

# Gretl User's Guide



Gnu Regression, Econometrics and Time-series Library

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## Chapter 1

# Introduction

### 1.1 Features at a glance

Gretl is an econometrics package, including a shared library, a command-line client program and a graphical user interface.

**User-friendly** Gretl offers an intuitive user interface; it is very easy to get up and running with econometric analysis. Thanks to its association with the econometrics textbooks by Ramu Ramanathan, Jeffrey Wooldridge, and James Stock and Mark Watson, the package offers many practice data files and command scripts. These are well annotated and accessible. Two other useful resources for gretl users are the available documentation and the [gretl-users](#) mailing list.

**Flexible** You can choose your preferred point on the spectrum from interactive point-and-click to batch processing, and can easily combine these approaches.

**Cross-platform** Gretl's "home" platform is Linux but it is also available for MS Windows and Mac OS X, and should work on any unix-like system that has the appropriate basic libraries (see [Appendix C](#)).

**Open source** The full source code for gretl is available to anyone who wants to critique it, patch it, or extend it. See [Appendix C](#).

**Sophisticated** Gretl offers a full range of least-squares based estimators, either for single equations and for systems, including vector autoregressions and vector error correction models. Several specific maximum likelihood estimators (e.g. probit, ARIMA, GARCH) are also provided natively; more advanced estimation methods can be implemented by the user via generic maximum likelihood or nonlinear GMM.

**Extensible** Users can enhance gretl by writing their own functions and procedures in gretl's scripting language, which includes a wide range of matrix functions.

**Accurate** Gretl has been thoroughly tested on several benchmarks, among which the NIST reference datasets. See [Appendix D](#).

**Internet ready** Gretl can access and fetch databases from a server at Wake Forest University. The MS Windows version comes with an updater program which will detect when a new version is available and offer the option of auto-updating.

**International** Gretl will produce its output in English, French, Italian, Spanish, Polish, Portuguese, German, Basque, Turkish or Russian depending on your computer's native language setting.

### 1.2 Acknowledgements

The gretl code base originally derived from the program ESL ("Econometrics Software Library"), written by Professor Ramu Ramanathan of the University of California, San Diego. We are much in debt to Professor Ramanathan for making this code available under the GNU General Public Licence and for helping to steer gretl's early development.

We are also grateful to the authors of several econometrics textbooks for permission to package for gretl various datasets associated with their texts. This list currently includes William Greene, author of *Econometric Analysis*; Jeffrey Wooldridge (*Introductory Econometrics: A Modern Approach*); James Stock and Mark Watson (*Introduction to Econometrics*); Damodar Gujarati (*Basic Econometrics*); Russell Davidson and James MacKinnon (*Econometric Theory and Methods*); and Marno Verbeek (*A Guide to Modern Econometrics*).

GARCH estimation in gretl is based on code deposited in the archive of the *Journal of Applied Econometrics* by Professors Fiorentini, Calzolari and Panattoni, and the code to generate  $p$ -values for Dickey-Fuller tests is due to James MacKinnon. In each case we are grateful to the authors for permission to use their work.

With regard to the internationalization of gretl, thanks go to Ignacio Díaz-Emparanza (Spanish), Michel Robitaille and Florent Bresson (French), Cristian Rigamonti (Italian), Tadeusz Kufel and Pawel Kufel (Polish), Markus Hahn and Sven Schreiber (German), Hélio Guilherme and Henrique Andrade (Portuguese), Susan Orbe (Basque), Talha Yalta (Turkish) and Alexander Gedranovich (Russian).

Gretl has benefitted greatly from the work of numerous developers of free, open-source software: for specifics please see Appendix C. Our thanks are due to Richard Stallman of the Free Software Foundation, for his support of free software in general and for agreeing to “adopt” gretl as a GNU program in particular.

Many users of gretl have submitted useful suggestions and bug reports. In this connection particular thanks are due to Ignacio Díaz-Emparanza, Tadeusz Kufel, Pawel Kufel, Alan Isaac, Cri Rigamonti, Sven Schreiber, Talha Yalta, Andreas Rosenblad, and Dirk Eddebuettel, who maintains the gretl package for Debian GNU/Linux.

## 1.3 Installing the programs

### Linux

On the Linux<sup>1</sup> platform you have the choice of compiling the gretl code yourself or making use of a pre-built package. Building gretl from the source is necessary if you want to access the development version or customize gretl to your needs, but this takes quite a few skills; most users will want to go for a pre-built package.

Some Linux distributions feature gretl as part of their standard offering: Debian, for example, or Ubuntu (in the *universe* repository). If this is the case, all you need to do is install gretl through your package manager of choice (e.g. synaptic).

Ready-to-run packages are available in rpm format (suitable for Red Hat Linux and related systems) on the gretl webpage <http://gretl.sourceforge.net>.

However, we're hopeful that some users with coding skills may consider gretl sufficiently interesting to be worth improving and extending. The documentation of the libgretl API is by no means complete, but you can find some details by following the link “Libgretl API docs” on the gretl homepage. People interested in the gretl development are welcome to subscribe to the [gretl-devel](#) mailing list.

If you prefer to compile your own (or are using a unix system for which pre-built packages are not available), instructions on building gretl can be found in Appendix C.

### MS Windows

The MS Windows version comes as a self-extracting executable. Installation is just a matter of downloading `gretl_install.exe` and running this program. You will be prompted for a location to install the package.

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<sup>1</sup>In this manual we use “Linux” as shorthand to refer to the GNU/Linux operating system. What is said herein about Linux mostly applies to other unix-type systems too, though some local modifications may be needed.

**Updating**

If your computer is connected to the Internet, then on start-up gretl can query its home website at Wake Forest University to see if any program updates are available; if so, a window will open up informing you of that fact. If you want to activate this feature, check the box marked “Tell me about gretl updates” under gretl’s “Tools, Preferences, General” menu.

The MS Windows version of the program goes a step further: it tells you that you can update gretl automatically if you wish. To do this, follow the instructions in the popup window: close gretl then run the program titled “gretl updater” (you should find this along with the main gretl program item, under the Programs heading in the Windows Start menu). Once the updater has completed its work you may restart gretl.

## **Part I**

# **Running the program**

## Chapter 2

# Getting started

### 2.1 Let's run a regression

This introduction is mostly angled towards the graphical client program; please see Chapter 40 below and the *Gretl Command Reference* for details on the command-line program, `gretlcli`.

You can supply the name of a data file to open as an argument to `gretl`, but for the moment let's not do that: just fire up the program.<sup>1</sup> You should see a main window (which will hold information on the data set but which is at first blank) and various menus, some of them disabled at first.

What can you do at this point? You can browse the supplied data files (or databases), open a data file, create a new data file, read the help items, or open a command script. For now let's browse the supplied data files. Under the File menu choose “Open data, Sample file”. A second notebook-type window will open, presenting the sets of data files supplied with the package (see Figure 2.1). Select the first tab, “Ramanathan”. The numbering of the files in this section corresponds to the chapter organization of [Ramanathan \(2002\)](#), which contains discussion of the analysis of these data. The data will be useful for practice purposes even without the text.

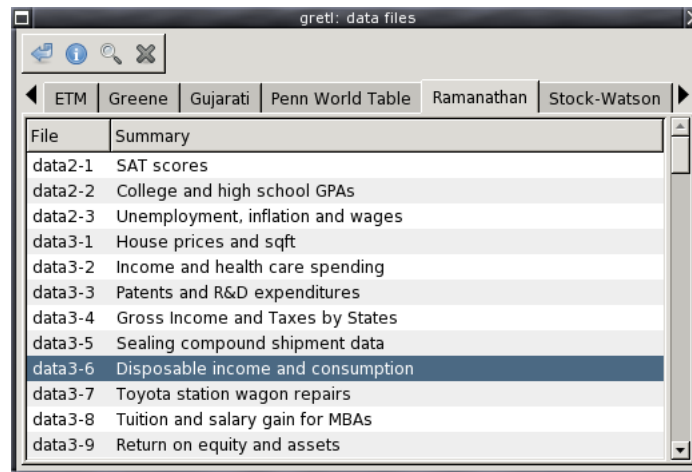



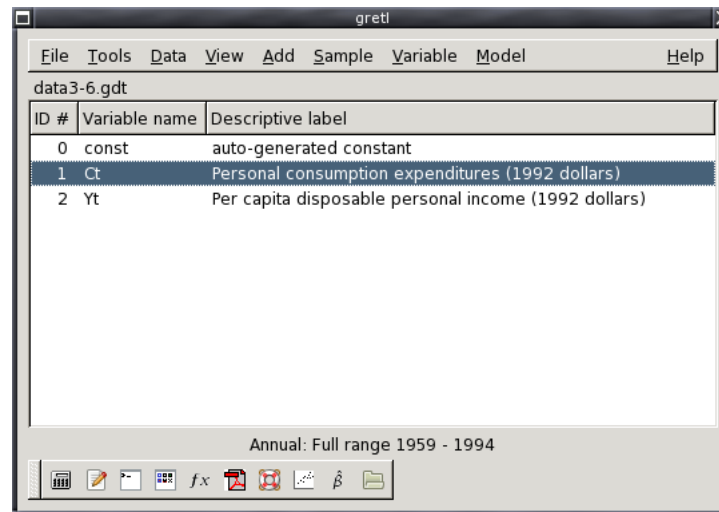
Figure 2.1: Practice data files window

If you select a row in this window and click on “Info” this opens a window showing information on the data set in question (for example, on the sources and definitions of the variables). If you find a file that is of interest, you may open it by clicking on “Open”, or just double-clicking on the file name. For the moment let's open data3-6.

 In `gretl` windows containing lists, double-clicking on a line launches a default action for the associated list entry: e.g. displaying the values of a data series, opening a file.

<sup>1</sup>For convenience we refer to the graphical client program simply as `gretl` in this manual. Note, however, that the specific name of the program differs according to the computer platform. On Linux it is called `gretl_x11` while on MS Windows it is `gretlw32.exe`. On Linux systems a wrapper script named `gretl` is also installed — see also the *Gretl Command Reference*.

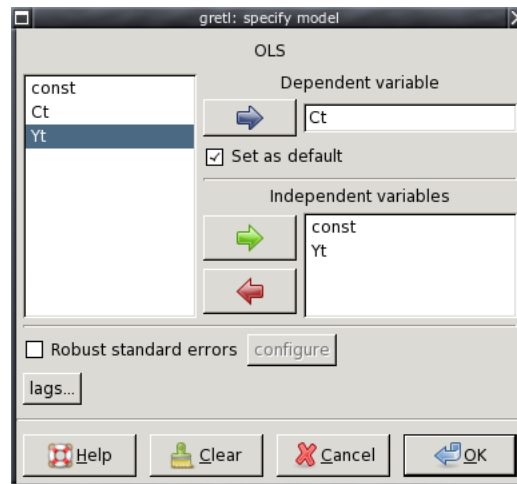
This file contains data pertaining to a classic econometric “chestnut”, the consumption function. The data window should now display the name of the current data file, the overall data range and sample range, and the names of the variables along with brief descriptive tags — see Figure 2.2.



**Figure 2.2:** Main window, with a practice data file open

OK, what can we do now? Hopefully the various menu options should be fairly self explanatory. For now we’ll dip into the Model menu; a brief tour of all the main window menus is given in Section 2.3 below.

gretl’s Model menu offers numerous various econometric estimation routines. The simplest and most standard is Ordinary Least Squares (OLS). Selecting OLS pops up a dialog box calling for a *model specification* — see Figure 2.3.



**Figure 2.3:** Model specification dialog

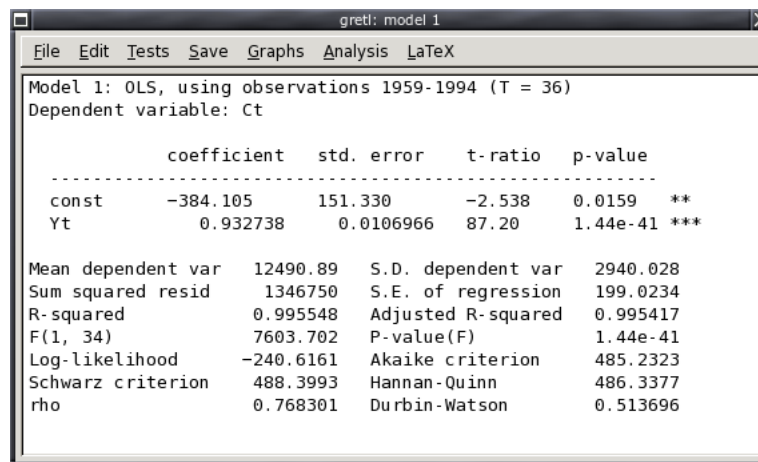
To select the dependent variable, highlight the variable you want in the list on the left and click the arrow that points to the Dependent variable slot. If you check the “Set as default” box this variable will be pre-selected as dependent when you next open the model dialog box. Shortcut: double-clicking on a variable on the left selects it as dependent and also sets it as the default. To select independent variables, highlight them on the left and click the green arrow (or right-click the



highlighted variable); to remove variables from the selected list, use the rad arrow. To select several variable in the list box, drag the mouse over them; to select several non-contiguous variables, hold down the Ctrl key and click on the variables you want. To run a regression with consumption as the dependent variable and income as independent, click Ct into the Dependent slot and add Yt to the Independent variables list.

## 2.2 Estimation output

Once you've specified a model, a window displaying the regression output will appear. The output is reasonably comprehensive and in a standard format (Figure 2.4).



	coefficient	std. error	t-ratio	p-value	
const	-384.105	151.330	-2.538	0.0159	**
Yt	0.932738	0.0106966	87.20	1.44e-41	***
Mean dependent var	12490.89	S.D. dependent var	2940.028		
Sum squared resid	1346750	S.E. of regression	199.0234		
R-squared	0.995548	Adjusted R-squared	0.995417		
F(1, 34)	7603.702	P-value(F)	1.44e-41		
Log-likelihood	-240.6161	Akaike criterion	485.2323		
Schwarz criterion	488.3993	Hannan-Quinn	486.3377		
rho	0.768301	Durbin-Watson	0.513696		

Figure 2.4: Model output window

The output window contains menus that allow you to inspect or graph the residuals and fitted values, and to run various diagnostic tests on the model.

For most models there is also an option to print the regression output in  $\text{\LaTeX}$  format. See Chapter 34 for details.

To import gretl output into a word processor, you may copy and paste from an output window, using its Edit menu (or Copy button, in some contexts) to the target program. Many (not all) gretl windows offer the option of copying in RTF (Microsoft's "Rich Text Format") or as  $\text{\LaTeX}$ . If you are pasting into a word processor, RTF may be a good option because the tabular formatting of the output is preserved.<sup>2</sup> Alternatively, you can save the output to a (plain text) file then import the file into the target program. When you finish a gretl session you are given the option of saving all the output from the session to a single file.

Note that on the gnome desktop and under MS Windows, the File menu includes a command to send the output directly to a printer.

☞ When pasting or importing plain text gretl output into a word processor, select a monospaced or typewriter-style font (e.g. Courier) to preserve the output's tabular formatting. Select a small font (10-point Courier should do) to prevent the output lines from being broken in the wrong place.

<sup>2</sup>Note that when you copy as RTF under MS Windows, Windows will only allow you to paste the material into applications that "understand" RTF. Thus you will be able to paste into MS Word, but not into notepad. Note also that there appears to be a bug in some versions of Windows, whereby the paste will not work properly unless the "target" application (e.g. MS Word) is already running prior to copying the material in question.

## 2.3 The main window menus

Reading left to right along the main window's menu bar, we find the File, Tools, Data, View, Add, Sample, Variable, Model and Help menus.



- File menu

- Open data: Open a native gretl data file or import from other formats. See Chapter 4.
- Append data: Add data to the current working data set, from a gretl data file, a comma-separated values file or a spreadsheet file.
- Save data: Save the currently open native gretl data file.
- Save data as: Write out the current data set in native format, with the option of using gzip data compression. See Chapter 4.
- Export data: Write out the current data set in Comma Separated Values (CSV) format, or the formats of GNU R or GNU Octave. See Chapter 4 and also Appendix E.
- Send to: Send the current data set as an e-mail attachment.
- New data set: Allows you to create a blank data set, ready for typing in values or for importing series from a database. See below for more on databases.
- Clear data set: Clear the current data set out of memory. Generally you don't have to do this (since opening a new data file automatically clears the old one) but sometimes it's useful.
- Script files: A "script" is a file containing a sequence of gretl commands. This item contains entries that let you open a script you have created previously ("User file"), open a sample script, or open an editor window in which you can create a new script.
- Session files: A "session" file contains a snapshot of a previous gretl session, including the data set used and any models or graphs that you saved. Under this item you can open a saved session or save the current session.
- Databases: Allows you to browse various large databases, either on your own computer or, if you are connected to the internet, on the gretl database server. See Section 4.2 for details.
- Function files: Handles "function packages" (see Section 11.5), which allow you to access functions written by other users and share the ones written by you.
- Exit: Quit the program. You'll be prompted to save any unsaved work.

- Tools menu

- Statistical tables: Look up critical values for commonly used distributions (normal or Gaussian,  $t$ , chi-square,  $F$  and Durbin-Watson).
- P-value finder: Look up p-values from the Gaussian,  $t$ , chi-square,  $F$ , gamma, binomial or Poisson distributions. See also the `pvalue` command in the *Gretl Command Reference*.
- Distribution graphs: Produce graphs of various probability distributions. In the resulting graph window, the pop-up menu includes an item "Add another curve", which enables you to superimpose a further plot (for example, you can draw the  $t$  distribution with various different degrees of freedom).
- Test statistic calculator: Calculate test statistics and p-values for a range of common hypothesis tests (population mean, variance and proportion; difference of means, variances and proportions).
- Nonparametric tests: Calculate test statistics for various nonparametric tests (Sign test, Wilcoxon rank sum test, Wilcoxon signed rank test, Runs test).

- Seed for random numbers: Set the seed for the random number generator (by default this is set based on the system time when the program is started).
  - Command log: Open a window containing a record of the commands executed so far.
  - Gretl console: Open a “console” window into which you can type commands as you would using the command-line program, `gretlcli` (as opposed to using point-and-click).
  - Start Gnu R: Start R (if it is installed on your system), and load a copy of the data set currently open in gretl. See Appendix E.
  - Sort variables: Rearrange the listing of variables in the main window, either by ID number or alphabetically by name.
  - NIST test suite: Check the numerical accuracy of gretl against the reference results for linear regression made available by the (US) National Institute of Standards and Technology.
  - Preferences: Set the paths to various files gretl needs to access. Choose the font in which gretl displays text output. Activate or suppress gretl’s messaging about the availability of program updates, and so on. See the *Gretl Command Reference* for further details.
- Data menu
    - Select all: Several menu items act upon those variables that are currently selected in the main window. This item lets you select all the variables.
    - Display values: Pops up a window with a simple (not editable) printout of the values of the selected variable or variables.
    - Edit values: Opens a spreadsheet window where you can edit the values of the selected variables.
    - Add observations: Gives a dialog box in which you can choose a number of observations to add at the end of the current dataset; for use with forecasting.
    - Remove extra observations: Active only if extra observations have been added automatically in the process of forecasting; deletes these extra observations.
    - Read info, Edit info: “Read info” just displays the summary information for the current data file; “Edit info” allows you to make changes to it (if you have permission to do so).
    - Print description: Opens a window containing a full account of the current dataset, including the summary information and any specific information on each of the variables.
    - Add case markers: Prompts for the name of a text file containing “case markers” (short strings identifying the individual observations) and adds this information to the data set. See Chapter 4.
    - Remove case markers: Active only if the dataset has case markers identifying the observations; removes these case markers.
    - Dataset structure: invokes a series of dialog boxes which allow you to change the structural interpretation of the current dataset. For example, if data were read in as a cross section you can get the program to interpret them as time series or as a panel. See also section 4.4.
    - Compact data: For time-series data of higher than annual frequency, gives you the option of compacting the data to a lower frequency, using one of four compaction methods (average, sum, start of period or end of period).
    - Expand data: For time-series data, gives you the option of expanding the data to a higher frequency.
    - Transpose data: Turn each observation into a variable and vice versa (or in other words, each row of the data matrix becomes a column in the modified data matrix); can be useful with imported data that have been read in “sideways”.
  - View menu

- **Icon view:** Opens a window showing the content of the current session as a set of icons; see section 3.4.
  - **Graph specified vars:** Gives a choice between a time series plot, a regular X-Y scatter plot, an X-Y plot using impulses (vertical bars), an X-Y plot “with factor separation” (i.e. with the points colored differently depending to the value of a given dummy variable), boxplots, and a 3-D graph. Serves up a dialog box where you specify the variables to graph. See Chapter 8 for details.
  - **Multiple graphs:** Allows you to compose a set of up to six small graphs, either pairwise scatter-plots or time-series graphs. These are displayed together in a single window.
  - **Summary statistics:** Shows a full set of descriptive statistics for the variables selected in the main window.
  - **Correlation matrix:** Shows the pairwise correlation coefficients for the selected variables.
  - **Cross Tabulation:** Shows a cross-tabulation of the selected variables. This works only if at least two variables in the data set have been marked as discrete (see Chapter 9).
  - **Principal components:** Produces a Principal Components Analysis for the selected variables.
  - **Mahalanobis distances:** Computes the Mahalanobis distance of each observation from the centroid of the selected set of variables.
  - **Cross-correlogram:** Computes and graphs the cross-correlogram for two selected variables.
- **Add menu** Offers various standard transformations of variables (logs, lags, squares, etc.) that you may wish to add to the data set. Also gives the option of adding random variables, and (for time-series data) adding seasonal dummy variables (e.g. quarterly dummy variables for quarterly data).
  - **Sample menu**
    - **Set range:** Select a different starting and/or ending point for the current sample, within the range of data available.
    - **Restore full range:** self-explanatory.
    - **Define, based on dummy:** Given a dummy (indicator) variable with values 0 or 1, this drops from the current sample all observations for which the dummy variable has value 0.
    - **Restrict, based on criterion:** Similar to the item above, except that you don’t need a pre-defined variable: you supply a Boolean expression (e.g. `sqft > 1400`) and the sample is restricted to observations satisfying that condition. See the entry for `genr` in the *Gretl Command Reference* for details on the Boolean operators that can be used.
    - **Random sub-sample:** Draw a random sample from the full dataset.
    - **Drop all obs with missing values:** Drop from the current sample all observations for which at least one variable has a missing value (see Section 4.6).
    - **Count missing values:** Give a report on observations where data values are missing. May be useful in examining a panel data set, where it’s quite common to encounter missing values.
    - **Set missing value code:** Set a numerical value that will be interpreted as “missing” or “not available”. This is intended for use with imported data, when `gretl` has not recognized the missing-value code used.
  - **Variable menu** Most items under here operate on a single variable at a time. The “active” variable is set by highlighting it (clicking on its row) in the main data window. Most options will be self-explanatory. Note that you can rename a variable and can edit its descriptive label under “Edit attributes”. You can also “Define a new variable” via a formula (e.g. involving

some function of one or more existing variables). For the syntax of such formulae, look at the online help for “Generate variable syntax” or see the *genr* command in the *Gretl Command Reference*. One simple example:

```
foo = x1 * x2
```

will create a new variable *foo* as the product of the existing variables *x1* and *x2*. In these formulae, variables must be referenced by name, not number.

- **Model menu** For details on the various estimators offered under this menu please consult the *Gretl Command Reference*. Also see Chapter 19 regarding the estimation of nonlinear models.
- **Help menu** Please use this as needed! It gives details on the syntax required in various dialog entries.

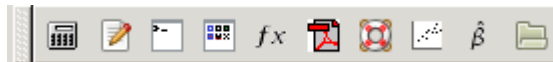
## 2.4 Keyboard shortcuts

When working in the main *gretl* window, some common operations may be performed using the keyboard, as shown in the table below.

Return	Opens a window displaying the values of the currently selected variables: it is the same as selecting “Data, Display Values”.
Delete	Pressing this key has the effect of deleting the selected variables. A confirmation is required, to prevent accidental deletions.
e	Has the same effect as selecting “Edit attributes” from the “Variable” menu.
F2	Same as “e”. Included for compatibility with other programs.
g	Has the same effect as selecting “Define new variable” from the “Variable” menu (which maps onto the <i>genr</i> command).
h	Opens a help window for <i>gretl</i> commands.
F1	Same as “h”. Included for compatibility with other programs.
r	Refreshes the variable list in the main window.
t	Graphs the selected variable; a line graph is used for time-series datasets, whereas a distribution plot is used for cross-sectional data.

## 2.5 The *gretl* toolbar

At the bottom left of the main window sits the toolbar.



The icons have the following functions, reading from left to right:

1. Launch a calculator program. A convenience function in case you want quick access to a calculator when you’re working in *gretl*. The default program is *calc.exe* under MS Windows, or *xcalc* under the X window system. You can change the program under the “Tools, Preferences, General” menu, “Programs” tab.
2. Start a new script. Opens an editor window in which you can type a series of commands to be sent to the program as a batch.
3. Open the *gretl* console. A shortcut to the “Gretl console” menu item (Section 2.3 above).
4. Open the *gretl* session icon window.

5. Open a window displaying available gretl function packages.
6. Open this manual in PDF format.
7. Open the help item for script commands syntax (i.e. a listing with details of all available commands).
8. Open the dialog box for defining a graph.
9. Open the dialog box for estimating a model using ordinary least squares.
10. Open a window listing the sample datasets supplied with gretl, and any other data file collections that have been installed.

## Chapter 3

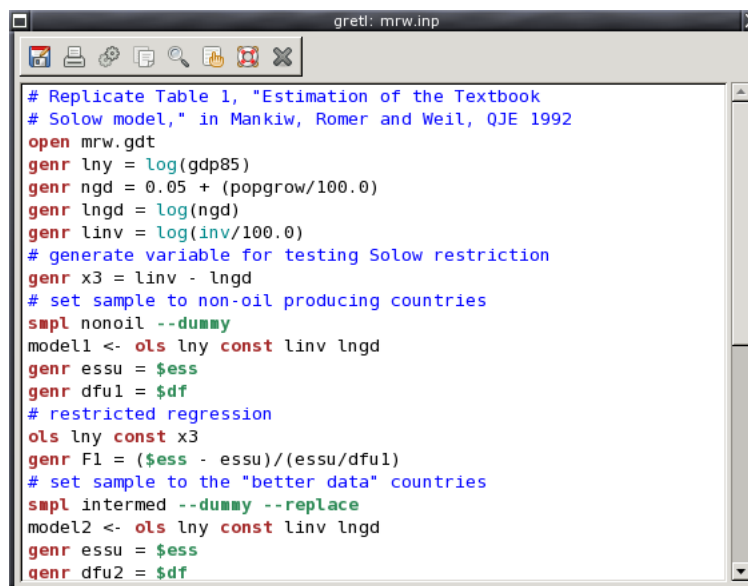
# Modes of working

### 3.1 Command scripts

As you execute commands in gretl, using the GUI and filling in dialog entries, those commands are recorded in the form of a “script” or batch file. Such scripts can be edited and re-run, using either gretl or the command-line client, gretlcli.

To view the current state of the script at any point in a gretl session, choose “Command log” under the Tools menu. This log file is called `session.inp` and it is overwritten whenever you start a new session. To preserve it, save the script under a different name. Script files will be found most easily, using the GUI file selector, if you name them with the extension “.inp”.

To open a script you have written independently, use the “File, Script files” menu item; to create a script from scratch use the “File, Script files, New script” item or the “new script” toolbar button. In either case a script window will open (see Figure 3.1).



```
# Replicate Table 1, "Estimation of the Textbook
# Solow model," in Mankiw, Romer and Weil, QJE 1992
open mrw.gdt
genr lny = log(gdp85)
genr ngd = 0.05 + (popgrow/100.0)
genr lngd = log(ngd)
genr linv = log(inv/100.0)
# generate variable for testing Solow restriction
genr x3 = linv - lngd
# set sample to non-oil producing countries
smpl nonoil --dummy
model1 <- ols lny const linv lngd
genr essu = $ess
genr dfu1 = $df
# restricted regression
ols lny const x3
genr F1 = ($ess - essu)/($ess/dfu1)
# set sample to the "better data" countries
smpl intermed --dummy --replace
model2 <- ols lny const linv lngd
genr essu = $ess
genr dfu2 = $df
```

**Figure 3.1:** Script window, editing a command file

The toolbar at the top of the script window offers the following functions (left to right): (1) Save the file; (2) Save the file under a specified name; (3) Print the file (this option is not available on all platforms); (4) Execute the commands in the file; (5) Copy selected text; (6) Paste the selected text; (7) Find and replace text; (8) Undo the last Paste or Replace action; (9) Help (if you place the cursor in a command word and press the question mark you will get help on that command); (10) Close the window.

When you execute the script, by clicking on the Execute icon or by pressing Ctrl-r, all output is directed to a single window, where it can be edited, saved or copied to the clipboard. To learn more about the possibilities of scripting, take a look at the gretl Help item “Command reference,”

or start up the command-line program `gretlcli` and consult its help, or consult the *Gretl Command Reference*.

If you run the script when part of it is highlighted, `gretl` will only run that portion. Moreover, if you want to run just the current line, you can do so by pressing Ctrl-Enter.<sup>1</sup>

Clicking the right mouse button in the script editor window produces a pop-up menu. This gives you the option of executing either the line on which the cursor is located, or the selected region of the script if there's a selection in place. If the script is editable, this menu also gives the option of adding or removing comment markers from the start of the line or lines.

The `gretl` package includes over 70 “practice” scripts. Most of these relate to [Ramanathan \(2002\)](#), but they may also be used as a free-standing introduction to scripting in `gretl` and to various points of econometric theory. You can explore the practice files under “File, Script files, Practice file” There you will find a listing of the files along with a brief description of the points they illustrate and the data they employ. Open any file and run it to see the output. Note that long commands in a script can be broken over two or more lines, using backslash as a continuation character.

You can, if you wish, use the GUI controls and the scripting approach in tandem, exploiting each method where it offers greater convenience. Here are two suggestions.

- Open a data file in the GUI. Explore the data — generate graphs, run regressions, perform tests. Then open the Command log, edit out any redundant commands, and save it under a specific name. Run the script to generate a single file containing a concise record of your work.
- Start by establishing a new script file. Type in any commands that may be required to set up transformations of the data (see the `genr` command in the *Gretl Command Reference*). Typically this sort of thing can be accomplished more efficiently via commands assembled with forethought rather than point-and-click. Then save and run the script: the GUI data window will be updated accordingly. Now you can carry out further exploration of the data via the GUI. To revisit the data at a later point, open and rerun the “preparatory” script first.

### Scripts and data files

One common way of doing econometric research with `gretl` is as follows: compose a script; execute the script; inspect the output; modify the script; run it again — with the last three steps repeated as many times as necessary. In this context, note that when you open a data file this clears out most of `gretl`'s internal state. It's therefore probably a good idea to have your script start with an open command: the data file will be re-opened each time, and you can be confident you're getting “fresh” results.

One further point should be noted. When you go to open a new data file via the graphical interface, you are always prompted: opening a new data file will lose any unsaved work, do you really want to do this? When you execute a script that opens a data file, however, you are *not* prompted. The assumption is that in this case you're not going to lose any work, because the work is embodied in the script itself (and it would be annoying to be prompted at each iteration of the work cycle described above).

This means you should be careful if you've done work using the graphical interface and then decide to run a script: the current data file will be replaced without any questions asked, and it's your responsibility to save any changes to your data first.

---

<sup>1</sup>This feature is not unique to `gretl`; other econometric packages offer the same facility. However, experience shows that while this can be remarkably useful, it can also lead to writing dinosaur scripts that are never meant to be executed all at once, but rather used as a chaotic repository to cherry-pick snippets from. Since `gretl` allows you to have several script windows open at the same time, you may want to keep your scripts tidy and reasonably small.



## 3.2 Saving script objects

When you estimate a model using point-and-click, the model results are displayed in a separate window, offering menus which let you perform tests, draw graphs, save data from the model, and so on. Ordinarily, when you estimate a model using a script you just get a non-interactive printout of the results. You can, however, arrange for models estimated in a script to be “captured”, so that you can examine them interactively when the script is finished. Here is an example of the syntax for achieving this effect:

```
Model1 <- ols Ct 0 Yt
```

That is, you type a name for the model to be saved under, then a back-pointing “assignment arrow”, then the model command. The assignment arrow is composed of the less-than sign followed by a dash; it must be separated by spaces from both the preceding name and the following command. The name for a saved object may include spaces, but in that case it must be wrapped in double quotes:

```
"Model 1" <- ols Ct 0 Yt
```

Models saved in this way will appear as icons in the gretl icon view window (see Section 3.4) after the script is executed. In addition, you can arrange to have a named model displayed (in its own window) automatically as follows:

```
Model1.show
```

Again, if the name contains spaces it must be quoted:

```
"Model 1".show
```

The same facility can be used for graphs. For example the following will create a plot of Ct against Yt, save it under the name “CrossPlot” (it will appear under this name in the icon view window), and have it displayed:

```
CrossPlot <- gnpplot Ct Yt  
CrossPlot.show
```

You can also save the output from selected commands as named pieces of text (again, these will appear in the session icon window, from where you can open them later). For example this command sends the output from an augmented Dickey-Fuller test to a “text object” named ADF1 and displays it in a window:

```
ADF1 <- adf 2 x1  
ADF1.show
```

Objects saved in this way (whether models, graphs or pieces of text output) can be destroyed using the command `.free` appended to the name of the object, as in `ADF1.free`.

## 3.3 The gretl console

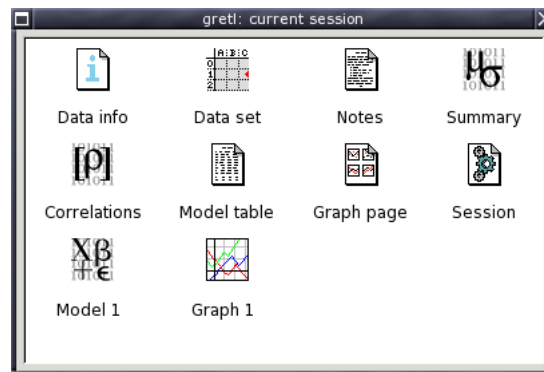
A further option is available for your computing convenience. Under gretl’s “Tools” menu you will find the item “Gretl console” (there is also an “open gretl console” button on the toolbar in the main window). This opens up a window in which you can type commands and execute them one by one (by pressing the Enter key) interactively. This is essentially the same as gretlcli’s mode of operation, except that the GUI is updated based on commands executed from the console, enabling you to work back and forth as you wish.

In the console, you have “command history”; that is, you can use the up and down arrow keys to navigate the list of command you have entered to date. You can retrieve, edit and then re-enter a previous command.

In console mode, you can create, display and free objects (models, graphs or text) as described above for script mode.

### 3.4 The Session concept

gretl offers the idea of a “session” as a way of keeping track of your work and revisiting it later. The basic idea is to provide an iconic space containing various objects pertaining to your current working session (see Figure 3.2). You can add objects (represented by icons) to this space as you go along. If you save the session, these added objects should be available again if you re-open the session later.



**Figure 3.2:** Icon view: one model and one graph have been added to the default icons

If you start *gretl* and open a data set, then select “Icon view” from the View menu, you should see the basic default set of icons: these give you quick access to information on the data set (if any), correlation matrix (“Correlations”) and descriptive summary statistics (“Summary”). All of these are activated by double-clicking the relevant icon. The “Data set” icon is a little more complex: double-clicking opens up the data in the built-in spreadsheet, but you can also right-click on the icon for a menu of other actions.

To add a model to the Icon view, first estimate it using the Model menu. Then pull down the File menu in the model window and select “Save to session as icon...” or “Save as icon and close”. Simply hitting the S key over the model window is a shortcut to the latter action.

To add a graph, first create it (under the View menu, “Graph specified vars”, or via one of *gretl*’s other graph-generating commands). Click on the graph window to bring up the graph menu, and select “Save to session as icon”.

Once a model or graph is added its icon will appear in the Icon view window. Double-clicking on the icon redisplay the object, while right-clicking brings up a menu which lets you display or delete the object. This popup menu also gives you the option of editing graphs.

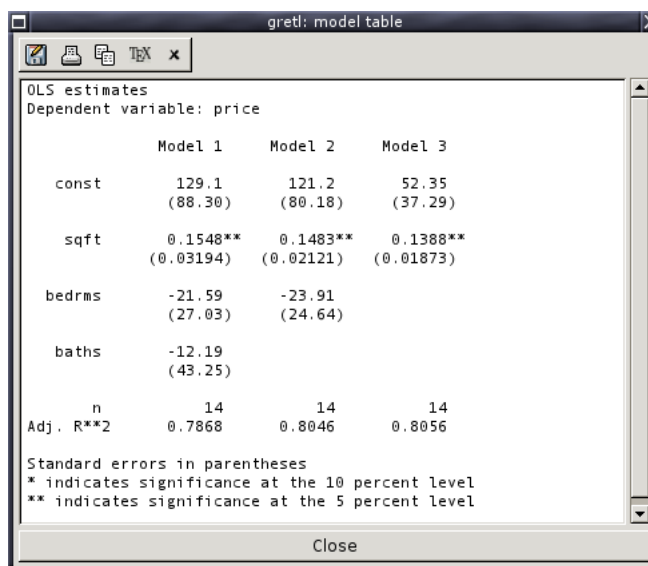
#### The model table

In econometric research it is common to estimate several models with a common dependent variable — the models differing in respect of which independent variables are included, or perhaps in respect of the estimator used. In this situation it is convenient to present the regression results in the form of a table, where each column contains the results (coefficient estimates and standard errors) for a given model, and each row contains the estimates for a given variable across the models.

In the Icon view window `gretl` provides a means of constructing such a table (and copying it in plain text,  $\text{\LaTeX}$  or Rich Text Format). The procedure is outlined below. (The model table can also be built non-interactively, in script mode. For details, see the entry for `modeltab` in the *Gretl Command Reference*.)

1. Estimate a model which you wish to include in the table, and in the model display window, under the File menu, select “Save to session as icon” or “Save as icon and close”.
2. Repeat step 1 for the other models to be included in the table (up to a total of six models).
3. When you are done estimating the models, open the icon view of your `gretl` session, by selecting “Icon view” under the View menu in the main `gretl` window, or by clicking the “session icon view” icon on the `gretl` toolbar.
4. In the Icon view, there is an icon labeled “Model table”. Decide which model you wish to appear in the left-most column of the model table and add it to the table, either by dragging its icon onto the Model table icon, or by right-clicking on the model icon and selecting “Add to model table” from the pop-up menu.
5. Repeat step 4 for the other models you wish to include in the table. The second model selected will appear in the second column from the left, and so on.
6. When you are finished composing the model table, display it by double-clicking on its icon. Under the Edit menu in the window which appears, you have the option of copying the table to the clipboard in various formats.
7. If the ordering of the models in the table is not what you wanted, right-click on the model table icon and select “Clear table”. Then go back to step 4 above and try again.

A simple instance of `gretl`'s model table is shown in Figure 3.3.



	Model 1	Model 2	Model 3
const	129.1 (88.30)	121.2 (80.18)	52.35 (37.29)
sqft	0.1548** (0.03194)	0.1483** (0.02121)	0.1388** (0.01873)
bedrms	-21.59 (27.03)	-23.91 (24.64)	
baths	-12.19 (43.25)		
n	14	14	14
Adj. R**2	0.7868	0.8046	0.8056

Standard errors in parentheses  
 \* indicates significance at the 10 percent level  
 \*\* indicates significance at the 5 percent level

Figure 3.3: Example of model table

### The graph page

The “graph page” icon in the session window offers a means of putting together several graphs for printing on a single page. This facility will work only if you have the  $\text{\LaTeX}$  typesetting system

installed, and are able to generate and view either PDF or PostScript output. The output format is controlled by your choice of program for compiling T<sub>E</sub>X files, which can be found under the “Programs” tab in the Preferences dialog box (under the “Tools” menu in the main window). Usually this should be pdf<sub>l</sub>atex for PDF output or latex for PostScript. In the latter case you must have a working set-up for handling PostScript, which will usually include dvips, ghostscript and a viewer such as gv, ggv or kghostview.

In the Icon view window, you can drag up to eight graphs onto the graph page icon. When you double-click on the icon (or right-click and select “Display”), a page containing the selected graphs (in PDF or EPS format) will be composed and opened in your viewer. From there you should be able to print the page.

To clear the graph page, right-click on its icon and select “Clear”.

As with the model table, it is also possible to manipulate the graph page via commands in script or console mode — see the entry for the `graphpg` command in the *Gretl Command Reference*.

### **Saving and re-opening sessions**

If you create models or graphs that you think you may wish to re-examine later, then before quitting `gretl` select “Session files, Save session” from the File menu and give a name under which to save the session. To re-open the session later, either

- Start `gretl` then re-open the session file by going to the “File, Session files, Open session”, or
- From the command line, type `gretl -r sessionfile`, where *sessionfile* is the name under which the session was saved, or
- Drag the icon representing a `gretl` session file onto `gretl`.

## Chapter 4

# Data files

### 4.1 Data file formats

gretl has its own format for data files. Most users will probably not want to read or write such files outside of `gretl` itself, but occasionally this may be useful and full details on the file formats are given in Appendix A.

`gretl` will read various other data formats.

- Plain text (ASCII) files. These can be brought in using `gretl`'s "File, Open Data, Import ASCII..." menu item, or the `import` script command. For details on what `gretl` expects of such files, see Section 4.3.
- Comma-Separated Values (CSV) files. These can be imported using `gretl`'s "File, Open Data, Import CSV..." menu item, or the `import` script command. See also Section 4.3.
- Spreadsheets: MS Excel, Gnumeric and Open Document (ODS). These are also brought in using `gretl`'s "File, Open Data, Import" menu. The requirements for such files are given in Section 4.3.
- Stata data files (.dta).
- SPSS data files (.sav).
- Eviews workfiles (.wf1).<sup>1</sup>
- JMulTi data files.

When you import data from the ASCII or CSV formats, `gretl` opens a "diagnostic" window, reporting on its progress in reading the data. If you encounter a problem with ill-formatted data, the messages in this window should give you a handle on fixing the problem.

Note that `gretl` has a facility for writing out data in the native formats of GNU R, Octave, JMulTi and PcGive (see Appendix E). In the GUI client this option is found under the "File, Export data" menu; in the command-line client use the `store` command with the appropriate option flag.

### 4.2 Databases

For working with large amounts of data `gretl` is supplied with a database-handling routine. A *database*, as opposed to a *data file*, is not read directly into the program's workspace. A database can contain series of mixed frequencies and sample ranges. You open the database and select series to import into the working dataset. You can then save those series in a native format data file if you wish. Databases can be accessed via `gretl`'s menu item "File, Databases".

For details on the format of `gretl` databases, see Appendix A.

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<sup>1</sup>See [http://www.ecn.wfu.edu/eviews\\_format/](http://www.ecn.wfu.edu/eviews_format/).

### Online access to databases

As of version 0.40, gretl is able to access databases via the internet. Several databases are available from Wake Forest University. Your computer must be connected to the internet for this option to work. Please see the description of the “data” command under gretl’s Help menu.

☞ Visit the gretl [data page](#) for details and updates on available data.

### Foreign database formats

Thanks to Thomas Doan of *Estima*, who made available the specification of the database format used by RATS 4 (Regression Analysis of Time Series), gretl can handle such databases — or at least, a subset of same, namely time-series databases containing monthly and quarterly series.

gretl can also import data from PcGive databases. These take the form of a pair of files, one containing the actual data (with suffix `.bn7`) and one containing supplementary information (`.in7`).

In addition, gretl offers ODBC connectivity. Be warned: this feature is meant for somewhat advanced users; there is currently no GUI interface. Interested readers will find more info in appendix [B](#).

## 4.3 Creating a dataset from scratch

There are several ways of doing this:

1. Find, or create using a text editor, a plain text data file and open it with gretl’s “Import ASCII” option.
2. Use your favorite spreadsheet to establish the data file, save it in Comma Separated Values format if necessary (this should not be necessary if the spreadsheet format is MS Excel, Gnumeric or Open Document), then use one of gretl’s “Import” options.
3. Use gretl’s built-in spreadsheet.
4. Select data series from a suitable database.
5. Use your favorite text editor or other software tools to create a data file in gretl format independently.

Here are a few comments and details on these methods.

### Common points on imported data

Options (1) and (2) involve using gretl’s “import” mechanism. For gretl to read such data successfully, certain general conditions must be satisfied:

- The first row must contain valid variable names. A valid variable name is of 15 characters maximum; starts with a letter; and contains nothing but letters, numbers and the underscore character, `_`. (Longer variable names will be truncated to 15 characters.) Qualifications to the above: First, in the case of an ASCII or CSV import, if the file contains no row with variable names the program will automatically add names, `v1`, `v2` and so on. Second, by “the first row” is meant the first *relevant* row. In the case of ASCII and CSV imports, blank rows and rows beginning with a hash mark, `#`, are ignored. In the case of Excel and Gnumeric imports, you are presented with a dialog box where you can select an offset into the spreadsheet, so that gretl will ignore a specified number of rows and/or columns.

- Data values: these should constitute a rectangular block, with one variable per column (and one observation per row). The number of variables (data columns) must match the number of variable names given. See also section 4.6. Numeric data are expected, but in the case of importing from ASCII/CSV, the program offers limited handling of character (string) data: if a given column contains character data only, consecutive numeric codes are substituted for the strings, and once the import is complete a table is printed showing the correspondence between the strings and the codes.
- Dates (or observation labels): Optionally, the *first* column may contain strings such as dates, or labels for cross-sectional observations. Such strings have a maximum of 8 characters (as with variable names, longer strings will be truncated). A column of this sort should be headed with the string *obs* or *date*, or the first row entry may be left blank.

For dates to be recognized as such, the date strings must adhere to one or other of a set of specific formats, as follows. For *annual* data: 4-digit years. For *quarterly* data: a 4-digit year, followed by a separator (either a period, a colon, or the letter Q), followed by a 1-digit quarter. Examples: 1997.1, 2002:3, 1947Q1. For *monthly* data: a 4-digit year, followed by a period or a colon, followed by a two-digit month. Examples: 1997.01, 2002:10.

CSV files can use comma, space or tab as the column separator. When you use the “Import CSV” menu item you are prompted to specify the separator. In the case of “Import ASCII” the program attempts to auto-detect the separator that was used.

If you use a spreadsheet to prepare your data you are able to carry out various transformations of the “raw” data with ease (adding things up, taking percentages or whatever): note, however, that you can also do this sort of thing easily — perhaps more easily — within gretl, by using the tools under the “Add” menu.

### Appending imported data

You may wish to establish a gretl dataset piece by piece, by incremental importation of data from other sources. This is supported via the “File, Append data” menu items: gretl will check the new data for conformability with the existing dataset and, if everything seems OK, will merge the data. You can add new variables in this way, provided the data frequency matches that of the existing dataset. Or you can append new observations for data series that are already present; in this case the variable names must match up correctly. Note that by default (that is, if you choose “Open data” rather than “Append data”), opening a new data file closes the current one.

### Using the built-in spreadsheet

Under gretl’s “File, New data set” menu you can choose the sort of dataset you want to establish (e.g. quarterly time series, cross-sectional). You will then be prompted for starting and ending dates (or observation numbers) and the name of the first variable to add to the dataset. After supplying this information you will be faced with a simple spreadsheet into which you can type data values. In the spreadsheet window, clicking the right mouse button will invoke a popup menu which enables you to add a new variable (column), to add an observation (append a row at the foot of the sheet), or to insert an observation at the selected point (move the data down and insert a blank row.)

Once you have entered data into the spreadsheet you import these into gretl’s workspace using the spreadsheet’s “Apply changes” button.

Please note that gretl’s spreadsheet is quite basic and has no support for functions or formulas. Data transformations are done via the “Add” or “Variable” menus in the main gretl window.

### Selecting from a database

Another alternative is to establish your dataset by selecting variables from a database.

Begin with gretl's "File, Databases" menu item. This has four forks: "Gretl native", "RATS 4", "PcGive" and "On database server". You should be able to find the file `fedst1.bin` in the file selector that opens if you choose the "Gretl native" option — this file, which contains a large collection of US macroeconomic time series, is supplied with the distribution.

You won't find anything under "RATS 4" unless you have purchased RATS data.<sup>2</sup> If you do possess RATS data you should go into gretl's "Tools, Preferences, General" dialog, select the Databases tab, and fill in the correct path to your RATS files.

If your computer is connected to the internet you should find several databases (at Wake Forest University) under "On database server". You can browse these remotely; you also have the option of installing them onto your own computer. The initial remote databases window has an item showing, for each file, whether it is already installed locally (and if so, if the local version is up to date with the version at Wake Forest).

Assuming you have managed to open a database you can import selected series into gretl's workspace by using the "Series, Import" menu item in the database window, or via the popup menu that appears if you click the right mouse button, or by dragging the series into the program's main window.

### Creating a gretl data file independently

It is possible to create a data file in one or other of gretl's own formats using a text editor or software tools such as `awk`, `sed` or `perl`. This may be a good choice if you have large amounts of data already in machine readable form. You will, of course, need to study the gretl data formats (XML format or "traditional" format) as described in Appendix A.

## 4.4 Structuring a dataset

Once your data are read by gretl, it may be necessary to supply some information on the nature of the data. We distinguish between three kinds of datasets:

1. Cross section
2. Time series
3. Panel data

The primary tool for doing this is the "Data, Dataset structure" menu entry in the graphical interface, or the `setobs` command for scripts and the command-line interface.

### Cross sectional data

By a cross section we mean observations on a set of "units" (which may be firms, countries, individuals, or whatever) at a common point in time. This is the default interpretation for a data file: if gretl does not have sufficient information to interpret data as time-series or panel data, they are automatically interpreted as a cross section. In the unlikely event that cross-sectional data are wrongly interpreted as time series, you can correct this by selecting the "Data, Dataset structure" menu item. Click the "cross-sectional" radio button in the dialog box that appears, then click "Forward". Click "OK" to confirm your selection.

### Time series data

When you import data from a spreadsheet or plain text file, gretl will make fairly strenuous efforts to glean time-series information from the first column of the data, if it looks at all plausible that such information may be present. If time-series structure is present but not recognized, again you

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<sup>2</sup>See [www.estima.com](http://www.estima.com)



can use the “Data, Dataset structure” menu item. Select “Time series” and click “Forward”; select the appropriate data frequency and click “Forward” again; then select or enter the starting observation and click “Forward” once more. Finally, click “OK” to confirm the time-series interpretation if it is correct (or click “Back” to make adjustments if need be).

Besides the basic business of getting a data set interpreted as time series, further issues may arise relating to the frequency of time-series data. In a gretl time-series data set, all the series must have the same frequency. Suppose you wish to make a combined dataset using series that, in their original state, are not all of the same frequency. For example, some series are monthly and some are quarterly.

Your first step is to formulate a strategy: Do you want to end up with a quarterly or a monthly data set? A basic point to note here is that “compacting” data from a higher frequency (e.g. monthly) to a lower frequency (e.g. quarterly) is usually unproblematic. You lose information in doing so, but in general it is perfectly legitimate to take (say) the average of three monthly observations to create a quarterly observation. On the other hand, “expanding” data from a lower to a higher frequency is not, in general, a valid operation.

In most cases, then, the best strategy is to start by creating a data set of the *lower* frequency, and then to compact the higher frequency data to match. When you import higher-frequency data from a database into the current data set, you are given a choice of compaction method (average, sum, start of period, or end of period). In most instances “average” is likely to be appropriate.

You *can* also import lower-frequency data into a high-frequency data set, but this is generally not recommended. What gretl does in this case is simply replicate the values of the lower-frequency series as many times as required. For example, suppose we have a quarterly series with the value 35.5 in 1990:1, the first quarter of 1990. On expansion to monthly, the value 35.5 will be assigned to the observations for January, February and March of 1990. The expanded variable is therefore useless for fine-grained time-series analysis, outside of the special case where you know that the variable in question does in fact remain constant over the sub-periods.

When the current data frequency is appropriate, gretl offers both “Compact data” and “Expand data” options under the “Data” menu. These options operate on the whole data set, compacting or expanding all series. They should be considered “expert” options and should be used with caution.

### Panel data

Panel data are inherently three dimensional — the dimensions being variable, cross-sectional unit, and time-period. For example, a particular number in a panel data set might be identified as the observation on capital stock for General Motors in 1980. (A note on terminology: we use the terms “cross-sectional unit”, “unit” and “group” interchangeably below to refer to the entities that compose the cross-sectional dimension of the panel. These might, for instance, be firms, countries or persons.)

For representation in a textual computer file (and also for gretl’s internal calculations) the three dimensions must somehow be flattened into two. This “flattening” involves taking layers of the data that would naturally stack in a third dimension, and stacking them in the vertical dimension.

Gretl always expects data to be arranged “by observation”, that is, such that each row represents an observation (and each variable occupies one and only one column). In this context the flattening of a panel data set can be done in either of two ways:

- Stacked time series: the successive vertical blocks each comprise a time series for a given unit.
- Stacked cross sections: the successive vertical blocks each comprise a cross-section for a given period.

You may input data in whichever arrangement is more convenient. Internally, however, gretl always stores panel data in the form of stacked time series.

## 4.5 Panel data specifics

When you import panel data into `gretl` from a spreadsheet or comma separated format, the panel nature of the data will not be recognized automatically (most likely the data will be treated as “undated”). A panel interpretation can be imposed on the data using the graphical interface or via the `setobs` command.

In the graphical interface, use the menu item “Data, Dataset structure”. In the first dialog box that appears, select “Panel”. In the next dialog you have a three-way choice. The first two options, “Stacked time series” and “Stacked cross sections” are applicable if the data set is already organized in one of these two ways. If you select either of these options, the next step is to specify the number of cross-sectional units in the data set. The third option, “Use index variables”, is applicable if the data set contains two variables that index the units and the time periods respectively; the next step is then to select those variables. For example, a data file might contain a country code variable and a variable representing the year of the observation. In that case `gretl` can reconstruct the panel structure of the data regardless of how the observation rows are organized.

The `setobs` command has options that parallel those in the graphical interface. If suitable index variables are available you can do, for example

```
setobs unitvar timevar --panel-vars
```

where `unitvar` is a variable that indexes the units and `timevar` is a variable indexing the periods. Alternatively you can use the form `setobs freq 1:1 structure`, where `freq` is replaced by the “block size” of the data (that is, the number of periods in the case of stacked time series, or the number of units in the case of stacked cross-sections) and `structure` is either `--stacked-time-series` or `--stacked-cross-section`. Two examples are given below: the first is suitable for a panel in the form of stacked time series with observations from 20 periods; the second for stacked cross sections with 5 units.

```
setobs 20 1:1 --stacked-time-series
setobs 5 1:1 --stacked-cross-section
```

### Panel data arranged by variable

Publicly available panel data sometimes come arranged “by variable.” Suppose we have data on two variables, `x1` and `x2`, for each of 50 states in each of 5 years (giving a total of 250 observations per variable). One textual representation of such a data set would start with a block for `x1`, with 50 rows corresponding to the states and 5 columns corresponding to the years. This would be followed, vertically, by a block with the same structure for variable `x2`. A fragment of such a data file is shown below, with quinquennial observations 1965–1985. Imagine the table continued for 48 more states, followed by another 50 rows for variable `x2`.

	x1				
	1965	1970	1975	1980	1985
AR	100.0	110.5	118.7	131.2	160.4
AZ	100.0	104.3	113.8	120.9	140.6

If a datafile with this sort of structure is read into `gretl`,<sup>3</sup> the program will interpret the columns as distinct variables, so the data will not be usable “as is.” But there is a mechanism for correcting the situation, namely the `stack` function within the `genr` command.

Consider the first data column in the fragment above: the first 50 rows of this column constitute a cross-section for the variable `x1` in the year 1965. If we could create a new variable by stacking the

<sup>3</sup>Note that you will have to modify such a datafile slightly before it can be read at all. The line containing the variable name (in this example `x1`) will have to be removed, and so will the initial row containing the years, otherwise they will be taken as numerical data.

first 50 entries in the second column underneath the first 50 entries in the first, we would be on the way to making a data set “by observation” (in the first of the two forms mentioned above, stacked cross-sections). That is, we’d have a column comprising a cross-section for  $x_1$  in 1965, followed by a cross-section for the same variable in 1970.

The following gretl script illustrates how we can accomplish the stacking, for both  $x_1$  and  $x_2$ . We assume that the original data file is called `panel.txt`, and that in this file the columns are headed with “variable names”  $p_1, p_2, \dots, p_5$ . (The columns are not really variables, but in the first instance we “pretend” that they are.)

```
open panel.txt
genr x1 = stack(p1..p5) --length=50
genr x2 = stack(p1..p5) --offset=50 --length=50
setobs 50 1:1 --stacked-cross-section
store panel.gdt x1 x2
```

The second line illustrates the syntax of the `stack` function. The double dots within the parentheses indicate a range of variables to be stacked: here we want to stack all 5 columns (for all 5 years).<sup>4</sup> The full data set contains 100 rows; in the stacking of variable  $x_1$  we wish to read only the first 50 rows from each column: we achieve this by adding `--length=50`. Note that if you want to stack a non-contiguous set of columns you can give a comma-separated list of variable names, as in

```
genr x = stack(p1,p3,p5)
```

or you can provide within the parentheses the name of a previously created list (see chapter 13).

On line 3 we do the stacking for variable  $x_2$ . Again we want a `length` of 50 for the components of the stacked series, but this time we want gretl to start reading from the 50th row of the original data, and we specify `--offset=50`. Line 4 imposes a panel interpretation on the data; finally, we save the data in gretl format, with the panel interpretation, discarding the original “variables”  $p_1$  through  $p_5$ .

The illustrative script above is appropriate when the number of variable to be processed is small. When then are many variables in the data set it will be more efficient to use a command loop to accomplish the stacking, as shown in the following script. The setup is presumed to be the same as in the previous section (50 units, 5 periods), but with 20 variables rather than 2.

```
open panel.txt
loop i=1..20
  genr k = ($i - 1) * 50
  genr x$i = stack(p1..p5) --offset=k --length=50
endloop
setobs 50 1.01 --stacked-cross-section
store panel.gdt x1 x2 x3 x4 x5 x6 x7 x8 x9 x10 \
  x11 x12 x13 x14 x15 x16 x17 x18 x19 x20
```

### Panel data marker strings

It can be helpful with panel data to have the observations identified by mnemonic markers. A special function in the `genr` command is available for this purpose.

In the example above, suppose all the states are identified by two-letter codes in the left-most column of the original datafile. When the stacking operation is performed, these codes will be stacked along with the data values. If the first row is marked AR for Arkansas, then the marker AR will end up being shown on each row containing an observation for Arkansas. That’s all very well, but these markers don’t tell us anything about the date of the observation. To rectify this we could do:

---

<sup>4</sup>You can also specify a list of series using the wildcard ‘\*’; for example `stack(p*)` would stack all series whose names begin with ‘p’.

```

genr time
genr year = 1960 + (5 * time)
genr markers = "%s:%d", marker, year

```

The first line generates a 1-based index representing the period of each observation, and the second line uses the `time` variable to generate a variable representing the year of the observation. The third line contains this special feature: if (and only if) the name of the new “variable” to generate is `markers`, the portion of the command following the equals sign is taken as a C-style format string (which must be wrapped in double quotes), followed by a comma-separated list of arguments. The arguments will be printed according to the given format to create a new set of observation markers. Valid arguments are either the names of variables in the dataset, or the string `marker` which denotes the pre-existing observation marker. The format specifiers which are likely to be useful in this context are `%s` for a string and `%d` for an integer. Strings can be truncated: for example `%.3s` will use just the first three characters of the string. To chop initial characters off an existing observation marker when constructing a new one, you can use the syntax `marker + n`, where `n` is a positive integer: in the case the first `n` characters will be skipped.

After the commands above are processed, then, the observation markers will look like, for example, `AR:1965`, where the two-letter state code and the year of the observation are spliced together with a colon.

### Panel dummy variables

In a panel study you may wish to construct dummy variables of one or both of the following sorts: (a) dummies as unique identifiers for the units or groups, and (b) dummies as unique identifiers for the time periods. The former may be used to allow the intercept of the regression to differ across the units, the latter to allow the intercept to differ across periods.

Two special functions are available to create such dummies. These are found under the “Add” menu in the GUI, or under the `genr` command in script mode or `gretlcli`.

1. “unit dummies” (script command `genr unitdum`). This command creates a set of dummy variables identifying the cross-sectional units. The variable `du_1` will have value 1 in each row corresponding to a unit 1 observation, 0 otherwise; `du_2` will have value 1 in each row corresponding to a unit 2 observation, 0 otherwise; and so on.
2. “time dummies” (script command `genr timedum`). This command creates a set of dummy variables identifying the periods. The variable `dt_1` will have value 1 in each row corresponding to a period 1 observation, 0 otherwise; `dt_2` will have value 1 in each row corresponding to a period 2 observation, 0 otherwise; and so on.

If a panel data set has the `YEAR` of the observation entered as one of the variables you can create a periodic dummy to pick out a particular year, e.g. `genr dum = (YEAR=1960)`. You can also create periodic dummy variables using the modulus operator, `%`. For instance, to create a dummy with value 1 for the first observation and every thirtieth observation thereafter, 0 otherwise, do

```

genr index
genr dum = ((index-1) % 30) = 0

```

### Lags, differences, trends

If the time periods are evenly spaced you may want to use lagged values of variables in a panel regression (but see also chapter 18); you may also wish to construct first differences of variables of interest.

Once a dataset is identified as a panel, `gretl` will handle the generation of such variables correctly. For example the command `genr x1_1 = x1(-1)` will create a variable that contains the first lag

of `x1` where available, and the missing value code where the lag is not available (e.g. at the start of the time series for each group). When you run a regression using such variables, the program will automatically skip the missing observations.

When a panel data set has a fairly substantial time dimension, you may wish to include a trend in the analysis. The command `genr time` creates a variable named `time` which runs from 1 to  $T$  for each unit, where  $T$  is the length of the time-series dimension of the panel. If you want to create an index that runs consecutively from 1 to  $m \times T$ , where  $m$  is the number of units in the panel, use `genr index`.

### Basic statistics by unit

Gretl contains functions which can be used to generate basic descriptive statistics for a given variable, on a per-unit basis; these are `pnobs()` (number of valid cases), `pmin()` and `pmax()` (minimum and maximum) and `pmean()` and `psd()` (mean and standard deviation).

As a brief illustration, suppose we have a panel data set comprising 8 time-series observations on each of  $N$  units or groups. Then the command

```
genr pmx = pmean(x)
```

creates a series of this form: the first 8 values (corresponding to unit 1) contain the mean of  $x$  for unit 1, the next 8 values contain the mean for unit 2, and so on. The `psd()` function works in a similar manner. The sample standard deviation for group  $i$  is computed as

$$s_i = \sqrt{\frac{\sum (x - \bar{x}_i)^2}{T_i - 1}}$$

where  $T_i$  denotes the number of valid observations on  $x$  for the given unit,  $\bar{x}_i$  denotes the group mean, and the summation is across valid observations for the group. If  $T_i < 2$ , however, the standard deviation is recorded as 0.

One particular use of `psd()` may be worth noting. If you want to form a sub-sample of a panel that contains only those units for which the variable  $x$  is time-varying, you can either use

```
smp1 (pmin(x) < pmax(x)) --restrict
```

or

```
smp1 (psd(x) > 0) --restrict
```

## 4.6 Missing data values

### Representation and handling

Missing values are represented internally as `DBL_MAX`, the largest floating-point number that can be represented on the system (which is likely to be at least 10 to the power 300, and so should not be confused with legitimate data values). In a native-format data file they should be represented as `NA`. When importing CSV data `gretl` accepts several common representations of missing values including `-999`, the string `NA` (in upper or lower case), a single dot, or simply a blank cell. Blank cells should, of course, be properly delimited, e.g. `120.6`, `, 5.38`, in which the middle value is presumed missing.

As for handling of missing values in the course of statistical analysis, `gretl` does the following:

- In calculating descriptive statistics (mean, standard deviation, etc.) under the `summary` command, missing values are simply skipped and the sample size adjusted appropriately.

- In running regressions `gretl` first adjusts the beginning and end of the sample range, truncating the sample if need be. Missing values at the beginning of the sample are common in time series work due to the inclusion of lags, first differences and so on; missing values at the end of the range are not uncommon due to differential updating of series and possibly the inclusion of leads.

If `gretl` detects any missing values “inside” the (possibly truncated) sample range for a regression, the result depends on the character of the dataset and the estimator chosen. In many cases, the program will automatically skip the missing observations when calculating the regression results. In this situation a message is printed stating how many observations were dropped. On the other hand, the skipping of missing observations is not supported for all procedures: exceptions include all autoregressive estimators, system estimators such as SUR, and nonlinear least squares. In the case of panel data, the skipping of missing observations is supported only if their omission leaves a balanced panel. If missing observations are found in cases where they are not supported, `gretl` gives an error message and refuses to produce estimates.

### Manipulating missing values

Some special functions are available for the handling of missing values. The boolean function `missing()` takes the name of a variable as its single argument; it returns a series with value 1 for each observation at which the given variable has a missing value, and value 0 otherwise (that is, if the given variable has a valid value at that observation). The function `ok()` is complementary to `missing`; it is just a shorthand for `!missing` (where `!` is the boolean NOT operator). For example, one can count the missing values for variable `x` using

```
scalar nmiss_x = sum(missing(x))
```

The function `zeromiss()`, which again takes a single series as its argument, returns a series where all zero values are set to the missing code. This should be used with caution — one does not want to confuse missing values and zeros — but it can be useful in some contexts. For example, one can determine the first valid observation for a variable `x` using

```
genr time
scalar x0 = min(zeromiss(time * ok(x)))
```

The function `misszero()` does the opposite of `zeromiss`, that is, it converts all missing values to zero.

It may be worth commenting on the propagation of missing values within `genr` formulae. The general rule is that in arithmetical operations involving two variables, if either of the variables has a missing value at observation  $t$  then the resulting series will also have a missing value at  $t$ . The one exception to this rule is multiplication by zero: zero times a missing value produces zero (since this is mathematically valid regardless of the unknown value).

## 4.7 Maximum size of data sets

Basically, the size of data sets (both the number of variables and the number of observations per variable) is limited only by the characteristics of your computer. `Gretl` allocates memory dynamically, and will ask the operating system for as much memory as your data require. Obviously, then, you are ultimately limited by the size of RAM.

Aside from the multiple-precision OLS option, `gretl` uses double-precision floating-point numbers throughout. The size of such numbers in bytes depends on the computer platform, but is typically eight. To give a rough notion of magnitudes, suppose we have a data set with 10,000 observations on 500 variables. That's 5 million floating-point numbers or 40 million bytes. If we define the

megabyte (MB) as  $1024 \times 1024$  bytes, as is standard in talking about RAM, it's slightly over 38 MB. The program needs additional memory for workspace, but even so, handling a data set of this size should be quite feasible on a current PC, which at the time of writing is likely to have at least 256 MB of RAM.

If RAM is not an issue, there is one further limitation on data size (though it's very unlikely to be a binding constraint). That is, variables and observations are indexed by signed integers, and on a typical PC these will be 32-bit values, capable of representing a maximum positive value of  $2^{31} - 1 = 2,147,483,647$ .

The limits mentioned above apply to gretl's "native" functionality. There are tighter limits with regard to two third-party programs that are available as add-ons to gretl for certain sorts of time-series analysis including seasonal adjustment, namely TRAMO/SEATS and X-12-ARIMA. These programs employ a fixed-size memory allocation, and can't handle series of more than 600 observations.

## 4.8 Data file collections

If you're using gretl in a teaching context you may be interested in adding a collection of data files and/or scripts that relate specifically to your course, in such a way that students can browse and access them easily.

There are three ways to access such collections of files:

- For data files: select the menu item "File, Open data, Sample file", or click on the folder icon on the gretl toolbar.
- For script files: select the menu item "File, Script files, Practice file".

When a user selects one of the items:

- The data or script files included in the gretl distribution are automatically shown (this includes files relating to Ramanathan's *Introductory Econometrics* and Greene's *Econometric Analysis*).
- The program looks for certain known collections of data files available as optional extras, for instance the datafiles from various econometrics textbooks (Davidson and MacKinnon, Gujarati, Stock and Watson, Verbeek, Wooldridge) and the Penn World Table (PWT 5.6). (See [the data page](#) at the gretl website for information on these collections.) If the additional files are found, they are added to the selection windows.
- The program then searches for valid file collections (not necessarily known in advance) in these places: the "system" data directory, the system script directory, the user directory, and all first-level subdirectories of these. For reference, typical values for these directories are shown in Table 4.1. (Note that PERSONAL is a placeholder that is expanded by Windows, corresponding to "My Documents" on English-language systems.)

	Linux	MS Windows
system data dir	/usr/share/gretl/data	c:\Program Files\gretl\data
system script dir	/usr/share/gretl/scripts	c:\Program Files\gretl/scripts
user dir	\$HOME/gretl	PERSONAL\gretl

**Table 4.1:** Typical locations for file collections

Any valid collections will be added to the selection windows. So what constitutes a valid file collection? This comprises either a set of data files in gretl XML format (with the .gdt suffix) or a set of

script files containing gretl commands (with `.inp` suffix), in each case accompanied by a “master file” or catalog. The gretl distribution contains several example catalog files, for instance the file `descriptions` in the `misc` sub-directory of the gretl data directory and `ps_descriptions` in the `misc` sub-directory of the scripts directory.

If you are adding your own collection, data catalogs should be named `descriptions` and script catalogs should be named `ps_descriptions`. In each case the catalog should be placed (along with the associated data or script files) in its own specific sub-directory (e.g. `/usr/share/gretl/data/mydata` or `c:\userdata\gretl\data\mydata`).

The catalog files are plain text; if they contain non-ASCII characters they must be encoded as UTF-8. The syntax of such files is straightforward. Here, for example, are the first few lines of gretl’s “misc” data catalog:

```
# Gretl: various illustrative datafiles
"arma","artificial data for ARMA script example"
"ects_nls","Nonlinear least squares example"
"hamilton","Prices and exchange rate, U.S. and Italy"
```

The first line, which must start with a hash mark, contains a short name, here “Gretl”, which will appear as the label for this collection’s tab in the data browser window, followed by a colon, followed by an optional short description of the collection.

Subsequent lines contain two elements, separated by a comma and wrapped in double quotation marks. The first is a datafile name (leave off the `.gdt` suffix here) and the second is a short description of the content of that datafile. There should be one such line for each datafile in the collection.

A script catalog file looks very similar, except that there are three fields in the file lines: a filename (without its `.inp` suffix), a brief description of the econometric point illustrated in the script, and a brief indication of the nature of the data used. Again, here are the first few lines of the supplied “misc” script catalog:

```
# Gretl: various sample scripts
"arma","ARMA modeling","artificial data"
"ects_nls","Nonlinear least squares (Davidson)","artificial data"
"leverage","Influential observations","artificial data"
"longley","Multicollinearity","US employment"
```

If you want to make your own data collection available to users, these are the steps:

1. Assemble the data, in whatever format is convenient.
2. Convert the data to gretl format and save as `gdt` files. It is probably easiest to convert the data by importing them into the program from plain text, CSV, or a spreadsheet format (MS Excel or Gnumeric) then saving them. You may wish to add descriptions of the individual variables (the “Variable, Edit attributes” menu item), and add information on the source of the data (the “Data, Edit info” menu item).
3. Write a descriptions file for the collection using a text editor.
4. Put the datafiles plus the descriptions file in a subdirectory of the gretl data directory (or user directory).
5. If the collection is to be distributed to other people, package the data files and catalog in some suitable manner, e.g. as a zipfile.

If you assemble such a collection, and the data are not proprietary, we would encourage you to submit the collection for packaging as a gretl optional extra.



## 4.9 Assembling data from multiple sources

In many contexts researchers need to bring together data from multiple source files, and in some cases these sources are not organized such that the data can simply be “stuck together” by appending rows or columns to a base dataset. In `gretl`, the `join` command can be used for this purpose; this command is discussed in detail in [chapter 5](#).

## Chapter 5

# Joining data sources

### 5.1 Introduction

As of version 1.9.10 gretl has a new command, `join`. The basic function of this command is to pull data from file into an existing in-memory dataset; it therefore overlaps to some degree with the `append` command, but `join` is much more flexible and sophisticated. This chapter gives an overview of the functionality of the new command along with a detailed account of its syntax and options. We provide several toy examples and discuss one real-world case.

First, a point on terminology: in the following we use the terms “left-hand” and “inner” to refer to the dataset that is already in memory, and the terms “right-hand” and “outer” to refer to the dataset in the file from which data are to be drawn.

Two main things are new in `join`:

- “Key” variables can be used to match specific observations (rows) in the inner and outer datasets, and this match need not be 1 to 1.
- A row filter may be applied to screen out unwanted observations in the outer dataset.

As will be explained below, these two features support rather complex concatenation and manipulation of data from different sources. The potential complexity of a `join` operation, when several options are activated, means that it is not possible to support batch importation of several series with a single command. In contrast with the `append` command, which by default imports the entire content of a data file, `join` imports one series at a time. A command loop can be used to apply `join` to multiple series.

A related aspect of `join` should be noted—one that makes this command particularly useful when dealing with very large datafiles. That is, when gretl executes a `join` it does not, in general, read into memory the entire content of the right-hand side dataset. Only those columns that are actually needed for the operation are read in full. This makes the `join` operation faster and less demanding of RAM than the methods available in most other software. On the other hand, gretl’s asymmetrical treatment of the “inner” and “outer” datasets in `join` may require some getting used to, for users of other packages.

### 5.2 Basic syntax

The minimal invocation of `join` is

```
join filename varname
```

where *filename* is the name of a delimited text data file and *varname* is the name of the series to be imported. Only column-delimited text files are supported at present; the delimiter may be comma, space, tab or semicolon. A series named *varname* may already be present in the left-hand dataset, but that is not required. The series to be imported may be numerical or string-valued.

The effect of the minimal version of `join` is this: gretl looks for a data column labeled *varname* in the specified file; if such a column is found and the number of observations on the right matches the number of observations in the current sample range on the left, then the values from the right are copied into the relevant range of observations on the left. If *varname* does not already exist

on the left, any observations outside of the current sample are set to NA; if it exists already then observations outside of the current sample are left unchanged.

The case where you want to rename a series on import is handled by the `--data` option. This option has one required argument, the name by which the series is known on the right. While the *varname* argument must be a valid gretl variable name, the right-hand data name need not be;<sup>1</sup> for example it can contain embedded spaces (in which case it must be enclosed in double quotes). For example, the command

```
join foo.csv x --data="12. Some name"
```

will look for a column headed "12. Some name" on the right and import it as x.

### 5.3 Filtering

Rows from the outer dataset can be filtered using the `--filter` option, which has a required argument of the form

*term1 op term2*

(with or without spaces). At least one of *term1* and *term2* must be the name of a series (column) present in the right-hand side dataset. The other may also be the name of a right-hand series, or it may be a numerical or string constant (with the type matching the specified series). For numerical data *op* can be one of

`==, >, <, >=, <=, or !=`

where these symbols have their usual meanings. If the series term in the filter is string-valued, the following subset of operators is supported: `==` and `!=` (the strings compare equal and unequal respectively), `>=` (the first string compares equal to the second up to the length of the latter, but may be longer than the second) and `<=` (the second string compares equal with the first up to the length of the first, but may be longer).

The filter specifies a Boolean condition in terms of either two right-hand side variables or one right-hand variable and a constant, and only those rows on which the condition is satisfied are imported. If the filter string contains spaces or an equals sign it must be double-quoted, otherwise double-quoting is optional. As with the data option, the names of series in the outer dataset need not be valid gretl identifiers.

Note that only a single filter, of binary form, is supported—this may be generalized in the future. However, in some cases the effect of a more elaborate filter may be achieved through subsampling the left-hand dataset (see section 5.8 below).

Examples of potentially valid filter options (assuming that the specified right-hand side columns are found):

```
--filter="x15<=x17"
```

```
--filter="SEX==F"
```

```
--filter=nkids>2
```

### 5.4 Matching with keys

Things begin to get interesting when we come to key-matching. The purpose of this facility is perhaps best introduced by example. Suppose that (as with many survey and census-based datasets) we have a dataset that is composed of two or more related files, each having a different unit of observation; for example we have a “persons” data file and a “households” datafile. Table 5.1 shows a

---

<sup>1</sup>But see section 5.7 below.

simple, artificial case. The file `people.csv` contains a unique identifier for the individuals, `pid`. The households file, `hholds.csv`, contains the unique household identifier `hid`, which is also present in the persons file.

As a first example of join with keys, let's add the household-level variable `xh` to the persons dataset:

```
open people.csv --quiet
join hholds.csv xh --ikey=hid
print --byobs
```

The basic key option is named `ikey`; this indicates “inner key”, that is, the key variable found in the left-hand or inner dataset. By default it is assumed that the right-hand dataset contains a column of the same name, though as we'll see below that assumption can be overridden. The `join` command above says, find a series named `xh` in the right-hand dataset and add it to the left-hand one, using the values of `hid` to match rows. Looking at the data in Table 5.1 we can see how this should work. Persons 1 and 2 are both members of household 1, so they should both get values of 1 for `xh`; persons 3 and 4 are members of household 2, so that `xh = 4`; and so on. Note that the order in which the key values occur on the right-hand side does not matter. The `gretl` output from the `print` command is shown in the lower panel of Table 5.1.

people.csv				hholds.csv			
pid,hid,gender,age,xp				hid,country,xh			
1	1	M	50	1	US	1	
2	1	F	40	6	IT	12	
3	2	M	30	3	UK	6	
4	2	F	25	4	IT	8	
5	3	M	40	2	US	4	
6	4	F	35	5	IT	10	
7	4	M	70				
8	4	F	60				
9	5	F	20				
10	6	M	40				
pid	hid			xh			
1	1			1			
2	1			1			
3	2			4			
4	2			4			
5	3			6			
6	4			8			
7	4			8			
8	4			8			
9	5			10			
10	6			12			

**Table 5.1:** Two linked CSV data files, and the effect of a `join`

Note that key variables are treated conceptually as integers. If a specified key contains fractional values these are truncated.

Three extensions of the basic key mechanism are available.

- If the outer dataset contains a relevant key variable but it goes under a different name from the inner key, you can use the `--okey` option to specify the outer key. (As with other right-hand names, this does not have to be a valid gretl identifier.) So, for example, if `hholds.csv` contained the `hid` information, but under the name `HHOLD`, the `join` command above could be modified as

```
join hholds.csv xh --ikey=hid --okey=HHOLD
```

- If a single key is not sufficient to generate the matches you want, you can specify a double key in the form of two series names separated by a comma; in this case the importation of data is restricted to those rows on which both keys match. The syntax here is, for example

```
join foo.csv x --ikey=key1,key2
```

Again, the `--okey` option may be used if the corresponding right-hand columns are named differently. The same number of keys must be given on the left and the right, but when a double key is used and only one of the key names differs on the right, the name that is in common may be omitted (although the comma separator must be retained). For example, the second of the following lines is acceptable shorthand for the first:

```
join foo.csv x --ikey=key1,Lkey2 --okey=key1,Rkey2
join foo.csv x --ikey=key1,Lkey2 --okey=,Rkey2
```

- The example above is an instance of a 1 to 1 match, in the sense that applying the matching criterion produces exactly one value of the variable `xh` corresponding to each row of the inner dataset. Two other possibilities arise.

First, it may be that some rows in the inner dataset have no match on the right: by default such observations get NA for the imported data. In some cases, the appropriate value to record in the absence of a match may be zero rather than NA. For example, consider a query on “number of hours worked” when the inner dataset contains individuals and the outer file contains data on jobs: if an individual does not appear in the jobs file, the number of hours worked is implicitly zero. In such cases gretl’s `misszero()` function can be used to adjust the imported data.

Second, some left-hand rows may have more than one match on the right; we refer to this as 1 to  $n$  matching. In that case it is necessary to specify an “aggregation method”. This is the job of the `--aggr` option, discussed below.

## 5.5 Aggregation

The `--aggr` option for 1 to  $n$  matching of rows takes a single argument, which must be one of the following:

<i>Code</i>	<i>Value returned</i>
<code>count</code>	count of matches
<code>avg</code>	mean of matching values
<code>sum</code>	sum of matching values
<code>min</code>	minimum of matching values
<code>max</code>	maximum of matching values
<code>seq:i</code>	the $i^{\text{th}}$ matching value (e.g. <code>seq:2</code> )

Note that the `count` aggregation method is special, in that there is no need for a “data series” on the right; the imported series is simply a function of the specified key(s). All the other methods

require that “actual data” are found on the right. Also note that when `count` is used, the value returned when no match is found is (as one might expect) zero rather than NA.

With 1:*n* matching, it may be that the number of matches differs across the observations on the left. The `seq` method returns NA when the (1-based) sequence parameter *i* exceeds the number of matches for a given observation.

Referring again to the data in Table 5.1, suppose we want to import data from the `people` file into a dataset established at household level. Here’s an example where we use the individual age data from `people.csv` to add the average and minimum age of household members.

```
open hholds.csv --quiet
join people.csv avgage --ikey=hid --data=age --aggr=avg
join people.csv minage --ikey=hid --data=age --aggr=min
```

Here’s a further example where we add to the household data the sum of the personal data `xp`, with the twist that we apply filters to get the sum specifically for household members under the age of 40, and for women.

```
open hholds.csv --quiet
join people.csv young_xp --ikey=hid --filter="age<40" --data=xp --aggr=sum
join people.csv female_xp --ikey=hid --filter="gender==F" --data=xp --aggr=sum
```

## 5.6 String-valued key variables

The examples above use numerical variables (household and individual ID numbers) in the matching process. It is also possible to use string-valued variables, in which case a match means that the string values of the key variables compare equal (with case sensitivity). When using double keys, you can mix numerical and string keys, but naturally you cannot mix a string variable on the left (via `ikey`) with a numerical one on the right (via `okey`), or vice versa.

Here’s a simple example. Suppose that alongside `hholds.csv` we have a file `countries.csv` with the following content:

```
country,GDP
UK,100
US,500
IT,150
FR,180
```

The variable `country`, which is also found in `hholds.csv`, is string-valued. We can pull the GDP of the country in which the household resides into our households dataset with

```
open hholds.csv -q
join countries.csv GDP --ikey=country
```

which gives

	hid	country	GDP
1	1	1	500
2	6	2	150
3	3	3	100
4	4	2	150
5	2	1	500
6	5	2	150

## 5.7 Right-hand column names

As noted above, the column names in the datafile from which data are to be joined do not have to be valid gretl identifiers (that is, composed of nothing but ASCII letters, numbers and the underscore character, starting with a letter and with a maximum length of 15 characters). However, there are limits.

- Names that include a comma will break the double-key mechanism, in which a comma is used to separate the two keys in the `okey` option.
- Names that include any of the characters used in the operators for the `filter` option will break that option.
- In reading a delimited text file, gretl truncates strings at 71 bytes.

## 5.8 A real-world case

For a real use-case for `join`, we turn to the Bank of Italy's *Survey on Household Income and Wealth* (SHIW).<sup>2</sup> In ASCII form the 2010 survey results comprise 47 MB of data in 29 files. In this exercise we will draw on five of the SHIW files to construct a replica of the dataset used in Thomas Mroz's famous paper (*Econometrica*, 1987) on women's labor force participation, which contains data on married women between the age of 30 and 60 along with certain characteristics of their households and husbands.

Our general strategy is as follows: we create a "core" dataset by opening the file `carcom10.csv`, which contains basic data on the individuals. After dropping unwanted individuals (all but married women), we use the resulting dataset as a base for pulling in further data via the `join` command.

The complete script to do the job is given in the Appendix to this chapter; here we walk through the script with comments interspersed. We assume that all the relevant files from the Bank of Italy survey are contained in a subdirectory called SHIW.

Starting with `carcom10.csv`, we use the `--cols` option to the `open` command to import specific series,<sup>3</sup> namely NQUEST (household ID number), NORD (sequence number for individuals within each household), SEX (male = 1, female = 2), PARENT (status in household: 1 = head of household, 2 = spouse of head, etc.), STACIV (marital status: married = 1), STUDIO (educational level, coded from 1 to 8) and ETA (age in years).

```
open SHIW/carcom10.csv --cols=1,2,3,4,9,10,29
```

We then restrict the sample to married women from 30 to 60 years of age, and additionally restrict the sample of women to those who are either heads of households or spouses of the head.

```
smp1 SEX==2 && ETA>=30 && ETA<=60 && STACIV==1 --restrict
smp1 PARENT<3 --restrict
```

For compatibility with the Mroz dataset as presented in the gretl datafile `mroz87.gdt`, we rename the age and education variables as `WA` and `WE` respectively, then we store the reduced base dataset in gretl format.

```
rename ETA WA
rename STUDIO WE
store mroz_rep.gdt
```

---

<sup>2</sup>Details of the survey can be found at <http://www.bancaditalia.it/statistiche/indcamp/bilfait/dismicro>. The ASCII (CSV) data files for the 2010 survey are available at [http://www.bancaditalia.it/statistiche/indcamp/bilfait/dismicro/annuale/ascii/ind10\\_ascii.zip](http://www.bancaditalia.it/statistiche/indcamp/bilfait/dismicro/annuale/ascii/ind10_ascii.zip).

<sup>3</sup>This is a new usage of `cols`; see section 5.9 for details.

The next step will be to get data on working hours from the jobs file `allb1.csv`. There's a complication here. We need the total hours worked over the course of the year (for both the women and their husbands). This is not available as such, but the variables `ORETOT` and `MESILAV` give, respectively, average hours worked per week and the number of months worked in 2010, each on a per-job basis. If each person held at most one job over the year we could compute his or her annual hours as

```
HRS = ORETOT * 52 * MESILAV/12
```

However, some people had more than one job, and in this case what we want is the sum of annual hours across their jobs. We could use `join` with the `seq` aggregation method to construct this sum, but it is probably more straightforward to read the `allb1` data, compute the HRS values per job as shown above, and save the results to a temporary CSV file.

```
open SHIW/allb1.csv --cols=1,2,8,11 --quiet
series HRS = misszero(ORETOT) * 52 * misszero(MESILAV)/12
store HRS.csv NQUEST NORD HRS
```

Now we can reopen the base dataset and join the hours variable from `HRS.csv`. Note that we need a double key here: the women are uniquely identified by the combination of `NQUEST` and `NORD`. We don't need an `okey` specification since these keys go under the same names in the right-hand file. We define labor force participation, `LFP`, based on hours.

```
open mroz_rep.gdt
join HRS.csv WHRS --ikey=NQUEST,NORD --data=HRS --aggr=sum
WHRS = misszero(WHRS)
LFP = WHRS > 0
```

For reference, here's how we could have used `seq` to avoid writing a temporary file:

```
join SHIW/allb1.csv njobs --ikey=NQUEST,NORD --data=ORETOT --aggr=count
series WHRS = 0
loop i=1..max(njobs) -q
  join SHIW/allb1.csv htmp --ikey=NQUEST,NORD --data=ORETOT --aggr="seq:$i"
  join SHIW/allb1.csv mtmp --ikey=NQUEST,NORD --data=MESILAV --aggr="seq:$i"
  WHRS += misszero(htmp) * 52 * misszero(mtmp)/12
endloop
```

To generate the work experience variable, `AX`, we use the file `lavoro.csv`: this contains a variable named `ETALAV` which records the age at which the person first started work.

```
join SHIW/lavoro.csv ETALAV --ikey=NQUEST,NORD
series AX = misszero(WA - ETALAV)
```

We compute the woman's hourly wage, `WW`, as the ratio of total employment income to annual working hours. This requires drawing the series `YL` (payroll income) and `YM` (net self-employment income) from the persons file `rper10.csv`.

```
join SHIW/rper10.csv YL --ikey=NQUEST,NORD --aggr=sum
join SHIW/rper10.csv YM --ikey=NQUEST,NORD --aggr=sum
series WW = LFP ? (YL + YM)/WHRS : 0
```

The family's net disposable income is available as `Y` in the file `rfam10.csv`; we import this as `FAMINC`.

```
join SHIW/rfam10.csv FAMINC --ikey=NQUEST --data=Y
```



Data on number of children are now obtained by applying the `count` method. For the Mroz replication we want the number of children under the age of 6, and also the number aged 6 to 18.

```
join SHIW/carcom10.csv KIDS --ikey=NQUEST --aggr=count --filter="ETA<=18"
join SHIW/carcom10.csv KL6 --ikey=NQUEST --aggr=count --filter=ETA<6
series K618 = KIDS - KL6
```

We want to add data on the women's husbands, but how do we find them? To do this we create an additional inner key which we'll call `H_ID` (husband ID), by sub-sampling in turn on the observations falling into each of two classes: (a) those where the woman is recorded as head of household and (b) those where the husband has that status. In each case we want the individual ID (`NORD`) of the household member whose status is complementary to that of the woman in question. So for case (a) we subsample using `PARENT==1` (head of household) and filter the join using `PARENT==2` (spouse of head); in case (b) we do the converse. We thus construct `H_ID` piece-wise.<sup>4</sup>

```
# for women who are household heads
smp1 PARENT==1 --restrict --replace
join SHIW/carcom10.csv H_ID --ikey=NQUEST --data=NORD --filter="PARENT==2"
# for women who are not household heads
smp1 PARENT==2 --restrict --replace
join SHIW/carcom10.csv H_ID --ikey=NQUEST --data=NORD --filter="PARENT==1"
smp1 full
```

Now we can use our new inner key to retrieve the husbands' data, matching `H_ID` on the left with `NORD` on the right within each household.

```
join SHIW/carcom10.csv HA --ikey=NQUEST,H_ID --okey=NQUEST,NORD --data=ETA
join SHIW/carcom10.csv HE --ikey=NQUEST,H_ID --okey=NQUEST,NORD --data=STUDIO
join HRS.csv HHRS --ikey=NQUEST,H_ID --okey=NQUEST,NORD --data=HRS --aggr=sum
HHRS = misszero(HHRS)
```

The remainder of the script is straightforward and does not require discussion here: we recode the education variables for compatibility; delete some intermediate series that are not needed any more; add informative labels; and save the final product. See the Appendix for details.

To compare the results from this dataset with those from the earlier US data used by Mroz, one can copy the input file `heckit.inp` (supplied with the `gretl` package) and substitute `mroz_rep.gdt` for `mroz87.gdt`.<sup>5</sup> It turns out that the results are qualitatively very similar.

## 5.9 A related change

Alongside the introduction of the `join` command, some changes have been made to the operation of the `open` command. The one that concerns us here (and the only one that is backward-incompatible) is a revised interpretation of the `--cols` option.

Up to `gretl` 1.9.9, this option was specific to the reading of fixed-format datafiles. In that context the parameter to the option—a list of comma-separated numbers—was interpreted as a set of pairs of the form (start, width), telling `gretl` at which byte on each line to start reading, and how many bytes to read, to get the value for a given variable.

As of `gretl` 1.9.10, the facility just described is still available but the option has been renamed as `--fixed-cols`. The parameter to the plain `--cols` option is now interpreted as a (1-based) list of

<sup>4</sup>In principle the husband ID variable could be constructed without subsampling if more complex filtering were supported, but as noted above the `join` filter is at present limited to a binary expression involving only right-hand side variables and constants.

<sup>5</sup>One other change is needed: in William Greene's specification of the `heckit` model an additional regressor named `CIT` is used. You can simply comment this out.

the columns to be read from a delimited text datafile (e.g. CSV). Note that if the first column in a CSV file is an observations column, it is not included in the count: the first actual data column is treated as column 1.

## Appendix: the full Mroz data script

```
# start with everybody; get gender, age and a few other variables
# directly while we're at it
open SHIW/carcom10.csv --cols=1,2,3,4,9,10,29

# subsample on married women between the ages of 30 and 60
smp1 SEX==2 && ETA>=30 && ETA<=60 && STACIV==1 --restrict
# for simplicity, restrict to heads of households and their spouses
smp1 PARENT<3 --restrict

# rename the age and education variables for compatibility; then
# save the reduced base dataset
rename ETA WA
rename STUDIO WE
store mroz_rep.gdt

# make a temp file holding annual hours worked per job
open SHIW/allb1.csv --cols=1,2,8,11 --quiet
series HRS = misszero(ORETOT) * 52 * misszero(MESILAV)/12
store HRS.csv NQUEST NORD HRS

# reopen the base dataset and begin drawing assorted data in
open mroz_rep.gdt

# women's annual hours (summed across jobs)
join HRS.csv WHRS --ikey=NQUEST,NORD --data=HRS --aggr=sum
WHRS = misszero(WHRS)

# labor force participation
LFP = WHRS > 0

# work experience: ETALAV = age when started first job
join SHIW/lavoro.csv ETALAV --ikey=NQUEST,NORD
series AX = misszero(WA - ETALAV)

# women's hourly wages
join SHIW/rper10.csv YL --ikey=NQUEST,NORD --aggr=sum
join SHIW/rper10.csv YM --ikey=NQUEST,NORD --aggr=sum
series WW = LFP ? (YL + YM)/WHRS : 0

# family income (Y = net disposable income)
join SHIW/rfam10.csv FAMINC --ikey=NQUEST --data=Y

# get data on children using the "count" method
join SHIW/carcom10.csv KIDS --ikey=NQUEST --aggr=count --filter="ETA<=18"
join SHIW/carcom10.csv KL6 --ikey=NQUEST --aggr=count --filter="ETA<6"
series K618 = KIDS - KL6

# data on husbands: we first construct an auxiliary inner key for
# husbands, using the little trick of subsampling the inner dataset
#
# for women who are household heads
smp1 PARENT==1 --restrict --replace
join SHIW/carcom10.csv H_ID --ikey=NQUEST --data=NORD --filter="PARENT==2"
```

```

# for women who are not household heads
smp1 PARENT==2 --restrict --replace
join SHIW/carcom10.csv H_ID --ikey=NQUEST --data=NORD --filter="PARENT==1"
smp1 full

# add husbands' data via the newly-added secondary inner key
join SHIW/carcom10.csv HA --ikey=NQUEST,H_ID --okey=NQUEST,NORD --data=ETA
join SHIW/carcom10.csv HE --ikey=NQUEST,H_ID --okey=NQUEST,NORD --data=STUDIO
join HRS.csv HHRS --ikey=NQUEST,H_ID --okey=NQUEST,NORD --data=HRS --aggr=sum
HHRS = misszero(HHRS)

# final cleanup begins

# recode educational attainment as years of education
matrix eduyrs = {0, 5, 8, 11, 13, 16, 18, 21}
series WE = replace(WE, seq(1,8), eduyrs)
series HE = replace(HE, seq(1,8), eduyrs)

# cut some cruft
delete SEX STACIV KIDS YL YM PARENT H_ID ETALAV

# add some labels for the series
setinfo LFP -d "1 if woman worked in 2010"
setinfo WHRS -d "Wife's hours of work in 2010"
setinfo KL6 -d "Number of children less than 6 years old in household"
setinfo K618 -d "Number of children between ages 6 and 18 in household"
setinfo WA -d "Wife's age"
setinfo WE -d "Wife's educational attainment, in years"
setinfo WW -d "Wife's average hourly earnings, in 2010 euros"
setinfo HHRS -d "Husband's hours worked in 2010"
setinfo HA -d "Husband's age"
setinfo HE -d "Husband's educational attainment, in years"
setinfo FAMINC -d "Family income, in 2010 euros"
setinfo AX -d "Actual years of wife's previous labor market experience"

# save the final product
store mroz_rep.gdt

```

## Chapter 6

# Special functions in genr

### 6.1 Introduction

The `genr` command provides a flexible means of defining new variables. It is documented in the *Gretl Command Reference*. This chapter offers a more expansive discussion of some of the special functions available via `genr` and some of the finer points of the command.

### 6.2 Long-run variance

As is well known, the variance of the average of  $T$  random variables  $x_1, x_2, \dots, x_T$  with equal variance  $\sigma^2$  equals  $\sigma^2/T$  if the data are uncorrelated. In this case, the sample variance of  $x_t$  over the sample size provides a consistent estimator.

If, however, there is serial correlation among the  $x_t$ s, the variance of  $\bar{X} = T^{-1} \sum_{t=1}^T x_t$  must be estimated differently. One of the most widely used statistics for this purpose is a nonparametric kernel estimator with the Bartlett kernel defined as

$$\hat{\omega}^2(k) = T^{-1} \sum_{t=k}^{T-k} \left[ \sum_{i=-k}^k w_i (x_t - \bar{X})(x_{t-i} - \bar{X}) \right], \quad (6.1)$$

where the integer  $k$  is known as the window size and the  $w_i$  terms are the so-called *Bartlett weights*, defined as  $w_i = 1 - \frac{|i|}{k+1}$ . It can be shown that, for  $k$  large enough,  $\hat{\omega}^2(k)/T$  yields a consistent estimator of the variance of  $\bar{X}$ .

Gretl implements this estimator by means of the function `lrvar()`, which takes two arguments: the series whose long-run variance must be estimated and the scalar  $k$ . If  $k$  is negative, the popular choice  $T^{1/3}$  is used.

