Jason H Moore

List of Publications by Year
in descending order

626 papers	33,850 citations	5574 82 h-index	5539 163 g-index
668 all docs	668 docs citations	668 times ranked	37942 citing authors

#	Article	IF	Citations
1	Multifactor-Dimensionality Reduction Reveals High-Order Interactions among Estrogen-Metabolism Genes in Sporadic Breast Cancer. American Journal of Human Genetics, 2001, 69, 138-147.	6.2	1,745
2	Missing heritability and strategies for finding the underlying causes of complex disease. Nature Reviews Genetics, 2010, 11, 446-450.	16.3	1,511
3	The Genetic Structure and History of Africans and African Americans. Science, 2009, 324, 1035-1044.	12.6	1,267
4	Multifactor dimensionality reduction software for detecting geneâ€“gene and geneâ€“environment interactions. Bioinformatics, 2003, 19, 376-382.	4.1	1,067
5	Chapter 11: Genome-Wide Association Studies. PLoS Computational Biology, 2012, 8, e1002822.	3.2	950
6	Relief-based feature selection: Introduction and review. Journal of Biomedical Informatics, 2018, 85, 189-203.	4.3	723
7	Characterization of MicroRNA Expression Levels and Their Biological Correlates in Human Cancer Cell Lines. Cancer Research, 2007, 67, 2456-2468.	0.9	669
8	The Ubiquitous Nature of Epistasis in Determining Susceptibility to Common Human Diseases. Human Heredity, 2003, 56, 73-82.	0.8	662
9	Proteomic patterns of tumour subsets in non-small-cell lung cancer. Lancet, The, 2003, 362, 433-439.	13.7	597
10	A flexible computational framework for detecting, characterizing, and interpreting statistical patterns of epistasis in genetic studies of human disease susceptibility. Journal of Theoretical Biology, 2006, 241, 252-261.	1.7	576
11	Power of multifactor dimensionality reduction for detecting geneâ€gene interactions in the presence of genotyping error, missing data, phenocopy, and genetic heterogeneity. Genetic Epidemiology, 2003, 24, 150-157.	1.3	515
12	Bioinformatics challenges for genome-wide association studies. Bioinformatics, 2010, 26, 445-455.	4.1	477
13	A High-Density Admixture Map for Disease Gene Discovery in African Americans. American Journal of Human Genetics, 2004, 74, 1001-1013.	6.2	416
14	Alzheimer's Disease Neuroimaging Initiative biomarkers as quantitative phenotypes: Genetics core aims, progress, and plans. Alzheimer's and Dementia, 2010, 6, 265-273.	0.8	378
15	New strategies for identifying gene-gene interactions in hypertension. Annals of Medicine, 2002, 34, 88-95.	3.8	377
16	Breast cancer riskâ€“associated SNPs modulate the affinity of chromatin for FOXA1 and alter gene expression. Nature Genetics, 2012, 44, 1191-1198.	21.4	357
17	Renin-Angiotensin System Gene Polymorphisms and Atrial Fibrillation. Circulation, 2004, 109, 1640-1646.	1.6	343
18	Whole genome association study of brain-wide imaging phenotypes for identifying quantitative trait loci in MCI and AD: A study of the ADNI cohort. NeuroImage, 2010, 53, 1051-1063.	4.2	340

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19	A balanced accuracy function for epistasis modeling in imbalanced datasets using multifactor dimensionality reduction. Genetic Epidemiology, 2007, 31, 306-315.	1.3	337
20	Epistasis and Its Implications for Personal Genetics. American Journal of Human Genetics, 2009, 85, 309-320.	6.2	326
21	Epigenomic Enhancer Profiling Defines a Signature of Colon Cancer. Science, 2012, 336, 736-739.	12.6	304
22	Traversing the conceptual divide between biological and statistical epistasis: systems biology and a more modern synthesis. BioEssays, 2005, 27, 637-646.	2.5	301
23	Evaluation of a Tree-based Pipeline Optimization Tool for Automating Data Science. , 2016, , .		290
24	Serial Analysis of the Gut and Respiratory Microbiome in Cystic Fibrosis in Infancy: Interaction between Intestinal and Respiratory Tracts and Impact of Nutritional Exposures. MBio, 2012, 3, .	4.1	281
25	Gut microbial colonisation in premature neonates predicts neonatal sepsis. Archives of Disease in Childhood: Fetal and Neonatal Edition, 2012, 97, F456-F462.	2.8	273
26	Scaling tree-based automated machine learning to biomedical big data with a feature set selector. Bioinformatics, 2020, 36, 250-256.	4.1	245
27	Association of Cesarean Delivery and Formula Supplementation With the Intestinal Microbiome of 6-Week-Old Infants. JAMA Pediatrics, 2016, 170, 212.	6.2	238
28	Pathway analysis of genomic data: concepts, methods, and prospects for future development. Trends in Genetics, 2012, 28, 323-332.	6.7	237
29	Computational analysis of gene-gene interactions using multifactor dimensionality reduction. Expert Review of Molecular Diagnostics, 2004, 4, 795-803.	3.1	235
30	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	21.4	232
31	Genetics, statistics and human disease: analytical retooling for complexity. Trends in Genetics, 2004, 20, 640-647.	6.7	230
32	Failure to Replicate a Genetic Association May Provide Important Clues About Genetic Architecture. PLoS ONE, 2009, 4, e5639.	2.5	227
33	A global view of epistasis. Nature Genetics, 2005, 37, 13-14.	21.4	221
34	Proteomic-Based Prognosis of Brain Tumor Patients Using Direct-Tissue Matrix-Assisted Laser Desorption Ionization Mass Spectrometry. Cancer Research, 2005, 65, 7674-7681.	0.9	221
35	Amplification and overâ€expression of the EGFR and erbBâ€2 genes in human esophageal adenocarcinomas. International Journal of Cancer, 1993, 54, 213-219.	5.1	209
36	Machine Learning for Detecting Gene-Gene Interactions. Applied Bioinformatics, 2006, 5, 77-88.	1.6	209

