

Zeit	Dienstag 11. März 2014					Mittwoch 12. März 2014					Donnerstag 13. März 2014																			
	Session 1	Session 2	Session 3	Session 4	Session 5	Session 1	Session 2	Session 3	Session 4	Session 5	Session 1	Session 2	Session 3	Session 4	Session 5															
08:50		08:50				08:50					08:50																			
09:00		Statistical Tests in a Pharmaceutical Environment	Statistical Applications in Genetics and Molecular Biology			Young Statisticians	Lehre und Didaktik 1: "Methoden"				Education for Statistics in Practice 1 "Analysis of Longitudinal Data" (G Molenberghs)	Survival Methoden	Incomplete Data: Missing Values and Censoring	Boosting																
09:10																														
09:20																														
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09:50				09:10	New Measures for the Assessment of Risk and Prognostic Factors			09:10	Combined Analysis of Multiple Data Sources	Multiple Testing in Clinical Trials					09:10	Adaptive Sample Size Reassessment														
10:00																														
10:10	BREAK					BREAK					BREAK																			
10:20	BREAK					BREAK					BREAK																			
10:30	BREAK					BREAK					BREAK																			
10:40	Opening Ceremony (N Breslow)					10:40	Nachwuchspreise	Research Ethics (G Williams)	Statistical Tests	Wahlauszählung		10:40	Education for Statistics in Practice 2 "Analysis of Longitudinal Data" (G Molenberghs)	Sequential Designs in Clinical Trials	Multivariate Methods (A Bathke)	Resampling and Machine Learning	Adaptive Designs with Several Treatments, Endpoints or Subgroups													
10:50						BREAK					BREAK					BREAK														
11:00						BREAK					BREAK					BREAK														
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12:00	LUNCH					LUNCH & Poster Poster Presence at poster required from 12:45-13:30					LUNCH																			
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13:30	13:30	Meta-Analysis	Clinical Studies in a Regulatory Environment	Spatio-Temporal Methods (A Gelfand)	Efficient Use of Secondary Data 2 (S Evans)	Mixed Models for Marker-Based Analysis Breeding and Genetics (F v Eeuwijk)	IBS 60+					13:30	Regression and Repeated Measurement Analysis in Clinical Trials	Latent Variable Models	Nonparametric Statistics	Integrative Analysis for High Dimensional Data Sets (M Vanucci)	Lehre und Didaktik 2: Curricula													
13:40	BREAK					BREAK					BREAK																			
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15:20	15:20	Network-Meta-Analysis	Evaluation of Surrogate Endpoints and Multistate Models in Clinical Trials (G Molenberghs)	Genetic Epidemiology (F Theis)	Disease Registries (E Pukkala)	Statistical Issues of Personalized Medicine	15:20	100 Jahre Wilcoxon Test	Generalized Additive Model for Location, Scale and Shape	Mixed Models and Extensions for Breeding Experiments and Epidemiological Studies	Multiple Testing with Dependent or Non-Uniform p-Values	Closing Ceremony (D Altman)																		
15:30	BREAK					BREAK					BREAK																			
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17:10	17:10	Statistical Modelling	Discussion EMA Transparency Policy	Statistical Analysis of Gene Expression Data	Analysis of Epidemiological Mega Studies (Cairns BJ)	Mixed Models and Extensions for Agricultural and Biological Experiments	IBS Annual General Meeting					BREAK																		
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19:30	19:30-21:30					19:30-23:30					19:30-23:30																			
20:00	Welcome Town Hall					Conference Dinner					BREAK																			
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60. Biometrisches Kolloquium der Deutschen Region der Internationalen Biometrischen Gesellschaft (IBS-DR)

Date: Monday, 10/Mar/2014

9:00am - 12:00pm	Mo11: Tutorial: Informative Graphics with R
12:00pm - 1:00pm	Lunch
1:00pm - 5:30pm	Mo21: Tutorial: Informative Graphics with R
1:00pm - 5:30pm	Mo22: Tutorial: Datenstrukturen moderner molekularer diagnostischer Technologien
1:30pm - 5:30pm	Vorstand/Beirat IBS-DR
6:00pm - 7:30pm	Der Nutzen großer Kohortenstudien in Deutschland - Der Bremer Beitrag zur Nationalen Kohorte
7:00pm - 11:30pm	Get-Together (Young Researchers)
7:30pm - 11:30pm	Get-Together

Date: Tuesday, 11/Mar/2014

8:50am - 10:10am Tu11: Statistical Tests in a Pharmaceutical Environment

A simple alternative to Fisher's Exact Test under inverse sampling for very small event rates with applications to sequential designs.

Günter Heimann¹, Mauro Gasparini², Mark Von Tress³

¹Novartis Pharma AG, Schweiz; ²Politecnico di Torino; ³Alcon Laboratories;
quenter.heimann@novartis.com

A permutation based conditional exact test for interaction

Joachim Röhmel

Ohne, Deutschland; joachim.roehmel@gmx.de

Statistical rationale for sampling procedures for process validation

Annika Laser^{1,2}

¹Universität Ulm, Deutschland; ²Roche Diagnostics GmbH, Mannheim; annika.laser@uni-ulm.de

An instructive example for poor asymptotic behavior of the logrank test

Ekkehard Glimm

Novartis Pharma, Basel, Schweiz; ekkehard.glimm@novartis.com

8:50am - 10:10am Tu12: Statistical Applications in Genetics and Molecular Biology

Statistical methods for the analysis and interpretation of large-scale gene expression data sets in toxicogenomics

Marianna Grinberg¹, Eugen Rempel¹, Jan Hengstler², Jörg Rahnenführer¹

¹Technische Universität Dortmund, Deutschland; ²Leibniz-Institut für Arbeitsforschung an der TU Dortmund (IfADo); grinberg@statistik.tu-dortmund.de

Bestimmung von Clustern in Netzwerkgraphen mittels korrelationsbasiertem Markov-Cluster-Algorithmus

Martin Jäger, Ronja Foraita

Leibniz-Institut für Präventionsforschung und Epidemiologie - BIPS GmbH, Deutschland;
jaeger@bips.uni-bremen.de

Zipf's law in RNA sequencing

Paul Eilers

Erasmus University Medical Center, Niederlande; p.eilers@erasmusmc.nl

Multiscale DNA partitioning: statistical evidence for segments

Andreas Futschik¹, Thomas Hotz³, Axel Munk², Hannes Sieling²

¹Inst. of Applied Statistics, Johannes Kepler University Linz; ²Institute for Mathematical Stochastics, Georgia Augusta University of Goettingen; ³Institute of Mathematics, Technische Universität Ilmenau;
andreas.futschik@jku.at

9:10am - 10:10am Tu13: Efficient Use of Secondary Data 1

Variance estimates in logistic regression models with random effects

Dirk Enders¹, Christoph Ohlmeier¹, Rafael Mikolajczyk^{2,3}

¹Leibniz-Institute for Prevention Research and Epidemiology - BIPS; ²Helmholtz Centre for Infection Research; ³Hannover Medical School; enders@bips.uni-bremen.de

Planung der Stichproben nach § 42 Risikostrukturausgleichsverordnung (RSAV)

Thomas Schäfer

Westfälische Hochschule, Deutschland; thomas.schaefer@w-hs.de

Schätzung des Verlaufs der HIV-Inzidenz aus Daten des AIDS-Fallregisters und der bestätigten HIV-Diagnosen nach Infektionsschutzgesetz

Matthias an der Heiden, Christian Kollan, Lieselotte Voß, Uli Marcus, Osamah Hamouda

Abteilung für Infektionsepidemiologie, Robert Koch-Institut, Berlin, Deutschland;
anderHeidenM@rki.de

