Jan Hasenauer

List of Publications by Year
in descending order

		136740	189595
129 papers	3,985 citations	32 h-index	50 g-index
170 all docs	170 docs citations	170 times ranked	4856 citing authors

#	Article	IF	Citations
1	Characterization of Rare, Dormant, and Therapy-Resistant Cells in Acute Lymphoblastic Leukemia. Cancer Cell, 2016, 30, 849-862.	7.7	215
2	Data2Dynamics: a modeling environment tailored to parameter estimation in dynamical systems. Bioinformatics, 2015, 31, 3558-3560.	1.8	206
3	Network plasticity of pluripotency transcription factors in embryonic stem cells. Nature Cell Biology, 2015, 17, 1235-1246.	4.6	130
4	Scalable Parameter Estimation for Genome-Scale Biochemical Reaction Networks. PLoS Computational Biology, 2017, 13, e1005331.	1.5	125
5	Efficient Parameter Estimation Enables the Prediction of Drug Response Using a Mechanistic Pan-Cancer Pathway Model. Cell Systems, 2018, 7, 567-579.e6.	2.9	99
6	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	2.4	99
7	Determinants of robustness in spindle assembly checkpoint signalling. Nature Cell Biology, 2013, 15, 1328-1339.	4.6	92
8	Benchmarking optimization methods for parameter estimation in large kinetic models. Bioinformatics, 2019, 35, 830-838.	1.8	90
9	Identification of models of heterogeneous cell populations from population snapshot data. BMC Bioinformatics, 2011, 12, 125.	1.2	88
10	Method of conditional moments (MCM) for the Chemical Master Equation. Journal of Mathematical Biology, 2014, 69, 687-735.	0.8	86
11	Inferring population dynamics from single-cell RNA-sequencing time series data. Nature Biotechnology, 2019, 37, 461-468.	9.4	85
12	PESTO: Parameter EStimation TOolbox. Bioinformatics, 2018, 34, 705-707.	1.8	83
13	pyABC: distributed, likelihood-free inference. Bioinformatics, 2018, 34, 3591-3593.	1.8	79
14	Inference for Stochastic Chemical Kinetics Using Moment Equations and System Size Expansion. PLoS Computational Biology, 2016, 12, e1005030.	1.5	77
15	GenSSI 2.0: multi-experiment structural identifiability analysis of SBML models. Bioinformatics, 2018, 34, 1421-1423.	1.8	75
16	Multi-experiment nonlinear mixed effect modeling of single-cell translation kinetics after transfection. Npj Systems Biology and Applications, 2018, 4, 1.	1.4	66
17	Parallelization and High-Performance Computing Enables Automated Statistical Inference of Multi-scale Models. Cell Systems, 2017, 4, 194-206.e9.	2.9	62
18	Benchmark problems for dynamic modeling of intracellular processes. Bioinformatics, 2019, 35, 3073-3082.	1.8	61

