Dario Pescini

List of Publications by Year
in descending order

59 papers	942 citations	471371 17 h-index	526166 27 g-index
69 all docs	69 docs citations	69 times ranked	794 citing authors

#	Article	IF	Citations
1	ExTaxsI: an exploration tool of biodiversity molecular data. GigaScience, 2022, 11, .	3.3	2
2	INTEGRATE: Model-based multi-omics data integration to characterize multi-level metabolic regulation. PLoS Computational Biology, 2022, 18, e1009337.	1.5	24
3	Accelerated global sensitivity analysis of genome-wide constraint-based metabolic models. BMC Bioinformatics, 2021, 22, 78.	1.2	5
4	GPRuler: Metabolic gene-protein-reaction rules automatic reconstruction. PLoS Computational Biology, 2021, 17, e1009550.	1.5	11
5	MaREA4Galaxy: Metabolic reaction enrichment analysis and visualization of RNA-seq data within Galaxy. Computational and Structural Biotechnology Journal, 2020, 18, 993-999.	1.9	7
6	Single-cell Digital Twins for Cancer Preclinical Investigation. Methods in Molecular Biology, 2020, 2088, 331-343.	0.4	17
7	Global Sensitivity Analysis of Constraint-Based Metabolic Models. Lecture Notes in Computer Science, 2020, , 179-186.	1.0	2
8	Integration of Single-Cell RNA-Sequencing Data into Flux Balance Cellular Automata. Lecture Notes in Computer Science, 2020, , 207-215.	1.0	1
9	Synchronization Effects in a Metabolism-Driven Model of Multi-cellular System. Communications in Computer and Information Science, 2019, , 115-126.	0.4	1
10	Integration of single-cell RNA-seq data into population models to characterize cancer metabolism. PLoS Computational Biology, 2019, 15, e1006733.	1.5	70
11	The Influence of Nutrients Diffusion on a Metabolism-driven Model of a Multi-cellular System. Fundamenta Informaticae, 2019, 171, 279-295.	0.3	0
12	Emerging ensembles of kinetic parameters to characterize observed metabolic phenotypes. BMC Bioinformatics, 2018, 19, 251.	1.2	2
13	Linking Alterations in Metabolic Fluxes with Shifts in Metabolite Levels by Means of Kinetic Modeling. Communications in Computer and Information Science, 2017, , 138-148.	0.4	1
14	Constraining Mechanism Based Simulations to Identify Ensembles of Parametrizations to Characterize Metabolic Features. Lecture Notes in Computer Science, 2017, , 107-117.	1.0	0
15	popFBA: tackling intratumour heterogeneity with Flux Balance Analysis. Bioinformatics, 2017, 33, i311-i318.	1.8	31
16	A metabolic core model elucidates how enhanced utilization of glucose and glutamine, with enhanced glutamine-dependent lactate production, promotes cancer cell growth: The WarburQ effect. PLoS Computational Biology, 2017, 13, e1005758.	1.5	64
17	Constraint-Based Modeling and Simulation of Cell Populations. Communications in Computer and Information Science, 2017, , 126-137.	0.4	3
18	Zooming-in on cancer metabolic rewiring with tissue specific constraint-based models. Computational Biology and Chemistry, 2016, 62, 60-69.	1.1	36

