

# Heinz Koeppel

## List of Publications by Year in descending order

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Version: 2024-02-01

125  
papers

2,027  
citations

331538

21  
h-index

315616

38  
g-index

134  
all docs

134  
docs citations

134  
times ranked

2310  
citing authors

#	ARTICLE	IF	CITATIONS
1	Yeast cell segmentation in microstructured environments with deep learning. <i>BioSystems</i> , 2022, 211, 104557.	0.9	15
2	Motif-based mean-field approximation of interacting particles on clustered networks. <i>Physical Review E</i> , 2022, 105, L042301.	0.8	3
3	Functional Nanopore Screen: A Versatile High-Throughput Assay to Study and Engineer Protein Nanopores in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2022, 11, 2070-2079.	1.9	4
4	Improving Daily Routine Recognition in Hearing Aids Using Sequence Learning. <i>IEEE Access</i> , 2021, 9, 93237-93247.	2.6	2
5	Daily Routine Recognition for Hearing Aid Personalization. <i>SN Computer Science</i> , 2021, 2, 1.	2.3	2
6	On the Throughput Optimization in Large-Scale Batch-Processing Systems. <i>Performance Evaluation Review</i> , 2021, 48, 128-129.	0.4	0
7	Tensor-train approximation of the chemical master equation and its application for parameter inference. <i>Journal of Chemical Physics</i> , 2021, 155, 034102.	1.2	9
8	Functionalizing Cell-Free Systems with CRISPR-Associated Proteins: Application to RNA-Based Circuit Engineering. <i>ACS Synthetic Biology</i> , 2021, 10, 2138-2150.	1.9	3
9	A finite volume method for continuum limit equations of nonlocally interacting active chiral particles. <i>Journal of Computational Physics</i> , 2021, 440, 110275.	1.9	7
10	Multi-StyleGAN: Towards Image-Based Simulation of Time-Lapse Live-Cell Microscopy. <i>Lecture Notes in Computer Science</i> , 2021, , 476-486.	1.0	4
11	Automated Design of Robust Genetic Circuits: Structural Variants and Parameter Uncertainty. <i>ACS Synthetic Biology</i> , 2021, 10, 3316-3329.	1.9	10
12	Discrete-Time Mean Field Control with Environment States. , 2021, , .		3
13	Active learning of continuous-time Bayesian networks through interventions*. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2021, 2021, 124001.	0.9	0
14	Hybrid master equation for jump-diffusion approximation of biomolecular reaction networks. <i>BIT Numerical Mathematics</i> , 2020, 60, 261-294.	1.0	3
15	Poisson channel with binary Markov input and average sojourn time constraint. , 2020, , .		1
16	On the Throughput Optimization in Large-scale Batch-processing Systems. <i>Performance Evaluation</i> , 2020, 144, 102142.	0.9	4
17	Traveling bands, clouds, and vortices of chiral active matter. <i>Physical Review E</i> , 2020, 102, 022604.	0.8	18
18	Multiclass Yeast Segmentation in Microstructured Environments with Deep Learning. , 2020, , .		9

