Jason H Moore

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

580 papers	26,332 citations	75 h-index	149 g-index
667 ext. papers	30,534 ext. citations	5 avg, IF	7.28 L-index

#	Paper	IF	Citations
580	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	4.1	
579	Gene-Interaction-Sensitive enrichment analysis in congenital heart disease.. *BioData Mining*, **2022**, 15, 4	4.3	
578	AddGBoost: A gradient boosting-style algorithm based on strong learners. *Machine Learning With Applications*, **2022**, 7, 100243	6.5	0
577	Single-cell multi-omics analysis of human pancreatic islets reveals novel cellular states in type 1 diabetes.. *Nature Metabolism*, **2022**, 4, 284-299	14.6	2
576	Shared Genetic Architecture and Causal Relationship Between Asthma and Cardiovascular Diseases: A Large-Scale Cross-Trait Analysis.. *Frontiers in Genetics*, **2021**, 12, 775591	4.5	2
575	Multi-task learning based structured sparse canonical correlation analysis for brain imaging genetics. *Medical Image Analysis*, **2021**, 76, 102297	15.4	1
574	TargetTox: A Feature Selection Pipeline for Identifying Predictive Targets Associated with Drug Toxicity. *Journal of Chemical Information and Modeling*, **2021**, 61, 5386-5394	6.1	0
573	PMLB v1.0: An open-source dataset collection for benchmarking machine learning methods. *Bioinformatics*, **2021**,	7.2	3
572	Plasma biomarkers associated with adverse outcomes in patients with calcific aortic stenosis. *European Journal of Heart Failure*, **2021**,	12.3	3
571	A semantic genetic programming framework based on dynamic targets. *Genetic Programming and Evolvable Machines*, **2021**, 22, 463	2	
570	The promise of automated machine learning for the genetic analysis of complex traits. *Human Genetics*, **2021**, 1	6.3	0
569	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	8.6	24
568	International Comparisons of Harmonized Laboratory Value Trajectories to Predict Severe COVID-19: Leveraging the 4CE Collaborative Across 342 Hospitals and 6 Countries: A Retrospective Cohort Study **2021**,		9
567	TPOT-NN: augmenting tree-based automated machine learning with neural network estimators. *Genetic Programming and Evolvable Machines*, **2021**, 22, 207	2	2
566	REGENS: an open source Python package for simulating realistic autosomal genotypes. *Journal of Open Source Software*, **2021**, 6, 2743	5.2	
565	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	7.6	13
564	Symbolic-regression boosting. *Genetic Programming and Evolvable Machines*, **2021**, 22, 357-381	2	1

563	The phenomics and genetics of addictive and affective comorbidity in opioid use disorder. *Drug and Alcohol Dependence*, **2021**, 221, 108602	4.9	1
562	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	4	1
561	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	11	7
560	The Translational Machine: A novel machine-learning approach to illuminate complex genetic architectures. *Genetic Epidemiology*, **2021**, 45, 485-536	2.6	
559	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	8.6	15
558	Why Is the Electronic Health Record So Challenging for Research and Clinical Care?. *Methods of Information in Medicine*, **2021**, 60, 32-48	1.5	0
557	Novel EDGE encoding method enhances ability to identify genetic interactions. *PLoS Genetics*, **2021** , 17, e1009534	6	0
556	International Analysis of Electronic Health Records of Children and Youth Hospitalized With COVID-19 Infection in 6 Countries. *JAMA Network Open*, **2021**, 4, e2112596	10.4	12
555	Towards effective GP multi-class classification based on dynamic targets **2021**,		1
554	Case contamination in electronic health records based case-control studies. *Biometrics*, **2021**, 77, 67-77	1.8	3
553	Anticancer Therapy at the End of Life: Lessons From a Community Cancer Institute. *Journal of Palliative Care*, **2021**, 36, 87-92	1.8	1
552	treeheatr: an R package for interpretable decision tree visualizations. *Bioinformatics*, **2021**, 37, 282-284	7.2	3
551	Evaluating recommender systems for AI-driven biomedical informatics. *Bioinformatics*, **2021**, 37, 250-256	7.2	4
550	Lossless integration of multiple electronic health records for identifying pleiotropy using summary statistics. *Nature Communications*, **2021**, 12, 168	17.4	1
549	Metabolomics Insights in Early Childhood Caries. *Journal of Dental Research*, **2021**, 100, 615-622	8.1	6
548	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*, **2021**, PP,	3	1
547	The Cosmos Collaborative: A Vendor-Facilitated Electronic Health Record Data Aggregation Platform.. *ACI Open*, **2021**, 5, e36-e46	0.8	5
546	The Role of Genetic Ancestry as a Risk Factor for Primary Open-angle Glaucoma in African Americans **2021**, 62, 28		4

