Daniela Besozzi

List of Publications by Year
in descending order

56 papers	1,250 citations	471509 17 h-index	414414 32 g-index
60 all docs	60 docs citations	60 times ranked	1305 citing authors

#	Article	IF	Citations
1	SMGen: A Generator of Synthetic Models of Biochemical Reaction Networks. Symmetry, 2022, 14, 119.	2.2	6
2	The Multi-Level Mechanism of Action of a Pan-Ras Inhibitor Explains its Antiproliferative Activity on Cetuximab-Resistant Cancer Cells. Frontiers in Molecular Biosciences, 2021, 8, 625979.	3.5	7
3	Screening for Combination Cancer Therapies With Dynamic Fuzzy Modeling and Multi-Objective Optimization. Frontiers in Genetics, 2021, 12, 617935.	2.3	5
4	HyperBeta: characterizing the structural dynamics of proteins and self-assembling peptides. Scientific Reports, 2021, 11, 7783.	3.3	0
5	Selected papers from the 15th and 16th international conference on Computational Intelligence Methods for Bioinformatics and Biostatistics. BMC Bioinformatics, 2021, 22, 90.	2.6	1
6	Editorial: Network-Oriented Approaches to Anticancer Drug Response. Frontiers in Bioengineering and Biotechnology, 2021, 9, 692369.	4.1	0
7	Analysis of single-cell RNA sequencing data based on autoencoders. BMC Bioinformatics, 2021, 22, 309.	2.6	15
8	The Impact of Representation on the Optimization of Marker Panels for Single-cell RNA Data. , 2021, , .		5
9	If You Canâ€™t Beat It, Squash It: Simplify Global Optimization by Evolving Dilation Functions. , 2021, , .		5
10	FiCoS: A fine-grained and coarse-grained GPU-powered deterministic simulator for biochemical networks. PLoS Computational Biology, 2021, 17, e1009410.	3.2	1
11	A comparison of multi-objective optimization algorithms to identify drug target combinations. , 2021, , .		0
12	An Experimental and Computational Protocol to Study Cell Proliferation in Human Acute Myeloid Leukemia Xenografts. Methods in Molecular Biology, 2021, 2185, 241-258.	0.9	1
13	Coupling Mechanistic Approaches and Fuzzy Logic to Model and Simulate Complex Systems. IEEE Transactions on Fuzzy Systems, 2020, 28, 1748-1759.	9.8	13
14	Fuzzy modeling and global optimization to predict novel therapeutic targets in cancer cells. Bioinformatics, 2020, 36, 2181-2188.	4.1	10
15	ACDC: Automated Cell Detection and Counting for Time-Lapse Fluorescence Microscopy. Applied Sciences (Switzerland), 2020, 10, 6187.	2.5	9
16	cuProCell: GPU-Accelerated Analysis of Cell Proliferation With Flow Cytometry Data. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 3173-3181.	6.3	2
17	On the automatic calibration of fully analogical spiking neuromorphic chips. , 2020, , .		2
18	Which random is the best random? A study on sampling methods in Fourier surrogate modeling. , 2020, , .		3

