

Corrado Priami

List of Publications by Year in descending order

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83
papers

2,053
citations

331670

21
h-index

276875

41
g-index

90
all docs

90
docs citations

90
times ranked

2680
citing authors

#	ARTICLE	IF	CITATIONS
1	Controlling astrocyte-mediated synaptic pruning signals for schizophrenia drug repurposing with deep graph networks. <i>PLoS Computational Biology</i> , 2022, 18, e1009531.	3.2	1
2	Computational approaches to understanding nutrient metabolism and metabolic disorders. <i>Current Opinion in Biotechnology</i> , 2021, 70, 7-14.	6.6	0
3	QSPcc reduces bottlenecks in computational model simulations. <i>Communications Biology</i> , 2021, 4, 1022.	4.4	2
4	Early outcome detection for COVID-19 patients. <i>Scientific Reports</i> , 2021, 11, 18464.	3.3	5
5	A comparison of deterministic and stochastic approaches for sensitivity analysis in computational systems biology. <i>Briefings in Bioinformatics</i> , 2020, 21, 527-540.	6.5	7
6	High-Precision Biomedical Relation Extraction for Reducing Human Curation Efforts in Industrial Applications. <i>IEEE Access</i> , 2020, 8, 150999-151011.	4.2	5
7	A Public Dataset of 24-h Multi-Levels Psycho-Physiological Responses in Young Healthy Adults. <i>Data</i> , 2020, 5, 91.	2.3	19
8	Stochastic simulation algorithms for computational systems biology: Exact, approximate, and hybrid methods. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2019, 11, e1459.	6.6	13
9	Regulatory Crosstalk of Doxorubicin, Estradiol and TNF α Combined Treatment in Breast Cancer-derived Cell Lines. <i>Scientific Reports</i> , 2019, 9, 15172.	3.3	2
10	Cross-disease analysis of Alzheimer's disease and type-2 Diabetes highlights the role of autophagy in the pathophysiology of two highly comorbid diseases. <i>Scientific Reports</i> , 2019, 9, 3965.	3.3	66
11	The 5-formyltetrahydrofolate futile cycle reduces pathway stochasticity in an extended hybrid-stochastic model of folate-mediated one-carbon metabolism. <i>Scientific Reports</i> , 2019, 9, 4322.	3.3	13
12	Efficient formulation of the rejection-based algorithm for biochemical reactions with delays. <i>International Journal of Bioinformatics Research and Applications</i> , 2019, 15, 159.	0.2	0
13	A network-based approach to identify deregulated pathways and drug effects in metabolic syndrome. <i>Nature Communications</i> , 2019, 10, 5215.	12.8	47
14	Multi-omics integration—a comparison of unsupervised clustering methodologies. <i>Briefings in Bioinformatics</i> , 2019, 20, 1269-1279.	6.5	105
15	Consensus Clustering of temporal profiles for the identification of metabolic markers of pre-diabetes in childhood (EarlyBird 73). <i>Scientific Reports</i> , 2018, 8, 1393.	3.3	10
16	Clinical and Vitamin Response to a Short-Term Multi-Micronutrient Intervention in Brazilian Children and Teens: From Population Data to Interindividual Responses. <i>Molecular Nutrition and Food Research</i> , 2018, 62, e1700613.	3.3	27
17	Efficient finite-difference method for computing sensitivities of biochemical reactions. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2018, 474, 20180303.	2.1	3
18	Incorporating extrinsic noise into the stochastic simulation of biochemical reactions: A comparison of approaches. <i>Journal of Chemical Physics</i> , 2018, 148, 064111.	3.0	8

