

Giorgio Valentini

List of Publications by Year in descending order

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Version: 2024-02-01

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	Automated image analysis to assess hygienic behaviour of honeybees. PLoS ONE, 2022, 17, e0263183.	2.5	2
2	Heterogeneous data integration methods for patient similarity networks. Briefings in Bioinformatics, 2022, 23, .	6.5	12
3	Semi-automatic Column Type Inference for CSV Table Understanding. Lecture Notes in Computer Science, 2021, , 535-549.	1.3	5
4	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
5	HEMDAG: a family of modular and scalable hierarchical ensemble methods to improve Gene Ontology term prediction. Bioinformatics, 2021, 37, 4526-4533.	4.1	2
6	Interpretable prioritization of splice variants in diagnostic next-generation sequencing. American Journal of Human Genetics, 2021, 108, 1564-1577.	6.2	36
7	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
8	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
9	Protein function prediction as a graph-transduction game. Pattern Recognition Letters, 2020, 134, 96-105.	4.2	8
10	parSMURF, a high-performance computing tool for the genome-wide detection of pathogenic variants. GigaScience, 2020, 9, .	6.4	11
11	Explainable Machine Learning for Early Assessment of COVID-19 Risk Prediction in Emergency Departments. IEEE Access, 2020, 8, 196299-196325.	4.2	55
12	Complex Data Imputation by Auto-Encoders and Convolutional Neural Networks – A Case Study on Genome Gap-Filling. Computers, 2020, 9, 37.	3.3	9
13	Network modeling of patients' biomolecular profiles for clinical phenotype/outcome prediction. Scientific Reports, 2020, 10, 3612.	3.3	11
14	Multitask Hopfield Networks. Lecture Notes in Computer Science, 2020, , 349-365.	1.3	0
15	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
16	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
17	A Graphical Tool for the Exploration and Visual Analysis of Biomolecular Networks. Lecture Notes in Computer Science, 2020, , 88-98.	1.3	0
18	Committee-Based Active Learning to Select Negative Examples for Predicting Protein Functions. Lecture Notes in Computer Science, 2020, , 80-87.	1.3	0

#	ARTICLE	IF	CITATIONS
19	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
20	Disease-aware Genes Must Guide Data Source Integration in the Gene Prioritization Process. Lecture Notes in Computer Science, 2019, , 60-69.	1.3	0
21	Ensembling Descendant Term Classifiers to Improve Gene - Abnormal Phenotype Predictions. Lecture Notes in Computer Science, 2019, , 70-80.	1.3	2
22	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
23	A GPU-based algorithm for fast node label learning in large and unbalanced biomolecular networks. BMC Bioinformatics, 2018, 19, 353.	2.6	2
24	COSNet: An R package for label prediction in unbalanced biological networks. Neurocomputing, 2017, 237, 397-400.	5.9	8
25	Imbalance-Aware Machine Learning for Predicting Rare and Common Disease-Associated Non-Coding Variants. Scientific Reports, 2017, 7, 2959.	3.3	63
26	Prediction of Human Phenotype Ontology terms by means of hierarchical ensemble methods. BMC Bioinformatics, 2017, 18, 449.	2.6	22
27	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
28	A Whole-Genome Analysis Framework for Effective Identification of Pathogenic Regulatory Variants in Mendelian Disease. American Journal of Human Genetics, 2016, 99, 595-606.	6.2	223
29	Multi-species protein function prediction. , 2016, , .		2
30	Learning node labels with multi-category Hopfield networks. Neural Computing and Applications, 2016, 27, 1677-1692.	5.6	5
31	<i>RANKS</i> : a flexible tool for node label ranking and classification in biological networks. Bioinformatics, 2016, 32, 2872-2874.	4.1	30
32	UNIPred: Unbalance-Aware Network Integration and Prediction of Protein Functions. Journal of Computational Biology, 2015, 22, 1057-1074.	1.6	17
33	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
34	A Hierarchical Ensemble Method for DAG-Structured Taxonomies. Lecture Notes in Computer Science, 2015, , 15-26.	1.3	8
35	Hierarchical Ensemble Methods for Protein Function Prediction. , 2014, 2014, 1-34.		32
36	GOssTo: a stand-alone application and a web tool for calculating semantic similarities on the Gene Ontology. Bioinformatics, 2014, 30, 2235-2236.	4.1	44

