

# Geoffrey I Webb

## List of Publications by Year in descending order

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207  
papers

10,734  
citations

53794

45  
h-index

42399

92  
g-index

219  
all docs

219  
docs citations

219  
times ranked

7630  
citing authors

#	ARTICLE	IF	CITATIONS
1	Not So Naive Bayes: Aggregating One-Dependence Estimators. <i>Machine Learning</i> , 2005, 58, 5-24.	5.4	570
2	MultiBoosting: A Technique for Combining Boosting and Wagging. <i>Machine Learning</i> , 2000, 40, 159-196.	5.4	556
3	InceptionTime: Finding AlexNet for time series classification. <i>Data Mining and Knowledge Discovery</i> , 2020, 34, 1936-1962.	3.7	542
4	<i>Feature</i> : a Python package and web server for features extraction and selection from protein and peptide sequences. <i>Bioinformatics</i> , 2018, 34, 2499-2502.	4.1	481
5	ROCKET: exceptionally fast and accurate time series classification using random convolutional kernels. <i>Data Mining and Knowledge Discovery</i> , 2020, 34, 1454-1495.	3.7	359
6	Temporal Convolutional Neural Network for the Classification of Satellite Image Time Series. <i>Remote Sensing</i> , 2019, 11, 523.	4.0	306
7	iLearn: an integrated platform and meta-learner for feature engineering, machine-learning analysis and modeling of DNA, RNA and protein sequence data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1047-1057.	6.5	294
8	Characterizing concept drift. <i>Data Mining and Knowledge Discovery</i> , 2016, 30, 964-994.	3.7	285
9	Machine Learning for User Modeling. <i>User Modeling and User-Adapted Interaction</i> , 2001, 11, 19-29.	3.8	278
10	PROSPER: An Integrated Feature-Based Tool for Predicting Protease Substrate Cleavage Sites. <i>PLoS ONE</i> , 2012, 7, e50300.	2.5	265
11	Multistrategy ensemble learning: reducing error by combining ensemble learning techniques. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2004, 16, 980-991.	5.7	206
12	Discovering Significant Patterns. <i>Machine Learning</i> , 2007, 68, 1-33.	5.4	195
13	Discretization for naive-Bayes learning: managing discretization bias and variance. <i>Machine Learning</i> , 2009, 74, 39-74.	5.4	187
14	Lazy Learning of Bayesian Rules. <i>Machine Learning</i> , 2000, 41, 53-84.	5.4	185
15	A novel selective naïve Bayes algorithm. <i>Knowledge-Based Systems</i> , 2020, 192, 105361.	7.1	185
16	GlycoMine: a machine learning-based approach for predicting N-, C- and O-linked glycosylation in the human proteome. <i>Bioinformatics</i> , 2015, 31, 1411-1419.	4.1	167
17	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. <i>Briefings in Bioinformatics</i> , 2019, 20, 638-658.	6.5	166
18	Cascleave: towards more accurate prediction of caspase substrate cleavage sites. <i>Bioinformatics</i> , 2010, 26, 752-760.	4.1	148