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19	A closed-loop multi-level model of glucose homeostasis. PLoS ONE, 2018, 13, e0190627.	2.5	14
20	Combined use of protein biomarkers and network analysis unveils deregulated regulatory circuits in Duchenne muscular dystrophy. PLoS ONE, 2018, 13, e0194225.	2.5	23
21	Efficient Constant-Time Complexity Algorithm for Stochastic Simulation of Large Reaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 657-667.	3.0	20
22	Mechanistic interplay between ceramide and insulin resistance. Scientific Reports, 2017, 7, 41231.	3.3	38
23	Efficient stochastic simulation of biochemical reactions with noise and delays. Journal of Chemical Physics, 2017, 146, 084107.	3.0	14
24	A hybrid stochastic model of folate-mediated one-carbon metabolism: Effect of the common C677T MTHFR variant on de novo thymidylate biosynthesis. Scientific Reports, 2017, 7, 797.	3.3	22
25	Graphical Modeling Meets Systems Pharmacology. Gene Regulation and Systems Biology, 2017, 11, 117762501769193.	2.3	4
26	Optimization Algorithms for Computational Systems Biology. Frontiers in Applied Mathematics and Statistics, 2017, 3, .	1.3	34
27	H Simulator: Hybrid Stochastic/Deterministic Simulation of Biochemical Reaction Networks. Complexity, 2017, 2017, 1-12.	1.6	1
28	Exploring the Limitations of Peripheral Blood Transcriptional Biomarkers in Predicting Influenza Vaccine Responsiveness. Complexity, 2017, 2017, 1-9.	1.6	2
29	Identification of an early transcriptomic signature of insulin resistance and related diseases in lymphomonocytes of healthy subjects. PLoS ONE, 2017, 12, e0182559.	2.5	11
30	Simulation Algorithms for Computational Systems Biology. Texts in Theoretical Computer Science, 2017, , .	0.8	29
31	Systems view of adipogenesis via novel omics-driven and tissue-specific activity scoring of network functional modules. Scientific Reports, 2016, 6, 28851.	3.3	17
32	Accelerating rejection-based simulation of biochemical reactions with bounded acceptance probability. Journal of Chemical Physics, 2016, 144, 224108.	3.0	10
33	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 645-653.	0.8	72
34	A Novel Insulin/Glucose Model after a Mixed-Meal Test in Patients with Type 1 Diabetes on Insulin Pump Therapy. Scientific Reports, 2016, 6, 36029.	3.3	10
35	HRSSA – Efficient hybrid stochastic simulation for spatially homogeneous biochemical reaction networks. Journal of Computational Physics, 2016, 317, 301-317.	3.8	26
36	Novel drug target identification for the treatment of dementia using multi-relational association mining. Scientific Reports, 2015, 5, 11104.	3.3	11

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37	On the rejection-based algorithm for simulation and analysis of large-scale reaction networks. <i>Journal of Chemical Physics</i> , 2015, 142, 244106.	3.0	25
38	Simulation of biochemical reactions with time-dependent rates by the rejection-based algorithm. <i>Journal of Chemical Physics</i> , 2015, 143, 054104.	3.0	43
39	The role of breast-feeding in infant immune system: a systems perspective on the intestinal microbiome. <i>Microbiome</i> , 2015, 3, 41.	11.1	81
40	Qualitative and Quantitative Protein Complex Prediction Through Proteome-Wide Simulations. <i>PLoS Computational Biology</i> , 2015, 11, e1004424.	3.2	21
41	Systems biology approaches to study the molecular effects of caloric restriction and polyphenols on aging processes. <i>Genes and Nutrition</i> , 2015, 10, 58.	2.5	18
42	SCUIDO: a tool for signature-based clustering of expression profiles. <i>Nucleic Acids Research</i> , 2015, 43, W188-W192.	14.5	15
43	Graphical Modeling Tools for Systems Biology. <i>ACM Computing Surveys</i> , 2015, 47, 1-21.	23.0	13
44	\$\$ell \$\$: An Imperative DSL to Stochastically Simulate Biological Systems. <i>Lecture Notes in Computer Science</i> , 2015, , 354-374.	1.3	3
45	Network Analysis of Neurodegenerative Disease Highlights a Role of Toll-Like Receptor Signaling. <i>BioMed Research International</i> , 2014, 2014, 1-16.	1.9	19
46	Efficient rejection-based simulation of biochemical reactions with stochastic noise and delays. <i>Journal of Chemical Physics</i> , 2014, 141, 134116.	3.0	39
47	Biological network inference for drug discovery. <i>Drug Discovery Today</i> , 2013, 18, 256-264.	6.4	31
48	Inferring biochemical reaction pathways: the case of the gemcitabine pharmacokinetics. <i>BMC Systems Biology</i> , 2012, 6, 51.	3.0	8
49	Algorithmic Modeling Quantifies the Complementary Contribution of Metabolic Inhibitions to Gemcitabine Efficacy. <i>PLoS ONE</i> , 2012, 7, e50176.	2.5	17
50	Network Inference from Time-Dependent Omics Data. <i>Methods in Molecular Biology</i> , 2011, 719, 435-455.	0.9	6
51	Process algebra-based computational tools in ecological modelling. <i>Ecological Complexity</i> , 2011, 8, 357-363.	2.9	14
52	Stochastic simulation of the spatio-temporal dynamics of reaction-diffusion systems: the case for the bicoid gradient. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	7
53	Calibration of dynamic models of biological systems with KInfer. <i>European Biophysics Journal</i> , 2010, 39, 1019-1039.	2.2	20
54	Snazer: the simulations and networks analyzer. <i>BMC Systems Biology</i> , 2010, 4, 1.	3.0	175

