Model selection procedures for genome wide association studies

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Till today the analysis of genome wide association studies (GWAS) is almost exclusively performed using single marker tests, which means that the association of each single nucleotide polymorphism (SNP) is tested individually. The results from a comprehensive simulation study based on real SNP data illustrate the shortcomings of single marker tests for complex traits, i.e. traits which are influenced by a larger number of genetic factors. Model selection helps to overcome some of these difficulties. We will discuss the statistical concepts underlying the software packages HLASSO, GWASelect and MOSGWA, and compare their performance in the context of case control studies. Discussion of MOSGWA will include the introduction of FDR-controlling modifications of the Bayesian information criterion. After describing some heuristic search procedures which try to minimize this criterion over the extremely large model space in GWAS we will finally discuss some potential directions in which to extend MOSGWA.

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