

Giorgio Valentini

List of Publications by Year in descending order

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96
papers

2,758
citations

201674

27
h-index

206112

48
g-index

105
all docs

105
docs citations

105
times ranked

3287
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	A Whole-Genome Analysis Framework for Effective Identification of Pathogenic Regulatory Variants in Mendelian Disease. <i>American Journal of Human Genetics</i> , 2016, 99, 595-606.	6.2	223
4	Ensembles of Learning Machines. <i>Lecture Notes in Computer Science</i> , 2002, , 3-20.	1.3	166
5	True Path Rule Hierarchical Ensembles for Genome-Wide Gene Function Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 832-847.	3.0	104
6	Cancer recognition with bagged ensembles of support vector machines. <i>Neurocomputing</i> , 2004, 56, 461-466.	5.9	79
7	Fuzzy ensemble clustering based on random projections for DNA microarray data analysis. <i>Artificial Intelligence in Medicine</i> , 2009, 45, 173-183.	6.5	79
8	Synergy of multi-label hierarchical ensembles, data fusion, and cost-sensitive methods for gene functional inference. <i>Machine Learning</i> , 2012, 88, 209-241.	5.4	67
9	Bio-molecular cancer prediction with random subspace ensembles of support vector machines. <i>Neurocomputing</i> , 2005, 63, 535-539.	5.9	65
10	Imbalance-Aware Machine Learning for Predicting Rare and Common Disease-Associated Non-Coding Variants. <i>Scientific Reports</i> , 2017, 7, 2959.	3.3	63
11	An Experimental Bias-Variance Analysis of SVM Ensembles Based on Resampling Techniques. <i>IEEE Transactions on Systems, Man, and Cybernetics</i> , 2005, 35, 1252-1271.	5.0	60
12	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
13	An extensive analysis of disease-gene associations using network integration and fast kernel-based gene prioritization methods. <i>Artificial Intelligence in Medicine</i> , 2014, 61, 63-78.	6.5	49
14	Support vector machines for candidate nodules classification. <i>Neurocomputing</i> , 2005, 68, 281-288.	5.9	45
15	Mosclust: a software library for discovering significant structures in bio-molecular data. <i>Bioinformatics</i> , 2007, 23, 387-389.	4.1	44
16	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
17	Ensemble Methods. <i>Chapman & Hall/CRC Data Mining and Knowledge Discovery Series</i> , 2012, , .	0.2	44
18	A neural network algorithm for semi-supervised node label learning from unbalanced data. <i>Neural Networks</i> , 2013, 43, 84-98.	5.9	43

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19	A Novel Approach to the Problem of Non-uniqueness of the Solution in Hierarchical Clustering. IEEE Transactions on Neural Networks and Learning Systems, 2013, 24, 1166-1173.	11.3	42
20	Gene expression data analysis of human lymphoma using support vector machines and output coding ensembles. Artificial Intelligence in Medicine, 2002, 26, 281-304.	6.5	40
21	Model order selection for bio-molecular data clustering. BMC Bioinformatics, 2007, 8, S7.	2.6	36
22	Network-Based Drug Ranking and Repositioning with Respect to DrugBank Therapeutic Categories. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1359-1371.	3.0	36
23	Interpretable prioritization of splice variants in diagnostic next-generation sequencing. American Journal of Human Genetics, 2021, 108, 1564-1577.	6.2	36
24	A Fast Ranking Algorithm for Predicting Gene Functions in Biomolecular Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1812-1818.	3.0	33
25	Effectiveness of Error Correcting Output Codes in Multiclass Learning Problems. Lecture Notes in Computer Science, 2000, , 107-116.	1.3	33
26	Hierarchical Ensemble Methods for Protein Function Prediction. , 2014, 2014, 1-34.		32
27	Randomized maps for assessing the reliability of patients clusters in DNA microarray data analyses. Artificial Intelligence in Medicine, 2006, 37, 85-109.	6.5	31
28	<i>RANKS</i>: a flexible tool for node label ranking and classification in biological networks. Bioinformatics, 2016, 32, 2872-2874.	4.1	30
29	True Path Rule Hierarchical Ensembles. Lecture Notes in Computer Science, 2009, , 232-241.	1.3	28
30	Regeneration-associated WNT Signaling Is Activated in Long-term Reconstituting AC133bright Acute Myeloid Leukemia Cells. Neoplasia, 2012, 14, 1236-IN45.	5.3	26
31	Clusterv: a tool for assessing the reliability of clusters discovered in DNA microarray data. Bioinformatics, 2006, 22, 369-370.	4.1	25
32	Prediction of Human Phenotype Ontology terms by means of hierarchical ensemble methods. BMC Bioinformatics, 2017, 18, 449.	2.6	22
33	XML-based approaches for the integration of heterogeneous bio-molecular data. BMC Bioinformatics, 2009, 10, S7.	2.6	21
34	COSNet: A Cost Sensitive Neural Network for Semi-supervised Learning in Graphs. Lecture Notes in Computer Science, 2011, , 219-234.	1.3	21
35	NEUROObjects: an object-oriented library for neural network development. Neurocomputing, 2002, 48, 623-646.	5.9	20
36	Integration of heterogeneous data sources for gene function prediction using decision templates and ensembles of learning machines. Neurocomputing, 2010, 73, 1533-1537.	5.9	20

