

# 70th Biometric Colloquium

Date: Wednesday, 28/Feb/2024

8:30am - 10:30am	<b>IBS-DR: Vorstandssitzung</b> Location: <b>C4-S03</b>									
9:00am - 12:00pm	<b>Tutorial: Introduction to Causal Inference and Target Trial Emulation</b> Location: <b>AM S1</b>  <u>Didelez, Vanessa;</u> <u>Braitmaier, Malte</u>		<b>Tutorial: An Introduction to Estimands and Estimand-Aligned Estimation</b> Location: <b>AM S2</b>  <u>Mütze, Tobias;</u> <u>Friede, Tim</u>		<b>Tutorial: Multiple Endpoints and Prioritized Outcomes - Nonparametric analysis methods using generalized pairwise comparisons</b> Location: <b>AM S3</b>  <u>Brunner, Edgar;</u> <u>Brannath, Werner</u>		<b>Tutorial: Advanced Data Visualization in R: (Re)producing professional plots with ggplot2 and the tidyverse</b> Location: <b>C4-S04</b>  <u>Schmidt, Paul</u>			
10:30am - 12:30pm	<b>IBS-DR: Beiratssitzung</b> Location: <b>C4-S03</b>									
12:00pm - 1:00pm	<b>Lunchbreak</b>	<b>AG Statistische Methoden in der Epidemiologie</b> Location: <b>AM 1 Empore</b>	<b>AG Statistische Methoden in der Medizin</b> Location: <b>AM 1 Empore</b>	<b>AG Ethik und Verantwortung</b> Location: <b>AM 2</b>	<b>AG Non-Clinical Statistics</b> Location: <b>AM S1</b>	<b>AG Pharmazeutische Forschung</b> Location: <b>AM S2</b>	<b>AG DAGStat</b> Location: <b>AM S3</b>	<b>AG Nachwuchs</b> Location: <b>C4-S01</b>	<b>AG Bayes-Methodik</b> Location: <b>C4-S02</b>	<b>AG Statistik Stochastischer Prozesse</b> Location: <b>C4-S04</b>
1:00pm - 2:20pm	<b>Opening Session &amp; Keynote Michael Love</b> Location: <b>AM 1</b> Chair: <b>Silke Szymczak</b> Chair: <b>Inke Regina Koenig</b>  <b>Pragmatic Biometrics for Transcriptomics: Rigor, Reproducibility, and Readability</b>									
2:20pm - 2:40pm	<b>Break</b>									
2:40pm - 4:00pm	<b>Invited: Synthetic Data with Privacy Guarantees: from Applied Statistics to Generative Machine Learning</b> Location: <b>AM 1</b> Chair: <b>Andreas Ziegler</b> Chair: <b>Harald Binder</b>  <b>2:40pm - 3:20pm</b> <b>Generative machine learning in biostatistics</b> <u>Wright, Marvin N.</u>  <b>3:20pm - 3:40pm</b> <b>A simple-to-use R package for mimicking study data by simulations</b> <u>Koliopanos, Georgios;</u> <u>Ojeda, Francisco;</u> <u>Ziegler, Andreas</u>  <b>3:40pm - 4:00pm</b> <b>A representation of longitudinal data for enabling synthetic data</b>	<b>Estimands</b> Location: <b>AM 2</b> Chair: <b>Ina Rondak</b> Chair: <b>Vanessa Didelez</b>  <b>2:40pm - 3:00pm</b> <b>Treatment effect measures in clinical trials with time-to-event outcomes: it is time to apply estimand thinking</b>  <b>3:00pm - 3:20pm</b> <b>Causal Inference with Continuous Interventions</b>  <b>3:20pm - 3:40pm</b> <b>The estimand framework for diagnostic accuracy studies</b>  <b>3:40pm - 4:00pm</b> <b>Estimande in early phase studies, with an</b>	<b>Complex Models</b> Location: <b>AM S1</b> Chair: <b>Frank Konietzschke</b> Chair: <b>Dennis Dobler</b>  <b>2:40pm - 3:00pm</b> <b>Multiple contrast tests for possible overdispersed count data: small sample approximations</b>  <b>3:00pm - 3:20pm</b> <b>Personalized patient-specific mechanistic mathematical models of acute myeloid leukaemia disease dynamics</b>  <b>3:20pm - 3:40pm</b> <b>Flexible Modeling of Biomarker Ratios with Correlated Components</b>  <b>3:40pm - 4:00pm</b> <b>Comparative analysis of proportional odds</b>	<b>Preclinical Drug Development and Toxicology 1</b> Location: <b>AM S2</b> Chair: <b>Jörg Rahnenführer</b> Chair: <b>Frank Schaarschmidt</b>  <b>2:40pm - 3:00pm</b> <b>Interaction effects of UVA with UVB irradiation at the gene expression level in human skin cells</b>  <b>3:00pm - 3:20pm</b> <b>Design of optimal concentrations for in vitro cytotoxicity experiments</b>  <b>3:20pm - 3:40pm</b> <b>Probabilistic Approaches for Modeling Patient-Specific Effects of</b>	<b>Statistics in Epidemiology</b> Location: <b>AM S3</b> Chair: <b>Irene Schmidtman</b> Chair: <b>André Scherag</b>  <b>2:40pm - 3:00pm</b> <b>Post-selection inference in case-control sampling designs: Results from the TORONTO Monte Carlo simulation study</b>  <b>3:00pm - 3:20pm</b> <b>Maximum likelihood estimation for aggregated current status data: Simulation study using the illness-death model for chronic diseases with duration dependency</b>  <b>3:20pm - 3:40pm</b> <b>Recent methodological</b>					

