Jason H Moore

List of Publications by Year
in descending order

626	33,850	5558	5519
papers	citations	82 h-index	163 g-index

668	668	668	37942
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic Analysis of Coronary Artery Disease Using Tree-Based Automated Machine Learning Informed By Biology-Based Feature Selection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1379-1386.	1.9	9
2	PMLB v1.0: an open-source dataset collection for benchmarking machine learning methods. Bioinformatics, 2022, 38, 878-880.	1.8	15
3	The promise of automated machine learning for the genetic analysis of complex traits. Human Genetics, 2022, 141, 1529-1544.	1.8	9
4	Multi-task learning based structured sparse canonical correlation analysis for brain imaging genetics. Medical Image Analysis, 2022, 76, 102297.	7.0	13
5	AddGBoost: A gradient boosting-style algorithm based on strong learners. Machine Learning With Applications, 2022, 7, 100243.	3.0	7
6	Antihypertensive effects of yoga in a general patient population: real-world evidence from electronic health records, a retrospective case-control study. BMC Public Health, 2022, 22, 186.	1.2	1
7	Gene-Interaction-Sensitive enrichment analysis in congenital heart disease. BioData Mining, 2022, 15, 4.	2.2	2
8	Single-cell multi-omics analysis of human pancreatic islets reveals novel cellular states in type 1 diabetes. Nature Metabolism, 2022, 4, 284-299.	5.1	52
9	Multisite learning of high-dimensional heterogeneous data with applications to opioid use disorder study of 15,000 patients across 5 clinical sites. Scientific Reports, 2022, 12, .	1.6	0
10	Automating Predictive Toxicology Using ComptoxAI. Chemical Research in Toxicology, 2022, 35, 1370-1382.	1.7	5
11	Novel digital approaches to the assessment of problematic opioid use. BioData Mining, 2022, 15, .	2.2	0
12	Case contamination in electronic health records based caseâ€control studies. Biometrics, 2021, 77, 67-77.	0.8	5
13	Anticancer Therapy at the End of Life: Lessons From a Community Cancer Institute. Journal of Palliative Care, 2021, 36, 87-92.	0.4	2
14	treeheatr: an R package for interpretable decision tree visualizations. Bioinformatics, 2021, 37, 282-284.	1.8	13
15	Evaluating recommender systems for AI-driven biomedical informatics. Bioinformatics, 2021, 37, 250-256.	1.8	13
16	Lossless integration of multiple electronic health records for identifying pleiotropy using summary statistics. Nature Communications, 2021, 12, 168.	5.8	2
17	Metabolomics Insights in Early Childhood Caries. Journal of Dental Research, 2021, 100, 615-622.	2.5	23
18	Empowering the data science scientist. BioData Mining, 2021, 14, 8.	2.2	1

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19	The Cosmos Collaborative: A Vendor-Facilitated Electronic Health Record Data Aggregation Platform. ACI Open, 2021, 05, e36-e46.	0.2	16
20	The Role of Genetic Ancestry as a Risk Factor for Primary Open-angle Glaucoma in African Americans. , 2021, 62, 28.		18
21	Conservation machine learning: a case study of random forests. Scientific Reports, 2021, 11, 3629.	1.6	19
22	Ten important roles for academic leaders to promote equity, diversity, and inclusion in data science. BioData Mining, 2021, 14, 22.	2.2	3
23	TPOT-NN: augmenting tree-based automated machine learning with neural network estimators. Genetic Programming and Evolvable Machines, 2021, 22, 207-227.	1.5	13
24	REGENS: an open source Python package for simulating realistic autosomal genotypes. Journal of Open Source Software, 2021, 6, 2743.	2.0	0
25	What Every Reader Should Know About Studies Using Electronic Health Record Data but May Be Afraid to Ask. Journal of Medical Internet Research, 2021, 23, e22219.	2.1	61
26	Symbolic-regression boosting. Genetic Programming and Evolvable Machines, 2021, 22, 357-381.	1.5	4
27	The phenomics and genetics of addictive and affective comorbidity in opioid use disorder. Drug and Alcohol Dependence, 2021, 221, 108602.	1.6	11
28	Leveraging Automated Machine Learning for the Analysis of Global Public Health Data: A Case Study in Malaria. International Journal of Public Health, 2021, 66, 614296.	1.0	2
29	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	2.6	18
30	The Translational Machine: A novel machineâ€learning approach to illuminate complex genetic architectures. Genetic Epidemiology, 2021, 45, 485-536.	0.6	0
31	Validation of an internationally derived patient severity phenotype to support COVID-19 analytics from electronic health record data. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1411-1420.	2.2	37
32	Why Is the Electronic Health Record So Challenging for Research and Clinical Care?. Methods of Information in Medicine, 2021, 60, 032-048.	0.7	13
33	Novel EDGE encoding method enhances ability to identify genetic interactions. PLoS Genetics, 2021, 17, e1009534.	1.5	5
34	International Analysis of Electronic Health Records of Children and Youth Hospitalized With COVID-19 Infection in 6 Countries. JAMA Network Open, 2021, 4, e2112596.	2.8	33
35	Towards effective GP multi-class classification based on dynamic targets. , 2021, , .		3
36	EBIC.JL. , 2021, , .		2