545	Conservation machine learning: a case study of random forests. *Scientific Reports*, **2021**, 11, 3629	4.9	4
544	Harnessing electronic health records to study emerging environmental disasters: a proof of concept with perfluoroalkyl substances (PFAS). *Npj Digital Medicine*, **2021**, 4, 122	15.7	0
543	Socio-cognitive Evolution Strategies. *Lecture Notes in Computer Science*, **2021**, 329-342	0.9	
542	A comparison of methods for interpreting random forest models of genetic association in the presence of non-additive interactions. *BioData Mining*, **2021**, 14, 9	4.3	7
541	Estimating prevalence of human traits among populations from polygenic risk scores.. *Human Genomics*, **2021**, 15, 70	6.8	0
540	Recommendations to enhance rigor and reproducibility in biomedical research. *GigaScience*, **2020**, 9,	7.6	20
539	1 Personalized medicine **2020**, 1-14		
538	Multiple Plasma Biomarkers for Risk´Stratification in Patients With Heart´Failure´and Preserved Ejection Fraction. *Journal of the American College of Cardiology*, **2020**, 75, 1281-1295	15.1	49
537	Learning feature spaces for regression with genetic programming. *Genetic Programming and Evolvable Machines*, **2020**, 21, 433-467	2	5
536	Electronic health records and polygenic risk scores for predicting disease risk. *Nature Reviews Genetics*, **2020**, 21, 493-502	30.1	32
535	How Computational Experiments Can Improve Our Understanding of the Genetic Architecture of Common Human Diseases. *Artificial Life*, **2020**, 26, 23-37	1.4	2
534	Image feature learning with a genetic programming autoencoder **2020**,		3
533	SGP-DT **2020**,		3
532	Genetic programming approaches to learning fair classifiers **2020**,		2
531	Benchmarking Manifold Learning Methods on a Large Collection of Datasets. *Lecture Notes in Computer Science*, **2020**, 135-150	0.9	2
530	Coevolving Artistic Images Using OMNIREP. *Lecture Notes in Computer Science*, **2020**, 165-178	0.9	
529	New Pathways in Coevolutionary Computation. *Genetic and Evolutionary Computation*, **2020**, 295-305	0.8	
528	SGP-DT: Semantic Genetic Programming Based on Dynamic Targets. *Lecture Notes in Computer Science*, **2020**, 167-183	0.9	7

527	Image Feature Learning with Genetic Programming. *Lecture Notes in Computer Science*, **2020**, 63-78	0.9	4
526	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	8.6	5
525	Global identifiability of latent class models with applications to diagnostic test accuracy studies: A GrБner basis approach. *Biometrics*, **2020**, 76, 98-108	1.8	1
524	Embracing study heterogeneity for finding genetic interactions in large-scale research consortia. *Genetic Epidemiology*, **2020**, 44, 52-66	2.6	1
523	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	8.6	0
522	Regional imaging genetic enrichment analysis. *Bioinformatics*, **2020**, 36, 2554-2560	7.2	8
521	Model selection for metabolomics: predicting diagnosis of coronary artery disease using automated machine learning. *Bioinformatics*, **2020**, 36, 1772-1778	7.2	18
520	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	8.6	27
519	Embedding covariate adjustments in tree-based automated machine learning for biomedical big data analyses. *BMC Bioinformatics*, **2020**, 21, 430	3.6	3
518	H3K27ac acetylome signatures reveal the epigenomic reorganization in remodeled non-failing human hearts. *Clinical Epigenetics*, **2020**, 12, 106	7.7	9
517	Integration of molecular and cellular pathogenesis - a bioinformatics approach **2020**, 201-207		
516	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	8.6	16
515	Diagnostic biomarkers to differentiate sepsis from cytokine release syndrome in critically ill children. *Blood Advances*, **2020**, 4, 5174-5183	7.8	10
514	International electronic health record-derived COVID-19 clinical course profiles: the 4CE consortium. *Npj Digital Medicine*, **2020**, 3, 109	15.7	61
513	Transfer learning with chest X-rays for ER patient classification. *Scientific Reports*, **2020**, 10, 20900	4.9	4
512	Gamorithm. *IEEE Transactions on Games*, **2020**, 12, 115-118	1.2	0
511	Genetic programming theory and practice: a fifteen-year trajectory. *Genetic Programming and Evolvable Machines*, **2020**, 21, 169-179	2	2
510	Scaling tree-based automated machine learning to biomedical big data with a feature set selector. *Bioinformatics*, **2020**, 36, 250-256	7.2	99

