

Jörg RAHNENFÜHRER

Technische Universität Dortmund
Fakultät Statistik
Vogelpothsweg 87
44221 Dortmund
Phone: (0049) 231/755-3121
Fax: (0049) 231/755-5303
Email: rahnenfuehrer@statistik.tu-dortmund.de
URL: www.statistik.tu-dortmund.de/rahnenfuehrer.html



Personal details

Date of birth: May 19, 1971
Place of birth: Köln (Germany)
Marital status: Married, three children (2005, 2008, 2011)
Nationality: German

Education

October 24, 2006	Habilitation, Bioinformatics, University of the Saarland: <i>Statistical methods for the biological interpretation of genome-wide measurements</i> , Advisor: Prof. Dr. Thomas Lengauer
January 29, 1999	Ph.D., Mathematics, University of Düsseldorf (Germany)
1995 - 1999	Ph.D. thesis, Department of Mathematical Statistics and Probability Theory, Mathematical Institute, Heinrich-Heine-University Düsseldorf: <i>Tests auf Unabhängigkeit in bivariaten Hazardmodellen mit zensierten Daten</i> (Tests of independence in bivariate hazard models with censored data), Supervisor: Prof. Dr. Arnold Janssen
October 9, 1995	Diploma (equivalent to M.sc.), Mathematics, University of Düsseldorf (Germany)
1994 - 1995	Diploma thesis, Mathematical Institute, University of Düsseldorf: <i>Über die Gütefunktion des Kolmogorov-Smirnov-Tests beim Signalerkennungsproblem</i> (On the power function of the Kolmogorov-Smirnov test for the signal detection problem), Supervisor: Prof. Dr. Arnold Janssen
1990 - 1995	Study of Mathematics and Psychology, University of Düsseldorf
June 9, 1990	Final examination (Abitur, 1.0), High school in Dormagen, (Bettina-von-Arnim-Gymnasium, Germany)
1981 - 1990	High school in Dormagen (Bettina-von-Arnim-Gymnasium)
Sep.-Dec. 1987	Exchange student in Ottawa, Canada, Colonel By Secondary School
1977 - 1981	Elementary school in Nievenheim (Germany)

Professional history

- 4/2007 - Full Professor for *Statistische Methoden in der Gernetik und Chemometrie* (Statistical Methods in Genetics and Chemometrics), Technische Universität Dortmund, Fakultät Statistik.
- 10/2002 - 3/2007 Research Scientist, Max-Planck-Institut für Informatik, Saarbrücken, Computational Biology and Applied Algorithmics group.
Advisor and consultation for PhD and master theses related to statistical methods in bioinformatics.
- 10/2001 - 9/2002 Consultant, Eppley Institute for Research in Cancer and Allied Diseases and Center for Human Molecular Genetics, University of Nebraska Medical Center.
- 10/2000 - 9/2002 Post-doctoral Researcher, University of California, Berkeley, Department of Biostatistics and Department of Statistics (funded by *Deutsche Forschungsgemeinschaft* (DFG)).
- 3/1999 - 8/1999 Research Assistant (Postdoc), Vienna University of Economics and Business Administration (Austria), SFB 010: Adaptive Information Systems and Modelling in Economics and Management Science (funded by Austrian Science Foundation (FWF)).
- 10/1995 - 9/2000 Teaching Assistant, University of Düsseldorf, Mathematical Institute, Department of Mathematical Statistics and Probability Theory;
Advisor and consultation for PhD and master theses in the fields of Bootstrap tests, permutation tests, signal detection problems and LAN-theory.

