



**Basel Biometric Section of the Austro-Swiss Region
of the International Biometric Society**

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BBS Seminar

Basel, 30 Nov 2010, 16:00 – 17:30

***Seminar Room 3, Swiss TPH
Socinstrasse 55a, Basel***

PROGRAM

16:00 Welcome

16:00 – 16:45 Dr Harald Binder (Institute of Medical Biometry and Medical Informatics,
University Medical Center Freiburg)

Fitting and evaluating risk prediction models with high-dimensional molecular data

Abstract

Analysis of molecular data promises identification of biomarkers for improving prognostic models, thus potentially enabling better patient management. For identifying such biomarkers, risk prediction models can be employed that link high-dimensional molecular covariate data to a clinical endpoint. In low-dimensional settings, a multitude of statistical techniques already exists for building such models, e.g., allowing for variable selection or for quantifying the added value of a new biomarker. We consider componentwise likelihood-based boosting techniques that transfer some of the underlying ideas towards high-dimensional settings, with a focus on models for time-to-event endpoints. Techniques for incorporating specific covariate structure are discussed, as well as techniques for dealing with more complex endpoints. Evaluation of prediction performance is an important part of developing high-dimensional risk prediction models. For example, erroneously evaluating models on the same data that were employed for model fitting can result in substantial overoptimism. Time-to-event endpoints pose additional challenges for performance evaluation. We illustrate how bootstrap .632+ prediction error curve estimates can avoid overoptimism and adequately deal with complex time-to-event structure. Techniques for fitting as well as evaluation of risk prediction models are illustrated using microarray survival data from patients with diffuse large B-cell lymphoma and from patients with bladder cancer.

16:45 – 17:30 Dr Martin Wolkewitz (Institute of Medical Biometry and Medical Informatics,
University Medical Center Freiburg)

Healthcare epidemiology, hospital-acquired infections, statistical modeling of outbreaks

Abstract

Hospital-acquired infections are a major public-health problem. They are associated with an increased mortality and extra length of hospital stay. The statistical analysis is challenging because the data are highly time-dependent. All patients could experience time-dependent events such as admission, infection, discharge or death. Thus, one is confronted with time-dependent exposures and competing events. Multistate models address the chronological order and give insights into the temporal dynamics. By using real data, I will discuss statistical modeling of outbreaks as well as typical pitfalls which should be avoided.