509	Semantic variation operators for multidimensional genetic programming **2019**,		5
508	Solution and Fitness Evolution (SAFE): A Study of Multiobjective Problems **2019**,		1
507	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	4	4
506	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	5.2	5
505	SNCA and mTOR Pathway Single Nucleotide Polymorphisms Interact to Modulate the Age at Onset of Parkinson's Disease. *Movement Disorders*, **2019**, 34, 1333-1344	7	14
504	Solution and Fitness Evolution (SAFE): Coevolving Solutions and Their Objective Functions. *Lecture Notes in Computer Science*, **2019**, 146-161	0.9	4
503	A comparison of two workflows for regulome and transcriptome-based prioritization of genetic variants associated with myocardial mass. *Genetic Epidemiology*, **2019**, 43, 717-726	2.6	1
502	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	8.6	8
501	How to increase our belief in discovered statistical interactions via large-scale association studies?. *Human Genetics*, **2019**, 138, 293-305	6.3	10
500	A Probabilistic and Multi-Objective Analysis of Lexicase Selection and -Lexicase Selection. *Evolutionary Computation*, **2019**, 27, 377-402	4.3	17
499	Gene-Gene Interactions: An Essential Component to Modeling Complexity for Precision Medicine **2019**, 171-177		
498	Comparing drug safety of hepatitis C therapies using post-market data. *BMC Medical Informatics and Decision Making*, **2019**, 19, 147	3.6	2
497	OMNIREP: Originating Meaning by Coevolving Encodings and Representations. *Memetic Computing*, **2019**, 11, 251-261	3.4	4
496	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	8.6	2
495	Scalable biclustering - the future of big data exploration?. *GigaScience*, **2019**, 8,	7.6	6
494	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	3	5
493	Exploration of a diversity of computational and statistical measures of association for genome-wide genetic studies. *BioData Mining*, **2019**, 12, 14	4.3	2
492	TPOT: A Tree-Based Pipeline Optimization Tool for Automating Machine Learning. *The Springer Series on Challenges in Machine Learning*, **2019**, 151-160	7.3	59

491	Why mind-body medicine is poised to set a new standard for clinical research. *Journal of Clinical Epidemiology*, **2019**, 116, 167-170	5.7	2
490	Using Machine Learning on Home Health Care Assessments to Predict Fall Risk. *Studies in Health Technology and Informatics*, **2019**, 264, 684-688	0.5	8
489	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	1.3	7
488	Automated discovery of test statistics using genetic programming. *Genetic Programming and Evolvable Machines*, **2019**, 20, 127-137	2	
487	Interpretation of machine learning predictions for patient outcomes in electronic health records **2019**, 2019, 572-581	0.7	7
486	Preparing next-generation scientists for biomedical big data: artificial intelligence approaches. *Personalized Medicine*, **2019**, 16, 247-257	2.2	11
485	Prevalence and Characterization of Yoga Mentions in the Electronic Health Record. *Journal of the American Board of Family Medicine*, **2019**, 32, 790-800	1.6	2
484	Mining Regional Imaging Genetic Associations via Voxel-wise Enrichment Analysis. *IEEE-EMBS International Conference on Biomedical and Health Informatics*, **2019**, 2019,	1.9	3
483	Automated discovery of test statistics using genetic programming. *Genetic Programming and Evolvable Machines*, **2019**, 20, 127-137	2	1
482	EBIC: an open source software for high-dimensional and big data analyses. *Bioinformatics*, **2019**, 35, 3181-3183	7.2	4
481	STatistical Inference Relief (STIR) feature selection. *Bioinformatics*, **2019**, 35, 1358-1365	7.2	28
480	Multidimensional genetic programming for multiclass classification. *Swarm and Evolutionary Computation*, **2019**, 44, 260-272	9.8	26
479	GPU Accelerated Browser for Neuroimaging Genomics. *Neuroinformatics*, **2018**, 16, 393-402	3.2	1
478	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	8.6	2
477	Data-driven advice for applying machine learning to bioinformatics problems **2018**,		52
476	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	8.6	6
475	DNAp: A Pipeline for DNA-seq Data Analysis. *Scientific Reports*, **2018**, 8, 6793	4.9	11
474	Collective feature selection to identify crucial epistatic variants. *BioData Mining*, **2018**, 11, 5	4.3	12