	<p><b>generation via transformers</b>  <u>Farhadyar, Kiana; Königs, Lukas; Binder, Harald</u></p>	<p><b>example in atopic dermatitis</b></p>	<p><b>models in a simulation study. A robust alternative to linear regression?</b></p>	<p><b>Antihypertensive Medication</b></p>	<p><b>trends in Epidemiology: No need for data-driven variable selection?</b></p>
					<p><b>3:40pm - 4:00pm</b>  <b>The evaluation of clinical prediction models – methodological pitfalls illustrated with an application to peripartum depression</b></p>
<b>4:00pm - 4:20pm</b>	<b>Break</b>				
<b>4:20pm - 5:40pm</b>	<p><b>Invited: Copula Regression for Time-to-Event Data</b>  Location: <b>AM 1</b>  Chair: <b>Nadja Klein</b>  Chair: <b>Andreas Mayr</b></p> <p><b>4:20pm - 5:00pm</b>  <b>Copula based Cox proportional hazards models for dependent censoring</b>  <u>Van Keilegom, Ingrid; Deresa, Negera Wakgari</u></p> <p><b>5:00pm - 5:20pm</b>  <b>Boosting distributional copula regression models for bivariate time-to-event data</b>  <u>Briseno Sanchez, Guillermo; Klein, Nadja; Mayr, Andreas; Groll, Andreas</u></p> <p><b>5:20pm - 5:40pm</b>  <b>A model-based boosting approach to deal with dependent censoring</b>  <u>Strömer, Annika; Klein, Nadja; Mayr, Andreas</u></p>	<p><b>Young Statisticians</b>  Location: <b>AM 2</b>  Chair: <b>Stefanie Peschel</b>  Chair: <b>Moritz Fabian Danzer</b></p> <p><b>4:20pm - 4:40pm</b>  <b>Sample size calculation and recalculation for non-inferiority trials in the ‘gold standard’ design using the studentized permutation test</b></p> <p><b>4:40pm - 5:00pm</b>  <b>A statistical deconvolution method with an application to secretomic and proteomic data</b></p> <p><b>5:00pm - 5:20pm</b>  <b>Evaluation of Time-To-Event-Endpoints in Oncology Biosimilar Trials – A Simulation Study</b></p> <p><b>5:20pm - 5:40pm</b>  <b>Real world vs. controlled diagnosis: The example of response in oncology</b></p>	<p><b>Missing Data</b>  Location: <b>AM S1</b>  Chair: <b>Maren Vens</b>  Chair: <b>Louis Rodrigue Macias</b></p> <p><b>4:20pm - 4:40pm</b>  <b>Recoverability of Causal Effects in a Longitudinal Study under Presence of Missing Data</b></p> <p><b>4:40pm - 5:00pm</b>  <b>Comparing propensity score methods combined with multiple imputation for controlling confounding: a case study on mantle cell lymphoma treatment regimens</b></p> <p><b>5:00pm - 5:20pm</b>  <b>Various approaches to deal with missing data when estimating causal effects with targeted maximum likelihood estimation</b></p> <p><b>5:20pm - 5:40pm</b>  <b>Adaptive predictor-set linear model: an imputation-free method for linear regression prediction on datasets with missing values</b></p>	<p><b>Preclinical Drug Development and Toxicology 2</b>  Location: <b>AM S2</b>  Chair: <b>Richardus Vonk</b>  Chair: <b>Katja Ickstadt</b></p> <p><b>4:20pm - 4:40pm</b>  <b>Shift from Frequentist to Bayesian Dose-Response modelling</b></p> <p><b>4:40pm - 5:00pm</b>  <b>Testing for similarity of multivariate mixed outcomes with application to efficacy-toxicity responses</b></p> <p><b>5:00pm - 5:20pm</b>  <b>Prediction intervals for counted observations and their application in toxicological and medical quality control charts</b></p> <p><b>5:20pm - 5:40pm</b>  <b>Methods of model selection for models with common parameters</b></p>	<p><b>Clinical Epidemiology</b>  Location: <b>AM S3</b>  Chair: <b>Stefan Wagenpfeil</b>  Chair: <b>Arne Bathke</b></p> <p><b>4:20pm - 4:40pm</b>  <b>First effects of HPV vaccination on cervical cancer incidence in Germany - an age-period-cohort analysis based on population-based cancer registry data</b></p> <p><b>4:40pm - 5:00pm</b>  <b>The Skellam Distribution revisited - Estimating the unobserved incoming and outgoing ICU COVID-19 patients on a regional level in Germany</b></p> <p><b>5:00pm - 5:20pm</b>  <b>When will I be cured from cancer? – An application of cure models to cancer registry data from Schleswig-Holstein charts</b></p>
<b>5:40pm - 6:30pm</b>	<b>Break</b>				

**6:30pm - 8:30pm** **Social Event: Town Hall Reception**

Adress: Breite Straße 62, 23552 Lübeck

**9:30pm - 11:00pm** **Social Event: Night Watchman Tour**

Remaining tickets are only available at the conference registration desk in Lübeck.

Meeting point: Holstentor, Holstentorplatz, 23552 Lübeck

Meeting time: Please arrive latest at 21:25.

