

Dr. Finja Wrzodek (former Büchel)



Background

- November 2008 - August 2013: Research assistant at the Centre of Bioinformatics (ZBIT), University of Tübingen
- October 2011 - December 2011: Software developer in the [Computational Systems Neurobiology Group](#) from [Nicolas Le Novère](#) at the EMBL - European Bioinformatics Institute (EBI), Wellcome Trust Genome Campus in Hinxton, United Kingdom
- April 2008 - October 2008: Bioinformatics student assistant at the department of Computer Architecture at the University of Tübingen
- October 2003 - October 2008: Computer science student at the University of Tübingen
- September 1994 - July 2003: [Gymnasium Hemsbach](#)

Research Interests

My research focuses on understanding and modeling of disturbed cellular processes in neurodegenerative diseases, especially in Parkinson's disease. I am particularly interested in:

- Systems biology, investigation and modelling of metabolic, signaling and gene regulatory networks
- Meta-analysis of genome-wide association studies (GWAS)
- Prediction of protein-protein interactions
- Visualization and conversion of biochemical networks

Current Project

The following project is funded by the Federal Ministry of Education and Research (*Bundesministerium für Bildung und Forschung*, [BMBF](#), Germany):

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

Software products

Main projects:

- BioPAX2SBML: Translation of BioPAX into SBML including the Qualitative Models extension.
- GWAS Pathway Identifier: Combining genome-wide association study SNP data, pathway, known and predicted protein-interaction data to identify disease specific pathways.
- ProDGe: Investigating protein-protein interactions at the domain level.

Contributions:

- KEGGtranslator: Visualizing and converting the KEGG PATHWAY database to various formats.
- InCroMAP: [Integrated](#) analysis of [Cross-platform](#) [MicroArray](#) and [Pathway](#) data.
- MACLEAPS: Machine Learning Analysis Pipeline for Genome-Wide Association Study SNP data.
- [JSBML](#): A flexible Java library for working with SBML.
- CpG island feature generator: Generating features to distinct between methylated and unmethylated CpG islands

Awards and honors

- 2011: [Baden-Württemberg-Zertifikat für Hochschuldidaktik](#) (Certificate for special skills in university teaching didactics).
- 2003: Award for outstanding marks in science (math, biology, computer science, micro controllers) by Gymnasium Hemsbach (Secondary school).

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] 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] Claudine Chaouiya, Duncan Bérenguier, Sarah M. Keating, Aurélien Naldi, Martijn P. van Iersel, Nicolas Rodriguez, Andreas Dräger, Finja Büchel, Thomas Cokelaer, Bryan Kowal, Benjamin Wicks, Emanuel Gonçalves, Julien Dorier, Michel Page, Pedro T. Monteiro, Axel von Kamp, Ioannis Xenarios, Hidde de Jong, Michael Hucka, Steffen Klamt, Dennis Thierffry, Nicolas Le Novère, Julio Saez-Rodriguez, and Tomáš Helikar. SBML Qualitative Models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. *BMC Systems Biology*, 7(1):135, December 2013. [[DOI](#) | [arXiv](#) | [link](#) | [pdf](#)]
- [4] 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](#)]
- [5] Finja Büchel, Sandra Saliger, Andreas Dräger, Stephanie Hoffmann, Clemens Wrzodek, Andreas Zell, and Philipp J. Kahle. Parkinson's disease: dopaminergic nerve cell model is consistent with experimental finding of increased extracellular transport of α -synuclein. *BMC Neuroscience*, 14(136), November 2013. [[DOI](#) | [link](#) | [pdf](#)]
- [6] 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](#)]
- [7] Suzana Gispert, Dajana Parganlija, Michael Klinkenberg, Stefan Dröse, Ilka Wittig, Michel Mittelbronn, Pawel Grzmil, Sebastian Koob, Andrea Hamann, Michael Walter, Finja Büchel, Thure Adler, Martin Hrabé de Angelis, Dirk H. Busch, Andreas Zell, Andreas S. Reichert, Ulrich Brandt, Heinz D. Osiewacz, Marina Jendrach, and Georg Auburger. Loss of mitochondrial peptidase clpp leads to infertility, hearing loss plus growth retardation via accumulation of CLPX, mtDNA, and inflammatory factors. *Human Molecular Genetics*, July 2013. [[DOI](#) | [arXiv](#) | [link](#)]
- [8] Clemens Wrzodek, Finja Büchel, Manuel Ruff, Andreas Dräger, and Andreas Zell. Precise generation of systems biology models from KEGG pathways. *BMC Systems Biology*, 7(1):15, January 2013. [[DOI](#) | [link](#) | [pdf](#)]
- [9] 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](#)]
- [10] 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](#)]
- [11] 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](#)]
- [12] 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](#)]
- [13] 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](#)]
- [14] 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](#)]
- [15] 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](#)]

Theses

Hardwaremodellierung einer Handprothese mit System C
Studienarbeit, University of Tübingen, 2008

Visualisierung von Domäne-Domäne-Interaktionsnetzwerken
Diplomarbeit, University of Tübingen, 2008

Posters

ProDGe: a Sequence and Protein Interaction Viewer
Finja Büchel, Gabrielle Doan, Andreas Dräger, Adrian Schröder and Andreas Zell
1st Annual Meeting of the Program of Medical Genome Research 2008, München, Germany

Press

Interviewed for SWR2 Dschungel: "[Dem Rausch auf den Grund gehen](#)" - Alexander Deeg, Jan Krassowski und Phillip Frost, Machete 18.6.2009

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