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55	On the computational power of BlenX. Theoretical Computer Science, 2010, 411, 542-565.	0.9	1
56	Algorithmic systems biology. Communications of the ACM, 2009, 52, 80-88.	4.5	100
57	Elucidation of functional consequences of signalling pathway interactions. BMC Bioinformatics, 2009, 10, 370.	2.6	5
58	Deducing Chemical Reaction Rate Constants and Their Regions of Confidence from Noisy Measurements of Time Series of Concentration. , 2009, , .		7
59	Communicating by compatibility. The Journal of Logic and Algebraic Programming, 2008, 75, 167-181.	1.4	2
60	An Automatic Translation of SBML into Beta-Binders. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 80-90.	3.0	5
61	The Beta Workbench: a computational tool to study the dynamics of biological systems. Briefings in Bioinformatics, 2008, 9, 437-449.	6.5	68
62	Modelling and simulation of biological processes in BlenX. Performance Evaluation Review, 2008, 35, 32-39.	0.6	22
63	Control Flow Analysis for BioAmbients. Electronic Notes in Theoretical Computer Science, 2007, 180, 65-79.	0.9	18
64	Cell Cycle Control in Eukaryotes: A BioSpi model. Electronic Notes in Theoretical Computer Science, 2007, 180, 51-63.	0.9	28
65	Biological Transactions for Quantitative Models. Electronic Notes in Theoretical Computer Science, 2007, 171, 55-67.	0.9	6
66	The Decidability of the Structural Congruence for Beta-binders. Electronic Notes in Theoretical Computer Science, 2007, 171, 155-170.	0.9	4
67	Process Calculi and Life Science. Electronic Notes in Theoretical Computer Science, 2006, 162, 301-304.	0.9	7
68	Performance Evaluation of Security Protocols Specified in LySa. Electronic Notes in Theoretical Computer Science, 2005, 112, 167-189.	0.9	6
69	A Quantitative Study of Two Attacks. Electronic Notes in Theoretical Computer Science, 2005, 121, 65-85.	0.9	6
70	Checking security policies through an enhanced Control Flow Analysis. Journal of Computer Security, 2005, 13, 49-85.	0.8	2
71	Shape Spaces in Formal Interactions. Complexus, 2004, 2, 128-139.	0.6	3
72	A Formal Language for Computational Systems Biology. OMICS A Journal of Integrative Biology, 2004, 8, 370-380.	2.0	17

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73	Modelling the dynamics of biosystems. <i>Briefings in Bioinformatics</i> , 2004, 5, 259-269.	6.5	49
74	Preface to the special issue on Security in global computing. <i>International Journal of Information Security</i> , 2004, 2, 125-125.	3.4	1
75	A Logical Approach to Security in the Context of Ambient Calculus. <i>Electronic Notes in Theoretical Computer Science</i> , 2004, 99, 3-29.	0.9	2
76	Toward Extracting π -calculus from UML Sequence and State Diagrams. <i>Electronic Notes in Theoretical Computer Science</i> , 2004, 101, 51-72.	0.9	11
77	Language-based Performance Prediction for Distributed and Mobile Systems. <i>Information and Computation</i> , 2002, 175, 119-145.	0.7	14
78	Application of a stochastic name-passing calculus to representation and simulation of molecular processes. <i>Information Processing Letters</i> , 2001, 80, 25-31.	0.6	361
79	Causality for debugging mobile agents. <i>Acta Informatica</i> , 1999, 36, 335-374.	0.5	7
80	LR techniques for handling syntax errors. <i>Computer Languages, Systems and Structures</i> , 1998, 24, 73-98.	0.3	1
81	Automatic verification of distributed systems: The process algebra approach. <i>Formal Methods in System Design</i> , 1996, 8, 7-38.	0.8	11
82	Comparison of syntactic error handling in LR parsers. <i>Software - Practice and Experience</i> , 1995, 25, 657-679.	3.6	18
83	Automatizing Parametric Reasoning on Distributed Concurrent Systems. <i>Formal Aspects of Computing</i> , 1994, 6, 676-695.	1.8	7