**Date: Thursday, 29/Feb/2024**

<p><b>9:00am - 10:20am</b></p> <p><b>Invited: Developing guidance for statistical analysis in observational research - a STRATOS Initiative update</b> Location: <b>AM 1</b> Chair: <b>Matthias Schmid</b> Chair: <b>Carsten Oliver Schmidt</b></p> <p><b>9:00am - 9:20am</b></p> <p><b>Evaluating biostatistical methods before use - each phase is important</b> <b>Heinze, Georg;</b> <b>Boulesteix, Anne-Laure;</b> <b>Kammer, Michael;</b> <b>Morris, Tim P.;</b> <b>White, Ian R.</b></p> <p><b>9:20am - 9:40am</b></p> <p><b>Initial Data Analysis, Data Quality Assessments and proper Information Management to Improve the Transparency of Statistical Analyses</b> <b>Schmidt, Carsten Oliver;</b> <b>Lusa, Lara;</b> <b>Huebner, Marianne</b></p> <p><b>9:40am - 10:00am</b></p> <p><b>Recent developments in measurement error modelling</b> <b>Küchenhoff, Helmut</b></p> <p><b>10:00am - 10:20am</b></p> <p><b>The STRATOS Open Science panel</b> <b>Hoffmann, Sabine;</b> <b>Boulesteix, Anne-Laure;</b> <b>Dunkler, Daniela;</b> <b>Hornung, Roman;</b> <b>Kammer, Michael;</b> <b>Luijken, Kim</b></p>	<p><b>Panel Discussion (AG-Nachwuchs)</b> Location: <b>AM 2</b> Chair: <b>Ina Dormuth</b> Chair: <b>Julia Christin Duda</b> Navigating the Academic Odyssey: Early Career Challenges</p>	<p><b>Meta-Analysis 1</b> Location: <b>AM S1</b> Chair: <b>Tim Friede</b> Chair: <b>Gerta Rücker</b></p> <p><b>9:00am - 9:20am</b></p> <p><b>Overall and landmark survival estimates by stage for patients with non-small cell lung cancer treated with either surgery alone or surgery plus adjuvant systemic anticancer treatment – an analysis based on German cancer registry data</b></p> <p><b>9:20am - 9:40am</b></p> <p><b>A discrete time-to-event model for the meta-analysis of full ROC curves</b></p> <p><b>9:40am - 10:00am</b></p> <p><b>Identifying the risk of sample overlap in meta-analysis of registry-based studies</b></p> <p><b>10:00am - 10:20am</b></p> <p><b>Addressing Challenges in Subgroup-Specific Treatment Effects and Aggregation Bias in Meta-Analysis</b></p>	<p><b>Clinical Trials</b> Location: <b>AM S2</b> Chair: <b>Thomas Asendorf</b> Chair: <b>Cornelia Ursula Kunz</b></p> <p><b>9:00am - 9:20am</b></p> <p><b>“Randomize the first patient” - old, but still most important concept</b></p> <p><b>9:20am - 9:40am</b></p> <p><b>A holistic approach to improve chronic kidney disease trials - unlocking the potential of hierarchical composite endpoints</b></p> <p><b>9:40am - 10:00am</b></p> <p><b>Sample size calculation for cluster randomized trial with heterogeneous cluster size within cluster variances</b></p> <p><b>10:00am - 10:20am</b></p> <p><b>Optimal standardization as an alternative to matching using propensity scores</b></p>	<p><b>High Dimensional Molecular Data</b> Location: <b>AM S3</b> Chair: <b>Stefan Böhringer</b> Chair: <b>Michael Love</b></p> <p><b>9:00am - 9:20am</b></p> <p><b>Robust statistical detection of interaction effects in high-throughput sequencing data</b></p> <p><b>9:20am - 9:40am</b></p> <p><b>Using gene-set tests on expression data of mRNA targets to predict miRNAs involved during West Nile virus infections</b></p> <p><b>9:40am - 10:00am</b></p> <p><b>Development of metabolomic risk scores for Alzheimer's Disease</b></p> <p><b>10:00am - 10:20am</b></p> <p><b>Evaluating deep learning models for cell detection and multi-class cell classification: a comparative analysis of metrics and solutions</b></p>
<p><b>10:20am - 10:40am</b></p>	<p><b>Break</b></p>			
<p><b>10:40am - 11:40am</b></p>	<p><b>Keynote Ina Rondak</b> Location: <b>AM 1</b> Chair: <b>Anne-Laure Boulesteix</b> Chair: <b>Anika Großhennig</b></p> <p><b>Wider access to more informative data and the key role of methodological experts in this endeavour</b></p>			

11:40am  
-  
12:40pm

**Poster**

Location: **AM 1**

Chair: **Björn-Hergen Laabs**

11:40-12:05 h Speed Session

**Comparison of genetic maps from different cattle breeds (Poster ID 01)**

**Wittenburg, Dörte**; Ding, Xi; Melzer, Nina; Schwarzenbacher, Hermann; Seefried, Franz R.

**Bayesian borrowing using mixture prior: frequentist operating characteristics (Poster ID 02)**

**Weru, Vivienne**; Calderazzo, Silvia; Wiesenfarth, Manuel; Kopp-Schneider, Annette

**A multi-omics differentiation pattern analysis of CCl4-treated mice data (Poster ID 03)**

**Heiner, Jonas**; Hengstler, Jan; Groll, Andreas

**Combining recurrent and terminal events into a composite endpoint may be problematic (Poster ID 04)**

**Liu, Xiaofei**; Koch, Armin

**Quantification of prior impact in terms of effective sample size targeting test decisions (Poster ID 05)**

**Wiesenfarth, Manuel**; Kopp-Schneider, Annette; Calderazzo, Silvia

**BACE2 polymorphisms are associated with memory impairment in a general population cohort SHIP-TREND (Poster ID 06)**

**Bonk, Sarah**; Kirchner, Kevin; Garvert, Linda; Völzke, Henry; Grabe, Hans Jörgen; Van der Auwera, Sandra

**Paradoxes of Inter-Rater Reliability Measures of skewed ordinal Data (Poster ID 07)**

**Mönch, Maximilian**; Grittner, Ulrike; Unger, Nina; Keller, Theresa; Breitenstein, Caterina; Schulze, Daniel; Pigorsch, Mareen

