David CorrÃªa Martins

List of Publications by Year
in descending order

33 papers	432 citations	840119 11 h-index	794141 19 g-index
36 all docs	36 docs citations	36 times ranked	457 citing authors

#	Article	IF	Citations
1	Feature selection environment for genomic applications. BMC Bioinformatics, 2008, 9, 451.	1.2	46
2	A feature selection technique for inference of graphs from their known topological properties: Revealing scale-free gene regulatory networks. Information Sciences, 2014, 272, 1-15.	4.0	44
3	Intrinsically Multivariate Predictive Genes. IEEE Journal on Selected Topics in Signal Processing, 2008, 2, 424-439.	7.3	41
4	Multidimensional integrative analysis uncovers driver candidates and biomarkers in penile carcinoma. Scientific Reports, 2017, 7, 6707.	1.6	35
5	Transcriptome Analysis of Mesenchymal Stem Cells from Multiple Myeloma Patients Reveals Downregulation of Genes Involved in Cell Cycle Progression, Immune Response, and Bone Metabolism. Scientific Reports, 2019, 9, 1056.	1.6	28
6	W-operator window design by minimization of mean conditional entropy. Pattern Analysis and Applications, 2006, 9, 139-153.	3.1	26
7	Assessment of complementarity of WGCNA and NERI results for identification of modules associated to schizophrenia spectrum disorders. PLoS ONE, 2019, 14, e0210431.	1.1	23
8	U-curve: A branch-and-bound optimization algorithm for U-shaped cost functions on Boolean lattices applied to the feature selection problem. Pattern Recognition, 2010, 43, 557-568.	5.1	21
9	Gene regulatory networks inference using a multi-GPU exhaustive search algorithm. BMC Bioinformatics, 2013, 14, S5.	1.2	21
10	Initial findings of striatum tripartite model in OCD brain samples based on transcriptome analysis. Scientific Reports, 2019, 9, 3086.	1.6	17
11	Signaling transcript profile of the asexual intraerythrocytic development cycle of Plasmodium falciparum induced by melatonin and cAMP. Genes and Cancer, 2016, 7, 323-339.	0.6	16
12	NERI: network-medicine based integrative approach for disease gene prioritization by relative importance. BMC Bioinformatics, 2015, 16, S9.	1.2	9
13	Signal propagation in Bayesian networks and its relationship with intrinsically multivariate predictive variables. Information Sciences, 2013, 225, 18-34.	4.0	8
14	Genome-wide analysis of the human malaria parasite *Plasmodium falciparum* transcription factor PfNF-YB shows interaction with a CCAAT motif. Oncotarget, 2017, 8, 113987-114001.	0.8	8
15	Identifying dense subgraphs in protein–protein interaction network for gene selection from microarray data. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	1.2	7
16	Finding exact hitting set solutions for systems biology applications using heterogeneous GPU clusters. Future Generation Computer Systems, 2017, 67, 418-429.	4.9	7
17	Generating segmented meshes from textured color images. Journal of Visual Communication and Image Representation, 2009, 20, 190-203.	1.7	5
18	Gene Networks Inference through One Genetic Algorithm Per Gene. , 2014, , .		4

#	Article	IF	Citations
19	One genetic algorithm per gene to infer gene networks from expression data. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	1.2	4
20	A Multi-GPU Hitting Set Algorithm for GRNs Inference. , 2015, , .		4
21	A feature selection approach for identification of signature genes from SAGE data. BMC Bioinformatics, 2007, 8, 169.	1.2	3
22	Accelerating gene regulatory networks inference through GPU/CUDA programming. , 2012, , .		3
23	Gene Networks Inference through Linear Grouping of Variables. , 2014, , .		3
24	Multiview Clustering on PPI Network for Gene Selection and Enrichment from Microarray Data. , 2014, , .		3
25	Gene expression profile of whole blood cells differs in pregnant women with positive screening and negative diagnosis for gestational diabetes. BMJ Open Diabetes Research and Care, 2016, 4, e000273.	1.2	3
26	Shortest paths ranking methodology to identify alterations in PPI networks of complex diseases. , 2012, , .		2
27	GeNICE: A Novel Framework for Gene Network Inference by Clustering, Exhaustive Search, and Multivariate Analysis. Journal of Computational Biology, 2017, 24, 809-830.	0.8	2
28	A hybrid CPUâ€GPUâ€MIC algorithm for minimal hitting set enumeration. Concurrency Computation Practice and Experience, 2019, 31, e5087.	1.4	2
29	Multi-GPU Approach for Large-Scale Multiple Sequence Alignment. Lecture Notes in Computer Science, 2021, , 560-575.	1.0	1
30	Inference of Restricted Stochastic Boolean GRNâ€™s by Bayesian Error and Entropy Based Criteria. Lecture Notes in Computer Science, 2010, , 144-152.	1.0	0
31	Network-Based Disease Gene Prioritization by Hitting Time Analysis. , 2014, , .		0
32	Linear grouping of predictor instances to infer gene networks. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	1.2	0
33	Finding Attractors in Biological Models Based on Boolean Dynamical Systems Using Hitting Set. , 2019, , .		0