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37	Rapid prototyping of evolution-driven biclustering methods in Julia. , 2021, , .		0
38	Harnessing electronic health records to study emerging environmental disasters: a proof of concept with perfluoroalkyl substances (PFAS). Npj Digital Medicine, 2021, 4, 122.	5.7	4
39	Socio-cognitive Evolution Strategies. Lecture Notes in Computer Science, 2021, , 329-342.	1.0	1
40	A comparison of methods for interpreting random forest models of genetic association in the presence of non-additive interactions. BioData Mining, 2021, 14, 9.	2.2	18
41	Use of electronic health records to support a public health response to the COVID-19 pandemic in the United States: a perspective from 15 academic medical centers. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 393-401.	2.2	54
42	Plasma biomarkers associated with adverse outcomes in patients with calcific aortic stenosis. European Journal of Heart Failure, 2021, 23, 2021-2032.	2.9	18
43	A semantic genetic programming framework based on dynamic targets. Genetic Programming and Evolvable Machines, 2021, 22, 463-493.	1.5	1
44	Human Intrigue: Meta-analysis approaches for big questions with big data while shaking up the peer review process. , 2021, , .		0
45	TargetTox: A Feature Selection Pipeline for Identifying Predictive Targets Associated with Drug Toxicity. Journal of Chemical Information and Modeling, 2021, 61, 5386-5394.	2.5	7
46	Shared Genetic Architecture and Causal Relationship Between Asthma and Cardiovascular Diseases: A Large-Scale Cross-Trait Analysis. Frontiers in Genetics, 2021, 12, 775591.	1.1	9
47	Estimating prevalence of human traits among populations from polygenic risk scores. Human Genomics, 2021, 15, 70.	1.4	5
48	Gamorithm. IEEE Transactions on Games, 2020, 12, 115-118.	1.2	1
49	Genetic programming theory and practice: a fifteen-year trajectory. Genetic Programming and Evolvable Machines, 2020, 21, 169-179.	1.5	4
50	Scaling tree-based automated machine learning to biomedical big data with a feature set selector. Bioinformatics, 2020, 36, 250-256.	1.8	245
51	A maximum likelihood approach to electronic health record phenotyping using positive and unlabeled patients. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 119-126.	2.2	13
52	Global identifiability of latent class models with applications to diagnostic test accuracy studies: A GrÃ¶bner basis approach. Biometrics, 2020, 76, 98-108.	0.8	5
53	Embracing study heterogeneity for finding genetic interactions in largeâ€scale research consortia. Genetic Epidemiology, 2020, 44, 52-66.	0.6	4
54	An augmented estimation procedure for EHR-based association studies accounting for differential misclassification. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 244-253.	2.2	9

