Dr. Alexander Dörr

Background

- Since Mai 2012: Research assistant at the Center for Bioinformatics (ZBIT), Department of Cognitive Systems, University of Tübingen
- 2009 - 2012: Master of Science in Bioinformatics at the University of Tübingen
- 2006 - 2009: Bachelor of Science in Bioinformatics at the University of Tübingen

Research Interests

- Systems Biology
- Machine Learning in Cheminformatics

Current Projects

Publications

[1] Alexander Dörr, Sebastian Otte, and Andreas Zell. Investigating Recurrent Neural Networks for Feature-less Computational Drug Design. In *International Conference on Artificial Neural Networks (ICANN)*, Barcelona, Spain, September 2016. (accepted for publication).

[2] Tamer M. Ibrahim, Matthias R. Bauer, Alexander Dörr, Erdem Veyisoglu, and Frank M. Boeckler. proc-chemotype plots enhance the interpretability of benchmarking results in structure-based virtual screening. *Journal of Chemical Information and Modeling*, October 2015. [DOI | link]

[3] Alexander Dörr, Lars Rosenbaum, and Andreas Zell. A ranking method for the concurrent learning of compounds with various activity profiles. *J. Cheminf.*, 7(1), January 2015.

[4] Alexander Dörr, Roland Keller, Andreas Zell, and Andreas Dräger. SBMLsimulator: a Java tool for model simulation and parameter estimation in systems biology. *Computation*, 2(4):246--257, December 2014. [DOI | link | link]

[5] 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]

[6] Lars Rosenbaum, Alexander Dörr, Matthias R. Bauer, Frank M. Boeckler, and Andreas Zell. Inferring multi-target QSAR models with taxonomy-based multi-task learning. *J. Cheminf.*, 5:33, 2013.

[7] Lars Rosenbaum, Andreas Jahn, Alexander Dörr, and Andreas Zell. Optimization and visualization of the edge weights in optimal assignment methods for virtual screening. *BioData Mining*, 6:7, 2013.

[8] Andreas Dräger, Nicolas Rodriguez, Marine Dumousseau, Alexander Dörr, Clemens Wrzodek, Nicolas Le Novère, Andreas Zell, and Michael Hucka. JSBML: a flexible Java library for working with SBML. *Bioinformatics*, 27(15):2167--2168, June 2011. [DOI | link | pdf]

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