Federico Divina

List of Publications by Year
in descending order

60	848	840728 11	526264 27
papers	citations	h-index	g-index

66	66	66	872
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Distribution level electric current consumption and meteorological data set of the east region of Paraguay. Data in Brief, 2022, 40, 107699.	1.0	1
2	Analysis of Electric Energy Consumption Profiles Using a Machine Learning Approach: A Paraguayan Case Study. Electronics (Switzerland), 2022, 11, 267.	3.1	7
3	A multi-GPU biclustering algorithm for binary datasets. Journal of Parallel and Distributed Computing, 2021, 147, 209-219.	4.1	8
4	Analysis of Student Achievement Scores via Cluster Analysis. Advances in Intelligent Systems and Computing, 2021, , 399-408.	0.6	1
5	Advanced Optimization Methods and Big Data Applications in Energy Demand Forecast. Applied Sciences (Switzerland), 2021, 11, 1261.	2.5	0
6	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
7	Technical analysis strategy optimization using a machine learning approach in stock market indices. Knowledge-Based Systems, 2021, 225, 107119.	7.1	55
8	Genome-wide prediction of topoisomerase IIÎ² binding by architectural factors and chromatin accessibility. PLoS Computational Biology, 2021, 17, e1007814.	3.2	8
9	A Trust-Based Methodology to Evaluate Deep Learning Models for Automatic Diagnosis of Ocular Toxoplasmosis from Fundus Images. Diagnostics, 2021, 11, 1951.	2.6	1
10	Adjacent Inputs With Different Labels and Hardness in Supervised Learning. IEEE Access, 2021, 9, 162487-162498.	4.2	1
11	Hybridizing Deep Learning and Neuroevolution: Application to the Spanish Short-Term Electric Energy Consumption Forecasting. Applied Sciences (Switzerland), 2020, 10, 5487.	2.5	15
12	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
13	A Comparative Study of Supervised Machine Learning Algorithms for the Prediction of Long-Range Chromatin Interactions. Genes, 2020, 11, 985.	2.4	9
14	Computational Methods for the Analysis of Genomic Data and Biological Processes. Genes, 2020, 11, 1230.	2.4	2
15	Identifying livestock behavior patterns based on accelerometer dataset. Journal of Computational Science, 2020, 41, 101076.	2.9	23
16	Biclustering of Smart Building Electric Energy Consumption Data. Applied Sciences (Switzerland), 2019, 9, 222.	2.5	6
17	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
18	A multivariate approach to the symmetrical uncertainty measure: Application to feature selection problem. Information Sciences, 2019, 494, 1-20.	6.9	25

#	Article	IF	Citations
19	Special Issue on Machine Learning for Biomedical Data Analysis. Applied Sciences (Switzerland), 2019, 9, 4676.	2.5	0
20	Computational Inference of Gene Co-Expression Networks for the identification of Lung Carcinoma Biomarkers: An Ensemble Approach. Genes, 2019, 10, 962.	2.4	4
21	Ensemble and Greedy Approach for the Reconstruction of Large Gene Co-Expression Networks. Entropy, 2019, 21, 1139.	2.2	2
22	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
23	Soft Computing for Analysis of Biomedical Data. Computational and Mathematical Methods in Medicine, 2018, 2018, 1-2.	1.3	1
24	Stacking Ensemble Learning for Short-Term Electricity Consumption Forecasting. Energies, 2018, 11, 949.	3.1	142
25	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
26	Bioinformatics from a Big Data Perspective: Meeting the Challenge. Lecture Notes in Computer Science, 2017, , 349-359.	1.3	0
27	Feature Selection Using Approximate Multivariate Markov Blankets. Lecture Notes in Computer Science, 2016, , 114-125.	1.3	4
28	Feature Selection via Approximated Markov Blankets Using the CFS Method. , 2015, , .		6
29	Evolutionary decision rules for predicting protein contact maps. Pattern Analysis and Applications, 2014, 17, 725-737.	4.6	4
30	An efficient decision rule-based system for the protein residue-residue contact prediction. , 2013, , .		0
31	Improving the Efficiency of MECoMaP: A Protein Residue-Residue Contact Predictor. Lecture Notes in Computer Science, 2013, , 166-173.	1.3	0
32	Contact map prediction using a large-scale ensemble of rule sets and the fusion of multiple predicted structural features. Bioinformatics, 2012, 28, 2441-2448.	4.1	36
33	An effective measure for assessing the quality of biclusters. Computers in Biology and Medicine, 2012, 42, 245-256.	7.0	38
34	A NSGA-II Algorithm for the Residue-Residue Contact Prediction. Lecture Notes in Computer Science, 2012, , 234-244.	1.3	3
35	A multi-objective genetic algorithm for the Protein Structure Prediction. , 2011, , .		1
36	A novel probabilistic encoding for EAs applied to biclustering of microarray data. , 2011, , .		2

