

**Publications:****Summary (h-Index: 14, google scholar, 10/17)**

Peer-reviewed articles in scientific journals:	32
Reviewed conference proceedings:	15
Books (Dissertations):	1
Book contributions:	4
Others:	5
<b>Sum</b>	<b>57</b>

**Peer-reviewed articles in scientific journals**

[57] Geissen E, Hasenauer J, Radde N. Inference of finite mixture models and the effect of binning, *Statist Appl Genet Mol Biol*, submitted.

[56] Jensch A, Frey Y, Bitschar K, Weber P, Schmid S, Hausser A, Olayioye M\*, Radde N\*. Feedback control of PKD activity and Golgi secretory function by the tumor suppressor DLC1, submitted. (\*joint last authors)

[55] Rehm M, Apweiler R, Beissbarth T, Berthold M, Bluethgen N, Burmeister Y, Dammann O, Deutsch A, Feuerhake F, Franke A, Hasenauer J, Hoffmann S, Höfer T, Jansen P, Kaderali L, Klingmüller U, Koch I, Kohlbacher O, Küpfer L, Lammert F, Maier D, Pfeifer N, Radde N, Röder I, Saez-Rodriguez J, Sax U, Schmeck B, Schuppert A, Seilheimer B, Theis F, Vera-González J, Wolkenhauer O (2017). Whither Systems Medicine? **Exp & Mol Med**, to appear.

[54] Jensch A, Thomaseth C, Radde N (2017). Sampling-based Bayesian approaches reveal the importance of quasi-bistable behavior in cellular decision processes on the example of the MAPK signaling pathway, **BMC Syst Biol** (2017), 11:11, doi:10.1186/s12918-017-0392-6.

[53] Thomaseth C, Kuritz K, Allgöwer F, Radde N (2016). The circuit-breaking algorithm for monotone systems, **Math Biosci**, 284, 80-91, doi:10.1016/j.mbs.2016.09.002.

[52] Radde N, Hütt M-T (2016). The Physics behind Systems Biology, **Eur Phys J Nonlin Biomed Phys**, 4(7), 1-19, doi: 10.1140/epjnbp/s40366-016-0034-8.

[51] Kirch J, Thomaseth C, Jensch A, Radde N (2016). The effect of model rescaling and normalization on sensitivity analysis on an example of a MAPK pathway model, **Eur Phys J Nonlin Biomed Phys** 4(3), 1-23.

[50] Geissen EM, Hasenauer J, Heinrich S, Hauf S, Radde N (2016). MEMO - Multi-experiment mixture model analysis for censored data, **Bioinformatics** 32(16), 2464-72, doi:10.1093/bioinformatics/bwt190.

[49] Weber P, Hornjik M, Olayioye MA, Hausser, A, Radde N (2015). A computational model of PKD and CERT interactions at the trans-Golgi network of mammalian cells, **BMC Syst Biol**, 9:9, doi:10.1186/s12918-015-0147-1.

[48] Kramer A, Stathopoulos V, Girolami M, Radde N (2014). MCMC\_CLIB: An advanced MCMC sampling package for ode models with highly correlated parameters, **Bioinformatics** 30(20):2991-2, doi: 10.1093/bioinformatics/btu429.

[47] Kramer A, Calderhead B, Radde N (2014). Hamiltonian Monte Carlo Methods for Efficient Parameter Estimation in Steady State Dynamical Systems, **BMC Bioinf** 2014, 15(1):253, doi:10.1186/1471-2105-15-253.

[46] Heinrich S, Geissen E-M, Kamenz J, Trautmann S, Widmer C, Drewe P, Knop M, Radde N, Hasenauer J, Hauf S (2013). Determinants for robustness in spindle assembly checkpoint signalling, **Nat Cell Biol** 15(11), 1328-39, doi:10.1038/ncb2864.

[45] Thomaseth C, Weber P, Hamm T, Kashima K, Radde N (2013). Modeling sphingomyelin synthase 1 driven conversion of ceramide to sphingomyelin at the Golgi apparatus can be explained by a positive feedback mechanism, **J Theor Biol** 337, 174-180, DOI: 10.1016/j.jtbi.2013.08.022.

[44] Offtermatt J, Radde N (2013). Convergence of posteriors for structurally non-identifiable problems

using results from the theory of inverse problems. **J Inverse Ill-Posed P** 22(2), 251-276, ISSN (Online) 1569 – 3945, ISSN (Print) 0928-0219, doi:10.1515/jip-2012-0057.