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19	POSSUM: a bioinformatics toolkit for generating numerical sequence feature descriptors based on PSSM profiles. <i>Bioinformatics</i> , 2017, 33, 2756-2758.	4.1	145
20	Dynamic Time Warping Averaging of Time Series Allows Faster and More Accurate Classification. , 2014, , .		137
21	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. <i>Bioinformatics</i> , 2018, 34, 684-687.	4.1	131
22	MiniRocket. , 2021, , .		130
23	PREvall, an integrative approach for inferring catalytic residues using sequence, structural, and network features in a machine-learning framework. <i>Journal of Theoretical Biology</i> , 2018, 443, 125-137.	1.7	124
24	iLearnPlus: a comprehensive and automated machine-learning platform for nucleic acid and protein sequence analysis, prediction and visualization. <i>Nucleic Acids Research</i> , 2021, 49, e60-e60.	14.5	124
25	Efficient search for association rules. , 2000, , .		113
26	TS-CHIEF: a scalable and accurate forest algorithm for time series classification. <i>Data Mining and Knowledge Discovery</i> , 2020, 34, 742-775.	3.7	112
27	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. <i>Bioinformatics</i> , 2020, 36, 1057-1065.	4.1	102
28	K-Optimal Rule Discovery. <i>Data Mining and Knowledge Discovery</i> , 2005, 10, 39-79.	3.7	100
29	Proximity Forest: an effective and scalable distance-based classifier for time series. <i>Data Mining and Knowledge Discovery</i> , 2019, 33, 607-635.	3.7	100
30	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. <i>Briefings in Bioinformatics</i> , 2019, 20, 2267-2290.	6.5	99
31	Comprehensive review and assessment of computational methods for predicting RNA post-transcriptional modification sites from RNA sequences. <i>Briefings in Bioinformatics</i> , 2020, 21, 1676-1696.	6.5	98
32	Naïve Bayes. , 2011, , 713-714.		92
33	Faster and more accurate classification of time series by exploiting a novel dynamic time warping averaging algorithm. <i>Knowledge and Information Systems</i> , 2016, 47, 1-26.	3.2	92
34	Generating Synthetic Time Series to Augment Sparse Datasets. , 2017, , .		84
35	Computational analysis and prediction of lysine malonylation sites by exploiting informative features in an integrative machine-learning framework. <i>Briefings in Bioinformatics</i> , 2019, 20, 2185-2199.	6.5	82
36	On detecting differences between groups. , 2003, , .		80

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37	Extremely Fast Decision Tree. , 2018, , .		79
38	On the Application of ROC Analysis to Predict Classification Performance Under Varying Class Distributions. Machine Learning, 2005, 58, 25-32.	5.4	75
39	Learning by extrapolation from marginal to full-multivariate probability distributions: decreasingly naive Bayesian classification. Machine Learning, 2012, 86, 233-272.	5.4	72
40	PhosphoPredict: A bioinformatics tool for prediction of human kinase-specific phosphorylation substrates and sites by integrating heterogeneous feature selection. Scientific Reports, 2017, 7, 6862.	3.3	72
41	Accurate in silico identification of species-specific acetylation sites by integrating protein sequence-derived and functional features. Scientific Reports, 2014, 4, 5765.	3.3	71
42	Procleave: Predicting Protease-specific Substrate Cleavage Sites by Combining Sequence and Structural Information. Genomics, Proteomics and Bioinformatics, 2020, 18, 52-64.	6.9	71
43	Twenty years of bioinformatics research for protease-specific substrate and cleavage site prediction: a comprehensive revisit and benchmarking of existing methods. Briefings in Bioinformatics, 2019, 20, 2150-2166.	6.5	70
44	Discovering significant rules. , 2006, , .		69
45	GlycoMinestruct: a new bioinformatics tool for highly accurate mapping of the human N-linked and O-linked glycoproteomes by incorporating structural features. Scientific Reports, 2016, 6, 34595.	3.3	69
46	Proportional k-Interval Discretization for Naive-Bayes Classifiers. Lecture Notes in Computer Science, 2001, , 564-575.	1.3	66
47	Discovering associations with numeric variables. , 2001, , .		65
48	Analyzing concept drift and shift from sample data. Data Mining and Knowledge Discovery, 2018, 32, 1179-1199.	3.7	65
49	Systematic analysis and prediction of type IV secreted effector proteins by machine learning approaches. Briefings in Bioinformatics, 2019, 20, 931-951.	6.5	65
50	Positive-unlabelled learning of glycosylation sites in the human proteome. BMC Bioinformatics, 2019, 20, 112.	2.6	60
51	Subsumption resolution: an efficient and effective technique for semi-naive Bayesian learning. Machine Learning, 2012, 87, 93-125.	5.4	56
52	Self-sufficient itemsets. ACM Transactions on Knowledge Discovery From Data, 2010, 4, 1-20.	3.5	54
53	Comprehensive assessment and performance improvement of effector protein predictors for bacterial secretion systems III, IV and VI. Briefings in Bioinformatics, 2018, 19, bbw100.	6.5	51
54	On Why Discretization Works for Naive-Bayes Classifiers. Lecture Notes in Computer Science, 2003, , 440-452.	1.3	49

