

Publications:*Summary*

Peer-reviewed articles in scientific journals:	28
Reviewed conference proceedings:	15
Books (Dissertations):	1
Book contributions:	4
Others:	3
Sum	51

Peer-reviewed articles in scientific journals

[51] Thomaseth C, Kuritz K, Allgöwer F, Radde N (2016). The circuit-breaking algorithm for monotone systems, **Math Biosci**, accepted for publication.

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

[49] 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(1), 1-23.

[48] 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.

[47] 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.

[46] 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.

[45] 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.

[44] 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, 1328-39, doi:10.1038/ncb2864.

[43] 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.

[42] 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.

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[40] 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.

[39] 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.

[38] 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.

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[30] 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.

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[24] 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 (Conference Proceedings)

[23] Thomaseth C, Radde N (2016). The effect of data normalization on model calibration, Fosbe 2016, Magdeburg, Proc. of Foundations of Systems Biology in Engineering (Fosbe2016), Magdeburg, Germany, provisionally accepted.

[22] 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, provisionally accepted.

[21] Radde N, Klaus S (2015). Bifurcation analysis for intracellular regulation networks based on their circuit structure, 9th 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.

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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.

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[14] 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.

[13] 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

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Miscellaneous

[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.

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Theses

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

Submitted/in revision/under review/in progress

- Jensch A, Bitschar K, Olayioye M, [Radde N](#). DLC1 regulation mechanisms, in preparation.
- Jensch A, Thomaseth C, [Radde N](#). 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, under review.