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E-mail: nicole.radde@ist.uni-stuttgart.de**Academic Education** 1996 Studies of Physics and Mathematics, TU Darmstadt
Diploma Physics and 1. State Examination
2002 Physics/Mathematics, TU Darmstadt
2007 Doctorate, Non-linear dynamic phenomena in biochemical systems, University of Cologne**Professional Career** 2003–2007 Research Assistant, Center for Applied Informatics, University of Cologne
2007–2008 Postdoctoral Researcher, Institute for Medical Informatics, Statistics and Epidemiology, University of Leipzig
2008–2015 Junior Professor for Systems Theory in Systems Biology, University of Stuttgart
since 2009 Member of the Board of Directors of the Stuttgart Research Center Systems Biology (SRCSB), formerly Center Systems Biology (CSB)
since 2012 Principal Investigator and member of the Advisory Board EXC 310
2015 Full Professor for Systems Theory in Systems Biology, University of Stuttgart
since 2017 Gender Equality Officer of the University of Stuttgart
since 2019 Vice Director of the Stuttgart Research Center Systems Biology (SRCSB)
since 2019 Member of the Board of Directors of the Excellence Cluster EXC 2075**Funding (last 5 years)****DFG-EXC 2075** 2019–2026 Data-integrated modeling to provide novel solutions for individualizing cancer therapy and predicting treatment success
DFG 2019–2021 Design of synthetic, methylation based, epigenetic gene circuits in bacteria (RA1840/2-1)
DFG-EXC 310/2 2014–2018 Regulation mechanisms of DLC1 and their role in tumour cell migration
Wilhelm-und-Else Heraeus Stiftung 2015 Summer School The Physics behind Systems Biology
DFG-TRR 141 2014–2018 Structural design with biological methods
BMBF e:Bio 2013–2016 Holistic multi-scale modeling of targeted protein therapeutics action

Publications (max. 10 most relevant)

1. I. Eisenkolb, A. Jensch, K. Eisenkolb, A. Kramer, P. Buchholz, J. Pleiss, A. Spiess, and N. **Radde**. “Modeling of biocatalytic reactions: A workflow for model calibration, selection and validation using Bayesian statistics”. In: *AiChE J* e16866 (2019)
2. C. Thomaseth, D. Fey, T. Santra, O. S. Rukhlenko, N. E. **Radde**, and B. N. Kholodenko. “Impact of measurement noise, experimental design, and estimation methods on Modular Response Analysis based network reconstruction”. In: *Scientific reports* 8.1 (2018), p. 16217. DOI: 10.1038/s41598-018-34353-3
3. A. Jensch, Y. Frey, K. Bitschar, P. Weber, S. Schmid, A. Hausser, M. A. Olayioye, and N. E. **Radde**. “The tumor suppressor protein DLC1 maintains protein kinase D activity and Golgi secretory function”. In: *The Journal of Biological Chemistry* 293.37 (2018), pp. 14407–14416. DOI: 10.1074/jbc.RA118.003787
4. A. Jensch, C. Thomaseth, and N. E. **Radde**. “Sampling-based Bayesian approaches reveal the importance of quasi-bistable behavior in cellular decision processes on the example of the MAPK signaling pathway in PC-12 cell lines”. In: *BMC Systems Biology* 11 (2017). DOI: 10.1186/s12918-017-0392-6
5. C. Thomaseth, K. Kuritz, F. Allgöwer, and N. **Radde**. “The circuit-breaking algorithm for monotone systems”. In: *Mathematical biosciences* 284 (2017), pp. 80–91. DOI: 10.1016/j.mbs.2016.09.002
6. E.-M. Geissen, J. Hasenauer, S. Heinrich, S. Hauf, F. J. Theis, and N. E. **Radde**. “MEMO: multi-experiment mixture model analysis of censored data”. In: *Bioinformatics (Oxford, England)* 32.16 (2016), pp. 2464–2472. DOI: 10.1093/bioinformatics/btw190
7. P. Weber, M. Hornjik, M. A. Olayioye, A. Hausser, and N. E. **Radde**. “A computational model of PKD and CERT interactions at the trans-Golgi network of mammalian cells”. In: *BMC Systems Biology* 9 (2015), p. 9. DOI: 10.1186/s12918-015-0147-1
8. A. Kramer, B. Calderhead, and N. **Radde**. “Hamiltonian Monte Carlo methods for efficient parameter estimation in steady state dynamical systems”. In: *BMC bioinformatics* 15 (2014), p. 253. DOI: 10.1186/1471-2105-15-253
9. S. Heinrich, E.-M. Geissen, J. Kamenz, S. Trautmann, C. Widmer, P. Drewe, M. Knop, N. **Radde**, J. Hasenauer, and S. Hauf. “Determinants of robustness in spindle assembly checkpoint signalling”. In: *Nature cell biology* 15.11 (2013), pp. 1328–1339. DOI: 10.1038/ncb2864
10. N. **Radde**. “Fixed point characterization of biological networks with complex graph topology”. In: *Bioinformatics (Oxford, England)* 26.22 (2010), pp. 2874–2880. DOI: 10.1093/bioinformatics/btq517