

Dr. Fabian Fröhlich

Private Address:

Karlsruher Strasse 54
69126 Heidelberg
Mobile: +49 167 45296749

Professional Address :

Institute for Computational Biomedicine
Im Neuenheimer Feld 130.3
69120 Heidelberg
E-mail: fabian_froehlich@hms.harvard.edu



Education & Research Activity

web	Visiting Fellow at University Hospital Heidelberg, Heidelberg, DE Research Group: Systems Biomedicine, Institute for Computational Biomedicine Focus: Structure based modeling, data-driven models of heterogeneity, automated model formulation PI: Julio Saez-Rodriguez, PhD	since 2022
web	Postdoctoral Fellow at Harvard Medical School, Boston, MA, USA Research Group: Laboratory of Systems Pharmacology, Harvard Institute for Therapeutic Science Focus: Adaptive resistance in melanoma, model interpretability, protein-structure based modeling PI: Peter Sorger, PhD	since 2018
web	PhD Candidate at the Helmholtz Zentrum München, Munich, Germany Research Group: Data-Driven Computational Modeling, Institute for Computational Biology Focus: Scalable simulation and estimation for ODE models, efficient description of cell-to-cell variability Thesis: Scalable Methods for Parameter Estimation in Systems Biology (Defense Date: 29.03.2018) Degree Granting Institution: Technische Universität München PI: Prof. Dr. Jan Hasenauer	2013-2018
web	Graduate School Quantitative Biosciences Munich (QBM), Munich, Germany Course Work: Monthly lecture series and journal clubs with external speakers, monthly life sciences primer Workshops: Scientific Writing, Grant Writing, Presentation Skills, Poster Design	2013-2018
web	Master of Science at the Technische Universität München, Munich, Germany Principal Subject: Mathematics in Bioscience Focus: Parameter inference, biophysics, numerical methods Thesis: Approximation and Analysis of Probability Densities using Radial Basis Functions Thesis Advisor: Prof. Dr. Jan Hasenauer	2011-2013
web	Bachelor of Science at the Technische Universität München, Munich, Germany Principal Subject: Mathematics Secondary Subject: Physics Focus: Mathematical modeling, image processing, dynamical systems Thesis: Modelling and Analysis of DDEs for Hysteresis in Bacterial Quorum Sensing Thesis Advisor: Prof. Dr. Christina Kuttler	2008-2011

Awards & Fellowships

web	MTZ®-Award for Medical Systems Biology 2020 (PhD Thesis)	2020
web	3-year Long-Term Fellowship from the Human Frontier Science Program (HFSP)	2019-present
	3-year PhD fellowship from the German Research Foundation (DFG)	2013-2016
web	International Genetically Engineered Machine Competition (iGEM) Best Wiki (overgraduate division, worldwide)	2014
web	International Genetically Engineered Machine Competition (iGEM) 1st Runner Up (undergraduate, Europe ; second best of 27 international teams) 1st Runner Up (undergraduate, worldwide ; second best of 112 international teams) Best Environment Project (undergraduate, Europe + worldwide), Best Wiki (undergraduate, Europe)	2013

Teaching & Mentoring Experience

	Mentor of Graduate Student during Summer Internship Student: Javiera Cortes	2022
web	Dana-Farber/Harvard Cancer Center – Harvard Medical School Mentor Training Courses: Assessing, Understanding and Maintaining Effective Communication; Designing Short Term Research Projects; Equity, Inclusion and Navigating Research Culture	2019
	Mentor of PhD Candidate Student: Paul Stapor	2016-2018
web	Foundation Level Certificate of Teaching in Higher Education (60 hours) Courses: Designing and Conducting Examinations, Fostering Students Self-Directed Learning, Principles of Professional Teaching in Higher Education, Presentation Techniques, Role as Lecturer	2014-2018
	Teaching Assistant at the Technische Universität München Lectures: Statistical Inference for Dynamical Systems, Parameter Estimation for Dynamic Biological Systems I, Parameter Estimation for Dynamic Biological Systems II Responsibility: Lectures (substitute) and tutorials, conception and grading of exercises and examinations	2015-2017

Presentations (invited, oral)

