

Dr. Florian Mittag



Background

- 04/2003 - 12/2008: Study of computer science at [TU Kaiserslautern](#) (Kaiserslautern, Germany)
- 05/2008 - 12/2008: Diploma thesis on "Performant Trust and Similarity Metrics for Inconsistent Knowledge-bases" ([Knowledge-based Systems Group](#), [TU Kaiserslautern/DFKI](#))
- Since 05/2009: Research assistant at the Department of Computer Architecture, University of Tübingen

Research Interests

- Metabolic and gene-regulatory networks
- Machine Learning
- Semantic Web
- Autonomous agents

Current Project

- German National Genome Research Network (NGFN-Plus): medical genome research with focus on Parkinson's disease

Publications

- [1] Florian Mittag, Michael Römer, and Andreas Zell. Influence of Feature Encoding and Choice of Classifier on Disease Risk Prediction in Genome-Wide Association Studies. *PLoS ONE*, 10(8):e0135832, August 2015. [[DOI](#) | [link](#)]
- [2] 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](#)]
- [3] Finja Büchel, Nicolas Rodriguez, Neil Swainston, Clemens Wrzodek, Tobias Czauderna, Roland Keller, Florian Mittag, Michael Schubert, Mihai Glont, Martin Golebiewski, Martijn van Iersel, Sarah M. Keating, Matthias Rall, Michael Wybrow, Henning Hermjakob, Michael Hucka, Douglas B Kell, Wolfgang Müller, Pedro Mendes, Andreas Zell, Claudine Chaouiya, Julio Saez-Rodriguez, Falk Schreiber, Camille Laibe, Andreas Dräger, and Nicolas Le Novère. Path2Models: large-scale generation of computational models from biochemical pathway maps. *BMC Systems Biology*, 7(1):116, November 2013. [[DOI](#) | [link](#) | [pdf](#)]
- [4] Finja Büchel, Florian Mittag, Clemens Wrzodek, Andreas Zell, Thomas Gasser, and Manu Sharma. Integrative pathway-based approach for genome-wide association studies: identification of new pathways for rheumatoid arthritis and type 1 diabetes. *PLoS ONE*, 8(10), September 2013. [[DOI](#) | [link](#)]
- [5] Peter Holmans, Valentina Moskvina, Lesley Jones, Manu Sharma, The International Parkinson's Disease Genomics Consortium (IPDGC), Alexey Vedernikov, Finja Büchel, Mohamad Sadd, Jose M. Bras, Francesco Bettella, Nayia Nicolaou, Javier Simón-Sánchez, Florian Mittag, J. Raphael Gibbs, Claudia Schulte, Alexandra Durr, Rita Guerreiro, Dena Hernandez, Alexis Brice, Hreinn Stefánsson, Kari Majamaa, Thomas Gasser, Peter Heutink, Nicholas W. Wood, Maria Martinez, Andrew B. Singleton, Michael A. Nalls, John Hardy, Huw R. Morris, and Nigel M. Williams. A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. *Human Molecular Genetics*, December 2012. [[DOI](#) | [link](#) | [pdf](#)]

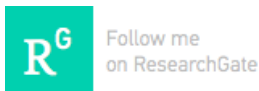
- [6] Finja Büchel, Clemens Wrzodek, Florian Mittag, Andreas Dräger, Johannes Eichner, Nicolas Rodriguez, Nicolas Le Novère, and Andreas Zell. Qualitative translation of relations from BioPAX to SBML qual. *Bioinformatics*, 28(20):2648--2653, August 2012. [[DOI](#) | [link](#) | [pdf](#)]
- [7] Florian Mittag, Finja Büchel, Mohamad Saad, Andreas Jahn, Claudia Schulte, Zoltan Bochdanovits, Javier Simón-Sánchez, Mike A Nalls, Margaux Keller, Dena Hernandez, Raphael Gibbs, Suzanne Lesage, Alexis Brice, Peter Heutink, Maria Martinez, Nicholas W Wood, John Hardy, Andrew B. Singleton, Andreas Zell, Thomas Gasser, and Manu Sharma. Use of Support Vector Machines for Disease Risk Prediction in Genome-Wide Association Studies: Concerns and Opportunities. *Human Mutation*, 33(12):1708--1718, June 2012. [[DOI](#) | [link](#)]
- [8] Margaux F. Keller, Mohamad Saad, Jose M. Bras, Francesco Bettella, Nayia Nicolaou, Javier Simón-Sánchez, Florian Mittag, Finja Büchel, Manu Sharma, J. Raphael Gibbs, Claudia Schulte, Valentina Moskvina, Alexandra Durr, Peter Holmans, Laura L. Kilarski, Rita Guerreiro, Dena Hernandez, Alexis Brice, Pauli Ylikotila, Hreinn Stefánsson, Kari Majamaa, Huw R. Morris, Nigel Williams, Thomas Gasser, Peter Heutink, Nick Wood, John Hardy, Maria Martinez, Andrew B. Singleton, and Michael A. Nalls. Using genome-wide complex trait analysis 1 to quantify 'missing heritability' in parkinson's disease. *Human Molecular Genetics*, 21(22):4996--5009, 2012. [[DOI](#) | [link](#) | [pdf](#)]
- [9] 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](#)]
- [10] 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](#)]
- [11] Georg Buscher, Andreas Dengel, Ludger van Elst, and Florian Mittag. Generating and using gaze-based document annotations. In *Proceedings and Extended Abstracts of the Conference on Human Factors in Computing Systems*, pages 3045--3050. ACM, 2008.
- [12] Thomas Roth-Berghofer and Florian Mittag. ReduxExp: A justification-based explanation-support server. In Miltos Petridis, Frans Coenen, and Max Bramer, editors, *Research and Development in Intelligent Systems XXV. Twenty-eighth SGAI International Conference on Artificial Intelligence (AI-2008), November 9-11, Cambridge, United Kingdom*. Springer Verlag, London, UK, 2008.

Diploma Thesis

Performant Trust and Similarity Metrics for Inconsistent Knowledge-bases

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