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55	Layered critical values: a powerful direct-adjustment approach to discovering significant patterns. <i>Machine Learning</i> , 2008, 71, 307-323.	5.4	45
56	MultiRocket: multiple pooling operators and transformations for fast and effective time series classification. <i>Data Mining and Knowledge Discovery</i> , 2022, 36, 1623-1646.	3.7	45
57	Feature-subspace aggregating: ensembles for stable and unstable learners. <i>Machine Learning</i> , 2011, 82, 375-397.	5.4	41
58	Survey of distance measures for quantifying concept drift and shift in numeric data. <i>Knowledge and Information Systems</i> , 2019, 60, 591-615.	3.2	40
59	Prodepth: Predict Residue Depth by Support Vector Regression Approach from Protein Sequences Only. <i>PLoS ONE</i> , 2009, 4, e7072.	2.5	40
60	Efficient lazy elimination for averaged one-dependence estimators. , 2006, , .		39
61	The Need for Low Bias Algorithms in Classification Learning from Large Data Sets. <i>Lecture Notes in Computer Science</i> , 2002, , 62-73.	1.3	39
62	Feature Based Modelling: A methodology for producing coherent, consistent, dynamically changing models of agents' competencies. <i>User Modeling and User-Adapted Interaction</i> , 1996, 5, 117-150.	3.8	38
63	To Select or To Weigh: A Comparative Study of Linear Combination Schemes for SuperParent-One-Dependence Estimators. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2007, 19, 1652-1665.	5.7	38
64	SecretEPDB: a comprehensive web-based resource for secreted effector proteins of the bacterial types III, IV and VI secretion systems. <i>Scientific Reports</i> , 2017, 7, 41031.	3.3	38
65	PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact. <i>Briefings in Bioinformatics</i> , 2020, 21, 1069-1079.	6.5	38
66	A tutorial on statistically sound pattern discovery. <i>Data Mining and Knowledge Discovery</i> , 2019, 33, 325-377.	3.7	37
67	Anthem: a user customised tool for fast and accurate prediction of binding between peptides and HLA class I molecules. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	37
68	RCPdb: An evolutionary classification and codon usage database for repeat-containing proteins. <i>Genome Research</i> , 2007, 17, 1118-1127.	5.5	36
69	TANGLE: Two-Level Support Vector Regression Approach for Protein Backbone Torsion Angle Prediction from Primary Sequences. <i>PLoS ONE</i> , 2012, 7, e30361.	2.5	36
70	Crysalis: an integrated server for computational analysis and design of protein crystallization. <i>Scientific Reports</i> , 2016, 6, 21383.	3.3	35
71	Filtered association discovery. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2011, 1, 183-192.	6.8	34
72	Indexing and classifying gigabytes of time series under time warping. , 2017, , 282-290.		33

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73	Discretization Methods. , 2009, , 101-116.		32
74	Time series extrinsic regression. Data Mining and Knowledge Discovery, 2021, 35, 1032-1060.	3.7	32
75	Ensemble Selection for SuperParent-One-Dependence Estimators. Lecture Notes in Computer Science, 2005, , 102-112.	1.3	32
76	BIOINFORMATIC APPROACHES FOR PREDICTING SUBSTRATES OF PROTEASES. Journal of Bioinformatics and Computational Biology, 2011, 09, 149-178.	0.8	31
77	Structural and dynamic properties that govern the stability of an engineered fibronectin type III domain. Protein Engineering, Design and Selection, 2015, 28, 67-78.	2.1	31
78	A Deep Learning-Based Method for Identification of Bacteriophage-Host Interaction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1801-1810.	3.0	31
79	The Efficacy of a Low-Level Program Visualization Tool for Teaching Programming Concepts to Novice C Programmers. Journal of Educational Computing Research, 2000, 22, 187-215.	5.5	30
80	Skopus: Mining top-k sequential patterns under leverage. Data Mining and Knowledge Discovery, 2016, 30, 1086-1111.	3.7	30
81	Using Decision Trees for Agent Modeling: Improving Prediction Performance. User Modeling and User-Adapted Interaction, 1998, 8, 131-152.	3.8	28
82	The enantioselective hydrogenation of methylacetoacetate over nickel catalysts modified with tartaric acid.. Catalysis Today, 1991, 10, 363-370.	4.4	26
83	Positive-unlabeled learning in bioinformatics and computational biology: a brief review. Briefings in Bioinformatics, 2022, 23, .	6.5	26
84	PROSPECT: A web server for predicting protein histidine phosphorylation sites. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050018.	0.8	25
85	Live fuel moisture content estimation from MODIS: A deep learning approach. ISPRS Journal of Photogrammetry and Remote Sensing, 2021, 179, 81-91.	11.1	25
86	Asymmetric hydrogenation of methyl acetoacetate using Ni/SiO <sub>2</sub> modified with tartaric acid and alanine. Journal of Molecular Catalysis, 1992, 73, 91-95.	1.2	24
87	Identifying markers of pathology in SAXS data of malignant tissues of the brain. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2005, 548, 140-146.	1.6	24
88	An Experimental Evaluation of Integrating Machine Learning with Knowledge Acquisition. Machine Learning, 1999, 35, 5-23.	5.4	22
89	Classifying under computational resource constraints: anytime classification using probabilistic estimators. Machine Learning, 2007, 69, 35-53.	5.4	22
90	Smoothing a rugged protein folding landscape by sequence-based redesign. Scientific Reports, 2016, 6, 33958.	3.3	22

