

Marco Frasca

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

1,365
citations

567281

15
h-index

377865

34
g-index

66
all docs

66
docs citations

66
times ranked

1368
citing authors

#	ARTICLE	IF	CITATIONS
1	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
2	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
3	Specifying and enforcing access control policies for XML document sources. <i>World Wide Web</i> , 2000, 3, 139-151.	4.0	135
4	A matching algorithm for measuring the structural similarity between an XML document and a DTD and its applications. <i>Information Systems</i> , 2004, 29, 23-46.	3.6	79
5	Explainable Machine Learning for Early Assessment of COVID-19 Risk Prediction in Emergency Departments. <i>IEEE Access</i> , 2020, 8, 196299-196325.	4.2	55
6	GOssTo: a stand-alone application and a web tool for calculating semantic similarities on the Gene Ontology. <i>Bioinformatics</i> , 2014, 30, 2235-2236.	4.1	44
7	A neural network algorithm for semi-supervised node label learning from unbalanced data. <i>Neural Networks</i> , 2013, 43, 84-98.	5.9	43
8	Protection and administration of XML data sources. <i>Data and Knowledge Engineering</i> , 2002, 43, 237-260.	3.4	33
9	<i>i>RANKS</i>: a flexible tool for node label ranking and classification in biological networks. <i>Bioinformatics</i>, 2016, 32, 2872-2874.</i>	4.1	30
10	Participatory knowledge-management design: A semiotic approach. <i>Journal of Visual Languages and Computing</i> , 2012, 23, 103-115.	1.8	24
11	XML-based approaches for the integration of heterogeneous bio-molecular data. <i>BMC Bioinformatics</i> , 2009, 10, S7.	2.6	21
12	COSNet: A Cost Sensitive Neural Network for Semi-supervised Learning in Graphs. <i>Lecture Notes in Computer Science</i> , 2011, , 219-234.	1.3	21
13	Measuring the structural similarity among XML documents and DTDs. <i>Journal of Intelligent Information Systems</i> , 2008, 30, 55-92.	3.9	20
14	UNIPred: Unbalance-Aware Network Integration and Prediction of Protein Functions. <i>Journal of Computational Biology</i> , 2015, 22, 1057-1074.	1.6	17
15	A novel computational method for automatic segmentation, quantification and comparative analysis of immunohistochemically labeled tissue sections. <i>BMC Bioinformatics</i> , 2018, 19, 357.	2.6	17
16	Multitask Protein Function Prediction through Task Dissimilarity. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1550-1560.	3.0	15
17	Automated gene function prediction through gene multifunctionality in biological networks. <i>Neurocomputing</i> , 2015, 162, 48-56.	5.9	14
18	A neural network based algorithm for gene expression prediction from chromatin structure. , 2013, , .		13

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19	Web accessibility legislation in Italy: a survey 10 years after the Stanca Act. <i>Universal Access in the Information Society</i> , 2018, 17, 211-222.	3.0	13
20	Think globally and solve locally: secondary memory-based network learning for automated multi-species function prediction. <i>GigaScience</i> , 2014, 3, 5.	6.4	12
21	Heterogeneous data integration methods for patient similarity networks. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	12
22	parSMURF, a high-performance computing tool for the genome-wide detection of pathogenic variants. <i>GigaScience</i> , 2020, 9, .	6.4	11
23	Network modeling of patients' biomolecular profiles for clinical phenotype/outcome prediction. <i>Scientific Reports</i> , 2020, 10, 3612.	3.3	11
24	Ontology-Based Consistent Specification of Sensor Data Acquisition Plans in Cross-Domain IoT Platforms. <i>IEEE Access</i> , 2019, 7, 176141-176169.	4.2	10
25	DESIGN OF KNOWLEDGE DRIVEN INTERFACES IN CULTURAL CONTEXTS. <i>International Journal of Semantic Computing</i> , 2008, 02, 525-553.	0.5	9
26	UNIPred-Web: a web tool for the integration and visualization of biomolecular networks for protein function prediction. <i>BMC Bioinformatics</i> , 2019, 20, 422.	2.6	9
27	“There's no Reason why” A Campaign to Raise Cancer Awareness among Adolescents. <i>Tumori</i> , 2016, 102, 270-275.	1.1	8
28	COSNet: An R package for label prediction in unbalanced biological networks. <i>Neurocomputing</i> , 2017, 237, 397-400.	5.9	8
29	Protein function prediction as a graph-transduction game. <i>Pattern Recognition Letters</i> , 2020, 134, 96-105.	4.2	8
30	Identification of Breast Cancer Subtype-Specific Biomarkers by Integrating Copy Number Alterations and Gene Expression Profiles. <i>Medicina (Lithuania)</i> , 2021, 57, 261.	2.0	8
31	Table understanding approaches for extracting knowledge from heterogeneous tables. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2021, 11, e1407.	6.8	8
32	A Hierarchical Ensemble Method for DAG-Structured Taxonomies. <i>Lecture Notes in Computer Science</i> , 2015, , 15-26.	1.3	8
33	Gene2DisCo: Gene to disease using disease commonalities. <i>Artificial Intelligence in Medicine</i> , 2017, 82, 34-46.	6.5	6
34	Learning node labels with multi-category Hopfield networks. <i>Neural Computing and Applications</i> , 2016, 27, 1677-1692.	5.6	5
35	Semi-automatic Column Type Inference for CSV Table Understanding. <i>Lecture Notes in Computer Science</i> , 2021, , 535-549.	1.3	5
36	Visual design of dialogue flows for conversational interfaces. <i>Behaviour and Information Technology</i> , 2021, 40, 1008-1023.	4.0	5

