Establishment of a seed orchard of *Acacia mearnsii* in Pietermartizburg, South Africa in 2019 using the ONA scheme. Photo by courtesy of Julian Chan, ICFR company.

Seed orchard layouts for advanced generations

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Milan Lstibůrek

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Chaloupková K., Stejskal J., El-Kassaby Y.A., Frampton J. & Lstibůrek M. (2019). Current Advances in Seed Orchard Layouts: Two Case Studies in Conifers. *Forests* 10(2): 93.

Chaloupková K., Stejskal J., El-Kassaby Y.A. & Lstibůrek M. (2016). Optimum neighborhood seed orchard design. *Tree Genetics & Genomes* 12(6): 105.

Lstibůrek M., Stejskal J., Misevicius A., Korecký J. & El-Kassaby Y.A. (2015). Expansion of the minimum-inbreeding seed orchard design to operational scale. *Tree Genetics & Genomes* 11(1): 12.

El-Kassaby Y. A., Fayed M., Klápště J. & Lstibůrek M. (2014). Randomized, replicated, staggered clonal-row (R^2SCR) seed orchard design. *Tree Genetics & Genomes* 10(3): 555-563.

Funda T., Lstibůrek M., Klápště J. & El-Kassaby Y.A. (2012). Optimization of genetic gain and diversity in seed orchard crops considering variation in seed germination. *Scandinavian Journal of Forest Research* 27(8): 787-793.

Lstibůrek M., El-Kassaby Y.A. (2010). Minimum Inbreeding Seed Orchard Design. *Forest Science* 56(6): 603–608.

Funda T., Lstibůrek M., Lachout Petr, Klápště J., El-Kassaby Y.A. (2009). Optimization of combined genetic gain and diversity for collection and deployment of seed orchards crops. *Tree Genetics & Genomes* 5(4): 583-593.

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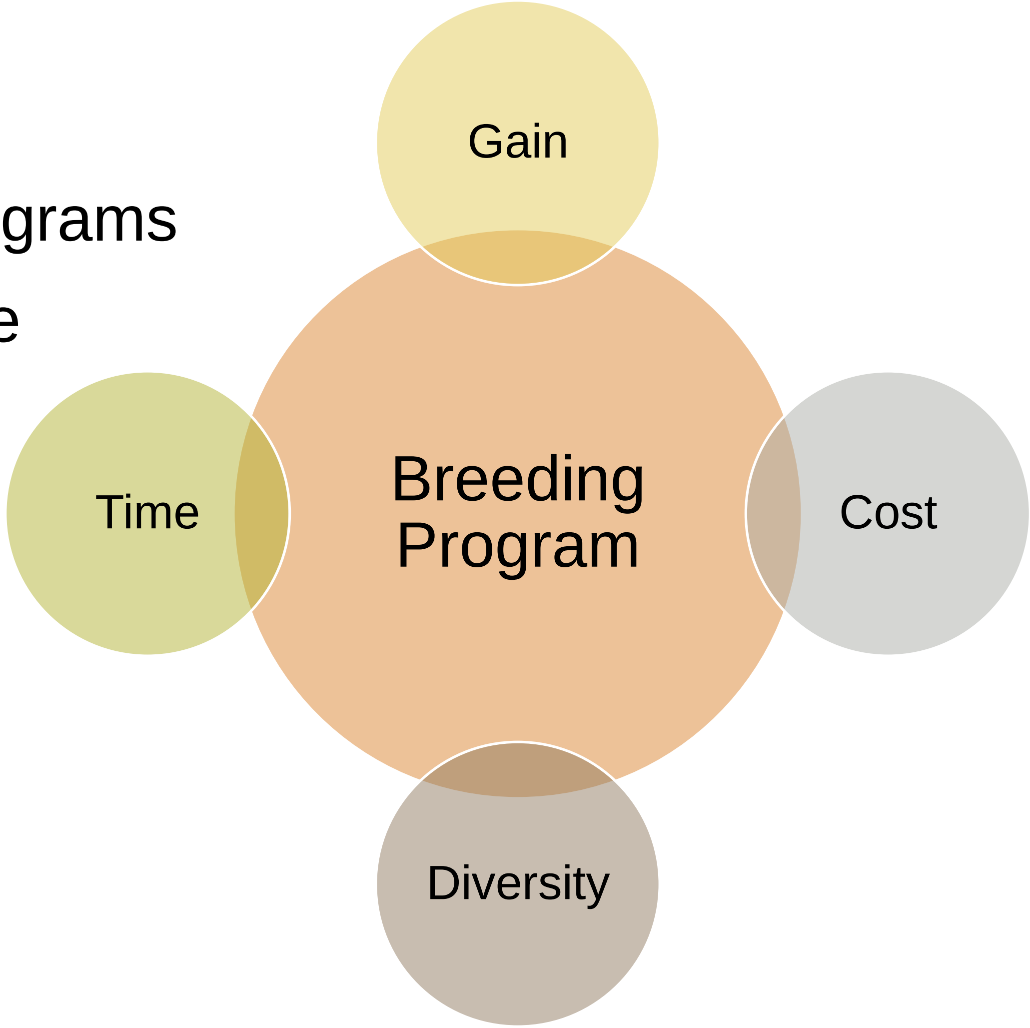
Breeding and deployment

- in line with the evolutionary framework?
- delineation and structure of breeding programs
- impact of environmental (climate) change
- utility of genomics and phenomics?



OP seed orchard deployment

- genetic improvement considering additive gene effects only,
- not utilizing non-additive components and GxE components,
- assuming constant environmental conditions (within a breeding zone),
- avoidance of inbreeding depression – reduced selection intensity,
- high error rate of the gain x diversity in particular seed crop,
- **in summary: not efficient deployment scheme for advanced generations.**

Criteria in the SO design

- maximize genetic gain while maintaining acceptable genetic diversity,
- provide for random mating,
- minimize inbreeding,
- minimize impact of selection errors (maintain flexibility for roguing).

Hodge and White, 1993

Genetic gain perspective (1)

- contributions are calculated as a compromise between high gain and „acceptable“ diversity,
- „optimum“ contribution in advanced generations is not linearly related to the breeding value,
- „optimum“ is in reference to a particular model (likely not the real system it represents),
- additional variables can be included to the calculation of contributions (Funda et al. 2009).

Genetic gain perspective (2)

