

Dr. Jochen Supper

Background

- since 04/2005 research assistant at the Centre for Bioinformatics (ZBIT), University of Tübingen
- 07/2003-03/2005 cont. University of Tübingen, diploma in Computer Science (Bioinformatics).
- 02/2004-04/2004 Internship at the Biofrontera AG, Leverkusen,
- 11/2002-06/2003 Graduate student at the University of Washington
- 10/1999-10/2002 Computer science student at the University of Tübingen



Research Interests

- Decipher regulatory signals controlling gene expression
- Analyze the robustness of Signaling pathways
- Cluster multi-conditioned microarray datasets
- Immunoinformatics

Current Projects

- Robustness analysis of signal transduction models in collaboration with Christian Lorenz Müller, Computational Biophysics Lab ETH Zurich
- Identifying Gene Expression Modules in *Arabidopsis thaliana* in collaboration with Prof. Dr. Harter, ZMBP Tübingen
- BMBF-Project: [NGFN 2](#) (National Genome Research Network): Explorative Project - Inferring Genetic Networks from Gene Expression Data

Publications

- [1] Adrian Schröder, Johannes Eichner, Jochen Supper, Jonas Eichner, Dierk Wanke, Carsten Hennekes, and Andreas Zell. Predicting DNA-Binding Specificities of Eukaryotic Transcription Factors. *PLoS ONE*, 5(11):e13876, November 2010. [[DOI](#) | [link](#)]
- [2] Hannes Planatscher, Jochen Supper, Oliver Poetz, Dieter Stoll, Thomas Joos, Markus Templin, and Andreas Zell. Optimal selection of epitopes for txp-immunoaffinity mass spectrometry. *Algorithms for Molecular Biology*, 5(1):28, June 2010. [[DOI](#) | [link](#)]
- [3] Jochen Supper, Lucía Spangenberg, Hannes Planatscher, Andreas Dräger, Adrian Schröder, and Andreas Zell. BowTieBuilder: modeling signal transduction pathways. *BMC Systems Biology*, 3(1):67, June 2009. [[DOI](#) | [link](#) | [pdf](#)]
- [4] Andreas Dräger, Marcel Kronfeld, Michael J. Ziller, Jochen Supper, Hannes Planatscher, Jørgen B. Magnus, Marco Oldiges, Oliver Kohlbacher, and Andreas Zell. Modeling metabolic networks in *C. glutamicum*: a comparison of rate laws in combination with various parameter optimization strategies. *BMC Systems Biology*, 3(5):5, January 2009. [[DOI](#) | [link](#) | [pdf](#)]
- [5] Andreas Dräger, Nadine Hassis, Jochen Supper, Adrian Schröder, and Andreas Zell. SBMLsqueezer: a CellDesigner plug-in to generate kinetic rate equations for biochemical networks. *BMC Systems Biology*, 2(1):39, April 2008. [[DOI](#) | [link](#) | [pdf](#)]
- [6] Andreas Dräger, Marcel Kronfeld, Jochen Supper, Hannes Planatscher, Jørgen B. Magnus, Marco Oldiges, and Andreas Zell. Benchmarking Evolutionary Algorithms on Convenience Kinetics Models of the Valine and Leucine Biosynthesis in *C. glutamicum*. In Dipti Srinivasan and Lipo Wang, editors, *IEEE Congress on Evolutionary Computation (CEC 2007)*, pages 896--903, Singapore, September 2007. IEEE Computational Intelligence Society, IEEE Press. [[DOI](#) | [link](#)]
- [7] Andreas Dräger, Jochen Supper, Hannes Planatscher, Jørgen B. Magnus, Marco Oldiges, and Andreas Zell. Comparing Various Evolutionary Algorithms on the Parameter Optimization of the Valine and Leucine Biosynthesis in *Corynebacterium glutamicum*. In Dipti Srinivasan and Lipo Wang, editors, *IEEE Congress on Evolutionary Computation (CEC 2007)*, pages 620--627, Singapore, September 2007. IEEE Computational Intelligence Society, IEEE Press. [[DOI](#) | [link](#)]

- [8] Martin Strauch, Jochen Supper, Christian Spieth, Dierk Wanke, Joachim Kilian, Klaus Harter, and Andreas Zell. A two-step clustering for 3-d gene expression data reveals the main features of the arabidopsis stress response. *Journal of Integrative Bioinformatics*, 4(1), 2007. [[DOI](#) | [pdf](#)]
- [9] Jochen Supper, Holger Fröhlich, Christian Spieth, Andreas Dräger, and Andreas Zell. Inferring gene regulatory networks by machine learning methods. In David Sankoff, Lusheng Wang, and Francis Chin, editors, *Proceedings of the 5th Asia-Pacific Bioinformatics Conference (APBC 2007)*, volume 5 of *Series on Advances in Bioinformatics and Computational Biology*, pages 247--256, 57 Shelton Street, Covent Garden, London WC2H 9HE, UK, January 2007. Imperial College Press. [[DOI](#) | [link](#)]
- [10] Jochen Supper, Holger Fröhlich, and Andreas Zell. Gene regulatory network inference via regression based topological refinement. In David Sankoff, Lusheng Wang, and Francis Chin, editors, *Asia-Pacific Bioinformatics Conference (APBC 2007)*, volume 5 of *Advances in Bioinformatics and Computational Biology*, pages 267--276, Hong Kong, China, January 2007. Imperial College Press.
- [11] Jochen Supper, Christian Spieth, and Andreas Zell. Reconstructing linear gene regulatory networks. In Elena Marchiori, Jason H. Moore, and Jagath C. Rajapakse, editors, *Proceedings of the 5th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO 2007)*, volume 4447 of *Lecture Notes in Computer Science*, pages 270--279, Valencia, Spain, 2007. Springer.
- [12] Jochen Supper, Martin Strauch, Dierk Wanke, Klaus Harter, and Andreas Zell. EDISA: extracting biclusters from multiple time-series of gene expression profiles. *BMC Bioinformatics*, 8(1):334, 2007. [[DOI](#) | [link](#)]
- [13] Christian Spieth, Nadine Hassis, Felix Streichert, Jochen Supper, Nora Speer, Klaus Beyreuther, and Andreas Zell. Comparing mathematical models on the problem of network inference. In *Genetic and Evolutionary Computation Conference (GECCO 2006)*, Lecture Notes in Computer Science, pages 305--306, Seattle, USA, 2006. Springer.
- [14] Christian Spieth, Jochen Supper, Felix Streichert, Nora Speer, and Andreas Zell. JCell - a java-based framework for inferring regulatory networks from time series data. *Bioinformatics*, 22(16):2051--2052, 2006. [[link](#)]
- [15] Christian Spieth, Felix Streichert, Jochen Supper, Nora Speer, and Andreas Zell. Feedback memetic algorithms for modelling gene regulatory networks. In *IEEE Symposium on Computational Intelligence and Computational Biology*, pages 61--67, San Diego, USA, November 2005. IEEE Press.
- [16] Jochen Supper, Christian Spieth, and Andreas Zell. Reverse engineering non-linear gene regulatory networks based on the bacteriophage lambda ci circuit. In *Proceedings of the 2005 IEEE Symposium on Computational Intelligence and Computational Biology (CIBCB '05)*, pages 325--332, San Diego, USA, November 2005. IEEE. [[DOI](#)]

Theses

Predicting MHC class I binding peptides based on amino acid properties using decision trees and support vector machines

Studienarbeit, University of Tübingen, 2005

Reconstruction of pseudo-linear under-determined networks

Master thesis, University of Tübingen, 2004

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