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37	Exploiting Negative Sample Selection for Prioritizing Candidate Disease Genes. <i>Genomics and Computational Biology</i> , 2017, 3, 47.	0.7	5
38	Multi-resolution visualization and analysis of biomolecular networks through hierarchical community detection and web-based graphical tools. <i>PLoS ONE</i> , 2020, 15, e0244241.	2.5	5
39	A Mathematical Model for the Validation of Gene Selection Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1385-1392.	3.0	4
40	An editable live ETL system for Ambient Intelligence environments. , 2015, , .		4
41	Compression strategies and space-conscious representations for deep neural networks. , 2021, , .		4
42	Artificial Intelligence in Predicting Clinical Outcome in COVID-19 Patients from Clinical, Biochemical and a Qualitative Chest X-Ray Scoring System. <i>Reports in Medical Imaging</i> , 0, Volume 14, 27-39.	0.8	4
43	Identification of key miRNAs in prostate cancer progression based on miRNA-mRNA network construction. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 864-873.	4.1	4
44	Protection and composition of crossmedia content in collaborative environments. <i>Multimedia Tools and Applications</i> , 2018, 77, 2083-2114.	3.9	3
45	Report on the EDBT/ICDT 2010 workshop on updates in XML. <i>SIGMOD Record</i> , 2010, 39, 54-57.	1.2	2
46	MergeGraphs. , 2015, , .		2
47	Gene-Disease Prioritization Through Cost-Sensitive Graph-Based Methodologies. <i>Lecture Notes in Computer Science</i> , 2016, , 739-751.	1.3	2
48	Multi-species protein function prediction. , 2016, , .		2
49	Analysis of Informative Features for Negative Selection in Protein Function Prediction. <i>Lecture Notes in Computer Science</i> , 2017, , 267-276.	1.3	2
50	Evaluating the impact of topological protein features on the negative examples selection. <i>BMC Bioinformatics</i> , 2018, 19, 417.	2.6	2
51	A GPU-based algorithm for fast node label learning in large and unbalanced biomolecular networks. <i>BMC Bioinformatics</i> , 2018, 19, 353.	2.6	2
52	Ensembling Descendant Term Classifiers to Improve Gene - Abnormal Phenotype Predictions. <i>Lecture Notes in Computer Science</i> , 2019, , 70-80.	1.3	2
53	Transcriptional Profiling of Hippocampus Identifies Network Alterations in Alzheimer's Disease. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 5035.	2.5	2
54	REPORT on the EDBT'04 workshop on database technologies for handling XML information on the web. <i>SIGMOD Record</i> , 2004, 33, 132-134.	1.2	1

#	ARTICLE	IF	CITATIONS
55	End-User Development for Lifelogging and eWellness. , 2016, , .		1
56	Reproducing the Sparse Huffman Address Map Compression for Deep Neural Networks. Lecture Notes in Computer Science, 2021, , 161-166.	1.3	1
57	A Neural Procedure for Gene Function Prediction. Smart Innovation, Systems and Technologies, 2013, , 179-188.	0.6	1
58	Making the Analysis of the Italian Legislative System Easy: The ILMA Web Portal. Journal of Information Technology and Politics, 2015, 12, 88-102.	2.9	0
59	Diseaseâ€“Genes Must Guide Data Source Integration in the Gene Prioritization Process. Lecture Notes in Computer Science, 2019, , 60-69.	1.3	0
60	Analysis of Novel Annotations in the Gene Ontology for Boosting the Selection of Negative Examples. , 2019, , .		0
61	Multitask Hopfield Networks. Lecture Notes in Computer Science, 2020, , 349-365.	1.3	0
62	A Graphical Tool for the Exploration and Visual Analysis of Biomolecular Networks. Lecture Notes in Computer Science, 2020, , 88-98.	1.3	0
63	Committee-Based Active Learning to Select Negative Examples for Predicting Protein Functions. Lecture Notes in Computer Science, 2020, , 80-87.	1.3	0