

Corrado Priami

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	Snazer: the simulations and networks analyzer. <i>BMC Systems Biology</i> , 2010, 4, 1.	3.0	175
3	Multi-omics integration—a comparison of unsupervised clustering methodologies. <i>Briefings in Bioinformatics</i> , 2019, 20, 1269-1279.	6.5	105
4	Algorithmic systems biology. <i>Communications of the ACM</i> , 2009, 52, 80-88.	4.5	100
5	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
6	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2016, 12, 645-653.	0.8	72
7	The Beta Workbench: a computational tool to study the dynamics of biological systems. <i>Briefings in Bioinformatics</i> , 2008, 9, 437-449.	6.5	68
8	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
9	Modelling the dynamics of biosystems. <i>Briefings in Bioinformatics</i> , 2004, 5, 259-269.	6.5	49
10	A network-based approach to identify deregulated pathways and drug effects in metabolic syndrome. <i>Nature Communications</i> , 2019, 10, 5215.	12.8	47
11	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
12	Efficient rejection-based simulation of biochemical reactions with stochastic noise and delays. <i>Journal of Chemical Physics</i> , 2014, 141, 134116.	3.0	39
13	Mechanistic interplay between ceramide and insulin resistance. <i>Scientific Reports</i> , 2017, 7, 41231.	3.3	38
14	Optimization Algorithms for Computational Systems Biology. <i>Frontiers in Applied Mathematics and Statistics</i> , 2017, 3, .	1.3	34
15	Biological network inference for drug discovery. <i>Drug Discovery Today</i> , 2013, 18, 256-264.	6.4	31
16	Simulation Algorithms for Computational Systems Biology. <i>Texts in Theoretical Computer Science</i> , 2017, . .	0.8	29
17	Cell Cycle Control in Eukaryotes: A BioSpi model. <i>Electronic Notes in Theoretical Computer Science</i> , 2007, 180, 51-63.	0.9	28
18	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

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19	HRSSA – Efficient hybrid stochastic simulation for spatially homogeneous biochemical reaction networks. <i>Journal of Computational Physics</i> , 2016, 317, 301-317.	3.8	26
20	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
21	Combined use of protein biomarkers and network analysis unveils deregulated regulatory circuits in Duchenne muscular dystrophy. <i>PLoS ONE</i> , 2018, 13, e0194225.	2.5	23
22	A hybrid stochastic model of folate-mediated one-carbon metabolism: Effect of the common C677T MTHFR variant on de novo thymidylate biosynthesis. <i>Scientific Reports</i> , 2017, 7, 797.	3.3	22
23	Modelling and simulation of biological processes in BlenX. <i>Performance Evaluation Review</i> , 2008, 35, 32-39.	0.6	22
24	Qualitative and Quantitative Protein Complex Prediction Through Proteome-Wide Simulations. <i>PLoS Computational Biology</i> , 2015, 11, e1004424.	3.2	21
25	Calibration of dynamic models of biological systems with KInfer. <i>European Biophysics Journal</i> , 2010, 39, 1019-1039.	2.2	20
26	Efficient Constant-Time Complexity Algorithm for Stochastic Simulation of Large Reaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 657-667.	3.0	20
27	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
28	A Public Dataset of 24-h Multi-Levels Psycho-Physiological Responses in Young Healthy Adults. <i>Data</i> , 2020, 5, 91.	2.3	19
29	Comparison of syntactic error handling in LR parsers. <i>Software - Practice and Experience</i> , 1995, 25, 657-679.	3.6	18
30	Control Flow Analysis for BioAmbients. <i>Electronic Notes in Theoretical Computer Science</i> , 2007, 180, 65-79.	0.9	18
31	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
32	A Formal Language for Computational Systems Biology. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 370-380.	2.0	17
33	Systems view of adipogenesis via novel omics-driven and tissue-specific activity scoring of network functional modules. <i>Scientific Reports</i> , 2016, 6, 28851.	3.3	17
34	Algorithmic Modeling Quantifies the Complementary Contribution of Metabolic Inhibitions to Gemcitabine Efficacy. <i>PLoS ONE</i> , 2012, 7, e50176.	2.5	17
35	SCUDO: a tool for signature-based clustering of expression profiles. <i>Nucleic Acids Research</i> , 2015, 43, W188-W192.	14.5	15
36	Language-based Performance Prediction for Distributed and Mobile Systems. <i>Information and Computation</i> , 2002, 175, 119-145.	0.7	14