9:10am - 10:10am	Tu14: New Measures for the Assessment of Risk and Prognostic Factors
	<p>Conditional Survival - a useful concept to provide information on prognosis <u>Martin Schumacher</u>¹, <u>Stefanie Hieke</u>¹, <u>Christine König</u>², <u>Martina Kleber</u>², <u>Monika Engelhardt</u>² ¹Institute of Medical Biometry and Statistics, University Medical Center Freiburg; ²Department of Medicine I, Hematology, Oncology and Stem Cell Transplantation, University Medical Center Freiburg; ms@imbi.uni-freiburg.de</p> <hr/> <p>Interpretation of linear regression coefficients under model miss-specification <u>Werner Brannath</u>, <u>Martin Scharpenberg</u> Universität Bremen, Deutschland; brannath@math.uni-bremen.de</p> <hr/> <p>Dichotomizing the survival endpoint in biomarker screening: a good idea? <u>Natalia Becker</u>, <u>Axel Benner</u> DKFZ, Deutschland; natalia.becker@dkfz.de</p>
10:10am - 10:40am	Coffee break
10:40am - 12:00pm	Tu21: Opening Ceremony
Lecture Hall (big)	<p>The case-control study: origins, conception and extensions <u>Norman Breslow</u> University of Washington, Seattle; norm@uw.edu</p>
12:00pm - 1:30pm	Lunch
1:30pm - 2:50pm	Tu31: Meta Analyses
	<p>Statistical methods for meta-analysis to compare two diagnostic tests to a common gold standard <u>Annika Hoyer</u>, <u>Oliver Kuß</u> Deutsches Diabetes-Zentrum (DDZ), Leibniz-Zentrum für Diabetes Forschung an der Heinrich-Heine-Universität Düsseldorf, Deutschland; annika.hoyer@ddz.uni-duesseldorf.de</p> <hr/> <p>A method for IPD meta-analysis of treatment-covariate interaction with a continuous predictor in randomised trials <u>Willi Sauerbrei</u>¹, <u>Patrick Royston</u>², <u>Benjamin Kasenda</u>³, <u>Matthias Briel</u>³ ¹Department für Medizinische Biometrie und Informatik, Universitätsklinikum Freiburg, Deutschland; ²Hub for Trials Methodology Research, MRC Clinical Trials Unit and University College London, London, UK; ³Institute for Clinical Epidemiology and Biostatistics, University Hospital Basel, Basel, Switzerland; wfs@imbi.uni-freiburg.de</p> <hr/> <p>Berechnung von Konfidenzintervallen für Risikodifferenzen mit Hilfe von MOVER-R <u>Ralf Bender</u>¹, <u>Robert G. Newcombe</u>² ¹Ressort "Medizinische Biometrie", Institut für Qualität und Wirtschaftlichkeit im Gesundheitswesen (IQWiG), Köln, Deutschland; ²Cochrane Institute of Primary Care & Public Health, Cardiff University, Cardiff, Wales, UK; Ralf.Bender@iqwig.de</p> <hr/> <p>A Bayesian approach to inferring heterogeneity in meta-analyses <u>Christian Röver</u>, <u>Tim Friede</u> Universitätsmedizin Göttingen; christian.roever@med.uni-goettingen.de</p>
1:30pm - 2:50pm	Tu32: Clinical Studies in a Regulatory Environment
	<p>Quantifizierung des Ausmaßes des Zusatznutzens von neuen Arzneimitteln: „gering“ – „beträchtlich“ – „erheblich“? <u>Werner Vach</u> Klinische Epidemiologie, Department für Medizinische Biometrie und Medizinische Informatik, Universitätsklinikum Freiburg; wv@imbi.uni-freiburg.de</p> <hr/> <p>Sample size planning for Phase 2 / Phase 3 development programs</p>

Heiko Götte¹, Armin Schüler¹, Marietta Kirchner², Meinhard Kieser²

¹Merck KGaA, Deutschland; ²Institut für Medizinische Biometrie und Informatik, Ruprecht-Karls Universität Heidelberg; heiko.goette@merckgroup.com

Analyzing the change of red blood cell (RBC) transfusion requirement in clinical studies – a comparison of different methods

Norbert Hollaender, Viktoriya Stalbovskaya

Novartis Pharma AG, Schweiz; norbert.hollaender@novartis.com

Schätzung der Interobserver-Variabilität in Diagnosestudien: kappa vs. Krippendorffs alpha

Antonia Zapf

Universitätsmedizin Göttingen, Deutschland; antonia.zapf@med.uni-goettingen.de

1:30pm - 2:50pm

Tu33: Spatio-Temporal Methods

Fusing point and areal level space-time data with application to wet deposition

Alan Gelfand

Duke University, United States of America; alan@stat.duke.edu

From retrospective intervention detection towards online monitoring in INGARCH models for time series of counts

Tobias Liboschik, Roland Fried

Technische Universität Dortmund, Deutschland; liboschik@statistik.tu-dortmund.de

Erfassung der räumlichen Verfügbarkeit von urbanen Punktcharakteristika zur Erklärung von körperlicher Aktivität bei Kindern: Evaluation von Kerndichte und Nachbarschaft

Christoph Buck¹, Thomas Kneib², Tobias Tkaczick³, Kenn Konstabel⁴, Iris Pigeot¹

¹Leibniz-Institut für Präventionsforschung und Epidemiologie - BIPS, Deutschland; ²Georg-August-Universität Göttingen; ³Institut für Geographie, Universität Bremen; ⁴National Institute for Health Development, Tallinn; buck@bips.uni-bremen.de

1:30pm - 2:50pm

Tu34: Efficient Use of Secondary Data 2

To be announced

Stephen Evans

London School of Hygiene & Tropical Medicine, Vereinigtes Königreich; stephen.evans@lshtm.ac.uk

Application of instrumental variable analysis to administrative data of statutory health insurances: potential and limitations

Bianca Kollhorst, Edeltraut Garbe, Iris Pigeot

Leibniz-Institut für Präventionsforschung und Epidemiologie - BIPS, Deutschland; kollhorst@bips.uni-bremen.de

Efficient ungrouping of coarsely grouped count data with the penalized composite link model

Silvia Rizzi¹, Jutta Gampe¹, Paul H.C. Eilers²

¹Max Planck Institute for Demographic Research, Germany; ²Department of Biostatistics, Erasmus Medical Center, Rotterdam, The Netherlands; rizzi@demogr.mpg.de

1:30pm - 2:50pm

Tu35: Mixed Models for Marker-Based Analysis in Breeding and Genetics

Mixed models for genotype by environment interactions in linkage and linkage disequilibrium QTL mapping and genomic prediction

Fred A. van Eeuwijk, Marcos Malosetti, Willem Kruijer, Martin Boer

Wageningen University, The Netherlands; Fred.vanEeuwijk@wur.nl

Marker-based estimation of heritability in Arabidopsis thaliana

Willem Kruijer¹, Martin Boer¹, Marcos Malosetti¹, Bas Engel¹, Pdraic Flood³, Rik Kooke², Joost Keurentjes^{3,4}, Fred van Eeuwijk¹

¹Biometris, Wageningen University and Research Centre, Wageningen, Netherlands; ²Laboratory of Plant Physiology, Wageningen University and Research Centre, Wageningen, Netherlands;

³Laboratory of Genetics, Wageningen University and Research Centre, Wageningen, Netherlands;
⁴University of Amsterdam, Netherlands; willem.kruijer@wur.nl

Investigations on significance of genomic effects

Dörte Wittenburg, Nina Melzer

Leibniz-Institut für Nutztierbiologie, Institut für Genetik und Biometrie, 18196 Dummerstorf, Deutschland; wittenburg@fbn-dummerstorf.de

