

Mario R Guarracino

List of Publications by Year in descending order

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89
papers

1,075
citations

471061

17
h-index

525886

27
g-index

96
all docs

96
docs citations

96
times ranked

1638
citing authors

#	ARTICLE	IF	CITATIONS
1	A classification method based on generalized eigenvalue problems. Optimization Methods and Software, 2007, 22, 73-81.	1.6	74
2	Cold adaptation shapes the robustness of metabolic networks in <i>Drosophila melanogaster</i> . Evolution; International Journal of Organic Evolution, 2014, 68, 3505-3523.	1.1	65
3	Glycosphingolipid metabolic reprogramming drives neural differentiation. EMBO Journal, 2018, 37, .	3.5	56
4	From trash to treasure: detecting unexpected contamination in unmapped NGS data. BMC Bioinformatics, 2019, 20, 168.	1.2	54
5	Integrating imaging and omics data: A review. Biomedical Signal Processing and Control, 2019, 52, 264-280.	3.5	41
6	Characterization of the Duodenal Mucosal Microbiome in Obese Adult Subjects by 16S rRNA Sequencing. Microorganisms, 2020, 8, 485.	1.6	36
7	Prediction of the responsiveness to pharmacological chaperones: lysosomal human alpha-galactosidase, a case of study. Orphanet Journal of Rare Diseases, 2010, 5, 36.	1.2	35
8	Foraging rules of flower selection applied by colonies of <i>Apis mellifera</i> : ranking and associations of floral sources. Functional Ecology, 2012, 26, 1186-1196.	1.7	34
9	Oropharyngeal microbiome evaluation highlights Neisseria abundance in active celiac patients. Scientific Reports, 2018, 8, 11047.	1.6	33
10	Studio comparativo con esame TC contrastografico e con PET-TC del tumore polmonare non a piccole cellule. Medical Science Monitor, 2013, 19, 95-101.	0.5	33
11	CAOS: a numerical simulation tool for astronomical adaptive optics (and beyond). , 2004, , .		31
12	Adaptive phenotype drives resistance to androgen deprivation therapy in prostate cancer. Cell Communication and Signaling, 2017, 15, 51.	2.7	29
13	Long Non-Coding RNA MAGI2-AS3 is a New Player with a Tumor Suppressive Role in High Grade Serous Ovarian Carcinoma. Cancers, 2019, 11, 2008.	1.7	27
14	SDI+: A Novel Algorithm for Segmenting Dermoscopic Images. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 481-488.	3.9	25
15	Robust generalized eigenvalue classifier with ellipsoidal uncertainty. Annals of Operations Research, 2014, 216, 327-342.	2.6	24
16	Integration of transcriptomic data in a genome-scale metabolic model to investigate the link between obesity and breast cancer. BMC Bioinformatics, 2019, 20, 162.	1.2	22
17	A hnRNP ϵ -AR-Related Signature Reflects Progression toward Castration-Resistant Prostate Cancer. International Journal of Molecular Sciences, 2018, 19, 1920.	1.8	19
18	Incremental Classification with Generalized Eigenvalues. Journal of Classification, 2007, 24, 205-219.	1.2	18

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19	Long Non-Coding RNA HAND2-AS1 Acts as a Tumor Suppressor in High-Grade Serous Ovarian Carcinoma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4059.	1.8	18
20	Pooled testing with replication as a mass testing strategy for the COVID-19 pandemics. <i>Scientific Reports</i> , 2021, 11, 3459.	1.6	18
21	miR-138/miR-222 Overexpression Characterizes the miRNome of Amniotic Mesenchymal Stem Cells in Obesity. <i>Stem Cells and Development</i> , 2017, 26, 4-14.	1.1	17
22	Genetic diversity in a collection of Italian long storage tomato landraces as revealed by SNP markers array. <i>Plant Biosystems</i> , 2019, 153, 288-297.	0.8	17
23	A Grid Enabled PSE for Medical Imaging: Experiences on MedGrid. , 0, , .		16
24	Netpro2vec: A Graph Embedding Framework for Biomedical Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 729-740.	1.9	16
25	Classification and Characterization of Gene Expression Data with Generalized Eigenvalues. <i>Journal of Optimization Theory and Applications</i> , 2009, 141, 533-545.	0.8	14
26	Transcriptator: An Automated Computational Pipeline to Annotate Assembled Reads and Identify Non Coding RNA. <i>PLoS ONE</i> , 2015, 10, e0140268.	1.1	14
27	Duodenal Metatranscriptomics to Define Human and Microbial Functional Alterations Associated with Severe Obesity: A Pilot Study. <i>Microorganisms</i> , 2020, 8, 1811.	1.6	13
28	Model simplification for supervised classification of metabolic networks. <i>Annals of Mathematics and Artificial Intelligence</i> , 2020, 88, 91-104.	0.9	12
29	Supervised Classification of Metabolic Networks. , 2018, , .		11
30	Classification of cancer cell death with spectral dimensionality reduction and generalized eigenvalues. <i>Artificial Intelligence in Medicine</i> , 2011, 53, 119-125.	3.8	10
31	Effects of Mecp2 loss of function in embryonic cortical neurons: a bioinformatics strategy to sort out non-neuronal cells variability from transcriptome profiling. <i>BMC Bioinformatics</i> , 2016, 17, 14.	1.2	10
32	Clustering analysis of tumor metabolic networks. <i>BMC Bioinformatics</i> , 2020, 21, 349.	1.2	10
33	Current classification algorithms for biomedical applications. <i>CRM Proceedings & Lecture Notes</i> , 2008, , 109-127.	0.1	10
34	Multiclass Generalized Eigenvalue Proximal Support Vector Machines. , 2010, , .		9
35	Sex-Comparative Analysis of the miRNome of Human Amniotic Mesenchymal Stem Cells During Obesity. <i>Stem Cells and Development</i> , 2017, 26, 1-3.	1.1	9
36	Exploiting single-cell RNA sequencing data to link alternative splicing and cancer heterogeneity: A computational approach. <i>International Journal of Biochemistry and Cell Biology</i> , 2019, 108, 51-60.	1.2	8