### 6.3 Cumulative densities and p-values

The two functions `cdf` and `pvalue` provide complementary means of examining values from several probability distributions: the standard normal, Student's  $t$ ,  $\chi^2$ ,  $F$ , gamma, and binomial. The syntax of these functions is set out in the *Gretl Command Reference*; here we expand on some subtleties.

The cumulative density function or CDF for a random variable is the integral of the variable's density from its lower limit (typically either  $-\infty$  or 0) to any specified value  $x$ . The p-value (at least the one-tailed, right-hand p-value as returned by the `pvalue` function) is the complementary probability, the integral from  $x$  to the upper limit of the distribution, typically  $+\infty$ .

In principle, therefore, there is no need for two distinct functions: given a CDF value  $p_0$  you could easily find the corresponding p-value as  $1 - p_0$  (or vice versa). In practice, with finite-precision computer arithmetic, the two functions are not redundant. This requires a little explanation. In `gretl`, as in most statistical programs, floating point numbers are represented as “doubles” — double-precision values that typically have a storage size of eight bytes or 64 bits. Since there are only so many bits available, only so many floating-point numbers can be represented: *doubles do not model the real line*. Typically doubles can represent numbers over the range (roughly)  $\pm 1.7977 \times 10^{308}$ , but only to about 15 digits of precision.

Suppose you're interested in the left tail of the  $\chi^2$  distribution with 50 degrees of freedom: you'd like to know the CDF value for  $x = 0.9$ . Take a look at the following interactive session:

```
? genr p1 = cdf(X, 50, 0.9)
Generated scalar p1 (ID 2) = 8.94977e-35
? genr p2 = pvalue(X, 50, 0.9)
Generated scalar p2 (ID 3) = 1
? genr test = 1 - p2
Generated scalar test (ID 4) = 0
```

The `cdf` function has produced an accurate value, but the `pvalue` function gives an answer of 1, from which it is not possible to retrieve the answer to the CDF question. This may seem surprising at first, but consider: if the value of `p1` above is correct, then the correct value for `p2` is  $1 - 8.94977 \times 10^{-35}$ . But there's no way that value can be represented as a double: that would require over 30 digits of precision.

Of course this is an extreme example. If the  $x$  in question is not too far off into one or other tail of the distribution, the `cdf` and `pvalue` functions will in fact produce complementary answers, as shown below:

```
? genr p1 = cdf(X, 50, 30)
Generated scalar p1 (ID 2) = 0.0111648
? genr p2 = pvalue(X, 50, 30)
Generated scalar p2 (ID 3) = 0.988835
? genr test = 1 - p2
Generated scalar test (ID 4) = 0.0111648
```

But the moral is that if you want to examine extreme values you should be careful in selecting the function you need, in the knowledge that values very close to zero can be represented as doubles while values very close to 1 cannot.

## 6.4 Retrieving internal variables

The `genr` command provides a means of retrieving various values calculated by the program in the course of estimating models or testing hypotheses. The variables that can be retrieved in this way are listed in the *Gretl Command Reference*; here we say a bit more about the special variables `$test` and `$pvalue`.

These variables hold, respectively, the value of the last test statistic calculated using an explicit testing command and the p-value for that test statistic. If no such test has been performed at the time when these variables are referenced, they will produce the missing value code. The “explicit testing commands” that work in this way are as follows: `add` (joint test for the significance of variables added to a model); `adf` (Augmented Dickey-Fuller test, see below); `arch` (test for ARCH); `chow` (Chow test for a structural break); `coeffsum` (test for the sum of specified coefficients); `cusum` (the Harvey-Collier  $t$ -statistic); `kpss` (KPSS stationarity test, no p-value available); `lmtest` (see below); `meantest` (test for difference of means); `omit` (joint test for the significance of variables omitted from a model); `reset` (Ramsey's RESET); `restrict` (general linear restriction); `runs` (runs test for randomness); `testuhat` (test for normality of residual); and `vartest` (test for difference of variances). In most cases both a `$test` and a `$pvalue` are stored; the exception is the KPSS test, for which a p-value is not currently available.

An important point to notice about this mechanism is that the internal variables `$test` and `$pvalue` are over-written each time one of the tests listed above is performed. If you want to reference these values, you must do so at the correct point in the sequence of `gretl` commands.

A related point is that some of the test commands generate, by default, more than one test statistic and p-value; in these cases only the last values are stored. To get proper control over the retrieval of values via `$test` and `$pvalue` you should formulate the test command in such a way that the result is unambiguous. This comment applies in particular to the `adf` and `lmtest` commands.

- By default, the `adf` command generates three variants of the Dickey-Fuller test: one based on a regression including a constant, one using a constant and linear trend, and one using a constant and a quadratic trend. When you wish to reference `$test` or `$pvalue` in connection with this command, you can control the variant that is recorded by using one of the flags `--nc`, `--c`, `--ct` or `--ctt` with `adf`.
- By default, the `lmtest` command (which must follow an OLS regression) performs several diagnostic tests on the regression in question. To control what is recorded in `$test` and `$pvalue` you should limit the test using one of the flags `--logs`, `--autocorr`, `--squares` or `--white`.

As an aid in working with values retrieved using `$test` and `$pvalue`, the nature of the test to which these values relate is written into the descriptive label for the generated variable. You can read the label for the variable using the `label` command (with just one argument, the name of the variable), to check that you have retrieved the right value. The following interactive session illustrates this point.

```
? adf 4 x1 --c
Augmented Dickey-Fuller tests, order 4, for x1
sample size 59
unit-root null hypothesis: a = 1
  test with constant
  model: (1 - L)y = b0 + (a-1)*y(-1) + ... + e
  estimated value of (a - 1): -0.216889
  test statistic: t = -1.83491
  asymptotic p-value 0.3638
P-values based on MacKinnon (JAE, 1996)
? genr pv = $pvalue
Generated scalar pv (ID 13) = 0.363844
? label pv
pv=Dickey-Fuller pvalue (scalar)
```

## 6.5 The discrete Fourier transform

The discrete Fourier transform can be best thought of as a linear, invertible transform of a complex vector. Hence, if  $\mathbf{x}$  is an  $n$ -dimensional vector whose  $k$ -th element is  $x_k = a_k + ib_k$ , then the output of the discrete Fourier transform is a vector  $\mathbf{f} = \mathcal{F}(\mathbf{x})$  whose  $k$ -th element is

$$f_k = \sum_{j=0}^{n-1} e^{-i\omega(j,k)} x_j$$

where  $\omega(j, k) = 2\pi i \frac{jk}{n}$ . Since the transformation is invertible, the vector  $\mathbf{x}$  can be recovered from  $\mathbf{f}$  via the so-called inverse transform

$$x_k = \frac{1}{n} \sum_{j=0}^{n-1} e^{i\omega(j,k)} f_j.$$

The Fourier transform is used in many diverse situations on account of this key property: the convolution of two vectors can be performed efficiently by multiplying the elements of their Fourier transforms and inverting the result. If

$$z_k = \sum_{j=1}^n x_j y_{k-j},$$

then

$$\mathcal{F}(\mathbf{z}) = \mathcal{F}(\mathbf{x}) \odot \mathcal{F}(\mathbf{y}).$$

That is,  $\mathcal{F}(\mathbf{z})_k = \mathcal{F}(\mathbf{x})_k \mathcal{F}(\mathbf{y})_k$ .

For computing the Fourier transform, `gretl` uses the external library `fftw3`: see [Frigo and Johnson \(2005\)](#). This guarantees extreme speed and accuracy. In fact, the CPU time needed to perform the transform is  $O(n \log n)$  for any  $n$ . This is why the array of numerical techniques employed in `fftw3` is commonly known as the *Fast* Fourier Transform.

`Gretl` provides two matrix functions<sup>1</sup> for performing the Fourier transform and its inverse: `fft` and `ffti`. In fact, `gretl`'s implementation of the Fourier transform is somewhat more specialized: the input to the `fft` function is understood to be real. Conversely, `ffti` takes a complex argument and delivers a real result. For example:

```
x1 = { 1 ; 2 ; 3 }
# perform the transform
f = fft(a)
# perform the inverse transform
x2 = ffti(f)
```

yields

$$x_1 = \begin{bmatrix} 1 \\ 2 \\ 3 \end{bmatrix} \quad f = \begin{bmatrix} 6 & 0 \\ -1.5 & 0.866 \\ -1.5 & -0.866 \end{bmatrix} \quad x_2 = \begin{bmatrix} 1 \\ 2 \\ 3 \end{bmatrix}$$

where the first column of  $f$  holds the real part and the second holds the complex part. In general, if the input to `fft` has  $n$  columns, the output has  $2n$  columns, where the real parts are stored in the odd columns and the complex parts in the even ones. Should it be necessary to compute the Fourier transform on several vectors with the same number of elements, it is numerically more efficient to group them into a matrix rather than invoking `fft` for each vector separately.

As an example, consider the multiplication of two polynomials:

$$\begin{aligned} a(x) &= 1 + 0.5x \\ b(x) &= 1 + 0.3x - 0.8x^2 \\ c(x) = a(x) \cdot b(x) &= 1 + 0.8x - 0.65x^2 - 0.4x^3 \end{aligned}$$

The coefficients of the polynomial  $c(x)$  are the convolution of the coefficients of  $a(x)$  and  $b(x)$ ; the following `gretl` code fragment illustrates how to compute the coefficients of  $c(x)$ :

```
# define the two polynomials
a = { 1, 0.5, 0, 0 }'
b = { 1, 0.3, -0.8, 0 }'
# perform the transforms
fa = fft(a)
fb = fft(b)
# complex-multiply the two transforms
fc = cmult(fa, fb)
# compute the coefficients of c via the inverse transform
c = ffti(fc)
```

Maximum efficiency would have been achieved by grouping `a` and `b` into a matrix. The computational advantage is so little in this case that the exercise is a bit silly, but the following alternative may be preferable for a large number of rows/columns:

```
# define the two polynomials
a = { 1 ; 0.5 ; 0 ; 0 }
b = { 1 ; 0.3 ; -0.8 ; 0 }
```

---

<sup>1</sup>See chapter 14.

```
# perform the transforms jointly
f = fft(a ~ b)
# complex-multiply the two transforms
fc = cmult(f[,1:2], f[,3:4])
# compute the coefficients of c via the inverse transform
c = ffti(fc)
```

Traditionally, the Fourier transform in econometrics has been mostly used in time-series analysis, the periodogram being the best known example. Example script [6.1](#) shows how to compute the periodogram of a time series via the `fft` function.

**Example 6.1:** Periodogram via the Fourier transform

---

```
nulldata 50
# generate an AR(1) process
series e = normal()
series x = 0
x = 0.9*x(-1) + e
# compute the periodogram
scale = 2*pi*$nobs
X = { x }
F = fft(X)
S = sumr(F.^2)
S = S[2:($nobs/2)+1]/scale
omega = seq(1,($nobs/2))' .* (2*pi/$nobs)
omega = omega ~ S
# compare the built-in command
pergm x
print omega
```

---



## Chapter 7

# Sub-sampling a dataset

### 7.1 Introduction

Some subtle issues can arise here. This chapter attempts to explain the issues.

A sub-sample may be defined in relation to a full data set in two different ways: we will refer to these as “setting” the sample and “restricting” the sample; these methods are discussed in sections 7.2 and 7.3 respectively. In addition section 7.4 discusses resampling with replacement, which is useful in the context of bootstrapping test statistics.

The following discussion focuses on the command-line approach. But you can also invoke the methods outlined here via the items under the Sample menu in the GUI program.

### 7.2 Setting the sample

By “setting” the sample we mean defining a sub-sample simply by means of adjusting the starting and/or ending point of the current sample range. This is likely to be most relevant for time-series data. For example, one has quarterly data from 1960:1 to 2003:4, and one wants to run a regression using only data from the 1970s. A suitable command is then

```
smp1 1970:1 1979:4
```

Or one wishes to set aside a block of observations at the end of the data period for out-of-sample forecasting. In that case one might do

```
smp1 ; 2000:4
```

where the semicolon is shorthand for “leave the starting observation unchanged”. (The semicolon may also be used in place of the second parameter, to mean that the ending observation should be unchanged.) By “unchanged” here, we mean unchanged relative to the last `smp1` setting, or relative to the full dataset if no sub-sample has been defined up to this point. For example, after

```
smp1 1970:1 2003:4  
smp1 ; 2000:4
```

the sample range will be 1970:1 to 2000:4.

An incremental or relative form of setting the sample range is also supported. In this case a relative offset should be given, in the form of a signed integer (or a semicolon to indicate no change), for both the starting and ending point. For example

```
smp1 +1 ;
```

will advance the starting observation by one while preserving the ending observation, and

```
smp1 +2 -1
```

will both advance the starting observation by two and retard the ending observation by one.

An important feature of “setting” the sample as described above is that it necessarily results in the selection of a subset of observations that are contiguous in the full dataset. The structure of the dataset is therefore unaffected (for example, if it is a quarterly time series before setting the sample, it remains a quarterly time series afterwards).

### 7.3 Restricting the sample

By “restricting” the sample we mean selecting observations on the basis of some Boolean (logical) criterion, or by means of a random number generator. This is likely to be most relevant for cross-sectional or panel data.

Suppose we have data on a cross-section of individuals, recording their gender, income and other characteristics. We wish to select for analysis only the women. If we have a `gender` dummy variable with value 1 for men and 0 for women we could do

```
smp1 gender=0 --restrict
```

to this effect. Or suppose we want to restrict the sample to respondents with incomes over \$50,000. Then we could use

```
smp1 income>50000 --restrict
```

A question arises here. If we issue the two commands above in sequence, what do we end up with in our sub-sample: all cases with income over 50000, or just women with income over 50000? By default, in a `gretl` script, the answer is the latter: women with income over 50000. The second restriction augments the first, or in other words the final restriction is the logical product of the new restriction and any restriction that is already in place. If you want a new restriction to replace any existing restrictions you can first recreate the full dataset using

```
smp1 --full
```

Alternatively, you can add the `replace` option to the `smp1` command:

```
smp1 income>50000 --restrict --replace
```

This option has the effect of automatically re-establishing the full dataset before applying the new restriction.

Unlike a simple “setting” of the sample, “restricting” the sample may result in selection of non-contiguous observations from the full data set. It may also change the structure of the data set.

This can be seen in the case of panel data. Say we have a panel of five firms (indexed by the variable `firm`) observed in each of several years (identified by the variable `year`). Then the restriction

```
smp1 year=1995 --restrict
```

produces a dataset that is not a panel, but a cross-section for the year 1995. Similarly

```
smp1 firm=3 --restrict
```

produces a time-series dataset for firm number 3.

For these reasons (possible non-contiguity in the observations, possible change in the structure of the data), `gretl` acts differently when you “restrict” the sample as opposed to simply “setting” it. In the case of setting, the program merely records the starting and ending observations and uses these

as parameters to the various commands calling for the estimation of models, the computation of statistics, and so on. In the case of restriction, the program makes a reduced copy of the dataset and by default treats this reduced copy as a simple, undated cross-section.<sup>1</sup>

If you wish to re-impose a time-series or panel interpretation of the reduced dataset you can do so using the `setobs` command, or the GUI menu item “Data, Dataset structure”.

The fact that “restricting” the sample results in the creation of a reduced copy of the original dataset may raise an issue when the dataset is very large (say, several thousands of observations). With such a dataset in memory, the creation of a copy may lead to a situation where the computer runs low on memory for calculating regression results. You can work around this as follows:

1. Open the full data set, and impose the sample restriction.
2. Save a copy of the reduced data set to disk.
3. Close the full dataset and open the reduced one.
4. Proceed with your analysis.

### Random sub-sampling

Besides restricting the sample on some deterministic criterion, it may sometimes be useful (when working with very large datasets, or perhaps to study the properties of an estimator) to draw a random sub-sample from the full dataset. This can be done using, for example,

```
smp1 100 --random
```

to select 100 cases. If you want the sample to be reproducible, you should set the seed for the random number generator first, using `set`. This sort of sampling falls under the “restriction” category: a reduced copy of the dataset is made.

## 7.4 Resampling and bootstrapping

Given an original data series  $x$ , the command

```
series xr = resample(x)
```

creates a new series each of whose elements is drawn at random from the elements of  $x$ . If the original series has 100 observations, each element of  $x$  is selected with probability 1/100 at each drawing. Thus the effect is to “shuffle” the elements of  $x$ , with the twist that each element of  $x$  may appear more than once, or not at all, in  $xr$ .

The primary use of this function is in the construction of bootstrap confidence intervals or p-values. Here is a simple example. Suppose we estimate a simple regression of  $y$  on  $x$  via OLS and find that the slope coefficient has a reported  $t$ -ratio of 2.5 with 40 degrees of freedom. The two-tailed p-value for the null hypothesis that the slope parameter equals zero is then 0.0166, using the  $t(40)$  distribution. Depending on the context, however, we may doubt whether the ratio of coefficient to standard error truly follows the  $t(40)$  distribution. In that case we could derive a bootstrap p-value as shown in Example 7.1.

Under the null hypothesis that the slope with respect to  $x$  is zero,  $y$  is simply equal to its mean plus an error term. We simulate  $y$  by resampling the residuals from the initial OLS and re-estimate the model. We repeat this procedure a large number of times, and record the number of cases where the absolute value of the  $t$ -ratio is greater than 2.5: the proportion of such cases is our bootstrap p-value. For a good discussion of simulation-based tests and bootstrapping, see Davidson and MacKinnon (2004, chapter 4).

<sup>1</sup>With one exception: if you start with a balanced panel dataset and the restriction is such that it preserves a balanced

**Example 7.1:** Calculation of bootstrap p-value

---

```
ols y 0 x
# save the residuals
genr ui = $uhat
scalar ybar = mean(y)
# number of replications for bootstrap
scalar replics = 10000
scalar tcount = 0
series ysim = 0
loop replics --quiet
  # generate simulated y by resampling
  ysim = ybar + resample(ui)
  ols ysim 0 x
  scalar tsim = abs($coeff(x) / $stderr(x))
  tcount += (tsim > 2.5)
endloop
printf "proportion of cases with |t| > 2.5 = %g\n", tcount / replics
```

---

---

panel — for example, it results in the deletion of all the observations for one cross-sectional unit — then the reduced dataset is still, by default, treated as a panel.

## Chapter 8

# Graphs and plots

### 8.1 Gnuplot graphs

A separate program, `gnuplot`, is called to generate graphs. Gnuplot is a very full-featured graphing program with myriad options. It is available from [www.gnuplot.info](http://www.gnuplot.info) (but note that a suitable copy of `gnuplot` is bundled with the packaged versions of `gretl` for MS Windows and Mac OS X). `gretl` gives you direct access, via a graphical interface, to a subset of `gnuplot`'s options and it tries to choose sensible values for you; it also allows you to take complete control over graph details if you wish.

With a graph displayed, you can click on the graph window for a pop-up menu with the following options.

- **Save as PNG:** Save the graph in Portable Network Graphics format (the same format that you see on screen).
- **Save as postscript:** Save in encapsulated postscript (EPS) format.
- **Save as Windows metafile:** Save in Enhanced Metafile (EMF) format.
- **Save to session as icon:** The graph will appear in iconic form when you select “Icon view” from the View menu.
- **Zoom:** Lets you select an area within the graph for closer inspection (not available for all graphs).
- **Print:** (Current GTK or MS Windows only) lets you print the graph directly.
- **Copy to clipboard:** MS Windows only, lets you paste the graph into Windows applications such as MS Word.
- **Edit:** Opens a controller for the plot which lets you adjust many aspects of its appearance.
- **Close:** Closes the graph window.

#### Displaying data labels

For simple X-Y scatter plots, some further options are available if the dataset includes “case markers” (that is, labels identifying each observation).<sup>1</sup> With a scatter plot displayed, when you move the mouse pointer over a data point its label is shown on the graph. By default these labels are transient: they do not appear in the printed or copied version of the graph. They can be removed by selecting “Clear data labels” from the graph pop-up menu. If you want the labels to be affixed permanently (so they will show up when the graph is printed or copied), select the option “Freeze data labels” from the pop-up menu; “Clear data labels” cancels this operation. The other label-related option, “All data labels”, requests that case markers be shown for all observations. At present the display of case markers is disabled for graphs containing more than 250 data points.

---

<sup>1</sup>For an example of such a dataset, see the Ramanathan file `data4-10`: this contains data on private school enrollment for the 50 states of the USA plus Washington, DC; the case markers are the two-letter codes for the states.

### GUI plot editor

Selecting the Edit option in the graph popup menu opens an editing dialog box, shown in Figure 8.1. Notice that there are several tabs, allowing you to adjust many aspects of a graph's appearance: font, title, axis scaling, line colors and types, and so on. You can also add lines or descriptive labels to a graph (under the Lines and Labels tabs). The “Apply” button applies your changes without closing the editor; “OK” applies the changes and closes the dialog.

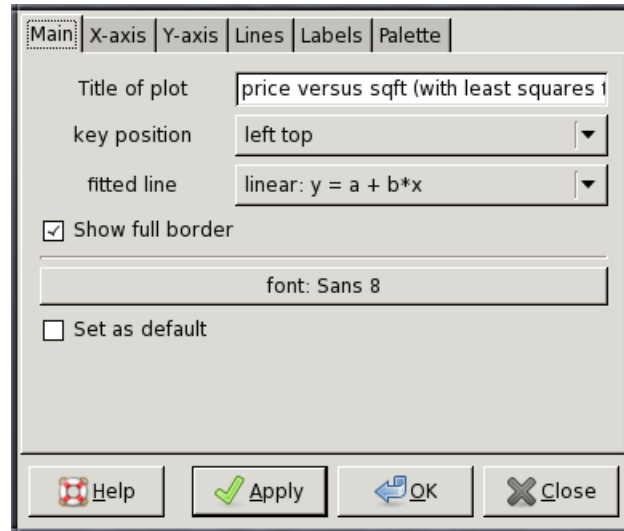


Figure 8.1: gretl's gnuplot controller

### Publication-quality graphics: advanced options

The GUI plot editor has two limitations. First, it cannot represent all the myriad options that gnuplot offers. Users who are sufficiently familiar with gnuplot to know what they're missing in the plot editor presumably don't need much help from gretl, so long as they can get hold of the gnuplot command file that gretl has put together. Second, even if the plot editor meets your needs, in terms of fine-tuning the graph you see on screen, a few details may need further work in order to get optimal results for publication.

Either way, the first step in advanced tweaking of a graph is to get access to the graph command file.

- In the graph display window, right-click and choose “Save to session as icon”.
- If it's not already open, open the icon view window — either via the menu item View/Icon view, or by clicking the “session icon view” button on the main-window toolbar.
- Right-click on the icon representing the newly added graph and select “Edit plot commands” from the pop-up menu.
- You get a window displaying the plot file (Figure 8.2).

Here are the basic things you can do in this window. Obviously, you can edit the file you just opened. You can also send it for processing by gnuplot, by clicking the “Execute” (cogwheel) icon in the toolbar. Or you can use the “Save as” button to save a copy for editing and processing as you wish.

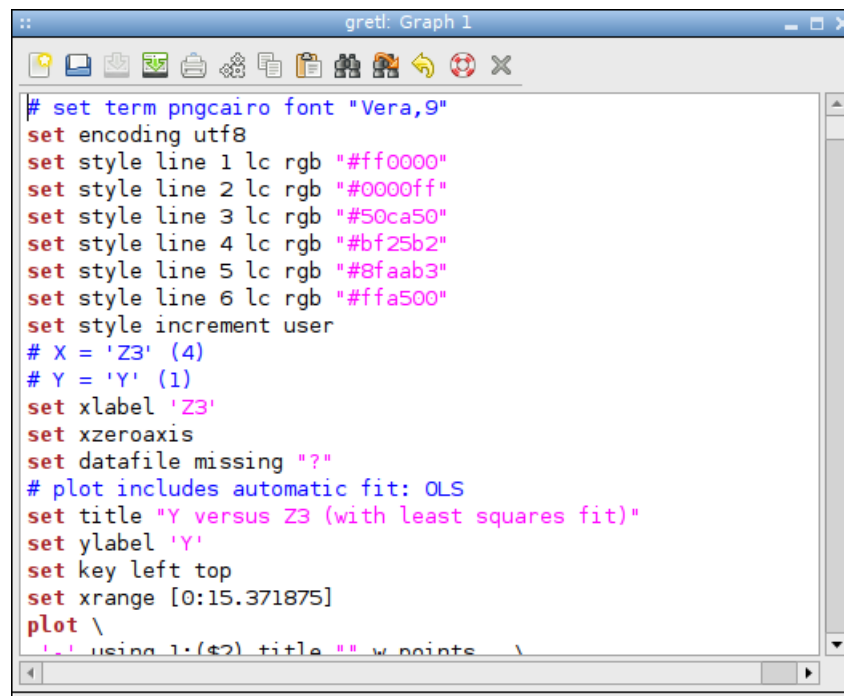


Figure 8.2: Plot commands editor

Unless you're a gnuplot expert, most likely you'll only need to edit a couple of lines at the top of the file, specifying a driver (plus options) and an output file. We offer here a brief summary of some points that may be useful.

First, gnuplot's output mode is set via the command `set term` followed by the name of a supported driver ("terminal" in gnuplot parlance) plus various possible options. (The top line in the plot commands window shows the `set term` line that gretl used to make a PNG file, commented out.) The graphic formats that are most suitable for publication are PDF and EPS. These are supported by the gnuplot term types `pdf`, `pdfcairo` and `postscript` (with the `eps` option). The `pdfcairo` driver has the virtue that it behaves in a very similar manner to the PNG one, the output of which you see on screen. This is provided by the version of gnuplot that is included in the gretl packages for MS Windows and Mac OS X; if you're on Linux it may or may be supported. If `pdfcairo` is not available, the `pdf` terminal may be available; the `postscript` terminal is almost certainly available.

Besides selecting a term type, if you want to get gnuplot to write the actual output file you need to append a `set output` line giving a filename. Here are a few examples of the first two lines you might type in the window editing your plot commands. We'll make these more "realistic" shortly.

```

set term pdfcairo
set output 'mygraph.pdf'

set term pdf
set output 'mygraph.pdf'

set term postscript eps
set output 'mygraph.eps'

```

There are a couple of things worth remarking here. First, you may want to adjust the size of the graph, and second you may want to change the font. The default sizes produced by the above drivers are 5 inches by 3 inches for `pdfcairo` and `pdf`, and 5 inches by 3.5 inches for `postscript eps`. In each case you can change this by giving a size specification, which takes the form `XX,YY` (examples below).

You may ask, why bother changing the size in the gnuplot command file? After all, PDF and EPS are both vector formats, so the graphs can be scaled at will. True, but a uniform scaling will also affect the font size, which may end looking wrong. You can get optimal results by experimenting with the `font` and `size` options to gnuplot's `set term` command. Here are some examples (comments follow below).

```
# pdfcairo, regular size, slightly amended
set term pdfcairo font "Sans,6" size 5in,3.5in
# or small size
set term pdfcairo font "Sans,5" size 3in,2in

# pdf, regular size, slightly amended
set term pdf font "Helvetica,8" size 5in,3.5in
# or small
set term pdf font "Helvetica,6" size 3in,2in

# postscript, regular
set term post eps solid font "Helvetica,16"
# or small
set term post eps solid font "Helvetica,12" size 3in,2in
```

On the first line we set a sans serif font for `pdfcairo` at a suitable size for a  $5 \times 3.5$  inch plot (which you may find looks better than the rather “letterboxy” default of  $5 \times 3$ ). And on the second we illustrate what you might do to get a smaller  $3 \times 2$  inch plot. You can specify the plot size in centimeters if you prefer, as in

```
set term pdfcairo font "Sans,6" size 6cm,4cm
```

We then repeat the exercise for the `pdf` terminal. Notice that here we’re specifying one of the 35 standard PostScript fonts, namely Helvetica. Unlike `pdfcairo`, the plain `pdf` driver is unlikely to be able to find fonts other than these.

In the third pair of lines we illustrate options for the `postscript` driver (which, as you see, can be abbreviated as `post`). Note that here we have added the option `solid`. Unlike most other drivers, this one uses dashed lines unless you specify the `solid` option. Also note that we’ve (apparently) specified a much larger font in this case. That’s because the `eps` option in effect tells the `postscript` driver to work at half-size (among other things), so we need to double the font size.

Table 8.1 summarizes the basics for the three drivers we have mentioned.

Terminal	default size (inches)	suggested font
<code>pdfcairo</code>	$5 \times 3$	Sans,6
<code>pdf</code>	$5 \times 3$	Helvetica,8
<code>post eps</code>	$5 \times 3.5$	Helvetica,16

**Table 8.1:** Drivers for publication-quality graphics

To find out more about gnuplot visit [www.gnuplot.info](http://www.gnuplot.info). This site has documentation for the current version of the program in various formats.

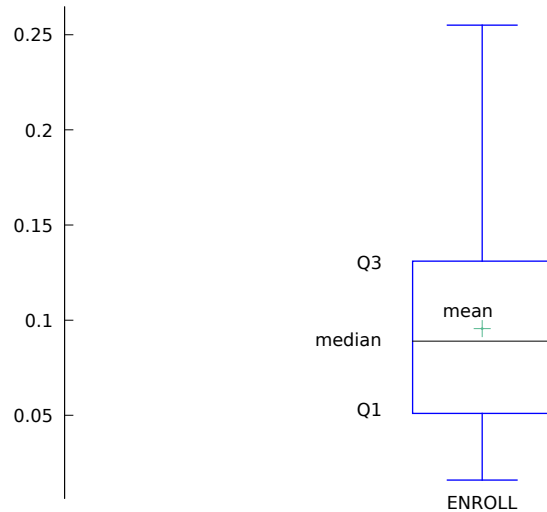
### Additional tips

To be written. Line widths, enhanced text. Show a “before and after” example.



## 8.2 Boxplots

These plots (after Tukey and Chambers) display the distribution of a variable. The central box encloses the middle 50 percent of the data, i.e. it is bounded by the first and third quartiles. The “whiskers” extend to the minimum and maximum values. A line is drawn across the box at the median and a “+” sign identifies the mean — see Figure 8.3.



**Figure 8.3:** Sample boxplot

In the case of boxplots with confidence intervals, dotted lines show the limits of an approximate 90 percent confidence interval for the median. This is obtained by the bootstrap method, which can take a while if the data series is very long.

After each variable specified in the boxplot command, a parenthesized boolean expression may be added, to limit the sample for the variable in question. A space must be inserted between the variable name or number and the expression. Suppose you have salary figures for men and women, and you have a dummy variable GENDER with value 1 for men and 0 for women. In that case you could draw comparative boxplots with the following line in the boxplots dialog:

```
salary (GENDER=1) salary (GENDER=0)
```

## Chapter 9

# Discrete variables

When a variable can take only a finite, typically small, number of values, then the variable is said to be *discrete*. Some gretl commands act in a slightly different way when applied to discrete variables; moreover, gretl provides a few commands that only apply to discrete variables. Specifically, the `dummify` and `xtab` commands (see below) are available only for discrete variables, while the `freq` (frequency distribution) command produces different output for discrete variables.

### 9.1 Declaring variables as discrete

Gretl uses a simple heuristic to judge whether a given variable should be treated as discrete, but you also have the option of explicitly marking a variable as discrete, in which case the heuristic check is bypassed.

The heuristic is as follows: First, are all the values of the variable “reasonably round”, where this is taken to mean that they are all integer multiples of 0.25? If this criterion is met, we then ask whether the variable takes on a “fairly small” set of distinct values, where “fairly small” is defined as less than or equal to 8. If both conditions are satisfied, the variable is automatically considered discrete.

To mark a variable as discrete you have two options.

1. From the graphical interface, select “Variable, Edit Attributes” from the menu. A dialog box will appear and, if the variable seems suitable, you will see a tick box labeled “Treat this variable as discrete”. This dialog box can also be invoked via the context menu (right-click on a variable) or by pressing the F2 key.
2. From the command-line interface, via the `discrete` command. The command takes one or more arguments, which can be either variables or list of variables. For example:

```
list xlist = x1 x2 x3
discrete z1 xlist z2
```

This syntax makes it possible to declare as discrete many variables at once, which cannot presently be done via the graphical interface. The switch `--reverse` reverses the declaration of a variable as discrete, or in other words marks it as continuous. For example:

```
discrete foo
# now foo is discrete
discrete foo --reverse
# now foo is continuous
```

The command-line variant is more powerful, in that you can mark a variable as discrete even if it does not seem to be suitable for this treatment.

Note that marking a variable as discrete does not affect its content. It is the user’s responsibility to make sure that marking a variable as discrete is a sensible thing to do. Note that if you want to recode a continuous variable into classes, you can use the `genr` command and its arithmetic functions, as in the following example:

```

nulldata 100
# generate a variable with mean 2 and variance 1
genr x = normal() + 2
# split into 4 classes
genr z = (x>0) + (x>2) + (x>4)
# now declare z as discrete
discrete z

```

Once a variable is marked as discrete, this setting is remembered when you save the file.

## 9.2 Commands for discrete variables

### The **dummify** command

The **dummify** command takes as argument a series  $x$  and creates dummy variables for each distinct value present in  $x$ , which must have already been declared as discrete. Example:

```

open greene22_2
discrete Z5 # mark Z5 as discrete
dummify Z5

```

The effect of the above command is to generate 5 new dummy variables, labeled DZ5\_1 through DZ5\_5, which correspond to the different values in Z5. Hence, the variable DZ5\_4 is 1 if Z5 equals 4 and 0 otherwise. This functionality is also available through the graphical interface by selecting the menu item “Add, Dummies for selected discrete variables”.

The **dummify** command can also be used with the following syntax:

```
list dlist = dummify(x)
```

This not only creates the dummy variables, but also a named list (see section 13.1) that can be used afterwards. The following example computes summary statistics for the variable Y for each value of Z5:

```

open greene22_2
discrete Z5 # mark Z5 as discrete
list foo = dummify(Z5)
loop foreach i foo
    smpl $i --restrict --replace
    summary Y
endloop
smpl --full

```

Since **dummify** generates a list, it can be used directly in commands that call for a list as input, such as **ols**. For example:

```

open greene22_2
discrete Z5 # mark Z5 as discrete
ols Y 0 dummify(Z5)

```

### The **freq** command

The **freq** command displays absolute and relative frequencies for a given variable. The way frequencies are counted depends on whether the variable is continuous or discrete. This command is also available via the graphical interface by selecting the “Variable, Frequency distribution” menu entry.

For discrete variables, frequencies are counted for each distinct value that the variable takes. For continuous variables, values are grouped into “bins” and then the frequencies are counted for each bin. The number of bins, by default, is computed as a function of the number of valid observations in the currently selected sample via the rule shown in Table 9.1. However, when the command is invoked through the menu item “Variable, Frequency Plot”, this default can be overridden by the user.

Observations	Bins
$8 \leq n < 16$	5
$16 \leq n < 50$	7
$50 \leq n \leq 850$	$\lceil \sqrt{n} \rceil$
$n > 850$	29

**Table 9.1:** Number of bins for various sample sizes

For example, the following code

```
open greene19_1
freq TUCE
discrete TUCE # mark TUCE as discrete
freq TUCE
```

yields

```
Read datafile /usr/local/share/gretl/data/greene/greene19_1.gdt
periodicity: 1, maxobs: 32,
observations range: 1-32
```

Listing 5 variables:

```
0) const    1) GPA        2) TUCE        3) PSI        4) GRADE
```

```
? freq TUCE
```

```
Frequency distribution for TUCE, obs 1-32
number of bins = 7, mean = 21.9375, sd = 3.90151
```

interval	midpt	frequency	rel.	cum.
< 13.417	12.000	1	3.12%	3.12% *
13.417 - 16.250	14.833	1	3.12%	6.25% *
16.250 - 19.083	17.667	6	18.75%	25.00% *****
19.083 - 21.917	20.500	6	18.75%	43.75% *****
21.917 - 24.750	23.333	9	28.12%	71.88% *****
24.750 - 27.583	26.167	7	21.88%	93.75% *****
>= 27.583	29.000	2	6.25%	100.00% **

```
Test for null hypothesis of normal distribution:
```

```
Chi-square(2) = 1.872 with p-value 0.39211
```

```
? discrete TUCE # mark TUCE as discrete
```

```
? freq TUCE
```

```
Frequency distribution for TUCE, obs 1-32
```

	frequency	rel.	cum.
12	1	3.12%	3.12% *
14	1	3.12%	6.25% *
17	3	9.38%	15.62% ***

19	3	9.38%	25.00%	***
20	2	6.25%	31.25%	**
21	4	12.50%	43.75%	*****
22	2	6.25%	50.00%	**
23	4	12.50%	62.50%	*****
24	3	9.38%	71.88%	***
25	4	12.50%	84.38%	*****
26	2	6.25%	90.62%	**
27	1	3.12%	93.75%	*
28	1	3.12%	96.88%	*
29	1	3.12%	100.00%	*

Test for null hypothesis of normal distribution:  
Chi-square(2) = 1.872 with p-value 0.39211

As can be seen from the sample output, a Doornik-Hansen test for normality is computed automatically. This test is suppressed for discrete variables where the number of distinct values is less than 10.

This command accepts two options: `--quiet`, to avoid generation of the histogram when invoked from the command line and `--gamma`, for replacing the normality test with Locke's nonparametric test, whose null hypothesis is that the data follow a Gamma distribution.

If the distinct values of a discrete variable need to be saved, the `values()` matrix construct can be used (see chapter 14).

### The `xtab` command

The `xtab` command can be invoked in either of the following ways. First,

```
xtab ylist ; xlist
```

where `ylist` and `xlist` are lists of discrete variables. This produces cross-tabulations (two-way frequencies) of each of the variables in `ylist` (by row) against each of the variables in `xlist` (by column). Or second,

```
xtab xlist
```

In the second case a full set of cross-tabulations is generated; that is, each variable in `xlist` is tabulated against each other variable in the list. In the graphical interface, this command is represented by the "Cross Tabulation" item under the View menu, which is active if at least two variables are selected.

Here is an example of use:

```
open greene22_2
discrete Z* # mark Z1-Z8 as discrete
xtab Z1 Z4 ; Z5 Z6
```

which produces

Cross-tabulation of Z1 (rows) against Z5 (columns)

	[ 1]	[ 2]	[ 3]	[ 4]	[ 5]	TOT.
[ 0]	20	91	75	93	36	315
[ 1]	28	73	54	97	34	286
TOTAL	48	164	129	190	70	601

Pearson chi-square test = 5.48233 (4 df, p-value = 0.241287)

Cross-tabulation of Z1 (rows) against Z6 (columns)

	[ 9][ 12][ 14][ 16][ 17][ 18][ 20]	TOT.
[ 0]	4 36 106 70 52 45 2	315
[ 1]	3 8 48 45 37 67 78	286
TOTAL	7 44 154 115 89 112 80	601

Pearson chi-square test = 123.177 (6 df, p-value = 3.50375e-24)

Cross-tabulation of Z4 (rows) against Z5 (columns)

	[ 1][ 2][ 3][ 4][ 5]	TOT.
[ 0]	17 60 35 45 14	171
[ 1]	31 104 94 145 56	430
TOTAL	48 164 129 190 70	601

Pearson chi-square test = 11.1615 (4 df, p-value = 0.0248074)

Cross-tabulation of Z4 (rows) against Z6 (columns)

	[ 9][ 12][ 14][ 16][ 17][ 18][ 20]	TOT.
[ 0]	1 8 39 47 30 32 14	171
[ 1]	6 36 115 68 59 80 66	430
TOTAL	7 44 154 115 89 112 80	601

Pearson chi-square test = 18.3426 (6 df, p-value = 0.0054306)

Pearson's  $\chi^2$  test for independence is automatically displayed, provided that all cells have expected frequencies under independence greater than  $10^{-7}$ . However, a common rule of thumb states that this statistic is valid only if the expected frequency is 5 or greater for at least 80 percent of the cells. If this condition is not met a warning is printed.

Additionally, the `--row` or `--column` options can be given: in this case, the output displays row or column percentages, respectively.

If you want to cut and paste the output of `xtab` to some other program, e.g. a spreadsheet, you may want to use the `--zeros` option; this option causes cells with zero frequency to display the number 0 instead of being empty.

## Chapter 10

# Loop constructs

### 10.1 Introduction

The command `loop` opens a special mode in which `gretl` accepts a block of commands to be repeated zero or more times. This feature may be useful for, among other things, Monte Carlo simulations, bootstrapping of test statistics and iterative estimation procedures. The general form of a loop is:

```
loop control-expression [ --progressive | --verbose | --quiet ]
    loop body
endloop
```

Five forms of control-expression are available, as explained in section 10.2.

Not all `gretl` commands are available within loops. The commands that are not presently accepted in this context are shown in Table 10.1.

**Table 10.1:** Commands not usable in loops

corrgm	cusum	eqnprint	function	hurst	include	leverage	nulldata
rmplot	run	setmiss	setobs	tabprint	vif		

By default, the `genr` command operates quietly in the context of a loop (without printing information on the variable generated). To force the printing of feedback from `genr` you may specify the `--verbose` option to `loop`. The `--quiet` option suppresses the usual printout of the number of iterations performed, which may be desirable when loops are nested.

The `--progressive` option to `loop` modifies the behavior of the commands `print` and `store`, and certain estimation commands, in a manner that may be useful with Monte Carlo analyses (see Section 10.3).

The following sections explain the various forms of the loop control expression and provide some examples of use of loops.

☞ If you are carrying out a substantial Monte Carlo analysis with many thousands of repetitions, memory capacity and processing time may be an issue. To minimize the use of computer resources, run your script using the command-line program, `gretlcli`, with output redirected to a file.

### 10.2 Loop control variants

#### Count loop

The simplest form of loop control is a direct specification of the number of times the loop should be repeated. We refer to this as a “count loop”. The number of repetitions may be a numerical constant, as in `loop 1000`, or may be read from a scalar variable, as in `loop replics`.

In the case where the loop count is given by a variable, say `replics`, in concept `replics` is an

integer; if the value is not integral, it is converted to an integer by truncation. Note that `replics` is evaluated only once, when the loop is initially compiled.

### While loop

A second sort of control expression takes the form of the keyword `while` followed by a boolean expression. For example,

```
loop while essdiff > .00001
```

Execution of the commands within the loop will continue so long as (a) the specified condition evaluates as true and (b) the number of iterations does not exceed the value of the internal variable `loop_maxiter`. By default this equals 250, but you can specify a different value via the `set` command (see the *Gretl Command Reference*).

### Index loop

A third form of loop control uses an index variable, for example `i`.<sup>1</sup> In this case you specify starting and ending values for the index, which is incremented by one each time round the loop. The syntax looks like this: `loop i=1..20`.

The index variable may be a pre-existing scalar; if this is not the case, the variable is created automatically and is destroyed on exit from the loop.

The index may be used within the loop body in either of two ways: you can access the integer value of `i` (see Example 10.4) or you can use its string representation, `$i` (see Example 10.5).

The starting and ending values for the index can be given in numerical form, by reference to pre-defined scalar variables, or as expressions that evaluate to scalars. In the latter two cases the variables are evaluated once, at the start of the loop. In addition, with time series data you can give the starting and ending values in the form of dates, as in `loop i=1950:1..1999:4`.

This form of loop control is intended to be quick and easy, and as such it is subject to certain limitations. In particular, the index variable is always incremented by one at each iteration. If, for example, you have

```
loop i=m..n
```

where `m` and `n` are scalar variables with values `m > n` at the time of execution, the index will not be decremented; rather, the loop will simply be bypassed.

If you need more complex loop control, see the “for” form below.

The index loop is particularly useful in conjunction with the `values()` matrix function when some operation must be carried out for each value of some discrete variable (see chapter 9). Consider the following example:

```
open greene22_2
discrete Z8
v8 = values(Z8)
loop i=1..rows(v8)
  scalar xi = v8[i]
  smpl (Z8=xi) --restrict --replace
  printf "mean(Y | Z8 = %g) = %8.5f, sd(Y | Z8 = %g) = %g\n", \
    xi, mean(Y), xi, sd(Y)
endloop
```

---

<sup>1</sup>It is common programming practice to use simple, one-character names for such variables. However, you may use any name that is acceptable by `gretl`: up to 15 characters, starting with a letter, and containing nothing but letters, numerals and the underscore character.



In this case, we evaluate the conditional mean and standard deviation of the variable *Y* for each value of *Z8*.

### Foreach loop

The fourth form of loop control also uses an index variable, in this case to index a specified list of strings. The loop is executed once for each string in the list. This can be useful for performing repetitive operations on a list of variables. Here is an example of the syntax:

```
loop foreach i peach pear plum
  print "$i"
endloop
```

This loop will execute three times, printing out “peach”, “pear” and “plum” on the respective iterations. The numerical value of the index starts at 1 and is incremented by 1 at each iteration.

If you wish to loop across a list of variables that are contiguous in the dataset, you can give the names of the first and last variables in the list, separated by “..”, rather than having to type all the names. For example, say we have 50 variables *AK*, *AL*, ..., *WY*, containing income levels for the states of the US. To run a regression of income on time for each of the states we could do:

```
genr time
loop foreach i AL..WY
  ols $i const time
endloop
```

This loop variant can also be used for looping across the elements in a *named list* (see chapter 13). For example:

```
list ylist = y1 y2 y3
loop foreach i ylist
  ols $i const x1 x2
endloop
```

Note that if you use this idiom inside a function (see chapter 11), looping across a list that has been supplied to the function as an argument, it is necessary to use the syntax *listname.\$i* to reference the list-member variables. In the context of the example above, this would mean replacing the third line with

```
ols ylist.$i const x1 x2
```

### For loop

The final form of loop control emulates the *for* statement in the C programming language. The syntax is `loop for`, followed by three component expressions, separated by semicolons and surrounded by parentheses. The three components are as follows:

1. Initialization: This is evaluated only once, at the start of the loop. Common example: setting a scalar control variable to some starting value.
2. Continuation condition: this is evaluated at the top of each iteration (including the first). If the expression evaluates as true (non-zero), iteration continues, otherwise it stops. Common example: an inequality expressing a bound on a control variable.
3. Modifier: an expression which modifies the value of some variable. This is evaluated prior to checking the continuation condition, on each iteration after the first. Common example: a control variable is incremented or decremented.

Here's a simple example:

```
loop for (r=0.01; r<.991; r+=.01)
```

In this example the variable `r` will take on the values 0.01, 0.02, ..., 0.99 across the 99 iterations. Note that due to the finite precision of floating point arithmetic on computers it may be necessary to use a continuation condition such as the above, `r<.991`, rather than the more “natural” `r<=.99`. (Using double-precision numbers on an x86 processor, at the point where you would expect `r` to equal 0.99 it may in fact have value 0.9900000000000001.)

Any or all of the three expressions governing a `for` loop may be omitted — the minimal form is `(; ;)`. If the continuation test is omitted it is implicitly true, so you have an infinite loop unless you arrange for some other way out, such as a `break` statement.

If the initialization expression in a `for` loop takes the common form of setting a scalar variable to a given value, the string representation of that scalar's value is made available within the loop via the accessor `$varname`.

### 10.3 Progressive mode

If the `--progressive` option is given for a command loop, special behavior is invoked for certain commands, namely, `print`, `store` and simple estimation commands. By “simple” here we mean commands which (a) estimate a single equation (as opposed to a system of equations) and (b) do so by means of a single command statement (as opposed to a block of statements, as with `nl`s and `mle`). The paradigm is `ols`; other possibilities include `tsls`, `wls`, `logit` and so on.

The special behavior is as follows.

**Estimators:** The results from each individual iteration of the estimator are not printed. Instead, after the loop is completed you get a printout of (a) the mean value of each estimated coefficient across all the repetitions, (b) the standard deviation of those coefficient estimates, (c) the mean value of the estimated standard error for each coefficient, and (d) the standard deviation of the estimated standard errors. This makes sense only if there is some random input at each step.

**print:** When this command is used to print the value of a variable, you do not get a print each time round the loop. Instead, when the loop is terminated you get a printout of the mean and standard deviation of the variable, across the repetitions of the loop. This mode is intended for use with variables that have a scalar value at each iteration, for example the error sum of squares from a regression. Data series cannot be printed in this way, and neither can matrices.

**store:** This command writes out the values of the specified scalars, from each time round the loop, to a specified file. Thus it keeps a complete record of their values across the iterations. For example, coefficient estimates could be saved in this way so as to permit subsequent examination of their frequency distribution. Only one such `store` can be used in a given loop.

### 10.4 Loop examples

#### Monte Carlo example

A simple example of a Monte Carlo loop in “progressive” mode is shown in Example [10.1](#).

This loop will print out summary statistics for the ‘a’ and ‘b’ estimates and  $R^2$  across the 100 repetitions. After running the loop, `coeffs.gdt`, which contains the individual coefficient estimates from all the runs, can be opened in `gretl` to examine the frequency distribution of the estimates in detail.

The command `nulldata` is useful for Monte Carlo work. Instead of opening a “real” data set, `nulldata 50` (for instance) opens a dummy data set, containing just a constant and an index variable, with a series length of 50. Constructed variables can then be added using the `genr` command. See the `set` command for information on generating repeatable pseudo-random series.

**Example 10.1:** Simple Monte Carlo loop

---

```

nulldata 50
set seed 547
genr x = 100 * uniform()
# open a "progressive" loop, to be repeated 100 times
loop 100 --progressive
  genr u = 10 * normal()
  # construct the dependent variable
  genr y = 10*x + u
  # run OLS regression
  ols y const x
  # grab the coefficient estimates and R-squared
  genr a = $coeff(const)
  genr b = $coeff(x)
  genr r2 = $rsq
  # arrange for printing of stats on these
  print a b r2
  # and save the coefficients to file
  store coeffs.gdt a b
endloop

```

---

**Iterated least squares**

Example 10.2 uses a “while” loop to replicate the estimation of a nonlinear consumption function of the form

$$C = \alpha + \beta Y^\gamma + \epsilon$$

as presented in [Greene \(2000\)](#), Example 11.3. This script is included in the `gretl` distribution under the name `greene11_3.inp`; you can find it in `gretl` under the menu item “File, Script files, Practice file, Greene...”.

The option `--print-final` for the `ols` command arranges matters so that the regression results will not be printed each time round the loop, but the results from the regression on the last iteration will be printed when the loop terminates.

Example 10.3 shows how a loop can be used to estimate an ARMA model, exploiting the “outer product of the gradient” (OPG) regression discussed by Davidson and MacKinnon in their *Estimation and Inference in Econometrics*.

**Indexed loop examples**

Example 10.4 shows an indexed loop in which the `smp1` is keyed to the index variable `i`. Suppose we have a panel dataset with observations on a number of hospitals for the years 1991 to 2000 (where the year of the observation is indicated by a variable named `year`). We restrict the sample to each of these years in turn and print cross-sectional summary statistics for variables 1 through 4.

Example 10.5 illustrates string substitution in an indexed loop.

The first time round this loop the variable `V` will be set to equal `COMP1987` and the dependent variable for the `ols` will be `PBT1987`. The next time round `V` will be redefined as equal to `COMP1988` and the dependent variable in the regression will be `PBT1988`. And so on.

**Example 10.2:** Nonlinear consumption function

---

```
open greene11_3.gdt
# run initial OLS
ols C 0 Y
genr essbak = $ess
genr essdiff = 1
genr beta = $coeff(Y)
genr gamma = 1
# iterate OLS till the error sum of squares converges
loop while essdiff > .00001
  # form the linearized variables
  genr C0 = C + gamma * beta * Y^gamma * log(Y)
  genr x1 = Y^gamma
  genr x2 = beta * Y^gamma * log(Y)
  # run OLS
  ols C0 0 x1 x2 --print-final --no-df-corr --vcv
  genr beta = $coeff(x1)
  genr gamma = $coeff(x2)
  genr ess = $ess
  genr essdiff = abs(ess - essbak)/essbak
  genr essbak = ess
endloop
# print parameter estimates using their "proper names"
set echo off
printf "alpha = %g\n", $coeff(0)
printf "beta  = %g\n", beta
printf "gamma = %g\n", gamma
```

---

**Example 10.3:** ARMA 1, 1

---

```

open armaloop.gdt

genr c = 0
genr a = 0.1
genr m = 0.1

series e = 1.0
genr de_c = e
genr de_a = e
genr de_m = e

genr crit = 1
loop while crit > 1.0e-9

    # one-step forecast errors
    genr e = y - c - a*y(-1) - m*e(-1)

    # log-likelihood
    genr loglik = -0.5 * sum(e^2)
    print loglik

    # partials of forecast errors wrt c, a, and m
    genr de_c = -1 - m * de_c(-1)
    genr de_a = -y(-1) - m * de_a(-1)
    genr de_m = -e(-1) - m * de_m(-1)

    # partials of l wrt c, a and m
    genr sc_c = -de_c * e
    genr sc_a = -de_a * e
    genr sc_m = -de_m * e

    # OPG regression
    ols const sc_c sc_a sc_m --print-final --no-df-corr --vcv

    # Update the parameters
    genr dc = $coeff(sc_c)
    genr c = c + dc
    genr da = $coeff(sc_a)
    genr a = a + da
    genr dm = $coeff(sc_m)
    genr m = m + dm

    printf "    constant          = %.8g (gradient = %#.6g)\n", c, dc
    printf "    ar1 coefficient = %.8g (gradient = %#.6g)\n", a, da
    printf "    ma1 coefficient = %.8g (gradient = %#.6g)\n", m, dm

    genr crit = $T - $ess
    print crit
endloop

genr se_c = $stderr(sc_c)
genr se_a = $stderr(sc_a)
genr se_m = $stderr(sc_m)

set echo off
printf "\n"
printf "constant = %.8g (se = %#.6g, t = %.4f)\n", c, se_c, c/se_c
printf "ar1 term = %.8g (se = %#.6g, t = %.4f)\n", a, se_a, a/se_a
printf "ma1 term = %.8g (se = %#.6g, t = %.4f)\n", m, se_m, m/se_m

```

---

**Example 10.4:** Panel statistics

---

```
open hospitals.gdt
loop i=1991..2000
  smpl (year=i) --restrict --replace
  summary 1 2 3 4
endloop
```

---

**Example 10.5:** String substitution

---

```
open bea.dat
loop i=1987..2001
  genr V = COMP$i
  genr TC = GOC$i - PBT$i
  genr C = TC - V
  ols PBT$i const TC V
endloop
```

---

# Chapter 11

## User-defined functions

### 11.1 Defining a function

Gretl offers a mechanism for defining functions, which may be called via the command line, in the context of a script, or (if packaged appropriately, see section 11.5) via the program's graphical interface.

The syntax for defining a function looks like this:<sup>1</sup>

```
function return-type function-name (parameters)  
    function body  
end function
```

The opening line of a function definition contains these elements, in strict order:

1. The keyword `function`.
2. *return-type*, which states the type of value returned by the function, if any. This must be one of `void` (if the function does not return anything), `scalar`, `series`, `matrix`, `list` or `string`.
3. *function-name*, the unique identifier for the function. Names must start with a letter. They have a maximum length of 31 characters; if you type a longer name it will be truncated. Function names cannot contain spaces. You will get an error if you try to define a function having the same name as an existing gretl command.
4. The functions's *parameters*, in the form of a comma-separated list enclosed in parentheses. This may be run into the function name, or separated by white space as shown.

Function parameters can be of any of the types shown below.<sup>2</sup>

Type	Description
<code>bool</code>	scalar variable acting as a Boolean switch
<code>int</code>	scalar variable acting as an integer
<code>scalar</code>	scalar variable
<code>series</code>	data series
<code>list</code>	named list of series
<code>matrix</code>	matrix or vector
<code>string</code>	string variable or string literal
<code>bundle</code>	all-purpose container (see section 12.7)

Each element in the listing of parameters must include two terms: a type specifier, and the name by which the parameter shall be known within the function. An example follows:

---

<sup>1</sup>The syntax given here differs from the standard prior to gretl version 1.8.4. For reasons of backward compatibility the old syntax is still supported; see section 11.6 for details.

<sup>2</sup>An additional parameter type is available for GUI use, namely `obs`; this is equivalent to `int` except for the way it is represented in the graphical interface for calling a function.

```
function scalar myfunc (series y, list xvars, bool verbose)
```

Each of the type-specifiers, with the exception of `list` and `string`, may be modified by prepending an asterisk to the associated parameter name, as in

```
function scalar myfunc (series *y, scalar *b)
```

The meaning of this modification is explained below (see section 11.4); it is related to the use of pointer arguments in the C programming language.

### Function parameters: optional refinements

Besides the required elements mentioned above, the specification of a function parameter may include some additional fields, as follows:

- The `const` modifier.
- For `scalar` or `int` parameters: minimum, maximum and default values; or for `bool` parameters, just a default value.
- For optional pointer and list arguments (see section 11.4), the special default value `null`.
- For all parameters, a descriptive string.
- For `int` parameters with minimum and maximum values specified, a set of strings to associate with the allowed numerical values (value labels).

The first two of these options may be useful in many contexts; the last two may be helpful if a function is to be packaged for use in the `gretl` GUI (but probably not otherwise). We now expand on each of the options.

- The `const` modifier: must be given as a prefix to the basic parameter specification, as in

```
const matrix M
```

This constitutes a promise that the corresponding argument will not be modified within the function; `gretl` will flag an error if the function attempts to modify the argument.

- Minimum, maximum and default values for `scalar` or `int` types: These values should directly follow the name of the parameter, enclosed in square brackets and with the individual elements separated by colons. For example, suppose we have an integer parameter `order` for which we wish to specify a minimum of 1, a maximum of 12, and a default of 4. We can write

```
int order[1:12:4]
```

If you wish to omit any of the three specifiers, leave the corresponding field empty. For example `[1::4]` would specify a minimum of 1 and a default of 4 while leaving the maximum unlimited.

For a parameter of type `bool` (whose values are just zero or non-zero), you can specify a default of 1 (true) or 0 (false), as in

```
bool verbose[0]
```

- Descriptive string: This will show up as an aid to the user if the function is packaged (see section 11.5 below) and called via `gretl`'s graphical interface. The string should be enclosed in double quotes and separated from the preceding elements of the parameter specification with a space, as in

```
series y "dependent variable"
```



- Value labels: These may be used only with `int` parameters for which minimum and maximum values have been specified, so there is a fixed number of admissible values, and the number of labels must match the number of values. They will show up in the graphical interface in the form of a drop-down list, making the function writer's intent clearer when an integer argument represents a categorical selection. A set of value labels must be enclosed in braces, and the individual labels must be enclosed in double quotes and separated by commas or spaces. For example:

```
int case[1:3:1] {"Fixed effects", "Between model", "Random effects"}
```

If two or more of the trailing optional fields are given in a parameter specification, they must be given in the order shown above: min-max-default, description, value labels. Note that there is no facility for “escaping” characters within descriptive strings or value labels; these may contain spaces but they cannot contain the double-quote character.

Here is an example of a well-formed function specification using all the elements mentioned above:

```
function matrix myfunc (series y "dependent variable",
                        list X "regressors",
                        int p[0::1] "lag order",
                        int c[1:2:1] "criterion" {"AIC", "BIC"},
                        bool quiet[0])
```

One advantage of specifying default values for parameters, where applicable, is that in script or command-line mode users may omit trailing arguments that have defaults. For example, `myfunc` above could be invoked with just two arguments, corresponding to `y` and `X`; implicitly `p = 1`, `c = 1` and `quiet` is false.

### Functions taking no parameters

You may define a function that has no parameters (these are called “routines” in some programming languages). In this case, use the keyword `void` in place of the listing of parameters:

```
function matrix myfunc2 (void)
```

### The function body

The *function body* is composed of `gretl` commands, or calls to user-defined functions (that is, function calls may be nested). A function may call itself (that is, functions may be recursive). While the function body may contain function calls, it may not contain function definitions. That is, you cannot define a function inside another function. For further details, see section [11.4](#).

## 11.2 Calling a function

A user function is called by typing its name followed by zero or more arguments enclosed in parentheses. If there are two or more arguments these should be separated by commas.

There are automatic checks in place to ensure that the number of arguments given in a function call matches the number of parameters, and that the types of the given arguments match the types specified in the definition of the function. An error is flagged if either of these conditions is violated. One qualification: allowance is made for omitting arguments at the end of the list, provided that default values are specified in the function definition. To be precise, the check is that the number of arguments is at least equal to the number of *required* parameters, and is no greater than the total number of parameters.

A scalar, series or matrix argument to a function may be given either as the name of a pre-existing variable or as an expression which evaluates to a variable of the appropriate type. Scalar arguments may also be given as numerical values. List arguments must be specified by name.

The following trivial example illustrates a function call that correctly matches the function definition.

```
# function definition
function scalar ols_ess(series y, list xvars)
  ols y 0 xvars --quiet
  scalar myess = $ess
  printf "ESS = %g\n", myess
  return myess
end function
# main script
open data4-1
list xlist = 2 3 4
# function call (the return value is ignored here)
ols_ess(price, xlist)
```

The function call gives two arguments: the first is a data series specified by name and the second is a named list of regressors. Note that while the function offers the variable `myess` as a return value, it is ignored by the caller in this instance. (As a side note here, if you want a function to calculate some value having to do with a regression, but are not interested in the full results of the regression, you may wish to use the `--quiet` flag with the estimation command as shown above.)

A second example shows how to write a function call that assigns a return value to a variable in the caller:

```
# function definition
function series get_uhat(series y, list xvars)
  ols y 0 xvars --quiet
  series uh = $uhat
  return uh
end function
# main script
open data4-1
list xlist = 2 3 4
# function call
series resid = get_uhat(price, xlist)
```

### 11.3 Deleting a function

If you have defined a function and subsequently wish to clear it out of memory, you can do so using the keywords `delete` or `clear`, as in

```
function myfunc delete
function get_uhat clear
```

Note, however, that if `myfunc` is already a defined function, providing a new definition automatically overwrites the previous one, so it should rarely be necessary to delete functions explicitly.

### 11.4 Function programming details

#### Variables versus pointers

Series, scalar, and matrix arguments to functions can be passed in two ways: “as they are”, or as pointers. For example, consider the following:

```
function series triple1(series x)
  return 3*x
```

```

end function

function series triple2(series *x)
  return 3*x
end function

```

These two functions are nearly identical (and yield the same result); the only difference is that you need to feed a series into `triple1`, as in `triple1(myseries)`, while `triple2` must be supplied a *pointer* to a series, as in `triple2(&myseries)`.

Why make the distinction? There are two main reasons for doing so: modularity and performance.

By modularity we mean the insulation of a function from the rest of the script which calls it. One of the many benefits of this approach is that your functions are easily reusable in other contexts. To achieve modularity, *variables created within a function are local to that function, and are destroyed when the function exits*, unless they are made available as return values and these values are “picked up” or assigned by the caller.

In addition, functions do not have access to variables in “outer scope” (that is, variables that exist in the script from which the function is called) except insofar as these are explicitly passed to the function as arguments.

By default, when a variable is passed to a function as an argument, what the function actually “gets” is a *copy* of the outer variable, which means that the value of the outer variable is not modified by anything that goes on inside the function. But the use of pointers allows a function and its caller to cooperate such that an outer variable can be modified by the function. In effect, this allows a function to “return” more than one value (although only one variable can be returned directly — see below). The parameter in question is marked with a prefix of `*` in the function definition, and the corresponding argument is marked with the complementary prefix `&` in the caller. For example,

```

function series get_uhat_and_ess(series y, list xvars, scalar *ess)
  ols y 0 xvars --quiet
  ess = $ess
  series uh = $uhat
  return uh
end function
# main script
open data4-1
list xlist = 2 3 4
# function call
scalar SSR
series resid = get_uhat_and_ess(price, xlist, &SSR)

```

In the above, we may say that the function is given the *address* of the scalar variable `SSR`, and it assigns a value to that variable (under the local name `ess`). (For anyone used to programming in C: note that it is not necessary, or even possible, to “dereference” the variable in question within the function using the `*` operator. Unadorned use of the name of the variable is sufficient to access the variable in outer scope.)

An “address” parameter of this sort can be used as a means of offering optional information to the caller. (That is, the corresponding argument is not strictly needed, but will be used if present). In that case the parameter should be given a default value of `null` and the the function should test to see if the caller supplied a corresponding argument or not, using the built-in function `isnull()`. For example, here is the simple function shown above, modified to make the filling out of the `ess` value optional.

```

function series get_uhat_and_ess(series y, list xvars, scalar *ess[null])
  ols y 0 xvars --quiet
  if !isnull(ess)
    ess = $ess

```

```

    endif
    return $uhat
end function

```

If the caller does not care to get the `ess` value, it can use `null` in place of a real argument:

```
series resid = get_uhat_and_ess(price, xlist, null)
```

Alternatively, trailing function arguments that have default values may be omitted, so the following would also be a valid call:

```
series resid = get_uhat_and_ess(price, xlist)
```

Pointer arguments may also be useful for optimizing performance: even if a variable is not modified inside the function, it may be a good idea to pass it as a pointer if it occupies a lot of memory. Otherwise, the time `gretl` spends transcribing the value of the variable to the local copy may be non-negligible, compared to the time the function spends doing the job it was written for.

Example 11.1 takes this to the extreme. We define two functions which return the number of rows of a matrix (a pretty fast operation). One function gets a matrix as argument, the other one a pointer to a matrix. The two functions are evaluated on a matrix with 2000 rows and 2000 columns; on a typical system, floating-point numbers take 8 bytes of memory, so the space occupied by the matrix is roughly 32 megabytes.

Running the code in example 11.1 will produce output similar to the following (the actual numbers depend on the machine you're running the example on):

```

Elapsed time:
    without pointers (copy) = 3.66 seconds,
    with pointers (no copy) = 0.01 seconds.

```

If a pointer argument is used for this sort of purpose — and the object to which the pointer points is not modified by the function — it is a good idea to signal this to the user by adding the `const` qualifier, as shown for function `b` in Example 11.1. When a pointer argument is qualified in this way, any attempt to modify the object within the function will generate an error.

One limitation on the use of pointer-type arguments should be noted: you cannot supply a given variable as a pointer argument more than once in any given function call. For example, suppose we have a function that takes two matrix-pointer arguments,

```
function scalar pointfunc (matrix *a, matrix *b)
```

And suppose we have two matrices, `x` and `y`, at the caller level. The call

```
pointfunc(&x, &y)
```

is OK, but the call

```
pointfunc(&x, &x) # will not work
```

will generate an error.

### List arguments

The use of a named list as an argument to a function gives a means of supplying a function with a set of variables whose number is unknown when the function is written — for example, sets of regressors or instruments. Within the function, the list can be passed on to commands such as `ols`.

**Example 11.1:** Performance comparison: values versus pointer

---

```
function scalar a(matrix X)
    return rows(X)
end function

function scalar b(const matrix *X)
    return rows(X)
end function

nulldata 10
set echo off
set messages off
X = zeros(2000,2000)
r = 0

set stopwatch
loop 100
    r = a(X)
endloop
fa = $stopwatch

set stopwatch
loop 100
    r = b(&X)
endloop
fb = $stopwatch

printf "Elapsed time:\n\
\twithout pointers (copy) = %g seconds,\n\
\twith pointers (no copy) = %g seconds.\n", fa, fb
```

---

A list argument can also be “unpacked” using a `foreach` loop construct, but this requires some care. For example, suppose you have a list `X` and want to calculate the standard deviation of each variable in the list. You can do:

```
loop foreach i X
  scalar sd_$i = sd(X.$i)
endloop
```

*Please note:* a special piece of syntax is needed in this context. If we wanted to perform the above task on a list in a regular script (not inside a function), we could do

```
loop foreach i X
  scalar sd_$i = sd($i)
endloop
```

where `$i` gets the name of the variable at position `i` in the list, and `sd($i)` gets its standard deviation. But inside a function, working on a list supplied as an argument, if we want to reference an individual variable in the list we must use the syntax *listname.varname*. Hence in the example above we write `sd(X.$i)`.

This is necessary to avoid possible collisions between the name-space of the function and the name-space of the caller script. For example, suppose we have a function that takes a list argument, and that defines a local variable called `y`. Now suppose that this function is passed a list containing a variable named `y`. If the two name-spaces were not separated either we’d get an error, or the external variable `y` would be silently over-written by the local one. It is important, therefore, that list-argument variables should not be “visible” by name within functions. To “get hold of” such variables you need to use the form of identification just mentioned: the name of the list, followed by a dot, followed by the name of the variable.

**Constancy of list arguments** When a named list of variables is passed to a function, the function is actually provided with a copy of the list. The function may modify this copy (for instance, adding or removing members), but the original list at the level of the caller is not modified.

**Optional list arguments** If a list argument to a function is optional, this should be indicated by appending a default value of `null`, as in

```
function scalar myfunc (scalar y, list X[null])
```

In that case, if the caller gives `null` as the list argument (or simply omits the last argument) the named list `X` inside the function will be empty. This possibility can be detected using the `nelem()` function, which returns 0 for an empty list.

### String arguments

String arguments can be used, for example, to provide flexibility in the naming of variables created within a function. In the following example the function `mavg` returns a list containing two moving averages constructed from an input series, with the names of the newly created variables governed by the string argument.

```
function list mavg (series y, string vname)
  series @vname_2 = (y+y(-1)) / 2
  series @vname_4 = (y+y(-1)+y(-2)+y(-3)) / 4
  list retlist = @vname_2 @vname_4
  return retlist
end function
```

```
open data9-9
list malist = mavg(nocars, "nocars")
print malist --byobs
```

The last line of the script will print two variables named `nocars_2` and `nocars_4`. For details on the handling of named strings, see chapter 13.

If a string argument is considered optional, it may be given a `null` default value, as in

```
function scalar foo (series y, string vname[null])
```

### Retrieving the names of arguments

The variables given as arguments to a function are known inside the function by the names of the corresponding parameters. For example, within the function whose signature is

```
function void somefun (series y)
```

we have the series known as `y`. It may be useful, however, to be able to determine the names of the variables provided as arguments. This can be done using the function `argname`, which takes the name of a function parameter as its single argument and returns a string. Here is a simple illustration:

```
function void namefun (series y)
  printf "the series given as 'y' was named %s\n", argname(y)
end function

open data9-7
namefun(QNC)
```

This produces the output

```
the series given as 'y' was named QNC
```

Please note that this will not always work: the arguments given to functions may be anonymous variables, created on the fly, as in `somefun(log(QNC))` or `somefun(CPI/100)`. In that case the `argname` function fails to return a string. Function writers who wish to make use of this facility should check the return from `argname` using the `isstring()` function, which returns 1 when given the name of a string variable, 0 otherwise.

### Return values

Functions can return nothing (just printing a result, perhaps), or they can return a single variable — a scalar, series, list, matrix, string, or bundle (see section 12.7). The return value, if any, is specified via a statement within the function body beginning with the keyword `return`, followed by either the name of a variable (which must be of the type announced on the first line of the function definition) or an expression which produces a value of the correct type.

Having a function return a list or bundle is a way of permitting the “return” of more than one variable. For example, you can define several series inside a function and package them as a list; in this case they are not destroyed when the function exits. Here is a simple example, which also illustrates the possibility of setting the descriptive labels for variables generated in a function.

```
function list make_cubes (list xlist)
  list cubes = null
  loop foreach i xlist --quiet
```

```

        series $i3 = (xlist.$i)^3
        setinfo $i3 -d "cube of $i"
        list cubes += $i3
    endloop
    return cubes
end function

open data4-1
list xlist = price sqft
list cubelist = make_cubes(xlist)
print xlist cubelist --byobs
labels

```

A `return` statement causes the function to return (exit) at the point where it appears within the body of the function. A function may also exit when (a) the end of the function code is reached (in the case of a function with no return value), (b) a `gretl` error occurs, or (c) a `funcerr` statement is reached.

The `funcerr` keyword, which may be followed by a string enclosed in double quotes, causes a function to exit with an error flagged. If a string is provided, this is printed on exit, otherwise a generic error message is printed. This mechanism enables the author of a function to pre-empt an ordinary execution error and/or offer a more specific and helpful error message. For example,

```

if nelem(xlist) = 0
    funcerr "xlist must not be empty"
endif

```

A function may contain more than one `return` statement, as in

```

function scalar multi (bool s)
    if s
        return 1000
    else
        return 10
    endif
end function

```

However, it is recommended programming practice to have a single return point from a function unless this is very inconvenient. The simple example above would be better written as

```

function scalar multi (bool s)
    return s ? 1000 : 10
end function

```

### Error checking

When `gretl` first reads and “compiles” a function definition there is minimal error-checking: the only checks are that the function name is acceptable, and, so far as the body is concerned, that you are not trying to define a function inside a function (see Section 11.1). Otherwise, if the function body contains invalid commands this will become apparent only when the function is called and its commands are executed.

### Debugging

The usual mechanism whereby `gretl` echoes commands and reports on the creation of new variables is by default suppressed when a function is being executed. If you want more verbose output from a particular function you can use either or both of the following commands within the function:



```
set echo on
set messages on
```

Alternatively, you can achieve this effect for all functions via the command `set debug 1`. Usually when you set the value of a state variable using the `set` command, the effect applies only to the current level of function execution. For instance, if you do `set messages on` within function `f1`, which in turn calls function `f2`, then messages will be printed for `f1` but not `f2`. The debug variable, however, acts globally; all functions become verbose regardless of their level.

Further, you can do `set debug 2`: in addition to command `echo` and the printing of messages, this is equivalent to setting `max_verbos` (which produces verbose output from the BFGS maximizer) at all levels of function execution.

## 11.5 Function packages

Since gretl 1.6.0 there has been a mechanism to package functions and make them available to other users of gretl. Here is a walk-through of the process.

### Load a function in memory

There are several ways to load a function:

- If you have a script file containing function definitions, open that file and run it.
- Create a script file from scratch. Include at least one function definition, and run the script.
- Open the GUI console and type a function definition interactively. This method is not particularly recommended; you are probably better composing a function non-interactively.

For example, suppose you decide to package a function that returns the percentage change of a time series. Open a script file and type

```
function series pc(series y "Series to process")
  return 100 * diff(y)/y(-1)
end function
```

In this case, we have appended a string to the function argument, as explained in section 11.1, so as to make our interface more informative. This is not obligatory: if you omit the descriptive string, gretl will supply a predefined one.

Now run your function. You may want to make sure it works properly by running a few tests. For example, you may open the console and type

```
genr x = uniform()
genr dpcx = pc(x)
print x dpcx --byobs
```

You should see something similar to figure 11.1. The function seems to work ok. Once your function is debugged, you may proceed to the next stage.

### Create a package

We first present the mechanism for creating a function package via gretl's graphical interface. This can also be done via the command line, which offers some additional functionality for package authors; an explanation is given later in this section.

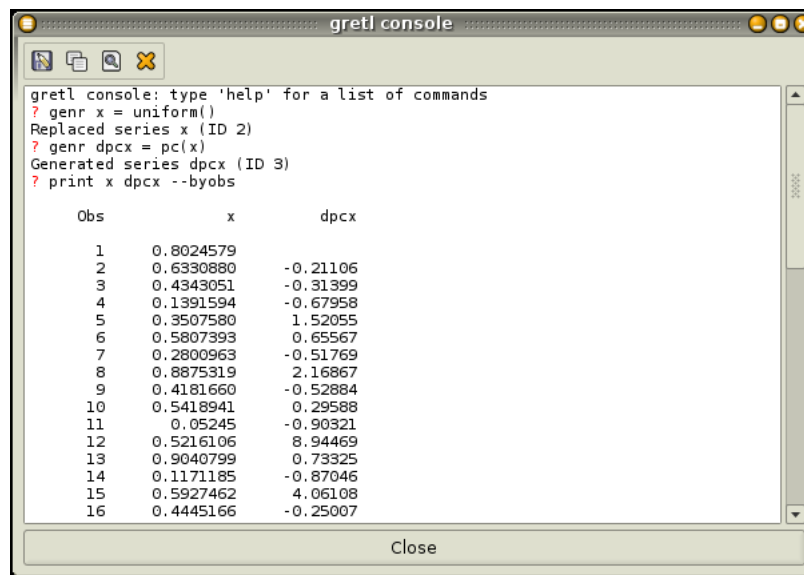


Figure 11.1: Output of function check

Start the GUI program and take a look at the “File, Function files” menu. This menu contains four items: “On local machine”, “On server”, “Edit package”, “New package”.

Select “New package”. (This will produce an error message unless at least one user-defined function is currently loaded in memory — see the previous point.) In the first dialog you get to select:

- A public function to package.
- Zero or more “private” helper functions.

Public functions are directly available to users; private functions are part of the “behind the scenes” mechanism in a function package.

On clicking “OK” a second dialog should appear (see Figure 11.2), where you get to enter the package information (author, version, date, and a short description). You can also enter help text for the public interface. You have a further chance to edit the code of the function(s) to be packaged, by clicking on “Edit function code”. (If the package contains more than one function, a drop-down selector will be shown.) And you get to add a sample script that exercises your package. This will be helpful for potential users, and also for testing. A sample script is required if you want to upload the package to the gretl server (for which a check-box is supplied).

You won’t need it right now, but the button labeled “Save as script” allows you to “reverse engineer” a function package, writing out a script that contains all the relevant function definitions.

Clicking “Save” in this dialog leads you to a File Save dialog. All being well, this should be pointing towards a directory named `functions`, either under the gretl system directory (if you have write permission on that) or the gretl user directory. This is the recommended place to save function package files, since that is where the program will look in the special routine for opening such files (see below).

Needless to say, the menu command “File, Function files, Edit package” allows you to make changes to a local function package.

A word on the file you just saved. By default, it will have a `.gfn` extension. This is a “function package” file: unlike an ordinary gretl script file, it is an XML file containing both the function code and the extra information entered in the packager. Hackers might wish to write such a file from scratch rather than using the GUI packager, but most people are likely to find it awkward. Note

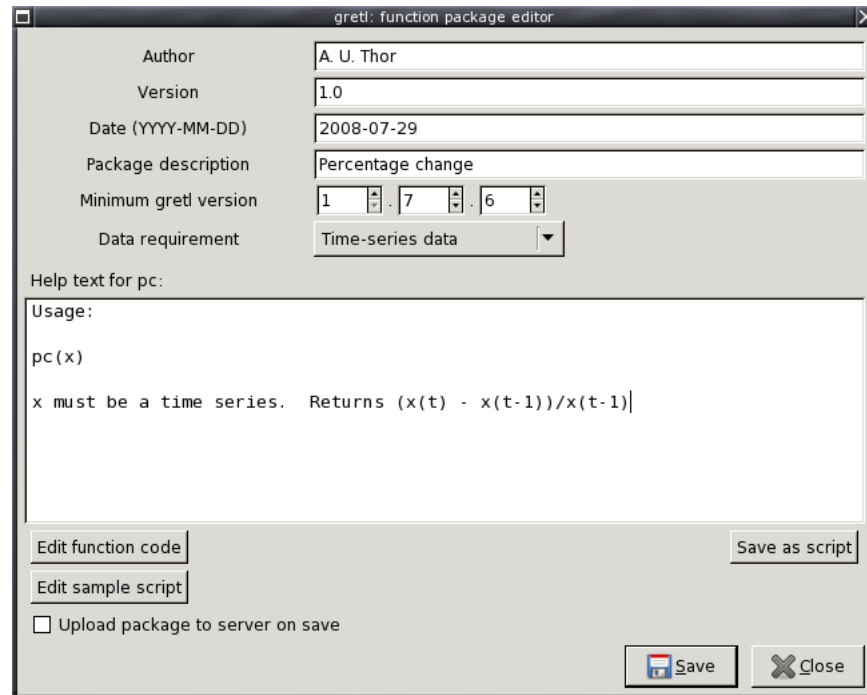


Figure 11.2: The package editor window

that XML-special characters in the function code have to be escaped, e.g. `&` must be represented as `&amp;`. Also, some elements of the function syntax differ from the standard script representation: the parameters and return values (if any) are represented in XML. Basically, the function is pre-parsed, and ready for fast loading using libxml.

### Load a package

Why package functions in this way? To see what's on offer so far, try the next phase of the walk-through.

Close gretl, then re-open it. Now go to “File, Function files, On local machine”. If the previous stage above has gone OK, you should see the file you packaged and saved, with its short description. If you click on “Info” you get a window with all the information gretl has gleaned from the function package. If you click on the “View code” icon in the toolbar of this new window, you get a script view window showing the actual function code. Now, back to the “Function packages” window, if you click on the package's name, the relevant functions are loaded into gretl's workspace, ready to be called by clicking on the “Call” button.

After loading the function(s) from the package, open the GUI console. Try typing `help foo`, replacing `foo` with the name of the public interface from the loaded function package: if any help text was provided for the function, it should be presented.

In a similar way, you can browse and load the function packages available on the gretl server, by selecting “File, Function files, On server”.

Once your package is installed on your local machine, you can use the function it contains via the graphical interface as described above, or by using the CLI, namely in a script or through the console. In the latter case, you load the function via the `include` command, specifying the package file as the argument, complete with the `.gfn` extension.

To continue with our example, load the file `np.gdt` (supplied with gretl among the sample datasets). Suppose you want to compute the rate of change for the variable `iproduct` via your new function and

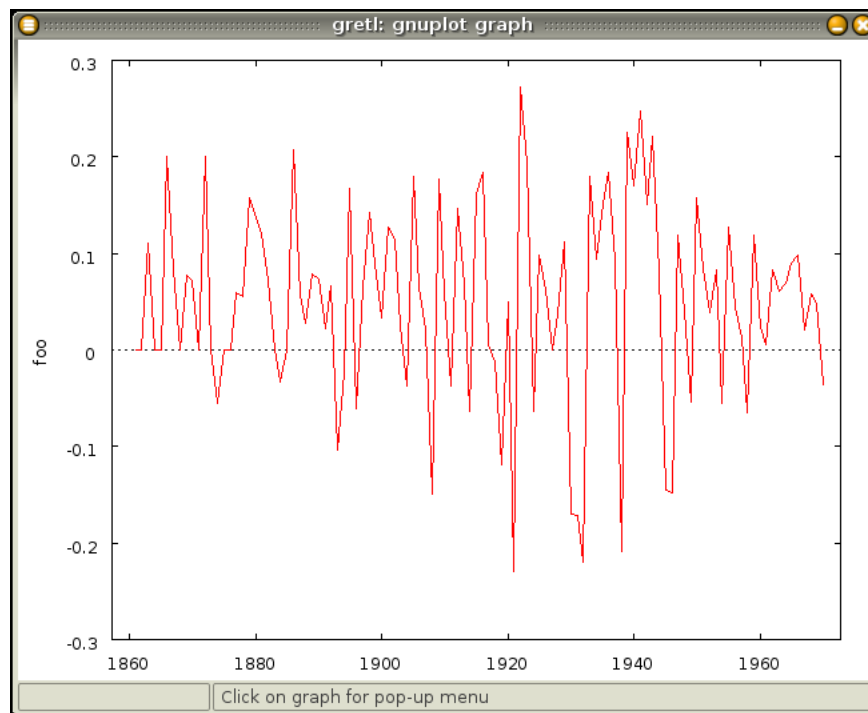


**Figure 11.3:** Using your package

store the result in a series named `foo`.

Go to “File, Function files, On local machine”. You will be shown a list of the installed packages, including the one you have just created. If you select it and click on “Execute” (or double-click on the name of the function package), a window similar to the one shown in figure 11.3 will appear. Notice that the description string “Series to process”, supplied with the function definition, appears to the left of the top series chooser.

Click “Ok” and the series `foo` will be generated (see figure 11.4). Under some circumstances you might have to press the “r” key (refresh) to have your new variable show up the main window variable list.



**Figure 11.4:** Percent change in industrial production

Alternatively, the same could have been accomplished by the script

```
include pc.gfn
open np
foo = pc(iprod)
```

### Creating a package via the command line

The mechanism described above, for creating function packages using the GUI, is likely to be convenient for small to medium-sized packages but may be too cumbersome for ambitious packages that include a large hierarchy of private functions. To facilitate the building of such packages gretl offers the `makepkg` command.

To use `makepkg` you create three files: a driver script that loads all the functions you want to package and invokes `makepkg`; a small, plain-text specification file that contains the required package details (author, version, etc.); and (in the simplest case) a plain text help file. You run the driver script and gretl writes the package (`.gfn`) file.

We first illustrate with a simple notional package. We have a gretl script file named `foo.inp` that contains a function, `foo`, that we want to package. Our driver script would then look like this

```
include foo.inp
makepkg foo.gfn
```

Note that the `makepkg` command takes one argument, the name of the package file to be created. The package *specification file* should have the same basename but the extension `.spec`. In this case gretl will therefore look for `foo.spec`. It should look something like this:

```
# foo.spec
author = A. U. Thor
version = 1.0
date = 2011-02-01
description = Does something with time series
public = foo
help = foohelp.txt
sample-script = example.inp
min-version = 1.9.3
data-requirement = needs-time-series-data
```

As you can see, the format of each line in this file is `key = value`, with two qualifications: blank lines are permitted (and ignored, as are comment lines that start with `#`).

All the fields included in the above example are required, with the exception of `data-requirement`, though the order in which they appear is immaterial. Here's a run-down of the basic fields:

- **author:** the name(s) of the author(s). Accented or other non-ASCII characters should be given as UTF-8.
- **version:** the version number of the package, which should be limited to two integers separated by a period.
- **date:** the release date of the current version of the package, in ISO 8601 format: YYYY-MM-DD.
- **description:** a brief description of the functionality offered by the package. This will be displayed in the GUI function packages window so it should be just one short line.
- **public:** the listing of public functions.
- **help:** the name of a plain text (UTF-8) file containing help; all packages must provide help.
- **sample-script:** the name of a sample script that illustrates use of the package; all packages must supply a sample script.

- `min-version`: the minimum version of gretl required for the package to work correctly. If you're unsure about this, the conservative thing is to give the current gretl version.

The `public` field indicates which function or functions are to be made directly available to users (as opposed to private “helper” functions). In the example above there is just one public function. Note that any functions in memory when `makepkg` is invoked, other than those designated as public, are assumed to be private functions that should also be included in the package. That is, the list of private functions (if any) is implicit.

The `data-requirement` field should be specified if the package requires time-series or panel data, or alternatively if no dataset is required. If the `data-requirement` field is omitted, the assumption is that the package needs a dataset in place, but it doesn't matter what kind; if the packaged functions do not use any series or lists this requirement can be explicitly relaxed. Valid values for this field are:

<code>needs-time-series-data</code>	(any time-series data OK)
<code>needs-qm-data</code>	(must be quarterly or monthly)
<code>needs-panel-data</code>	(must be a panel)
<code>no-data-ok</code>	(no dataset is needed)

For a more complex example, let's look at the `gig` (GARCH-in-gretl) package. The driver script for building `gig` looks something like this:

```
set echo off
set messages off
include gig_mle.inp
include gig_setup.inp
include gig_estimate.inp
include gig_printout.inp
include gig_plot.inp
makepkg gig.gfn
```

In this case the functions to be packaged (of which there are many) are distributed across several script files, each of which is the target of an `include` command. The `set` commands at the top are included to cut down on the verbosity of the output.

The content of `gig.spec` is as follows:

```
author = Riccardo "Jack" Lucchetti and Stefano Baliotti
version = 2.0
date = 2010-12-21
description = An assortment of univariate GARCH models
public = GUI_gig \
    gig_setup gig_set_dist gig_set_pq gig_set_vQR \
    gig_print gig_estimate \
    gig_plot gig_dplot \
    gig_bundle_print GUI_gig_plot

gui-main = GUI_gig
bundle-print = gig_bundle_print
bundle-plot = GUI_gig_plot
help = gig.pdf
sample-script = examples/example1.inp
min-version = 1.9.3
data-requirement = needs-time-series-data
```

Note that backslash continuation can be used for the elements of the `public` function listing.

In addition to the fields shown in the simple example above, `gig.spec` includes three optional fields: `gui-main`, `bundle-print` and `bundle-plot`. These keywords are used to designate certain functions as playing a special role in the gretl graphical interface. A function picked out in this way must be in the `public` list and must satisfy certain further requirements.

- `gui-main`: this specifies a function as the one which will be presented automatically to GUI users (instead of users' being faced with a choice of interfaces). This makes sense only for packages that have multiple public functions. In addition, the `gui-main` function must return a `bundle` (see section 12.7).
- `bundle-print`: this picks out a function that should be used to print the contents of a bundle returned by the `gui-main` function. It must take a pointer-to-bundle as its first argument. The second argument, if present, should be an `int` switch, with two or more valid values, that controls the printing in some way. Any further arguments must have default values specified so that they can be omitted.
- `bundle-plot`: selects a function for the role of producing a plot or graph based on the contents of a returned bundle. The requirements on this function are as for `bundle-print`.

The "GUI special" tags support a user-friendly mode of operation. On a successful call to `gui-main`, gretl opens a window displaying the contents of the returned bundle (formatted via `bundle-print`). Menus in this window give the user the option of saving the entire bundle (in which case it's represented as an icon in the "icon view" window) or of extracting specific elements from the bundle (series or matrices, for example).

If the package has a `bundle-plot` function, the bundle window also has a Graph menu. In `gig`, for example, the `bundle-plot` function has this signature:

```
function void GUI_gig_plot(bundle *model, int ptype[0:1:0] \
                          "Plot type" {"Time series", "Density"})
```

The `ptype` switch is used to choose between a time-series plot of the residual and its conditional variance, and a kernel density plot of the innovation against the theoretical distribution it is supposed to follow. The use of the value-labels `Time series` and `Density` means that the Graph menu will display these two choices.

One other feature of the `gig spec` file is noteworthy: the `help` field specifies `gig.pdf`, documentation in PDF format. Unlike plain-text help, this cannot be rolled into the `gfn` (XML) file produced by the `makepkg` command; rather, both `gig.gfn` and `gig.pdf` are packaged into a zip archive for distribution. This represents a form of package which is new in gretl 1.9.4. More details will be made available before long.

## 11.6 Memo: updating old-style functions

As mentioned at the start of this chapter, different rules were in force for defining functions prior to gretl 1.8.4. While the old syntax is still supported to date, this may not always be the case. But it is straightforward to convert a function to the new style. The only thing that must be changed for compatibility with the new syntax is the declaration of the function's return type. Previously this was placed inline in the `return` statement, whereas now it is placed right after the `function` keyword. For example:

```
# old style
function triple (series x)
  y = 3*x
  return series y # note the "series" here
end function
```

```
# new style
function series triple (series x)
  y = 3*x
  return y
end function
```

Note also that the role of the `return` statement has changed (and its use has become more flexible):

- The `return` statement now causes the function to return directly, and you can have more than one such statement, wrapped in conditionals. Before there could only be one `return` statement, and its role was just to specify the type available for assignment by the caller.
- The final element in the `return` statement can now be an expression that evaluates to a value of the advertised return type; before, it had to be the name of a pre-defined variable.



## Chapter 12

# Gretl data types

### 12.1 Introduction

Gretl offers the following data types:

<code>scalar</code>	holds a single numerical value
<code>series</code>	holds $n$ numerical values, where $n$ is the number of observations in the current dataset
<code>matrix</code>	holds a rectangular array of numerical values, of any dimensions
<code>list</code>	holds the ID numbers of a set of series
<code>string</code>	holds an array of characters
<code>bundle</code>	holds a variable number of objects of various types

The “numerical values” mentioned above are all double-precision floating point numbers.

In this chapter we give a run-down of the basic characteristics of each of these types and also explain their “life cycle” (creation, modification and destruction). The list and matrix types, whose uses are relatively complex, are discussed at greater length in the following two chapters.

### 12.2 Series

We begin with the `series` type, which is the oldest and in a sense the most basic type in gretl. When you open a data file in the gretl GUI, what you see in the main window are the ID numbers, names (and descriptions, if available) of the series read from the file. All the series existing at any point in a gretl session are of the same length, although some may have missing values. The variables that can be added via the items under the Add menu in the main window (logs, squares and so on) are also series.

For a gretl session to contain any series, a common series length must be established. This is usually achieved by opening a data file, or importing a series from a database, in which case the length is set by the first import. But one can also use the `nulldata` command, which takes as its single argument the desired length, a positive integer.

Each series has these basic attributes: an ID number, a name, and of course  $n$  numerical values. In addition a series may have a description (which is shown in the main window and is also accessible via the `labels` command), a “display name” for use in graphs, a record of the compaction method used in reducing the variable’s frequency (for time-series data only) and a flag marking the variable as discrete. These attributes can be edited in the GUI by choosing Edit Attributes (either under the Variable menu or via right-click), or by means of the `setinfo` command.

In the context of most commands you are able to reference series by name or by ID number as you wish. The main exception is the definition or modification of variables via a formula; here you must use names since ID numbers would get confused with numerical constants.

Note that series ID numbers are always consecutive, and the ID number for a given series will change if you delete a lower-numbered series. In some contexts, where gretl is liable to get confused by such changes, deletion of low-numbered series is disallowed.

### 12.3 Scalars

The scalar type is relatively simple: just a convenient named holder for a single numerical value. Scalars have none of the additional attributes pertaining to series, do not have public ID numbers, and must be referenced by name. A common use of scalar variables is to record information made available by gretl commands for further processing, as in `scalar s2 = $sigma^2` to record the square of the standard error of the regression following an estimation command such as `ols`.

You can define and work with scalars in gretl without having any dataset in place.

In the gretl GUI, scalar variables can be inspected and their values edited via the “Icon view” (see the View menu in the main window).

### 12.4 Matrices

Matrices in gretl work much as in other mathematical software (e.g. MATLAB, Octave). Like scalars they have no public ID numbers and must be referenced by name, and they can be used without any dataset in place. Matrix indexing is 1-based: the top-left element of matrix A is `A[1,1]`. Matrices are discussed at length in chapter 14; advanced users of gretl will want to study this chapter in detail.

Matrices have one optional attribute beyond their numerical content: they may have column names attached, which are displayed when the matrix is printed. See the `colnames` function for details.

In the gretl GUI, matrices can be inspected, analysed and edited via the `Icon view` item under the View menu in the main window: each currently defined matrix is represented by an icon.

### 12.5 Lists

As with matrices, lists merit an explication of their own (see chapter 13). Briefly, named lists can (and should!) be used to make commands scripts less verbose and repetitious, and more easily modifiable. Since lists are in fact lists of series ID numbers they can be used only when a dataset is in place.

In the gretl GUI, named lists can be inspected and edited under the Data menu in the main window, via the item `Define or edit list`.

### 12.6 Strings

String variables may be used for labeling, or for constructing commands. They are discussed in chapter 13. They must be referenced by name; they can be defined in the absence of a dataset.

Such variables can be created and modified via the command-line in the gretl console or via script; there is no means of editing them via the gretl GUI.

### 12.7 Bundles

A `bundle` is a container or wrapper for various sorts of objects — specifically, scalars, series, matrices, strings and bundles. (Yes, a bundle can contain other bundles). A bundle takes the form of a hash table or associative array: each item placed in the bundle is associated with a key string which can be used to retrieve it subsequently. We begin by explaining the mechanics of bundles then offer some thoughts on what they are good for.

To use a bundle you must first “declare” it, as in

```
bundle foo
```

To add an object to a bundle you assign to a compound left-hand value: the name of the bundle followed by the key string in square brackets. For example, the statement

```
foo["matrix1"] = m
```

adds an object called `m` (presumably a matrix) to bundle `foo` under the key `matrix1`. To get an item out of a bundle, again use the name of the bundle followed by the bracketed key, as in

```
matrix bm = foo["matrix1"]
```

A bundle key may be given as a double-quoted string literal, as shown above, or as the name of a pre-defined string variable. Key strings have a maximum length of 15 characters and cannot contain spaces.

Note that the key identifying an object within a given bundle is necessarily unique. If you reuse an existing key in a new assignment, the effect is to replace the object which was previously stored under the given key. It is not required that the type of the replacement object is the same as that of the original.

Also note that when you add an object to a bundle, what in fact happens is that the bundle acquires a copy of the object. The external object retains its own identity and is unaffected if the bundled object is replaced by another. Consider the following script fragment:

```
bundle foo
matrix m = I(3)
foo["mykey"] = m
scalar x = 20
foo["mykey"] = x
```

After the above commands are completed bundle `foo` does not contain a matrix under `mykey`, but the original matrix `m` is still in good health.

To delete an object from a bundle use the `delete` command, as in

```
delete foo["mykey"]
```

This destroys the object associated with the key and removes the key from the hash table.

Besides adding, accessing, replacing and deleting individual items, the other operations that are supported for bundles are union, printing and deletion. As regards union, if bundles `b1` and `b2` are defined you can say

```
bundle b3 = b1 + b2
```

to create a new bundle that is the union of the two others. The algorithm is: create a new bundle that is a copy of `b1`, then add any items from `b2` whose keys are not already present in the new bundle. (This means that bundle union is not commutative if the bundles have one or more key strings in common.)

If `b` is a bundle and you say `print b`, you get a listing of the bundle's keys along with the types of the corresponding objects, as in

```
? print b
bundle b:
  x (scalar)
  mat (matrix)
  inside (bundle)
```

### What are bundles good for?

Bundles are unlikely to be of interest in the context of standalone gretl scripts, but they can be very useful in the context of complex function packages where a good deal of information has to be passed around between the component functions. Instead of using a lengthy list of individual arguments, function *A* can bundle up the required data and pass it to functions *B* and *C*, where relevant information can be extracted via a mnemonic key.