2:50pm - 3:20pm **Coffee break**

3:20pm - 4:40pm **Tu41: Network Meta Analyses**

Network meta-analysis for cluster-randomized trials

Lorenz Uhlmann, Katrin Jensen, Meinhard Kieser

Universität Heidelberg, Deutschland; uhlmann@imbi.uni-heidelberg.de

Reduce dimension or reduce weights? Comparing two approaches to multi-armed studies in network meta-analysis

Gerta Rücker, Guido Schwarzer

University Medical Center Freiburg, Deutschland; ruecker@imbi.uni-freiburg.de

Detection of Inconsistency in Network Meta-Analysis Based on Random Effects Modelling

Ulrike Krahn, Harald Binder, Jochem König

Institute of Medical Biostatistics, Epidemiology and Informatics (IMBEI), University Medical Center Johannes Gutenberg University Mainz, Germany; krahn@uni-mainz.de

Investigating consistency of mixed treatment comparisons by approximating sub-networks

Jochem König, Ulrike Krahn, Harald Binder

Unimedizin der Johannes Gutenberg Universität Mainz, Deutschland; koenig@uni-mainz.de

3:20pm - 4:40pm **Tu42: Evaluation of Surrogate Endpoints and Multistate Models in Clinical Trials**

The Statistical Evaluation of Surrogate Endpoints in Clinical Trials

Geert Molenberghs

Universiteit Hasselt & KU Leuven, Belgium; geert.molenberghs@uhasselt.be

The multistate model as nested competing risks experiments with an application to hematopoietic cell transplantation data

Susanna Di Termini¹, Martin Schumacher¹, Jan Bayersmann²

¹Institut für Medizinische Biometrie und Medizinische Informatik Universitätsklinikum Freiburg, Deutschland; ²Institute of Statistics, Ulm University; susanna@fdm.uni-freiburg.de

Subgroup identification in oncology trials based on multistate modeling

Salome Friedel¹, Birgit Gaschler-Markefski¹, Jan Beyersmann², Patricia Glomb¹

¹Boehringer Ingelheim Pharma GmbH & Co. KG, Deutschland; ²Universität Ulm, Ulm, Deutschland; salome.friedel@gmail.com

3:20pm - 4:40pm **Tu43: Genetic Epidemiology**

Integrating omics data in cohort studies: beyond univariate analyses

Fabian Theis

Helmholtz Zentrum München, Deutschland; fabian.theis@helmholtz-muenchen.de

From Epilepsies to Autism: Finding the “Missing Heritability” Through a Novel Computational Biostatistics Approach

Knut M. Wittkowski¹, Benedetta Bigio¹, Mona Katharina Tonn²

¹The Rockefeller University, USA; ²Hochschule Koblenz; kmw@rockefeller.edu

Robust association tests and model selection for the X chromosome

Christina Loley¹, Inke R. König¹, Andreas Ziegler^{1,2}

¹Institut für Medizinische Biometrie und Statistik, Universität zu Lübeck, Universitätsklinikum Schleswig-Holstein, Campus Lübeck, Lübeck, Germany; ²Zentrum für Klinische Studien Lübeck, Universität zu Lübeck, Lübeck, Germany; christina.loley@imbs.uni-luebeck.de

3:20pm - 4:40pm

Tu44: Disease Registries

To be announced

Eero Pukkala

Finnish Cancer Registry, Finland; Eero.pukkala@cancer.fi

Use of simulation methods in the assessment of competing analysis strategies for disease registries accounting for calendar time effects

David Ellenberger, Tim Friede

Universitätsmedizin Göttingen, Deutschland; david.ellenberger@med.uni-goettingen.de

Coupled variable selection in regression models for data from a clinical cancer registry

Irene Schmidtman¹, Arndt Weinmann², Harald Binder¹

¹Institut für Medizinische Biometrie, Epidemiologie und Informatik, Universitätsmedizin Mainz, Deutschland; ²I. Medizinische Klinik, Universitätsmedizin Mainz, Deutschland; Irene.Schmidtman@uni-mainz.de

3:20pm - 4:40pm

Tu45: Statistical Issues of Personalized Medicine

Analyzing treatment-by-subgroup interactions in time-to-event data - comparison of three multivariate approaches

Anne-Sophie Stöhlker, Harriet Sommer, Martin Grupp, Martin Schumacher

University Medical Center Freiburg, Deutschland; stoehlker@imbi.uni-freiburg.de

Entscheidungskriterien für die prospektive Validierung eines Biomarkers in einer Therapiestudie

Anika Großhennig, Armin Koch

Medizinische Hochschule Hannover, Deutschland; grosshennig.anika@mh-hannover.de

Comparing a marker based stratified treatment strategy with the standard treatment in a randomized clinical trial

Hong Sun¹, Frank Bretz², Werner Vach¹

¹Department für Medizinische Biometrie und Medizinische Informatik, Universitätsklinikums Freiburg, Deutschland; ²Novartis Pharma AG, Switzerland; sun@imbi.uni-freiburg.de

Construction of target ranges in transplantation data

Markus Harden¹, Byron Jones², Tim Friede¹

¹Universitätsmedizin Göttingen, Deutschland; ²Novartis, Basel, Switzerland; markus.harden@med.uni-goettingen.de

4:40pm - 5:10pm

Coffee break

5:10pm - 6:30pm

Tu51: Statistical Modelling

Multivariate Bayesian Gaussian distributional regression

Nadja Klein

Georg-August-Universität Göttingen, Deutschland; nklein@uni-goettingen.de

Assessment of strategies for modelling two continuous covariates with a spike at zero

Carolin Jenkner¹, Eva Lorenz², Heiko Becher², Willi Sauerbrei¹

¹University Medical Center, Institute for Medical Biometry and Statistics, Freiburg, Deutschland; ²University of Heidelberg, Institute of Public Health; jenkner@imbi.uni-freiburg.de

Robust quantification of non-linear dependencies

Martin Scharpenberg, Werner Brannath

Universität Bremen, Deutschland; mscharpenberg@uni-bremen.de

Graphical tools for investigating variable selection instability caused by correlated variables

Sam Doerken¹, **Riccardo De Bin²**, **Anne-Laure Boulesteix²**, **Willi Sauerbrei¹**

¹Department of Medical Biometry and Statistics, University Medical Center Freiburg; ²Department of Medical Informatics, Biometry and Epidemiology, University of Munich; doerken@imbi.uni-freiburg.de

5:10pm - 6:30pm

Tu53: Statistical Analysis of Gene Expression Data

Combined Analysis of Different Types of Genetic and Clinical Data in NSCLC

Helena König¹, **Katja Ickstadt¹**, **Jan G. Hengstler²**, **Patrick Micke³**

¹TU Dortmund, Germany; ²Leibniz-Institut für Arbeitsforschung, University of Dortmund, Germany; ³Uppsala University, Sweden; hkoenig@statistik.tu-dortmund.de

A correlation approach for including interactions into prognostic model for high-dimensional molecular data

Isabell Hoffmann, **Murat Sariyar**, **Harald Binder**

Institut für medizinische Biometrie, Epidemiologie und Informatik, Universitätsmedizin Mainz, Deutschland; Isabell.Hoffmann@unimedizin-mainz.de

Quality control in public gene expression datasets: Identification of sample misannotations with a male-female classifier

Jörg Rahnenführer, **Miriam Lohr**

Fakultät Statistik, Technische Universität Dortmund, Deutschland; rahenfuehrer@statistik.tu-dortmund.de

Extreme value analysis meets biometrics: The peaks over threshold method in gene expression analysis

