

Giancarlo Mauri

List of Publications by Year in descending order

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Version: 2024-02-01

364
papers

6,392
citations

94433

37
h-index

128289

60
g-index

400
all docs

400
docs citations

400
times ranked

6188
citing authors

#	ARTICLE	IF	CITATIONS
1	On the complexity of approximately matching a string to a directed graph. Information and Computation, 2022, 288, 104748.	0.7	2
2	Top-k overlapping densest subgraphs: approximation algorithms and computational complexity. Journal of Combinatorial Optimization, 2021, 41, 80-104.	1.3	18
3	HyperBeta: characterizing the structural dynamics of proteins and self-assembling peptides. Scientific Reports, 2021, 11, 7783.	3.3	0
4	Alternative space definitions for P systems with active membranes. Journal of Membrane Computing, 2021, 3, 87-96.	1.8	5
5	FiCoS: A fine-grained and coarse-grained GPU-powered deterministic simulator for biochemical networks. PLoS Computational Biology, 2021, 17, e1009410.	3.2	1
6	A Low-Dose CT-Based Radiomic Model to Improve Characterization and Screening Recall Intervals of Indeterminate Prevalent Pulmonary Nodules. Diagnostics, 2021, 11, 1610.	2.6	10
7	Explainable Attentional Neural Recommendations for Personalized Social Learning. Lecture Notes in Computer Science, 2021, , 67-79.	1.3	1
8	A CUDA-powered method for the feature extraction and unsupervised analysis of medical images. Journal of Supercomputing, 2021, 77, 8514-8531.	3.6	6
9	A framework for validating AI in precision medicine: considerations from the European ITFoC consortium. BMC Medical Informatics and Decision Making, 2021, 21, 274.	3.0	28
10	Depth-two P systems can simulate Turing machines with NP oracles. Theoretical Computer Science, 2021, , .	0.9	1
11	Subroutines in P systems and closure properties of their complexity classes. Theoretical Computer Science, 2020, 805, 193-205.	0.9	4
12	Coupling Mechanistic Approaches and Fuzzy Logic to Model and Simulate Complex Systems. IEEE Transactions on Fuzzy Systems, 2020, 28, 1748-1759.	9.8	13
13	Fuzzy modeling and global optimization to predict novel therapeutic targets in cancer cells. Bioinformatics, 2020, 36, 2181-2188.	4.1	10
14	ACDC: Automated Cell Detection and Counting for Time-Lapse Fluorescence Microscopy. Applied Sciences (Switzerland), 2020, 10, 6187.	2.5	9
15	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
16	Simulating counting oracles with cooperation. Journal of Membrane Computing, 2020, 2, 303-310.	1.8	3
17	MaREA4Galaxy: Metabolic reaction enrichment analysis and visualization of RNA-seq data within Galaxy. Computational and Structural Biotechnology Journal, 2020, 18, 993-999.	4.1	7
18	Online Social Space Identification. A Computational Tool for Optimizing Social Recommendations. Applied Sciences (Switzerland), 2020, 10, 3024.	2.5	0

