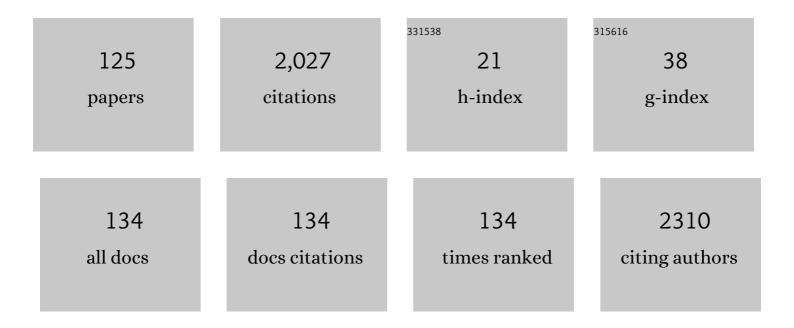
List of Publications by Year in descending order

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HEINZ KOEDDI

#	Article	IF	CITATIONS
1	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	9.0	209
2	Moment-based inference predicts bimodality in transient gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8340-8345.	3.3	207
3	Scalable inference of heterogeneous reaction kinetics from pooled single-cell recordings. Nature Methods, 2014, 11, 197-202.	9.0	131
4	Strengths and limitations of microarray-based phenotype prediction: lessons learned from the IMPROVER Diagnostic Signature Challenge. Bioinformatics, 2013, 29, 2892-2899.	1.8	108
5	Verification of systems biology research in the age of collaborative competition. Nature Biotechnology, 2011, 29, 811-815.	9.4	83
6	â€~Glocal' Robustness Analysis and Model Discrimination for Circadian Oscillators. PLoS Computational Biology, 2009, 5, e1000534.	1.5	57
7	Effect of Network Architecture on Synchronization and Entrainment Properties of the Circadian Oscillations in the Suprachiasmatic Nucleus. PLoS Computational Biology, 2012, 8, e1002419.	1.5	50
8	A Cellular System for Spatial Signal Decoding in Chemical Gradients. Developmental Cell, 2015, 35, 458-470.	3.1	50
9	Spatial Simulations in Systems Biology: From Molecules to Cells. International Journal of Molecular Sciences, 2012, 13, 7798-7827.	1.8	49
10	Lumpability abstractions of rule-based systems. Theoretical Computer Science, 2012, 431, 137-164.	0.5	45
11	Uncoupled Analysis of Stochastic Reaction Networks in Fluctuating Environments. PLoS Computational Biology, 2014, 10, e1003942.	1.5	42
12	Attention-Based Transformers for Instance Segmentation of Cells in Microstructures. , 2020, , .		40
13	Jump-Diffusion Approximation of Stochastic Reaction Dynamics: Error Bounds and Algorithms. Multiscale Modeling and Simulation, 2015, 13, 1390-1419.	0.6	35
14	Cell-Free Prototyping of AND-Logic Gates Based on Heterogeneous RNA Activators. ACS Synthetic Biology, 2019, 8, 2163-2173.	1.9	35
15	Spatial Modeling of Vesicle Transport and the Cytoskeleton: The Challenge of Hitting the Right Road. PLoS ONE, 2012, 7, e29645.	1.1	34
16	Digitally enhanced analog circuits: System aspects. , 2008, , .		33
17	Parallel feedback loops control the basal activity of the HOG MAPK signaling cascade. Integrative Biology (United Kingdom), 2015, 7, 412-422.	0.6	29
18	Hybrid spatial Gillespie and particle tracking simulation. Bioinformatics, 2012, 28, i549-i555.	1.8	27