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37	Process algebra-based computational tools in ecological modelling. <i>Ecological Complexity</i> , 2011, 8, 357-363.	2.9	14
38	Efficient stochastic simulation of biochemical reactions with noise and delays. <i>Journal of Chemical Physics</i> , 2017, 146, 084107.	3.0	14
39	A closed-loop multi-level model of glucose homeostasis. <i>PLoS ONE</i> , 2018, 13, e0190627.	2.5	14
40	Graphical Modeling Tools for Systems Biology. <i>ACM Computing Surveys</i> , 2015, 47, 1-21.	23.0	13
41	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
42	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
43	Automatic verification of distributed systems: The process algebra approach. <i>Formal Methods in System Design</i> , 1996, 8, 7-38.	0.8	11
44	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
45	Novel drug target identification for the treatment of dementia using multi-relational association mining. <i>Scientific Reports</i> , 2015, 5, 11104.	3.3	11
46	Identification of an early transcriptomic signature of insulin resistance and related diseases in lymphomonocytes of healthy subjects. <i>PLoS ONE</i> , 2017, 12, e0182559.	2.5	11
47	Accelerating rejection-based simulation of biochemical reactions with bounded acceptance probability. <i>Journal of Chemical Physics</i> , 2016, 144, 224108.	3.0	10
48	A Novel Insulin/Glucose Model after a Mixed-Meal Test in Patients with Type 1 Diabetes on Insulin Pump Therapy. <i>Scientific Reports</i> , 2016, 6, 36029.	3.3	10
49	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
50	Inferring biochemical reaction pathways: the case of the gemcitabine pharmacokinetics. <i>BMC Systems Biology</i> , 2012, 6, 51.	3.0	8
51	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
52	Automatizing Parametric Reasoning on Distributed Concurrent Systems. <i>Formal Aspects of Computing</i> , 1994, 6, 676-695.	1.8	7
53	Causality for debugging mobile agents. <i>Acta Informatica</i> , 1999, 36, 335-374.	0.5	7
54	Process Calculi and Life Science. <i>Electronic Notes in Theoretical Computer Science</i> , 2006, 162, 301-304.	0.9	7

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55	Deducing Chemical Reaction Rate Constants and Their Regions of Confidence from Noisy Measurements of Time Series of Concentration. , 2009, , .		7
56	Stochastic simulation of the spatio-temporal dynamics of reaction-diffusion systems: the case for the bicoid gradient. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	7
57	A comparison of deterministic and stochastic approaches for sensitivity analysis in computational systems biology. Briefings in Bioinformatics, 2020, 21, 527-540.	6.5	7
58	Performance Evaluation of Security Protocols Specified in LySa. Electronic Notes in Theoretical Computer Science, 2005, 112, 167-189.	0.9	6
59	A Quantitative Study of Two Attacks. Electronic Notes in Theoretical Computer Science, 2005, 121, 65-85.	0.9	6
60	Biological Transactions for Quantitative Models. Electronic Notes in Theoretical Computer Science, 2007, 171, 55-67.	0.9	6
61	Network Inference from Time-Dependent Omics Data. Methods in Molecular Biology, 2011, 719, 435-455.	0.9	6
62	An Automatic Translation of SBML into Beta-Binders. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 80-90.	3.0	5
63	Elucidation of functional consequences of signalling pathway interactions. BMC Bioinformatics, 2009, 10, 370.	2.6	5
64	High-Precision Biomedical Relation Extraction for Reducing Human Curation Efforts in Industrial Applications. IEEE Access, 2020, 8, 150999-151011.	4.2	5
65	Early outcome detection for COVID-19 patients. Scientific Reports, 2021, 11, 18464.	3.3	5
66	The Decidability of the Structural Congruence for Beta-binders. Electronic Notes in Theoretical Computer Science, 2007, 171, 155-170.	0.9	4
67	Graphical Modeling Meets Systems Pharmacology. Gene Regulation and Systems Biology, 2017, 11, 117762501769193.	2.3	4
68	Shape Spaces in Formal Interactions. Complexus, 2004, 2, 128-139.	0.6	3
69	Efficient finite-difference method for computing sensitivities of biochemical reactions. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2018, 474, 20180303.	2.1	3
70	\$\$ell \$\$: An Imperative DSL to Stochastically Simulate Biological Systems. Lecture Notes in Computer Science, 2015, , 354-374.	1.3	3
71	A Logical Approach to Security in the Context of Ambient Calculus. Electronic Notes in Theoretical Computer Science, 2004, 99, 3-29.	0.9	2
72	Checking security policies through an enhanced Control Flow Analysis. Journal of Computer Security, 2005, 13, 49-85.	0.8	2

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73	Communicating by compatibility. <i>The Journal of Logic and Algebraic Programming</i> , 2008, 75, 167-181.	1.4	2
74	Exploring the Limitations of Peripheral Blood Transcriptional Biomarkers in Predicting Influenza Vaccine Responsiveness. <i>Complexity</i> , 2017, 2017, 1-9.	1.6	2
75	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
76	QSPcc reduces bottlenecks in computational model simulations. <i>Communications Biology</i> , 2021, 4, 1022.	4.4	2
77	LR techniques for handling syntax errors. <i>Computer Languages, Systems and Structures</i> , 1998, 24, 73-98.	0.3	1
78	Preface to the special issue on Security in global computing. <i>International Journal of Information Security</i> , 2004, 2, 125-125.	3.4	1
79	On the computational power of BlenX. <i>Theoretical Computer Science</i> , 2010, 411, 542-565.	0.9	1
80	HSimulator: Hybrid Stochastic/Deterministic Simulation of Biochemical Reaction Networks. <i>Complexity</i> , 2017, 2017, 1-12.	1.6	1
81	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
82	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
83	Computational approaches to understanding nutrient metabolism and metabolic disorders. <i>Current Opinion in Biotechnology</i> , 2021, 70, 7-14.	6.6	0