**Performance of different Interpolation Methods on self-reported symptoms in the context of Digital Allergology (Poster ID 08)**

**Hernandez-Toro, Camilo Jose**; Grittner, Ulrike; Caminiti, Lucia; Charpin, Denis; Delgado, Luís; Dramburg, Stephanie; Kalpaklioglu, Fusun; Nieto, Antonio; Papadopoulos, Nikolaos G.; Pelosi, Simone; Potapova, Ekaterina; Priftanji, Alfred; Travaglini, Alessandro; Tripodi, Salvatore; Matricardi, Paolo Maria

**A MAP prior approach for piecewise constant hazards and competing risks (Poster ID 09)**

**Stemke, Alexander**; Sailer, Oliver

**Using early or baseline data in a trial with missingness in a continuous primary endpoint (Poster ID 10)**

**Basu, Joydeep**; Stallard, Nigel

**Simultaneous inference of multiple binary endpoints in biomedical research: small sample properties of multiple marginal models and a resampling approach (Poster ID 11)**

**Budig, Sören**; Schaarschmidt, Frank

**Kirstine.jl: A Julia Package for Bayesian Optimal Design of Experiments (Poster ID 12)**

**Sandig, Ludger**

**{cases} - an R package for simultaneous evaluation of multiple diagnostic tests or prediction models regarding co-primary endpoints sensitivity and specificity (Poster ID 13)**

**Westphal, Max**; Zapf, Antonia

**{mldesign} - an R package to conduct meaningful data splitting in applied machine learning (Poster ID 14)**

**Westphal, Max**

**Multivariate modelling of water quality parameters in nigeria (Poster ID 15)**

**Dosumu, Ebun Adegbola**

**A unified parametric approach to the estimation of dependence and marginal distributions in bivariate competing risks survival data (Poster ID 16)**

**Zhang, Hyun-Soo; Jung, Inkyung; Nam, Chung Mo**

**Sample size re-examination for clinical trials with survival endpoints (Poster ID 17)**

**Dormuth, Ina; Liu, Tiantian; Chen, Zijian; Ditzhaus, Marc; Pauly, Markus; Xu, Jin**

**Improvement in population-based survival in cutaneous malignant melanoma after the introduction of new therapies (Poster ID 18)**

**Eisemann, Nora; Schumann, Laura; Baltus, Hannah; Labohm, Louisa; Kraywinkel, Klaus; Katalinic, Alexander**

**"Initiative Biokybernetik" - ten years later (Poster ID 19)**

**Mau, Jochen**

**Structured evaluation of drug prescription data from Schleswig-Holstein in a networked big data context (Poster ID 20)**

**Schuster, Reinhard; Emcke, Timo; Burmester, Mareike**

**High Degree of Agreement but Low Measures - Problems of Inter-Rater Reliability Measures for Unbalanced Ordinal Data (Poster ID 21)**

**Grittner, Ulrike; Schulze, Daniel; Unger, Nina; Keller, Theresa; Breitenstein, Caterina; Pigorsch, Mareen; Mönch, Maximilian**

**Time-dependent change in risk through an exposure and possible estimands of interest: A simulation study using two clinically motivated examples (Poster ID 23)**

**Meiszl, Katharina; Tokic, Marianne C.; Timmesfeld, Nina**

12:00pm

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12:40pm

12:40pm

-

1:20pm

1:20pm

-

2:40pm

**AG Öffentlichkeitsarbeit**

Location: **AM S2**

**Lunchbreak**

**AG Leitersitzung**

Location: **AM S1**

**Invited: Risk Prediction meets Causal Inference**

Location: **AM 1**  
Chair: **Vanessa Didelez**  
Chair: **Michael Schomaker**

**1:20pm - 2:00pm**

**Causal blind spots in risk-based medical decision making**

**Invited: Innovative Clinical Trial Designs: Estimands and Operating Characteristics**

Location: **AM 2**  
Chair: **Silvia Calderazzo**  
Chair: **Christian Röver**

**1:20pm - 2:00pm**

**Estimands and Complex Innovative Designs**

**Machine Learning 1**

Location: **AM S1**  
Chair: **Marvin N. Wright**  
Chair: **Inke Regina Koenig**