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19	cuTauLeaping: A GPU-Powered Tau-Leaping Stochastic Simulator for Massive Parallel Analyses of Biological Systems. PLoS ONE, 2014, 9, e91963.	1.1	28
20	Computational Strategies for a System-Level Understanding of Metabolism. Metabolites, 2014, 4, 1034-1087.	1.3	54
21	An ensemble evolutionary constraint-based approach to understand the emergence of metabolic phenotypes. Natural Computing, 2014, 13, 321-331.	1.8	18
22	Molecular Diffusion and Compartmentalization in Signal Transduction Pathways: An Application of Membrane Systems to the Study of Bacterial Chemotaxis. Emergence, Complexity and Computation, 2014, , 65-96.	0.2	1
23	In vivo and in silico analysis of PCNA ubiquitylation in the activation of the Post Replication Repair pathway in S. cerevisiae. BMC Systems Biology, 2013, 7, 24.	3.0	7
24	Reverse engineering of kinetic reaction networks by means of Cartesian Genetic Programming and Particle Swarm Optimization. , 2013, , .		13
25	cupSODA: A CUDA-Powered Simulator of Mass-Action Kinetics. Lecture Notes in Computer Science, 2013, , 344-357.	1.0	13
26	Estimating reaction constants in stochastic biological systems with a multi-swarm PSO running on GPUs. , 2012, , .		19
27	The role of feedback control mechanisms on the establishment of oscillatory regimes in the Ras/cAMP/PKA pathway in S. cerevisiae. Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 10.	1.4	26
28	Simulation of the Ras/cAMP/PKA pathway in budding yeast highlights the establishment of stable oscillatory states. Biotechnology Advances, 2012, 30, 99-107.	6.0	28
29	A GPU-Based Multi-swarm PSO Method for Parameter Estimation in Stochastic Biological Systems Exploiting Discrete-Time Target Series. Lecture Notes in Computer Science, 2012, , 74-85.	1.0	30
30	MODELING DIFFUSION IN A SIGNAL TRANSDUCTION PATHWAY: THE USE OF VIRTUAL VOLUMES IN P SYSTEMS. International Journal of Foundations of Computer Science, 2011, 22, 89-96.	0.8	6
31	BioSimWare: A Software for the Modeling, Simulation and Analysis of Biological Systems. Lecture Notes in Computer Science, 2010, , 119-143.	1.0	7
32	Computing with energy and chemical reactions. Natural Computing, 2010, 9, 493-512.	1.8	6
33	BioSimWare: A Simulation Environment for Stochastic Modelling of Complex Biological Systems. Journal of Biotechnology, 2010, 150, 519-520.	1.9	0
34	Simulation of the Ras/cAMP/PKA Pathway in Budding Yeast Evidences the Presence of Stable Oscillatory States. Journal of Biotechnology, 2010, 150, 545-545.	1.9	0
35	A Novel Variant of P Systems for the Modelling and Simulation of Biochemical Systems. Lecture Notes in Computer Science, 2010, , 210-226.	1.0	3
36	Modelling Spatial Heterogeneity and Macromolecular Crowding with Membrane Systems. Lecture Notes in Computer Science, 2010, , 285-304.	1.0	6

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37	(Tissue) P systems with cell polarity. Mathematical Structures in Computer Science, 2009, 19, 1141-1160.	0.5	2
38	Stochastic Simulations on a Grid Framework for Parameter Sweep Applications in Biological Models. , 2009, , .		5
39	A Multi-volume Approach to Stochastic Modeling with Membrane Systems. Natural Computing Series, 2009, , 519-542.	2.2	6
40	First Steps Towards a Wet Implementation for Ï„-DPP. Lecture Notes in Computer Science, 2009, , 355-373.	1.0	2
41	A Comparison of Genetic Algorithms and Particle Swarm Optimization for Parameter Estimation in Stochastic Biochemical Systems. Lecture Notes in Computer Science, 2009, , 116-127.	1.0	24
42	Modelling metapopulations with stochastic membrane systems. BioSystems, 2008, 91, 499-514.	0.9	45
43	Modeling and stochastic simulation of the Ras/cAMP/PKA pathway in the yeast Saccharomyces cerevisiae evidences a key regulatory function for intracellular guanine nucleotides pools. Journal of Biotechnology, 2008, 133, 377-385.	1.9	46
44	Membrane systems in systems biology. , 2008, , .		2
45	Seasonal variance in P system models for metapopulations. Progress in Natural Science: Materials International, 2007, 17, 392-400.	1.8	8
46	Cycles and communicating classes in membrane systems and molecular dynamics. Theoretical Computer Science, 2007, 372, 242-266.	0.5	6
47	A new technique for fluid velocimetry based on near field scattering. Optics and Lasers in Engineering, 2006, 44, 722-731.	2.0	6
48	A new particle sizing technique based on near field scattering. Nuclear Physics, Section B, Proceedings Supplements, 2006, 150, 334-338.	0.5	3
49	DYNAMICAL PROBABILISTIC P SYSTEMS. International Journal of Foundations of Computer Science, 2006, 17, 183-204.	0.8	79
50	Towards a P Systems Pseudomonas Quorum Sensing Model. Lecture Notes in Computer Science, 2006, , 197-214.	1.0	13
51	Tau Leaping Stochastic Simulation Method in P Systems. Lecture Notes in Computer Science, 2006, , 298-313.	1.0	28
52	Towards Probabilistic Model Checking on P Systems Using PRISM. Lecture Notes in Computer Science, 2006, , 477-495.	1.0	21
53	Investigating local evolutions in dynamical probabilistic P systems. , 2005, , .		7
54	Heterodyne near-field scattering: A technique for complex fluids. Physical Review E, 2004, 70, 041405.	0.8	57

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55	A novel particle sizing technique based on near field scattering. , 2004, , .		1
56	GPU-powered Simulation Methodologies for Biological Systems. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 130, 87-91.	0.8	2
57	An Analysis on the Influence of Network Topologies on Local and Global Dynamics of Metapopulation Systems. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 33, 1-17.	0.8	5
58	A study on the combined interplay between stochastic fluctuations and the number of flagella in bacterial chemotaxis. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 6, 47-62.	0.8	5
59	An ensemble approach to the study of the emergence of metabolic and proliferative disorders via Flux Balance Analysis. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 130, 92-97.	0.8	0