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19	Shallow laconic P systems can count. Journal of Membrane Computing, 2020, 2, 49-58.	1.8	8
20	Surfing on Fitness Landscapes: A Boost on Optimization by Fourier Surrogate Modeling. Entropy, 2020, 22, 285.	2.2	14
21	A Turing machine simulation by P systems without charges. Journal of Membrane Computing, 2020, 2, 71-79.	1.8	15
22	Single-cell Digital Twins for Cancer Preclinical Investigation. Methods in Molecular Biology, 2020, 2088, 331-343.	0.9	17
23	CNN-Based Prostate Zonal Segmentation on T2-Weighted MR Images: A Cross-Dataset Study. Smart Innovation, Systems and Technologies, 2020, , 269-280.	0.6	20
24	Infinite Brain MR Images: PGGAN-Based Data Augmentation for Tumor Detection. Smart Innovation, Systems and Technologies, 2020, , 291-303.	0.6	46
25	Attentional Neural Mechanisms for Social Recommendations in Educational Platforms. , 2020, ,		1
26	Complexity Issues of String to Graph Approximate Matching. Lecture Notes in Computer Science, 2020, , 248-259.	1.3	3
27	Integration of Single-Cell RNA-Sequencing Data into Flux Balance Cellular Automata. Lecture Notes in Computer Science, 2020, , 207-215.	1.3	1
28	An Attention-based Architecture for EEG Classification. , 2020, ,		2
29	Kernel Machines: Introduction. , 2019, , 495-502.		3
30	Kernel Methods: Support Vector Machines. , 2019, , 503-510.		12
31	Kernel Machines: Applications. , 2019, , 511-518.		0
32	Graph Algorithms. , 2019, , 940-949.		3
33	ginSODA: massive parallel integration of stiff ODE systems on GPUs. Journal of Supercomputing, 2019, 75, 7844-7856.	3.6	5
34	Graph Isomorphism. , 2019, , 933-939.		0
35	HaraliCU: GPU-Powered Haralick Feature Extraction on Medical Images Exploiting the Full Dynamics of Gray-Scale Levels. Lecture Notes in Computer Science, 2019, , 304-318.	1.3	10
36	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

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37	Characterizing PSPACE with shallow non-confluent P systems. Journal of Membrane Computing, 2019, 1, 75-84.	1.8	20
38	System of Nudge Theory-Based ICT Applications for Older Citizens: The SENIOR Project. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2019, , 29-42.	0.3	1
39	Comparing incomplete sequences via longest common subsequence. Theoretical Computer Science, 2019, 796, 272-285.	0.9	2
40	Combining Noise-to-Image and Image-to-Image GANs: Brain MR Image Augmentation for Tumor Detection. IEEE Access, 2019, 7, 156966-156977.	4.2	138
41	Computational Methods for Resting-State EEG of Patients With Disorders of Consciousness. Frontiers in Neuroscience, 2019, 13, 807.	2.8	17
42	ProCell: Investigating cell proliferation with Swarm Intelligence. , 2019, , .		3
43	A Computational Model for Promoting Targeted Communication and Supplying Social Explainable Recommendations. , 2019, , .		2
44	Synchronization Effects in a Metabolism-Driven Model of Multi-cellular System. Communications in Computer and Information Science, 2019, , 115-126.	0.5	1
45	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
46	GenHap: a novel computational method based on genetic algorithms for haplotype assembly. BMC Bioinformatics, 2019, 20, 172.	2.6	26
47	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
48	Integration of single-cell RNA-seq data into population models to characterize cancer metabolism. PLoS Computational Biology, 2019, 15, e1006733.	3.2	70
49	On the tractability of finding disjoint clubs in a network. Theoretical Computer Science, 2019, 777, 243-251.	0.9	10
50	Modeling cell proliferation in human acute myeloid leukemia xenografts. Bioinformatics, 2019, 35, 3378-3386.	4.1	8
51	High Performance Computing for Haplotyping: Models and Platforms. Lecture Notes in Computer Science, 2019, , 650-661.	1.3	1
52	MedGA: A novel evolutionary method for image enhancement in medical imaging systems. Expert Systems With Applications, 2019, 119, 387-399.	7.6	85
53	Towards Human Cell Simulation. Lecture Notes in Computer Science, 2019, , 221-249.	1.3	6
54	Optimized Social Explanation for Educational Platforms. , 2019, , .		2