Grants

- 5/2011 - 4/2014 DFG research grant "Improved prognostic signatures from microarray studies by choosing genes with characteristic distributions".
- 5/2011 - 4/2014 DFG research grant "Clinical prognoses on the basis of gene-regulatory networks"
- 1/2011 - 12/2014 Principal Investigator within the Collaborative Research Center SFB 876 "Providing Information by Resource-Constrained Data Analysis".
- 1/2009 - 6/2013 DFG graduate school: Principal investigator within the Research Training Group (Graduiertenkolleg) "Statistical Modelling".
- 7/2008 - 6/2013 BMBF grant: Project partner in NGFNplus (Nationales Genomforschungsnetzwerk) Verbundantrag "Deciphering oncogene dependencies in human cancer oncogene mutation space": Project leader of Subproject 6: Statistical modeling of drug response and pathway alterations.
- 11/2004 - 04/2008 BMBF grant No. 01GR0453: Project partner in NGFN II (Nationales Genomforschungsnetzwerk), SMP (Systematic Methodological Platform) Bioinformatics. Coordination of "Subproject 2.3: Method development for enhanced biological interpretation of gene expression data". Partner in "Subproject 3.2: Practical Microarray Data Analysis Courses": The "NGFN Microarray Data Analysis Resource" aims to improve the bioinformatics and statistics support for the design and analysis of gene expression data in the NGFN. Basic techniques are taught in regularly held courses on the analysis of gene expression data.
- 2/2002 - 9/2002 Consultancy on NIH grant R01HD037804-04 (Prof. Dr. Claudia Kappen): Support regarding statistical aspects in the design and analysis of microarray experiments.
- 10/2001 - 9/2002 DFG Research stipend RA 870/2-2: Extension of part I: "Nonparametric testing theory in multivariate survival analysis - applications in genetic statistics", funded by "Deutsche Forschungsgemeinschaft" (DFG).
- 10/2000 - 9/2001 DFG Research stipend RA 870/2-1: "Nonparametric testing theory in multivariate survival analysis" (Nichtparametrische Testtheorie in der multivariaten Survivalanalyse), funded by "Deutsche Forschungsgemeinschaft" (DFG).

Teaching

SS 2011	Course	Statistische Methoden in der Bioinformatik
SS 2011	Course	Datenanalyse mit SAS
WS 2010/11	Course	Klinische Studien
WS 2010/11	Course	Multivariate Verfahren
WS 2009/10	Course	Klinische Studien
WS 2009/10	Seminar	Modellwahlkriterien
SS 2009	Course	Statistische Methoden in der Bioinformatik
SS 2009	Seminar	Bioinformatik
WS 2008/09	Course	Klinische Studien
WS 2008/09	Course	Multivariate Verfahren
SS 2008	Course	Statistische Methoden in der Bioinformatik
SS 2008	Course	Fallstudien II
SS 2008	Seminar	Bioinformatik
WS 2007/08	Course	Klinische Studien
SS 2007	Course	Statistische Lernverfahren
SS 2007	Seminar	Überlebenszeitanalyse
SS 2006	Course	Selected Topics in Computational Biology: The Elements of Statistical Learning II
SS 2005	Course	Selected Topics in Computational Biology: The Elements of Statistical Learning II
SS 2004	Course	Selected Topics in Computational Biology: The Elements of Statistical Learning II
SS 2004	Tutorial	The Elements of Statistical Learning
WS 2002/03	Tutorial	The Elements of Statistical Learning
SS 2000	Tutorial	Einführung in die Stochastik
WS 1999/00	Tutorial	Mathematik für Biologen
WS 1998/99	Seminar	Praxis der Stochastik
SS 1998	Tutorial	Einführung in die Stochastik
WS 1997/98	Tutorial	Einführung zur Mathematik für Biologen
SS 1997	Tutorial	Zeitreihenanalyse (mit praktischen Übungen in SAS)
WS 1996/97	Seminar	Statistik
SS 1996	Seminar	Statistisches Labor: Einführung in SAS
WS 1995/96	Tutorial	Wahrscheinlichkeitstheorie

2003 - 2008 Member of the teaching faculty of 'Courses in Practical DNA Microarray Analysis', funded by the NGFN (Nationales Genomforschungsnetzwerk)

Supervised PhD theses (ongoing)

Michel Lang: *Methods for Efficient Resource Utilization in Machine Learning Algorithms*, started 2011.

Miriam Lohr: *Differential biological networks*, started 2010.

André König: *Dimension reduction for high dimensional genetic measurements with gene group tests*, started 2009.

Eugen Rempel: *Support-Vector-Machines for bioinformatic applications*, started 2009.

Birte Hellwig: *Joint statistical analysis of gene expression data and survival data for breast cancer patients*, started 2009.

Christian Netzer: *Statistical modeling of drug response and pathway alterations*, started 2008.

Kai Kammers: *Survival analysis with high dimensional genetic covariates*, started 2007.

