Francisco GÃ³mez-Vela

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Stacking Ensemble Learning for Short-Term Electricity Consumption Forecasting. Energies, 2018, 11, 949.	3.1	142
2	Computational methods for Gene Regulatory Networks reconstruction and analysis: A review. Artificial Intelligence in Medicine, 2019, 95, 133-145.	6.5	127
3	High-dimensional feature selection via feature grouping: A Variable Neighborhood Search approach. Information Sciences, 2016, 326, 102-118.	6.9	99
4	A Comparative Study of Time Series Forecasting Methods for Short Term Electric Energy Consumption Prediction in Smart Buildings. Energies, 2019, 12, 1934.	3.1	65
5	Pangenome of Acinetobacter baumannii uncovers two groups of genomes, one of them with genes involved in CRISPR/Cas defence systems associated with the absence of plasmids and exclusive genes for biofilm formation. Microbial Genomics, 2019, 5, .	2.0	42
6	An effective measure for assessing the quality of biclusters. Computers in Biology and Medicine, 2012, 42, 245-256.	7.0	38
7	Social symbol grounding and language evolution. Interaction Studies, 2007, 8, 31-52.	0.6	31
8	A multivariate approach to the symmetrical uncertainty measure: Application to feature selection problem. Information Sciences, 2019, 494, 1-20.	6.9	25
9	Identifying livestock behavior patterns based on accelerometer dataset. Journal of Computational Science, 2020, 41, 101076.	2.9	23
10	Hybridizing Deep Learning and Neuroevolution: Application to the Spanish Short-Term Electric Energy Consumption Forecasting. Applied Sciences (Switzerland), 2020, 10, 5487.	2.5	15
11	GNC–app: A new Cytoscape app to rate gene networks biological coherence using gene–gene indirect relationships. BioSystems, 2018, 166, 61-65.	2.0	14
12	Gene network coherence based on prior knowledge using direct and indirect relationships. Computational Biology and Chemistry, 2015, 56, 142-151.	2.3	11
13	Incorporating biological knowledge for construction of fuzzy networks of gene associations. Applied Soft Computing Journal, 2016, 42, 144-155.	7.2	10
14	A Comparative Study of Supervised Machine Learning Algorithms for the Prediction of Long-Range Chromatin Interactions. Genes, 2020, 11, 985.	2.4	9
15	Genome-wide prediction of topoisomerase IIÎ ² binding by architectural factors and chromatin accessibility. PLoS Computational Biology, 2021, 17, e1007814.	3.2	8
16	GFD-Net: A novel semantic similarity methodology for the analysis of gene networks. Journal of Biomedical Informatics, 2017, 68, 71-82.	4.3	7
17	Analysis of Electric Energy Consumption Profiles Using a Machine Learning Approach: A Paraguayan Case Study. Electronics (Switzerland), 2022, 11, 267.	3.1	7
18	Gene Network Biological Validity Based on Gene-Gene Interaction Relevance. Scientific World Journal, The. 2014, 2014, 1-11.	2.1	6

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19	Structure Optimization for Large Gene Networks Based on Greedy Strategy. Computational and Mathematical Methods in Medicine, 2018, 2018, 1-11.	1.3	6
20	Biclustering of Smart Building Electric Energy Consumption Data. Applied Sciences (Switzerland), 2019, 9, 222.	2.5	6
21	Computational Analysis of the Global Effects of Ly6E in the Immune Response to Coronavirus Infection Using Gene Networks. Genes, 2020, 11, 831.	2.4	6
22	Automatic Diagnosis of Ocular Toxoplasmosis from Fundus Images with Residual Neural Networks. Studies in Health Technology and Informatics, 2021, 281, 173-177.	0.3	5
23	Computational Inference of Gene Co-Expression Networks for the identification of Lung Carcinoma Biomarkers: An Ensemble Approach. Genes, 2019, 10, 962.	2.4	4
24	Pattern Recognition in Biological Time Series. Lecture Notes in Computer Science, 2011, , 164-172.	1.3	4
25	Ensemble and Greedy Approach for the Reconstruction of Large Gene Co-Expression Networks. Entropy, 2019, 21, 1139.	2.2	2
26	Analysis of Student Achievement Scores: A Machine Learning Approach. Advances in Intelligent Systems and Computing, 2020, , 275-284.	0.6	2
27	Computational Methods for the Analysis of Genomic Data and Biological Processes. Genes, 2020, 11, 1230.	2.4	2
28	A multi-objective genetic algorithm for the Protein Structure Prediction. , 2011, , .		1
29	Feature Grouping and Selection on High-Dimensional Microarray Data. , 2015, , .		1
30	BIGO: A web application to analyse gene enrichment analysis results. Computational Biology and Chemistry, 2018, 76, 169-178.	2.3	1
31	gMSR: A Multi-GPU Algorithm to Accelerate a Massive Validation of Biclusters. Electronics (Switzerland), 2020, 9, 1782.	3.1	1
32	Gene Regulatory Networks Validation Framework Based in KEGG. Lecture Notes in Computer Science, 2011, , 279-286.	1.3	1
33	Distribution level electric current consumption and meteorological data set of the east region of Paraguay. Data in Brief, 2022, 40, 107699.	1.0	1
34	A multi-objective Evolutionary Concept Learner. , 2010, , .		0
35	Gene Networks Validation based on Metabolic Pathways. , 2011, , .		0
36	Gene-gene interaction based clustering method for microarray data. , 2011, , .		0

3

#	Article	IF	CITATIONS
37	An efficient decision rule-based system for the protein residue-residue contact prediction. , 2013, , .		0
38	Bioinformatics from a Big Data Perspective: Meeting the Challenge. Lecture Notes in Computer Science, 2017, , 349-359.	1.3	0
39	Special Issue on Machine Learning for Biomedical Data Analysis. Applied Sciences (Switzerland), 2019, 9, 4676.	2.5	Ο
40	Advanced Optimization Methods and Big Data Applications in Energy Demand Forecast. Applied Sciences (Switzerland), 2021, 11, 1261.	2.5	0
41	Analysis of Relevance and Redundance onÂTopoisomerase 2b (TOP2B) Binding Sites: A Feature Selection Approach. Lecture Notes in Computer Science, 2018, , 86-101.	1.3	0
42	Redundancy Is Not Necessarily Detrimental in Classification Problems. Mathematics, 2021, 9, 2899.	2.2	0