

Rank-based model selection in locating multiple interacting QTL

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In this talk we will discuss the problem of localizing genes influencing quantitative traits, so called Quantitative Trait Loci (QTL). QTL are located with respect to genetic markers, whose positions on the chromosome are known. The relationship between marker genotypes and trait values can be often described by a multiple regression model and the task of locating QTL relies on identifying important regressors. The main difficulty arises from the fact that the search for QTL must be performed within a huge data base of marker genotypes collected in large genome scans. It was shown that in such case a popular model selection criterion, Schwarz BIC, overestimates QTL number. In [1] a suitable modification of BIC, mBIC, was proposed, which also allows to estimate two-way gene interactions. mBIC was derived under the standard assumption that the distribution of the error term is normal and its performance deteriorates when this distribution is heavy-tailed or the data set contains certain proportion of outliers. In this talk we will present a new, robust version of mBIC, based on ranks, which was originally proposed in [2]. The rank version of mBIC, rBIC, allows controlling the family wise error rate and has good power of detecting QTL, independently on the distribution of the error term. The simulation study shows that rBIC is almost as efficient as standard techniques when the error term is normally distributed, and works much better when data comes from a heavy-tailed distribution or include a proportion of outliers.

References

- [1] Bogdan M, Ghosh JK, Doerge RW (2004) Modifying the Schwarz Bayesian Information Criterion to Locate Multiple Interacting Quantitative Trait Loci. *Genetics* 167:989-999
- [2] Żak M, Baierl A, Bogdan M, Futschik A (2007) Locating Multiple Interacting Quantitative Trait Loci Using Rank-Based Model Selection. *Genetics* 176:1845-1854