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19	Dynamical properties of Discrete Reaction Networks. Journal of Mathematical Biology, 2014, 69, 55-72.	0.8	27
20	Quasi-Steady-State Approximations Derived from the Stochastic Model of Enzyme Kinetics. Bulletin of Mathematical Biology, 2019, 81, 1303-1336.	0.9	24
21	Minimum Mean-Square Error Equalization for Second-Order Volterra Systems. IEEE Transactions on Signal Processing, 2008, 56, 4729-4737.	3.2	23
22	Accounting for extrinsic variability in the estimation of stochastic rate constants. International Journal of Robust and Nonlinear Control, 2012, 22, 1103-1119.	2.1	23
23	Self-propelled chimeras. Physical Review E, 2018, 98, .	0.8	23
24	A tightly regulated and adjustable CRISPR-dCas9 based AND gate in yeast. Nucleic Acids Research, 2019, 47, 509-520.	6.5	22
25	An Efficient Scheme for Nonlinear Modeling and Predistortion in Mixed-Signal Systems. IEEE Transactions on Circuits and Systems Part 2: Express Briefs, 2006, 53, 1368-1372.	2.3	21
26	A variational approach to moment-closure approximations for the kinetics of biomolecular reaction networks. Journal of Chemical Physics, 2018, 148, 014105.	1.2	21
27	Global injectivity and multiple equilibria in uni- and bi-molecular reaction networks. Discrete and Continuous Dynamical Systems - Series B, 2012, 17, 2153-2170.	0.5	20
28	Traveling bands, clouds, and vortices of chiral active matter. Physical Review E, 2020, 102, 022604.	0.8	18
29	A game theoretical model of deforestation in human–environment relationships. Journal of Theoretical Biology, 2009, 258, 127-134.	0.8	16
30	ROC'n'Ribo: Characterizing a Riboswitching Expression System by Modeling Single-Cell Data. ACS Synthetic Biology, 2017, 6, 1211-1224.	1.9	16
31	Inferring gene expression networks with hubs using a degree weighted Lasso approach. Bioinformatics, 2019, 35, 987-994.	1.8	16
32	Trajectory enclosures for nonlinear systems with uncertain initial conditions and parameters. , 2012, , .		15
33	Bayesian inference of reaction kinetics from single-cell recordings across a heterogeneous cell population. Methods, 2015, 85, 22-35.	1.9	15
34	Yeast cell segmentation in microstructured environments with deep learning. BioSystems, 2022, 211, 104557.	0.9	15
35	Deterministic characterization of phase noise in biomolecular oscillators. Physical Biology, 2011, 8, 055008.	0.8	14
36	Almost sure stability and stabilization of discrete-time stochastic systems. Systems and Control Letters, 2015, 82, 26-32.	1.3	14

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37	Optimal Kullback–Leibler Aggregation via Information Bottleneck. IEEE Transactions on Automatic Control, 2015, 60, 1010-1022.	3.6	14
38	Transitions: A Protocol-Independent View of the Future Internet. Proceedings of the IEEE, 2019, 107, 835-846.	16.4	14
39	Markov chain aggregation and its applications to combinatorial reaction networks. Journal of Mathematical Biology, 2014, 69, 767-797.	0.8	13
40	A low-rate identification method for digital predistorters based on Volterra kernel interpolation. , 0, , .		12
41	Volterra kernel interpolation for system modeling and predistortion purposes. , 0, , .		12
42	Combining Model Reductions. Electronic Notes in Theoretical Computer Science, 2010, 265, 73-96.	0.9	12
43	Mapping behavioral specifications to model parameters in synthetic biology. BMC Bioinformatics, 2013, 14, S9.	1.2	12
44	Marginal process framework: A model reduction tool for Markov jump processes. Physical Review E, 2018, 97, 062147.	0.8	12
45	Solitary states in the mean-field limit. Chaos, 2020, 30, 111104.	1.0	12
46	Reconstructing dynamic molecular states from single-cell time series. Journal of the Royal Society Interface, 2016, 13, 20160533.	1.5	11
47	Context in synthetic biology: Memory effects of environments with mono-molecular reactions. Journal of Chemical Physics, 2019, 150, 024106.	1.2	11
48	Microfluidic platforms for the dynamic characterisation of synthetic circuitry. Current Opinion in Biotechnology, 2020, 63, 167-176.	3.3	11
49	Under-Approximating Cut Sets for Reachability in Large Scale Automata Networks. Lecture Notes in Computer Science, 2013, , 69-84.	1.0	11
50	Recursive Bayesian estimation of stochastic rate constants from heterogeneous cell populations. , 2011, , .		10
51	Automated Design of Robust Genetic Circuits: Structural Variants and Parameter Uncertainty. ACS Synthetic Biology, 2021, 10, 3316-3329.	1.9	10
52	Inverse problems from biomedicine. Journal of Mathematical Biology, 2013, 67, 143-168.	0.8	9
53	Multiclass Yeast Segmentation in Microstructured Environments with Deep Learning. , 2020, , .		9
54	Tensor-train approximation of the chemical master equation and its application for parameter inference. Journal of Chemical Physics, 2021, 155, 034102.	1.2	9