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19	Microfluidic platforms for the dynamic characterisation of synthetic circuitry. <i>Current Opinion in Biotechnology</i> , 2020, 63, 167-176.	3.3	11
20	Generalized Cost-Based Job Scheduling in Very Large Heterogeneous Cluster Systems. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2020, 31, 2594-2604.	4.0	5
21	Stabilized Reconstruction of Signaling Networks from Single-Cell Cue-Response Data. <i>Scientific Reports</i> , 2020, 10, 1233.	1.6	1
22	Solitary states in the mean-field limit. <i>Chaos</i> , 2020, 30, 111104.	1.0	12
23	Attention-Based Transformers for Instance Segmentation of Cells in Microstructures. , 2020, , .		40
24	Cell-Free Prototyping of AND-Logic Gates Based on Heterogeneous RNA Activators. <i>ACS Synthetic Biology</i> , 2019, 8, 2163-2173.	1.9	35
25	CBA: Contextual Quality Adaptation for Adaptive Bitrate Video Streaming. , 2019, , .		8
26	Transitions: A Protocol-Independent View of the Future Internet. <i>Proceedings of the IEEE</i> , 2019, 107, 835-846.	16.4	14
27	Quasi-Steady-State Approximations Derived from the Stochastic Model of Enzyme Kinetics. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 1303-1336.	0.9	24
28	Provisioning and Performance Evaluation of Parallel Systems with Output Synchronization. <i>ACM Transactions on Modeling and Performance Evaluation of Computing Systems</i> , 2019, 4, 1-31.	0.8	3
29	Daily Routine Recognition with Visual Interactive Labeling by Fusing Acceleration and Audio Signals. , 2019, , .		2
30	Approximate lumpability for Markovian agent-based models using local symmetries. <i>Journal of Applied Probability</i> , 2019, 56, 647-671.	0.4	8
31	Inferring gene expression networks with hubs using a degree weighted Lasso approach. <i>Bioinformatics</i> , 2019, 35, 987-994.	1.8	16
32	Context in synthetic biology: Memory effects of environments with mono-molecular reactions. <i>Journal of Chemical Physics</i> , 2019, 150, 024106.	1.2	11
33	A tightly regulated and adjustable CRISPR-dCas9 based AND gate in yeast. <i>Nucleic Acids Research</i> , 2019, 47, 509-520.	6.5	22
34	A variational approach to moment-closure approximations for the kinetics of biomolecular reaction networks. <i>Journal of Chemical Physics</i> , 2018, 148, 014105.	1.2	21
35	A Bayesian Approach to Policy Recognition and State Representation Learning. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2018, 40, 1295-1308.	9.7	2
36	Reinforcement learning in a continuum of agents. <i>Swarm Intelligence</i> , 2018, 12, 23-51.	1.3	3

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37	Collaborative Uploading in Heterogeneous Networks: Optimal and Adaptive Strategies. , 2018, , .		4
38	Network Reconstruction From Time-Course Perturbation Data Using Multivariate Gaussian Processes. , 2018, , .		0
39	Collapsed Variational Inference for Nonparametric Bayesian Group Factor Analysis. , 2018, , .		0
40	Self-propelled chimeras. Physical Review E, 2018, 98, .	0.8	23
41	Marginal process framework: A model reduction tool for Markov jump processes. Physical Review E, 2018, 97, 062147.	0.8	12
42	Maximizing information gain for the characterization of biomolecular circuits. , 2018, , .		8
43	Non-Parametric Bayesian Inference for Change Point Detection in Neural Spike Trains. , 2018, , .		2
44	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
45	ROCa€™nâ€™Ribo: Characterizing a Riboswitching Expression System by Modeling Single-Cell Data. ACS Synthetic Biology, 2017, 6, 1211-1224.	1.9	16
46	Cross-Layer QoE-Based Incentive Mechanism for Video Streaming in Multi-Hop Wireless Networks. , 2017, , .		3
47	Optimizing stochastic scheduling in fork-join queueing models: Bounds and applications. , 2017, , .		7
48	Enabling crowdsourced live event coverage with adaptive collaborative upload strategies. , 2016, , .		7
49	Graph reconstruction using covariance-based methods. Eurasip Journal on Bioinformatics and Systems Biology, 2016, 2016, 19.	1.4	7
50	A diagram technique for cumulant equations in biomolecular reaction networks with mass-action kinetics. , 2016, , .		0
51	Scalable inference using PMCMC and parallel tempering for high-throughput measurements of biomolecular reaction networks. , 2016, , .		1
52	Analysing and leveraging client heterogeneity in swarming-based live streaming. , 2016, , .		2
53	Efficient simulation of multiscale reaction networks: A multilevel partitioning approach. , 2016, , .		1
54	Reconstructing dynamic molecular states from single-cell time series. Journal of the Royal Society Interface, 2016, 13, 20160533.	1.5	11