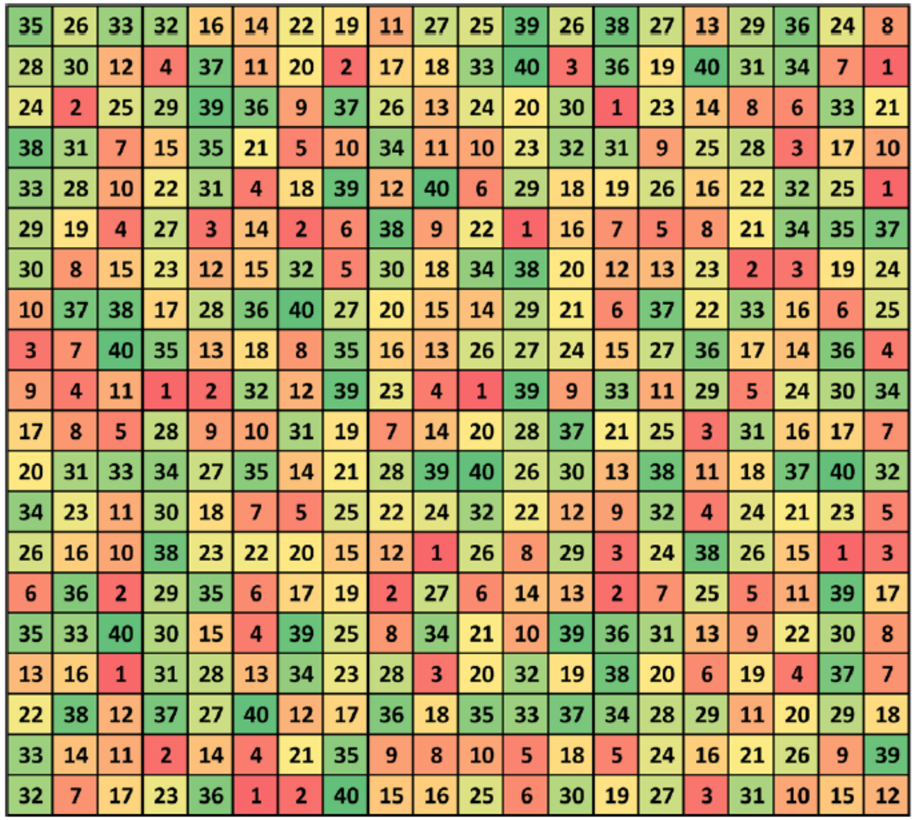
- clonal contributions should be determined within the selection algorithm (one-step approach),
- contributions are function of unknown (predicted) breeding values, so there is an error associated with contributions (should not be treated as constants),
- genetic response and diversity are each associated with prediction error:

Random mating

- good admixture, no preferential mating,
- “random” vs. mathematical random,
- is not 100% in line with the inbreeding minimization criterium,
- not realistically feasible with **many** added constraints (large clonal contributions, variation in clonal contributions, spatial adjustment accounting for relatedness),
- real outcome dependent on variation in fecundity and flowering phenology and additional variables (contamination, pollen dispersal etc.).

Optimum-Neighborhood Design

40 unrelated clones, 10 ramets each



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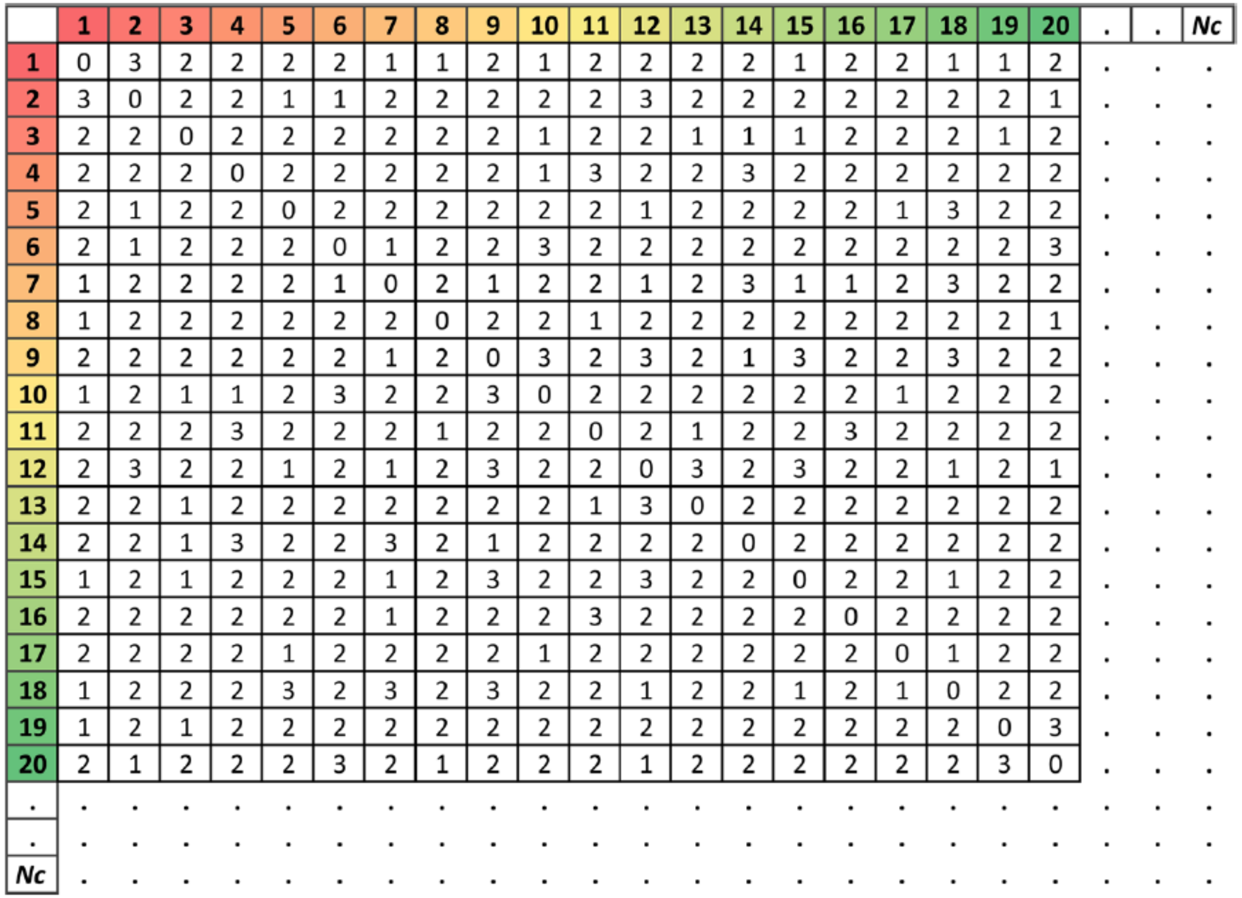

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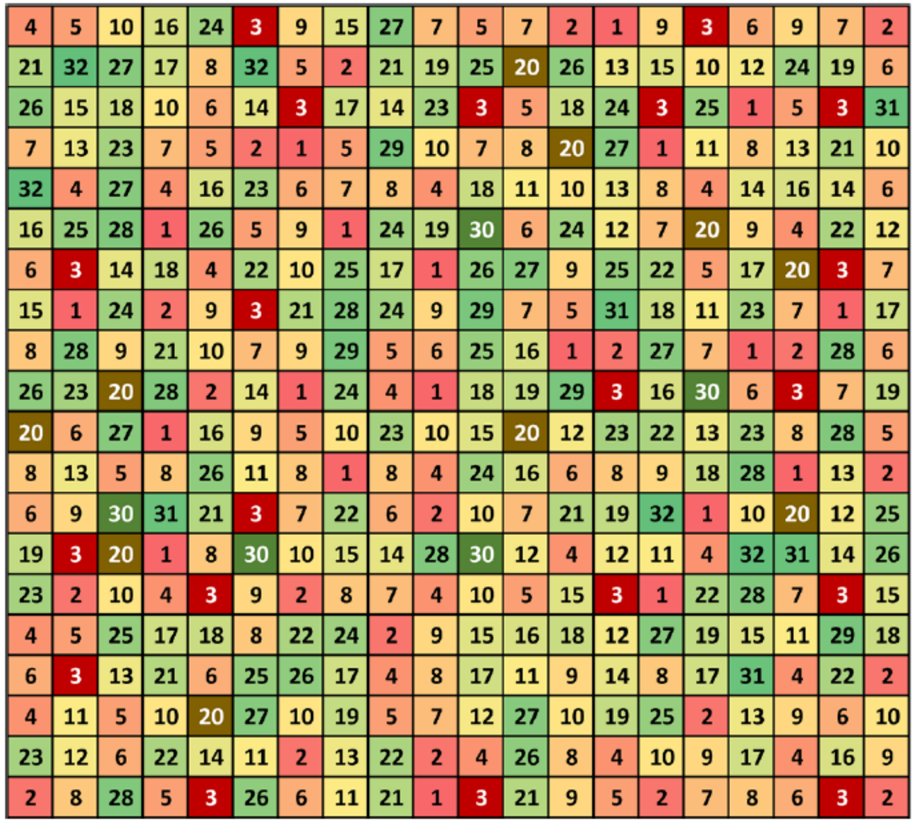
Chaloupková et al., 2016

