Optimal selection procedures in genome wide association studies

Abstract

The use of genome-wide association studies (GWAS) to identify common genetic factors that influence health and disease are becoming ever more important. For this purpose the Clinical Institute for Neurology of the Medical University of Vienna is currently acquiring the latest gene chip technology, which allows genotyping of up to a million single nucleotide polymorphisms (SNPs) in patients. The statistical challenges of analysing GWAS-data are considerable, both from a theoretical as well as from a practical perspective. Retrieving useful information from such studies requires close cooperation between medical researchers, computer scientists and statisticians. The purpose of this project is to gain further theoretical understanding of statistical procedures involved, and to provide efficient implementations of these methods to perform improved GWAS data analysis in the future.

Keywords:
model selection, Bayesian statistics, genetic association study

---

Principal Investigator:	Florian Frommlet
Institution:	University Vienna
Further collaborators:	Malgorzata Bogdan (TU Wroclaw) Alexander Zimprich (Medical University of Vienna)

Status: Completed (01.03.2010 - 31.08.2014) 54 months

Funding volume: EUR 372,000

Further links about the involved persons and regarding the project you can find at
https://archiv.wwtf.at/programmes/mathematics/MA09-007