Wiener Biometrische Sektion (WBS)
der Internationalen Biometrischen Gesellschaft
Region Österreich – Schweiz (ROeS)

http://www.meduniwien.ac.at/wbs/

WBS Herbst Seminar 2016

Jointly organized with the EU FP7 project IDeAl and Asterix

Datum: Mittwoch, 9. November
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: 11:45 Uhr
Organisatoren: Franz König & Martin Posch (CeMSIIS, Med. Univ. Wien)

AGENDA

9:00-10:30 Session 1, Chair: Franz König

- **R. A. Bailey,** University of St Andrews
  The design of blocked experiments when the average replication is very low
- **Christopher Jennison**, University of Bath, UK
  Designing an adaptive trial with treatment selection and a survival endpoint
- **Ralf-Dieter Hilgers**, Department of Medical Statistics RWTH Aachen University
  The selection of a randomization procedure to avoid the impact of bias on the test result in clinical trials – A case study!

10:30 – 10:45 *Break (Foyer)*

10:45:-11:45 Session 2, Chair: Martin Posch

- **Stephen Senn**, Luxembourg Institute of Health
  On being Bayesian
- **Kit Roes**, Julius Center for Health Sciences and Primary Care, Biostatistics and Research Support University Medical Center Utrecht
  Hybrid Bayesian-frequentist approaches for small sample trial design: examples and discussion on concepts.

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

The design of blocked experiments when the average replication is very low
R. A. Bailey, University of St Andrews
In breeding trials of new crop varieties, typically there is very little seed of each of the new varieties. Traditionally, an experiment has one plot for each new variety and several plots for a well-established ``control''. On the other hand, the usual statistical wisdom of equal replication suggests replacing many occurrences of the control by double replicates of a small number of new varieties, especially if comparisons with control are of no interest. This is an improvement if there are no blocks. However, recent work shows that when there are blocks and the average replication is less than 2 then the best designs are far from obvious.

Designing an adaptive trial with treatment selection and a survival endpoint
Christopher Jennison, University of Bath, UK
We consider a clinical trial in which two versions of a new treatment are compared against control with the primary endpoint of overall survival. At an interim analysis, mid-way through the trial, one of the two treatments is selected, based on the short term response of progression free survival. For such an adaptive design the familywise type I error rate can be protected by use of a closed testing procedure to deal with the two null hypotheses and combination tests to combine data from before and after the interim analysis. However, with the primary endpoint of overall survival, there is still a danger of inflating the type I error rate: we present a way of applying the combination test that solves this problem simply and effectively. With the methodology in place, we then assess the potential benefits of treatment selection in this adaptive trial design.

The selection of a randomization procedure to avoid the impact of bias on the test result in clinical trials – A case study!
Ralf-Dieter Hilgers, Department of Medical Statistics RWTH Aachen University
Randomization is the most important design techniques to avoid bias in clinical trials. Up to now the choice of the randomization procedure seem to depend on the research opinion and not on sound scientific arguments.
In this talk, I will show that randomization procedures differ with respect to the impact of bias on the study result. A case study will be conducted to plan a clinical trial.

On being Bayesian
Stephen Senn, Luxembourg Institute of Health
Thanks partly to progress in computing but also in statistical understanding, the last quarter of a century has seen a dramatic rise in the use of "Bayesian" methods. The use of the inverted commas is deliberate. What all these analyses share in common is the use of Bayes theorem to combine prior distributions and data to form a posterior probability statement. However, this is not enough to make the process pass the requirement of Bayesian coherence and most of them would not pass this test.
My talk will be in two main parts. In the first part I shall take two apparently simple examples and show that things are perhaps not so simple after all and that apparently elementary problems can have disturbing implications. In the second part I shall take a (potentially) important problem in drug development, the use of historical data, to try and illustrate what a true Bayesian analysis really needs.
I conclude with some suggestions as to how one might approach the process of thinking about and constructing prior distributions.

Hybrid Bayesian-frequentist approaches for small sample trial design:
examples and discussion on concepts.
Kit Roes, Julius Center for Health Sciences and Primary Care, Biostatistics and Research Support University Medical Center Utrecht

In clinical trials that aim to provide confirmatory evidence for new treatments for rare diseases, the available sample size is often a crucial limitation. In a regulatory (drug approval) setting decision making based on evidence from a limited number of small trials is challenging. The totality of evidence is commonly taken into account, although in an informal fashion. One direction of research in this respect, is to develop methods that prospectively include prior information into the design and analysis of a (confirmatory) trial. This leads to design and analysis procedures which use Bayesian methods, but of which we would like to assess and control frequentist properties. Two examples will be described. As this is a direction of research more broadly explored, some discussion on the conceptual challenges will be included.