Diana Tichy

German Cancer Research Center, Heidelberg, Germany; d.tichy@dkfz.de

5:10pm - 6:30pm

Tu54: Analysis of Epidemiological Mega Studies

Just more of the same? Statistical challenges in the Million Women Study and other large-scale cohorts

Benjamin J. Cairns

University of Oxford, United Kingdom; ben.cairns@ceu.ox.ac.uk

A simulation approach to power calculation for large cohort studies based on multistate models

Bastian Jenny, **Martin Schumacher**

Institute of Medical Biometry and Medical Informatics, University Medical Center Freiburg, Germany; bastian_jenny@web.de

Full cohort, nested case-control or case-cohort study? - Impact on sample size and precision of risk estimates

Kristin Ohneberg¹, **Jan Beyersmann²**, **Martin Wolkewitz¹**, **Martin Schumacher¹**

¹Department für Medizinische Biometrie und Medizinische Informatik, Universitätsklinikum Freiburg, Deutschland; ²Institut für Statistik, Universität Ulm, Deutschland; ohneberg@imbi.uni-freiburg.de

5:10pm - 6:30pm

Tu55: Mixed Models and Extensions for Agricultural and Biological Experiments

Basisfunktionsansätze und Regularisierung in Regressionsmodellen zur Auswertung von Kartierungsversuchen

Manuela Reichelt, **Friedrich Teuscher**, **Norbert Reinsch**

Leibniz-Institut für Nutztierbiologie, Deutschland; reichelt@fhn-dummerstorf.de

A classification study for hygienic bees with mixed model pre-processing

Henrik Rudolf^{1,2}, **Norbert Reinsch¹**

¹Leibniz-Institut für Nutztierbiologie, Deutschland; ²Ruhr-Universität Bochum, Deutschland; rudolf@amib.ruhr-uni-bochum.de

Optimal block design with nested rows and columns

Maria Kozłowska

Poznan University of Life Sciences, Poland; markoz@up.poznan.pl

Inter-block information: To recover or not to recover it?

Jens Möhring, Hans-Peter Piepho

Universität Hohenheim, Deutschland; moehring@uni-hohenheim.de

5:10pm - 6:30pm
Lecture Hall (big)

Tu52: Discussion EMA Transparency Policy

Offenlegung klinischer Studiendaten – Statistische Herausforderungen hinsichtlich der EMA Transparency Policy und anderer Initiativen

Frank Langer¹, Christoph Gerlinger², Hans-Jürgen Lomp³

¹Lilly Deutschland GmbH; ²Bayer Pharma AG; ³Boehringer Ingelheim Pharma KG; langner@lilly.com

7:30pm - 9:30pm

Welcome to Town Hall

Date: Wednesday, 12/Mar/2014

8:50am - 10:10am We11: Young Statisticians

Simulation von rekurrenten Ereigniszeitdaten im Total-Time-Model

Ann-Kathrin Ozga¹, Katharina Ingel², Antje Jahn²

¹Fachhochschule Koblenz (RheinAhrCampus), Deutschland; ²Institut für Medizinische Biometrie, Epidemiologie und Informatik, Mainz; A.Ozga@gmx.net

Detektion von Nanoobjekten in Graustufenbildern und Bildsequenzen mittels robuster Zeitreihenmethoden zur Strukturbruchererkennung

Sermad Abbas

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Application of spatial Bayesian Poisson regression to identify associations between EHEC incidence and socio-economic variables

Maïke Tahden¹, Juliane Manitz², Thomas Kneib², Guido Hegasy³

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Statistical Learning from Imbalanced Datasets - Comparison of Different Strategies for Multivariate Classification Methods

Laura Schlieker¹, Anna Telaar², Katja Ickstadt¹, Carmen Theek²

¹TU Dortmund, Deutschland; ²Protagen AG, Dortmund, Deutschland; laura.schlieker@uni-dortmund.de

8:50am - 10:10am We12: Lehre und Didaktik 1: "Methoden"

Prüfungsmöglichkeit in einem Statistiksoftware-Kurs

Rainer Muche, Beate Einsiedler, Marianne Meule, Benjamin Mayer

Institut für Epidemiologie und Med. Biometrie, Universität Ulm, Deutschland; rainer.muche@uni-ulm.de

Motivate students with exciting findings: How to find short, interesting, and published papers?

Jochen Kruppa

Georg-August-University Göttingen, Animal Breeding and Genetics Group, Göttingen; jkruppa@gwdg.de

Aufgaben in der Vorlesung

Reinhard Vonthein

Universität zu Lübeck, Deutschland; Reinhard.Vonthein@imbs.uni-luebeck.de

Erhöhen Youtube-Videos auch Deinen Puls? – Erfahrungsbericht einer randomisierten, klinischen Studie

Theodor Framke

Medizinische Hochschule Hannover, Deutschland; framke.theodor@mh-hannover.de

9:10am - 10:10am We13: Combined Analysis of Multiple Data Sources

Choosing efficient stratifications in logistic two-phase studies based on administrative data

Sigrid Behr, Walter Schill, Iris Pigeot

Leibniz-Institut für Präventionsforschung und Epidemiologie - BIPS, Deutschland; behr@bips.uni-bremen.de

Using the whole cohort in the analysis of case-control data: application to the women's health initiative

Norman Breslow¹, Gustavo Amorim², Mary Pettinger³, Jacques Roussow⁴

¹University of Washington, Seattle, USA; ²University of Auckland, New Zealand; ³Fred Hutchinson Cancer Research Center, Seattle, USA; ⁴National Heart, Lung and Blood Institute, Bethesda, MD, USA; norm@uw.edu

Computing adjusted attributable fractions from two-phase case-control data

Walter Schill¹, Pascal Wild², Karsten Drescher³

¹Leibniz-Institut für Präventionsforschung und Epidemiologie - BIPS, Deutschland; ²INRS, Vandoeuvre, Frankreich; ³Statistisches Landesamt Bremen, Deutschland; schill@bips.uni-bremen.de

9:10am - 10:10am **We14: Multiple Testing in Clinical Trials**

Informative Konfidenzintervalle für hierarchische Tests

Sylvia Schmidt, Werner Brannath

Universität Bremen, Deutschland; sylviaschmidt@math.uni-bremen.de

Multiple Tests of Nonlinear Models

Georg Gutjahr¹, Björn Bornkamp²

¹Universität Bremen, Deutschland; ²Novartis Pharma AG, Schweiz; georg.gutjahr@math.uni-bremen.de

Matroids & testing in families of algebraically dependent and contextually related hypotheses

Florian Klinglmueller¹, Willi Maurer²

¹Medizinische Universität Wien, Österreich; ²Novartis AG; florian.klinglmueller@meduniwien.ac.at

10:10am - 10:40am **Coffee break**

10:40am - 11:40am **We23: Statistical Tests**

Tailoring goodness-of-fit tests with local levels

Sandra Landwehr^{1,2}, Veronika Gotscharuk^{1,2}, Helmut Finner²

¹Department of Statistics in Medicine, Faculty of Medicine, Heinrich Heine University Düsseldorf; ²Institute for Biometrics and Epidemiology, German Diabetes Center, Leibniz Center for Diabetes Research at the Heinrich Heine University Düsseldorf; sandra.landwehr@ddz.uni-duesseldorf.de

Vergleich verschiedener Methoden zur Berechnung von Konfidenzintervallen für das relative Risiko

Daniela Zöller¹, Ralf Bender²

¹Hochschule Koblenz, Standort RheinAhrCampus Remagen, Deutschland; ²Ressort Medizinische Biometrie, Institut für Qualität und Wirtschaftlichkeit im Gesundheitswesen (IQWiG), Köln; daniela.zoeller@outlook.de