13	Maximum likelihood estimation and profile likelihoods Workshop on Statistical Inference for Dynamical Systems, Berlin, DE	2022
12	Mechanistic Models for Data-Driven Drug Sensitivity Prediction Francis Crick Institute, London, UK	2022
11	A Mechanistic Model of MAPK Signaling Reveals how Allostery and Rewiring Contribute to Drug Resistance Pfizer Systems Modeling & Simulation Network Webinar, Virtual (US)	2022
10	Dynamic Models for Data-Driven Drug Sensitivity Prediction Department of Protein Science, KTH Royal Institute of Technology, Virtual (SE)	2022
9	Kinetic Models for Data-Driven Drug Sensitivity Prediction Faculty of Science, Stockholm University, Virtual (SE)	2022
8	Mechanistic Models for Individualized Prediction of Resistance to Targeted Anti-Cancer Drugs VIB Cancer Biology Lecture Series, VIB-KU Leuven Center for Cancer Biology, BE	2021
7	Mechanistic Models for Personalized Drug Sensitivity Prediction LySiM status seminar (MTZAward Ceremony), Virtual (DE)	2021
6	Causal Deconvolution of a Mechanistic Model of EGFR and ERK Signaling explains Adaptive and Genetic Resistance in Melanoma Novartis Institutes for Biomedical Research, Virtual (US)	2020
5	In search of insight: Understanding large mechanistic models Timmer Group, University of Freiburg, DE	2019
4	In search of insight: Understanding large kinetic models BioQuant, Heidelberg, DE	2019
3	Unraveling Complexity in Large Kinetic Models Department of Computational and Systems Biology, University of Pittsburgh, US	2019
2	Efficient Parameterization of Large-Scale Mechanistic Models Enables Drug Response Prediction for Cancer Cell Lines Instituto de Investigaciones Mariñas, Consejo Superior de Investigaciones Científicas, ES	2017
1	Accounting for Variability in Cell Populations BioQuant, Heidelberg, DE	2015

Presentations (contributed, oral)

21	A Mechanistic model of EGFR and ERK signaling reveals how allostery and rewiring contribute to drug resistance ICSB 2022, Berlin, DE	2022
20	A Mechanistic Model of EGFR and ERK Signaling Reveals how Allostery and Rewiring Contribute to RAF and MEK Inhibitor Resistance ECMTB 2022, Heidelberg, DE	2022
19	Scalable Calibration of Large Cancer Related Signaling Pathway Models in HPC Environments ECCB 2022, Simulating Cellular Behaviours Workshop, Virtual	2022
18	Fides: Reliable Trust-Region Optimization for Parameter Estimation of Ordinary Differential Equation Models COMBINE 2021, Virtual	2021
17	Causal Deconvolution of a Thermodynamic Model of MAPK Signaling explains Adaptive and Genetic Resistance to Targeted Drugs in BRAF-mutant Cancers INCOME2021 Conference and Hackathon, Virtual	2021
16	Causal Deconvolution of a Mechanistic Model of EGFR and ERK Signaling Explains Adaptive and Genetic Resistance in Melanoma Computational Approaches for Cancer Workshop, Virtual	2020
15	A thermodynamic Model of EGFR and ERK Signaling explains Adaptive and Genetic Resistance in Melanoma COMBINE 2020, Virtual	2020
14	Making Sense of Large Kinetic Models Intelligent Systems for Molecular Biology (ISMB), Basel, CH	2019
13	Simulation and Sensitivity Analysis for Large Kinetic Models in AMICI COMBINE 2019, Heidelberg, DE	2019
12	Hierarchical Modularization of Rule-Based Modeling Enables Construction of Complex Mechanistic Models CSHL Meeting: Cellular Dynamics & Models, Cold Spring Harbor, US	2019