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55	Reconstructing species-based dynamics from reduced stochastic rule-based models. , 2012, , .		8
56	CBA: Contextual Quality Adaptation for Adaptive Bitrate Video Streaming. , 2019, , .		8
57	Approximate lumpability for Markovian agent-based models using local symmetries. Journal of Applied Probability, 2019, 56, 647-671.	0.4	8
58	Maximizing information gain for the characterization of biomolecular circuits. , 2018, , .		8
59	Parallelized agent-based simulation on CPU and graphics hardware for spatial and stochastic models in biology. , 2011, , .		7
60	Finding invariant sets for biological systems using monomial domination. , 2012, , .		7
61	From microscopy data to in silico environments for in vivo-oriented simulations. Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 7.	1.4	7
62	Enabling crowdsourced live event coverage with adaptive collaborative upload strategies. , 2016, , .		7
63	Graph reconstruction using covariance-based methods. Eurasip Journal on Bioinformatics and Systems Biology, 2016, 2016, 19.	1.4	7
64	Optimizing stochastic scheduling in fork-join queueing models: Bounds and applications. , 2017, , .		7
65	A finite volume method for continuum limit equations of nonlocally interacting active chiral particles. Journal of Computational Physics, 2021, 440, 110275.	1.9	7
66	Marginal dynamics of stochastic biochemical networks in random environments. , 2013, , .		7
67	Reaction schemes, escape times and geminate recombinations in particle-based spatial simulations of biochemical reactions. Physical Biology, 2013, 10, 046005.	0.8	5
68	From biochemical reaction networks to 3D dynamics in the cell: The ZigCell3D modeling, simulation and visualisation framework. , 2013, , .		5
69	Generalized Cost-Based Job Scheduling in Very Large Heterogeneous Cluster Systems. IEEE Transactions on Parallel and Distributed Systems, 2020, 31, 2594-2604.	4.0	5
70	Coarse-Grained Brownian Dynamics Simulation of Rule-Based Models. Lecture Notes in Computer Science, 2013, , 64-77.	1.0	5
71	The Cramer-Rao Bound and DMT Signal Optimisation for the Identification of a Wiener-Type Model. Eurasip Journal on Advances in Signal Processing, 2004, 2004, 1.	1.0	4
72	Network Inference by Combining Biologically Motivated Regulatory Constraints with Penalized Regression. Annals of the New York Academy of Sciences, 2009, 1158, 114-124.	1.8	4

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73	Rational Design of Robust Biomolecular Circuits: from Specification to Parameters. , 2011, , 253-279.		4
74	Collaborative Uploading in Heterogeneous Networks: Optimal and Adaptive Strategies. , 2018, , .		4
75	On the Throughput Optimization in Large-scale Batch-processing Systems. Performance Evaluation, 2020, 144, 102142.	0.9	4
76	Multi-StyleGAN: Towards Image-Based Simulation of Time-Lapse Live-Cell Microscopy. Lecture Notes in Computer Science, 2021, , 476-486.	1.0	4
77	Functional Nanopore Screen: A Versatile High-Throughput Assay to Study and Engineer Protein Nanopores in <i>Escherichia coli</i> . ACS Synthetic Biology, 2022, 11, 2070-2079.	1.9	4
78	A Local Nonlinear Model for the Approximation and Identification of a Class of Systems. IEEE Transactions on Circuits and Systems II: Express Briefs, 2009, 56, 315-319.	2.2	3
79	Probability metrics to calibrate stochastic chemical kinetics. , 2010, , .		3
80	Optimal Perturbations for the Identification of Stochastic Reaction Dynamics. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2012, 45, 686-691.	0.4	3
81	Model Decomposition and Stochastic Fragments. Electronic Notes in Theoretical Computer Science, 2012, 284, 105-124.	0.9	3
82	Optimal variational perturbations for the inference of stochastic reaction dynamics. , 2012, , .		3
83	Cross-Layer QoE-Based Incentive Mechanism for Video Streaming in Multi-Hop Wireless Networks. , 2017, , .		3
84	Reinforcement learning in a continuum of agents. Swarm Intelligence, 2018, 12, 23-51.	1.3	3
85	Provisioning and Performance Evaluation of Parallel Systems with Output Synchronization. ACM Transactions on Modeling and Performance Evaluation of Computing Systems, 2019, 4, 1-31.	0.8	3
86	Hybrid master equation for jump-diffusion approximation of biomolecular reaction networks. BIT Numerical Mathematics, 2020, 60, 261-294.	1.0	3
87	Functionalizing Cell-Free Systems with CRISPR-Associated Proteins: Application to RNA-Based Circuit Engineering. ACS Synthetic Biology, 2021, 10, 2138-2150.	1.9	3
88	Discrete-Time Mean Field Control with Environment States. , 2021, , .		3
89	Motif-based mean-field approximation of interacting particles on clustered networks. Physical Review E, 2022, 105, L042301.	0.8	3