473	Considerations for automated machine learning in clinical metabolic profiling: Altered homocysteine plasma concentration associated with metformin exposure **2018**,		6
472	Relief-based feature selection: Introduction and review. *Journal of Biomedical Informatics*, **2018**, 85, 189-203	10.2	352
471	Benchmarking relief-based feature selection methods for bioinformatics data mining. *Journal of Biomedical Informatics*, **2018**, 85, 168-188	10.2	82
470	Investigating the parameter space of evolutionary algorithms. *BioData Mining*, **2018**, 11, 2	4.3	31
469	Improving machine learning reproducibility in genetic association studies with proportional instance cross validation (PICV). *BioData Mining*, **2018**, 11, 6	4.3	6
468	A multidimensional genetic programming approach for identifying epsistatic gene interactions **2018**,		2
467	Integration of Molecular and Cellular Pathogenesis **2018**, 243-249		
466	Eleven quick tips for architecting biomedical informatics workflows with cloud computing. *PLoS Computational Biology*, **2018**, 14, e1005994	5	6
465	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	1.3	4
464	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	1.3	2
463	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	1.3	15
462	Data-driven advice for applying machine learning to bioinformatics problems. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2018**, 23, 192-203	1.3	47
461	Characterizing and Managing Missing Structured Data in Electronic Health Records: Data Analysis. *JMIR Medical Informatics*, **2018**, 6, e11	3.6	55
460	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	0.8	
459	Problem Driven Machine Learning by Co-evolving Genetic Programming Trees and Rules in a Learning Classifier System. *Genetic and Evolutionary Computation*, **2018**, 55-71	0.8	0
458	A System for Accessible Artificial Intelligence. *Genetic and Evolutionary Computation*, **2018**, 121-134	0.8	7
457	Mapping Patient Trajectories using Longitudinal Extraction and Deep Learning in the MIMIC-III Critical Care Database **2018**,		4
456	Attribute tracking **2018**,		3

455	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	2.3	6
454	Druggability of Coronary Artery Disease Risk Loci. *Circulation Genomic and Precision Medicine*, **2018**, 11, e001977	5.2	12
453	Where are we now? **2018**,		33
452	Grammatical Evolution Strategies for Bioinformatics and Systems Genomics **2018**, 395-405		
451	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	3.2	61
450	EBIC: an evolutionary-based parallel biclustering algorithm for pattern discovery. *Bioinformatics*, **2018**, 34, 3719-3726	7.2	16
449	Bootstrapped Sparse Canonical Correlation Analysis **2018**, 101-117		
448	Leveraging epigenomics and contactomics data to investigate SNP pairs in GWAS. *Human Genetics*, **2018**, 137, 413-425	6.3	7
447	runibic: a Bioconductor package for parallel row-based biclustering of gene expression data. *Bioinformatics*, **2018**, 34, 4302-4304	7.2	7
446	THE TRAINING OF NEXT GENERATION DATA SCIENTISTS IN BIOMEDICINE. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2017**, 22, 640-645	1.3	5
445	MISSING DATA IMPUTATION IN THE ELECTRONIC HEALTH RECORD USING DEEPLY LEARNED AUTOENCODERS. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2017**, 22, 207-218	1.3	54
444	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6,	6	65
443	Tissue-specific network-based genome wide study of amygdala imaging phenotypes to identify functional interaction modules. *Bioinformatics*, **2017**, 33, 3250-3257	7.2	18
442	Genetic Programming Representations for Multi-dimensional Feature Learning in Biomedical Classification. *Lecture Notes in Computer Science*, **2017**, 158-173	0.9	7
441	A General Feature Engineering Wrapper for Machine Learning Using (epsilon)-Lexicase Survival. *Lecture Notes in Computer Science*, **2017**, 80-95	0.9	5
440	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. *Nature Communications*, **2017**, 8, 1167	17.4	23
439	Evolutionarily derived networks to inform disease pathways. *Genetic Epidemiology*, **2017**, 41, 866-875	2.6	1
438	Phenotype validation in electronic health records based genetic association studies. *Genetic Epidemiology*, **2017**, 41, 790-800	2.6	5