Nearly exact sample size calculation for powerful nonrandomized tests for differences between binomial proportions

Stefan Wellek^{1,2}

¹Dept. of Biostatistics, CIMH Mannheim, Mannheim Medical School of the Univ. of Heidelberg; ²Dept. of Med. Biostatistics, Epidemiology and Informatics, University Medical Center, Univ. of Mainz; stefan.wellek@zi-mannheim.de

10:40am - 12:00pm **We22: Research Ethics**

To be announced

Garrath Williams

Lancaster University, Vereinigtes Königreich; g.d.williams@lancaster.ac.uk
To be announced

10:40am - 12:00pm **We21: Nachwuchspreise**
Lecture Hall (big)

12:00pm - 1:30pm **Lunch**

12:45pm - 1:30pm **We31: Poster Session**

A clustering-based test for non-additivity in an unreplicated two-way layout

Waqas Ahmed Malik¹, Jens Möhring², Hans-Peter Piepho³

¹Universität Hohenheim, Germany; ²Universität Hohenheim, Germany; ³Universität Hohenheim,

Germany; w.malik@uni-hohenheim.de

Trial designs balancing patient-orientation and randomization - theoretical considerations and simulations

Constanze Schulz

Competence center for clinical trials Bremen, Deutschland; conschul@math.uni-bremen.de

Looking for the hump – How can differences in the shape of distribution be detected?

Carmen Theek, Anna Telaar

Protagen AG, Deutschland; carmen.theek@protagen.com

Sind Meta-Analysen orientierend oder konfirmatorisch?

Wilhelm Gaus, Benjamin Mayer, Rainer Muehe

Universität Ulm, Institut für Epidemiologie und Medizinische Biometrie, Deutschland; wilhelm.gaus@uni-ulm.de

Sample size determination for studies designed to estimate covariate-dependent reference quantile curves

Christine Jennen-Steinmetz

Zentralinstitut für Seelische Gesundheit, Medizinische Fakultät Mannheim /Universität Heidelberg, Deutschland; christine.jennen-steinmetz@zi-mannheim.de

Untersuchung einer Fallzahlformel in einem meta-analytisch prädiktiven Bayes-Modell als Maß des Extrapolationsgehalts historischer Studienergebnisse

Raphael Koch, Gerß Joachim

Institut für Biometrie und Klinische Forschung, Deutschland; Raphael.Koch@ukmuenster.de

A SNP genotyping study reveals an association of mt-ND4 11719 A/G polymorphism with ulcerative colitis in two German cohorts

Theresa Holste¹, Torsten Schröder², Steffen Möller³, Xinhua Yu^{4,5}, David Ellinghaus⁶, Florian Bär², Bandik Föh², Saujanya R. Ventrapragada², Kilian von Medem², Jürgen Büning², Klaus Fellermann², Hendrik Lehnert², Stefan Schreiber⁶, Andre Franke⁶, Christian Sina², Saleh M. Ibrahim³, Inke R. König¹

¹Institute of Medical Biometry and Statistics, University Lübeck, University Hospital Schleswig-Holstein, Campus Lübeck, Germany; ²Department of Medicine I, University Hospital Schleswig-Holstein, Campus Lübeck, Germany; ³Department of Dermatology, University Hospital Schleswig-Holstein, Campus Lübeck, Germany; ⁴Department of Immunology and Cell Biology, Research Center Borstel, Germany; ⁵Laboratory of Autoimmunity, The Medical College of Xiamen University, China; ⁶Institute of Clinical Molecular Biology, Christian-Albrechts-University of Kiel, Germany; theresa.holste@imbs.uni-luebeck.de

Asymptotic distribution of the MAX gTDT statistic for association testing in case-parent trio studies

Philipp Berger, Holger Schwender

Mathematisches Institut, Heinrich-Heine-Universität Düsseldorf; philipp.berger@uni-duesseldorf.de

Comparison of variable importance measures for Partial Least Squares Discriminant Analysis

Anna Telaar, Carmen Theek

Protagen AG, Deutschland; anna.telaar@protagen.com

Simultaneous small-sample inference in longitudinal settings using multiple contrasts

Philip Pallmann

Leibniz Universität Hannover, Deutschland; pallmann@biostat.uni-hannover.de

The analysis of longitudinal pain data in cancer pain studies: results from a systematic literature review.

Odile Sauzet¹, Maren Klein¹, John E. Williams², Joy R. Ross^{3,4}

¹Epidemiologie & International Public Health, Universität Bielefeld, Deutschland; ²Department of Anaesthetics and Pain Management, Royal Marsden NHS Foundation Trust, London, UK; ³Royal Marsden and Royal Brompton Palliative Care Service, Royal Marsden NHS Foundation Trust, London, UK; ⁴National Heart and Lung Institute, Imperial College, London, UK; odile.sauzet@uni-bielefeld.de

Eine Erweiterung der "Trim und Fill-Methode" in Meta-Analysen diagnostischer Studien

Julia Rey, Eva Herrmann

Institut für Biostatistik und Mathematische Modellierung, Goethe Universität Frankfurt, Deutschland; Rey@med.uni-frankfurt.de

Imputation von fehlenden Werten für die Schätzung der Inzidenz bei der web-basierten prospektiven Erfassung von akuten Atemwegserkrankungen

Nicole Rübsamen, Manas Akmatov, Rafael Mikolajczyk

Arbeitsgruppe „Epidemiologische und statistische Methoden“, Helmholtz-Zentrum für Infektionsforschung, Braunschweig, Deutschland; nru13@helmholtz-hzi.de

Analyzing Case-Parent Trio Data with Sparse Group Lasso

Timo Stöcker, Holger Schwender

Mathematical Institute, Heinrich Heine University Düsseldorf, Deutschland; stoecker@math.uni-duesseldorf.de

Wissenschaftliche Politikberatung - wie unsicher ist sicher

Olaf Mosbach-Schulz

Europäische Behörde für Lebensmittelsicherheit (EFSA), Italien; olaf.mosbach-schulz@efsa.europa.eu

Die Area under the ROC-Curve (AUC) als Selektionsparameter zur Identifizierung von prognostischen und diagnostischen Faktoren in einer epidemiologischen Feldstudie

Michael Schneider, Luksche Nicole, Zehnder Andreas, Jakob Franz, Seefried Lothar

Orthopädisches Zentrum für Muskuloskelettale Forschung, Universität Würzburg; m-schneider.klh@uni-wuerzburg.de

Can we draw sound conclusions from extension trials?

Stefan Hantel

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Vergleich von Konfidenzintervall-Schätzungen für Wahrscheinlichkeiten bei Meta-Analysen

Julia Rey, Eva Herrmann

Institut für Biostatistik und Mathematische Modellierung, Goethe Universität Frankfurt, Deutschland; Rey@med.uni-frankfurt.de

A two-stage hierarchical multiple test procedure based on the asymptotically optimal rejection curve

Konstantin Schildknecht

Humboldt-Universität zu Berlin, Deutschland; schildkn@mathematik.hu-berlin.de

Probability estimation for binary and multi-category outcome using machine learning methods

Jochen Kruppa¹, Theresa Holste², Andreas Ziegler²

¹Georg-August-University Göttingen, Animal Breeding and Genetics Group, Göttingen; ²Universität zu Lübeck, Institut für Medizinische Biometrie und Statistik, Lübeck; jkruppa@gwdg.de

1:30pm - 2:50pm
Lecture Hall (big)

We41: IBS 60+

Geschichte der Deutschen Region der Internationalen Biometrischen Gesellschaft

Hanspeter Thöni

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Biometrie in der DDR

Jürgen Läuter

Otto-von-Guericke-Universität Magdeburg, Deutschland; juergen.laeuter@med.ovgu.de

Biometrie in der Klinischen Forschung in Deutschland

Lutz Edler

Abt Biostatistik, Deutsches Krebsforschungszentrum, Heidelberg, Deutschland; edler@dkfz.de

Die Epidemiologie in Deutschland. 60+

Maria Blettner

IMBEI, Deutschland; blettner-sekretariat@imbei.uni-mainz.de

2:50pm - 3:20pm Coffee break

3:20pm - 4:20pm We51: 100 Jahre Wilcoxon-Test

100 Jahre Wilcoxon-Test

Markus Neuhäuser

RheinAhrCampus, Deutschland; neuhaeuser@rheinahrcampus.de

Der Wilcoxon-Mann-Whitney Test - Die Entwicklung ab 1950 -

Edgar Brunner

Universitätsmedizin Göttingen, Deutschland; ebrunne1@gwdg.de

New results for Wilcoxon type tests: More than a tool box?

