Wiener Biometrische Sektion
der Internationalen Biometrischen Gesellschaft
Region Österreich – Schweiz

Einladung zum

Biometrischen Kolloquium

am **Donnerstag, 12. Juli 2012** um **10:00 Uhr** (s.t.)
(CAVE! Geänderter Termin!)

in der Informatik-Bibliothek (Ebene 3, Raum 88.03.806) des
Zentrums für Medizinische Statistik, Informatik und Intelligente
Systeme (CeMSIIS) der Medizinischen Universität Wien
Spitalgasse 23, 1090 Wien
(Plan siehe http://www.muw.ac.at/cemsiis/allgemeines/anschrift/)

Vortragende:
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TU Wroclaw

Logic regression for localizing
interacting quantitative trait loci

Wir freuen uns auf zahlreichen Besuch.

Gerhard Svolba   Franz König
Präsident   Sekretär

Logic regression for localizing interacting quantitative trait loci

Malgorzata Bogdan
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Abstract:

Logic regression was introduced by RUCZINSKI *et al.* 2003 to identify important gene-gene interactions in association studies based on SNP data. The logic regression model can be understood as a natural extension of the standard generalized linear model. The role of regressors is played by logic expressions, dependent on the genotypes of one or several interacting SNPs. Thus, logic regression models allow for a natural description of gene-gene interactions, under which the mean value of the trait (or the disease risk) is modified only under a certain specific combination of genotypes of several SNPs. From the mathematical point of view, every logic regression model can be represented by a generalized linear model (GLM) with interactions and some restrictions on regression coefficients. However, standard estimation procedures for GLM, which do not use these restrictions, introduce unnecessary noise as compared to the analysis with the proper logic regression model. This results in a larger number of degrees of freedom for the corresponding likelihood ratio statistics and a lower power to detect the group of influential genes. Also, when using GLM, the natural logic predictors are projected both on the main effects and classical interactions, which additionally leads to a loss of power of detection of interacting effects. In this article we discuss the properties of logic regression in the context of localizing quantitative trait loci (QTL) in experimental populations. We will present some theoretical results as well as the results of a simulation study and real data analysis comparing the performance of the classical methods of localizing QTL, based on standard GLM models, with *logicFS* of SCHWENDER et. al. 2008, based on logic regression.

This is a joint work with Magdalena Malina from Wroclaw University and Katja Ickstadt and Holger Schwender from TU Dortmund University.

References:

1. Ruczinski, I., C. Kooperberg, M. LeBlanc, 2003 Logic regression. J. Comput. Graphical Statist. **12(3):** 474 -- 511.
2. Schwender, H. and K. Ickstadt, 2008 Identification of SNP interactions using logic regression. Biostatistics **9:** 187--198.