437	Analysis of Gene-Gene Interactions. *Current Protocols in Human Genetics*, **2017**, 95, 1.14.1-1.14.10	3.2	10
436	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. *BioData Mining*, **2017**, 10, 25	4.3	5
435	PMLB: a large benchmark suite for machine learning evaluation and comparison. *BioData Mining*, **2017**, 10, 36	4.3	95
434	Artificial intelligence: more human with human. *BioData Mining*, **2017**, 10, 34	4.3	
433	Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. *American Journal of Epidemiology*, **2017**, 186, 771-777	3.8	13
432	Toward the automated analysis of complex diseases in genome-wide association studies using genetic programming **2017**,		11
431	A Pilot Characterization of the Human Chronobiome. *Scientific Reports*, **2017**, 7, 17141	4.9	48
430	On meta- and mega-analyses for gene-environment interactions. *Genetic Epidemiology*, **2017**, 41, 876-886	2.6	2
429	Grid-based stochastic search for hierarchical gene-gene interactions in population-based genetic studies of common human diseases. *BioData Mining*, **2017**, 10, 19	4.3	8
428	Variant Set Enrichment: an R package to identify disease-associated functional genomic regions. *BioData Mining*, **2017**, 10, 9	4.3	16
427	Multi-class computational evolution: development, benchmark evaluation and application to RNA-Seq biomarker discovery. *BioData Mining*, **2017**, 10, 13	4.3	9
426	Gene Set Enrichment Analyses: lessons learned from the heart failure phenotype. *BioData Mining*, **2017**, 10, 18	4.3	3
425	Identifying gene-gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. *Human Genetics*, **2017**, 136, 165-178	6.3	8
424	Two-dimensional enrichment analysis for mining high-level imaging genetic associations. *Brain Informatics*, **2017**, 4, 27-37	5.9	9
423	NO-BOUNDARY THINKING IN BIOINFORMATICS. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2017**, 22, 646-648	1.3	1
422	Evolutionary computation: the next major transition of artificial intelligence?. *BioData Mining*, **2017**, 10, 26	4.3	8
421	Ensemble representation learning **2017**,		6
420	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	6	19

419	Comparing Different Adverse Effects Among Multiple Drugs Using FAERS Data. *Studies in Health Technology and Informatics*, **2017**, 245, 1268	0.5	0
418	EVE: Cloud-Based Annotation of Human Genetic Variants. *Lecture Notes in Computer Science*, **2017**, 83-95	0.9	
417	Improving the Reproducibility of Genetic Association Results Using Genotype Resampling Methods. *Lecture Notes in Computer Science*, **2017**, 96-108	0.9	
416	Genetic Effects on the Correlation Structure of´CVD Risk Factors: Exome-Wide Data From a Ghanaian Population. *Global Heart*, **2017**, 12, 133-140	2.9	2
415	Fetal exposures and perinatal influences on the stool microbiota of premature infants. *Journal of Maternal-Fetal and Neonatal Medicine*, **2016**, 29, 99-105	2	36
414	Adapting bioinformatics curricula for big data. *Briefings in Bioinformatics*, **2016**, 17, 43-50	13.4	37
413	Evaluation of a Tree-based Pipeline Optimization Tool for Automating Data Science **2016**,		149
412	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. *Npj Genomic Medicine*, **2016**, 1,	6.2	11
411	A global test for gene-gene interactions based on random matrix theory. *Genetic Epidemiology*, **2016**, 40, 689-701	2.6	2
410	Complex systems analysis of bladder cancer susceptibility reveals a role for decarboxylase activity in two genome-wide association studies. *BioData Mining*, **2016**, 9, 40	4.3	4
409	Structured sparse CCA for brain imaging genetics via graph OSCAR. *BMC Systems Biology*, **2016**, 10 Suppl 3, 68	3.5	8
408	Evolutionary triangulation: informing genetic association studies with evolutionary evidence. *BioData Mining*, **2016**, 9, 12	4.3	4
407	A call for biological data mining approaches in epidemiology. *BioData Mining*, **2016**, 9, 1	4.3	18
406	The golden era of biomedical informatics has begun. *BioData Mining*, **2016**, 9, 15	4.3	4
405	Detecting gene-gene interactions using a permutation-based random forest method. *BioData Mining*, **2016**, 9, 14	4.3	37
404	Association of Cesarean Delivery and Formula Supplementation With the Intestinal Microbiome of 6-Week-Old Infants. *JAMA Pediatrics*, **2016**, 170, 212-9	8.3	170
403	Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. *Genetics*, **2016**, 202, 457-70	4	13
402	A Locus at 5q33.3 Confers Resistance to Tuberculosis in Highly Susceptible Individuals. *American Journal of Human Genetics*, **2016**, 98, 514-524	11	53