**1:20pm - 1:40pm**

**Achieving explainable machine learning by functional decomposition of black-box models**

**Meta-Analysis 2**

Location: **AM S2**  
Chair: **Tim Mathes**  
Chair: **Johannes Rauh**

**1:20pm - 1:40pm**

**Trials and triangles - The geometric interpretation of multi-arm studies in network meta-analysis**

**Application with Molecular Data**

Location: **AM S3**  
Chair: **Klaus Jung**  
Chair: **Silke Szymczak**

**1:20pm - 1:40pm**

**Companion diagnostics in oncology clinical trials: lessons from the practice**

	<p><u>van Geloven, Nan</u></p> <p><b>2:00pm - 2:20pm</b></p> <p>Methods for obtaining causal predictions and quantifying associated uncertainty</p> <p><u>DiazOrdaz, Karla</u></p> <p><b>2:20pm - 2:40pm</b></p> <p>Causal effect estimation and risk prediction - the example of screening colonoscopy and colorectal cancer</p> <p><u>Braitmaier, Malte;</u> <u>Didelez, Vanessa</u></p>	<p><u>Bretz, Frank</u></p> <p><b>2:00pm - 2:20pm</b></p> <p>Multiplicity Issues in Platform Trials – adjusting for what? Looking forward and benefiting from the past</p> <p><u>Koenig, Franz;</u> <u>Posch, Martin;</u> <u>Zehetmayer, Sonja</u></p> <p><b>2:20pm - 2:40pm</b></p> <p>Modeling strategies for analysing platform trials with non-concurrent controls</p> <p><u>Bofill Roig, Marta</u></p>	<p>into explainable predictor effects</p> <p><b>1:40pm - 2:00pm</b></p> <p>Red-light crossing or bank robbery? On the bias in model performance estimates resulting from incorrect optimization of algorithm and preprocessing hyperparameters</p> <p><b>2:00pm - 2:20pm</b></p> <p>Using background knowledge from previous studies in model building: the good, the bad and the ugly</p> <p><b>2:20pm - 2:40pm</b></p> <p>Random forests more data hungry than logistic regression models? A confirmatory, large-scale, real-data study on the link between the number of events per variable and prediction performance</p>	<p><b>1:40pm - 2:00pm</b></p> <p>A comparison of different software tools to support systematic reviews - considering the size of the training dataset and the machine learning methods used.</p> <p><b>2:00pm - 2:20pm</b></p> <p>Path-Based Approach for Detecting and Assessing Inconsistency in Network Meta-Analysis: A Novel Method</p> <p><b>2:20pm - 2:40pm</b></p> <p>A re-analysis of about 60.000 sparse data meta-analyses suggests that using an adequate method for pooling matters.</p>	<p><b>1:40pm - 2:00pm</b></p> <p>Genome-wide association studies on hedonic eating behaviour</p> <p><b>2:00pm - 2:20pm</b></p> <p>Partial interaction analysis in case-only defined clusters for high-dimensional biomarkers</p> <p><b>2:20pm - 2:40pm</b></p> <p>Is the early microbiome linked to childhood obesity? – A network perspective</p>
<b>2:40pm - 3:00pm</b>	Break				
<b>3:00pm - 4:20pm</b>	<p><b>IBS-DR: Nachwuchspreise</b></p> <p>Location: <b>AM 1</b></p> <p>Chair: Annette Kopp-Schneider</p> <p>Chair: Anne-Laure Boulesteix</p> <p><b>Infusing structural assumptions into dimension reduction for single-cell RNA sequencing data to identify small gene sets</b></p> <p><u>Brunn, Niklas</u></p> <p><b>Evaluation of Index-based Response-adaptive Randomization</b></p>	<p>Invited: Stochastic Processes in Time-to-Event Analysis and Biostatistics</p> <p>Location: <b>AM 2</b></p> <p>Chair: Dennis Dobler</p> <p>Chair: Jan Feifel</p> <p><b>3:00pm - 3:40pm</b></p> <p>Counting processes in stochastic epidemic models: the link with survival analysis</p> <p><u>Putter, Hein;</u> <u>Goeman, Jelle;</u> <u>Wallinga, Jacco</u></p> <p><b>3:40pm - 4:00pm</b></p> <p>Identifying alert concentrations</p>	<p><b>Machine Learning 2</b></p> <p>Location: <b>AM S1</b></p> <p>Chair: Jörg Rahnenführer</p> <p>Chair: Björn-Hergen Laabs</p> <p><b>3:00pm - 3:20pm</b></p> <p>Adversarial random forests for imputing missing values</p> <p><b>3:20pm - 3:40pm</b></p> <p>Confidence intervals for tree-structured varying coefficients based on parametric bootstrap</p>	<p><b>Special: IQWiG/IQTIG: Statistical analyses based on aggregated data</b></p> <p>Location: <b>AM S2</b></p> <p>Chair: Tim Friede</p> <p>Chair: Ralf Bender</p> <p>Chair: Jona Cederbaum</p> <p><b>3:00pm - 3:20pm</b></p> <p>Performing subgroup analyses in HTA applications</p> <p><u>Grouven, Ulrich;</u> <u>Skipka, Guido</u></p> <p><b>3:20pm - 3:40pm</b></p> <p>Using meta-regression for investigating</p>	<p><b>Genetic Epidemiology</b></p> <p>Location: <b>AM S3</b></p> <p>Chair: Silke Szymczak</p> <p>Chair: Amke Caliebe</p> <p><b>3:00pm - 3:20pm</b></p> <p>Clinical utility of polygenic scores: A critical 2023 appraisal</p> <p><b>3:20pm - 3:40pm</b></p> <p>Tools for predicting the effects of genetic variants: a systematic review and practical guide</p>

	<p><b>Procedures in Clinical Trials</b>  <u>Drescher, Sonja;</u>  <u>Kunz, Cornelia</u>  <u>Ursula; Walther, Andrea</u></p>	<p><b>using a model-based bootstrap approach</b>  <u>Möllenhoff, Kathrin;</u>  <u>Schorning, Kirsten;</u>  <u>Kappenberg, Franziska</u></p>	<p>3:40pm - 4:00pm  <b>On the handling of method failure in comparison studies</b></p>	<p><b>subgroups in a meta-analysis</b>  <u>Röver, Christian;</u>  <u>Kramer, Malte;</u>  <u>Friede, Tim</u></p>	<p>3:40pm - 4:00pm  <b>Detecting interactions in High Dimensional Data using Cross Leverage Scores</b></p>
	<p><b>Functional Additive Models on Manifolds of Planar Shapes and Forms</b>  <u>Stöcker, Almond</u></p>	<p>4:00pm - 4:20pm  <b>Resampling-based inference for the average treatment effect in time-to-event data</b>  <u>Rühl, Jasmin;</u>  <u>Friedrich, Sarah</u></p>	<p>4:00pm - 4:20pm  <b>An empirical study of the performance of semi-supervised machine learning methods in systematic review tools for abstract and title screening</b></p>	<p>3:40pm - 4:00pm  <b>Statistical analysis of aggregate results of health care providers</b>  <u>Rauh, Johannes</u></p>	<p>4:00pm - 4:20pm  <b>Estimating sparse graphical models in high dimensions</b></p>
	<p><b>A connection between survival multistate models and causal inference for external treatment interruptions</b>  <u>Erdmann, Alexandra;</u>  <u>Loos, Anja;</u>  <u>Beyersmann, Jan</u></p>			<p>4:00pm - 4:20pm  <b>Volume-outcome analyses based on aggregated data</b>  <u>Gutzeit, Maurilio;</u>  <u>Rauh, Johannes;</u>  <u>Cederbaum, Jona</u></p>	
4:20pm - 4:30pm	Break				
4:30pm - 6:00pm	<b>IBS-DR: Mitgliederversammlung</b> Location: <b>AM 1</b>				
6:00pm - 7:00pm	Break				
7:00pm - 10:00pm	<b>Social Event: Conference Dinner</b> Adress: Breite Straße 2, 23552 Lübeck				



