

Andrea Passerini

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

1,988
citations

393982

19
h-index

264894

42
g-index

80
all docs

80
docs citations

80
times ranked

3052
citing authors

#	ARTICLE	IF	CITATIONS
1	An efficient procedure for mining egocentric temporal motifs. <i>Data Mining and Knowledge Discovery</i> , 2022, 36, 355-378.	2.4	10
2	Skeptical Learning – An Algorithm and a Platform for Dealing with Mislabeling in Personal Context Recognition. <i>Algorithms</i> , 2022, 15, 109.	1.2	0
3	Give more data, awareness and control to individual citizens, and they will help COVID-19 containment. <i>Ethics and Information Technology</i> , 2021, 23, 1-6.	2.3	33
4	A review and experimental analysis of active learning over crowdsourced data. <i>Artificial Intelligence Review</i> , 2021, 54, 5283-5305.	9.7	11
5	Learning Modulo Theories for constructive preference elicitation. <i>Artificial Intelligence</i> , 2021, 295, 103454.	3.9	2
6	Learning Aggregation Functions. , 2021, , .		3
7	Putting human behavior predictability in context. <i>EPJ Data Science</i> , 2021, 10, .	1.5	12
8	Hybrid Probabilistic Inference with Logical and Algebraic Constraints: a Survey. , 2021, , .		0
9	Towards Visual Semantics. <i>SN Computer Science</i> , 2021, 2, 1.	2.3	5
10	Deep Learning for Classification and Localization of COVID-19 Markers in Point-of-Care Lung Ultrasound. <i>IEEE Transactions on Medical Imaging</i> , 2020, 39, 2676-2687.	5.4	422
11	Learning in the Wild with Incremental Skeptical Gaussian Processes. , 2020, , .		2
12	Learning Weighted Model Integration Distributions. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2020, 34, 5224-5231.	3.6	1
13	Combining learning and constraints for genome-wide protein annotation. <i>BMC Bioinformatics</i> , 2019, 20, 338.	1.2	1
14	Advanced SMT techniques for weighted model integration. <i>Artificial Intelligence</i> , 2019, 275, 1-27.	3.9	8
15	Counts-of-counts similarity for prediction and search in relational data. <i>Data Mining and Knowledge Discovery</i> , 2019, 33, 1254-1297.	2.4	0
16	Automating Layout Synthesis with Constructive Preference Elicitation. <i>Lecture Notes in Computer Science</i> , 2019, , 254-270.	1.0	1
17	Fixing Mislabeling by Human Annotators Leveraging Conflict Resolution and Prior Knowledge. , 2019, 3, 1-23.		16
18	A Big Data and machine learning approach for network monitoring and security. <i>Security and Privacy</i> , 2019, 2, e53.	1.9	5

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19	The pywmi Framework and Toolbox for Probabilistic Inference using Weighted Model Integration. , 2019, , .		1
20	No more ready-made deals. , 2018, , .		6
21	Constructive Preference Elicitation. Frontiers in Robotics and AI, 2018, 4, .	2.0	11
22	Learning SMT(LRA) Constraints using SMT Solvers. , 2018, , .		17
23	Pyconstruct: Constraint Programming Meets Structured Prediction. , 2018, , .		3
24	Structured learning modulo theories. Artificial Intelligence, 2017, 244, 166-187.	3.9	32
25	Introduction to the special issue on Combining Constraint Solving with Mining and Learning. Artificial Intelligence, 2017, 244, 1-5.	3.9	4
26	Group-level spatio-temporal pattern recovery in MEG decoding using multi-task joint feature learning. Journal of Neuroscience Methods, 2017, 285, 97-108.	1.3	17
27	Investigating the association between social interactions and personality states dynamics. Royal Society Open Science, 2017, 4, 170194.	1.1	8
28	Constructive Preference Elicitation for Multiple Users with Setwise Max-margin. Lecture Notes in Computer Science, 2017, , 3-17.	1.0	6
29	Efficient Weighted Model Integration via SMT-Based Predicate Abstraction. , 2017, , .		4
30	Guest editorsâ€™ introduction to the EcmlPkdd 2016 journal track special issue of Machine Learning. Data Mining and Knowledge Discovery, 2016, 30, 995-997.	2.4	0
31	Guest editorsâ€™ introduction to the EcmlPkdd 2016 journal track special issue of Machine Learning. Machine Learning, 2016, 104, 149-150.	3.4	0
32	RNAcommender: genome-wide recommendation of RNAâ€™protein interactions. Bioinformatics, 2016, 32, 3627-3634.	1.8	31
33	Interpretability of Multivariate Brain Maps in Linear Brain Decoding: Definition, and Heuristic Quantification in Multivariate Analysis of MEG Time-Locked Effects. Frontiers in Neuroscience, 2016, 10, 619.	1.4	16
34	Learning Modulo Theories. Lecture Notes in Computer Science, 2016, , 113-146.	1.0	0
35	Three distinct ribosome assemblies modulated by translation are the building blocks of polysomes. Journal of Cell Biology, 2015, 208, 581-596.	2.3	44
36	Joint probabilistic-logical refinement of multiple protein feature predictors. BMC Bioinformatics, 2014, 15, 16.	1.2	15