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55	Regional imaging genetic enrichment analysis. Bioinformatics, 2020, 36, 2554-2560.	1.8	16
56	Model selection for metabolomics: predicting diagnosis of coronary artery disease using automated machine learning. Bioinformatics, 2020, 36, 1772-1778.	1.8	42
57	Learning from electronic health records across multiple sites: A communication-efficient and privacy-preserving distributed algorithm. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 376-385.	2.2	61
58	Embedding covariate adjustments in tree-based automated machine learning for biomedical big data analyses. BMC Bioinformatics, 2020, 21, 430.	1.2	15
59	WellExplorer: an integrative resource linking hydraulic fracturing chemicals with hormonal pathways and geographic location. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	0
60	H3K27ac acetylome signatures reveal the epigenomic reorganization in remodeled non-failing human hearts. Clinical Epigenetics, 2020, 12, 106.	1.8	20
61	Translational Bioinformatics: Integrating Electronic Health Record and Omics Data. , 2020, , .		1
62	Integration of molecular and cellular pathogenesis - a bioinformatics approach. , 2020, , 201-207.		0
63	Learning from local to global: An efficient distributed algorithm for modeling time-to-event data. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1028-1036.	2.2	46
64	Diagnostic biomarkers to differentiate sepsis from cytokine release syndrome in critically ill children. Blood Advances, 2020, 4, 5174-5183.	2.5	30
65	International electronic health record-derived COVID-19 clinical course profiles: the 4CE consortium. Npj Digital Medicine, 2020, 3, 109.	5.7	128
66	Conservation machine learning. BioData Mining, 2020, 13, 9.	2.2	4
67	Transfer learning with chest X-rays for ER patient classification. Scientific Reports, 2020, 10, 20900.	1.6	10
68	An Automated Functional Annotation Pipeline That Rapidly Prioritizes Clinically Relevant Genes for Autism Spectrum Disorder. International Journal of Molecular Sciences, 2020, 21, 9029.	1.8	1
69	Ten important roles for academic leaders in data science. BioData Mining, 2020, 13, 18.	2.2	0
70	Ideas for how informaticians can get involved with COVID-19 research. BioData Mining, 2020, 13, 3.	2.2	20
71	Recommendations to enhance rigor and reproducibility in biomedical research. GigaScience, 2020, 9, .	3.3	83
72	1 Personalized medicine. , 2020, , 1-14.		0

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73	Multiple Plasma Biomarkers for RiskÂStratification in Patients With HeartÂFailureÂand Preserved Ejection Fraction. Journal of the American College of Cardiology, 2020, 75, 1281-1295.	1.2	116
74	Learning feature spaces for regression with genetic programming. Genetic Programming and Evolvable Machines, 2020, 21, 433-467.	1.5	23
75	Electronic health records and polygenic risk scores for predicting disease risk. Nature Reviews Genetics, 2020, 21, 493-502.	7.7	78
76	How Computational Experiments Can Improve Our Understanding of the Genetic Architecture of Common Human Diseases. Artificial Life, 2020, 26, 23-37.	1.0	4
77	SGP-DT: Semantic Genetic Programming Based on Dynamic Targets. Lecture Notes in Computer Science, 2020, , 167-183.	1.0	10
78	Image Feature Learning with Genetic Programming. Lecture Notes in Computer Science, 2020, , 63-78.	1.0	6
79	Image feature learning with a genetic programming autoencoder. , 2020, , .		4
80	SGP-DT. , 2020, , .		4
81	Genetic programming approaches to learning fair classifiers. , 2020, , .		11
82	New Pathways in Coevolutionary Computation. Genetic and Evolutionary Computation, 2020, , 295-305.	1.0	0
83	Benchmarking Manifold Learning Methods on a Large Collection of Datasets. Lecture Notes in Computer Science, 2020, , 135-150.	1.0	6
84	Coevolving Artistic Images Using OMNIREP. Lecture Notes in Computer Science, 2020, , 165-178.	1.0	0
85	Large scale biomedical data analysis with tree-based automated machine learning. , 2020, , .		0
86	Ten simple rules for writing a paper about scientific software. PLoS Computational Biology, 2020, 16, e1008390.	1.5	1
87	A Probabilistic and Multi-Objective Analysis of Lexicase Selection and Îµ-Lexicase Selection. Evolutionary Computation, 2019, 27, 377-402.	2.3	43
88	Gene-Gene Interactions: An Essential Component to Modeling Complexity for Precision Medicine. , 2019, , 171-177.		0
89	Comparing drug safety of hepatitis C therapies using post-market data. BMC Medical Informatics and Decision Making, 2019, 19, 147.	1.5	7
90	OMNIREP: originating meaning by coevolving encodings and representations. Memetic Computing, 2019, 11, 251-261.	2.7	7

