Geoffrey I Webb

List of Publications by Year
in descending order

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	An accurate and fully-automated ensemble model for weekly time series forecasting. International Journal of Forecasting, 2023, 39, 641-658.	6.5	3
2	Positive-unlabeled learning in bioinformatics and computational biology: a brief review. Briefings in Bioinformatics, 2022, 23, .	6.5	26
3	Robust Variational Learning for Multiclass Kernel Models With Stein Refinement. IEEE Transactions on Knowledge and Data Engineering, 2022, 34, 4425-4438.	5.7	1
4	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	11
5	An eager splitting strategy for online decision trees in ensembles. Data Mining and Knowledge Discovery, 2022, 36, 566-619.	3.7	4
6	ASPIRER: a new computational approach for identifying non-classical secreted proteins based on deep learning. Briefings in Bioinformatics, 2022, 23, .	6.5	11
7	Smooth Perturbations for Time Series Adversarial Attacks. Lecture Notes in Computer Science, 2022, , 485-496.	1.3	3
8	Cell graph neural networks enable the precise prediction of patient survival in gastric cancer. Npj Precision Oncology, 2022, 6, .	5.4	22
9	MultiRocket: multiple pooling operators and transformations for fast and effective time series classification. Data Mining and Knowledge Discovery, 2022, 36, 1623-1646.	3.7	45
10	DeepBL: a deep learning-based approach for *in silico* discovery of beta-lactamases. Briefings in Bioinformatics, 2021, 22, .	6.5	9
11	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
12	Anthem: a user customised tool for fast and accurate prediction of binding between peptides and HLA class I molecules. Briefings in Bioinformatics, 2021, 22, .	6.5	37
13	*iLearnPlus:* a comprehensive and automated machine-learning platform for nucleic acid and protein sequence analysis, prediction and visualization. Nucleic Acids Research, 2021, 49, e60-e60.	14.5	124
14	Time series extrinsic regression. Data Mining and Knowledge Discovery, 2021, 35, 1032-1060.	3.7	32
15	HEAL: an automated deep learning framework for cancer histopathology image analysis. Bioinformatics, 2021, 37, 4291-4295.	4.1	18
16	OCTID: a one-class learning-based Python package for tumor image detection. Bioinformatics, 2021, 37, 3986-3988.	4.1	8
17	Tight lower bounds for dynamic time warping. Pattern Recognition, 2021, 115, 107895.	8.1	9
18	MiniRocket. , 2021, , .		130

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19	Ensembles of localised models for time series forecasting. Knowledge-Based Systems, 2021, 233, 107518.	7.1	16
20	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
21	Ultra fast warping window optimization for Dynamic Time Warping. , 2021, , .		2
22	iLearn: an integrated platform and meta-learner for feature engineering, machine-learning analysis and modeling of DNA, RNA and protein sequence data. Briefings in Bioinformatics, 2020, 21, 1047-1057.	6.5	294
23	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. Bioinformatics, 2020, 36, 1057-1065.	4.1	102
24	Comprehensive review and assessment of computational methods for predicting RNA post-transcriptional modification sites from RNA sequences. Briefings in Bioinformatics, 2020, 21, 1676-1696.	6.5	98
25	FastEE: Fast Ensembles of Elastic Distances for time series classification. Data Mining and Knowledge Discovery, 2020, 34, 231-272.	3.7	21
26	A novel selective naÃ¯ve Bayes algorithm. Knowledge-Based Systems, 2020, 192, 105361.	7.1	185
27	ROCKET: exceptionally fast and accurate time series classification using random convolutional kernels. Data Mining and Knowledge Discovery, 2020, 34, 1454-1495.	3.7	359
28	InceptionTime: Finding AlexNet for time series classification. Data Mining and Knowledge Discovery, 2020, 34, 1936-1962.	3.7	542
29	On the Effectiveness of Discretizing Quantitative Attributes in Linear Classifiers. IEEE Access, 2020, 8, 198856-198871.	4.2	9
30	Procleave: Predicting Protease-specific Substrate Cleavage Sites by Combining Sequence and Structural Information. Genomics, Proteomics and Bioinformatics, 2020, 18, 52-64.	6.9	71
31	PROSPECT: A web server for predicting protein histidine phosphorylation sites. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050018.	0.8	25
32	TS-CHIEF: a scalable and accurate forest algorithm for time series classification. Data Mining and Knowledge Discovery, 2020, 34, 742-775.	3.7	112
33	PCA-based drift and shift quantification framework for multidimensional data. Knowledge and Information Systems, 2020, 62, 2835-2854.	3.2	7
34	PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact. Briefings in Bioinformatics, 2020, 21, 1069-1079.	6.5	38
35	AI for monitoring the Sustainable Development Goals and supporting and promoting action and policy development. , 2020, , .		5
36	Unsupervised Domain Adaptation Techniques for Classification of Satellite Image Time Series. , 2020, , .		5

