

Statistical Computing 2014 - Workshop Program

07/20/14		07/21/14	07/22/14	07/23/14
	9:00 9:20	Thomas Villman (Mittweida): Statistical Quality Measures and ROC-Optimization by Learning Vector Quantization Classifiers	Eric Sträng (Ulm): Di-methylation is necessary for a sharp Notch response	Rainer Dangi (Wien): A Web Application for Generating Benchmarking Data
	9:20 9:40	Giuseppe Casalicchio (München): Beyond discrimination and calibration: why the predictiveness curve is not sufficient for assessing the performance of prediction models	Melanie Grieb (Ulm): Predicting new Phenotypes with a Boolean Network incorporating uncertainty	Riccardo De Bin (München): Subsampling versus bootstrap in resampling-based model selection for multivariable regression
	9:40 10:00	Marianna Grinberg (Dortmund): Statistical methods for large-scale gene expression data sets in toxicogenomics	Alexander Groß (Ulm): Predicting the dynamic behavior of Wnt/ β -catenin and Wnt/JNK signaling by a rule based probabilistic modeling approach	Johann Kraus (Ulm): Semantic clustering
	10:00 10:20	Matthias Kuhn (Dresden): Specific identification of small genomic structural variations using next generation sequencing data	Markus Maucher (Ulm): A critical noise level for the reconstruction of Boolean functions from time series data	Florian Schmid (Ulm): Semantic multi-classifier systems
	10:20 10:50	Coffee break	Coffee break	Coffee break
	10:50 11:10	Andre Burkovski (Ulm): Rank aggregation of heterogeneous data for identification of common genesets	Julia Schiffner (Düsseldorf): A Mixture of Experts Approach for the Analysis of SNP Data	Ludwig Lausser (Ulm): Fold change classifiers
	11:10 11:30	Werner Adler (Erlangen): Comparing Classifiers for Optical Tissue Differentiation	Katrin Madjar (München): Subgroup-specific survival analysis in high-dimensional datasets	Sebastian Krey (Dortmund): An Statistical approach for Modelling of Low Frequency Oscillations in Electricity Networks
	11:30 11:50	Jörn Lötsch (Frankfurt), Alfred Ultsch (Marburg): What do all those MIRnas do?	Andreas Mayr (Erlangen): Boosting the concordance index for survival data	Axel Fürstberger (Ulm): Interactive zoomable alignment graphs for pairwise wild base nucleotide protein alignment
	12:00 13:30	Lunch	Lunch	Lunch
	13:30 14:30	Eyke Hüllermeier (Paderborn): Learning from imprecise and fuzzy data	Axel Benner (Heidelberg): Genomic Biomarkers for Personalised Medicine: Identification and Validation	
	14:30 14:40	Tutorials: Teasers	Anthony Rossini (Basel): Putting Statistics back into Statistical Computing	
	14:40 15:00	Coffee break		
	15:00 15:30	Social Activities: Schwörmontag (Self-organization)	Coffee break	
	15:30 15:50		Manuela Zucknick (Heidelberg): Non-identical Twins: Comparison of Frequentist and Bayesian Lasso for Cox Models	
	15:50 16:10		Michael Glodek (Ulm): Inequality-constraint Multi-class Fuzzy-in Fuzzy-out Support vector machines	
	16:10 16:30		Markus Kächele (Ulm): Importance based hierarchical Langrange multiplier filtering for the parallel training of Support Vector machines	
	16:30 16:50		Tutorials: Teasers	
	16:50 17:50		Working group meeting on Statistical Computing 2015 and other topics (all welcome)	
Dinner	18:00 20:00		Dinner	
Ulrich Mansmann (München): Genes and Function: Prediction, Regression and systems' modelling	20:00 20:30		Tutorials: C. Müssel, L. Lausser (Ulm): Boolean networks	
	20:30 21:00	J. Mazur, A. Gerhold-Ay (Mainz): Statistical Workflows for Sequencing Data	B. Bischl (München), F. Schmid (Ulm): Algorithm Configuration / Tuning with R	
	21:00 21:30			