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91	A regression framework to uncover pleiotropy in large-scale electronic health record data. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1083-1090.	2.2	9
92	Scalable biclustering â€" the future of big data exploration?. GigaScience, 2019, 8, .	3.3	12
93	Artificial Intelligence Based Approaches to Identify Molecular Determinants of Exceptional Health and Life Span-An Interdisciplinary Workshop at the National Institute on Aging. Frontiers in Artificial Intelligence, 2019, 2, 12.	2.0	12
94	Exploration of a diversity of computational and statistical measures of association for genome-wide genetic studies. BioData Mining, 2019, 12, 14.	2.2	3
95	EBIC. , 2019, , .		2
96	TPOT: A Tree-Based Pipeline Optimization Tool for Automating Machine Learning. The Springer Series on Challenges in Machine Learning, 2019, , 151-160.	10.4	149
97	Why mind-body medicine is poised to set a new standard for clinical research. Journal of Clinical Epidemiology, 2019, 116, 167-170.	2.4	3
98	Semantic variation operators for multidimensional genetic programming. , 2019, , .		14
99	Solution and Fitness Evolution (SAFE): A Study of Multiobjective Problems. , 2019, , .		1
100	Discovering test statistics using genetic programming. , 2019, , .		0
101	Machine Learning to Predict Toxicity in Head and Neck Cancer Patients Treated with Definitive Chemoradiation. International Journal of Radiation Oncology Biology Physics, 2019, 105, E139-E140.	0.4	8
102	Strategies for improving performance of evolutionary biclustering algorithm EBIC. , 2019, , .		1
103	Integrative Functional Annotation of 52 Genetic Loci Influencing Myocardial Mass Identifies Candidate Regulatory Variants and Target Genes. Circulation Genomic and Precision Medicine, 2019, 12, e002328.	1.6	7
104	SNCA and mTOR Pathway Single Nucleotide Polymorphisms Interact to Modulate the Age at Onset of Parkinson's Disease. Movement Disorders, 2019, 34, 1333-1344.	2.2	21
105	Solution and Fitness Evolution (SAFE): Coevolving Solutions and Their Objective Functions. Lecture Notes in Computer Science, 2019, , 146-161.	1.0	5
106	A comparison of two workflows for regulome and transcriptomeâ€based prioritization of genetic variants associated with myocardial mass. Genetic Epidemiology, 2019, 43, 717-726.	0.6	1
107	Integration of genetic and clinical information to improve imputation of data missing from electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1056-1063.	2.2	17
108	How to increase our belief in discovered statistical interactions via large-scale association studies?. Human Genetics, 2019, 138, 293-305.	1.8	12