Arnold Janssen

Heinrich-Heine Universität Düsseldorf, Deutschland; janssena@math.uni-duesseldorf.de

3:20pm - 4:20pm We52: Generalized Additive Model for Location, Scale and Shape

Modeling DNA methylation data using generalized additive models for location, scale and shape

Simone Wahl¹, Nora Fenske², Sonja Zeilinger¹, Annette Peters^{1,3}, Melanie Waldenberger¹, Harald Grallert¹, Matthias Schmid²

¹Research Unit of Molecular Epidemiology, Helmholtz Zentrum München, Neuherberg, Germany;

²Department of Statistics, Ludwig-Maximilians-Universität München, Munich, Germany; ³Institute of Epidemiology II, Helmholtz Zentrum München, Neuherberg, Germany; simone.wahl@helmholtz-muenchen.de

Analysing the age-dependent increase of skinfold thickness in children and its interaction with the FTO polymorphism rs9939609 using semiparametric expectile regression in the IDEFICS study

Fabian Sobotka¹, Ronja Foraita², Alfonso Siani³, Fabio Lauria³, Paola Russo³, Stefaan De Henauw⁴, Michael Tornaritis⁵, Dénes Molnár⁶, Luis A Moreno⁷, Lauren Lissner⁸, Toomas Veidebaum⁹, Licia Iacoviello¹⁰, Yannis Pitsiladis¹¹, Iris Pigeot²

¹Universität Göttingen, Deutschland; ²Leibniz Institute for Prevention Research and Epidemiology – BIPS; ³National Research Council, Institute of Food Science, Epidemiology and Population Genetics, Avellino, Italy; ⁴Ghent University, Department of Public Health, Ghent, Belgium; ⁵Research and Education Institute of Child Health, Strovolos, Cyprus; ⁶University of Pécs, Department of Pediatrics, Pécs, Hungary; ⁷University of Zaragoza, Growth, Exercise, Nutrition and Development (GENUD) Research Group, Zaragoza, Spain; ⁸University of Gothenburg, Department of Pediatrics, Institution of clinical sciences, Gothenburg, Sweden; ⁹National Institute for Health Development, Department of Chronic Diseases, Tallinn, Estonia; ¹⁰Department of Epidemiology and Prevention, IRCCS Istituto Neurologico Mediterraneo Neuromed, Pozzilli, Italy; ¹¹University of Brighton, School of Sport and Service Management, Eastbourne, UK; fabian.sobotka@wiwi.uni-goettingen.de

How to develop and evaluate spirometric reference values by using GAMLSS

Anke Hüls¹, Ursula Krämer¹, Monika Gappa², Christine Müller-Brandes³, Gabriele Seitner-Sorge¹, Andrea von Berg², Barbara Hoffmann^{1,4}, Antje Schuster⁵, Matthias Wisbauer⁶, Dietrich Berdel²

¹IUF Leibniz Institute for Environmental Medicine, Düsseldorf; ²Marien Hospital Wesel, Children's Hospital and Research Institute, Wesel; ³Medical School of Hanover, Department of Anaesthesiology and Intensive Care Medicine, Hanover; ⁴Medical Faculty, Heinrich-Heine University of Düsseldorf, Düsseldorf; ⁵Heinrich-Heine University, University Children's Hospital, Düsseldorf; ⁶Helios Clinic Wuppertal, Department of Pediatric Cardiology and Pneumology, Wuppertal; Anke.Huels@IUF-Duesseldorf.de

3:20pm - 4:20pm We53: Mixed Models and Extensions for Breeding Experiments and Epidemiological Studies

Dissecting genetic and non-genetic sources of long-term yield trend in German

official cultivar trials

Hans-Peter Piepho¹, Friedrich Laidig², Drobek Thomas², Meyer Uwe²

¹Universität Hohenheim, Deutschland; ²Bundessortenamt, Hannover, Deutschland; hans-peter.piepho@uni-hohenheim.de

Hierarchien und Zähldaten: Erfahrungen mit unterschiedlichen Modellierungsstrategien in einer epidemiologischen Querschnittsstudie

Cornelia Frömke, Johanna Hering, Katja Hille, Christiane von Münchhausen, Lothar Kreienbrock

Stiftung Tierärztliche Hochschule Hannover, Deutschland; cornelia.froemke@tiho-hannover.de

Exakte SNP-basierte Berechnung der additiven und dominanten genetischen Streuung von Nachkommen in der Anpaarungsplanung

Sarah Bonk, Friedrich Teuscher, **Norbert Reinsch**

Leibniz-Institut für Nutztierforschung, Deutschland; reinsch@fhn-dummerstorf.de

3:20pm - 4:20pm

We54: Multiple Testing with Dependent or Non-Uniform p-Values

Randomized p -values for multiple testing of composite null hypotheses

Thorsten Dickhaus

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On control of the FWER of some adaptive procedures under dependency

Veronika Gontscharuk^{1,2}, Helmut Finner²

¹Department of Statistics in Medicine, Faculty of Medicine, Heinrich-Heine-University Duesseldorf;

²Institute for Biometrics and Epidemiology, German Diabetes Center at the Heinrich-Heine-University Duesseldorf, Leibniz Center for Diabetes Research; veronika.gontscharuk@ddz.uni-duesseldorf.de

On the Simes Test Under Dependence

Helmut Finner, Klaus Strassburger

Deutsches Diabetes-Zentrum an der Heinrich-Heine-Universität Düsseldorf, Leibniz-Zentrum für Diabetes-Forschung, Deutschland; finner@ddz.uni-duesseldorf.de

4:20pm - 4:30pm

Short break

4:30pm - 6:30pm

IBS-DR Annual General Meeting

Lecture Hall (big)

7:30pm - 11:30pm

Conference Dinner

Date: Thursday, 13/Mar/2014

8:50am - 10:10am Th12: Survival Methods

On the choice and influence of the number of boosting steps

Heidi Seibold, Anne-Laure Boulesteix, Riccardo De Bin

IBE, LMU Munich, Deutschland; Heidi.Seibold@campus.lmu.de

The use of historical data for estimation of parameters in survival analysis

Joachim Röhmel¹, **Dietrich Knoerzer**², Sandra Klawitter², Claus Garbe³

¹ehem. BfArM; ²Roche Pharma AG, Grenzach; ³Universitätsklinikum Tübingen;
dietrich.knoerzer@roche.com

Dichotomising using a distributional method: what benefits for results of a clinical or observational study?

