## Selecting explanatory variables with the modified version of Bayesian Information Criterion

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Abstract

We consider the situation when a large data base needs to be searched to identify a few important predictors of a given quantitative response variable. There is a lot of evidence that in this case classical model selection criteria, like Akaike Information Criterion (AIC) or Bayesian Information Criterion (BIC), have a strong tendency to overestimate the number of regressors. As discussed in [1], this phenomenon is closely related to the well known issue of multiple testing. To solve this problem, a modified version of BIC (mBIC), which allows for incorporating a prior knowledge on a number of regressors, was proposed. In a series of papers ([1],[2],[3],[4],[5]) mBIC was successfully used for large scale genome scans identifying genes influencing quantitative traits. In this talk we will present mBIC and illustrate its optimality properties with theoretical asymptotic results and computer simulations.

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[2] Baierl A, Bogdan M, Frommlet F, Futschik A. On Locating Multiple Interacting Quantitative Trait Loci in Intercross Designs. Genetics, 2006; 173: 1693-1703.

[3] Baierl A, Futschik A, Bogdan M, Biecek P. Locating Multiple Interacting Quantitative Trait Loci Using Robust Model Selection, Computational Statistics and Data Analysis, 2007; 51: 6423-6434.

[4] Zak M, Baierl A, Bogdan M, Futschik A. Locating Multiple Interacting Quantitative Trait Loci Using Rank-Based Model Selection. Genetics 2007; 176: 1845-1854.

[5] Bogdan M, Frommlet F, Biecek P, Cheng R, Ghosh JK, Doerge RW Extending the Modified Bayesian Information Criterion (mBIC) to dense markers and multiple interval mapping, to appear in Biometrics, 2008.