11	Large-Scale Mechanistic Modeling Enables Robust Prediction of Cancer Cell Drug Response Intelligent Systems for Molecular Biology (ISMB), Prague, CZ	2017
10	Large-Scale Mechanistic Modeling Enables Robust Prediction of Cancer Cell Drug Response Interdisciplinary Signalling Workshop (ISW), Visegrad, HU	2017
9	Large-scale Modeling of Cancer Signaling: Mechanistic Modeling Meets Big Data 2016 International Conference on Systems Biology (ICSB), Barcelona, ES	2016
8	AMICI: An ODE Simulation Framework for Sensitivity Analysis of Large-scale Models COMBINE 2016, Newcastle, UK	2016
7	Think Adjoint – Methods Facilitating Parameter Estimation for Genome-scale Mechanistic Dynamic Models 6th Conference on Systems Biology of Mammalian Cells (SBMC), Munich, DE	2016
6	Parameter Estimation for Genome-Scale Mechanistic Models Workshop e:Med PG "Informatics & Modelling", Heidelberg, DE	2015
5	Parameter Estimation for Heterogeneous Populations Numerical Methods for Optimal Control and Inverse Problems (OCIP 2015), Munich, DE	2015
4	Parameter Estimation for the System Size Expansion 9th European Conference on Mathematical and Theoretical Biology (ECMTB), Gothenburg, SE	2014
3	Radial Basis Function Approximation of Bayesian Parameter Posterior Densities for Uncertainty Analysis 12th Conference on Computational Methods in Systems Biology (CMSB), Manchester, UK	2014
2	Uncertainty Analysis for Non-Identifiable Dynamical Systems: Profile Likelihoods, Bootstrapping and More 12th Conference on Computational Methods in Systems Biology (CMSB), Manchester, UK	2014
1	Uncertainty Analysis for Dynamical Systems using Radial Basis Functions Numerical Methods for Optimal Control and Inverse Problems (OCIP 2014), Munich, DE	2014

Publications

25	Fröhlich, F.* ; Gerosa, L.*; Muhlich, J.; Sorger, P. K.; Mechanistic model of MAPK signaling reveals how drug resistance arises from allostery and rewiring. <i>bioRxiv</i>	2022
24	Fröhlich, F.# ; Sorger, P.K.#; Fides: Reliable optimization for parameter estimation of ordinary differential equation models. <i>Accepted for publication in PLoS Comp. Bio.</i>	.