Supervised PhD theses (finished)

Henrike Feuersenger: *Entwicklung eines Isotonen Regressionstrendtests für Multi-State Modelle in der Überlebenszeitanalyse*, 05.06.2009.

Member of PhD committees

Nils Raabe, 11.03.2011.

Anika Buchholz, 05.07.2010.

Sabine Mersmann, 02.07.2010.

Arno Fritsch, 11.06.2010.

Andre Altmann, *Ranking of anti-HIV Combination Therapies and Planning of Treatment Schedules*, Universität des Saarlands, 3rd referee report, 08.06.2010.

Tina Müller, *Local Analysis of High Dimensional Genetic Data Considering Interactions*, 2nd referee report, 22.01.2010.

Dominik Wied, 18.12.2009.

Björn Bornkamp, 26.11.2009.

Raluca Ilinca Schmitt: *Learning diagnostic rules with multivariate classification algorithms*, 2nd referee report, 19.10.2009.

Andreas Keller: *Understanding Cancer with Bioinformatics*, Universität des Saarlands, 3rd referee report, 02.04.2009.

Priti Talwar: *Development of Computational Methods for Metabolic Network Analysis based on*

Metabolomics Data, Universität des Saarlands, 2nd referee report, 26.11.2008

Matthias Arnold, 24.06.2008

Markus Ruschhaupt: *Erzeugung von positiv definiten Matrizen mit Nebenbedingungen zur Validierung von Netzwerkalgorithmen für Microarray-Daten*, LMU München, 2nd referee report, 22.01.2008

Barbara Sarholz: *Microarray Experiments to estimate Heterosis: Design, Transformations, Models*, 3rd referee report, 28.09.2007.

Sibylle Sturtz, 11.09.2007.

Nina Kirschbaum, 02.07.2007.

Habilitation reports

Harald Binder: *Konstruktion und Bewertung von Modellen zur klinischen Vorhersage auf Basis hochdimensionaler molekularer Daten*, Medizinische Fakultät der Albert-Ludwigs-Universität in Freiburg im Breisgau, 2010.

Uwe Saint-Mont: *Statistik im Forschungszirkel: Induktion, Information und Invarianz*, Fachbereich I der Universität Trier, 2010.

Ingo Roeder: *Model-Based Analysis of Stem Cell Dynamics - An Application of Medical Systems Biology*, Medizinische Fakultät der Universität Leipzig, 2008.

Supervised bachelor, master and diploma theses

Katrin Madjar: Vorhersage von Brustkrebsfällen anhand von Ultraschalluntersuchungen, Bachelorarbeit, Februar 2011.

Ying Chen: Linkszensierte Datenanalyse für Metallbelastungen bei Schweißverfahren und deren gesundheitliche Auswirkungen, Diplomarbeit, Februar 2011.

Max Kullack: Klassifikation von Brustkrebspatientinnen mit Baummodellen und vorausgewählten Genen, Diplomarbeit, Dezember 2010.

Kathrin Pytel: Vergleich der Ergebnisse von Überlebenszeitanalysen verschiedener Brustkrebskohorten, Bachelorarbeit, Dezember 2010.

Robert Krausche: Bewertung von Vorhersagemodellen mit dem Brier-Score bei Vorliegen hochdimensionaler genetischen Daten, Diplomarbeit, Dezember 2010.

Jessica Priebe: Phänotypische Charakterisierung eines genomweit genotypisierten Patientenkollektivs mit malignem Melanom, Bachelorarbeit, November 2010.

Michel Lang: Korrelierte Gengruppen als Kovariablen in Überlebenszeitmodellen, Diplomarbeit, November 2010.

Corinna Wrede: Validierung von Nomogrammen für Prostatakrebspatienten, Diplomarbeit, Oktober 2010.

Maike Ahrens: Fallzahlplanung bei individualisierten Therapien, Diplomarbeit, September 2010.

Claudia Köllmann: Stabilität von Ergebnissen aus Biclustering-Algorithmen, Diplomarbeit, August 2010.

Idrissa N'Diaye: Statistische Auswertung einer Studie zur Erkennung von Tuberkulosefällen, Bachelorarbeit, August 2010.

Lars Koppers: Vergleich von Methoden zur Imputation fehlender Daten, Bachelorarbeit, Juli 2010.

Inga Bayh: Marginal structural models for survival analysis of hemodialysis patients, Diplomarbeit, Mai 2010.