Optimum-Neighborhood Design

10, 18, 4 clones with 20, 10, 5 ramets



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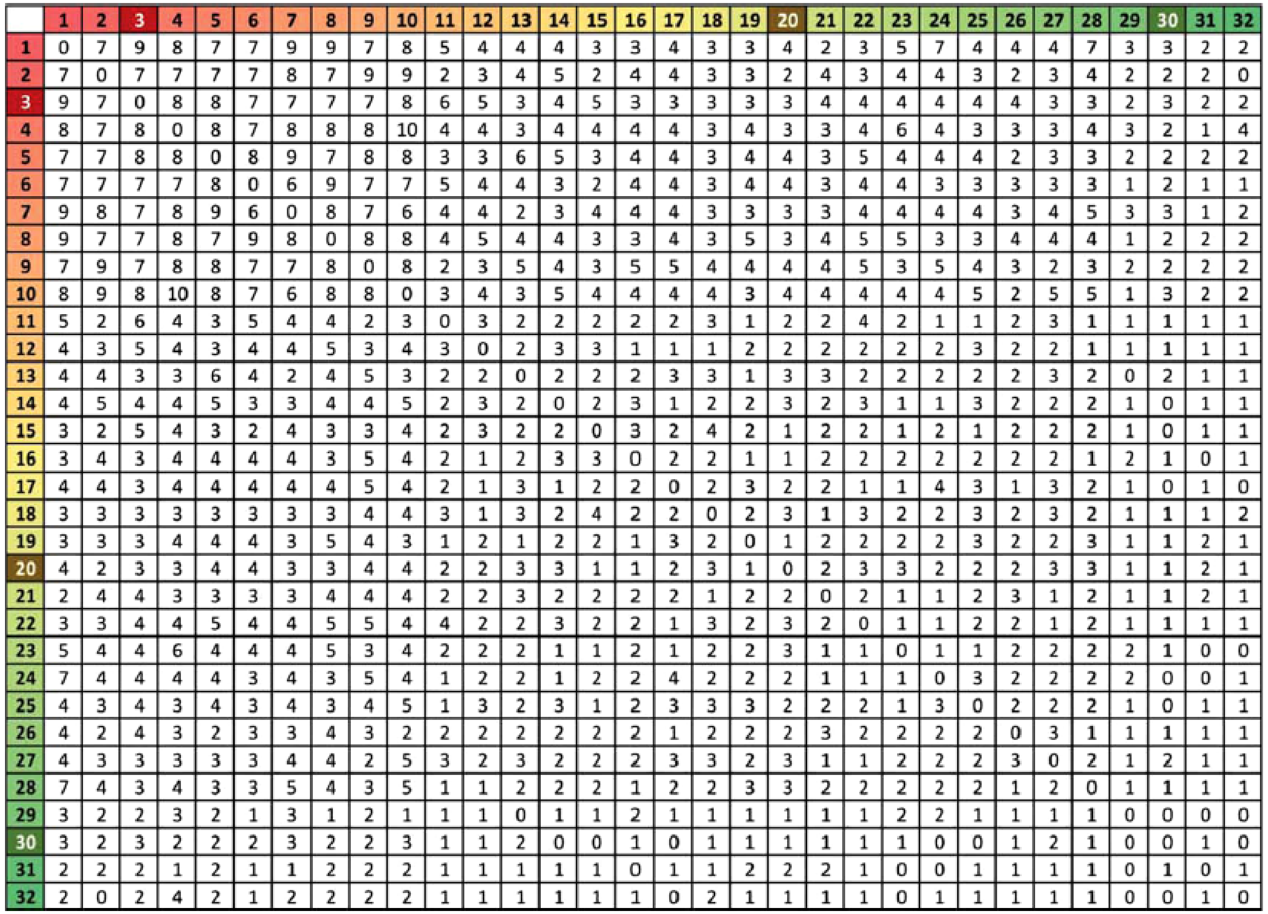

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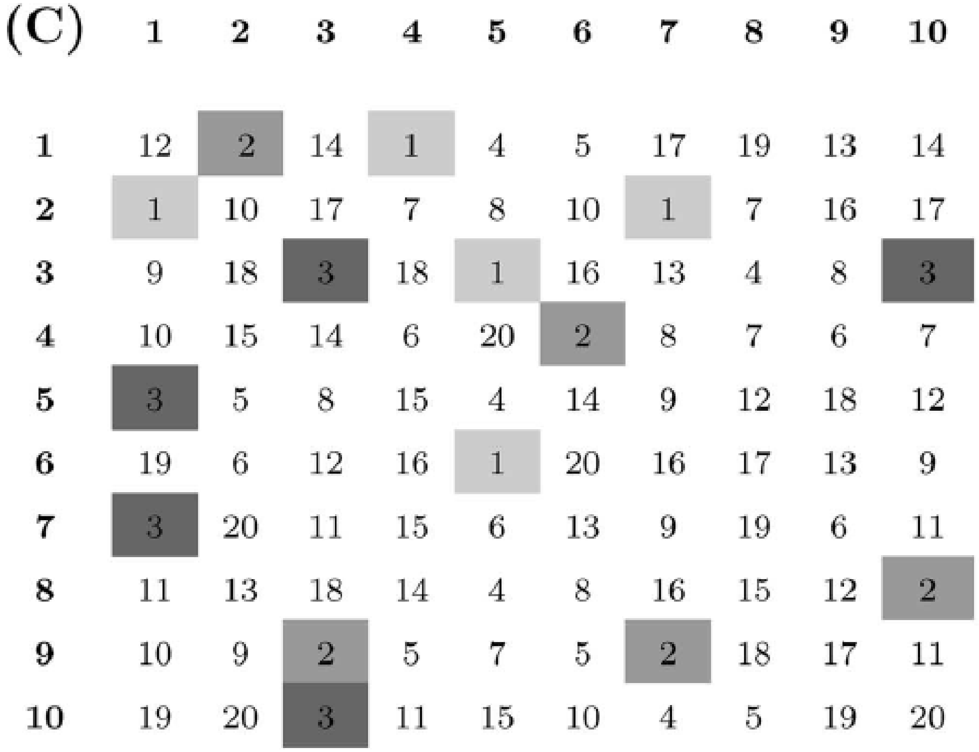
Chaloupková et al., 2016

Avoidance of inbreeding

- consequence of relatedness within and among parents in SO,
- knowledge of the negative impact of inbreeding (including selfing) on target traits (inbreeding depression),
- minimization is not 100% in line with the random mating objective,
- not realistically feasible with **many** added constraints (large clonal contributions, variation in clonal contributions, many related clones),
- real outcome dependent on variation in fecundity and flowering phenology and additional variables (contamination, pollen dispersal etc.).