23	Shaikh, B.; Smith, L.P.; Vasilescu, D.; Marupilla, G.; Wilson, M.; Agmon, E.; Agnew, H.; Andrews, S.S.; Anwar, A.; Beber, M.E.; Bergmann, F.T.; Brooks, D.; Brusch, L.; Calzone, L.; Choi, K.; Cooper, J.; Detloff, J.; Drawert, B.; Dumontier, M.; Ermentrout, M.G.; Faeder, J.R.; Freiburger, A.P.; Fröhlich, F. ; Funahashi, A.; Garny, A.; Gennari, J.H.; Gleeson, P.; Goelzer, A.; Haiman, Z.; Hellerstein, J.L.; Hoops, S.; Ison, J.C.; Jahn, D.; Jakubowski, H.V.; Jordan, R.; Kalaš, M.; König, M.; Liebermeister, W.; Mandal, S.; McDougal, R.; J Medley, K.; Mendes, P.; Müller, R.; Myers, C.J.; Naldi, A.; Nguyen, T.V.; Nickerson, D.P.; Olivier, B.G.; Patoliya, D.; Paulevé, L.; Petzold, L.R.; Priya, A.; Rampadarath, A.K.; Rohwer, J.M.; Saglam, A.S.; Singh, D.; Sinha, A.; Snoep, J.; Sorby, H.; Spangler, R.; Starruß, J.; Thomas, P.J.; David Niekerk, V.; Weindl, D.; Zhang, F.; Zhukova, A.; Goldberg, A.P.; Blinov, M.L.; Sauro, H.M.; Moraru, I.I.; Karr, J.R.; BioSimulators: a central registry of simulation engines and services for recommending specific tools. <i>Nucleic Acids Research</i> 50(1): W108-W114	2022
22	Villaverde, A.F.; Pathirana, D.; Fröhlich, F. ; Hasenauer, J.; Banga J.R.; A protocol for dynamic model calibration. <i>Brief. Bioinformatics</i> 23(1), 1-19	2022
21	Schmucker, R.; Farina, G.; Faeder, J.; Fröhlich, F. ; Saglam, A.S.; Sandholm, T.; Combination treatment optimization using a pan-cancer pathway model. <i>PLoS Comp. Bio.</i> 17(12): e1009689	2021
20	Fröhlich, F.# ; Weindl, D.; Schälte, Y.; Pathirana, D.; Paszkowski, Ł.; Lines, G. T.; Stapor, P.; Hasenauer, J.#; AMICI: High-performance sensitivity analysis for large ordinary differential equation models. <i>Bioinformatics</i> 37(20), 3676-3677	2021
19	Schmiester, L.; Schälte, Y.; Bergmann, F.T.; Camba, T.; Dudkin, E.; Egert, J.; Fröhlich, F. ; Fuhrmann, L.; Hauber, A.L.; Kemmer, S.; Lakrisenko, P.; Loos, C.; Merkt, S.; Pathirana, D.; Raimúndez, E.; Refisch, L.; Rosenblatt, M.; Städter, P.; Wang, D.; Wieland, F.G.; Banga, J.R.; Timmer, J.; Villaverde, A.F.; Sahle, S.; Kreutz, C.; Hasenauer, J.; Weindl, D.; PEtab – interoperable specification of parameter estimation problems in systems biology. <i>PLoS Comp. Bio.</i> 17(1): e1008646	2021
18	Gerosa, L.; Chidley, C.; Fröhlich, F.; Sanchez, G.; Lim, S.K.; Muhlich, J.; Chen, J.Y.; Baker, G.J.; Schapiro, D.; Shi, T.; Yi, L.; Nicora, C.D.; Claas, A.; Lauffenburger, D.A.; Qian, W.J.; Wiley, H.S.; Sorger, P.K.; Sporadic ERK pulses drive non-genetic resistance in drug-adapted BRAFV600E melanoma cells. <i>Cell Systems</i> 11(5), 478-494	2020
17	Schmiester, L.; Schälte, Y.; Fröhlich, F.; Hasenauer, J.; Weindl, D.; Efficient parameterization of large-scale dynamic models based on relative measurements. <i>Bioinformatics</i> 36(2), 594-602	2020

