

David Corrâ Martins

List of Publications by Citations

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Version: 2024-04-25

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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.

32
papers

317
citations

11
h-index

16
g-index

36
ext. papers

377
ext. citations

3.5
avg, IF

3.06
L-index

#	Paper	IF	Citations
32	Feature selection environment for genomic applications. <i>BMC Bioinformatics</i> , 2008 , 9, 451	3.6	38
31	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
30	Intrinsically Multivariate Predictive Genes. <i>IEEE Journal on Selected Topics in Signal Processing</i> , 2008 , 2, 424-439	7.5	33
29	Multidimensional integrative analysis uncovers driver candidates and biomarkers in penile carcinoma. <i>Scientific Reports</i> , 2017 , 7, 6707	4.9	24
28	W-operator window design by minimization of mean conditional entropy. <i>Pattern Analysis and Applications</i> , 2006 , 9, 139-153	2.3	22
27	Gene regulatory networks inference using a multi-GPU exhaustive search algorithm. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 18, S5	3.6	18
26	U-curve: A branch-and-bound optimization algorithm for U-shaped cost functions on Boolean lattices applied to the feature selection problem. <i>Pattern Recognition</i> , 2010 , 43, 557-568	7.7	17
25	Assessment of complementarity of WGCNA and NERI results for identification of modules associated to schizophrenia spectrum disorders. <i>PLoS ONE</i> , 2019 , 14, e0210431	3.7	16
24	Constructing Probabilistic Genetic Networks of Plasmodium falciparum from Dynamical Expression Signals of the Intraerythrocytic Development Cycle 2007 , 11-26		16
23	Signaling transcript profile of the asexual intraerythrocytic development cycle of induced by melatonin and cAMP. <i>Genes and Cancer</i> , 2016 , 7, 323-339	2.9	14
22	Transcriptome Analysis of Mesenchymal Stem Cells from Multiple Myeloma Patients Reveals Downregulation of Genes Involved in Cell Cycle Progression, Immune Response, and Bone Metabolism. <i>Scientific Reports</i> , 2019 , 9, 1056	4.9	13
21	Signal propagation in Bayesian networks and its relationship with intrinsically multivariate predictive variables. <i>Information Sciences</i> , 2013 , 225, 18-34	7.7	8
20	Initial findings of striatum tripartite model in OCD brain samples based on transcriptome analysis. <i>Scientific Reports</i> , 2019 , 9, 3086	4.9	8
19	NERI: network-medicine based integrative approach for disease gene prioritization by relative importance. <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 19, S9	3.6	7
18	Finding exact hitting set solutions for systems biology applications using heterogeneous GPU clusters. <i>Future Generation Computer Systems</i> , 2017 , 67, 418-429	7.5	6
17	Genome-wide analysis of the human malaria parasite transcription factor PfNF-YB shows interaction with a CCAAT motif. <i>Oncotarget</i> , 2017 , 8, 113987-114001	3.3	6
16	Identifying dense subgraphs in protein-protein interaction network for gene selection from microarray data. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015 , 4, 1	1.6	5

15	A Multi-GPU Hitting Set Algorithm for GRNs Inference 2015 ,		3
14	Gene Networks Inference through Linear Grouping of Variables 2014 ,		3
13	Multiview Clustering on PPI Network for Gene Selection and Enrichment from Microarray Data 2014 ,		3
12	Gene Networks Inference through One Genetic Algorithm Per Gene 2014 ,		3
11	Generating segmented meshes from textured color images. <i>Journal of Visual Communication and Image Representation</i> , 2009 , 20, 190-203	2.7	3
10	Accelerating gene regulatory networks inference through GPU/CUDA programming 2012 ,		3
9	Gene expression profile of whole blood cells differs in pregnant women with positive screening and negative diagnosis for gestational diabetes. <i>BMJ Open Diabetes Research and Care</i> , 2016 , 4, e000273	4.5	3
8	One genetic algorithm per gene to infer gene networks from expression data. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015 , 4, 1	1.6	2
7	Shortest paths ranking methodology to identify alterations in PPI networks of complex diseases 2012 ,		2
6	GeNICE: A Novel Framework for Gene Network Inference by Clustering, Exhaustive Search, and Multivariate Analysis. <i>Journal of Computational Biology</i> , 2017 , 24, 809-830	1.7	1
5	A feature selection approach for identification of signature genes from SAGE data. <i>BMC Bioinformatics</i> , 2007 , 8, 169	3.6	1
4	A hybrid CPU-GPU-MIC algorithm for minimal hitting set enumeration. <i>Concurrency Computation Practice and Experience</i> , 2019 , 31, e5087	1.4	0
3	Linear grouping of predictor instances to infer gene networks. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015 , 4, 1	1.6	
2	Inference of Restricted Stochastic Boolean GRNs by Bayesian Error and Entropy Based Criteria. <i>Lecture Notes in Computer Science</i> , 2010 , 144-152	0.9	
1	Multi-GPU Approach for Large-Scale Multiple Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2021 , 560-575	0.9	