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19	High-dimensional Bayesian parameter estimation: Case study for a model of JAK2/STAT5 signaling. Mathematical Biosciences, 2013, 246, 293-304.	0.9	56
20	PEtab—Interoperable specification of parameter estimation problems in systems biology. PLoS Computational Biology, 2021, 17, e1008646.	1.5	55
21	A protocol for dynamic model calibration. Briefings in Bioinformatics, 2022, 23, .	3.2	54
22	HER2 Expression, Test Deviations, and Their Impact on Survival in Metastatic Gastric Cancer: Results From the Prospective Multicenter VARIANZ Study. Journal of Clinical Oncology, 2021, 39, 1468-1478.	0.8	54
23	Domain Model Explains Propagation Dynamics and Stability of Histone H3K27 and H3K36 Methylation Landscapes. Cell Reports, 2020, 30, 1223-1234.e8.	2.9	54
24	In Search of the SARS-CoV-2 Protection Correlate: Head-to-Head Comparison of Two Quantitative S1 Assays in Pre-characterized Oligo-/Asymptomatic Patients. Infectious Diseases and Therapy, 2021, 10, 1505-1518.	1.8	53
25	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	3.2	53
26	Robust parameter estimation for dynamical systems from outlier-corrupted data. Bioinformatics, 2017, 33, 718-725.	1.8	49
27	Whither systems medicine?. Experimental and Molecular Medicine, 2018, 50, e453-e453.	3.2	49
28	Community-driven roadmap for integrated disease maps. Briefings in Bioinformatics, 2019, 20, 659-670.	3.2	48
29	Prevalence and Risk Factors of Infection in the Representative COVID-19 Cohort Munich. International Journal of Environmental Research and Public Health, 2021, 18, 3572.	1.2	47
30	AMICI: high-performance sensitivity analysis for large ordinary differential equation models. Bioinformatics, 2021, 37, 3676-3677.	1.8	45
31	ODE Constrained Mixture Modelling: A Method for Unraveling Subpopulation Structures and Dynamics. PLoS Computational Biology, 2014, 10, e1003686.	1.5	44
32	Dominant Negative Effects of Tumor Necrosis Factor (TNF)-related Apoptosis-inducing Ligand (TRAIL) Receptor 4 on TRAIL Receptor 1 Signaling by Formation of Heteromeric Complexes. Journal of Biological Chemistry, 2014, 289, 16576-16587.	1.6	44
33	A Hierarchical, Data-Driven Approach to Modeling Single-Cell Populations Predicts Latent Causes of Cell-To-Cell Variability. Cell Systems, 2018, 6, 593-603.e13.	2.9	42
34	Protocol of a population-based prospective COVID-19 cohort study Munich, Germany (KoCo19). BMC Public Health, 2020, 20, 1036.	1.2	42
35	Wound-healing growth factor, basic FGF, induces Erk1/2-dependent mechanical hyperalgesia. Pain, 2013, 154, 2216-2226.	2.0	41
36	PKA-RII subunit phosphorylation precedes activation by cAMP and regulates activity termination. Journal of Cell Biology, 2018, 217, 2167-2184.	2.3	40

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37	Parameter identification, experimental design and model falsification for biological network models using semidefinite programming. IET Systems Biology, 2010, 4, 119-130.	0.8	39
38	Data-Driven Modelling of Biological Multi-Scale Processes. Journal of Coupled Systems and Multiscale Dynamics, 2015, 3, 101-121.	0.2	37
39	Parameter estimation for dynamical systems with discrete events and logical operations. Bioinformatics, 2017, 33, 1049-1056.	1.8	36
40	CERENA: ChEmical REaction Network Analyzer—A Toolbox for the Simulation and Analysis of Stochastic Chemical Kinetics. PLoS ONE, 2016, 11, e0146732.	1.1	35
41	Analysis of CFSE time-series data using division-, age- and label-structured population models. Bioinformatics, 2016, 32, 2321-2329.	1.8	35
42	Increasing Neural Stem Cell Division Asymmetry and Quiescence Are Predicted to Contribute to the Age-Related Decline in Neurogenesis. Cell Reports, 2018, 25, 3231-3240.e8.	2.9	35
43	Comprehensive benchmarking of Markov chain Monte Carlo methods for dynamical systems. BMC Systems Biology, 2017, 11, 63.	3.0	34
44	Uncertainty Analysis for Non-identifiable Dynamical Systems: Profile Likelihoods, Bootstrapping and More. Lecture Notes in Computer Science, 2014, , 61-72.	1.0	33
45	Pain modulators regulate the dynamics of PKA-RII phosphorylation in subgroups of sensory neurons. Journal of Cell Science, 2014, 127, 216-29.	1.2	32
46	Efficient parameterization of large-scale dynamic models based on relative measurements. Bioinformatics, 2020, 36, 594-602.	1.8	32
47	Tailored parameter optimization methods for ordinary differential equation models with steady-state constraints. BMC Systems Biology, 2016, 10, 80.	3.0	30
48	Seroepidemiology and model-based prediction of SARS-CoV-2 in Ethiopia: longitudinal cohort study among front-line hospital workers and communities. The Lancet Global Health, 2021, 9, e1517-e1527.	2.9	30
49	Analysis and Simulation of Division- and Label-Structured Population Models. Bulletin of Mathematical Biology, 2012, 74, 2692-732.	0.9	29
50	Benchmarking of numerical integration methods for ODE models of biological systems. Scientific Reports, 2021, 11, 2696.	1.6	28
51	Analysis of heterogeneous cell populations: A density-based modeling and identification framework. Journal of Process Control, 2011, 21, 1417-1425.	1.7	24
52	Hierarchical optimization for the efficient parametrization of ODE models. Bioinformatics, 2018, 34, 4266-4273.	1.8	24
53	Optimization and profile calculation of ODE models using second order adjoint sensitivity analysis. Bioinformatics, 2018, 34, i151-i159.	1.8	23
54	Scalable Inference of Ordinary Differential Equation Models of Biochemical Processes. Methods in Molecular Biology, 2019, 1883, 385-422.	0.4	22

