Optimum neighborhood seed orchard design -software package

Kateřina Chaloupková, Jan Stejskal, Milan Lstibůrek Czech University of Life Sciences, Prague, Czech Republic

Introduction

Seed orchards (SO) represent the link between operation forestry and tree improvement. Globally, SO are the most common deployment scenario in forest tree breeding programs. Variety of available designs have been used for new SO establishment and most of them are primary focused on minimizing inbreeding. In our opinion, good quality design should promote random mating too. With this in mind, Optimum Neighborhood Algorithm (ONA) was developed Chaloupková et. al (2016).

Software package

The current version of the software was programmed in the R language and the code is connected to a simple interface in Microsoft Excel. The end user works almost exclusively in Excel file, which includes all necessary instructions.

Input Parameters:

- SO grid
- number of clones, their ID and sizes,
- number of iterations and additional parameters controlling the heuristics.

Possibilities of using ONA

In its current basic form, the ONA is specifically suited for the establishment of the first generation SO. It allows creating layouts of any sizes and shapes. It also works efficiently with variable clonal sizes (i.e., different numbers of ramets per clone). ONA can also be utilized to improve existing SO if mortality occurs or in conjunction with additional design.

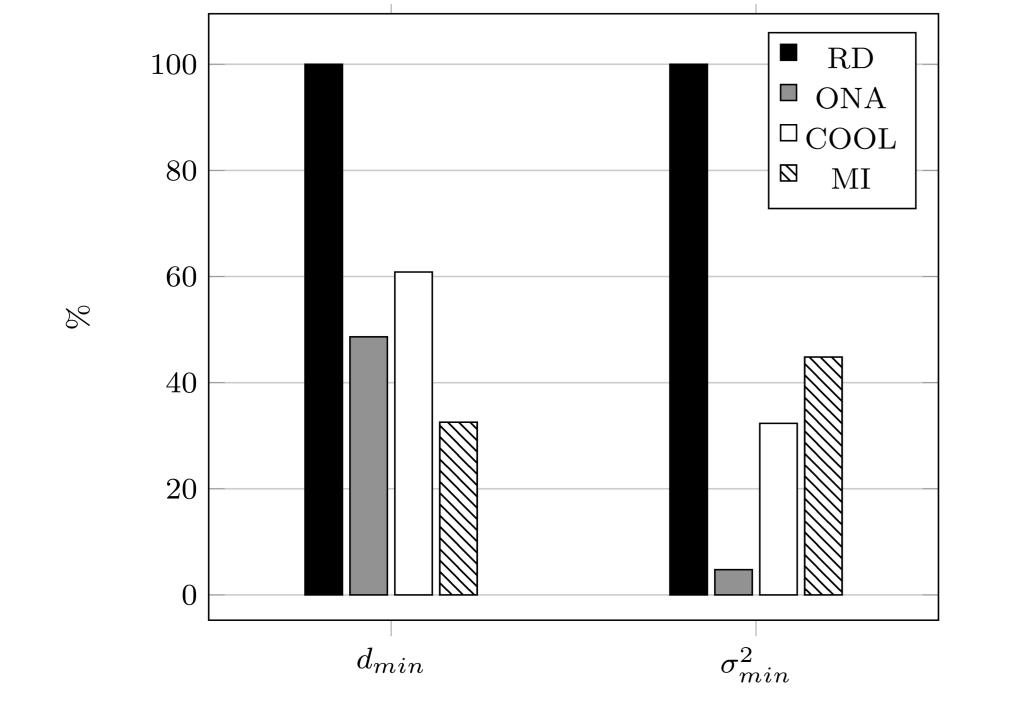
Software extensions are under continuous development and the software link is being updated. Extensions should include, in particular, the addition of assortative positive/negative mating, and relatedness. Therefore, ONA will become suitable for the establishment of advanced-generation SO.

ONA promotes panmixia in SO due to the original heuristic algorithm, which is based on the fact that most frequent gametic exchange occurs among close neighbors. Benefits of the ONA are exemplified in Fig. 1, where it is compared to additional commonly used designs.



These parameters are automatically forwarded to the R software and the resulting scheme with the matrix of direct neighborhoods are forwarded back to MS Excel (Fig. 2). All these steps are done using simple keyboard shortcuts as described in the instructions.

The software is freely available at: https://katedry.czu.cz/en/kgfld/software **References:** Chaloupková, K., et al. 2016. Optimum neighborhood seed orchard design. Tree Genetics & Genomes 12:105.



6	1	2	1	17	5	1	4	19	21	3	12	16	20	5	9	4	2	5	19	8	4	3	2	5
8	11	14	3	23	6	7	2	14	5	24	26	10	7	3	8	10	24	9	12	10	6	9	19	6
10	2	13	12	7	8	13	26	15	4	17	13	6	15	26	25	9	18	23	16	4	7	22	1	17
11	12	16	14	17	11	3	9	5	11	15	16	4	2	12	11	10	2	21	25	13	3	4	2	24
15	24	7	1	10	4	21	15	6	22	5	8	22	8	6	24	7	17	5	9	17	19	1	14	25
1	6	16	15	20	13	8	14	2	7	18	14	24	26	10	3	22	9	20	4	6	15	3	6	13
26	18	12	6	23	1	9	5	23	13	3	5	20	4	5	16	2	8	12	2	21	4	18	1	5
4	1	21	22	25	15	7	14	4	1	21	11	1	12	6	4	5	1	3	8	26	23	11	8	13
2	10	14	11	1	12	4	11	16	7	12	22	5	3	25	20	23	10	25	2	3	9	16	14	20
3	6	3	16	9	14	6	1	19	2	18	13	10	16	18	19	2	7	5	13	15	11	6	15	3

Fig. 1. Relative comparison of ONA design with minimum inbreeding (MI), replicated randomized staggered clonal rows (R²SCR), and randomized (RD) designs using d_{min} and σ^2_{min} parameters for layout with balanced clonal sizes (Chaloupková et al. 2016).

Fig. 2. The resulting ONA layout with 250 positions. 26 clones were allocated, with clonal numbers: 6, 10, and 10, and respective clonal sizes: 15, 10 and 6.