Miriam Lohr: Netzwerkanalysen von Brustkrebsdaten, Diplomarbeit, April 2010.

Maike Horster: Modellierung des Einflusses von Begleitmedikation auf klinische Endpunkte, Diplomarbeit, Januar 2010.

Hui Ding: Analyse beruflicher Risikofaktoren für Blasenkrebs in der europäischen EPIC-Kohorte, Masterarbeit, Januar 2010.

Anne Weber: Klassifikation von Lungenkrebstypen anhand von molekularen Signaturen von kombinierten Schadstoffwirkungen, Diplomarbeit, Dezember 2009.

Qing Wang: Statistische Evaluierung des Tumormarkers NMP22 in einem Früherkennungspro-

gramm für Harnblasenkrebs, Diplomarbeit, November 2009.

Birte Weibert: Genexpressionsdaten als Kovariablen in Überlebenszeitmodellen für Brustkrebspatientinnen, Diplomarbeit, March 2009.

Theodor Framke: Modellierung und Analyse von DNA-Strangbrüchen (Comet Assay-Daten) im Rahmen der Humanstudie Bitumen, Diplomarbeit, March 2009.

André König: Regularisierte Gengruppentests für Affymetrix GeneChip Zeitreihendaten, Diplomarbeit, March 2009.

Elisabeth Kociemba: Modellierung des Faktors Rauchen für histologische Subtypen von Lungenkrebs, Diplomarbeit, February 2009.

Carolin Sturtz: Analyse einer Kohortenstudie zur Früherkennung von Harnblasenkrebs mit statistischen Lernverfahren, Diplomarbeit, December 2008.

Christian Netzer: *Statistische Analyse der Signifikanz des Genetischen Progressions-Scores für Überlebenszeiten von Hirntumorpatienten*, Diplomarbeit, October 2008.

Jasmina Bogojeska: *Stability analysis for oncogenetic trees*, master thesis, January 2007.

Laura Toloşi: *Analysis of arrayCGH data for the estimation of genetic tumor progression*, master thesis, June 2006.

Adrian Alexa: *Integrating the GO graph structure in scoring the significance of gene ontology terms*, master thesis, March 2005.

Junming Yin: *Model selection for mixtures of mutagenetic trees*, master thesis (Co-Supervisor: Niko Beerenwinkel), March 2005.

Jumamurat Bayjanov: *Scoring pathway activity from gene expression data*, master thesis, September 2004.

Publications

Wolfgang A. Schulz, Marc Ingenwerth, Carolle E Djuidje, Christiane Hader, Jörg Rahnenführer, Rainer Engers: **Changes in cortical cytoskeletal and extracellular matrix gene expression in prostate cancer are related to oncogenic ERG deregulation**, *BMC Cancer* 10(1):505, 2010.

Kai Kammers, Jörg Rahnenführer: **Improved Interpretability of Survival Models with Gene Groups as Covariates**, *Technical Report 2/2010*, TU Dortmund, Department of Statistics, 2010.

Cristina Cadenas, Dennis Franckenstein, Marcus Schmidt, Mathias Gehrmann, Matthias Hermes, Bettina Geppert, Wiebke Schormann, Lindsey J. Maccoux, Markus Schug, Anika Schumann, Christian Wilhelm, Evgenia Freis, Katja Ickstadt, Jörg Rahnenführer, Jörg I. Baumbach, Albert Sickmann, and Jan G. Hengstler: **Role of thioredoxin reductase 1 and thioredoxin interacting protein in prognosis of breast cancer**, *Breast Cancer Research* 12(3):R44, 2010.

Sebastian Briesemeister, Jörg Rahnenführer, Oliver Kohlbacher: **YLoc - an interpretable web server for predicting subcellular localization**, *Nucleic Acids Research* 38(Web Server issue):W497-W502, 2010.

Christian Netzer, Jörg Rahnenführer: **Sample size estimation for cancer progression models**, *International Journal of Computational Bioscience*, accepted, 2010.

Marco Grzegorzczuk, Dirk Husmeier, Jörg Rahnenführer: **Modelling non-stationary dynamic gene regulatory processes with the BGM model**, *Computational Statistics*, DOI: 10.1007/s00180-010-0201-9, 2010.

