

# Dr. Adrian Schröder



## Background

- since 01/2007 research assistant at the Centre for Bioinformatics (ZBIT), University of Tübingen
- 10/2000-10/2006 Computer science student at the University of Tübingen
- 01/2005-10/2006 assistant at Synovo GmbH

## Research Interests

- Data mining and modelling in systems biology
- New approaches to pharmacogenomics and systems genetics
- Machine learning based methods for transcription factor binding site prediction and cis-regulatory module detection
- Data and knowledge based inference of gene regulatory mechanisms
- Dynamic modeling of complex biochemical systems

## Current Projects

- Virtual Liver: Subproject A3.4: Linking signaling to metabolic functions; subproject B5: Impact of cytokines on detoxifying functions in primary human hepatocytes
- Genomics of ADME gene expression: Mapping quantitative trait loci relevant for absorption, distribution, metabolism and excretion of drugs
- MARCAR: bioMARKers and molecular tumor classification for non-genotoxic CARcinogenesis
- Spher4Sys: Systems biology based approach for preclinical lead compound development using an in-vivo like spheroid test system
- [HepatoSys](#): A systems biology approach to decipher statin-induced gene regulatory mechanisms in primary human hepatocytes

## Publications

- [1] Adrian Schröder. *Inference of gene-regulatory networks in primary human hepatocytes*. PhD thesis, University of Tuebingen, Tübingen, Germany, November 2011. [ [link](#) ]
- [2] Adrian Schröder, Kathrin Klein, Stefan Winter, Matthias Schwab, Michael Bonin, Andreas Zell, and Ulrich M. Zanger. Genomics of ADME gene expression: mapping expression quantitative trait loci relevant for absorption, distribution, metabolism and excretion of drugs in human liver. *The Pharmacogenomics Journal*, pages 1473--1150, September 2011. [ [DOI](#) | [link](#) | [pdf](#) ]
- [3] Finja Büchel, Clemens Wrzodek, Florian Mittag, Andreas Dräger, Adrian Schröder, and Andreas Zell. ProDGe: investigating protein-protein interactions at the domain level. Technical report, Nature Precedings, August 2011. [ [DOI](#) | [link](#) | [pdf](#) ]
- [4] Adrian Schröder, Johannes Wollnik, Clemens Wrzodek, Andreas Dräger, Michael Bonin, Oliver Burk, Maria Thomas, Wolfgang E. Thasler, Ulrich M. Zanger, and Andreas Zell. Inferring statin-induced gene regulatory relationships in primary human hepatocytes. *Bioinformatics*, 27(18):2473--2477, July 2011. [ [DOI](#) | [link](#) | [pdf](#) ]
- [5] Adrian Schröder, Clemens Wrzodek, Johannes Wollnik, Andreas Dräger, Dierk Wanke, Kenneth W. Berendzen, and Andreas Zell. Inferring transcriptional regulators for sets of co-expressed genes by multi-objective evolutionary optimization. In *IEEE Congress on Evolutionary Computation (CEC 2011)*, New Orleans, USA, June 2011. IEEE. [ [DOI](#) | [link](#) ]

- [6] 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](#) ]
- [7] Andreas Dräger, Adrian Schröder, and Andreas Zell. *Systems Biology for Signaling Networks*, volume 1 of *Systems Biology*, chapter Automating mathematical modeling of biochemical reaction networks, pages 159--205. Springer-Verlag, July 2010. [ [DOI](#) | [link](#) ]
- [8] Clemens Wrzodek, Adrian Schröder, Andreas Dräger, Dierk Wanke, Kenneth W. Berendzen, Marcel Kronfeld, Klaus Harter, and Andreas Zell. ModuleMaster: A new tool to decipher transcriptional regulatory networks. *Biosystems*, 99(1):79--81, January 2010. [ [DOI](#) | [link](#) ]
- [9] 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](#) ]
- [10] Andreas Dräger, Hannes Planatscher, Dieudonné Motsou Wouamba, Adrian Schröder, Michael Hucka, Lukas Ender, Martin Golebiewski, Wolfgang Müller, and Andreas Zell. SBML2L<sup>A</sup>T<sub>E</sub>X: Conversion of SBML files into human-readable reports. *Bioinformatics*, 25(11):1455--1456, April 2009. [ [DOI](#) | [link](#) | [pdf](#) ]
- [11] 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](#) ]

## Theses

- [1] Adrian Schröder. *Inference of gene-regulatory networks in primary human hepatocytes*. PhD thesis, University of Tuebingen, Tübingen, Germany, November 2011.
- [2] *Integration of CH - PI Interactions into a grid based genetic docking algorithm*. Studienarbeit, University of Tübingen, 2005
- [3] *Construction of a Dynamic Model of the T-Cell Signal Transduction*. Master thesis, University of Tübingen, 2006

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