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37	Cutting Edge: Molecular Portrait of Human Autoimmune Disease. Journal of Immunology, 2002, 169, 5-9.	0.8	193
38	Optimizationof neural network architecture using genetic programming improvesdetection and modeling of gene-gene interactions in studies of humandiseases. BMC Bioinformatics, 2003, 4, 28.	2.6	190
39	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
40	PMLB: a large benchmark suite for machine learning evaluation and comparison. BioData Mining, 2017, 10, 36.	4.0	188
41	GAMETES: a fast, direct algorithm for generating pure, strict, epistatic models with random architectures. BioData Mining, 2012, 5, 16.	4.0	184
42	Multifactor-dimensionality reduction shows a two-locus interaction associated with Type 2 diabetes mellitus. Diabetologia, 2004, 47, 549-554.	6.3	183
43	Analysis of the RELN gene as a genetic risk factor for autism. Molecular Psychiatry, 2005, 10, 563-571.	7.9	181
44	Learning Classifier Systems: A Complete Introduction, Review, and Roadmap. Journal of Artificial Evolution and Applications, 2009, 2009, 1-25.	1.8	173
45	Automating Biomedical Data Science Through Tree-Based Pipeline Optimization. Lecture Notes in Computer Science, 2016, , 123-137.	1.3	170
46	Shadows of complexity: what biological networks reveal about epistasis and pleiotropy. BioEssays, 2009, 31, 220-227.	2.5	162
47	Concordance of multiple analytical approaches demonstrates a complex relationship between DNA repair gene SNPs, smoking and bladder cancer susceptibility. Carcinogenesis, 2006, 27, 1030-1037.	2.8	161
48	Genetic analysis of quantitative phenotypes in AD and MCI: imaging, cognition and biomarkers. Brain Imaging and Behavior, 2014, 8, 183-207.	2.1	161
49	Big Data Bioinformatics. Journal of Cellular Physiology, 2014, 229, 1896-1900.	4.1	161
50	Benchmarking relief-based feature selection methods for bioinformatics data mining. Journal of Biomedical Informatics, 2018, 85, 168-188.	4.3	156
51	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
52	Multilocus Analysis of Hypertension: A Hierarchical Approach. Human Heredity, 2004, 57, 28-38.	0.8	146
53	Evidence for epistasis between SLC6A4 and ITGB3 in autism etiology and in the determination of platelet serotonin levels. Human Genetics, 2007, 121, 243-256.	3.8	135
54	The Challenges of Whole-Genome Approaches to Common Diseases. JAMA - Journal of the American Medical Association, 2004, 291, 1642-1643.	7.4	133