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37	No Cloud on the Horizon: Probabilistic Gap Filling in Satellite Image Series. , 2020, , .		2
38	Computational analysis and prediction of lysine malonylation sites by exploiting informative features in an integrative machine-learning framework. Briefings in Bioinformatics, 2019, 20, 2185-2199.	6.5	82
39	Using Sentinel-2 Image Time Series to map the State of Victoria, Australia. , 2019, , .		5
40	Exploring Data Quantity Requirements for Domain Adaptation in the Classification of Satellite Image Time Series. , 2019, , .		3
41	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
42	Positive-unlabelled learning of glycosylation sites in the human proteome. BMC Bioinformatics, 2019, 20, 112.	2.6	60
43	Temporal Convolutional Neural Network for the Classification of Satellite Image Time Series. Remote Sensing, 2019, 11, 523.	4.0	306
44	Proximity Forest: an effective and scalable distance-based classifier for time series. Data Mining and Knowledge Discovery, 2019, 33, 607-635.	3.7	100
45	Elastic bands across the path: A new framework and method to lower bound DTW. , 2019, , 522-530.		14
46	SIMLIN: a bioinformatics tool for prediction of S-sulphenylation in theÂhuman proteome based on multi-stage ensemble-learning models. BMC Bioinformatics, 2019, 20, 602.	2.6	10
47	Deep Learning for the Classification of Sentinel-2 Image Time Series. , 2019, , .		13
48	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
49	Survey of distance measures for quantifying concept drift and shift in numeric data. Knowledge and Information Systems, 2019, 60, 591-615.	3.2	40
50	A tutorial on statistically sound pattern discovery. Data Mining and Knowledge Discovery, 2019, 33, 325-377.	3.7	37
51	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. Briefings in Bioinformatics, 2019, 20, 2267-2290.	6.5	99
52	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. Briefings in Bioinformatics, 2019, 20, 638-658.	6.5	166
53	Systematic analysis and prediction of type IV secreted effector proteins by machine learning approaches. Briefings in Bioinformatics, 2019, 20, 931-951.	6.5	65
54	Adaptive online extreme learning machine by regulating forgetting factor by concept drift map. Neurocomputing, 2019, 343, 141-153.	5.9	19

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55	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
56	*iFeature*: a Python package and web server for features extraction and selection from protein and peptide sequences. Bioinformatics, 2018, 34, 2499-2502.	4.1	481
57	PREvaIL, an integrative approach for inferring catalytic residues using sequence, structural, and network features in a machine-learning framework. Journal of Theoretical Biology, 2018, 443, 125-137.	1.7	124
58	Mining significant crisp-fuzzy spatial association rules. International Journal of Geographical Information Science, 2018, 32, 1247-1270.	4.8	10
59	Analyzing concept drift and shift from sample data. Data Mining and Knowledge Discovery, 2018, 32, 1179-1199.	3.7	65
60	Critical evaluation of bioinformatics tools for the prediction of protein crystallization propensity. Briefings in Bioinformatics, 2018, 19, 838-852.	6.5	22
61	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. Bioinformatics, 2018, 34, 684-687.	4.1	131
62	Efficient search of the best warping window for Dynamic Time Warping. , 2018, , 225-233.		20
63	Efficient and Effective Accelerated Hierarchical Higher-Order Logistic Regression for Large Data Quantities. , 2018, , 459-467.		2
64	Extremely Fast Decision Tree. , 2018, , .		79
65	Structural Capacitance in Protein Evolution and Human Diseases. Journal of Molecular Biology, 2018, 430, 3200-3217.	4.2	3
66	Tamping Effectiveness Prediction Using Supervised Machine Learning Techniques. , 2018, , .		0
67	Robust Bayesian Kernel Machine via Stein Variational Gradient Descent for Big Data. , 2018, , .		5
68	Accurate parameter estimation for Bayesian network classifiers using hierarchical Dirichlet processes. Machine Learning, 2018, 107, 1303-1331.	5.4	16
69	Selective AnDE for large data learning: a low-bias memory constrained approach. Knowledge and Information Systems, 2017, 50, 475-503.	3.2	18
70	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
71	SecretEPDB: a comprehensive web-based resource for secreted effector proteins of the bacterial types III, IV and VI secretion systems. Scientific Reports, 2017, 7, 41031.	3.3	38
72	Efficient parameter learning of Bayesian network classifiers. Machine Learning, 2017, 106, 1289-1329.	5.4	19