90 An Adaptive Cellular Network for Subspace Extraction. , 2006, , .

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#	Article	IF	CITATIONS
91	The Composition Rule for Multivariate Volterra Operators and its Application to Circuit Analysis. , 2007, , .		2
92	A low-rate identification method for digital predistorters based on Volterra kernel interpolation. Analog Integrated Circuits and Signal Processing, 2008, 56, 107-115.	0.9	2
93	Analysis and design of biological circuits and systems. , 2009, , .		2
94	Learning diagnostic signatures from microarray data using L1-regularized logistic regression. Systems Biomedicine (Austin, Tex ), 2013, 1, 240-246.	0.7	2
95	Approximate model reductions for combinatorial reaction systems. , 2013, , .		2
96	Error bound and simulation algorithm for piecewise deterministic approximations of stochastic reaction systems. , 2015, , .		2
97	Analysing and leveraging client heterogeneity in swarming-based live streaming. , 2016, , .		2
98	A Bayesian Approach to Policy Recognition and State Representation Learning. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2018, 40, 1295-1308.	9.7	2
99	Daily Routine Recognition with Visual Interactive Labeling by Fusing Acceleration and Audio Signals. , 2019, , .		2
100	Improving Daily Routine Recognition in Hearing Aids Using Sequence Learning. IEEE Access, 2021, 9, 93237-93247.	2.6	2
101	Daily Routine Recognition for Hearing Aid Personalization. SN Computer Science, 2021, 2, 1.	2.3	2
102	Lumpability Abstractions of Rule-based Systems. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 40, 142-161.	0.8	2
103	Non-Parametric Bayesian Inference for Change Point Detection in Neural Spike Trains. , 2018, , .		2
104	Automatic Reduction of Stochastic Rules-Based Models in a Nutshell. , 2010, , .		1
105	Computationally implementable sufficient conditions for the synchronisation of coupled dynamical systems with time delays in the coupling. , 2011, , .		1
106	Stochastic Semantics of Signaling as a Composition of Agent-view Automata. Electronic Notes in Theoretical Computer Science, 2011, 272, 3-17.	0.9	1
107	Computing enclosures for uncertain biochemical systems. IET Systems Biology, 2012, 6, 232-240.	0.8	1
108	Scalable inference using PMCMC and parallel tempering for high-throughput measurements of biomolecular reaction networks. , 2016, , .		1

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109	Efficient simulation of multiscale reaction networks: A multilevel partitioning approach. , 2016, , .		1
110	Policy recognition via expectation maximization. , 2016, , .		1
111	Sensitivity estimation for stochastic models of biochemical reaction networks in the presence of extrinsic variability. Journal of Chemical Physics, 2017, 146, 124122.	1.2	1
112	Poisson channel with binary Markov input and average sojourn time constraint. , 2020, , .		1
113	Stabilized Reconstruction of Signaling Networks from Single-Cell Cue-Response Data. Scientific Reports, 2020, 10, 1233.	1.6	1
114	Guaranteed and Randomized Methods for Stability Analysis of Uncertain Metabolic Networks. Lecture Notes in Control and Information Sciences, 2010, , 297-307.	0.6	1
115	Information Rate Maximization over a Resistive Grid. , 0, , .		Ο
116	A Bio-inspired Computer Fovea Model based on Hexagonal-type Cellular Neural Networks. , 0, , .		0
117	Information Rate Maximization over a Resistive Grid. , 2006, , .		0
118	A Bio-inspired Computer Fovea Model based on Hexagonal-type Cellular Neural Networks. , 2006, , .		0
119	Sparse Learning of Markovian Population Models in Random Environments. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2014, 47, 1723-1728.	0.4	0
120	A diagram technique for cumulant equations in biomolecular reaction networks with mass-action kinetics. , 2016, , .		0
121	Network Reconstruction From Time-Course Perturbation Data Using Multivariate Gaussian Processes. , 2018, , .		Ο
122	Collapsed Variational Inference for Nonparametric Bayesian Group Factor Analysis. , 2018, , .		0
123	On the Throughput Optimization in Large-Scale Batch-Processing Systems. Performance Evaluation Review, 2021, 48, 128-129.	0.4	0
124	Stochastic Simulations in Systems Biology. Advances in Computer and Electrical Engineering Book Series, 2012, , 267-286.	0.2	0
125	Active learning of continuous-time Bayesian networks through interventions*. Journal of Statistical Mechanics: Theory and Experiment, 2021, 2021, 124001.	0.9	0