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55	Covering a Graph with Clubs. Journal of Graph Algorithms and Applications, 2019, 23, 271-292.	0.4	12
56	Computer-Assisted Approaches for Uterine Fibroid Segmentation in MRgFUS Treatments: Quantitative Evaluation and Clinical Feasibility Analysis. Smart Innovation, Systems and Technologies, 2019, , 229-241.	0.6	1
57	Solving QSAT in Sublinear Depth. Lecture Notes in Computer Science, 2019, , 188-201.	1.3	0
58	Top k 2-Clubs in a Network: A Genetic Algorithm. Lecture Notes in Computer Science, 2019, , 656-663.	1.3	0
59	A Gentle Introduction to Membrane Systems and Their Computational Properties. , 2019, , 1-32.		0
60	MTGO: PPI Network Analysis Via Topological and Functional Module Identification. Scientific Reports, 2018, 8, 5499.	3.3	103
61	Fuzzy Self-Tuning PSO: A settings-free algorithm for global optimization. Swarm and Evolutionary Computation, 2018, 39, 70-85.	8.1	171
62	NeXt for neuro-radiosurgery: A fully automatic approach for necrosis extraction in brain tumor MRI using an unsupervised machine learning technique. International Journal of Imaging Systems and Technology, 2018, 28, 21-37.	4.1	41
63	GTVcut for neuro-radiosurgery treatment planning: an MRI brain cancer seeded image segmentation method based on a cellular automata model. Natural Computing, 2018, 17, 521-536.	3.0	32
64	Integration of transcriptomic data and metabolic networks in cancer samples reveals highly significant prognostic power. Journal of Biomedical Informatics, 2018, 87, 37-49.	4.3	28
65	A survey on space complexity of P systems with active membranes. International Journal of Advances in Engineering Sciences and Applied Mathematics, 2018, 10, 221-229.	1.1	11
66	Computational Intelligence for Parameter Estimation of Biochemical Systems. , 2018, , .		21
67	GAN-based synthetic brain MR image generation. , 2018, , .		173
68	Distributed Heuristics for Optimizing Cohesive Groups: A Support for Clinical Patient Engagement in Social Network Analysis. , 2018, , .		0
69	Emerging ensembles of kinetic parameters to characterize observed metabolic phenotypes. BMC Bioinformatics, 2018, 19, 251.	2.6	2
70	In-Silico Integration Approach to Identify a Key miRNA Regulating a Gene Network in Aggressive Prostate Cancer. International Journal of Molecular Sciences, 2018, 19, 910.	4.1	11
71	Fully Automatic Multispectral MR Image Segmentation of Prostate Gland Based on the Fuzzy C-Means Clustering Algorithm. Smart Innovation, Systems and Technologies, 2018, , 23-37.	0.6	8
72	Solving a Special Case of the P Conjecture Using Dependency Graphs with Dissolution. Lecture Notes in Computer Science, 2018, , 196-213.	1.3	3

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73	Optimizing Social Interaction. , 2018, , .		2
74	Covering with Clubs: Complexity and Approximability. Lecture Notes in Computer Science, 2018, , 153-164.	1.3	1
75	Computational complexity of finite asynchronous cellular automata. Theoretical Computer Science, 2017, 664, 131-143.	0.9	19
76	Gillespie's Stochastic Simulation Algorithm on MIC coprocessors. Journal of Supercomputing, 2017, 73, 676-686.	3.6	4
77	Proteomic profiles of thyroid tumors by mass spectrometry-imaging on tissue microarrays. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 817-827.	2.3	23
78	A toolbox for simpler active membrane algorithms. Theoretical Computer Science, 2017, 673, 42-57.	0.9	8
79	Linking Alterations in Metabolic Fluxes with Shifts in Metabolite Levels by Means of Kinetic Modeling. Communications in Computer and Information Science, 2017, , 138-148.	0.5	1
80	From protein-protein interactions to protein co-expression networks: a new perspective to evaluate large-scale proteomic data. Eurasip Journal on Bioinformatics and Systems Biology, 2017, 2017, 6.	1.4	81
81	A fully automatic approach for multimodal PET and MR image segmentation in gamma knife treatment planning. Computer Methods and Programs in Biomedicine, 2017, 144, 77-96.	4.7	39
82	Constraining Mechanism Based Simulations to Identify Ensembles of Parametrizations to Characterize Metabolic Features. Lecture Notes in Computer Science, 2017, , 107-117.	1.3	0
83	COSYS: A Computational Infrastructure for Systems Biology. Lecture Notes in Computer Science, 2017, , 82-92.	1.3	1
84	Accelerated Analysis of Biological Parameters Space Using GPUs. Lecture Notes in Computer Science, 2017, , 70-81.	1.3	3
85	Area-based cell colony surviving fraction evaluation: A novel fully automatic approach using general-purpose acquisition hardware. Computers in Biology and Medicine, 2017, 89, 454-465.	7.0	19
86	GPU-powered model analysis with PySB/cupSODA. Bioinformatics, 2017, 33, 3492-3494.	4.1	17
87	Characterising the complexity of tissue P systems with fission rules. Journal of Computer and System Sciences, 2017, 90, 115-128.	1.2	20
88	Orthology Correction for Gene Tree Reconstruction: Theoretical and Experimental Results. Procedia Computer Science, 2017, 108, 1115-1124.	2.0	17
89	The counting power of P systems with antimatter. Theoretical Computer Science, 2017, 701, 161-173.	0.9	14
90	Tissue P Systems with Small Cell Volume. Fundamenta Informaticae, 2017, 154, 261-275.	0.4	5