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55	Policy recognition via expectation maximization. , 2016, , .		1
56	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	9.0	209
57	Parallel feedback loops control the basal activity of the HOG MAPK signaling cascade. Integrative Biology (United Kingdom), 2015, 7, 412-422.	0.6	29
58	Almost sure stability and stabilization of discrete-time stochastic systems. Systems and Control Letters, 2015, 82, 26-32.	1.3	14
59	Jump-Diffusion Approximation of Stochastic Reaction Dynamics: Error Bounds and Algorithms. Multiscale Modeling and Simulation, 2015, 13, 1390-1419.	0.6	35
60	Error bound and simulation algorithm for piecewise deterministic approximations of stochastic reaction systems. , 2015, , .		2
61	A Cellular System for Spatial Signal Decoding in Chemical Gradients. Developmental Cell, 2015, 35, 458-470.	3.1	50
62	Optimal Kullback-Leibler Aggregation via Information Bottleneck. IEEE Transactions on Automatic Control, 2015, 60, 1010-1022.	3.6	14
63	Bayesian inference of reaction kinetics from single-cell recordings across a heterogeneous cell population. Methods, 2015, 85, 22-35.	1.9	15
64	Uncoupled Analysis of Stochastic Reaction Networks in Fluctuating Environments. PLoS Computational Biology, 2014, 10, e1003942.	1.5	42
65	Dynamical properties of Discrete Reaction Networks. Journal of Mathematical Biology, 2014, 69, 55-72.	0.8	27
66	Markov chain aggregation and its applications to combinatorial reaction networks. Journal of Mathematical Biology, 2014, 69, 767-797.	0.8	13
67	Scalable inference of heterogeneous reaction kinetics from pooled single-cell recordings. Nature Methods, 2014, 11, 197-202.	9.0	131
68	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
69	Inverse problems from biomedicine. Journal of Mathematical Biology, 2013, 67, 143-168.	0.8	9
70	Reaction schemes, escape times and geminate recombinations in particle-based spatial simulations of biochemical reactions. Physical Biology, 2013, 10, 046005.	0.8	5
71	Strengths and limitations of microarray-based phenotype prediction: lessons learned from the IMPROVER Diagnostic Signature Challenge. Bioinformatics, 2013, 29, 2892-2899.	1.8	108
72	Mapping behavioral specifications to model parameters in synthetic biology. BMC Bioinformatics, 2013, 14, S9.	1.2	12

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73	From biochemical reaction networks to 3D dynamics in the cell: The ZigCell3D modeling, simulation and visualisation framework. , 2013, , .		5
74	Learning diagnostic signatures from microarray data using L1-regularized logistic regression. Systems Biomedicine (Austin, Tex ), 2013, 1, 240-246.	0.7	2
75	Approximate model reductions for combinatorial reaction systems. , 2013, , .		2
76	Under-Approximating Cut Sets for Reachability in Large Scale Automata Networks. Lecture Notes in Computer Science, 2013, , 69-84.	1.0	11
77	Coarse-Grained Brownian Dynamics Simulation of Rule-Based Models. Lecture Notes in Computer Science, 2013, , 64-77.	1.0	5
78	Marginal dynamics of stochastic biochemical networks in random environments. , 2013, , .		7
79	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
80	Spatial Simulations in Systems Biology: From Molecules to Cells. International Journal of Molecular Sciences, 2012, 13, 7798-7827.	1.8	49
81	Hybrid spatial Gillespie and particle tracking simulation. Bioinformatics, 2012, 28, i549-i555.	1.8	27
82	Computing enclosures for uncertain biochemical systems. IET Systems Biology, 2012, 6, 232-240.	0.8	1
83	Finding invariant sets for biological systems using monomial domination. , 2012, , .		7
84	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
85	Model Decomposition and Stochastic Fragments. Electronic Notes in Theoretical Computer Science, 2012, 284, 105-124.	0.9	3
86	Optimal variational perturbations for the inference of stochastic reaction dynamics. , 2012, , .		3
87	Reconstructing species-based dynamics from reduced stochastic rule-based models. , 2012, , .		8
88	Trajectory enclosures for nonlinear systems with uncertain initial conditions and parameters. , 2012, , .		15
89	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
90	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