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55	Cell differentiation modeled via a coupled two-switch regulatory network. Chaos, 2010, 20, 045121.	1.0	21
56	Model predictive control using reduced order models: Guaranteed stability for constrained linear systems. Journal of Process Control, 2014, 24, 1647-1659.	1.7	21
57	Head-to-head evaluation of seven different seroassays including direct viral neutralisation in a representative cohort for SARS-CoV-2. Journal of General Virology, 2021, 102, .	1.3	21
58	Alveolar macrophage transcriptomic profiling in COPD shows major lipid metabolism changes. ERJ Open Research, 2021, 7, 00915-2020.	1.1	20
59	From first to second wave: follow-up of the prospective COVID-19 cohort (KoCo19) in Munich (Germany). BMC Infectious Diseases, 2021, 21, 925.	1.3	20
60	Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. Cell Systems, 2016, 2, 49-58.	2.9	19
61	Mathematical modeling of variability in intracellular signaling. Current Opinion in Systems Biology, 2019, 16, 17-24.	1.3	19
62	Efficient exact inference for dynamical systems with noisy measurements using sequential approximate Bayesian computation. Bioinformatics, 2020, 36, i551-i559.	1.8	18
63	Integration based profile likelihood calculation for PDE constrained parameter estimation problems. Inverse Problems, 2016, 32, 125009.	1.0	17
64	Sharpening of expression domains induced by transcription and microRNA regulationwithin a spatio-temporal model of mid-hindbrain boundary formation. BMC Systems Biology, 2013, 7, 48.	3.0	16
65	Evaluation of epidermal growth factor receptor signaling effects in gastric cancer cell lines by detailed motility-focused phenotypic characterization linked with molecular analysis. BMC Cancer, 2017, 17, 845.	1.1	16
66	Comparison of null models for combination drug therapy reveals Hand model as biochemically most plausible. Scientific Reports, 2019, 9, 3002.	1.6	16
67	COVID-19 outbreak in Wuhan demonstrates the limitations of publicly available case numbers for epidemiological modeling. Epidemics, 2021, 34, 100439.	1.5	16
68	Modeling of 2D diffusion processes based on microscopy data: parameter estimation and practical identifiability analysis. BMC Bioinformatics, 2013, 14, S7.	1.2	15
69	An adaptive scheduling scheme for calculating Bayes factors with thermodynamic integration using Simpson's rule. Statistics and Computing, 2016, 26, 663-677.	0.8	15
70	Effects of trastuzumab and afatinib on kinase activity in gastric cancer cell lines. Molecular Oncology, 2018, 12, 441-462.	2.1	15
71	Guaranteed steady state bounds for uncertain (bio-)chemical processes using infeasibility certificates. Journal of Process Control, 2010, 20, 1076-1083.	1.7	14
72	Bayesian parameter estimation for biochemical reaction networks using region-based adaptive parallel tempering. Bioinformatics, 2018, 34, i494-i501.	1.8	14