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91	Critical evaluation of bioinformatics tools for the prediction of protein crystallization propensity. Briefings in Bioinformatics, 2018, 19, 838-852.	6.5	22
92	Cell graph neural networks enable the precise prediction of patient survival in gastric cancer. Npj Precision Oncology, 2022, 6, .	5.4	22
93	Identifying Approximate Itemsets of Interest in Large Databases. Applied Intelligence, 2003, 18, 91-104.	5.3	21
94	FastEE: Fast Ensembles of Elastic Distances for time series classification. Data Mining and Knowledge Discovery, 2020, 34, 231-272.	3.7	21
95	Integrating machine learning with knowledge acquisition through direct interaction with domain experts. Knowledge-Based Systems, 1996, 9, 253-266.	7.1	20
96	Efficient Discovery of the Most Interesting Associations. ACM Transactions on Knowledge Discovery From Data, 2014, 8, 1-31.	3.5	20
97	Efficient search of the best warping window for Dynamic Time Warping. , 2018, , 225-233.		20
98	Mining Negative Rules Using GRD. Lecture Notes in Computer Science, 2004, , 161-165.	1.3	19
99	Efficient parameter learning of Bayesian network classifiers. Machine Learning, 2017, 106, 1289-1329.	5.4	19
100	Sample-Based Attribute Selective A\$n\$ DE for Large Data. IEEE Transactions on Knowledge and Data Engineering, 2017, 29, 172-185.	5.7	19
101	Adaptive online extreme learning machine by regulating forgetting factor by concept drift map. Neurocomputing, 2019, 343, 141-153.	5.9	19
102	Stochastic Attribute Selection Committees. Lecture Notes in Computer Science, 1998, , 321-332.	1.3	18
103	Selective AnDE for large data learning: a low-bias memory constrained approach. Knowledge and Information Systems, 2017, 50, 475-503.	3.2	18
104	HEAL: an automated deep learning framework for cancer histopathology image analysis. Bioinformatics, 2021, 37, 4291-4295.	4.1	18
105	Efficient large-scale protein sequence comparison and gene matching to identify orthologs and co-orthologs. Nucleic Acids Research, 2012, 40, e44-e44.	14.5	17
106	Knowledge-transfer learning for prediction of matrix metalloprotease substrate-cleavage sites. Scientific Reports, 2017, 7, 5755.	3.3	17
107	MetalExplorer, a Bioinformatics Tool for the Improved Prediction of Eight Types of Metal-Binding Sites Using a Random Forest Algorithm with Two- Step Feature Selection. Current Bioinformatics, 2017, 12, .	1.5	17
108	Accurate parameter estimation for Bayesian network classifiers using hierarchical Dirichlet processes. Machine Learning, 2018, 107, 1303-1331.	5.4	16