Miriam Lohr, Patricio Godoy, Jan G. Hengstler, Jörg Rahnenführer, Marco Grzegorzczuk: **Extracting differential regulatory sub-networks from genome-wide microarray expression data**, In: T. Manninen et al. (eds.): *Proceedings of the Seventh International Workshop on Computational Systems Biology*, 63-66, WCSB 2010, Luxembourg, 2010.

Marco Grzegorzczuk, Dirk Husmeier, Jörg Rahnenführer: **Modelling non-stationary gene regulatory processes**, *Advances in Bioinformatics*, Article ID 749848, doi:10.1155/2010/749848, 2010.

Birte Hellwig, Jan G. Hengstler, Marcus Schmidt, Mathias C. Gehrmann, Wiebke Schormann, Jörg Rahnenführer: **Comparison of scores for bimodality of gene expression distributions and genome-wide evaluation of the prognostic relevance of high-scoring genes**, *BMC Bioinformatics* 11:276, 2010.

Katharina Podwojski, Martin Eisenacher, Michael Kohl, Michael Turewicz, Helmut E. Meyer, Jörg Rahnenführer, Christian Stephan: **Peek a peak: a glance at statistics for quantitative label-free proteomics**, *Expert Review of Proteomics* 7(2):249-261, 2010.

Jan C. Brase, Marcus Schmidt, Thomas Fischbach, Holger Sültmann, Hans Bojar, Heinz Koelbl, Birte Hellwig, Jörg Rahnenführer, Jan G. Hengstler, Mathias C. Gehrmann: **ERBB2 and TOP2A in breast cancer: A comprehensive analysis of gene amplification, RNA levels, and protein expression and their influence on prognosis and prediction**, *Clin-*

ical Cancer Research 16(8):2391-2401, 2010.

Marcus Schmidt, Ilka B. Petry, Daniel Böhm, Antje Lebrecht, Christian von Törne, Susanne Gebhard, Aslihan Gerhold-Ay, Christina Cotarelo, Marco Battista, Wiebke Schormann, Evgenia Freis, Silvia Selinski, Katja Ickstadt, Jörg Rahnenführer, Martin Sebastian, Martin Schuler, Heinz Koelbl, Mathias Gehrman, Jan G. Hengstler: **Ep-CAM RNA expression predicts metastasis-free survival in three cohorts of untreated node-negative breast cancer**, *Breast Cancer Research and Treatment* 2010 Mar 30. [Epub ahead of print], DOI: 10.1007/s10549-010-0856-5.

Briesemeister S, Rahnenführer J, Kohlbacher O: **Going from where to why - interpretable prediction of protein subcellular localization**, *Bioinformatics* 26(9): 1232-1238, 2010.

Wuest, S.E., Vijverberg, K., Schmidt, A., Weiss, M., Gheyselinck, J., Lohr, M., Wellmer, F., Rahnenführer, J., von Mering, C., Grossniklaus, U.: **Arabidopsis female gametophyte gene expression map reveals similarities between plant and animal gametes**, *Current Biology* 20(6): 506-512, 2010.

Peifer, M., Weiss, J., Sos, M.L., Koker, M., Heynck, S., Netzer, C., Fischer, S., Rode, H., Rauh, D., Rahnenführer, J., Thomas, R.K.: **Analysis of compound synergy in high-throughput cellular screens by population-based lifetime modeling**, *PLoS One* 5(1):e8919, 2010.

Petry, I.B., Fieber, E., Schmidt, M., Gehrman, M., Gebhard, S., Hermes, M., Schormann, W., Selinski, S., Freis, E., Schwender, H., Brulport, M., Ickstadt, K., Rahnenführer, J., Maccoux, L., West, J., Kölbl, H., Schuler, M., Hengstler, J.G.: **ERBB2 induces an antiapoptotic expression pattern of Bcl-2 family members in node-negative breast cancer**, *Clinical Cancer Research* 16(2): 451-460, 2010.

Freis, E., Selinski, S., Weibert, B., Krahn, U., Schmidt, S., Gehrman, M., Hermes, M., Maccoux, L., West, J., Schwender, H., Rahnenführer, J., Hengstler, J.G., Ickstadt, K.: **Effects of metagene calculation on survival: An integrative approach using cluster and promoter analysis**, *Proceedings of the Sixth International Workshop on Computational Systems Biology (WCSB 2009)*, TICSP series #42, p. 47-50, Aarhus, Denmark, June 10-12, 2009.