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91	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
92	Lumpability abstractions of rule-based systems. Theoretical Computer Science, 2012, 431, 137-164.	0.5	45
93	Spatial Modeling of Vesicle Transport and the Cytoskeleton: The Challenge of Hitting the Right Road. PLoS ONE, 2012, 7, e29645.	1.1	34
94	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
95	Stochastic Simulations in Systems Biology. Advances in Computer and Electrical Engineering Book Series, 2012, , 267-286.	0.2	0
96	Computationally implementable sufficient conditions for the synchronisation of coupled dynamical systems with time delays in the coupling. , 2011, , .		1
97	Rational Design of Robust Biomolecular Circuits: from Specification to Parameters. , 2011, , 253-279.		4
98	Stochastic Semantics of Signaling as a Composition of Agent-view Automata. Electronic Notes in Theoretical Computer Science, 2011, 272, 3-17.	0.9	1
99	Parallelized agent-based simulation on CPU and graphics hardware for spatial and stochastic models in biology. , 2011, , .		7
100	Recursive Bayesian estimation of stochastic rate constants from heterogeneous cell populations. , 2011, , .		10
101	Deterministic characterization of phase noise in biomolecular oscillators. Physical Biology, 2011, 8, 055008.	0.8	14
102	Verification of systems biology research in the age of collaborative competition. Nature Biotechnology, 2011, 29, 811-815.	9.4	83
103	Combining Model Reductions. Electronic Notes in Theoretical Computer Science, 2010, 265, 73-96.	0.9	12
104	Probability metrics to calibrate stochastic chemical kinetics. , 2010, , .		3
105	Automatic Reduction of Stochastic Rules-Based Models in a Nutshell. , 2010, , .		1
106	Guaranteed and Randomized Methods for Stability Analysis of Uncertain Metabolic Networks. Lecture Notes in Control and Information Sciences, 2010, , 297-307.	0.6	1
107	Analysis and design of biological circuits and systems. , 2009, , .		2
108	Global Robustness Analysis and Model Discrimination for Circadian Oscillators. PLoS Computational Biology, 2009, 5, e1000534.	1.5	57

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109	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
110	A game theoretical model of deforestation in humanâ€environment relationships. Journal of Theoretical Biology, 2009, 258, 127-134.	0.8	16
111	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
112	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
113	Digitally enhanced analog circuits: System aspects. , 2008, , .		33
114	Minimum Mean-Square Error Equalization for Second-Order Volterra Systems. IEEE Transactions on Signal Processing, 2008, 56, 4729-4737.	3.2	23
115	The Composition Rule for Multivariate Volterra Operators and its Application to Circuit Analysis. , 2007, , .		2
116	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
117	Information Rate Maximization over a Resistive Grid. , 2006, , .		0
118	An Adaptive Cellular Network for Subspace Extraction. , 2006, , .		2
119	A Bio-inspired Computer Fovea Model based on Hexagonal-type Cellular Neural Networks. , 2006, , .		0
120	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
121	A low-rate identification method for digital predistorters based on Volterra kernel interpolation. , 0, , .		12
122	Volterra kernel interpolation for system modeling and predistortion purposes. , 0, , .		12
123	Information Rate Maximization over a Resistive Grid. , 0, , .		0
124	A Bio-inspired Computer Fovea Model based on Hexagonal-type Cellular Neural Networks. , 0, , .		0
125	Lumpability Abstractions of Rule-based Systems. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 40, 142-161.	0.8	2