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91	Efficient Simulation of Reaction Systems on Graphics Processing Units. Fundamenta Informaticae, 2017, 154, 307-321.	0.4	13
92	LASSIE: simulating large-scale models of biochemical systems on GPUs. BMC Bioinformatics, 2017, 18, 246.	2.6	22
93	popFBA: tackling intratumour heterogeneity with Flux Balance Analysis. Bioinformatics, 2017, 33, i311-i318.	4.1	31
94	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.	3.2	64
95	Pathway-based classification of breast cancer subtypes. Frontiers in Bioscience - Landmark, 2017, 22, 1697-1712.	3.0	17
96	SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. International Journal of Molecular Sciences, 2017, 18, 274.	4.1	50
97	Automated Prostate Gland Segmentation Based on an Unsupervised Fuzzy C-Means Clustering Technique Using Multispectral T1w and T2w MR Imaging. Information (Switzerland), 2017, 8, 49.	2.9	48
98	Shallow Non-confluent P Systems. Lecture Notes in Computer Science, 2017, , 307-316.	1.3	4
99	DIABESITY: A Study for mHealth Integrated Solutions. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2017, , 195-199.	0.3	1
100	Constraint-Based Modeling and Simulation of Cell Populations. Communications in Computer and Information Science, 2017, , 126-137.	0.5	3
101	mHealth and eHealth for Obesity and Types 2 and 1 Diabetes. Journal of Diabetes Research, 2016, 2016, 1-1.	2.3	6
102	A Support Vector Machine Classification of Thyroid Bioptic Specimens Using MALDI-MSI Data. Advances in Bioinformatics, 2016, 2016, 1-7.	5.7	17
103	Multimodal medical image registration using Particle Swarm Optimization: A review. , 2016, , .		25
104	How interacting pathways are regulated by miRNAs in breast cancer subtypes. BMC Bioinformatics, 2016, 17, 348.	2.6	20
105	Parallel implementation of efficient search schemes for the inference of cancer progression models. , 2016, , .		5
106	Trend of FEV1 in Cystic Fibrosis patients: A telehomecare experience. , 2016, , .		0
107	MP85-19 URINARY PEPTIDOME AND PROTEOME ALTERATIONS RELATED TO TUMOR PROGRESSION AND INVASION IN RCC. Journal of Urology, 2016, 195, .	0.4	0
108	Ordering cancer mutational profiles of cross-sectional copy number alterations. International Journal of Data Mining and Bioinformatics, 2016, 15, 59.	0.1	1