**Date: Friday, 01/Mar/2024**

<p><b>9:00am - 10:20am</b></p> <p><b>Invited: Biometric Research Outside High-Income Settings</b> Location: <b>AM 1</b> Chair: <b>Michael Schomaker</b> Chair: <b>Martje Rave</b></p> <p><b>9:00am - 9:40am</b> <b>Assessment of the treat-all public health approach in Eswatini – challenges and opportunities</b> <b>Kerschberger, Bernhard;</b> <b>Ciglenecki, Iza</b></p> <p><b>9:40am - 10:00am</b> <b>The South African HIV Cancer Match (SAM) Study: a unique resource for cancer research among people with HIV in South Africa</b> <b>Rohner, Eliane;</b> <b>Olago, Victor;</b> <b>Ruffieux, Yann;</b> <b>Metekoua, Carole;</b> <b>Tombe-Nyahuma, Tinashe;</b> <b>Mwansa-Kambafwile, Judith;</b> <b>Egger, Matthias;</b> <b>Muchengeti, Mazvita</b></p> <p><b>10:00am - 10:20am</b> <b>Interplay between Applied Biostatistics and Public Health in Humanitarian Settings</b> <b>Luque Fernandez, Miguel Angel</b></p>	<p><b>Statistics in Practice 1</b> Location: <b>AM 2</b> Diagnostic Accuracy Studies: Basic and Advanced Statistical Methods</p>	<p><b>Time-to-Event 1</b> Location: <b>AM S1</b> Chair: <b>Annika Hoyer</b> Chair: <b>Sarah Friedrich</b></p> <p><b>9:00am - 9:20am</b> <b>On historically controlled survival trials</b></p> <p><b>9:20am - 9:40am</b> <b>Conditional survival of younger patients with mantle cell lymphoma: novel insights into disease course and dynamic prediction by baseline and time-dependent prognostic factors</b></p> <p><b>9:40am - 10:00am</b> <b>The challenge of time-to-event analysis for multiple events: Which method of analysis can we trust?</b></p> <p><b>10:00am - 10:20am</b> <b>Unleashing the power of adjusted survival curves: Introducing the adjustedCurves R-package</b></p>	<p><b>Agricultural and Biological Statistics 1</b> Location: <b>AM S2</b> Chair: <b>Klaus Jung</b> Chair: <b>Dörte Wittenburg</b></p> <p><b>9:00am - 9:20am</b> <b>A random-regression model for analyzing the genetic variance of litter weight in mice</b></p> <p><b>9:20am - 9:40am</b> <b>Optimising sampling efforts in hierarchical Lincoln-Petersen experiment: Towards precise population size estimation</b></p> <p><b>9:40am - 10:00am</b> <b>Optimizing Genetic Gain and Haplotype Diversity in Genomic Selection through Mendelian Sampling-Based Similarity Matrices</b></p> <p><b>10:00am - 10:20am</b> <b>Challenges in statistical consulting for Animal Science</b></p>	<p><b>Multiple Testing</b> Location: <b>AM S3</b> Chair: <b>Werner Brannath</b> Chair: <b>Edgar Brunner</b></p> <p><b>9:00am - 9:20am</b> <b>Surviving the multiple testing problem: RMST-based tests in general factorial designs</b></p> <p><b>9:20am - 9:40am</b> <b>Informative simultaneous confidence intervals for graphical test procedures</b></p> <p><b>9:40am - 10:00am</b> <b>Multiple contrast testing procedures for semiparametric MANCOVA</b></p> <p><b>10:00am - 10:20am</b> <b>Asymptotic online familywise error rate control for dependent test statistics</b></p>	<p><b>School 1 (only for pupils)</b> Location: <b>AM S4</b> Workshop: Künstliche Intelligenz – Spielerisch lernen</p>
<p><b>10:20am - 10:40am</b></p> <p><b>Break</b></p>					
<p><b>10:40am - 12:00pm</b></p> <p><b>Invited: Statistical Issues in Animal Testing</b> Location: <b>AM 1</b> Chair: <b>Bernd-Wolfgang</b></p>	<p><b>Statistics in Practice 2</b> Location: <b>AM 2</b> Diagnostic Accuracy Studies: Basic and</p>	<p><b>Time-to-Event 2</b> Location: <b>AM S1</b> Chair: <b>Irene Schmidtman</b></p>	<p><b>Agricultural and Biological Statistics 2</b> Location: <b>AM S2</b> Chair: <b>Hans-Peter</b></p>	<p><b>Simulation Studies</b> Location: <b>AM S3</b> Chair: <b>Maarten van Smeden</b></p>	<p><b>School 2 (only for pupils)</b> Location: <b>AM S4</b> Workshop: Künstliche</p>