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109	Ensembles of localised models for time series forecasting. Knowledge-Based Systems, 2021, 233, 107518.	7.1	16
110	Discretization Methods. , 2005, , 113-130.		15
111	Periscope: quantitative prediction of soluble protein expression in the periplasm of Escherichia coli. Scientific Reports, 2016, 6, 21844.	3.3	15
112	Designing a more efficient, effective and safe Medical Emergency Team (MET) service using data analysis. PLoS ONE, 2017, 12, e0188688.	2.5	15
113	Raman signatures of the modern pigment (Zn,Cd)S <sup>1</sup> and glass matrix of a red bead from Magoro Hill, an archaeological site in Limpopo Province, South Africa, recalibrate the settlement chronology. Journal of Molecular Structure, 2012, 1023, 123-127.	3.6	14
114	Learning crew scheduling constraints from historical schedules. Transportation Research Part C: Emerging Technologies, 2013, 26, 214-232.	7.6	14
115	Mining significant association rules from uncertain data. Data Mining and Knowledge Discovery, 2016, 30, 928-963.	3.7	14
116	Toward Electronic Surveillance of Invasive Mold Diseases in Hematology-Oncology Patients: An Expert System Combining Natural Language Processing of Chest Computed Tomography Reports, Microbiology, and Antifungal Drug Data. JCO Clinical Cancer Informatics, 2017, 1, 1-10.	2.1	14
117	Elastic bands across the path: A new framework and method to lower bound DTW. , 2019, , 522-530.		14
118	A Comparative Study of Bandwidth Choice in Kernel Density Estimation for Naive Bayesian Classification. Lecture Notes in Computer Science, 2009, , 302-313.	1.3	14
119	Naive-Bayes Inspired Effective Pre-Conditioner for Speeding-Up Logistic Regression. , 2014, , .		13
120	A Multiple Test Correction for Streams and Cascades of Statistical Hypothesis Tests. , 2016, , .		13
121	An Incremental Construction of Deep Neuro Fuzzy System for Continual Learning of Non-stationary Data Streams. IEEE Transactions on Fuzzy Systems, 2019, , 1-1.	9.8	13
122	Deep Learning for the Classification of Sentinel-2 Image Time Series. , 2019, , .		13
123	Scaling Log-Linear Analysis to High-Dimensional Data. , 2013, , .		12
124	A Bayesian-inspired, deep learning-based, semi-supervised domain adaptation technique for land cover mapping. Machine Learning, 0, , 1.	5.4	12
125	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	11
126	ASPIRER: a new computational approach for identifying non-classical secreted proteins based on deep learning. Briefings in Bioinformatics, 2022, 23, .	6.5	11



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127	A knowledge-based approach to computer-aided learning. International Journal of Man-Machine Studies, 1988, 29, 257-285.	0.7	10
128	Contrary to Popular Belief Incremental Discretization can be Sound, Computationally Efficient and Extremely Useful for Streaming Data. , 2014, , .		10
129	Accelerated higher-order logistic regression. Machine Learning, 2016, 104, 151-194.	5.4	10
130	Mining significant crisp-fuzzy spatial association rules. International Journal of Geographical Information Science, 2018, 32, 1247-1270.	4.8	10
131	SIMLIN: a bioinformatics tool for prediction of S-sulphenylation in the human proteome based on multi-stage ensemble-learning models. BMC Bioinformatics, 2019, 20, 602.	2.6	10
132	Cost-sensitive specialization. Lecture Notes in Computer Science, 1996, , 23-34.	1.3	10
133	Highly Scalable Attribute Selection for Averaged One-Dependence Estimators. Lecture Notes in Computer Science, 2014, , 86-97.	1.3	10
134	Inducing diagnostic rules for glomerular disease with the DLG machine learning algorithm. Artificial Intelligence in Medicine, 1992, 4, 419-430.	6.5	9
135	DeepBL: a deep learning-based approach for <i>in silico</i> discovery of beta-lactamases. Briefings in Bioinformatics, 2021, 22, .	6.5	9
136	On the Effectiveness of Discretizing Quantitative Attributes in Linear Classifiers. IEEE Access, 2020, 8, 198856-198871.	4.2	9
137	Tight lower bounds for dynamic time warping. Pattern Recognition, 2021, 115, 107895.	8.1	9
138	To Select or To Weigh: A Comparative Study of Model Selection and Model Weighing for SPODE Ensembles. Lecture Notes in Computer Science, 2006, , 533-544.	1.3	8
139	OCTID: a one-class learning-based Python package for tumor image detection. Bioinformatics, 2021, 37, 3986-3988.	4.1	8
140	A Case Study in Feature Invention for Breast Cancer Diagnosis Using X-Ray Scatter Images. Lecture Notes in Computer Science, 2003, , 677-685.	1.3	8
141	Discarding Insignificant Rules during Impact Rule Discovery in Large, Dense Databases. , 2005, , .		8
142	EGM: encapsulated gene-by-gene matching to identify gene orthologs and homologous segments in genomes. Bioinformatics, 2010, 26, 2076-2084.	4.1	7
143	A Statistically Efficient and Scalable Method for Log-Linear Analysis of High-Dimensional Data. , 2014, , .		7
144	PCA-based drift and shift quantification framework for multidimensional data. Knowledge and Information Systems, 2020, 62, 2835-2854.	3.2	7