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73	POSSUM: a bioinformatics toolkit for generating numerical sequence feature descriptors based on PSSM profiles. Bioinformatics, 2017, 33, 2756-2758.	4.1	145
74	Indexing and classifying gigabytes of time series under time warping. , 2017, , 282-290.		33
75	Knowledge-transfer learning for prediction of matrix metalloprotease substrate-cleavage sites. Scientific Reports, 2017, 7, 5755.	3.3	17
76	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
77	Sample-Based Attribute Selective An DE for Large Data. IEEE Transactions on Knowledge and Data Engineering, 2017, 29, 172-185.	5.7	19
78	Specious rules: an efficient and effective unifying method for removing misleading and uninformative patterns in association rule mining. , 2017, , 309-317.		5
79	Generating Synthetic Time Series to Augment Sparse Datasets. , 2017, , .		84
80	A Fast Trust-Region Newton Method for Softmax Logistic Regression. , 2017, , 705-713.		3
81	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
82	Designing a more efficient, effective and safe Medical Emergency Team (MET) service using data analysis. PLoS ONE, 2017, 12, e0188688.	2.5	15
83	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
84	Evaluation of Learning Algorithms. , 2017, , 415-416.		0
85	Semi-naive Bayesian Learning. , 2017, , 1137-1142.		0
86	MultiBoosting. , 2017, , 863-864.		0
87	Generative and Discriminative Learning. , 2017, , 565-566.		0
88	Averaged One-Dependence Estimators. , 2017, , 85-87.		1
89	Algorithm Evaluation. , 2017, , 40-41.		0
90	A Multiple Test Correction for Streams and Cascades of Statistical Hypothesis Tests. , 2016, , .		13

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91	Crysalis: an integrated server for computational analysis and design of protein crystallization. Scientific Reports, 2016, 6, 21383.	3.3	35
92	Periscope: quantitative prediction of soluble protein expression in the periplasm of Escherichia coli. Scientific Reports, 2016, 6, 21844.	3.3	15
93	Skopus: Mining top-k sequential patterns under leverage. Data Mining and Knowledge Discovery, 2016, 30, 1086-1111.	3.7	30
94	ALR^n ALR n : accelerated higher-order logistic regression. Machine Learning, 2016, 104, 151-194.	5.4	10
95	Scalable Learning of Graphical Models. , 2016, , .		1
96	Smoothing a rugged protein folding landscape by sequence-based redesign. Scientific Reports, 2016, 6, 33958.	3.3	22
97	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
98	Characterizing concept drift. Data Mining and Knowledge Discovery, 2016, 30, 964-994.	3.7	285
99	Mining significant association rules from uncertain data. Data Mining and Knowledge Discovery, 2016, 30, 928-963.	3.7	14
100	Faster and more accurate classification of time series by exploiting a novel dynamic time warping averaging algorithm. Knowledge and Information Systems, 2016, 47, 1-26.	3.2	92
101	Generative and Discriminative Learning. , 2016, , 1-2.		1
102	Preconditioning an Artificial Neural Network Using Naïve Bayes. Lecture Notes in Computer Science, 2016, , 341-353.	1.3	4
103	Evaluation of Learning Algorithms. , 2016, , 1-2.		0
104	Scaling log-linear analysis to datasets with thousands of variables. , 2015, , .		6
105	GlycoMine: a machine learning-based approach for predicting N-, C- and O-linked glycosylation in the human proteome. Bioinformatics, 2015, 31, 1411-1419.	4.1	167
106	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
107	Introduction: special issue of selected papers of ACML 2013. Machine Learning, 2015, 99, 165-167.	5.4	0
108	Efficient Discovery of the Most Interesting Associations. ACM Transactions on Knowledge Discovery From Data, 2014, 8, 1-31.	3.5	20