	<p>Igl Chair: <b>Michael Lauseker</b></p> <p><b>10:40am - 11:20am</b></p> <p><b>Statistical Review of Animal trials in Ethics Committees</b> <b>Piper, Sophie K.; Konietschke, Frank; Zocholl, Dario; Röhle, Robert; Tölch, Ulf</b></p> <p><b>11:20am - 11:40am</b></p> <p><b>Sample size justification in preclinical animal studies</b> <b>Wilcke, Juliane C.; Boulesteix, Anne-Laure</b></p> <p><b>11:40am - 12:00pm</b></p> <p><b>3R initiatives in preclinical toxicology and research</b> <b>Lang, Tina; Vaas, Lea</b></p>	<p>Advanced Statistical Methods</p> <p>Chair: <b>Andreas Faldum</b></p> <p><b>10:40am - 11:00am</b></p> <p><b>Adaptive redesigning of combination testing procedures in survival analysis</b></p> <p><b>11:00am - 11:20am</b></p> <p><b>A new parametric accelerated failure time model for semi-competing risk data</b></p> <p><b>11:20am - 11:40am</b></p> <p><b>Dynamic prediction of the risk of preeclampsia – Landmarking with continuous time-dependent covariates in left-truncated competing risks data</b></p>	<p>Piepho Chair: <b>Sabine K. Schnabel</b></p> <p><b>10:40am - 11:00am</b></p> <p><b>Promises and limitations of applying structural equation modelling techniques from psychology in other disciplines exemplified in geocology</b></p> <p><b>11:00am - 11:20am</b></p> <p><b>Analysis of greenhouse gas emission and the effect on rainfall outcomes in nigeria</b></p> <p><b>11:20am - 11:40am</b></p> <p><b>Antibiotic resistance in pigs - analysis of the VetAmUR data to investigate the influence of antibiotic use on the temporal development of resistance in pig farming</b></p>	<p>Chair: <b>Anne-Laure Boulesteix</b></p> <p><b>10:40am - 11:00am</b></p> <p><b>Statistical Plasmode Simulations - Potentials, Challenges and Recommendations</b></p> <p><b>11:00am - 11:20am</b></p> <p><b>When is Plasmode simulation superior to parametric simulation?</b></p> <p><b>11:20am - 11:40am</b></p> <p><b>On the role of benchmarking data sets and simulations in method comparison studies</b></p> <p><b>11:40am - 12:00pm</b></p> <p><b>Translating methodological simulation studies into practice: a reproducible application</b></p>	<p>Intelligenz – Spielerisch lernen</p>	
<b>12:00pm - 12:30pm</b>	<p><b>Group photo</b> A group photo will be taken in front of the Audimax building.</p>					
<b>12:00pm - 1:00pm</b>	<p><b>Lunchbreak</b></p>					
<b>1:00pm - 2:20pm</b>	<p><b>Geburtstagsfeier (only German)</b> Location: <b>AM 1</b> Chair: <b>Annette Kopp-Schneider</b> Chair: <b>Anne-Laure Boulesteix</b></p> <p><b>Die wilden Achtziger und die</b></p>	<p><b>Diagnostic Studies</b> Location: <b>AM 2</b> Chair: <b>Annika Hoyer</b> Chair: <b>Maria Stark</b></p> <p><b>1:00pm - 1:20pm</b></p> <p><b>Unblinded sample size re-estimation in diagnostic test accuracy studies</b></p>	<p><b>Time-to-Event: Estimation</b> Location: <b>AM S1</b> Chair: <b>Kathrin Möllenhoff</b> Chair: <b>Alexandra Erdmann</b></p> <p><b>1:00pm - 1:20pm</b></p> <p><b>Implication of the choice of time scales in</b></p>	<p><b>Time Series and Longitudinal Data</b> Location: <b>AM S2</b> Chair: <b>Michael Lauseker</b> Chair: <b>Almond Stöcker</b></p> <p><b>1:00pm - 1:20pm</b></p> <p><b>On detecting change points in unlabelled</b></p>	<p><b>Nonparametric Methods</b> Location: <b>AM S3</b> Chair: <b>Frank Konietschke</b> Chair: <b>Ekkehard Glimm</b></p> <p><b>1:00pm - 1:20pm</b></p> <p><b>Inference for Random Effects in Nonparametric Repeated Measures Designs</b></p>	