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37	Cancer module genes ranking using kernelized score functions. BMC Bioinformatics, 2012, 13, S3.	2.6	20
38	Bias Variance Analysis and Ensembles of SVM. Lecture Notes in Computer Science, 2002, , 222-231.	1.3	18
39	Computational intelligence and machine learning in bioinformatics. Artificial Intelligence in Medicine, 2009, 45, 91-96.	6.5	17
40	UNIPred: Unbalance-Aware Network Integration and Prediction of Protein Functions. Journal of Computational Biology, 2015, 22, 1057-1074.	1.6	17
41	An experimental analysis of the dependence among codeword bit errors in ECOC learning machines. Neurocomputing, 2004, 57, 189-214.	5.9	16
42	Discovering multi-level structures in bio-molecular data through the Bernstein inequality. BMC Bioinformatics, 2008, 9, S4.	2.6	16
43	Random projections for assessing gene expression cluster stability. , 0, , .		14
44	HCGene: a software tool to support the hierarchical classification of genes. Bioinformatics, 2008, 24, 729-731.	4.1	14
45	Ensembles Based on Random Projections to Improve the Accuracy of Clustering Algorithms. Lecture Notes in Computer Science, 2006, , 31-37.	1.3	13
46	Ensemble Clustering with a Fuzzy Approach. Studies in Computational Intelligence, 2008, , 49-69.	0.9	13
47	Think globally and solve locally: secondary memory-based network learning for automated multi-species function prediction. GigaScience, 2014, 3, 5.	6.4	12
48	Heterogeneous data integration methods for patient similarity networks. Briefings in Bioinformatics, 2022, 23, .	6.5	12
49	parSMURF, a high-performance computing tool for the genome-wide detection of pathogenic variants. GigaScience, 2020, 9, .	6.4	11
50	Network modeling of patients' biomolecular profiles for clinical phenotype/outcome prediction. Scientific Reports, 2020, 10, 3612.	3.3	11
51	Classification of co-expressed genes from DNA regulatory regions. Information Fusion, 2009, 10, 233-241.	19.1	10
52	UNIPred-Web: a web tool for the integration and visualization of biomolecular networks for protein function prediction. BMC Bioinformatics, 2019, 20, 422.	2.6	9
53	Complex Data Imputation by Auto-Encoders and Convolutional Neural Networks A Case Study on Genome Gap-Filling. Computers, 2020, 9, 37.	3.3	9
54	Feature Selection Combined with Random Subspace Ensemble for Gene Expression Based Diagnosis of Malignancies. , 2005, , 29-35.		9

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55	Large Scale Ranking and Repositioning of Drugs with Respect to DrugBank Therapeutic Categories. Lecture Notes in Computer Science, 2012, , 225-236.	1.3	8
56	COSNet: An R package for label prediction in unbalanced biological networks. Neurocomputing, 2017, 237, 397-400.	5.9	8
57	Protein function prediction as a graph-transduction game. Pattern Recognition Letters, 2020, 134, 96-105.	4.2	8
58	FZD6 triggers Wnt signalling driven by WNT10B^{IVS1} expression and highlights new targets in T cell acute lymphoblastic leukemia. Hematological Oncology, 2021, 39, 364-379.	1.7	8
59	Dependence among Codeword Bits Errors in ECOC Learning Machines: An Experimental Analysis. Lecture Notes in Computer Science, 2001, , 158-167.	1.3	8
60	A Hierarchical Ensemble Method for DAG-Structured Taxonomies. Lecture Notes in Computer Science, 2015, , 15-26.	1.3	8
61	Fuzzy Ensemble Clustering for DNA Microarray Data Analysis. Lecture Notes in Computer Science, 2007, , 537-543.	1.3	8
62	Ensemble Based Data Fusion for Gene Function Prediction. Lecture Notes in Computer Science, 2009, , 448-457.	1.3	8
63	Random Aggregated and Bagged Ensembles of SVMs: An Empirical Bias-Variance Analysis. Lecture Notes in Computer Science, 2004, , 263-272.	1.3	5
64	Lung nodules detection and classification. , 2005, , .		5
65	Characterization of lung tumor subtypes through gene expression cluster validity assessment. RAIRO - Theoretical Informatics and Applications, 2006, 40, 163-176.	0.5	5
66	Gene expression modeling through positive boolean functions. International Journal of Approximate Reasoning, 2008, 47, 97-108.	3.3	5
67	Learning node labels with multi-category Hopfield networks. Neural Computing and Applications, 2016, 27, 1677-1692.	5.6	5
68	Semi-automatic Column Type Inference for CSV Table Understanding. Lecture Notes in Computer Science, 2021, , 535-549.	1.3	5
69	An Experimental Comparison of Hierarchical Bayes and True Path Rule Ensembles for Protein Function Prediction. Lecture Notes in Computer Science, 2010, , 294-303.	1.3	5
70	Multi-resolution visualization and analysis of biomolecular networks through hierarchical community detection and web-based graphical tools. PLoS ONE, 2020, 15, e0244241.	2.5	5
71	A Mathematical Model for the Validation of Gene Selection Methods. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1385-1392.	3.0	4
72	Artificial Intelligence in Predicting Clinical Outcome in COVID-19 Patients from Clinical, Biochemical and a Qualitative Chest X-Ray Scoring System. Reports in Medical Imaging, 0, Volume 14, 27-39.	0.8	4