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109	Testing the assumptions of parametric linear models: the need for biological data mining in disciplines such as human genetics. BioData Mining, 2019, 12, 6.	2.2	3
110	Preparing next-generation scientists for biomedical big data: artificial intelligence approaches. Personalized Medicine, 2019, 16, 247-257.	0.8	28
111	Prevalence and Characterization of Yoga Mentions in the Electronic Health Record. Journal of the American Board of Family Medicine, 2019, 32, 790-800.	0.8	5
112	Mining Regional Imaging Genetic Associations via Voxel-wise Enrichment Analysis. , 2019, 2019, .		4
113	Automated discovery of test statistics using genetic programming. Genetic Programming and Evolvable Machines, 2019, 20, 127-137.	1.5	3
114	EBIC: an open source software for high-dimensional and big data analyses. Bioinformatics, 2019, 35, 3181-3183.	1.8	7
115	STatistical Inference Relief (STIR) feature selection. Bioinformatics, 2019, 35, 1358-1365.	1.8	47
116	Multidimensional genetic programming for multiclass classification. Swarm and Evolutionary Computation, 2019, 44, 260-272.	4.5	36
117	Robust-ODAL: Learning from heterogeneous health systems without sharing patient-level data. , 2019, , .		5
118	Translational Bioinformatics: Biobanks in the Precision Medicine Era. , 2019, , .		4
119	Using Machine Learning on Home Health Care Assessments to Predict Fall Risk. Studies in Health Technology and Informatics, 2019, 264, 684-688.	0.2	14
120	ODAL: A one-shot distributed algorithm to perform logistic regressions on electronic health records data from multiple clinical sites. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 30-41.	0.7	7
121	Automated discovery of test statistics using genetic programming. Genetic Programming and Evolvable Machines, 2019, 20, 127-137.	1.5	0
122	Interpretation of machine learning predictions for patient outcomes in electronic health records. AMIA ... Annual Symposium proceedings, 2019, 2019, 572-581.	0.2	9
123	Reading Between the Genes: Computational Models to Discover Function from Noncoding DNA. , 2018, , .		0
124	GPU Accelerated Browser for Neuroimaging Genomics. Neuroinformatics, 2018, 16, 393-402.	1.5	1
125	Medication class enrichment analysis: a novel algorithm to analyze multiple pharmacologic exposures simultaneously using electronic health record data. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 780-789.	2.2	3
126	Data-driven advice for applying machine learning to bioinformatics problems. , 2018, , .		118

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127	PIE: A prior knowledge guided integrated likelihood estimation method for bias reduction in association studies using electronic health records data. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 345-352.	2.2	15
128	A heuristic method for simulating open-data of arbitrary complexity that can be used to compare and evaluate machine learning methods. , 2018, , .		4
129	DNAp: A Pipeline for DNA-seq Data Analysis. Scientific Reports, 2018, 8, 6793.	1.6	14
130	Collective feature selection to identify crucial epistatic variants. BioData Mining, 2018, 11, 5.	2.2	22
131	Considerations for automated machine learning in clinical metabolic profiling: Altered homocysteine plasma concentration associated with metformin exposure. , 2018, , .		16
132	Leveraging putative enhancer-promoter interactions to investigate two-way epistasis in Type 2 Diabetes GWAS. , 2018, , .		2
133	Mapping Patient Trajectories using Longitudinal Extraction and Deep Learning in the MIMIC-III Critical Care Database. , 2018, , .		22
134	Comparing adverse effects of Hepatitis C drugs using FAERS data. , 2018, , .		0
135	Attribute tracking. , 2018, , .		3
136	Retrieving Impressions from Semantic Memory Modeled with Associative Pulsing Neural Networks. , 2018, , .		0
137	Analysis validation has been neglected in the Age of Reproducibility. PLoS Biology, 2018, 16, e3000070.	2.6	13
138	To know the objective is not (necessarily) to know the objective function. BioData Mining, 2018, 11, 21.	2.2	5
139	Identification of epistatic interactions between the human RNA demethylases FTO and ALKBH5 with gene set enrichment analysis informed by differential methylation. BMC Proceedings, 2018, 12, 59.	1.8	7
140	Druggability of Coronary Artery Disease Risk Loci. Circulation Genomic and Precision Medicine, 2018, 11, e001977.	1.6	18
141	Where are we now?. , 2018, , .		72
142	Grammatical Evolution Strategies for Bioinformatics and Systems Genomics. , 2018, , 395-405.		0
143	The premature infant gut microbiome during the first 6 weeks of life differs based on gestational maturity at birth. Pediatric Research, 2018, 84, 71-79.	1.1	101
144	EBIC: an evolutionary-based parallel biclustering algorithm for pattern discovery. Bioinformatics, 2018, 34, 3719-3726.	1.8	28