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73	Evaluation of Derivative-Free Optimizers for Parameter Estimation in Systems Biology. IFAC-PapersOnLine, 2018, 51, 98-101.	0.5	13
74	pyABC: Efficient and robust easy-to-use approximate Bayesian computation. Journal of Open Source Software, 2022, 7, 4304.	2.0	13
75	Dynamical optimization using reduced order models: A method to guarantee performance. Journal of Process Control, 2012, 22, 1490-1501.	1.7	12
76	A Comparison of Methods for Quantifying Prediction Uncertainty in Systems Biology. IFAC-PapersOnLine, 2019, 52, 45-51.	0.5	12
77	Closing the gap between formats for storing layout information in systems biology. Briefings in Bioinformatics, 2020, 21, 1249-1260.	3.2	12
78	A maximum likelihood estimator for parameter distributions in heterogeneous cell populations. Procedia Computer Science, 2010, 1, 1655-1663.	1.2	11
79	Parameter Estimation and Identifiability of Biological Networks Using Relative Data. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2011, 44, 11648-11653.	0.4	11
80	iVUN: interactive Visualization of Uncertain biochemical reaction Networks. BMC Bioinformatics, 2013, 14, S2.	1.2	11
81	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	6.5	11
82	Estimation of biochemical network parameter distributions in cell populations. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2009, 42, 1265-1270.	0.4	10
83	Guaranteed Steady-State Bounds for Uncertain Chemical Processes. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2009, 42, 643-648.	0.4	10
84	Computation of the posterior entropy in a Bayesian framework for parameter estimation in biological networks. , 2010, , .		10
85	Challenges in the calibration of large-scale ordinary differential equation models. IFAC-PapersOnLine, 2019, 52, 58-64.	0.5	10
86	Cell-to-cell variability in JAK2/STAT5 pathway components and cytoplasmic volumes defines survival threshold in erythroid progenitor cells. Cell Reports, 2021, 36, 109507.	2.9	10
87	A Scheme for Adaptive Selection of Population Sizes in Approximate Bayesian Computation - Sequential Monte Carlo. Lecture Notes in Computer Science, 2017, , 128-144.	1.0	9
88	HCV Spread Kinetics Reveal Varying Contributions of Transmission Modes to Infection Dynamics. Viruses, 2021, 13, 1308.	1.5	9
89	The interplay of viral loads, clinical presentation, and serological responses in SARS-CoV-2 â€" Results from a prospective cohort of outpatient COVID-19 cases. Virology, 2022, 569, 37-43.	1.1	9
90	A visual analytics approach for models of heterogeneous cell populations. Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 4.	1.4	8

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91	Threshold-Free Population Analysis Identifies Larger DRG Neurons to Respond Stronger to NGF Stimulation. PLoS ONE, 2012, 7, e34257.	1.1	8
92	Determining the effects of trastuzumab, cetuximab and afatinib by phosphoprotein, gene expression and phenotypic analysis in gastric cancer cell lines. BMC Cancer, 2020, 20, 1039.	1.1	8
93	Parameterization of mechanistic models from qualitative data using an efficient optimal scaling approach. Journal of Mathematical Biology, 2020, 81, 603-623.	0.8	8
94	Model-based analysis of response and resistance factors of cetuximab treatment in gastric cancer cell lines. PLoS Computational Biology, 2020, 16, e1007147.	1.5	8
95	Mini-batch optimization enables training of ODE models on large-scale datasets. Nature Communications, 2022, 13, 34.	5.8	8
96	Modeling of stochastic biological processes with non-polynomial propensities using non-central conditional moment equation. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2014, 47, 1729-1735.	0.4	7
97	MEMO: multi-experiment mixture model analysis of censored data. Bioinformatics, 2016, 32, 2464-2472.	1.8	7
98	AsthmaMap: An interactive knowledge repository for mechanisms of asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 853-856.	1.5	6
99	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. Bioinformatics, 2021, 37, 3702-3706.	1.8	6
100	Efficient gradient-based parameter estimation for dynamic models using qualitative data. Bioinformatics, 2021, 37, 4493-4500.	1.8	6
101	Computational Methods in Systems Biology. Lecture Notes in Computer Science, 2016, , .	1.0	5
102	The mesoscale organization of syntaxin 1A and SNAP25 is determined by SNARE–SNARE interactions. ELife, 2021, 10, .	2.8	5
103	Uncertainty-aware visual analysis of biochemical reaction networks. , 2012, , .		4
104	Visualizing edge-edge relations in graphs. , 2013, , .		4
105	Radial Basis Function Approximations of Bayesian Parameter Posterior Densities for Uncertainty Analysis. Lecture Notes in Computer Science, 2014, , 73-85.	1.0	4
106	Efficient computation of steady states in large-scale ODE models of biochemical reaction networks. IFAC-PapersOnLine, 2019, 52, 32-37.	0.5	4
107	Approximate Bayesian Computation for Stochastic Single-Cell Time-Lapse Data Using Multivariate Test Statistics. Lecture Notes in Computer Science, 2015, , 52-63.	1.0	4
108	Combining gene expression analysis of gastric cancer cell lines and tumor specimens to identify biomarkers for anti-HER therapies—the role of HAS2, SHB and HBEGF. BMC Cancer, 2022, 22, 254.	1.1	4

