

Dr. Johannes Eichner



Background

- 06/2002: Abitur at the Remstal-Gymnasium Weinstadt
- 10/2002 - 09/2003: Study of computer science (business informatics) at [University of Mannheim](#)
- 10/2003 - 04/2009: Study of computer science (bioinformatics) at [University of Tübingen](#)
- 12/2007 - 01/2009: Student assistant at the [Friedrich Miescher Laboratory](#) of the [Max Planck Society Tübingen](#)
- 06/2008: Diploma thesis on "Analysis of alternative transcripts in *A. thaliana* with whole-genome arrays" at the [Friedrich Miescher Laboratory](#) of the [Max Planck Society Tübingen](#)
- 11/2008 - 12/2008: Consultant at [BIOBASE GmbH](#), Wolfenbüttel
- Since 04/2009: Research assistant at the Department of Computer Architecture, University of Tübingen

Research Interests

- Systems biology
- Biomarker discovery
- Drug design
- Machine learning

Current Project

- Spher4Sys: Systems biology based approach for preclinical lead compound development using an in-vivo like spheroid test system
- MARCAR: Biomarkers and molecular tumor classification for non-genotoxic carcinogenesis
- SABINE: Support vector regression-based method for the prediction of transcription factor binding specificities
- RA Galaxy Webservices: A web-based framework for bioinformatics tools.

Publications

- [1] Michael Römer, Johannes Eichner, Andreas Dräger, Clemens Wrzodek, Finja Wrzodek, and Andreas Zell. ZBIT Bioinformatics Toolbox: a Web-Platform for Systems Biology and Expression Data Analysis. *PLoS ONE*, 11(2):e0149263, February 2016. [[DOI](#) | [link](#)]
- [2] Andreas Dräger, Daniel C. Zielinski, Roland Keller, Matthias Rall, Johannes Eichner, Bernhard O. Palsson, and Andreas Zell. SBMLsqueezer 2: Context-sensitive creation of kinetic equations in biochemical networks. *BMC Systems Biology*, 9(1):1--17, September 2015. [[DOI](#) | [link](#) | [pdf](#)]
- [3] Nicolas Rodriguez, Alex Thomas, Leandro Watanabe, Ibrahim Y. Vazirabad, Victor Kofia, Harold F. Gómez, Florian Mittag, Jakob Matthes, Jan D. Rudolph, Finja Wrzodek, Eugen Netz, Alexander Diamantikos, Johannes Eichner, Roland Keller, Clemens Wrzodek, Sebastian Fröhlich, Nathan E. Lewis, Chris J. Myers, Nicolas Le Novère, Bernhard Ø. Palsson, Michael Hucka, and Andreas Dräger. JSBML 1.0: providing a smorgasbord of options to encode systems biology models. *Bioinformatics*, June 2015. [[DOI](#) | [arXiv](#) | [link](#) | [pdf](#)]
- [4] Bettina Grasl-Kraupp, Teresa Riegler, Marzieh Nejabat, Jakob Paur, Johannes Eichner, Michael Römer, Andreas Zell, Rolf Schulte-Hermann, and Wolfgang Huber. Abstract 810: Non-genotoxic hepatocarcinogens induce growth and anti-apoptotic pathways in hepatocytes via mesenchymal cytokines. *Cancer Research*, 75(15 Supplement):810, April 2015. [[DOI](#) | [link](#)]
- [5] Michael Römer, Linus Backert, Johannes Eichner, and Andreas Zell. Toxdbscan: Large-scale similarity screening of toxicological databases for drug candidates. *International Journal of Molecular Sciences*, 15(10):19037--19055, October 2014. [[DOI](#) | [link](#)]