In this context bundles should be passed in “pointer” form (see chapter 11) as illustrated in the following trivial example, where a bundle is created at one level then filled out by a separate function.

```
# modification of bundle (pointer) by user function

function void fill_out_bundle (bundle *b)
  b["mat"] = I(3)
  b["str"] = "foo"
  b["x"] = 32
end function

bundle my_bundle
fill_out_bundle(&my_bundle)
```

The bundle type can also be used to advantage as the *return value* from a packaged function, in cases where a package writer wants to give the user the option of accessing various results. In the gretl GUI, function packages that return a bundle are treated specially: the output window that displays the printed results acquires a menu showing the bundled items (their names and types), from which the user can save items of interest. For example, a function package that estimates a model might return a bundle containing a vector of parameter estimates, a residual series and a covariance matrix for the parameter estimates, among other possibilities.

As a refinement to support the use of bundles as a function return type, the `setnote` function can be used to add a brief explanatory note to a bundled item — such notes will then be shown in the GUI menu. This function takes three arguments: the name of a bundle, a key string, and the note. For example

```
setnote(b, "vcv", "covariance matrix")
```

After this, the object under the key `vcv` in bundle `b` will be shown as “covariance matrix” in a GUI menu.

## 12.8 The life cycle of gretl objects

### Creation

The most basic way to create a new variable of any type is by *declaration*, where one states the type followed by the name of the variable to create, as in

```
scalar x
series y
matrix A
```

and so forth. In that case the object in question is given a default initialization, as follows: a new scalar has value NA (missing); a new series is filled with NAs; a new matrix is null (zero rows and columns); a new string is empty; a new list has no members, and a new bundle is empty.

Declaration can be supplemented by a definite initialization, as in

```

scalar x = pi
series y = log(x)
matrix A = zeros(10,4)

```

With the exception of bundles (as noted above), new variables in `gretl` do not *have* to be declared by type. The traditional way of creating a new variable in `gretl` was via the `genr` command (which is still supported), as in

```
genr x = y/100
```

Here the type of `x` is left implicit and will be determined automatically depending on the context: if `y` is a scalar, a series or a matrix `x` will inherit `y`'s type (otherwise an error will be generated, since division is applicable to these types only). Moreover, the type of a new variable can be left implicit *without* use of `genr`:

```
x = y/100
```

In “modern” `gretl` scripting we recommend that you state the type of a new variable explicitly. This makes the intent clearer to a reader of the script and also guards against errors that might otherwise be difficult to understand (i.e. a certain variable turns out to be of the wrong type for some subsequent calculation, but you don't notice at first because you didn't say what type you needed). An exception to this rule might reasonably be granted for clear and simple cases where there's little possibility of confusion.

### Modification

Typically, the values of variables of all types are modified by assignment, using the `=` operator with the name of the variable on the left and a suitable value or formula on the right:

```

z = normal()
x = 100 * log(y) - log(y(-1))
M = qform(a, X)

```

By a “suitable” value we mean one that is conformable for the type in question. A `gretl` variable acquires its type when it is first created and this cannot be changed via assignment; for example, if you have a matrix `A` and later want a string `A`, you will have to delete the matrix first.

☞ One point to watch out for in `gretl` scripting is type conflicts having to do with the names of series brought in from a data file. For example, in setting up a command loop (see chapter 10) it is very common to call the loop index `i`. Now a loop index is a scalar (typically incremented each time round the loop). If you open a data file that happens to contain a series named `i` you will get a type error (“Types not conformable for operation”) when you try to use `i` as a loop index.

Although the type of an existing variable cannot be changed on the fly, `gretl` nonetheless tries to be as “understanding” as possible. For example if `x` is a series and you say

```
x = 100
```

`gretl` will give the series a constant value of 100 rather than complaining that you are trying to assign a scalar to a series. This issue is particularly relevant for the matrix type — see chapter 14 for details.

Besides using the regular assignment operator you also have the option of using an “inflected” equals sign, as in the C programming language. This is shorthand for the case where the new value of the variable is a function of the old value. For example,

```
x += 100 # in longhand: x = x + 100
x *= 100 # in longhand: x = x * 100
```

For scalar variables you can use a more condensed shorthand for simple increment or decrement by 1, namely trailing ++ or -- respectively:

```
x = 100
x--      # x now equals 99
x++      # x now equals 100
```

In the case of objects holding more than one value — series, matrices and bundles — you can modify particular values within the object using an expression within square brackets to identify the elements to access. We have discussed this above for the bundle type and chapter 14 goes into details for matrices. As for series, there are two ways to specify particular values for modification: you can use a simple 1-based index, or if the dataset is a time series or panel (or if it has marker strings that identify the observations) you can use an appropriate observation string. Such strings are displayed by gretl when you print data with the --byobs flag. Examples:

```
x[13]      = 100 # simple index: the 13th observation
x[1995:4]  = 100 # date: quarterly time series
x[2003:08] = 100 # date: monthly time series
x["AZ"]    = 100 # the observation with marker string "AZ"
x[3:15]    = 100 # panel: the 15th observation for the 3rd unit
```

Note that with quarterly or monthly time series there is no ambiguity between a simple index number and a date, since dates always contain a colon. With annual time-series data, however, such ambiguity exists and it is resolved by the rule that a number in brackets is always read as a simple index: `x[1905]` means the nineteen-hundred and fifth observation, *not* the observation for the year 1905. You can specify a year by quotation, as in `x["1905"]`.

## Destruction

Objects of the types discussed above, *with the important exception of named lists*, are all destroyed using the `delete` command: `delete objectname`.

Lists are an exception for this reason: in the context of gretl commands, a named list expands to the ID numbers of the member series, so if you say

```
delete L
```

for `L` a list, the effect is to delete all the series in `L`; the list itself is not destroyed, but ends up empty. To delete the list itself (without deleting the member series) you must invert the command and use the `list` keyword:

```
list L delete
```

## Chapter 13

# Named lists and strings

### 13.1 Named lists

Many `gretl` commands take one or more lists of series as arguments. To make this easier to handle in the context of command scripts, and in particular within user-defined functions, `gretl` offers the possibility of *named lists*.

#### Creating and modifying named lists

A named list is created using the keyword `list`, followed by the name of the list, an equals sign, and an expression that forms a list. The most basic sort of expression that works in this context is a space-separated list of variables, given either by name or by ID number. For example,

```
list xlist = 1 2 3 4
list reglist = income price
```

Note that the variables in question must be of the series type: you cannot include scalars in a named list.

Two abbreviations are available in defining lists:

- You can use the wildcard character, “\*”, to create a list of variables by name. For example, `dum*` can be used to indicate all variables whose names begin with `dum`.
- You can use two dots to indicate a range of variables. For example `income..price` indicates the set of variables whose ID numbers are greater than or equal to that of `income` and less than or equal to that of `price`.

In addition there are two special forms:

- If you use the keyword `null` on the right-hand side, you get an empty list.
- If you use the keyword `dataset` on the right, you get a list containing all the series in the current dataset (except the pre-defined `const`).

The name of the list must start with a letter, and must be composed entirely of letters, numbers or the underscore character. The maximum length of the name is 15 characters; list names cannot contain spaces.

Once a named list has been created, it will be “remembered” for the duration of the `gretl` session (unless you delete it), and can be used in the context of any `gretl` command where a list of variables is expected. One simple example is the specification of a list of regressors:

```
list xlist = x1 x2 x3 x4
ols y 0 xlist
```

To get rid of a list, you use the following syntax:

```
list xlist delete
```

Be careful: `delete xlist` will delete the variables contained in the list, so it implies data loss (which may not be what you want). On the other hand, `list xlist delete` will simply “undefine” the `xlist` identifier and the variables themselves will not be affected.

Similarly, to print the names of the variables in a list you have to invert the usual print command, as in

```
list xlist print
```

If you just say `print xlist` the list will be expanded and the values of all the member variables will be printed.

Lists can be modified in various ways. To *redefine* an existing list altogether, use the same syntax as for creating a list. For example

```
list xlist = 1 2 3
xlist = 4 5 6
```

After the second assignment, `xlist` contains just variables 4, 5 and 6.

To *append* or *prepend* variables to an existing list, we can make use of the fact that a named list stands in for a “longhand” list. For example, we can do

```
list xlist = xlist 5 6 7
xlist = 9 10 xlist 11 12
```

Another option for appending a term (or a list) to an existing list is to use `+=`, as in

```
xlist += cpi
```

To drop a variable from a list, use `-=`:

```
xlist -= cpi
```

In most contexts where lists are used in `gretl`, it is expected that they do not contain any duplicated elements. If you form a new list by simple concatenation, as in `list L3 = L1 L2` (where `L1` and `L2` are existing lists), it’s possible that the result may contain duplicates. To guard against this you can form a new list as the union of two existing ones:

```
list L3 = L1 || L2
```

The result is a list that contains all the members of `L1`, plus any members of `L2` that are not already in `L1`.

In the same vein, you can construct a new list as the intersection of two existing ones:

```
list L3 = L1 && L2
```

Here `L3` contains all the elements that are present in both `L1` and `L2`.

You can also subtract one list from another:

```
list L3 = L1 - L2
```

The result contains all the elements of `L1` that are not present in `L2`.



### Lists and matrices

Another way of forming a list is by assignment from a matrix. The matrix in question must be interpretable as a vector containing ID numbers of (series) variables. It may be either a row or a column vector, and each of its elements must have an integer part that is no greater than the number of variables in the data set. For example:

```
matrix m = {1,2,3,4}
list L = m
```

The above is OK provided the data set contains at least 4 variables.

### Querying a list

You can determine whether an unknown variable actually represents a list using the function `islist()`.

```
series x11 = log(x1)
series x12 = log(x2)
list xlogs = x11 x12
genr is1 = islist(xlogs)
genr is2 = islist(x11)
```

The first `genr` command above will assign a value of 1 to `is1` since `xlogs` is in fact a named list. The second `genr` will assign 0 to `is2` since `x11` is a data series, not a list.

You can also determine the number of variables or elements in a list using the function `nelem()`.

```
list xlist = 1 2 3
n1 = nelem(xlist)
```

The (scalar) variable `n1` will be assigned a value of 3 since `xlist` contains 3 members.

You can determine whether a given series is a member of a specified list using the function `inlist()`, as in

```
scalar k = inlist(L, y)
```

where `L` is a list and `y` a series. The series may be specified by name or ID number. The return value is the (1-based) position of the series in the list, or zero if the series is not present in the list.

### Generating lists of transformed variables

Given a named list of variables, you are able to generate lists of transformations of these variables using the functions `log`, `lags`, `diff`, `ldiff`, `sdiff` or `dummify`. For example

```
list xlist = x1 x2 x3
list lxlist = log(xlist)
list difflist = diff(xlist)
```

When generating a list of *lags* in this way, you specify the maximum lag order inside the parentheses, before the list name and separated by a comma. For example

```
list xlist = x1 x2 x3
list laglist = lags(2, xlist)
```

or

	YpcFR	YpcGE	YpcIT	NFR	NGE	NIT
1997	114.9	124.6	119.3	59830.635	82034.771	56890.372
1998	115.3	122.7	120.0	60046.709	82047.195	56906.744
1999	115.0	122.4	117.8	60348.255	82100.243	56916.317
2000	115.6	118.8	117.2	60750.876	82211.508	56942.108
2001	116.0	116.9	118.1	61181.560	82349.925	56977.217
2002	116.3	115.5	112.2	61615.562	82488.495	57157.406
2003	112.1	116.9	111.0	62041.798	82534.176	57604.658
2004	110.3	116.6	106.9	62444.707	82516.260	58175.310
2005	112.4	115.1	105.1	62818.185	82469.422	58607.043
2006	111.9	114.2	103.3	63195.457	82376.451	58941.499

**Table 13.1:** GDP per capita and population in 3 European countries (Source: Eurostat)

```
scalar order = 4
list laglist = lags(order, xlist)
```

These commands will populate `laglist` with the specified number of lags of the variables in `xlist`. You can give the name of a single series in place of a list as the second argument to `lags`: this is equivalent to giving a list with just one member.

The `dummiify` function creates a set of dummy variables coding for all but one of the distinct values taken on by the original variable, which should be discrete. (The smallest value is taken as the omitted category.) Like `lags`, this function returns a list even if the input is a single series.

### Generating series from lists

Once a list is defined, `gretl` offers several functions that apply to the list and return a series. In most cases, these functions also apply to single series and behave as natural extensions when applied to a list, but this is not always the case.

For recognizing and handling missing values, `Gretl` offers several functions (see the *Gretl Command Reference* for details). In this context, it is worth remarking that the `ok()` function can be used with a list argument. For example,

```
list xlist = x1 x2 x3
series xok = ok(xlist)
```

After these commands, the series `xok` will have value 1 for observations where none of `x1`, `x2`, or `x3` has a missing value, and value 0 for any observations where this condition is not met.

The functions `max`, `min`, `mean`, `sd`, `sum` and `var` behave horizontally rather than vertically when their argument is a list. For instance, the following commands

```
list Xlist = x1 x2 x3
series m = mean(Xlist)
```

produce a series `m` whose  $i$ -th element is the average of  $x_{1,i}$ ,  $x_{2,i}$  and  $x_{3,i}$ ; missing values, if any, are implicitly discarded.

In addition, `gretl` provides three functions for weighted operations: `wmean`, `wsd` and `wvar`. Consider as an illustration Table 13.1: the first three columns are GDP per capita for France, Germany and Italy; columns 4 to 6 contain the population for each country. If we want to compute an aggregate indicator of per capita GDP, all we have to do is

```
list Ypc = YpcFR YpcGE YpcIT
list N = NFR NGE NIT
y = wmean(Ypc, N)
```

so for example

$$y_{1996} = \frac{114.9 \times 59830.635 + 124.6 \times 82034.771 + 119.3 \times 56890.372}{59830.635 + 82034.771 + 56890.372} = 120.163$$

See the *Gretl Command Reference* for more details.

## 13.2 Named strings

For some purposes it may be useful to save a string (that is, a sequence of characters) as a named variable that can be reused. Versions of `gretl` higher than 1.6.0 offer this facility, but some of the refinements noted below are available only in `gretl` 1.7.2 and higher.

To *define* a string variable, you can use either of two commands, `string` or `sprintf`. The `string` command is simpler: you can type, for example,

```
string s1 = "some stuff I want to save"
string s2 = getenv("HOME")
string s3 = s1 + 11
```

The first field after `string` is the name under which the string should be saved, then comes an equals sign, then comes a specification of the string to be saved. This can be the keyword `null`, to produce an empty string, or may take any of the following forms:

- a string literal (enclosed in double quotes); or
- the name of an existing string variable; or
- a function that returns a string (see below); or
- any of the above followed by `+` and an integer offset.

The role of the integer offset is to use a substring of the preceding element, starting at the given character offset. An empty string is returned if the offset is greater than the length of the string in question.

To add to the end of an existing string you can use the operator `+=`, as in

```
string s1 = "some stuff I want to "
string s1 += "save"
```

or you can use the `~` operator to join two or more strings, as in

```
string s1 = "sweet"
string s2 = "Home, " ~ s1 ~ " home."
```

Note that when you define a string variable using a string literal, no characters are treated as “special” (other than the double quotes that delimit the string). Specifically, the backslash is not used as an escape character. So, for example,

```
string s = "\"
```

is a valid assignment, producing a string that contains a single backslash character. If you wish to use backslash-escapes to denote newlines, tabs, embedded double-quotes and so on, use `sprintf` instead.

The `sprintf` command is more flexible. It works exactly as `gretl`'s `printf` command except that the “format” string must be preceded by the name of a string variable. For example,

```
scalar x = 8
sprintf foo "var%d", x
```

To use the *value* of a string variable in a command, give the name of the variable preceded by the “at” sign, `@`. This notation is treated as a “macro”. That is, if a sequence of characters in a `gretl` command following the symbol `@` is recognized as the name of a string variable, the value of that variable is substituted literally into the command line before the regular parsing of the command is carried out. This is illustrated in the following interactive session:

```
? scalar x = 8
  scalar x = 8
Generated scalar x (ID 2) = 8
? sprintf foo "var%d", x
  Saved string as 'foo'
? print "@foo"
  var8
```

Note the effect of the quotation marks in the line `print "@foo"`. The line

```
? print @foo
```

would *not* print a literal “var8” as above. After pre-processing the line would read

```
print var8
```

It would therefore print the value(s) of the variable `var8`, if such a variable exists, or would generate an error otherwise.

In some contexts, however, one wants to treat string variables as variables in their own right: to do this, give the name of the variable without the leading `@` symbol. This is the way to handle such variables in the following contexts:

- When they appear among the arguments to the commands `printf` and `sprintf`.
- On the right-hand side of a string assignment.
- When they appear as an argument to the function taking a string argument.

Here is an illustration of the use of named string arguments with `printf`:

```
string vstr = "variance"
Generated string vstr
printf "vstr: %12s\n", vstr
vstr:      variance
```

Note that `vstr` should not be put in quotes in this context. Similarly with

```
? string vstr_copy = vstr
```

<code>gretl_dir</code>	the gretl installation directory
<code>workdir</code>	user's current gretl working directory
<code>dotdir</code>	the directory gretl uses for temporary files
<code>gnuplot</code>	path to, or name of, the <code>gnuplot</code> executable
<code>tramo</code>	path to, or name of, the <code>tramo</code> executable
<code>x12a</code>	path to, or name of, the <code>x-12-arma</code> executable
<code>tramodir</code>	tramo data directory
<code>x12adir</code>	x-12-arma data directory

Table 13.2: Built-in string variables

**Built-in strings**

Apart from any strings that the user may define, some string variables are defined by gretl itself. These may be useful for people writing functions that include shell commands. The built-in strings are as shown in Table 13.2.

**Reading strings from the environment**

In addition, it is possible to read into gretl's named strings, values that are defined in the external environment. To do this you use the function `getenv`, which takes the name of an environment variable as its argument. For example:

```
? string user = getenv("USER")
Saved string as 'user'
? string home = getenv("HOME")
Saved string as 'home'
? print "@user's home directory is @home"
cottrell's home directory is /home/cottrell
```

To check whether you got a non-empty value from a given call to `getenv`, you can use the function `strlen`, which retrieves the length of the string, as in

```
? string temp = getenv("TEMP")
Saved empty string as 'temp'
? scalar x = strlen(temp)
Generated scalar x (ID 2) = 0
```

The function `isstring` returns 1 if its argument is the name of a string variable, 0 otherwise. However, if the return is 1 the string may still be empty.

At present the `getenv` function can only be used on the right-hand side of a `string` assignment, as in the above illustrations.

**Capturing strings via the shell**

If shell commands are enabled in gretl, you can capture the output from such commands using the syntax

```
string stringname = $(shellcommand)
```

That is, you enclose a shell command in parentheses, preceded by a dollar sign.

**Reading from a file into a string**

You can read the content of a file into a string variable using the syntax

```
string stringname = readfile(filename)
```

The *filename* field may be given as a string variable. For example

```
? sprintf fname "%s/QNC.rts", x12adir
Generated string fname
? string foo = readfile(fname)
Generated string foo
```

The above could also be accomplished using the “macro” variant of a string variable, provided it is placed in quotation marks:

```
string foo = readfile("@x12adir/QNC.rts")
```

### The **strstr** function

Invocation of this function takes the form

```
string stringname = strstr(s1, s2)
```

The effect is to search *s1* for the first occurrence of *s2*. If no such occurrence is found, an empty string is returned; otherwise the portion of *s1* starting with *s2* is returned. For example:

```
? string hw = "hello world"
Saved string as 'hw'
? string w = strstr(hw, "o")
Saved string as 'w'
? print "@w"
o world
```

## Chapter 14

# Matrix manipulation

Together with the other two basic types of data (series and scalars), gretl offers a quite comprehensive array of matrix methods. This chapter illustrates the peculiarities of matrix syntax and discusses briefly some of the more complex matrix functions. For a full listing of matrix functions and a comprehensive account of their syntax, please refer to the *Gretl Command Reference*.

### 14.1 Creating matrices

Matrices can be created using any of these methods:

1. By direct specification of the scalar values that compose the matrix — in numerical form, by reference to pre-existing scalar variables, or using computed values.
2. By providing a list of data series.
3. By providing a *named list* of series.
4. Using a formula of the same general type that is used with the `genr` command, whereby a new matrix is defined in terms of existing matrices and/or scalars, or via some special functions.

To specify a matrix *directly in terms of scalars*, the syntax is, for example:

```
matrix A = { 1, 2, 3 ; 4, 5, 6 }
```

The matrix is defined by rows; the elements on each row are separated by commas and the rows are separated by semi-colons. The whole expression must be wrapped in braces. Spaces within the braces are not significant. The above expression defines a  $2 \times 3$  matrix. Each element should be a numerical value, the name of a scalar variable, or an expression that evaluates to a scalar. Directly after the closing brace you can append a single quote (') to obtain the transpose.

To specify a matrix *in terms of data series* the syntax is, for example,

```
matrix A = { x1, x2, x3 }
```

where the names of the variables are separated by commas. Besides names of existing variables, you can use expressions that evaluate to a series. For example, given a series `x` you could do

```
matrix A = { x, x^2 }
```

Each variable occupies a column (and there can only be one variable per column). You cannot use the semicolon as a row separator in this case: if you want the series arranged in rows, append the transpose symbol. The range of data values included in the matrix depends on the current setting of the sample range.

Instead of giving an explicit list of variables, you may instead provide the *name of a saved list* (see Chapter 13), as in

```
list xlist = x1 x2 x3
matrix A = { xlist }
```

When you provide a named list, the data series are by default placed in columns, as is natural in an econometric context: if you want them in rows, append the transpose symbol.

As a special case of constructing a matrix from a list of variables, you can say

```
matrix A = { dataset }
```

This builds a matrix using all the series in the current dataset, apart from the constant (variable 0). When this dummy list is used, it must be the sole element in the matrix definition {...}. You can, however, create a matrix that includes the constant along with all other variables using horizontal concatenation (see below), as in

```
matrix A = {const}~{dataset}
```

By default, when you build a matrix from series that include missing values the data rows that contain NAs are skipped. But you can modify this behavior via the command `set skip_missing off`. In that case NAs are converted to NaN (“Not a Number”). In the IEEE floating-point standard, arithmetic operations involving NaN always produce NaN. Alternatively, you can take greater control over the observations (data rows) that are included in the matrix using the “set” variable `matrix_mask`, as in

```
set matrix_mask msk
```

where `msk` is the name of a series. Subsequent commands that form matrices from series or lists will include only observations for which `msk` has non-zero (and non-missing) values. You can remove this mask via the command `set matrix_mask null`.

☞ Names of matrices must satisfy the same requirements as names of gretl variables in general: the name can be no longer than 15 characters, must start with a letter, and must be composed of nothing but letters, numbers and the underscore character.

## 14.2 Empty matrices

The syntax

```
matrix A = {}
```

creates an empty matrix — a matrix with zero rows and zero columns.

The main purpose of the concept of an empty matrix is to enable the user to define a starting point for subsequent concatenation operations. For instance, if `X` is an already defined matrix of any size, the commands

```
matrix A = {}
matrix B = A ~ X
```

result in a matrix `B` identical to `X`.

From an algebraic point of view, one can make sense of the idea of an empty matrix in terms of vector spaces: if a matrix is an ordered set of vectors, then  $A=\{\}$  is the empty set. As a consequence, operations involving addition and multiplications don’t have any clear meaning (arguably, they have none at all), but operations involving the cardinality of this set (that is, the dimension of the space spanned by `A`) are meaningful.



Legal operations on empty matrices are listed in Table 14.1. (All other matrix operations generate an error when an empty matrix is given as an argument.) In line with the above interpretation, some matrix functions return an empty matrix under certain conditions: the functions `diag`, `vec`, `vech`, `unvech` when the arguments is an empty matrix; the functions `I`, `ones`, `zeros`, `mnormal`, `muniform` when one or more of the arguments is 0; and the function `nullspace` when its argument has full column rank.

<i>Function</i>	<i>Return value</i>
<code>A'</code> , <code>transp(A)</code>	<code>A</code>
<code>rows(A)</code>	0
<code>cols(A)</code>	0
<code>rank(A)</code>	0
<code>det(A)</code>	NA
<code>ldet(A)</code>	NA
<code>tr(A)</code>	NA
<code>onenorm(A)</code>	NA
<code>infnorm(A)</code>	NA
<code>rcond(A)</code>	NA

**Table 14.1:** Valid functions on an empty matrix, `A`

### 14.3 Selecting sub-matrices

You can select sub-matrices of a given matrix using the syntax

`A[rows,cols]`

where *rows* can take any of these forms:

- |                                      |                                  |
|--------------------------------------|----------------------------------|
| 1. empty                             | selects all rows                 |
| 2. a single integer                  | selects the single specified row |
| 3. two integers separated by a colon | selects a range of rows          |
| 4. the name of a matrix              | selects the specified rows       |

With regard to option 2, the integer value can be given numerically, as the name of an existing scalar variable, or as an expression that evaluates to a scalar. With option 4, the index matrix given in the *rows* field must be either  $p \times 1$  or  $1 \times p$ , and should contain integer values in the range 1 to  $n$ , where  $n$  is the number of rows in the matrix from which the selection is to be made.

The *cols* specification works in the same way, *mutatis mutandis*. Here are some examples.

```
matrix B = A[1,]
matrix B = A[2:3,3:5]
matrix B = A[2,2]
matrix idx = { 1, 2, 6 }
matrix B = A[idx,]
```

The first example selects row 1 from matrix `A`; the second selects a  $2 \times 3$  submatrix; the third selects a scalar; and the fourth selects rows 1, 2, and 6 from matrix `A`.

If the matrix in question is  $n \times 1$  or  $1 \times m$ , it is OK to give just one index specifier and omit the comma. For example, `A[2]` selects the second element of `A` if `A` is a vector. Otherwise the comma is mandatory.

In addition there is a pre-defined index specification, `diag`, which selects the principal diagonal of a square matrix, as in `B[diag]`, where `B` is square.

You can use selections of this sort on either the right-hand side of a matrix-generating formula or the left. Here is an example of use of a selection on the right, to extract a  $2 \times 2$  submatrix  $B$  from a  $3 \times 3$  matrix  $A$ :

```
matrix A = { 1, 2, 3; 4, 5, 6; 7, 8, 9 }
matrix B = A[1:2,2:3]
```

And here are examples of selection on the left. The second line below writes a  $2 \times 2$  identity matrix into the bottom right corner of the  $3 \times 3$  matrix  $A$ . The fourth line replaces the diagonal of  $A$  with 1s.

```
matrix A = { 1, 2, 3; 4, 5, 6; 7, 8, 9 }
matrix A[2:3,2:3] = I(2)
matrix d = { 1, 1, 1 }
matrix A[diag] = d
```

## 14.4 Matrix operators

The following binary operators are available for matrices:

+	addition
-	subtraction
*	ordinary matrix multiplication
'	pre-multiplication by transpose
\	matrix “left division” (see below)
/	matrix “right division” (see below)
~	column-wise concatenation
	row-wise concatenation
**	Kronecker product
=	test for equality

In addition, the following operators (“dot” operators) apply on an element-by-element basis:

```
.+   .-   .*   ./   .^   .=   .>   .<   .>=   .<=
```

Here are explanations of the less obvious cases.

For matrix addition and subtraction, in general the two matrices have to be of the same dimensions but an exception to this rule is granted if one of the operands is a  $1 \times 1$  matrix or scalar. The scalar is implicitly promoted to the status of a matrix of the correct dimensions, all of whose elements are equal to the given scalar value. For example, if  $A$  is an  $m \times n$  matrix and  $k$  a scalar, then the commands

```
matrix C = A + k
matrix D = A - k
```

both produce  $m \times n$  matrices, with elements  $c_{ij} = a_{ij} + k$  and  $d_{ij} = a_{ij} - k$  respectively.

By “pre-multiplication by transpose” we mean, for example, that

```
matrix C = X'Y
```

produces the product of  $X$ -transpose and  $Y$ . In effect, the expression  $X'Y$  is shorthand for  $X'*Y$  (which is also valid).

In matrix “left division”, the statement

```
matrix X = A \ B
```

is interpreted as a request to find the matrix  $X$  that solves  $AX = B$ . If  $B$  is a square matrix, this is in principle equivalent to  $A^{-1}B$ , which fails if  $A$  is singular; the numerical method employed here is the LU decomposition. If  $A$  is a  $T \times k$  matrix with  $T > k$ , then  $X$  is the least-squares solution,  $X = (A'A)^{-1}A'B$ , which fails if  $A'A$  is singular; the numerical method employed here is the QR decomposition. Otherwise, the operation necessarily fails.

For matrix “right division”, as in  $X = A / B$ ,  $X$  is the matrix that solves  $XB = A$ , in principle equivalent to  $AB^{-1}$ .

In “dot” operations a binary operation is applied element by element; the result of this operation is obvious if the matrices are of the same size. However, there are several other cases where such operators may be applied. For example, if we write

```
matrix C = A .- B
```

then the result  $C$  depends on the dimensions of  $A$  and  $B$ . Let  $A$  be an  $m \times n$  matrix and let  $B$  be  $p \times q$ ; the result is as follows:

Case	Result
Dimensions match ( $m = p$ and $n = q$ )	$c_{ij} = a_{ij} - b_{ij}$
$A$ is a column vector; rows match ( $m = p$ ; $n = 1$ )	$c_{ij} = a_i - b_{ij}$
$B$ is a column vector; rows match ( $m = p$ ; $q = 1$ )	$c_{ij} = a_{ij} - b_i$
$A$ is a row vector; columns match ( $m = 1$ ; $n = q$ )	$c_{ij} = a_j - b_{ij}$
$B$ is a row vector; columns match ( $m = p$ ; $q = 1$ )	$c_{ij} = a_{ij} - b_j$
$A$ is a column vector; $B$ is a row vector ( $n = 1$ ; $p = 1$ )	$c_{ij} = a_i - b_j$
$A$ is a row vector; $B$ is a column vector ( $m = 1$ ; $q = 1$ )	$c_{ij} = a_j - b_i$
$A$ is a scalar ( $m = 1$ and $n = 1$ )	$c_{ij} = a - b_{ij}$
$B$ is a scalar ( $p = 1$ and $q = 1$ )	$c_{ij} = a_{ij} - b$

If none of the above conditions are satisfied the result is undefined and an error is flagged.

Note that this convention makes it unnecessary, in most cases, to use diagonal matrices to perform transformations by means of ordinary matrix multiplication: if  $Y = XV$ , where  $V$  is diagonal, it is computationally much more convenient to obtain  $Y$  via the instruction

```
matrix Y = X .* v
```

where  $v$  is a row vector containing the diagonal of  $V$ .

In *column-wise concatenation* of an  $m \times n$  matrix  $A$  and an  $m \times p$  matrix  $B$ , the result is an  $m \times (n+p)$  matrix. That is,

```
matrix C = A ~ B
```

produces  $C = \begin{bmatrix} A & B \end{bmatrix}$ .

*Row-wise concatenation* of an  $m \times n$  matrix  $A$  and an  $p \times n$  matrix  $B$  produces an  $(m+p) \times n$  matrix. That is,

```
matrix C = A | B
```

produces  $C = \begin{bmatrix} A \\ B \end{bmatrix}$ .

### 14.5 Matrix-scalar operators

For matrix  $A$  and scalar  $k$ , the operators shown in Table 14.2 are available. (Addition and subtraction were discussed in section 14.4 but we include them in the table for completeness.) In addition, for square  $A$  and integer  $k \geq 0$ ,  $B = A^k$  produces a matrix  $B$  which is  $A$  raised to the power  $k$ .

<i>Expression</i>	<i>Effect</i>
<code>matrix B = A * k</code>	$b_{ij} = ka_{ij}$
<code>matrix B = A / k</code>	$b_{ij} = a_{ij}/k$
<code>matrix B = k / A</code>	$b_{ij} = k/a_{ij}$
<code>matrix B = A + k</code>	$b_{ij} = a_{ij} + k$
<code>matrix B = A - k</code>	$b_{ij} = a_{ij} - k$
<code>matrix B = k - A</code>	$b_{ij} = k - a_{ij}$
<code>matrix B = A % k</code>	$b_{ij} = a_{ij} \text{ modulo } k$

**Table 14.2:** Matrix-scalar operators

### 14.6 Matrix functions

Most of the `gretl` functions available for scalars and series also apply to matrices in an element-by-element fashion, and as such their behavior should be pretty obvious. This is the case for functions such as `log`, `exp`, `sin`, etc. These functions have the effects documented in relation to the `genr` command. For example, if a matrix  $A$  is already defined, then

```
matrix B = sqrt(A)
```

generates a matrix such that  $b_{ij} = \sqrt{a_{ij}}$ . All such functions require a single matrix as argument, or an expression which evaluates to a single matrix.<sup>1</sup>

In this section, we review some aspects of `genr` functions that apply specifically to matrices. A full account of each function is available in the *Gretl Command Reference*.

#### Matrix reshaping

In addition to the methods discussed in sections 14.1 and 14.3, a matrix can also be created by re-arranging the elements of a pre-existing matrix. This is accomplished via the `mshape` function. It takes three arguments: the input matrix,  $A$ , and the rows and columns of the target matrix,  $r$  and  $c$  respectively. Elements are read from  $A$  and written to the target in column-major order. If  $A$  contains fewer elements than  $n = r \times c$ , they are repeated cyclically; if  $A$  has more elements, only the first  $n$  are used.

For example:

```
matrix a = mnormal(2,3)
a
matrix b = mshape(a,3,1)
b
```

<sup>1</sup>Note that to find the “matrix square root” you need the `cholesky` function (see below); moreover, the `exp` function computes the exponential element by element, and therefore does *not* return the matrix exponential unless the matrix is diagonal — to get the matrix exponential, use `mexp`.

<b>Creation and I/O</b>						
	colnames	diag	diagcat	I	lower	mnormal
	mread	muniform	mwrite	ones	rownames	seq
	unvech	upper	vec	vech	zeros	
<b>Shape/size/arrangement</b>						
	cols	dsort	mreverse	mshape	msortby	rows
	selifc	selifr	sort	trimr		
<b>Matrix algebra</b>						
	cdiv	cholesky	cmult	det	eigengen	eigensym
	eigsolve	fft	ffti	ginv	hdprod	infnorm
	inv	invpd	ldet	mexp	nullspace	onenorm
	polroots	psdroot	qform	qrdecomp	rank	rcond
	svd	toepsolv	tr	transp	varsimul	
<b>Statistics/transformations</b>						
	cdemean	corr	corrgm	cov	fcstats	ghk
	halton	imaxc	imaxr	iminc	iminr	irf
	kdensity	maxc	maxr	mcorr	mcov	mcovg
	meanc	meanr	minc	minr	mlag	mols
	mpols	mrls	mxtab	pergm	princomp	quantile
	ranking	resample	sd	sumc	sumr	uniq
	values					
<b>Data utilities</b>						
	isconst	ok	pshrink	replace		
<b>Filters</b>						
	filter	kfilter	ksimul	ksmooth	lrvar	
<b>Numerical methods</b>						
	BFGSmax	fdjac	NRmax	simann		
<b>Strings</b>						
	colname					
<b>Transformations</b>						
	chowlin	cum	lincomb			

Table 14.3: Matrix functions by category

```
matrix b = mshape(a,5,2)
b
```

produces

```
? a
a
      1.2323      0.99714      -0.39078
      0.54363      0.43928      -0.48467
```

```
? matrix b = mshape(a,3,1)
Generated matrix b
? b
b
```

```
      1.2323
      0.54363
      0.99714
```

```
? matrix b = mshape(a,5,2)
Replaced matrix b
? b
b
```

```
      1.2323      -0.48467
      0.54363      1.2323
      0.99714      0.54363
      0.43928      0.99714
      -0.39078      0.43928
```

### Complex multiplication and division

Gretl has no native provision for complex numbers. However, basic operations can be performed on vectors of complex numbers by using the convention that a vector of  $n$  complex numbers is represented as a  $n \times 2$  matrix, where the first column contains the real part and the second the imaginary part.

Addition and subtraction are trivial; the functions `cmult` and `cdiv` compute the complex product and division, respectively, of two input matrices,  $A$  and  $B$ , representing complex numbers. These matrices must have the same number of rows,  $n$ , and either one or two columns. The first column contains the real part and the second (if present) the imaginary part. The return value is an  $n \times 2$  matrix, or, if the result has no imaginary part, an  $n$ -vector.

For example, suppose you have  $z_1 = [1 + 2i, 3 + 4i]'$  and  $z_2 = [1, i]'$ :

```
? z1 = {1,2;3,4}
z1 = {1,2;3,4}
Generated matrix z1
? z2 = I(2)
z2 = I(2)
Generated matrix z2
? conj_z1 = z1 .* {1,-1}
conj_z1 = z1 .* {1,-1}
Generated matrix conj_z1
? eval cmult(z1,z2)
eval cmult(z1,z2)
      1      2
     -4      3
```

```
? eval cmult(z1,conj_z1)
eval cmult(z1,conj_z1)
5
25
```

### Multiple returns and the `null` keyword

Some functions take one or more matrices as arguments and compute one or more matrices; these are:

<code>eigensym</code>	Eigen-analysis of symmetric matrix
<code>eigen</code>	Eigen-analysis of general matrix
<code>mo1s</code>	Matrix OLS
<code>qrdecomp</code>	QR decomposition
<code>svd</code>	Singular value decomposition (SVD)

The general rule is: the “main” result of the function is always returned as the result proper. Auxiliary returns, if needed, are retrieved using pre-existing matrices, which are passed to the function as pointers (see 11.4). If such values are not needed, the pointer may be substituted with the keyword `null`.

The syntax for `qrdecomp`, `eigensym` and `eigen` is of the form

```
matrix B = func(A, &C)
```

The first argument, `A`, represents the input data, that is, the matrix whose decomposition or analysis is required. The second argument must be either the name of an existing matrix preceded by `&` (to indicate the “address” of the matrix in question), in which case an auxiliary result is written to that matrix, or the keyword `null`, in which case the auxiliary result is not produced, or is discarded.

In case a non-null second argument is given, the specified matrix will be over-written with the auxiliary result. (It is not required that the existing matrix be of the right dimensions to receive the result.)

The function `eigensym` computes the eigenvalues, and optionally the right eigenvectors, of a symmetric  $n \times n$  matrix. The eigenvalues are returned directly in a column vector of length  $n$ ; if the eigenvectors are required, they are returned in an  $n \times n$  matrix. For example:

```
matrix V
matrix E = eigensym(M, &V)
matrix E = eigensym(M, null)
```

In the first case `E` holds the eigenvalues of `M` and `V` holds the eigenvectors. In the second, `E` holds the eigenvalues but the eigenvectors are not computed.

The function `eigen` computes the eigenvalues, and optionally the eigenvectors, of a general  $n \times n$  matrix. The eigenvalues are returned directly in an  $n \times 2$  matrix, the first column holding the real components and the second column the imaginary components.

If the eigenvectors are required (that is, if the second argument to `eigen` is not `null`), they are returned in an  $n \times n$  matrix. The column arrangement of this matrix is somewhat non-trivial: the eigenvectors are stored in the same order as the eigenvalues, but the real eigenvectors occupy one column, whereas complex eigenvectors take two (the real part comes first); the total number of columns is still  $n$ , because the conjugate eigenvector is skipped. Example 14.1 provides a (hopefully) clarifying example (see also subsection 14.6).

**Example 14.1:** Complex eigenvalues and eigenvectors

---

```
set seed 34756

matrix v
A = mnormal(3,3)

/* do the eigen-analysis */
l = eigengen(A,&v)
/* eigenvalue 1 is real, 2 and 3 are complex conjugates */
print l
print v

/*
  column 1 contains the first eigenvector (real)
*/

B = A*v[,1]
c = l[1,1] * v[,1]
/* B should equal c */
print B
print c

/*
  columns 2:3 contain the real and imaginary parts
  of eigenvector 2
*/

B = A*v[,2:3]
c = cmult(ones(3,1)*(l[2,]),v[,2:3])
/* B should equal c */
print B
print c
```

---



The `qrdecomp` function computes the QR decomposition of an  $m \times n$  matrix  $A$ :  $A = QR$ , where  $Q$  is an  $m \times n$  orthogonal matrix and  $R$  is an  $n \times n$  upper triangular matrix. The matrix  $Q$  is returned directly, while  $R$  can be retrieved via the second argument. Here are two examples:

```
matrix R
matrix Q = qrdecomp(M, &R)
matrix Q = qrdecomp(M, null)
```

In the first example, the triangular  $R$  is saved as  $R$ ; in the second,  $R$  is discarded. The first line above shows an example of a “simple declaration” of a matrix:  $R$  is declared to be a matrix variable but is not given any explicit value. In this case the variable is initialized as a  $1 \times 1$  matrix whose single element equals zero.

The syntax for `svd` is

```
matrix B = func(A, &C, &D)
```

The function `svd` computes all or part of the singular value decomposition of the real  $m \times n$  matrix  $A$ . Let  $k = \min(m, n)$ . The decomposition is

$$A = U\Sigma V'$$

where  $U$  is an  $m \times k$  orthogonal matrix,  $\Sigma$  is an  $k \times k$  diagonal matrix, and  $V$  is an  $k \times n$  orthogonal matrix.<sup>2</sup> The diagonal elements of  $\Sigma$  are the singular values of  $A$ ; they are real and non-negative, and are returned in descending order. The first  $k$  columns of  $U$  and  $V$  are the left and right singular vectors of  $A$ .

The `svd` function returns the singular values, in a vector of length  $k$ . The left and/or right singular vectors may be obtained by supplying non-null values for the second and/or third arguments respectively. For example:

```
matrix s = svd(A, &U, &V)
matrix s = svd(A, null, null)
matrix s = svd(A, null, &V)
```

In the first case both sets of singular vectors are obtained, in the second case only the singular values are obtained; and in the third, the right singular vectors are obtained but  $U$  is not computed. *Please note:* when the third argument is non-null, it is actually  $V'$  that is provided. To reconstitute the original matrix from its SVD, one can do:

```
matrix s = svd(A, &U, &V)
matrix B = (U.*s)*V
```

Finally, the syntax for `mol`s is

```
matrix B = mol
```

s(Y, X, &U)

This function returns the OLS estimates obtained by regressing the  $T \times n$  matrix  $Y$  on the  $T \times k$  matrix  $X$ , that is, a  $k \times n$  matrix holding  $(X'X)^{-1}X'Y$ . The Cholesky decomposition is used. The matrix  $U$ , if not null, is used to store the residuals.

### Reading and writing matrices from/to text files

The two functions `mread` and `mwri`te can be used for basic matrix input/output. This can be useful to enable `gretl` to exchange data with other programs.

---

<sup>2</sup>This is not the only definition of the SVD: some writers define  $U$  as  $m \times m$ ,  $\Sigma$  as  $m \times n$  (with  $k$  non-zero diagonal elements) and  $V$  as  $n \times n$ .

The `mread` function accepts one string parameter: the name of the (plain text) file from which the matrix is to be read. The file in question may start with any number of comment lines, defined as lines that start with the hash mark, “#”; such lines are ignored. Beyond that, the content must conform to the following rules:

1. The first non-comment line must contain two integers, separated by a space or a tab, indicating the number of rows and columns, respectively.
2. The columns must be separated by spaces or tab characters.
3. The decimal separator must be the dot “.” character.

Should an error occur (such as the file being badly formatted or inaccessible), an empty matrix (see section 14.2) is returned.

The complementary function `mwrite` produces text files formatted as described above. The column separator is the tab character, so import into spreadsheets should be straightforward. Usage is illustrated in example 14.2. Matrices stored via the `mwrite` command can be easily read by other programs; the following table summarizes the appropriate commands for reading a matrix `A` from a file called `a.mat` in some widely-used programs.<sup>3</sup>

Program	Sample code
GAUSS	<pre>tmp[] = load a.mat; A = reshape(tmp[3:rows(tmp)],tmp[1],tmp[2]);</pre>
Octave	<pre>fd = fopen("a.mat"); [r,c] = fscanf(fd, "%d %d", "C"); A = reshape(fscanf(fd, "%g", r*c),c,r)'; fclose(fd);</pre>
Ox	<pre>decl A = loadmat("a.mat");</pre>
R	<pre>A &lt;- as.matrix(read.table("a.mat", skip=1))</pre>

## 14.7 Matrix accessors

In addition to the matrix functions discussed above, various “accessor” strings allow you to create copies of internal matrices associated with models previously estimated. These are set out in Table 14.4.

Many of the accessors in Table 14.4 behave somewhat differently depending on the sort of model that is referenced, as follows:

- Single-equation models: `$sigma` gets a scalar (the standard error of the regression); `$coeff` and `$stderr` get column vectors; `$uhat` and `$yhat` get series.
- System estimators: `$sigma` gets the cross-equation residual covariance matrix; `$uhat` and `$yhat` get matrices with one column per equation. The format of `$coeff` and `$stderr` depends on the nature of the system: for VARs and VECMs (where the matrix of regressors is the same for all equations) these return matrices with one column per equation, but for other system estimators they return a big column vector.
- VARs and VECMs: `$vcv` is not available, but  $X'X^{-1}$  (where  $X$  is the common matrix of regressors) is available as `$xtxinv`.

<sup>3</sup>Matlab users may find the Octave example helpful, since the two programs are mostly compatible with one another.

**Example 14.2:** Matrix input/output via text files

---

```

nulldata 64
scalar n = 3
string f1 = "a.csv"
string f2 = "b.csv"

matrix a = mnormal(n,n)
matrix b = inv(a)

err = mwrite(a, f1)

if err != 0
    fprintf "Failed to write %s\n", f1
else
    err = mwrite(b, f2)
endif

if err != 0
    fprintf "Failed to write %s\n", f2
else
    c = mread(f1)
    d = mread(f2)
    a = c*d
    printf "The following matrix should be an identity matrix\n"
    print a
endif

```

---

<code>\$coeff</code>	matrix of estimated coefficients
<code>\$compan</code>	companion matrix (after VAR or VECM estimation)
<code>\$jalpha</code>	matrix $\alpha$ (loadings) from Johansen's procedure
<code>\$jbeta</code>	matrix $\beta$ (cointegration vectors) from Johansen's procedure
<code>\$jvbeta</code>	covariance matrix for the unrestricted elements of $\beta$ from Johansen's procedure
<code>\$rho</code>	autoregressive coefficients for error process
<code>\$sigma</code>	residual covariance matrix
<code>\$stderr</code>	matrix of estimated standard errors
<code>\$uhat</code>	matrix of residuals
<code>\$vcv</code>	covariance matrix of parameter estimates
<code>\$vma</code>	VMA matrices in stacked form — see section 25.2 (after VAR or VECM estimation)
<code>\$yhat</code>	matrix of fitted values

**Table 14.4:** Matrix accessors for model data

If the accessors are given without any prefix, they retrieve results from the last model estimated, if any. Alternatively, they may be prefixed with the name of a saved model plus a period (`.`), in which case they retrieve results from the specified model. Here are some examples:

```
matrix u = $uhat
matrix b = m1.$coeff
matrix v2 = m1.$vcv[1:2,1:2]
```

The first command grabs the residuals from the last model; the second grabs the coefficient vector from model `m1`; and the third (which uses the mechanism of sub-matrix selection described above) grabs a portion of the covariance matrix from model `m1`.

If the model in question a VAR or VECM (only) `$compan` and `$vma` return the companion matrix and the VMA matrices in stacked form, respectively (see section 25.2 for details). After a vector error correction model is estimated via Johansen's procedure, the matrices `$jalpha` and `$jbeta` are also available. These have a number of columns equal to the chosen cointegration rank; therefore, the product

```
matrix Pi = $jalpha * $jbeta'
```

returns the reduced-rank estimate of  $A(1)$ . Since  $\beta$  is automatically identified via the Phillips normalization (see section 26.5), its unrestricted elements do have a proper covariance matrix, which can be retrieved through the `$jvbeta` accessor.

## 14.8 Namespace issues

Matrices share a common namespace with data series and scalar variables. In other words, no two objects of any of these types can have the same name. It is an error to attempt to change the type of an existing variable, for example:

```
scalar x = 3
matrix x = ones(2,2) # wrong!
```

It is possible, however, to delete or rename an existing variable then reuse the name for a variable of a different type:

```
scalar x = 3
delete x
matrix x = ones(2,2) # OK
```

## 14.9 Creating a data series from a matrix

Section 14.1 above describes how to create a matrix from a data series or set of series. You may sometimes wish to go in the opposite direction, that is, to copy values from a matrix into a regular data series. The syntax for this operation is

```
series sname = mspec
```

where *sname* is the name of the series to create and *mspec* is the name of the matrix to copy from, possibly followed by a matrix selection expression. Here are two examples.

```
series s = x
series u1 = U[,1]
```

It is assumed that `x` and `U` are pre-existing matrices. In the second example the series `u1` is formed from the first column of the matrix `U`.

For this operation to work, the matrix (or matrix selection) must be a vector with length equal to either the full length of the current dataset,  $n$ , or the length of the current sample range,  $n'$ . If  $n' < n$  then only  $n'$  elements are drawn from the matrix; if the matrix or selection comprises  $n$  elements, the  $n'$  values starting at element  $t_1$  are used, where  $t_1$  represents the starting observation of the sample range. Any values in the series that are not assigned from the matrix are set to the missing code.

### 14.10 Matrices and lists

To facilitate the manipulation of named lists of variables (see Chapter 13), it is possible to convert between matrices and lists. In section 14.1 above we mentioned the facility for creating a matrix from a list of variables, as in

```
matrix M = { listname }
```

That formulation, with the name of the list enclosed in braces, builds a matrix whose columns hold the variables referenced in the list. What we are now describing is a different matter: if we say

```
matrix M = listname
```

(without the braces), we get a row vector whose elements are the ID numbers of the variables in the list. This special case of matrix generation cannot be embedded in a compound expression. The syntax must be as shown above, namely simple assignment of a list to a matrix.

To go in the other direction, you can include a matrix on the right-hand side of an expression that defines a list, as in

```
list X1 = M
```

where M is a matrix. The matrix must be suitable for conversion; that is, it must be a row or column vector containing non-negative whole-number values, none of which exceeds the highest ID number of a variable (series or scalar) in the current dataset.

Example 14.3 illustrates the use of this sort of conversion to “normalize” a list, moving the constant (variable 0) to first position.

### 14.11 Deleting a matrix

To delete a matrix, just write

```
delete M
```

where M is the name of the matrix to be deleted.

### 14.12 Printing a matrix

To print a matrix, the easiest way is to give the name of the matrix in question on a line by itself, which is equivalent to using the `print` command:

```
matrix M = mnormal(100,2)
M
print M
```

You can get finer control on the formatting of output by using the `printf` command, as illustrated in the interactive session below:

**Example 14.3:** Manipulating a list

---

```

function void normalize_list (matrix *x)
  # If the matrix (representing a list) contains var 0,
  # but not in first position, move it to first position

  if (x[1] != 0)
    scalar k = cols(x)
    loop for (i=2; i<=k; i++) --quiet
      if (x[i] = 0)
        x[i] = x[1]
        x[1] = 0
        break
      endif
    endloop
  endif
end function

open data9-7
list X1 = 2 3 0 4
matrix x = X1
normalize_list(&x)
list X1 = x

```

---

```

? matrix Id = I(2)
matrix Id = I(2)
Generated matrix Id
? print Id
print Id
Id (2 x 2)

1  0
0  1

? printf "%10.3f", Id
1.000    0.000
0.000    1.000

```

For presentation purposes you may wish to give titles to the columns of a matrix. For this you can use the `colnames` function: the first argument is a matrix and the second is either a named list of variables, whose names will be used as headings, or a string that contains as many space-separated substrings as the matrix has columns. For example,

```

? matrix M = mnormal(3,3)
? colnames(M, "foo bar baz")
? print M
M (3 x 3)

      foo      bar      baz
1.7102 -0.76072  0.089406
-0.99780 -1.9003 -0.25123
-0.91762 -0.39237 -1.6114

```

### 14.13 Example: OLS using matrices

Example 14.4 shows how matrix methods can be used to replicate gretl's built-in OLS functionality.

**Example 14.4:** OLS via matrix methods

---

```
open data4-1
matrix X = { const, sqft }
matrix y = { price }
matrix b = invpd(X'X) * X'y
print "estimated coefficient vector"
b
matrix u = y - X*b
scalar SSR = u'u
scalar s2 = SSR / (rows(X) - rows(b))
matrix V = s2 * inv(X'X)
V
matrix se = sqrt(diag(V))
print "estimated standard errors"
se
# compare with built-in function
ols price const sqft --vcv
```

---

## Chapter 15

# Cheat sheet

This chapter explains how to perform some common — and some not so common — tasks in **gretl**'s scripting language. Some but not all of the techniques listed here are also available through the graphical interface. Although the graphical interface may be more intuitive and less intimidating at first, we encourage users to take advantage of the power of **gretl**'s scripting language as soon as they feel comfortable with the program.

### 15.1 Dataset handling

#### **“Weird” periodicities**

*Problem:* You have data sampled each 3 minutes from 9am onwards; you'll probably want to specify the hour as 20 periods.

*Solution:*

```
setobs 20 9:1 --special
```

*Comment:* Now functions like `sdiff()` (“seasonal” difference) or estimation methods like seasonal ARIMA will work as expected.

#### **Help, my data are backwards!**

*Problem:* Gretl expects time series data to be in chronological order (most recent observation last), but you have imported third-party data that are in reverse order (most recent first).

*Solution:*

```
setobs 1 1 --cross-section
genr sortkey = -obs
dataset sortby sortkey
setobs 1 1950 --time-series
```

*Comment:* The first line is required only if the data currently have a time series interpretation: it removes that interpretation, because (for fairly obvious reasons) the `dataset sortby` operation is not allowed for time series data. The following two lines reverse the data, using the negative of the built-in index variable `obs`. The last line is just illustrative: it establishes the data as annual time series, starting in 1950.

If you have a dataset that is mostly the right way round, but a particular variable is wrong, you can reverse that variable as follows:

```
genr x = sortby(-obs, x)
```

#### **Dropping missing observations selectively**

*Problem:* You have a dataset with many variables and want to restrict the sample to those observations for which there are no missing observations for the variables `x1`, `x2` and `x3`.



*Solution:*

```
list X = x1 x2 x3
smp1 --no missing X
```

*Comment:* You can now save the file via a `store` command to preserve a subsampled version of the dataset. Alternative solution based on the `ok` function, such as

```
list X = x1 x2 x3
genr sel = ok(X)
smp1 sel --restrict
```

are perhaps less obvious, but more flexible. Pick your poison.

### “By” operations

*Problem:* You have a discrete variable `d` and you want to run some commands (for example, estimate a model) by splitting the sample according to the values of `d`.

*Solution:*

```
matrix vd = values(d)
m = rows(vd)
loop i=1..m
    scalar sel = vd[i]
    smp1 (d=sel) --restrict --replace
    ols y const x
endloop
smp1 --full
```

*Comment:* The main ingredient here is a loop. You can have `gretl` perform as many instructions as you want for each value of `d`, as long as they are allowed inside a loop. Note, however, that if all you want is descriptive statistics, the `summary` command does have a `--by` option.

### Adding a time series to a panel

*Problem:* You have a panel dataset (comprising observations of  $n$  individuals in each of  $T$  periods) and you want to add a variable which is available in straight time-series form. For example, you want to add annual CPI data to a panel in order to deflate nominal income figures.

In `gretl` a panel is represented in stacked time-series format, so in effect the task is to create a new variable which holds  $n$  stacked copies of the original time series. Let's say the panel comprises 500 individuals observed in the years 1990, 1995 and 2000 ( $n = 500$ ,  $T = 3$ ), and we have these CPI data in the ASCII file `cpi.txt`:

```
date cpi
1990 130.658
1995 152.383
2000 172.192
```

What we need is for the CPI variable in the panel to repeat these three values 500 times.

*Solution:* Simple! With the panel dataset open in `gretl`,

```
append cpi.txt
```

*Comment:* If the length of the time series is the same as the length of the time dimension in the panel (3 in this example), `gretl` will perform the stacking automatically. Rather than using the `append` command you could use the “Append data” item under the File menu in the GUI program. For this to work, your main dataset must be recognized as a panel. This can be arranged via the `setobs` command or the “Dataset structure” item under the Data menu.

## 15.2 Creating/modifying variables

### Generating a dummy variable for a specific observation

*Problem:* Generate  $d_t = 0$  for all observation but one, for which  $d_t = 1$ .

*Solution:*

```
genr d = (t="1984:2")
```

*Comment:* The internal variable `t` is used to refer to observations in string form, so if you have a cross-section sample you may just use `d = (t="123")`; of course, if the dataset has data labels, use the corresponding label. For example, if you open the dataset `mrw.gdt`, supplied with `gretl` among the examples, a dummy variable for Italy could be generated via

```
genr DIta = (t="Italy")
```

Note that this method does not require scripting at all. In fact, you might as well use the GUI Menu “Add/Define new variable” for the same purpose, with the same syntax.

### Generating an ARMA(1,1)

*Problem:* Generate  $y_t = 0.9y_{t-1} + \varepsilon_t - 0.5\varepsilon_{t-1}$ , with  $\varepsilon_t \sim NIID(0, 1)$ .

*Recommended solution:*

```
alpha = 0.9
theta = -0.5
series y = filter(normal(), {1, theta}, alpha)
```

*“Bread and butter” solution:*

```
alpha = 0.9
theta = -0.5
series e = normal()
series y = 0
series y = alpha * y(-1) + e + theta * e(-1)
```

*Comment:* The `filter` function is specifically designed for this purpose so in most cases you’ll want to take advantage of its speed and flexibility. That said, in some cases you may want to generate the series in a manner which is more transparent (maybe for teaching purposes).

In the second solution, the statement `series y = 0` is necessary because the next statement evaluates `y` recursively, so `y[1]` must be set. Note that you must use the keyword `series` here instead of writing `genr y = 0` or simply `y = 0`, to ensure that `y` is a series and not a scalar.

### Recoding a variable

*Problem:* You want to recode a variable by classes. For example, you have the age of a sample of individuals ( $x_i$ ) and you need to compute age classes ( $y_i$ ) as

$$\begin{aligned} y_i &= 1 && \text{for } x_i < 18 \\ y_i &= 2 && \text{for } 18 \leq x_i < 65 \\ y_i &= 3 && \text{for } x_i \geq 65 \end{aligned}$$

*Solution:*

```
series y = 1 + (x >= 18) + (x >= 65)
```

*Comment:* True and false expressions are evaluated as 1 and 0 respectively, so they can be manipulated algebraically as any other number. The same result could also be achieved by using the conditional assignment operator (see below), but in most cases it would probably lead to more convoluted constructs.

### Conditional assignment

*Problem:* Generate  $y_t$  via the following rule:

$$y_t = \begin{cases} x_t & \text{for } d_t > a \\ z_t & \text{for } d_t \leq a \end{cases}$$

*Solution:*

```
series y = (d > a) ? x : z
```

*Comment:* There are several alternatives to the one presented above. One is a brute force solution using loops. Another one, more efficient but still suboptimal, would be

```
series y = (d>a)*x + (d<=a)*z
```

However, the ternary conditional assignment operator is not only the most numerically efficient way to accomplish what we want, it is also remarkably transparent to read when one gets used to it. Some readers may find it helpful to note that the conditional assignment operator works exactly the same way as the =IF() function in spreadsheets.

### Generating a time index for panel datasets

*Problem:* Gretl has a \$unit accessor, but not the equivalent for time. What should I use?

*Solution:*

```
series x = time
```

*Comment:* The special construct `genr time` and its variants are aware of whether a dataset is a panel.

## 15.3 Neat tricks

### Interaction dummies

*Problem:* You want to estimate the model  $y_i = \mathbf{x}_i\beta_1 + \mathbf{z}_i\beta_2 + d_i\beta_3 + (d_i \cdot \mathbf{z}_i)\beta_4 + \varepsilon_i$ , where  $d_i$  is a dummy variable while  $\mathbf{x}_i$  and  $\mathbf{z}_i$  are vectors of explanatory variables.

*Solution:*

```
list X = x1 x2 x3
list Z = z1 z2
list dZ = null
loop foreach i Z
  series d$i = d * $i
  list dZ = dZ d$i
endloop

ols y X Z d dZ
```

*Comment:* It's amazing what string substitution can do for you, isn't it?

**Realized volatility**

*Problem:* Given data by the minute, you want to compute the “realized volatility” for the hour as  $RV_t = \frac{1}{60} \sum_{\tau=1}^{60} y_{t:\tau}^2$ . Imagine your sample starts at time 1:1.

*Solution:*

```
smp1 --full
genr time
genr minute = int(time/60) + 1
genr second = time % 60
setobs minute second --panel
genr rv = psd(y)^2
setobs 1 1
smp1 second=1 --restrict
store foo rv
```

*Comment:* Here we trick `gretl` into thinking that our dataset is a panel dataset, where the minutes are the “units” and the seconds are the “time”; this way, we can take advantage of the special function `psd()`, panel standard deviation. Then we simply drop all observations but one per minute and save the resulting data (`store foo rv` translates as “store in the `gretl` datafile `foo.gdt` the series `rv`”).

**Looping over two paired lists**

*Problem:* Suppose you have two lists with the same number of elements, and you want to apply some command to corresponding elements over a loop.

*Solution:*

```
list L1 = a b c
list L2 = x y z

k1 = 1
loop foreach i L1 --quiet
  k2 = 1
  loop foreach j L2 --quiet
    if k1=k2
      ols $i 0 $j
    endif
    k2++
  endloop
  k1++
endloop
```

*Comment:* The simplest way to achieve the result is to loop over all possible combinations and filter out the unneeded ones via an `if` condition, as above. That said, in some cases variable names can help. For example, if

```
list Lx = x1 x2 x3
list Ly = y1 y2 y3
```

looping over the integers is quite intuitive and certainly more elegant:

```
loop i=1..3
  ols y$i const x$i
endloop
```

## **Part II**

# **Econometric methods**

## Chapter 16

# Robust covariance matrix estimation

### 16.1 Introduction

Consider (once again) the linear regression model

$$y = X\beta + u \quad (16.1)$$

where  $y$  and  $u$  are  $T$ -vectors,  $X$  is a  $T \times k$  matrix of regressors, and  $\beta$  is a  $k$ -vector of parameters. As is well known, the estimator of  $\beta$  given by Ordinary Least Squares (OLS) is

$$\hat{\beta} = (X'X)^{-1}X'y \quad (16.2)$$

If the condition  $E(u|X) = 0$  is satisfied, this is an unbiased estimator; under somewhat weaker conditions the estimator is biased but consistent. It is straightforward to show that when the OLS estimator is unbiased (that is, when  $E(\hat{\beta} - \beta) = 0$ ), its variance is

$$\text{Var}(\hat{\beta}) = E\left((\hat{\beta} - \beta)(\hat{\beta} - \beta)'\right) = (X'X)^{-1}X'\Omega X(X'X)^{-1} \quad (16.3)$$

where  $\Omega = E(uu')$  is the covariance matrix of the error terms.

Under the assumption that the error terms are independently and identically distributed (iid) we can write  $\Omega = \sigma^2 I$ , where  $\sigma^2$  is the (common) variance of the errors (and the covariances are zero). In that case (16.3) simplifies to the “classical” formula,

$$\text{Var}(\hat{\beta}) = \sigma^2 (X'X)^{-1} \quad (16.4)$$

If the iid assumption is not satisfied, two things follow. First, it is possible in principle to construct a more efficient estimator than OLS — for instance some sort of Feasible Generalized Least Squares (FGLS). Second, the simple “classical” formula for the variance of the least squares estimator is no longer correct, and hence the conventional OLS standard errors — which are just the square roots of the diagonal elements of the matrix defined by (16.4) — do not provide valid means of statistical inference.

In the recent history of econometrics there are broadly two approaches to the problem of non-iid errors. The “traditional” approach is to use an FGLS estimator. For example, if the departure from the iid condition takes the form of time-series dependence, and if one believes that this could be modeled as a case of first-order autocorrelation, one might employ an AR(1) estimation method such as Cochrane–Orcutt, Hildreth–Lu, or Prais–Winsten. If the problem is that the error variance is non-constant across observations, one might estimate the variance as a function of the independent variables and then perform weighted least squares, using as weights the reciprocals of the estimated variances.

While these methods are still in use, an alternative approach has found increasing favor: that is, use OLS but compute standard errors (or more generally, covariance matrices) that are robust with respect to deviations from the iid assumption. This is typically combined with an emphasis on using large datasets — large enough that the researcher can place some reliance on the (asymptotic) consistency property of OLS. This approach has been enabled by the availability of cheap computing power. The computation of robust standard errors and the handling of very large datasets were daunting tasks at one time, but now they are unproblematic. The other point favoring the newer methodology is that while FGLS offers an efficiency advantage in principle, it often involves making

additional statistical assumptions which may or may not be justified, which may not be easy to test rigorously, and which may threaten the consistency of the estimator — for example, the “common factor restriction” that is implied by traditional FGLS “corrections” for autocorrelated errors.

James Stock and Mark Watson’s *Introduction to Econometrics* illustrates this approach at the level of undergraduate instruction: many of the datasets they use comprise thousands or tens of thousands of observations; FGLS is downplayed; and robust standard errors are reported as a matter of course. In fact, the discussion of the classical standard errors (labeled “homoskedasticity-only”) is confined to an Appendix.

Against this background it may be useful to set out and discuss all the various options offered by `gretl` in respect of robust covariance matrix estimation. The first point to notice is that `gretl` produces “classical” standard errors by default (in all cases apart from GMM estimation). In script mode you can get robust standard errors by appending the `--robust` flag to estimation commands. In the GUI program the model specification dialog usually contains a “Robust standard errors” check box, along with a “configure” button that is activated when the box is checked. The configure button takes you to a configuration dialog (which can also be reached from the main menu bar: Tools → Preferences → General → HCCME). There you can select from a set of possible robust estimation variants, and can also choose to make robust estimation the default.

The specifics of the available options depend on the nature of the data under consideration — cross-sectional, time series or panel — and also to some extent the choice of estimator. (Although we introduced robust standard errors in the context of OLS above, they may be used in conjunction with other estimators too.) The following three sections of this chapter deal with matters that are specific to the three sorts of data just mentioned. Note that additional details regarding covariance matrix estimation in the context of GMM are given in chapter 21.

We close this introduction with a brief statement of what “robust standard errors” can and cannot achieve. They can provide for asymptotically valid statistical inference in models that are basically correctly specified, but in which the errors are not iid. The “asymptotic” part means that they may be of little use in small samples. The “correct specification” part means that they are not a magic bullet: if the error term is correlated with the regressors, so that the parameter estimates themselves are biased and inconsistent, robust standard errors will not save the day.

## 16.2 Cross-sectional data and the HCCME

With cross-sectional data, the most likely departure from iid errors is heteroskedasticity (non-constant variance).<sup>1</sup> In some cases one may be able to arrive at a judgment regarding the likely form of the heteroskedasticity, and hence to apply a specific correction. The more common case, however, is where the heteroskedasticity is of unknown form. We seek an estimator of the covariance matrix of the parameter estimates that retains its validity, at least asymptotically, in face of unspecified heteroskedasticity. It is not obvious, a priori, that this should be possible, but White (1980) showed that

$$\widehat{\text{Var}}_h(\hat{\beta}) = (X'X)^{-1}X'\hat{\Omega}X(X'X)^{-1} \quad (16.5)$$

does the trick. (As usual in statistics, we need to say “under certain conditions”, but the conditions are not very restrictive.)  $\hat{\Omega}$  is in this context a diagonal matrix, whose non-zero elements may be estimated using squared OLS residuals. White referred to (16.5) as a heteroskedasticity-consistent covariance matrix estimator (HCCME).

Davidson and MacKinnon (2004, chapter 5) offer a useful discussion of several variants on White’s HCCME theme. They refer to the original variant of (16.5) — in which the diagonal elements of  $\hat{\Omega}$  are estimated directly by the squared OLS residuals,  $\hat{u}_i^2$  — as HC0. (The associated standard errors are often called “White’s standard errors”.) The various refinements of White’s proposal share a common point of departure, namely the idea that the squared OLS residuals are likely to be “too

<sup>1</sup>In some specialized contexts spatial autocorrelation may be an issue. `Gretl` does not have any built-in methods to handle this and we will not discuss it here.

small” on average. This point is quite intuitive. The OLS parameter estimates,  $\hat{\beta}$ , satisfy by design the criterion that the sum of squared residuals,

$$\sum \hat{u}_t^2 = \sum (\mathcal{Y}_t - X_t \hat{\beta})^2$$

is minimized for given  $X$  and  $\mathcal{Y}$ . Suppose that  $\hat{\beta} \neq \beta$ . This is almost certain to be the case: even if OLS is not biased, it would be a miracle if the  $\hat{\beta}$  calculated from any finite sample were exactly equal to  $\beta$ . But in that case the sum of squares of the true, unobserved *errors*,  $\sum u_t^2 = \sum (\mathcal{Y}_t - X_t \beta)^2$  is bound to be greater than  $\sum \hat{u}_t^2$ . The elaborated variants on  $HC_0$  take this point on board as follows:

- $HC_1$ : Applies a degrees-of-freedom correction, multiplying the  $HC_0$  matrix by  $T/(T - k)$ .
- $HC_2$ : Instead of using  $\hat{u}_t^2$  for the diagonal elements of  $\hat{\Omega}$ , uses  $\hat{u}_t^2/(1 - h_t)$ , where  $h_t = X_t(X'X)^{-1}X'_t$ , the  $t^{\text{th}}$  diagonal element of the projection matrix,  $P$ , which has the property that  $P \cdot \mathcal{Y} = \hat{\mathcal{Y}}$ . The relevance of  $h_t$  is that if the variance of all the  $u_t$  is  $\sigma^2$ , the expectation of  $\hat{u}_t^2$  is  $\sigma^2(1 - h_t)$ , or in other words, the ratio  $\hat{u}_t^2/(1 - h_t)$  has expectation  $\sigma^2$ . As Davidson and MacKinnon show,  $0 \leq h_t < 1$  for all  $t$ , so this adjustment cannot reduce the the diagonal elements of  $\hat{\Omega}$  and in general revises them upward.
- $HC_3$ : Uses  $\hat{u}_t^2/(1 - h_t)^2$ . The additional factor of  $(1 - h_t)$  in the denominator, relative to  $HC_2$ , may be justified on the grounds that observations with large variances tend to exert a lot of influence on the OLS estimates, so that the corresponding residuals tend to be underestimated. See Davidson and MacKinnon for a fuller explanation.

The relative merits of these variants have been explored by means of both simulations and theoretical analysis. Unfortunately there is not a clear consensus on which is “best”. Davidson and MacKinnon argue that the original  $HC_0$  is likely to perform worse than the others; nonetheless, “White’s standard errors” are reported more often than the more sophisticated variants and therefore, for reasons of comparability,  $HC_0$  is the default HCCME in gretl.

If you wish to use  $HC_1$ ,  $HC_2$  or  $HC_3$  you can arrange for this in either of two ways. In script mode, you can do, for example,

```
set hc_version 2
```

In the GUI program you can go to the HCCME configuration dialog, as noted above, and choose any of these variants to be the default.

### 16.3 Time series data and HAC covariance matrices

Heteroskedasticity may be an issue with time series data too, but it is unlikely to be the only, or even the primary, concern.

One form of heteroskedasticity is common in macroeconomic time series, but is fairly easily dealt with. That is, in the case of strongly trending series such as Gross Domestic Product, aggregate consumption, aggregate investment, and so on, higher levels of the variable in question are likely to be associated with higher variability in absolute terms. The obvious “fix”, employed in many macroeconometric studies, is to use the logs of such series rather than the raw levels. Provided the *proportional* variability of such series remains roughly constant over time, the log transformation is effective.

Other forms of heteroskedasticity may resist the log transformation, but may demand a special treatment distinct from the calculation of robust standard errors. We have in mind here *autoregressive conditional* heteroskedasticity, for example in the behavior of asset prices, where large disturbances to the market may usher in periods of increased volatility. Such phenomena call for specific estimation strategies, such as GARCH (see chapter 24).



Despite the points made above, some residual degree of heteroskedasticity may be present in time series data: the key point is that in most cases it is likely to be combined with serial correlation (autocorrelation), hence demanding a special treatment. In White's approach,  $\hat{\Omega}$ , the estimated covariance matrix of the  $u_t$ , remains conveniently diagonal: the variances,  $E(u_t^2)$ , may differ by  $t$  but the covariances,  $E(u_t u_s)$ , are all zero. Autocorrelation in time series data means that at least some of the off-diagonal elements of  $\hat{\Omega}$  should be non-zero. This introduces a substantial complication and requires another piece of terminology; estimates of the covariance matrix that are asymptotically valid in face of both heteroskedasticity and autocorrelation of the error process are termed HAC (heteroskedasticity and autocorrelation consistent).

The issue of HAC estimation is treated in more technical terms in chapter 21. Here we try to convey some of the intuition at a more basic level. We begin with a general comment: residual autocorrelation is not so much a property of the data, as a symptom of an inadequate model. Data may be persistent though time, and if we fit a model that does not take this aspect into account properly, we end up with a model with autocorrelated disturbances. Conversely, it is often possible to mitigate or even eliminate the problem of autocorrelation by including relevant lagged variables in a time series model, or in other words, by specifying the dynamics of the model more fully. HAC estimation should *not* be seen as the first resort in dealing with an autocorrelated error process.

That said, the “obvious” extension of White's HCCME to the case of autocorrelated errors would seem to be this: estimate the off-diagonal elements of  $\hat{\Omega}$  (that is, the autocovariances,  $E(u_t u_s)$ ) using, once again, the appropriate OLS residuals:  $\hat{w}_{ts} = \hat{u}_t \hat{u}_s$ . This is basically right, but demands an important amendment. We seek a *consistent* estimator, one that converges towards the true  $\Omega$  as the sample size tends towards infinity. This can't work if we allow unbounded serial dependence. Bigger samples will enable us to estimate more of the true  $\omega_{ts}$  elements (that is, for  $t$  and  $s$  more widely separated in time) but will *not* contribute ever-increasing information regarding the maximally separated  $\omega_{ts}$  pairs, since the maximal separation itself grows with the sample size. To ensure consistency, we have to confine our attention to processes exhibiting temporally limited dependence, or in other words cut off the computation of the  $\hat{w}_{ts}$  values at some maximum value of  $p = t - s$  (where  $p$  is treated as an increasing function of the sample size,  $T$ , although it cannot increase in proportion to  $T$ ).

The simplest variant of this idea is to truncate the computation at some finite lag order  $p$ , where  $p$  grows as, say,  $T^{1/4}$ . The trouble with this is that the resulting  $\hat{\Omega}$  may not be a positive definite matrix. In practical terms, we may end up with negative estimated variances. One solution to this problem is offered by The Newey-West estimator (Newey and West, 1987), which assigns declining weights to the sample autocovariances as the temporal separation increases.

To understand this point it is helpful to look more closely at the covariance matrix given in (16.5), namely,

$$(X'X)^{-1}(X'\hat{\Omega}X)(X'X)^{-1}$$

This is known as a “sandwich” estimator. The bread, which appears on both sides, is  $(X'X)^{-1}$ . This is a  $k \times k$  matrix, and is also the key ingredient in the computation of the classical covariance matrix. The filling in the sandwich is

$$\begin{array}{ccccc} \hat{\Sigma} & = & X' & \hat{\Omega} & X \\ (k \times k) & & (k \times T) & (T \times T) & (T \times k) \end{array}$$

Since  $\Omega = E(uu')$ , the matrix being estimated here can also be written as

$$\Sigma = E(X'u u'X)$$

which expresses  $\Sigma$  as the long-run covariance of the random  $k$ -vector  $X'u$ .

From a computational point of view, it is not necessary or desirable to store the (potentially very large)  $T \times T$  matrix  $\hat{\Omega}$  as such. Rather, one computes the sandwich filling by summation as

$$\hat{\Sigma} = \hat{\Gamma}(0) + \sum_{j=1}^p w_j (\hat{\Gamma}(j) + \hat{\Gamma}'(j))$$

where the  $k \times k$  sample autocovariance matrix  $\hat{\Gamma}(j)$ , for  $j \geq 0$ , is given by

$$\hat{\Gamma}(j) = \frac{1}{T} \sum_{t=j+1}^T \hat{u}_t \hat{u}_{t-j}' X_t' X_{t-j}$$

and  $w_j$  is the weight given to the autocovariance at lag  $j > 0$ .

This leaves two questions. How exactly do we determine the maximum lag length or “bandwidth”,  $p$ , of the HAC estimator? And how exactly are the weights  $w_j$  to be determined? We will return to the (difficult) question of the bandwidth shortly. As regards the weights, *Gretl* offers three variants. The default is the Bartlett kernel, as used by Newey and West. This sets

$$w_j = \begin{cases} 1 - \frac{j}{p+1} & j \leq p \\ 0 & j > p \end{cases}$$

so the weights decline linearly as  $j$  increases. The other two options are the Parzen kernel and the Quadratic Spectral (QS) kernel. For the Parzen kernel,

$$w_j = \begin{cases} 1 - 6a_j^2 + 6a_j^3 & 0 \leq a_j \leq 0.5 \\ 2(1 - a_j)^3 & 0.5 < a_j \leq 1 \\ 0 & a_j > 1 \end{cases}$$

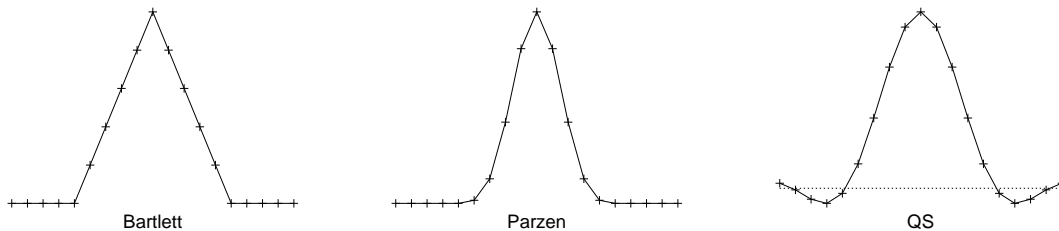
where  $a_j = j/(p+1)$ , and for the QS kernel,

$$w_j = \frac{25}{12\pi^2 d_j^2} \left( \frac{\sin m_j}{m_j} - \cos m_j \right)$$

where  $d_j = j/p$  and  $m_j = 6\pi d_j/5$ .

Figure 16.1 shows the weights generated by these kernels, for  $p = 4$  and  $j = 1$  to 9.

Figure 16.1: Three HAC kernels



In *gretl* you select the kernel using the `set` command with the `hac_kernel` parameter:

```
set hac_kernel parzen
set hac_kernel qs
set hac_kernel bartlett
```

### Selecting the HAC bandwidth

The asymptotic theory developed by Newey, West and others tells us in general terms how the HAC bandwidth,  $p$ , should grow with the sample size,  $T$  — that is,  $p$  should grow in proportion to some fractional power of  $T$ . Unfortunately this is of little help to the applied econometrician, working with a given dataset of fixed size. Various rules of thumb have been suggested, and *gretl* implements two such. The default is  $p = 0.75T^{1/3}$ , as recommended by [Stock and Watson \(2003\)](#). An alternative is  $p = 4(T/100)^{2/9}$ , as in [Wooldridge \(2002b\)](#). In each case one takes the integer part of the result. These variants are labeled `nw1` and `nw2` respectively, in the context of the `set` command with the `hac_lag` parameter. That is, you can switch to the version given by Wooldridge with

```
set hac_lag nw2
```

As shown in Table 16.1 the choice between nw1 and nw2 does not make a great deal of difference.

$T$	$p$ (nw1)	$p$ (nw2)
50	2	3
100	3	4
150	3	4
200	4	4
300	5	5
400	5	5

**Table 16.1:** HAC bandwidth: two rules of thumb

You also have the option of specifying a fixed numerical value for  $p$ , as in

```
set hac_lag 6
```

In addition you can set a distinct bandwidth for use with the Quadratic Spectral kernel (since this need not be an integer). For example,

```
set qs_bandwidth 3.5
```

### Prewhitening and data-based bandwidth selection

An alternative approach is to deal with residual autocorrelation by attacking the problem from two sides. The intuition behind the technique known as *VAR prewhitening* (Andrews and Monahan, 1992) can be illustrated by a simple example. Let  $x_t$  be a sequence of first-order autocorrelated random variables

$$x_t = \rho x_{t-1} + u_t$$

The long-run variance of  $x_t$  can be shown to be

$$V_{LR}(x_t) = \frac{V_{LR}(u_t)}{(1 - \rho)^2}$$

In most cases,  $u_t$  is likely to be less autocorrelated than  $x_t$ , so a smaller bandwidth should suffice. Estimation of  $V_{LR}(x_t)$  can therefore proceed in three steps: (1) estimate  $\rho$ ; (2) obtain a HAC estimate of  $\hat{u}_t = x_t - \hat{\rho}x_{t-1}$ ; and (3) divide the result by  $(1 - \rho)^2$ .

The application of the above concept to our problem implies estimating a finite-order Vector Autoregression (VAR) on the vector variables  $\xi_t = X_t \hat{u}_t$ . In general, the VAR can be of any order, but in most cases 1 is sufficient; the aim is not to build a watertight model for  $\xi_t$ , but just to “mop up” a substantial part of the autocorrelation. Hence, the following VAR is estimated

$$\xi_t = A\xi_{t-1} + \varepsilon_t$$

Then an estimate of the matrix  $X'\Omega X$  can be recovered via

$$(I - \hat{A})^{-1} \hat{\Sigma}_\varepsilon (I - \hat{A}')^{-1}$$

where  $\hat{\Sigma}_\varepsilon$  is any HAC estimator, applied to the VAR residuals.

You can ask for prewhitening in gretl using

```
set hac_prewhiten on
```

There is at present no mechanism for specifying an order other than 1 for the initial VAR.

A further refinement is available in this context, namely data-based bandwidth selection. It makes intuitive sense that the HAC bandwidth should not simply be based on the size of the sample, but should somehow take into account the time-series properties of the data (and also the kernel chosen). A nonparametric method for doing this was proposed by [Newey and West \(1994\)](#); a good concise account of the method is given in [Hall \(2005\)](#). This option can be invoked in gretl via

```
set hac_lag nw3
```

This option is the default when prewhitening is selected, but you can override it by giving a specific numerical value for `hac_lag`.

Even the Newey–West data-based method does not fully pin down the bandwidth for any particular sample. The first step involves calculating a series of residual covariances. The length of this series is given as a function of the sample size, but only up to a scalar multiple — for example, it is given as  $O(T^{2/9})$  for the Bartlett kernel. Gretl uses an implied multiple of 1.

### VARs: a special case

A well-specified vector autoregression (VAR) will generally include enough lags of the dependent variables to obviate the problem of residual autocorrelation, in which case HAC estimation is redundant — although there may still be a need to correct for heteroskedasticity. For that reason plain HCCME, and not HAC, is the default when the `--robust` flag is given in the context of the `var` command. However, if for some reason you need HAC you can force the issue by giving the option `--robust-hac`.

## 16.4 Special issues with panel data

Since panel data have both a time-series and a cross-sectional dimension one might expect that, in general, robust estimation of the covariance matrix would require handling both heteroskedasticity and autocorrelation (the HAC approach). In addition, some special features of panel data require attention.

- The variance of the error term may differ across the cross-sectional units.
- The covariance of the errors across the units may be non-zero in each time period.
- If the “between” variation is not removed, the errors may exhibit autocorrelation, not in the usual time-series sense but in the sense that the mean error for unit  $i$  may differ from that of unit  $j$ . (This is particularly relevant when estimation is by pooled OLS.)

Gretl currently offers two robust covariance matrix estimators specifically for panel data. These are available for models estimated via fixed effects, pooled OLS, and pooled two-stage least squares. The default robust estimator is that suggested by [Arellano \(2003\)](#), which is HAC provided the panel is of the “large  $n$ , small  $T$ ” variety (that is, many units are observed in relatively few periods). The Arellano estimator is

$$\hat{\Sigma}_A = (X'X)^{-1} \left( \sum_{i=1}^n X_i' \hat{u}_i \hat{u}_i' X_i \right) (X'X)^{-1}$$

where  $X$  is the matrix of regressors (with the group means subtracted, in the case of fixed effects)  $\hat{u}_i$  denotes the vector of residuals for unit  $i$ , and  $n$  is the number of cross-sectional units.<sup>2</sup> [Cameron and Trivedi \(2005\)](#) make a strong case for using this estimator; they note that the ordinary White HCCME can produce misleadingly small standard errors in the panel context because it fails to take

<sup>2</sup>This variance estimator is also known as the “clustered (over entities)” estimator.

autocorrelation into account. In addition [Stock and Watson \(2008\)](#) show that the White HCCME is inconsistent in the fixed-effects panel context for fixed  $T > 2$ .

In cases where autocorrelation is not an issue the estimator proposed by [Beck and Katz \(1995\)](#) and discussed by [Greene \(2003, chapter 13\)](#) may be appropriate. This estimator, which takes into account contemporaneous correlation across the units and heteroskedasticity by unit, is

$$\hat{\Sigma}_{BK} = (X'X)^{-1} \left( \sum_{i=1}^n \sum_{j=1}^n \hat{\sigma}_{ij} X_i' X_j \right) (X'X)^{-1}$$

The covariances  $\hat{\sigma}_{ij}$  are estimated via

$$\hat{\sigma}_{ij} = \frac{\hat{u}_i' \hat{u}_j}{T}$$

where  $T$  is the length of the time series for each unit. Beck and Katz call the associated standard errors “Panel-Corrected Standard Errors” (PCSE). This estimator can be invoked in `gretl` via the command

```
set pcse on
```

The Arellano default can be re-established via

```
set pcse off
```

(Note that regardless of the `pcse` setting, the robust estimator is not used unless the `--robust` flag is given, or the “Robust” box is checked in the GUI program.)

## 16.5 The cluster-robust estimator

One further variance estimator is available in `gretl`, namely the “cluster-robust” estimator. This may be appropriate (for cross-sectional data, mostly) when the observations naturally fall into groups or clusters, and one suspects that the error term may exhibit dependency within the clusters and/or have a variance that differs across clusters. Such clusters may be binary (e.g. employed versus unemployed workers), categorical with several values (e.g. products grouped by manufacturer) or ordinal (e.g. individuals with low, middle or high education levels).

For linear regression models estimated via least squares the cluster estimator is defined as

$$\hat{\Sigma}_C = (X'X)^{-1} \left( \sum_{j=1}^m X_j' \hat{u}_j \hat{u}_j' X_j \right) (X'X)^{-1}$$

where  $m$  denotes the number of clusters, and  $X_j$  and  $\hat{u}_j$  denote, respectively, the matrix of regressors and the vector of residuals that fall within cluster  $j$ . As noted above, the Arellano variance estimator for panel data models is a special case of this, where the clustering is by panel unit.

For models estimated by the method of Maximum Likelihood (in which case the standard variance estimator is the inverse of the negative Hessian,  $H$ ), the cluster estimator is

$$\hat{\Sigma}_C = H^{-1} \left( \sum_{j=1}^m G_j' G_j \right) H^{-1}$$

where  $G_j$  is the sum of the “score” (that is, the derivative of the loglikelihood with respect to the parameter estimates) across the observations falling within cluster  $j$ .

It is common to apply a degrees of freedom adjustment to these estimators (otherwise the variance may appear misleadingly small in comparison with other estimators, if the number of clusters is small). In the least squares case the factor is  $(m/(m-1)) \times (n-1)/(n-k)$ , where  $n$  is the total number of observations and  $k$  is the number of parameters estimated; in the case of ML estimation the factor is just  $m/(m-1)$ .

**Availability and syntax**

The cluster-robust estimator is currently available for models estimated via OLS and TSLS, and also for most ML estimators other than those specialized for time-series data: binary logit and probit, ordered logit and probit, multinomial logit, Tobit, interval regression, biprobit, count models and duration models. In all cases the syntax is the same: you give the option flag `--cluster=` followed by the name of the series to be used to define the clusters, as in

```
ols y 0 x1 x2 --cluster=cvar
```

The specified clustering variable must (a) be defined (not missing) at all observations used in estimating the model and (b) take on at least two distinct values over the estimation range. The clusters are defined as sets of observations having a common value for the clustering variable. It is generally expected that the number of clusters is substantially less than the total number of observations.

## Chapter 17

# Panel data

### 17.1 Estimation of panel models

#### Pooled Ordinary Least Squares

The simplest estimator for panel data is pooled OLS. In most cases this is unlikely to be adequate, but it provides a baseline for comparison with more complex estimators.

If you estimate a model on panel data using OLS an additional test item becomes available. In the GUI model window this is the item “panel diagnostics” under the Tests menu; the script counterpart is the `hausman` command.

To take advantage of this test, you should specify a model without any dummy variables representing cross-sectional units. The test compares pooled OLS against the principal alternatives, the fixed effects and random effects models. These alternatives are explained in the following section.

#### The fixed and random effects models

In gretl version 1.6.0 and higher, the fixed and random effects models for panel data can be estimated in their own right. In the graphical interface these options are found under the menu item “Model/Panel/Fixed and random effects”. In the command-line interface one uses the `panel` command, with or without the `--random-effects` option.

This section explains the nature of these models and comments on their estimation via gretl.

The pooled OLS specification may be written as

$$y_{it} = X_{it}\beta + u_{it} \quad (17.1)$$

where  $y_{it}$  is the observation on the dependent variable for cross-sectional unit  $i$  in period  $t$ ,  $X_{it}$  is a  $1 \times k$  vector of independent variables observed for unit  $i$  in period  $t$ ,  $\beta$  is a  $k \times 1$  vector of parameters, and  $u_{it}$  is an error or disturbance term specific to unit  $i$  in period  $t$ .

The fixed and random effects models have in common that they decompose the unitary pooled error term,  $u_{it}$ . For the *fixed effects* model we write  $u_{it} = \alpha_i + \varepsilon_{it}$ , yielding

$$y_{it} = X_{it}\beta + \alpha_i + \varepsilon_{it} \quad (17.2)$$

That is, we decompose  $u_{it}$  into a unit-specific and time-invariant component,  $\alpha_i$ , and an observation-specific error,  $\varepsilon_{it}$ .<sup>1</sup> The  $\alpha_i$ s are then treated as fixed parameters (in effect, unit-specific  $y$ -intercepts), which are to be estimated. This can be done by including a dummy variable for each cross-sectional unit (and suppressing the global constant). This is sometimes called the Least Squares Dummy Variables (LSDV) method. Alternatively, one can subtract the group mean from each of variables and estimate a model without a constant. In the latter case the dependent variable may be written as

$$\tilde{y}_{it} = y_{it} - \bar{y}_i$$

The “group mean”,  $\bar{y}_i$ , is defined as

$$\bar{y}_i = \frac{1}{T_i} \sum_{t=1}^{T_i} y_{it}$$

---

<sup>1</sup>It is possible to break a third component out of  $u_{it}$ , namely  $w_t$ , a shock that is time-specific but common to all the units in a given period. In the interest of simplicity we do not pursue that option here.

where  $T_i$  is the number of observations for unit  $i$ . An exactly analogous formulation applies to the independent variables. Given parameter estimates,  $\hat{\beta}$ , obtained using such de-meaned data we can recover estimates of the  $\alpha_i$ s using

$$\hat{\alpha}_i = \frac{1}{T_i} \sum_{t=1}^{T_i} (y_{it} - X_{it}\hat{\beta})$$

These two methods (LSDV, and using de-meaned data) are numerically equivalent. Gretl takes the approach of de-meaning the data. If you have a small number of cross-sectional units, a large number of time-series observations per unit, and a large number of regressors, it is more economical in terms of computer memory to use LSDV. If need be you can easily implement this manually. For example,

```
genr unitdum
ols y x du_*
```

(See Chapter 6 for details on `unitdum`).

The  $\hat{\alpha}_i$  estimates are not printed as part of the standard model output in gretl (there may be a large number of these, and typically they are not of much inherent interest). However you can retrieve them after estimation of the fixed effects model if you wish. In the graphical interface, go to the “Save” menu in the model window and select “per-unit constants”. In command-line mode, you can do `genr newname = $ahat`, where *newname* is the name you want to give the series.

For the *random effects* model we write  $u_{it} = v_i + \varepsilon_{it}$ , so the model becomes

$$y_{it} = X_{it}\beta + v_i + \varepsilon_{it} \quad (17.3)$$

In contrast to the fixed effects model, the  $v_i$ s are not treated as fixed parameters, but as random drawings from a given probability distribution.

The celebrated Gauss–Markov theorem, according to which OLS is the best linear unbiased estimator (BLUE), depends on the assumption that the error term is independently and identically distributed (IID). In the panel context, the IID assumption means that  $E(u_{it}^2)$ , in relation to equation 17.1, equals a constant,  $\sigma_u^2$ , for all  $i$  and  $t$ , while the covariance  $E(u_{is}u_{it})$  equals zero for all  $s \neq t$  and the covariance  $E(u_{jt}u_{it})$  equals zero for all  $j \neq i$ .

If these assumptions are not met — and they are unlikely to be met in the context of panel data — OLS is not the most efficient estimator. Greater efficiency may be gained using generalized least squares (GLS), taking into account the covariance structure of the error term.

Consider observations on a given unit  $i$  at two different times  $s$  and  $t$ . From the hypotheses above it can be worked out that  $\text{Var}(u_{is}) = \text{Var}(u_{it}) = \sigma_v^2 + \sigma_\varepsilon^2$ , while the covariance between  $u_{is}$  and  $u_{it}$  is given by  $E(u_{is}u_{it}) = \sigma_v^2$ .

In matrix notation, we may group all the  $T_i$  observations for unit  $i$  into the vector  $\mathbf{y}_i$  and write it as

$$\mathbf{y}_i = \mathbf{X}_i\beta + \mathbf{u}_i \quad (17.4)$$

The vector  $\mathbf{u}_i$ , which includes all the disturbances for individual  $i$ , has a variance–covariance matrix given by

$$\text{Var}(\mathbf{u}_i) = \Sigma_i = \sigma_\varepsilon^2 I + \sigma_v^2 J \quad (17.5)$$

where  $J$  is a square matrix with all elements equal to 1. It can be shown that the matrix

$$K_i = I - \frac{\theta_i}{T_i} J,$$

where  $\theta_i = 1 - \sqrt{\frac{\sigma_\varepsilon^2}{\sigma_\varepsilon^2 + T_i \sigma_v^2}}$ , has the property

$$K_i \Sigma_i K_i' = \sigma_\varepsilon^2 I$$



It follows that the transformed system

$$K_i \mathbf{y}_i = K_i \mathbf{X}_i \boldsymbol{\beta} + K_i \mathbf{u}_i \quad (17.6)$$

satisfies the Gauss–Markov conditions, and OLS estimation of (17.6) provides efficient inference. But since

$$K_i \mathbf{y}_i = \mathbf{y}_i - \theta_i \bar{\mathbf{y}}_i$$

GLS estimation is equivalent to OLS using “quasi-demeaned” variables; that is, variables from which we subtract a fraction  $\theta$  of their average.<sup>2</sup> Notice that for  $\sigma_\varepsilon^2 \rightarrow 0$ ,  $\theta \rightarrow 1$ , while for  $\sigma_v^2 \rightarrow 0$ ,  $\theta \rightarrow 0$ . This means that if all the variance is attributable to the individual effects, then the fixed effects estimator is optimal; if, on the other hand, individual effects are negligible, then pooled OLS turns out, unsurprisingly, to be the optimal estimator.

To implement the GLS approach we need to calculate  $\theta$ , which in turn requires estimates of the variances  $\sigma_\varepsilon^2$  and  $\sigma_v^2$ . (These are often referred to as the “within” and “between” variances respectively, since the former refers to variation within each cross-sectional unit and the latter to variation between the units). Several means of estimating these magnitudes have been suggested in the literature (see Baltagi, 1995); by default *gretl* uses the method of Swamy and Arora (1972):  $\sigma_\varepsilon^2$  is estimated by the residual variance from the fixed effects model, and the sum  $\sigma_\varepsilon^2 + T_i \sigma_v^2$  is estimated as  $T_i$  times the residual variance from the “between” estimator,

$$\bar{\mathbf{y}}_i = \bar{\mathbf{X}}_i \boldsymbol{\beta} + e_i$$

The latter regression is implemented by constructing a data set consisting of the group means of all the relevant variables. Alternatively, if the `--nerlove` option is given, *gretl* uses the method suggested by Nerlove (1971). In this case  $\sigma_v^2$  is estimated as the sample variance of the fixed effects,

$$\hat{\sigma}_v^2 = \frac{1}{n-1} \sum_{i=1}^n (\alpha_i - \bar{\alpha})^2$$

where  $n$  is the number of individuals and  $\bar{\alpha}$  is the mean of the fixed effects.

### Choice of estimator

Which panel method should one use, fixed effects or random effects?