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37	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
38	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
39	A neural network algorithm for semi-supervised node label learning from unbalanced data. <i>Neural Networks</i> , 2013, 43, 84-98.	5.9	43
40	Network-Based Drug Ranking and Repositioning with Respect to DrugBank Therapeutic Categories. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1359-1371.	3.0	36
41	A Novel Approach to the Problem of Non-uniqueness of the Solution in Hierarchical Clustering. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2013, 24, 1166-1173.	11.3	42
42	Large Scale Ranking and Repositioning of Drugs with Respect to DrugBank Therapeutic Categories. <i>Lecture Notes in Computer Science</i> , 2012, , 225-236.	1.3	8
43	Regeneration-associated WNT Signaling Is Activated in Long-term Reconstituting AC133bright Acute Myeloid Leukemia Cells. <i>Neoplasia</i> , 2012, 14, 1236-IN45.	5.3	26
44	A Fast Ranking Algorithm for Predicting Gene Functions in Biomolecular Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1812-1818.	3.0	33
45	Cancer module genes ranking using kernelized score functions. <i>BMC Bioinformatics</i> , 2012, 13, S3.	2.6	20
46	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
47	Ensemble Methods. <i>Chapman & Hall/CRC Data Mining and Knowledge Discovery Series</i> , 2012, , .	0.2	44
48	Random Walking on Functional Interaction Networks to Rank Genes Involved in Cancer. <i>International Federation for Information Processing</i> , 2012, , 66-75.	0.4	4
49	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
50	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
51	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
52	Integration of heterogeneous data sources for gene function prediction using decision templates and ensembles of learning machines. <i>Neurocomputing</i> , 2010, 73, 1533-1537.	5.9	20
53	An Experimental Comparison of Hierarchical Bayes and True Path Rule Ensembles for Protein Function Prediction. <i>Lecture Notes in Computer Science</i> , 2010, , 294-303.	1.3	5
54	Noise tolerance of multiple classifier systems in data integration-based gene function prediction. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	1

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55	XML-based approaches for the integration of heterogeneous bio-molecular data. BMC Bioinformatics, 2009, 10, S7.	2.6	21
56	Fuzzy ensemble clustering based on random projections for DNA microarray data analysis. Artificial Intelligence in Medicine, 2009, 45, 173-183.	6.5	79
57	Computational intelligence and machine learning in bioinformatics. Artificial Intelligence in Medicine, 2009, 45, 91-96.	6.5	17
58	Classification of co-expressed genes from DNA regulatory regions. Information Fusion, 2009, 10, 233-241.	19.1	10
59	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
60	True Path Rule Hierarchical Ensembles. Lecture Notes in Computer Science, 2009, , 232-241.	1.3	28
61	Ensemble Based Data Fusion for Gene Function Prediction. Lecture Notes in Computer Science, 2009, , 448-457.	1.3	8
62	Prediction of Gene Function Using Ensembles of SVMs and Heterogeneous Data Sources. Studies in Computational Intelligence, 2009, , 79-91.	0.9	2
63	Unsupervised Stability-Based Ensembles to Discover Reliable Structures in Complex Bio-molecular Data. Lecture Notes in Computer Science, 2009, , 25-43.	1.3	0
64	Gene expression modeling through positive boolean functions. International Journal of Approximate Reasoning, 2008, 47, 97-108.	3.3	5
65	Discovering multi-level structures in bio-molecular data through the Bernstein inequality. BMC Bioinformatics, 2008, 9, S4.	2.6	16
66	Dataset complexity can help to generate accurate ensembles of k-nearest neighbors. , 2008, , .		1
67	HCGene: a software tool to support the hierarchical classification of genes. Bioinformatics, 2008, 24, 729-731.	4.1	14
68	Ensemble Clustering with a Fuzzy Approach. Studies in Computational Intelligence, 2008, , 49-69.	0.9	13
69	Mosclust: a software library for discovering significant structures in bio-molecular data. Bioinformatics, 2007, 23, 387-389.	4.1	44
70	Model order selection for bio-molecular data clustering. BMC Bioinformatics, 2007, 8, S7.	2.6	36
71	Fuzzy Ensemble Clustering for DNA Microarray Data Analysis. Lecture Notes in Computer Science, 2007, , 537-543.	1.3	8
72	Discovering Significant Structures in Clustered Bio-molecular Data Through the Bernstein Inequality. Lecture Notes in Computer Science, 2007, , 886-891.	1.3	3