Odile Sauzet¹, Janet L. Peacock²

¹Universität Bielefeld, Deutschland; ²Division of Health and Social Care Research, King's College London, UK; odile.sauzet@uni-bielefeld.de

Adjusted excess length-of-stay in hospital due to hospital-acquired infections

Arthur Allignol¹, Martin Schumacher², Stephan Harbarth³, Jan Beyersmann¹

¹Institute for Statistics, Ulm University, Germany; ²Institute of Medical Biometry and Medical Informatics, University Medical Center Freiburg, Germany; ³Infection Control Program, University of Geneva Hospitals and Faculty of Medicine, Geneva, Switzerland; arthur.allignol@uni-ulm.de

8:50am - 10:10am Th13: Incomplete Data: Missing Values and Censoring

Semiparametric regression with missing responses

Ursula U. Müller

Texas A&M University, USA; uschi@stat.tamu.edu

Local variance estimation for uncensored and censored observations

Paola Gloria Ferrario

Universität zu Lübeck, Universitätsklinikum Schleswig-Holstein, Campus Lübeck, Deutschland;
paola.ferrario@imbs.uni-luebeck.de

Application of random forest for ordinal response data for prediction and variable selection

Silke Janitza¹, Gerhard Tutz², Anne-Laure Boulesteix¹

¹Institut für medizinische Informationsverarbeitung, Biometrie und Epidemiologie, Ludwig-Maximilians-Universität München, Deutschland; ²Institut für Statistik, Ludwig-Maximilians-Universität München, Deutschland; janitza@ibe.med.uni-muenchen.de

The integrated Brier score as an appropriate error measure in the variable importance of Random Survival Forests

Roman Hornung¹, Silke Janitza¹, Abdelilah El Hadad², Anne-Laure Boulesteix¹

¹Department of Medical Informatics, Biometry and Epidemiology, University of Munich, Marchioninstr. 15, 81377 Munich, Germany; ²Institute of Clinical Psychology and Psychotherapy, Dresden University of Technology, Chemnitz Str. 46, 01187 Dresden, Germany; hornung@ibe.med.uni-muenchen.de

8:50am - 10:10am Th14: Boosting

Effect of the overlap size on the selected molecular characteristics when integrating two molecular sources in a clinical risk prediction model

Stefanie Hieke^{1,2}, Martin Schumacher¹, Axel Benner³, Lars Bullinger⁴, Harald Binder^{1,5}

¹Institute of Medical Biometry and Statistics, University Medical Center Freiburg, Germany.; ²Freiburg Center for Data Analysis and Modeling, University Freiburg, Germany.; ³Division of Biostatistics, German Cancer Research Center, Heidelberg, Germany.; ⁴Department of Internal Medicine III, University Hospital of Ulm, Germany.; ⁵Institute of Medical Biostatistics, Epidemiology and Informatics, University Medical Center Johannes Gutenberg University Mainz, Germany.;
hieke@imbi.uni-freiburg.de

Stratified weighted regression for subgroup signatures from prognostic models with molecular data

Veronika Weyer, Harald Binder

Institute of Medical Biostatistics, Epidemiology and Informatics, University Medical Center Mainz, Germany; weyer@uni-mainz.de

Estimation of biomarker combinations by boosting the concordance index for survival data

Andreas Mayr¹, Matthias Schmid²

¹Institut für Medizininformatik, Biometrie und Epidemiologie, Friedrich-Alexander-Universität Erlangen-Nürnberg, Deutschland; ²Institut für Statistik, Ludwig-Maximilians-Universität München, Deutschland; andreas.mayr@fau.de

Controlling false discoveries in high dimensional situations: Boosting with stability selection

Benjamin Hofner

Institut für Medizininformatik, Biometrie und Epidemiologie; Friedrich-Alexander-Universität Erlangen-Nürnberg; Germany; benjamin.hofner@fau.de

8:50am - 10:10am Th11: Education for Statistics in Practice 1
Lecture Hall (big)

Longitudinal Data Analysis (1)

Geert Molenberghs

Universiteit Hasselt & KU Leuven, Belgien; geert.molenberghs@uhasselt.be

9:10am - 10:10am Th15: Adaptive Sample Size Reassessment

Die „Bayesian Predictive Power“ als Entscheidungskriterium in adaptiven Studiendesigns

Joachim Gerß, Andreas Faldum

Westfälische Wilhelms-Universität Münster, Deutschland; joachim.gerss@ukmuenster.de

Fallzahlenanpassungsstrategien für klinische Studien mit zeitvariierenden Zähldaten

Simon Schneider¹, Heinz Schmidli², Tim Friede¹

¹Universitätsmedizin Göttingen, Deutschland; ²Abteilung Statistical Methodology, Novartis Pharma AG, Schweiz; simon.schneider@med.uni-goettingen.de

Two-stage designs for crossover bioequivalence trials

Sven Schnaidt, Geraldine Rauch, Meinhard Kieser

Universität Heidelberg, Deutschland; schnaidt@imbi.uni-heidelberg.de

10:10am - 10:40am Coffee break

10:40am - 12:00pm Th22: Sequential Designs in Clinical Trials

Incorporating binary short-term endpoints in multi-stage phase II oncology trials

Cornelia Ursula Kunz¹, James Wason², Meinhard Kieser³

¹Warwick Medical School, University of Warwick, United Kingdom; ²Hub for Trials Methodology, MRC Biostatistics Unit Cambridge, United Kingdom; ³Institute for Medical Biometry and Informatics, University of Heidelberg, Germany; c.u.kunz@warwick.ac.uk

Extended futility boundaries in group sequential designs with two endpoints

Svenja Schüler, Meinhard Kieser, Geraldine Rauch

Universität Heidelberg, Deutschland; schueler@imbi.uni-heidelberg.de

A sequential triangular test of a correlation coefficient's null-hypothesis: $0 < \rho \leq \rho_0$

Berthold Schneider¹, Dieter Rasch², Klaus D. Kubinger³, Takuya Yanagida³

¹Institut für Biometrie, Medizinische Hochschule Hannover, Deutschland; ²Institut für Angewandte Statistik und EDV (IAS), Universität für Bodenkultur Wien, Österreich; ³Test- und Beratungsstelle des AB Psychologische Diagnostik, Fakultät für Psychologie, Universität Wien, Österreich; schneider.berthold@mh-hannover.de

Sequential meta-analyses of safety data

Daniel Saure, Katrin Jensen, Meinhard Kieser

Institut für Medizinische Biometrie und Informatik, Heidelberg, Deutschland; saure@imbi.uni-heidelberg.de

10:40am - 12:00pm **Th23: Multivariate Methods**

Making sense of multivariate data

Arne Bathke^{1,2}, Amanda Ellis², Woodrow Burchett², Solomon Harrar²

¹Universität Salzburg; ²University of Kentucky; Arne.Bathke@sbq.ac.at

Simultaneous confidence intervals for nonparametric effects in multivariate designs

Frank Konietzschke¹, Arne C. Bathke²

¹Universitätsmedizin Göttingen, Deutschland; ²University of Salzburg; fkoniet@gwdg.de

A nonparametric permutation test for high-dimensional data to detect signals of increased frequencies for adverse drug reactions in post-marketing drug safety surveillance.