One way of answering this question is in relation to the nature of the data set. If the panel comprises observations on a fixed and relatively small set of units of interest (say, the member states of the European Union), there is a presumption in favor of fixed effects. If it comprises observations on a large number of randomly selected individuals (as in many epidemiological and other longitudinal studies), there is a presumption in favor of random effects.

Besides this general heuristic, however, various statistical issues must be taken into account.

1. Some panel data sets contain variables whose values are specific to the cross-sectional unit but which do not vary over time. If you want to include such variables in the model, the fixed effects option is simply not available. When the fixed effects approach is implemented using dummy variables, the problem is that the time-invariant variables are perfectly collinear with the per-unit dummies. When using the approach of subtracting the group means, the issue is that after de-meaning these variables are nothing but zeros.
2. A somewhat analogous prohibition applies to the random effects estimator. This estimator is in effect a matrix-weighted average of pooled OLS and the “between” estimator. Suppose we have observations on  $n$  units or individuals and there are  $k$  independent variables of interest. If  $k > n$ , the “between” estimator is undefined — since we have only  $n$  effective observations — and hence so is the random effects estimator.

<sup>2</sup>In a balanced panel, the value of  $\theta$  is common to all individuals, otherwise it differs depending on the value of  $T_i$ .

If one does not fall foul of one or other of the prohibitions mentioned above, the choice between fixed effects and random effects may be expressed in terms of the two econometric *desiderata*, efficiency and consistency.

From a purely statistical viewpoint, we could say that there is a tradeoff between robustness and efficiency. In the fixed effects approach, we do not make any hypotheses on the “group effects” (that is, the time-invariant differences in mean between the groups) beyond the fact that they exist — and that can be tested; see below. As a consequence, once these effects are swept out by taking deviations from the group means, the remaining parameters can be estimated.

On the other hand, the random effects approach attempts to model the group effects as drawings from a probability distribution instead of removing them. This requires that individual effects are representable as a legitimate part of the disturbance term, that is, zero-mean random variables, uncorrelated with the regressors.

As a consequence, the fixed-effects estimator “always works”, but at the cost of not being able to estimate the effect of time-invariant regressors. The richer hypothesis set of the random-effects estimator ensures that parameters for time-invariant regressors can be estimated, and that estimation of the parameters for time-varying regressors is carried out more efficiently. These advantages, though, are tied to the validity of the additional hypotheses. If, for example, there is reason to think that individual effects may be correlated with some of the explanatory variables, then the random-effects estimator would be inconsistent, while fixed-effects estimates would still be valid. It is precisely on this principle that the Hausman test is built (see below): if the fixed- and random-effects estimates agree, to within the usual statistical margin of error, there is no reason to think the additional hypotheses invalid, and as a consequence, no reason *not* to use the more efficient RE estimator.

### Testing panel models

If you estimate a fixed effects or random effects model in the graphical interface, you may notice that the number of items available under the “Tests” menu in the model window is relatively limited. Panel models carry certain complications that make it difficult to implement all of the tests one expects to see for models estimated on straight time-series or cross-sectional data.

Nonetheless, various panel-specific tests are printed along with the parameter estimates as a matter of course, as follows.

When you estimate a model using *fixed effects*, you automatically get an  $F$ -test for the null hypothesis that the cross-sectional units all have a common intercept. That is to say that all the  $\alpha_i$ s are equal, in which case the pooled model (17.1), with a column of 1s included in the  $X$  matrix, is adequate.

When you estimate using *random effects*, the Breusch–Pagan and Hausman tests are presented automatically.

The Breusch–Pagan test is the counterpart to the  $F$ -test mentioned above. The null hypothesis is that the variance of  $\nu_i$  in equation (17.3) equals zero; if this hypothesis is not rejected, then again we conclude that the simple pooled model is adequate.

The Hausman test probes the consistency of the GLS estimates. The null hypothesis is that these estimates are consistent — that is, that the requirement of orthogonality of the  $\nu_i$  and the  $X_i$  is satisfied. The test is based on a measure,  $H$ , of the “distance” between the fixed-effects and random-effects estimates, constructed such that under the null it follows the  $\chi^2$  distribution with degrees of freedom equal to the number of time-varying regressors in the matrix  $X$ . If the value of  $H$  is “large” this suggests that the random effects estimator is not consistent and the fixed-effects model is preferable.

There are two ways of calculating  $H$ , the matrix-difference method and the regression method. The procedure for the matrix-difference method is this:

- Collect the fixed-effects estimates in a vector  $\tilde{\beta}$  and the corresponding random-effects estimates in  $\hat{\beta}$ , then form the difference vector  $(\tilde{\beta} - \hat{\beta})$ .
- Form the covariance matrix of the difference vector as  $\text{Var}(\tilde{\beta} - \hat{\beta}) = \text{Var}(\tilde{\beta}) - \text{Var}(\hat{\beta}) = \Psi$ , where  $\text{Var}(\tilde{\beta})$  and  $\text{Var}(\hat{\beta})$  are estimated by the sample variance matrices of the fixed- and random-effects models respectively.<sup>3</sup>
- Compute  $H = (\tilde{\beta} - \hat{\beta})' \Psi^{-1} (\tilde{\beta} - \hat{\beta})$ .

Given the relative efficiencies of  $\tilde{\beta}$  and  $\hat{\beta}$ , the matrix  $\Psi$  “should be” positive definite, in which case  $H$  is positive, but in finite samples this is not guaranteed and of course a negative  $\chi^2$  value is not admissible. The regression method avoids this potential problem. The procedure is:

- Treat the random-effects model as the restricted model, and record its sum of squared residuals as  $\text{SSR}_r$ .
- Estimate via OLS an unrestricted model in which the dependent variable is quasi-demeaned  $y$  and the regressors include both quasi-demeaned  $X$  (as in the RE model) and the de-meaned variants of all the time-varying variables (i.e. the fixed-effects regressors); record the sum of squared residuals from this model as  $\text{SSR}_u$ .
- Compute  $H = n (\text{SSR}_r - \text{SSR}_u) / \text{SSR}_u$ , where  $n$  is the total number of observations used. On this variant  $H$  cannot be negative, since adding additional regressors to the RE model cannot raise the SSR.

By default `gretl` computes the Hausman test via the regression method, but it uses the matrix-difference method if you pass the option `--matrix-diff` to the `panel` command.

### Robust standard errors

For most estimators, `gretl` offers the option of computing an estimate of the covariance matrix that is robust with respect to heteroskedasticity and/or autocorrelation (and hence also robust standard errors). In the case of panel data, robust covariance matrix estimators are available for the pooled and fixed effects model but not currently for random effects. Please see section 16.4 for details.

## 17.2 Autoregressive panel models

Special problems arise when a lag of the dependent variable is included among the regressors in a panel model. Consider a dynamic variant of the pooled model (17.1):

$$y_{it} = X_{it}\beta + \rho y_{it-1} + u_{it} \quad (17.7)$$

First, if the error  $u_{it}$  includes a group effect,  $v_i$ , then  $y_{it-1}$  is bound to be correlated with the error, since the value of  $v_i$  affects  $y_i$  at all  $t$ . That means that OLS applied to (17.7) will be inconsistent as well as inefficient. The fixed-effects model sweeps out the group effects and so overcomes this particular problem, but a subtler issue remains, which applies to both fixed and random effects estimation. Consider the de-meaned representation of fixed effects, as applied to the dynamic model,

$$\tilde{y}_{it} = \tilde{X}_{it}\beta + \rho \tilde{y}_{i,t-1} + \varepsilon_{it}$$

where  $\tilde{y}_{it} = y_{it} - \bar{y}_i$  and  $\varepsilon_{it} = u_{it} - \bar{u}_i$  (or  $u_{it} - \alpha_i$ , using the notation of equation 17.2). The trouble is that  $\tilde{y}_{i,t-1}$  will be correlated with  $\varepsilon_{it}$  via the group mean,  $\bar{y}_i$ . The disturbance  $\varepsilon_{it}$  influences  $y_{it}$  directly, which influences  $\bar{y}_i$ , which, by construction, affects the value of  $\tilde{y}_{it}$  for all  $t$ . The same issue arises in relation to the quasi-demeaning used for random effects. Estimators which ignore

<sup>3</sup>Hausman (1978) showed that the covariance of the difference takes this simple form when  $\hat{\beta}$  is an efficient estimator and  $\tilde{\beta}$  is inefficient.

this correlation will be consistent only as  $T \rightarrow \infty$  (in which case the marginal effect of  $\varepsilon_{it}$  on the group mean of  $y$  tends to vanish).

One strategy for handling this problem, and producing consistent estimates of  $\beta$  and  $\rho$ , was proposed by Anderson and Hsiao (1981). Instead of de-meaning the data, they suggest taking the first difference of (17.7), an alternative tactic for sweeping out the group effects:

$$\Delta y_{it} = \Delta X_{it}\beta + \rho\Delta y_{i,t-1} + \eta_{it} \quad (17.8)$$

where  $\eta_{it} = \Delta u_{it} = \Delta(v_i + \varepsilon_{it}) = \varepsilon_{it} - \varepsilon_{i,t-1}$ . We're not in the clear yet, given the structure of the error  $\eta_{it}$ : the disturbance  $\varepsilon_{i,t-1}$  is an influence on both  $\eta_{it}$  and  $\Delta y_{i,t-1} = y_{it} - y_{i,t-1}$ . The next step is then to find an instrument for the “contaminated”  $\Delta y_{i,t-1}$ . Anderson and Hsiao suggest using either  $y_{i,t-2}$  or  $\Delta y_{i,t-2}$ , both of which will be uncorrelated with  $\eta_{it}$  provided that the underlying errors,  $\varepsilon_{it}$ , are not themselves serially correlated.

The Anderson-Hsiao estimator is not provided as a built-in function in gretl, since gretl's sensible handling of lags and differences for panel data makes it a simple application of regression with instrumental variables — see Example 17.1, which is based on a study of country growth rates by Nerlove (1999).<sup>4</sup>

**Example 17.1:** The Anderson-Hsiao estimator for a dynamic panel model

---

```
# Penn World Table data as used by Nerlove
open penngrow.gdt
# Fixed effects (for comparison)
panel Y 0 Y(-1) X
# Random effects (for comparison)
panel Y 0 Y(-1) X --random-effects
# take differences of all variables
diff Y X
# Anderson-Hsiao, using Y(-2) as instrument
tsls d_Y d_Y(-1) d_X ; 0 d_X Y(-2)
# Anderson-Hsiao, using d_Y(-2) as instrument
tsls d_Y d_Y(-1) d_X ; 0 d_X d_Y(-2)
```

---

Although the Anderson-Hsiao estimator is consistent, it is not most efficient: it does not make the fullest use of the available instruments for  $\Delta y_{i,t-1}$ , nor does it take into account the differenced structure of the error  $\eta_{it}$ . It is improved upon by the methods of Arellano and Bond (1991) and Blundell and Bond (1998). These methods are taken up in the next chapter.

---

<sup>4</sup>Also see Clint Cummins' benchmarks page, <http://www.stanford.edu/~clint/bench/>.

## Chapter 18

# Dynamic panel models

As of `gretl` version 1.9.2, the primary command for estimating dynamic panel models is `dpanel`. The closely related `arbond` command has been available for some time, and is still present, but whereas `arbond` only supports the so-called “difference” estimator ([Arellano and Bond, 1991](#)), `dpanel` in addition offers the “system” estimator ([Blundell and Bond, 1998](#)), which has become the method of choice in the applied literature.

### 18.1 Introduction

#### Notation

A dynamic linear panel data model can be represented as follows (in notation based on [Arellano \(2003\)](#)):

$$y_{it} = \alpha y_{i,t-1} + \beta' x_{it} + \eta_i + v_{it} \quad (18.1)$$

The main idea on which the difference estimator is based is to get rid of the individual effect via differencing:<sup>1</sup> first-differencing eq. (18.1) yields

$$\Delta y_{it} = \alpha \Delta y_{i,t-1} + \beta' \Delta x_{it} + \Delta v_{it} = y' W_{it} + \Delta v_{it}, \quad (18.2)$$

in obvious notation. The error term of (18.2) is, by construction, autocorrelated and also correlated with the lagged dependent variable, so an estimator that takes both issues into account is needed. The endogeneity issue is solved by noting that all values of  $y_{i,t-k}$ , with  $k > 1$  can be used as instruments for  $\Delta y_{i,t-1}$ : unobserved values of  $y_{i,t-k}$  (because they could be missing, or pre-sample) can safely be substituted with 0. In the language of GMM, this amounts to using the relation

$$E(\Delta v_{it} \cdot y_{i,t-k}) = 0, \quad k > 1 \quad (18.3)$$

as an orthogonality condition.

Autocorrelation is dealt with by noting that, if  $v_{it}$  is a white noise, then the covariance matrix of the vector whose typical element is  $\Delta v_{it}$  is proportional to a matrix  $H$  that has 2 on the main diagonal,  $-1$  on the first subdiagonals and 0 elsewhere. In practice, one-step GMM estimation of equation (18.2) amounts to computing

$$\begin{aligned} \hat{y} = & \left[ \left( \sum_{i=1}^N \mathbf{w}_i' \mathbf{z}_i \right) \left( \sum_{i=1}^N \mathbf{z}_i' H \mathbf{z}_i \right)^{-1} \left( \sum_{i=1}^N \mathbf{z}_i' \mathbf{w}_i \right) \right]^{-1} \times \\ & \times \left( \sum_{i=1}^N \mathbf{w}_i' \mathbf{z}_i \right) \left( \sum_{i=1}^N \mathbf{z}_i' H \mathbf{z}_i \right)^{-1} \left( \sum_{i=1}^N \mathbf{z}_i' \Delta \mathbf{y}_i \right) \end{aligned} \quad (18.4)$$

---

<sup>1</sup>An alternative is “orthogonal deviations”: this is implemented in `arbond`, but not in `dpanel`, since it was a lot of work and OD is very rarely seen in the wild.

where

$$\begin{aligned}\Delta \mathbf{y}_i &= \begin{bmatrix} \Delta y_{i,3} & \cdots & \Delta y_{i,T} \end{bmatrix}' \\ \mathbf{W}_i &= \begin{bmatrix} \Delta y_{i,2} & \cdots & \Delta y_{i,T-1} \\ \Delta x_{i,3} & \cdots & \Delta x_{i,T} \end{bmatrix}' \\ \mathbf{Z}_i &= \begin{bmatrix} y_{i1} & 0 & 0 & \cdots & 0 & \Delta x_{i3} \\ 0 & y_{i1} & y_{i2} & \cdots & 0 & \Delta x_{i4} \\ & & \vdots & & & \\ 0 & 0 & 0 & \cdots & y_{i,T-2} & \Delta x_{iT} \end{bmatrix}'\end{aligned}$$

Once the 1-step estimator is computed, the sample covariance matrix of the estimated residuals can be used instead of  $H$  to obtain 2-step estimates, which are not only consistent but asymptotically efficient.<sup>2</sup> Standard GMM theory applies, except for one thing: [Windmeijer \(2005\)](#) has computed finite-sample corrections to the asymptotic covariance matrix of the parameters, which are nowadays almost universally used.

The difference estimator is consistent, but has been shown to have poor properties in finite samples when  $\alpha$  is near one. People these days prefer the so-called “system” estimator, which complements the differenced data (with lagged levels used as instruments) with data in levels (using lagged differences as instruments). The system estimator relies on an extra orthogonality condition which has to do with the earliest value of the dependent variable  $y_{i,1}$ . The interested reader is referred to [Blundell and Bond \(1998, pp. 124–125\)](#) for details, but here it suffices to say that this condition is satisfied in mean-stationary models and brings about efficiency that may be substantial in many cases.

The set of orthogonality conditions exploited in the system approach is not very much larger than with the difference estimator, the reason being that most of the possible orthogonality conditions associated with the equations in levels are redundant, given those already used for the equations in differences.

The key equations of the system estimator can be written as

$$\begin{aligned}\hat{\mathbf{y}} &= \left[ \left( \sum_{i=1}^N \tilde{\mathbf{W}}' \tilde{\mathbf{Z}} \right) \left( \sum_{i=1}^N \tilde{\mathbf{Z}}' H^* \tilde{\mathbf{Z}} \right)^{-1} \left( \sum_{i=1}^N \tilde{\mathbf{Z}}' \tilde{\mathbf{W}} \right) \right]^{-1} \times \\ &\quad \times \left( \sum_{i=1}^N \tilde{\mathbf{W}}' \tilde{\mathbf{Z}} \right) \left( \sum_{i=1}^N \tilde{\mathbf{Z}}' H^* \tilde{\mathbf{Z}} \right)^{-1} \left( \sum_{i=1}^N \tilde{\mathbf{Z}}' \Delta \tilde{\mathbf{y}}_i \right)\end{aligned}\tag{18.5}$$

---

<sup>2</sup>In theory, the process may be iterated, but nobody seems to be interested.

where

$$\begin{aligned}\Delta\tilde{\mathbf{y}}_i &= \begin{bmatrix} \Delta y_{i3} & \cdots & \Delta y_{iT} & y_{i3} & \cdots & y_{iT} \end{bmatrix}' \\ \tilde{\mathbf{W}}_i &= \begin{bmatrix} \Delta y_{i2} & \cdots & \Delta y_{i,T-1} & y_{i2} & \cdots & y_{i,T-1} \\ \Delta x_{i3} & \cdots & \Delta x_{iT} & x_{i3} & \cdots & x_{iT} \end{bmatrix}' \\ \tilde{\mathbf{Z}}_i &= \begin{bmatrix} y_{i1} & 0 & 0 & \cdots & 0 & 0 & \cdots & 0 & \Delta x_{i,3} \\ 0 & y_{i1} & y_{i2} & \cdots & 0 & 0 & \cdots & 0 & \Delta x_{i,4} \\ & & \vdots & & & & & & \\ 0 & 0 & 0 & \cdots & y_{i,T-2} & 0 & \cdots & 0 & \Delta x_{iT} \\ & & \vdots & & & & & & \\ 0 & 0 & 0 & \cdots & 0 & \Delta y_{i2} & \cdots & 0 & x_{i3} \\ & & \vdots & & & & & & \\ 0 & 0 & 0 & \cdots & 0 & 0 & \cdots & \Delta y_{i,T-1} & x_{iT} \end{bmatrix}'\end{aligned}$$

In this case choosing a precise form for the matrix  $H^*$  for the first step is no trivial matter. Its north-west block should be as similar as possible to the covariance matrix of the vector  $\Delta v_{it}$ , so the same choice as the “difference” estimator is appropriate. Ideally, the south-east block should be proportional to the covariance matrix of the vector  $\mathbf{u}\eta_i + \mathbf{v}$ , that is  $\sigma_v^2 I + \sigma_\eta^2 \mathbf{u}\mathbf{u}'$ ; but since  $\sigma_\eta^2$  is unknown and any positive definite matrix renders the estimator consistent, people just use  $I$ . The off-diagonal blocks should, in principle, contain the covariances between  $\Delta v_{is}$  and  $v_{it}$ , which would be an identity matrix if  $v_{it}$  is white noise. However, since the south-east block is typically given a conventional value anyway, the benefit in making this choice is not obvious. Some packages use  $I$ ; others use a zero matrix. Asymptotically, it should not matter, but on real datasets the difference between the resulting estimates can be noticeable.

### Rank deficiency

Both the difference estimator (18.4) and the system estimator (18.5) depend, for their existence, on the invertibility of  $A = \sum_{i=1}^N \tilde{\mathbf{Z}}_i' H^* \tilde{\mathbf{Z}}_i$ . This matrix may turn out to be singular for several reasons. However, this does not mean that the estimator is not computable: in some cases, adjustments are possible such that the estimator does exist, but the user must be aware that in these cases not all software packages use the same strategy and replication of results may prove difficult or even impossible.

A first reason why  $A$  may be singular could be the unavailability of instruments, chiefly because of missing observations. This case is easy to handle. If a particular row of  $\tilde{\mathbf{Z}}_i$  is zero for all units, the corresponding orthogonality condition (or the corresponding instrument if you prefer) is automatically dropped; of course, the overidentification rank is adjusted for testing purposes.

Even if no instruments are zero, however,  $A$  could be rank deficient. A trivial case occurs if there are collinear instruments, but a less trivial case may arise when  $T$  (the total number of time periods available) is not much smaller than  $N$  (the number of units), as, for example, in some macro datasets where the units are countries. The total number of potentially usable orthogonality conditions is  $O(T^2)$ , which may well exceed  $N$  in some cases. Of course  $A$  is the sum of  $N$  matrices which have, at most, rank  $2T - 3$  and therefore it could well happen that  $A$  is singular.

In all these cases, what we consider the “proper” way to go is to substitute the pseudo-inverse of  $A$  (Moore–Penrose) for its regular inverse. Again, our choice is shared by some software packages, but not all, so replication may be hard.

### Treatment of missing values

Textbooks seldom bother with missing values, but in some cases their treatment may be far from obvious. This is especially true if missing values are interspersed between valid observations. For example, consider the plain difference estimator with one lag, so

$$y_t = \alpha y_{t-1} + \eta + \epsilon_t$$

where the  $i$  index is omitted for clarity. Suppose you have an individual with  $t = 1 \dots 5$ , for which  $y_3$  is missing. It may seem that the data for this individual are unusable, because differencing  $y_t$  would produce something like

$t$	1	2	3	4	5
$y_t$	*	*	o	*	*
$\Delta y_t$	o	*	o	o	*

where  $*$  = nonmissing and  $o$  = missing. Estimation seems to be unfeasible, since there are no periods in which  $\Delta y_t$  and  $\Delta y_{t-1}$  are both observable.

However, we can use a  $k$ -difference operator and get

$$\Delta_k y_t = \alpha \Delta_k y_{t-1} + \Delta_k \epsilon_t$$

where  $\Delta_k = 1 - L^k$  and past levels of  $y_t$  are perfectly valid instruments. In this example, we can choose  $k = 3$  and use  $y_1$  as an instrument, so this unit is in fact perfectly usable.

Not all software packages seem to be aware of this possibility, so replicating published results may prove tricky if your dataset contains individuals with “gaps” between valid observations.

## 18.2 Usage

One of the concepts underlying the syntax of `dpanel` is that you get default values for several choices you may want to make, so that in a “standard” situation the command itself is very short to write (and read). The simplest case of the model (18.1) is a plain AR(1) process:

$$y_{i,t} = \alpha y_{i,t-1} + \eta_i + v_{it}. \quad (18.6)$$

If you give the command

```
dpanel 1 ; y
```

gretl assumes that you want to estimate (18.6) via the difference estimator (18.4), using as many orthogonality conditions as possible. The scalar 1 between `dpanel` and the semicolon indicates that only one lag of  $y$  is included as an explanatory variable; using 2 would give an AR(2) model. The syntax that `gretl` uses for the non-seasonal AR and MA lags in an ARMA model is also supported in this context.<sup>3</sup> For example, if you want the first and third lags of  $y$  (but not the second) included as explanatory variables you can say

```
dpanel {1 3} ; y
```

or you can use a pre-defined matrix for this purpose:

```
matrix ylags = {1, 3}
dpanel ylags ; y
```

To use a single lag of  $y$  other than the first you need to employ this mechanism:

<sup>3</sup>This represents an enhancement over the `arbond` command.



```
dpanel {3} ; y # only lag 3 is included
dpanel 3 ; y # compare: lags 1, 2 and 3 are used
```

To use the system estimator instead, you add the `--system` option, as in

```
dpanel 1 ; y --system
```

The level orthogonality conditions and the corresponding instrument are appended automatically (see eq. 18.5).

### Regressors

If we want to introduce additional regressors, we list them after the dependent variable in the same way as other `gretl` commands, such as `ols`.

For the difference orthogonality relations, `dpanel` takes care of transforming the regressors in parallel with the dependent variable. Note that this differs from `gretl`'s `arbond` command, where only the dependent variable is differenced automatically; it brings us more in line with other software.

One case of potential ambiguity is when an intercept is specified but the difference-only estimator is selected, as in

```
dpanel 1 ; y const
```

In this case the default `dpanel` behavior, which agrees with Stata's `xtabond2`, is to drop the constant (since differencing reduces it to nothing but zeros). However, for compatibility with the DPD package for Ox, you can give the option `--dpdstyle`, in which case the constant is retained (equivalent to including a linear trend in equation 18.1). A similar point applies to the period-specific dummy variables which can be added in `dpanel` via the `--time-dummies` option: in the differences-only case these dummies are entered in differenced form by default, but when the `--dpdstyle` switch is applied they are entered in levels.

The standard `gretl` syntax applies if you want to use lagged explanatory variables, so for example the command

```
dpanel 1 ; y const x(0 to -1) --system
```

would result in estimation of the model

$$y_{it} = \alpha y_{i,t-1} + \beta_0 + \beta_1 x_{it} + \beta_2 x_{i,t-1} + \eta_i + v_{it}.$$

### Instruments

The default rules for instruments are:

- lags of the dependent variable are instrumented using all available orthogonality conditions; and
- additional regressors are considered exogenous, so they are used as their own instruments.

If a different policy is wanted, the instruments should be specified in an additional list, separated from the regressors list by a semicolon. The syntax closely mirrors that for the `tsls` command, but in this context it is necessary to distinguish between “regular” instruments and what are often called “GMM-style” instruments (that, instruments that are handled in the same block-diagonal manner as lags of the dependent variable, as described above).

“Regular” instruments are transformed in the same way as regressors, and the contemporaneous value of the transformed variable is used to form an orthogonality condition. Since regressors are treated as exogenous by default, it follows that these two commands estimate the same model:

```
dpanel 1 ; y z
dpanel 1 ; y z ; z
```

The instrument specification in the second case simply confirms what is implicit in the first: that  $z$  is exogenous. Note, though, that if you have some additional variable  $z2$  which you want to add as a regular instrument, it then becomes necessary to include  $z$  in the instrument list if it is to be treated as exogenous:

```
dpanel 1 ; y z ; z2 # z is now implicitly endogenous
dpanel 1 ; y z ; z z2 # z is treated as exogenous
```

The specification of “GMM-style” instruments is handled by the special constructs `GMM()` and `GMMlevel()`. The first of these relates to instruments for the equations in differences, and the second to the equations in levels. The syntax for `GMM()` is

```
GMM(varname, minlag, maxlag)
```

where *varname* is replaced by the name of a series, and *minlag* and *maxlag* are replaced by the minimum and maximum lags to be used as instruments. The same goes for `GMMlevel()`.

One common use of `GMM()` is to limit the number of lagged levels of the dependent variable used as instruments for the equations in differences. It’s well known that although exploiting all possible orthogonality conditions yields maximal asymptotic efficiency, in finite samples it may be preferable to use a smaller subset (but see also [Okui \(2009\)](#)). For example, the specification

```
dpanel 1 ; y ; GMM(y, 2, 4)
```

ensures that no lags of  $y_t$  earlier than  $t - 4$  will be used as instruments.

A second use of `GMM()` is to exploit more fully the potential block-diagonal orthogonality conditions offered by an exogenous regressor, or a related variable that does not appear as a regressor. For example, in

```
dpanel 1 ; y x ; GMM(z, 2, 6)
```

the variable  $x$  is considered an endogenous regressor, and up to 5 lags of  $z$  are used as instruments. Note that in the following script fragment

```
dz = diff(z)
dpanel 1 ; y dz
dpanel 1 ; y dz ; GMM(z,0,0)
```

the two estimation commands should not be expected to give the same result, as the sets of orthogonality relationships are subtly different. In the latter case, you have  $T - 2$  separate orthogonality relationships pertaining to  $z_{it}$ , none of which has any implication for the other ones; in the former case, you only have one. In terms of the  $\mathbf{Z}_i$  matrix, the first form adds a single row to the bottom of the instruments matrix, while the second form adds a diagonal block with  $T - 2$  columns, that is

$$\begin{bmatrix} \Delta z_{i3} & \Delta z_{i4} & \cdots & \Delta z_{it} \end{bmatrix}$$

versus

$$\begin{bmatrix} \Delta z_{i3} & 0 & \cdots & 0 \\ 0 & \Delta z_{i4} & \cdots & 0 \\ & \ddots & \ddots & \\ 0 & 0 & \cdots & \Delta z_{it} \end{bmatrix}$$

### 18.3 Replication of DPD results

In this section we show how to replicate the results of some of the pioneering work with dynamic panel-data estimators by Arellano, Bond and Blundell. As the DPD manual (Doornik, Arellano and Bond, 2006) explains, it is difficult to replicate the original published results exactly, for two main reasons: not all of the data used in those studies are publicly available; and some of the choices made in the original software implementation of the estimators have been superseded. Here, therefore, our focus is on replicating the results obtained using the current DPD package and reported in the DPD manual.

The examples are based on the program files `abest1.ox`, `abest3.ox` and `bbest1.ox`. These are included in the DPD package, along with the Arellano-Bond database files `abdata.bn7` and `abdata.in7`.<sup>4</sup> The Arellano-Bond data are also provided with `gretl`, in the file `abdata.gdt`. In the following we do not show the output from DPD or `gretl`; it is somewhat voluminous, and is easily generated by the user. As of this writing the results from Ox/DPD and `gretl` are identical in all relevant respects for all of the examples shown.<sup>5</sup>

A complete Ox/DPD program to generate the results of interest takes this general form:

```
#include <oxstd.h>
#import <packages/dpd/dpd>

main()
{
    decl dpd = new DPD();

    dpd.Load("abdata.in7");
    dpd.SetYear("YEAR");

    // model-specific code here

    delete dpd;
}
```

In the examples below we take this template for granted and show just the model-specific code.

#### Example 1

The following Ox/DPD code—drawn from `abest1.ox`—replicates column (b) of Table 4 in Arellano and Bond (1991), an instance of the differences-only or GMM-DIF estimator. The dependent variable is the log of employment, `n`; the regressors include two lags of the dependent variable, current and lagged values of the log real-product wage, `w`, the current value of the log of gross capital, `k`, and current and lagged values of the log of industry output, `ys`. In addition the specification includes a constant and five year dummies; unlike the stochastic regressors, these deterministic terms are not differenced. In this specification the regressors `w`, `k` and `ys` are treated as exogenous and serve as their own instruments. In DPD syntax this requires entering these variables twice, on the `X_VAR` and `I_VAR` lines. The GMM-type (block-diagonal) instruments in this example are the second and subsequent lags of the level of `n`. Both 1-step and 2-step estimates are computed.

```
dpd.SetOptions(FALSE); // don't use robust standard errors
dpd.Select(Y_VAR, {"n", 0, 2});
dpd.Select(X_VAR, {"w", 0, 1, "k", 0, 0, "ys", 0, 1});
dpd.Select(I_VAR, {"w", 0, 1, "k", 0, 0, "ys", 0, 1});
```

<sup>4</sup>See <http://www.doornik.com/download.html>.

<sup>5</sup>To be specific, this is using Ox Console version 5.10, version 1.24 of the DPD package, and `gretl` built from CVS as of 2010-10-23, all on Linux.

```

dpd.Gmm("n", 2, 99);
dpd.SetDummies(D_CONSTANT + D_TIME);

print("\n\n***** Arellano & Bond (1991), Table 4 (b)");
dpd.SetMethod(M_1STEP);
dpd.Estimate();
dpd.SetMethod(M_2STEP);
dpd.Estimate();

```

Here is gretl code to do the same job:

```

open abdata.gdt
list X = w w(-1) k ys ys(-1)
dpanel 2 ; n X const --time-dummies --asy --dpdstyle
dpanel 2 ; n X const --time-dummies --asy --two-step --dpdstyle

```

Note that in gretl the switch to suppress robust standard errors is `--asymptotic`, here abbreviated to `--asy`.<sup>6</sup> The `--dpdstyle` flag specifies that the constant and dummies should not be differenced, in the context of a GMM-DIF model. With gretl's `dpanel` command it is not necessary to specify the exogenous regressors as their own instruments since this is the default; similarly, the use of the second and all longer lags of the dependent variable as GMM-type instruments is the default and need not be stated explicitly.

## Example 2

The DPD file `abest3.ox` contains a variant of the above that differs with regard to the choice of instruments: the variables `w` and `k` are now treated as predetermined, and are instrumented GMM-style using the second and third lags of their levels. This approximates column (c) of Table 4 in [Arellano and Bond \(1991\)](#). We have modified the code in `abest3.ox` slightly to allow the use of robust (Windmeijer-corrected) standard errors, which are the default in both DPD and gretl with 2-step estimation:

```

dpd.Select(Y_VAR, {"n", 0, 2});
dpd.Select(X_VAR, {"w", 0, 1, "k", 0, 0, "ys", 0, 1});
dpd.Select(I_VAR, {"ys", 0, 1});
dpd.SetDummies(D_CONSTANT + D_TIME);

dpd.Gmm("n", 2, 99);
dpd.Gmm("w", 2, 3);
dpd.Gmm("k", 2, 3);

print("\n***** Arellano & Bond (1991), Table 4 (c)\n");
print("      (but using different instruments!!)\n");
dpd.SetMethod(M_2STEP);
dpd.Estimate();

```

The gretl code is as follows:

```

open abdata.gdt
list X = w w(-1) k ys ys(-1)
list Ivars = ys ys(-1)
dpanel 2 ; n X const ; GMM(w,2,3) GMM(k,2,3) Ivars --time --two-step --dpd

```

Note that since we are now calling for an instrument set other than the default (following the second semicolon), it is necessary to include the `Ivars` specification for the variable `ys`. However, it is not necessary to specify `GMM(n,2,99)` since this remains the default treatment of the dependent variable.

---

<sup>6</sup>Option flags in gretl can always be truncated, down to the minimal unique abbreviation.

**Example 3**

Our third example replicates the DPD output from `bbest1.ox`: this uses the same dataset as the previous examples but the model specifications are based on [Blundell and Bond \(1998\)](#), and involve comparison of the GMM-DIF and GMM-SYS (“system”) estimators. The basic specification is slightly simplified in that the variable `ys` is not used and only one lag of the dependent variable appears as a regressor. The Ox/DPD code is:

```
dpd.Select(Y_VAR, {"n", 0, 1});
dpd.Select(X_VAR, {"w", 0, 1, "k", 0, 1});
dpd.SetDummies(D_CONSTANT + D_TIME);

print("\n\n***** Blundell & Bond (1998), Table 4: 1976-86 GMM-DIF");
dpd.Gmm("n", 2, 99);
dpd.Gmm("w", 2, 99);
dpd.Gmm("k", 2, 99);
dpd.SetMethod(M_2STEP);
dpd.Estimate();

print("\n\n***** Blundell & Bond (1998), Table 4: 1976-86 GMM-SYS");
dpd.GmmLevel("n", 1, 1);
dpd.GmmLevel("w", 1, 1);
dpd.GmmLevel("k", 1, 1);
dpd.SetMethod(M_2STEP);
dpd.Estimate();
```

Here is the corresponding gretl code:

```
open abdata.gdt
list X = w w(-1) k k(-1)

# Blundell & Bond (1998), Table 4: 1976-86 GMM-DIF
dpanel 1 ; n X const ; GMM(w,2,99) GMM(k,2,99) --time --two-step --dpd

# Blundell & Bond (1998), Table 4: 1976-86 GMM-SYS
dpanel 1 ; n X const ; GMM(w,2,99) GMM(k,2,99) \
  GMMlevel(w,1,1) GMMlevel(k,1,1) --time --two-step --dpd --system
```

Note the use of the `--system` option flag to specify GMM-SYS, including the default treatment of the dependent variable, which corresponds to `GMMlevel(n,1,1)`. In this case we also want to use lagged differences of the regressors `w` and `k` as instruments for the levels equations so we need explicit `GMMlevel` entries for those variables. If you want something other than the default treatment for the dependent variable as an instrument for the levels equations, you should give an explicit `GMMlevel` specification for that variable—and in that case the `--system` flag is redundant (but harmless).

For the sake of completeness, note that if you specify at least one `GMMlevel` term, `dpanel` will then include equations in levels, but it will not automatically add a default `GMMlevel` specification for the dependent variable unless the `--system` option is given.

**18.4 Cross-country growth example**

The previous examples all used the Arellano–Bond dataset; for this example we use the dataset `CEL.gdt`, which is also included in the gretl distribution. As with the Arellano–Bond data, there are numerous missing values. Details of the provenance of the data can be found by opening the dataset information window in the gretl GUI (Data menu, Dataset info item). This is a subset of the Barro–Lee 138-country panel dataset, an approximation to which is used in [Caselli, Esquivel and](#)

Lefort (1996) and Bond, Hoeffler and Temple (2001).<sup>7</sup> Both of these papers explore the dynamic panel-data approach in relation to the issues of growth and convergence of per capita income across countries.

The dependent variable is growth in real GDP per capita over successive five-year periods; the regressors are the log of the initial (five years prior) value of GDP per capita, the log-ratio of investment to GDP,  $s$ , in the prior five years, and the log of annual average population growth,  $n$ , over the prior five years plus 0.05 as stand-in for the rate of technical progress,  $g$ , plus the rate of depreciation,  $\delta$  (with the last two terms assumed to be constant across both countries and periods). The original model is

$$\Delta_5 y_{it} = \beta y_{i,t-5} + \alpha s_{it} + \gamma(n_{it} + g + \delta) + v_t + \eta_i + \epsilon_{it} \quad (18.7)$$

which allows for a time-specific disturbance  $v_t$ . The Solow model with Cobb–Douglas production function implies that  $\gamma = -\alpha$ , but this assumption is not imposed in estimation. The time-specific disturbance is eliminated by subtracting the period mean from each of the series.

Equation (18.7) can be transformed to an AR(1) dynamic panel-data model by adding  $y_{i,t-5}$  to both sides, which gives

$$y_{it} = (1 + \beta)y_{i,t-5} + \alpha s_{it} + \gamma(n_{it} + g + \delta) + \eta_i + \epsilon_{it} \quad (18.8)$$

where all variables are now assumed to be time-demeaned.

In (rough) replication of Bond *et al.* (2001) we now proceed to estimate the following two models: (a) equation (18.8) via GMM-DIF, using as instruments the second and all longer lags of  $y_{it}$ ,  $s_{it}$  and  $n_{it} + g + \delta$ ; and (b) equation (18.8) via GMM-SYS, using  $\Delta y_{i,t-1}$ ,  $\Delta s_{i,t-1}$  and  $\Delta(n_{i,t-1} + g + \delta)$  as additional instruments in the levels equations. We report robust standard errors throughout. (As a purely notational matter, we now use “ $t - 1$ ” to refer to values five years prior to  $t$ , as in Bond *et al.* (2001)).

The gretl script to do this job is shown below. Note that the final transformed versions of the variables (logs, with time-means subtracted) are named `ly` ( $y_{it}$ ), `linv` ( $s_{it}$ ) and `lngd` ( $n_{it} + g + \delta$ ).

```
open CEL.gdt

ngd = n + 0.05
ly = log(y)
linv = log(s)
lngd = log(ngd)

# take out time means
loop i=1..8 --quiet
  smpl (time == i) --restrict --replace
  ly -= mean(ly)
  linv -= mean(linv)
  lngd -= mean(lngd)
endloop

smpl --full
list X = linv lngd
# 1-step GMM-DIF
dpanel 1 ; ly X ; GMM(linv,2,99) GMM(lngd,2,99)
# 2-step GMM-DIF
dpanel 1 ; ly X ; GMM(linv,2,99) GMM(lngd,2,99) --two-step
# GMM-SYS
dpanel 1 ; ly X ; GMM(linv,2,99) GMM(lngd,2,99) \
  GMMlevel(linv,1,1) GMMlevel(lngd,1,1) --two-step --sys
```

<sup>7</sup>We say an “approximation” because we have not been able to replicate exactly the OLS results reported in the papers cited, though it seems from the description of the data in Caselli *et al.* (1996) that we ought to be able to do so. We note that Bond *et al.* (2001) used data provided by Professor Caselli yet did not manage to reproduce the latter’s results.

For comparison we estimated the same two models using Ox/DPD and the Stata command `xtabond2`. (In each case we constructed a comma-separated values dataset containing the data as transformed in the `gretl` script shown above, using a missing-value code appropriate to the target program.) For reference, the commands used with Stata are reproduced below:

```
insheet using CEL.csv
tsset unit time
xtabond2 ly L.ly linv lngd, gmm(L.ly, lag(1 99)) gmm(linv, lag(2 99))
      gmm(lngd, lag(2 99)) rob nolev
xtabond2 ly L.ly linv lngd, gmm(L.ly, lag(1 99)) gmm(linv, lag(2 99))
      gmm(lngd, lag(2 99)) rob nolev twostep
xtabond2 ly L.ly linv lngd, gmm(L.ly, lag(1 99)) gmm(linv, lag(2 99))
      gmm(lngd, lag(2 99)) rob nocons twostep
```

For the GMM-DIF model all three programs find 382 usable observations and 30 instruments, and yield identical parameter estimates and robust standard errors (up to the number of digits printed, or more); see Table 18.1.<sup>8</sup>

	1-step		2-step	
	coeff	std. error	coeff	std. error
ly(-1)	0.577564	0.1292	0.610056	0.1562
linv	0.0565469	0.07082	0.100952	0.07772
lngd	-0.143950	0.2753	-0.310041	0.2980

**Table 18.1:** GMM-DIF: Barro-Lee data

Results for GMM-SYS estimation are shown in Table 18.2. In this case we show two sets of `gretl` results: those labeled “`gretl(1)`” were obtained using `gretl`’s `--dpdstyle` option, while those labeled “`gretl(2)`” did not use that option—the intent being to reproduce the  $H$  matrices used by Ox/DPD and `xtabond2` respectively.

	gretl(1)	Ox/DPD	gretl(2)	xtabond2
ly(-1)	0.9237 (0.0385)	0.9167 (0.0373)	0.9073 (0.0370)	0.9073 (0.0370)
linv	0.1592 (0.0449)	0.1636 (0.0441)	0.1856 (0.0411)	0.1856 (0.0411)
lngd	-0.2370 (0.1485)	-0.2178 (0.1433)	-0.2355 (0.1501)	-0.2355 (0.1501)

**Table 18.2:** 2-step GMM-SYS: Barro-Lee data (standard errors in parentheses)

In this case all three programs use 479 observations; `gretl` and `xtabond2` use 41 instruments and produce the same estimates (when using the same  $H$  matrix) while Ox/DPD nominally uses 66.<sup>9</sup> It is noteworthy that with GMM-SYS plus “messy” missing observations, the results depend on the precise array of instruments used, which in turn depends on the details of the implementation of the estimator.

### Auxiliary test statistics

We have concentrated above on the parameter estimates and standard errors. It may be worth adding a few words on the additional test statistics that typically accompany both GMM-DIF and

<sup>8</sup>The coefficient shown for `ly(-1)` in the Tables is that reported directly by the software; for comparability with the original model (eq. 18.7) it is necessary to subtract 1, which produces the expected negative value indicating conditional convergence in per capita income.

<sup>9</sup>This is a case of the issue described in section 18.1: the full  $A$  matrix turns out to be singular and special measures must be taken to produce estimates.

GMM-SYS estimation. These include the Sargan test for overidentification, one or more Wald tests for the joint significance of the regressors, and time dummies if applicable, and tests for first- and second-order autocorrelation of the residuals from the equations in differences.

In general we see a good level of agreement between gretl, DPD and xtabond2 with regard to these statistics, with a few relatively minor exceptions. Specifically, xtabond2 computes both a “Sargan test” and a “Hansen test” for overidentification, but what it calls the Hansen test is what DPD and gretl call the Sargan test. (We have had difficulty determining from the xtabond2 documentation (Roodman, 2006) exactly how its Sargan test is computed.) In addition there are cases where the degrees of freedom for the Sargan test differ between DPD and gretl; this occurs when the  $A$  matrix is singular (section 18.1). In concept the df equals the number of instruments minus the number of parameters estimated; for the first of these terms gretl uses the rank of  $A$ , while DPD appears to use the full dimension of  $A$ .

### 18.5 Memo: dpanel options

<i>flag</i>	<i>effect</i>
<code>--asymptotic</code>	Suppresses the use of robust standard errors
<code>--two-step</code>	Calls for 2-step estimation (the default being 1-step)
<code>--system</code>	Calls for GMM-SYS, with default treatment of the dependent variable, as in <code>GMMlevel(y,1,1)</code>
<code>--time-dummies</code>	Includes period-specific dummy variables
<code>--dpdstyle</code>	Compute the $H$ matrix as in DPD; also suppresses differencing of automatic time dummies and omission of intercept in the GMM-DIF case
<code>--verbose</code>	When <code>--two-step</code> is selected, prints the 1-step estimates first
<code>--vcv</code>	Calls for printing of the covariance matrix
<code>--quiet</code>	Suppresses the printing of results



## Chapter 19

# Nonlinear least squares

### 19.1 Introduction and examples

Gretl supports nonlinear least squares (NLS) using a variant of the Levenberg–Marquardt algorithm. The user must supply a specification of the regression function; prior to giving this specification the parameters to be estimated must be “declared” and given initial values. Optionally, the user may supply analytical derivatives of the regression function with respect to each of the parameters. If derivatives are not given, the user must instead give a list of the parameters to be estimated (separated by spaces or commas), preceded by the keyword `params`. The tolerance (criterion for terminating the iterative estimation procedure) can be adjusted using the `set` command.

The syntax for specifying the function to be estimated is the same as for the `genr` command. Here are two examples, with accompanying derivatives.

```
# Consumption function from Greene
nls C = alpha + beta * Y^gamma
    deriv alpha = 1
    deriv beta = Y^gamma
    deriv gamma = beta * Y^gamma * log(Y)
end nls

# Nonlinear function from Russell Davidson
nls y = alpha + beta * x1 + (1/beta) * x2
    deriv alpha = 1
    deriv beta = x1 - x2/(beta*beta)
end nls --vcv
```

Note the command words `nls` (which introduces the regression function), `deriv` (which introduces the specification of a derivative), and `end nls`, which terminates the specification and calls for estimation. If the `--vcv` flag is appended to the last line the covariance matrix of the parameter estimates is printed.

### 19.2 Initializing the parameters

The parameters of the regression function must be given initial values prior to the `nls` command. This can be done using the `genr` command (or, in the GUI program, via the menu item “Variable, Define new variable”).

In some cases, where the nonlinear function is a generalization of (or a restricted form of) a linear model, it may be convenient to run an `ols` and initialize the parameters from the OLS coefficient estimates. In relation to the first example above, one might do:

```
ols C O Y
genr alpha = $coeff(0)
genr beta = $coeff(Y)
genr gamma = 1
```

And in relation to the second example one might do:

```

ols y 0 x1 x2
genr alpha = $coeff(0)
genr beta = $coeff(x1)

```

### 19.3 NLS dialog window

It is probably most convenient to compose the commands for NLS estimation in the form of a gretl script but you can also do so interactively, by selecting the item “Nonlinear Least Squares” under the “Model, Nonlinear models” menu. This opens a dialog box where you can type the function specification (possibly prefaced by `genr` lines to set the initial parameter values) and the derivatives, if available. An example of this is shown in Figure 19.1. Note that in this context you do not have to supply the `nls` and `end nls` tags.

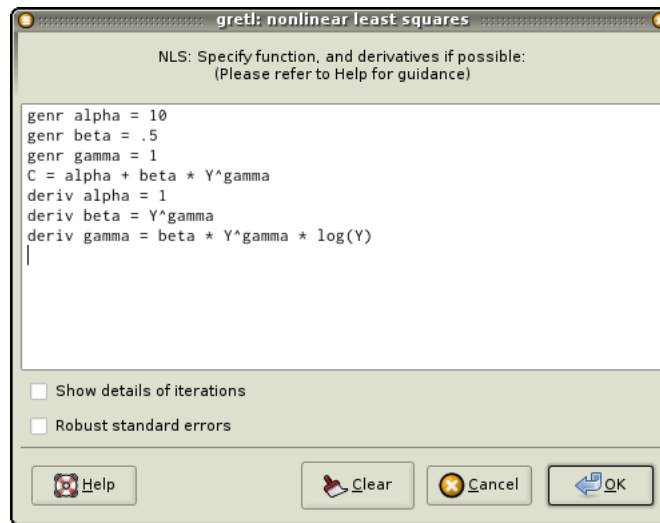


Figure 19.1: NLS dialog box

### 19.4 Analytical and numerical derivatives

If you are able to figure out the derivatives of the regression function with respect to the parameters, it is advisable to supply those derivatives as shown in the examples above. If that is not possible, gretl will compute approximate numerical derivatives. However, the properties of the NLS algorithm may not be so good in this case (see section 19.7).

This is done by using the `params` statement, which should be followed by a list of identifiers containing the parameters to be estimated. In this case, the examples above would read as follows:

```

# Greene
nls C = alpha + beta * Y^gamma
    params alpha beta gamma
end nls

# Davidson
nls y = alpha + beta * x1 + (1/beta) * x2
    params alpha beta
end nls

```

If analytical derivatives are supplied, they are checked for consistency with the given nonlinear function. If the derivatives are clearly incorrect estimation is aborted with an error message. If the

derivatives are “suspicious” a warning message is issued but estimation proceeds. This warning may sometimes be triggered by incorrect derivatives, but it may also be triggered by a high degree of collinearity among the derivatives.

Note that you cannot mix analytical and numerical derivatives: you should supply expressions for all of the derivatives or none.

## 19.5 Controlling termination

The NLS estimation procedure is an iterative process. Iteration is terminated when the criterion for convergence is met or when the maximum number of iterations is reached, whichever comes first.

Let  $k$  denote the number of parameters being estimated. The maximum number of iterations is  $100 \times (k + 1)$  when analytical derivatives are given, and  $200 \times (k + 1)$  when numerical derivatives are used.

Let  $\epsilon$  denote a small number. The iteration is deemed to have converged if at least one of the following conditions is satisfied:

- Both the actual and predicted relative reductions in the error sum of squares are at most  $\epsilon$ .
- The relative error between two consecutive iterates is at most  $\epsilon$ .

This default value of  $\epsilon$  is the machine precision to the power  $3/4$ ,<sup>1</sup> but it can be adjusted using the `set` command with the parameter `nls_tol`. For example

```
set nls_tol .0001
```

will relax the value of  $\epsilon$  to 0.0001.

## 19.6 Details on the code

The underlying engine for NLS estimation is based on the `minpack` suite of functions, available from [netlib.org](http://netlib.org). Specifically, the following `minpack` functions are called:

<code>lmdr</code>	Levenberg-Marquardt algorithm with analytical derivatives
<code>chkder</code>	Check the supplied analytical derivatives
<code>lmdif</code>	Levenberg-Marquardt algorithm with numerical derivatives
<code>fdjac2</code>	Compute final approximate Jacobian when using numerical derivatives
<code>dpmpar</code>	Determine the machine precision

On successful completion of the Levenberg-Marquardt iteration, a Gauss-Newton regression is used to calculate the covariance matrix for the parameter estimates. If the `--robust` flag is given a robust variant is computed. The documentation for the `set` command explains the specific options available in this regard.

Since NLS results are asymptotic, there is room for debate over whether or not a correction for degrees of freedom should be applied when calculating the standard error of the regression (and the standard errors of the parameter estimates). For comparability with OLS, and in light of the reasoning given in Davidson and MacKinnon (1993), the estimates shown in `gretl` do use a degrees of freedom correction.

---

<sup>1</sup>On a 32-bit Intel Pentium machine a likely value for this parameter is  $1.82 \times 10^{-12}$ .

## 19.7 Numerical accuracy

Table 19.1 shows the results of running the gretl NLS procedure on the 27 Statistical Reference Datasets made available by the U.S. National Institute of Standards and Technology (NIST) for testing nonlinear regression software.<sup>2</sup> For each dataset, two sets of starting values for the parameters are given in the test files, so the full test comprises 54 runs. Two full tests were performed, one using all analytical derivatives and one using all numerical approximations. In each case the default tolerance was used.<sup>3</sup>

Out of the 54 runs, gretl failed to produce a solution in 4 cases when using analytical derivatives, and in 5 cases when using numeric approximation. Of the four failures in analytical derivatives mode, two were due to non-convergence of the Levenberg–Marquardt algorithm after the maximum number of iterations (on MGH09 and Bennett5, both described by NIST as of “Higher difficulty”) and two were due to generation of range errors (out-of-bounds floating point values) when computing the Jacobian (on BoxBOD and MGH17, described as of “Higher difficulty” and “Average difficulty” respectively). The additional failure in numerical approximation mode was on MGH10 (“Higher difficulty”, maximum number of iterations reached).

The table gives information on several aspects of the tests: the number of outright failures, the average number of iterations taken to produce a solution and two sorts of measure of the accuracy of the estimates for both the parameters and the standard errors of the parameters.

For each of the 54 runs in each mode, if the run produced a solution the parameter estimates obtained by gretl were compared with the NIST certified values. We define the “minimum correct figures” for a given run as the number of significant figures to which the *least accurate* gretl estimate agreed with the certified value, for that run. The table shows both the average and the worst case value of this variable across all the runs that produced a solution. The same information is shown for the estimated standard errors.<sup>4</sup>

The second measure of accuracy shown is the percentage of cases, taking into account all parameters from all successful runs, in which the gretl estimate agreed with the certified value to at least the 6 significant figures which are printed by default in the gretl regression output.

Using analytical derivatives, the worst case values for both parameters and standard errors were improved to 6 correct figures on the test machine when the tolerance was tightened to  $1.0e-14$ . Using numerical derivatives, the same tightening of the tolerance raised the worst values to 5 correct figures for the parameters and 3 figures for standard errors, at a cost of one additional failure of convergence.

Note the overall superiority of analytical derivatives: on average solutions to the test problems were obtained with substantially fewer iterations and the results were more accurate (most notably for the estimated standard errors). Note also that the six-digit results printed by gretl are not 100 percent reliable for difficult nonlinear problems (in particular when using numerical derivatives). Having registered this caveat, the percentage of cases where the results were good to six digits or better seems high enough to justify their printing in this form.

<sup>2</sup>For a discussion of gretl's accuracy in the estimation of linear models, see Appendix D.

<sup>3</sup>The data shown in the table were gathered from a pre-release build of gretl version 1.0.9, compiled with gcc 3.3, linked against glibc 2.3.2, and run under Linux on an i686 PC (IBM ThinkPad A21m).

<sup>4</sup>For the standard errors, I excluded one outlier from the statistics shown in the table, namely Lanczos1. This is an odd case, using generated data with an almost-exact fit: the standard errors are 9 or 10 orders of magnitude smaller than the coefficients. In this instance gretl could reproduce the certified standard errors to only 3 figures (analytical derivatives) and 2 figures (numerical derivatives).

**Table 19.1:** Nonlinear regression: the NIST tests

	<i>Analytical derivatives</i>	<i>Numerical derivatives</i>
Failures in 54 tests	4	5
Average iterations	32	127
Mean of min. correct figures, parameters	8.120	6.980
Worst of min. correct figures, parameters	4	3
Mean of min. correct figures, standard errors	8.000	5.673
Worst of min. correct figures, standard errors	5	2
Percent correct to at least 6 figures, parameters	96.5	91.9
Percent correct to at least 6 figures, standard errors	97.7	77.3

## Chapter 20

# Maximum likelihood estimation

### 20.1 Generic ML estimation with gretl

Maximum likelihood estimation is a cornerstone of modern inferential procedures. Gretl provides a way to implement this method for a wide range of estimation problems, by use of the `mle` command. We give here a few examples.

To give a foundation for the examples that follow, we start from a brief reminder on the basics of ML estimation. Given a sample of size  $T$ , it is possible to define the density function<sup>1</sup> for the whole sample, namely the joint distribution of all the observations  $f(\mathbf{Y}; \theta)$ , where  $\mathbf{Y} = \{y_1, \dots, y_T\}$ . Its shape is determined by a  $k$ -vector of unknown parameters  $\theta$ , which we assume is contained in a set  $\Theta$ , and which can be used to evaluate the probability of observing a sample with any given characteristics.

After observing the data, the values  $\mathbf{Y}$  are given, and this function can be evaluated for any legitimate value of  $\theta$ . In this case, we prefer to call it the *likelihood* function; the need for another name stems from the fact that this function works as a density when we use the  $y_t$ s as arguments and  $\theta$  as parameters, whereas in this context  $\theta$  is taken as the function's argument, and the data  $\mathbf{Y}$  only have the role of determining its shape.

In standard cases, this function has a unique maximum. The location of the maximum is unaffected if we consider the logarithm of the likelihood (or log-likelihood for short): this function will be denoted as

$$\ell(\theta) = \log f(\mathbf{Y}; \theta)$$

The log-likelihood functions that gretl can handle are those where  $\ell(\theta)$  can be written as

$$\ell(\theta) = \sum_{t=1}^T \ell_t(\theta)$$

which is true in most cases of interest. The functions  $\ell_t(\theta)$  are called the log-likelihood contributions.

Moreover, the location of the maximum is obviously determined by the data  $\mathbf{Y}$ . This means that the value

$$\hat{\theta}(\mathbf{Y}) = \underset{\theta \in \Theta}{\text{Argmax}} \ell(\theta) \quad (20.1)$$

is some function of the observed data (a statistic), which has the property, under mild conditions, of being a consistent, asymptotically normal and asymptotically efficient estimator of  $\theta$ .

Sometimes it is possible to write down explicitly the function  $\hat{\theta}(\mathbf{Y})$ ; in general, it need not be so. In these circumstances, the maximum can be found by means of numerical techniques. These often rely on the fact that the log-likelihood is a smooth function of  $\theta$ , and therefore on the maximum its partial derivatives should all be 0. The *gradient vector*, or *score vector*, is a function that enjoys many interesting statistical properties in its own right; it will be denoted here as  $\mathbf{g}(\theta)$ . It is a

---

<sup>1</sup>We are supposing here that our data are a realization of continuous random variables. For discrete random variables, everything continues to apply by referring to the probability function instead of the density. In both cases, the distribution may be conditional on some exogenous variables.

$k$ -vector with typical element

$$g_i(\theta) = \frac{\partial \ell(\theta)}{\partial \theta_i} = \sum_{t=1}^T \frac{\partial \ell_t(\theta)}{\partial \theta_i}$$

Gradient-based methods can be shortly illustrated as follows:

1. pick a point  $\theta_0 \in \Theta$ ;
2. evaluate  $\mathbf{g}(\theta_0)$ ;
3. if  $\mathbf{g}(\theta_0)$  is “small”, stop. Otherwise, compute a direction vector  $d(\mathbf{g}(\theta_0))$ ;
4. evaluate  $\theta_1 = \theta_0 + d(\mathbf{g}(\theta_0))$ ;
5. substitute  $\theta_0$  with  $\theta_1$ ;
6. restart from 2.

Many algorithms of this kind exist; they basically differ from one another in the way they compute the direction vector  $d(\mathbf{g}(\theta_0))$ , to ensure that  $\ell(\theta_1) > \ell(\theta_0)$  (so that we eventually end up on the maximum).

The default method `gretl` uses to maximize the log-likelihood is a gradient-based algorithm known as the **BFGS** (Broyden, Fletcher, Goldfarb and Shanno) method. This technique is used in most econometric and statistical packages, as it is well-established and remarkably powerful. Clearly, in order to make this technique operational, it must be possible to compute the vector  $\mathbf{g}(\theta)$  for any value of  $\theta$ . In some cases this vector can be written explicitly as a function of  $\mathbf{Y}$ . If this is not possible or too difficult the gradient may be evaluated numerically. The alternative **Newton-Raphson** algorithm is also available, which is more effective under some circumstances but is also more fragile; see section 20.8 and chapter 30 for details.

The choice of the starting value,  $\theta_0$ , is crucial in some contexts and inconsequential in others. In general, however, it is advisable to start the algorithm from “sensible” values whenever possible. If a consistent estimator is available, this is usually a safe and efficient choice: this ensures that in large samples the starting point will be likely close to  $\hat{\theta}$  and convergence can be achieved in few iterations.

The maximum number of iterations allowed for the BFGS procedure, and the relative tolerance for assessing convergence, can be adjusted using the `set` command: the relevant variables are `bfgs_maxiter` (default value 500) and `bfgs_tol` (default value, the machine precision to the power 3/4).

### Covariance matrix and standard errors

By default the covariance matrix of the parameter estimates is based on the Outer Product of the Gradient. That is,

$$\widehat{\text{Var}}_{\text{OPG}}(\hat{\theta}) = \left( G'(\hat{\theta}) G(\hat{\theta}) \right)^{-1} \quad (20.2)$$

where  $G(\hat{\theta})$  is the  $T \times k$  matrix of contributions to the gradient. Two other options are available. If the `--hessian` flag is given, the covariance matrix is computed from a numerical approximation to the Hessian at convergence. If the `--robust` option is selected, the quasi-ML “sandwich” estimator is used:

$$\widehat{\text{Var}}_{\text{QML}}(\hat{\theta}) = H(\hat{\theta})^{-1} G'(\hat{\theta}) G(\hat{\theta}) H(\hat{\theta})^{-1}$$

where  $H$  denotes the numerical approximation to the Hessian.

## 20.2 Gamma estimation

Suppose we have a sample of  $T$  independent and identically distributed observations from a Gamma distribution. The density function for each observation  $x_t$  is

$$f(x_t) = \frac{\alpha^p}{\Gamma(p)} x_t^{p-1} \exp(-\alpha x_t) \quad (20.3)$$

The log-likelihood for the entire sample can be written as the logarithm of the joint density of all the observations. Since these are independent and identical, the joint density is the product of the individual densities, and hence its log is

$$\ell(\alpha, p) = \sum_{t=1}^T \log \left[ \frac{\alpha^p}{\Gamma(p)} x_t^{p-1} \exp(-\alpha x_t) \right] = \sum_{t=1}^T \ell_t \quad (20.4)$$

where

$$\ell_t = p \cdot \log(\alpha x_t) - \gamma(p) - \log x_t - \alpha x_t$$

and  $\gamma(\cdot)$  is the log of the gamma function. In order to estimate the parameters  $\alpha$  and  $p$  via ML, we need to maximize (20.4) with respect to them. The corresponding `gretl` code snippet is

```
scalar alpha = 1
scalar p = 1

mle logl = p*ln(alpha * x) - lngamma(p) - ln(x) - alpha * x
  params alpha p
end mle
```

The first two statements

```
alpha = 1
p = 1
```

are necessary to ensure that the variables `alpha` and `p` exist before the computation of `logl` is attempted. Inside the `mle` block these variables (which could be either scalars, vectors or a combination of the two — see below for an example) are identified as the parameters that should be adjusted to maximize the likelihood via the `params` keyword. Their values will be changed by the execution of the `mle` command; upon successful completion, they will be replaced by the ML estimates. The starting value is 1 for both; this is arbitrary and does not matter much in this example (more on this later).

The above code can be made more readable, and marginally more efficient, by defining a variable to hold  $\alpha \cdot x_t$ . This command can be embedded in the `mle` block as follows:

```
mle logl = p*ln(ax) - lngamma(p) - ln(x) - ax
  series ax = alpha*x
  params alpha p
end mle
```

The variable `ax` is not added to the `params` list, of course, since it is just an auxiliary variable to facilitate the calculations. You can insert as many such auxiliary lines as you require before the `params` line, with the restriction that they must contain either (a) commands to generate series, scalars or matrices or (b) print commands (which may be used to aid in debugging).

In a simple example like this, the choice of the starting values is almost inconsequential; the algorithm is likely to converge no matter what the starting values are. However, consistent method-of-moments estimators of  $p$  and  $\alpha$  can be simply recovered from the sample mean  $m$  and variance  $V$ : since it can be shown that

$$E(x_t) = p/\alpha \quad V(x_t) = p/\alpha^2$$



it follows that the following estimators

$$\begin{aligned}\bar{\alpha} &= m/V \\ \bar{p} &= m \cdot \bar{\alpha}\end{aligned}$$

are consistent, and therefore suitable to be used as starting point for the algorithm. The gretl script code then becomes

```
scalar m = mean(x)
scalar alpha = m/var(x)
scalar p = m*alpha

mle logl = p*ln(ax) - lngamma(p) - ln(x) - ax
series ax = alpha*x
params alpha p
end mle
```

Another thing to note is that sometimes parameters are constrained within certain boundaries: in this case, for example, both  $\alpha$  and  $p$  must be positive numbers. Gretl does not check for this: it is the user's responsibility to ensure that the function is always evaluated at an admissible point in the parameter space during the iterative search for the maximum. An effective technique is to define a variable for checking that the parameters are admissible and setting the log-likelihood as undefined if the check fails. An example, which uses the conditional assignment operator, follows:

```
scalar m = mean(x)
scalar alpha = m/var(x)
scalar p = m*alpha

mle logl = check ? p*ln(ax) - lngamma(p) - ln(x) - ax : NA
series ax = alpha*x
scalar check = (alpha>0) && (p>0)
params alpha p
end mle
```

### 20.3 Stochastic frontier cost function

When modeling a cost function, it is sometimes worthwhile to incorporate explicitly into the statistical model the notion that firms may be inefficient, so that the observed cost deviates from the theoretical figure not only because of unobserved heterogeneity between firms, but also because two firms could be operating at a different efficiency level, despite being identical under all other respects. In this case we may write

$$C_i = C_i^* + u_i + v_i$$

where  $C_i$  is some variable cost indicator,  $C_i^*$  is its “theoretical” value,  $u_i$  is a zero-mean disturbance term and  $v_i$  is the inefficiency term, which is supposed to be nonnegative by its very nature.

A linear specification for  $C_i^*$  is often chosen. For example, the Cobb–Douglas cost function arises when  $C_i^*$  is a linear function of the logarithms of the input prices and the output quantities.

The *stochastic frontier* model is a linear model of the form  $y_i = x_i\beta + \varepsilon_i$  in which the error term  $\varepsilon_i$  is the sum of  $u_i$  and  $v_i$ . A common postulate is that  $u_i \sim N(0, \sigma_u^2)$  and  $v_i \sim |N(0, \sigma_v^2)|$ . If independence between  $u_i$  and  $v_i$  is also assumed, then it is possible to show that the density function of  $\varepsilon_i$  has the form:

$$f(\varepsilon_i) = \sqrt{\frac{2}{\pi}} \Phi\left(\frac{\lambda \varepsilon_i}{\sigma}\right) \frac{1}{\sigma} \phi\left(\frac{\varepsilon_i}{\sigma}\right) \quad (20.5)$$

where  $\Phi(\cdot)$  and  $\phi(\cdot)$  are, respectively, the distribution and density function of the standard normal,  $\sigma = \sqrt{\sigma_u^2 + \sigma_v^2}$  and  $\lambda = \frac{\sigma_u}{\sigma_v}$ .

As a consequence, the log-likelihood for one observation takes the form (apart from an irrelevant constant)

$$\ell_t = \log \Phi \left( \frac{\lambda \varepsilon_i}{\sigma} \right) - \left[ \log(\sigma) + \frac{\varepsilon_i^2}{2\sigma^2} \right]$$

Therefore, a Cobb–Douglas cost function with stochastic frontier is the model described by the following equations:

$$\begin{aligned} \log C_i &= \log C_i^* + \varepsilon_i \\ \log C_i^* &= c + \sum_{j=1}^m \beta_j \log y_{ij} + \sum_{j=1}^n \alpha_j \log p_{ij} \\ \varepsilon_i &= u_i + v_i \\ u_i &\sim N(0, \sigma_u^2) \\ v_i &\sim |N(0, \sigma_v^2)| \end{aligned}$$

In most cases, one wants to ensure that the homogeneity of the cost function with respect to the prices holds by construction. Since this requirement is equivalent to  $\sum_{j=1}^n \alpha_j = 1$ , the above equation for  $C_i^*$  can be rewritten as

$$\log C_i - \log p_{in} = c + \sum_{j=1}^m \beta_j \log y_{ij} + \sum_{j=2}^n \alpha_j (\log p_{ij} - \log p_{in}) + \varepsilon_i \quad (20.6)$$

The above equation could be estimated by OLS, but it would suffer from two drawbacks: first, the OLS estimator for the intercept  $c$  is inconsistent because the disturbance term has a non-zero expected value; second, the OLS estimators for the other parameters are consistent, but inefficient in view of the non-normality of  $\varepsilon_i$ . Both issues can be addressed by estimating (20.6) by maximum likelihood. Nevertheless, OLS estimation is a quick and convenient way to provide starting values for the MLE algorithm.

Example 20.1 shows how to implement the model described so far. The `banks91` file contains part of the data used in Lucchetti, Papi and Zazzaro (2001).

The script in example 20.1 is relatively easy to modify to show how one can use vectors (that is, 1-dimensional matrices) for storing the parameters to optimize: example 20.2 holds essentially the same script in which the parameters of the cost function are stored together in a vector. Of course, this makes also possible to use variable lists and other refinements which make the code more compact and readable.

## 20.4 GARCH models

GARCH models are handled by `gretl` via a native function. However, it is instructive to see how they can be estimated through the `mle` command.<sup>2</sup>

The following equations provide the simplest example of a GARCH(1,1) model:

$$\begin{aligned} y_t &= \mu + \varepsilon_t \\ \varepsilon_t &= u_t \cdot \sigma_t \\ u_t &\sim N(0, 1) \\ h_t &= \omega + \alpha \varepsilon_{t-1}^2 + \beta h_{t-1}. \end{aligned}$$

Since the variance of  $y_t$  depends on past values, writing down the log-likelihood function is not simply a matter of summing the log densities for individual observations. As is common in time

<sup>2</sup>The `gig` addon, which handles other variants of conditionally heteroskedastic models, uses `mle` as its internal engine.

**Example 20.1:** Estimation of stochastic frontier cost function (with scalar parameters)

---

```
open banks91

# Cobb-Douglas cost function

ols cost const y p1 p2 p3

# Cobb-Douglas cost function with homogeneity restrictions

genr rcost = cost - p3
genr rp1 = p1 - p3
genr rp2 = p2 - p3

ols rcost const y rp1 rp2

# Cobb-Douglas cost function with homogeneity restrictions
# and inefficiency

scalar b0 = $coeff(const)
scalar b1 = $coeff(y)
scalar b2 = $coeff(rp1)
scalar b3 = $coeff(rp2)

scalar su = 0.1
scalar sv = 0.1

mle logl = ln(cnorm(e*lambda/ss)) - (ln(ss) + 0.5*(e/ss)^2)
    scalar ss = sqrt(su^2 + sv^2)
    scalar lambda = su/sv
    series e = rcost - b0*const - b1*y - b2*rp1 - b3*rp2
    params b0 b1 b2 b3 su sv
end mle
```

---

**Example 20.2:** Estimation of stochastic frontier cost function (with matrix parameters)

---

```
open banks91

# Cobb-Douglas cost function

ols cost const y p1 p2 p3

# Cobb-Douglas cost function with homogeneity restrictions

genr rcost = cost - p3
genr rp1 = p1 - p3
genr rp2 = p2 - p3

list X = const y rp1 rp2
ols rcost X

# Cobb-Douglas cost function with homogeneity restrictions
# and inefficiency

matrix b = $coeff
scalar su = 0.1
scalar sv = 0.1

mle logl = ln(cnorm(e*lambda/ss)) - (ln(ss) + 0.5*(e/ss)^2)
    scalar ss = sqrt(su^2 + sv^2)
    scalar lambda = su/sv
    series e = rcost - lincomb(X, b)
    params b su sv
end mle
```

---

series models,  $y_t$  cannot be considered independent of the other observations in our sample, and consequently the density function for the whole sample (the joint density for all observations) is not just the product of the marginal densities.

Maximum likelihood estimation, in these cases, is achieved by considering *conditional* densities, so what we maximize is a conditional likelihood function. If we define the information set at time  $t$  as

$$F_t = \{y_t, y_{t-1}, \dots\},$$

then the density of  $y_t$  conditional on  $F_{t-1}$  is normal:

$$y_t | F_{t-1} \sim N[\mu, h_t].$$

By means of the properties of conditional distributions, the joint density can be factorized as follows

$$f(y_t, y_{t-1}, \dots) = \left[ \prod_{t=1}^T f(y_t | F_{t-1}) \right] \cdot f(y_0)$$

If we treat  $y_0$  as fixed, then the term  $f(y_0)$  does not depend on the unknown parameters, and therefore the conditional log-likelihood can then be written as the sum of the individual contributions as

$$\ell(\mu, \omega, \alpha, \beta) = \sum_{t=1}^T \ell_t \quad (20.7)$$

where

$$\ell_t = \log \left[ \frac{1}{\sqrt{h_t}} \phi \left( \frac{y_t - \mu}{\sqrt{h_t}} \right) \right] = -\frac{1}{2} \left[ \log(h_t) + \frac{(y_t - \mu)^2}{h_t} \right]$$

The following script shows a simple application of this technique, which uses the data file `djc1close`; it is one of the example dataset supplied with `gretl` and contains daily data from the Dow Jones stock index.

```
open djc1close

series y = 100*1diff(djc1close)

scalar mu = 0.0
scalar omega = 1
scalar alpha = 0.4
scalar beta = 0.0

mle ll = -0.5*(log(h) + (e^2)/h)
  series e = y - mu
  series h = var(y)
  series h = omega + alpha*(e(-1))^2 + beta*h(-1)
  params mu omega alpha beta
end mle
```

## 20.5 Analytical derivatives

Computation of the score vector is essential for the working of the BFGS method. In all the previous examples, no explicit formula for the computation of the score was given, so the algorithm was fed numerically evaluated gradients. Numerical computation of the score for the  $i$ -th parameter is performed via a finite approximation of the derivative, namely

$$\frac{\partial \ell(\theta_1, \dots, \theta_n)}{\partial \theta_i} \simeq \frac{\ell(\theta_1, \dots, \theta_i + h, \dots, \theta_n) - \ell(\theta_1, \dots, \theta_i - h, \dots, \theta_n)}{2h}$$

where  $h$  is a small number.

In many situations, this is rather efficient and accurate. A better approximation to the true derivative may be obtained by forcing `mle` to use a technique known as *Richardson Extrapolation*, which gives extremely precise results, but is considerably more CPU-intensive. This feature may be turned on by using the `set` command as in

```
set bfgs_richardson on
```

However, one might want to avoid the approximation and specify an exact function for the derivatives. As an example, consider the following script:

```
nulldata 1000

genr x1 = normal()
genr x2 = normal()
genr x3 = normal()

genr ystar = x1 + x2 + x3 + normal()
genr y = (ystar > 0)

scalar b0 = 0
scalar b1 = 0
scalar b2 = 0
scalar b3 = 0

mle logl = y*ln(P) + (1-y)*ln(1-P)
    series ndx = b0 + b1*x1 + b2*x2 + b3*x3
    series P = cnorm(ndx)
    params b0 b1 b2 b3
end mle --verbose
```

Here, 1000 data points are artificially generated for an ordinary probit model:<sup>3</sup>  $y_t$  is a binary variable, which takes the value 1 if  $y_t^* = \beta_1 x_{1t} + \beta_2 x_{2t} + \beta_3 x_{3t} + \varepsilon_t > 0$  and 0 otherwise. Therefore,  $y_t = 1$  with probability  $\Phi(\beta_1 x_{1t} + \beta_2 x_{2t} + \beta_3 x_{3t}) = \pi_t$ . The probability function for one observation can be written as

$$P(y_t) = \pi_t^{y_t} (1 - \pi_t)^{1-y_t}$$

Since the observations are independent and identically distributed, the log-likelihood is simply the sum of the individual contributions. Hence

$$\ell = \sum_{t=1}^T y_t \log(\pi_t) + (1 - y_t) \log(1 - \pi_t)$$

The `--verbose` switch at the end of the `end mle` statement produces a detailed account of the iterations done by the BFGS algorithm.

In this case, numerical differentiation works rather well; nevertheless, computation of the analytical score is straightforward, since the derivative  $\frac{\partial \ell}{\partial \beta_i}$  can be written as

$$\frac{\partial \ell}{\partial \beta_i} = \frac{\partial \ell}{\partial \pi_t} \cdot \frac{\partial \pi_t}{\partial \beta_i}$$

via the chain rule, and it is easy to see that

$$\begin{aligned} \frac{\partial \ell}{\partial \pi_t} &= \frac{y_t}{\pi_t} - \frac{1 - y_t}{1 - \pi_t} \\ \frac{\partial \pi_t}{\partial \beta_i} &= \phi(\beta_1 x_{1t} + \beta_2 x_{2t} + \beta_3 x_{3t}) \cdot x_{it} \end{aligned}$$

<sup>3</sup>Again, `gretl` does provide a native `probit` command (see section 31.1), but a probit model makes for a nice example here.

The `mle` block in the above script can therefore be modified as follows:

```
mle logl = y*ln(P) + (1-y)*ln(1-P)
  series ndx = b0 + b1*x1 + b2*x2 + b3*x3
  series P = cnorm(ndx)
  series m = dnorm(ndx)*(y/P - (1-y)/(1-P))
  deriv b0 = m
  deriv b1 = m*x1
  deriv b2 = m*x2
  deriv b3 = m*x3
end mle --verbose
```

Note that the `params` statement has been replaced by a series of `deriv` statements; these have the double function of identifying the parameters over which to optimize and providing an analytical expression for their respective score elements.

## 20.6 Debugging ML scripts

We have discussed above the main sorts of statements that are permitted within an `mle` block, namely

- auxiliary commands to generate helper variables;
- `deriv` statements to specify the gradient with respect to each of the parameters; and
- a `params` statement to identify the parameters in case analytical derivatives are not given.

For the purpose of debugging ML estimators one additional sort of statement is allowed: you can print the value of a relevant variable at each step of the iteration. This facility is more restricted than the regular `print` command. The command word `print` should be followed by the name of just one variable (a scalar, series or matrix).

In the last example above a key variable named `m` was generated, forming the basis for the analytical derivatives. To track the progress of this variable one could add a `print` statement within the ML block, as in

```
series m = dnorm(ndx)*(y/P - (1-y)/(1-P))
print m
```

## 20.7 Using functions

The `mle` command allows you to estimate models that `gretl` does not provide natively: in some cases, it may be a good idea to wrap up the `mle` block in a user-defined function (see Chapter 11), so as to extend `gretl`'s capabilities in a modular and flexible way.

As an example, we will take a simple case of a model that `gretl` does not yet provide natively: the zero-inflated Poisson model, or ZIP for short.<sup>4</sup> In this model, we assume that we observe a mixed population: for some individuals, the variable  $y_t$  is (conditionally on a vector of exogenous covariates  $x_t$ ) distributed as a Poisson random variate; for some others,  $y_t$  is identically 0. The trouble is, we don't know which category a given individual belongs to.

For instance, suppose we have a sample of women, and the variable  $y_t$  represents the number of children that woman  $t$  has. There may be a certain proportion,  $\alpha$ , of women for whom  $y_t = 0$  with certainty (maybe out of a personal choice, or due to physical impossibility). But there may be other

<sup>4</sup>The actual ZIP model is in fact a bit more general than the one presented here. The specialized version discussed in this section was chosen for the sake of simplicity. For further details, see [Greene \(2003\)](#).

women for whom  $y_t = 0$  just as a matter of chance — they haven't happened to have any children at the time of observation.

In formulae:

$$P(y_t = k | x_t) = \alpha d_t + (1 - \alpha) \left[ e^{-\mu_t} \frac{\mu_t^{y_t}}{y_t!} \right]$$

$$\mu_t = \exp(x_t \beta)$$

$$d_t = \begin{cases} 1 & \text{for } y_t = 0 \\ 0 & \text{for } y_t > 0 \end{cases}$$

Writing a `mle` block for this model is not difficult:

```
mle ll = logprob
  series xb = exp(b0 + b1 * x)
  series d = (y=0)
  series poiprob = exp(-xb) * xb^y / gamma(y+1)
  series logprob = (alpha>0) && (alpha<1) ? \
    log(alpha*d + (1-alpha)*poiprob) : NA
  params alpha b0 b1
end mle -v
```

However, the code above has to be modified each time we change our specification by, say, adding an explanatory variable. Using functions, we can simplify this task considerably and eventually be able to write something easy like

```
list X = const x
zip(y, X)
```

### Example 20.3: Zero-inflated Poisson Model — user-level function

---

```
/*
  user-level function: estimate the model and print out
  the results
*/
function void zip(series y, list X)
  matrix coef_stde = zip_estimate(y, X)
  printf "\nZero-inflated Poisson model:\n"
  string parnames = "alpha,"
  string parnames += varname(X)
  modprint coef_stde parnames
end function
```

---

Let's see how this can be done. First we need to define a function called `zip()` that will take two arguments: a dependent variable `y` and a list of explanatory variables `X`. An example of such function can be seen in script [20.3](#). By inspecting the function code, you can see that the actual estimation does not happen here: rather, the `zip()` function merely uses the built-in `modprint` command to print out the results coming from another user-written function, namely `zip_estimate()`.

The function `zip_estimate()` is not meant to be executed directly; it just contains the number-crunching part of the job, whose results are then picked up by the end function `zip()`. In turn, `zip_estimate()` calls other user-written functions to perform other tasks. The whole set of “internal” functions is shown in the panel [20.4](#).



**Example 20.4:** Zero-inflated Poisson Model — internal functions

---

```

/* compute log probabilities for the plain Poisson model */
function series ln_poi_prob(series y, list X, matrix beta)
    series xb = lincomb(X, beta)
    return -exp(xb) + y*xb - lngamma(y+1)
end function

/* compute log probabilities for the zero-inflated Poisson model */
function series ln_zip_prob(series y, list X, matrix beta, scalar p0)
    # check if the probability is in [0,1]; otherwise, return NA
    if (p0>1) || (p0<0)
        series ret = NA
    else
        series ret = ln_poi_prob(y, X, beta) + ln(1-p0)
        series ret = (y=0) ? ln(p0 + exp(ret)) : ret
    endif
    return ret
end function

/* do the actual estimation (silently) */
function matrix zip_estimate(series y, list X)
    # initialize alpha to a "sensible" value: half the frequency
    # of zeros in the sample
    scalar alpha = mean(y=0)/2
    # initialize the coeffs (we assume the first explanatory
    # variable is the constant here)
    matrix coef = zeros(nelem(X), 1)
    coef[1] = mean(y) / (1-alpha)
    # do the actual ML estimation
    mle ll = ln_zip_prob(y, X, coef, alpha)
    params alpha coef
    end mle --hessian --quiet
    return $coeff ~ $stderr
end function

```

---

All the functions shown in 20.3 and 20.4 can be stored in a separate `inp` file and executed once, at the beginning of our job, by means of the `include` command. Assuming the name of this script file is `zip_est.inp`, the following is an example script which (a) includes the script file, (b) generates a simulated dataset, and (c) performs the estimation of a ZIP model on the artificial data.

```
set echo off
set messages off

# include the user-written functions
include zip_est.inp

# generate the artificial data
nulldata 1000
set seed 732237
scalar truep = 0.2
scalar b0 = 0.2
scalar b1 = 0.5
series x = normal()
series y = (uniform() < truep) ? 0 : genpois(exp(b0 + b1*x))
list X = const x

# estimate the zero-inflated Poisson model
zip(y, X)
```

The results are as follows:

Zero-inflated Poisson model:

	coefficient	std. error	z-stat	p-value	
alpha	0.203069	0.0238035	8.531	1.45e-17	***
const	0.257014	0.0417129	6.161	7.21e-10	***
x	0.466657	0.0321235	14.53	8.17e-48	***

A further step may then be creating a function package for accessing your new `zip()` function via gretl's graphical interface. For details on how to do this, see section 11.5.

## 20.8 Advanced use of `mle`: functions, analytical derivatives, algorithm choice

All the techniques described in the previous sections may be combined, and `mle` can be used for solving non-standard estimation problems (provided, of course, that one chooses maximum likelihood as the preferred inference method).

The strategy that, as of this writing, has proven most successful in designing scripts for this purpose is:

- Modularize your code as much as possible.
- Use analytical derivatives whenever possible.
- Choose your optimization method wisely.

In the rest of this section, we will expand on the probit example of section 20.5 to give the reader an idea of what a “heavy-duty” application of `mle` looks like. Most of the code fragments come from `mle-advanced.inp`, which is one of the sample scripts supplied with the standard installation of gretl (see under *File > Script files > Practice File*).

**BFGS with and without analytical derivatives**

The example in section 20.5 can be made more general by using matrices and user-written functions. Consider the following code fragment:

```
list X = const x1 x2 x3
matrix b = zeros(nelem(X),1)

mle logl = y*ln(P) + (1-y)*ln(1-P)
    series ndx = lincomb(X, b)
    series P = cnorm(ndx)
    params b
end mle
```

In this context, the fact that the model we are estimating has four explanatory variables is totally incidental: the code is written in such a way that we could change the content of the list *X* without having to make any other modification. This was made possible by:

1. gathering the parameters to estimate into a single vector *b* rather than using separate scalars;
2. using the `nelem()` function to initialize *b*, so that its dimension is kept track of automatically;
3. using the `lincomb()` function to compute the index function.

A parallel enhancement could be achieved in the case of analytically computed derivatives: since *b* is now a vector, `mle` expects the argument to the `deriv` keyword to be a matrix, in which each column is the partial derivative to the corresponding element of *b*. It is useful to re-write the score for the *i*-th observation as

$$\frac{\partial \ell_i}{\partial \beta} = m_i \mathbf{x}'_i \quad (20.8)$$

where  $m_i$  is the “signed Mills’ ratio”, that is

$$m_i = y_i \frac{\phi(\mathbf{x}'_i \beta)}{\Phi(\mathbf{x}'_i \beta)} - (1 - y_i) \frac{\phi(\mathbf{x}'_i \beta)}{1 - \Phi(\mathbf{x}'_i \beta)},$$

which was computed in section 20.5 via

```
series P = cnorm(ndx)
series m = dnorm(ndx)*(y/P - (1-y)/(1-P))
```

Here, we will code it in a somewhat terser way as

```
series m = y ? invmills(-ndx) : -invmills(ndx)
```

and make use of the conditional assignment operator and of the specialized function `invmills()` for efficiency. Building the score matrix is now easily achieved via

```
mle logl = y*ln(P) + (1-y)*ln(1-P)
    series ndx = lincomb(X, b)
    series P = cnorm(ndx)
    series m = y ? invmills(-ndx) : -invmills(ndx)
    matrix mX = {X}
    deriv b = mX .* {m}
end mle
```

in which the `{}` operator was used to turn series and lists into matrices (see chapter 14). However, proceeding in this way for more complex models than probit may imply inserting into the `mle`

block a long series of instructions; the example above merely happens to be short because the score matrix for the probit model is very easy to write in matrix form.

A better solution is writing a user-level function to compute the score and using that inside the `mle` block, as in

```
function matrix score(matrix b, series y, list X)
    series ndx = lincomb(X, b)
    series m = y ? invmills(-ndx) : -invmills(ndx)
    return {m} .* {X}
end function

[...]

mle logl = y*ln(P) + (1-y)*ln(1-P)
    series ndx = lincomb(X, b)
    series P = cnorm(ndx)
    deriv b = score(b, y, X)
end mle
```

In this way, no matter how complex the computation of the score is, the `mle` block remains nicely compact.

### Newton's method and the analytical Hessian

Since version 1.9.7, `gretl` offers the user the option of using Newton's method for maximizing the log-likelihood. In terms of the notation used in section 20.1, the direction for updating the initial parameter vector  $\theta_0$  is given by

$$d[\mathbf{g}(\theta_0)] = -\lambda \mathbf{H}(\theta_0)^{-1} \mathbf{g}(\theta_0), \quad (20.9)$$

where  $\mathbf{H}(\theta)$  is the Hessian of the total loglikelihood computed at  $\theta$  and  $0 < \lambda < 1$  is a scalar called the *step length*.

The above expression makes a few points clear:

1. At each step, it must be possible to compute not only the score  $\mathbf{g}(\theta)$ , but also its derivative  $\mathbf{H}(\theta)$ ;
2. the matrix  $\mathbf{H}(\theta)$  should be nonsingular;
3. it is assumed that for some positive value of  $\lambda$ ,  $\ell(\theta_1) > \ell(\theta_0)$ ; in other words, that going in the direction  $d[\mathbf{g}(\theta_0)]$  leads upwards for some step length.

The strength of Newton's method lies in the fact that, if the loglikelihood is globally concave, then (20.9) enjoys certain optimality properties and the number of iterations required to reach the maximum is often much smaller than it would be with other methods, such as BFGS. However, it may have some disadvantages: for a start, the Hessian  $\mathbf{H}(\theta)$  may be difficult or very expensive to compute; moreover, the loglikelihood may not be globally concave, so for some values of  $\theta$ , the matrix  $\mathbf{H}(\theta)$  is not negative definite or perhaps even singular. Those cases are handled by `gretl`'s implementation of Newton's algorithm by means of several heuristic techniques<sup>5</sup>, but a number of adverse consequences may occur, which range from *longer* computation time for optimization to non-convergence of the algorithm.

As a consequence, using Newton's method is advisable only when the computation of the Hessian is not too CPU-intensive and the nature of the estimator is such that it is known in advance that

<sup>5</sup>The gist of it is that, if  $\mathbf{H}$  is not negative definite, it is substituted by  $k \cdot \text{dg}(\mathbf{H}) + (1 - k) \cdot \mathbf{H}$ , where  $k$  is a suitable scalar; however, if you're interested in the precise details, you'll be much better off looking at the source code: the file you'll want to look at is `lib/src/gretl_bfgs.c`.

the loglikelihood is globally concave. The probit model satisfies both requisites, so we will expand the preceding example to illustrate how to use Newton's method in gretl.

A first example may be given simply by issuing the command

```
set optimizer newton
```

before the `mle` block.<sup>6</sup> This will instruct gretl to use Newton's method instead of BFGS. If the `deriv` keyword is used, gretl will differentiate the score function numerically; otherwise, if the score has to be computed itself numerically, gretl will calculate  $\mathbf{H}(\theta)$  by differentiating the loglikelihood numerically twice. The latter solution, though, is generally to be avoided, as may be extremely time-consuming and may yield imprecise results.

A much better option is to calculate the Hessian analytically and have gretl use its true value rather than a numerical approximation. In most cases, this is both much faster and numerically stable, but of course comes at the price of having to differentiate the loglikelihood twice to respect with the parameters and translate the resulting expressions into efficient `hansl` code.

Luckily, both tasks are relatively easy in the probit case: the matrix of second derivatives of  $\ell_i$  may be written as

$$\frac{\partial^2 \ell_i}{\partial \beta \partial \beta'} = -m_i (m_i + \mathbf{x}_i' \beta) \mathbf{x}_i \mathbf{x}_i'$$

so the total Hessian is

$$\sum_{i=1}^n \frac{\partial^2 \ell_i}{\partial \beta \partial \beta'} = -X' \begin{bmatrix} w_1 & & & \\ & w_2 & & \\ & & \ddots & \\ & & & w_n \end{bmatrix} X \quad (20.10)$$

where  $w_i = m_i (m_i + \mathbf{x}_i' \beta)$ . It can be shown that  $w_i > 0$ , so the Hessian is guaranteed to be negative definite in all sensible cases and the conditions are ideal for applying Newton's method.

A `hansl` translation of equation (20.10) may look like

```
function void Hess(matrix *H, matrix b, series y, list X)
/* computes the negative Hessian for a Probit model */
series ndx = lincomb(X, b)
series m = y ? invmills(-ndx) : -invmills(ndx)
series w = m*(m+ndx)
matrix mX = {X}
H = (mX .* {w})'mX
end function
```

There are two characteristics worth noting of the function above. For a start, it doesn't return anything: the result of the computation is simply stored in the matrix pointed at by the first argument of the function. Second, the result is not the Hessian proper, but rather its negative. This function becomes usable from within an `mle` block by the keyword `hessian`. The syntax is

```
mle ...
...
hessian funcname(&mat_addr, ...)
end mle
```

In other words, the `hessian` keyword must be followed by the call to a function whose first argument is a matrix pointer which is supposed to be filled with the *negative* of the Hessian at  $\theta$ .

Another feature worth noting is that gretl does not perform any numerical check on whether the function computes the Hessian correctly or not. On the one hand, this means that you can trick

<sup>6</sup>To go back to BFGS, you use `set optimizer bfgs`.

`mle` into using alternatives to the Hessian and thereby implement other optimization methods. For example, if you substitute in equation 20.9 the Hessian  $\mathbf{H}$  with the negative of the OPG matrix  $-\mathbf{G}'\mathbf{G}$ , as defined in (20.2), you get the so-called BHHH optimization method (see Berndt *et al.* (1974)). Again, the sample file `mle-advanced.inp` provides an example. On the other hand, you may want to perform a check of your analytically-computed  $\mathbf{H}$  matrix versus a numerical approximation.

If you have a function that computes the score, this is relatively simple to do by using the `fdjac` function, briefly described in section 30.4, which computes a numerical approximation to a derivative. In practice, you need a function computing  $\mathbf{g}(\theta)$  as a row vector and then use `fdjac` to differentiate it numerically with respect to  $\theta$ . The result can then be compared to your analytically-computed Hessian. The code fragment below shows an example of how this can be done in the probit case:

```
function matrix totalscore(matrix *b, series y, list X)
    /* computes the total score */
    return sumc(score(b, y, X))
end function

function void check(matrix b, series y, list X)
    /* compares the analytical Hessian to its numerical
    approximation obtained via fdjac */
    matrix aH
    Hess(&aH, b, y, X) # stores the analytical Hessian into aH

    matrix nH = fdjac(b, "totalscore(&b, y, X)")
    nH = 0.5*(nH + nH') # force symmetry

    printf "Numerical Hessian\n%16.6f\n", nH
    printf "Analytical Hessian (negative)\n%16.6f\n", aH
    printf "Check (should be zero)\n%16.6f\n", nH + aH
end function
```

## Chapter 21

# GMM estimation

### 21.1 Introduction and terminology

The Generalized Method of Moments (GMM) is a very powerful and general estimation method, which encompasses practically all the parametric estimation techniques used in econometrics. It was introduced in Hansen (1982) and Hansen and Singleton (1982); an excellent and thorough treatment is given in chapter 17 of Davidson and MacKinnon (1993).

The basic principle on which GMM is built is rather straightforward. Suppose we wish to estimate a scalar parameter  $\theta$  based on a sample  $x_1, x_2, \dots, x_T$ . Let  $\theta_0$  indicate the “true” value of  $\theta$ . Theoretical considerations (either of statistical or economic nature) may suggest that a relationship like the following holds:

$$E[x_t - g(\theta)] = 0 \Leftrightarrow \theta = \theta_0, \quad (21.1)$$

with  $g(\cdot)$  a continuous and invertible function. That is to say, there exists a function of the data and the parameter, with the property that it has expectation zero if and only if it is evaluated at the true parameter value. For example, economic models with rational expectations lead to expressions like (21.1) quite naturally.

If the sampling model for the  $x_t$ s is such that some version of the Law of Large Numbers holds, then

$$\bar{X} = \frac{1}{T} \sum_{t=1}^T x_t \xrightarrow{p} g(\theta_0);$$

hence, since  $g(\cdot)$  is invertible, the statistic

$$\hat{\theta} = g^{-1}(\bar{X}) \xrightarrow{p} \theta_0,$$

so  $\hat{\theta}$  is a consistent estimator of  $\theta$ . A different way to obtain the same outcome is to choose, as an estimator of  $\theta$ , the value that minimizes the objective function

$$F(\theta) = \left[ \frac{1}{T} \sum_{t=1}^T (x_t - g(\theta)) \right]^2 = [\bar{X} - g(\theta)]^2; \quad (21.2)$$

the minimum is trivially reached at  $\hat{\theta} = g^{-1}(\bar{X})$ , since the expression in square brackets equals 0.

The above reasoning can be generalized as follows: suppose  $\theta$  is an  $n$ -vector and we have  $m$  relations like

$$E[f_i(x_t, \theta)] = 0 \quad \text{for } i = 1 \dots m, \quad (21.3)$$

where  $E[\cdot]$  is a conditional expectation on a set of  $p$  variables  $z_t$ , called the *instruments*. In the above simple example,  $m = 1$  and  $f(x_t, \theta) = x_t - g(\theta)$ , and the only instrument used is  $z_t = 1$ . Then, it must also be true that

$$E[f_i(x_t, \theta) \cdot z_{j,t}] = E[f_{i,j,t}(\theta)] = 0 \quad \text{for } i = 1 \dots m \quad \text{and } j = 1 \dots p; \quad (21.4)$$

equation (21.4) is known as an *orthogonality condition*, or *moment condition*. The GMM estimator is defined as the minimum of the quadratic form

$$F(\theta, W) = \tilde{\mathbf{f}}' W \tilde{\mathbf{f}}, \quad (21.5)$$

where  $\bar{\mathbf{f}}$  is a  $(1 \times m \cdot p)$  vector holding the average of the orthogonality conditions and  $W$  is some symmetric, positive definite matrix, known as the *weights* matrix. A necessary condition for the minimum to exist is the order condition  $n \leq m \cdot p$ .

The statistic

$$\hat{\theta} = \underset{\theta}{\text{Argmin}} F(\theta, W) \quad (21.6)$$

is a consistent estimator of  $\theta$  whatever the choice of  $W$ . However, to achieve maximum asymptotic efficiency  $W$  must be proportional to the inverse of the long-run covariance matrix of the orthogonality conditions; if  $W$  is not known, a consistent estimator will suffice.