Sos, M.L., Michel, K., Zander, T., ..., 39 further co-authors, ..., Thomas, R.K.: **Predicting drug susceptibility of non-small cell lung cancers based on genetic lesions**, *Journal of Clinical Investigation* 119(6): 1727-1740, 2009.

Wemmert, S., Bettscheider, M., Alt, S., Ketter, R., Kammers, K., Feiden, W., Steudel, W.-I., Rahnenführer, J., Urbschat, S.: **p15 promotor methylation - A novel prognostic marker in glioblastoma patients**, *International Journal of Oncology* 34(6):1743-1748, 2009.

Podwojski, K., Fritsch, A., Chamrad, D.C., Paul, W., Sitek, B., Stühler, K., Mutzel, P., Stephan, C., Meyer, H.E., Urfer, W., Ickstadt, K., Rahnenführer, J.: **Retention time alignment algorithms for LC/MS data must consider non-linear shifts**, *Bioinformatics* 25(6): 758-764, 2009.

Karlowatz, R.-J., Scharhag, J., Rahnenführer, J., Schneider, U., Jakob, E., Kindermann, W., Zang, K.D.: **Polymorphisms in the IGF1 signalling pathway including the myostatin gene are associated with left ventricular mass in male athletes**, *British Journal of*

Sports Medicine Jan 9. [Epub ahead of print], 2009.

Schwender, H., Ickstadt, K., Rahnenführer, J.: **Classification with High-Dimensional Genetic Data: Assigning Patients and Genetic Features to Known Classes**, *Biometrical journal* 50(5), 911-926, 2008.

Rahnenführer, J.: **Locally optimal tests of independence for Archimedean copula families**, In: B.Schipp, W. Krämer (Eds.): *Festschrift in Honour of Götz Trenkler: Statistical Inference, Econometric Analysis and Matrix Algebra*, Physica-Verlag HD, 103-112, 2008.

Bogojeska, J., Alexa, A., Altmann, A., Lengauer, T., Rahnenführer, J.: **Rtreemix: an R package for estimating evolutionary pathways and genetic progression scores**, *Bioinformatics* 24(20): 2391-2392, 2008.

Bogojeska, J., Lengauer, T., Rahnenführer, J.: **Stability Analysis of Mixtures of Mutagenetic Trees**, *BMC Bioinformatics* 9: 165, 2008.

Hornstein, M., Hoffmann, M.J., Alexa, A., Yamanaka, M., Müller, M., Jung, V., Rahnenführer, J.; Schulz, W.A.: **Protein phosphatase and TRAIL receptor genes as new candidate tumor genes on chromosome 8p in prostate cancer**, *Cancer Genomics & Proteomics* 5(2): 123-136, 2008.

Podwojski, K., Fritsch, A., Chamrad, D., Paul, W., Mutzel, P., Ickstadt, K., Rahnenführer, J.: **A retention-time alignment algorithm for LC/MS data**, *Proceedings of the Fifth International Workshop on Computational Systems Biology (WCSB 2008)*, TICSP series #41, p. 129-132, Leipzig, June 11-13, 2008.

Ketter, R., Rahnenführer, J., Henn, W., Kim, Y.-J., Feiden, W., Steudel, W.-I., Zang, K.D., Urbschat, S.: **Correspondence of tumor localization with tumor recurrence and cytogenetic progression in meningiomas**, *Neurosurgery* 62(1): 61-70, 2008.

Domingues, F.S., Rahnenführer, J., Lengauer, T.: **Conformational analysis of alternative protein structures**, *Bioinformatics* 23(23): 3131-3138, 2007.

Kamradt, J., Jung, V., Wahrheit, K., Tološi, L., Rahnenführer, J., Schilling, M., Walker, R., Davis, S., Stöckle, M., Meltzer, P., Wullich, B.: **Detection of Novel Amplicons in Prostate Cancer by Comprehensive Genomic Profiling of Prostate Cancer Cell Lines Using Oligonucleotide-Based ArrayCGH**, *PLoS ONE* 2:e769, 2007.