- [6] Johannes Eichner, Yvonne Heubach, Manuel Ruff, Hella Kohlhof, Stefan Strobl, Barbara Mayer, Michael Pawlak, Markus F. Templin, and Andreas Zell. RPPApipe: A pipeline for the analysis of reverse-phase protein array data. *BioSystems*, June 2014. [[DOI](#) | [link](#) | [pdf](#)]
- [7] Johannes Eichner, Lars Rosenbaum, Clemens Wrzodek, Hans-Ulrich Häring, Andreas Zell, and Rainer Lehmann. Integrated enrichment analysis and pathway-centered visualization of metabolomics, proteomics, transcriptomics, and genomics data by using the InCroMAP software. *Journal of Chromatography B*, May 2014. [[DOI](#) | [link](#)]
- [8] Johannes Eichner, Clemens Wrzodek, Michael Römer, Heidrun Ellinger-Ziegelbauer, and Andreas Zell. Evaluation of toxicogenomics approaches for assessing the risk of nongenotoxic carcinogenicity in rat liver. *PLoS ONE*, 9(5):e97678, May 2014. [[DOI](#) | [link](#)]
- [9] Michael Römer, Johannes Eichner, Ute Metzger, Markus F. Templin, Simon Plummer, Heidrun Ellinger-Ziegelbauer, and Andreas Zell. Cross-platform toxicogenomics for the prediction of non-genotoxic hepatocarcinogenesis in rat. *PLoS ONE*, 9(5):e97640, May 2014. [[DOI](#) | [link](#)]
- [10] Elif B. Unterberger, Johannes Eichner, Clemens Wrzodek, Harri Lempäinen, Raphaëlle Luisier, Rémi Terranova, Ute Metzger, Simon Plummer, Thomas Knorpp, Albert Braeuning, Jonathan Moggs, Markus Templin, Valerie Honndorf, Martial Piotto, Andreas Zell, and Michael Schwarz. Metabolic Programs Orchestrated by the Activated Ha-ras and β -Catenin Oncoproteins in Mouse Liver Tumors. *International Journal of Cancer*, March 2014. [[DOI](#) | [link](#)]
- [11] Johannes Eichner, Florian Topf, Andreas Dräger, Clemens Wrzodek, Dierk Wanke, and Andreas Zell. TFpredict and SABINE: Sequence-Based Prediction of Structural and Functional Characteristics of Transcription Factors. *PLoS ONE*, 8(12):e82238, December 2013. [[DOI](#) | [link](#) | [link](#)]
- [12] Johannes Eichner. *Inference of Alternative Splicing from Tiling Array Data*, volume 1067 of *Methods in Molecular Biology*, pages 143--164. Humana Press, October 2013. [[link](#)]
- [13] Johannes Eichner, Nadine Kossler, Clemens Wrzodek, Arno Kalkuhl, Dorte Bach Toft, Nina Ostefeldt, Virgile Richard, and Andreas Zell. A Toxicogenomic Approach for the Prediction of Murine Hepatocarcinogenesis Using Ensemble Feature Selection. *PLoS ONE*, 8(9):e73938, September 2013. [[DOI](#) | [link](#)]
- [14] Clemens Wrzodek, Johannes Eichner, Finja Büchel, and Andreas Zell. InCroMAP: Integrated analysis of Cross-platform MicroArray and Pathway data. *Bioinformatics*, 29(4):506--508, December 2012. [[DOI](#) | [arXiv](#) | [link](#) | [pdf](#)]
- [15] Clemens Wrzodek, Johannes Eichner, and Andreas Zell. Pathway-based visualization of cross-platform microarray datasets. *Bioinformatics*, 28(23):3021--3026, September 2012. [[DOI](#) | [arXiv](#) | [link](#) | [pdf](#)]
- [16] Finja Büchel, Clemens Wrzodek, Florian Mittag, Andreas Dräger, Johannes Eichner, Nicolas Rodriguez, Nicolas Le Novère, and Andreas Zell. Qualitative translation of relations from BioPAX to SBML qual. *Bioinformatics*, 28(20):2648--2653, August 2012. [[DOI](#) | [link](#) | [pdf](#)]
- [17] Clemens Wrzodek, Finja Büchel, Georg Hinselmann, Johannes Eichner, Florian Mittag, and Andreas Zell. Linking the epigenome to the genome: Correlation of different features to DNA methylation of CpG islands. *PLoS ONE*, 7(4):e35327, 04 2012. [[DOI](#) | [link](#)]
- [18] Johannes Eichner, Georg Zeller, Sascha Laubinger, and Gunnar Raetsch. Support vector machines-based identification of alternative splicing in *Arabidopsis thaliana* from whole-genome tiling arrays. *BMC Bioinformatics*, 12(1):55, February 2011. [[DOI](#) | [link](#)]
- [19] Adrian Schröder, Johannes Eichner, Jochen Supper, Jonas Eichner, Dierk Wanke, Carsten Henneges, and Andreas Zell. Predicting DNA-Binding Specificities of Eukaryotic Transcription Factors. *PLoS ONE*, 5(11):e13876, November 2010. [[DOI](#) | [link](#)]

Theses

Untersuchung regulatorischer Zusammenhänge aus Expressionsdaten

Johannes Eichner

University of Tübingen, Prof. Dr. Andreas Zell, July 2007

*Analysis of alternative transcripts in *A. thaliana* with whole-genome arrays*

Johannes Eichner

Friedrich Miescher Laboratory of the Max Planck Society Tübingen, Dr. Gunnar Rättsch,

and University of Tübingen, Dr. Kay Nieselt, June 2008



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