Statistical Computing 2014
Abstracts der 46. Arbeitstagung

HA Kestler, M Schmid,
L Lausser, JM Kraus (eds)

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Genes and Function: Prediction, Regression and systems' modelling
Ulrich Mansmann

Statistical Quality Measures and ROC-Optimization by Learning Vector Quantization Classifiers
Michael Biehl, Marika Kaden, Thomas Villmann

Beyond discrimination and calibration: why the predictiveness curve is not sufficient for assessing the performance of prediction models
Giuseppe Casalicchio, Bernd Bischl, Matthias Schmid

Statistical methods for large-scale gene expression data sets in toxicogenomics
Marianna Grinberg, Eugen Rempel, Jan G. Hengstler, Jörg Rahnenführer

Specific identification of small genomic structural variations using next generation sequencing data
Matthias Kuhn

Rank aggregation of heterogeneous data for identification of common genesets
Andre Burkovski, Florian Schmid, Ludwig Lausser, Hans A. Kestler

Comparing Classifiers for Optical Tissue Differentiation.
Alexander Engelhardt, Rajesh Kanawade, Christian Knipfer, Matthias Schmid, Florian Stelzle, Werner Adler

What do all those MIRnas do?
Alfred Ultsch, Christian Pallasch, Sabine Herda, Jörn Lötsch

Learning from imprecise and fuzzy data
Eyke Hüllermeier

Statistical Workflows for Sequencing Data
Johanna Mazur, Aslihan Gerhold-Ay

Di-methylation is necessary for a sharp Notch response
Eric Sträng, Franz Oswald, Hans A. Kestler

Predicting new Phenotypes with a Boolean Network incorporating uncertainty
Melanie B. Grieb, Andre Burkovski, J. Eric Sträng, Johann M. Kraus, Alexander Groß, Susanne Kühl, Günther Palm, Michael Kühl and Hans A. Kestler

Predicting the dynamic behavior of Wnt/β-catenin and Wnt/JNK signaling by a rule based probabilistic modeling approach
Alexander Groß, Barbara Kracher, Johann M. Kraus, Katrin Luckert, Oliver Pötz, Thomas Joos, Luc de Raedt, Michael Kühl, Hans A. Kestler

A critical noise level for the reconstruction of Boolean functions from time series data
Markus Maucher, Hans A. Kestler

A Mixture of Experts Approach for the Analysis of SNP Data
Julia Schiffner, Holger Schwender
Subgroup-specific survival analysis in high-dimensional datasets
Katrin Madjar, Christian Netzer, Jörg Rahnenführer

Boosting the concordance index for survival data
Andreas Mayr, Matthias Schmid

Genomic Biomarkers for Personalised Medicine Identification and Validation
Axel Benner

Putting Statistics back into Statistical Computing
Anthony Rossini

Non-identical Twins: Comparison of Frequentist and Bayesian Lasso for Cox Models
Manuela Zucknick, Maral Saadati, Axel Benner

Inequality-constraint Multi-class Fuzzy-in Fuzzy-out Support vector machines
Michael Glodek, Markus Kächele, Friedhelm Schwenker

Importance based hierarchical Lagrange multiplier filtering for the parallel training of Support Vector Machines
Markus Kächele, Friedhelm Schwenker

Boolean networks
Christoph Müssel, Ludwig Lausser

Algorithm Configuration / Tuning with R
Bernd Bischl, Florian Schmid

A Web Application for Generating Benchmarking Data
Rainer Dangl, Friedrich Leisch

Subsampling versus bootstrap in resampling-based model selection for multivariable regression
Riccardo De Bin, Silke Janitza, Willi Sauerbrei, Anne-Laure Boulesteix

Semantic clustering
Johann M. Kraus, Ludwig Lausser, Hans A. Kestler

Semantic multi-classifier systems
Ludwig Lausser, Florian Schmid, Johann Kraus, Axel Fürstberger, Hans A. Kestler

Fold change classifiers
Ludwig Lausser, Hans A. Kestler

An Statistical approach for Modelling of Low Frequency Oscillations in Electricity Networks
Dirk Surmann, Sebastian Krey, Uwe Ligges, Claus Weihs

Interactive zoom-able alignment graphs for pairwise wild base nucleotide protein alignments
Axel Fürstberger, Hans A. Kestler