Statistical Methods for Quantitative Trait Localization Based on Genome Data

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A popular task in genetics is to identify genes influencing quantitative traits, like blood pressure or yield in agriculture. The talk will address two common approaches, one based on crossing experiments and the other on a population genetic approach.

With crossing experiments one obtains marker genotype data and measurements of the quantitative trait. The genotype data for a marker close to a QTL (i.e. a gene influencing a quantitative trait) can be expected to be correlated with the quantitative trait. One possibility to search for such markers is to set up a linear (ANOVA) model. Because of the usually large number of markers, and since it is important to take into account interaction effects, the resulting model becomes extremely high dimensional. We will discuss the need to modify classical model selection criteria in this context.

With population genetic data, it is sometimes possible to localize genes influencing a quantitative trait, without actually observing the trait. Such a situation occurs, when a trait of interest has been affected by selection. In this case, an option is to search for traces of selection in the genome.