COOL vs. Minimum Inbreeding

20 unrelated clones, 5 ramets each



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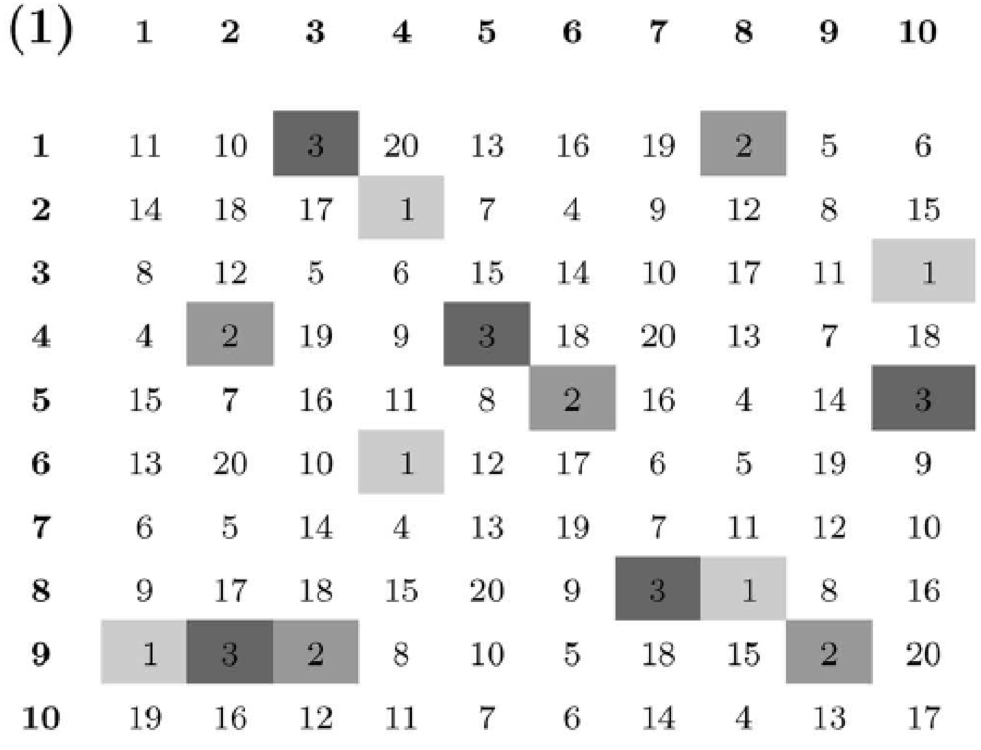
Bell and Fletcher, 1978



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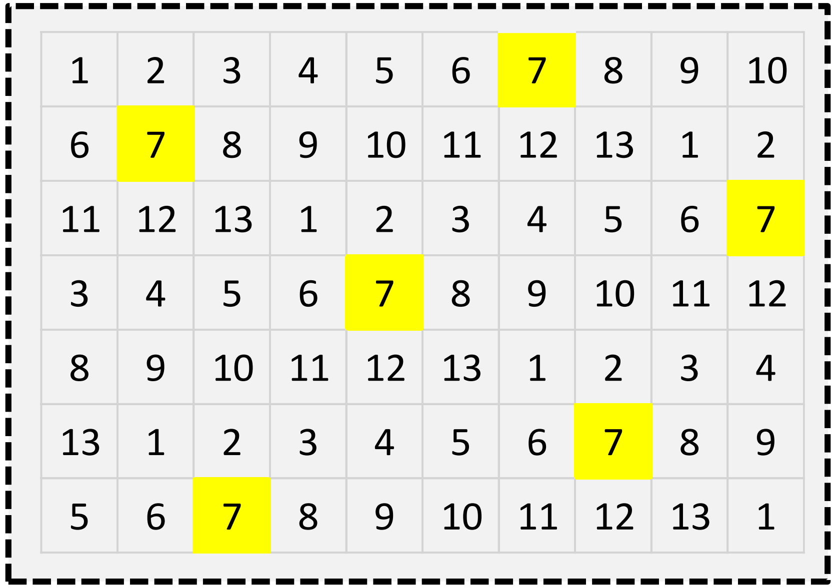
Lstibůrek and El-Kassaby, 2010

Minimum Inbreeding vs. Systematic scheme



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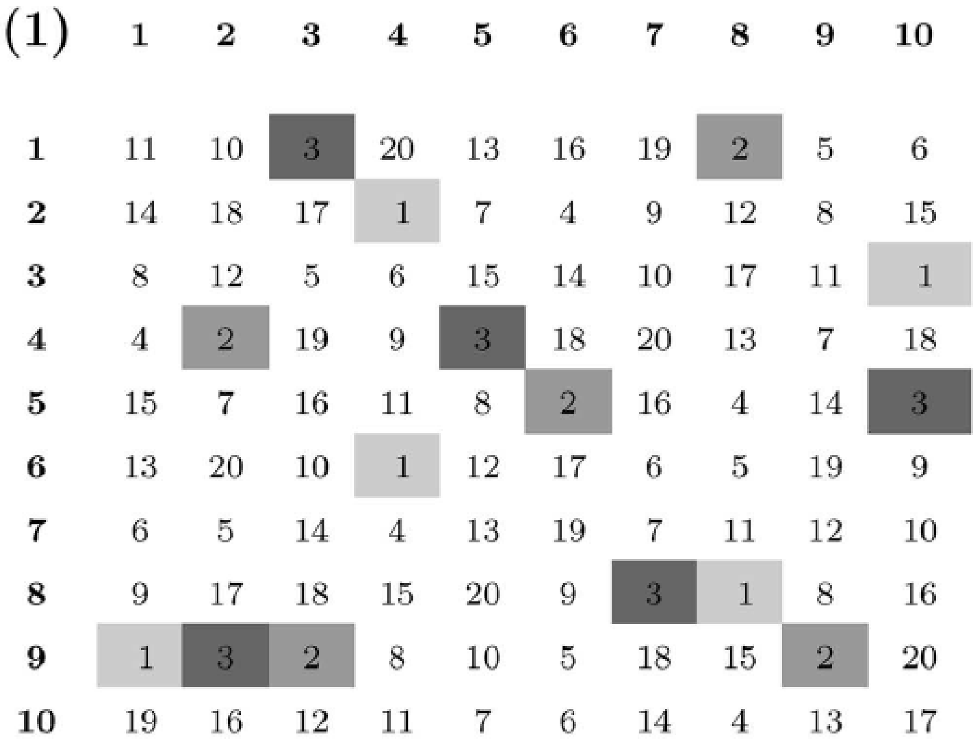
subset from Giertych, 1971