These considerations lead to the following empirical strategy:

1. Choose a positive definite  $W$  and compute the *one-step* GMM estimator  $\hat{\theta}_1$ . Customary choices for  $W$  are  $I_{m \cdot p}$  or  $I_m \otimes (Z'Z)^{-1}$ .
2. Use  $\hat{\theta}_1$  to estimate  $V(f_{i,j,t}(\theta))$  and use its inverse as the weights matrix. The resulting estimator  $\hat{\theta}_2$  is called the *two-step* estimator.
3. Re-estimate  $V(f_{i,j,t}(\theta))$  by means of  $\hat{\theta}_2$  and obtain  $\hat{\theta}_3$ ; iterate until convergence. Asymptotically, these extra steps are unnecessary, since the two-step estimator is consistent and efficient; however, the iterated estimator often has better small-sample properties and should be independent of the choice of  $W$  made at step 1.

In the special case when the number of parameters  $n$  is equal to the total number of orthogonality conditions  $m \cdot p$ , the GMM estimator  $\hat{\theta}$  is the same for any choice of the weights matrix  $W$ , so the first step is sufficient; in this case, the objective function is 0 at the minimum.

If, on the contrary,  $n < m \cdot p$ , the second step (or successive iterations) is needed to achieve efficiency, and the estimator so obtained can be very different, in finite samples, from the one-step estimator. Moreover, the value of the objective function at the minimum, suitably scaled by the number of observations, yields *Hansen's J statistic*; this statistic can be interpreted as a test statistic that has a  $\chi^2$  distribution with  $m \cdot p - n$  degrees of freedom under the null hypothesis of correct specification. See Davidson and MacKinnon (1993, section 17.6) for details.

In the following sections we will show how these ideas are implemented in gretl through some examples.

## 21.2 OLS as GMM

It is instructive to start with a somewhat contrived example: consider the linear model  $y_t = x_t\beta + u_t$ . Although most of us are used to read it as the sum of a hazily defined “systematic part” plus an equally hazy “disturbance”, a more rigorous interpretation of this familiar expression comes from the *hypothesis* that the conditional mean  $E(y_t|x_t)$  is linear and the *definition* of  $u_t$  as  $y_t - E(y_t|x_t)$ .

From the definition of  $u_t$ , it follows that  $E(u_t|x_t) = 0$ . The following orthogonality condition is therefore available:

$$E[f(\beta)] = 0, \quad (21.7)$$

where  $f(\beta) = (y_t - x_t\beta)x_t$ . The definitions given in the previous section therefore specialize here to:

- $\theta$  is  $\beta$ ;
- the instrument is  $x_t$ ;
- $f_{i,j,t}(\theta)$  is  $(y_t - x_t\beta)x_t = u_tx_t$ ; the orthogonality condition is interpretable as the requirement that the regressors should be uncorrelated with the disturbances;



- $W$  can be any symmetric positive definite matrix, since the number of parameters equals the number of orthogonality conditions. Let's say we choose  $I$ .
- The function  $F(\theta, W)$  is in this case

$$F(\theta, W) = \left[ \frac{1}{T} \sum_{t=1}^T (\hat{u}_t x_t) \right]^2$$

and it is easy to see why OLS and GMM coincide here: the GMM objective function has the same minimizer as the objective function of OLS, the residual sum of squares. Note, however, that the two functions are not equal to one another: at the minimum,  $F(\theta, W) = 0$  while the minimized sum of squared residuals is zero only in the special case of a perfect linear fit.

The code snippet contained in Example 21.1 uses `gretl`'s `gmm` command to make the above operational.

#### Example 21.1: OLS via GMM

```
/* initialize stuff */
series e = 0
scalar beta = 0
matrix W = I(1)

/* proceed with estimation */
gmm
  series e = y - x*beta
  orthog e ; x
  weights W
  params beta
end gmm
```

We feed `gretl` the necessary ingredients for GMM estimation in a command block, starting with `gmm` and ending with `end gmm`. After the `end gmm` statement two mutually exclusive options can be specified: `--two-step` or `--iterate`, whose meaning should be obvious.

Three elements are compulsory within a `gmm` block:

1. one or more `orthog` statements
2. one `weights` statement
3. one `params` statement

The three elements should be given in the stated order.

The `orthog` statements are used to specify the orthogonality conditions. They must follow the syntax

```
orthog x ; Z
```

where  $x$  may be a series, matrix or list of series and  $Z$  may also be a series, matrix or list. In example 21.1, the series `e` holds the “residuals” and the series `x` holds the regressor. If `x` had been a list (a matrix), the `orthog` statement would have generated one orthogonality condition for each element (column) of `x`. Note the structure of the orthogonality condition: it is assumed that the term to the left of the semicolon represents a quantity that depends on the estimated parameters (and so must be updated in the process of iterative estimation), while the term on the right is a constant function of the data.

The `weights` statement is used to specify the initial weighting matrix and its syntax is straightforward. But please note...

☞ In cases other than one-step estimation the specified weights matrix will be overwritten with the *final* weights on completion of the `gmm` command. If you wish to execute more than one GMM block with a common starting-point it is therefore necessary to reinitialize the weights matrix between runs.

The `params` statement specifies the parameters with respect to which the GMM criterion should be minimized; it follows the same logic and rules as in the `mle` and `nls` commands.

The minimum is found through numerical minimization via BFGS (see chapters 30 and 20). The progress of the optimization procedure can be observed by appending the `--verbose` switch to the end `gmm` line.

### 21.3 TSLS as GMM

Moving closer to the proper domain of GMM, we now consider two-stage least squares (TSLS) as a case of GMM.

TSLS is employed in the case where one wishes to estimate a linear model of the form  $y_t = X_t\beta + u_t$ , but where one or more of the variables in the matrix  $X$  are potentially endogenous — correlated with the error term,  $u$ . We proceed by identifying a set of instruments,  $Z_t$ , which are explanatory for the endogenous variables in  $X$  but which are plausibly uncorrelated with  $u$ . The classic two-stage procedure is (1) regress the endogenous elements of  $X$  on  $Z$ ; then (2) estimate the equation of interest, with the endogenous elements of  $X$  replaced by their fitted values from (1).

An alternative perspective is given by GMM. We define the residual  $\hat{u}_t$  as  $y_t - X_t\hat{\beta}$ , as usual. But instead of relying on  $E(u|X) = 0$  as in OLS, we base estimation on the condition  $E(u|Z) = 0$ . In this case it is natural to base the initial weighting matrix on the covariance matrix of the instruments. Example 21.2 presents a model from Stock and Watson's *Introduction to Econometrics*. The demand for cigarettes is modeled as a linear function of the logs of price and income; income is treated as exogenous while price is taken to be endogenous and two measures of tax are used as instruments. Since we have two instruments and one endogenous variable the model is over-identified and therefore the weights matrix will influence the solution. Partial output from this script is shown in 21.3. The estimated standard errors from GMM are robust by default; if we supply the `--robust` option to the `tsls` command we get identical results.<sup>1</sup>

### 21.4 Covariance matrix options

The covariance matrix of the estimated parameters depends on the choice of  $W$  through

$$\hat{\Sigma} = (J'WJ)^{-1}J'W\Omega WJ(J'WJ)^{-1} \quad (21.8)$$

where  $J$  is a Jacobian term

$$J_{ij} = \frac{\partial \tilde{f}_i}{\partial \theta_j}$$

and  $\Omega$  is the long-run covariance matrix of the orthogonality conditions.

Gretl computes  $J$  by numeric differentiation (there is no provision for specifying a user-supplied analytical expression for  $J$  at the moment). As for  $\Omega$ , a consistent estimate is needed. The simplest choice is the sample covariance matrix of the  $f_t$ s:

$$\hat{\Omega}_0(\theta) = \frac{1}{T} \sum_{t=1}^T f_t(\theta) f_t(\theta)' \quad (21.9)$$

<sup>1</sup>The data file used in this example is available in the Stock and Watson package for gretl. See [http://gretl.sourceforge.net/gretl\\_data.html](http://gretl.sourceforge.net/gretl_data.html).

**Example 21.2:** TSLS via GMM

---

```

open cig_ch10.gdt
# real avg price including sales tax
genr ravgprs = avgprs / cpi
# real avg cig-specific tax
genr rtax = tax / cpi
# real average total tax
genr rtaxs = taxes / cpi
# real average sales tax
genr rtaxso = rtaxs - rtax
# logs of consumption, price, income
genr lpackpc = log(packpc)
genr lravgprs = log(ravgprs)
genr lperinc = income / (pop*cpi)
genr lperinc = log(perinc)
# restrict sample to 1995 observations
smpl --restrict year=1995
# Equation (10.16) by tsls
list xlist = const lravgprs lperinc
list zlist = const rtaxso rtax lperinc
tsls lpackpc xlist ; zlist --robust

# setup for gmm
matrix Z = { zlist }
matrix W = inv(Z'Z)
series e = 0
scalar b0 = 1
scalar b1 = 1
scalar b2 = 1

gmm e = lpackpc - b0 - b1*lravgprs - b2*lperinc
    orthog e ; Z
    weights W
    params b0 b1 b2
end gmm

```

---

**Example 21.3:** TSLS via GMM: partial output

Model 1: TSLS estimates using the 48 observations 1-48

Dependent variable: lpackpc

Instruments: rtaxso rtax

Heteroskedasticity-robust standard errors, variant HCO

VARIABLE	COEFFICIENT	STDERROR	T STAT	P-VALUE
const	9.89496	0.928758	10.654	<0.00001 ***
lragvprs	-1.27742	0.241684	-5.286	<0.00001 ***
lperinc	0.280405	0.245828	1.141	0.25401

Model 2: 1-step GMM estimates using the 48 observations 1-48

e = lpackpc - b0 - b1\*lragvprs - b2\*lperinc

PARAMETER	ESTIMATE	STDERROR	T STAT	P-VALUE
b0	9.89496	0.928758	10.654	<0.00001 ***
b1	-1.27742	0.241684	-5.286	<0.00001 ***
b2	0.280405	0.245828	1.141	0.25401

GMM criterion = 0.0110046

This estimator is robust with respect to heteroskedasticity, but not with respect to autocorrelation. A heteroskedasticity- and autocorrelation-consistent (HAC) variant can be obtained using the Bartlett kernel or similar. A univariate version of this is used in the context of the `lrvvar()` function — see equation (6.1). The multivariate version is set out in equation (21.10).

$$\hat{\Omega}_k(\theta) = \frac{1}{T} \sum_{t=k}^{T-k} \left[ \sum_{i=-k}^k w_i f_t(\theta) f_{t-i}(\theta)' \right], \quad (21.10)$$

Gretl computes the HAC covariance matrix by default when a GMM model is estimated on time series data. You can control the kernel and the bandwidth (that is, the value of  $k$  in 21.10) using the `set` command. See chapter 16 for further discussion of HAC estimation. You can also ask `gretl` *not* to use the HAC version by saying

```
set force_hc on
```

## 21.5 A real example: the Consumption Based Asset Pricing Model

To illustrate `gretl`'s implementation of GMM, we will replicate the example given in chapter 3 of Hall (2005). The model to estimate is a classic application of GMM, and provides an example of a case when orthogonality conditions do not stem from statistical considerations, but rather from economic theory.

A rational individual who must allocate his income between consumption and investment in a financial asset must in fact choose the consumption path of his whole lifetime, since investment translates into future consumption. It can be shown that an optimal consumption path should satisfy the following condition:

$$pU'(c_t) = \delta^k E[r_{t+k}U'(c_{t+k})|\mathcal{F}_t], \quad (21.11)$$

where  $p$  is the asset price,  $U(\cdot)$  is the individual's utility function,  $\delta$  is the individual's subjective discount rate and  $r_{t+k}$  is the asset's rate of return between time  $t$  and time  $t+k$ .  $\mathcal{F}_t$  is the *information set* at time  $t$ ; equation (21.11) says that the utility “lost” at time  $t$  by purchasing the asset

instead of consumption goods must be matched by a corresponding increase in the (discounted) future utility of the consumption financed by the asset's return. Since the future is uncertain, the individual considers his expectation, conditional on what is known at the time when the choice is made.

We have said nothing about the nature of the asset, so equation (21.11) should hold whatever asset we consider; hence, it is possible to build a system of equations like (21.11) for each asset whose price we observe.

If we are willing to believe that

- the economy as a whole can be represented as a single gigantic and immortal representative individual, and
- the function  $U(x) = \frac{x^{\alpha-1}}{\alpha}$  is a faithful representation of the individual's preferences,

then, setting  $k = 1$ , equation (21.11) implies the following for any asset  $j$ :

$$E \left[ \delta \frac{r_{j,t+1}}{p_{j,t}} \left( \frac{C_{t+1}}{C_t} \right)^{\alpha-1} \middle| \mathcal{F}_t \right] = 1, \quad (21.12)$$

where  $C_t$  is aggregate consumption and  $\alpha$  and  $\delta$  are the risk aversion and discount rate of the representative individual. In this case, it is easy to see that the “deep” parameters  $\alpha$  and  $\delta$  can be estimated via GMM by using

$$e_t = \delta \frac{r_{j,t+1}}{p_{j,t}} \left( \frac{C_{t+1}}{C_t} \right)^{\alpha-1} - 1$$

as the moment condition, while any variable known at time  $t$  may serve as an instrument.

In the example code given in 21.4, we replicate selected portions of table 3.7 in Hall (2005). The variable `consrat` is defined as the ratio of monthly consecutive real per capita consumption (services and nondurables) for the US, and `ewr` is the return–price ratio of a fictitious asset constructed by averaging all the stocks in the NYSE. The instrument set contains the constant and two lags of each variable.

The command `set force_hc on` on the second line of the script has the sole purpose of replicating the given example: as mentioned above, it forces `gretl` to compute the long-run variance of the orthogonality conditions according to equation (21.9) rather than (21.10).

We run `gmm` four times: one-step estimation for each of two initial weights matrices, then iterative estimation starting from each set of initial weights. Since the number of orthogonality conditions (5) is greater than the number of estimated parameters (2), the choice of initial weights should make a difference, and indeed we see fairly substantial differences between the one-step estimates (Models 1 and 2). On the other hand, iteration reduces these differences almost to the vanishing point (Models 3 and 4).

Part of the output is given in 21.5. It should be noted that the  $J$  test leads to a rejection of the hypothesis of correct specification. This is perhaps not surprising given the heroic assumptions required to move from the microeconomic principle in equation (21.11) to the aggregate system that is actually estimated.

## 21.6 Caveats

A few words of warning are in order: despite its ingenuity, GMM is possibly the most fragile estimation method in econometrics. The number of non-obvious choices one has to make when using GMM is high, and in finite samples each of these can have dramatic consequences on the eventual output. Some of the factors that may affect the results are:

1. Orthogonality conditions can be written in more than one way: for example, if  $E(x_t - \mu) = 0$ , then  $E(x_t/\mu - 1) = 0$  holds too. It is possible that a different specification of the moment conditions leads to different results.

**Example 21.4:** Estimation of the Consumption Based Asset Pricing Model

---

```

open hall.gdt
set force_hc on

scalar alpha = 0.5
scalar delta = 0.5
series e = 0

list inst = const consrat(-1) consrat(-2) ewr(-1) ewr(-2)

matrix V0 = 100000*I(nelem(inst))
matrix Z = { inst }
matrix V1 = $nobs*inv(Z'Z)

gmm e = delta*ewr*consrat^(alpha-1) - 1
    orthog e ; inst
    weights V0
    params alpha delta
end gmm

gmm e = delta*ewr*consrat^(alpha-1) - 1
    orthog e ; inst
    weights V1
    params alpha delta
end gmm

gmm e = delta*ewr*consrat^(alpha-1) - 1
    orthog e ; inst
    weights V0
    params alpha delta
end gmm --iterate

gmm e = delta*ewr*consrat^(alpha-1) - 1
    orthog e ; inst
    weights V1
    params alpha delta
end gmm --iterate

```

---

**Example 21.5:** Estimation of the Consumption Based Asset Pricing Model — output

---

Model 1: 1-step GMM estimates using the 465 observations 1959:04-1997:12

$e = d*ewr*consrat^{(\alpha-1)} - 1$

PARAMETER	ESTIMATE	STDERROR	T STAT	P-VALUE
alpha	-3.14475	6.84439	-0.459	0.64590
d	0.999215	0.0121044	82.549	<0.00001 ***

GMM criterion = 2778.08

Model 2: 1-step GMM estimates using the 465 observations 1959:04-1997:12

$e = d*ewr*consrat^{(\alpha-1)} - 1$

PARAMETER	ESTIMATE	STDERROR	T STAT	P-VALUE
alpha	0.398194	2.26359	0.176	0.86036
d	0.993180	0.00439367	226.048	<0.00001 ***

GMM criterion = 14.247

Model 3: Iterated GMM estimates using the 465 observations 1959:04-1997:12

$e = d*ewr*consrat^{(\alpha-1)} - 1$

PARAMETER	ESTIMATE	STDERROR	T STAT	P-VALUE
alpha	-0.344325	2.21458	-0.155	0.87644
d	0.991566	0.00423620	234.070	<0.00001 ***

GMM criterion = 5491.78

J test: Chi-square(3) = 11.8103 (p-value 0.0081)

Model 4: Iterated GMM estimates using the 465 observations 1959:04-1997:12

$e = d*ewr*consrat^{(\alpha-1)} - 1$

PARAMETER	ESTIMATE	STDERROR	T STAT	P-VALUE
alpha	-0.344315	2.21359	-0.156	0.87639
d	0.991566	0.00423469	234.153	<0.00001 ***

GMM criterion = 5491.78

J test: Chi-square(3) = 11.8103 (p-value 0.0081)

---

2. As with all other numerical optimization algorithms, weird things may happen when the objective function is nearly flat in some directions or has multiple minima. BFGS is usually quite good, but there is no guarantee that it always delivers a sensible solution, if one at all.
3. The 1-step and, to a lesser extent, the 2-step estimators may be sensitive to apparently trivial details, like the re-scaling of the instruments. Different choices for the initial weights matrix can also have noticeable consequences.
4. With time-series data, there is no hard rule on the appropriate number of lags to use when computing the long-run covariance matrix (see section 21.4). Our advice is to go by trial and error, since results may be greatly influenced by a poor choice. Future versions of `gretl` will include more options on covariance matrix estimation.

One of the consequences of this state of things is that replicating various well-known published studies may be extremely difficult. Any non-trivial result is virtually impossible to reproduce unless all details of the estimation procedure are carefully recorded.



## Chapter 22

# Model selection criteria

### 22.1 Introduction

In some contexts the econometrician chooses between alternative models based on a formal hypothesis test. For example, one might choose a more general model over a more restricted one if the restriction in question can be formulated as a testable null hypothesis, and the null is rejected on an appropriate test.

In other contexts one sometimes seeks a criterion for model selection that somehow measures the balance between goodness of fit or likelihood, on the one hand, and parsimony on the other. The balancing is necessary because the addition of extra variables to a model cannot reduce the degree of fit or likelihood, and is very likely to increase it somewhat even if the additional variables are not truly relevant to the data-generating process.

The best known such criterion, for linear models estimated via least squares, is the adjusted  $R^2$ ,

$$\bar{R}^2 = 1 - \frac{\text{SSR}/(n - k)}{\text{TSS}/(n - 1)}$$

where  $n$  is the number of observations in the sample,  $k$  denotes the number of parameters estimated, and SSR and TSS denote the sum of squared residuals and the total sum of squares for the dependent variable, respectively. Compared to the ordinary coefficient of determination or unadjusted  $R^2$ ,

$$R^2 = 1 - \frac{\text{SSR}}{\text{TSS}}$$

the “adjusted” calculation penalizes the inclusion of additional parameters, other things equal.

### 22.2 Information criteria

A more general criterion in a similar spirit is Akaike’s (1974) “Information Criterion” (AIC). The original formulation of this measure is

$$\text{AIC} = -2\ell(\hat{\theta}) + 2k \quad (22.1)$$

where  $\ell(\hat{\theta})$  represents the maximum loglikelihood as a function of the vector of parameter estimates,  $\hat{\theta}$ , and  $k$  (as above) denotes the number of “independently adjusted parameters within the model.” In this formulation, with AIC negatively related to the likelihood and positively related to the number of parameters, the researcher seeks the minimum AIC.

The AIC can be confusing, in that several variants of the calculation are “in circulation.” For example, Davidson and MacKinnon (2004) present a simplified version,

$$\text{AIC} = \ell(\hat{\theta}) - k$$

which is just  $-2$  times the original: in this case, obviously, one wants to maximize AIC.

In the case of models estimated by least squares, the loglikelihood can be written as

$$\ell(\hat{\theta}) = -\frac{n}{2}(1 + \log 2\pi - \log n) - \frac{n}{2} \log \text{SSR} \quad (22.2)$$

Substituting (22.2) into (22.1) we get

$$\text{AIC} = n(1 + \log 2\pi - \log n) + n \log \text{SSR} + 2k$$

which can also be written as

$$\text{AIC} = n \log \left( \frac{\text{SSR}}{n} \right) + 2k + n(1 + \log 2\pi) \quad (22.3)$$

Some authors simplify the formula for the case of models estimated via least squares. For instance, William Greene writes

$$\text{AIC} = \log \left( \frac{\text{SSR}}{n} \right) + \frac{2k}{n} \quad (22.4)$$

This variant can be derived from (22.3) by dividing through by  $n$  and subtracting the constant  $1 + \log 2\pi$ . That is, writing  $\text{AIC}_G$  for the version given by Greene, we have

$$\text{AIC}_G = \frac{1}{n} \text{AIC} - (1 + \log 2\pi)$$

Finally, Ramanathan gives a further variant:

$$\text{AIC}_R = \left( \frac{\text{SSR}}{n} \right) e^{2k/n}$$

which is the exponential of the one given by Greene.

Gretl began by using the Ramanathan variant, but since version 1.3.1 the program has used the original Akaike formula (22.1), and more specifically (22.3) for models estimated via least squares.

Although the Akaike criterion is designed to favor parsimony, arguably it does not go far enough in that direction. For instance, if we have two nested models with  $k - 1$  and  $k$  parameters respectively, and if the null hypothesis that parameter  $k$  equals 0 is true, in large samples the AIC will nonetheless tend to select the less parsimonious model about 16 percent of the time (see Davidson and MacKinnon, 2004, chapter 15).

An alternative to the AIC which avoids this problem is the Schwarz (1978) “Bayesian information criterion” (BIC). The BIC can be written (in line with Akaike’s formulation of the AIC) as

$$\text{BIC} = -2\ell(\hat{\theta}) + k \log n$$

The multiplication of  $k$  by  $\log n$  in the BIC means that the penalty for adding extra parameters grows with the sample size. This ensures that, asymptotically, one will not select a larger model over a correctly specified parsimonious model.

A further alternative to AIC, which again tends to select more parsimonious models than AIC, is the Hannan–Quinn criterion or HQC (Hannan and Quinn, 1979). Written consistently with the formulations above, this is

$$\text{HQC} = -2\ell(\hat{\theta}) + 2k \log \log n$$

The Hannan–Quinn calculation is based on the law of the iterated logarithm (note that the last term is the log of the log of the sample size). The authors argue that their procedure provides a “strongly consistent estimation procedure for the order of an autoregression”, and that “compared to other strongly consistent procedures this procedure will underestimate the order to a lesser degree.”

Gretl reports the AIC, BIC and HQC (calculated as explained above) for most sorts of models. The key point in interpreting these values is to know whether they are calculated such that smaller values are better, or such that larger values are better. In gretl, smaller values are better: one wants to minimize the chosen criterion.

## Chapter 23

# Time series filters

In addition to the usual application of lags and differences, gretl provides fractional differencing and various filters commonly used in macroeconomics for trend-cycle decomposition: notably the Hodrick–Prescott filter (Hodrick and Prescott, 1997), the Baxter–King bandpass filter (Baxter and King, 1999) and the Butterworth filter (Butterworth, 1930).

### 23.1 Fractional differencing

The concept of differencing a time series  $d$  times is pretty obvious when  $d$  is an integer; it may seem odd when  $d$  is fractional. However, this idea has a well-defined mathematical content: consider the function

$$f(z) = (1 - z)^{-d},$$

where  $z$  and  $d$  are real numbers. By taking a Taylor series expansion around  $z = 0$ , we see that

$$f(z) = 1 + dz + \frac{d(d+1)}{2}z^2 + \dots$$

or, more compactly,

$$f(z) = 1 + \sum_{i=1}^{\infty} \psi_i z^i$$

with

$$\psi_k = \frac{\prod_{i=1}^k (d + i - 1)}{k!} = \psi_{k-1} \frac{d + k - 1}{k}$$

The same expansion can be used with the lag operator, so that if we defined

$$Y_t = (1 - L)^{0.5} X_t$$

this could be considered shorthand for

$$Y_t = X_t - 0.5X_{t-1} - 0.125X_{t-2} - 0.0625X_{t-3} - \dots$$

In gretl this transformation can be accomplished by the syntax

```
genr Y = fracdiff(X,0.5)
```

### 23.2 The Hodrick–Prescott filter

This filter is accessed using the `hpfilt()` function, which takes as its first argument the name of the variable to be processed. (A further optional argument is explained below.)

A time series  $y_t$  may be decomposed into a trend or growth component  $g_t$  and a cyclical component  $c_t$ .

$$y_t = g_t + c_t, \quad t = 1, 2, \dots, T$$

The Hodrick-Prescott filter effects such a decomposition by minimizing the following:

$$\sum_{t=1}^T (y_t - g_t)^2 + \lambda \sum_{t=2}^{T-1} ((g_{t+1} - g_t) - (g_t - g_{t-1}))^2.$$

The first term above is the sum of squared cyclical components  $c_t = y_t - g_t$ . The second term is a multiple  $\lambda$  of the sum of squares of the trend component's second differences. This second term penalizes variations in the growth rate of the trend component: the larger the value of  $\lambda$ , the higher is the penalty and hence the smoother the trend series.

Note that the `hpfilt` function in `gretl` produces the cyclical component,  $c_t$ , of the original series. If you want the smoothed trend you can subtract the cycle from the original:

```
genr ct = hpfilt(yt)
genr gt = yt - ct
```

Hodrick and Prescott (1997) suggest that a value of  $\lambda = 1600$  is reasonable for quarterly data. The default value in `gretl` is 100 times the square of the data frequency (which, of course, yields 1600 for quarterly data). The value can be adjusted using an optional second argument to `hpfilt()`, as in

```
genr ct = hpfilt(yt, 1300)
```

### 23.3 The Baxter and King filter

This filter is accessed using the `bkfilt()` function, which again takes the name of the variable to be processed as its first argument. The operation of the filter can be controlled via three further optional argument.

Consider the spectral representation of a time series  $y_t$ :

$$y_t = \int_{-\pi}^{\pi} e^{i\omega} dZ(\omega)$$

To extract the component of  $y_t$  that lies between the frequencies  $\underline{\omega}$  and  $\overline{\omega}$  one could apply a bandpass filter:

$$c_t^* = \int_{-\pi}^{\pi} F^*(\omega) e^{i\omega} dZ(\omega)$$

where  $F^*(\omega) = 1$  for  $\underline{\omega} < |\omega| < \overline{\omega}$  and 0 elsewhere. This would imply, in the time domain, applying to the series a filter with an infinite number of coefficients, which is undesirable. The Baxter and King bandpass filter applies to  $y_t$  a finite polynomial in the lag operator  $A(L)$ :

$$c_t = A(L)y_t$$

where  $A(L)$  is defined as

$$A(L) = \sum_{i=-k}^k a_i L^i$$

The coefficients  $a_i$  are chosen such that  $F(\omega) = A(e^{i\omega})A(e^{-i\omega})$  is the best approximation to  $F^*(\omega)$  for a given  $k$ . Clearly, the higher  $k$  the better the approximation is, but since  $2k$  observations have to be discarded, a compromise is usually sought. Moreover, the filter has also other appealing theoretical properties, among which the property that  $A(1) = 0$ , so a series with a single unit root is made stationary by application of the filter.

In practice, the filter is normally used with monthly or quarterly data to extract the “business cycle” component, namely the component between 6 and 36 quarters. Usual choices for  $k$  are 8 or

12 (maybe higher for monthly series). The default values for the frequency bounds are 8 and 32, and the default value for the approximation order,  $k$ , is 8. You can adjust these values using the full form of `bkfilt()`, which is

`bkfilt(seriesname, f1, f2, k)`

where  $f1$  and  $f2$  represent the lower and upper frequency bounds respectively.

### 23.4 The Butterworth filter

The Butterworth filter (Butterworth, 1930) is an approximation to an “ideal” square-wave filter. The ideal filter divides the spectrum of a time series into a pass-band (frequencies less than some chosen  $\omega^*$  for a low-pass filter, or frequencies greater than  $\omega^*$  for high-pass) and a stop-band; the gain is 1 for the pass-band and 0 for the stop-band. The ideal filter is unattainable in practice since it would require an infinite number of coefficients, but the Butterworth filter offers a remarkably good approximation. This filter is derived and persuasively advocated by Pollock (2000).

For data  $y$ , the filtered sequence  $x$  is given by

$$x = y - \lambda \Sigma Q (M + \lambda Q' \Sigma Q)^{-1} Q' y \quad (23.1)$$

where

$$\Sigma = \{2I_T - (L_T + L_T^{-1})\}^{T-2} \quad \text{and} \quad M = \{2I_T + (L_T + L_T^{-1})\}^T$$

$I_T$  denotes the identity matrix of order  $T$ ;  $L_T = [e_1, e_2, \dots, e_{T-1}, 0]$  is the finite-sample matrix version of the lag operator; and  $Q$  is defined such that pre-multiplication of a  $T$ -vector of data by  $Q'$  of order  $(T-2) \times T$  produces the second differences of the data. The matrix product

$$Q' \Sigma Q = \{2I_T - (L_T + L_T^{-1})\}^T$$

is a Toeplitz matrix.

The behavior of the Butterworth filter is governed by two parameters: the frequency cutoff  $\omega^*$  and an integer order,  $n$ , which determines the number of coefficients used. The  $\lambda$  that appears in (23.1) is  $\tan(\omega^*/2)^{-2n}$ . Higher values of  $n$  produce a better approximation to the ideal filter in principle (i.e. a sharper cut between the pass-band and the stop-band) but there is a downside: with a greater number of coefficients numerical instability may be an issue, and the influence of the initial values in the sample may be exaggerated.

In `gretl` the Butterworth filter is implemented by the `bwfilt()` function,<sup>1</sup> which takes three arguments: the series to filter, the order  $n$  and the frequency cutoff,  $\omega^*$ , expressed in degrees. The cutoff value must be greater than 0 and less than 180. This function operates as a low-pass filter; for the high-pass variant, subtract the filtered series from the original, as in

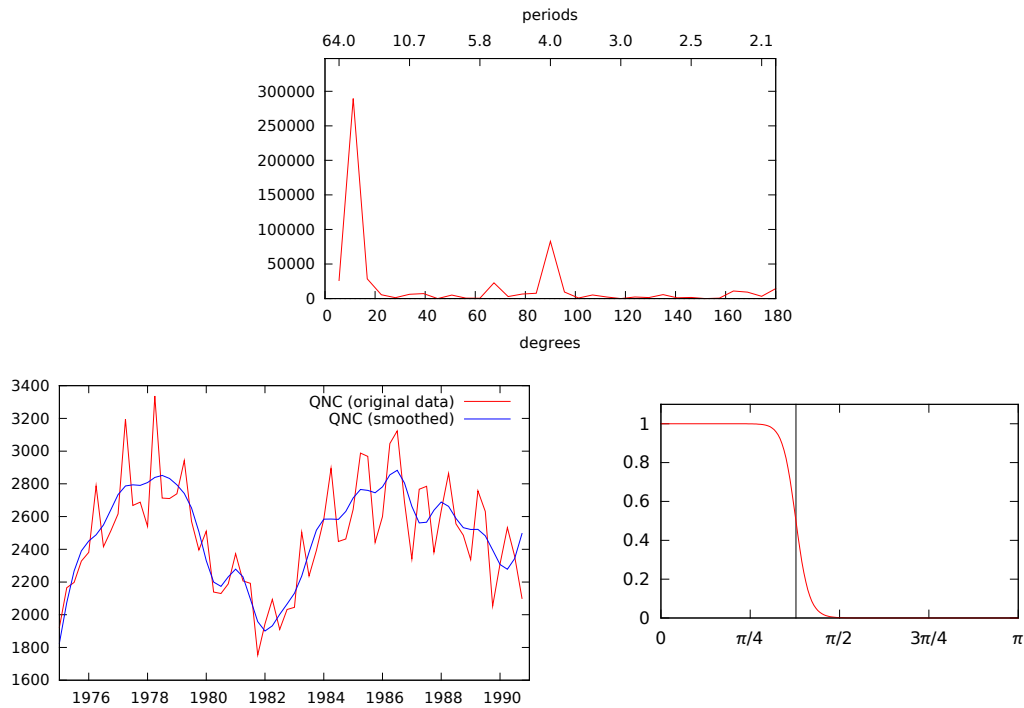
```
series bwcycle = y - bwfilt(y, 8, 67)
```

Pollock recommends that the parameters of the Butterworth filter be tuned to the data: one should examine the periodogram of the series in question (possibly after removal of a polynomial trend) in search of a “dead spot” of low power between the frequencies one wishes to exclude and the frequencies one wishes to retain. If  $\omega^*$  is placed in such a dead spot then the job of separation can be done with a relatively small  $n$ , hence avoiding numerical problems. By way of illustration, consider the periodogram for quarterly observations on new cars sales in the US,<sup>2</sup> 1975:1 to 1990:4 (the upper panel in Figure 23.1).

A seasonal pattern is clearly visible in the periodogram, centered at an angle of  $90^\circ$  or 4 periods. If we set  $\omega^* = 68^\circ$  (or thereabouts) we should be able to excise the seasonality quite cleanly using

<sup>1</sup>The code for this filter is based on D. S. G. Pollock's programs IDEOLOG and DETREND. The Pascal source code for the former is available from <http://www.le.ac.uk/users/dsgp1> and the C sources for the latter were kindly made available to us by the author.

<sup>2</sup>This is the variable QNC from the Ramanathan data file data9-7.



**Figure 23.1:** The Butterworth filter applied

$n = 8$ . The result is shown in the lower panel of the Figure, along with the frequency response or gain plot for the chosen filter. Note the smooth and reasonably steep drop-off in gain centered on the nominal cutoff of  $68^\circ \approx 3\pi/8$ .

The apparatus that supports this sort of analysis in the **gretl** GUI can be found under the **Variable** menu in the main window: the items **Periodogram** and **Filter**. In the periodogram dialog box you have the option of expressing the frequency axis in degrees, which is helpful when selecting a Butterworth filter; and in the Butterworth filter dialog you have the option of plotting the frequency response as well as the smoothed series and/or the residual or cycle.

## Chapter 24

# Univariate time series models

### 24.1 Introduction

Time series models are discussed in this chapter and the next two. Here we concentrate on ARIMA models, unit root tests, and GARCH. The following chapter deals with VARs, and chapter 26 with cointegration and error correction.

### 24.2 ARIMA models

#### Representation and syntax

The `arma` command performs estimation of AutoRegressive, Integrated, Moving Average (ARIMA) models. These are models that can be written in the form

$$\phi(L)y_t = \theta(L)\epsilon_t \quad (24.1)$$

where  $\phi(L)$ , and  $\theta(L)$  are polynomials in the lag operator,  $L$ , defined such that  $L^n x_t = x_{t-n}$ , and  $\epsilon_t$  is a white noise process. The exact content of  $y_t$ , of the AR polynomial  $\phi()$ , and of the MA polynomial  $\theta()$ , will be explained in the following.

#### Mean terms

The process  $y_t$  as written in equation (24.1) has, without further qualifications, mean zero. If the model is to be applied to real data, it is necessary to include some term to handle the possibility that  $y_t$  has non-zero mean. There are two possible ways to represent processes with nonzero mean: one is to define  $\mu_t$  as the *unconditional* mean of  $y_t$ , namely the central value of its marginal distribution. Therefore, the series  $\tilde{y}_t = y_t - \mu_t$  has mean 0, and the model (24.1) applies to  $\tilde{y}_t$ . In practice, assuming that  $\mu_t$  is a linear function of some observable variables  $x_t$ , the model becomes

$$\phi(L)(y_t - x_t\beta) = \theta(L)\epsilon_t \quad (24.2)$$

This is sometimes known as a “regression model with ARMA errors”; its structure may be more apparent if we represent it using two equations:

$$\begin{aligned} y_t &= x_t\beta + u_t \\ \phi(L)u_t &= \theta(L)\epsilon_t \end{aligned}$$

The model just presented is also sometimes known as “ARMAX” (ARMA + eXogenous variables). It seems to us, however, that this label is more appropriately applied to a different model: another way to include a mean term in (24.1) is to base the representation on the *conditional* mean of  $y_t$ , that is the central value of the distribution of  $y_t$  *given its own past*. Assuming, again, that this can be represented as a linear combination of some observable variables  $z_t$ , the model would expand to

$$\phi(L)y_t = z_t\gamma + \theta(L)\epsilon_t \quad (24.3)$$

The formulation (24.3) has the advantage that  $\gamma$  can be immediately interpreted as the vector of marginal effects of the  $z_t$  variables on the conditional mean of  $y_t$ . And by adding lags of  $z_t$  to

this specification one can estimate *Transfer Function models* (which generalize ARMA by adding the effects of exogenous variable distributed across time).

Gretl provides a way to estimate both forms. Models written as in (24.2) are estimated by maximum likelihood; models written as in (24.3) are estimated by conditional maximum likelihood. (For more on these options see the section on “Estimation” below.)

In the special case when  $x_t = z_t = 1$  (that is, the models include a constant but no exogenous variables) the two specifications discussed above reduce to

$$\phi(L)(y_t - \mu) = \theta(L)\epsilon_t \quad (24.4)$$

and

$$\phi(L)y_t = \alpha + \theta(L)\epsilon_t \quad (24.5)$$

respectively. These formulations are essentially equivalent, but if they represent one and the same process  $\mu$  and  $\alpha$  are, fairly obviously, not numerically identical; rather

$$\alpha = (1 - \phi_1 - \dots - \phi_p)\mu$$

The `gretl` syntax for estimating (24.4) is simply

```
arma p q ; y
```

The AR and MA lag orders,  $p$  and  $q$ , can be given either as numbers or as pre-defined scalars. The parameter  $\mu$  can be dropped if necessary by appending the option `--nc` (“no constant”) to the command. If estimation of (24.5) is needed, the switch `--conditional` must be appended to the command, as in

```
arma p q ; y --conditional
```

Generalizing this principle to the estimation of (24.2) or (24.3), you get that

```
arma p q ; y const x1 x2
```

would estimate the following model:

$$y_t - x_t\beta = \phi_1(y_{t-1} - x_{t-1}\beta) + \dots + \phi_p(y_{t-p} - x_{t-p}\beta) + \epsilon_t + \theta_1\epsilon_{t-1} + \dots + \theta_q\epsilon_{t-q}$$

where in this instance  $x_t\beta = \beta_0 + x_{t,1}\beta_1 + x_{t,2}\beta_2$ . Appending the `--conditional` switch, as in

```
arma p q ; y const x1 x2 --conditional
```

would estimate the following model:

$$y_t = x_t\gamma + \phi_1y_{t-1} + \dots + \phi_py_{t-p} + \epsilon_t + \theta_1\epsilon_{t-1} + \dots + \theta_q\epsilon_{t-q}$$

Ideally, the issue broached above could be made moot by writing a more general specification that nests the alternatives; that is

$$\phi(L)(y_t - x_t\beta) = z_t\gamma + \theta(L)\epsilon_t; \quad (24.6)$$

we would like to generalize the `arma` command so that the user could specify, for any estimation method, whether certain exogenous variables should be treated as  $x_t$ s or  $z_t$ s, but we’re not yet at that point (and neither are most other software packages).



### Seasonal models

A more flexible lag structure is desirable when analyzing time series that display strong seasonal patterns. Model (24.1) can be expanded to

$$\phi(L)\Phi(L^s)y_t = \theta(L)\Theta(L^s)\epsilon_t. \quad (24.7)$$

For such cases, a fuller form of the syntax is available, namely,

```
arma p q ; P Q ; y
```

where  $p$  and  $q$  represent the non-seasonal AR and MA orders, and  $P$  and  $Q$  the seasonal orders. For example,

```
arma 1 1 ; 1 1 ; y
```

would be used to estimate the following model:

$$(1 - \phi L)(1 - \Phi L^s)(y_t - \mu) = (1 + \theta L)(1 + \Theta L^s)\epsilon_t$$

If  $y_t$  is a quarterly series (and therefore  $s = 4$ ), the above equation can be written more explicitly as

$$y_t - \mu = \phi(y_{t-1} - \mu) + \Phi(y_{t-4} - \mu) - (\phi \cdot \Phi)(y_{t-5} - \mu) + \epsilon_t + \theta\epsilon_{t-1} + \Theta\epsilon_{t-4} + (\theta \cdot \Theta)\epsilon_{t-5}$$

Such a model is known as a “multiplicative seasonal ARMA model”.

### Gaps in the lag structure

The standard way to specify an ARMA model in `gretl` is via the AR and MA orders,  $p$  and  $q$  respectively. In this case all lags from 1 to the given order are included. In some cases one may wish to include only certain specific AR and/or MA lags. This can be done in either of two ways.

- One can construct a matrix containing the desired lags (positive integer values) and supply the name of this matrix in place of  $p$  or  $q$ .
- One can give a space-separated list of lags, enclosed in braces, in place of  $p$  or  $q$ .

The following code illustrates these options:

```
matrix pvec = {1, 4}
arma pvec 1 ; y
arma {1 4} 1 ; y
```

Both forms above specify an ARMA model in which AR lags 1 and 4 are used (but not 2 and 3).

This facility is available only for the non-seasonal component of the ARMA specification.

### Differencing and ARIMA

The above discussion presupposes that the time series  $y_t$  has already been subjected to all the transformations deemed necessary for ensuring stationarity (see also section 24.3). Differencing is the most common of these transformations, and `gretl` provides a mechanism to include this step into the `arma` command: the syntax

```
arma p d q ; y
```

would estimate an  $\text{ARMA}(p, q)$  model on  $\Delta^d y_t$ . It is functionally equivalent to

```

series tmp = y
loop i=1..d
    tmp = diff(tmp)
endloop
arma p q ; tmp

```

except with regard to forecasting after estimation (see below).

When the series  $y_t$  is differenced before performing the analysis the model is known as ARIMA (“I” for Integrated); for this reason, `gretl` provides the `arima` command as an alias for `arma`.

Seasonal differencing is handled similarly, with the syntax

```
arma p d q ; P D Q ; y
```

where `D` is the order for seasonal differencing. Thus, the command

```
arma 1 0 0 ; 1 1 1 ; y
```

would produce the same parameter estimates as

```

genr dsy = sdiff(y)
arma 1 0 ; 1 1 ; dsy

```

where we use the `sdiff` function to create a seasonal difference (e.g. for quarterly data,  $y_t - y_{t-4}$ ).

In specifying an ARIMA model with exogenous regressors we face a choice which relates back to the discussion of the variant models (24.2) and (24.3) above. If we choose model (24.2), the “regression model with ARMA errors”, how should this be extended to the case of ARIMA? The issue is whether or not the differencing that is applied to the dependent variable should also be applied to the regressors. Consider the simplest case, ARIMA with non-seasonal differencing of order 1. We may estimate either

$$\phi(L)(1-L)(y_t - X_t\beta) = \theta(L)\epsilon_t \quad (24.8)$$

or

$$\phi(L)((1-L)y_t - X_t\beta) = \theta(L)\epsilon_t \quad (24.9)$$

The first of these formulations can be described as a regression model with ARIMA errors, while the second preserves the levels of the  $X$  variables. As of `gretl` version 1.8.6, the default model is (24.8), in which differencing is applied to both  $y_t$  and  $X_t$ . However, when using the default estimation method (native exact ML, see below), the option `--y-diff-only` may be given, in which case `gretl` estimates (24.9).<sup>1</sup>

### Estimation

The default estimation method for ARMA models is exact maximum likelihood estimation (under the assumption that the error term is normally distributed), using the Kalman filter in conjunction with the BFGS maximization algorithm. The gradient of the log-likelihood with respect to the parameter estimates is approximated numerically. This method produces results that are directly comparable with many other software packages. The constant, and any exogenous variables, are treated as in equation (24.2). The covariance matrix for the parameters is computed using a numerical approximation to the Hessian at convergence.

The alternative method, invoked with the `--conditional` switch, is conditional maximum likelihood (CML), also known as “conditional sum of squares” (see Hamilton, 1994, p. 132). This method was exemplified in the script 10.3, and only a brief description will be given here. Given a sample of size  $T$ , the CML method minimizes the sum of squared one-step-ahead prediction errors generated

<sup>1</sup>Prior to `gretl` 1.8.6, the default model was (24.9). We changed this for the sake of consistency with other software.

by the model for the observations  $t_0, \dots, T$ . The starting point  $t_0$  depends on the orders of the AR polynomials in the model. The numerical maximization method used is BHHH, and the covariance matrix is computed using a Gauss-Newton regression.

The CML method is nearly equivalent to maximum likelihood under the hypothesis of normality; the difference is that the first  $(t_0 - 1)$  observations are considered fixed and only enter the likelihood function as conditioning variables. As a consequence, the two methods are asymptotically equivalent under standard conditions — except for the fact, discussed above, that our CML implementation treats the constant and exogenous variables as per equation (24.3).

The two methods can be compared as in the following example

```
open data10-1
arma 1 1 ; r
arma 1 1 ; r --conditional
```

which produces the estimates shown in Table 24.1. As you can see, the estimates of  $\phi$  and  $\theta$  are quite similar. The reported constants differ widely, as expected — see the discussion following equations (24.4) and (24.5). However, dividing the CML constant by  $1 - \phi$  we get 7.38, which is not far from the ML estimate of 6.93.

**Table 24.1:** ML and CML estimates

Parameter	ML		CML	
$\mu$	6.93042	(0.923882)	1.07322	(0.488661)
$\phi$	0.855360	(0.0511842)	0.852772	(0.0450252)
$\theta$	0.588056	(0.0986096)	0.591838	(0.0456662)

### Convergence and initialization

The numerical methods used to maximize the likelihood for ARMA models are not guaranteed to converge. Whether or not convergence is achieved, and whether or not the true maximum of the likelihood function is attained, may depend on the starting values for the parameters. Gretl employs one of the following two initialization mechanisms, depending on the specification of the model and the estimation method chosen.

1. Estimate a pure AR model by Least Squares (nonlinear least squares if the model requires it, otherwise OLS). Set the AR parameter values based on this regression and set the MA parameters to a small positive value (0.0001).
2. The Hannan-Rissanen method: First estimate an autoregressive model by OLS and save the residuals. Then in a second OLS pass add appropriate lags of the first-round residuals to the model, to obtain estimates of the MA parameters.

To see the details of the ARMA estimation procedure, add the `--verbose` option to the command. This prints a notice of the initialization method used, as well as the parameter values and log-likelihood at each iteration.

Besides the built-in initialization mechanisms, the user has the option of specifying a set of starting values manually. This is done via the `set` command: the first argument should be the keyword `initvals` and the second should be the name of a pre-specified matrix containing starting values. For example

```
matrix start = { 0, 0.85, 0.34 }
set initvals start
arma 1 1 ; y
```

The specified matrix should have just as many parameters as the model: in the example above there are three parameters, since the model implicitly includes a constant. The constant, if present, is always given first; otherwise the order in which the parameters are expected is the same as the order of specification in the `arma` or `arma` command. In the example the constant is set to zero,  $\phi_1$  to 0.85, and  $\theta_1$  to 0.34.

You can get `gretl` to revert to automatic initialization via the command `set initvals auto`.

Two variants of the BFGS algorithm are available in `gretl`. In general we recommend the default variant, which is based on an implementation by Nash (1990), but for some problems the alternative, limited-memory version (L-BFGS-B, see Byrd *et al.*, 1995) may increase the chances of convergence on the ML solution. This can be selected via the `--lbfgs` option to the `arma` command.

### Estimation via X-12-ARIMA

As an alternative to estimating ARMA models using “native” code, `gretl` offers the option of using the external program X-12-ARIMA. This is the seasonal adjustment software produced and maintained by the U.S. Census Bureau; it is used for all official seasonal adjustments at the Bureau.

`Gretl` includes a module which interfaces with X-12-ARIMA: it translates `arma` commands using the syntax outlined above into a form recognized by X-12-ARIMA, executes the program, and retrieves the results for viewing and further analysis within `gretl`. To use this facility you have to install X-12-ARIMA separately. Packages for both MS Windows and GNU/Linux are available from the `gretl` website, <http://gretl.sourceforge.net/>.

To invoke X-12-ARIMA as the estimation engine, append the flag `--x-12-arma`, as in

```
arma p q ; y --x-12-arma
```

As with native estimation, the default is to use exact ML but there is the option of using conditional ML with the `--conditional` flag. However, please note that when X-12-ARIMA is used in conditional ML mode, the comments above regarding the variant treatments of the mean of the process  $y_t$  *do not apply*. That is, when you use X-12-ARIMA the model that is estimated is (24.2), regardless of whether estimation is by exact ML or conditional ML. In addition, the treatment of exogenous regressors in the context of ARIMA differencing is always that shown in equation (24.8).

### Forecasting

ARMA models are often used for forecasting purposes. The autoregressive component, in particular, offers the possibility of forecasting a process “out of sample” over a substantial time horizon.

`Gretl` supports forecasting on the basis of ARMA models using the method set out by Box and Jenkins (1976).<sup>2</sup> The Box and Jenkins algorithm produces a set of integrated AR coefficients which take into account any differencing of the dependent variable (seasonal and/or non-seasonal) in the ARIMA context, thus making it possible to generate a forecast for the level of the original variable. By contrast, if you first difference a series manually and then apply ARMA to the differenced series, forecasts will be for the differenced series, not the level. This point is illustrated in Example 24.1. The parameter estimates are identical for the two models. The forecasts differ but are mutually consistent: the variable `fcdiff` emulates the ARMA forecast (static, one step ahead within the sample range, and dynamic out of sample).

<sup>2</sup>See in particular their “Program 4” on p. 505ff.

**Example 24.1:** ARIMA forecasting

---

```

open greenel8_2.gdt
# log of quarterly U.S. nominal GNP, 1950:1 to 1983:4
genr y = log(Y)
# and its first difference
genr dy = diff(y)
# reserve 2 years for out-of-sample forecast
smpl ; 1981:4
# Estimate using ARIMA
arima 1 1 1 ; y
# forecast over full period
smpl --full
fcast fc1
# Return to sub-sample and run ARMA on the first difference of y
smpl ; 1981:4
arma 1 1 ; dy
smpl --full
fcast fc2
genr fcdiff = (t<=1982:1)? (fc1 - y(-1)) : (fc1 - fc1(-1))
# compare the forecasts over the later period
smpl 1981:1 1983:4
print y fc1 fc2 fcdiff --byobs

```

---

The output from the last command is:

	y	fc1	fc2	fcdiff
1981:1	7.964086	7.940930	0.02668	0.02668
1981:2	7.978654	7.997576	0.03349	0.03349
1981:3	8.009463	7.997503	0.01885	0.01885
1981:4	8.015625	8.033695	0.02423	0.02423
1982:1	8.014997	8.029698	0.01407	0.01407
1982:2	8.026562	8.046037	0.01634	0.01634
1982:3	8.032717	8.063636	0.01760	0.01760
1982:4	8.042249	8.081935	0.01830	0.01830
1983:1	8.062685	8.100623	0.01869	0.01869
1983:2	8.091627	8.119528	0.01891	0.01891
1983:3	8.115700	8.138554	0.01903	0.01903
1983:4	8.140811	8.157646	0.01909	0.01909

### 24.3 Unit root tests

#### The ADF test

The Augmented Dickey-Fuller (ADF) test is, as implemented in `gretl`, the  $t$ -statistic on  $\varphi$  in the following regression:

$$\Delta y_t = \mu_t + \varphi y_{t-1} + \sum_{i=1}^p y_i \Delta y_{t-i} + \epsilon_t. \quad (24.10)$$

This test statistic is probably the best-known and most widely used unit root test. It is a one-sided test whose null hypothesis is  $\varphi = 0$  versus the alternative  $\varphi < 0$  (and hence large negative values of the test statistic lead to the rejection of the null). Under the null,  $y_t$  must be differenced at least once to achieve stationarity; under the alternative,  $y_t$  is already stationary and no differencing is required.

One peculiar aspect of this test is that its limit distribution is non-standard under the null hypothesis: moreover, the shape of the distribution, and consequently the critical values for the test, depends on the form of the  $\mu_t$  term. A full analysis of the various cases is inappropriate here: [Hamilton \(1994\)](#) contains an excellent discussion, but any recent time series textbook covers this topic. Suffice it to say that `gretl` allows the user to choose the specification for  $\mu_t$  among four different alternatives:

$\mu_t$	command option
0	--nc
$\mu_0$	--c
$\mu_0 + \mu_1 t$	--ct
$\mu_0 + \mu_1 t + \mu_1 t^2$	--ctt

These option flags are not mutually exclusive; when they are used together the statistic will be reported separately for each selected case. By default, `gretl` uses the combination `--c --ct`. For each case, approximate p-values are calculated by means of the algorithm developed in [MacKinnon \(1996\)](#).

The `gretl` command used to perform the test is `adf`; for example

```
adf 4 x1
```

would compute the test statistic as the  $t$ -statistic for  $\varphi$  in equation 24.10 with  $p = 4$  in the two cases  $\mu_t = \mu_0$  and  $\mu_t = \mu_0 + \mu_1 t$ .

The number of lags ( $p$  in equation 24.10) should be chosen as to ensure that (24.10) is a parametrization flexible enough to represent adequately the short-run persistence of  $\Delta y_t$ . Setting  $p$  too low results in size distortions in the test, whereas setting  $p$  too high leads to low power. As a convenience to the user, the parameter  $p$  can be automatically determined. Setting  $p$  to a negative number triggers a sequential procedure that starts with  $p$  lags and decrements  $p$  until the  $t$ -statistic for the parameter  $\gamma_p$  exceeds 1.645 in absolute value.

#### The ADF-GLS test

[Elliott, Rothenberg and Stock \(1996\)](#) proposed a variant of the ADF test which involves an alternative method of handling the parameters pertaining to the deterministic term  $\mu_t$ : these are estimated first via Generalized Least Squares, and in a second stage an ADF regression is performed using the GLS residuals. This variant offers greater power than the regular ADF test for the cases  $\mu_t = \mu_0$  and  $\mu_t = \mu_0 + \mu_1 t$ .

The ADF-GLS test is available in `gretl` via the `--gls` option to the `adf` command. When this option is selected the `--nc` and `--ctt` options become unavailable, and only one case can be selected at

a time; by default the constant-only model is used but a trend can be added using the `--ct` flag. When a trend is present in this test MacKinnon-type p-values are not available; instead we show critical values from Table 1 in [Elliott \*et al.\* \(1996\)](#).

### The KPSS test

The KPSS test ([Kwiatkowski, Phillips, Schmidt and Shin, 1992](#)) is a unit root test in which the null hypothesis is opposite to that in the ADF test: under the null, the series in question is stationary; the alternative is that the series is  $I(1)$ .

The basic intuition behind this test statistic is very simple: if  $y_t$  can be written as  $y_t = \mu + u_t$ , where  $u_t$  is some zero-mean stationary process, then not only does the sample average of the  $y_t$ s provide a consistent estimator of  $\mu$ , but the long-run variance of  $u_t$  is a well-defined, finite number. Neither of these properties hold under the alternative.

The test itself is based on the following statistic:

$$\eta = \frac{\sum_{t=1}^T S_t^2}{T^2 \bar{\sigma}^2} \quad (24.11)$$

where  $S_t = \sum_{s=1}^t e_s$  and  $\bar{\sigma}^2$  is an estimate of the long-run variance of  $e_t = (y_t - \bar{y})$ . Under the null, this statistic has a well-defined (nonstandard) asymptotic distribution, which is free of nuisance parameters and has been tabulated by simulation. Under the alternative, the statistic diverges.

As a consequence, it is possible to construct a one-sided test based on  $\eta$ , where  $H_0$  is rejected if  $\eta$  is bigger than the appropriate critical value; `gretl` provides the 90, 95 and 99 percent quantiles. The critical values are computed via the method presented by [Sephton \(1995\)](#), which offers greater accuracy than the values tabulated in [Kwiatkowski \*et al.\* \(1992\)](#).

Usage example:

```
kpss m y
```

where `m` is an integer representing the bandwidth or window size used in the formula for estimating the long run variance:

$$\bar{\sigma}^2 = \sum_{i=-m}^m \left(1 - \frac{|i|}{m+1}\right) \hat{y}_i$$

The  $\hat{y}_i$  terms denote the empirical autocovariances of  $e_t$  from order  $-m$  through  $m$ . For this estimator to be consistent,  $m$  must be large enough to accommodate the short-run persistence of  $e_t$ , but not too large compared to the sample size  $T$ . If the supplied `m` is non-positive a default value is computed, namely the integer part of  $4 \left(\frac{T}{100}\right)^{1/4}$ .

The above concept can be generalized to the case where  $y_t$  is thought to be stationary around a deterministic trend. In this case, formula (24.11) remains unchanged, but the series  $e_t$  is defined as the residuals from an OLS regression of  $y_t$  on a constant and a linear trend. This second form of the test is obtained by appending the `--trend` option to the `kpss` command:

```
kpss n y --trend
```

Note that in this case the asymptotic distribution of the test is different and the critical values reported by `gretl` differ accordingly.

### Panel unit root tests

The most commonly used unit root tests for panel data involve a generalization of the ADF procedure, in which the joint null hypothesis is that a given times series is non-stationary for all individuals in the panel.

In this context the ADF regression (24.10) can be rewritten as

$$\Delta y_{it} = \mu_{it} + \varphi_i y_{i,t-1} + \sum_{j=1}^{p_i} y_{ij} \Delta y_{i,t-j} + \epsilon_{it} \quad (24.12)$$

The model (24.12) allows for maximal heterogeneity across the individuals in the panel: the parameters of the deterministic term, the autoregressive coefficient  $\varphi$ , and the lag order  $p$  are all specific to the individual, indexed by  $i$ .

One possible modification of this model is to impose the assumption that  $\varphi_i = \varphi$  for all  $i$ ; that is, the individual time series share a common autoregressive root (although they may differ in respect of other statistical properties). The choice of whether or not to impose this assumption has an important bearing on the hypotheses under test. Under model (24.12) the joint null is  $\varphi_i = 0$  for all  $i$ , meaning that all the individual time series are non-stationary, and the alternative (simply the negation of the null) is that *at least one* individual time series is stationary. When a common  $\varphi$  is assumed, the null is that  $\varphi = 0$  and the alternative is that  $\varphi < 0$ . The null still says that all the individual series are non-stationary, but the alternative now says that they are *all* stationary. The choice of model should take this point into account, as well as the gain in power from forming a pooled estimate of  $\varphi$  and, of course, the plausibility of assuming a common AR(1) coefficient.<sup>3</sup>

In gretl, the formulation (24.12) is used automatically when the `adf` command is used on panel data. The joint test statistic is formed using the method of Im, Pesaran and Shin (2003). In this context the behavior of `adf` differs from regular time-series data: only one case of the deterministic term is handled per invocation of the command; the default is that  $\mu_{it}$  includes just a constant but the `--nc` and `--ct` flags can be used to suppress the constant or to include a trend, respectively; and the quadratic trend option `--ctt` is not available.

The alternative that imposes a common value of  $\varphi$  is implemented via the `levinlin` command. The test statistic is computed as per Levin, Lin and Chu (2002). As with the `adf` command, the first argument is the lag order and the second is the name of the series to test; and the default case for the deterministic component is a constant only. The options `--nc` and `--ct` have the same effect as with `adf`. One refinement is that the lag order may be given in either of two forms: if a scalar is given, this is taken to represent a common value of  $p$  for all individuals, but you may instead provide a vector holding a set of  $p_i$  values, hence allowing the order of autocorrelation of the series to differ by individual. So, for example, given

```
levinlin 2 y
levinlin {2,2,3,3,4,4} y
```

the first command runs a joint ADF test with a common lag order of 2, while the second (which assumes a panel with six individuals) allows for differing short-run dynamics. The first argument to `levinlin` can be given as a set of comma-separated integers enclosed in braces, as shown above, or as the name of an appropriately dimensioned pre-defined matrix (see chapter 14).

Besides variants of the ADF test, the KPSS test also can be used with panel data via the `kpss` command. In this case the test (of the null hypothesis that the given time series is *stationary* for all individuals) is implemented using the method of Choi (2001). This is an application of *meta-analysis*, the statistical technique whereby an overall or composite p-value for the test of a given null hypothesis can be computed from the p-values of a set of separate tests. Unfortunately, in the case of the KPSS test we are limited by the unavailability of precise p-values, although if an individual test statistic falls between the 10 percent and 1 percent critical values we are able to interpolate with a fair degree of confidence. This gives rise to four cases.

1. All the individual KPSS test statistics fall between the 10 percent and 1 percent critical values: the Choi method gives us a plausible composite p-value.

<sup>3</sup>If the assumption of a common  $\varphi$  seems excessively restrictive, bear in mind that we routinely assume common slope coefficients when estimating panel models, even if this is unlikely to be literally true.



2. Some of the KPSS test statistics exceed the 1 percent value and none fall short of the 10 percent value: we can give an upper bound for the composite p-value by setting the unknown p-values to 0.01.
3. Some of the KPSS test statistics fall short of the 10 percent critical value but none exceed the 1 percent value: we can give a lower bound to the composite p-value by setting the unknown p-values to 0.10.
4. None of the above conditions are satisfied: the Choi method fails to produce any result for the composite KPSS test.

## 24.4 Cointegration tests

The generally recommended test for cointegration is the Johansen test, which is discussed in detail in chapter 26. In this context we offer a few remarks on the cointegration test of Engle and Granger (1987), which builds on the ADF test discussed above (section 24.3).

For the Engle–Granger test, the procedure is:

1. Test each series for a unit root using an ADF test.
2. Run a “cointegrating regression” via OLS. For this we select one of the potentially cointegrated variables as dependent, and include the other potentially cointegrated variables as regressors.
3. Perform an ADF test on the residuals from the cointegrating regression.

The idea is that cointegration is supported if (a) the null of non-stationarity is *not* rejected for each of the series individually, in step 1, while (b) the null *is* rejected for the residuals at step 3. That is, each of the individual series is  $I(1)$  but some linear combination of the series is  $I(0)$ .

This test is implemented in gretl by the `coint` command, which requires an integer lag order (for the ADF tests) followed by a list of variables to be tested, the first of which will be taken as dependent in the cointegrating regression. Please see the online help for `coint`, or the *Gretl Command Reference*, for further details.

## 24.5 ARCH and GARCH

Heteroskedasticity means a non-constant variance of the error term in a regression model. Autoregressive Conditional Heteroskedasticity (ARCH) is a phenomenon specific to time series models, whereby the variance of the error displays autoregressive behavior; for instance, the time series exhibits successive periods where the error variance is relatively large, and successive periods where it is relatively small. This sort of behavior is reckoned to be common in asset markets: an unsettling piece of news can lead to a period of increased volatility in the market.

An ARCH error process of order  $q$  can be represented as

$$u_t = \sigma_t \varepsilon_t; \quad \sigma_t^2 \equiv E(u_t^2 | \Omega_{t-1}) = \alpha_0 + \sum_{i=1}^q \alpha_i u_{t-i}^2$$

where the  $\varepsilon_t$ s are independently and identically distributed (iid) with mean zero and variance 1, and where  $\sigma_t$  is taken to be the positive square root of  $\sigma_t^2$ .  $\Omega_{t-1}$  denotes the information set as of time  $t-1$  and  $\sigma_t^2$  is the conditional variance: that is, the variance conditional on information dated  $t-1$  and earlier.

It is important to notice the difference between ARCH and an ordinary autoregressive error process. The simplest (first-order) case of the latter can be written as

$$u_t = \rho u_{t-1} + \varepsilon_t; \quad -1 < \rho < 1$$

where the  $\varepsilon_t$ s are independently and identically distributed with mean zero and variance  $\sigma^2$ . With an AR(1) error, if  $\rho$  is positive then a positive value of  $u_t$  will tend to be followed by a positive  $u_{t+1}$ . With an ARCH error process, a disturbance  $u_t$  of large absolute value will tend to be followed by further large absolute values, but with no presumption that the successive values will be of the same sign. ARCH in asset prices is a “stylized fact” and is consistent with market efficiency; on the other hand autoregressive behavior of asset prices would violate market efficiency.

One can test for ARCH of order  $q$  in the following way:

1. Estimate the model of interest via OLS and save the squared residuals,  $\hat{u}_t^2$ .
2. Perform an auxiliary regression in which the current squared residual is regressed on a constant and  $q$  lags of itself.
3. Find the  $TR^2$  value (sample size times unadjusted  $R^2$ ) for the auxiliary regression.
4. Refer the  $TR^2$  value to the  $\chi^2$  distribution with  $q$  degrees of freedom, and if the p-value is “small enough” reject the null hypothesis of homoskedasticity in favor of the alternative of ARCH( $q$ ).

This test is implemented in gretl via the `modtest` command with the `--arch` option, which must follow estimation of a time-series model by OLS (either a single-equation model or a VAR). For example,

```
ols y 0 x
modtest 4 --arch
```

This example specifies an ARCH order of  $q = 4$ ; if the order argument is omitted,  $q$  is set equal to the periodicity of the data. In the graphical interface, the ARCH test is accessible from the “Tests” menu in the model window (again, for single-equation OLS or VARs).

## GARCH

The simple ARCH( $q$ ) process is useful for introducing the general concept of conditional heteroskedasticity in time series, but it has been found to be insufficient in empirical work. The dynamics of the error variance permitted by ARCH( $q$ ) are not rich enough to represent the patterns found in financial data. The generalized ARCH or GARCH model is now more widely used.

The representation of the variance of a process in the GARCH model is somewhat (but not exactly) analogous to the ARMA representation of the level of a time series. The variance at time  $t$  is allowed to depend on both past values of the variance and past values of the realized squared disturbance, as shown in the following system of equations:

$$y_t = X_t \beta + u_t \quad (24.13)$$

$$u_t = \sigma_t \varepsilon_t \quad (24.14)$$

$$\sigma_t^2 = \alpha_0 + \sum_{i=1}^q \alpha_i u_{t-i}^2 + \sum_{j=1}^p \delta_j \sigma_{t-j}^2 \quad (24.15)$$

As above,  $\varepsilon_t$  is an iid sequence with unit variance.  $X_t$  is a matrix of regressors (or in the simplest case, just a vector of 1s allowing for a non-zero mean of  $y_t$ ). Note that if  $p = 0$ , GARCH collapses to ARCH( $q$ ): the generalization is embodied in the  $\delta_j$  terms that multiply previous values of the error variance.

In principle the underlying innovation,  $\varepsilon_t$ , could follow any suitable probability distribution, and besides the obvious candidate of the normal or Gaussian distribution the Student’s  $t$  distribution has been used in this context. Currently gretl only handles the case where  $\varepsilon_t$  is assumed to be Gaussian. However, when the `--robust` option to the `garch` command is given, the estimator gretl

uses for the covariance matrix can be considered Quasi-Maximum Likelihood even with non-normal disturbances. See below for more on the options regarding the GARCH covariance matrix.

Example:

```
garch p q ; y const x
```

where  $p \geq 0$  and  $q > 0$  denote the respective lag orders as shown in equation (24.15). These values can be supplied in numerical form or as the names of pre-defined scalar variables.

### GARCH estimation

Estimation of the parameters of a GARCH model is by no means a straightforward task. (Consider equation 24.15: the conditional variance at any point in time,  $\sigma_t^2$ , depends on the conditional variance in earlier periods, but  $\sigma_t^2$  is not observed, and must be inferred by some sort of Maximum Likelihood procedure.) By default gretl uses native code that employs the BFGS maximizer; you also have the option (activated by the `--fcp` command-line switch) of using the method proposed by Fiorentini *et al.* (1996),<sup>4</sup> which was adopted as a benchmark in the study of GARCH results by McCullough and Renfro (1998). It employs analytical first and second derivatives of the log-likelihood, and uses a mixed-gradient algorithm, exploiting the information matrix in the early iterations and then switching to the Hessian in the neighborhood of the maximum likelihood. (This progress can be observed if you append the `--verbose` option to gretl's `garch` command.)

Several options are available for computing the covariance matrix of the parameter estimates in connection with the `garch` command. At a first level, one can choose between a “standard” and a “robust” estimator. By default, the Hessian is used unless the `--robust` option is given, in which case the QML estimator is used. A finer choice is available via the `set` command, as shown in Table 24.2.

**Table 24.2:** Options for the GARCH covariance matrix

<i>command</i>	<i>effect</i>
<code>set garch_vcv hessian</code>	Use the Hessian
<code>set garch_vcv im</code>	Use the Information Matrix
<code>set garch_vcv op</code>	Use the Outer Product of the Gradient
<code>set garch_vcv qml</code>	QML estimator
<code>set garch_vcv bw</code>	Bollerslev-Wooldridge “sandwich” estimator

It is not uncommon, when one estimates a GARCH model for an arbitrary time series, to find that the iterative calculation of the estimates fails to converge. For the GARCH model to make sense, there are strong restrictions on the admissible parameter values, and it is not always the case that there exists a set of values inside the admissible parameter space for which the likelihood is maximized.

The restrictions in question can be explained by reference to the simplest (and much the most common) instance of the GARCH model, where  $p = q = 1$ . In the GARCH(1, 1) model the conditional variance is

$$\sigma_t^2 = \alpha_0 + \alpha_1 u_{t-1}^2 + \delta_1 \sigma_{t-1}^2 \quad (24.16)$$

Taking the unconditional expectation of (24.16) we get

$$\sigma^2 = \alpha_0 + \alpha_1 \sigma^2 + \delta_1 \sigma^2$$

<sup>4</sup>The algorithm is based on Fortran code deposited in the archive of the *Journal of Applied Econometrics* by the authors, and is used by kind permission of Professor Fiorentini.

so that

$$\sigma^2 = \frac{\alpha_0}{1 - \alpha_1 - \delta_1}$$

For this unconditional variance to exist, we require that  $\alpha_1 + \delta_1 < 1$ , and for it to be positive we require that  $\alpha_0 > 0$ .

A common reason for non-convergence of GARCH estimates (that is, a common reason for the non-existence of  $\alpha_i$  and  $\delta_i$  values that satisfy the above requirements and at the same time maximize the likelihood of the data) is misspecification of the model. It is important to realize that GARCH, in itself, allows *only* for time-varying volatility in the data. If the *mean* of the series in question is not constant, or if the error process is not only heteroskedastic but also autoregressive, it is necessary to take this into account when formulating an appropriate model. For example, it may be necessary to take the first difference of the variable in question and/or to add suitable regressors,  $X_t$ , as in (24.13).

## Chapter 25

# Vector Autoregressions

Gretl provides a standard set of procedures for dealing with the multivariate time-series models known as VARs (*Vector AutoRegression*). More general models — such as VARMA, nonlinear models or multivariate GARCH models — are not provided as of now, although it is entirely possible to estimate them by writing custom procedures in the gretl scripting language. In this chapter, we will briefly review gretl's VAR toolbox.

### 25.1 Notation

A VAR is a structure whose aim is to model the time persistence of a vector of  $n$  time series,  $y_t$ , via a multivariate autoregression, as in

$$y_t = A_1 y_{t-1} + A_2 y_{t-2} + \cdots + A_p y_{t-p} + Bx_t + \epsilon_t \quad (25.1)$$

The number of lags  $p$  is called the *order* of the VAR. The vector  $x_t$ , if present, contains a set of exogenous variables, often including a constant, possibly with a time trend and seasonal dummies. The vector  $\epsilon_t$  is typically assumed to be a vector white noise, with covariance matrix  $\Sigma$ .

Equation (25.1) can be written more compactly as

$$A(L)y_t = Bx_t + \epsilon_t \quad (25.2)$$

where  $A(L)$  is a matrix polynomial in the lag operator, or as

$$\begin{bmatrix} y_t \\ y_{t-1} \\ \vdots \\ y_{t-p-1} \end{bmatrix} = \mathbf{A} \begin{bmatrix} y_{t-1} \\ y_{t-2} \\ \vdots \\ y_{t-p} \end{bmatrix} + \begin{bmatrix} B \\ 0 \\ \vdots \\ 0 \end{bmatrix} x_t + \begin{bmatrix} \epsilon_t \\ 0 \\ \vdots \\ 0 \end{bmatrix} \quad (25.3)$$

The matrix  $\mathbf{A}$  is known as the “companion matrix” and equals

$$\mathbf{A} = \begin{bmatrix} A_1 & A_2 & \cdots & A_p \\ I & 0 & \cdots & 0 \\ 0 & I & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \end{bmatrix}$$

Equation (25.3) is known as the “companion form” of the VAR.

Another representation of interest is the so-called “VMA representation”, which is written in terms of an infinite series of matrices  $\Theta_i$  defined as

$$\Theta_i = \frac{\partial y_t}{\partial \epsilon_{t-i}} \quad (25.4)$$

The  $\Theta_i$  matrices may be derived by recursive substitution in equation (25.1): for example, assuming for simplicity that  $B = 0$  and  $p = 1$ , equation (25.1) would become

$$y_t = Ay_{t-1} + \epsilon_t$$

which could be rewritten as

$$y_t = A^{n+1}y_{t-n-1} + \epsilon_t + A\epsilon_{t-1} + A^2\epsilon_{t-2} + \cdots + A^n\epsilon_{t-n}$$

In this case  $\Theta_i = A^i$ . In general, it is possible to compute  $\Theta_i$  as the  $n \times n$  north-west block of the  $i$ -th power of the companion matrix  $A$  (so  $\Theta_0$  is always an identity matrix).

The VAR is said to be *stable* if all the eigenvalues of the companion matrix  $A$  are smaller than 1 in absolute value, or equivalently, if the matrix polynomial  $A(L)$  in equation (25.2) is such that  $|A(z)| = 0$  implies  $|z| > 1$ . If this is the case,  $\lim_{n \rightarrow \infty} \Theta_n = 0$  and the vector  $y_t$  is stationary; as a consequence, the equation

$$y_t - E(y_t) = \sum_{i=0}^{\infty} \Theta_i \epsilon_{t-i} \quad (25.5)$$

is a legitimate Wold representation.

If the VAR is not stable, then the inferential procedures that are called for become somewhat more specialized, except for some simple cases. In particular, if the number of eigenvalues of  $A$  with modulus 1 is between 1 and  $n - 1$ , the canonical tool to deal with these models is the cointegrated VAR model, discussed in chapter 26.

## 25.2 Estimation

The `gretl` command for estimating a VAR is `var` which, in the command line interface, is invoked in the following manner:

```
[ modelname <- ] var p Ylist [; Xlist]
```

where  $p$  is a scalar (the VAR order) and `Ylist` is a list of variables describing the content of  $y_t$ . If the list `Xlist` is absent, the vector  $x_t$  is understood to contain a constant only; if present, must be separated from `Ylist` by a semi-colon and contains the other exogenous variables. Note, however, that a few common choices can be obtained in a simpler way via options: the options `gretl` provides are `--trend`, `--seasonals` and `--nc` (no constant). Either `Ylist` and `Xlist` may be named lists (see section 13.1). The “<-” construct can be used to store the model under a name (see section 3.2), if so desired. To estimate a VAR using the graphical interface, choose “Time Series, Vector Autoregression”, under the Model menu.

The parameters in eq. (25.1) are typically free from restrictions, which implies that multivariate OLS provides a consistent and asymptotically efficient estimator of all the parameters.<sup>1</sup> Given the simplicity of OLS, this is what every software package, including `gretl`, uses: example script 25.1 exemplifies the fact that the `var` command gives you exactly the output you would have from a battery of OLS regressions. The advantage of using the dedicated command is that, after estimation is done, it makes it much easier to access certain quantities and manage certain tasks. For example, the `$coeff` accessor returns the estimated coefficients as a matrix with  $n$  columns and `$sigma` returns an estimate of the matrix  $\Sigma$ , the covariance matrix of  $\epsilon_t$ .

Moreover, for each variable in the system an F test is automatically performed, in which the null hypothesis is that no lags of variable  $j$  are significant in the equation for variable  $i$ . This is commonly known as a **Granger causality** test.

In addition, two accessors become available for the companion matrix (`$companion`) and the VMA representation (`$vma`). The latter deserves a detailed description: since the VMA representation (25.5) is of infinite order, `gretl` defines a *horizon* up to which the  $\Theta_i$  matrices are computed automatically. By default, this is a function of the periodicity of the data (see table 25.1), but it can be set by the user to any desired value via the `set` command with the `horizon` parameter, as in

<sup>1</sup>In fact, under normality of  $\epsilon_t$  OLS is indeed the conditional ML estimator. You may want to use other methods if you need to estimate a VAR in which some parameters are constrained.

**Example 25.1:** Estimation of a VAR via OLS

Input:

```
open sw_ch14.gdt
genr infl = 400*sdiff(log(PUNEW))
```

```
scalar p = 2
list X = LHUR infl
list Xlag = lags(p,X)
```

```
loop foreach i X
  ols $i const Xlag
end loop
```

var p X

Output (selected portions):

Model 1: OLS, using observations 1960:3-1999:4 (T = 158)  
Dependent variable: LHUR

	coefficient	std. error	t-ratio	p-value	
const	0.113673	0.0875210	1.299	0.1960	
LHUR_1	1.54297	0.0680518	22.67	8.78e-51	***
LHUR_2	-0.583104	0.0645879	-9.028	7.00e-16	***
infl_1	0.0219040	0.00874581	2.505	0.0133	**
infl_2	-0.0148408	0.00920536	-1.612	0.1090	

Mean dependent var	6.019198	S.D. dependent var	1.502549
Sum squared resid	8.654176	S.E. of regression	0.237830

...

VAR system, lag order 2  
OLS estimates, observations 1960:3-1999:4 (T = 158)  
Log-likelihood = -322.73663  
Determinant of covariance matrix = 0.20382769  
AIC = 4.2119  
BIC = 4.4057  
HQC = 4.2906  
Portmanteau test: LB(39) = 226.984, df = 148 [0.0000]

Equation 1: LHUR

	coefficient	std. error	t-ratio	p-value	
const	0.113673	0.0875210	1.299	0.1960	
LHUR_1	1.54297	0.0680518	22.67	8.78e-51	***
LHUR_2	-0.583104	0.0645879	-9.028	7.00e-16	***
infl_1	0.0219040	0.00874581	2.505	0.0133	**
infl_2	-0.0148408	0.00920536	-1.612	0.1090	

Mean dependent var	6.019198	S.D. dependent var	1.502549
Sum squared resid	8.654176	S.E. of regression	0.237830

Periodicity	horizon
Quarterly	20 (5 years)
Monthly	24 (2 years)
Daily	3 weeks
All other cases	10

**Table 25.1:** VMA horizon as a function of the dataset periodicity

```
set horizon 30
```

Calling the horizon  $h$ , the `$vma` accessor returns an  $(h + 1) \times n^2$  matrix, in which the  $(i + 1)$ -th row is the vectorized form of  $\Theta_i$ .

### VAR order selection

In order to help the user choose the most appropriate VAR order, `gretl` provides a special syntax construct to the `var` command:

```
var p Ylist [; Xlist] --lagselect
```

When the command is invoked with the `--lagselect` option, estimation is performed for all lags up to  $p$  and a table is printed: it displays, for each order, a LR test for the order  $p$  versus  $p - 1$ , plus an array of information criteria (see chapter 22). For each information criterion in the table, a star indicates what appears to be the “best” choice. The same output can be obtained through the graphical interface via the “Time Series, VAR lag selection” entry under the Model menu.

Warning: in finite samples the choice of  $p$  may affect the outcome of the procedure. **This is not a bug**, but rather a nasty but unavoidable side effect of the way these comparisons should be made: if your sample contains  $T$  observations, the lag selection procedure, if invoked with parameter  $p$ , examines all VARs of order ranging from 1 to  $p$ , estimated on a sample of  $T - p$  observations. In other words, the comparison procedure does not use all the data available when estimating VARs of order less than  $p$  to make sure that all the models compared are estimated on the same data range. Under these circumstances, choosing a different value of  $p$  may alter the results, although this is unlikely to happen if your sample size is reasonably large.

An example of this unpleasant phenomenon is given in example script 25.2. As can be seen, according to the Hannan-Quinn criterion, order 2 seems preferable to order 1 if the maximum tested order is 4, but the situation is reversed if the maximum tested order is 6.

## 25.3 Structural VARs

As of today, `gretl` does not provide a native implementation for the class of models known as “Structural VARs”; however, it provides an implementation of the Cholesky decomposition-based approach, which is the most classic, and certainly most popular SVAR version.

### IRF and FEVD

Assume that the disturbance in equation (25.1) can be thought of as a linear function of a vector of *structural shocks*  $u_t$ , which are assumed to have unit variance and to be incorrelated to one another, so  $V(u_t) = I$ . If  $\epsilon_t = Ku_t$ , it follows that  $\Sigma = V(\epsilon_t) = KK'$ .

The main object of interest in this setting the sequence of matrices

$$C_k = \frac{\partial y_t}{\partial u_{t-i}} = \Theta_k K, \quad (25.6)$$



**Example 25.2:** VAR lag selection via Information Criteria

Input:

```
open denmark
list Y = 1 2 3 4
var 4 Y --lagselect
var 6 Y --lagselect
```

Output (selected portions):

VAR system, maximum lag order 4

The asterisks below indicate the best (that is, minimized) values of the respective information criteria, AIC = Akaike criterion, BIC = Schwarz Bayesian criterion and HQC = Hannan-Quinn criterion.

lags	loglik	p(LR)	AIC	BIC	HQC
1	609.15315		-23.104045	-22.346466*	-22.814552
2	631.70153	0.00013	-23.360844*	-21.997203	-22.839757*
3	642.38574	0.16478	-23.152382	-21.182677	-22.399699
4	653.22564	0.15383	-22.950025	-20.374257	-21.965748

VAR system, maximum lag order 6

The asterisks below indicate the best (that is, minimized) values of the respective information criteria, AIC = Akaike criterion, BIC = Schwarz Bayesian criterion and HQC = Hannan-Quinn criterion.

lags	loglik	p(LR)	AIC	BIC	HQC
1	594.38410		-23.444249	-22.672078*	-23.151288*
2	615.43480	0.00038	-23.650400*	-22.260491	-23.123070
3	624.97613	0.26440	-23.386781	-21.379135	-22.625083
4	636.03766	0.13926	-23.185210	-20.559827	-22.189144
5	658.36014	0.00016	-23.443271	-20.200150	-22.212836
6	669.88472	0.11243	-23.260601	-19.399743	-21.795797

known as the structural VMA representation. From the  $C_k$  matrices defined in equation (25.6) two quantities of interest may be derived: the **Impulse Response Function** (IRF) and the **Forecast Error Variance Decomposition** (FEVD).

The IRF of variable  $i$  to shock  $j$  is simply the sequence of the elements in row  $i$  and column  $j$  of the  $C_k$  matrices. In formulae:

$$I_{i,j,k} = \frac{\partial y_{i,t}}{\partial u_{j,t-k}}$$

As a rule, Impulse Response Functions are plotted as a function of  $k$ , and are interpreted as the effect that a shock has on an observable variable through time. Of course, what we observe are the estimated IRFs, so it is natural to endow them with confidence intervals: following common practice among econometric software, gretl computes the confidence intervals by using the bootstrap<sup>2</sup>; details are later in this section.

Another quantity of interest that may be computed from the structural VMA representation is the Forecast Error Variance Decomposition (FEVD). The forecast error variance after  $h$  steps is given by

$$\Omega_h = \sum_{k=0}^h C_k C_k'$$

hence the variance for variable  $i$  is

$$\omega_i^2 = [\Omega_h]_{i,i} = \sum_{k=0}^h \text{diag}(C_k C_k')_i = \sum_{k=0}^h \sum_{l=1}^n (k c_{i,l})^2$$

where  $k c_{i,l}$  is, trivially, the  $i, l$  element of  $C_k$ . As a consequence, the share of uncertainty on variable  $i$  that can be attributed to the  $j$ -th shock after  $h$  periods equals

$$\mathcal{VD}_{i,j,h} = \frac{\sum_{k=0}^h (k c_{i,j})^2}{\sum_{k=0}^h \sum_{l=1}^n (k c_{i,l})^2}.$$

This makes it possible to quantify which shocks are most important to determine a certain variable in the short and/or in the long run.

### Triangularization

The formula 25.6 takes  $K$  as known, while of course it has to be estimated. The estimation problem has been the subject of an enormous body of literature we will not even attempt to summarize here: see for example (Lütkepohl, 2005, chapter 9).

Suffice it to say that the most popular choice dates back to Sims (1980), and consists in assuming that  $K$  is lower triangular, so its estimate is simply the Cholesky decomposition of the estimate of  $\Sigma$ . The main consequence of this choice is that the ordering of variables within the vector  $y_t$  becomes meaningful: since  $K$  is also the matrix of Impulse Response Functions at lag 0, the triangularity assumption means that the first variable in the ordering responds instantaneously only to shock number 1, the second one only to shocks 1 and 2, and so forth. For this reason, each variable is thought to “own” one shock: variable 1 owns shock number 1, etcetera.

This is the reason why in this sort of exercises the ordering of the variables is important and the applied literature has developed the “most exogenous first” mantra. Where, in this setting, “exogenous” really means “instantaneously insensitive to structural shocks”<sup>3</sup>. To put it differently,

<sup>2</sup>It is possible, in principle, to compute analytical confidence intervals via an asymptotic approximation, but this is not a very popular choice: asymptotic formulae are known to often give a very poor approximation of the finite-sample properties.

<sup>3</sup>The word “exogenous” has caught on in this context, but it's a rather unfortunate choice: for a start, each shock impacts on every variable after one lag, so nothing is really exogenous here. A much better choice of words would probably have been something like “sturdy”, but it's too late now.

if variable `foo` comes before variable `bar` in the `Y` list, it follows that the shock owned by `foo` affects `bar` instantaneously, but the reverse does not happen.

Impulse Response Functions and the FEVD can be printed out via the command line interface by using the `--impulse-response` and `--variance-decomp` options, respectively. If you need to store them into matrices, you can compute the structural VMA and proceed from there. For example, the following code snippet shows you how to compute a matrix containing the IRFs:

```
open denmark
list Y = 1 2 3 4
scalar n = nelem(Y)
var 2 Y --quiet --impulse

matrix K = cholesky($sigma)
matrix V = $vma
matrix IRF = V * (K ** I(n))
print IRF
```

in which the equality

$$\text{vec}(C_k) = \text{vec}(\Theta_k K) = (K' \otimes I) \text{vec}(\Theta_k)$$

was used.

FIXME: show all the nice stuff we have under the GUI.

### IRF bootstrap

FIXME: todo

## Chapter 26

# Cointegration and Vector Error Correction Models

### 26.1 Introduction

The twin concepts of cointegration and error correction have drawn a good deal of attention in macroeconometrics over recent years. The attraction of the Vector Error Correction Model (VECM) is that it allows the researcher to embed a representation of economic equilibrium relationships within a relatively rich time-series specification. This approach overcomes the old dichotomy between (a) structural models that faithfully represented macroeconomic theory but failed to fit the data, and (b) time-series models that were accurately tailored to the data but difficult if not impossible to interpret in economic terms.

The basic idea of cointegration relates closely to the concept of unit roots (see section 24.3). Suppose we have a set of macroeconomic variables of interest, and we find we cannot reject the hypothesis that some of these variables, considered individually, are non-stationary. Specifically, suppose we judge that a subset of the variables are individually integrated of order 1, or I(1). That is, while they are non-stationary in their levels, their first differences are stationary. Given the statistical problems associated with the analysis of non-stationary data (for example, the threat of spurious regression), the traditional approach in this case was to take first differences of all the variables before proceeding with the analysis.

But this can result in the loss of important information. It may be that while the variables in question are I(1) when taken individually, there exists a linear combination of the variables that is stationary without differencing, or I(0). (There could be more than one such linear combination.) That is, while the ensemble of variables may be “free to wander” over time, nonetheless the variables are “tied together” in certain ways. And it may be possible to interpret these ties, or *cointegrating vectors*, as representing equilibrium conditions.

For example, suppose we find some or all of the following variables are I(1): money stock,  $M$ , the price level,  $P$ , the nominal interest rate,  $R$ , and output,  $Y$ . According to standard theories of the demand for money, we would nonetheless expect there to be an equilibrium relationship between real balances, interest rate and output; for example

$$m - p = \gamma_0 + \gamma_1 y + \gamma_2 r \quad \gamma_1 > 0, \gamma_2 < 0$$

where lower-case variable names denote logs. In equilibrium, then,

$$m - p - \gamma_1 y - \gamma_2 r = \gamma_0$$

Realistically, we should not expect this condition to be satisfied each period. We need to allow for the possibility of short-run disequilibrium. But if the system moves back towards equilibrium following a disturbance, it follows that the vector  $x = (m, p, y, r)'$  is bound by a cointegrating vector  $\beta' = (\beta_1, \beta_2, \beta_3, \beta_4)$ , such that  $\beta'x$  is stationary (with a mean of  $\gamma_0$ ). Furthermore, if equilibrium is correctly characterized by the simple model above, we have  $\beta_2 = -\beta_1$ ,  $\beta_3 < 0$  and  $\beta_4 > 0$ . These things are testable within the context of cointegration analysis.

There are typically three steps in this sort of analysis:

1. Test to determine the number of cointegrating vectors, the *cointegrating rank* of the system.
2. Estimate a VECM with the appropriate rank, but subject to no further restrictions.

3. Probe the interpretation of the cointegrating vectors as equilibrium conditions by means of restrictions on the elements of these vectors.

The following sections expand on each of these points, giving further econometric details and explaining how to implement the analysis using gretl.

## 26.2 Vector Error Correction Models as representation of a cointegrated system

Consider a VAR of order  $p$  with a deterministic part given by  $\mu_t$  (typically, a polynomial in time). One can write the  $n$ -variate process  $y_t$  as

$$y_t = \mu_t + A_1 y_{t-1} + A_2 y_{t-2} + \cdots + A_p y_{t-p} + \epsilon_t \quad (26.1)$$

But since  $y_{t-i} \equiv y_{t-1} - (\Delta y_{t-1} + \Delta y_{t-2} + \cdots + \Delta y_{t-i+1})$ , we can re-write the above as

$$\Delta y_t = \mu_t + \Pi y_{t-1} + \sum_{i=1}^{p-1} \Gamma_i \Delta y_{t-i} + \epsilon_t, \quad (26.2)$$

where  $\Pi = \sum_{i=1}^p A_i - I$  and  $\Gamma_i = -\sum_{j=i+1}^p A_j$ . This is the VECM representation of (26.1).

The interpretation of (26.2) depends crucially on  $r$ , the rank of the matrix  $\Pi$ .

- If  $r = 0$ , the processes are all I(1) and not cointegrated.
- If  $r = n$ , then  $\Pi$  is invertible and the processes are all I(0).
- Cointegration occurs in between, when  $0 < r < n$  and  $\Pi$  can be written as  $\alpha\beta'$ . In this case,  $y_t$  is I(1), but the combination  $z_t = \beta' y_t$  is I(0). If, for example,  $r = 1$  and the first element of  $\beta$  was  $-1$ , then one could write  $z_t = -y_{1,t} + \beta_2 y_{2,t} + \cdots + \beta_n y_{n,t}$ , which is equivalent to saying that

$$y_{1,t} = \beta_2 y_{2,t} + \cdots + \beta_n y_{n,t} - z_t$$

is a long-run equilibrium relationship: the deviations  $z_t$  may not be 0 but they are stationary. In this case, (26.2) can be written as

$$\Delta y_t = \mu_t + \alpha\beta' y_{t-1} + \sum_{i=1}^{p-1} \Gamma_i \Delta y_{t-i} + \epsilon_t. \quad (26.3)$$

If  $\beta$  were known, then  $z_t$  would be observable and all the remaining parameters could be estimated via OLS. In practice, the procedure estimates  $\beta$  first and then the rest.

The rank of  $\Pi$  is investigated by computing the eigenvalues of a closely related matrix whose rank is the same as  $\Pi$ : however, this matrix is by construction symmetric and positive semidefinite. As a consequence, all its eigenvalues are real and non-negative, and tests on the rank of  $\Pi$  can therefore be carried out by testing how many eigenvalues are 0.

If all the eigenvalues are significantly different from 0, then all the processes are stationary. If, on the contrary, there is at least one zero eigenvalue, then the  $y_t$  process is integrated, although some linear combination  $\beta' y_t$  might be stationary. At the other extreme, if no eigenvalues are significantly different from 0, then not only is the process  $y_t$  non-stationary, but the same holds for any linear combination  $\beta' y_t$ ; in other words, no cointegration occurs.

Estimation typically proceeds in two stages: first, a sequence of tests is run to determine  $r$ , the cointegration rank. Then, for a given rank the parameters in equation (26.3) are estimated. The two commands that gretl offers for estimating these systems are `coint2` and `vecm`, respectively.

The syntax for `coint2` is

```
coint2 p ylist [ ; xlist [ ; zlist ] ]
```

where  $p$  is the number of lags in (26.1);  $ylist$  is a list containing the  $y_t$  variables;  $xlist$  is an optional list of exogenous variables; and  $zlist$  is another optional list of exogenous variables whose effects are assumed to be confined to the cointegrating relationships.

The syntax for `vecm` is

```
vecm p r ylist [ ; xlist [ ; zlist ] ]
```

where  $p$  is the number of lags in (26.1);  $r$  is the cointegration rank; and the lists  $ylist$ ,  $xlist$  and  $zlist$  have the same interpretation as in `coint2`.

Both commands can be given specific options to handle the treatment of the deterministic component  $\mu_t$ . These are discussed in the following section.

### 26.3 Interpretation of the deterministic components

Statistical inference in the context of a cointegrated system depends on the hypotheses one is willing to make on the deterministic terms, which leads to the famous “five cases.”

In equation (26.2), the term  $\mu_t$  is usually understood to take the form

$$\mu_t = \mu_0 + \mu_1 \cdot t.$$

In order to have the model mimic as closely as possible the features of the observed data, there is a preliminary question to settle. Do the data appear to follow a deterministic trend? If so, is it linear or quadratic?

Once this is established, one should impose restrictions on  $\mu_0$  and  $\mu_1$  that are consistent with this judgement. For example, suppose that the data do not exhibit a discernible trend. This means that  $\Delta y_t$  is on average zero, so it is reasonable to assume that its expected value is also zero. Write equation (26.2) as

$$\Gamma(L)\Delta y_t = \mu_0 + \mu_1 \cdot t + \alpha z_{t-1} + \epsilon_t, \quad (26.4)$$

where  $z_t = \beta' y_t$  is assumed to be stationary and therefore to possess finite moments. Taking unconditional expectations, we get

$$0 = \mu_0 + \mu_1 \cdot t + \alpha m_z.$$

Since the left-hand side does not depend on  $t$ , the restriction  $\mu_1 = 0$  is a safe bet. As for  $\mu_0$ , there are just two ways to make the above expression true: either  $\mu_0 = 0$  with  $m_z = 0$ , or  $\mu_0$  equals  $-\alpha m_z$ . The latter possibility is less restrictive in that the vector  $\mu_0$  may be non-zero, but is constrained to be a linear combination of the columns of  $\alpha$ . In that case,  $\mu_0$  can be written as  $\alpha \cdot c$ , and one may write (26.4) as

$$\Gamma(L)\Delta y_t = \alpha \begin{bmatrix} \beta' & c \end{bmatrix} \begin{bmatrix} y_{t-1} \\ 1 \end{bmatrix} + \epsilon_t.$$

The long-run relationship therefore contains an intercept. This type of restriction is usually written

$$\alpha'_\perp \mu_0 = 0,$$

where  $\alpha_\perp$  is the left null space of the matrix  $\alpha$ .

An intuitive understanding of the issue can be gained by means of a simple example. Consider a series  $x_t$  which behaves as follows

$$x_t = m + x_{t-1} + \varepsilon_t$$

where  $m$  is a real number and  $\varepsilon_t$  is a white noise process:  $x_t$  is then a random walk with drift  $m$ . In the special case  $m = 0$ , the drift disappears and  $x_t$  is a pure random walk.

Consider now another process  $y_t$ , defined by

$$y_t = k + x_t + u_t$$

where, again,  $k$  is a real number and  $u_t$  is a white noise process. Since  $u_t$  is stationary by definition,  $x_t$  and  $y_t$  cointegrate: that is, their difference

$$z_t = y_t - x_t = k + u_t$$

is a stationary process. For  $k = 0$ ,  $z_t$  is simple zero-mean white noise, whereas for  $k \neq 0$  the process  $z_t$  is white noise with a non-zero mean.