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37	Evolutionary computation for the prediction of secondary protein structures. , 2011, , .		0
38	Protein secondary structures prediction based on evolutionary computation. ACM SIGAPP Applied Computing Review: A Publication of the Special Interest Group on Applied Computing, 2011, 11, 17-25.	0.9	1
39	An Evolutionary Approach for Protein Contact Map Prediction. Lecture Notes in Computer Science, 2011, , 101-110.	1.3	1
40	Residue-Residue Contact Prediction Based on Evolutionary Computation. Advances in Intelligent and Soft Computing, 2011, , 279-283.	0.2	0
41	A multi-objective Evolutionary Concept Learner. , 2010, , .		0
42	Alpha Helix Prediction Based on Evolutionary Computation. Lecture Notes in Computer Science, 2010, , 358-367.	1.3	1
43	Improved biclustering on expression data through overlapping control. International Journal of Intelligent Computing and Cybernetics, 2009, 2, 477-493.	2.7	7
44	Empirical evaluation of a new structure for AdaBoost. , 2008, , .		5
45	A Novel Approach for Avoiding Overlapping Among Biclusters in Expression Data. , 2008, , .		0
46	A multi-objective approach to discover biclusters in microarray data. , 2007, , .		39
47	Evolutionary Search of Biclusters by Minimal Intrafluctuation. IEEE International Conference on Fuzzy Systems, 2007, , .	0.0	6
48	Social symbol grounding and language evolution. Interaction Studies, 2007, 8, 31-52.	0.6	31
49	Virtual Error: A New Measure for Evolutionary Biclustering. , 2007, , 217-226.		23
50	Biclustering of expression data with evolutionary computation. IEEE Transactions on Knowledge and Data Engineering, 2006, 18, 590-602.	5.7	152
51	GA-based approach to discover meaningful biclusters. , 2005, , .		0
52	Evolutionary computation for biclustering of gene expression. , 2005, , .		7
53	Evolutionary Biclustering of Microarray Data. Lecture Notes in Computer Science, 2005, , 1-10.	1.3	8
54	Handling Continuous Attributes in an Evolutionary Inductive Learner. IEEE Transactions on Evolutionary Computation, 2005, 9, 31-43.	10.0	11

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55	Assessing the Effectiveness of Incorporating Knowledge in an Evolutionary Concept Learner. Lecture Notes in Computer Science, 2005, , 13-24.	1.3	2
56	Perceptually Grounded Lexicon Formation Using Inconsistent Knowledge. Lecture Notes in Computer Science, 2005, , 644-654.	1.3	1
57	Knowledge discovery from doctor-patient relationship. , 2004, , .		4
58	Experimental Evaluation of Discretization Schemes for Rule Induction. Lecture Notes in Computer Science, 2004, , 828-839.	1.3	2
59	A Method for Handling Numerical Attributes in GA-Based Inductive Concept Learners. Lecture Notes in Computer Science, 2003, , 898-908.	1.3	9
60	Non-universal Suffrage Selection Operators Favor Population Diversity in Genetic Algorithms. Lecture Notes in Computer Science, 2003, , 1574-1575.	1.3	3