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37	Predicting virus mutations through statistical relational learning. BMC Bioinformatics, 2014, 15, 309.	1.2	6
38	Active Learning of Pareto Fronts. IEEE Transactions on Neural Networks and Learning Systems, 2014, 25, 506-519.	7.2	31
39	Improving Activity Recognition by Segmental Pattern Mining. IEEE Transactions on Knowledge and Data Engineering, 2014, 26, 889-902.	4.0	18
40	Improved multi-level protein-protein interaction prediction with semantic-based regularization. BMC Bioinformatics, 2014, 15, 103.	1.2	16
41	PTRcombiner: mining combinatorial regulation of gene expression from post-transcriptional interaction maps. BMC Genomics, 2014, 15, 304.	1.2	4
42	Ego-centric Graphlets for Personality and Affective States Recognition. , 2013, , .		8
43	Type Extension Trees for feature construction and learning in relational domains. Artificial Intelligence, 2013, 204, 30-55.	3.9	6
44	Navigating the topical structure of academic search results via the Wikipedia category network. , 2013, , .		5
45	A Fully Unsupervised Approach to Activity Discovery. Lecture Notes in Computer Science, 2013, , 77-88.	1.0	3
46	Using Machine Learning and Information Retrieval Techniques to Improve Software Maintainability. Communications in Computer and Information Science, 2013, , 117-134.	0.4	3
47	Kernel Methods for Structured Data. Intelligent Systems Reference Library, 2013, , 283-333.	1.0	0
48	Predicting Metal-Binding Sites from Protein Sequence. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 203-213.	1.9	20
49	Improving activity recognition by segmental pattern mining. , 2012, , .		5
50	Widespread uncoupling between transcriptome and translome variations after a stimulus in mammalian cells. BMC Genomics, 2012, 13, 220.	1.2	113
51	Metal Binding in Proteins: Machine Learning Complements X-Ray Absorption Spectroscopy. Lecture Notes in Computer Science, 2012, , 854-857.	1.0	1
52	MetalDetector v2.0: predicting the geometry of metal binding sites from protein sequence. Nucleic Acids Research, 2011, 39, W288-W292.	6.5	58
53	Active Learning of Combinatorial Features for Interactive Optimization. Lecture Notes in Computer Science, 2011, , 336-350.	1.0	2
54	Relational Feature Mining with Hierarchical Multitask kFOIL. Fundamenta Informaticae, 2011, 113, 151-177.	0.3	4

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55	Relational information gain. <i>Machine Learning</i> , 2011, 83, 219-239.	3.4	3
56	Characterization of metalloproteins by high-throughput X-ray absorption spectroscopy. <i>Genome Research</i> , 2011, 21, 898-907.	2.4	41
57	Fast learning of relational kernels. <i>Machine Learning</i> , 2010, 78, 305-342.	3.4	25
58	Brainâ€“Computer Evolutionary Multiobjective Optimization: A Genetic Algorithm Adapting to the Decision Maker. <i>IEEE Transactions on Evolutionary Computation</i> , 2010, 14, 671-687.	7.5	118
59	Automatic prediction of catalytic residues by modeling residue structural neighborhood. <i>BMC Bioinformatics</i> , 2010, 11, 115.	1.2	17
60	An On/Off Lattice Approach to Protein Structure Prediction from Contact Maps. <i>Lecture Notes in Computer Science</i> , 2010, , 368-379.	1.0	2
61	From On-Going to Complete Activity Recognition Exploiting Related Activities. <i>Lecture Notes in Computer Science</i> , 2010, , 26-37.	1.0	1
62	Adapting to a Realistic Decision Maker: Experiments towards a Reactive Multi-objective Optimizer. <i>Lecture Notes in Computer Science</i> , 2010, , 338-341.	1.0	6
63	A semiparametric generative model for efficient structured-output supervised learning. <i>Annals of Mathematics and Artificial Intelligence</i> , 2008, 54, 207-222.	0.9	0
64	A simplified approach to disulfide connectivity prediction from protein sequences. <i>BMC Bioinformatics</i> , 2008, 9, 20.	1.2	20
65	MetalDetector: a web server for predicting metal-binding sites and disulfide bridges in proteins from sequence. <i>Bioinformatics</i> , 2008, 24, 2094-2095.	1.8	47
66	On the Convergence of Protein Structure and Dynamics. <i>Statistical Learning Studies of Pseudo Folding Pathways</i> . , 2008, , 200-211.		1
67	Feature Discovery with Type Extension Trees. <i>Lecture Notes in Computer Science</i> , 2008, , 122-139.	1.0	2
68	Learning with Kernels and Logical Representations. <i>Lecture Notes in Computer Science</i> , 2008, , 56-91.	1.0	6
69	Predicting zinc binding at the proteome level. <i>BMC Bioinformatics</i> , 2007, 8, 39.	1.2	89
70	DISULFIND: a disulfide bonding state and cysteine connectivity prediction server. <i>Nucleic Acids Research</i> , 2006, 34, W177-W181.	6.5	306
71	Identifying cysteines and histidines in transition-metal-binding sites using support vector machines and neural networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 305-316.	1.5	86
72	Learning to discriminate between ligand-bound and disulfide-bound cysteines. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 367-373.	1.0	18

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73	New Results on Error Correcting Output Codes of Kernel Machines. IEEE Transactions on Neural Networks, 2004, 15, 45-54.	4.8	116
74	Predicting the Disulfide Bonding State of Cysteines with Combinations of Kernel Machines. Journal of Signal Processing Systems, 2003, 35, 287-295.	1.0	19
75	A Combination of Support Vector Machines and Bidirectional Recurrent Neural Networks for Protein Secondary Structure Prediction. Lecture Notes in Computer Science, 2003, , 142-153.	1.0	4