

# David Corrâ Martins

## 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.

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	Multi-GPU Approach for Large-Scale Multiple Sequence Alignment. <i>Lecture Notes in Computer Science</i> , <b>2021</b> , 560-575	0.9	
31	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> , <b>2019</b> , 9, 1056	4.9	13
30	Initial findings of striatum tripartite model in OCD brain samples based on transcriptome analysis. <i>Scientific Reports</i> , <b>2019</b> , 9, 3086	4.9	8
29	Assessment of complementarity of WGCNA and NERI results for identification of modules associated to schizophrenia spectrum disorders. <i>PLoS ONE</i> , <b>2019</b> , 14, e0210431	3.7	16
28	A hybrid CPU-GPU-MIC algorithm for minimal hitting set enumeration. <i>Concurrency Computation Practice and Experience</i> , <b>2019</b> , 31, e5087	1.4	0
27	Finding exact hitting set solutions for systems biology applications using heterogeneous GPU clusters. <i>Future Generation Computer Systems</i> , <b>2017</b> , 67, 418-429	7.5	6
26	GeNICE: A Novel Framework for Gene Network Inference by Clustering, Exhaustive Search, and Multivariate Analysis. <i>Journal of Computational Biology</i> , <b>2017</b> , 24, 809-830	1.7	1
25	Multidimensional integrative analysis uncovers driver candidates and biomarkers in penile carcinoma. <i>Scientific Reports</i> , <b>2017</b> , 7, 6707	4.9	24
24	Genome-wide analysis of the human malaria parasite transcription factor PfNF-YB shows interaction with a CCAAT motif. <i>Oncotarget</i> , <b>2017</b> , 8, 113987-114001	3.3	6
23	Signaling transcript profile of the asexual intraerythrocytic development cycle of induced by melatonin and cAMP. <i>Genes and Cancer</i> , <b>2016</b> , 7, 323-339	2.9	14
22	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> , <b>2016</b> , 4, e000273	4.5	3
21	One genetic algorithm per gene to infer gene networks from expression data. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , <b>2015</b> , 4, 1	1.6	2
20	A Multi-GPU Hitting Set Algorithm for GRNs Inference <b>2015</b> ,		3
19	Identifying dense subgraphs in protein-protein interaction network for gene selection from microarray data. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , <b>2015</b> , 4, 1	1.6	5
18	Linear grouping of predictor instances to infer gene networks. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , <b>2015</b> , 4, 1	1.6	
17	NERI: network-medicine based integrative approach for disease gene prioritization by relative importance. <i>BMC Bioinformatics</i> , <b>2015</b> , 16 Suppl 19, S9	3.6	7
16	A feature selection technique for inference of graphs from their known topological properties: Revealing scale-free gene regulatory networks. <i>Information Sciences</i> , <b>2014</b> , 272, 1-15	7.7	37

15	Gene Networks Inference through Linear Grouping of Variables <b>2014</b> ,		3
14	Multiview Clustering on PPI Network for Gene Selection and Enrichment from Microarray Data <b>2014</b> ,		3
13	Gene Networks Inference through One Genetic Algorithm Per Gene <b>2014</b> ,		3
12	Signal propagation in Bayesian networks and its relationship with intrinsically multivariate predictive variables. <i>Information Sciences</i> , <b>2013</b> , 225, 18-34	7.7	8
11	Gene regulatory networks inference using a multi-GPU exhaustive search algorithm. <i>BMC Bioinformatics</i> , <b>2013</b> , 14 Suppl 18, S5	3.6	18
10	Shortest paths ranking methodology to identify alterations in PPI networks of complex diseases <b>2012</b> ,		2
9	Accelerating gene regulatory networks inference through GPU/CUDA programming <b>2012</b> ,		3
8	Inference of Restricted Stochastic Boolean GRN by Bayesian Error and Entropy Based Criteria. <i>Lecture Notes in Computer Science</i> , <b>2010</b> , 144-152	0.9	
7	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> , <b>2010</b> , 43, 557-568	7.7	17
6	Generating segmented meshes from textured color images. <i>Journal of Visual Communication and Image Representation</i> , <b>2009</b> , 20, 190-203	2.7	3
5	Intrinsically Multivariate Predictive Genes. <i>IEEE Journal on Selected Topics in Signal Processing</i> , <b>2008</b> , 2, 424-439	7.5	33
4	Feature selection environment for genomic applications. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 451	3.6	38
3	A feature selection approach for identification of signature genes from SAGE data. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 169	3.6	1
2	Constructing Probabilistic Genetic Networks of Plasmodium falciparum from Dynamical Expression Signals of the Intraerythrocytic Development Cycle <b>2007</b> , 11-26		16
1	W-operator window design by minimization of mean conditional entropy. <i>Pattern Analysis and Applications</i> , <b>2006</b> , 9, 139-153	2.3	22