Ketter, R., Urbschat, S., Henn, W., Kim, Y.-J., Feiden, W., Beerenwinkel, N., Lengauer, T., Steudel, W.-I., Zang, K.D., Rahnenführer, J.: **Application of oncogenetic trees mixtures as a biostatistical model of the clonal cytogenetic evolution of meningiomas**, *International Journal of Cancer* 121(7): 1473-1480, 2007.

Schlicker, A., Rahnenführer, J., Albrecht, M., Lengauer, T., Domingues, F.S.: **GOTax: Investigating biological processes and biochemical activities along the taxonomic tree**, *Genome Biology* 8: R33, 2007.

Schulz, W.A., Alexa, A., Jung, V., Hader, C., Hoffmann, M.J., Yamanaka, M., Fritzsche, S., Wlazlinski, A., Müller, M., Lengauer, T., Engers, R., Florl, A.R., Wullich, B., Rahnenführer, J.: **Factor interaction analysis for chromosome 8 and DNA methylation alterations highlights innate immune response suppression and cytoskeletal changes in prostate**

cancer, *Molecular Cancer* 6: 14, 2007.

Ketter, R., Kim, Y.-J., Storck, S., Rahnenführer, J., Romeike, B.F.M., Steudel, W.-I., Zang, K.D., Henn, W.: **Hyperdiploidy defines a distinct cytogenetic entity of meningiomas**, *Journal of Neuro-Oncology* 83(2): 213-221, 2007.

Yin, J., Beerenwinkel, N., Rahnenführer, J., Lengauer, T.: **Model selection for mixtures of mutagenetic trees**, *Statistical Applications in Genetics and Molecular Biology*: Vol. 5: No. 1, Article 17, 2006.

Schlicker, A., Domingues, F.S., Rahnenführer, J., Lengauer, T.: **A new Measure for functional Similarity of Gene Products based on Gene Ontology**, *BMC Bioinformatics* 7: 302, 2006.

Alexa, A., Rahnenführer, J., Lengauer, T.: **Improved scoring of functional groups from gene expression data by decorrelating GO graph structure**, *Bioinformatics* 22(13): 1600-1607, 2006.

Wemmert, S., Ketter, R., Rahnenführer, J., Strowitzki, M., Feiden, W., Hartmann, C., Lengauer, T., Stockhammer, F., Zang, K.D., Meese, E., Steudel, W., von Deimling, A., Urbschat, S.: **Patients with high grade gliomas harboring deletions of chromosomes 9p and 10q benefit from temozolomide treatment**, *Neoplasia* 7(10): 883-893, 2005.

Beerenwinkel, N., Sing, T., Lengauer, T., Rahnenführer, J., Roomp, K., Savenkov, I., Fischer, R., Hoffmann, D., Selbig, J., Korn, K., Schmidt, B., Walter, H., Berg, T., Braun, P., Fätkenheuer, G., Oette, M., Rockstroh, J., Kupfer, B., Kaiser, R., Däumer, M.: **Computational methods for the design of effective therapies against drug resistant HIV strains**, *Bioinformatics* 21(21): 3943-3950, 2005.

Beerenwinkel, N., Rahnenführer, J., Däumer, M., Hoffmann, D., Kaiser, R., Selbig, J., Lengauer, T.: **Learning multiple evolutionary pathways from cross-sectional data**, *Journal of Computational Biology* 12(6): 584-598, 2005.

Rahnenführer, J.: **Clustering algorithms and other exploratory methods for microarray data analysis**, *Methods of Information in Medicine* 44(3): 444-448, 2005.

Rahnenführer, J.: **Image analysis for cDNA microarrays**, *Methods of Information in Medicine* 44(3): 405-407, 2005.

Rahnenführer, J., Beerenwinkel, N., Schulz, W.A., Hartmann, C., von Deimling, A., Wullich, B., Lengauer, T.: **Estimating cancer survival and clinical outcome based on genetic tumor progression scores**, *Bioinformatics* 21(10): 2438-2446, 2005.

Hahn, A., Rahnenführer, J., Talwar, P., Lengauer, T.: **Confirmation of human protein interaction data by human expression data**, *BMC Bioinformatics* 6: 112, 2005.

Beerenwinkel, N., Däumer, M., Sing, T., Rahnenführer, J., Lengauer, T., Selbig, J., Hoffmann, D., Kaiser, R.: **Estimating HIV evolutionary pathways and the genetic barrier to drug resistance**, *The Journal of Infectious Diseases* 191(11): 1953-1960, 2005.