After some simple substitutions, the two equations above can be represented jointly as a VAR(1) system

$$\begin{bmatrix} y_t \\ x_t \end{bmatrix} = \begin{bmatrix} k + m \\ m \end{bmatrix} + \begin{bmatrix} 0 & 1 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} y_{t-1} \\ x_{t-1} \end{bmatrix} + \begin{bmatrix} u_t + \varepsilon_t \\ \varepsilon_t \end{bmatrix}$$

or in VECM form

$$\begin{aligned} \begin{bmatrix} \Delta y_t \\ \Delta x_t \end{bmatrix} &= \begin{bmatrix} k + m \\ m \end{bmatrix} + \begin{bmatrix} -1 & 1 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} y_{t-1} \\ x_{t-1} \end{bmatrix} + \begin{bmatrix} u_t + \varepsilon_t \\ \varepsilon_t \end{bmatrix} = \\ &= \begin{bmatrix} k + m \\ m \end{bmatrix} + \begin{bmatrix} -1 \\ 0 \end{bmatrix} \begin{bmatrix} 1 & -1 \end{bmatrix} \begin{bmatrix} y_{t-1} \\ x_{t-1} \end{bmatrix} + \begin{bmatrix} u_t + \varepsilon_t \\ \varepsilon_t \end{bmatrix} = \\ &= \mu_0 + \alpha \beta' \begin{bmatrix} y_{t-1} \\ x_{t-1} \end{bmatrix} + \eta_t = \mu_0 + \alpha z_{t-1} + \eta_t, \end{aligned}$$

where  $\beta$  is the cointegration vector and  $\alpha$  is the “loadings” or “adjustments” vector.

We are now ready to consider three possible cases:

1.  $m \neq 0$ : In this case  $x_t$  is trended, as we just saw; it follows that  $y_t$  also follows a linear trend because on average it keeps at a fixed distance  $k$  from  $x_t$ . The vector  $\mu_0$  is unrestricted.
2.  $m = 0$  and  $k \neq 0$ : In this case,  $x_t$  is not trended and as a consequence neither is  $y_t$ . However, the mean distance between  $y_t$  and  $x_t$  is non-zero. The vector  $\mu_0$  is given by

$$\mu_0 = \begin{bmatrix} k \\ 0 \end{bmatrix}$$

which is not null and therefore the VECM shown above does have a constant term. The constant, however, is subject to the restriction that its second element must be 0. More generally,  $\mu_0$  is a multiple of the vector  $\alpha$ . Note that the VECM could also be written as

$$\begin{bmatrix} \Delta y_t \\ \Delta x_t \end{bmatrix} = \begin{bmatrix} -1 \\ 0 \end{bmatrix} \begin{bmatrix} 1 & -1 & -k \end{bmatrix} \begin{bmatrix} y_{t-1} \\ x_{t-1} \\ 1 \end{bmatrix} + \begin{bmatrix} u_t + \varepsilon_t \\ \varepsilon_t \end{bmatrix}$$

which incorporates the intercept into the cointegration vector. This is known as the “restricted constant” case.

3.  $m = 0$  and  $k = 0$ : This case is the most restrictive: clearly, neither  $x_t$  nor  $y_t$  are trended, and the mean distance between them is zero. The vector  $\mu_0$  is also 0, which explains why this case is referred to as “no constant.”

In most cases, the choice between these three possibilities is based on a mix of empirical observation and economic reasoning. If the variables under consideration seem to follow a linear trend

then we should not place any restriction on the intercept. Otherwise, the question arises of whether it makes sense to specify a cointegration relationship which includes a non-zero intercept. One example where this is appropriate is the relationship between two interest rates: generally these are not trended, but the VAR might still have an intercept because the difference between the two (the “interest rate spread”) might be stationary around a non-zero mean (for example, because of a risk or liquidity premium).

The previous example can be generalized in three directions:

1. If a VAR of order greater than 1 is considered, the algebra gets more convoluted but the conclusions are identical.
2. If the VAR includes more than two endogenous variables the cointegration rank  $r$  can be greater than 1. In this case,  $\alpha$  is a matrix with  $r$  columns, and the case with restricted constant entails the restriction that  $\mu_0$  should be some linear combination of the columns of  $\alpha$ .
3. If a linear trend is included in the model, the deterministic part of the VAR becomes  $\mu_0 + \mu_1 t$ . The reasoning is practically the same as above except that the focus now centers on  $\mu_1$  rather than  $\mu_0$ . The counterpart to the “restricted constant” case discussed above is a “restricted trend” case, such that the cointegration relationships include a trend but the first differences of the variables in question do not. In the case of an unrestricted trend, the trend appears in both the cointegration relationships and the first differences, which corresponds to the presence of a quadratic trend in the variables themselves (in levels).

In order to accommodate the five cases, `gretl` provides the following options to the `coint2` and `vecm` commands:

$\mu_t$	option flag	description
0	--nc	no constant
$\mu_0, \alpha'_\perp \mu_0 = 0$	--rc	restricted constant
$\mu_0$	--uc	unrestricted constant
$\mu_0 + \mu_1 t, \alpha'_\perp \mu_1 = 0$	--crt	constant + restricted trend
$\mu_0 + \mu_1 t$	--ct	constant + unrestricted trend

Note that for this command the above options are mutually exclusive. In addition, you have the option of using the `--seasonal` options, for augmenting  $\mu_t$  with centered seasonal dummies. In each case, p-values are computed via the approximations devised by [Doornik \(1998\)](#).

## 26.4 The Johansen cointegration tests

The two Johansen tests for cointegration are used to establish the rank of  $\beta$ ; in other words, how many cointegration vectors the system has. These are the “ $\lambda$ -max” test, for hypotheses on individual eigenvalues, and the “trace” test, for joint hypotheses. Suppose that the eigenvalues  $\lambda_i$  are sorted from largest to smallest. The null hypothesis for the  $\lambda$ -max test on the  $i$ -th eigenvalue is that  $\lambda_i = 0$ . The corresponding trace test, instead, considers the hypothesis  $\lambda_j = 0$  for all  $j \geq i$ .

The `gretl` command `coint2` performs these two tests. The corresponding menu entry in the GUI is “Model, Time Series, Cointegration Test, Johansen”.

As in the ADF test, the asymptotic distribution of the tests varies with the deterministic component  $\mu_t$  one includes in the VAR (see section 26.3 above). The following code uses the `denmark` data file, supplied with `gretl`, to replicate Johansen’s example found in his 1995 book.

```
open denmark
coint2 2 LRM LRY IBO IDE --rc --seasonal
```



In this case, the vector  $y_t$  in equation (26.2) comprises the four variables LRM, LRY, IBO, IDE. The number of lags equals  $p$  in (26.2) (that is, the number of lags of the model written in VAR form). Part of the output is reported below:

```
Johansen test:
Number of equations = 4
Lag order = 2
Estimation period: 1974:3 - 1987:3 (T = 53)

Case 2: Restricted constant
Rank Eigenvalue Trace test p-value Lmax test p-value
0 0.43317 49.144 [0.1284] 30.087 [0.0286]
1 0.17758 19.057 [0.7833] 10.362 [0.8017]
2 0.11279 8.6950 [0.7645] 6.3427 [0.7483]
3 0.043411 2.3522 [0.7088] 2.3522 [0.7076]
```

Both the trace and  $\lambda$ -max tests accept the null hypothesis that the smallest eigenvalue is 0 (see the last row of the table), so we may conclude that the series are in fact non-stationary. However, some linear combination may be  $I(0)$ , since the  $\lambda$ -max test rejects the hypothesis that the rank of  $\Pi$  is 0 (though the trace test gives less clear-cut evidence for this, with a p-value of 0.1284).

## 26.5 Identification of the cointegration vectors

The core problem in the estimation of equation (26.2) is to find an estimate of  $\Pi$  that has by construction rank  $r$ , so it can be written as  $\Pi = \alpha\beta'$ , where  $\beta$  is the matrix containing the cointegration vectors and  $\alpha$  contains the “adjustment” or “loading” coefficients whereby the endogenous variables respond to deviation from equilibrium in the previous period.

Without further specification, the problem has multiple solutions (in fact, infinitely many). The parameters  $\alpha$  and  $\beta$  are under-identified: if all columns of  $\beta$  are cointegration vectors, then any arbitrary linear combinations of those columns is a cointegration vector too. To put it differently, if  $\Pi = \alpha_0\beta_0'$  for specific matrices  $\alpha_0$  and  $\beta_0$ , then  $\Pi$  also equals  $(\alpha_0 Q)(Q^{-1}\beta_0')$  for any conformable non-singular matrix  $Q$ . In order to find a unique solution, it is therefore necessary to impose some restrictions on  $\alpha$  and/or  $\beta$ . It can be shown that the minimum number of restrictions that is necessary to guarantee identification is  $r^2$ . Normalizing one coefficient per column to 1 (or  $-1$ , according to taste) is a trivial first step, which also helps in that the remaining coefficients can be interpreted as the parameters in the equilibrium relations, but this only suffices when  $r = 1$ .

The method that gretl uses by default is known as the “Phillips normalization”, or “triangular representation”.<sup>1</sup> The starting point is writing  $\beta$  in partitioned form as in

$$\beta = \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix},$$

where  $\beta_1$  is an  $r \times r$  matrix and  $\beta_2$  is  $(n - r) \times r$ . Assuming that  $\beta_1$  has full rank,  $\beta$  can be post-multiplied by  $\beta_1^{-1}$ , giving

$$\hat{\beta} = \begin{bmatrix} I \\ \beta_2\beta_1^{-1} \end{bmatrix} = \begin{bmatrix} I \\ -B \end{bmatrix},$$

The coefficients that gretl produces are  $\hat{\beta}$ , with  $B$  known as the matrix of unrestricted coefficients. In terms of the underlying equilibrium relationship, the Phillips normalization expresses the system

<sup>1</sup>For comparison with other studies, you may wish to normalize  $\beta$  differently. Using the `set` command you can do `set vecm_norm diag` to select a normalization that simply scales the columns of the original  $\beta$  such that  $\beta_{ij} = 1$  for  $i = j$  and  $i \leq r$ , as used in the empirical section of Boswijk and Doornik (2004). Another alternative is `set vecm_norm first`, which scales  $\beta$  such that the elements on the first row equal 1. To suppress normalization altogether, use `set vecm_norm none`. (To return to the default: `set vecm_norm phillips`.)

of  $r$  equilibrium relations as

$$\begin{aligned} y_{1,t} &= b_{1,r+1}y_{r+1,t} + \dots + b_{1,n}y_{n,t} \\ y_{2,t} &= b_{2,r+1}y_{r+1,t} + \dots + b_{2,n}y_{n,t} \\ &\vdots \\ y_{r,t} &= b_{r,r+1}y_{r+1,t} + \dots + b_{r,n}y_{n,t} \end{aligned}$$

where the first  $r$  variables are expressed as functions of the remaining  $n - r$ .

Although the triangular representation ensures that the statistical problem of estimating  $\beta$  is solved, the resulting equilibrium relationships may be difficult to interpret. In this case, the user may want to achieve identification by specifying manually the system of  $r^2$  constraints that gretl will use to produce an estimate of  $\beta$ .

As an example, consider the money demand system presented in section 9.6 of Verbeek (2004). The variables used are *m* (the log of real money stock M1), *infl* (inflation), *cpr* (the commercial paper rate), *y* (log of real GDP) and *tbr* (the Treasury bill rate).<sup>2</sup>

Estimation of  $\beta$  can be performed via the commands

```
open money.gdt
smp1 1954:1 1994:4
vecm 6 2 m infl cpr y tbr --rc
```

and the relevant portion of the output reads

```
Maximum likelihood estimates, observations 1954:1-1994:4 (T = 164)
Cointegration rank = 2
Case 2: Restricted constant

beta (cointegrating vectors, standard errors in parentheses)

m          1.0000      0.0000
           (0.0000)    (0.0000)
infl       0.0000      1.0000
           (0.0000)    (0.0000)
cpr        0.56108     -24.367
           (0.10638)   (4.2113)
y          -0.40446    -0.91166
           (0.10277)   (4.0683)
tbr        -0.54293     24.786
           (0.10962)   (4.3394)
const      -3.7483     16.751
           (0.78082)   (30.909)
```

Interpretation of the coefficients of the cointegration matrix  $\beta$  would be easier if a meaning could be attached to each of its columns. This is possible by hypothesizing the existence of two long-run relationships: a money demand equation

$$m = c_1 + \beta_1 \text{infl} + \beta_2 y + \beta_3 \text{tbr}$$

and a risk premium equation

$$\text{cpr} = c_2 + \beta_4 \text{infl} + \beta_5 y + \beta_6 \text{tbr}$$

<sup>2</sup>This data set is available in the verbeek data package; see [http://gretl.sourceforge.net/gretl\\_data.html](http://gretl.sourceforge.net/gretl_data.html).

which imply that the cointegration matrix can be normalized as

$$\beta = \begin{bmatrix} -1 & 0 \\ \beta_1 & \beta_4 \\ 0 & -1 \\ \beta_2 & \beta_5 \\ \beta_3 & \beta_6 \\ c_1 & c_2 \end{bmatrix}$$

This renormalization can be accomplished by means of the `restrict` command, to be given after the `vecm` command or, in the graphical interface, by selecting the “Test, Linear Restrictions” menu entry. The syntax for entering the restrictions should be fairly obvious:<sup>3</sup>

```
restrict
  b[1,1] = -1
  b[1,3] = 0
  b[2,1] = 0
  b[2,3] = -1
end restrict
```

which produces

Cointegrating vectors (standard errors in parentheses)

m	-1.0000	0.0000
	(0.0000)	(0.0000)
infl	-0.023026	0.041039
	(0.0054666)	(0.027790)
cpr	0.0000	-1.0000
	(0.0000)	(0.0000)
y	0.42545	-0.037414
	(0.033718)	(0.17140)
tbr	-0.027790	1.0172
	(0.0045445)	(0.023102)
const	3.3625	0.68744
	(0.25318)	(1.2870)

## 26.6 Over-identifying restrictions

One purpose of imposing restrictions on a VECM system is simply to achieve identification. If these restrictions are simply normalizations, they are not testable and should have no effect on the maximized likelihood. In addition, however, one may wish to formulate constraints on  $\beta$  and/or  $\alpha$  that derive from the economic theory underlying the equilibrium relationships; substantive restrictions of this sort are then testable via a likelihood-ratio statistic.

Gretl is capable of testing general linear restrictions of the form

$$R_b \text{vec}(\beta) = q \quad (26.5)$$

and/or

$$R_a \text{vec}(\alpha) = 0 \quad (26.6)$$

Note that the  $\beta$  restriction may be non-homogeneous ( $q \neq 0$ ) but the  $\alpha$  restriction must be homogeneous. Nonlinear restrictions are not supported, and neither are restrictions that cross between

<sup>3</sup>Note that in this context we are bending the usual matrix indexation convention, using the leading index to refer to the *column* of  $\beta$  (the particular cointegrating vector). This is standard practice in the literature, and defensible insofar as it is the columns of  $\beta$  (the cointegrating relations or equilibrium errors) that are of primary interest.

$\beta$  and  $\alpha$ . In the case where  $r > 1$  such restrictions may be in common across all the columns of  $\beta$  (or  $\alpha$ ) or may be specific to certain columns of these matrices. This is the case discussed in [Boswijk \(1995\)](#) and [Boswijk and Doornik \(2004\)](#), section 4.4.

The restrictions (26.5) and (26.6) may be written in explicit form as

$$\text{vec}(\beta) = H\phi + h_0 \quad (26.7)$$

and

$$\text{vec}(\alpha') = G\psi \quad (26.8)$$

respectively, where  $\phi$  and  $\psi$  are the free parameter vectors associated with  $\beta$  and  $\alpha$  respectively. We may refer to the free parameters collectively as  $\theta$  (the column vector formed by concatenating  $\phi$  and  $\psi$ ). Gretl uses this representation internally when testing the restrictions.

If the list of restrictions that is passed to the `restrict` command contains more constraints than necessary to achieve identification, then an LR test is performed; moreover, the `restrict` command can be given the `--full` switch, in which case full estimates for the restricted system are printed (including the  $\Gamma_i$  terms), and the system thus restricted becomes the “current model” for the purposes of further tests. Thus you are able to carry out cumulative tests, as in Chapter 7 of [Johansen \(1995\)](#).

### Syntax

The full syntax for specifying the restriction is an extension of that exemplified in the previous section. Inside a `restrict...end restrict` block, valid statements are of the form

$$\textit{parameter linear combination} = \textit{scalar}$$

where a parameter linear combination involves a weighted sum of individual elements of  $\beta$  or  $\alpha$  (but not both in the same combination); the scalar on the right-hand side must be 0 for combinations involving  $\alpha$ , but can be any real number for combinations involving  $\beta$ . Below, we give a few examples of valid restrictions:

```
b[1,1] = 1.618
b[1,4] + 2*b[2,5] = 0
a[1,3] = 0
a[1,1] - a[1,2] = 0
```

Special syntax is used when a certain constraint should be applied to all columns of  $\beta$ : in this case, one index is given for each `b` term, and the square brackets are dropped. Hence, the following syntax

```
restrict
  b1 + b2 = 0
end restrict
```

corresponds to

$$\beta = \begin{bmatrix} \beta_{11} & \beta_{21} \\ -\beta_{11} & -\beta_{21} \\ \beta_{13} & \beta_{23} \\ \beta_{14} & \beta_{24} \end{bmatrix}$$

The same convention is used for  $\alpha$ : when only one index is given for an `a` term the restriction is presumed to apply to all  $r$  columns of  $\alpha$ , or in other words the variable associated with the given row of  $\alpha$  is weakly exogenous. For instance, the formulation

```

restrict
  a3 = 0
  a4 = 0
end restrict

```

specifies that variables 3 and 4 do not respond to the deviation from equilibrium in the previous period.<sup>4</sup>

A variant on the single-index syntax for common restrictions on  $\alpha$  and  $\beta$  is available: you can replace the index number with the name of the corresponding variable, in square brackets. For example, instead of `a3 = 0` one could write `a[cpr] = 0`, if the third variable in the system is named `cpr`.

Finally, a short-cut is available for setting up complex restrictions (but currently only in relation to  $\beta$ ): you can specify  $R_b$  and  $q$ , as in  $R_b \text{vec}(\beta) = q$ , by giving the names of previously defined matrices. For example,

```

matrix I4 = I(4)
matrix vR = I4**(I4~zeros(4,1))
matrix vq = mshape(I4,16,1)
restrict
  R = vR
  q = vq
end restrict

```

which manually imposes Phillips normalization on the  $\beta$  estimates for a system with cointegrating rank 4.

### An example

[Brand and Cassola \(2004\)](#) propose a money demand system for the Euro area, in which they postulate three long-run equilibrium relationships:

money demand	$m = \beta_l l + \beta_y y$
Fisher equation	$\pi = \phi l$
Expectation theory of interest rates	$l = s$

where  $m$  is real money demand,  $l$  and  $s$  are long- and short-term interest rates,  $y$  is output and  $\pi$  is inflation.<sup>5</sup> (The names for these variables in the `gretl` data file are `m_p`, `r_l`, `rs`, `y` and `infl`, respectively.)

The cointegration rank assumed by the authors is 3 and there are 5 variables, giving 15 elements in the  $\beta$  matrix.  $3 \times 3 = 9$  restrictions are required for identification, and a just-identified system would have  $15 - 9 = 6$  free parameters. However, the postulated long-run relationships feature only three free parameters, so the over-identification rank is 3.

Example 26.1 replicates Table 4 on page 824 of the Brand and Cassola article.<sup>6</sup> Note that we use the `$lnl` accessor after the `vecm` command to store the unrestricted log-likelihood and the `$rlnl` accessor after `restrict` for its restricted counterpart.

<sup>4</sup>Note that when two indices are given in a restriction on  $\alpha$  the indexation is consistent with that for  $\beta$  restrictions: the leading index denotes the cointegrating vector and the trailing index the equation number.

<sup>5</sup>A traditional formulation of the Fisher equation would reverse the roles of the variables in the second equation, but this detail is immaterial in the present context; moreover, the expectation theory of interest rates implies that the third equilibrium relationship should include a constant for the liquidity premium. However, since in this example the system is estimated with the constant term unrestricted, the liquidity premium gets merged in the system intercept and disappears from  $z_t$ .

<sup>6</sup>Modulo what appear to be a few typos in the article.

**Example 26.1:** Estimation of a money demand system with constraints on  $\beta$ 

Input:

```

open brand_cassola.gdt

# perform a few transformations
m_p = m_p*100
y = y*100
infl = infl/4
rs = rs/4
r1 = r1/4

# replicate table 4, page 824
vecm 2 3 m_p infl r1 rs y -q
genr l10 = $lnl

restrict --full
  b[1,1] = 1
  b[1,2] = 0
  b[1,4] = 0
  b[2,1] = 0
  b[2,2] = 1
  b[2,4] = 0
  b[2,5] = 0
  b[3,1] = 0
  b[3,2] = 0
  b[3,3] = 1
  b[3,4] = -1
  b[3,5] = 0
end restrict
genr l11 = $rlnl

```

Partial output:

```

Unrestricted loglikelihood (lu) = 116.60268
Restricted loglikelihood (lr) = 115.86451
2 * (lu - lr) = 1.47635
P(Chi-Square(3) > 1.47635) = 0.68774

```

beta (cointegrating vectors, standard errors in parentheses)

m_p	1.0000	0.0000	0.0000
	(0.0000)	(0.0000)	(0.0000)
infl	0.0000	1.0000	0.0000
	(0.0000)	(0.0000)	(0.0000)
r1	1.6108	-0.67100	1.0000
	(0.62752)	(0.049482)	(0.0000)
rs	0.0000	0.0000	-1.0000
	(0.0000)	(0.0000)	(0.0000)
y	-1.3304	0.0000	0.0000
	(0.030533)	(0.0000)	(0.0000)

The example continues in script 26.2, where we perform further testing to check whether (a) the income elasticity in the money demand equation is 1 ( $\beta_y = 1$ ) and (b) the Fisher relation is homogeneous ( $\phi = 1$ ). Since the `--full` switch was given to the initial `restrict` command, additional restrictions can be applied without having to repeat the previous ones. (The second script contains a few `printf` commands, which are not strictly necessary, to format the output nicely.) It turns out that both of the additional hypotheses are rejected by the data, with p-values of 0.002 and 0.004.

**Example 26.2:** Further testing of money demand system

Input:

```
restrict
  b[1,5] = -1
end restrict
genr ll_uie = $rlnl

restrict
  b[2,3] = -1
end restrict
genr ll_hfh = $rlnl

# replicate table 5, page 824
printf "Testing zero restrictions in cointegration space:\n"
printf "  LR-test, rank = 3: chi^2(3) = %6.4f [%6.4f]\n", 2*(ll0-ll1), \
  pvalue(X, 3, 2*(ll0-ll1))

printf "Unit income elasticity: LR-test, rank = 3:\n"
printf "  chi^2(4) = %g [%6.4f]\n", 2*(ll0-ll_uie), \
  pvalue(X, 4, 2*(ll0-ll_uie))

printf "Homogeneity in the Fisher hypothesis:\n"
printf "  LR-test, rank = 3: chi^2(4) = %6.3f [%6.4f]\n", 2*(ll0-ll_hfh), \
  pvalue(X, 4, 2*(ll0-ll_hfh))
```

Output:

```
Testing zero restrictions in cointegration space:
  LR-test, rank = 3: chi^2(3) = 1.4763 [0.6877]
Unit income elasticity: LR-test, rank = 3:
  chi^2(4) = 17.2071 [0.0018]
Homogeneity in the Fisher hypothesis:
  LR-test, rank = 3: chi^2(4) = 15.547 [0.0037]
```

Another type of test that is commonly performed is the “weak exogeneity” test. In this context, a variable is said to be weakly exogenous if all coefficients on the corresponding row in the  $\alpha$  matrix are zero. If this is the case, that variable does not adjust to deviations from any of the long-run equilibria and can be considered an autonomous driving force of the whole system.

The code in Example 26.3 performs this test for each variable in turn, thus replicating the first column of Table 6 on page 825 of [Brand and Cassola \(2004\)](#). The results show that weak exogeneity might perhaps be accepted for the long-term interest rate and real GDP (p-values 0.07 and 0.08 respectively).

### Identification and testability

One point regarding VECM restrictions that can be confusing at first is that identification (does the restriction identify the system?) and testability (is the restriction testable?) are quite separate matters. Restrictions can be identifying but not testable; less obviously, they can be testable but not identifying.

**Example 26.3:** Testing for weak exogeneity

Input:

```

restrict
  a1 = 0
end restrict
ts_m = 2*(110 - $rln1)

restrict
  a2 = 0
end restrict
ts_p = 2*(110 - $rln1)

restrict
  a3 = 0
end restrict
ts_l = 2*(110 - $rln1)

restrict
  a4 = 0
end restrict
ts_s = 2*(110 - $rln1)

restrict
  a5 = 0
end restrict
ts_y = 2*(110 - $rln1)

loop foreach i m p l s y --quiet
  printf "\Delta $i\t%6.3f [%6.4f]\n", ts_$i, pvalue(X, 6, ts_$i)
endloop

```

Output (variable, LR test, p-value):

\Delta m	18.111	[0.0060]
\Delta p	21.067	[0.0018]
\Delta l	11.819	[0.0661]
\Delta s	16.000	[0.0138]
\Delta y	11.335	[0.0786]



This can be seen quite easily in relation to a rank-1 system. The restriction  $\beta_1 = 1$  is identifying (it pins down the scale of  $\beta$ ) but, being a pure scaling, it is not testable. On the other hand, the restriction  $\beta_1 + \beta_2 = 0$  is testable — the system with this requirement imposed will almost certainly have a lower maximized likelihood — but it is not identifying; it still leaves open the scale of  $\beta$ .

We said above that the number of restrictions must equal at least  $r^2$ , where  $r$  is the cointegrating rank, for identification. This is a necessary and not a sufficient condition. In fact, when  $r > 1$  it can be quite tricky to assess whether a given set of restrictions is identifying. *Gretl* uses the method suggested by [Doornik \(1995\)](#), where identification is assessed via the rank of the information matrix.

It can be shown that for restrictions of the sort (26.7) and (26.8) the information matrix has the same rank as the Jacobian matrix

$$J(\theta) = \left[ (I_p \otimes \beta)G : (\alpha \otimes I_{p_1})H \right]$$

A sufficient condition for identification is that the rank of  $J(\theta)$  equals the number of free parameters. The rank of this matrix is evaluated by examination of its singular values at a randomly selected point in the parameter space. For practical purposes we treat this condition as if it were both necessary and sufficient; that is, we disregard the special cases where identification could be achieved without this condition being met.<sup>7</sup>

## 26.7 Numerical solution methods

In general, the ML estimator for the restricted VECM problem has no closed form solution, hence the maximum must be found via numerical methods.<sup>8</sup> In some cases convergence may be difficult, and *gretl* provides several choices to solve the problem.

### Switching and LBFGS

Two maximization methods are available in *gretl*. The default is the switching algorithm set out in [Boswijk and Doornik \(2004\)](#). The alternative is a limited-memory variant of the BFGS algorithm (LBFGS), using analytical derivatives. This is invoked using the `--lbfgs` flag with the `restrict` command.

The switching algorithm works by explicitly maximizing the likelihood at each iteration, with respect to  $\hat{\phi}$ ,  $\hat{\psi}$  and  $\hat{\Omega}$  (the covariance matrix of the residuals) in turn. This method shares a feature with the basic Johansen eigenvalues procedure, namely, it can handle a set of restrictions that does not fully identify the parameters.

LBFGS, on the other hand, requires that the model be fully identified. When using LBFGS, therefore, you may have to supplement the restrictions of interest with normalizations that serve to identify the parameters. For example, one might use all or part of the Phillips normalization (see section 26.5).

Neither the switching algorithm nor LBFGS is guaranteed to find the global ML solution.<sup>9</sup> The optimizer may end up at a local maximum (or, in the case of the switching algorithm, at a saddle point).

The solution (or lack thereof) may be sensitive to the initial value selected for  $\theta$ . By default, *gretl* selects a starting point using a deterministic method based on [Boswijk \(1995\)](#), but two further

<sup>7</sup>See [Boswijk and Doornik \(2004\)](#), pp. 447–8 for discussion of this point.

<sup>8</sup>The exception is restrictions that are homogeneous, common to all  $\beta$  or all  $\alpha$  (in case  $r > 1$ ), and involve either  $\beta$  only or  $\alpha$  only. Such restrictions are handled via the modified eigenvalues method set out by [Johansen \(1995\)](#). We solve directly for the ML estimator, without any need for iterative methods.

<sup>9</sup>In developing *gretl*'s VECM-testing facilities we have considered a fair number of “tricky cases” from various sources. We'd like to thank Luca Fanelli of the University of Bologna and Sven Schreiber of Goethe University Frankfurt for their help in devising torture-tests for *gretl*'s VECM code.

options are available: the initialization may be adjusted using simulated annealing, or the user may supply an explicit initial value for  $\theta$ .

The default initialization method is:

1. Calculate the unrestricted ML  $\hat{\beta}$  using the Johansen procedure.
2. If the restriction on  $\beta$  is non-homogeneous, use the method proposed by Boswijk:

$$\phi_0 = -[(I_r \otimes \hat{\beta}_\perp)' H]^+ (I_r \otimes \hat{\beta}_\perp)' h_0 \quad (26.9)$$

where  $\hat{\beta}_\perp' \hat{\beta} = 0$  and  $A^+$  denotes the Moore-Penrose inverse of  $A$ . Otherwise

$$\phi_0 = (H' H)^{-1} H' \text{vec}(\hat{\beta}) \quad (26.10)$$

3.  $\text{vec}(\beta_0) = H\phi_0 + h_0$ .
4. Calculate the unrestricted ML  $\hat{\alpha}$  conditional on  $\beta_0$ , as per Johansen:

$$\hat{\alpha} = S_{01} \beta_0 (\beta_0' S_{11} \beta_0)^{-1} \quad (26.11)$$

5. If  $\alpha$  is restricted by  $\text{vec}(\alpha') = G\psi$ , then  $\psi_0 = (G' G)^{-1} G' \text{vec}(\hat{\alpha}')$  and  $\text{vec}(\alpha'_0) = G\psi_0$ .

### Alternative initialization methods

As mentioned above, `gretl` offers the option of adjusting the initialization using **simulated annealing**. This is invoked by adding the `--jitter` option to the `restrict` command.

The basic idea is this: we start at a certain point in the parameter space, and for each of  $n$  iterations (currently  $n = 4096$ ) we randomly select a new point within a certain radius of the previous one, and determine the likelihood at the new point. If the likelihood is higher, we jump to the new point; otherwise, we jump with probability  $P$  (and remain at the previous point with probability  $1 - P$ ). As the iterations proceed, the system gradually “cools” — that is, the radius of the random perturbation is reduced, as is the probability of making a jump when the likelihood fails to increase.

In the course of this procedure many points in the parameter space are evaluated, starting with the point arrived at by the deterministic method, which we’ll call  $\theta_0$ . One of these points will be “best” in the sense of yielding the highest likelihood: call it  $\theta^*$ . This point may or may not have a greater likelihood than  $\theta_0$ . And the procedure has an end point,  $\theta_n$ , which may or may not be “best”.

The rule followed by `gretl` in selecting an initial value for  $\theta$  based on simulated annealing is this: use  $\theta^*$  if  $\theta^* > \theta_0$ , otherwise use  $\theta_n$ . That is, if we get an improvement in the likelihood via annealing, we make full use of this; on the other hand, if we fail to get an improvement we nonetheless allow the annealing to randomize the starting point. Experiments indicated that the latter effect can be helpful.

Besides annealing, a further alternative is **manual initialization**. This is done by passing a predefined vector to the `set` command with parameter `initvals`, as in

```
set initvals myvec
```

The details depend on whether the switching algorithm or LBFGS is used. For the switching algorithm, there are two options for specifying the initial values. The more user-friendly one (for most people, we suppose) is to specify a matrix that contains  $\text{vec}(\beta)$  followed by  $\text{vec}(\alpha)$ . For example:

```
open denmark.gdt
vecm 2 1 LRM LRY IBO IDE --rc --seasonals

matrix BA = {1, -1, 6, -6, -6, -0.2, 0.1, 0.02, 0.03}
```

```

set initvals BA
restrict
  b[1] = 1
  b[1] + b[2] = 0
  b[3] + b[4] = 0
end restrict

```

In this example — from [Johansen \(1995\)](#) — the cointegration rank is 1 and there are 4 variables. However, the model includes a restricted constant (the `--rc` flag) so that  $\beta$  has 5 elements. The  $\alpha$  matrix has 4 elements, one per equation. So the matrix BA may be read as

$$(\beta_1, \beta_2, \beta_3, \beta_4, \beta_5, \alpha_1, \alpha_2, \alpha_3, \alpha_4)$$

The other option, which is compulsory when using LBFGS, is to specify the initial values in terms of the free parameters,  $\phi$  and  $\psi$ . Getting this right is somewhat less obvious. As mentioned above, the implicit-form restriction  $R\text{vec}(\beta) = q$  has explicit form  $\text{vec}(\beta) = H\phi + h_0$ , where  $H = R_\perp$ , the right nullspace of  $R$ . The vector  $\phi$  is shorter, by the number of restrictions, than  $\text{vec}(\beta)$ . The savvy user will then see what needs to be done. The other point to take into account is that if  $\alpha$  is unrestricted, the *effective* length of  $\psi$  is 0, since it is then optimal to compute  $\alpha$  using Johansen's formula, conditional on  $\beta$  (equation 26.11 above). The example above could be rewritten as:

```

open denmark.gdt
vecm 2 1 LRM LRY IBO IDE --rc --seasonals

matrix phi = {-8, -6}
set initvals phi
restrict --lbfgs
  b[1] = 1
  b[1] + b[2] = 0
  b[3] + b[4] = 0
end restrict

```

In this more economical formulation the initializer specifies only the two free parameters in  $\phi$  (5 elements in  $\beta$  minus 3 restrictions). There is no call to give values for  $\psi$  since  $\alpha$  is unrestricted.

### Scale removal

Consider a simpler version of the restriction discussed in the previous section, namely,

```

restrict
  b[1] = 1
  b[1] + b[2] = 0
end restrict

```

This restriction comprises a substantive, testable requirement — that  $\beta_1$  and  $\beta_2$  sum to zero — and a normalization or scaling,  $\beta_1 = 1$ . The question arises, might it be easier and more reliable to maximize the likelihood without imposing  $\beta_1 = 1$ ?<sup>10</sup> If so, we could record this normalization, remove it for the purpose of maximizing the likelihood, then reimpose it by scaling the result.

Unfortunately it is not possible to say in advance whether “scale removal” of this sort will give better results, for any particular estimation problem. However, this does seem to be the case more often than not. Gretl therefore performs scale removal where feasible, unless you

- explicitly forbid this, by giving the `--no-scaling` option flag to the restrict command; or
- provide a specific vector of initial values; or

<sup>10</sup>As a numerical matter, that is. In principle this should make no difference.

- select the LBFGS algorithm for maximization.

Scale removal is deemed infeasible if there are any cross-column restrictions on  $\beta$ , or any non-homogeneous restrictions involving more than one element of  $\beta$ .

In addition, experimentation has suggested to us that scale removal is inadvisable if the system is just identified with the normalization(s) included, so we do not do it in that case. By “just identified” we mean that the system would not be identified if any of the restrictions were removed. On that criterion the above example is not just identified, since the removal of the second restriction would not affect identification; and *gretl* would in fact perform scale removal in this case unless the user specified otherwise.

## Chapter 27

# Multivariate models

By a multivariate model we mean one that includes more than one dependent variable. Certain specific types of multivariate model for time-series data are discussed elsewhere: chapter 25 deals with VARs and chapter 26 with VECMs. Here we discuss two general sorts of multivariate model, implemented in `gretl` via the `system` command: SUR systems (Seemingly Unrelated Regressions), in which all the regressors are taken to be exogenous and interest centers on the covariance of the error term across equations; and simultaneous systems, in which some regressors are assumed to be endogenous.

In this chapter we give an account of the syntax and use of the `system` command and its companions, `restrict` and `estimate`; we also explain the options and accessors available in connection with multivariate models.

### 27.1 The `system` command

The specification of a multivariate system takes the form of a block of statements, starting with `system` and ending with `end system`. Once a system is specified it can be estimated via various methods, using the `estimate` command, with or without restrictions, which may be imposed via the `restrict` command.

#### Starting a system block

The first line of a system block may be augmented in either (or both) of two ways:

- An estimation method is specified for the system. This is done by following `system` with an expression of the form `method=estimator`, where *estimator* must be one of `ols` (Ordinary Least Squares), `tsls` (Two-Stage Least Squares), `sur` (Seemingly Unrelated Regressions), `3sls` (Three-Stage Least Squares), `liml` (Limited Information Maximum Likelihood) or `fiml` (Full Information Maximum Likelihood). Two examples:

```
system method=sur
system method=fiml
```

OLS, TSLS and LIML are, of course, single-equation methods rather than true system estimators; they are included to facilitate comparisons.

- The system is assigned a name. This is done by giving the name first, followed by a back-arrow, “<-”, followed by `system`. If the name contains spaces it must be enclosed in double-quotes. Here are two examples:

```
sys1 <- system
"System 1" <- system
```

Note, however, that this naming method is not available within a user-defined function, only in the main body of a `gretl` script.

If the initial `system` line is augmented in the first way, the effect is that the system is estimated as soon as its definition is completed, using the specified method. The effect of the second option is

that the system can then be referenced by the assigned name for the purposes of the `restrict` and `estimate` commands; in the gretl GUI an additional effect is that an icon for the system is added to the “Session view”.

These two possibilities can be combined, as in

```
msysys <- system method=3sls
```

In this example the system is estimated immediately via Three-Stage Least Squares, and is also available for subsequent use under the name `msysys`.

If the system is not named via the back-arrow mechanism, it is still available for subsequent use via `restrict` and `estimate`; in this case you should use the generic name `$system` to refer to the last-defined multivariate system.

### The body of a system block

The most basic element in the body of a `system` block is the `equation` statement, which is used to specify each equation within the system. This takes the same form as the regression specification for single-equation estimators, namely a list of series with the dependent variable given first, followed by the regressors, with the series given either by name or by ID number (order in the dataset). A system block must contain at least two `equation` statements, and for systems without endogenous regressors these statements are all that is required. So, for example, a minimal SUR specification might look like this:

```
system method=sur
  equation y1 const x1
  equation y2 const x2
end system
```

For simultaneous systems it is necessary to determine which regressors are endogenous and which exogenous. By default all regressors are treated as exogenous, except that any variable that appears as the dependent variable in one equation is automatically treated as endogenous if it appears as a regressor elsewhere. However, an explicit list of endogenous regressors may be supplied following the equations lines: this takes the form of the keyword `endog` followed by the names or ID numbers of the relevant regressors.

When estimation is via TSLS or 3SLS it is possible to specify a particular set of instruments for each equation. This is done by giving the `equation` lists in the format used with the `tsls` command: first the dependent variable, then the regressors, then a semicolon, then the instruments, as in

```
system method=3sls
  equation y1 const x11 x12 ; const x11 z1
  equation y2 const x21 x22 ; const x21 z2
end system
```

In this case, as in `tsls`, any regressors that are not also listed as instruments are treated as endogenous, so in the example above `x11` and `x21` are treated as exogenous while `x12` and `x22` are endogenous, and instrumented by `z1` and `z2` respectively.

One more sort of statement is allowed in a `system` block: that is, the keyword `identity` followed by an equation that defines an accounting relationship, rather than a stochastic one, between variables. For example,

```
identity Y = C + I + G + X
```

There can be more than one `identity` in a system block. But note that these statements are specific to estimation via FIML; they are ignored for other estimators.

### Equation systems within functions

It is also possible to define a multivariate system in a programmatic way. This is useful if the precise specification of the system depends on some input parameters that are not known in advance, but are given when the script is actually run.<sup>1</sup>

The relevant syntax is given by the `equations` keyword (note the plural), which replaces the block of `equation` lines in the standard form. An `equations` line requires two list arguments. The first list must contain all series on the left-hand side of the system; thus the number of elements in this first list determines the number of equations in the system. The second list is a “list of lists”, which is a special variant of the list data type. That is, for each equation of the system you must provide a list of right-hand side variables, and the lists for all equations must be joined by assigning them to another list object; in that assignment, they must be separated by a semicolon. Here is an example for a two-equation system:

```
list syslist = xlist1 ; xlist2
```

Therefore, specifying a system generically in this way just involves building the necessary list arguments, as shown in the following example:

```
open denmark
list LHS = LRM LRY
list RHS1 = const LRM(-1) IBO(-1) IDE(-1)
list RHS2 = const LRY(-1) IBO(-1)
list RHS = RHS1 ; RHS2
system method=ols
    equations LHS RHS
end system
```

As mentioned above, the option of assigning a specific name to a system is not available within functions, but the generic identifier `$system` can be used to similar effect. The following example shows how one can define a system, estimate it via two methods, apply a restriction, then re-estimate it subject to the restriction.

```
function void anonsys(series x, series y)
    system
        equation x const
        equation y const
    end system
    estimate $system method=ols
    estimate $system method=sur
    restrict $system
        b[1,1] - b[2,1] = 0
    end restrict
    estimate $system method=ols
end function
```

## 27.2 Restriction and estimation

The behavior of the `restrict` command is a little different for multivariate systems as compared with single-equation models.

In the single-equation case, `restrict` refers to the last-estimated model, and once the command is completed the restriction is tested. In the multivariate case, you must give the name of the system to which the restriction is to be applied (or `$system` to refer to the last-defined system), and the

<sup>1</sup>This feature was added in version 1.9.7 of gretl.

effect of the command is just to attach the restriction to the system; testing is not done until the next `estimate` command is given. In addition, in the system case the default is to produce full estimates of the restricted model; if you are not interested in the full estimates and just want the test statistic you can append the `--quiet` option to `estimate`.

A given system restriction remains in force until it is replaced or removed. To return a system to its unrestricted state you can give an empty `restrict` block, as in

```
restrict sysname
end restrict
```

As illustrated above, you can use the `method` tag to specify an estimation method with the `estimate` command. If the system has already been estimated you can omit this tag and the previous method is used again.

The `estimate` command is the main locus for options regarding the details of estimation. The available options are as follows:

- If the estimation method is SUR or 3SLS and the `--iterate` flag is given, the estimator will be iterated. In the case of SUR, if the procedure converges the results are maximum likelihood estimates. Iteration of three-stage least squares, however, does not in general converge on the full-information maximum likelihood results. This flag is ignored for other estimators.
- If the equation-by-equation estimators OLS or TSLS are chosen, the default is to apply a degrees of freedom correction when calculating standard errors. This can be suppressed using the `--no-df-corr` flag. This flag has no effect with the other estimators; no degrees of freedom correction is applied in any case.
- By default, the formula used in calculating the elements of the cross-equation covariance matrix is

$$\hat{\sigma}_{ij} = \frac{\hat{u}_i' \hat{u}_j}{T}$$

where  $T$  is the sample size and  $\hat{u}_i$  is the vector of residuals from equation  $i$ . But if the `--geomean` flag is given, a degrees of freedom correction is applied: the formula is

$$\hat{\sigma}_{ij} = \frac{\hat{u}_i' \hat{u}_j}{\sqrt{(T - k_i)(T - k_j)}}$$

where  $k_i$  denotes the number of independent parameters in equation  $i$ .

- If an iterative method is specified, the `--verbose` option calls for printing of the details of the iterations.
- When the system estimator is SUR or 3SLS the cross-equation covariance matrix is initially estimated via OLS or TSLS, respectively. In the case of a system subject to restrictions the question arises: should the initial single-equation estimator be restricted or unrestricted? The default is the former, but the `--unrestrict-init` flag can be used to select unrestricted initialization. (Note that this is unlikely to make much difference if the `--iterate` option is given.)

### 27.3 System accessors

After system estimation various matrices may be retrieved for further analysis. Let  $g$  denote the number of equations in the system and let  $K$  denote the total number of estimated parameters ( $K = \sum_i k_i$ ). The accessors `$uhat` and `$yhat` get  $T \times g$  matrices holding the residuals and fitted values respectively. The accessor `$coeff` gets the stacked  $K$ -vector of parameter estimates; `$vcv`



gets the  $K \times K$  variance matrix of the parameter estimates; and `$sigma` gets the  $g \times g$  cross-equation covariance matrix,  $\hat{\Sigma}$ .

A test statistic for the hypothesis that  $\Sigma$  is diagonal can be retrieved as `$diagtest` and its p-value as `$diagpval`. This is the Breusch-Pagan test except when the estimator is (unrestricted) iterated SUR, in which case it's a Likelihood Ratio test. The Breusch-Pagan test is computed as

$$\text{LM} = T \sum_{i=2}^g \sum_{j=1}^{i-1} r_{ij}^2$$

where  $r_{ij} = \hat{\sigma}_{ij} / \sqrt{\hat{\sigma}_{ii} \hat{\sigma}_{jj}}$ ; the LR test is

$$\text{LR} = T \left( \sum_{i=1}^g \log \hat{\sigma}_i^2 - \log |\hat{\Sigma}| \right)$$

where  $\hat{\sigma}_i^2$  is  $\hat{u}_i' \hat{u}_i / T$  from the individual OLS regressions. In both cases the test statistic is distributed asymptotically as  $\chi^2$  with  $g(g-1)/2$  degrees of freedom.

### Structural and reduced forms

Systems of simultaneous systems can be represented in structural form as

$$\Gamma y_t = A_1 y_{t-1} + A_2 y_{t-2} + \cdots + A_p y_{t-p} + B x_t + \epsilon_t$$

where  $y_t$  represents the vector of endogenous variables in period  $t$ ,  $x_t$  denotes the vector of exogenous variables, and  $p$  is the maximum lag of the endogenous regressors. The structural-form matrices can be retrieved as `$sysGamma`, `$sysA` and `$sysB` respectively. If  $y_t$  is  $m \times 1$  and  $x_t$  is  $n \times 1$ , then  $\Gamma$  is  $m \times m$  and  $B$  is  $m \times n$ . If the system contains no lags of the endogenous variables then the  $A$  matrix is not defined, otherwise  $A$  is the horizontal concatenation of  $A_1, \dots, A_p$ , and is therefore  $m \times mp$ .

From the structural form it is straightforward to obtain the reduced form, namely,

$$y_t = \Gamma^{-1} \left( \sum_{i=1}^p A_i y_{t-i} \right) + \Gamma^{-1} B x_t + v_t$$

where  $v_t \equiv \Gamma^{-1} \epsilon_t$ . The reduced form is used by `gretl` to generate forecasts in response to the `fcast` command. This means that — in contrast to single-equation estimation — the values produced via `fcast` for a static, within-sample forecast will in general differ from the fitted values retrieved via `$yhat`. The fitted values for equation  $i$  represent the expectation of  $y_{ti}$  conditional on the contemporaneous values of all the regressors, while the `fcast` values are conditional on the exogenous and predetermined variables only.

The above account has to be qualified for the case where a system is set up for estimation via TSLS or 3SLS using a specific list of instruments per equation, as described in section 27.1. In that case it is possible to include more endogenous regressors than explicit equations (although, of course, there must be sufficient instruments to achieve identification). In such systems endogenous regressors that have no associated explicit equation are treated “as if” exogenous when constructing the structural-form matrices. This means that forecasts are conditional on the observed values of the “extra” endogenous regressors rather than solely on the values of the exogenous and predetermined variables.

## Chapter 28

# Forecasting

### 28.1 Introduction

In some econometric contexts forecasting is the prime objective: one wants estimates of the future values of certain variables to reduce the uncertainty attaching to current decision making. In other contexts where real-time forecasting is not the focus prediction may nonetheless be an important moment in the analysis. For example, out-of-sample prediction can provide a useful check on the validity of an econometric model. In other cases we are interested in questions of “what if”: for example, how might macroeconomic outcomes have differed over a certain period if a different policy had been pursued? In the latter cases “prediction” need not be a matter of actually projecting into the future but in any case it involves generating fitted values from a given model. The term “postdiction” might be more accurate but it is not commonly used; we tend to talk of prediction even when there is no true forecast in view.

This chapter offers an overview of the methods available within `gretl` for forecasting or prediction (whether forward in time or not) and explicates some of the finer points of the relevant commands.

### 28.2 Saving and inspecting fitted values

In the simplest case, the “predictions” of interest are just the (within sample) fitted values from an econometric model. For the single-equation linear model,  $y_t = X_t\beta + u_t$ , these are  $\hat{y}_t = X_t\hat{\beta}$ .

In command-line mode, the  $\hat{y}$  series can be retrieved, after estimating a model, using the accessor `$yhat`, as in

```
series yh = $yhat
```

If the model in question takes the form of a system of equations, `$yhat` returns a matrix, each column of which contains the fitted values for a particular dependent variable. To extract the fitted series for, e.g., the dependent variable in the second equation, do

```
matrix Yh = $yhat
series yh2 = Yh[,2]
```

Having obtained a series of fitted values, you can use the `fcstats` function to produce a vector of statistics that characterize the accuracy of the predictions (see section [28.4](#) below).

The `gretl` GUI offers several ways of accessing and examining within-sample predictions. In the model display window the `Save` menu contains an item for saving fitted values, the `Graphs` menu allows plotting of fitted versus actual values, and the `Analysis` menu offers a display of actual, fitted and residual values.

### 28.3 The `fcast` command

The `fcast` command generates predictions based on the last estimated model. Several questions arise here: How to control the range over which predictions are generated? How to control the forecasting method (where a choice is available)? How to control the printing and/or saving of the results? Basic answers can be found in the *Gretl Command Reference*; we add some more details here.

### The forecast range

The range defaults to the currently defined sample range. If this remains unchanged following estimation of the model in question, the forecast will be “within sample” and (with some qualifications noted below) it will essentially duplicate the information available via the retrieval of fitted values (see section 28.2 above).

A common situation is that a model is estimated over a given sample and then forecasts are wanted for a subsequent out-of-sample range. The simplest way to accomplish this is via the `--out-of-sample` option to `fcast`. For example, assuming we have a quarterly time-series dataset containing observations from 1980:1 to 2008:4, four of which are to be reserved for forecasting:

```
# reserve the last 4 observations
smpl 1980:1 2007:4
ols y 0 xlist
fcast --out-of-sample
```

This will generate a forecast from 2008:1 to 2008:4.

There are two other ways of adjusting the forecast range, offering finer control:

- Use the `smpl` command to adjust the sample range prior to invoking `fcast`.
- Use the optional *startobs* and *endobs* arguments to `fcast` (which should come right after the command word). These values set the forecast range independently of the sample range.

What if one wants to generate a true forecast that goes beyond the available data? In that case one can use the `dataset` command with the `addobs` parameter to add extra observations before forecasting. For example:

```
# use the entire dataset, which ends in 2008:4
ols y 0 xlist
dataset addobs 4
fcast 2009:1 2009:4
```

But this will work as stated only if the set of regressors in `xlist` does not contain any stochastic regressors other than lags of `y`. The `dataset addobs` command attempts to detect and extrapolate certain common deterministic variables (e.g., time trend, periodic dummy variables). In addition, lagged values of the dependent variable can be supported via a dynamic forecast (see below for discussion of the static/dynamic distinction). But “future” values of any other included regressors must be supplied before such a forecast is possible. Note that specific values in a series can be set directly by date, for example: `x1[2009:1] = 120.5`. Or, if the assumption of no change in the regressors is warranted, one can do something like this:

```
loop t=2009:1..2009:4
  loop foreach i xlist
    $i[t] = $i[2008:4]
  endloop
endloop
```

### Static, dynamic and rolling forecasts

The distinction between static and dynamic forecasts applies only to dynamic models, i.e., those that feature one or more lags of the dependent variable. The simplest case is the AR(1) model,

$$y_t = \alpha_0 + \alpha_1 y_{t-1} + \epsilon_t \quad (28.1)$$

In some cases the presence of a lagged dependent variable is implicit in the dynamics of the error term, for example

$$\begin{aligned} y_t &= \beta + u_t \\ u_t &= \rho u_{t-1} + \epsilon_t \end{aligned}$$

which implies that

$$y_t = (1 - \rho)\beta + \rho y_{t-1} + \epsilon_t$$

Suppose we want to forecast  $y$  for period  $s$  using a dynamic model, say (28.1) for example. If we have data on  $y$  available for period  $s - 1$  we could form a fitted value in the usual way:  $\hat{y}_s = \hat{\alpha}_0 + \hat{\alpha}_1 y_{s-1}$ . But suppose that data are available only up to  $s - 2$ . In that case we can apply the chain rule of forecasting:

$$\begin{aligned} \hat{y}_{s-1} &= \hat{\alpha}_0 + \hat{\alpha}_1 y_{s-2} \\ \hat{y}_s &= \hat{\alpha}_0 + \hat{\alpha}_1 \hat{y}_{s-1} \end{aligned}$$

This is what is called a dynamic forecast. A static forecast, on the other hand, is simply a fitted value (even if it happens to be computed out-of-sample).

### Printing and saving forecasts

To be written.

## 28.4 Univariate forecast evaluation statistics

Let  $y_t$  be the value of a variable of interest at time  $t$  and let  $f_t$  be a forecast of  $y_t$ . We define the forecast error as  $e_t = y_t - f_t$ . Given a series of  $T$  observations and associated forecasts we can construct several measures of the overall accuracy of the forecasts. Some commonly used measures are the Mean Error (ME), Mean Squared Error (MSE), Root Mean Squared Error (RMSE), Mean Absolute Error (MAE), Mean Percentage Error (MPE) and Mean Absolute Percentage Error (MAPE). These are defined as follows.

$$\begin{aligned} \text{ME} &= \frac{1}{T} \sum_{t=1}^T e_t & \text{MSE} &= \frac{1}{T} \sum_{t=1}^T e_t^2 & \text{RMSE} &= \sqrt{\frac{1}{T} \sum_{t=1}^T e_t^2} & \text{MAE} &= \frac{1}{T} \sum_{t=1}^T |e_t| \\ \text{MPE} &= \frac{1}{T} \sum_{t=1}^T 100 \frac{e_t}{y_t} & \text{MAPE} &= \frac{1}{T} \sum_{t=1}^T 100 \frac{|e_t|}{y_t} \end{aligned}$$

A further relevant statistic is Theil's  $U$  (Theil, 1966), defined as the positive square root of

$$U^2 = \frac{1}{T} \sum_{t=1}^{T-1} \left( \frac{f_{t+1} - y_{t+1}}{y_t} \right)^2 \cdot \left[ \frac{1}{T} \sum_{t=1}^{T-1} \left( \frac{y_{t+1} - y_t}{y_t} \right)^2 \right]^{-1}$$

The more accurate the forecasts, the lower the value of Theil's  $U$ , which has a minimum of 0.<sup>1</sup> This measure can be interpreted as the ratio of the RMSE of the proposed forecasting model to the RMSE of a naïve model which simply predicts  $y_{t+1} = y_t$  for all  $t$ . The naïve model yields  $U = 1$ ; values less than 1 indicate an improvement relative to this benchmark and values greater than 1 a deterioration.

<sup>1</sup>This statistic is sometimes called  $U_2$ , to distinguish it from a related but different  $U$  defined in an earlier work by Theil (1961). It seems to be generally accepted that the later version of Theil's  $U$  is a superior statistic, so we ignore the earlier version here.

In addition, Theil (1966, pp. 33–36) proposed a decomposition of the MSE which can be useful in evaluating a set of forecasts. He showed that the MSE could be broken down into three non-negative components as follows

$$\text{MSE} = (\bar{f} - \bar{y})^2 + (s_f - r s_y)^2 + (1 - r^2) s_y^2$$

where  $\bar{f}$  and  $\bar{y}$  are the sample means of the forecasts and the observations,  $s_f$  and  $s_y$  are the respective standard deviations (using  $T$  in the denominator), and  $r$  is the sample correlation between  $y$  and  $f$ . Dividing through by MSE we get

$$\frac{(\bar{f} - \bar{y})^2}{\text{MSE}} + \frac{(s_f - r s_y)^2}{\text{MSE}} + \frac{(1 - r^2) s_y^2}{\text{MSE}} = 1 \quad (28.2)$$

Theil labeled the three terms on the left-hand side of (28.2) the bias proportion ( $U^M$ ), regression proportion ( $U^R$ ) and disturbance proportion ( $U^D$ ), respectively. If  $y$  and  $f$  represent the in-sample observations of the dependent variable and the fitted values from a linear regression then the first two components,  $U^M$  and  $U^R$ , will be zero (apart from rounding error), and the entire MSE will be accounted for by the unsystematic part,  $U^D$ . In the case of out-of-sample prediction, however (or “prediction” over a sub-sample of the data used in the regression),  $U^M$  and  $U^R$  are not necessarily close to zero, although this is a desirable property for a forecast to have.  $U^M$  differs from zero if and only if the mean of the forecasts differs from the mean of the realizations, and  $U^R$  is non-zero if and only if the slope of a simple regression of the realizations on the forecasts differs from 1.

The above-mentioned statistics are printed as part of the output of the `fcast` command. They can also be retrieved in the form of a column vector using the function `fcstats`, which takes two series arguments corresponding to  $y$  and  $f$ . The vector returned is

$$\left( \text{ME} \quad \text{MSE} \quad \text{MAE} \quad \text{MPE} \quad \text{MAPE} \quad U \quad U^M \quad U^R \quad U^D \right)'$$

(Note that the RMSE is not included since it can easily be obtained given the MSE.) The series given as arguments to `fcstats` must not contain any missing values in the currently defined sample range; use the `smp1` command to adjust the range if needed.

## 28.5 Forecasts based on VAR models

To be written.

## 28.6 Forecasting from simultaneous systems

To be written.

## Chapter 29

# The Kalman Filter

### 29.1 Preamble

The Kalman filter has been used “behind the scenes” in gretl for quite some time, in computing ARMA estimates. But user access to the Kalman filter is new and it has not yet been tested to any great extent. We have run some tests of relatively simple cases against the benchmark of SsfPack Basic. This is state-space software written by Koopman, Shephard and Doornik and documented in [Koopman, Shephard and Doornik \(1999\)](#). It requires Doornik’s ox program. Both ox and SsfPack are available as free downloads for academic use but neither is open-source; see <http://www.ssfpack.com>. Since Koopman is one of the leading researchers in this area, presumably the results from SsfPack are generally reliable. To date we have been able to replicate the SsfPack results in gretl with a high degree of precision.

We welcome both success reports and bug reports.

### 29.2 Notation

It seems that in econometrics everyone is happy with  $y = X\beta + u$ , but we can’t, as a community, make up our minds on a standard notation for state-space models. [Harvey \(1989\)](#), [Hamilton \(1994\)](#), [Harvey and Proietti \(2005\)](#) and [Pollock \(1999\)](#) all use different conventions. The notation used here is based on James Hamilton’s, with slight variations.

A state-space model can be written as

$$\boldsymbol{\xi}_{t+1} = \mathbf{F}_t \boldsymbol{\xi}_t + \mathbf{v}_t \quad (29.1)$$

$$\mathbf{y}_t = \mathbf{A}_t' \mathbf{x}_t + \mathbf{H}_t' \boldsymbol{\xi}_t + \mathbf{w}_t \quad (29.2)$$

where (29.1) is the state transition equation and (29.2) is the observation or measurement equation. The state vector,  $\boldsymbol{\xi}_t$ , is  $(r \times 1)$  and the vector of observables,  $\mathbf{y}_t$ , is  $(n \times 1)$ ;  $\mathbf{x}_t$  is a  $(k \times 1)$  vector of exogenous variables. The  $(r \times 1)$  vector  $\mathbf{v}_t$  and the  $(n \times 1)$  vector  $\mathbf{w}_t$  are assumed to be vector white noise:

$$\begin{aligned} E(\mathbf{v}_t \mathbf{v}_s') &= \mathbf{Q}_t \text{ for } t = s, \text{ otherwise } \mathbf{0} \\ E(\mathbf{w}_t \mathbf{w}_s') &= \mathbf{R}_t \text{ for } t = s, \text{ otherwise } \mathbf{0} \end{aligned}$$

The number of time-series observations will be denoted by  $T$ . In the special case when  $\mathbf{F}_t = \mathbf{F}$ ,  $\mathbf{H}_t = \mathbf{H}$ ,  $\mathbf{A}_t = \mathbf{A}$ ,  $\mathbf{Q}_t = \mathbf{Q}$  and  $\mathbf{R}_t = \mathbf{R}$ , the model is said to be *time-invariant*.

#### The Kalman recursions

Using this notation, and assuming for the moment that  $\mathbf{v}_t$  and  $\mathbf{w}_t$  are mutually independent, the Kalman recursions can be written as follows.

Initialization is via the unconditional mean and variance of  $\boldsymbol{\xi}_1$ :

$$\begin{aligned} \hat{\boldsymbol{\xi}}_{1|0} &= E(\boldsymbol{\xi}_1) \\ \mathbf{P}_{1|0} &= E \left\{ [\boldsymbol{\xi}_1 - E(\boldsymbol{\xi}_1)] [\boldsymbol{\xi}_1 - E(\boldsymbol{\xi}_1)]' \right\} \end{aligned}$$

Usually these are given by  $\hat{\boldsymbol{\xi}}_{1|0} = \mathbf{0}$  and

$$\text{vec}(\mathbf{P}_{1|0}) = [\mathbf{I}_{r^2} - \mathbf{F} \otimes \mathbf{F}]^{-1} \cdot \text{vec}(\mathbf{Q}) \quad (29.3)$$

but see below for further discussion of the initial variance.

Iteration then proceeds in two steps.<sup>1</sup> First we update the estimate of the state

$$\hat{\boldsymbol{\xi}}_{t+1|t} = \mathbf{F}_t \hat{\boldsymbol{\xi}}_{t|t-1} + \mathbf{K}_t \mathbf{e}_t \quad (29.4)$$

where  $\mathbf{e}_t$  is the prediction error for the observable:

$$\mathbf{e}_t = \mathbf{y}_t - \mathbf{A}_t' \mathbf{x}_t - \mathbf{H}_t' \hat{\boldsymbol{\xi}}_{t|t-1}$$

and  $\mathbf{K}_t$  is the gain matrix, given by

$$\mathbf{K}_t = \mathbf{F}_t \mathbf{P}_{t|t-1} \mathbf{H}_t \boldsymbol{\Sigma}_t^{-1} \quad (29.5)$$

with

$$\boldsymbol{\Sigma}_t = \mathbf{H}_t' \mathbf{P}_{t|t-1} \mathbf{H}_t + \mathbf{R}_t$$

The second step then updates the estimate of the variance of the state using

$$\mathbf{P}_{t+1|t} = \mathbf{F}_t \mathbf{P}_{t|t-1} \mathbf{F}_t' - \mathbf{K}_t \boldsymbol{\Sigma}_t \mathbf{K}_t' + \mathbf{Q}_t \quad (29.6)$$

### Cross-correlated disturbances

The formulation given above assumes mutual independence of the disturbances in the state and observation equations,  $\mathbf{v}_t$  and  $\mathbf{w}_t$ . This assumption holds good in many practical applications, but a more general formulation allows for cross-correlation. In place of (29.1)–(29.2) we may write

$$\begin{aligned} \boldsymbol{\xi}_{t+1} &= \mathbf{F}_t \boldsymbol{\xi}_t + \mathbf{B}_t \boldsymbol{\varepsilon}_t \\ \mathbf{y}_t &= \mathbf{A}_t' \mathbf{x}_t + \mathbf{H}_t' \boldsymbol{\xi}_t + \mathbf{C}_t \boldsymbol{\varepsilon}_t \end{aligned}$$

where  $\boldsymbol{\varepsilon}_t$  is a  $(p \times 1)$  disturbance vector, all the elements of which have unit variance,  $\mathbf{B}_t$  is  $(r \times p)$  and  $\mathbf{C}_t$  is  $(n \times p)$ .

The no-correlation case is nested thus: define  $\mathbf{v}_t^*$  and  $\mathbf{w}_t^*$  as modified versions of  $\mathbf{v}_t$  and  $\mathbf{w}_t$ , scaled such that each element has unit variance, and let

$$\boldsymbol{\varepsilon}_t = \begin{bmatrix} \mathbf{v}_t^* \\ \mathbf{w}_t^* \end{bmatrix}$$

so that  $p = r + n$ . Then (suppressing time subscripts for simplicity) let

$$\begin{aligned} \mathbf{B} &= \begin{bmatrix} \boldsymbol{\Gamma}_{r \times r} & \vdots & \mathbf{0}_{r \times n} \end{bmatrix} \\ \mathbf{C} &= \begin{bmatrix} \mathbf{0}_{n \times r} & \vdots & \boldsymbol{\Lambda}_{n \times n} \end{bmatrix} \end{aligned}$$

where  $\boldsymbol{\Gamma}$  and  $\boldsymbol{\Lambda}$  are lower triangular matrices satisfying  $\mathbf{Q} = \boldsymbol{\Gamma} \boldsymbol{\Gamma}'$  and  $\mathbf{R} = \boldsymbol{\Lambda} \boldsymbol{\Lambda}'$  respectively. The zero sub-matrices in the above expressions for  $\mathbf{B}$  and  $\mathbf{C}$  produce the case of mutual independence; this corresponds to the condition  $\mathbf{B} \mathbf{C}' = \mathbf{0}$ .

In the general case  $p$  is not necessarily equal to  $r + n$ , and  $\mathbf{B} \mathbf{C}'$  may be non-zero. This means that the Kalman gain equation (29.5) must be modified as

$$\mathbf{K}_t = (\mathbf{F}_t \mathbf{P}_{t|t-1} \mathbf{H}_t + \mathbf{B}_t \mathbf{C}_t') \boldsymbol{\Sigma}_t^{-1} \quad (29.7)$$

Otherwise, the equations given earlier hold good, if we write  $\mathbf{B} \mathbf{B}'$  in place of  $\mathbf{Q}$  and  $\mathbf{C} \mathbf{C}'$  in place of  $\mathbf{R}$ .

In the account of gretl's Kalman facility below we take the uncorrelated case as the baseline, but add remarks on how to handle the correlated case where applicable.

<sup>1</sup>For a justification of the following formulae see the classic book by Anderson and Moore (1979) or, for a more modern treatment, Pollock (1999) or Hamilton (1994). A transcription of R. E. Kalman's original paper (Kalman, 1960) is available at <http://www.cs.unc.edu/~welch/kalman/kalmanPaper.html>.

### 29.3 Intended usage

The Kalman filter can be used in three ways: two of these are the classic forward and backward pass, or filtering and smoothing respectively; the third use is simulation. In the filtering/smoothing case you have the data  $\mathbf{y}_t$  and you want to reconstruct the states  $\boldsymbol{\xi}_t$  (and the forecast errors as a by-product), but we may also have a computational apparatus that does the reverse: given artificially-generated series  $\mathbf{w}_t$  and  $\mathbf{v}_t$ , generate the states  $\boldsymbol{\xi}_t$  (and the observables  $\mathbf{y}_t$  as a by-product).

The usefulness of the classical filter is well known; the usefulness of the Kalman filter as a simulation tool may be huge too. Think for instance of Monte Carlo experiments, simulation-based inference—see [Gourieroux and Monfort \(1996\)](#)—or Bayesian methods, especially in the context of the estimation of DSGE models.

### 29.4 Overview of syntax

Using the Kalman filter in `gretl` is a two-step process. First you set up your filter, using a block of commands starting with `kalman` and ending with `end kalman`—much like the `gmm` command. Then you invoke the functions `kfilter`, `ksmooth` or `ksimul` to do the actual work. The next two sections expand on these points.

### 29.5 Defining the filter

Each line within the `kalman ... end kalman` block takes the form

*keyword value*

where *keyword* represents a matrix, as shown below. (An additional matrix which may be useful in some cases is introduced later under the heading “Constant term in the state transition”).

Keyword	Symbol	Dimensions
<code>obsy</code>	$\mathbf{y}$	$T \times n$
<code>obsymat</code>	$\mathbf{H}$	$r \times n$
<code>obsx</code>	$\mathbf{x}$	$T \times k$
<code>obsxmat</code>	$\mathbf{A}$	$k \times n$
<code>obsvar</code>	$\mathbf{R}$	$n \times n$
<code>statemat</code>	$\mathbf{F}$	$r \times r$
<code>statevar</code>	$\mathbf{Q}$	$r \times r$
<code>inistate</code>	$\hat{\boldsymbol{\xi}}_{1 0}$	$r \times 1$
<code>inivar</code>	$\mathbf{P}_{1 0}$	$r \times r$

For the data matrices  $\mathbf{y}$  and  $\mathbf{x}$  the corresponding *value* may be the name of a predefined matrix, the name of a data series, or the name of a list of series.<sup>2</sup>

For the other inputs, *value* may be the name of a predefined matrix or, if the input in question happens to be  $(1 \times 1)$ , the name of a scalar variable or a numerical constant. If the *value* of a coefficient matrix is given as the name of a matrix or scalar variable, the input is not “hard-wired” into the Kalman structure, rather a record is made of the *name* of the variable and on each run of a Kalman function (as described below) its value is re-read. It is therefore possible to write one `kalman` block and then do several filtering or smoothing passes using different sets of coefficients.<sup>3</sup>

<sup>2</sup>Note that the data matrices `obsy` and `obsx` have  $T$  rows. That is, the column vectors  $\mathbf{y}_t$  and  $\mathbf{x}_t$  in (29.1) and (29.2) are in fact the transposes of the  $t$ -dated rows of the full matrices.

<sup>3</sup>Note, however, that the dimensions of the various input matrices are defined via the initial `kalman` set-up and it is an error if any of the matrices are changed in size.



An example of this technique is provided later, in the example scripts [29.1](#) and [29.2](#). This facility to alter the values of the coefficients between runs of the filter is to be distinguished from the case of *time-varying* matrices, which is discussed below.

Not all of the above-mentioned inputs need be specified in every case; some are optional. (In addition, you can specify the matrices in any order.) The mandatory elements are **y**, **H**, **F** and **Q**, so the minimal `kalman` block looks like this:

```
kalman
  obsy y
  obsymat H
  statemat F
  statevar Q
end kalman
```

The optional matrices are listed below, along with the implication of omitting the given matrix.

Keyword	If omitted...
<code>obsx</code>	no exogenous variables in observation equation
<code>obsxmat</code>	no exogenous variables in observation equation
<code>obsvar</code>	no disturbance term in observation equation
<code>inistate</code>	$\hat{\mathbf{x}}_{1 0}$ is set to a zero vector
<code>inivar</code>	$\mathbf{P}_{1 0}$ is set automatically

It might appear that the `obsx` (**x**) and `obsxmat` (**A**) matrices must go together—either both are given or neither is given. But an exception is granted for convenience. If the observation equation includes a constant but no additional exogenous variables, you can give a  $(1 \times n)$  value for **A** without having to specify `obsx`. More generally, if the row dimension of **A** is 1 greater than the column dimension of **x**, it is assumed that the first element of **A** is associated with an implicit column of 1s.

Regarding the automatic initialization of  $\mathbf{P}_{1|0}$  (in case no `inivar` input is given): by default this is done as in equation (29.3). However, this method is applicable only if all the eigenvalues of **F** lie inside the unit circle. If this condition is not satisfied we instead apply a diffuse prior, setting  $\mathbf{P}_{1|0} = \kappa \mathbf{I}_r$  with  $\kappa = 10^7$ . If you wish to impose this diffuse prior from the outset, append the option flag `--diffuse` to the end `kalman` statement.<sup>4</sup>

### Time-varying matrices

Any or all of the matrices `obsymat`, `obsxmat`, `obsvar`, `statemat` and `statevar` may be time-varying. In that case the *value* corresponding to the matrix keyword should be given in a special form: the name of an existing matrix plus a function call which modifies that matrix, separated by a semicolon. Note that in this case you must use a matrix variable, even if the matrix in question happens to be  $1 \times 1$ .

For example, suppose the matrix **H** is time-varying. Then we might write

```
obsymat H ; modify_H(&H, theta)
```

where `modify_H` is a user-defined function which modifies matrix **H** (and `theta` is a suitable additional argument to that function, if required).

<sup>4</sup>Initialization of the Kalman filter outside of the case where equation (29.3) applies has been the subject of much discussion in the literature—see for example [de Jong \(1991\)](#), [Koopman \(1997\)](#). At present `gretl` does not implement any of the more elaborate proposals that have been made.

The above is just an illustration: the matrix argument does not have to come first, and the function can have as many arguments as you like. The essential point is that the function must modify the specified matrix, which requires that it be given as an argument in “pointer” form (preceded by &). The function need not return any value directly; if it does, that value is ignored.

Such matrix-modifying functions will be called at each time-step of the filter operation, prior to performing any calculations. They have access to the current time-step of the Kalman filter via the internal variable `$kalman_t`, which has value 1 on the first step, 2 on the second, and so on, up to step  $T$ . They also have access to the previous  $n$ -vector of forecast errors,  $\mathbf{e}_{t-1}$ , under the name `$kalman_uhat`. When  $t = 1$  this will be a zero vector.

### Correlated disturbances

Defining a filter in which the disturbances  $\mathbf{v}_t$  and  $\mathbf{w}_t$  are correlated involves one modification to the account given above. If you append the `--cross` option flag to the end `kalman` statement, then the matrices corresponding to the keywords `statevar` and `obsvar` are interpreted not as  $\mathbf{Q}$  and  $\mathbf{R}$  but rather as  $\mathbf{B}$  and  $\mathbf{C}$  as discussed in section 29.2. Gretl then computes  $\mathbf{Q} = \mathbf{B}\mathbf{B}'$  and  $\mathbf{R} = \mathbf{C}\mathbf{C}'$  as well as the cross-product  $\mathbf{B}\mathbf{C}'$  and utilizes the modified expression for the gain as given in equation (29.7). As mentioned above,  $\mathbf{B}$  should be  $(r \times p)$  and  $\mathbf{C}$  should be  $(n \times p)$ , where  $p$  is the number of elements in the combined disturbance vector  $\boldsymbol{\varepsilon}_t$ .

### Constant term in the state transition

In some applications it is useful to be able to represent a constant term in the state transition equation explicitly; that is, equation (29.1) becomes

$$\boldsymbol{\xi}_{t+1} = \boldsymbol{\mu} + \mathbf{F}_t \boldsymbol{\xi}_t + \mathbf{v}_t \quad (29.8)$$

This is never strictly necessary; the system (29.1) and (29.2) is general enough to accommodate such a term, by absorbing it as an extra (unvarying) element in the state vector. But this comes at the cost of expanding all the matrices that touch the state ( $\boldsymbol{\xi}$ ,  $\mathbf{F}$ ,  $\mathbf{v}$ ,  $\mathbf{Q}$ ,  $\mathbf{H}$ ), making the model relatively awkward to formulate and forecasts relatively expensive to compute.

As a simple illustration, consider a univariate model in which the state,  $s_t$ , is just a random walk with drift  $\mu$  and the observed variable,  $y_t$ , is the state plus white noise:

$$s_{t+1} = \mu + s_t + v_t \quad (29.9)$$

$$y_t = s_t + w_t \quad (29.10)$$

Putting this into the standard form of (29.1) and (29.2) we get:

$$\begin{bmatrix} s_{t+1} \\ \mu \end{bmatrix} = \begin{bmatrix} 1 & 1 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} s_t \\ \mu \end{bmatrix} + \begin{bmatrix} v_t \\ 0 \end{bmatrix}, \quad \mathbf{Q} = \begin{bmatrix} \sigma_v^2 & 0 \\ 0 & 0 \end{bmatrix}$$

$$y_t = \begin{bmatrix} 1 & 0 \end{bmatrix} \begin{bmatrix} s_t \\ \mu \end{bmatrix} + w_t$$

In such a simple case the notational and computational burden is not very great; nonetheless it is clearly more “natural” to express this system in the form of (29.9) and (29.10) and in a multivariate model the gain in parsimony could be substantial.

For this reason we support the use of an additional named matrix in the `kalman` setup, namely `stconst`. This corresponds to  $\boldsymbol{\mu}$  in equation (29.8); it should be an  $r \times 1$  vector (or if  $r = 1$  may be given as the name of a scalar variable). The use of `stconst` in setting up a filter corresponding to (29.9) and (29.10) is shown below.

```
matrix H = {1}
matrix R = {1}
```

```

matrix F = {1}
matrix Q = {1}
matrix mu = {0.05}

kalman
  obsy y
  obsmat H
  obsvar R
  statemat F
  statevar Q
  stconst mu
end kalman

```

### Handling of missing values

It is acceptable for the data matrices, `obsy` and `obsx`, to contain missing values. In this case the filtering operation will work around the missing values, and the `ksmooth` function can be used to obtain estimates of these values. However, there are two points to note.

First, gretl's default behavior is to skip missing observations when constructing matrices from data series. To change this, use the `set` command thus:

```
set skip_missing off
```

Second, the handling of missing values is not yet quite right for the case where the observable vector  $\mathbf{y}_t$  contains more than one element. At present, if any of the elements of  $\mathbf{y}_t$  are missing the entire observation is ignored. Clearly it should be possible to make use of any non-missing elements, and this is not very difficult in principle, it's just awkward and is not implemented yet.

### Persistence and identity of the filter

At present there is no facility to create a "named filter". Only one filter can exist at any point in time, namely the one created by the last `kalman` block.<sup>5</sup> If a filter is already defined, and you give a new `kalman` block, the old filter is over-written. Otherwise the existing filter persists (and remains available for the `kfilter`, `ksmooth` and `ksimul` functions) until either (a) the gretl session is terminated or (b) the command `delete kalman` is given.

## 29.6 The `kfilter` function

Once a filter is established, as discussed in the previous section, `kfilter` can be used to run a forward, forecasting pass. This function returns a scalar code: 0 for successful completion, or 1 if numerical problems were encountered. On successful completion, two scalar accessor variables become available: `$kalman_ln1`, which gives the overall log-likelihood under the joint normality assumption,

$$\ell = -\frac{1}{2} \left[ nT \log(2\pi) + \sum_{t=1}^T \log |\Sigma_t| + \sum_{t=1}^T \mathbf{e}_t' \Sigma_t^{-1} \mathbf{e}_t \right]$$

and `$kalman_s2`, which gives the estimated variance,

$$\hat{\sigma}^2 = \frac{1}{nT} \sum_{t=1}^T \mathbf{e}_t' \Sigma_t^{-1} \mathbf{e}_t$$

<sup>5</sup>This is not quite true: more precisely, there can be no more than one Kalman filter *at each level of function execution*. That is, if a gretl script creates a Kalman filter, a user-defined function called from that script may also create a filter, without interfering with the original one.

(but see below for modifications to these formulae for the case of a diffuse prior). In addition the accessor `$kalman_llt` gives a  $(T \times 1)$  vector, element  $t$  of which is

$$\ell_t = -\frac{1}{2} \left[ n \log(2\pi) + \log |\Sigma_t| + \mathbf{e}_t' \Sigma_t^{-1} \mathbf{e}_t \right]$$

The `kfilter` function does not require any arguments, but up to five matrix quantities may be retrieved via optional pointer arguments. Each of these matrices has  $T$  rows, one for each time-step; the contents of the rows are shown in the following listing.

1. Forecast errors for the observable variables:  $\mathbf{e}_t'$ ,  $n$  columns.
2. Variance matrix for the forecast errors:  $\text{vech}(\Sigma_t)'$ ,  $n(n+1)/2$  columns.
3. Estimate of the state vector:  $\hat{\boldsymbol{\xi}}_{t|t-1}'$ ,  $r$  columns.
4. MSE of estimate of the state vector:  $\text{vech}(\mathbf{P}_{t|t-1})'$ ,  $r(r+1)/2$  columns.
5. Kalman gain:  $\text{vec}(\mathbf{K}_t)'$ ,  $rn$  columns.

Unwanted trailing arguments can be omitted, otherwise unwanted arguments can be skipped by using the keyword `null`. For example, the following call retrieves the forecast errors in the matrix `E` and the estimate of the state vector in `S`:

```
matrix E S
kfilter(&E, null, &S)
```

Matrices given as pointer arguments do not have to be correctly dimensioned in advance; they will be resized to receive the specified content.

Further note: in general, the arguments to `kfilter` should all be matrix-pointers, but under two conditions you can give a pointer to a series variable instead. The conditions are: (i) the matrix in question has just one column in context (for example, the first two matrices will have a single column if the length of the observables vector,  $n$ , equals 1) and (ii) the time-series length of the filter is equal to the current `gretl` sample size.

### Likelihood under the diffuse prior

There seems to be general agreement in the literature that the log-likelihood calculation should be modified in the case of a diffuse prior for  $\mathbf{P}_{1|0}$ . However, it is not clear to us that there is a well-defined “correct” method for this. At present we emulate `SsfPack` (see [Koopman \*et al.\* \(1999\)](#) and section 29.1). In case  $\mathbf{P}_{1|0} = \kappa \mathbf{I}_r$ , we set  $d = r$  and calculate

$$\ell = -\frac{1}{2} \left[ (nT - d) \log(2\pi) + \sum_{t=1}^T \log |\Sigma_t| + \sum_{t=1}^T \mathbf{e}_t' \Sigma_t^{-1} \mathbf{e}_t - d \log(\kappa) \right]$$

and

$$\hat{\sigma}^2 = \frac{1}{nT - d} \sum_{t=1}^T \mathbf{e}_t' \Sigma_t^{-1} \mathbf{e}_t$$

### 29.7 The `ksmooth` function

This function returns the  $(T \times r)$  matrix of smoothed estimates of the state vector—that is, estimates based on all  $T$  observations: row  $t$  of this matrix holds  $\hat{\boldsymbol{\xi}}_{t|T}'$ . This function has no required arguments but it offers one optional matrix-pointer argument, which retrieves the variance of the smoothed state estimate,  $\mathbf{P}_{t|T}$ . The latter matrix is  $(T \times r(r+1)/2)$ ; each row is in transposed `vech` form. Examples:

```

matrix S = ksmooth() # smoothed state only
matrix P
S = ksmooth(&P)      # the variance is wanted

```

These values are computed via a backward pass of the filter, from  $t = T$  to  $t = 1$ , as follows:

$$\begin{aligned}
 \mathbf{L}_t &= \mathbf{F}_t - \mathbf{K}_t \mathbf{H}_t' \\
 \mathbf{u}_{t-1} &= \mathbf{H}_t \boldsymbol{\Sigma}_t^{-1} \mathbf{e}_t + \mathbf{L}_t' \mathbf{u}_t \\
 \mathbf{U}_{t-1} &= \mathbf{H}_t \boldsymbol{\Sigma}_t^{-1} \mathbf{H}_t' + \mathbf{L}_t' \mathbf{U}_t \mathbf{L}_t \\
 \hat{\boldsymbol{\xi}}_{t|T} &= \hat{\boldsymbol{\xi}}_{t|t-1} + \mathbf{P}_{t|t-1} \mathbf{u}_{t-1} \\
 \mathbf{P}_{t|T} &= \mathbf{P}_{t|t-1} - \mathbf{P}_{t|t-1} \mathbf{U}_{t-1} \mathbf{P}_{t|t-1}
 \end{aligned}$$

with initial values  $\mathbf{u}_T = 0$  and  $\mathbf{U}_T = 0$ .<sup>6</sup>

This iteration is preceded by a special forward pass in which the matrices  $\mathbf{K}_t$ ,  $\boldsymbol{\Sigma}_t^{-1}$ ,  $\hat{\boldsymbol{\xi}}_{t|t-1}$  and  $\mathbf{P}_{t|t-1}$  are stored for all  $t$ . If  $\mathbf{F}$  is time-varying, its values for all  $t$  are stored on the forward pass, and similarly for  $\mathbf{H}$ .

## 29.8 The ksimul function

This simulation function takes up to three arguments. The first, mandatory, argument is a  $(T \times r)$  matrix containing artificial disturbances for the state transition equation: row  $t$  of this matrix represents  $\mathbf{v}_t'$ . If the current filter has a non-null  $\mathbf{R}$  (obsvar) matrix, then the second argument should be a  $(T \times n)$  matrix containing artificial disturbances for the observation equation, on the same pattern. Otherwise the second argument should be given as `null`. If  $r = 1$  you may give a series for the first argument, and if  $n = 1$  a series is acceptable for the second argument.

Provided that the current filter does not include exogenous variables in the observation equation (obsx), the  $T$  for simulation need not equal that defined by the original obsy data matrix: in effect  $T$  is temporarily redefined by the row dimension of the first argument to `ksimul`. Once the simulation is completed, the  $T$  value associated with the original data is restored.

The value returned by `ksimul` is a  $(T \times n)$  matrix holding simulated values for the observables at each time step. A third optional matrix-pointer argument allows you to retrieve a  $(T \times r)$  matrix holding the simulated state vector. Examples:

```

matrix Y = ksimul(V)      # obsvar is null
Y = ksimul(V, W)          # obsvar is non-null
matrix S
Y = ksimul(V, null, &S) # the simulated state is wanted

```

The initial value  $\boldsymbol{\xi}_1$  is calculated thus: we find the matrix  $\mathbf{T}$  such that  $\mathbf{T}\mathbf{T}' = \mathbf{P}_{1|0}$  (as given by the `inivar` element in the `kalman` block), multiply it into  $\mathbf{v}_1$ , and add the result to  $\boldsymbol{\xi}_{1|0}$  (as given by `inistate`).

If the disturbances are correlated across the two equations the arguments to `ksimul` must be revised: the first argument should be a  $(T \times p)$  matrix, each row of which represents  $\boldsymbol{\varepsilon}_t'$  (see section 29.2), and the second argument should be given as `null`.

## 29.9 Example 1: ARMA estimation

As is well known, the Kalman filter provides a very efficient way to compute the likelihood of ARMA models; as an example, take an ARMA(1,1) model

$$y_t = \phi y_{t-1} + \varepsilon_t + \theta \varepsilon_{t-1}$$

<sup>6</sup>See I. Karibzhanov's exposition at <http://www.econ.umn.edu/~karib003/help/kalcv5.htm>.

One of the ways the above equation can be cast in state-space form is by defining a latent process  $\xi_t = (1 - \phi L)^{-1} \varepsilon_t$ . The observation equation corresponding to (29.2) is then

$$y_t = \xi_t + \theta \xi_{t-1} \quad (29.11)$$

and the state transition equation corresponding to (29.1) is

$$\begin{bmatrix} \xi_t \\ \xi_{t-1} \end{bmatrix} = \begin{bmatrix} \phi & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} \xi_{t-1} \\ \xi_{t-2} \end{bmatrix} + \begin{bmatrix} \varepsilon_t \\ 0 \end{bmatrix}$$

The gretl syntax for a corresponding `kalman` block would be

```
matrix H = {1; theta}
matrix F = {phi, 0; 1, 0}
matrix Q = {s^2, 0; 0, 0}

kalman
  obsy y
  obsymat H
  statemat F
  statevar Q
end kalman
```

Note that the observation equation (29.11) does not include an “error term”; this is equivalent to saying that  $V(\mathbf{w}_t) = 0$  and, as a consequence, the `kalman` block does not include an `obsvar` keyword.

Once the filter is set up, all it takes to compute the log-likelihood for given values of  $\phi$ ,  $\theta$  and  $\sigma^2$  is to execute the `kfilter()` function and use the `$kalman_ln1` accessor (which returns the total log-likelihood) or, more appropriately if the likelihood has to be maximized through `mle`, the `$kalman_llt` accessor, which returns the series of individual contribution to the log-likelihood for each observation. An example is shown in script 29.1.

### 29.10 Example 2: local level model

Suppose we have a series  $y_t = \mu_t + \varepsilon_t$ , where  $\mu_t$  is a random walk with normal increments of variance  $\sigma_1^2$  and  $\varepsilon_t$  is a normal white noise with variance  $\sigma_2^2$ , independent of  $\mu_t$ . This is known as the “local level” model in Harvey’s (1989) terminology, and it can be cast in state-space form as equations (29.1)-(29.2) with  $\mathbf{F} = 1$ ,  $\mathbf{v}_t \sim N(0, \sigma_1^2)$ ,  $\mathbf{H} = 1$  and  $\mathbf{w}_t \sim N(0, \sigma_2^2)$ . The translation to a `kalman` block is

```
kalman
  obsy y
  obsymat 1
  statemat 1
  statevar s2
  obsvar s1
end kalman --diffuse
```

The two unknown parameters  $\sigma_1^2$  and  $\sigma_2^2$  can be estimated via maximum likelihood. Script 29.2 provides an example of simulation and estimation of such a model. For the sake of brevity, simulation is carried out via ordinary gretl commands, rather than the state-space apparatus described above.

The example contains two functions: the first one carries out the estimation of the unknown parameters  $\sigma_1^2$  and  $\sigma_2^2$  via maximum likelihood; the second one uses these estimates to compute a smoothed estimate of the unobservable series  $\mu_t$  called `muhat`. A plot of  $\mu_t$  and its estimate is presented in Figure 29.1.

**Example 29.1:** ARMA estimation

---

```

function void arma11_via_kalman(series y)
  /* parameter initialization */
  phi = 0
  theta = 0
  sigma = 1

  /* Kalman filter setup */
  matrix H = {1; theta}
  matrix F = {phi, 0; 1, 0}
  matrix Q = {sigma^2, 0; 0, 0}

  kalman
    obsy y
    obsymat H
    statemat F
    statevar Q
  end kalman

  /* maximum likelihood estimation */
  mle logl = ERR ? NA : $kalman_llt
    H[2] = theta
    F[1,1] = phi
    Q[1,1] = sigma^2
    ERR = kfilter()
    params phi theta sigma
  end mle -h
end function

# ----- main -----

open arma.gdt      # open the "arma" example dataset
arma11_via_kalman(y) # estimate an arma(1,1) model
arma 1 1 ; y --nc   # check via native command

```

---

**Example 29.2:** Local level model

---

```

function matrix local_level (series y)
  /* starting values */
  scalar s1 = 1
  scalar s2 = 1

  /* Kalman filter set-up */
  kalman
    obsy y
    obsymat 1
    statemat 1
    statevar s2
    obsvar s1
  end kalman --diffuse

  /* ML estimation */
  mle ll = ERR ? NA : $kalman_llt
    ERR = kfilter()
    params s1 s2
  end mle

  return s1 ~ s2
end function

function series loclev_sm (series y, scalar s1, scalar s2)
  /* return the smoothed estimate of \mu_t */
  kalman
    obsy y
    obsymat 1
    statemat 1
    statevar s2
    obsvar s1
  end kalman --diffuse
  series ret = ksmooth()
  return ret
end function

/* ----- main script ----- */

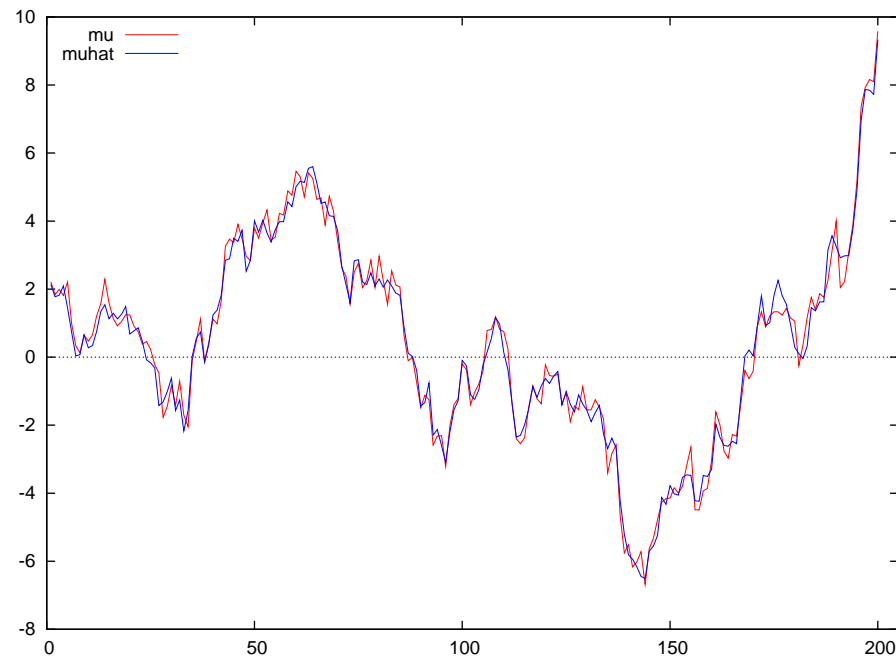
nulldata 200
set seed 202020
setobs 1 1 --special
true_s1 = 0.25
true_s2 = 0.5
v = normal() * sqrt(true_s1)
w = normal() * sqrt(true_s2)
mu = 2 + cum(w)
y = mu + v

matrix Vars = local_level(y)          # estimate the variances
muhat = loclev_sm(y, Vars[1], Vars[2]) # compute the smoothed state

```

---





**Figure 29.1:** Local level model:  $\mu_t$  and its smoothed estimate

By appending the following code snippet to the example in Table 29.2, one may check the results against the R command `StructTS`.

```
foreign language=R --send-data
y <- gretldata[, "y"]
a <- StructTS(y, type="level")
a
StateFromR <- as.ts(tsSmooth(a))
gretl.export(StateFromR)
end foreign

append @dotdir/StateFromR.csv

ols muhat 0 StateFromR --simple
```

## Chapter 30

# Numerical methods

Several functions are available to aid in the construction of special-purpose estimators: one group of functions are used to maximize user-supplied functions via numerical methods: BFGS, Newton-Raphson and Simulated Annealing. Another relevant function is `fdjac`, which produces a forward-difference approximation to the Jacobian.

### 30.1 BFGS

The `BFGSmax` function has two required arguments: a vector holding the initial values of a set of parameters, and a call to a function that calculates the (scalar) criterion to be maximized, given the current parameter values and any other relevant data. If the object is in fact minimization, this function should return the negative of the criterion. On successful completion, `BFGSmax` returns the maximized value of the criterion and the matrix given via the first argument holds the parameter values which produce the maximum. It is assumed here that the objective function is a user-defined function (see Chapter 11) with the following general set-up:

```
function scalar ObjFunc (matrix *theta, matrix *X)
  scalar val = ... # do some computation
  return val
end function
```

The first argument contains the arguments upon which the maximization has to take place, while the second argument may be used to hold “extra” values that are necessary to compute the objective function, but are not the variables of the optimization problem. For example, if the objective function were a loglikelihood, the first argument would contain the parameters and the second one the data. Or, for more economic-theory inclined readers, if the objective function were the utility of a consumer, the first argument would contain the quantities of goods and the second one their prices and disposable income.

#### Example 30.1: Finding the minimum of the Rosenbrock function

---

```
function scalar Rosenbrock(matrix *param)
  scalar x = param[1]
  scalar y = param[2]
  return -(1-x)^2 - 100 * (y - x^2)^2
end function

matrix theta = { 0, 0 }

set max_verbose 1
M = BFGSmax(theta, Rosenbrock(&theta))

print theta
```

---

The operation of BFGS can be adjusted using the set variables `bfgs_maxiter` and `bfgs_tol` (see Chapter 20). In addition you can provoke verbose output from the maximizer by assigning a positive value to `max_verbose`, again via the set command.

The Rosenbrock function is often used as a test problem for optimization algorithms. It is also known as “Rosenbrock’s Valley” or “Rosenbrock’s Banana Function”, on account of the fact that its contour lines are banana-shaped. It is defined by:

$$f(x, y) = (1 - x)^2 + 100(y - x^2)^2$$

The function has a global minimum at  $(x, y) = (1, 1)$  where  $f(x, y) = 0$ . Example 30.1 shows a gretl script that discovers the minimum using `BFGSmax` (giving a verbose account of progress). Note that, in this particular case, the function to be maximized only depends on the parameters, so the second parameter is omitted from the definition of the function `Rosenbrock`.

### Limited-memory variant

See [Byrd \*et al.\* \(1995\)](#) (...FIXME: expand a little here ...)

### Supplying analytical derivatives for BFGS

An optional third argument to the `BFGSmax` function enables the user to supply analytical derivatives of the criterion function with respect to the parameters (without which a numerical approximation to the gradient is computed). This argument is similar to the second one in that it specifies a function call. In this case the function that is called must have the following signature.

Its first argument should be a pre-defined matrix correctly dimensioned to hold the gradient; that is, if the parameter vector contains  $k$  elements, the gradient matrix must also be a  $k$ -vector. This matrix argument must be given in “pointer” form so that its content can be modified by the function. (Note that unlike the parameter vector, where the choice of initial values can be important, the initial values given to the gradient are immaterial and do not affect the results.)

In addition the gradient function must have as one of its argument the parameter vector. This may be given in pointer form (which enhances efficiency) but that is not required. Additional arguments may be specified if necessary.

Given the current parameter values, the function call must fill out the gradient vector appropriately. It is not required that the gradient function returns any value directly; if it does, that value is ignored.

Example 30.2 illustrates, showing how the Rosenbrock script can be modified to use analytical derivatives. (Note that since this is a minimization problem the values written into `g[1]` and `g[2]` in the function `Rosen_grad` are in fact the derivatives of the negative of the Rosenbrock function.)

## 30.2 Newton-Raphson

BFGS, discussed above, is an excellent all-purpose maximizer, and about as robust as possible given the limitations of digital computer arithmetic. The Newton-Raphson maximizer is not as robust, but may converge much faster than BFGS for problems where the maximand is reasonably well behaved — in particular, where it is anything like quadratic (see below). The case for using Newton-Raphson is enhanced if it is possible to supply a function to calculate the Hessian analytically.