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73	Characterization of lung tumor subtypes through gene expression cluster validity assessment. RAIRO - Theoretical Informatics and Applications, 2006, 40, 163-176.	0.5	5
74	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
75	Clusterv: a tool for assessing the reliability of clusters discovered in DNA microarray data. Bioinformatics, 2006, 22, 369-370.	4.1	25
76	Ensembles Based on Random Projections to Improve the Accuracy of Clustering Algorithms. Lecture Notes in Computer Science, 2006, , 31-37.	1.3	13
77	Biological Specifications for a Synthetic Gene Expression Data Generation Model. Lecture Notes in Computer Science, 2006, , 277-283.	1.3	1
78	Bio-molecular cancer prediction with random subspace ensembles of support vector machines. Neurocomputing, 2005, 63, 535-539.	5.9	65
79	Support vector machines for candidate nodules classification. Neurocomputing, 2005, 68, 281-288.	5.9	45
80	Lung nodules detection and classification. , 2005, , .		5
81	An Experimental Bias-Variance Analysis of SVM Ensembles Based on Resampling Techniques. IEEE Transactions on Systems, Man, and Cybernetics, 2005, 35, 1252-1271.	5.0	60
82	Feature Selection Combined with Random Subspace Ensemble for Gene Expression Based Diagnosis of Malignancies. , 2005, , 29-35.		9
83	Random Aggregated and Bagged Ensembles of SVMs: An Empirical Bias-Variance Analysis. Lecture Notes in Computer Science, 2004, , 263-272.	1.3	5
84	Cancer recognition with bagged ensembles of support vector machines. Neurocomputing, 2004, 56, 461-466.	5.9	79
85	An experimental analysis of the dependence among codeword bit errors in ECOC learning machines. Neurocomputing, 2004, 57, 189-214.	5.9	16
86	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
87	Ensembles of Learning Machines. Lecture Notes in Computer Science, 2002, , 3-20.	1.3	166
88	NEUROObjects: an object-oriented library for neural network development. Neurocomputing, 2002, 48, 623-646.	5.9	20
89	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
90	Bias-Variance Analysis and Ensembles of SVM. Lecture Notes in Computer Science, 2002, , 222-231.	1.3	18

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91	Boosting and Classification of Electronic Nose Data. Lecture Notes in Computer Science, 2002, , 262-271.	1.3	3
92	Dependence among Codeword Bits Errors in ECOC Learning Machines: An Experimental Analysis. Lecture Notes in Computer Science, 2001, , 158-167.	1.3	8
93	Effectiveness of Error Correcting Output Codes in Multiclass Learning Problems. Lecture Notes in Computer Science, 2000, , 107-116.	1.3	33
94	Random projections for assessing gene expression cluster stability. , 0, , .		14
95	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
96	Data Integration Issues and Opportunities in Biological XML Data Management. , 0, , 263-286.		4