Wiener Biometrische Sektion (WBS)
der Internationalen Biometrischen Gesellschaft
Region Österreich – Schweiz (ROeS)
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MEDICAL UNIVERSITY OF VIENNA

Agenda für das WBS Seminar 2019

"Update your prior: The power of Bayesian Tools for Research"

des Zentrums für Medizinische Statistik, Informatik und Intelligente Systeme und der
Wiener Biometrischen Sektion (WBS) der Internationalen Biometrischen Gesellschaft (IBS),
Region Österreich – Schweiz (ROeS)

Datum: Freitag, 22. Februar
Ort: Jugendstilhörsaal der Medizinischen Universität Wien,
Bauteil 88 – Ebene 3, Spitalgasse 23, 1090 Wien
Plan siehe http://cemsiis.meduniwien.ac.at/allgemeines/anschrift/
Beginn: 9:00 Uhr (s.t.)
Ende: 12:00 Uhr
Organisatoren: Franz König, Elias Meyer, Martin Posch (Med Uni Wien), Simon Wandel (Novartis, Basel)

9:00-10:30 Session 1, Chair: Martin Posch

- **Helga Wagner**, Department of Applied Statistics, Johannes Keppler Universität Linz
  Bayesian effect fusion for categorical predictors in regression
- **Gertraud Malsiner-Walli,** Institute of Statistics and Mathematics, WU Vienna University of Economics and Business
  Bayesianische Modellierung von Mischmodellen angewandt auf medizinische Fragestellungen
- **Florian Frommlet**, CeMSIIS, Medical University of Vienna
  Deep Bayesian Regression

10:30 – 10:45 *Break (Foyer)*

10:45:-12:00 Session 2, Chair: Franz König

- **Beat Neuenschwander**, Novartis, Basel
  Predictive evidence threshold scaling (PETS): does the evidence meet a confirmatory standard?
- **Simon Wandel**, Novartis Basel
  Model averaging for robust extrapolation in evidence synthesis

No registration and fee. Please feel free to distribute the announcement to colleagues. The WBS runs a mailing list for announcing talks in the field of biostatistics. For subscription to the mailing list, send an e-mail to harald.herkner@meduniwien.ac.at.

ABSTRACTS

Helga Wagner (Department of Applied Statistics, Johannes Keppler Universität Linz)

Bayesian effect fusion for categorical predictors in regression

Sparse modelling and variable selection is one of the most important issues in regression type models, as in applications often a large number of covariates on comparably few subjects are available. Many methods have been developed, which allow to identify regressors with a non-negligible effect. These are however not appropriate for a categorical covariate, where the effect is captured by a group of level effects and sparsity cannot only be achieved by excluding single irrelevant effects or the whole group of level effects but also by fusing levels which have essentially the same effect on the response.

In a Bayesian approach a sparse representation of the effect of a categorical predictor can be achieved by specifying appropriate prior distributions. We present two different specifications of the prior on level effects that encourage sparsity by selection and effect fusion: The first is a multivariate Normal distribution with a precision matrix that allows for either almost perfect or almost zero dependence of level effects. As an alternative we consider a sparse finite mixture prior where a spike at zero is combined with a location mixture of spiky components to allow clustering of level effects. For both priors Bayesian inference is feasible by MCMC methods. Performance of the methods is illustrated on simulated as well as a data set on the recurrence of breast cancer.

Gertraud Malsiner-Walli (Institute of Statistics and Mathematics, WU Vienna)

Bayesianische Modellierung von Mischmodellen angewandt auf medizinische Fragestellungen

Latent class analysis uses mixture models to model multivariate categorical data where dependencies between variables are observed due to the presence of latent groups. Each latent group corresponds to a component in the mixture model and the variable distributions are independent within components. Applications of the latent class model are widespread within fields where categorical data are frequently collected such as medicine or the social sciences. Crucial issues in performing latent class analysis are to select a suitable number of filled components and the variables which are most informative for distinguishing between the components.

Within a Bayesian context we propose an approach which addresses these two issues simultaneously. We specify suitable shrinkage priors for the component weights as well as the component-specific success probabilities which induce sparsity with respect to the number of filled components as well as heterogeneity of the success probabilities across components. Standard estimation methods for Bayesian mixture models are employed because the only difference to a standard Bayesian latent class analysis lies in the specification of suitable hierarchical priors with appropriate hyperparameter values.

The application of this approach is investigated using simulation studies as well as illustrated using some real data.

Florian Frommlet (CeMSIIS, Medical University of Vienna)

Deep Bayesian Regression

One of the most exciting recent developments in data analysis is deep learning. Multilayer networks have become extremely successful in performing prediction tasks and are successfully applied in many different areas. However, the resulting prediction models often difficult to interpret and potentially suffer from overfitting. The aim of this paper is to bring the ideas of deep learning into a statistical framework which yields more parsimonious models and allows to quantify model uncertainty. To this end we introduce the class of deep Bayesian regression models (DBRM) consisting of a generalized linear model combined with a comprehensive non-linear feature space, where non-linear features are generated just like in deep learning. DBRM can easily be extended to include latent Gaussian variables to model complex correlation structures between observations, which seems to be not easily possible with existing deep learning approaches. Two different algorithms based on MCMC are introduced to fit DBRM and to perform Bayesian inference. The predictive performance of these algorithms is compared with a large number of state of the art learning algorithms. Furthermore we illustrate how DBRM can be used for model inference in various applications.

Beat Neuenschwander (Novartis Pharma AG, Basel, Switzerland)

Predictive evidence threshold scaling (PETS): does the evidence meet a confirmatory standard?

Making better use of evidence is one of the tenets of modern drug development. This calls for an understanding of the evidential strength of non-confirmatory data relative to a confirmatory standard. Predictive evidence threshold scaling (PETS) provides a framework for such a comparison. Under PETS, the evidence meets a confirmatory standard if the predictive probability of a positive effect reaches the predictive evidence threshold from hypothetical confirmatory data. Obtaining these probabilities requires hierarchical models with plausible heterogeneity and bias assumptions. After introducing the methodology, I will illustrate PETS for a recent FDA breakthrough designation of Crizotinib for non-small-cell lung cancer (NSCLC). The example shows that the evidential strength of non-confirmatory data can meet a confirmatory standard. This finding is encouraging for modern drug development, which aims to use various types of evidence to inform licensing decisions.

Simon Wandel (Novartis Pharma AG, Switzerland)
joint work with Dr. Christian Röver and Prof. Tim Friede, University Medical Center Göttingen

Model averaging for robust extrapolation in evidence synthesis

Extrapolation from a source (e.g. children) to a target (e.g. adults) is a promising approach to utilize external information. In the context of meta-analyses, especially when dealing with a small number of studies, relevant additional information may be available and could be utilized. Here, we describe an extrapolation strategy using a model-averaging technique. This has the nice feature that the fundamental model remains a random-effects model, yet allowing to leverage existing information on the parameters. The method is robust in the sense that a potential prior-data conflict (discrepancy between source and target data) is explicitly anticipated.
A case study and insight from simulations will be discussed, accompanied with some code snippets.