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145	Early abandoning and pruning for elastic distances including dynamic time warping. Data Mining and Knowledge Discovery, 0, , 1.	3.7	7
146	Anytime classification for a pool of instances. Machine Learning, 2009, 77, 61-102.	5.4	6
147	Scaling log-linear analysis to datasets with thousands of variables. , 2015, , .		6
148	SimUSF: an efficient and effective similarity measure that is invariant to violations of the interval scale assumption. Data Mining and Knowledge Discovery, 2017, 31, 264-286.	3.7	6
149	Candidate Elimination Criteria for Lazy Bayesian Rules. Lecture Notes in Computer Science, 2001, , 545-556.	1.3	6
150	Finding the Right Family: Parent and Child Selection for Averaged One-Dependence Estimators. Lecture Notes in Computer Science, 2007, , 490-501.	1.3	6
151	A Comparison of First-Order and Zeroth-Order Induction for Input-Output Agent Modelling. , 1997, , 347-358.		6
152	Specious rules: an efficient and effective unifying method for removing misleading and uninformative patterns in association rule mining. , 2017, , 309-317.		5
153	Robust Bayesian Kernel Machine via Stein Variational Gradient Descent for Big Data. , 2018, , .		5
154	Using Sentinel-2 Image Time Series to map the State of Victoria, Australia. , 2019, , .		5
155	Evaluation of Feature Based Modelling in subtraction. Lecture Notes in Computer Science, 1992, , 269-276.	1.3	5
156	Fast and Effective Single Pass Bayesian Learning. Lecture Notes in Computer Science, 2013, , 149-160.	1.3	5
157	AI for monitoring the Sustainable Development Goals and supporting and promoting action and policy development. , 2020, , .		5
158	Unsupervised Domain Adaptation Techniques for Classification of Satellite Image Time Series. , 2020, , .		5
159	Statistically sound pattern discovery. , 2014, , .		4
160	Generality Is Predictive of Prediction Accuracy. Lecture Notes in Computer Science, 2006, , 1-13.	1.3	4
161	Preconditioning an Artificial Neural Network Using Naive Bayes. Lecture Notes in Computer Science, 2016, , 341-353.	1.3	4
162	Solving Regression Problems Using Competitive Ensemble Models. Lecture Notes in Computer Science, 2002, , 511-522.	1.3	4

