

Proposal number:	MA14-007
Title:	Improving genetic inference by modelling population structure
Keywords:	Association studies, population genetics, mixed models, statistical genetics
Principal Investigator:	Mr. Florian Frommlet
Home Institution:	Medical University of Vienna
Website:	http://statistics.msi.meduniwien.ac.at/

Abstract:

While the problem of population structure in genome wide association studies (GWAS) has received considerable attention, there are still many open questions. In this project we will focus on spatially distributed populations that are subject to natural selection. Essentially all populations are spatially structured, which means that the genotype of an individual depends on where it was sampled. Natural selection also often acts in a spatial manner, leading to local adaptation, so that the genotype of loci under selection will also depend on where the individual was sampled, but in a different manner. The resulting dependencies make statistical inference of which loci are causally related to a phenotype, or which loci have been subject to selection, rather difficult. Estimates of effect size at truly causal loci may be inflated because of correlations with other causal loci induced by selection. On the other hand regions exhibiting signs of selection might do so simply due to population structure. Though these problems are well known, existing statistical methods either ignore them or attempt to handle them using very crude models of population structure. Here, we plan to utilize explicit models of population structure and of selection to improve our ability to identify loci being responsible for particular traits or being under selection. Specifically, we will integrate recently developed methods from population genetics into GWAS analysis.

Project duration:	48 months
WWTF funding requested (in €1,000):	649.00