The gretl function `NRmax`, which implements the Newton-Raphson method, has a maximum of four arguments. The first two (required) arguments are exactly as for BFGS: an initial parameter vector, and a function call which returns the maximand given the parameters. The (optional) third argument is again as in BFGS: a function call that calculates the gradient. Specific to `NRmax` is an optional fourth argument, namely a function call to calculate the (negative) Hessian. The first argument of this function must be a pre-defined matrix of the right dimension to hold the Hessian — that is, a  $k \times k$  matrix, where  $k$  is the length of the parameter vector — given in “pointer” form.

**Example 30.2:** Rosenbrock function with analytical gradient

---

```

function scalar Rosenbrock (matrix *param)
    scalar x = param[1]
    scalar y = param[2]
    return -(1-x)^2 - 100 * (y - x^2)^2
end function

function void Rosen_grad (matrix *g, matrix *param)
    scalar x = param[1]
    scalar y = param[2]
    g[1] = 2*(1-x) + 2*x*(200*(y-x^2))
    g[2] = -200*(y - x^2)
end function

matrix theta = { 0, 0 }
matrix grad = { 0, 0 }

set max_verbose 1
M = BFGSmax(theta, Rosenbrock(&theta), Rosen_grad(&grad, &theta))

print theta
print grad

```

---

The second argument should be the parameter vector (optionally in pointer form). Other data may be passed as additional arguments as needed. Similarly to the case with the gradient, if the fourth argument to NRmax is omitted then a numerical approximation to the Hessian is constructed.

What is ultimately required in Newton-Raphson is the negative inverse of the Hessian. Note that if you give the optional fourth argument, your function should compute the negative Hessian, but should not invert it; NRmax takes care of inversion, with special handling for the case where the matrix is not negative definite, which can happen far from the maximum.

Script 30.3 extends the Rosenbrock example, using NRmax with a function Rosen\_hess to compute the Hessian. The functions Rosenbrock and Rosen\_grad are just the same as in Example 30.2 and are omitted for brevity.

The idea behind Newton-Raphson is to exploit a quadratic approximation to the maximand, under the assumption that it is concave. If this is true, the method is very effective. However, if the algorithm happens to evaluate the function at a point where the Hessian is not negative definite, things may go wrong. Script 30.4 exemplifies this by using a normal density, which is concave in the interval  $(-1, 1)$  and convex elsewhere. If the algorithm is started from within the interval everything goes well and NR is (slightly) more effective than BFGS. If, however, the Hessian is positive at the starting point BFGS converges with only little more difficulty, while Newton-Raphson fails.

### 30.3 Simulated Annealing

Simulated annealing — as implemented by the gretl function `simann` — is not a full-blown maximization method in its own right, but can be a useful auxiliary tool in problems where convergence depends sensitively on the initial values of the parameters. The idea is that you supply initial values and the simulated annealing mechanism tries to improve on them via controlled randomization.

The `simann` function takes up to three arguments. The first two (required) are the same as for BFGSmax and NRmax: an initial parameter vector and a function that computes the maximand. The

**Example 30.3:** Rosenbrock function via Newton-Raphson

---

```

function void Rosen_hess (matrix *H, matrix *param)
    scalar x = param[1]
    scalar y = param[2]
    H[1,1] = 2 - 400*y + 1200*x^2
    H[1,2] = -400*x
    H[2,1] = -400*x
    H[2,2] = 200
end function

matrix theta = { 0, 0 }
matrix g = { 0, 0 }
matrix H = zeros(2, 2)

set max_verbose 1
M = NRmax(theta, Rosenbrock(&theta), Rosen_grad(&g, &theta),
          Rosen_hess(&H, &theta))

print theta
print grad

```

---

**Example 30.4:** Maximization of a Gaussian density

---

```

function scalar ND(matrix x)
    scalar z = x[1]
    return exp(-0.5*z*z)
end function

set max_verbose 1

x = {0.75}
A = BFGSmax(x, ND(x))

x = {0.75}
A = NRmax(x, ND(x))

x = {1.5}
A = BFGSmax(x, ND(x))

x = {1.5}
A = NRmax(x, ND(x))

```

---

optional third argument is a positive integer giving the maximum number of iterations,  $n$ , which defaults to 1024.

Starting from the specified point in the parameter space, for each of  $n$  iterations we select at random a new point within a certain radius of the previous one and determine the value of the criterion at the new point. If the criterion is higher we jump to the new point; otherwise, we jump with probability  $P$  (and remain at the previous point with probability  $1 - P$ ). As the iterations proceed, the system gradually “cools” — that is, the radius of the random perturbation is reduced, as is the probability of making a jump when the criterion fails to increase.

In the course of this procedure  $n + 1$  points in the parameter space are evaluated: call them  $\theta_i, i = 0, \dots, n$ , where  $\theta_0$  is the initial value given by the user. Let  $\theta^*$  denote the “best” point among  $\theta_1, \dots, \theta_n$  (highest criterion value). The value written into the parameter vector on completion is then  $\theta^*$  if  $\theta^*$  is better than  $\theta_0$ , otherwise  $\theta_n$ . In other words, failing an actual improvement in the criterion, `simann` randomizes the starting point, which may be helpful in tricky optimization problems.

Example 30.5 shows `simann` at work as a helper for `BFGSmax` in finding the maximum of a bimodal function. Unaided, `BFGSmax` requires 60 function evaluations and 55 evaluations of the gradient, while after simulated annealing the maximum is found with 7 function evaluations and 6 evaluations of the gradient.<sup>1</sup>

#### Example 30.5: BFGS with initialization via Simulated Annealing

---

```
function scalar bimodal (matrix x, matrix A)
    scalar ret = exp(-qform((x-1)', A))
    ret += 2*exp(-qform((x+4)', A))
    return ret
end function

set seed 12334
set max_verbose on

scalar k = 2
matrix A = 0.1 * I(k)
matrix x0 = {3; -5}

x = x0
u = BFGSmax(x, bimodal(x, A))
print x

x = x0
u = simann(x, bimodal(x, A), 1000)
print x
u = BFGSmax(x, bimodal(x, A))
print x
```

---

### 30.4 Computing a Jacobian

Gretl offers the possibility of differentiating numerically a user-defined function via the `fdjac` function.

This function takes two arguments: an  $n \times 1$  matrix holding initial parameter values and a function

<sup>1</sup>Your mileage may vary: these figures are somewhat compiler- and machine-dependent.

call that calculates and returns an  $m \times 1$  matrix, given the current parameter values and any other relevant data. On successful completion it returns an  $m \times n$  matrix holding the Jacobian. For example,

```
matrix Jac = fdjac(theta, SumOC(&theta, &X))
```

where we assume that SumOC is a user-defined function with the following structure:

```
function matrix SumOC (matrix *theta, matrix *X)
  matrix V = ... # do some computation
  return V
end function
```

This may come in handy in several cases: for example, if you use BFGSmax to estimate a model, you may wish to calculate a numerical approximation to the relevant Jacobian to construct a covariance matrix for your estimates.

Another example is the delta method: if you have a consistent estimator of a vector of parameters  $\hat{\theta}$ , and a consistent estimate of its covariance matrix  $\Sigma$ , you may need to compute estimates for a nonlinear continuous transformation  $\psi = g(\theta)$ . In this case, a standard result in asymptotic theory is that

$$\left\{ \begin{array}{c} \hat{\theta} \xrightarrow{p} \theta \\ \sqrt{T}(\hat{\theta} - \theta) \xrightarrow{d} N(0, \Sigma) \end{array} \right\} \Rightarrow \left\{ \begin{array}{c} \hat{\psi} = g(\hat{\theta}) \xrightarrow{p} \psi = g(\theta) \\ \sqrt{T}(\hat{\psi} - \psi) \xrightarrow{d} N(0, J\Sigma J') \end{array} \right\}$$

where  $T$  is the sample size and  $J$  is the Jacobian  $\left. \frac{\partial g(x)}{\partial x} \right|_{x=\theta}$ .

Script 30.6 exemplifies such a case: the example is taken from [Greene \(2003\)](#), section 9.3.1. The slight differences between the results reported in the original source and what gretl returns are due to the fact that the Jacobian is computed numerically, rather than analytically as in the book.

On the subject of numerical versus analytical derivatives, one may wonder what difference it makes to use one method or another. Simply put, the answer is: analytical derivatives may be painful to derive and to translate into code, but in most cases they are much faster than using fdjac; as a consequence, if you need to use derivatives as part of an algorithm that requires iteration (such as numerical optimization, or a Monte Carlo experiment), you'll definitely want to use analytical derivatives.

Analytical derivatives are also, in most cases, more precise than numerical ones, but this advantage may or may not be negligible in practice depending on the practical details: the two fundamental aspects to take in consideration are nonlinearity and machine precision.

As an example, consider the derivative of a highly nonlinear function such as the matrix inverse. In order to keep the example simple, let's focus on  $2 \times 2$  matrices and define the function

```
function matrix vecinv(matrix x)
  A = mshape(x,2,2)
  return vec(inv(A))'
end function
```

which, given  $\text{vec}(A)$ , returns  $\text{vec}(A^{-1})$ . As is well known (see for example [Magnus and Neudecker \(1988\)](#)),

$$\frac{\partial \text{vec}(A^{-1})}{\partial \text{vec}(A)} = -(A^{-1})' \otimes (A^{-1}),$$

which is rather easy to code in hansl as

```
function matrix grad(matrix x)
  iA = inv(mshape(x,2,2))
  return -iA' ** iA
end function
```

**Example 30.6:** Delta Method

---

```

function matrix MPC(matrix *param, matrix *Y)
    beta = param[2]
    gamma = param[3]
    y = Y[1]
    return beta*gamma*y^(gamma-1)
end function

# William Greene, Econometric Analysis, 5e, Chapter 9
set echo off
set messages off
open greene5_1.gdt

# Use OLS to initialize the parameters
ols realcons 0 realdpi --quiet
genr a = $coeff(0)
genr b = $coeff(realdpi)
genr g = 1.0

# Run NLS with analytical derivatives
nls realcons = a + b * (realdpi^g)
    deriv a = 1
    deriv b = realdpi^g
    deriv g = b * realdpi^g * log(realdpi)
end nls

matrix Y = realdpi[2000:4]
matrix theta = $coeff
matrix V = $vcv

mpc = MPC(&theta, &Y)
matrix Jac = fdjac(theta, MPC(&theta, &Y))
Sigma = qform(Jac, V)

printf "\nmpc = %g, std.err = %g\n", mpc, sqrt(Sigma)
scalar teststat = (mpc-1)/sqrt(Sigma)
printf "\nTest for MPC = 1: %g (p-value = %g)\n", \
    teststat, pvalue(n,abs(teststat))

```

---



Using the `fdjac` function to obtain the same result is even easier: you just invoke it like

```
fdjac(a, "vecinv(a)")
```

In order to see what the difference is, in terms of precision, between analytical and numerical Jacobians, start from  $A = \begin{bmatrix} 2 & 1 \\ 1 & 1 \end{bmatrix}$ ; the following code

```
a = {2; 1; 1; 1}
ia = vecinv(a)
ag = grad(a)
ng = fdjac(a, "vecinv(a)")
dg = ag - ng
print ag ng dg
```

gives

```
ag (4 x 4)
```

```
-1    1    1   -1
 1   -2   -1    2
 1   -1   -2    2
-1    2    2   -4
```

```
ng (4 x 4)
```

```
-1    1    1   -1
 1   -2   -1    2
 1   -1   -2    2
-1    2    2   -4
```

```
dg (4 x 4)
```

```
-3.3530e-08 -3.7251e-08 -3.7251e-08 -3.7255e-08
 2.6079e-08  5.2150e-08  3.7251e-08  6.7060e-08
 2.6079e-08  3.7251e-08  5.2150e-08  6.7060e-08
-2.2354e-08 -5.9600e-08 -5.9600e-08 -1.4902e-07
```

in which the analytically-computed derivative and its numerical approximation are essentially the same. If, however, you set  $A = \begin{bmatrix} 1.0001 & 1 \\ 1 & 1 \end{bmatrix}$  you end up evaluating the function at a point in which the function itself is considerably more nonlinear since the matrix is much closer to being singular. As a consequence, the numerical approximation becomes much less satisfactory:

```
ag (4 x 4)
```

```
-1.0000e+08  1.0000e+08  1.0000e+08 -1.0000e+08
 1.0000e+08 -1.0001e+08 -1.0000e+08  1.0001e+08
 1.0000e+08 -1.0000e+08 -1.0001e+08  1.0001e+08
-1.0000e+08  1.0001e+08  1.0001e+08 -1.0002e+08
```

```
ng (4 x 4)
```

```
-9.9985e+07  1.0001e+08  1.0001e+08 -9.9985e+07
 9.9985e+07 -1.0002e+08 -1.0001e+08  9.9995e+07
 9.9985e+07 -1.0001e+08 -1.0002e+08  9.9995e+07
-9.9985e+07  1.0002e+08  1.0002e+08 -1.0001e+08
```

dg (4 x 4)

-14899.	-14901.	-14901.	-14900.
14899.	14903.	14901.	14902.
14899.	14901.	14903.	14902.
-14899.	-14903.	-14903.	-14903.

Moreover, machine precision may have its impact: if you take  $A = 0.00001 \times \begin{bmatrix} 2 & 1 \\ 1 & 1 \end{bmatrix}$ , the matrix itself is not singular at all, but the order of magnitude of its elements is close enough to machine precision to provoke problems:

ag (4 x 4)

-1.0000e+10	1.0000e+10	1.0000e+10	-1.0000e+10
1.0000e+10	-2.0000e+10	-1.0000e+10	2.0000e+10
1.0000e+10	-1.0000e+10	-2.0000e+10	2.0000e+10
-1.0000e+10	2.0000e+10	2.0000e+10	-4.0000e+10

ng (4 x 4)

-1.0000e+10	1.0000e+10	1.0000e+10	-1.0000e+10
1.0000e+10	-2.0000e+10	-1.0000e+10	2.0000e+10
1.0000e+10	-1.0000e+10	-2.0000e+10	2.0000e+10
-1.0000e+10	2.0000e+10	2.0000e+10	-4.0000e+10

dg (4 x 4)

-488.30	-390.60	-390.60	-195.33
634.79	781.21	390.60	585.98
634.79	488.26	683.55	585.98
-781.27	-976.52	-781.21	-1367.3

## Chapter 31

# Discrete and censored dependent variables

This chapter deals with models for dependent variables that are discrete or censored or otherwise limited (as in event counts or durations, which must be positive) and that therefore call for estimation methods other than the classical linear model. We discuss several estimators (mostly based on the Maximum Likelihood principle), adding some details and examples to complement the material on these methods in the *Gretl Command Reference*.

### 31.1 Logit and probit models

It often happens that one wants to specify and estimate a model in which the dependent variable is not continuous, but discrete. A typical example is a model in which the dependent variable is the occupational status of an individual (1 = employed, 0 = unemployed). A convenient way of formalizing this situation is to consider the variable  $y_i$  as a Bernoulli random variable and analyze its distribution conditional on the explanatory variables  $x_i$ . That is,

$$y_i = \begin{cases} 1 & P_i \\ 0 & 1 - P_i \end{cases} \quad (31.1)$$

where  $P_i = P(y_i = 1|x_i)$  is a given function of the explanatory variables  $x_i$ .

In most cases, the function  $P_i$  is a cumulative distribution function  $F$ , applied to a linear combination of the  $x_i$ s. In the probit model, the normal cdf is used, while the logit model employs the logistic function  $\Lambda(\cdot)$ . Therefore, we have

$$\text{probit} \quad P_i = F(z_i) = \Phi(z_i) \quad (31.2)$$

$$\text{logit} \quad P_i = F(z_i) = \Lambda(z_i) = \frac{1}{1 + e^{-z_i}} \quad (31.3)$$

$$z_i = \sum_{j=1}^k x_{ij}\beta_j \quad (31.4)$$

where  $z_i$  is commonly known as the *index* function. Note that in this case the coefficients  $\beta_j$  cannot be interpreted as the partial derivatives of  $E(y_i|x_i)$  with respect to  $x_{ij}$ . However, for a given value of  $x_i$  it is possible to compute the vector of “slopes”, that is

$$\text{slope}_j(\tilde{x}) = \left. \frac{\partial F(z)}{\partial x_j} \right|_{z=\tilde{z}}$$

Gretl automatically computes the slopes, setting each explanatory variable at its sample mean.

Another, equivalent way of thinking about this model is in terms of an unobserved variable  $y_i^*$  which can be described thus:

$$y_i^* = \sum_{j=1}^k x_{ij}\beta_j + \varepsilon_i = z_i + \varepsilon_i \quad (31.5)$$

We observe  $y_i = 1$  whenever  $y_i^* > 0$  and  $y_i = 0$  otherwise. If  $\varepsilon_i$  is assumed to be normal, then we have the probit model. The logit model arises if we assume that the density function of  $\varepsilon_i$  is

$$\lambda(\varepsilon_i) = \frac{\partial \Lambda(\varepsilon_i)}{\partial \varepsilon_i} = \frac{e^{-\varepsilon_i}}{(1 + e^{-\varepsilon_i})^2}$$

Both the probit and logit model are estimated in `gretl` via maximum likelihood, where the log-likelihood can be written as

$$L(\beta) = \sum_{y_i=0} \ln[1 - F(z_i)] + \sum_{y_i=1} \ln F(z_i), \quad (31.6)$$

which is always negative, since  $0 < F(\cdot) < 1$ . Since the score equations do not have a closed form solution, numerical optimization is used. However, in most cases this is totally transparent to the user, since usually only a few iterations are needed to ensure convergence. The `--verbose` switch can be used to track the maximization algorithm.

**Example 31.1:** Estimation of simple logit and probit models

---

```
open greene19_1
```

```
logit GRADE const GPA TUCE PSI
probit GRADE const GPA TUCE PSI
```

---

As an example, we reproduce the results given in chapter 21 of [Greene \(2000\)](#), where the effectiveness of a program for teaching economics is evaluated by the improvements of students' grades. Running the code in example 31.1 gives the output reported in Table 31.1; note that, for the probit model, a conditional moment test on skewness and kurtosis is printed out automatically as a test for normality.

In this context, the `$uhat` accessor function takes a special meaning: it returns generalized residuals as defined in [Gourieroux, Monfort, Renault and Trognon \(1987\)](#), which can be interpreted as unbiased estimators of the latent disturbances  $\varepsilon_i$ . These are defined as

$$u_i = \begin{cases} y_i - \hat{P}_i & \text{for the logit model} \\ y_i \cdot \frac{\phi(\hat{z}_i)}{\Phi(\hat{z}_i)} - (1 - y_i) \cdot \frac{\phi(\hat{z}_i)}{1 - \Phi(\hat{z}_i)} & \text{for the probit model} \end{cases} \quad (31.7)$$

Among other uses, generalized residuals are often used for diagnostic purposes. For example, it is very easy to set up an omitted variables test equivalent to the familiar LM test in the context of a linear regression; example 31.2 shows how to perform a variable addition test.

**Example 31.2:** Variable addition test in a probit model

---

```
open greene19_1
```

```
probit GRADE const GPA PSI
series u = $uhat
%$
ols u const GPA PSI TUCE -q
printf "Variable addition test for TUCE:\n"
printf "Rsqr * T = %g (p. val. = %g)\n", $trsqr, pvalue(X,1,$trsqr)
```

---

### The perfect prediction problem

One curious characteristic of logit and probit models is that (quite paradoxically) estimation is not feasible if a model fits the data perfectly; this is called the *perfect prediction problem*. The reason

Model 1: Logit estimates using the 32 observations 1-32  
Dependent variable: GRADE

VARIABLE	COEFFICIENT	STDERROR	T STAT	SLOPE (at mean)
const	-13.0213	4.93132	-2.641	
GPA	2.82611	1.26294	2.238	0.533859
TUCE	0.0951577	0.141554	0.672	0.0179755
PSI	2.37869	1.06456	2.234	0.449339

Mean of GRADE = 0.344

Number of cases 'correctly predicted' = 26 (81.2%)

$f(\beta'x)$  at mean of independent vars = 0.189

McFadden's pseudo-R-squared = 0.374038

Log-likelihood = -12.8896

Likelihood ratio test: Chi-square(3) = 15.4042 (p-value 0.001502)

Akaike information criterion (AIC) = 33.7793

Schwarz Bayesian criterion (BIC) = 39.6422

Hannan-Quinn criterion (HQC) = 35.7227

	Predicted	
	0	1
Actual 0	18	3
1	3	8

Model 2: Probit estimates using the 32 observations 1-32  
Dependent variable: GRADE

VARIABLE	COEFFICIENT	STDERROR	T STAT	SLOPE (at mean)
const	-7.45232	2.54247	-2.931	
GPA	1.62581	0.693883	2.343	0.533347
TUCE	0.0517288	0.0838903	0.617	0.0169697
PSI	1.42633	0.595038	2.397	0.467908

Mean of GRADE = 0.344

Number of cases 'correctly predicted' = 26 (81.2%)

$f(\beta'x)$  at mean of independent vars = 0.328

McFadden's pseudo-R-squared = 0.377478

Log-likelihood = -12.8188

Likelihood ratio test: Chi-square(3) = 15.5459 (p-value 0.001405)

Akaike information criterion (AIC) = 33.6376

Schwarz Bayesian criterion (BIC) = 39.5006

Hannan-Quinn criterion (HQC) = 35.581

	Predicted	
	0	1
Actual 0	18	3
1	3	8

Test for normality of residual -

Null hypothesis: error is normally distributed

Test statistic: Chi-square(2) = 3.61059

with p-value = 0.164426

**Table 31.1:** Example logit and probit

why this problem arises is easy to see by considering equation (31.6): if for some vector  $\beta$  and scalar  $k$  it's the case that  $z_i < k$  whenever  $y_i = 0$  and  $z_i > k$  whenever  $y_i = 1$ , the same thing is true for any multiple of  $\beta$ . Hence,  $L(\beta)$  can be made arbitrarily close to 0 simply by choosing enormous values for  $\beta$ . As a consequence, the log-likelihood has no maximum, despite being bounded.

Gretl has a mechanism for preventing the algorithm from iterating endlessly in search of a non-existent maximum. One sub-case of interest is when the perfect prediction problem arises because of a single binary explanatory variable. In this case, the offending variable is dropped from the model and estimation proceeds with the reduced specification. Nevertheless, it may happen that no single “perfect classifier” exists among the regressors, in which case estimation is simply impossible and the algorithm stops with an error. This behavior is triggered during the iteration process if

$$\max_{i:y_i=0} z_i < \min_{i:y_i=1} z_i$$

If this happens, unless your model is trivially mis-specified (like predicting if a country is an oil exporter on the basis of oil revenues), it is normally a small-sample problem: you probably just don't have enough data to estimate your model. You may want to drop some of your explanatory variables.

This problem is well analyzed in [Stokes \(2004\)](#); the results therein are replicated in the example script `murder_rates.inp`.

## 31.2 Ordered response models

These models constitute a simple variation on ordinary logit/probit models, and are usually applied when the dependent variable is a discrete and ordered measurement — not simply binary, but on an ordinal rather than an interval scale. For example, this sort of model may be applied when the dependent variable is a qualitative assessment such as “Good”, “Average” and “Bad”.

In the general case, consider an ordered response variable,  $y$ , that can take on any of the  $J+1$  values  $0, 1, 2, \dots, J$ . We suppose, as before, that underlying the observed response is a latent variable,

$$y^* = X\beta + \varepsilon = z + \varepsilon$$

Now define “cut points”,  $\alpha_1 < \alpha_2 < \dots < \alpha_J$ , such that

$$\begin{aligned} y &= 0 & \text{if } y^* \leq \alpha_1 \\ y &= 1 & \text{if } \alpha_1 < y^* \leq \alpha_2 \\ &\vdots \\ y &= J & \text{if } y^* > \alpha_J \end{aligned}$$

For example, if the response takes on three values there will be two such cut points,  $\alpha_1$  and  $\alpha_2$ .

The probability that individual  $i$  exhibits response  $j$ , conditional on the characteristics  $x_i$ , is then given by

$$P(y_i = j | x_i) = \begin{cases} P(y^* \leq \alpha_1 | x_i) = F(\alpha_1 - z_i) & \text{for } j = 0 \\ P(\alpha_j < y^* \leq \alpha_{j+1} | x_i) = F(\alpha_{j+1} - z_i) - F(\alpha_j - z_i) & \text{for } 0 < j < J \\ P(y^* > \alpha_J | x_i) = 1 - F(\alpha_J - z_i) & \text{for } j = J \end{cases} \quad (31.8)$$

The unknown parameters  $\alpha_j$  are estimated jointly with the  $\beta$ s via maximum likelihood. The  $\hat{\alpha}_j$  estimates are reported by gretl as `cut1`, `cut2` and so on. For the probit variant, a conditional moment test for normality constructed in the spirit of [Chesher and Irish \(1987\)](#) is also included.

Note that the  $\alpha_j$  parameters can be shifted arbitrarily by adding a constant to  $z_i$ , so the model is under-identified if there is some linear combination of the explanatory variables which is constant. The most obvious case in which this occurs is when the model contains a constant term; for this

reason, gretl drops automatically the intercept if present. However, it may happen that the user inadvertently specifies a list of regressors that may be combined in such a way to produce a constant (for example, by using a full set of dummy variables for a discrete factor). If this happens, gretl will also drop any offending regressors.

In order to apply these models in gretl, the dependent variable must either take on only non-negative integer values, or be explicitly marked as discrete. (In case the variable has non-integer values, it will be recoded internally.) Note that gretl does not provide a separate command for ordered models: the `logit` and `probit` commands automatically estimate the ordered version if the dependent variable is acceptable, but not binary.

Example 31.3 reproduces the results presented in section 15.10 of Wooldridge (2002a). The question of interest in this analysis is what difference it makes, to the allocation of assets in pension funds, whether individual plan participants have a choice in the matter. The response variable is an ordinal measure of the weight of stocks in the pension portfolio. Having reported the results of estimation of the ordered model, Wooldridge illustrates the effect of the `choice` variable by reference to an “average” participant. The example script shows how one can compute this effect in gretl.

After estimating ordered models, the `$uhat` accessor yields generalized residuals as in binary models; additionally, the `$yhat` accessor function returns  $\hat{z}_i$ , so it is possible to compute an unbiased estimator of the latent variable  $y_i^*$  simply by adding the two together.

### 31.3 Multinomial logit

When the dependent variable is not binary and does not have a natural ordering, *multinomial* models are used. Multinomial logit is supported in gretl via the `--multinomial` option to the `logit` command. Simple models can also be handled via the `mle` command (see chapter 20). We give here an example of such a model. Let the dependent variable,  $y_i$ , take on integer values  $0, 1, \dots, p$ . The probability that  $y_i = k$  is given by

$$P(y_i = k | x_i) = \frac{\exp(x_i \beta_k)}{\sum_{j=0}^p \exp(x_i \beta_j)}$$

For the purpose of identification one of the outcomes must be taken as the “baseline”; it is usually assumed that  $\beta_0 = 0$ , in which case

$$P(y_i = k | x_i) = \frac{\exp(x_i \beta_k)}{1 + \sum_{j=1}^p \exp(x_i \beta_j)}$$

and

$$P(y_i = 0 | x_i) = \frac{1}{1 + \sum_{j=1}^p \exp(x_i \beta_j)}.$$

Example 31.4 reproduces Table 15.2 in Wooldridge (2002a), based on data on career choice from Keane and Wolpin (1997). The dependent variable is the occupational status of an individual (0 = in school; 1 = not in school and not working; 2 = working), and the explanatory variables are education and work experience (linear and square) plus a “black” binary variable. The full data set is a panel; here the analysis is confined to a cross-section for 1987.

**Example 31.3:** Ordered probit model

---

```

/*
  Replicate the results in Wooldridge, Econometric Analysis of Cross
  Section and Panel Data, section 15.10, using pension-plan data from
  Papke (AER, 1998).

  The dependent variable, pctstck (percent stocks), codes the asset
  allocation responses of "mostly bonds", "mixed" and "mostly stocks"
  as {0, 50, 100}.

  The independent variable of interest is "choice", a dummy indicating
  whether individuals are able to choose their own asset allocations.
*/

open pension.gdt

# demographic characteristics of participant
list DEMOG = age educ female black married
# dummies coding for income level
list INCOME = finc25 finc35 finc50 finc75 finc100 finc101

# Papke's OLS approach
ols pctstck const choice DEMOG INCOME wealth89 prftshr
# save the OLS choice coefficient
choice_ols = $coeff(choice)

# estimate ordered probit
probit pctstck choice DEMOG INCOME wealth89 prftshr

k = $ncoeff
matrix b = $coeff[1:k-2]
a1 = $coeff[k-1]
a2 = $coeff[k]

/*
  Wooldridge illustrates the 'choice' effect in the ordered probit
  by reference to a single, non-black male aged 60, with 13.5 years
  of education, income in the range $50K - $75K and wealth of $200K,
  participating in a plan with profit sharing.
*/
matrix X = {60, 13.5, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 200, 1}

# with 'choice' = 0
scalar Xb = (0 ~ X) * b
P0 = cdf(N, a1 - Xb)
P50 = cdf(N, a2 - Xb) - P0
P100 = 1 - cdf(N, a2 - Xb)
E0 = 50 * P50 + 100 * P100

# with 'choice' = 1
Xb = (1 ~ X) * b
P0 = cdf(N, a1 - Xb)
P50 = cdf(N, a2 - Xb) - P0
P100 = 1 - cdf(N, a2 - Xb)
E1 = 50 * P50 + 100 * P100

printf "\nWith choice, E(y) = %.2f, without E(y) = %.2f\n", E1, E0
printf "Estimated choice effect via ML = %.2f (OLS = %.2f)\n", E1 - E0,
choice_ols

```

---



**Example 31.4:** Multinomial logit

Input:

```
open keane.gdt
smpl (year=87) --restrict
logit status 0 educ exper expersq black --multinomial
```

Output (selected portions):

Model 1: Multinomial Logit, using observations 1-1738 (n = 1717)  
 Missing or incomplete observations dropped: 21  
 Dependent variable: status  
 Standard errors based on Hessian

	coefficient	std. error	z	p-value	
-----					
status = 2					
const	10.2779	1.13334	9.069	1.20e-19	***
educ	-0.673631	0.0698999	-9.637	5.57e-22	***
exper	-0.106215	0.173282	-0.6130	0.5399	
expersq	-0.0125152	0.0252291	-0.4961	0.6199	
black	0.813017	0.302723	2.686	0.0072	***
status = 3					
const	5.54380	1.08641	5.103	3.35e-07	***
educ	-0.314657	0.0651096	-4.833	1.35e-06	***
exper	0.848737	0.156986	5.406	6.43e-08	***
expersq	-0.0773003	0.0229217	-3.372	0.0007	***
black	0.311361	0.281534	1.106	0.2687	
Mean dependent var	2.691322	S.D. dependent var	0.573502		
Log-likelihood	-907.8572	Akaike criterion	1835.714		
Schwarz criterion	1890.198	Hannan-Quinn	1855.874		

Number of cases 'correctly predicted' = 1366 (79.6%)  
 Likelihood ratio test: Chi-square(8) = 583.722 [0.0000]

### 31.4 Bivariate probit

The bivariate probit model is simply a two-equation system in which each equation is a probit model, but the two disturbance terms may not be independent. In formulae,

$$y_{1,i}^* = \sum_{j=1}^{k_1} x_{ij}\beta_j + \varepsilon_{1,i} \quad y_{1,i} = 1 \iff y_{1,i}^* > 0 \quad (31.9)$$

$$y_{2,i}^* = \sum_{j=1}^{k_2} z_{ij}\gamma_j + \varepsilon_{2,i} \quad y_{2,i} = 1 \iff y_{2,i}^* > 0 \quad (31.10)$$

$$\begin{bmatrix} \varepsilon_{1,i} \\ \varepsilon_{2,i} \end{bmatrix} \sim N \left[ 0, \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix} \right] \quad (31.11)$$

- The explanatory variables for the first equation  $x$  and for the second equation  $z$  may overlap
- example contained in `biprobit.inp`
- `$uhat` and `$yhat` are matrices

FIXME: expand.

### 31.5 The Tobit model

The Tobit model is used when the dependent variable of a model is *censored*. Assume a latent variable  $y_i^*$  can be described as

$$y_i^* = \sum_{j=1}^k x_{ij}\beta_j + \varepsilon_i,$$

where  $\varepsilon_i \sim N(0, \sigma^2)$ . If  $y_i^*$  were observable, the model's parameters could be estimated via ordinary least squares. On the contrary, suppose that we observe  $y_i$ , defined as

$$y_i = \begin{cases} a & \text{for } y_i^* \leq a \\ y_i^* & \text{for } a < y_i^* < b \\ b & \text{for } y_i^* \geq b \end{cases} \quad (31.12)$$

In most cases found in the applied literature,  $a = 0$  and  $b = \infty$ , so in practice negative values of  $y_i^*$  are not observed and are replaced by zeros.

In this case, regressing  $y_i$  on the  $x_i$ s does not yield consistent estimates of the parameters  $\beta$ , because the conditional mean  $E(y_i|x_i)$  is not equal to  $\sum_{j=1}^k x_{ij}\beta_j$ . It can be shown that restricting the sample to non-zero observations would not yield consistent estimates either. The solution is to estimate the parameters via maximum likelihood. The syntax is simply

```
tobit depvar indvars
```

As usual, progress of the maximization algorithm can be tracked via the `--verbose` switch, while `$uhat` returns the generalized residuals. Note that in this case the generalized residual is defined as  $\hat{u}_i = E(\varepsilon_i|y_i = 0)$  for censored observations, so the familiar equality  $\hat{u}_i = y_i - \hat{y}_i$  only holds for uncensored observations, that is, when  $y_i > 0$ .

An important difference between the Tobit estimator and OLS is that the consequences of non-normality of the disturbance term are much more severe: non-normality implies inconsistency for the Tobit estimator. For this reason, the output for the Tobit model includes the [Chesher and Irish \(1987\)](#) normality test by default.

The general case in which  $a$  is nonzero and/or  $b$  is finite can be handled by using the options `--llimit` and `--rlimit`. So, for example,

```
tobit depvar indvars --llimit=10
```

would tell gretl that the left bound  $a$  is set to 10.

### 31.6 Interval regression

The interval regression model arises when the dependent variable is unobserved for some (possibly all) observations; what we observe instead is an interval in which the dependent variable lies. In other words, the data generating process is assumed to be

$$y_i^* = x_i\beta + \epsilon_i$$

but we only know that  $m_i \leq y_i^* \leq M_i$ , where the interval may be left- or right-unbounded (but not both). If  $m_i = M_i$ , we effectively observe  $y_i^*$  and no information loss occurs. In practice, each observation belongs to one of four categories:

1. left-unbounded, when  $m_i = -\infty$ ,
2. right-unbounded, when  $M_i = \infty$ ,
3. bounded, when  $-\infty < m_i < M_i < \infty$  and
4. point observations when  $m_i = M_i$ .

It is interesting to note that this model bears similarities to other models in several special cases:

- When all observations are point observations the model trivially reduces to the ordinary linear regression model.
- The interval model could be thought of an ordered probit model (see 31.2) in which the cut points (the  $\alpha_j$  coefficients in eq. 31.8) are observed and don't need to be estimated.
- The Tobit model (see 31.5) is a special case of the interval model in which  $m_i$  and  $M_i$  do not depend on  $i$ , that is, the censoring limits are the same for all observations. As a matter of fact, gretl's `tobit` commands is handled internally as a special case of the interval model.

The gretl command `intreg` estimates interval models by maximum likelihood, assuming normality of the disturbance term  $\epsilon_i$ . Its syntax is

```
intreg minvar maxvar X
```

where `minvar` contains the  $m_i$  series, with NAs for left-unbounded observations, and `maxvar` contains  $M_i$ , with NAs for right-unbounded observations. By default, standard errors are computed using the negative inverse of the Hessian. If the `--robust` flag is given, then QML or Huber-White standard errors are calculated instead. In this case the estimated covariance matrix is a “sandwich” of the inverse of the estimated Hessian and the outer product of the gradient.

If the model specification contains regressors other than just a constant, the output includes a chi-square statistic for testing the joint null hypothesis that none of these regressors has any effect on the outcome. This is a Wald statistic based on the estimated covariance matrix. If you wish to construct a likelihood ratio test, this is easily done by estimating both the full model and the null model (containing only the constant), saving the log-likelihood in both cases via the `$lnl` accessor, and then referring twice the difference between the two log-likelihoods to the chi-square distribution with  $k$  degrees of freedom, where  $k$  is the number of additional regressors (see the `pvalue` command in the *Gretl Command Reference*). Also included is a conditional moment normality test, similar to those provided for the probit, ordered probit and Tobit models (see above). An example is contained in the sample script `wtp.inp`, provided with the gretl distribution.

**Example 31.5:** Interval model on artificial data

Input:

```

nulldata 100
# generate artificial data
set seed 201449
x = normal()
epsilon = 0.2*normal()
ystar = 1 + x + epsilon
lo_bound = floor(ystar)
hi_bound = ceil(ystar)

# run the interval model
intreg lo_bound hi_bound const x

# estimate ystar
gen_resid = $uhat
yhat = $yhat + gen_resid
corr ystar yhat

```

Output (selected portions):

Model 1: Interval estimates using the 100 observations 1-100  
 Lower limit: lo\_bound, Upper limit: hi\_bound

	coefficient	std. error	t-ratio	p-value
const	0.993762	0.0338325	29.37	1.22e-189 ***
x	0.986662	0.0319959	30.84	8.34e-209 ***
Chi-square(1)	950.9270	p-value		8.3e-209
Log-likelihood	-44.21258	Akaike criterion		94.42517
Schwarz criterion	102.2407	Hannan-Quinn		97.58824

```

sigma = 0.223273
Left-unbounded observations: 0
Right-unbounded observations: 0
Bounded observations: 100
Point observations: 0

```

...

```

corr(ystar, yhat) = 0.98960092
Under the null hypothesis of no correlation:
t(98) = 68.1071, with two-tailed p-value 0.0000

```

As with the probit and Tobit models, after a model has been estimated the `$uhat` accessor returns the generalized residual, which is an estimate of  $\epsilon_i$ : more precisely, it equals  $y_i - x_i\hat{\beta}$  for point observations and  $E(\epsilon_i|m_i, M_i, x_i)$  otherwise. Note that it is possible to compute an unbiased predictor of  $y_i^*$  by summing this estimate to  $x_i\hat{\beta}$ . Script 31.5 shows an example. As a further similarity with Tobit, the interval regression model may deliver inconsistent estimates if the disturbances are non-normal; hence, the [Chesher and Irish \(1987\)](#) test for normality is included by default here too.

### 31.7 Sample selection model

In the sample selection model (also known as “Tobit II” model), there are two latent variables:

$$y_i^* = \sum_{j=1}^k x_{ij} \beta_j + \varepsilon_i \quad (31.13)$$

$$s_i^* = \sum_{j=1}^p z_{ij} \gamma_j + \eta_i \quad (31.14)$$

and the observation rule is given by

$$y_i = \begin{cases} y_i^* & \text{for } s_i^* > 0 \\ \blacklozenge & \text{for } s_i^* \leq 0 \end{cases} \quad (31.15)$$

In this context, the  $\blacklozenge$  symbol indicates that for some observations we simply do not have data on  $y$ :  $y_i$  may be 0, or missing, or anything else. A dummy variable  $d_i$  is normally used to set censored observations apart.

One of the most popular applications of this model in econometrics is a wage equation coupled with a labor force participation equation: we only observe the wage for the employed. If  $y_i^*$  and  $s_i^*$  were (conditionally) independent, there would be no reason not to use OLS for estimating equation (31.13); otherwise, OLS does not yield consistent estimates of the parameters  $\beta_j$ .

Since conditional independence between  $y_i^*$  and  $s_i^*$  is equivalent to conditional independence between  $\varepsilon_i$  and  $\eta_i$ , one may model the co-dependence between  $\varepsilon_i$  and  $\eta_i$  as

$$\varepsilon_i = \lambda \eta_i + v_i;$$

substituting the above expression in (31.13), you obtain the model that is actually estimated:

$$y_i = \sum_{j=1}^k x_{ij} \beta_j + \lambda \hat{\eta}_i + v_i,$$

so the hypothesis that censoring does not matter is equivalent to the hypothesis  $H_0 : \lambda = 0$ , which can be easily tested.

The parameters can be estimated via maximum likelihood under the assumption of joint normality of  $\varepsilon_i$  and  $\eta_i$ ; however, a widely used alternative method yields the so-called *Heckit* estimator, named after Heckman (1979). The procedure can be briefly outlined as follows: first, a probit model is fit on equation (31.14); next, the generalized residuals are inserted in equation (31.13) to correct for the effect of sample selection.

Gretl provides the `heckit` command to carry out estimation; its syntax is

```
heckit y X ; d Z
```

where  $y$  is the dependent variable,  $X$  is a list of regressors,  $d$  is a dummy variable holding 1 for uncensored observations and  $Z$  is a list of explanatory variables for the censoring equation.

Since in most cases maximum likelihood is the method of choice, by default `gretl` computes ML estimates. The 2-step Heckit estimates can be obtained by using the `--two-step` option. After estimation, the `$uhat` accessor contains the generalized residuals. As in the ordinary Tobit model, the residuals equal the difference between actual and fitted  $y_i$  only for uncensored observations (those for which  $d_i = 1$ ).

Example 31.6 shows two estimates from the dataset used in Mroz (1987): the first one replicates Table 22.7 in Greene (2003),<sup>1</sup> while the second one replicates table 17.1 in Wooldridge (2002a).

<sup>1</sup>Note that the estimates given by `gretl` do not coincide with those found in the printed volume. They do, however, match those found on the errata web page for Greene's book: <http://pages.stern.nyu.edu/~wgreene/Text/Errata/ERRATA5.htm>.

**Example 31.6:** Heckit model

---

```

open mroz87.gdt

genr EXP2 = AX^2
genr WA2 = WA^2
genr KIDS = (KL6+K618)>0

# Greene's specification

list X = const AX EXP2 WE CIT
list Z = const WA WA2 FAMINC KIDS WE

heckit WW X ; LFP Z --two-step
heckit WW X ; LFP Z

# Wooldridge's specification

series NWINC = FAMINC - WW*WHRS
series lww = log(WW)
list X = const WE AX EXP2
list Z = X NWINC WA KL6 K618

heckit lww X ; LFP Z --two-step

```

---

**31.8 Count data**

Here the dependent variable is assumed to be a non-negative integer, so a probabilistic description of  $y_i|x_i$  must hinge on some discrete distribution. The most common model is the Poisson model, in which

$$P(y_i = Y|x_i) = \frac{e^{-\mu_i} \mu_i^Y}{Y!}$$

$$\mu_i = \exp\left(\sum_j x_{ij}\beta_j\right)$$

In some cases, an “offset” variable is needed. The number of occurrences of  $y_i$  in a given time is assumed to be strictly proportional to the offset variable  $n_i$ . In the epidemiology literature, the offset is known as “population at risk”. In this case, the model becomes

$$\mu_i = n_i \exp\left(\sum_j x_{ij}\beta_j\right)$$

Another way to look at the offset variable is to consider its natural log as just another explanatory variable whose coefficient is constrained to be one.

Estimation is carried out by maximum likelihood and follows the syntax

```
poisson depvar indep
```

If an offset variable is needed, it has to be specified at the end of the command, separated from the list of explanatory variables by a semicolon, as in

```
poisson depvar indep ; offset
```

It should be noted that the `poisson` command does not use, internally, the same optimization engines as most other `gretl` command, such as `arma` or `tobit`. As a consequence, some details may differ: the `--verbose` option will yield different output and settings such as `bfgs_tol` will not work.

### Overdispersion

In the Poisson model,  $E(y_i|x_i) = V(y_i|x_i) = \mu_i$ , that is, the conditional mean equals the conditional variance by construction. In many cases, this feature is at odds with the data, as the conditional variance is often larger than the mean; this phenomenon is called “overdispersion”. The output from the `poisson` command includes a conditional moment test for overdispersion (as per [Davidson and MacKinnon \(2004\)](#), section 11.5), which is printed automatically after estimation.

Overdispersion can be attributed to unmodeled heterogeneity between individuals. Two data points with the same observable characteristics  $x_i = x_j$  may differ because of some unobserved scale factor  $s_i \neq s_j$  so that

$$E(y_i|x_i, s_i) = \mu_i s_i \neq \mu_j s_j = E(y_j|x_j, s_j)$$

even though  $\mu_i = \mu_j$ . In other words,  $y_i$  is a Poisson random variable conditional on both  $x_i$  and  $s_i$ , but since  $s_i$  is unobservable, the only thing we can use,  $P(y_i|x_i)$ , will not follow the Poisson distribution.

It is often assumed that  $s_i$  can be represented as a gamma random variable with mean 1 and variance  $\alpha$ : the parameter  $\alpha$  is estimated together with the vector  $\beta$ , and measures the degree of heterogeneity between individuals.

In this case, the conditional probability for  $y_i$  given  $x_i$  can be shown to be

$$P(y_i|x_i) = \frac{\Gamma(y_i + \alpha^{-1})}{\Gamma(\alpha^{-1})\Gamma(y_i + 1)} \left[ \frac{\mu_i}{\mu_i + \alpha^{-1}} \right]^{y_i} \left[ \frac{\alpha^{-1}}{\mu_i + \alpha^{-1}} \right]^{\alpha^{-1}} \quad (31.16)$$

which is known as the “Negative Binomial Model”. The conditional mean is still  $E(y_i|x_i) = \mu_i$ , but the variance equals  $V(y_i|x_i) = \mu_i (1 + \mu_i \alpha)$ . The `gretl` command for this model is `negbin depvar indep`.

- There is also a less used variant of the negative binomial model, in which the conditional variance is a scalar multiple of the conditional mean, that is  $V(y_i|x_i) = \mu_i (1 + \gamma)$ . To distinguish between the two, the model (31.16) is termed “Type 2”. `Gretl` implements model 1 via the option `--model1`.
- A script which exemplifies the above models is included among `gretl`’s sample scripts, under the name `camtriv.inp`.

FIXME: expand.

## 31.9 Duration models

In some contexts we wish to apply econometric methods to measurements of the duration of certain states. Classic examples include the following:

- From engineering, the “time to failure” of electronic or mechanical components: how long do, say, computer hard drives last until they malfunction?
- From the medical realm: how does a new treatment affect the time from diagnosis of a certain condition to exit from that condition (where “exit” might mean death or full recovery)?
- From economics: the duration of strikes, or of spells of unemployment.

In each case we may be interested in how the durations are distributed, and how they are affected by relevant covariates. There are several approaches to this problem; the one we discuss here — which is currently the only one supported by `gretl` — is estimation of a parametric model by means of Maximum Likelihood. In this approach we hypothesize that the durations follow some definite probability law and we seek to estimate the parameters of that law, factoring in the influence of covariates.

We may express the density (PDF) of the durations as  $f(t, X, \theta)$ , where  $t$  is the length of time in the state in question,  $X$  is a matrix of covariates, and  $\theta$  is a vector of parameters. The likelihood for a sample of  $n$  observations indexed by  $i$  is then

$$L = \prod_{i=1}^n f(t_i, x_i, \theta)$$

Rather than working with the density directly, however, it is standard practice to factor  $f(\cdot)$  into two components, namely a *hazard function*,  $\lambda$ , and a *survivor function*,  $S$ . The survivor function gives the probability that a state lasts at least as long as  $t$ ; it is therefore  $1 - F(t, X, \theta)$  where  $F$  is the CDF corresponding to the density  $f(\cdot)$ . The hazard function addresses this question: given that a state has persisted as long as  $t$ , what is the likelihood that it ends within a short increment of time beyond  $t$  — that is, it ends between  $t$  and  $t + \Delta$ ? Taking the limit as  $\Delta$  goes to zero, we end up with the ratio of the density to the survivor function:<sup>2</sup>

$$\lambda(t, X, \theta) = \frac{f(t, X, \theta)}{S(t, X, \theta)} \quad (31.17)$$

so the log-likelihood can be written as

$$\ell = \sum_{i=1}^n \log f(t_i, x_i, \theta) = \sum_{i=1}^n \log \lambda(t_i, x_i, \theta) + \log S(t_i, x_i, \theta) \quad (31.18)$$

One point of interest is the shape of the hazard function, in particular its dependence (or not) on time since the state began. If  $\lambda$  does not depend on  $t$  we say the process in question exhibits *duration independence*: the probability of exiting the state at any given moment neither increases nor decreases based simply on how long the state has persisted to date. The alternatives are positive duration dependence (the likelihood of exiting the state rises, the longer the state has persisted) or negative duration dependence (exit becomes less likely, the longer it has persisted). Finally, the behavior of the hazard with respect to time need not be monotonic; some parameterizations allow for this possibility and some do not.

Since durations are inherently positive the probability distribution used in modeling must respect this requirement, giving a density of zero for  $t \leq 0$ . Four common candidates are the exponential, Weibull, log-logistic and log-normal, the Weibull being the most common choice. The table below displays the density and the hazard function for each of these distributions as they are commonly parameterized, written as functions of  $t$  alone. ( $\phi$  and  $\Phi$  denote, respectively, the Gaussian PDF and CDF.)

	density, $f(t)$	hazard, $\lambda(t)$
Exponential	$\gamma \exp(-\gamma t)$	$\gamma$
Weibull	$\alpha \gamma^\alpha t^{\alpha-1} \exp[-(\gamma t)^\alpha]$	$\alpha \gamma^\alpha t^{\alpha-1}$
Log-logistic	$\gamma \alpha \frac{(\gamma t)^{\alpha-1}}{[1 + (\gamma t)^\alpha]^2}$	$\gamma \alpha \frac{(\gamma t)^{\alpha-1}}{[1 + (\gamma t)^\alpha]}$
Log-normal	$\frac{1}{\sigma t} \phi[(\log t - \mu)/\sigma]$	$\frac{1}{\sigma t} \frac{\phi[(\log t - \mu)/\sigma]}{\Phi[-(\log t - \mu)/\sigma]}$

<sup>2</sup>For a fuller discussion see, for example, Davidson and MacKinnon (2004).



The hazard is constant for the exponential distribution. For the Weibull, it is monotone increasing in  $t$  if  $\alpha > 1$ , or monotone decreasing for  $\alpha < 1$ . (If  $\alpha = 1$  the Weibull collapses to the exponential.) The log-logistic and log-normal distributions allow the hazard to vary with  $t$  in a non-monotonic fashion.

Covariates are brought into the picture by allowing them to govern one of the parameters of the density, so that the durations are not identically distributed across cases. For example, when using the log-normal distribution it is natural to make  $\mu$ , the expected value of  $\log t$ , depend on the covariates,  $X$ . This is typically done via a linear index function:  $\mu = X\beta$ .

Note that the expressions for the log-normal density and hazard contain the term  $(\log t - \mu)/\sigma$ . Replacing  $\mu$  with  $X\beta$  this becomes  $(\log t - X\beta)/\sigma$ . It turns out that this constitutes a useful simplifying change of variables for all of the distributions discussed here. As in [Kalbfleisch and Prentice \(2002\)](#), we define

$$w_i \equiv (\log t_i - x_i\beta)/\sigma$$

The interpretation of the scale factor,  $\sigma$ , in this expression depends on the distribution. For the log-normal,  $\sigma$  represents the standard deviation of  $\log t$ ; for the Weibull and the log-logistic it corresponds to  $1/\alpha$ ; and for the exponential it is fixed at unity. For distributions other than the log-normal,  $X\beta$  corresponds to  $-\log \gamma$ , or in other words  $\gamma = \exp(-X\beta)$ .

With this change of variables, the density and survivor functions may be written compactly as follows (the exponential is the same as the Weibull).

	density, $f(w_i)$	survivor, $S(w_i)$
Weibull	$\exp(w_i - e^{w_i})$	$\exp(-e^{w_i})$
Log-logistic	$e^{w_i} (1 + e^{w_i})^{-2}$	$(1 + e^{w_i})^{-1}$
Log-normal	$\phi(w_i)$	$\Phi(-w_i)$

In light of the above we may think of the generic parameter vector  $\theta$ , as in  $f(t, X, \theta)$ , as composed of the coefficients on the covariates,  $\beta$ , plus (in all cases apart from the exponential) the additional parameter  $\sigma$ .

A complication in estimation of  $\theta$  is posed by “incomplete spells”. That is, in some cases the state in question may not have ended at the time the observation is made (e.g. some workers remain unemployed, some components have not yet failed). If we use  $t_i$  to denote the time from entering the state to either (a) exiting the state or (b) the observation window closing, whichever comes first, then all we know of the “right-censored” cases (b) is that the duration was at least as long as  $t_i$ . This can be handled by rewriting the the log-likelihood (compare [31.18](#)) as

$$\ell_i = \sum_{i=1}^n \delta_i \log S(w_i) + (1 - \delta_i) [-\log \sigma + \log f(w_i)] \quad (31.19)$$

where  $\delta_i$  equals 1 for censored cases (incomplete spells), and 0 for complete observations. The rationale for this is that the log-density equals the sum of the log hazard and the log survivor function, but for the incomplete spells only the survivor function contributes to the likelihood. So in [\(31.19\)](#) we are adding up the log survivor function alone for the incomplete cases, plus the full log density for the completed cases.

### Implementation in gretl and illustration

The `duration` command accepts a list of series on the usual pattern: dependent variable followed by covariates. If right-censoring is present in the data this should be represented by a dummy variable corresponding to  $\delta_i$  above, separated from the covariates by a semicolon. For example,

```
duration durat 0 X ; cens
```

where `durat` measures durations, 0 represents the constant (which is required for such models), `X` is a named list of regressors, and `cens` is the censoring dummy.

By default the Weibull distribution is used; you can substitute any of the other three distributions discussed here by appending one of the option flags `--exponential`, `--loglogistic` or `--lognormal`.

Interpreting the coefficients in a duration model requires some care, and we will work through an illustrative case. The example comes from section 20.3 of Wooldridge (2002a), and it concerns criminal recidivism.<sup>3</sup> The data (filename `recid.gdt`) pertain to a sample of 1,445 convicts released from prison between July 1, 1977 and June 30, 1978. The dependent variable is the time in months until they are again arrested. The information was gathered retrospectively by examining records in April 1984; the maximum possible length of observation is 81 months. Right-censoring is important: when the data were compiled about 62 percent had not been arrested. The dataset contains several covariates, which are described in the data file; we will focus below on interpretation of the `married` variable, a dummy which equals 1 if the respondent was married when imprisoned.

Example 31.7 shows the `gretl` commands for a Weibull model along with most of the output. Consider first the scale factor,  $\sigma$ . The estimate is 1.241 with a standard error of 0.048. (We don't print a  $z$  score and  $p$ -value for this term since  $H_0 : \sigma = 0$  is not of interest.) Recall that  $\sigma$  corresponds to  $1/\alpha$ ; we can be confident that  $\alpha$  is less than 1, so recidivism displays negative duration dependence. This makes sense: it is plausible that if a past offender manages to stay out of trouble for an extended period his risk of engaging in crime again diminishes. (The exponential model would therefore not be appropriate in this case.)

On a priori grounds, however, we may doubt the monotonic decline in hazard that is implied by the Weibull specification. Even if a person is liable to return to crime, it seems relatively unlikely that he would do so straight out of prison. In the data, we find that only 2.6 percent of those followed were rearrested within 3 months. The log-normal specification, which allows the hazard to rise and then fall, may be more appropriate. Using the `duration` command again with the same covariates but the `--lognormal` flag, we get a log-likelihood of  $-1597$  as against  $-1633$  for the Weibull, confirming that the log-normal gives a better fit.

Let us now focus on the `married` coefficient, which is positive in both specifications but larger and more sharply estimated in the log-normal variant. The first thing is to get the interpretation of the sign right. Recall that  $X\beta$  enters negatively into the intermediate variable  $w$ . The Weibull hazard is  $\lambda(w_i) = e^{w_i}$ , so being married reduces the hazard of re-offending, or in other words lengthens the expected duration out of prison. The same qualitative interpretation applies for the log-normal.

To get a better sense of the `married` effect, it is useful to show its impact on the hazard across time. We can do this by plotting the hazard for two values of the index function  $X\beta$ : in each case the values of all the covariates other than `married` are set to their means (or some chosen values) while `married` is set first to 0 then to 1. Example 31.8 provides a script that does this, and the resulting plots are shown in Figure 31.1. Note that when computing the hazards we need to multiply by the Jacobian of the transformation from  $t_i$  to  $w_i = \log(t_i - x_i\beta)/\sigma$ , namely  $1/t$ . Note also that the estimate of  $\sigma$  is available via the accessor `$sigma`, but it is also present as the last element in the coefficient vector obtained via `$coeff`.

A further difference between the Weibull and log-normal specifications is illustrated in the plots. The Weibull is an instance of a *proportional hazard* model. This means that for any sets of values of the covariates,  $x_i$  and  $x_j$ , the ratio of the associated hazards is invariant with respect to duration. In this example the Weibull hazard for unmarried individuals is always 1.1637 times that for married. In the log-normal variant, on the other hand, this ratio gradually declines from 1.6703 at one month to 1.1766 at 100 months.

<sup>3</sup>Germán Rodríguez of Princeton University has a page discussing this example and displaying estimates from Stata at <http://data.princeton.edu/pop509a/recid1.html>.

**Example 31.7:** Weibull model for recidivism data

Input:

```
open recid.gdt
list X = workprg priors tserved felon alcohol drugs \
      black married educ age
duration durat 0 X ; cens
duration durat 0 X ; cens --lognormal
```

Partial output:

Model 1: Duration (Weibull), using observations 1-1445

Dependent variable: durat

	coefficient	std. error	z	p-value	
-----					
const	4.22167	0.341311	12.37	3.85e-35 ***	
workprg	-0.112785	0.112535	-1.002	0.3162	
priors	-0.110176	0.0170675	-6.455	1.08e-10 ***	
tserve <sup>d</sup>	-0.0168297	0.00213029	-7.900	2.78e-15 ***	
felon	0.371623	0.131995	2.815	0.0049 ***	
alcohol	-0.555132	0.132243	-4.198	2.69e-05 ***	
drugs	-0.349265	0.121880	-2.866	0.0042 ***	
black	-0.563016	0.110817	-5.081	3.76e-07 ***	
married	0.188104	0.135752	1.386	0.1659	
educ	0.0289111	0.0241153	1.199	0.2306	
age	0.00462188	0.000664820	6.952	3.60e-12 ***	
sigma	1.24090	0.0482896			
-----					
Chi-square(10)	165.4772	p-value		2.39e-30	
Log-likelihood	-1633.032	Akaike criterion		3290.065	

Model 2: Duration (log-normal), using observations 1-1445

Dependent variable: durat

	coefficient	std. error	z	p-value	
-----					
const	4.09939	0.347535	11.80	4.11e-32 ***	
workprg	-0.0625693	0.120037	-0.5213	0.6022	
priors	-0.137253	0.0214587	-6.396	1.59e-10 ***	
tserve <sup>d</sup>	-0.0193306	0.00297792	-6.491	8.51e-11 ***	
felon	0.443995	0.145087	3.060	0.0022 ***	
alcohol	-0.634909	0.144217	-4.402	1.07e-05 ***	
drugs	-0.298159	0.132736	-2.246	0.0247 **	
black	-0.542719	0.117443	-4.621	3.82e-06 ***	
married	0.340682	0.139843	2.436	0.0148 **	
educ	0.0229194	0.0253974	0.9024	0.3668	
age	0.00391028	0.000606205	6.450	1.12e-10 ***	
sigma	1.81047	0.0623022			
-----					
Chi-square(10)	166.7361	p-value		1.31e-30	
Log-likelihood	-1597.059	Akaike criterion		3218.118	

**Example 31.8:** Create plots showing conditional hazards

---

```

open recid.gdt -q

# leave 'married' separate for analysis
list X = workprg priors tserve felon alcohol drugs \
    black educ age

# Weibull variant
duration durat 0 X married ; cens
# coefficients on all Xs apart from married
matrix beta_w = $coeff[1:$ncoeff-2]
# married coefficient
scalar mc_w = $coeff[$ncoeff-1]
scalar s_w = $sigma

# Log-normal variant
duration durat 0 X married ; cens --lognormal
matrix beta_n = $coeff[1:$ncoeff-2]
scalar mc_n = $coeff[$ncoeff-1]
scalar s_n = $sigma

list allX = 0 X
# evaluate X\beta at means of all variables except marriage
scalar Xb_w = meanc({allX}) * beta_w
scalar Xb_n = meanc({allX}) * beta_n

# construct two plot matrices
matrix mat_w = zeros(100, 3)
matrix mat_n = zeros(100, 3)

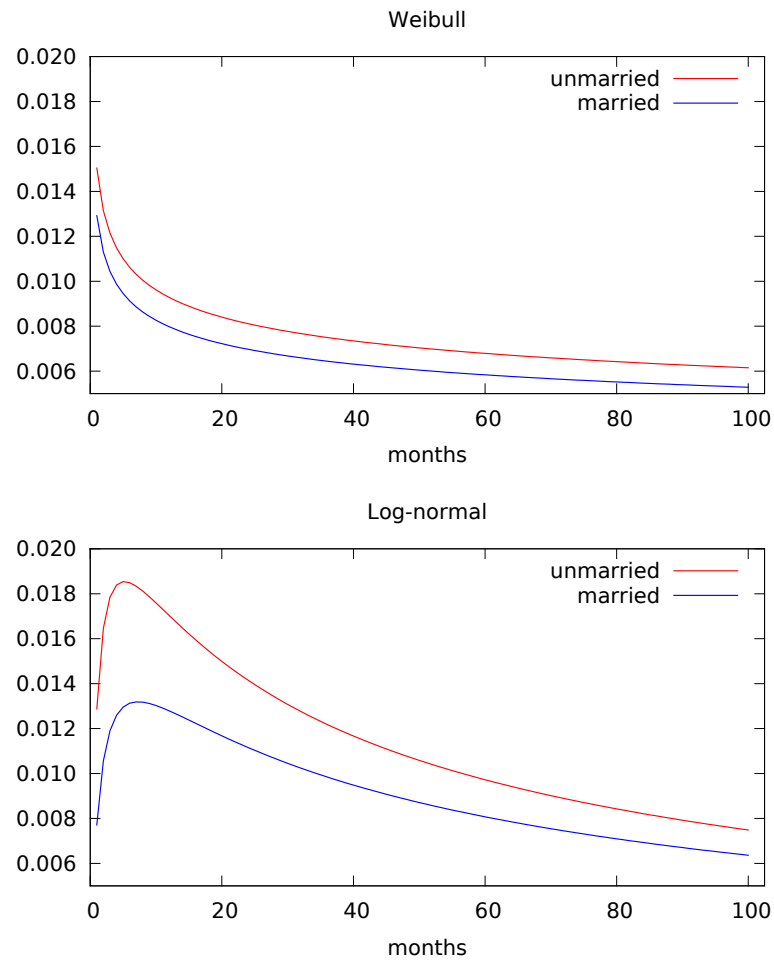
loop t=1..100 -q
    # first column, duration
    mat_w[t, 1] = t
    mat_n[t, 1] = t
    wi_w = (log(t) - Xb_w)/s_w
    wi_n = (log(t) - Xb_n)/s_n
    # second col: hazard with married = 0
    mat_w[t, 2] = (1/t) * exp(wi_w)
    mat_n[t, 2] = (1/t) * pdf(z, wi_n) / cdf(z, -wi_n)
    wi_w = (log(t) - (Xb_w + mc_w))/s_w
    wi_n = (log(t) - (Xb_n + mc_n))/s_n
    # third col: hazard with married = 1
    mat_w[t, 3] = (1/t) * exp(wi_w)
    mat_n[t, 3] = (1/t) * pdf(z, wi_n) / cdf(z, -wi_n)
endloop

colnames(mat_w, "months unmarried married")
colnames(mat_n, "months unmarried married")

gnuplot 2 3 1 --with-lines --supp --matrix=mat_w --output=weibull.plt
gnuplot 2 3 1 --with-lines --supp --matrix=mat_n --output=lognorm.plt

```

---



**Figure 31.1:** Recidivism hazard estimates for married and unmarried ex-convicts

### Alternative representations of the Weibull model

One point to watch out for with the Weibull duration model is that the estimates may be represented in different ways. The representation given by `gretl` is sometimes called the *accelerated failure-time* (AFT) metric. An alternative that one sometimes sees is the *log relative-hazard* metric; in fact this is the metric used in Wooldridge's presentation of the recidivism example. To get from AFT estimates to log relative-hazard form it is necessary to multiply the coefficients by  $-\sigma^{-1}$ . For example, the married coefficient in the Weibull specification as shown here is 0.188104 and  $\hat{\sigma}$  is 1.24090, so the alternative value is  $-0.152$ , which is what Wooldridge shows (2002a, Table 20.1).

### Fitted values and residuals

By default, `gretl` computes fitted values (accessible via `$yhat`) as the conditional mean of duration. The formulae are shown below (where  $\Gamma$  denotes the gamma function, and the exponential variant is just Weibull with  $\sigma = 1$ ).

Weibull	Log-logistic	Log-normal
$\exp(X\beta)\Gamma(1 + \sigma)$	$\exp(X\beta)\frac{\pi\sigma}{\sin(\pi\sigma)}$	$\exp(X\beta + \sigma^2/2)$

The expression given for the log-logistic mean, however, is valid only for  $\sigma < 1$ ; otherwise the expectation is undefined, a point that is not noted in all software.<sup>4</sup>

Alternatively, if the `--medians` option is given, `gretl`'s `duration` command will produce conditional medians as the content of `$yhat`. For the Weibull the median is  $\exp(X\beta)(\log 2)^\sigma$ ; for the log-logistic and log-normal it is just  $\exp(X\beta)$ .

The values we give for the accessor `$uhat` are generalized (Cox-Snell) residuals, computed as the integrated hazard function, which equals the negative of the log of the survivor function:

$$\hat{u}_i = \Lambda(t_i, x_i, \theta) = -\log S(t_i, x_i, \theta)$$

Under the null of correct specification of the model these generalized residuals should follow the unit exponential distribution, which has mean and variance both equal to 1 and density  $e^{-1}$ . See Cameron and Trivedi (2005) for further discussion.

---

<sup>4</sup>The `predict` adjunct to the `streg` command in Stata 10, for example, gaily produces large negative values for the log-logistic mean in duration models with  $\sigma > 1$ .

## Chapter 32

# Quantile regression

### 32.1 Introduction

In Ordinary Least Squares (OLS) regression, the fitted values,  $\hat{y}_i = X_i\hat{\beta}$ , represent the *conditional mean* of the dependent variable — conditional, that is, on the regression function and the values of the independent variables. In median regression, by contrast and as the name implies, fitted values represent the *conditional median* of the dependent variable. It turns out that the principle of estimation for median regression is easily stated (though not so easily computed), namely, choose  $\hat{\beta}$  so as to minimize the sum of absolute residuals. Hence the method is known as Least Absolute Deviations or LAD. While the OLS problem has a straightforward analytical solution, LAD is a linear programming problem.

Quantile regression is a generalization of median regression: the regression function predicts the conditional  $\tau$ -quantile of the dependent variable — for example the first quartile ( $\tau = .25$ ) or the ninth decile ( $\tau = .90$ ).

If the classical conditions for the validity of OLS are satisfied — that is, if the error term is independently and identically distributed, conditional on  $X$  — then quantile regression is redundant: all the conditional quantiles of the dependent variable will march in lockstep with the conditional mean. Conversely, if quantile regression reveals that the conditional quantiles behave in a manner quite distinct from the conditional mean, this suggests that OLS estimation is problematic.

As of version 1.7.5, gretl offers quantile regression functionality (in addition to basic LAD regression, which has been available since early in gretl's history via the `lad` command).<sup>1</sup>

### 32.2 Basic syntax

The basic invocation of quantile regression is

```
quantreg tau reglist
```

where

- *reglist* is a standard gretl regression list (dependent variable followed by regressors, including the constant if an intercept is wanted); and
- *tau* is the desired conditional quantile, in the range 0.01 to 0.99, given either as a numerical value or the name of a pre-defined scalar variable (but see below for a further option).

Estimation is via the Frisch–Newton interior point solver (Portnoy and Koenker, 1997), which is substantially faster than the “traditional” Barrodale–Roberts (1974) simplex approach for large problems.

---

<sup>1</sup>We gratefully acknowledge our borrowing from the `quantreg` package for GNU R (version 4.17). The core of the `quantreg` package is composed of Fortran code written by Roger Koenker; this is accompanied by various driver and auxiliary functions written in the R language by Koenker and Martin Mächler. The latter functions have been re-worked in C for gretl. We have added some guards against potential numerical problems in small samples.

By default, standard errors are computed according to the asymptotic formula given by [Koenker and Bassett \(1978\)](#). Alternatively, if the `--robust` option is given, we use the sandwich estimator developed in [Koenker and Zhao \(1994\)](#).<sup>2</sup>

### 32.3 Confidence intervals

An option `--intervals` is available. When this is given we print confidence intervals for the parameter estimates instead of standard errors. These intervals are computed using the rank inversion method and in general they are asymmetrical about the point estimates — that is, they are not simply “plus or minus so many standard errors”. The specifics of the calculation are inflected by the `--robust` option: without this, the intervals are computed on the assumption of IID errors ([Koenker, 1994](#)); with it, they use the heteroskedasticity-robust estimator developed by [Koenker and Machado \(1999\)](#).

By default, 90 percent intervals are produced. You can change this by appending a confidence value (expressed as a decimal fraction) to the intervals option, as in

```
quantreg tau reglist --intervals=.95
```

When the confidence intervals option is selected, the parameter estimates are calculated using the Barrodale–Roberts method. This is simply because the Frisch–Newton code does not currently support the calculation of confidence intervals.

Two further details. First, the mechanisms for generating confidence intervals for quantile estimates require that the model has at least two regressors (including the constant). If the `--intervals` option is given for a model containing only one regressor, an error is flagged. Second, when a model is estimated in this mode, you can retrieve the confidence intervals using the accessor `$coeff_ci`. This produces a  $k \times 2$  matrix, where  $k$  is the number of regressors. The lower bounds are in the first column, the upper bounds in the second. See also section 32.5 below.

### 32.4 Multiple quantiles

As a further option, you can give *tau* as a matrix — either the name of a predefined matrix or in numerical form, as in `{.05, .25, .5, .75, .95}`. The given model is estimated for all the  $\tau$  values and the results are printed in a special form, as shown below (in this case the `--intervals` option was also given).

Model 1: Quantile estimates using the 235 observations 1-235

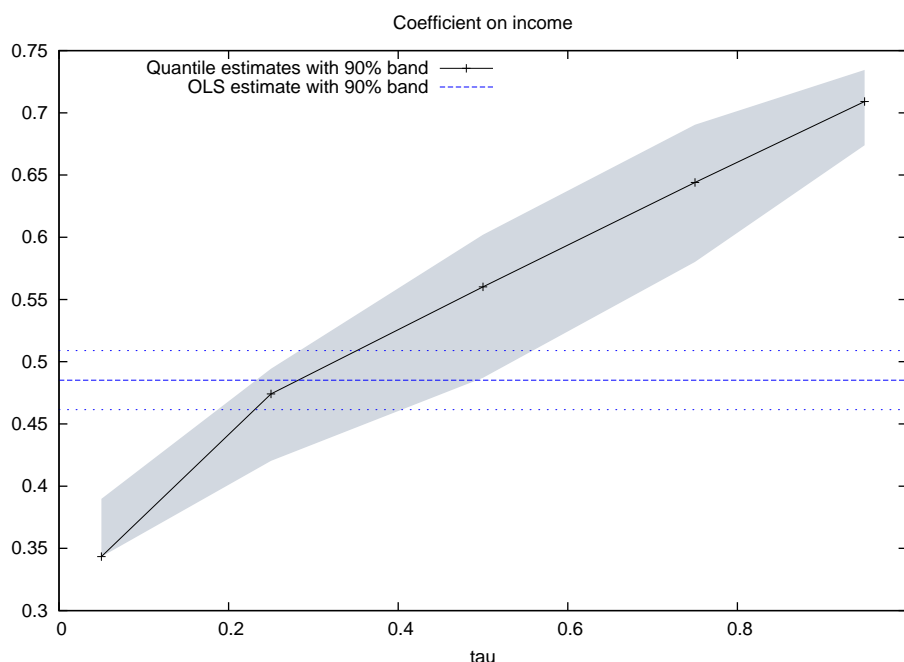
Dependent variable: foodexp

With 90 percent confidence intervals

VARIABLE	TAU	COEFFICIENT	LOWER	UPPER
const	0.05	124.880	98.3021	130.517
	0.25	95.4835	73.7861	120.098
	0.50	81.4822	53.2592	114.012
	0.75	62.3966	32.7449	107.314
	0.95	64.1040	46.2649	83.5790
income	0.05	0.343361	0.343327	0.389750
	0.25	0.474103	0.420330	0.494329
	0.50	0.560181	0.487022	0.601989
	0.75	0.644014	0.580155	0.690413
	0.95	0.709069	0.673900	0.734441

<sup>2</sup>These correspond to the `iid` and `nid` options in R's `quantreg` package, respectively.





**Figure 32.1:** Regression of food expenditure on income; Engel's data

The `gretl` GUI has an entry for Quantile Regression (under `/Model/Robust estimation`), and you can select multiple quantiles there too. In that context, just give space-separated numerical values (as per the predefined options, shown in a drop-down list).

When you estimate a model in this way most of the standard menu items in the model window are disabled, but one extra item is available — graphs showing the  $\tau$  sequence for a given coefficient in comparison with the OLS coefficient. An example is shown in Figure 32.1. This sort of graph provides a simple means of judging whether quantile regression is redundant (OLS is fine) or informative.

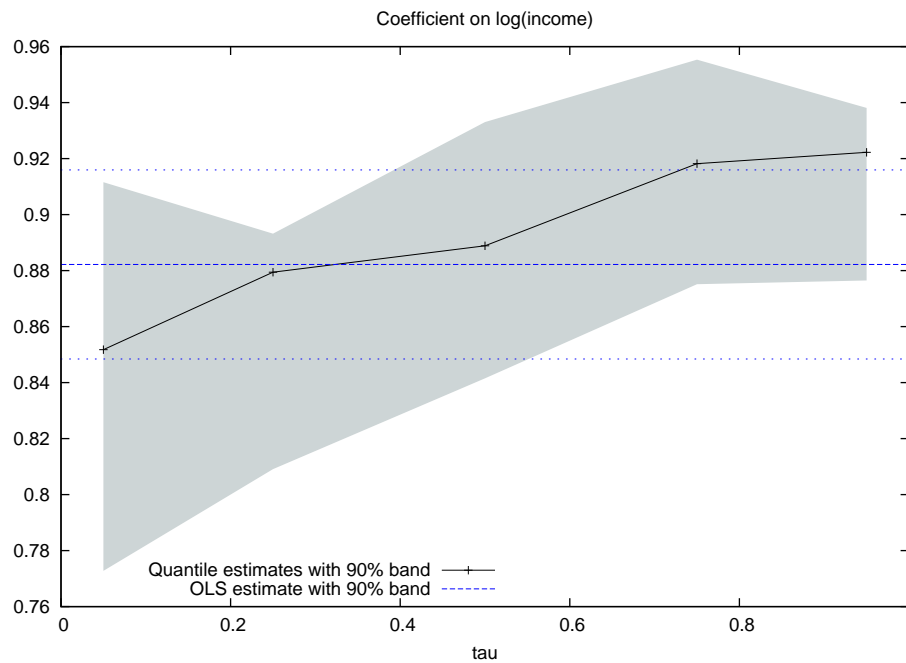
In the example shown — based on data on household income and food expenditure gathered by Ernst Engel (1821–1896) — it seems clear that simple OLS regression is potentially misleading. The “crossing” of the OLS estimate by the quantile estimates is very marked.

However, it is not always clear what implications should be drawn from this sort of conflict. With the Engel data there are two issues to consider. First, Engel's famous “law” claims an income-elasticity of food consumption that is less than one, and talk of elasticities suggests a logarithmic formulation of the model. Second, there are two apparently anomalous observations in the data set: household 105 has the third-highest income but unexpectedly low expenditure on food (as judged from a simple scatter plot), while household 138 (which also has unexpectedly low food consumption) has much the highest income, almost twice that of the next highest.

With  $n = 235$  it seems reasonable to consider dropping these observations. If we do so, and adopt a log-log formulation, we get the plot shown in Figure 32.2. The quantile estimates still cross the OLS estimate, but the “evidence against OLS” is much less compelling: the 90 percent confidence bands of the respective estimates overlap at all the quantiles considered.

### 32.5 Large datasets

As noted above, when you give the `--intervals` option with the `quantreg` command, which calls for estimation of confidence intervals via rank inversion, `gretl` switches from the default Frisch-Newton algorithm to the Barrodale–Roberts simplex method.



**Figure 32.2:** Log-log regression; 2 observations dropped from full Engel data set.

This is OK for moderately large datasets (up to, say, a few thousand observations) but on very large problems the simplex algorithm may become seriously bogged down. For example, [Koenker and Hallock \(2001\)](#) present an analysis of the determinants of birth weights, using 198377 observations and with 15 regressors. Generating confidence intervals via Barrodale–Roberts for a single value of  $\tau$  took about half an hour on a Lenovo Thinkpad T60p with 1.83GHz Intel Core 2 processor.

If you want confidence intervals in such cases, you are advised not to use the `--intervals` option, but to compute them using the method of “plus or minus so many standard errors”. (One Frisch–Newton run took about 8 seconds on the same machine, showing the superiority of the interior point method.) The script below illustrates:

```
quantreg .10 y 0 xlist
scalar crit = qnorm(.95)
matrix ci = $coeff - crit * $stderr
ci = ci~($coeff + crit * $stderr)
print ci
```

The matrix `ci` will contain the lower and upper bounds of the (symmetrical) 90 percent confidence intervals.

To avoid a situation where `gretl` becomes unresponsive for a very long time we have set the maximum number of iterations for the Barrodale–Roberts algorithm to the (somewhat arbitrary) value of 1000. We will experiment further with this, but for the meantime if you really want to use this method on a large dataset, and don’t mind waiting for the results, you can increase the limit using the `set` command with parameter `rq_maxiter`, as in

```
set rq_maxiter 5000
```

## Chapter 33

# Nonparametric methods

The main focus of `gretl` is on parametric estimation, but we offer a selection of nonparametric methods. The most basic of these

- various tests for difference in distribution (Sign test, Wilcoxon rank-sum test, Wilcoxon signed-rank test);
- the Runs test for randomness; and
- nonparametric measures of association: Spearman's rho and Kendall's tau.

Details on the above can be found by consulting the help for the commands `diffstest`, `runs`, `corr` and `spearman`. In the GUI program these items are found under the Tools menu and the Robust estimation item under the Model menu.

In this chapter we concentrate on two relatively complex methods for nonparametric curve-fitting and prediction, namely William Cleveland's "loess" (also known as "lowess") and the Nadaraya-Watson estimator.

### 33.1 Locally weighted regression (loess)

Loess (Cleveland, 1979) is a nonparametric smoother employing locally weighted polynomial regression. It is intended to yield an approximation to  $g(\cdot)$  when the dependent variable,  $y$ , can be expressed as

$$y_i = g(x_i) + \epsilon_i$$

for some smooth function  $g(\cdot)$ .

Given a sample of  $n$  observations on the variables  $y$  and  $x$ , the procedure is to run a weighted least squares regression (a polynomial of order  $d = 0, 1$  or  $2$  in  $x$ ) localized to each data point,  $i$ . In each such regression the sample consists of the  $r$  nearest neighbors (in the  $x$  dimension) to the point  $i$ , with weights that are inversely related to the distance  $|x_i - x_k|$ ,  $k = 1, \dots, r$ . The predicted value  $\hat{y}_i$  is then obtained by evaluating the estimated polynomial at  $x_i$ . The most commonly used order is  $d = 1$ .

A bandwidth parameter  $0 < q \leq 1$  controls the proportion of the total number of data points used in each regression; thus  $r = qn$  (rounded up to an integer). Larger values of  $q$  lead to a smoother fitted series, smaller values to a series that tracks the actual data more closely;  $0.25 \leq q \leq 0.5$  is often a suitable range.

In `gretl`'s implementation of loess the weighting scheme is that given by Cleveland, namely,

$$w_k(x_i) = W(h_i^{-1}(x_k - x_i))$$

where  $h_i$  is the distance between  $x_i$  and its  $r^{\text{th}}$  nearest neighbor, and  $W(\cdot)$  is the tricube function,

$$W(x) = \begin{cases} (1 - |x|^3)^3 & \text{for } |x| < 1 \\ 0 & \text{for } |x| \geq 1 \end{cases}$$

The local regression can be made robust via an adjustment based on the residuals,  $e_i = y_i - \hat{y}_i$ . Robustness weights,  $\delta_k$ , are defined by

$$\delta_k = B(e_k/6s)$$

where  $s$  is the median of the  $|e_i|$  and  $B(\cdot)$  is the bisquare function,

$$B(x) = \begin{cases} (1 - x^2)^2 & \text{for } |x| < 1 \\ 0 & \text{for } |x| \geq 1 \end{cases}$$

The polynomial regression is then re-run using weight  $\delta_k w_k(x_i)$  at  $(x_k, y_k)$ .

The `loess()` function in `gretl` takes up to five arguments as follows: the  $y$  series, the  $x$  series, the order  $d$ , the bandwidth  $q$ , and a boolean switch to turn on the robust adjustment. The last three arguments are optional: if they are omitted the default values are  $d = 1$ ,  $q = 0.5$  and no robust adjustment. An example of a full call to `loess()` is shown below; in this case a quadratic in  $x$  is specified, three quarters of the data points will be used in each local regression, and robustness is turned on:

```
series yh = loess(y, x, 2, 0.75, 1)
```

An illustration of loess is provided in Example 33.1: we generate a series that has a deterministic sine wave component overlaid with noise uniformly distributed on  $(-1, 1)$ . Loess is then used to retrieve a good approximation to the sine function. The resulting graph is shown in Figure 33.1.

#### Example 33.1: Loess script

---

```
nulldata 120
series x = index
scalar n = $nobs
series y = sin(2*pi*x/n) + uniform(-1, 1)
series yh = loess(y, x, 2, 0.75, 0)
gnuplot y yh x --output=display --with-lines=yh
```

---

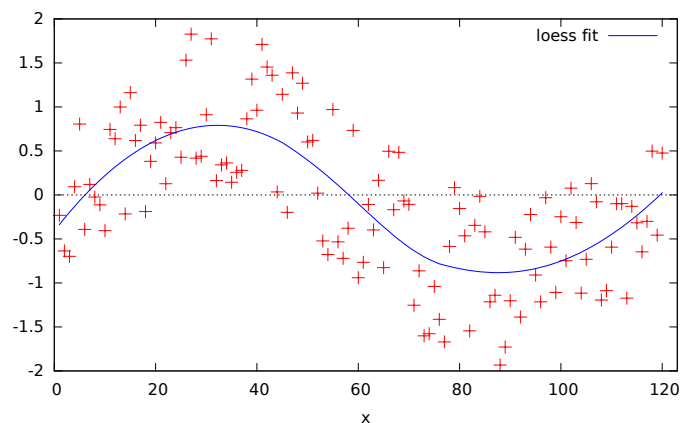


Figure 33.1: Loess: retrieving a sine wave

### 33.2 The Nadaraya–Watson estimator

The Nadaraya–Watson nonparametric estimator (Nadaraya, 1964; Watson, 1964) is an estimator for the conditional mean of a variable  $Y$ , available in a sample of size  $n$ , for a given value of a conditioning variable  $X$ , and is defined as

$$m(X) = \frac{\sum_{j=1}^n y_j \cdot K_h(X - x_j)}{\sum_{j=1}^n K_h(X - x_j)}$$

where  $K_h(\cdot)$  is the so-called *kernel function*, which is usually some simple transform of a density function that depends on a scalar called the *bandwidth*. The one `gretl` uses is given by

$$K_h(x) = \exp\left(-\frac{x^2}{2h}\right)$$

for  $|x| < \tau$  and zero otherwise. The scalar  $\tau$  is used to prevent numerical problems when the kernel function is evaluated too far away from zero and is called the trim parameter.

#### Example 33.2: Nadaraya–Watson example

---

```
# Nonparametric regression example: husband's age on wife's age
open mroz87.gdt

# initial value for the bandwidth
scalar h = $nobs^(-0.2)
# three increasingly smoother estimates
series m0 = nadarwat(HA, WA, h)
series m1 = nadarwat(HA, WA, h * 5)
series m2 = nadarwat(HA, WA, h * 10)

# produce the graph
dataset sortby WA
gnuplot m0 m1 m2 HA WA --output=display --with=lines
```

---

Example 33.2 produces the graph shown in Figure 33.2 (after some slight editing).

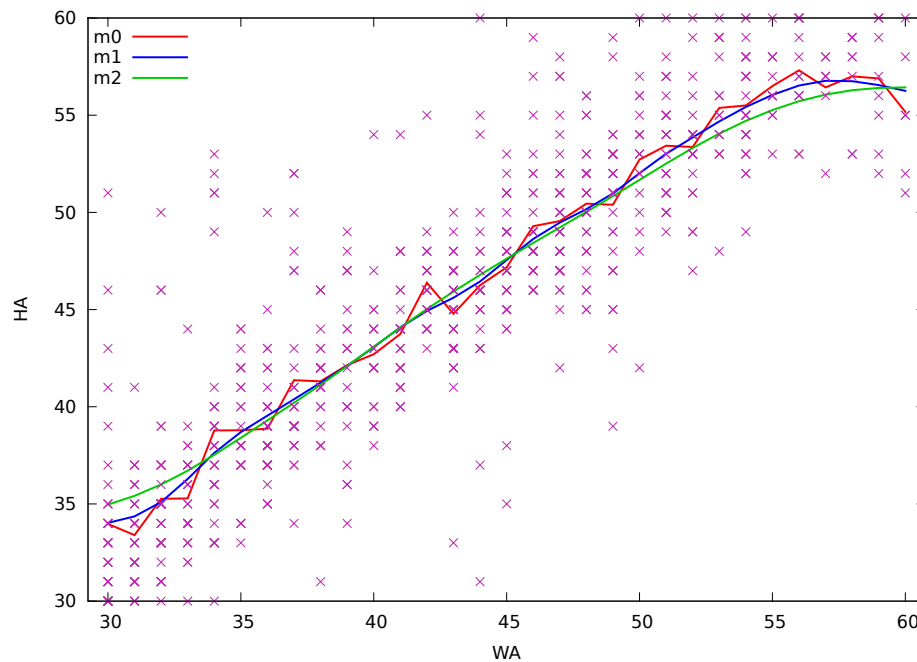
The choice of the bandwidth is up to the user: larger values of  $h$  lead to a smoother  $m(\cdot)$  function; smaller values make the  $m(\cdot)$  function follow the  $y_i$  values more closely, so that the function appears more “jagged”. In fact, as  $h \rightarrow \infty$ ,  $m(x_i) \rightarrow \bar{Y}$ ; on the contrary, if  $h \rightarrow 0$ , observations for which  $x_i \neq X$  are not taken into account at all when computing  $m(X)$ .

Also, the statistical properties of  $m(\cdot)$  vary with  $h$ : its variance can be shown to be decreasing in  $h$ , while its squared bias is increasing in  $h$ . It can be shown that choosing  $h \sim n^{-1/5}$  minimizes the RMSE, so that value is customarily taken as a reference point.

Note that the kernel function has its tails “trimmed”. The scalar  $\tau$ , which controls the level at which trimming occurs is set by default at  $4 \cdot h$ ; this setting, however, may be changed via the `set` command. For example,

```
set nadarwat_trim 10
```

sets  $\tau = 10 \cdot h$ . This may at times produce more sensible results in regions of  $X$  with sparse support; however, you should be aware that in those same cases machine precision (division by numerical zero) may render your results spurious. The default is relatively safe, but experimenting with larger values may be a sensible strategy in some cases.



**Figure 33.2:** Nadaraya-Watson example for several choices of the bandwidth parameter

A common variant of the Nadaraya-Watson estimator is the so-called “leave-one-out” estimator: this is a variant of the estimator that does not use the  $i$ -th observation for evaluating  $m(x_i)$ . This makes the estimator more robust numerically and its usage is often advised for inference purposes. In formulae, the leave-one-out estimator is

$$m(x_i) = \frac{\sum_{j \neq i} y_j \cdot K_h(x_i - x_j)}{\sum_{j \neq i} K_h(x_i - x_j)}$$

In order to have `gretl` compute the leave-one-out estimator, just reverse the sign of  $h$ : if we changed example 33.2 by substituting

```
scalar h = $nobs^(-0.2)
```

with

```
scalar h = -($nobs^(-0.2))
```

the rest of the example would have stayed unchanged, the only difference being the usage of the leave-one-out estimator.

Although  $X$  could be, in principle, any value, in the typical usage of this estimator you want to compute  $m(X)$  for  $X$  equal to one or more values actually observed in your sample, that is  $m(x_i)$ . If you need a point estimate of  $m(X)$  for some value of  $X$  which is not present among the valid observations of your dependent variable, you may want to add some “fake” observations to your dataset in which  $y$  is missing and  $x$  contains the values you want  $m(x)$  evaluated at. For example, the following script evaluates  $m(x)$  at regular intervals between -2.0 and 2.0:

```
nulldata 120
set seed 120496

# first part of the sample: actual data
smpl 1 100
```

```

x = normal()
y = x^2 + sin(x) + normal()

# second part of the sample: fake x data
smp1 101 120
x = (obs-110) / 5

# compute the Nadaraya-Watson estimate
# with bandwidth equal to 0.4 (note that
#  $100^{(-0.2)} = 0.398$ )
smp1 full
m = nadarwat(y, x, 0.4)

# show m(x) for the fake x values only
smp1 101 120
print x m -o

```

and running it produces

	x	m
101	-1.8	1.165934
102	-1.6	0.730221
103	-1.4	0.314705
104	-1.2	0.026057
105	-1.0	-0.131999
106	-0.8	-0.215445
107	-0.6	-0.269257
108	-0.4	-0.304451
109	-0.2	-0.306448
110	0.0	-0.238766
111	0.2	-0.038837
112	0.4	0.354660
113	0.6	0.908178
114	0.8	1.485178
115	1.0	2.000003
116	1.2	2.460100
117	1.4	2.905176
118	1.6	3.380874
119	1.8	3.927682
120	2.0	4.538364

## **Part III**

# **Technical details**



## Chapter 34

# Gretl and T<sub>E</sub>X

### 34.1 Introduction

T<sub>E</sub>X — initially developed by Donald Knuth of Stanford University and since enhanced by hundreds of contributors around the world — is the gold standard of scientific typesetting. Gretl provides various hooks that enable you to preview and print econometric results using the T<sub>E</sub>X engine, and to save output in a form suitable for further processing with T<sub>E</sub>X.

This chapter explains the finer points of gretl's T<sub>E</sub>X-related functionality. The next section describes the relevant menu items; section 34.3 discusses ways of fine-tuning T<sub>E</sub>X output; and section 34.4 gives some pointers on installing (and learning) T<sub>E</sub>X if you do not already have it on your computer. (Just to be clear: T<sub>E</sub>X is not included with the gretl distribution; it is a separate package, including several programs and a large number of supporting files.)

Before proceeding, however, it may be useful to set out briefly the stages of production of a final document using T<sub>E</sub>X. For the most part you don't have to worry about these details, since, in regard to previewing at any rate, gretl handles them for you. But having some grasp of what is going on behind the scenes will enable you to understand your options better.

The first step is the creation of a plain text “source” file, containing the text or mathematics to be typeset, interspersed with mark-up that defines how it should be formatted. The second step is to run the source through a processing engine that does the actual formatting. Typically this is either:

- a program called latex that generates so-called DVI (device-independent) output, or
- (more commonly nowadays) a program called pdflatex that generates PDF output.<sup>1</sup>

For previewing, one uses either a DVI viewer (typically xdvi on GNU/Linux systems) or a PDF viewer (for example, Adobe's Acrobat Reader or xpdf), depending on how the source was processed. If the DVI route is taken, there's then a third step to produce printable output, typically using the program dvips to generate a PostScript file. If the PDF route is taken, the output is ready for printing without any further processing.

On MS Windows and Mac OS X, gretl calls pdflatex to process the source file, and expects the operating system to be able to find the default viewer for PDF output; DVI is not supported. On GNU/Linux the default is also to produce PDF, but if you prefer the DVI/PostScript route you can do the following: select the menu item “Tools, Preferences, General” then the “Programs” tab. Find the item titled “Command to compile TeX files”, and set this to latex. In the same window, Make sure the commands to view DVI and PostScript files are set to something appropriate for your system.

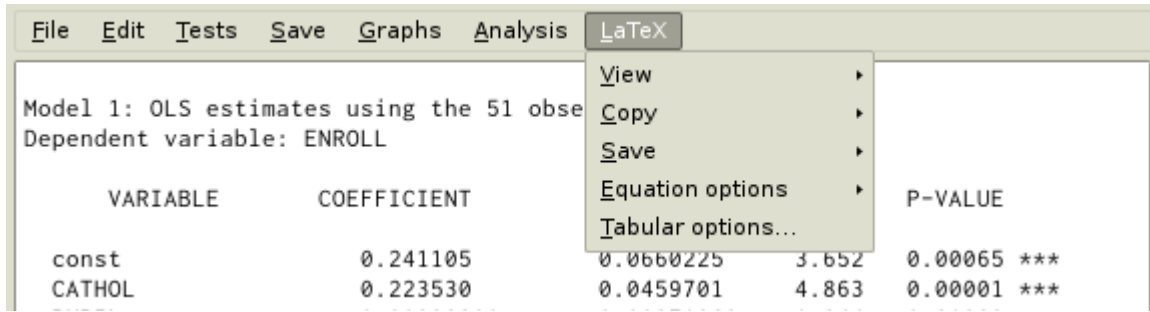
### 34.2 T<sub>E</sub>X-related menu items

#### The model window

The fullest T<sub>E</sub>X support in gretl is found in the GUI model window. This has a menu item titled “LaTeX” with sub-items “View”, “Copy”, “Save” and “Equation options” (see Figure 34.1).

---

<sup>1</sup>Experts will be aware of something called “plain T<sub>E</sub>X”, which is processed using the program tex. The great majority of T<sub>E</sub>X users, however, use the L<sup>A</sup>T<sub>E</sub>X macros, initially developed by Leslie Lamport. Gretl does not support plain T<sub>E</sub>X.

**Figure 34.1:** L<sup>A</sup>T<sub>E</sub>X menu in model window

The first three sub-items have branches titled “Tabular” and “Equation”. By “Tabular” we mean that the model is represented in the form of a table; this is the fullest and most explicit presentation of the results. See Table 34.1 for an example; this was pasted into the manual after using the “Copy, Tabular” item in gretl (a few lines were edited out for brevity).

**Table 34.1:** Example of L<sup>A</sup>T<sub>E</sub>X tabular output

Model 1: OLS estimates using the 51 observations 1-51  
Dependent variable: ENROLL

Variable	Coefficient	Std. Error	t-statistic	p-value
const	0.241105	0.0660225	3.6519	0.0007
CATHOL	0.223530	0.0459701	4.8625	0.0000
PUPIL	-0.00338200	0.00271962	-1.2436	0.2198
WHITE	-0.152643	0.0407064	-3.7499	0.0005
Mean of dependent variable			0.0955686	
S.D. of dependent variable			0.0522150	
Sum of squared residuals			0.0709594	
Standard error of residuals ( $\hat{\sigma}$ )			0.0388558	
Unadjusted $R^2$			0.479466	
Adjusted $\bar{R}^2$			0.446241	
$F(3, 47)$			14.4306	

The “Equation” option is fairly self-explanatory — the results are written across the page in equation format, as below:

$$\widehat{\text{ENROLL}} = 0.241105 + 0.223530 \text{ CATHOL} - 0.00338200 \text{ PUPIL} - 0.152643 \text{ WHITE}$$

$(0.066022) \quad (0.04597) \quad (0.0027196) \quad (0.040706)$   
 $T = 51 \quad \bar{R}^2 = 0.4462 \quad F(3, 47) = 14.431 \quad \hat{\sigma} = 0.038856$   
 (standard errors in parentheses)

The distinction between the “Copy” and “Save” options (for both tabular and equation) is twofold. First, “Copy” puts the T<sub>E</sub>X source on the clipboard while with “Save” you are prompted for the name of a file into which the source should be saved. Second, with “Copy” the material is copied as a

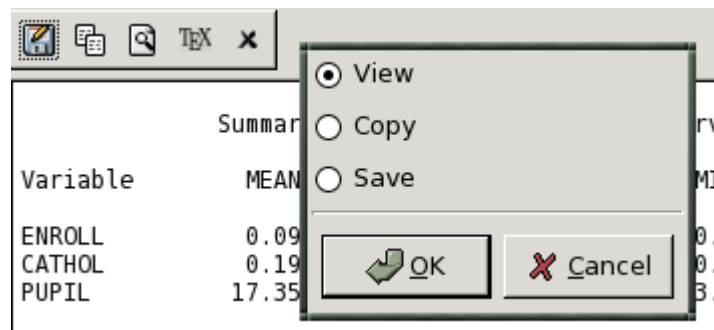
“fragment” while with “Save” it is written as a complete file. The point is that a well-formed T<sub>E</sub>X source file must have a header that defines the `documentclass` (article, report, book or whatever) and tags that say `\begin{document}` and `\end{document}`. This material is included when you do “Save” but not when you do “Copy”, since in the latter case the expectation is that you will paste the data into an existing T<sub>E</sub>X source file that already has the relevant apparatus in place.