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109	Contrary to Popular Belief Incremental Discretization can be Sound, Computationally Efficient and Extremely Useful for Streaming Data. , 2014, , .		10
110	A Statistically Efficient and Scalable Method for Log-Linear Analysis of High-Dimensional Data. , 2014, , .		7
111	Dynamic Time Warping Averaging of Time Series Allows Faster and More Accurate Classification. , 2014, , .		137
112	Does social good justify risking personal privacy?. , 2014, , .		1
113	Naive-Bayes Inspired Effective Pre-Conditioner for Speeding-Up Logistic Regression. , 2014, , .		13
114	Statistically sound pattern discovery. , 2014, , .		4
115	A Data Scientist's Guide to Start-Ups. Big Data, 2014, 2, 117-128.	3.4	1
116	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
117	Highly Scalable Attribute Selection for Averaged One-Dependence Estimators. Lecture Notes in Computer Science, 2014, , 86-97.	1.3	10
118	Scaling Log-Linear Analysis to High-Dimensional Data. , 2013, , .		12
119	Learning crew scheduling constraints from historical schedules. Transportation Research Part C: Emerging Technologies, 2013, 26, 214-232.	7.6	14
120	Fast and Effective Single Pass Bayesian Learning. Lecture Notes in Computer Science, 2013, , 149-160.	1.3	5
121	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
122	Raman signatures of the modern pigment (Zn,Cd)S1−xSex 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
123	TANGLE: Two-Level Support Vector Regression Approach for Protein Backbone Torsion Angle Prediction from Primary Sequences. PLoS ONE, 2012, 7, e30361.	2.5	36
124	Subsumption resolution: an efficient and effective technique for semi-naive Bayesian learning. Machine Learning, 2012, 87, 93-125.	5.4	56
125	Learning by extrapolation from marginal to full-multivariate probability distributions: decreasingly naive Bayesian classification. Machine Learning, 2012, 86, 233-272.	5.4	72
126	Non-Disjoint Discretization for Aggregating One-Dependence Estimator Classifiers. Lecture Notes in Computer Science, 2012, , 151-162.	1.3	2

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127	PROSPER: An Integrated Feature-Based Tool for Predicting Protease Substrate Cleavage Sites. PLoS ONE, 2012, 7, e50300.	2.5	265
128	Techniques for Efficient Learning without Search. Lecture Notes in Computer Science, 2012, , 50-61.	1.3	1
129	Discovery of Amino Acid Motifs for Thrombin Cleavage and Validation Using a Model Substrate. Biochemistry, 2011, 50, 10499-10507.	2.5	3
130	NaÃ¯ve Bayes. , 2011, , 713-714.		92
131	Filteredâ€top â€‹<i>k</i> association discovery. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2011, 1, 183-192.	6.8	34
132	Feature-subspace aggregating: ensembles for stable andÂunstable learners. Machine Learning, 2011, 82, 375-397.	5.4	41
133	The history of IRPAâ€"up to the millennium. Journal of Radiological Protection, 2011, 31, 177-204.	1.1	3
134	BIOINFORMATIC APPROACHES FOR PREDICTING SUBSTRATES OF PROTEASES. Journal of Bioinformatics and Computational Biology, 2011, 09, 149-178.	0.8	31
135	EGM: encapsulated gene-by-gene matching to identify gene orthologs and homologous segments in genomes. Bioinformatics, 2010, 26, 2076-2084.	4.1	7
136	Cascleave: towards more accurate prediction of caspase substrate cleavage sites. Bioinformatics, 2010, 26, 752-760.	4.1	148
137	Self-sufficient itemsets. ACM Transactions on Knowledge Discovery From Data, 2010, 4, 1-20.	3.5	54
138	Association discovery. , 2010, , .		0
139	Discretization for naive-Bayes learning: managingÂdiscretization bias and variance. Machine Learning, 2009, 74, 39-74.	5.4	187
140	Anytime classification for a pool of instances. Machine Learning, 2009, 77, 61-102.	5.4	6
141	Discretization Methods. , 2009, , 101-116.		32
142	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
143	Prodepth: Predict Residue Depth by Support Vector Regression Approach from Protein Sequences Only. PLoS ONE, 2009, 4, e7072.	2.5	40
144	FaSS: Ensembles for Stable Learners. Lecture Notes in Computer Science, 2009, , 364-374.	1.3	0