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109	Neuro-Radiosurgery Treatments: MRI Brain Tumor Seeded Image Segmentation Based on a Cellular Automata Model. Lecture Notes in Computer Science, 2016, , 323-333.	1.3	4
110	Monodirectional P systems. Natural Computing, 2016, 15, 551-564.	3.0	25
111	Gene switching rate determines response to extrinsic perturbations in the self-activation transcriptional network motif. Scientific Reports, 2016, 6, 26980.	3.3	10
112	BITS 2015: the annual meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2016, 17, 396.	2.6	0
113	Machine learning approaches in MALDI-MSI: clinical applications. Expert Review of Proteomics, 2016, 13, 685-696.	3.0	22
114	CABeRNET: a Cytoscape app for augmented Boolean models of gene regulatory NETworks. BMC Bioinformatics, 2016, 17, 64.	2.6	13
115	Algorithmic methods to infer the evolutionary trajectories in cancer progression. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4025-34.	7.1	80
116	Zooming-in on cancer metabolic rewiring with tissue specific constraint-based models. Computational Biology and Chemistry, 2016, 62, 60-69.	2.3	36
117	TRONCO: an R package for the inference of cancer progression models from heterogeneous genomic data. Bioinformatics, 2016, 32, 1911-1913.	4.1	39
118	Clique Editing to Support Case Versus Control Discrimination. Smart Innovation, Systems and Technologies, 2016, , 27-36.	0.6	6
119	Design of the TRONCO BioConductor Package for TRanslational ONCOlogy. R Journal, 2016, 8, 39.	1.8	3
120	Tumor size, stage and grade alterations of urinary peptidome in RCC. Journal of Translational Medicine, 2015, 13, 332.	4.4	38
121	Recent complexity-theoretic results on P systems with active membranes. Journal of Logic and Computation, 2015, 25, 1047-1071.	0.8	7
122	Social media and mobile applications in chronic disease prevention and management. Frontiers in Psychology, 2015, 6, 567.	2.1	53
123	New Technologies for the Management and Rehabilitation of Chronic Diseases and Conditions. BioMed Research International, 2015, 2015, 1-2.	1.9	17
124	CoGNAC: A Chaste Plugin for the Multiscale Simulation of Gene Regulatory Networks Driving the Spatial Dynamics of Tissues and Cancer. Cancer Informatics, 2015, 14s4, CIN.S19965.	1.9	12
125	Managing chronic pathologies with a stepped mHealth-based approach in clinical psychology and medicine. Frontiers in Psychology, 2015, 06, 407.	2.1	32
126	Proactive Particles in Swarm Optimization: A self-tuning algorithm based on Fuzzy Logic. , 2015, , .		18

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127	Foreword: asynchronous behavior of cellular automata and discrete models. Natural Computing, 2015, 14, 505-506.	3.0	0
128	Robust Conclusions in Mass Spectrometry Analysis. Procedia Computer Science, 2015, 51, 683-692.	2.0	0
129	Membrane Division, Oracles, and the Counting Hierarchy. Fundamenta Informaticae, 2015, 138, 97-111.	0.4	24
130	CAPRI: efficient inference of cancer progression models from cross-sectional data. Bioinformatics, 2015, 31, 3016-3026.	4.1	90
131	Restricted and Swap Common Superstring: A Multivariate Algorithmic Perspective. Algorithmica, 2015, 72, 914-939.	1.3	1
132	Tissue P Systems Can be Simulated Efficiently with Counting Oracles. Lecture Notes in Computer Science, 2015, , 251-261.	1.3	4
133	Complexity Classes for Membrane Systems: A Survey. Lecture Notes in Computer Science, 2015, , 56-69.	1.3	0
134	Telemedicine Home Program in Patients with Cystic Fibrosis: Results after 10 Years. Clinica Terapeutica, 2015, 166, e384-8.	0.3	8
135	cuTauLeaping: A GPU-Powered Tau-Leaping Stochastic Simulator for Massive Parallel Analyses of Biological Systems. PLoS ONE, 2014, 9, e91963.	2.5	28
136	Integration of mRNA Expression Profile, Copy Number Alterations, and microRNA Expression Levels in Breast Cancer to Improve Grade Definition. PLoS ONE, 2014, 9, e97681.	2.5	53
137	Urinary Signatures of Renal Cell Carcinoma Investigated by Peptidomic Approaches. PLoS ONE, 2014, 9, e106684.	2.5	30
138	Inferring Tree Causal Models of Cancer Progression with Probability Raising. PLoS ONE, 2014, 9, e108358.	2.5	57
139	Computational Strategies for a System-Level Understanding of Metabolism. Metabolites, 2014, 4, 1034-1087.	2.9	54
140	Self-adaptive simulation time for sensitivity analysis of a stochastic computational model. , 2014, , .		0
141	A memetic hybrid method for the Molecular Distance Geometry Problem with incomplete information. , 2014, , .		3
142	Constant-Space P Systems with Active Membranes. Fundamenta Informaticae, 2014, 134, 111-128.	0.4	11
143	Massive Exploration of Perturbed Conditions of the Blood Coagulation Cascade through GPU Parallelization. BioMed Research International, 2014, 2014, 1-20.	1.9	10
144	Towards the Use of Genetic Programming for the Prediction of Survival in Cancer. , 2014, , 177-192.		2