Beerenwinkel, N., Rahnenführer, J., Kaiser, R., Hoffmann, D., Selbig, J., Lengauer, T.: **Mtreemix: a software package for learning and using mixture models of mutagenetic trees**,

Bioinformatics 21(9): 2106-2107, 2005.

Das, A.V., James, J., Rahnenführer, J., Thoreson, W.B., Bhattacharya, S., Zhao, X., Ahmad, I.: **Retinal properties and potential of the adult mammalian ciliary epithelium stem cells**, *Vision Research* 45(13): 1653-1666, 2005.

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Refereeing work

Algorithms in Molecular Biology

Archives of Toxicology

Bioinformatics

BioData Mining

Biometrical Journal

Biostatistics

BioTechniques

BMC Bioinformatics

BMC Genomics

BMC Medical Genomics

Briefings in Bioinformatics

Cancer Informatics

Computational Statistics and Data Analysis

Genome Biology

IEEE/ACM Transactions on Computational Biology and Bioinformatics

International Journal of Cancer

Journal of the American Statistical Association (JASA)

Journal of Bioinformatics and Computational Biology

Journal of Computational Biology

Methods of Information in Medicine

Molecular Medicine

Nucleic Acids Research

Quality and Reliability Engineering International

Statistical Applications in Genetics and Molecular Biology

Statistical Papers

Statistics in Medicine

The Computer Journal

ECCB03,06-08 (European Conference in Computational Biology)

GCB03-05 (German Conference in Bioinformatics)

ISMB10 (International Conference on Intelligent Systems for Molecular Biology)

ISMB/ECCB07,09

RECOMB03-06,08 (Research in Computational Molecular Biology)

Referee for Research Proposals of 'Deutsche Forschungsgemeinschaft' (DFG), 'Helmholtz Gemeinschaft', and 'Swiss National Science Foundation'

Organizing work

ISMB 2010: Eighteenth Annual International Conference on Intelligent Systems for Molecular Biology, July 2010, Boston, USA: Member of program committee.

DAGStat 2010: Statistik unter einem Dach: Zweite gemeinsame Tagung Deutsche Arbeitsgemeinschaft Statistik, Dortmund, Germany: Chair of Local Organizing Committee.

WCSB 2009, Sixth International Workshop on Computational Systems Biology, June 2009, Aarhus, Denmark: Member of Scientific Committee.

ISMB 2008, Sixteenth Annual International Conference on Intelligent Systems for Molecular Biology, July 2008, Toronto, Canada: Member of program committee.

ECCB 2008, European Conference on Computational Biology, September 2008, Cagliari, Sardinia, Italy: Member of program committee.

WCSB 2008, Fifth International Workshop on Computational Systems Biology, June 2008, Leipzig, Germany: Member of Scientific Committee.

Annual Conference of the Working Group "Statistical Methods in Bioinformatics" of the German Region of the International Biometric Society, November 2007, München, Germany: Member of Organizing Committee.

ISMB/ECCB 2007, Fifteenth International Conference on Intelligent Systems for Molecular Biology, July 2007, Wien, Austria: Member of program committee.

gmds 2006, 51. Jahrestagung der Deutschen Gesellschaft für Medizinische Informatik, Biometrie und Epidemiologie, September 2006, Leipzig, Germany: Member of program committee.

Frankfurter Stochastiktag 2006, March 2006, Frankfurt, Germany: Organizer of *Sektion 11: Statistik in Biowissenschaften und Medizin*.

Journal positions

Biometrical Journal: Associate Editor (since 2007).

BioData Mining: Member of Editorial Board (since 2007).

Memberships

Deutsche Region der Internationalen Biometrischen Gesellschaft (IBS) (International Biometric Society)

International Society for Computational Biology (ISCB)

Deutsche Mathematiker-Vereinigung (DMV) (German National Mathematical Society)

DMV-Fachgruppe Stochastik

Industry consulting

Signature Diagnostics, Potsdam: *Statistical consulting in biometry and biostatistics* (since 2010).

BASF AG, Ludwigshafen: *Modelling and analysis of biological High Throughput Screening (HTS) data* (2006-2008).

Patents

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Dortmund, April 12, 2011