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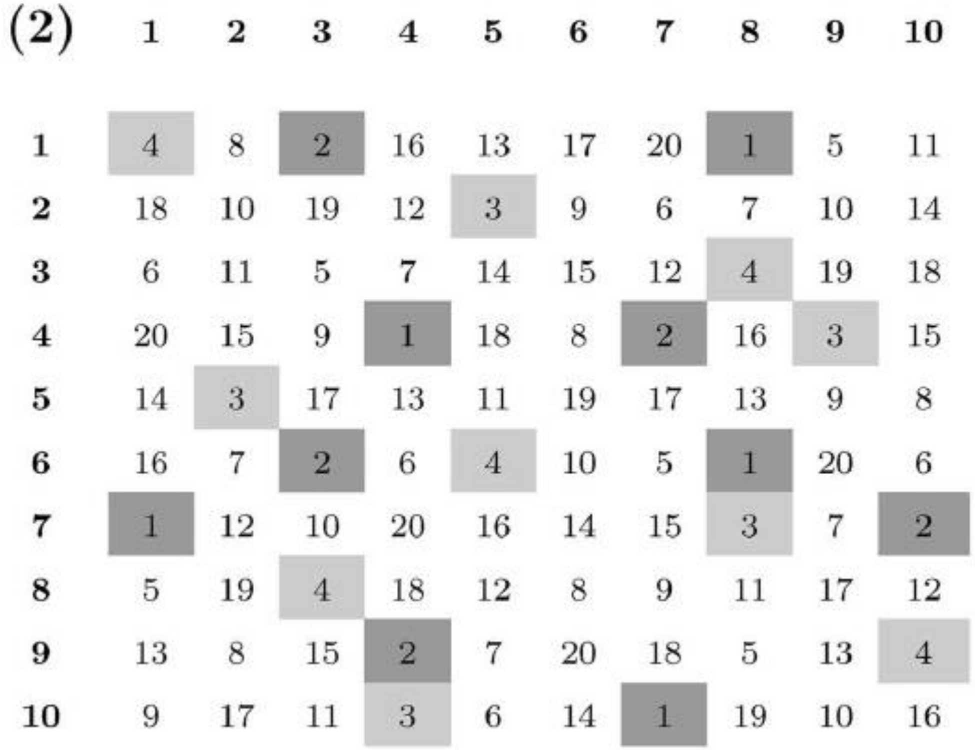
7	6	5	14	4	13	19	7	11	12	10
8	9	17	18	15	20	9	3	1	8	16
9	1	3	2	8	10	5	18	15	2	20
10	19	16	12	11	7	6	14	4	13	17

Lstibůrek and El-Kassaby, 2010

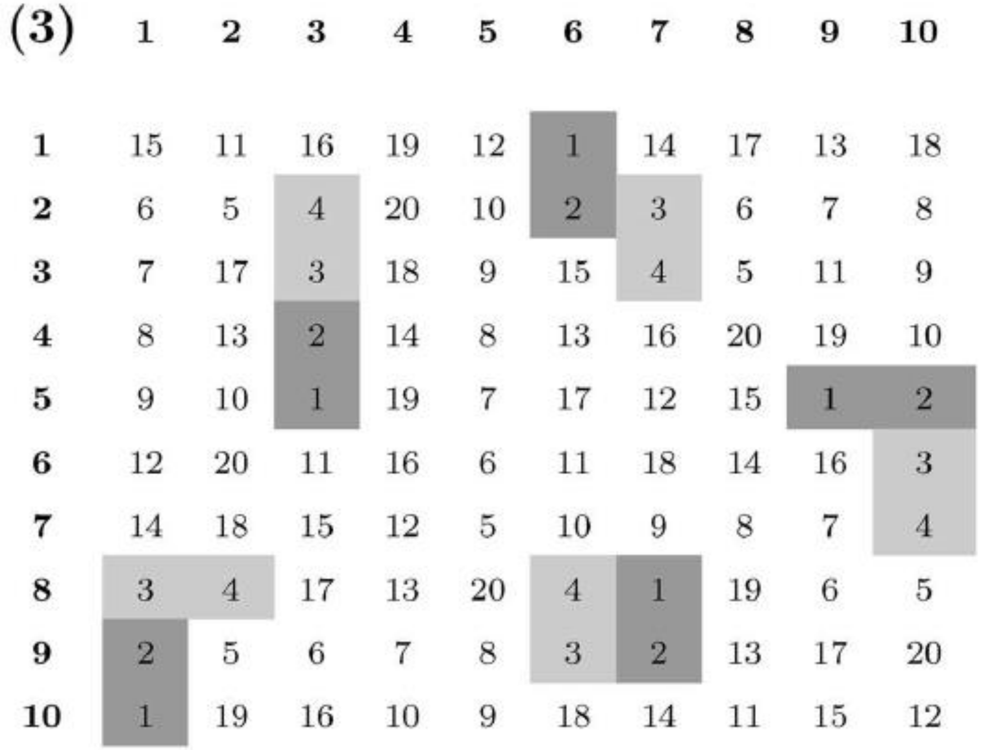
Minimum Inbreeding

20 clones: 10 pairs of half-sibs (1-2, …, 19-20)



(2)	1	2	3	4	5	6	7	8	9	10
1	4	8	2	16	13	17	20	1	5	11
2	18	10	19	12	3	9	6	7	10	14
3	6	11	5	7	14	15	12	4	19	18
4	20	15	9	1	18	8	2	16	3	15
5	14	3	17	13	11	19	17	13	9	8
6	16	7	2	6	4	10	5	1	20	6
7	1	12	10	20	16	14	15	3	7	2
8	5	19	4	18	12	8	9	11	17	12
9	13	8	15	2	7	20	18	5	13	4
10	9	17	11	3	6	14	1	19	10	16

20 unrelated clones, preferential mating (1-2, …, 9-10)

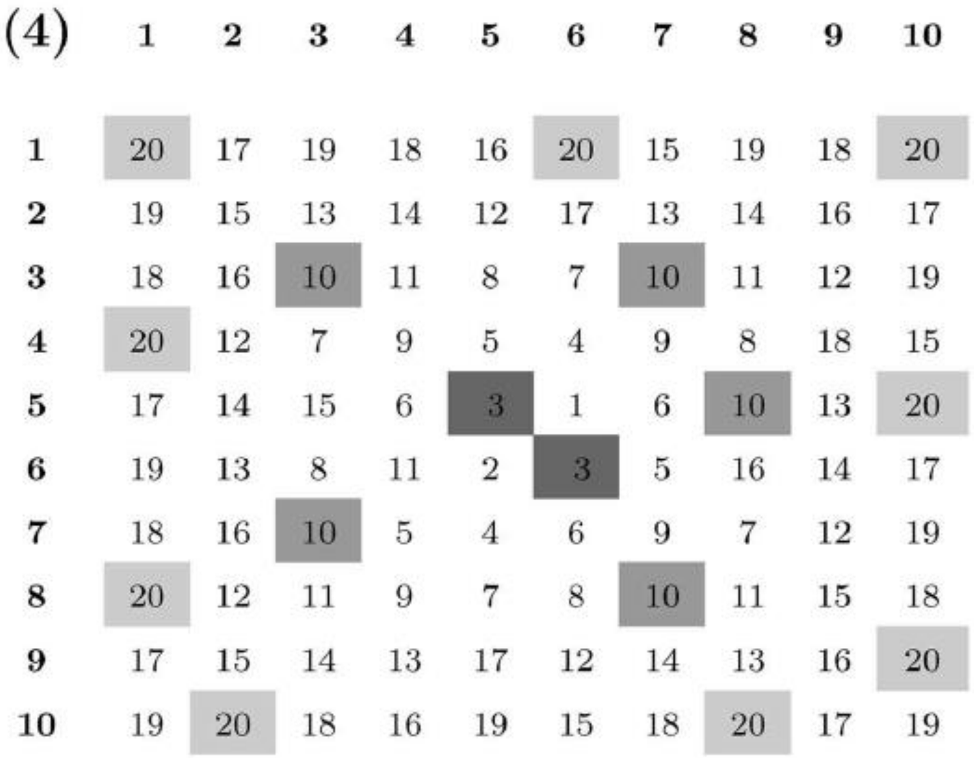


(3)	1	2	3	4	5	6	7	8	9	10
1	15	11	16	19	12	1	14	17	13	18
2	6	5	4	20	10	2	3	6	7	8
3	7	17	3	18	9	15	4	5	11	9
4	8	13	2	14	8	13	16	20	19	10
5	9	10	1	19	7	17	12	15	1	2
6	12	20	11	16	6	11	18	14	16	3
7	14	18	15	12	5	10	9	8	7	4
8	3	4	17	13	20	4	1	19	6	5
9	2	5	6	7	8	3	2	13	17	20
10	1	19	16	10	9	18	14	11	15	12