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145	Stochastic Hybrid Automata with delayed transitions to model biochemical systems with delays. Information and Computation, 2014, 236, 19-34.	0.7	6
146	A study of search algorithmsâ€™ optimization speed. Journal of Combinatorial Optimization, 2014, 27, 256-270.	1.3	2
147	Combined analysis of chromosomal instabilities and gene expression for colon cancer progression inference. Journal of Clinical Bioinformatics, 2014, 4, 2.	1.2	15
148	Space complexity equivalence of P systems with active membranes and Turing machines. Theoretical Computer Science, 2014, 529, 69-81.	0.9	27
149	GPU-accelerated simulations of mass-action kinetics models with cupSODA. Journal of Supercomputing, 2014, 69, 17-24.	3.6	44
150	Simulation and Analysis of the Blood Coagulation Cascade Accelerated on GPU. , 2014, , .		0
151	A local landscape mapping method for protein structure prediction in the HP model. Natural Computing, 2014, 13, 309-319.	3.0	1
152	An ensemble evolutionary constraint-based approach to understand the emergence of metabolic phenotypes. Natural Computing, 2014, 13, 321-331.	3.0	18
153	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.	0.3	1
154	Simulating Elementary Active Membranes. Lecture Notes in Computer Science, 2014, , 284-299.	1.3	19
155	Flattening in (Tissue) P Systems. Lecture Notes in Computer Science, 2014, , 173-188.	1.3	20
156	Enzymatic Numerical P Systems Using Elementary Arithmetic Operations. Lecture Notes in Computer Science, 2014, , 249-264.	1.3	5
157	Introducing a Space Complexity Measure for P Systems. International Journal of Computers, Communications and Control, 2014, 4, 301.	1.8	22
158	SPECIAL ISSUE ON MEMBRANE COMPUTING, Seventh Brainstorming Week on Membrane Computing. International Journal of Computers, Communications and Control, 2014, 4, 204.	1.8	0
159	P Systems with Active Membranes Working in Sublinear Space. Lecture Notes in Computer Science, 2014, , 35-47.	1.3	0
160	Elementary Active Membranes Have the Power of Counting. , 2014, , 194-206.		0
161	Availability of MudPIT data for classification of biological samples. Journal of Clinical Bioinformatics, 2013, 3, 1.	1.2	14
162	m-Asynchronous cellular automata: from fairness to quasi-fairness. Natural Computing, 2013, 12, 561-572.	3.0	33