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145	Bootstrapped Sparse Canonical Correlation Analysis. , 2018, , 101-117.		0
146	Leveraging epigenomics and contactomics data to investigate SNP pairs in GWAS. Human Genetics, 2018, 137, 413-425.	1.8	8
147	runibic: a Bioconductor package for parallel row-based biclustering of gene expression data. Bioinformatics, 2018, 34, 4302-4304.	1.8	17
148	Relief-based feature selection: Introduction and review. Journal of Biomedical Informatics, 2018, 85, 189-203.	2.5	723
149	How computational thought experiments can improve our understanding of the genetic architecture of common human diseases. , 2018, , .		2
150	Evolutionary computation. , 2018, , .		1
151	Benchmarking relief-based feature selection methods for bioinformatics data mining. Journal of Biomedical Informatics, 2018, 85, 168-188.	2.5	156
152	Investigating the parameter space of evolutionary algorithms. BioData Mining, 2018, 11, 2.	2.2	51
153	Improving machine learning reproducibility in genetic association studies with proportional instance cross validation (PICV). BioData Mining, 2018, 11, 6.	2.2	6
154	EBIC. , 2018, , .		5
155	A multidimensional genetic programming approach for identifying epsistatic gene interactions. , 2018, , .		2
156	Integration of Molecular and Cellular Pathogenesis. , 2018, , 243-249.		0
157	Eleven quick tips for architecting biomedical informatics workflows with cloud computing. PLoS Computational Biology, 2018, 14, e1005994.	1.5	9
158	A System for Accessible Artificial Intelligence. Genetic and Evolutionary Computation, 2018, , 121-134.	1.0	13
159	Characterizing and Managing Missing Structured Data in Electronic Health Records: Data Analysis. JMIR Medical Informatics, 2018, 6, e11.	1.3	104
160	Identifying and Harnessing the Building Blocks of Machine Learning Pipelines for Sensible Initialization of a Data Science Automation Tool. Genetic and Evolutionary Computation, 2018, , 211-223.	1.0	0
161	Problem Driven Machine Learning by Co-evolving Genetic Programming Trees and Rules in a Learning Classifier System. Genetic and Evolutionary Computation, 2018, , 55-71.	1.0	2
162	Workshop during the Pacific Symposium of Biocomputing, Jan 3-7, 2019: Reading between the genes: interpreting non-coding DNA in high-throughput. , 2018, , .		0

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163	Translational informatics of population health: How large biomolecular and clinical datasets unite. , 2018, , .		0
164	ODAL: A one-shot distributed algorithm to perform logistic regressions on electronic health records data from multiple clinical sites. , 2018, , .		13
165	A heuristic method for simulating open-data of arbitrary complexity that can be used to compare and evaluate machine learning methods. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 259-267.	0.7	4
166	Leveraging putative enhancer-promoter interactions to investigate two-way epistasis in Type 2 Diabetes GWAS. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 548-558.	0.7	2
167	Considerations for automated machine learning in clinical metabolic profiling: Altered homocysteine plasma concentration associated with metformin exposure. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 460-471.	0.7	16
168	Data-driven advice for applying machine learning to bioinformatics problems. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 192-203.	0.7	53
169	THE TRAINING OF NEXT GENERATION DATA SCIENTISTS IN BIOMEDICINE. , 2017, 22, 640-645.		9
170	MISSING DATA IMPUTATION IN THE ELECTRONIC HEALTH RECORD USING DEEPLY LEARNED AUTOENCODERS. , 2017, 22, 207-218.		89
171	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
172	Tissue-specific network-based genome wide study of amygdala imaging phenotypes to identify functional interaction modules. Bioinformatics, 2017, 33, 3250-3257.	1.8	23
173	Genetic Programming Representations for Multi-dimensional Feature Learning in Biomedical Classification. Lecture Notes in Computer Science, 2017, , 158-173.	1.0	9
174	A General Feature Engineering Wrapper for Machine Learning Using $$epsilon $$ -Lexicase Survival. Lecture Notes in Computer Science, 2017, , 80-95.	1.0	9
175	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. Nature Communications, 2017, 8, 1167.	5.8	40
176	Evolutionarily derived networks to inform disease pathways. Genetic Epidemiology, 2017, 41, 866-875.	0.6	1
177	Phenotype validation in electronic health records based genetic association studies. Genetic Epidemiology, 2017, 41, 790-800.	0.6	8
178	Analysis of Geneâ€Gene Interactions. Current Protocols in Human Genetics, 2017, 95, 1.14.1-1.14.10.	3.5	34
179	Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 771-777.	1.6	23
180	Toward the automated analysis of complex diseases in genome-wide association studies using genetic programming. , 2017, , .		19