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145	Layered critical values: a powerful direct-adjustment approach to discovering significant patterns. Machine Learning, 2008, 71, 307-323.	5.4	45
146	RCPdb: An evolutionary classification and codon usage database for repeat-containing proteins. Genome Research, 2007, 17, 1118-1127.	5.5	36
147	To Select or To Weigh: A Comparative Study of Linear Combination Schemes for SuperParent-One-Dependence Estimators. IEEE Transactions on Knowledge and Data Engineering, 2007, 19, 1652-1665.	5.7	38
148	Nairn conference supplement. Journal of Radiological Protection, 2007, 27, A1-A2.	1.1	0
149	Discovering Significant Patterns. Machine Learning, 2007, 68, 1-33.	5.4	195
150	Classifying under computational resource constraints: anytime classification using probabilistic estimators. Machine Learning, 2007, 69, 35-53.	5.4	22
151	Finding the Right Family: Parent and Child Selection for Averaged One-Dependence Estimators. Lecture Notes in Computer Science, 2007, , 490-501.	1.3	6
152	Finding the Real Patterns. , 2007, , 6-6.		0
153	ICRP comes up trumps. Journal of Radiological Protection, 2006, 26, 251-252.	1.1	0
154	Adsorption of Chiral 2,2â€˜-Substituted-1,1â€™-Binaphthalenes onto Silica-Supported Palladium and Nickel. Adsorption Science and Technology, 2006, 24, 257-268.	3.2	0
155	Efficient lazy elimination for averaged one-dependence estimators. , 2006, , .		39
156	Discovering significant rules. , 2006, , .		69
157	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
158	Generality Is Predictive of Prediction Accuracy. Lecture Notes in Computer Science, 2006, , 1-13.	1.3	4
159	Efficiently Identifying Exploratory Rulesâ€™ Significance. Lecture Notes in Computer Science, 2006, , 64-77.	1.3	0
160	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
161	K-Optimal Rule Discovery. Data Mining and Knowledge Discovery, 2005, 10, 39-79.	3.7	100
162	On the Application of ROC Analysis to Predict Classification Performance Under Varying Class Distributions. Machine Learning, 2005, 58, 25-32.	5.4	75

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163	Not So Naive Bayes: Aggregating One-Dependence Estimators. Machine Learning, 2005, 58, 5-24.	5.4	570
164	Discretization Methods. , 2005, , 113-130.		15
165	Ensemble Selection for SuperParent-One-Dependence Estimators. Lecture Notes in Computer Science, 2005, , 102-112.	1.3	32
166	Discarding Insignificant Rules during Impact Rule Discovery in Large, Dense Databases. , 2005, , .		8
167	K-Optimal Pattern Discovery: An Efficient and Effective Approach to Exploratory Data Mining. Lecture Notes in Computer Science, 2005, , 1-2.	1.3	1
168	Multistrategy ensemble learning: reducing error by combining ensemble learning techniques. IEEE Transactions on Knowledge and Data Engineering, 2004, 16, 980-991.	5.7	206
169	Mining Negative Rules Using GRD. Lecture Notes in Computer Science, 2004, , 161-165.	1.3	19
170	Selective Augmented Bayesian Network Classifiers Based on Rough Set Theory. Lecture Notes in Computer Science, 2004, , 319-328.	1.3	3
171	Identifying Approximate Itemsets of Interest in Large Databases. Applied Intelligence, 2003, 18, 91-104.	5.3	21
172	On detecting differences between groups. , 2003, , .		80
173	On Why Discretization Works for Naive-Bayes Classifiers. Lecture Notes in Computer Science, 2003, , 440-452.	1.3	49
174	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
175	A New Restricted Bayesian Network Classifier. Lecture Notes in Computer Science, 2003, , 265-270.	1.3	1
176	The Need for Low Bias Algorithms in Classification Learning from Large Data Sets. Lecture Notes in Computer Science, 2002, , 62-73.	1.3	39
177	Solving Regression Problems Using Competitive Ensemble Models. Lecture Notes in Computer Science, 2002, , 511-522.	1.3	4
178	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
179	Machine Learning for User Modeling. User Modeling and User-Adapted Interaction, 2001, 11, 19-29.	3.8	278
180	Discovering associations with numeric variables. , 2001, , .		65