[43] Vehlow C, Hasenauer J, Kramer A, Raue A, Hug S, Timmer J, Radde N, Theis FJ, Weiskopf D (2013). iVUN: Interactive Visualization of Uncertain biochemical reaction Networks. **BMC Bioinf** 2013, 14(Suppl) 19: S2, doi:10.1186/1471-2105-14-S19-S2.

[42] Weber P, Dingler C, Kramer A, Radde N (2012). Trajectory-oriented Bayesian experiment design versus Fisher A-optimal design: An in depth comparison study. **Bioinformatics** 28:i535-i541, doi: 10.1093/bioinformatics/bts377.

[41] Radde N (2012). Analyzing fixed points of intracellular regulation networks with complex feedback topology. **BMC Syst Biol** 6:57, doi:10.1186/1752-0509-6-57.

[40] Hasenauer J, Waldherr S, Doszczak M, Scheurich P, Radde N and Allgöwer F (2011). Analysis of heterogeneous cell populations: A density-based modeling and identification framework. **J Process Contr** 21(10), 1417-25. doi:10.1016/j.jprocont.2011.06.020.

[39] Radde N (2011). The role of feedback mechanisms in biological network models – A tutorial. **Asian J Control** 13(5), 597-610, doi:10.1002/asjc.376.

[38] Hasenauer J, Waldherr S, Doszczak M, Radde N, Scheurich P and Allgöwer F (2011). Identification of models of heterogeneous cell populations from population snapshot data. **BMC Bioinf** 2011, 12:125, doi:10.1186/1471-2105-12-125.

[37] Radde N (2010). Fixed point characterization of biological networks with complex graph topology. **Bioinformatics** 26(22), 2874-2880, doi: 10.1093/bioinformatics/btq517.

[36] Bar NS, Radde N (2009). Long-term prediction of fish growth under varying ambient temperature using a multi-scale dynamic model. **BMC Syst Biol** 3:107, doi:10.1186/1752-0509-3-107.

[35] Radde N, Bar NS, Banaji M (2009). Graphical methods for analysing feedback in biological networks - A survey - **Int J Syst Sci** 41(1), 35-46, DOI: 10.1080/00207720903151326.

[34] Radde N (2008). The impact of time-delays on the robustness of biological oscillators and the effect of bifurcations on the inverse problem. **Eurasip J Bioinf Syst Biol**, vol. 2009, article ID 327503, doi:10.1155/2009/327503.

[33] Radde N (2008). The effect of time scale differences and time-delays on the structural stability of oscillations in a two-gene network. **Adv Complex Syst** 11(3), 471-83,

[32] Radde N, Gebert J, Faigle U, Schrader R, Schnetz K (2008). Modeling feedback loops in the H-NS-mediated regulation of the *Escherichia coli* bgl operon. **J Theor Biol** 250(2), 298-306.

[31] Radde N, Kaderali L (2008). Inference of an oscillating model for the yeast cell cycle. **Discrete Appl Math** 157 (10), 2285-2295, doi:10.1016/j.dam.2008.06.036.

[30] Gebert J, Radde N, Faigle U, Strösser J, Burkovski A (2008). Modelling and simulation of nitrogen regulation in *Corynebacterium glutamicum*. **Discrete Appl Math** 157 (10), 2232-2243, doi:10.1016/j.dam.2008.06.055.

[29] Gebert J, Radde N, Weber GW (2007). Modelling gene regulatory networks with piecewise linear differential equations. **Eur J Oper Res** 18(3), 1148-1165.

[28] Radde N, Gebert J, Forst CV (2006). Systematic component selection for gene-network refinement. **Bioinformatics** 22(21), 2674-2680.

[27] Ergenc T, Pickl SW, Radde N, Weber GW (2005). Generalized semi-infinite optimization and anticipatory systems. **Int J Comput Anticipatory Syst** 15, Chaos, 3-30.

[26] Gebert J, Öktem H, Pickl SW, Radde N, Weber GW, Yilmaz FB (2004). Inference of gene expression patterns by using a hybrid system formulation - an algorithmic approach to local state transition matrices. *Anticipative & Predictive Models in Systems Science* 1, 63-66, GE Lasker, DM Dubois (eds.), Canada, 63-66.

