Software to facilitate estimation of genetic parameters and breeding values for honey bees

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In short

Effective breeding requires knowledge of heritabilities and estimation of breeding values. Recent theory shows how these can be estimated for honey bees (Brascamp & Bijma, 2014; Bernstein *et al.* 2018). Here we provide software for this purpose.

The software uses inputs that are routinely available in most bee breeding programs and experiments, and provides output files that allow straightforward application of standard software packages for genetic analysis (such as ASReml).
This poster describes the ideas behind the software.

The software

The software concerns two R-programmes.

The first programme builds a **pedigree file**.
Inputs are the IDs of the yellow blocks in Figures 1-3, their years of birth, and for each mating the number of drone-producing queens and also the number of drones in average fertilizing a queen. The number of drone-producing queens may vary from 1 (as in Figure 2) and very large (as in case of open mating, Figure 3).
The output pedigree file consists of entries colony, queen or sire with their respective dam and sire. The output serves as input for the second programme.

The second programme computes the matrix with additive genetic relationships between all members of the pedigree, and its inverse **AINV**. The inverse is calculated using a method based on Mendelian sampling terms (Brascamp & Bijma, 2014).

AINV can be used as input for **standard software like ASReml**, along with a declaration of the statistical model and observations, to estimate genetic parameters and breeding values. The programmes by now have been used to analyse a variety of datasets.

The programmes are available on request: pim.brascamp@wur.nl.

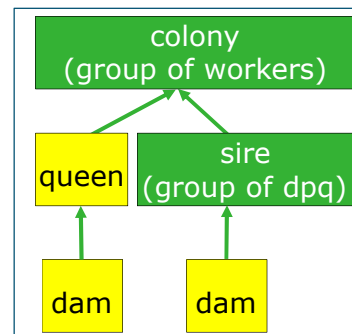## Alternative elements of pedigrees

Figure 1. Members of a pedigree with drone producing queens (dpq) that are full sibs. Yellow blocks are input, green blocks are added to complete a pedigree. A sire consists of a group of dpq descending from a single dam.
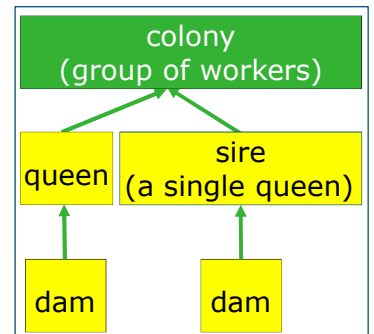

Figure 2. Members of a pedigree with a single sire. Yellow blocks are input, the green block is added to complete a pedigree. The software facilitates sires used for single-drone-insemination, but also for multi-drone-insemination.
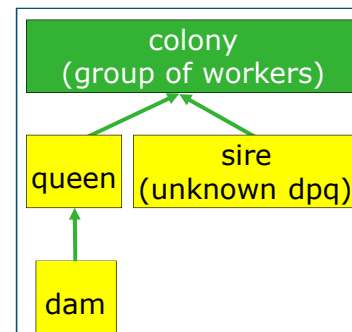

Figure 3. Members of a pedigree with a sire consisting of non-identified drone producing queens. Yellow blocks are input, the green block is added to complete a pedigree. This case facilitates, for example, open mating.

In the pedigrees in Figures 1-3 yellow blocks are input. The green blocks are added to complete pedigrees. The queen heading the colony and its dam always are input.

The software facilitates three alternative mating structures each leading to its own input:
- In Figure 1 drones are produced by drone-producing queens reared from one single colony (full sibs).
- In Figure 2 the sire is a single queen.
- In Figure 3 the sire consists of non-identified drone-producing queens, as with open mating.

The software allows for alternative assumptions on the additive genetic relationship between drone-producing queens with unknown parents. A paper on this issue (Brascamp & Bijma, 2018) was submitted to GSE.

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