Name	Position Title
LEBIEDZ, Dirk	Prof. Dr. rer. nat. habil.
	Full Professor
	Institute for Numerical Mathematics &
	Ulm Center for Scientific Computing

EDUCATION/TRAINING

Institution and Location	Degree	Year(s)	Field of Study
University of Freiburg, Germany	Habilitation	2010	Mathematics
University of Freiburg, Germany	Venia leg.	2007	Systems Biology
University of Heidelberg, Germany	Habilitation	2007	Chemistry
University of Münster, Germany	Diploma	2002	Mathematics
University of Münster, Germany	Dr. rer. nat.	2001	Chemistry
University of Münster, Germany	Diploma	1998	(Bio)Chemistry

A.   Positions and Honours

Employment/Experience

since 2012	W3 professorship (Applied Mathematics), University of Ulm
2009 - 2010	Visiting Professor (W3), Replacement of the Chair Reactive Flows, Interdisciplinary Center for Scientific Computing, University of Heidelberg, Germany
since 2007	Lecturer (A13, Akadem. Rat) and Research Group Leader at the Zentrum für Biosystemanalyse (ZBSA), University of Freiburg, Germany
2002 - 2007	Assistant Professor (C1), Interdisciplinary Center for Scientific Computing, University of Heidelberg, Germany
1999 - 2001	Ph.D. Student, Department of Physical Chemistry, University of Münster
1998 - 1999	Scientific coworker at the Institute for Cell Biology, University of Münster, Germany

Honors, Awards, and Scholarships

2011	Offer of a W3 professorship (Scientific Computing, Modeling and Simulation), University of Ulm (accepted)
2011	Offer of a W2 professorship (Applied Mathematics), University of Greifswald (rejected)
1996	Member of the Studienstiftung des Deutschen Volkes

Other Scientific Activities

2008	Assembly of a Master of Science study program "Bioinformatics and Systems Biology", University of Freiburg, Germany
since 2007	Member of the Deutsche Mathematiker Vereinigung
2006 - 2007	Adoption of the basic education in Mathematics in the Bachelor of Science program "Molecular Biotechnology", University of Heidelberg, Germany
2003 - 2007	Member and project leader in SFB 568, Technical University of Darmstadt, Germany
2003	Member of SFB 359, University of Heidelberg, Germany
since 2003	Interdisciplinary lecture courses in Mathematics, Scientific Computing, Modeling and Optimization, System Biology

10 selected Publications

Kasenda, B., Rehberg, M. Thürmann, P., Franzem, M., Veelken, H., Fritsch, K., Schorb. E., Finke, J., **Lebiedz. D.**, Illerhaus, G. The prognostic value of serum methotrexate area under curve in elderly primary CNS lymphoma patients. Ann. Hematol. 2012 (in press), DOI: 10.1007/s00277-012-1441-2

Skanda, D., **Lebiedz, D.** A robust optimization approach to experimental design for model discrimination of dynamical systems. Math. Prog. 2012 (in press), DOI: 10.1007/s10107-012-0532-0

Lebiedz, D., Siehr, J. Unger, J. A Variational principle for computing slow invariant manifolds in dissipative dynamical systems. SIAM J. Sci. Comput. 33, 703 (2011)

Skanda, D., **Lebiedz, D.** An optimal experimental design approach to model discrimination in dynamic biochemical systems. Bioinformatics 26, 939-945 (2010)

Vladimirov, N., **Lebiedz, D.**, Sourjik, V. Predicted auxiliary navigation mechanism of peritrichously flagellated chemotactic bacteria. PloS Comput. Biol. 6, e1000717 (2010)

Slaby, O., **Lebiedz, D.** Oscillatory NAD(P)H waves and calcium oscillations in neutrophils ? A modeling study of feasibility. Biophys. J. 96, 417 (2009)

Mommer, M. S., **Lebiedz, D.** Modeling subdiffusion using reaction diffusion systems. SIAM J. Appl. Math. 70, 112 (2009)

Løvdok, L., Bentele, K., Vladimirov, N., Müller, A., Pop, F. S., **Lebiedz, D.**,Kollmann, M., Sourjik, V. Role of translational coupling in robustness of bacterial chemotaxis pathway. PLoS Biol. 7, e1000171 (2009)

Schulmeister, S., Ruttorf, M., Thiem, S., Kentner, D., **Lebiedz, D.**, Sourjik, V. Protein exchange dynamics at chemoreceptor clusters in Escherichia coli. Proc. Natl. Acad. Sci. USA 29, 6403 (2008)

Shaik, O. S., Sager, S., Slaby, O., **Lebiedz, D.** Phase tracking and restoration of circadian rhythms by model-based optimal control. IET Syst. Biol. 2, 16 (2008)

NephAge project:

Finding suitable models of dynamic biochemical systems is an important task in the biosciences.

On the one hand a correct model can explain the underlying mechanisms, on the other hand one can use the model to predict the behavior of a biological system under various circumstances.

Typically, before the correct model of a biochemical system is found different hypothetical models might be possible. All the models have in common that they fit one initial series of measurements.

The main goal now is to find the best suited model out of different hypotheses. This is usually done by iterative measurements and successive fitting of the different models to the collectivity of all series of measurements. This is repeated until all "wrong" models do not fit to the collectivity of all series of measurements any more. Thus the "wrong" models are falsified. The whole process is called model discrimination.

We are developing a new computational framework to compute optimal experiments in the context of model discrimination. Usability and parallelization are in the current scope of the project.

This framework is promoted to the experimental Nephage team members to assist in the process of modelling and statistical analysis.The groups also deals with the issue of model reduction and the application of it to biochemical systems.

Programming and the Algorithmic design is developed by Dominik Skanda, PhD student and team member of "Lebiedz group: Modeling and Scientific Computing"