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181	A Pilot Characterization of the Human Chronobiome. Scientific Reports, 2017, 7, 17141.	1.6	70
182	On metaâ€•and megaâ€analyses for geneâ€“environment interactions. Genetic Epidemiology, 2017, 41, 876-886.	0.6	2
183	Grid-based stochastic search for hierarchical gene-gene interactions in population-based genetic studies of common human diseases. BioData Mining, 2017, 10, 19.	2.2	12
184	Variant Set Enrichment: an R package to identify disease-associated functional genomic regions. BioData Mining, 2017, 10, 9.	2.2	17
185	Multi-class computational evolution: development, benchmark evaluation and application to RNA-Seq biomarker discovery. BioData Mining, 2017, 10, 13.	2.2	10
186	Gene Set Enrichment Analyses: lessons learned from the heart failure phenotype. BioData Mining, 2017, 10, 18.	2.2	4
187	Identifying geneâ€“gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. Human Genetics, 2017, 136, 165-178.	1.8	11
188	Two-dimensional enrichment analysis for mining high-level imaging genetic associations. Brain Informatics, 2017, 4, 27-37.	1.8	13
189	NO-BOUNDARY THINKING IN BIOINFORMATICS. , 2017, 22, 646-648.		1
190	Evolutionary computation: the next major transition of artificial intelligence?. BioData Mining, 2017, 10, 26.	2.2	16
191	Ensemble representation learning. , 2017, , .		8
192	Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. PLoS Genetics, 2017, 13, e1006945.	1.5	3
193	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	2.2	7
194	PMLB: a large benchmark suite for machine learning evaluation and comparison. BioData Mining, 2017, 10, 36.	2.2	188
195	Artificial intelligence: more human with human. BioData Mining, 2017, 10, 34.	2.2	0
196	Genetic Effects on the Correlation Structure of CVD Risk Factors: Exome-Wide Data From a Ghanaian Population. Global Heart, 2017, 12, 133.	0.9	4
197	A chromosome 5q31.1 locus associates with tuberculin skin test reactivity in HIV-positive individuals from tuberculosis hyper-endemic regions in east Africa. PLoS Genetics, 2017, 13, e1006710.	1.5	28
198	EVE: Cloud-Based Annotation of Human Genetic Variants. Lecture Notes in Computer Science, 2017, , 83-95.	1.0	0

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199	Improving the Reproducibility of Genetic Association Results Using Genotype Resampling Methods. Lecture Notes in Computer Science, 2017, , 96-108.	1.0	0
200	Comparing Different Adverse Effects Among Multiple Drugs Using FAERS Data. Studies in Health Technology and Informatics, 2017, 245, 1268.	0.2	1
201	Meta-dimensional data integration identifies critical pathways for susceptibility, tumorigenesis and progression of endometrial cancer. Oncotarget, 2016, 7, 55249-55263.	0.8	14
202	Embracing Complex Associations in Common Traits: Critical Considerations for Precision Medicine. Trends in Genetics, 2016, 32, 470-484.	2.9	31
203	Pareto Inspired Multi-objective Rule Fitness for Adaptive Rule-based Machine Learning. , 2016, , .		0
204	The tip of the iceberg: challenges of accessing hospital electronic health record data for biological data mining. BioData Mining, 2016, 9, 29.	2.2	6
205	AN INTEGRATED NETWORK APPROACH TO IDENTIFYING BIOLOGICAL PATHWAYS AND ENVIRONMENTAL EXPOSURE INTERACTIONS IN COMPLEX DISEASES. , 2016, , .		1
206	Bicliques in Graphs with Correlated Edges: From Artificial to Biological Networks. Lecture Notes in Computer Science, 2016, , 138-155.	1.0	2
207	Automating Biomedical Data Science Through Tree-Based Pipeline Optimization. Lecture Notes in Computer Science, 2016, , 123-137.	1.0	170
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