Wiener Biometrische Sektion
der Internationalen Biometrischen Gesellschaft
Region Österreich – Schweiz
http://www.meduniwien.ac.at/wbs/

Einladung zum

Biometrischen Kolloquium

am Montag, 26. März 2012 um 14:00 Uhr (s.t.)

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/)

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Integration of multiple genomic data sources in Bayesian Regression Models for Prediction and Biomarker Selection

Wir freuen uns auf zahlreichen Besuch.

Georg Heinze	Gerhard Svolba
Präsident	Sekretär

Integration of multiple genomic data sources in Bayesian Regression Models for Prediction and Biomarker Selection

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Bayesian variable selection (BVS) models are an alternative to well-known sparse regularisation methods like lasso regression for prognostic modelling based on high-dimensional input spaces. A common application is the prediction of clinical endpoints like therapy response with simultaneous biomarker selection using microarray gene expression data.

High-throughput microarray technologies are also available for many other types of genomic data, and in recent years clinical researchers have begun to systematically collect genome-wide data from various sources on the DNA- and RNA-level. If data from several sources are available for the same set of biological samples, they can be analysed together in an integrative manner, with the aim of providing a more comprehensive picture of the disease biology and improving the performance of clinical prediction models.

For example, the integration of copy number variation data into gene-expression-based prognostic models promises to improve both prognostic value and interpretability of the model, because genomic aberrations are known to affect expression levels of corresponding genes. In fact, the deletion of chromosomal regions harbouring important tumour suppressor genes is a well-known cause of certain cancers.

BVS models are very flexible in their setup and are naturally well-suited to extensions allowing the integration of additional data sources. I will propose such extensions for the integration of CNV or methylation data with gene expression data in prognostic models. Model behaviour and the influence of prior specifications will be investigated through simulation studies. The model will be illustrated in applications to pediatric brain tumour data.