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181	Proportional k-Interval Discretization for Naive-Bayes Classifiers. Lecture Notes in Computer Science, 2001, , 564-575.	1.3	66
182	Candidate Elimination Criteria for Lazy Bayesian Rules. Lecture Notes in Computer Science, 2001, , 545-556.	1.3	6
183	Further Pruning for Efficient Association Rule Discovery. Lecture Notes in Computer Science, 2001, , 605-618.	1.3	2
184	Lazy Learning of Bayesian Rules. Machine Learning, 2000, 41, 53-84.	5.4	185
185	MultiBoosting: A Technique for Combining Boosting and Wagging. Machine Learning, 2000, 40, 159-196.	5.4	556
186	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
187	Efficient search for association rules. , 2000, , .		113
188	Learning Lazy Rules to Improve the Performance of Classifiers. , 2000, , 122-131.		1
189	An Experimental Evaluation of Integrating Machine Learning with Knowledge Acquisition. Machine Learning, 1999, 35, 5-23.	5.4	22
190	Using Decision Trees for Agent Modeling: Improving Prediction Performance. User Modeling and User-Adapted Interaction, 1998, 8, 131-152.	3.8	28
191	Stochastic Attribute Selection Committees. Lecture Notes in Computer Science, 1998, , 321-332.	1.3	18
192	Evaluation of Data Aging: A Technique for Discounting Old Data during Student Modeling. Lecture Notes in Computer Science, 1998, , 384-393.	1.3	2
193	A Comparison of First-Order and Zeroth-Order Induction for Input-Output Agent Modelling. , 1997, , 347-358.		6
194	Using decision trees for agent modelling: A study on resolving conflicting predictions. Lecture Notes in Computer Science, 1997, , 349-358.	1.3	0
195	Integrating machine learning with knowledge acquisition through direct interaction with domain experts. Knowledge-Based Systems, 1996, 9, 253-266.	7.1	20
196	Feature Based Modelling: A methodology for producing coherent, consistent, dynamically changing models of agents' competencies. User Modeling and User-Adapted Interaction, 1996, 5, 117-150.	3.8	38
197	Cost-sensitive specialization. Lecture Notes in Computer Science, 1996, , 23-34.	1.3	10
198	Application of machine learning to a renal biopsy database. Nephrology Dialysis Transplantation, 1992, , .	0.7	1

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199	Asymmetric hydrogenation of methyl acetoacetate using Ni/SiO2 modified with tartaric acid and alanine. Journal of Molecular Catalysis, 1992, 73, 91-95.	1.2	24
200	Inducing diagnostic rules for glomerular disease with the DLG machine learning algorithm. Artificial Intelligence in Medicine, 1992, 4, 419-430.	6.5	9
201	Evaluation of Feature Based Modelling in subtraction. Lecture Notes in Computer Science, 1992, , 269-276.	1.3	5
202	The enantioselective hydrogenation of methylacetoacetate over nickel catalysts modified with tartaric acid.. Catalysis Today, 1991, 10, 363-370.	4.4	26
203	Improving the efficiency of rule-based expert systems by rule activation. Journal of Experimental and Theoretical Artificial Intelligence, 1990, 2, 369-380.	2.8	0
204	Techniques for efficient empirical induction. Lecture Notes in Computer Science, 1990, , 225-239.	1.3	1
205	A knowledge-based approach to computer-aided learning. International Journal of Man-Machine Studies, 1988, 29, 257-285.	0.7	10
206	A Bayesian-inspired, deep learning-based, semi-supervised domain adaptation technique for land cover mapping. Machine Learning, 0, , 1.	5.4	12
207	Early abandoning and pruning for elastic distances including dynamic time warping. Data Mining and Knowledge Discovery, 0, , 1.	3.7	7