Günter Heimann, Rossella Belleli, Roland Fisch, Jouni Kerman

Novartis Pharma AG, Schweiz; guenter.heimann@novartis.com

10:40am - 12:00pm **Th24: Resampling and Machine Learning**

Tests performed on bootstrap samples have increased type I error: causes and practical consequences in biometrical applications

Silke Janitza, Susanne Rospleszcz, Anne-Laure Boulesteix

Ludwig-Maximilians-Universität München, Deutschland; boulesteix@ibe.med.uni-muenchen.de

Comparison of variable selection methods in random forests for genomic data sets

Silke Szymczak¹, James D Malley², Andre Franke¹

¹Institute of Clinical Molecular Biology, Christian-Albrechts-University of Kiel, Kiel, Germany; ²Center for Information Technology, National Institutes of Health, Bethesda, MD, USA; s.szymczak@ikmb.uni-kiel.de

Pathogenicity prediction via machine learning

Carlus Deneke, Bernhard Renard

Robert Koch Institut, Deutschland; DenekeC@rki.de

Re-sampling schemes for error rate estimation as $\$U\$$ -statistics and estimation of their variance

Mathias Fuchs

Ludwig-Maximilians-Universität München, Germany; fuchs@ibe.med.uni-muenchen.de

10:40am - 12:00pm **Th25: Adaptive Designs with Several Treatments, Endpoints or Subgroups**

Adaptive designs to improve the interpretation a composite endpoints by addressing the main component or a subcomposite

Geraldine Rauch, Meinhard Kieser

Universität Heidelberg, Deutschland; rauch@imbi.uni-heidelberg.de

Adaptive three-stage phase II/III designs with endpoint and treatment selection

Cornelia Ursula Kunz¹, Tim Friede², Nicholas Parsons¹, Susan Todd³, Nigel Stallard¹

¹Warwick Medical School, United Kingdom; ²Department of Medical Statistics, University Medical Center Göttingen, Germany; ³Department of Mathematics and Statistics, University of Reading, United Kingdom; c.u.kunz@warwick.ac.uk

Adaptive and sequential methods based on the average hazard ratio

Matthias Brückner, Werner Brannath

Universität Bremen, Deutschland; mwb@math.uni-bremen.de

Performance of decision rules for selecting the target population in adaptive enrichment designs

Johannes Krisam, Meinhard Kieser

Universität Heidelberg, Deutschland; krisam@imbi.uni-heidelberg.de

10:40am - 12:00pm **Th21: Education for Statistics in Practice 2**
Lecture Hall (big)

Longitudinal Data Analysis (2)

Geert Molenberghs

Universiteit Hasselt & KU Leuven, Belgien; geert.molenberghs@uhasselt.be

12:00pm - 1:30pm **Lunch**

1:30pm - 2:50pm **Th31: Regression and Repeated Measurement Analysis in Clinical Trials**

Spline based analysis and design of dose-finding studies with active control

Hans-Joachim Helms¹, Norbert Benda², Jörg Zinserling², Thomas Kneib³, Tim Friede¹

¹Department of Medical Statistics, University Medical Center Göttingen; ²Federal Institute for Drugs and Medical Devices, Bonn; ³Faculty of Economic Sciences, Georg-August-University Göttingen; Hans-Joachim.Helms@med.uni-goettingen.de

Unimodal spline regression in various application areas

Claudia Köllmann¹, Björn Bornkamp², Katja Ickstadt¹

¹Fakultät Statistik, TU Dortmund, Deutschland; ²Novartis Pharma AG, Basel, Schweiz; koellmann@statistik.tu-dortmund.de

Global tests for high-dimensional repeated measures under weak distributional assumptions

Benjamin Becker

Universität Göttingen, Deutschland; b.becker1@stud.uni-goettingen.de

Exploring time-dependency of a gene-signature for breast cancer patients

Anika Buchholz, Willi Sauerbrei

Center for Medical Biometry and Medical Informatics, Medical Center - University of Freiburg, Germany; ab@imbi.uni-freiburg.de

1:30pm - 2:50pm **Th32: Latent Variable Models**

Generalised method of moments estimation of mediation models and structural mean models

Tom Michael Palmer

University of Warwick, United Kingdom; t.m.palmer@warwick.ac.uk

On the statistical comparison of diagnostic tests

Todor Dinev

Universität Trier, Deutschland; dinev@uni-trier.de

Statistical investigation of the immune response in non-human primate models

Annika Laser

University of Wisconsin-Milwaukee, MI (US); annika.laser@uni-ulm.de

Bayesianische Bestimmung des familiären Darmkrebsrisikos

Anna Rieger, Ulrich Mansmann

Institut für Medizinische Informatik, Biometrie und Epidemiologie (IBE), LMU München, Deutschland; riegera@ibe.med.uni-muenchen.de

1:30pm - 2:50pm **Th33: Nonparametric Statistics**

Non-parametric Bayesian prediction of the time to reach a given number of events

Gerhard Nehmiz, Birgit Gaschler-Markefski

Boehringer Ingelheim Pharma GmbH&Co. KG, 88397 Biberach, Deutschland; gerhard.nehmiz@boehringer-ingelheim.com

Nonparametric simultaneous inference for factorial repeated measures designs

Marius Placzek

Universitätsmedizin Göttingen, Deutschland; marius.placzek@stud.uni-goettingen.de

Non-parametric Multiple Contrast Tests with Covariates

Thomas Asendorf

Universitätsmedizin Göttingen, Deutschland; thomas.asendorf@med.uni-goettingen.de

Confidence bounds for the mean of success probabilities

Christoph Tasto

Universität Trier, Deutschland; tasto@uni-trier.de

1:30pm - 2:50pm

Th34: Integrative Analysis for High Dimensional Data Sets

Bayesian Models for Integrative Genomics

Marina Vannucci

Rice University, United States of America; marina@rice.edu

Integrative analysis of histone ChIP-seq and gene expression data using Bayesian mixture models

Martin Schäfer¹, Hans-Ulrich Klein², Holger Schwender¹, Martin Dugas², Katja Ickstadt³

¹Heinrich-Heine-Universität Düsseldorf, Germany; ²Westfälische Wilhelms-Universität Münster, Germany; ³Technische Universität Dortmund, Germany; martin.schaefer@udo.edu

A Bayesian method for detecting increased frequencies of safety signals in post-marketing safety surveillance

Roland Fisch, Rossella Belleli, Conny Berlin, Guenter Heimann, Jouni Kerman

Novartis Pharma AG, Schweiz; roland.fisch@novartis.com

1:30pm - 2:50pm

Th35: Lehre und Didaktik 2: "Curricula"

A blended learning module for medical biometry in an online master study programme

Benjamin Mayer¹, Christina Ring², Dietrich Rothenbacher¹, Uta Schmidt-Straßburger³, Rainer Muche¹

¹Institut für Epidemiologie und Medizinische Biometrie, Universität Ulm, Deutschland; ²Leicester, Großbritannien; ³Dekanat der Medizinischen Fakultät, Universität Ulm, Deutschland; benjamin.mayer@uni-ulm.de

Grundvorlesung Biometrie und Epidemiologie - Welche Anforderungen stellen Lehrende der Veterinärmedizin an das Curriculum?

Ramona Zeimet¹, Lothar Kreienbrock¹, Marcus G. Doherr²

¹Stiftung Tierärztliche Hochschule Hannover, Deutschland; ²Vetsuisse Fakultät, Universität Bern, Schweiz; Ramona.Zeimet@tiho-hannover.de

Wie wird man Biometriker? Berufsbegleitender Masterstudiengang Medical Biometry/Biostatistics an der Universität Heidelberg

Marietta Kirchner, Geraldine Rauch, Andreas Deckert, Meinhard Kieser

Institut für medizinische Biometrie, Universität Heidelberg, Deutschland; kirchner@imbi.uni-heidelberg.de

Kompetenzorientierte Biometrielehre für Biologen

Udo Rempe

Zoologisches Institut, Uni Kiel, Deutschland; Rempe-Udo@T-Online.DE

2:50pm - 3:20pm

Coffee break

3:20pm - 4:40pm

Th41: Closing Ceremony

Lecture Hall (big)

To be announced

Doug Altman

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