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Construction of linkage maps for outbreeding based on haplotype
reconstruction - Jansen, J.

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Construction of linkage maps for outbreeding species based on haplotype reconstruction

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In outbreeding species the construction of linkage maps is far more complicated than in progenies derived from pure lines. Maliepaard *et al.* (1997) provide an overview of all possible configurations of marker pairs in a full-sib family and provide formula for the maximum likelihood estimators of pair-wise recombination frequencies. The current approach for constructing linkage maps is based on pair-wise estimates of recombination frequencies. For large numbers of markers, the use of multi-point maximum likelihood would be computationally intractable.

In this presentation, the construction of linkage maps is considered as a combinatorial optimisation problem based on haplotype reconstruction. The aim is to minimise the number of recombination events between adjacent markers. In this approach, incomplete marker data and phase information are considered as restrictions on haplotypes. Jansen *et al.* (2001) used a simple version of simulated annealing in conjunction with spatial sampling to obtain the best marker order in the case of a back-cross population. This method can be extended to more general populations. This requires optimisation in more than one direction (marker order, phase and haplotype). Practical examples will be used to illustrate the methods.

Jansen, J., A.G. de Jong & J.W. van Ooijen (2001) Constructing dense genetic linkage maps. *Theoretical and Applied Genetics*, **102**: 1113 - 1122.

Maliepaard, C., J. Jansen & J.W. van Ooijen (1997) Linkage analysis in a full-sib family of an outbreeding plant species: overview and consequences for applications. *Genetical Research, Cambridge*, **70**: 237 - 250.

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QTL analysis in pedigrees and related crosses of apple

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In plants, QTL analysis has been carried out predominantly in experimental populations (BC, F₂, RIL). A novel approach is to use all available breeding material by incorporating information about genetic relationships between individuals (pedigree information). The advantage of this approach is that QTL are identified in the breeding material and can be employed directly in decisions about future crosses.

Apple (*Malus domestica* Borkh.) is an outbreeding species ($n = 2x = 34$) with a long juvenile period. Apple cultivars consist of clones, where multiplication occurs by (bud) grafting. Apple breeding started in the 19th century and many of the old varieties are still present in orchards.

In this presentation, we will look at different methods that are advocated for QTL analysis in pedigrees and discuss their merits and drawbacks in the analysis of apple pedigrees.