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73	Data Integration Issues and Opportunities in Biological XML Data Management. , 0, , 263-286.		4
74	Random Walking on Functional Interaction Networks to Rank Genes Involved in Cancer. International Federation for Information Processing, 2012, , 66-75.	0.4	4
75	Supervised learning with word embeddings derived from PubMed captures latent knowledge about protein kinases and cancer. NAR Genomics and Bioinformatics, 2021, 3, lqab113.	3.2	4
76	Prediction of Human Gene - Phenotype Associations by Exploiting the Hierarchical Structure of the Human Phenotype Ontology. Lecture Notes in Computer Science, 2015, , 66-77.	1.3	3
77	Boosting and Classification of Electronic Nose Data. Lecture Notes in Computer Science, 2002, , 262-271.	1.3	3
78	Discovering Significant Structures in Clustered Bio-molecular Data Through the Bernstein Inequality. Lecture Notes in Computer Science, 2007, , 886-891.	1.3	3
79	A stability-based algorithm to validate hierarchical clusters of genes. International Journal of Knowledge Engineering and Soft Data Paradigms, 2009, 1, 318.	0.0	2
80	Multi-species protein function prediction. , 2016, , .		2
81	A GPU-based algorithm for fast node label learning in large and unbalanced biomolecular networks. BMC Bioinformatics, 2018, 19, 353.	2.6	2
82	Ensembling Descendant Term Classifiers to Improve Gene - Abnormal Phenotype Predictions. Lecture Notes in Computer Science, 2019, , 70-80.	1.3	2
83	HEMDAG: a family of modular and scalable hierarchical ensemble methods to improve Gene Ontology term prediction. Bioinformatics, 2021, 37, 4526-4533.	4.1	2
84	Prediction of Gene Function Using Ensembles of SVMs and Heterogeneous Data Sources. Studies in Computational Intelligence, 2009, , 79-91.	0.9	2
85	Abdominal Computed Tomography Imaging Findings in Hospitalized COVID-19 Patients: A Year-Long Experience and Associations Revealed by Explainable Artificial Intelligence. Journal of Imaging, 2021, 7, 258.	3.0	2
86	Automated image analysis to assess hygienic behaviour of honeybees. PLoS ONE, 2022, 17, e0263183.	2.5	2
87	Dataset complexity can help to generate accurate ensembles of k-nearest neighbors. , 2008, , .		1
88	An Application of Low Bias Bagged SVMs to the Classification of Heterogeneous Malignant Tissues. Lecture Notes in Computer Science, 2003, , 316-321.	1.3	1
89	Biological Specifications for a Synthetic Gene Expression Data Generation Model. Lecture Notes in Computer Science, 2006, , 277-283.	1.3	1
90	Bayesian Optimization Improves Tissue-Specific Prediction of Active Regulatory Regions with Deep Neural Networks. Lecture Notes in Computer Science, 2020, , 600-612.	1.3	1

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91	Noise tolerance of multiple classifier systems in data integration-based gene function prediction. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	1
92	Diseaseâ€“Genes Must Guide Data Source Integration in the Gene Prioritization Process. Lecture Notes in Computer Science, 2019, , 60-69.	1.3	0
93	Unsupervised Stability-Based Ensembles to Discover Reliable Structures in Complex Bio-molecular Data. Lecture Notes in Computer Science, 2009, , 25-43.	1.3	0
94	Multitask Hopfield Networks. Lecture Notes in Computer Science, 2020, , 349-365.	1.3	0
95	A Graphical Tool for the Exploration and Visual Analysis of Biomolecular Networks. Lecture Notes in Computer Science, 2020, , 88-98.	1.3	0
96	Committee-Based Active Learning to Select Negative Examples for Predicting Protein Functions. Lecture Notes in Computer Science, 2020, , 80-87.	1.3	0