**Further refereed publications (peer-reviewed Conference Proceedings)**

- [25] Thomaseth C, Radde N (2016). Normalization of Western blot data affects the statistics of estimators, Proc. of Foundations of Systems Biology in Engineering (Fosbe2016), Magdeburg, Germany, IFAC-PapersOnline 49(26), 56-62, doi:0.1016/j.ifacol.2016.12.1031.
- [24] Paul D, Radde N (2016). Robustness and filtering properties of ubiquitous signaling network motifs, Proc. of Foundations of Systems Biology in Engineering (Fosbe2016), Magdeburg, Germany, IFAC-PapersOnline 49(26), 120-127.
- [23] Radde N, Klaus S (2015). Bifurcation analysis for intracellular regulation networks based on their circuit structure, 9<sup>th</sup> IFAC Symp on Biological and Medical Systems 48(20), Aug 31 – Sept 2, Berlin, Germany, p.165-70, doi:10.1016/j.ifacol.2015.10.133.
- [22] Vehlow C, Hasenauer J, Kramer A, Heinrich J, Radde N, Allgöwer F, Weiskopf D (2012). Uncertainty-aware visual analysis of biochemical reaction networks. In Proc. Of the IEEE Symp onn Biolog Data Visualization, Seattle, USA, p.79-82, Oct. 2012, doi: 10.1109/BioVis.2012.6378598.
- [21] Radde N (2012). Identification of feedback circuits that are connected to multiple fixed points in biological networks, Conf Proc of the 9<sup>th</sup> Workshop of Comput Syst Biol (WCSB12), June 4-5 2012, Ulm, Germany, p.59-62.
- [20] Weber P, Hasenauer J, Allgöwer F and Radde N (2011). Parameter Estimation and Identifiability of Biological Networks Using Relative Data. Conf. Proc. of the 18th World Congress of the International Federation of Automatic Control (IFAC 2011), August 28 - September 1 2011, Milano, Italy, 11648-11653, 10.3182/20110828-6-IT-1002.01007.
- [19] Waldherr S, Allgöwer F, Radde N (2010). Generic bifurcations in the dynamics of biochemical networks. IEEE Multi-Conference on Systems and Control (MCS 2010), September 8-10, Yokohama, Japan, 135-141, doi: 10.1109/CCA.2010.5611139.
- [18] Kramer A, Hasenauer J, Radde N (2010). Computation of the posterior entropy in a Bayesian framework for parameter estimation in biological networks. IEEE Multi-Conference on Systems and Control (MCS 2010), September 8-10, Yokohama, Japan (2010), 493-498, doi: 10.1109/CCA.2010.5611198
- [17] Kramer A, Radde N (2010). Towards experimental design using a Bayesian framework for parameter identification in dynamic intracellular network models. Procedia Comput Sci 1(1), 1639-1647, doi: 10.1016/j.procs.2010.04.184.
- [16] Hasenauer J, Waldherr S, Radde N, Doszczak M, Scheurich P, Allgöwer F (2010). A maximum likelihood estimator for parameter distributions in heterogeneous cell populations. Procedia Comput Sci 1(1), 1659-1667, doi: 10.1016/j.procs.2010.04.185.
- [15] Kramer A, Radde N (2010). A statistical framework for noise separation in dynamical models of intracellular networks. AIP Proc. of 9th Int. Conf. on Comput Anticipatory Syst (Casys09), August 3-9, Liege, Belgium, vol. 1303, 68-73, doi: 10.1063/1.3527187
- [14] Radde N, Bar NS, Tresch A (2009). A comparison of likelihoods for dynamic stochastic models of biological networks. Proc. of Workshop of Comput Syst Biol (WCSB09), Aarhus, Denmark, 131-134.
- [13] Radde N, Kaderali L (2007). Bayesian inference of gene regulatory networks using gene expression time series data. Lecture Notes in Bioinf (LNBI) 4414, Bird07, Springer Verlag, 1-15.
- [12] Gebert J, Radde N (2006). A new approach for modeling prokaryotic biochemical networks with differential equations. Conf Proc of 7th Int Conf on Comput Anticipatory Syst (Casys05), Liege, Belgium, 526-533.
- [11] Gebert J, Lätsch M, Pickl SW, Radde N, Weber GW, Wünschiers R (2004). Genetic networks and anticipation of gene expression patterns. AIP Conf Proc of Comput Anticipatory Syst (Casys03), 718, 474-485.

**Miscellaneous**

- [10] Vogel M (2017). Gehirntumore besser verstehen. FORSCHUNG LEBEN, Magazin der Universität

Stuttgart, Nr. 8.