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37	Data Mining in Psychiatric Research. <i>Methods in Molecular Biology</i> , 2012, 829, 593-603.	0.4	8
38	Dynamic clustering detection through multi-valued descriptors of dermoscopic images. <i>Statistics in Medicine</i> , 2011, 30, 2536-2550.	0.8	7
39	Var2GO: a web-based tool for gene variants selection. <i>BMC Bioinformatics</i> , 2016, 17, 376.	1.2	7
40	Beta-Binomial Model for the Detection of Rare Mutations in Pooled Next-Generation Sequencing Experiments. <i>Journal of Computational Biology</i> , 2017, 24, 357-367.	0.8	7
41	RankerGUI: A Computational Framework to Compare Differential Gene Expression Profiles Using Rank Based Statistics. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6098.	1.8	7
42	Glioma Grade Classification via Omics Imaging. , 2020, , .		7
43	Network Distances for Weighted Digraphs. <i>Communications in Computer and Information Science</i> , 2020, , 389-408.	0.4	7
44	Application Oriented Brokering in Medical Imaging: Algorithms and Software Architecture. <i>Lecture Notes in Computer Science</i> , 2005, , 972-981.	1.0	6
45	Predicting Protein-Protein Interactions with K-Nearest Neighbors Classification Algorithm. <i>Lecture Notes in Computer Science</i> , 2010, , 139-150.	1.0	6
46	A generalized eigenvalues classifier with embedded feature selection. <i>Optimization Letters</i> , 2017, 11, 299-311.	0.9	6
47	Ensemble of rankers for efficient gene signature extraction in smoke exposure classification. <i>BMC Bioinformatics</i> , 2018, 19, 48.	1.2	6
48	Setup of Quantitative PCR for Oral Neisseria spp. Evaluation in Celiac Disease Diagnosis. <i>Diagnostics</i> , 2020, 10, 12.	1.3	6
49	A new approach to brain imaging, based on an open and distributed environment. , 0, , .		5
50	A parallel classification method for genomic and proteomic problems. , 2006, , .		5
51	Supervised classification of distributed data streams for smart grids. <i>Energy Systems</i> , 2012, 3, 95-108.	1.8	5
52	An integrated approach to infer cross-talks between intracellular protein transport and signaling pathways. <i>BMC Bioinformatics</i> , 2018, 19, 58.	1.2	5
53	Application of Support Vector Machines to Melissopalynological Data for Honey Classification. <i>International Journal of Agricultural and Environmental Information Systems</i> , 2010, 1, 85-94.	1.8	5
54	Learning from Metabolic Networks: Current Trends and Future Directions for Precision Medicine. <i>Current Medicinal Chemistry</i> , 2021, 28, 6619-6653.	1.2	5