	<p>goldenen Neunziger  <u>Rücker, Gerta;</u>  <u>Pigeot, Iris;</u>  <u>Kreienbrock, Lothar</u></p> <p>AG Nachwuchs: Rückblicke, Einblicke, Ausblicke  <u>AG Nachwuchs, Verschiedene Mitglieder</u></p>	<p>1:20pm - 1:40pm</p> <p>Comparing methods to handle missing values in the index test in diagnostic studies - a simulation study</p> <p>1:40pm - 2:00pm</p> <p>Covariate adjustment, factorial designs and clustered data in diagnostic accuracy studies</p> <p>2:00pm - 2:20pm</p> <p>Power and sample size estimation for comparing diagnostic methods with imperfect reference standards</p>	<p>survival analysis</p> <p>1:20pm - 1:40pm</p> <p>Hazards: key quantities for analysis, interpretation and understanding of time-to-event data</p> <p>1:40pm - 2:00pm</p> <p>Piecewise constant hazard estimation with the fused lasso</p> <p>2:00pm - 2:20pm</p> <p>Estimation Within The Responder Stratified Exponential Survival Model</p>	<p>multivariate time series</p> <p>1:20pm - 1:40pm</p> <p>Deep mixture of linear mixed models for complex longitudinal data</p> <p>1:40pm - 2:00pm</p> <p>Type-I-error rate inflation in mixed models for repeated measures caused by ambiguous or incomplete model specifications</p> <p>2:00pm - 2:20pm</p> <p>Function-on-Scalar Regression (FoSR) with Wavelet Basis Functions for the analysis of Periodic Time-Series</p>	<p>with Missing Data via Randomization</p> <p>1:20pm - 1:40pm</p> <p>NANCOVA: Nonparametric Analysis of Covariance for Rare Disease Research  <u>I</u></p> <p>1:40pm - 2:00pm</p> <p>Sample size planning for rank-based multiple contrast tests</p> <p>2:00pm - 2:20pm</p> <p>A non-parametric proportional risk model to assess a treatment effect in an application to long-term carcinogenicity assays</p>
2:20pm - 2:40pm	Break				
2:40pm - 4:00pm	<p>Invited: Advanced Statistical Modelling for Polygenic Risk Scores to Enhance their Transferability to Underrepresented Populations  Location: <b>AM 1</b>  Chair: Christian Staerk  Chair: Andreas Mayr</p> <p>2:40pm - 3:20pm</p> <p>Power of inclusion: Enhancing polygenic prediction with admixed individuals  <u>Tanigawa, Yosuke;</u>  <u>Kellis, Manolis</u></p> <p>3:20pm - 3:40pm</p>	<p>Data Sharing and Reproducibility  Location: <b>AM 2</b>  Chair: Matthias Schmid  Chair: Max Westphal</p> <p>2:40pm - 3:00pm</p> <p>Federated Generalized Additive Models for Location, Scale and Shape in DataSHIELD</p> <p>3:00pm - 3:20pm</p> <p>The CodeClub at the MPI of Psychiatry – better code</p>	<p>Time-to-Event: Machine Learning  Location: <b>AM S1</b>  Chair: Moritz Maximilian Berger  Chair: Jan Beyersmann</p> <p>2:40pm - 3:00pm</p> <p>A Large-Scale Neutral Comparison Study of Survival Models</p> <p>3:00pm - 3:20pm</p> <p>Integrating Fine &amp; Gray's Subdistribution Weights into Random Survival Forests for</p>	<p>Special: Statistics in Toxicology  Location: <b>AM S2</b>  Chair: Bernd-Wolfgang Igl  Chair: Tina Lang</p> <p>2:40pm - 3:00pm</p> <p>How to benefit from statistics in toxicology  <u>Rahmenführer, Jörg;</u>  <u>Kappenberg, Franziska</u></p> <p>3:00pm - 3:20pm</p> <p>Virtual Control Groups in Toxicity Studies</p>	<p>Teaching Statistics  Location: <b>AM S3</b>  Chair: André Scherag  Chair: Cornelia Frömke</p> <p>2:40pm - 3:00pm</p> <p>The Power of Data: A Story by global Biostatistics and Data Sciences (gBDS)</p> <p>3:00pm - 3:20pm</p> <p>The Alienator App: Unveiling Data Science in Clinical Trials to a Lay Audience</p>

	<p><b>Bridging the performance gap for underrepresented populations: How to account for population structure in polygenic risk modelling?</b>  <u>Klinkhammer, Hannah</u>; Maj, Carlo; Staerk, Christian; Krawitz, Peter; Mayr, Andreas</p>	<p>and better reproducibility</p> <p>3:20pm - 3:40pm</p> <p>Simple tips for writing and publishing clear code to ensure reproducible results</p>	<p>Competing Event Analysis</p> <p>3:20pm - 3:40pm</p> <p>A random forest pseudo-value approach for modeling restricted mean survival times</p>	<p><u>Vaas, Lea A.I.</u>; Gurjanov, Alexander; Ulbrich, Hannes-Friedrich; Kreuchwig, Annika; Steger-Hartmann, Thomas</p> <p>3:20pm - 3:40pm</p> <p><u>Robust and simple experimental designs for fitting dose response curves in toxicology</u>  <u>Holland-Letz, Tim</u></p> <p>3:40pm - 4:00pm</p> <p>How to benefit from high-dimensional expression data in toxicology  <u>Kappenberg, Franziska</u>; Schorning, Kirsten; Rahnenführer, Jörg</p>	<p>3:20pm - 3:40pm</p> <p>If four programs do the same thing, it's still not the same... (A model building catalog)</p> <hr/> <p>3:40pm - 4:00pm</p> <p>Overview over 5 years of Academia meets Industry Workshop</p>
	<p>3:40pm - 4:00pm</p> <p><b>Boosting European and Multi-ancestry polygenic models: an analysis across different phenotypes of the UK Biobank</b>  <u>Maj, Carlo</u>; Klinkhammer, Hannah; Staerk, Christian; Krawitz, Peter; Mayr, Andreas</p>	<p>3:40pm - 4:00pm</p> <p>Addressing researcher degrees of freedom through adjustment for the multiplicity of analysis strategies</p>	<p>3:40pm - 4:00pm</p> <p>Oversimplifying machine learning on event time data – results of a literature and software review</p>		
4:00pm - 5:20pm	<p><b>Closing Session &amp; Keynote Maarten van Smeden</b>  Location: <b>AM 1</b>  Chair: Jan Beyersmann</p>				
	<p><b>Clinical prediction modeling in the era of AI: a blessing and a curse</b></p>				
5:20pm - 6:00pm	<p>Break</p>				
6:00pm - 7:00pm	<p><b>Vortrag für die Öffentlichkeit: "Sich selbst mit dem Smartphone behandeln: Wie gut funktioniert das?"</b>  Location: <b>AM 1</b>  Chair: Inke Regina Koenig  Speaker: Prof. Dr. med. Stefan Sauerland</p>				