[9] Radde N, Paul D, Bischoff M (2017). Abstrahieren statt Kopieren - Auf der Suche nach der Erfolgsformel. Begleitband zur Ausstellung 'baubionik – biologie beflügelt architektur', Knippers J, Schmid U, Speck T (eds), Stuttgarter Beiträge zur Naturkunde, Serie C, Bd. 82, 125-29.

[8] Weber P, Kuritz K, Kramer A, Allgöwer F, Olayioye M, Hausser A, Radde N (2014). Mit Simulationstechnik zu neuen Erkenntnissen in der Systembiologie. Beitrag zum Themenheft Forschung der Universität Stuttgart, 2014.

[7] Radde N (2009). Fixed point analysis in biological networks of coupled feedback. Oberwolfach reports 11/2009, doi:10.4171/OWR/2009/11.

### Book Contributions

[6] Paul D, Dehkordi LKF, von Scheven M, Bischoff M, Radde N (2016). Structural design with biological methods: Optimality, multi-functionality and robustness, Springer book series, edited volume, accepted.

[5] Radde N, Kaderali L (2010). A Bayes Regularized ODE Model for the Inference of Gene Regulatory Networks. In: Das S, Caragea D, Hsu WH, Welch SM (eds.), 'Computational Methods in Gene Regulatory Networks', IGI Global, Chapter 6, pp. 139-168.

[4] Ahdesmäki M, Strimmer K, Radde N, Rahnenführer J, Klemm K, Lähdesmäki H, and Yli-Harja O (eds), 2008. Proc of the 5th Int Workshop on Comput Syst Biol (WCSB08), June 11-13, Leipzig, Germany.

[3] Kaderali L, Radde N (2007). Inferring Gene Regulatory Networks from Gene Expression Data. In 'Computational Intelligence in Bioinformatics', Chapter 2, Studies in Computational Intelligence (SCI) series, Springer-Verlag, Berlin.

### Theses

[2] Radde N (2007). Modeling non-linear dynamic phenomena in biochemical networks. PhD thesis in applied mathematics, Center of Applied Computer Science, University of Cologne, Germany.

[1] Radde N (2002). Neutrino-Transport in Proto-Neutronen-Sternen. Diploma thesis in physics, Department of Nuclear Physics, Technical University of Darmstadt, Germany.

### Selected Talks

[52] **Radde N** (2017). Phosphorylation cascade motifs are robust intrinsic noise filters. 15<sup>th</sup> International Conference on Molecular Systems Biology (ICMSB), July 26-28, Raitenhaslach, Germany.

[51] **Radde N** (2016). Cells are smart – what can we learn from them? A systems-theoretic perspective. Inaugural lecture, October 26, 2016, U Stuttgart.

[50] **Radde N** (2016). Introduction into Systems Medicine. HEC 2016 Workshop 'From Biomedical Informatics to Medical Bioinformatics', September 1, 2016, LMU Munich.

[49] **Radde N** (2016). Sampling-based Bayesian approaches for model calibration on the example of a MAPK signaling pathway model. Seminar in the Group 'Bioinspired Communication Systems', July 1, 2016, TU Darmstadt.

[48] **Radde N** (2016). The effect of model rescaling and normalization on sensitivity analysis on an example of a MAPK pathway model. 80. DPG Jahrestagung, March 6-11, 2016, Universität Regensburg.

[47] **Radde N** (2016). Quasi-bistability in cellular decision processes. Institute Seminar, Freiburg Institute for Advanced Studies, February 2, University of Freiburg.

[46] **Radde N** (2016). Quasi-bistability in cellular decision processes. Helmholtz-Kolloquium, January 21, Helmholtz-Institut für Biomedizinische Technik, RWTH Aachen.