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163	Candidate biomarkers for response to tamoxifen in breast cancer metastatic patients. , 2013, , .		1
164	G<sc>e</sc>S<sc>to</sc>D<sc>ifferent</sc>: a Cytoscape plugin for the generation and the identification of gene regulatory networks describing a stochastic cell differentiation process. Bioinformatics, 2013, 29, 513-514.	4.1	6
165	The<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.gif" display="inline" overflow="scroll"><mml:mi>l</mml:mi></mml:math>-Diversity problem: Tractability and approximability. Theoretical Computer Science, 2013, 511, 159-171.	0.9	9
166	Reverse engineering of kinetic reaction networks by means of Cartesian Genetic Programming and Particle Swarm Optimization. , 2013, , .		13
167	cupSODA: A CUDA-Powered Simulator of Mass-Action Kinetics. Lecture Notes in Computer Science, 2013, , 344-357.	1.3	13
168	Combination of gene expression and genome copy number alteration has a prognostic value for breast cancer. , 2013, 2013, 608-11.		15
169	Evolutionary inference of biochemical reaction networks accelerated on graphics processing units. , 2013, , .		0
170	RESEARCH FRONTIERS OF MEMBRANE COMPUTING: OPEN PROBLEMS AND RESEARCH TOPICS. International Journal of Foundations of Computer Science, 2013, 24, 547-623.	1.1	48
171	SENSITIVITY ANALYSIS FOR STUDYING THE RELATION BETWEEN BIOCHEMICAL REACTIONS AND METABOLIC PHENOTYPES. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340002.	0.8	2
172	The Interplay of Intrinsic and Extrinsic Bounded Noises in Biomolecular Networks. PLoS ONE, 2013, 8, e51174.	2.5	41
173	Bounded Extrinsic Noises Affecting Biochemical Networks with Low Molecule Numbers. Modeling and Simulation in Science, Engineering and Technology, 2013, , 201-221.	0.6	1
174	Sublinear-Space PÃSystems with Active Membranes. Lecture Notes in Computer Science, 2013, , 342-357.	1.3	19
175	CopyÃNumber Alterations for Tumor Progression Inference. Lecture Notes in Computer Science, 2013, , 104-109.	1.3	11
176	Cancer cell growth and survival as a system-level property sustained by enhanced glycolysis and mitochondrial metabolic remodeling. Frontiers in Physiology, 2012, 3, 362.	2.8	24
177	Estimating reaction constants in stochastic biological systems with a multi-swarm PSO running on GPUs. , 2012, , .		19
178	Mutual Information Optimization for Mass Spectra Data Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 934-939.	3.0	7
179	An Empirical Study of Parallel and Distributed Particle Swarm Optimization. Studies in Computational Intelligence, 2012, , 125-150.	0.9	3
180	A new clustering approach for learning transcriptional modules. International Journal of Data Mining and Bioinformatics, 2012, 6, 304.	0.1	2

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181	Poster: Characterization of distinguishing regions for Renal Cell Carcinoma discrimination. , 2012, , .		0
182	The role of feedback control mechanisms on the establishment of oscillatory regimes in the Ras/cAMP/PKA pathway in <i>S. cerevisiae</i> . Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 10.	1.4	26
183	An excursion in reaction systems: From computer science to biology. Theoretical Computer Science, 2012, 454, 95-108.	0.9	42
184	A study on learning robustness using asynchronous 1D cellular automata rules. Natural Computing, 2012, 11, 289-302.	3.0	6
185	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
186	A study of the neutrality of Boolean function landscapes in genetic programming. Theoretical Computer Science, 2012, 425, 34-57.	0.9	13
187	A distance between populations for one-point crossover in genetic algorithms. Theoretical Computer Science, 2012, 429, 213-221.	0.9	4
188	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.	1.3	30
189	m-Asynchronous Cellular Automata. Lecture Notes in Computer Science, 2012, , 653-662.	1.3	8
190	Restricted and Swap Common Superstring: A Parameterized View. Lecture Notes in Computer Science, 2012, , 49-60.	1.3	1
191	Ordering copy number alteration data to analyze colorectal cancer progression. EMBnet Journal, 2012, 18, 84.	0.6	0
192	Chromosome instability for tumor progression inference. EMBnet Journal, 2012, 18, 97.	0.6	0
193	Picture Languages Generated by Assembling Tiles. Fundamenta Informaticae, 2011, 110, 77-93.	0.4	0
194	P systems with active membranes: trading time for space. Natural Computing, 2011, 10, 167-182.	3.0	20
195	A Comparative Study of Four Parallel and Distributed PSO Methods. New Generation Computing, 2011, 29, 129-161.	3.3	23
196	A comparison of machine learning techniques for survival prediction in breast cancer. BioData Mining, 2011, 4, 12.	4.0	41
197	PSYSTEMS WITH ACTIVE MEMBRANES WORKING IN POLYNOMIAL SPACE. International Journal of Foundations of Computer Science, 2011, 22, 65-73.	1.1	22
198	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.	1.1	6

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199	A New Evolutionary Gene Regulatory Network Reverse Engineering Tool. Lecture Notes in Computer Science, 2011, , 13-24.	1.3	2
200	Elementary Active Membranes Have the Power of Counting. International Journal of Natural Computing Research, 2011, 2, 35-48.	0.5	14
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