The items under “Equation options” should be self-explanatory: when printing the model in equation form, do you want standard errors or *t*-ratios displayed in parentheses under the parameter estimates? The default is to show standard errors; if you want *t*-ratios, select that item.

### Other windows

Several other sorts of output windows also have T<sub>E</sub>X preview, copy and save enabled. In the case of windows having a graphical toolbar, look for the T<sub>E</sub>X button. Figure 34.2 shows this icon (second from the right on the toolbar) along with the dialog that appears when you press the button.

Figure 34.2: T<sub>E</sub>X icon and dialog



One aspect of gretl’s T<sub>E</sub>X support that is likely to be particularly useful for publication purposes is the ability to produce a typeset version of the “model table” (see section 3.4). An example of this is shown in Table 34.2.

### 34.3 Fine-tuning typeset output

There are three aspects to this: adjusting the appearance of the output produced by gretl in L<sup>A</sup>T<sub>E</sub>X preview mode; adjusting the formatting of gretl’s tabular output for models when using the `tabprint` command; and incorporating gretl’s output into your own T<sub>E</sub>X files.

#### Previewing in the GUI

As regards *preview mode*, you can control the appearance of gretl’s output using a file named `gretlpre.tex`, which should be placed in your gretl user directory (see the *Gretl Command Reference*). If such a file is found, its contents will be used as the “preamble” to the T<sub>E</sub>X source. The default value of the preamble is as follows:

```
\documentclass[11pt]{article}
\usepackage[utf8]{inputenc}
\usepackage{amsmath}
\usepackage{dcolumn,longtable}
\begin{document}
\thispagestyle{empty}
```

**Table 34.2:** Example of model table output

OLS estimates			
Dependent variable: ENROLL			
	Model 1	Model 2	Model 3
const	0.2907** (0.07853)	0.2411** (0.06602)	0.08557 (0.05794)
CATHOL	0.2216** (0.04584)	0.2235** (0.04597)	0.2065** (0.05160)
PUPIL	−0.003035 (0.002727)	−0.003382 (0.002720)	−0.001697 (0.003025)
WHITE	−0.1482** (0.04074)	−0.1526** (0.04071)	
ADMEXP	−0.1551 (0.1342)		
<i>n</i>	51	51	51
$\bar{R}^2$	0.4502	0.4462	0.2956
$\ell$	96.09	95.36	88.69

Standard errors in parentheses

\* indicates significance at the 10 percent level

\*\* indicates significance at the 5 percent level

Note that the `amsmath` and `dcolumn` packages are required. (For some sorts of output the `longtable` package is also needed.) Beyond that you can, for instance, change the type size or the font by altering the `documentclass` declaration or including an alternative font package.

In addition, if you wish to typeset `gretl` output in more than one language, you can set up per-language preamble files. A “localized” preamble file is identified by a name of the form `gretlpre_xx.tex`, where `xx` is replaced by the first two letters of the current setting of the `LANG` environment variable. For example, if you are running the program in Polish, using `LANG=pl_PL`, then `gretl` will do the following when writing the preamble for a T<sub>E</sub>X source file.

1. Look for a file named `gretlpre_pl.tex` in the `gretl` user directory. If this is not found, then
2. look for a file named `gretlpre.tex` in the `gretl` user directory. If this is not found, then
3. use the default preamble.

Conversely, suppose you usually run `gretl` in a language other than English, and have a suitable `gretlpre.tex` file in place for your native language. If on some occasions you want to produce T<sub>E</sub>X output in English, then you could create an additional file `gretlpre_en.tex`: this file will be used for the preamble when `gretl` is run with a language setting of, say, `en_US`.

### Command-line options

After estimating a model via a script — or interactively via the `gretl` console or using the command-line program `gretlcli` — you can use the commands `tabprint` or `eqnprint` to print the model to file in tabular format or equation format respectively. These options are explained in the *Gretl Command Reference*.

If you wish alter the appearance of `gretl`’s tabular output for models in the context of the `tabprint` command, you can specify a custom row format using the `--format` flag. The format string must be enclosed in double quotes and must be tied to the flag with an equals sign. The pattern for the format string is as follows. There are four fields, representing the coefficient, standard error, *t*-ratio and *p*-value respectively. These fields should be separated by vertical bars; they may contain a `printf`-type specification for the formatting of the numeric value in question, or may be left blank to suppress the printing of that column (subject to the constraint that you can’t leave all the columns blank). Here are a few examples:

```
--format="%.4f|%.4f|%.4f|%.4f"
--format="%.4f|%.4f|%.3f|"
--format="%.5f|%.4f| |%.4f"
--format="%.8g|%.8g| |%.4f"
```

The first of these specifications prints the values in all columns using 4 decimal places. The second suppresses the *p*-value and prints the *t*-ratio to 3 places. The third omits the *t*-ratio. The last one again omits the *t*, and prints both coefficient and standard error to 8 significant figures.

Once you set a custom format in this way, it is remembered and used for the duration of the `gretl` session. To revert to the default formatting you can use the special variant `--format=default`.

### Further editing

Once you have pasted `gretl`’s T<sub>E</sub>X output into your own document, or saved it to file and opened it in an editor, you can of course modify the material in any wish you wish. In some cases, machine-generated T<sub>E</sub>X is hard to understand, but `gretl`’s output is intended to be human-readable and -editable. In addition, it does not use any non-standard style packages. Besides the standard L<sup>A</sup>T<sub>E</sub>X document classes, the only files needed are, as noted above, the `amsmath`, `dcolumn` and `longtable` packages. These should be included in any reasonably full T<sub>E</sub>X implementation.

### 34.4 Installing and learning T<sub>E</sub>X

This is not the place for a detailed exposition of these matters, but here are a few pointers.

So far as we know, every GNU/Linux distribution has a package or set of packages for T<sub>E</sub>X, and in fact these are likely to be installed by default. Check the documentation for your distribution. For MS Windows, several packaged versions of T<sub>E</sub>X are available: one of the most popular is MiK<sub>T</sub><sub>E</sub>X at <http://www.miktex.org/>. For Mac OS X a nice implementation is i<sub>T</sub><sub>E</sub>XMac, at <http://itexmac.sourceforge.net/>. An essential starting point for online T<sub>E</sub>X resources is the Comprehensive T<sub>E</sub>X Archive Network (CTAN) at <http://www.ctan.org/>.

As for learning T<sub>E</sub>X, many useful resources are available both online and in print. Among online guides, Tony Roberts' "L<sub>A</sub>T<sub>E</sub>X: from quick and dirty to style and finesse" is very helpful, at

<http://www.sci.usq.edu.au/staff/robertsa/LaTeX/latexintro.html>

An excellent source for advanced material is *The L<sub>A</sub>T<sub>E</sub>X Companion* (Goossens *et al.*, 2004).

## Chapter 35

# Gretl and R

### 35.1 Introduction

R is, by far, the largest free statistical project.<sup>1</sup> Like gretl, it is a GNU project and the two have a lot in common; however, gretl's approach focuses on ease of use much more than R, which instead aims to encompass the widest possible range of statistical procedures.

As is natural in the free software ecosystem, we don't view ourselves as competitors to R,<sup>2</sup> but rather as projects sharing a common goal who should support each other whenever possible. For this reason, gretl provides a way to interact with R and thus enable users to pool the capabilities of the two packages.

In this chapter, we will explain how to exploit R's power from within gretl. We assume that the reader has a working installation of R available and a basic grasp of R's syntax.<sup>3</sup>

Despite several valiant attempts, no graphical shell has gained wide acceptance in the R community: by and large, the standard method of working with R is by writing scripts, or by typing commands at the R prompt, much in the same way as one would write gretl scripts or work with the gretl console. In this chapter, the focus will be on the methods available to execute R commands without leaving gretl.

### 35.2 Starting an interactive R session

The easiest way to use R from gretl is in interactive mode. Once you have your data loaded in gretl, you can select the menu item "Tools, Start GNU R" and an interactive R session will be started, with your dataset automatically pre-loaded.

#### A simple example: OLS on cross-section data

For this example we use Ramanathan's dataset data4-1, one of the sample files supplied with gretl. We first run, in gretl, an OLS regression of price on sqft, bedrms and baths. The basic results are shown in Table 35.1.

Table 35.1: OLS house price regression via gretl

Variable	Coefficient	Std. Error	t-statistic	p-value
const	129.062	88.3033	1.4616	0.1746
sqft	0.154800	0.0319404	4.8465	0.0007
bedrms	-21.587	27.0293	-0.7987	0.4430
baths	-12.192	43.2500	-0.2819	0.7838

<sup>1</sup>R's homepage is at <http://www.r-project.org/>.

<sup>2</sup>OK, who are we kidding? But it's *friendly* competition!

<sup>3</sup>The main reference for R documentation is <http://cran.r-project.org/manuals.html>. In addition, R tutorials abound on the Net; as always, Google is your friend.

We will now replicate the above results using R. Select the menu item “Tools, Start GNU R”. A window similar to the one shown in figure 35.1 should appear.

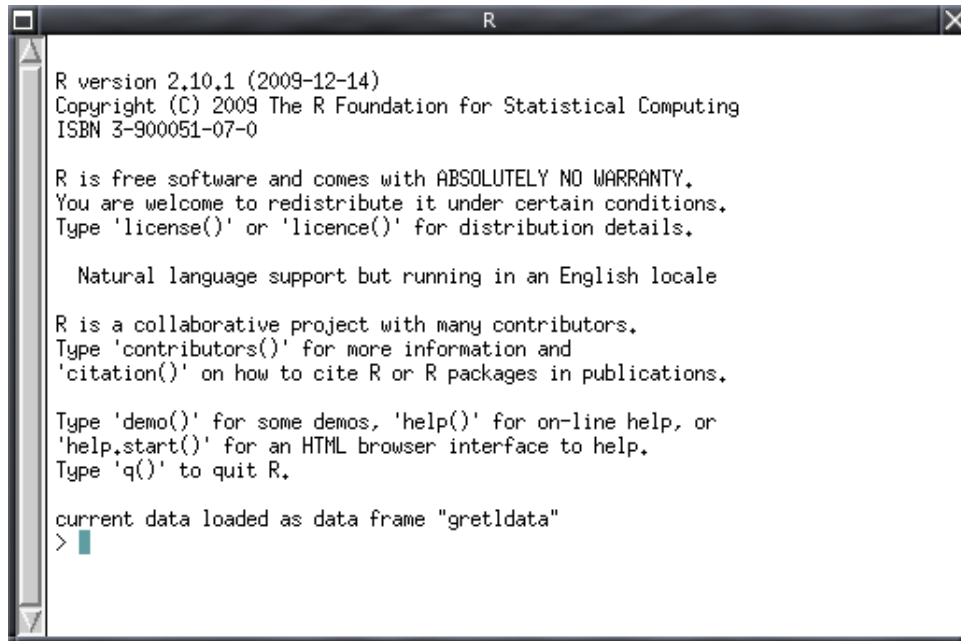


Figure 35.1: R window

The actual look of the R window may be somewhat different from what you see in Figure 35.1 (especially for Windows users), but this is immaterial. The important point is that you have a window where you can type commands to R. If the above procedure doesn't work and no R window opens, it means that gretl was unable to launch R. You should ensure that R is installed and working on your system and that gretl knows where it is. The relevant settings can be found by selecting the “Tools, Preferences, General” menu entry, under the “Programs” tab.

Assuming R was launched successfully, you will see notification that the data from gretl are available. In the background, gretl has arranged for two R commands to be executed, one to load the gretl dataset in the form of a *data frame* (one of several forms in which R can store data) and one to *attach* the data so that the variable names defined in the gretl workspace are available as valid identifiers within R.

In order to replicate gretl's OLS estimation, go into the R window and type at the prompt

```
model <- lm(price ~ sqft + bedrms + baths)
summary(model)
```

You should see something similar to Figure 35.2. Surprise — the estimates coincide! To get out, just close the R window or type `q()` at the R prompt.

### Time series data

We now turn to an example which uses time series data: we will compare gretl's and R's estimates of Box and Jenkins' immortal “airline” model. The data are contained in the `bjg` sample dataset. The following gretl code

```
open bjg
arima 0 1 1 ; 0 1 1 ; lg --nc
```

produces the estimates shown in Table 35.2.



```

> model <- lm(price ~ sqft + bedrms + baths)
> summary(model)

Call:
lm(formula = price ~ sqft + bedrms + baths)

Residuals:
    Min       1Q   Median       3Q      Max
-55.533 -16.219  -6.093   22.432   68.703

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) 129.06163   88.30326   1.462 0.174559
sqft         0.15480    0.03194   4.847 0.000675 ***
bedrms      -21.58752   27.02933  -0.799 0.443037
baths       -12.19276   43.25000  -0.282 0.783758
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 40.87 on 10 degrees of freedom
Multiple R-squared:  0.836,    Adjusted R-squared:  0.7868
F-statistic: 16.99 on 3 and 10 DF,  p-value: 0.0002986

> █

```

Figure 35.2: OLS regression on house prices via R

Table 35.2: Airline model from Box and Jenkins (1976) — selected portion of gretl's estimates

Variable	Coefficient	Std. Error	<i>t</i> -statistic	p-value
$\theta_1$	-0.401824	0.0896421	-4.4825	0.0000
$\Theta_1$	-0.556936	0.0731044	-7.6184	0.0000
Variance of innovations			0.00134810	
Log-likelihood			244.696	
Akaike information criterion			-483.39	

If we now open an R session as described in the previous subsection, the data-passing mechanism is slightly different. Since our data were defined in gretl as time series, we use an R *time-series* object (*ts* for short) for the transfer. In this way we can retain in R useful information such as the periodicity of the data and the sample limits. The downside is that the names of individual series, as defined in gretl, are not valid identifiers. In order to extract the variable *lg*, one needs to use the syntax `lg <- gretldata[, "lg"]`.

ARIMA estimation can be carried out by issuing the following two R commands:

```
lg <- gretldata[, "lg"]
arima(lg, c(0,1,1), seasonal=c(0,1,1))
```

which yield

```
Coefficients:
      ma1      sma1
    -0.4018  -0.5569
s.e.    0.0896   0.0731

sigma^2 estimated as 0.001348:  log likelihood = 244.7,  aic = -483.4
```

Happily, the estimates again coincide.

### 35.3 Running an R script

Opening an R window and keying in commands is a convenient method when the job is small. In some cases, however, it would be preferable to have R execute a script prepared in advance. One way to do this is via the `source()` command in R. Alternatively, gretl offers the facility to edit an R script and run it, having the current dataset pre-loaded automatically. This feature can be accessed via the “File, Script Files” menu entry. By selecting “User file”, one can load a pre-existing R script; if you want to create a new script instead, select the “New script, R script” menu entry.

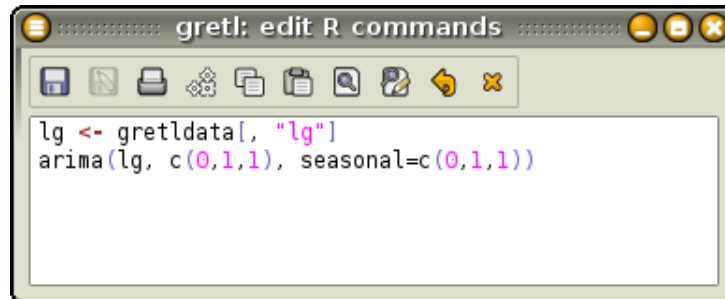


Figure 35.3: Editing window for R scripts

In either case, you are presented with a window very similar to the editor window used for ordinary gretl scripts, as in Figure 35.3.

There are two main differences. First, you get syntax highlighting for R's syntax instead of gretl's. Second, clicking on the Execute button (the gears icon), launches an instance of R in which your commands are executed. Before R is actually run, you are asked if you want to run R interactively or not (see Figure 35.4).

An interactive run opens an R instance similar to the one seen in the previous section: your data will be pre-loaded (if the “pre-load data” box is checked) and your commands will be executed. Once this is done, you will find yourself at the R prompt, where you can enter more commands.

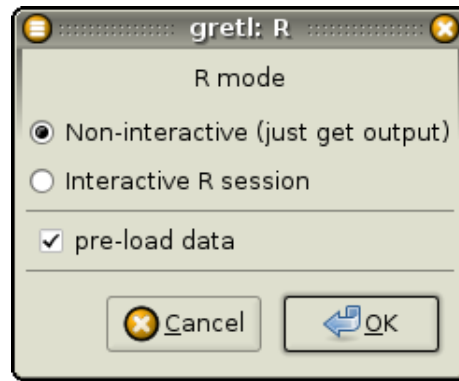


Figure 35.4: Editing window for R scripts

A non-interactive run, on the other hand, will execute your script, collect the output from R and present it to you in an output window; R will be run in the background. If, for example, the script in Figure 35.3 is run non-interactively, a window similar to Figure 35.5 will appear.

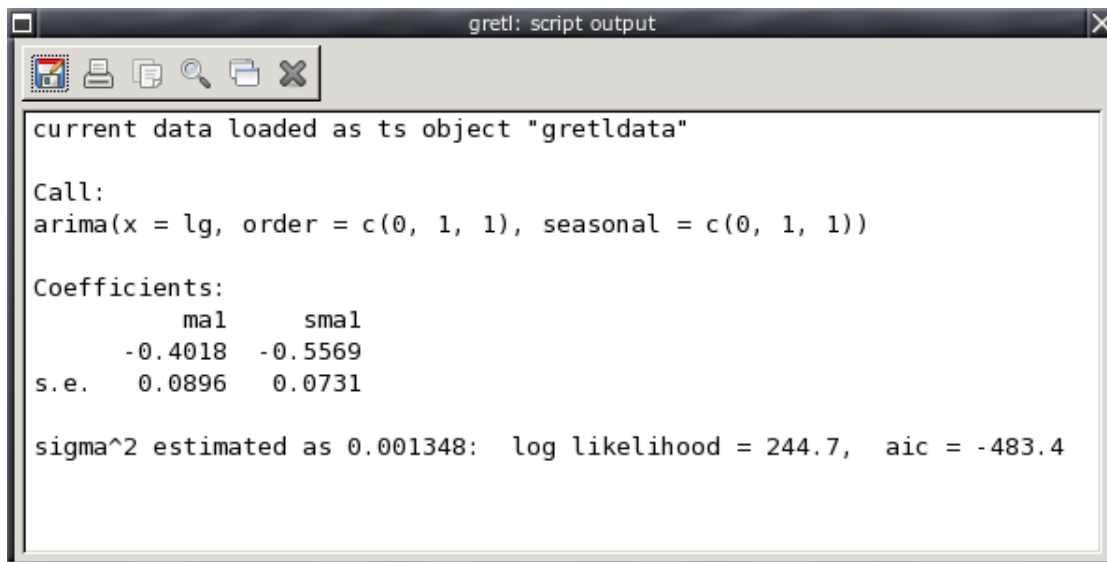


Figure 35.5: Output from a non-interactive R run

### 35.4 Taking stuff back and forth

As regards the passing of data between the two programs, so far we have only considered passing series from gretl to R. In order to achieve a satisfactory degree of interoperability, more is needed. In the following sub-sections we see how matrices can be exchanged, and how data can be passed from R back to gretl.

### Passing matrices from gretl to R

For passing matrices from gretl to R, you can use the `mwrite` matrix function described in section 14.6. For example, the following gretl code fragment generates the matrix

$$A = \begin{bmatrix} 3 & 7 & 11 \\ 4 & 8 & 12 \\ 5 & 9 & 13 \\ 6 & 10 & 14 \end{bmatrix}$$

and stores it into the file `mymatfile.mat`.

```
matrix A = mshape(seq(3,14),4,3)
err = mwrite(A, "mymatfile.mat")
```

In order to retrieve this matrix from R, all you have to do is

```
A <- as.matrix(read.table("mymatfile.mat", skip=1))
```

Although in principle you can give your matrix file any valid filename, a couple of conventions may prove useful. First, you may want to use an informative file suffix such as `.mat`, but this is a matter of taste. More importantly, the exact location of the file created by `mwrite` could be an issue. By default, if no path is specified in the file name, gretl stores matrix files in the current work directory. However, it may be wise for the purpose at hand to use the directory in which gretl stores all its temporary files, whose name is stored in the built-in string `dotdir` (see section 13.2). The value of this string is automatically passed to R as the string variable `gretl.dotdir`, so the above example may be rewritten more cleanly as

Gretl side:

```
matrix A = mshape(seq(3,14),4,3)
err = mwrite(A, "@dotdir/mymatfile.mat")
```

R side:

```
fname <- paste(gretl.dotdir, "mymatfile.mat", sep="")
A <- as.matrix(read.table(fname, skip=1))
```

### Passing data from R to gretl

For passing data in the opposite direction, gretl defines a special function that can be used in the R environment. An R object will be written as a temporary file in gretl's `dotdir` directory, from where it can be easily retrieved from within gretl.

The name of this function is `gretl.export()`, and it accepts one argument, the object to be exported. At present, the objects that can be exported with this method are matrices, data frames and time-series objects. The function creates a text file, with the same name as the exported object, in gretl's temporary directory. Data frames and time-series objects are stored as CSV files, and can be retrieved by using gretl's `append` command. Matrices are stored in a special text format that is understood by gretl (see section 14.6); the file suffix is in this case `.mat`, and to read the matrix in gretl you must use the `mread()` function.

As an example, we take the airline data and use them to estimate a structural time series model à la Harvey (1989). The model we will use is the *Basic Structural Model* (BSM), in which a time series is decomposed into three terms:

$$y_t = \mu_t + \gamma_t + \varepsilon_t$$

where  $\mu_t$  is a trend component,  $y_t$  is a seasonal component and  $\varepsilon_t$  is a noise term. In turn, the following is assumed to hold:

$$\begin{aligned}\Delta\mu_t &= \beta_{t-1} + \eta_t \\ \Delta\beta_t &= \zeta_t \\ \Delta_s y_t &= \Delta\omega_t\end{aligned}$$

where  $\Delta_s$  is the seasonal differencing operator,  $(1 - L^s)$ , and  $\eta_t$ ,  $\zeta_t$  and  $\omega_t$  are mutually uncorrelated white noise processes. The object of the analysis is to estimate the variances of the noise components (which may be zero) and to recover estimates of the latent processes  $\mu_t$  (the “level”),  $\beta_t$  (the “slope”) and  $y_t$ .

Gretl does not provide (yet) a command for estimating this class of models, so we will use R’s `StructTS` command and import the results back into gretl. Once the `bjg` dataset is loaded in gretl, we pass the data to R and execute the following script:

```
# extract the log series
y <- gretldata[, "lg"]
# estimate the model
strmod <- StructTS(y)
# save the fitted components (smoothed)
compon <- as.ts(tsSmooth(strmod))
# save the estimated variances
vars <- as.matrix(strmod$coef)

# export into gretl's temp dir
gretl.export(compon)
gretl.export(vars)
```

Running this script via gretl produces minimal output:

```
current data loaded as ts object "gretldata"
wrote /home/cottrell/.gretl/compon.csv
wrote /home/cottrell/.gretl/vars.mat
```

However, we are now able to pull the results back into gretl by executing the following commands, either from the console or by creating a small script:<sup>4</sup>

```
append @dotdir/compon.csv
vars = mread("@dotdir/vars.mat")
```

The first command reads the estimated time-series components from a CSV file, which is the format that the passing mechanism employs for series. The matrix `vars` is read from the file `vars.mat`.

After the above commands have been executed, three new series will have appeared in the gretl workspace, namely the estimates of the three components; by plotting them together with the original data, you should get a graph similar to Figure 35.6. The estimates of the variances can be seen by printing the `vars` matrix, as in

```
? print vars
vars (4 x 1)

0.00077185
0.0000
0.0013969
0.0000
```

<sup>4</sup>This example will work on Linux and presumably on OSX without modifications. On the Windows platform, you may have to substitute the “/” character with “\”.

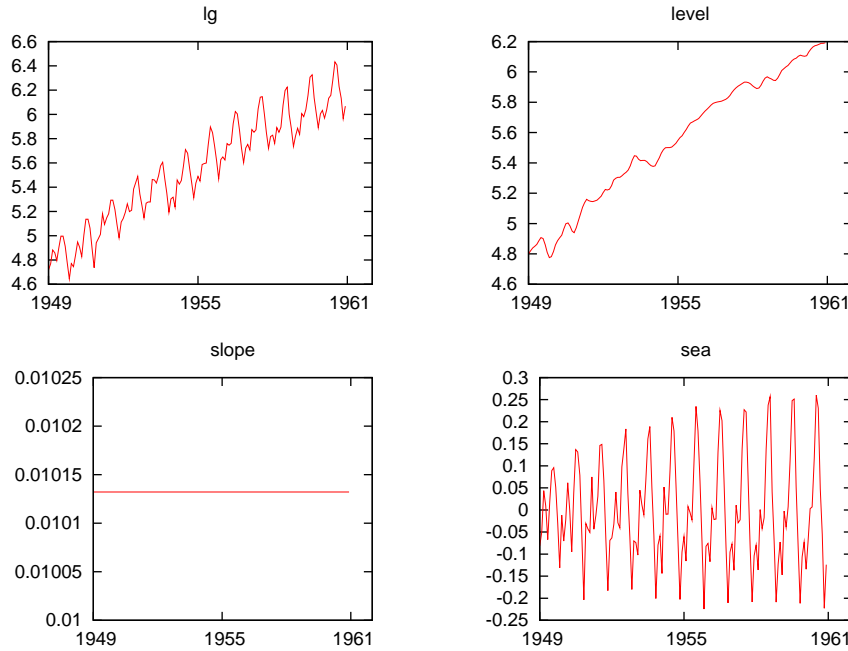


Figure 35.6: Estimated components from BSM

That is,

$$\hat{\sigma}_\eta^2 = 0.00077185, \quad \hat{\sigma}_\xi^2 = 0, \quad \hat{\sigma}_\omega^2 = 0.0013969, \quad \hat{\sigma}_\varepsilon^2 = 0$$

Notice that, since  $\hat{\sigma}_\xi^2 = 0$ , the estimate for  $\beta_t$  is constant and the level component is simply a random walk with a drift.

### 35.5 Interacting with R from the command line

Up to this point we have spoken only of interaction with R via the GUI program. In order to do the same from the command line interface, gretl provides the `foreign` command. This enables you to embed non-native commands within a gretl script.

A “foreign” block takes the form

```
foreign language=R [--send-data] [--quiet]
... R commands ...
end foreign
```

and achieves the same effect as submitting the enclosed R commands via the GUI in the non-interactive mode (see section 35.3 above). The `--send-data` option arranges for auto-loading of the data present in the gretl session. The `--quiet` option prevents the output from R from being echoed in the gretl output.

Using this method, replicating the example in the previous subsection is rather easy: basically, all it takes is encapsulating the content of the R script in a `foreign...end foreign` block; see example 35.1.

The above syntax, despite being already quite useful by itself, shows its full power when it is used in conjunction with user-written functions. Example 35.2 shows how to define a gretl function that calls R internally.

**Example 35.1:** Estimation of the Basic Structural Model — simple

---

```

open bjg.gdt

foreign language=R --send-data
  y <- gretldata[, "lg"]
  strmod <- StructTS(y)
  compon <- as.ts(tsSmooth(strmod))
  vars <- as.matrix(strmod$coef)

  gretl.export(compon)
  gretl.export(vars)
end foreign

append @dotdir/compon.csv
rename level lg_level
rename slope lg_slope
rename sea lg_seas

vars = mread("@dotdir/vars.mat")

```

---

**Example 35.2:** Estimation of the Basic Structural Model — via a function

---

```

function list RStructTS(series myseries)

  smp1 ok(myseries) --restrict
  sx = argname(myseries)

  foreign language=R --send-data --quiet
    @sx <- gretldata[, "myseries"]
    strmod <- StructTS(@sx)
    compon <- as.ts(tsSmooth(strmod))
    gretl.export(compon)
  end foreign

  append @dotdir/compon.csv
  rename level @sx_level
  rename slope @sx_slope
  rename sea @sx_seas

  list ret = @sx_level @sx_slope @sx_seas
  return ret
end function

# ----- main -----

open bjg.gdt
list X = RStructTS(lg)

```

---

## 35.6 Performance issues with R

R is a large and complex program, which takes an appreciable time to initialize itself.<sup>5</sup> In interactive use this not a significant problem, but if you have a gretl script that calls R repeatedly the cumulated start-up costs can become bothersome. To get around this, gretl calls the R shared library by preference; in this case the start-up cost is borne only once, on the first invocation of R code from within gretl.

Support for the R shared library is built into the gretl packages for MS Windows and OS X — but the advantage is realized only if the library is in fact available at run time. If you are building gretl yourself on Linux and wish to make use of the R library, you should ensure (a) that R has been built with the shared library enabled (specify `--enable-R-shlib` when configuring your build of R), and (b) that the `pkg-config` program is able to detect your R installation. We do not link to the R library at build time, rather we open it dynamically on demand. The gretl GUI has an item under the Tools/Preferences menu which enables you to select the path to the library, if it is not detected automatically.

If you have the R shared library installed but want to force gretl to call the R executable instead, you can do

```
set R_lib off
```

## 35.7 Further use of the R library

Besides improving performance, as noted above, use of the R shared library makes possible a further refinement. That is, you can define functions in R, within a `foreign` block, then call those functions later in your script much as if they were gretl functions. This is illustrated below.

```
set R_functions on
foreign language=R
  plus_one <- function(q) {
    z = q+1
    invisible(z)
  }
end foreign

scalar b=R.plus_one(2)
```

The R function `plus_one` is obviously trivial in itself, but the example shows a couple of points. First, for this mechanism to work you need to enable `R_functions` via the `set` command. Second, to avoid collision with the gretl function namespace, calls to functions defined in this way must be prefixed with “R.”, as in `R.plus_one`.

Built-in R functions may also be called in this way, once `R_functions` is set on. For example one can invoke R’s `choose` function, which computes binomial coefficients:

```
set R_functions on
scalar b=R.choose(10,4)
```

Note, however, that the possibilities for use of built-in R functions are limited; only functions whose arguments and return values are sufficiently generic (basically scalars or matrices) will work.

---

<sup>5</sup>About one third of a second on an Intel Core Duo machine of 2009 vintage.



## Chapter 36

# Gretl and Ox

### 36.1 Introduction


Ox, written by Jurgen A. Doornik (see [Doornik, 2007](#)), is described by its author as “an object-oriented statistical system. At its core is a powerful matrix language, which is complemented by a comprehensive statistical library. Among the special features of Ox are its speed [and] well-designed syntax. . . . Ox comes in two versions: Ox Professional and Ox Console. Ox is available for Windows, Linux, Mac (OS X), and several Unix platforms.” ([www.doornik.com](http://www.doornik.com))

Ox is proprietary, closed-source software. The command-line version of the program is, however, available free of charge for academic users. Quoting again from Doornik’s website: “The Console (command line) versions may be used freely for academic research and teaching purposes only. . . . The Ox syntax is public, and, of course, you may do with your own Ox code whatever you wish.” If you wish to use Ox in conjunction with gretl please refer to [doornik.com](http://www.doornik.com) for further details on licensing.

As the reader will no doubt have noticed, all the other software that we discuss in this Guide is open-source and freely available for all users. We make an exception for Ox on the grounds that it is indeed fast and well designed, and that its statistical library — along with various add-on packages that are also available — has exceptional coverage of cutting-edge techniques in econometrics. The gretl authors have used Ox for benchmarking some of gretl’s more advanced features such as dynamic panel models and the state space models.<sup>1</sup>

### 36.2 Ox support in gretl

The support offered for Ox in gretl is similar to that offered for R, as discussed in chapter 35, but with a few differences. The first difference to note is that Ox support is not on by default; it must be enabled explicitly.

 To enable support for Ox, go to the Tools/Preferences/General menu item and check the box labeled “Enable Ox support”. Click “OK” in the preferences dialog, then quit and restart gretl. You will now find, under the Programs tab in the Tools/Preferences/General dialog, an entry for specifying the path to the oxl executable, that is, the program that runs Ox files (on MS Windows it is called oxl.exe). Make sure that path is right, and you’re ready to go.

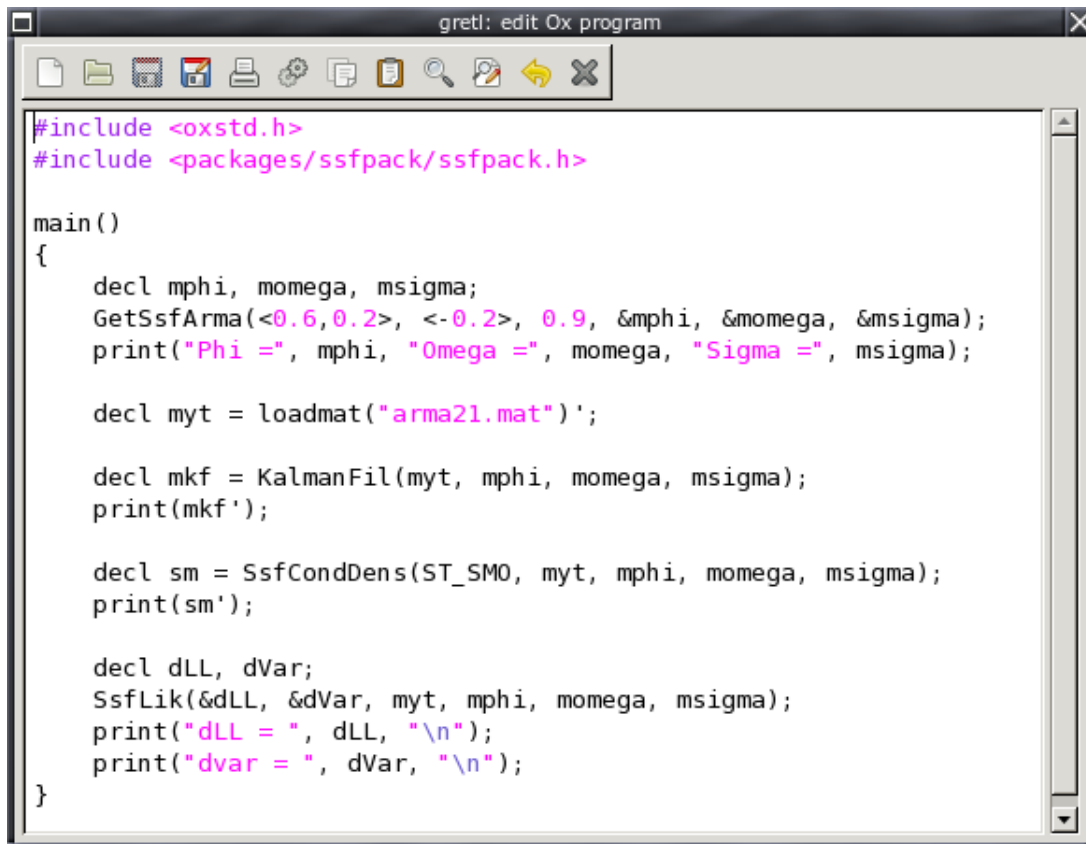
With support enabled, you can open and edit Ox programs in the gretl GUI. Clicking the “execute” icon in the editor window will send your code to Ox for execution. Figures 36.1 and Figure 36.2 show an Ox program and part of its output.

In addition you can embed Ox code within a gretl script using a `foreign` block, as described in connection with R. A trivial example, which simply prints the gretl data matrix within Ox, is shown below:

```
open data4-1
matrix m = { dataset }
mwrite(m, "@dotdir/gretl.mat")
```

---

<sup>1</sup>For a review of Ox, see [Cribari-Neto and Zarkos \(2003\)](#) and for a (somewhat dated) comparison of Ox with other matrix-oriented packages such as GAUSS, see [Steinhaus \(1999\)](#).



```

#include <oxstd.h>
#include <packages/ssfpack/ssfpack.h>

main()
{
    decl mphi, momega, msigma;
    GetSsfArma(<0.6,0.2>, <-0.2>, 0.9, &mphi, &momega, &msigma);
    print("Phi =", mphi, "Omega =", momega, "Sigma =", msigma);

    decl myt = loadmat("arma21.mat");

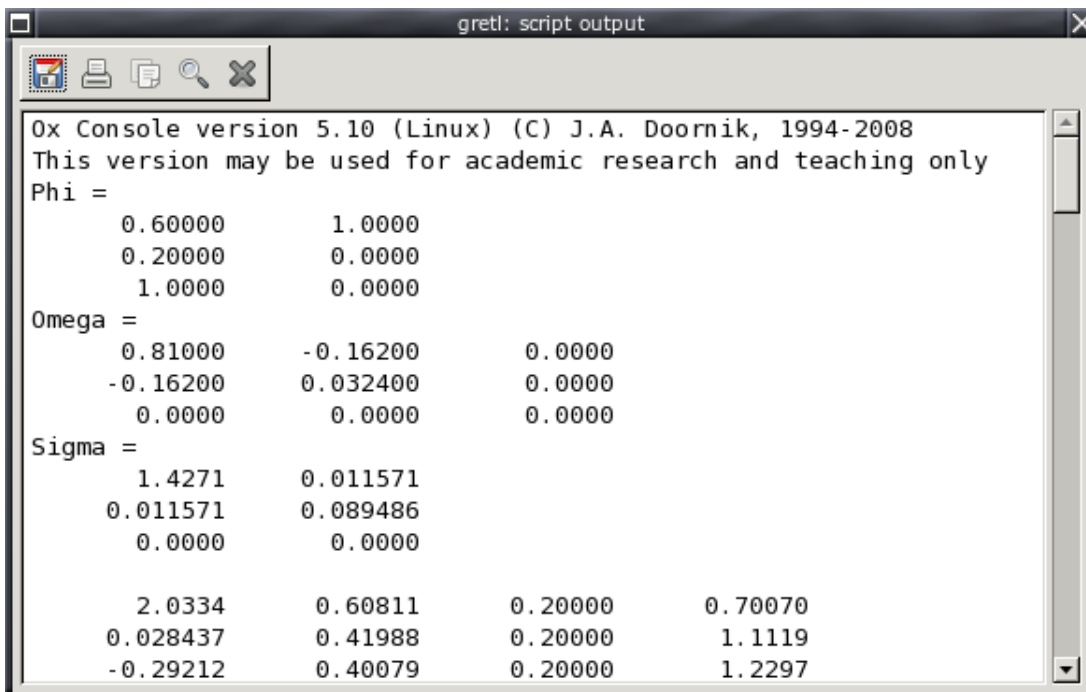
    decl mkf = KalmanFil(myt, mphi, momega, msigma);
    print(mkf');

    decl sm = SsfCondDens(ST_SMO, myt, mphi, momega, msigma);
    print(sm');

    decl dLL, dVar;
    SsfLik(&dLL, &dVar, myt, mphi, momega, msigma);
    print("dLL = ", dLL, "\n");
    print("dvar = ", dVar, "\n");
}

```

Figure 36.1: Ox editing window



```

Ox Console version 5.10 (Linux) (C) J.A. Doornik, 1994-2008
This version may be used for academic research and teaching only
Phi =
    0.60000    1.0000
    0.20000    0.0000
    1.0000    0.0000
Omega =
    0.81000   -0.16200    0.0000
   -0.16200    0.032400    0.0000
    0.0000    0.0000    0.0000
Sigma =
    1.4271    0.011571
    0.011571    0.089486
    0.0000    0.0000

    2.0334    0.60811    0.20000    0.70070
    0.028437    0.41988    0.20000    1.1119
   -0.29212    0.40079    0.20000    1.2297

```

Figure 36.2: Output from Ox

```

foreign language=Ox
#include <oxstd.h>
main()
{
    decl gmat = gretl_loadmat("gretl.mat");
    print(gmat);
}
end foreign

```

The above example illustrates how a matrix can be passed from gretl to Ox. We use the `mwrite` function to write a matrix into the user's "dotdir" (see section 13.2), then in Ox we use the function `gretl_loadmat` to retrieve the matrix.

How does `gretl_loadmat` come to be defined? When gretl writes out the Ox program corresponding to your `foreign` block it does two things in addition. First, it writes a small utility file named `gretl_io.ox` into your dotdir. This contains a definition for `gretl_loadmat` and also for the function `gretl_export` (see below). Second, gretl interpolates into your Ox code a line which includes this utility file (it is inserted right after the inclusion of `oxstd.h`, which is needed in all Ox programs). Note that `gretl_loadmat` expects to find the named file in the user's dotdir.

### 36.3 Illustration: replication of DPD model

Example 36.1 shows a more ambitious case. This script replicates one of the dynamic panel data models in Arellano and Bond (1991), first using gretl and then using Ox; we then check the relative differences between the parameter estimates produced by the two programs (which turn out to be reassuringly small).

Unlike the previous example, in this case we pass the dataset from gretl to Ox as a CSV file in order to preserve the variable names. Note the use of the internal variable `csv_na` to get the right representation of missing values for use with Ox — and also note that the `--send-data` option for the `foreign` command is not available in connection with Ox.

We get the parameter estimates back from Ox using `gretl_export` on the Ox side and `mread` on the gretl side. The `gretl_export` function takes two arguments, a matrix and a file name. The file is written into the user's dotdir, from where it can be picked up using `mread`. The final portion of the output from Example 36.1 is shown below:

```

? matrix oxparm = mread("/home/cottrell/.gretl/oxparm.mat")
Generated matrix oxparm
? eval abs((parm - oxparm) ./ oxparm)
1.4578e-13
3.5642e-13
5.0672e-15
1.6091e-13
8.9808e-15
2.0450e-14
1.0218e-13
2.1048e-13
9.5898e-15
1.8658e-14
2.1852e-14
2.9451e-13
1.9398e-13

```

**Example 36.1:** Estimation of dynamic panel data model via gretl and Ox

---

```

open abdata.gdt

# Take first differences of the independent variables
genr Dw = diff(w)
genr Dk = diff(k)
genr Dys = diff(ys)

# 1-step GMM estimation
arbond 2 ; n Dw Dw(-1) Dk Dys Dys(-1) 0 --time-dummies
matrix parm = $coeff

# Write CSV file for Ox
set csv_na .NaN
store @dotdir/abdata.csv

# Replicate using the Ox DPD package
foreign language=Ox
#include <oxstd.h>
#import <packages/dpd/dpd>

main ()
{
    decl dpd = new DPD();
    dpd.Load("@dotdir/abdata.csv");
    dpd.SetYear("YEAR");

    dpd.Select(Y_VAR, {"n", 0, 2});
    dpd.Select(X_VAR, {"w", 0, 1, "k", 0, 0, "ys", 0, 1});
    dpd.Select(I_VAR, {"w", 0, 1, "k", 0, 0, "ys", 0, 1});

    dpd.Gmm("n", 2, 99); // GMM-type instrument
    dpd.SetDummies(D_CONSTANT + D_TIME);
    dpd.SetTest(2, 2); // Sargan, AR 1-2 tests
    dpd.Estimate(); // 1-step estimation
    decl parm = dpd.GetPar();
    gretl_export(parm, "oxparm.mat");

    delete dpd;
}
end foreign

# Compare the results
matrix oxparm = mread("@dotdir/oxparm.mat")
eval abs((parm - oxparm) ./ oxparm)

```

---

## Chapter 37

# Gretl and Octave

### 37.1 Introduction

GNU Octave, written by John W. Eaton and others, is described as “a high-level language, primarily intended for numerical computations.” The program is oriented towards “solving linear and nonlinear problems numerically” and “performing other numerical experiments using a language that is mostly compatible with Matlab.” ([www.gnu.org/software/octave](http://www.gnu.org/software/octave)) Octave is available in source-code form (naturally, for GNU software) and also in the form of binary packages for MS Windows and Mac OS X. Numerous contributed packages that extend Octave’s functionality in various ways can be found at [octave.sf.net](http://octave.sf.net).

### 37.2 Octave support in gretl

The support offered for Octave in gretl is similar to that offered for R (chapter 35). For example, you can open and edit Octave scripts in the gretl GUI. Clicking the “execute” icon in the editor window will send your code to Octave for execution. Figures 37.1 and Figure 37.2 show an Octave script and its output; in this example we use the function `logistic_regression` to replicate some results from [Greene \(2000\)](#).

In addition you can embed Octave code within a gretl script using a `foreign` block, as described in connection with R. A trivial example, which simply loads and prints the gretl data matrix within Octave, is shown below. (Note that in Octave, appending “;” to a line suppresses verbose output; leaving off the semicolon results in printing of the object that is produced, if any.)

```
open data4-1
matrix m = { dataset }
mwrite(m, "@dotdir/gretl.mat")

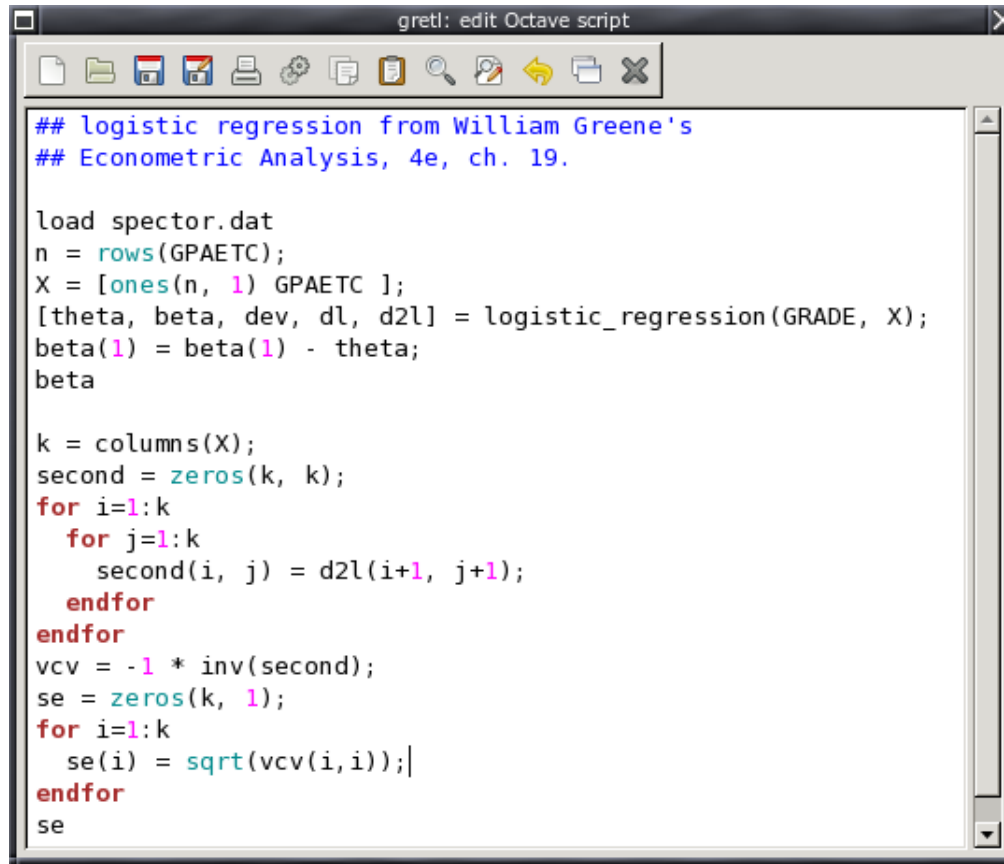
foreign language=Octave
  gmat = gretl_loadmat("gretl.mat")
end foreign
```

We use the `mwrite` function to write a matrix into the user’s “dotdir” (see section 13.2), then in Octave we use the function `gretl_loadmat` to retrieve the matrix. The “magic” behind `gretl_loadmat` works in essentially the same way as for Ox (chapter 36).

### 37.3 Illustration: spectral methods

We now present a more ambitious example which exploits Octave’s handling of the frequency domain (and also its ability to use code written for MATLAB), namely estimation of the spectral coherence of two time series. For this illustration we require two extra Octave packages from [octave.sf.net](http://octave.sf.net), namely those supporting spectral functions (`specfun`) and signal processing (`signal`). After downloading the packages you can install them from within Octave as follows (using version numbers as of March 2010):

```
pkg install specfun-1.0.8.tar.gz
pkg install signal-1.0.10.tar.gz
```

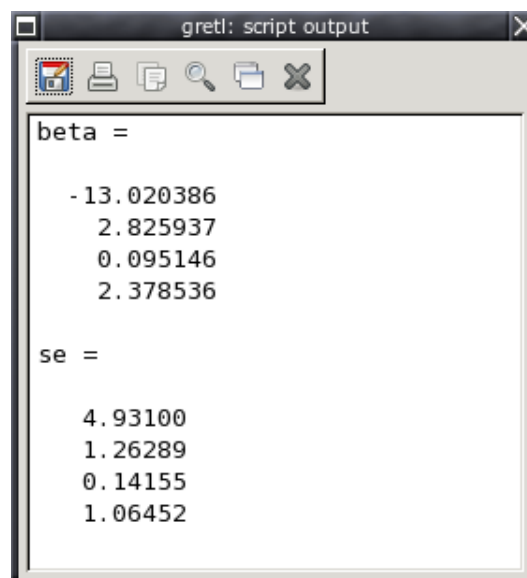
The image shows a window titled 'gretl: edit Octave script'. It contains a script for logistic regression. The script starts with comments, then loads a data file 'spector.dat'. It calculates the number of rows 'n' and creates a matrix 'X' with a column of ones. It then performs a logistic regression on 'GRADE' using 'X'. The results are stored in 'theta', 'beta', 'dev', 'dl', and 'd2l'. The script then calculates the variance-covariance matrix 'vcv' and the standard errors 'se' for the coefficients.

```
## logistic regression from William Greene's
## Econometric Analysis, 4e, ch. 19.

load spector.dat
n = rows(GPAETC);
X = [ones(n, 1) GPAETC ];
[theta, beta, dev, dl, d2l] = logistic_regression(GRADE, X);
beta(1) = beta(1) - theta;
beta

k = columns(X);
second = zeros(k, k);
for i=1:k
    for j=1:k
        second(i, j) = d2l(i+1, j+1);
    endfor
endfor
vcv = -1 * inv(second);
se = zeros(k, 1);
for i=1:k
    se(i) = sqrt(vcv(i,i));
endfor
se
```

Figure 37.1: Octave editing window

The image shows a window titled 'gretl: script output'. It displays the results of the Octave script. The 'beta' coefficients are shown as a column vector, and the 'se' (standard errors) are shown as a column vector.

```
beta =

-13.020386
  2.825937
  0.095146
  2.378536

se =

 4.93100
 1.26289
 0.14155
 1.06452
```

Figure 37.2: Output from Octave

In addition we need some specialized MATLAB files made available by Mario Forni of the University of Modena, at [http://www.economia.unimore.it/forni\\_mario/matlab.htm](http://www.economia.unimore.it/forni_mario/matlab.htm). The files needed are `coheren2.m`, `coheren.m`, `coher.m`, `cospec.m`, `crosscov.m`, `crosspec.m`, `crosspe.m` and `spec.m`. These are in a form appropriate for MS Windows. On Linux you could run the following shell script to get the files and remove the Windows end-of-file character (which prevents the files from running under Octave):

```
SITE=http://www.economia.unimore.it/forni_mario/MYPROG
# download files and delete trailing Ctrl-Z
for f in \
  coheren2.m \
  coheren.m \
  coher.m \
  cospec.m \
  crosscov.m \
  crosspec.m \
  crosspe.m \
  spec.m ; do
  wget $SITE/$f && \
  cat $f | tr -d '\032' > tmp.m && mv tmp.m $f
done
```

The Forni files should be placed in some appropriate directory, and you should tell Octave where to find them by adding that directory to Octave's `loadpath`. On Linux this can be done via an entry in one's `~/.octaverc` file. For example

```
addpath("~/stats/octave/forni");
```

Alternatively, an `addpath` directive can be written into the Octave script that calls on these files.

With everything set up on the Octave side we now write a `gretl` script (see Example 37.1) which opens a time-series dataset, constructs and writes a matrix containing two series, and defines a `foreign` block containing the Octave statements needed to produce the spectral coherence matrix. The matrix is exported via the `gretl_export` function, which is automatically defined for you; this function takes two arguments, a matrix and a file name. The file is written into the user's "dotdir", from where it can be picked up using `mread`. Finally, we produce a graph from the matrix in `gretl`. In the script this is sent to the screen; Figure 37.3 shows the same graph in PDF format.

**Example 37.1:** Estimation of spectral coherence via Octave

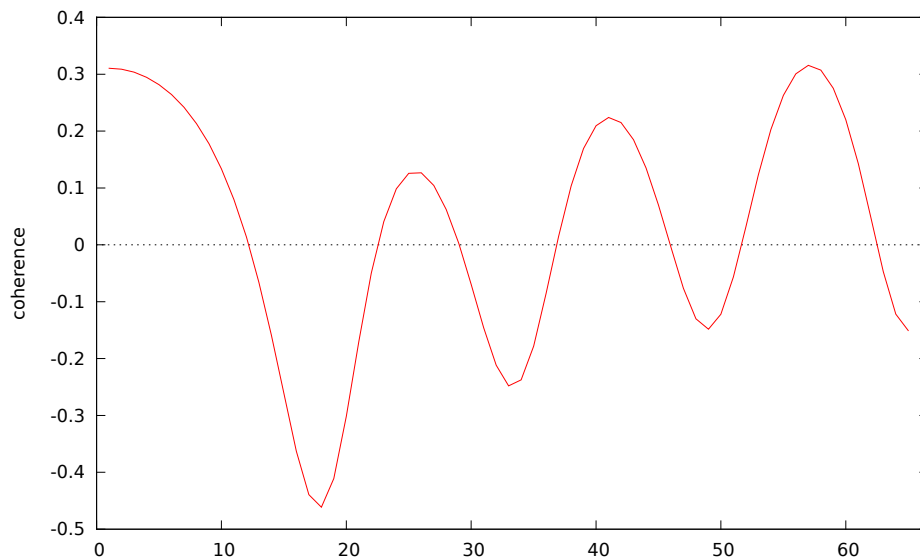
---

```
open data9-7
matrix xy = { PRIME, UNEMP }
mwrite(xy, "@dotdir/xy.mat")

foreign language=Octave
# uncomment and modify the following if necessary
# addpath("~/stats/octave/forni");
xy = gretl_loadmat("xy.mat");
x = xy(:,1);
y = xy(:,2);
# note: the last parameter is the Bartlett window size
h = coher(x, y, 8);
gretl_export(h, "h.mat");
end foreign

h = mread("@dotdir/h.mat")
colnames(h, "coherence")
gnuplot 1 --time-series --with-lines --matrix=h --output=display
```

---

**Figure 37.3:** Spectral coherence estimated via Octave



## Chapter 38

# Gretl and Stata

Stata ([www.stata.com](http://www.stata.com)) is closed-source, proprietary (and expensive) software and as such is not a natural companion to gretl. Nonetheless, given Stata's popularity it is desirable to have a convenient way of comparing results across the two programs, and to that end we provide limited support for Stata code under the `foreign` command.

The following example illustrates what's available. You can send the current gretl dataset to Stata using the `--send-data` flag. And having defined a matrix within Stata you can export it for use with gretl via the `gretl_export` command: this takes two arguments, the name of the matrix to export and the filename to use; the file is written to the user's "dotdir", from where it can be retrieved using the `mread()` function.<sup>1</sup> To suppress printed output from Stata you can add the `--quiet` flag to the `foreign` block.

### Example 38.1: Comparison of clustered standard errors with Stata

---

```
function matrix stata_reorder (matrix se)
  # stata puts the intercept last, but gretl puts it first
  scalar n = rows(se)
  return se[n] | se[1:n-1]
end function

open data4-1
ols 1 0 2 3 --cluster=bedrms
matrix se = $stderr

foreign language=stata --send-data
  regress price sqft bedrms, vce(cluster bedrms)
  matrix vcv = e(V)
  gretl_export vcv "vcv.mat"
end foreign

matrix stata_vcv = mread("@dotdir/vcv.mat")
stata_se = stata_reorder(sqrt(diag(stata_vcv)))
matrix check = se - stata_se
print check
```

---

Note that there is no support for editing Stata scripts via the gretl GUI. Neither is there a way of specifying the path to the stata executable in the gretl GUI; the executable must be in your PATH. Also note that Stata coerces all variable names to lower-case on data input, so even if series names in gretl are upper-case, or of mixed case, it's necessary to use all lower-case in Stata.

---

<sup>1</sup>We do not currently offer the complementary functionality of `gretl_loadmat`, which enables reading of matrices written by gretl's `mwrite()` function in Ox and Octave. This is not at all easy to implement in Stata code.

## Chapter 39

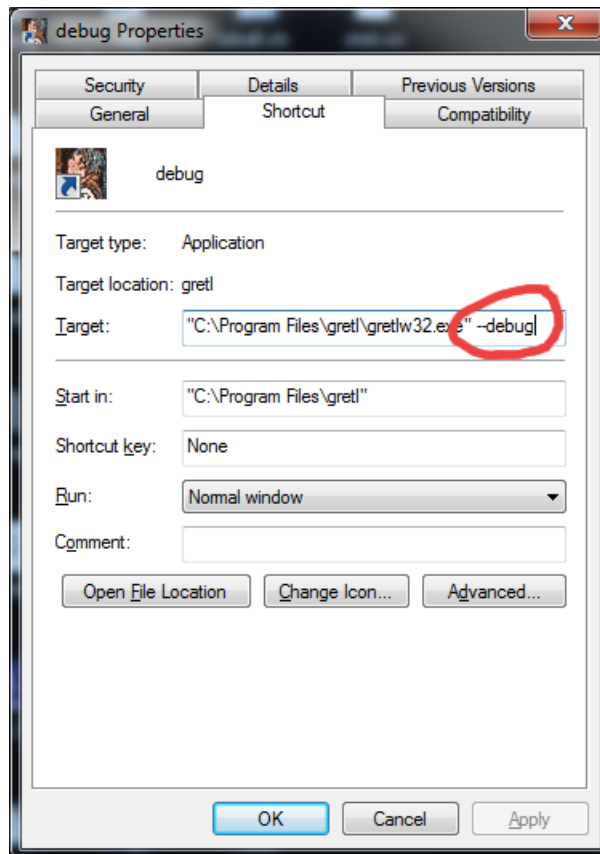
# Troubleshooting gretl

### 39.1 Bug reports

Bug reports are welcome — well, if not exactly welcome then useful and appreciated. Hopefully, you are unlikely to find bugs in the actual calculations done by gretl (although this statement does not constitute any sort of warranty). You may, however, come across bugs or oddities in the behavior of the graphical interface. Please remember that the usefulness of bug reports is greatly enhanced if you can be as specific as possible: what *exactly* went wrong, under what conditions, and on what operating system? If you saw an error message, what precisely did it say?

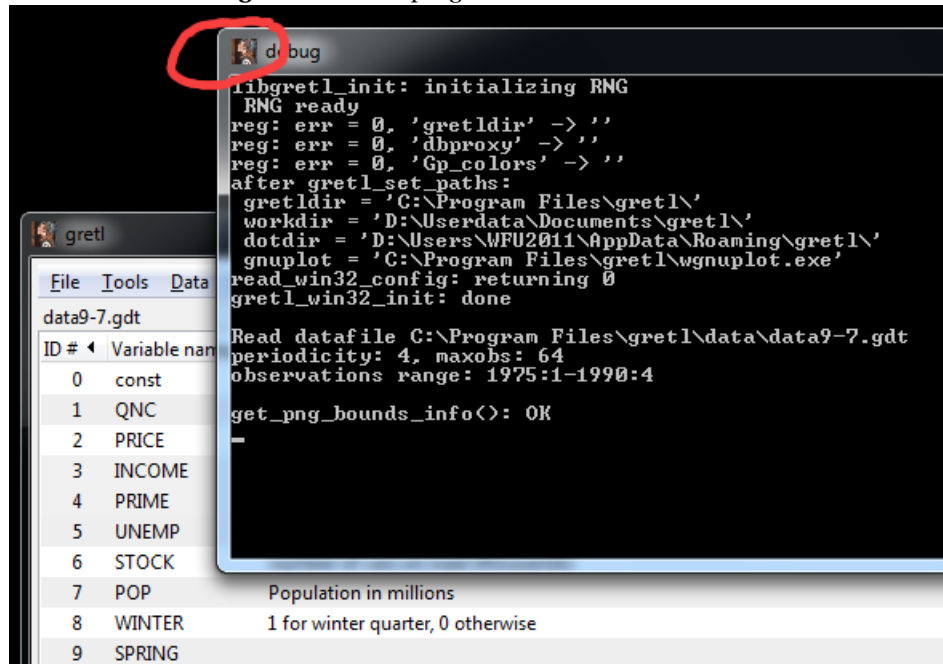
One way of making a bug report more useful is to run the program in such a way that you can see (and copy) any additional information that gets printed to the `stderr` output stream. On Linux and Mac OS X that's just a matter of launching gretl from the command prompt in a terminal window. On MS Windows it's a bit more complicated since `stderr` is by default “invisible.” However, you can quite easily set up a special gretl shortcut that does the job. On the Windows desktop, right-click and select “New shortcut.” In the dialog box that appears, browse to find `gretlw32.exe` and append the `--debug` flag, as shown in Figure 39.1. Note that there are two dashes before “debug”.

Figure 39.1: Creating a debugging shortcut



When you start gretl in this mode, a “console window” appears as well as the gretl window, and `stderr` output goes to the console. To copy this output, click at the top left of the console window for a menu (Figure 39.2): first do “Select all”, then “Copy.” You can paste the results into Notepad or similar.

Figure 39.2: The program with console window



## 39.2 Auxiliary programs

As mentioned above, gretl calls some other programs to accomplish certain tasks (gnuplot for graphing, L<sup>A</sup>T<sub>E</sub>X for high-quality typesetting of regression output, GNU R). If something goes wrong with such external links, it is not always easy for gretl to produce an informative error message. If such a link fails when accessed from the gretl graphical interface, you may be able to get more information by starting gretl from the command prompt rather than via a desktop menu entry or icon. On the X window system, start gretl from the shell prompt in an xterm; on MS Windows, start the program `gretlwin32.exe` from a console window or “DOS box” using the `-g` or `--debug` option flag. Additional error messages may be displayed on the terminal window.

Also please note that for most external calls, gretl assumes that the programs in question are available in your “path” — that is, that they can be invoked simply via the name of the program, without supplying the program’s full location.<sup>1</sup> Thus if a given program fails, try the experiment of typing the program name at the command prompt, as shown below.

	<i>Graphing</i>	<i>Typesetting</i>	<i>GNU R</i>
X window system	gnuplot	pdflatex	R
MS Windows	wgnuplot.exe	pdflatex	RGui.exe

If the program fails to start from the prompt, it’s not a gretl issue but rather that the program’s home directory is not in your path, or the program is not installed (properly). For details on modifying your path please see the documentation or online help for your operating system or shell.

<sup>1</sup>The exception to this rule is the invocation of gnuplot under MS Windows, where a full path to the program is given.

## Chapter 40

# The command line interface

The `gretl` package includes the command-line program `gretlcli`. On Linux it can be run from a terminal window (`xterm`, `rxvt`, or similar), or at the text console. Under MS Windows it can be run in a console window (sometimes inaccurately called a “DOS box”). `gretlcli` has its own help file, which may be accessed by typing “help” at the prompt. It can be run in batch mode, sending output directly to a file (see also the *Gretl Command Reference*).

If `gretlcli` is linked to the `readline` library (this is automatically the case in the MS Windows version; also see Appendix C), the command line is recallable and editable, and offers command completion. You can use the Up and Down arrow keys to cycle through previously typed commands. On a given command line, you can use the arrow keys to move around, in conjunction with Emacs editing keystrokes.<sup>1</sup> The most common of these are:

<i>Keystroke</i>	<i>Effect</i>
Ctrl-a	go to start of line
Ctrl-e	go to end of line
Ctrl-d	delete character to right

where “Ctrl-a” means press the “a” key while the “Ctrl” key is also depressed. Thus if you want to change something at the beginning of a command, you *don’t* have to backspace over the whole line, erasing as you go. Just hop to the start and add or delete characters. If you type the first letters of a command name then press the Tab key, `readline` will attempt to complete the command name for you. If there’s a unique completion it will be put in place automatically. If there’s more than one completion, pressing Tab a second time brings up a list.

Probably the most useful mode for heavy-duty work with `gretlcli` is batch (non-interactive) mode, in which the program reads and processes a script, and sends the output to file. For example

```
gretlcli -b scriptfile > outputfile
```

Note that *scriptfile* is treated as a program argument; only the output file requires redirection (>). Don’t forget the `-b` (batch) switch, otherwise the program will wait for user input after executing the script (and if output is redirected, the program will appear to “hang”).

---

<sup>1</sup>Actually, the key bindings shown below are only the defaults; they can be customized. See the [readline manual](#).

## **Part IV**

# **Appendices**

## Appendix A

# Data file details

### A.1 Basic native format

In gretl's native data format, a data set is stored in XML (extensible mark-up language). Data files correspond to the simple DTD (document type definition) given in `gretldata.dtd`, which is supplied with the gretl distribution and is installed in the system data directory (e.g. `/usr/share/gretl/data` on Linux.) Data files may be plain text or gzipped. They contain the actual data values plus additional information such as the names and descriptions of variables, the frequency of the data, and so on.

Most users will probably not have need to read or write such files other than via gretl itself, but if you want to manipulate them using other software tools you should examine the DTD and also take a look at a few of the supplied practice data files: `data4-1.gdt` gives a simple example; `data4-10.gdt` is an example where observation labels are included.

### A.2 Traditional ESL format

For backward compatibility, gretl can also handle data files in the “traditional” format inherited from Ramu Ramanathan's ESL program. In this format a data set is represented by two text files; one contains the actual data and the other information on how the data should be read. To be more specific:

1. *Actual data*: A rectangular matrix of white-space separated numbers. By default, each column represents a variable, each row an observation. The data columns can be separated by spaces or tabs. Traditionally the data filename has no extension/suffix.
2. *Header*: The data file must be accompanied by a header file which has the same basename as the data file plus the suffix `.hdr`. This file contains, in order:
  - (Optional) *comments* on the data, set off by the opening string `(*` and the closing string `*)`, each of these strings to occur on lines by themselves.
  - (Required) a list of the *names of the variables* in the data file, separated by white space. Names are limited to 8 characters, must start with a letter, and are limited to alphanumeric characters plus the underscore. The list may continue over more than one line; it should be terminated with a semicolon.
  - (Required) an *observations* line of the form `1 1 85`. The first element gives the data frequency (1 for undated or annual data, 4 for quarterly, 12 for monthly). The second and third elements give the starting and ending observations. These should be 1 and the number of observations, respectively, for undated data. For time-series data one can use dates of the form `1959.1` (quarterly, one digit after the point) or `1967.03` (monthly, two digits after the point).
  - The keyword `BYOBS` (but see below).

Here is an example of a well-formed data header file; the corresponding data file contains three columns of data, each having 90 entries.

```
(*
  DATA9-6:
  Data on log(money), log(income) and interest rate from US.
  Source: Stock and Watson (1993) Econometrica
  (unsmoothed data) Period is 1900-1989 (annual data).
  Data compiled by Graham Elliott.
*)
lmoney lincome intrate ;
1 1900 1989 BYOBS
```

Three further features of the traditional ESL data format may be noted.

1. If the BYOBS keyword is replaced by BYVAR this indicates that in the corresponding data file the data are written out by variable rather than by observation.
2. If BYOBS is followed by the keyword MARKERS, gretl expects a data file in which the *first column* contains strings (8 characters maximum) used to identify the observations. This may be useful in the case of cross-sectional data where the units of observation are identifiable: countries, states, cities or whatever. It can also be useful for irregular time series data, such as daily stock price data where some days are not trading days — in this case the observations can be marked with a date string such as 10/01/98. (Remember the 8-character maximum.) Note that BYVAR and MARKERS are mutually exclusive flags. Also note that the “markers” are not considered to be a variable: this column does not have a corresponding entry in the list of variable names in the header file.
3. If a file with the same base name as the data file and header files, but with the suffix `.lbl`, is found, it is read to fill out the descriptive labels for the data series. The format of the label file is simple: each line contains the name of one variable (as found in the header file), followed by one or more spaces, followed by the descriptive label. Here is an example, giving a label for a variable named “price”: price New car price index, 1982 base year

If you want to save data in traditional format, use the `--traditional` flag with the `store` command, either in the command-line program or in the console window of the GUI program.

### A.3 Binary database details

A gretl database consists of two parts: an ASCII index file (with filename suffix `.idx`) containing information on the series, and a binary file (suffix `.bin`) containing the actual data. Two examples of the format for an entry in the `idx` file are shown below:

```
GOM910 Composite index of 11 leading indicators (1987=100)
M 1948.01 - 1995.11 n = 575
currbal Balance of Payments: Balance on Current Account; SA
Q 1960.1 - 1999.4 n = 160
```

The first field is the series name. The second is a description of the series (maximum 128 characters). On the second line the first field is a frequency code: M for monthly, Q for quarterly, A for annual, B for business-daily (daily with five days per week) and D for daily (seven days per week). No other frequencies are accepted at present. Then comes the starting date (N.B. with two digits following the point for monthly data, one for quarterly data, none for annual), a space, a hyphen, another space, the ending date, the string “n = ” and the integer number of observations. In the case of daily data the starting and ending dates should be given in the form YYYY/MM/DD. This format must be respected exactly.

Optionally, the first line of the index file may contain a short comment (up to 64 characters) on the source and nature of the data, following a hash mark. For example:

# Federal Reserve Board (interest rates)

The corresponding binary database file holds the data values, represented as “floats”, that is, single-precision floating-point numbers, typically taking four bytes apiece. The numbers are packed “by variable”, so that the first  $n$  numbers are the observations of variable 1, the next  $m$  the observations on variable 2, and so on.



## Appendix B

# Data import via ODBC

Since version 1.7.5, gretl provides a method for retrieving data from databases which support the Open Database Connectivity (ODBC) standard. Most users won't be interested in this, but there may be some for whom this feature matters a lot — typically, those who work in an environment where huge data collections are accessible via a Data Base Management System (DBMS).

In the following section we explain what is needed for ODBC support in gretl. We provide some background information on how ODBC works in section [B.2](#), and explain the details of getting gretl to retrieve data from a database in section [B.3](#).

### B.1 ODBC support

The piece of software that bridges between gretl and the ODBC system is a dynamically loaded “plugin”. This is included in the gretl packages for MS Windows and Mac OS X (on OS X support was added in gretl 1.9.0). On other unix-type platforms (notably Linux) you will have to build gretl from source to get ODBC support. This is because the gretl plugin depends on having unixODBC installed, which we cannot assume to be the case on typical Linux systems. To enable the ODBC plugin when building gretl, you must pass the option `--with-odbc` to gretl's configure script. In addition, if unixODBC is installed in a non-standard location you will have to specify its installation prefix using `--with-ODBC-prefix`, as in (for example)

```
./configure --with-odbc --with-ODBC-prefix=/opt/ODBC
```

### B.2 ODBC base concepts

ODBC is short for *Open DataBase Connectivity*, a group of software methods that enable a *client* to interact with a database *server*. The most common operation is when the client fetches some data from the server. ODBC acts as an intermediate layer between client and server, so the client “talks” to ODBC rather than accessing the server directly (see Figure [B.1](#)).

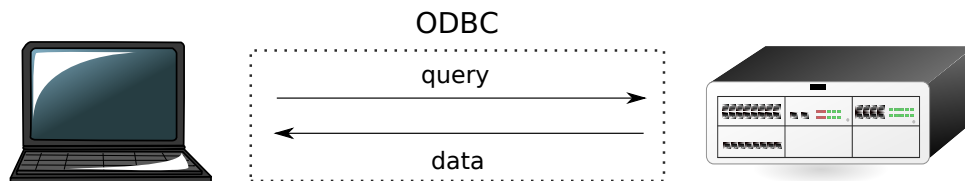


Figure B.1: Retrieving data via ODBC

For the above mechanism to work, it is necessary that the relevant ODBC software is installed and working on the client machine (contact your DB administrator for details). At this point, the database (or databases) that the server provides will be accessible to the client as a *data source* with a specific identifier (a Data Source Name or DSN); in most cases, a username and a password are required to connect to the data source.

Once the connection is established, the user sends a *query* to ODBC, which contacts the database manager, collects the results and sends them back to the user. The query is almost invariably

formulated in a special language used for the purpose, namely SQL.<sup>1</sup> We will not provide here an SQL tutorial: there are many such tutorials on the Net; besides, each database manager tends to support its own SQL dialect so the precise form of an SQL query may vary slightly if the DBMS on the other end is Oracle, MySQL, PostgreSQL or something else.

Suffice it to say that the main statement for retrieving data is the SELECT statement. Within a DBMS, data are organized in *tables*, which are roughly equivalent to spreadsheets. The SELECT statement returns a subset of a table, which is itself a table. For example, imagine that the database holds a table called “NatAccounts”, containing the data shown in Table B.1.

year	qtr	gdp	consump	tradebal
1970	1	584763	344746.9	−5891.01
1970	2	597746	350176.9	−7068.71
1970	3	604270	355249.7	−8379.27
1970	4	609706	361794.7	−7917.61
1971	1	609597	362490	−6274.3
1971	2	617002	368313.6	−6658.76
1971	3	625536	372605	−4795.89
1971	4	630047	377033.9	−6498.13

**Table B.1:** The “NatAccounts” table

The SQL statement

```
SELECT qtr, tradebal, gdp FROM NatAccounts WHERE year=1970;
```

produces the subset of the original data shown in Table B.2.

qtr	tradebal	gdp
1	−5891.01	584763
2	−7068.71	597746
3	−8379.27	604270
4	−7917.61	609706

**Table B.2:** Result of a SELECT statement

Gretl provides a mechanism for forwarding your query to the DBMS via ODBC and including the results in your currently open dataset.

### B.3 Syntax

At present gretl does not offer a graphical interface for ODBC import; this must be done via the command line interface. The two commands used for fetching data via an ODBC connection are `open` and `data`.

The `open` command is used for connecting to a DBMS: its syntax is

```
open dsn=database [user=username] [password=password] --odbc
```

The `user` and `password` items are optional; the effect of this command is to initiate an ODBC connection. It is assumed that the machine gretl runs on has a working ODBC client installed.

In order to actually retrieve the data, the `data` command is used. Its syntax is:

<sup>1</sup>See <http://en.wikipedia.org/wiki/SQL>.

```
data series [obs-format=format-string] query=query-string --odbc
```

where:

**series** is a list of names of gretl series to contain the incoming data, separated by spaces. Note that these series need not exist prior to the ODBC import.

**format-string** is an optional parameter, used to handle cases when a “rectangular” organisation of the database cannot be assumed (more on this later);

**query-string** is a string containing the SQL statement used to extract the data.<sup>2</sup>

There should be no spaces around the equals signs in the `obs-format` and `query` fields in the `data` command.

The `query-string` can, in principle, contain any valid SQL statement which results in a table. This string may be specified directly within the command, as in

```
data x query="SELECT foo FROM bar" --odbc
```

which will store into the gretl variable `x` the content of the column `foo` from the table `bar`. However, since in a real-life situation the string containing the SQL statement may be rather long, it may be best to store it in a string variable. For example:

```
string SqlQry = "SELECT foo1, foo2 FROM bar"
data x y query=SqlQry --odbc
```

### The observation format specifier

If the optional parameter `obs-format` is absent, as in the above example, the SQL query should return  $k$  columns of data, where  $k$  is the number of series names listed in the `data` command. It may be necessary to include a `smp1` command before the `data` command to set up the right “window” for the incoming data. In addition, if one cannot assume that the data will be delivered in the correct order (typically, chronological order), the SQL query should contain an appropriate `ORDER BY` clause.

The optional format string is used for those cases when there is no certainty that the data from the query will arrive in the same order as the gretl dataset. This may happen when missing values are interspersed within a column, or with data that do not have a natural ordering, e.g. cross-sectional data. In this case, the SQL statement should return a table with  $m + k$  columns, where the first  $m$  columns are used to identify the observation or row in the gretl dataset into which the actual data values in the final  $k$  columns should be placed. The `obs-format` string is used to translate the first  $m$  fields into a string which matches the string gretl uses to identify observations in the currently open dataset. Up to three columns can be used for this purpose ( $m \leq 3$ ).

Note that the strings gretl uses to identify observations can be seen by printing any variable “by observation”, as in

```
print index --byobs
```

(The series named `index` is automatically added to a dataset created via the `nulldata` command.)

The format specifiers available for use with `obs-format` are as follows:

<code>%d</code>	print an integer value
<code>%s</code>	print an string value
<code>%g</code>	print a floating-point value

<sup>2</sup>Prior to gretl 1.8.8, the tag “`query=`” was not required (or accepted) before the query string, and only one series could be imported at a time. This variant is still accepted for the sake of backward compatibility.

In addition the format can include literal characters to be passed through, such as slashes or colons, to make the resulting string compatible with gretl's observation identifiers.

For example, consider the following fictitious case: we have a 5-days-per-week dataset, to which we want to add the stock index for the Verdurian market;<sup>3</sup> it so happens that in Verduria Saturdays are working days but Wednesdays are not. We want a column which does *not* contain data on Saturdays, because we wouldn't know where to put them, but at the same time we want to place missing values on all the Wednesdays.

In this case, the following syntax could be used

```
string QRY="SELECT year,month,day,VerdSE FROM AlmeaIndexes"
data y obs-format="%d/%d/%d" query=QRY --odbc
```

The column VerdSE holds the data to be fetched, which will go into the gretl series *y*. The first three columns are used to construct a string which identifies the day. Daily dates take the form YYYY/MM/DD in gretl. If a row from the DBMS produces the observation string 2008/04/01 this will match OK (it's a Tuesday), but 2008/04/05 will not match since it is a Saturday; the corresponding row will therefore be discarded. On the other hand, since no string 2008/04/23 will be found in the data coming from the DBMS (it's a Wednesday), that entry is left blank in our series *y*.

## B.4 Examples

Table Consump

Field	Type
time	decimal(7,2)
income	decimal(16,6)
consump	decimal(16,6)

Table DATA

Field	Type
year	decimal(4,0)
qtr	decimal(1,0)
varname	varchar(16)
xval	decimal(20,10)

**Table B.3:** Example AWM database – structure

Table Consump

1970.00	424278.975500	344746.944000
1970.25	433218.709400	350176.890400
1970.50	440954.219100	355249.672300
1970.75	446278.664700	361794.719900
1971.00	447752.681800	362489.970500
1971.25	453553.860100	368313.558500
1971.50	460115.133100	372605.015300
...		

Table DATA

1970	1	CAN	-517.9085000000
1970	2	CAN	662.5996000000
1970	3	CAN	1130.4155000000
1970	4	CAN	467.2508000000
1970	1	COMPR	18.4000000000
1970	2	COMPR	18.6341000000
1970	3	COMPR	18.3000000000
1970	4	COMPR	18.2663000000
1970	1	D1	1.0000000000
1970	2	D1	0.0000000000
...			

**Table B.4:** Example AWM database — data

In the following examples, we will assume that access is available to a database known to ODBC with the data source name “AWM”, with username “Otto” and password “Bingo”. The database “AWM” contains quarterly data in two tables (see B.3 and B.4):

<sup>3</sup>See <http://www.almeopedia.com/index.php/Verduria>.

The table `Consump` is the classic “rectangular” dataset; that is, its internal organization is the same as in a spreadsheet or econometrics package: each row is a data point and each column is a variable. The structure of the `DATA` table is different: each record is one figure, stored in the column `xval`, and the other fields keep track of which variable it belongs to, for which date.

**Example B.1:** Simple query from a rectangular table

---

```
nulldata 160
setobs 4 1970:1 --time
open dsn=AWM user=Otto password=Bingo --odbc

string Qry = "SELECT consump, income FROM Consump"
data cons inc query=Qry --odbc
```

---

Example [B.1](#) shows a query for two series: first we set up an empty quarterly dataset. Then we connect to the database using the `open` statement. Once the connection is established we retrieve two columns from the `Consump` table. No observation string is required because the data already have a suitable structure; we need only import the relevant columns.

**Example B.2:** Simple query from a non-rectangular table

---

```
string S = "select year, qtr, xval from DATA \
           where varname='WLN' ORDER BY year, qtr"
data wln obs-format="%d:%d" query=S --odbc
```

---

In example [B.2](#), by contrast, we make use of the observation string since we are drawing from the `DATA` table, which is not rectangular. The SQL statement stored in the string `S` produces a table with three columns. The `ORDER BY` clause ensures that the rows will be in chronological order, although this is not strictly necessary in this case.

**Example B.3:** Handling of missing values for a non-rectangular table

---

```
string foo = "select year, qtr, xval from DATA \
  where varname='STN' AND qtr>1"
data bar obs-format="%d:%d" query=foo --odbc
print bar --byobs
```

---

Example B.3 shows what happens if the rows in the outcome from the SELECT statement do not match the observations in the currently open gretl dataset. The query includes a condition which filters out all the data from the first quarter. The query result (invisible to the user) would be something like

year	qtr	xval
1970	2	7.8705000000
1970	3	7.5600000000
1970	4	7.1892000000
1971	2	5.8679000000
1971	3	6.2442000000
1971	4	5.9811000000
1972	2	4.6883000000
1972	3	4.6302000000
...		

Internally, gretl fills the variable `bar` with the corresponding value if it finds a match; otherwise, NA is used. Printing out the variable `bar` thus produces

Obs	bar
1970:1	
1970:2	7.8705
1970:3	7.5600
1970:4	7.1892
1971:1	
1971:2	5.8679
1971:3	6.2442
1971:4	5.9811
1972:1	
1972:2	4.6883
1972:3	4.6302
...	

## Appendix C

# Building gretl

### C.1 Requirements

Gretl is written in the C programming language, abiding as far as possible by the ISO/ANSI C Standard (C90) although the graphical user interface and some other components necessarily make use of platform-specific extensions.

The program was developed under Linux. The shared library and command-line client should compile and run on any platform that supports ISO/ANSI C and has the libraries listed in Table C.1. If the GNU readline library is found on the host system this will be used for gretcli, providing a much enhanced editable command line. See the [readline homepage](#).

<i>Library</i>	<i>purpose</i>	<i>website</i>
zlib	data compression	<a href="#">info-zip.org</a>
libxml2	XML manipulation	<a href="#">xmlsoft.org</a>
LAPACK	linear algebra	<a href="#">netlib.org</a>
FFTW3	Fast Fourier Transform	<a href="#">fftw.org</a>
glib-2.0	Numerous utilities	<a href="#">gtk.org</a>

**Table C.1:** Libraries required for building gretl

The graphical client program should compile and run on any system that, in addition to the above requirements, offers GTK version 2.4.0 or higher (see [gtk.org](#)).<sup>1</sup>

Gretl calls gnuplot for graphing. You can find gnuplot at [gnuplot.info](#). As of this writing the most recent official release is 4.2.6 (of September, 2009). The gretl packages for MS Windows and Mac OS X come with current CVS gnuplot (version 4.5), and the gretl website offers information on building or installing gnuplot 4.5 on Linux.

Some features of gretl make use of portions of Adrian Feguin's gtkextra library. The relevant parts of this package are included (in slightly modified form) with the gretl source distribution.

A binary version of the program is available for the Microsoft Windows platform (Windows 2000 or higher). This version was cross-compiled under Linux using mingw (the GNU C compiler, gcc, ported for use with win32) and linked against the Microsoft C library, msvcrt.dll. The (free, open-source) Windows installer program is courtesy of Jordan Russell ([jrsoftware.org](#)).

### C.2 Build instructions: a step-by-step guide

In this section we give instructions detailed enough to allow a user with only a basic knowledge of a Unix-type system to build gretl. These steps were tested on a fresh installation of Debian Etch. For other Linux distributions (especially Debian-based ones, like Ubuntu and its derivatives) little should change. Other Unix-like operating systems such as MacOSX and BSD would probably require more substantial adjustments.

In this guided example, we will build gretl complete with documentation. This introduces a few

---

<sup>1</sup>Up till version 1.5.1, gretl could also be built using GTK 1.2. Support for this was dropped at version 1.6.0 of gretl.

more requirements, but gives you the ability to modify the documentation files as well, like the help files or the manuals.

### Installing the prerequisites

We assume that the basic GNU utilities are already installed on the system, together with these other programs:

- some  $\text{T}_{\text{E}}\text{X}/\text{L}_{\text{A}}\text{T}_{\text{E}}\text{X}$  system (texlive will do beautifully)
- Gnuplot
- ImageMagick

We also assume that the user has administrative privileges and knows how to install packages. The examples below are carried out using the `apt-get` shell command, but they can be performed with menu-based utilities like `aptitude`, `dselect` or the GUI-based program `synaptic`. Users of Linux distributions which employ rpm packages (e.g. Red Hat/Fedora, Mandriva, SuSE) may want to refer to the [dependencies](#) page on the gretl website.

The first step is installing the C compiler and related basic utilities, if these are not already in place. On a Debian system, these are contained in a bunch of packages that can be installed via the command

```
apt-get install gcc autoconf automake1.9 libtool flex bison gcc-doc \
libc6-dev libc-dev gfortran gettext pkgconfig
```

Then it is necessary to install the “development” (dev) packages for the libraries that gretl uses:

<i>Library</i>	<i>command</i>
GLIB	<code>apt-get install libglib2.0-dev</code>
GTK 2.0	<code>apt-get install libgtk2.0-dev</code>
PNG	<code>apt-get install libpng12-dev</code>
XSLT	<code>apt-get install libxslt1-dev</code>
LAPACK	<code>apt-get install liblapack-dev</code>
FFTW	<code>apt-get install libfftw3-dev</code>
READLINE	<code>apt-get install libreadline-dev</code>
ZLIB	<code>apt-get install zlib1g-dev</code>
XML	<code>apt-get install libxml2-dev</code>
GMP	<code>apt-get install libgmp3-dev</code>
CURL	<code>apt-get install libcurl-dev</code>
MPFR	<code>apt-get install libmpfr-dev</code>

(MPFR is optional, but recommended.) The dev packages for these libraries are necessary to *compile* gretl — you’ll also need the plain, non-dev library packages to *run* gretl, but most of these should already be part of a standard installation. In order to enable other optional features, like audio support, you may need to install more libraries.

☞ The above steps can be much simplified on Linux systems that provide deb-based package managers, such as Debian and its derivatives (Ubuntu, Knoppix and other distributions). The command

```
apt-get build-dep gretl
```

will download and install all the necessary packages for building the version of gretl that is currently present in your APT sources. Technically, this does not guarantee that all the software necessary to build the CVS



version is included, because the version of gretl on your repository may be quite old and build requirements may have changed in the meantime. However, the chances of a mismatch are rather remote for a reasonably up-to-date system, so in most cases the above command should take care of everything correctly.

### Getting the source: release or CVS

At this point, it is possible to build from the source. You have two options here: obtain the latest released source package, or retrieve the current CVS version of gretl (CVS = Concurrent Versions System). The usual caveat applies to the CVS version, namely, that it may not build correctly and may contain “experimental” code; on the other hand, CVS often contains bug-fixes relative to the released version. If you want to help with testing and to contribute bug reports, we recommend using CVS gretl.

To work with the released source:

1. Download the gretl source package from [gretl.sourceforge.net](http://gretl.sourceforge.net).
2. Unzip and untar the package. On a system with the GNU utilities available, the command would be `tar xvfz gretl-N.tar.gz` (replace N with the specific version number of the file you downloaded at step 1).
3. Change directory to the gretl source directory created at step 2 (e.g. `gretl-1.6.6`).
4. Proceed to the next section, “Configure and make”.

To work with CVS you’ll first need to install the cvs client program if it’s not already on your system. Relevant resources you may wish to consult include the CVS website at [www.nongnu.org/cvs](http://www.nongnu.org/cvs), general information on sourceforge CVS on the [SourceForge CVS page](#), and instructions specific to gretl at the [SF gretl CVS page](#).

When grabbing the CVS sources *for the first time*, you should first decide where you want to store the code. For example, you might create a directory called cvs under your home directory. Open a terminal window, cd into this directory, and type the following commands:

```
cvs -d:pserver:anonymous@gretl.cvs.sourceforge.net:/cvsroot/gretl login
cvs -z3 -d:pserver:anonymous@gretl.cvs.sourceforge.net:/cvsroot/gretl co -P gretl
```

After the first command you will be prompted for a password: just hit the Enter key. After the second command, cvs should create a subdirectory named gretl and fill it with the current sources.

When you want to *update the source*, this is very simple: just move into the gretl directory and type

```
cvs update -d -P
```

Assuming you’re now in the CVS gretl directory, you can proceed in the same manner as with the released source package.

### Configure the source

The next command you need is `./configure`; this is a complex script that detects which tools you have on your system and sets things up. The configure command accepts many options; you may want to run

```
./configure --help
```

first to see what options are available. One option you may wish to tweak is `--prefix`. By default the installation goes under `/usr/local` but you can change this. For example

```
./configure --prefix=/usr
```

will put everything under the /usr tree. Another useful option refers to the fact that, by default, gretl offers support for the gnome desktop. If you want to suppress the gnome-specific features you can pass the option `--without-gnome` to `configure`.

In order to have the documentation built, we need to pass the relevant option to `configure`, as in

```
./configure --enable-build-doc
```

But please note that this option will work only if you are using the CVS source.

You will see a number of checks being run, and if everything goes according to plan, you should see a summary similar to that displayed in Example C.1.

**Example C.1:** Output from `./configure --enable-build-doc`

---

Configuration:

```

Installation path:           /usr/local
Use readline library:       yes
Use gnuplot for graphs:     yes
Use PNG for gnuplot graphs: yes
Use LaTeX for typesetting output: yes
Gnu Multiple Precision support: yes
MPFR support:               no
LAPACK support:             yes
FFTW3 support:              yes
Build with GTK version:     2.0
Script syntax highlighting: yes
Use installed gtksourceview: yes
Build with gnome support:   no
Build gretl documentation:  yes
Build message catalogs:    yes
Gnome installation prefix:  NA
X-12-ARIMA support:         yes
TRAMO/SEATS support:        yes
Experimental audio support: no

```

Now type 'make' to build gretl.

---

☞ If you're using CVS, it's a good idea to re-run the `configure` script after doing an update. This is not always necessary, but sometimes it is, and it never does any harm. For this purpose, you may want to write a little shell script that calls `configure` with any options you want to use.

### Build and install

We are now ready to undertake the compilation proper: this is done by running the `make` command, which takes care of compiling all the necessary source files in the correct order. All you need to do is type

```
make
```

This step will likely take several minutes to complete; a lot of output will be produced on screen. Once this is done, you can install your freshly baked copy of gretl on your system via

```
make install
```

On most systems, the `make install` command requires you to have administrative privileges. Hence, either you log in as `root` before launching `make install` or you may want to use the `sudo` utility:

```
sudo make install
```

## Appendix D

# Numerical accuracy

Gretl uses double-precision arithmetic throughout — except for the multiple-precision plugin invoked by the menu item “Model, Other linear models, High precision OLS” which represents floating-point values using a number of bits given by the environment variable GRETL\_MP\_BITS (default value 256).

The normal equations of Least Squares are by default solved via Cholesky decomposition, which is highly accurate provided the matrix of cross-products of the regressors,  $X'X$ , is not very ill conditioned. If this problem is detected, gretl automatically switches to use QR decomposition.

The program has been tested rather thoroughly on the statistical reference datasets provided by NIST (the U.S. National Institute of Standards and Technology) and a full account of the results may be found on the gretl website (follow the link “Numerical accuracy”).

To date, two published reviews have discussed gretl’s accuracy: Giovanni Baiocchi and Walter Di-taso (2003), and Talha Yalta and Yasemin Yalta (2007). We are grateful to these authors for their careful examination of the program. Their comments have prompted several modifications including the use of Stephen Moshier’s *cephes* code for computing p-values and other quantities relating to probability distributions (see [netlib.org](http://netlib.org)), changes to the formatting of regression output to ensure that the program displays a consistent number of significant digits, and attention to compiler issues in producing the MS Windows version of gretl (which at one time was slightly less accurate than the Linux version).

Gretl now includes a “plugin” that runs the NIST linear regression test suite. You can find this under the “Tools” menu in the main window. When you run this test, the introductory text explains the expected result. If you run this test and see anything other than the expected result, please send a bug report to [cottrell@wfu.edu](mailto:cottrell@wfu.edu).

All regression statistics are printed to 6 significant figures in the current version of gretl (except when the multiple-precision plugin is used, in which case results are given to 12 figures). If you want to examine a particular value more closely, first save it (for example, using the `genr` command) then print it using `printf`, to as many digits as you like (see the *Gretl Command Reference*).

## Appendix E

# Related free software

Gretl's capabilities are substantial, and are expanding. Nonetheless you may find there are some things you can't do in gretl, or you may wish to compare results with other programs. If you are looking for complementary functionality in the realm of free, open-source software we recommend the following programs. The self-description of each program is taken from its website.

- **GNU R** [r-project.org](http://r-project.org): "R is a system for statistical computation and graphics. It consists of a language plus a run-time environment with graphics, a debugger, access to certain system functions, and the ability to run programs stored in script files... It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS." Comment: There are numerous add-on packages for R covering most areas of statistical work.
- **GNU Octave** [www.octave.org](http://www.octave.org): "GNU Octave is a high-level language, primarily intended for numerical computations. It provides a convenient command line interface for solving linear and nonlinear problems numerically, and for performing other numerical experiments using a language that is mostly compatible with Matlab. It may also be used as a batch-oriented language."
- **JMulTi** [www.jmulti.de](http://www.jmulti.de): "JMulTi was originally designed as a tool for certain econometric procedures in time series analysis that are especially difficult to use and that are not available in other packages, like Impulse Response Analysis with bootstrapped confidence intervals for VAR/VEC modelling. Now many other features have been integrated as well to make it possible to convey a comprehensive analysis." Comment: JMulTi is a java GUI program: you need a java run-time environment to make use of it.

As mentioned above, gretl offers the facility of exporting data in the formats of both Octave and R. In the case of Octave, the gretl data set is saved as a single matrix, X. You can pull the X matrix apart if you wish, once the data are loaded in Octave; see the Octave manual for details. As for R, the exported data file preserves any time series structure that is apparent to gretl. The series are saved as individual structures. The data should be brought into R using the `source()` command.

In addition, gretl has a convenience function for moving data quickly into R. Under gretl's "Tools" menu, you will find the entry "Start GNU R". This writes out an R version of the current gretl data set (in the user's gretl directory), and sources it into a new R session. The particular way R is invoked depends on the internal gretl variable `Rcommand`, whose value may be set under the "Tools, Preferences" menu. The default command is `RGui.exe` under MS Windows. Under X it is `xterm -e R`. Please note that at most three space-separated elements in this command string will be processed; any extra elements are ignored.

## Appendix F

# Listing of URLs

Below is a listing of the full URLs of websites mentioned in the text.

**Estima (RATS)** <http://www.estima.com/>  
**FFTW3** <http://www.fftw.org/>  
**Gnome desktop homepage** <http://www.gnome.org/>  
**GNU Multiple Precision (GMP) library** <http://gmplib.org/>  
**CURL library** <http://curl.haxx.se/libcurl/>  
**GNU Octave homepage** <http://www.octave.org/>  
**GNU R homepage** <http://www.r-project.org/>  
**GNU R manual** <http://cran.r-project.org/doc/manuals/R-intro.pdf>  
**Gnuplot homepage** <http://www.gnuplot.info/>  
**Gnuplot manual** <http://ricardo.ecn.wfu.edu/gnuplot.html>  
**Gretl data page** [http://gretl.sourceforge.net/gretl\\_data.html](http://gretl.sourceforge.net/gretl_data.html)  
**Gretl homepage** <http://gretl.sourceforge.net/>  
**GTK+ homepage** <http://www.gtk.org/>  
**GTK+ port for win32** <http://www.gimp.org/~tml/gimp/win32/>  
**InfoZip homepage** <http://www.info-zip.org/pub/infozip/zlib/>  
**JMulTi homepage** <http://www.jmulti.de/>  
**JRSoftware** <http://www.jrsoftware.org/>  
**Mingw (gcc for win32) homepage** <http://www.mingw.org/>  
**Minpack** <http://www.netlib.org/minpack/>  
**Penn World Table** <http://pwt.econ.upenn.edu/>  
**Readline homepage** <http://cnswww.cns.cwru.edu/~chet/readline/rltop.html>  
**Readline manual** <http://cnswww.cns.cwru.edu/~chet/readline/readline.html>  
**Xmlsoft homepage** <http://xmlsoft.org/>

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