Lstibůrek and El-Kassaby, 2010

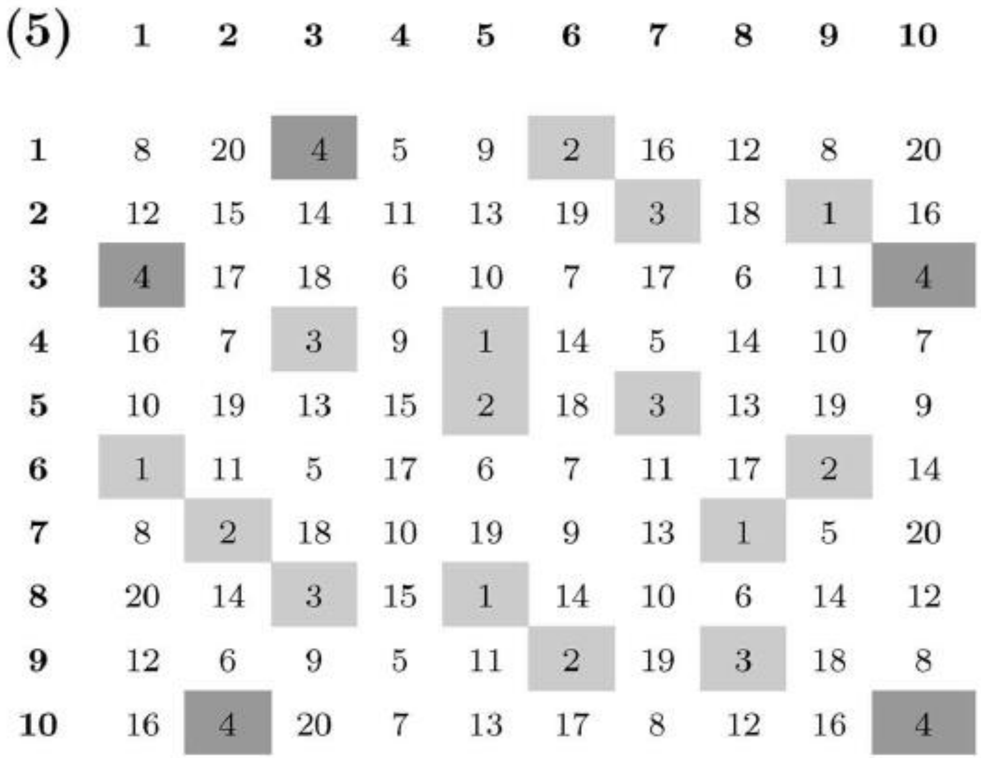
Minimum Inbreeding

20 clones: proportional deployment



(4)	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
1	20	17	19	18	16	20	15	19	18	20
2	19	15	13	14	12	17	13	14	16	17
3	18	16	10	11	8	7	10	11	12	19
4	20	12	7	9	5	4	9	8	18	15
5	17	14	15	6	3	1	6	10	13	20
6	19	13	8	11	2	3	5	16	14	17
7	18	16	10	5	4	6	9	7	12	19
8	20	12	11	9	7	8	10	11	15	18
9	17	15	14	13	17	12	14	13	16	20
10	19	20	18	16	19	15	18	20	17	19

5 unrelated groups: parent and clones from 3 half-sibs



(5)	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
1	8	20	4	5	9	2	16	12	8	20
2	12	15	14	11	13	19	3	18	1	16
3	4	17	18	6	10	7	17	6	11	4
4	16	7	3	9	1	14	5	14	10	7
5	10	19	13	15	2	18	3	13	19	9
6	1	11	5	17	6	7	11	17	2	14
7	8	2	18	10	19	9	13	1	5	20
8	20	14	3	15	1	14	10	6	14	12
9	12	6	9	5	11	2	19	3	18	8
10	16	4	20	7	13	17	8	12	16	4

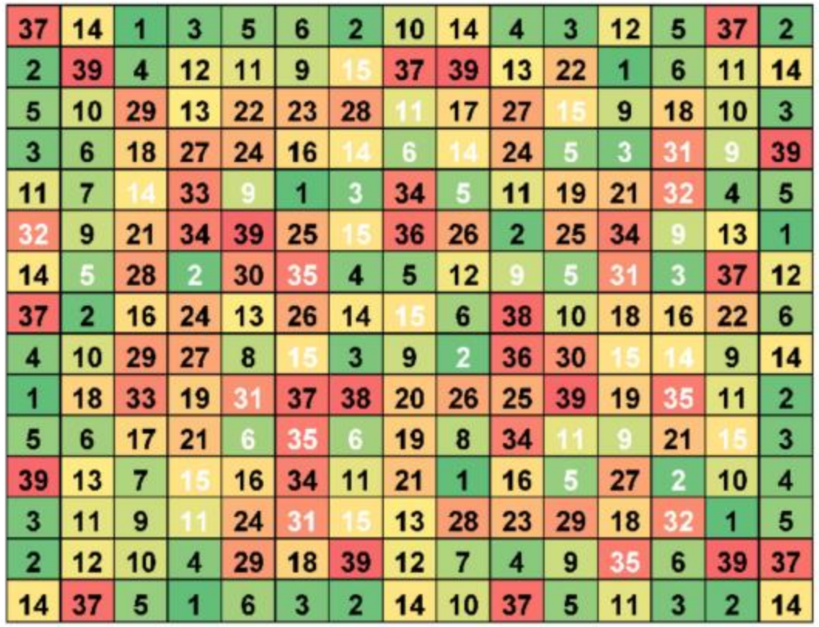
#ramets:
1-1-2-2-3-3-4-4-4-5-5-6-6-6-7-7-8-8-9-9

Lstibůrek and El-Kassaby, 2010

Flexibility for genetic thinning

- impact of genetic thinning limited unless the selection intensity is high,
- high selection intensity is drastically reducing seed production,
- more complex designs needed to accommodate multiple variables in advanced generation SO, thus thinning is becoming more problematic,
- complex pedigrees + clonal replication in advanced generation genetic testing (both traditional and genomic evaluation): higher accuracy of forward selection,
- generally better to avoid genetic thinning in advanced generation SOs, better alternatives: SMP, CMP, selective seed harvest.

Flexibility for genetic thinning



37	14	1	3	5	6	2	10	14	4	3	12	5	37	2
2	39	4	12	11	9	15	37	39	13	22	1	6	11	14
5	10	29	13	22	23	28	11	17	27	15	9	18	10	3
3	6	18	27	24	16	14	6	14	24	5	3	31	9	39
11	7	14	33	9	1	3	34	5	11	19	21	32	4	5
32	9	21	34	39	25	15	36	26	2	25	34	9	13	1
14	5	28	2	30	35	4	5	12	9	5	31	3	37	12
37	2	16	24	13	26	14	15	6	38	10	18	16	22	6
4	10	29	27	8	15	3	9	2	36	30	15	14	9	14
1	18	33	19	31	37	38	20	26	25	39	19	35	11	2
5	6	17	21	6	35	6	19	8	34	11	9	21	15	3
39	13	7	15	16	34	11	21	1	16	5	27	2	10	4
3	11	9	11	24	31	15	13	28	23	29	18	32	1	5
2	12	10	4	29	18	39	12	7	4	9	35	6	39	37
14	37	5	1	6	3	2	14	10	37	5	11	3	2	14

Figure 1. Example of the Optimum Neighborhood Algorithm design for refilling empty positions in an existing orchard. Numbers designate individual clones' IDs. Numbers in white color represent refilled positions utilizing the ONA algorithm.

