

Dr. Max Flöttmann

Curriculum Vitæ

Berlin
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Professional Experience

- since 06.2013 **Post Doc**, *Humboldt-Universität zu Berlin*.
Modeling of the host-pathogen-interaction during influenza A infection
- 2012–2013 **Founder**, *Webpgr Project*.
Co-founder of a web technology startup (<http://www.webpgr.com>)
- 2011–2012 **IT-Consultant**, *Diehl und Brüser Handelskonzepte GmbH*, Düsseldorf.
Technical consulting in the creation of an innovative retail solution (www.emmas-enkel.de)
- 2011 **Mentor**, *Google Summer of Code*, Berlin/San Francisco, CA.
Mentor in the project Biographer (<http://code.google.com/p/biographer>)
- 05.2009–06.2013 **Graduate student**, *Humboldt-Universität zu Berlin*.
Theoretical Biophysics
- 06–07.2007 **Scientific Exchange**, *Virginia Bioinformatics Institute, Virginia Tech*, Blacksburg, VA, USA.
- 2007–2008 **Working Student**, *Kinetic Modeling Group, Max-Planck-Institute for Molecular Genetics*, Berlin.
Software Development, Modeling
- 2005–2007 **Working Student**, *Institute for Biometrics, Charité*, Berlin.
Creation of a web-based e-learning platform
- 2005 **Practical**, *Institute for Biometrics, Charité*, Berlin.
Statistical analysis of clinical trials.
- 2002–2003 **Community service**, *Children's home Sankt Mauritz*, Münster.
- 1997–2000 **Web designer**, *Dino-Graphics/Netcentric*, Arnsberg.
Web design for local businesses

Education

- 06.2013 **Dr. rer. nat.**, *Humboldt-Universität zu Berlin*.
Theoretical Biophysics
- 10.2006–08.2008 **M.Sc.**, *Freie Universität*, Berlin.
Master course in Bioinformatics specializing in mathematical modeling and scientific visualization.
- 10.2003–06.2006 **B.Sc.**, *Freie Universität*, Berlin.
Bachelor Bioinformatics

Dissertation

- Title Functional Analysis of High-Throughput Data for Dynamic Modeling in Eukaryotic Systems.
- Adviser Prof. Dr. Dr. h.c. Edda Klipp

Teaching Experience

- 2010–2014 **Python for natural sciences**, *Humboldt-Universität zu Berlin*.
Organizer and teacher of a two weeks course on Python, Linux, bioinformatic web services, matplotlib, etc. (for bachelor and master students)
- 2013 **ODE modeling in Matlab**, *Humboldt-Universität zu Berlin*.
A one week course on dynamic pathway modeling in Matlab.
- 2011 **Statistics using R**, *Humboldt-Universität zu Berlin*.
Course for Phd. students on micro-array analysis
- 2010 **Electrodynamics**, *Humboldt-Universität zu Berlin*.
Tutor in the bachelor's course in Biophysics

Honours and Awards

- 2013 **Dissertation**, *Humboldt-Universität zu Berlin*.
My dissertation was honoured with highest praise (summa cum laude).
- 2010 **Travel Grant**, *German Cancer Research Center*.
This grant allowed me to visit the conference "Systems Biology of Human Disease" in Boston.

IT Skills

- Programming Python, JavaScript, C, C++, Java
- Modeling COPASI, Matlab, R, Scipy, Cain, STEPS
- Data Analysis Bioconductor, Biopython, Pandas, dplyr
- Network Analysis NetworkX, Cytoscape, Pajek
- Visualization ggplot2, D3.js, POV-Ray, Adobe CS
- Operating Systems Linux, Apple OS X, Microsoft Windows
- Productivity Latex, version control systems (Git, Mercurial, Subversion)

Publications

Peer Reviewed Journals

- [1] **Max Flöttmann**, Jörg Schaber, Stephan Hoops, Edda Klipp, and Pedro Mendes. ModelMage: A Tool for Automatic Model Generation, Selection and Management. In *Genome Informatics*, pages 52–63, 2008.
- [2] Nancy Mah, Ying Wang, Mei-Chih Liao, Alessandro Prigione, Justyna Jozefczuk, Björn Lichtner, Katharina Wolfrum, Manuela Haltmeier, **Max Flöttmann**, Martin Schaefer, Alexander Hahn, Ralf Mrowka, Edda Klipp, Miguel a Andrade-Navarro, and James Adjaye. Molecular Insights into Reprogramming-Initiation Events Mediated by the OSKM Gene Regulatory Network. *PLoS ONE*, 6(8):e24351, January 2011.
- [3] Jörg Schaber, **Max Flöttmann**, Jian Li, Carl-Fredrik Tiger, Stefan Hohmann, and Edda Klipp. Automated Ensemble Modeling with modelMaGe: Analyzing Feedback Mechanisms in the Sho1 Branch of the HOG Pathway. *PLoS ONE*, 6(3):e14791, March 2011.
- [4] Christian Waltermann, **Max Flöttmann**, and Edda Klipp. G1 and G2 Arrests in Response to Osmotic Shock are Robust Properties of the Budding Yeast Cell Cycle. In *Genome Informatics*, pages 204–217, 2011.
- [5] **Max Flöttmann**, Till Scharp, and Edda Klipp. A stochastic model of epigenetic dynamics in somatic cell reprogramming. *Frontiers in physiology*, 3(June):216, January 2012.
- [6] Falko Krause, Marvin Schulz, Ben Ripkens, **Max Flöttmann**, Marcus Krantz, Edda Klipp, and Thomas Handorf. Biographer: web-based editing and rendering of SBGN compliant biochemical networks. *Bioinformatics (Oxford, England)*, 29(11):1467–8, June 2013.
- [7] **Max Flöttmann**, Falko Krause, Edda Klipp, and Marcus Krantz. Reaction-contingency based bipartite Boolean modelling. *BMC systems biology*, 7:58, January 2013.
- [8] **Max Flöttmann**, Susann Kummer, Björn Schwanhäusser, Michael Veit, Matthias Selbach, Edda Klipp, and Andreas Herrmann. Alteration of protein levels during influenza virus h1n1 infection in host cells: A proteomic survey of host and virus reveals differential dynamics. *PLoS One*, 2014.
- [9] **Max Flöttmann**, Jannis Uhlendorf, Till Scharp, Edda Klipp, and Thomas W Spiesser. SensA: web-based sensitivity analysis of SBML models. *Bioinformatics (Oxford, England)*, June 2014.

Others

- [10] **Max Floettmann**, Till Scharp, and Edda Klipp. Computational Modeling of Biochemical Processes and Cell Differentiation. In *STEM CELLS From Mechanisms to Technologies*, pages 3–31. 2011.

- [11] **Max Floettmann**, Till Scharp, Ying Wang, Katharina Drews, Xinlai Cheng, Stefan Wölfl, Alexander Hahn, Sheraz Gul, Nancy Mah, Miguel Andrade-Navarro, Edda Klipp, Gunter Wolf, James Adjaye, and Ralf Mrowka. Wie aus Hautzellen Leberzellen werden. *systembiologie.de*, (04):1–108, 2012.