16	Fröhlich, F.; Loos, C.; Hasenauer, J.; Scalable Inference of Ordinary Differential Equation Models of Biochemical Processes. <i>Gene Regulatory Networks</i> , 385-422	2019
15	Villaverde, A.F.; Fröhlich, F.; Weindl, D.; Hasenauer, J.; Banga J.R.; Benchmarking Optimization Methods for Parameter Estimation in Large Kinetic Models. <i>Bioinformatics</i> 35(5), 830-838	2019
14	Fröhlich, F.*; Reiser, A.*; Fink, L.; Woschke, D.; Ligon, T.; Theis, F.J.; Rädler, J.; Hasenauer, J.; Multi-Experiment Nonlinear Mixed Effect Modeling of Single-Cell Translation Kinetics after Transfection. <i>npj Syst. Biol. Appl.</i> 5(1), 1	2018
13	Fröhlich, F.*; Kessler, T.*; Weindl, D.; Shadrin, S.; Schmiester, L.; Hache, H.; Muradyan, A.; Schuette, M.; Lim, J.H.; Heinig, M.; Theis, F.J.; Lehrach, H.; Wierling, C.; Lange, B.; Hasenauer, J.; Efficient Parameter Estimation enables the Prediction of Drug Response using a Mechanistic Pan-Cancer Pathway Model. <i>Cell Systems</i> 7(6), 567-579	2018
12	Stapor, P.; Fröhlich, F.; Hasenauer, J.; Optimization and profile calculation of ODE models using second order adjoint sensitivity analysis. <i>Bioinformatics</i> 34(13), i151-159	2018
11	Loos, C.; Möller, K.; Fröhlich, F.; Hucho, T.; Hasenauer, J.; A Hierarchical, Data-Driven Approach to Modeling Single-Cell Populations Predicts Latent Causes of Cell-To-Cell Variability. <i>Cell Systems</i> , 6(5), 593-603. e13	2018
10	Ligon, T.; Fröhlich, F.; Chis, O.; Banga, J.; Balsa-Canto, E.; Hasenauer, J.; GenSSI 2.0: Multi-experiment structural identifiability analysis of SBML models. <i>Bioinformatics</i> 34(8), 1421-1423	2018
9	Stapor, P.; Weindl, D.; Ballnus, B.; Hug, S.; Loos, C.; Fiedler, A.; Krause, S.; Hroß, S.; Fröhlich, F.; Hasenauer, J.; PESTO: Parameter ESTimation TOOLbox. <i>Bioinformatics</i> 34(4), 705-707	2018
8	Fröhlich, F.; Kaltenbacher, B.; Theis, F.J.; Hasenauer, J.; Scalable parameter estimation for genome-scale biochemical reaction networks. <i>PLoS Comp. Bio.</i> 13(1): e1005331.	2017
7	Fröhlich, F.; Theis, F.J.; Rädler, J.O.; Hasenauer, J.; Parameter estimation for dynamical Systems with discrete events and logical operations. <i>Bioinformatics</i> 33(7), 1049-1056.	2017
6	Fröhlich, F.; Thomas, P.; Kazeroonian, A.; Theis, F.J.; Grima, R.; Hasenauer, J.; Inference for stochastic chemical kinetics using moment equations and system size expansion. <i>PLoS Comp. Bio.</i> 12(7): e1005030.	2016
5	Kazeroonian, A.; Fröhlich, F.; Raue, A.; Theis, F.J.; Hasenauer, J.; CERENA: ChEmical REaction Network Analyzer – A toolbox for the simulation and analysis of stochastic chemical kinetics. <i>PLoS ONE</i> 11: e0146732.	2016
4	Fröhlich, F.; Hross, S.; Theis, F.J.; Hasenauer, J.; Radial basis function approximation of bayesaian parameter posterior densities for uncertainty analysis. <i>Lecture Notes Comp. Sci.</i> 8859, 73-85.	2014
3	Fröhlich, F.; Theis, F.J.; Hasenauer, J.; Uncertainty analysis for non-Identifiable dynamical systems: profile likelihoods, bootstrapping and more. <i>Lecture Notes Comp. Sci.</i> 8859, 61-72.	2014
2	Morath, V.; Truong, D.J.J.; Albrecht, F.; Polte, I.; Ciccone, R.A.; Funke, L.F.; Reichart, L.; Wolf, C.G.; Brunner, A.D.; Fischer, K.; Schneider, P.C.; Brüggenthies, J.B.; Fröhlich, F.; Wiedemann, G.; Reski, R.; Skerra, A.; Design and characterization of a modular membrane protein anchor to functionalize the moss <i>Physcomitrella patens</i> with extracellular catalytic and/or binding activities. <i>ACS Synth. Biol.</i> 3, 990-994.	2014
1	Bongini, M.; Fornasier, M.; Fröhlich, F.; Haghverdi, L.; Sparse control of force field dynamics. <i>International Conference on NETwork Games, COntrol and OPTimization</i> , 195-200.	2014

Software

web	AMICI – Advanced MATLAB Interface for CVODES and IDAS (lead developer)
web	Fides – Reliable Trust Region Optimization in Python (lead developer)
web	MEMOIR – MATLAB toolbox for Mixed Effect Model InfeRence (lead developer)
web	pyPESTO – Parameter ESTimation Toolbox (developer)
web	PEtab – Data Format for Parameter Estimation Problems (developer)
web	CERENA – ChEmical REaction Network Analyzer (developer)
web	GenSSI – Generating Series for testing Structural Identifiability (developer)

Service & Leadership

Reviewer for Cell Systems, eLife, PLoS Computational Biology, Bioinformatics, Complexity, BMC Systems Biology, IEEE Access, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Journal of the Royal Society Interface, Journal of the Royal Society Proceedings A

Grant Referee for the Marsden Fund	
Program Committee Member for CMSB2016 , ISMB2018 , ISBM2019 , ISMB2020 , ISMB2021 , ISMB2022	
Elected member of the editorial board for the PEtab format	2021-2023
Judge for the international Genetically Engineered Machine (iGEM) competition	2018-2019
Student representative in the Life Sciences Graduate Network	2016-2018
Student representative in the QBM Graduate School managing board	2014-2018