Dr. Hannes Planatscher

Background

- 10/1999-4/2006 Computer science student at the University of Tübingen
- since 05/2006 research assistant at the Centre for Bioinformatics (ZBIT), University of Tübingen

Research Interests

- Systems Biology
- Machine Learning
- Combinatorial Optimization
- Mass Spectrometry

Current Projects

- JavaEva: A Java based framework for Evolutionary Algorithms

Publications

[1] Andreas Dräger and Hannes Planatscher. *Encyclopedia of Systems Biology*, chapter Metabolic Networks, pages 1249--1251. Springer-Verlag, Springer New York Heidelberg Dorodrecht London, August 2013. [DOI | link]

[2] Andreas Dräger and Hannes Planatscher. *Encyclopedia of Systems Biology*, chapter Parameter Estimation, Metabolic Network Modeling, pages 1627--1631. Springer-Verlag, Springer New York Heidelberg Dorodrecht London, August 2013. [DOI | link]

[3] Roland Keller, Alexander Dörr, Akito Tabira, Akira Funahashi, Michael J. Ziller, Richard Adams, Nicolas Rodriguez, Nicolas Le Novère, Noriko Hiroi, Hannes Planatscher, Andreas Zell, and Andreas Dräger. The systems biology simulation core algorithm. *BMC Systems Biology*, 7:55, July 2013. [DOI | link | pdf]

[4] Sibylle Hoeppe, Thomas D. Schreiber, Hannes Planatscher, Andreas Zell, Markus F. Templin, Dieter Stoll, Thomas O. Joos, and Oliver Poetz. Targeting peptide termini, a novel immunoaffinity approach to reduce complexity in mass spectrometric protein identification. *Mol Cell Proteomics*, 10(2):M110.002857, February 2011. [DOI | link | pdf]

[5] 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]

[6] Marcel Kronfeld, Hannes Planatscher, and Andreas Zell. The EvA2 optimization framework. In Christian Blum and Roberto Battiti, editors, *Learning and Intelligent Optimization Conference, Special Session on Software for Optimization (LION-SWOP)*, number 6073 in Lecture Notes in Computer Science, LNCS, pages 247--250, Venice, Italy, January 2010. Springer Verlag.

[7] 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]

[8] Andreas Dräger, Hannes Planatscher, Dieudonné Motsou Wouamba, Adrian Schröder, Michael Hucka, Lukas Endler, Martin Golebiewski, Wolfgang Müller, and Andreas Zell. SBML2L^{A}T$_{E}$X: Conversion of SBML files into human-readable reports. *Bioinformatics*, 25(11):1455--1456, April 2009. [DOI | link | pdf]

[9] 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]

[10] 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]

[11] 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]

[12] Felix Streichert, Hannes Planatscher, Christian Spieth, Holger Ulmer, and Andreas Zell. Comparing genetic programming and evolution strategies on inferring gene regulatory networks. In *Genetic and Evolutionary Computation (GECCO 2004)*, volume 3102 of *Lecture Notes in Computer Science*, pages 471--480, Seattle, USA, June 2004. Springer.

Address, Phone, Fax, Email

Eberhard-Karls-Universität Tübingen
Wilhelm-Schickard-Institut für Informatik
Lehrstuhl Rechnerarchitektur
Sand 1
D - 72076 Tübingen

Germany

Tel: (+49/0) 7071 / 29 78982
Fax: (+49/0) 7071 / 29 5091
Email: hannes at planatscher.net