Chaloupková et al., 2019

Which design is the best? (1)

- mathematically none, as there are multiple objectives (criteria),
- over the past decade, new designs were developed to account for additional variables in advanced-generation programs:
  - variable number of clones/sizes,
  - layout shape/spacing variation,
  - complex genetic relationship within and among clones,
  - could utilize additional information on flowering synchronization, assortative mating, etc.
- so one could think about these as reference solutions providing optimal (textbook) configurations.

Which design is the best? (2)

- earlier schemes: mostly sufficient under simple scenarios in the 1th and 2nd gens combined with linear deployment and further assumptions,
- one may put different emphasis on the 4 (or more) criteria and design a particular orchard as a „good“ compromise, often utilizing a hybrid scheme,
- reproductive biology is a key component and provides useful insight.

Comparison of layouts (1)

$$d_{min} = \sum_{l=1}^{N_c} \sum_{i=1}^{N_k} \sum_{j=i+1}^{N_k} \frac{1}{d_{il,jl}^2}, \tag{3}$$

where d is the distance between the i^{th} and the j^{th} ramet of the l^{th} clone, N_c is the number of clones, and N_k is the number of ramets within a clone. The d_{min} represents the inverse sum of squares of all possible distances between any two ramets of the same clone and across all clones. The closer the distance between any two ramets of the same clone, the higher the value and, conversely, the further the distance, the lower the value (Lstibůrek and El-Kassaby 2010).

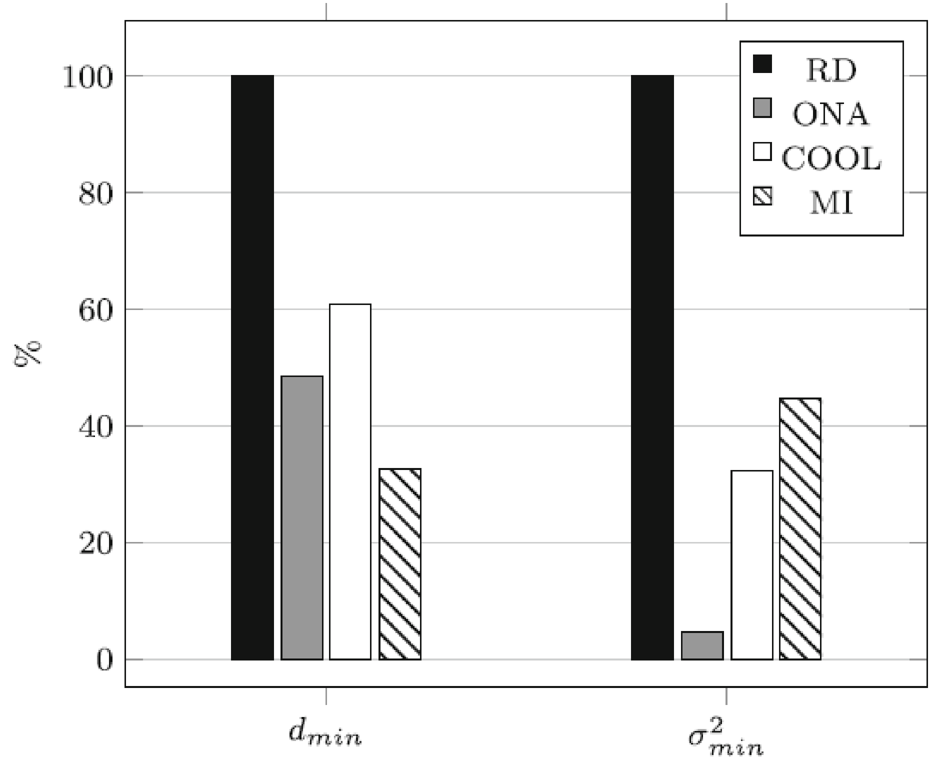


Fig. 4 Relative comparison of optimum neighbourhood (ONA) with minimum inbreeding (MI), replicated randomized staggered clonal rows (R^2SCR), and randomized (RD) designs using a balanced completely random layout

Chaloupková et al., 2016

Comparison of layouts (2)

$$d_{min} = \sum_{l=1}^{N_c} \sum_{i=1}^{N_k} \sum_{j=i+1}^{N_k} \frac{1}{d_{il,jl}^2}, \tag{3}$$

where d is the distance between the i^{th} and the j^{th} ramet of the l^{th} clone, N_c is the number of clones, and N_k is the number of ramets within a clone. The d_{min} represents the inverse sum of squares of all possible distances between any two ramets of the same clone and across all clones. The closer the distance between any two ramets of the same clone, the higher the value and, conversely, the further the distance, the lower the value (Lstibůrek and El-Kassaby 2010).