401	Structured sparse canonical correlation analysis for brain imaging genetics: an improved GraphNet method. *Bioinformatics*, **2016**, 32, 1544-51	7.2	66
400	Cardiovascular Disease Risk Factors in Ghana during the Rural-to-Urban Transition: A Cross-Sectional Study. *PLoS ONE*, **2016**, 11, e0162753	3.7	30
399	AN INTEGRATED NETWORK APPROACH TO IDENTIFYING BIOLOGICAL PATHWAYS AND ENVIRONMENTAL EXPOSURE INTERACTIONS IN COMPLEX DISEASES. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2016**, 21, 9-20	1.3	2
398	Evolution of Active Categorical Image Classification via Saccadic Eye Movement. *Lecture Notes in Computer Science*, **2016**, 581-590	0.9	1
397	Meta-dimensional data integration identifies critical pathways for susceptibility, tumorigenesis and progression of endometrial cancer. *Oncotarget*, **2016**, 7, 55249-55263	3.3	12
396	Embracing Complex Associations in Common Traits: Critical Considerations for Precision Medicine. *Trends in Genetics*, **2016**, 32, 470-484	8.5	22
395	Bicliques in Graphs with Correlated Edges: From Artificial to Biological Networks. *Lecture Notes in Computer Science*, **2016**, 138-155	0.9	1
394	Automating Biomedical Data Science Through Tree-Based Pipeline Optimization. *Lecture Notes in Computer Science*, **2016**, 123-137	0.9	107
393	Harnessing publicly available genetic data to prioritize lipid modifying therapeutic targets for prevention of coronary heart disease based on dysglycemic risk. *Human Genetics*, **2016**, 135, 453-467	6.3	9
392	Identifying significant gene-environment interactions using a combination of screening testing and hierarchical false discovery rate control. *Genetic Epidemiology*, **2016**, 40, 544-557	2.6	15
391	Pareto Inspired Multi-objective Rule Fitness for Noise-Adaptive Rule-Based Machine Learning. *Lecture Notes in Computer Science*, **2016**, 514-524	0.9	2
390	Plasminogen Activator Inhibitor-1 and Diagnosis of the Metabolic Syndrome in a West African Population. *Journal of the American Heart Association*, **2016**, 5,	6	14
389	Studying the Genetics of Complex Disease With Ancestry-Specific Human Phenotype Networks: The Case of Type 2 Diabetes in East Asian Populations. *Genetic Epidemiology*, **2016**, 40, 293-303	2.6	10
388	Big data - a 21st century science Maginot Line? No-boundary thinking: shifting from the big data paradigm. *BioData Mining*, **2015**, 8, 7	4.3	5
387	A systems genetics approach to dyslipidemia in children and adolescents. *OMICS A Journal of Integrative Biology*, **2015**, 19, 248-59	3.8	4
386	Delay-tolerant networks and network coding: Comparative studies on simulated and real-device experiments. *Computer Networks*, **2015**, 83, 349-362	5.4	2
385	Hippocampal transcriptome-guided genetic analysis of correlated episodic memory phenotypes in Alzheimer's disease. *Frontiers in Genetics*, **2015**, 6, 117	4.5	18
384	ExSTraCS 2.0: Description and Evaluation of a Scalable Learning Classifier System. *Evolutionary Intelligence*, **2015**, 8, 89-116	1.7	57

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