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55	Decision rules for efficient classification of biological data. Optimization Letters, 2009, 3, 357-366.	0.9	4
56	Fuzzy regularized generalized eigenvalue classifier with a novel membership function. Information Sciences, 2013, 245, 53-62.	4.0	4
57	Prediction of Rare Single-Nucleotide Causative Mutations for Muscular Diseases in Pooled Next-Generation Sequencing Experiments. Journal of Computational Biology, 2014, 21, 665-675.	0.8	4
58	On the regularization of generalized eigenvalues classifiers. AIP Conference Proceedings, 2016, , .	0.3	4
59	Semi-supervised generalized eigenvalues classification. Annals of Operations Research, 2019, 276, 249-266.	2.6	4
60	Multidimensional Scaling for Genomic Data. Springer Optimization and Its Applications, 2016, , 129-139.	0.6	4
61	Fuzzy Hyperinference-Based Pattern Recognition. Studies in Fuzziness and Soft Computing, 2013, , 223-240.	0.6	4
62	Application of Multi-Objective Optimization to Pooled Experiments of Next Generation Sequencing for Detection of Rare Mutations. PLoS ONE, 2014, 9, e104992.	1.1	4
63	Parallel, distributed and network-based processing. Journal of Systems Architecture, 2008, 54, 841-842.	2.5	3
64	DecontaMiner: A Pipeline for the Detection and Analysis of Contaminating Sequences in Human NGS Sequencing Data. , 2016, , 137-148.		3
65	A web-oriented software for the optimization of pooled experiments in NGS for detection of rare mutations. BMC Research Notes, 2016, 9, 111.	0.6	3
66	A computational integrative approach based on alternative splicing analysis to compare immortalized and primary cancer cells. International Journal of Biochemistry and Cell Biology, 2017, 91, 116-123.	1.2	3
67	A Framework Based on Metabolic Networks and Biomedical Images Data to Discriminate Glioma Grades. Communications in Computer and Information Science, 2021, , 165-189.	0.4	3
68	The MetaboX Library: Building Metabolic Networks from KEGG Database. Lecture Notes in Computer Science, 2015, , 565-576.	1.0	3
69	Efficient Prediction of Protein-Protein Interactions Using Sequence Information. , 2010, , .		2
70	A Novel Feature Selection Method for Classification Using a Fuzzy Criterion. Lecture Notes in Computer Science, 2013, , 455-467.	1.0	2
71	Transcriptator: Computational Pipeline to Annotate Transcripts and Assembled Reads from RNA-Seq Data. Lecture Notes in Computer Science, 2015, , 156-169.	1.0	2
72	An adaptable learning technology system for mathematical models. , 0, , .		1

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73	Integrating Medical Imaging into a Grid Based Computing Infrastructure. Lecture Notes in Computer Science, 2004, , 505-514.	1.0	1
74	Incremental Learning and Decremental Characterization of Gene Expression Data Analysis. , 2008, , .		1
75	A sparse nonsymmetric eigensolver for distributed memory architectures. International Journal of Parallel, Emergent and Distributed Systems, 2008, 23, 259-270.	0.7	1
76	An Atlas of annotations of Hydra vulgaris transcriptome. BMC Bioinformatics, 2016, 17, 360.	1.2	1
77	A Web Resource on Skeletal Muscle Transcriptome of Primates. Lecture Notes in Computer Science, 2016, , 273-284.	1.0	1
78	From Separating to Proximal Plane Classifiers: A Review. Springer Optimization and Its Applications, 2014, , 167-180.	0.6	1
79	Raman Spectroscopy Using a Multiclass Extension of Fisher-Based Feature Selection Support Vector Machines (FFS-SVM) for Characterizing In-Vitro Apoptotic Cell Death Induced by Paclitaxel. Lecture Notes in Computer Science, 2014, , 306-323.	1.0	1
80	A Parallel Classification and Feature Reduction Method for Biomedical Applications. , 2008, , 1210-1219.		1
81	On the parallelization of a commercial PSE for scientific computing. , 2003, , .		0
82	Detection of Rare Mutations Using Beta-Binomial and Empirical Quantile Models in Next-Generation Sequencing Experiments. , 2016, , 89-99.		0
83	Comparison of Gene Expression Signature Using Rank Based Statistical Inference. Lecture Notes in Computer Science, 2016, , 28-41.	1.0	0
84	A mixed integer programming-based global optimization framework for analyzing gene expression data. Journal of Global Optimization, 2017, 69, 727-744.	1.1	0
85	A Supervised Learning Technique and Its Applications to Computational Biology. Lecture Notes in Computer Science, 2009, , 275-283.	1.0	0
86	Prior Knowledge in the Classification of Biomedical Data. Advances in Intelligent and Soft Computing, 2010, , 1-8.	0.2	0
87	Mathematical Models of Supervised Learning and Application to Medical Diagnosis. Fields Institute Communications, 2013, , 67-81.	0.6	0
88	Classification of Data Chunks Using Proximal Vector Machines and Singular Value Decomposition. Studies in Classification, Data Analysis, and Knowledge Organization, 2013, , 55-62.	0.1	0
89	IGV-plus: A Java Software for the Analysis and Visualization of Next-Generation Sequencing Data. Springer Proceedings in Mathematics and Statistics, 2014, , 149-160.	0.1	0