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163	An eager splitting strategy for online decision trees in ensembles. Data Mining and Knowledge Discovery, 2022, 36, 566-619.	3.7	4
164	Processes Occurring during Deactivation/Regeneration of a Vanadia/Alumina Catalyst under Propane Dehydrogenation Conditions. Studies in Surface Science and Catalysis, 2001, 139, 271-278.	1.5	3
165	Selective Augmented Bayesian Network Classifiers Based on Rough Set Theory. Lecture Notes in Computer Science, 2004, , 319-328.	1.3	3
166	Discovery of Amino Acid Motifs for Thrombin Cleavage and Validation Using a Model Substrate. Biochemistry, 2011, 50, 10499-10507.	2.5	3
167	The history of IRPA up to the millennium. Journal of Radiological Protection, 2011, 31, 177-204.	1.1	3
168	A Fast Trust-Region Newton Method for Softmax Logistic Regression. , 2017, , 705-713.		3
169	Structural Capacitance in Protein Evolution and Human Diseases. Journal of Molecular Biology, 2018, 430, 3200-3217.	4.2	3
170	Exploring Data Quantity Requirements for Domain Adaptation in the Classification of Satellite Image Time Series. , 2019, , .		3
171	An accurate and fully-automated ensemble model for weekly time series forecasting. International Journal of Forecasting, 2023, 39, 641-658.	6.5	3
172	Smooth Perturbations for Time Series Adversarial Attacks. Lecture Notes in Computer Science, 2022, , 485-496.	1.3	3
173	Efficient and Effective Accelerated Hierarchical Higher-Order Logistic Regression for Large Data Quantities. , 2018, , 459-467.		2
174	Non-Disjoint Discretization for Aggregating One-Dependence Estimator Classifiers. Lecture Notes in Computer Science, 2012, , 151-162.	1.3	2
175	Further Pruning for Efficient Association Rule Discovery. Lecture Notes in Computer Science, 2001, , 605-618.	1.3	2
176	Evaluation of Data Aging: A Technique for Discounting Old Data during Student Modeling. Lecture Notes in Computer Science, 1998, , 384-393.	1.3	2
177	No Cloud on the Horizon: Probabilistic Gap Filling in Satellite Image Series. , 2020, , .		2
178	Ultra fast warping window optimization for Dynamic Time Warping. , 2021, , .		2
179	Application of machine learning to a renal biopsy database. Nephrology Dialysis Transplantation, 1992, , .	0.7	1
180	Does social good justify risking personal privacy?. , 2014, , .		1

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181	A Data Scientist's Guide to Start-Ups. <i>Big Data</i> , 2014, 2, 117-128.	3.4	1
182	Scalable Learning of Graphical Models. , 2016, , .		1
183	Generative and Discriminative Learning. , 2016, , 1-2.		1
184	Learning Lazy Rules to Improve the Performance of Classifiers. , 2000, , 122-131.		1
185	A New Restricted Bayesian Network Classifier. <i>Lecture Notes in Computer Science</i> , 2003, , 265-270.	1.3	1
186	K-Optimal Pattern Discovery: An Efficient and Effective Approach to Exploratory Data Mining. <i>Lecture Notes in Computer Science</i> , 2005, , 1-2.	1.3	1
187	Techniques for Efficient Learning without Search. <i>Lecture Notes in Computer Science</i> , 2012, , 50-61.	1.3	1
188	Techniques for efficient empirical induction. <i>Lecture Notes in Computer Science</i> , 1990, , 225-239.	1.3	1
189	Averaged One-Dependence Estimators. , 2017, , 85-87.		1
190	Robust Variational Learning for Multiclass Kernel Models With Stein Refinement. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2022, 34, 4425-4438.	5.7	1
191	Improving the efficiency of rule-based expert systems by rule activation. <i>Journal of Experimental and Theoretical Artificial Intelligence</i> , 1990, 2, 369-380.	2.8	0
192	ICRP comes up trumps. <i>Journal of Radiological Protection</i> , 2006, 26, 251-252.	1.1	0
193	Adsorption of Chiral 2,2â€-Substituted-1,1â€™-Binaphthalenes onto Silica-Supported Palladium and Nickel. <i>Adsorption Science and Technology</i> , 2006, 24, 257-268.	3.2	0
194	Nairn conference supplement. <i>Journal of Radiological Protection</i> , 2007, 27, A1-A2.	1.1	0
195	Introduction: special issue of selected papers of ACML 2013. <i>Machine Learning</i> , 2015, 99, 165-167.	5.4	0
196	Tamping Effectiveness Prediction Using Supervised Machine Learning Techniques. , 2018, , .		0
197	Efficiently Identifying Exploratory Rulesâ€™ Significance. <i>Lecture Notes in Computer Science</i> , 2006, , 64-77.	1.3	0
198	FaSS: Ensembles for Stable Learners. <i>Lecture Notes in Computer Science</i> , 2009, , 364-374.	1.3	0

#	ARTICLE	IF	CITATIONS
199	Association discovery. , 2010, , .		0
200	Using decision trees for agent modelling: A study on resolving conflicting predictions. Lecture Notes in Computer Science, 1997, , 349-358.	1.3	0
201	Evaluation of Learning Algorithms. , 2016, , 1-2.		0
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