

Fabricio Martins Lopes

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44
papers

618
citations

11
h-index

24
g-index

50
ext. papers

842
ext. citations

3.2
avg, IF

4.36
L-index

#	Paper	IF	Citations
44	Analysis of co-authorship networks among Brazilian graduate programs in computer science.. <i>PLoS ONE</i> , 2022 , 17, e0261200	3.7	1
43	A Feature Extraction Approach Based on LBP Operator and Complex Networks for Face Recognition. <i>Lecture Notes in Computer Science</i> , 2021 , 440-450	0.9	
42	Assessing Active Learning Strategies to Improve the Quality Control of the Soybean Seed Vigor. <i>IEEE Transactions on Industrial Electronics</i> , 2021 , 68, 1675-1683	8.9	2
41	Computational Analysis of Transposable Elements and CircRNAs in Plants. <i>Methods in Molecular Biology</i> , 2021 , 2362, 147-172	1.4	1
40	Feature extraction approaches for biological sequences: a comparative study of mathematical features. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	4
39	A Simplified Complex Network-Based Approach to mRNA and ncRNA Transcript Classification. <i>Lecture Notes in Computer Science</i> , 2020 , 192-203	0.9	3
38	Classification of texture based on Bag-of-Visual-Words through complex networks. <i>Expert Systems With Applications</i> , 2019 , 133, 215-224	7.8	13
37	Brazilian-adapted soybean Bradyrhizobium strains uncover IS elements with potential impact on biological nitrogen fixation. <i>FEMS Microbiology Letters</i> , 2019 , 366,	2.9	2
36	Contributing to agriculture by using soybean seed data from the tetrazolium test. <i>Data in Brief</i> , 2019 , 23, 103652	1.2	8
35	Inference of Gene Regulatory Networks by Topological Prior Information and Data Integration 2019 , 265-304		0
34	Feature Extraction of Long Non-coding RNAs: A Fourier and Numerical Mapping Approach. <i>Lecture Notes in Computer Science</i> , 2019 , 469-479	0.9	2
33	BASiNET-Biological Sequences NETWORK: a case study on coding and non-coding RNAs identification. <i>Nucleic Acids Research</i> , 2018 , 46, e96	20.1	21
32	An Efficient Approach to Explore and Discriminate Anomalous Regions in Bacterial Genomes Based on Maximum Entropy. <i>Journal of Computational Biology</i> , 2017 , 24, 1125-1133	1.7	1
31	RNA-Seq differential expression analysis: An extended review and a software tool. <i>PLoS ONE</i> , 2017 , 12, e0190152	3.7	243
30	Evolutionary computation and swarm intelligence for the inference of gene regulatory networks. <i>International Journal of Innovative Computing and Applications</i> , 2016 , 7, 225	0.4	1
29	A feature extraction approach based on complex networks for genomic sequences recognition 2016 ,		1
28	Combining SURF descriptor and complex networks for face recognition 2016 ,		3

27	A Computer Vision Approach for Automatic Measurement of the Inter-plant Spacing. <i>Lecture Notes in Computer Science</i> , 2015 , 219-227	0.9	1
26	A Complex Network-Based Approach to the Analysis and Classification of Images. <i>Lecture Notes in Computer Science</i> , 2015 , 322-330	0.9	4
25	A Feature Selection Approach for Evaluate the Inference of GRNs Through Biological Data Integration - A Case Study on A. Thaliana. <i>Lecture Notes in Computer Science</i> , 2015 , 667-675	0.9	
24	A database for the taxonomic and phylogenetic identification of the genus Bradyrhizobium using multilocus sequence analysis. <i>BMC Genomics</i> , 2015 , 16 Suppl 5, S10	4.5	15
23	Brazilian bibliometric coauthorship networks. <i>Journal of the Association for Information Science and Technology</i> , 2014 , 65, 1424-1445	2.7	38
22	A feature selection technique for inference of graphs from their known topological properties: Revealing scale-free gene regulatory networks. <i>Information Sciences</i> , 2014 , 272, 1-15	7.7	37
21	Entropic Biological Score: a cell cycle investigation for GRNs inference. <i>Gene</i> , 2014 , 541, 129-37	3.8	13
20	SFFS-SW: A Feature Selection Algorithm Exploring the Small-World Properties of GNs. <i>Lecture Notes in Computer Science</i> , 2014 , 60-71	0.9	3
19	CoffeeBEST: an integrated resource for Coffea spp expressed sequence tags. <i>Genetics and Molecular Research</i> , 2014 , 13, 10913-20	1.2	
18	Networking the host immune response in Plasmodium vivax malaria. <i>Malaria Journal</i> , 2013 , 12, 69	3.6	47
17	Ptaquiloside reduces NK cell activities by enhancing metallothionein expression, which is prevented by selenium. <i>Toxicology</i> , 2013 , 304, 100-8	4.4	11
16	Combining Texture and Shape Descriptors for Bioimages Classification: A Case of Study in ImageCLEF Dataset. <i>Lecture Notes in Computer Science</i> , 2013 , 431-438	0.9	5
15	Assessing the gain of biological data integration in gene networks inference. <i>BMC Genomics</i> , 2012 , 13 Suppl 6, S7	4.5	6
14	Reverse engineering of GRNs 2012 ,		7
13	Inference of gene regulatory networks from time series by Tsallis entropy. <i>BMC Systems Biology</i> , 2011 , 5, 61	3.5	26
12	Gene expression complex networks: synthesis, identification, and analysis. <i>Journal of Computational Biology</i> , 2011 , 18, 1353-67	1.7	31
11	The effect of certain Boolean functions in stability of networks with varying topology 2011 ,		1
10	3D facial expression analysis by using 2D AND 3D wavelet transforms 2011 ,		5

9	Improvement of GNs inference through biological data integration 2011 ,		1
8	SFFS-MR: A Floating Search Strategy for GRNs Inference. <i>Lecture Notes in Computer Science</i> , 2010 , 407-418		6
7	Comparative study of GRNS inference methods based on feature selection by mutual information 2009 ,		2
6	Analysis of the GRNs Inference by Using Tsallis Entropy and a Feature Selection Approach. <i>Lecture Notes in Computer Science</i> , 2009 , 473-480	0.9	2
5	Feature selection environment for genomic applications. <i>BMC Bioinformatics</i> , 2008 , 9, 451	3.6	38
4	AGN Simulation and Validation Model. <i>Lecture Notes in Computer Science</i> , 2008 , 169-173	0.9	7
3	A RBFN Perceptive Model for Image Thresholding 2005 ,		3
2	Inference of Gene Regulatory Networks by Topological Prior Information and Data Integration. <i>Advances in Medical Technologies and Clinical Practice Book Series</i> ,1-51	0.3	
1	Feature Extraction Approaches for Biological Sequences: A Comparative Study of Mathematical Models		2