- [45] **Radde N** (2016). Quasi-bistable behavior in cellular decision processes on the example of the MAPK signaling pathway module. ICB Seminar, January 18, Helmholtz Center Munich.
- [44] **Radde N** (2015). Sampling-based approaches for tracking uncertainty for intracellular processes. Invited lecture at the International Max Planck Research School for "Advanced Methods in Process and Systems Engineering - IMPRS ProEng", August 31-September 4, University of Magdeburg.
- [43] **Radde N** (2015). Bifurcation analysis for intracellular regulation networks based on their circuit structure, 9<sup>th</sup> IFAC Symp on Biological and Medical Systems, Aug 31 – Sept 2, Berlin, Germany.
- [42] **Radde N** (2015). Sampling-based approaches for the calibration of intracellular processes using Western blot data: From semi-quantitative data to quantitative dynamic models. Invited talk at the Open BIOMS Seminar Series, March 2, University of Heidelberg.
- [41] **Radde N** (2014). Intracellular processes: From qualitative models to a quantitative dynamic understanding with mathematical approaches. December 16, Weihnachtskolloquium, Institut für Sportwissenschaften, University of Stuttgart.
- [40] **Radde N** (2014). Netzwerkstrukturen biologischer Systeme. 1. Arbeitstreffen zur Initiative Biokybernetik, Großkarlbach, Pfalz, November 20-21.
- [39] **Radde N** (2014). Mit mathematischen Modellen intrazellulären Mechanismen und Prozessen auf der Spur. Tag der Technischen Biologie, November 7, University of Stuttgart.
- [38] **Radde N** and Weber P (2012). Trajectory-oriented Bayesian experiment design versus Fisher A-optimal design: An in-depth comparison study. 11<sup>th</sup> European Conference on Computational Biology (ECCB2012), September 9-12, Basel, Switzerland.
- [37] **Radde N** (2012). Analysis of feedback structures in intracellular networks. Invited talk, University of Genf, June 21, Switzerland.
- [36] **Radde N** (2012). Using statistical Bayesian approaches for the identification of intracellular networks. Invited talk in the lecture series "Computational Methods in Systems Biology", June 14, University of Bonn, Germany.
- [35] **Radde N** (2012). Identification of feedback circuits that are connected to multiple fixed points in biological networks – A systemic approach. 9<sup>th</sup> International Workshop on Computational Systems Biology (WCSB2012), Ulm, Germany, June 4-6.
- [34] **Radde N** (2011). The role of protein kinase D in the balance between lipid homeostasis and secretory activity in mammalian cells – A systemic approach. Invited talk at Böhlinger Ingelheim, Biberach a.d. Riss, Germany, Dec 13.
- [33] **Radde N** (2011). Introduction of the Center Systems Biology, Tag der industriellen Biotechnologie am Zentrum für Bioverfahrenstechnik, University of Stuttgart, Germany, Nov 25.
- [32] **Radde N** (2011). New SimTech vision 'Integrated overall human model'. SimTech Status seminar in Bad Boll, Germany, 21.-23.11.2011.
- [31] Kramer A, **Radde N** (2011). Systems Biology investigates the properties of biochemical reaction networks. Joint Workshop 'Statistical and dynamical models in biology and medicine' of the GmdS/IBS working groups 'Statistical methods in bioinformatics' and 'Mathematical models in medicine', October 27-28, Göttingen, Germany.
- [30] **Radde N**, 2011. Fixed point characterization of biological networks with complex graph topology. Institute for Automatic Control, February 1, ETH Zürich, Switzerland.
- [29] **Radde N**, 2011. Fixed point characterization of biological networks with complex graph topology. B-IT Kolloquium 'Algorithmic Bioinformatics' at the Bonn-Aachen International Center for Information Technology, January 27, University of Bonn, Germany.
- [28] **Radde N**, 2011. A systemic modeling approach towards understanding the protein kinase D-mediated balance between lipid homeostasis and secretory activity in mammalian cells. Workshop 'Systembiologie zwischen Forschung und Anwendung' jointly organized by DECHEMA and Vereinigung deutscher Biotechnologie-Unternehmen (VBU), January 18-19, Frankfurt am Main, Germany.