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19	Surfing on Fitness Landscapes: A Boost on Optimization by Fourier Surrogate Modeling. Entropy, 2020, 22, 285.	2.2	14
20	Efficient and Settings-Free Calibration of Detailed Kinetic Metabolic Models with Enzyme Isoforms Characterization. Lecture Notes in Computer Science, 2020, , 187-202.	1.3	3
21	Simpful: A User-Friendly Python Library for Fuzzy Logic. International Journal of Computational Intelligence Systems, 2020, 13, 1687.	2.7	32
22	Fourier Surrogate Models of Dilated Fitness Landscapes in Systems Biology : or how we learned to torture optimization problems until they confess. , 2020, , .		0
23	ginSODA: massive parallel integration of stiff ODE systems on GPUs. Journal of Supercomputing, 2019, 75, 7844-7856.	3.6	5
24	USE-Net: Incorporating Squeeze-and-Excitation blocks into U-Net for prostate zonal segmentation of multi-institutional MRI datasets. Neurocomputing, 2019, 365, 31-43.	5.9	185
25	ProCell: Investigating cell proliferation with Swarm Intelligence. , 2019, , .		3
26	Biochemical parameter estimation vs. benchmark functions: A comparative study of optimization performance and representation design. Applied Soft Computing Journal, 2019, 81, 105494.	7.2	45
27	GenHap: a novel computational method based on genetic algorithms for haplotype assembly. BMC Bioinformatics, 2019, 20, 172.	2.6	26
28	A novel framework for MR image segmentation and quantification by using MedGA. Computer Methods and Programs in Biomedicine, 2019, 176, 159-172.	4.7	43
29	Modeling cell proliferation in human acute myeloid leukemia xenografts. Bioinformatics, 2019, 35, 3378-3386.	4.1	8
30	Computational Intelligence for Life Sciences. Fundamenta Informaticae, 2019, 171, 57-80.	0.4	5
31	MedGA: A novel evolutionary method for image enhancement in medical imaging systems. Expert Systems With Applications, 2019, 119, 387-399.	7.6	85
32	Fuzzy Self-Tuning PSO: A settings-free algorithm for global optimization. Swarm and Evolutionary Computation, 2018, 39, 70-85.	8.1	171
33	Computational Intelligence for Parameter Estimation of Biochemical Systems. , 2018, , .		21
34	Graphics processing units in bioinformatics, computational biology and systems biology. Briefings in Bioinformatics, 2017, 18, bbw058.	6.5	84
35	Gillespie's Stochastic Simulation Algorithm on MIC coprocessors. Journal of Supercomputing, 2017, 73, 676-686.	3.6	4
36	GPU-powered model analysis with PySB/cupSODA. Bioinformatics, 2017, 33, 3492-3494.	4.1	17

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37	LASSIE: simulating large-scale models of biochemical systems on GPUs. BMC Bioinformatics, 2017, 18, 246.	2.6	22
38	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. Npj Systems Biology and Applications, 2016, 2, 16011.	3.0	21
39	GPU-powered and settings-free parameter estimation of biochemical systems. , 2016, , .		4
40	Reaction-Based Models of Biochemical Networks. Lecture Notes in Computer Science, 2016, , 24-34.	1.3	6
41	The impact of particles initialization in PSO: Parameter estimation as a case in point. , 2015, , .		27
42	Proactive Particles in Swarm Optimization: A self-tuning algorithm based on Fuzzy Logic. , 2015, , .		18
43	cuTauLeaping: A GPU-Powered Tau-Leaping Stochastic Simulator for Massive Parallel Analyses of Biological Systems. PLoS ONE, 2014, 9, e91963.	2.5	28
44	Computational Strategies for a System-Level Understanding of Metabolism. Metabolites, 2014, 4, 1034-1087.	2.9	54
45	Massive Exploration of Perturbed Conditions of the Blood Coagulation Cascade through GPU Parallelization. BioMed Research International, 2014, 2014, 1-20.	1.9	10
46	GPU-accelerated simulations of mass-action kinetics models with cupSODA. Journal of Supercomputing, 2014, 69, 17-24.	3.6	44
47	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
48	cupSODA: A CUDA-Powered Simulator of Mass-Action Kinetics. Lecture Notes in Computer Science, 2013, , 344-357.	1.3	13
49	Estimating reaction constants in stochastic biological systems with a multi-swarm PSO running on GPUs. , 2012, , .		19
50	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
51	Simulation of the Ras/cAMP/PKA pathway in budding yeast highlights the establishment of stable oscillatory states. Biotechnology Advances, 2012, 30, 99-107.	11.7	28
52	BioSimWare: A Software for the Modeling, Simulation and Analysis of Biological Systems. Lecture Notes in Computer Science, 2010, , 119-143.	1.3	7
53	A Comparison of Genetic Algorithms and Particle Swarm Optimization for Parameter Estimation in Stochastic Biochemical Systems. Lecture Notes in Computer Science, 2009, , 116-127.	1.3	24
54	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.	3.8	46

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55	Cycles and communicating classes in membrane systems and molecular dynamics. Theoretical Computer Science, 2007, 372, 242-266.	0.9	6
56	Modeling Calcium Signaling in S. cerevisiae Highlights the Role and Regulation of the Calmodulin-Calcineurin Pathway in Response to Hypotonic Shock. Frontiers in Molecular Biosciences, 0, 9, .	3.5	1