THE QUALITY OF GENETIC LINKAGE MAPS

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High quality genetic linkage maps are a prerequisite for the success of many genetic studies, *e.g.* QTL analysis, map-based cloning of genes. They are also important for marker-assisted breeding. However, publications of genetic linkage maps hardly ever show how the authors arrived at their results (other than by referring to a computer package) or how reliable genetic linkage maps really are. Often, published maps are considered as 100% true.

A genetic linkage map is a representation of the relative positions of molecular genetic markers on the chromosomes. It can be constructed using estimates of recombination frequencies: the frequencies at which in the meiosis, marker alleles of the same parental origin are inherited together or become separated by genetic recombination. Estimates of recombination frequencies have to be obtained using observations on molecular genetic markers in segregating populations of individuals.

The major cause of problems in the construction of genetic linkage maps are imperfect observations on molecular genetic markers: a part of the observations are wrong, incomplete or missing. Imperfect observations may occur in various ways. They affect the estimates of recombination frequencies between molecular genetic markers and as a consequence lead to problems when positioning the molecular genetic markers on the genetic linkage map. Even a small percentage of errors may lead to major problems, especially if the distances between the markers are small.

In this paper we will go through the process of constructing genetic linkage maps, and show how various statistical-genetic tools (often in the form of graphs) can be used to identify and solve problems and check the quality of intermediate and final results.