- [27] Weber P, **Radde N** (2010). Parameter estimation and identifiability of biological networks using relative data. Joint Workshop 'Statistical and dynamical models in biology and medicine' of the GmdS/IBS working groups 'Statistical methods in bioinformatics' and 'Mathematical models in medicine', October 21-22, Heidelberg, Germany.
- [26] **Radde N** (2010). A statistical Bayesian framework for identification of biological networks from perturbation experiments. European Conference on Computational Biology (ECCB 2010), September 26-29, Ghent, Belgium.
- [25] **Radde N** (2010). Generic bifurcations in the dynamics of biochemical networks. IEEE Multi-Conference on Systems and Control (MCS 2010), September 8-10, Yokohama, Japan.
- [24] **Radde N** (2010). Computation of the posterior entropy in a Bayesian framework for parameter estimation in biological networks. IEEE Multi-Conference on Systems and Control (MCS 2010), September 8-10, Yokohama, Japan.
- [23] Kramer A, **Radde N** (2010). Towards optimal experimental design using a Bayesian framework for parameter identification in dynamic intracellular network models. International Conference on Computational Systems (ICCS2010), May 29-31, Amsterdam, Netherlands.
- [22] Kramer A, **Radde N** (2010) Optimal Experimental Design Using a Bayesian Framework for the Identification of Dynamic Intracellular Network Models. DAGStat 2010, 2. gemeinsame Tagung der Deutschen Arbeitsgemeinschaft Statistik 'Statistik unter einem Dach', March 23-26, Dortmund, Germany.
- [21] **Radde, N** (2010) Analyse von Feedback-Mechanismen in biologischen Netzwerken. 6. Elgersburg Workshop, March 1-4, Elgersburg, Germany.
- [20] **Radde, N** (2009). Systems Biology - A New Application Field in Systems Theory. Kolloquium des Exzellenzclusters 'Simulation Technology', December 22, University of Stuttgart, Germany.
- [19] **Radde N** (2009). Statistical approaches for the inference of biological networks. GmdS Jahrestagung, September 7-10, Essen, Germany.
- [18] **Radde N** (2009). A statistical framework for noise separation in dynamic models of intracellular networks. 9th Int Conf on Anticipatory Syst, August 3-7, Liege, Belgium.
- [17] **Radde N** (2009). Systemtheoretische Ansätze zur Untersuchung von Feedback-Mechanismen in biologischen Netzwerken. Seminarvortrag, July 15, University of Hohenheim, Germany.
- [16] **Radde N** (2009). Statistical approaches for the inference of biological networks. Invited seminar talk, June 26, MPI Magdeburg, Germany.
- [15] **Radde N** (2009). A comparison of likelihood functions for dynamic stochastic models of biological networks. Invited seminar talk, June 25, University of Magdeburg, Germany.
- [14] **Radde N** (2009). A comparison of likelihood functions for dynamic stochastic models of biological networks. Workshop on Comput Syst Biol, June 10-12, Aarhus, Denmark.
- [13] **Radde N** (2009). Systemtheoretische Ansätze zur Analyse komplexer biologischer Systeme. Workshop 'System und Komplexität: Kulturalistische vs. Naturalistische Aspekte' May 29, University of Stuttgart, Germany.
- [12] **Radde N** (2009). Antrittsvorlesung: Warum sind Zellen komplex? April 30, University of Stuttgart, Germany.
- [11] **Radde N** (2009). Fixed point analysis in biological networks of coupled feedback. Oberwolfach Workshop: Control Theory: On the Way to New Application Fields, February 22-28, Oberwolfach, Germany.
- [10] **Radde N** (2009). Statistical Bayesian approaches for dynamic network inference. Workshop on Computational Approaches to Stem Cell Biology, January 12-14, Leipzig, Germany.
- [9] **Radde N** (2008). Fixed point analysis in biological networks with interlocked feedback circuits. Workshop on Gene Regulatory Network Inference, September 25-26, Jena, Germany.

- [8] **Radde N** (2008). Fixed point analysis in biological networks with interlocked feedback circuits. European Conference on Mathematical and Theoretical Biology, June 29 - July 4, Edinburgh, Scotland.
- [7] **Radde N** (2008). Inference of oscillating regulatory networks using time series data. Workshop on integrative network analysis: Network structure and biological function - reconstruction, modelling and statistical approaches, April 10-11, Potsdam, Germany.
- [6] **Radde N** (2007). Robustness of Oscillations in Biological Networks. Annual Conference of the Working Group 'Statistical Bioinformatics', November 22-23, Munich, Germany.
- [5] **Radde N** (2007). Bayesian Inference of Gene Regulatory Networks using Gene Expression Time Series Data. Bioinformatics Research and Development (BIRD07), March 12-14, Berlin, Germany.
- [4] **Radde N** (2006). Hierarchical Bayesian Inference of Oscillating Gene Regulatory Networks. International Conference on Molecular Systems Biology (ICMSB06), July 31 - August 4, Munich, Germany.
- [3] **Radde N** (2006). Ein Bayessches Lernverfahren für genregulatorische Netze. Kolloquium über Parallelverarbeitung in technisch-naturwissenschaftlichen Anwendungen, May 15, Jülich, Germany.
- [2] **Radde N** (2006). Hierarchical Bayesian Inference of Gene Regulatory Networks. 30. Annual Conference of the German Classification Society (GfKI06), March 8-10, Berlin, Germany.
- [1] **Radde N** (2005). Graph Theory Applied to Biological Networks. Cologne-Twente Workshop (CTW) on Graphs and Combinatorial Optimization, May 18-20, Cologne, Germany.