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109	Trajectory-based model reduction of nonlinear biochemical networks employing the observability normal form. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2011, 44, 10442-10447.	0.4	3
110	Continuous analogue to iterative optimization for PDE-constrained inverse problems. Inverse Problems in Science and Engineering, 2019, 27, 710-734.	1.2	3
111	Density-based modeling and identification of biochemical networks in cell populations. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2010, 43, 320-325.	0.4	2
112	Quantitative comparison of competing PDE models for Pom1p dynamics in fission yeast * *The authors acknowledge financial support from the Postdoctoral Fellowship Program (PFP) of the Helmholtz Zentrum Munchen.. IFAC-PapersOnLine, 2016, 49, 264-269.	0.5	2
113	A scalable moment-closure approximation for large-scale biochemical reaction networks. Bioinformatics, 2017, 33, i293-i300.	1.8	2
114	Mechanistic description of spatial processes using integrative modelling of noise-corrupted imaging data. Journal of the Royal Society Interface, 2018, 15, 20180600.	1.5	2
115	Abstract 2615: Heterogeneity of HER2 expression in gastric cancer (GC) leads to high deviation rates between local and central testing and hampers efficacy of anti-HER2 therapy: Survival results from the VARIANZ study. , 2018, , .		2
116	Approximative classification of regions in parameter spaces of nonlinear ODEs yielding different qualitative behavior. , 2010, , .		1
117	Dirac mixture distributions for the approximation of mixed effects models. IFAC-PapersOnLine, 2019, 52, 200-206.	0.5	1
118	Robust calibration of hierarchical population models for heterogeneous cell populations. Journal of Theoretical Biology, 2020, 488, 110118.	0.8	1
119	yaml2sbml: Human-readable and -writable specification of ODE models and their conversion to SBML. Journal of Open Source Software, 2021, 6, 3215.	2.0	1
120	Global Uncertainty Analysis for a Model of TNF-Induced NF-κB Signalling. Lecture Notes in Control and Information Sciences, 2010, , 365-377.	0.6	1
121	Parameter Estimation for Reaction Rate Equation Constrained Mixture Models. Lecture Notes in Computer Science, 2016, , 186-200.	1.0	1
122	Identifiability analysis for models of the translation kinetics after mRNA transfection. Journal of Mathematical Biology, 2022, 84, 56.	0.8	1
123	Steady state stability preserving nonlinear model reduction using sequential convex optimization. , 2011, , .		0
124	LNA++: Linear Noise Approximation with First and Second Order Sensitivities. Lecture Notes in Computer Science, 2018, , 300-306.	1.0	0
125	Inference of finite mixture models and the effect of binning. Statistical Applications in Genetics and Molecular Biology, 2019, 18, .	0.2	0
126	Model Falsification, Semidefinite Programming. , 2013, , 1391-1395.		0

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127	Feasibility. , 2013, , 736-737.		0
128	Quadratic Decomposition. , 2013, , 1803-1803.		0
129	Convex Optimization. , 2013, , 501-502.		0