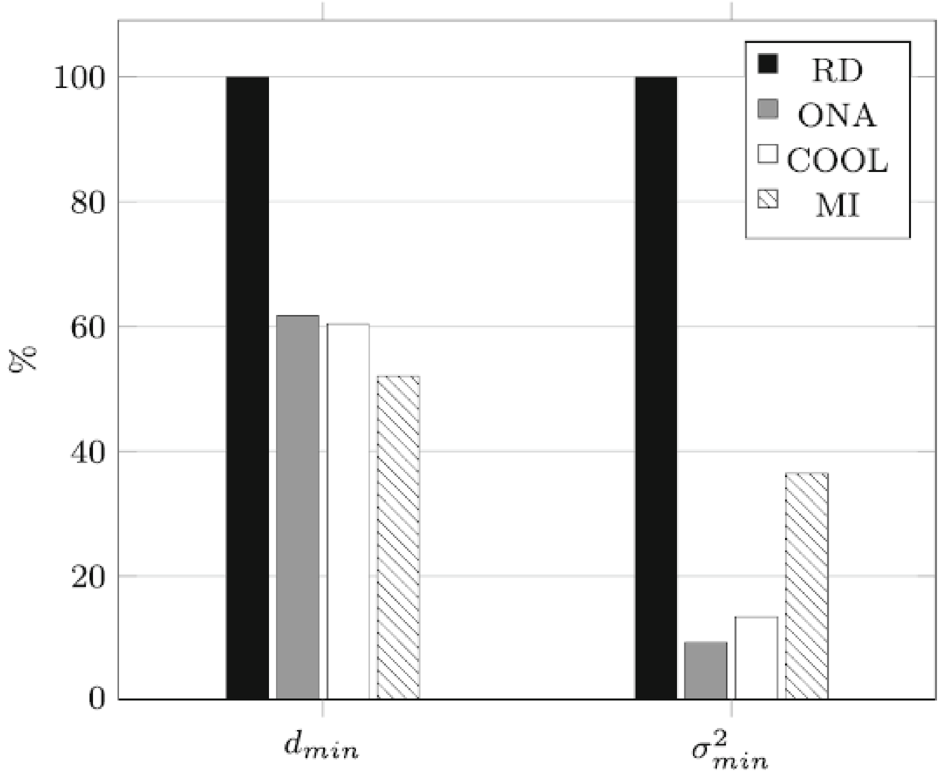
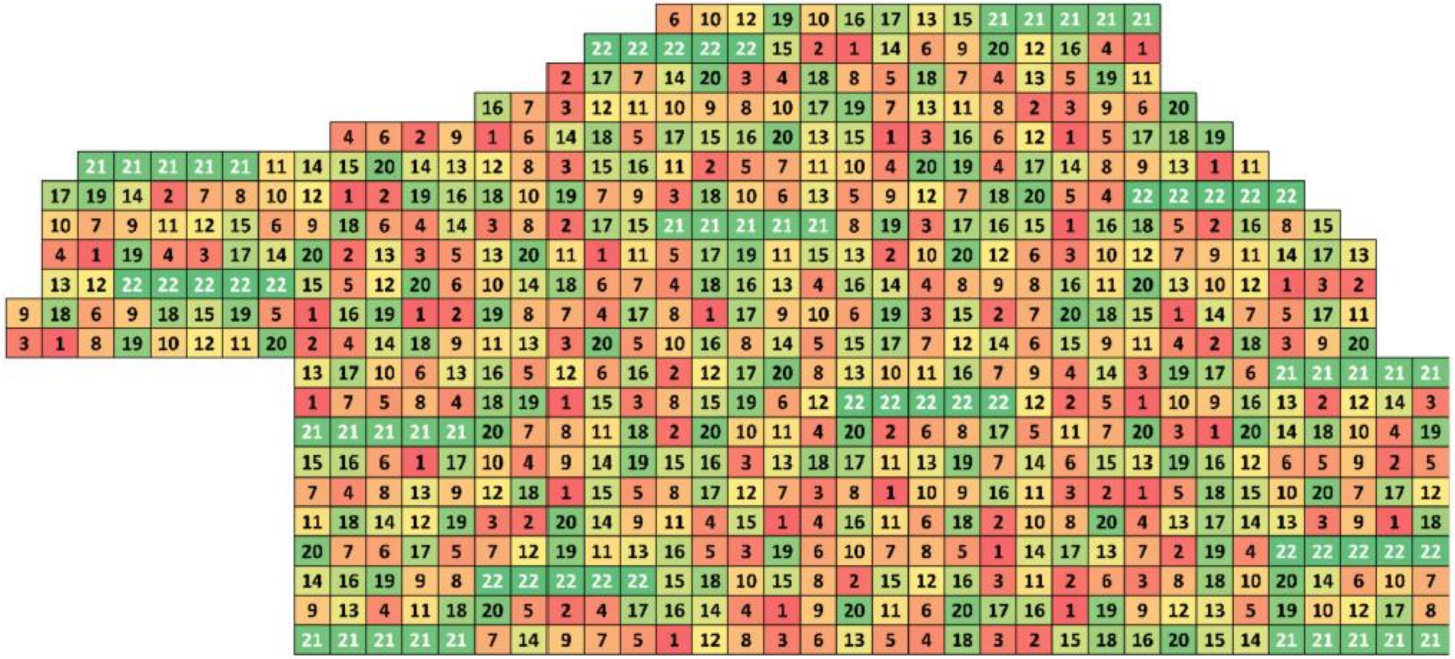


Fig. 5 Relative comparison of optimum neighbourhood (ONA) with minimum inbreeding (MI), replicated randomized staggered clonal rows (R^2SCR), and randomized (RD) designs using an unbalanced completely random layout

Chaloupková et al., 2016

Hybrid layout MI & ONA



																		6	10	12	19	10	16	17	13	15	21	21	21	21	21								
																22	22	22	22	22	15	2	1	14	6	9	20	12	16	4	1								
															2	17	7	14	20	3	4	18	8	5	18	7	4	13	5	19	11								
													16	7	3	12	11	10	9	8	10	17	19	7	13	11	8	2	3	9	6	20							
									4	6	2	9	1	6	14	18	5	17	15	16	20	13	15	1	3	16	6	12	1	5	17	18	19						
		21	21	21	21	21	11	14	15	20	14	13	12	8	3	15	16	11	2	5	7	11	10	4	20	19	4	17	14	8	9	13	1	11					
	17	19	14	2	7	8	10	12	1	2	19	16	18	10	19	7	9	3	18	10	6	13	5	9	12	7	18	20	5	4	22	22	22	22	22				
	10	7	9	11	12	15	6	9	18	6	4	14	3	8	2	17	15	21	21	21	21	21	8	19	3	17	16	15	1	16	18	5	2	16	8	15			
	4	1	19	4	3	17	14	20	2	13	3	5	13	20	11	1	11	5	17	19	11	15	13	2	10	20	12	6	3	10	12	7	9	11	14	17	13		
	13	12	22	22	22	22	22	15	5	12	20	6	10	14	18	6	7	4	18	16	13	4	16	14	4	8	9	8	16	11	20	13	10	12	1	3	2		
9	18	6	9	18	15	19	5	1	16	19	1	2	19	8	7	4	17	8	1	17	9	10	6	19	3	15	2	7	20	18	15	1	14	7	5	17	11		
3	1	8	19	10	12	11	20	2	4	14	18	9	11	13	3	20	5	10	16	8	14	5	15	17	7	12	14	6	15	9	11	4	2	18	3	9	20		
								13	17	10	6	13	16	5	12	6	16	2	12	17	20	8	13	10	11	16	7	9	4	14	3	19	17	6	21	21	21	21	21
								1	7	5	8	4	18	19	1	15	3	8	15	19	6	12	22	22	22	22	22	12	2	5	1	10	9	16	13	2	12	14	3
								21	21	21	21	21	20	7	8	11	18	2	20	10	11	4	20	2	6	8	17	5	11	7	20	3	1	20	14	18	10	4	19
								15	16	6	1	17	10	4	9	14	19	15	16	3	13	18	17	11	13	19	7	14	6	15	13	19	16	12	6	5	9	2	5
								7	4	8	13	9	12	18	1	15	5	8	17	12	7	3	8	1	10	9	16	11	3	2	1	5	18	15	10	20	7	17	12
								11	18	14	12	19	3	2	20	14	9	11	4	15	1	4	16	11	6	18	2	10	8	20	4	13	17	14	13	3	9	1	18
								20	7	6	17	5	7	12	19	11	13	16	5	3	19	6	10	7	8	5	1	14	17	13	7	2	19	4	22	22	22	22	22
								14	16	19	9	8	22	22	22	22	22	15	18	10	15	8	2	15	12	16	3	11	2	6	3	8	18	10	20	14	6	10	7
								9	13	4	11	18	20	5	2	4	17	16	14	4	1	9	20	11	6	20	17	16	1	19	9	12	13	5	19	10	12	17	8
								21	21	21	21	21	7	14	9	7	5	1	12	8	3	6	13	5	4	18	3	2	15	18	16	20	15	14	21	21	21	21	21

Figure 2. Design combining both Minimum Inbreeding and Optimum Neighborhood Algorithm designs. Numbers designate individual clones' IDs. Numbers in white color represent clonal rows utilizing MI algorithm. Remaining entries where optimized by ONA algorithm.

Chaloupková et al., 2019

General advice

- **absence of constraints:** some of the earlier designs could still be used, such as the COOL or systematic layouts,
- **presence of constraints:** Minimum Inbreeding, R^2SCR, ONA or hybrid schemes were designed for complex scenarios, selection should be made based on the preferred criteria,
- **important:** mathematically feasible solution is not at all times biologically feasible, the design should be verified using biology and common sense, constraints should be reduced when possible,
- **failure:** no feasible design: OP seed orchard may not be appropriate.

Questions?