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55	Associations between Gut Microbial Colonization in Early Life and Respiratory Outcomes in Cystic Fibrosis. Journal of Pediatrics, 2015, 167, 138-147.e3.	1.8	131
56	Recurrent Tissue-Specific mtDNA Mutations Are Common in Humans. PLoS Genetics, 2013, 9, e1003929.	3.5	130
57	Why epistasis is important for tackling complex human disease genetics. Genome Medicine, 2014, 6, 124.	8.2	130
58	Drinking-Water Arsenic Exposure Modulates Gene Expression in Human Lymphocytes from a U.S. Population. Environmental Health Perspectives, 2008, 116, 524-531.	6.0	129
59	Spatially Uniform ReliefF (SURF) for computationally-efficient filtering of gene-gene interactions. BioData Mining, 2009, 2, 5.	4.0	129
60	International electronic health record-derived COVID-19 clinical course profiles: the 4CE consortium. Npj Digital Medicine, 2020, 3, 109.	10.9	128
61	An application of conditional logistic regression and multifactor dimensionality reduction for detecting gene-gene Interactions on risk of myocardial infarction: The importance of model validation. BMC Bioinformatics, 2004, 5, 49.	2.6	127
62	Pathways-based analyses of whole-genome association study data in bipolar disorder reveal genes mediating ion channel activity and synaptic neurotransmission. Human Genetics, 2009, 125, 63-79.	3.8	126
63	A gene expression signature for recent onset rheumatoid arthritis in peripheral blood mononuclear cells. Annals of the Rheumatic Diseases, 2004, 63, 1387-1392.	0.9	124
64	Data-driven advice for applying machine learning to bioinformatics problems. , 2018, , .		118
65	Relative impact of CYP3A genotype and concomitant medication on the severity of atorvastatin-induced muscle damage. Pharmacogenetics and Genomics, 2005, 15, 415-421.	1.5	117
66	Tuning ReliefF for Genome-Wide Genetic Analysis. , 2007, , 166-175.		117
67	A gene expression fingerprint of C. elegans embryonic motor neurons. BMC Genomics, 2005, 6, 42.	2.8	116
68	Multiple Plasma Biomarkers for RiskÂStratification in Patients With HeartÂFailureÂand Preserved Ejection Fraction. Journal of the American College of Cardiology, 2020, 75, 1281-1295.	2.8	116
69	Integrative functional genomics identifies an enhancer looping to the SOX9 gene disrupted by the 17q24.3 prostate cancer risk locus. Genome Research, 2012, 22, 1437-1446.	5.5	115
70	A novel method to identify geneâ€“gene effects in nuclear families: the MDRâ€PDT. Genetic Epidemiology, 2006, 30, 111-123.	1.3	112
71	Acceleration of Cardiovascular Disease by a Dysfunctional Prostacyclin Receptor Mutation. Circulation Research, 2008, 102, 986-993.	4.5	112
72	Reninâ€“angiotensin system gene polymorphisms and coronary artery disease in a large angiographic cohort: Detection of high order geneâ€“gene interaction. Atherosclerosis, 2007, 195, 172-180.	0.8	107

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73	Admixture Mapping in Lupus Identifies Multiple Functional Variants within IFIH1 Associated with Apoptosis, Inflammation, and Autoantibody Production. PLoS Genetics, 2013, 9, e1003222.	3.5	107
74	Combinatorial Pharmacogenetics. Nature Reviews Drug Discovery, 2005, 4, 911-918.	46.4	106
75	Characterizing genetic interactions in human disease association studies using statistical epistasis networks. BMC Bioinformatics, 2011, 12, 364.	2.6	106
76	Characterizing and Managing Missing Structured Data in Electronic Health Records: Data Analysis. JMIR Medical Informatics, 2018, 6, e11.	2.6	104
77	Single-Nucleotide Polymorphisms for Diagnosis of Salt-Sensitive Hypertension. Clinical Chemistry, 2006, 52, 352-360.	3.2	103
78	A training-testing approach to the molecular classification of resected non-small cell lung cancer. Clinical Cancer Research, 2003, 9, 4695-704.	7.0	102
79	DNA Repair Polymorphisms Modify Bladder Cancer Risk: A Multi-factor Analytic Strategy. Human Heredity, 2008, 65, 105-118.	0.8	101
80	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.	2.3	101
81	Structured sparse canonical correlation analysis for brain imaging genetics: an improved GraphNet method. Bioinformatics, 2016, 32, 1544-1551.	4.1	96
82	The Interaction of Four Genes in the Inflammation Pathway Significantly Predicts Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 2563-2568.	2.5	91
83	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	1.4	90
84	MISSING DATA IMPUTATION IN THE ELECTRONIC HEALTH RECORD USING DEEPLY LEARNED AUTOENCODERS. , 2017, 22, 207-218.		89
85	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
86	ExSTraCS 2.0: description and evaluation of a scalable learning classifier system. Evolutionary Intelligence, 2015, 8, 89-116.	3.6	88
87	Bladder cancer SNP panel predicts susceptibility and survival. Human Genetics, 2009, 125, 527-539.	3.8	85
88	Symbolic discriminant analysis of microarray data in autoimmune disease. Genetic Epidemiology, 2002, 23, 57-69.	1.3	84
89	Elevated male European and female African contributions to the genomes of African American individuals. Human Genetics, 2006, 120, 713-722.	3.8	84
90	Exploiting the proteome to improve the genome-wide genetic analysis of epistasis in common human diseases. Human Genetics, 2008, 124, 19-29.	3.8	83

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91	Recommendations to enhance rigor and reproducibility in biomedical research. GigaScience, 2020, 9, .	6.4	83
92	A Simple and Computationally Efficient Approach to Multifactor Dimensionality Reduction Analysis of Gene-Gene Interactions for Quantitative Traits. PLoS ONE, 2013, 8, e66545.	2.5	82
93	The use of animal models in the study of complex disease: all else is never equal or why do so many human studies fail to replicate animal findings?. BioEssays, 2004, 26, 170-179.	2.5	81
94	A computationally efficient hypothesis testing method for epistasis analysis using multifactor dimensionality reduction. Genetic Epidemiology, 2009, 33, 87-94.	1.3	80
95	A Locus at 5q33.3 Confers Resistance to Tuberculosis in Highly Susceptible Individuals. American Journal of Human Genetics, 2016, 98, 514-524.	6.2	78
96	Electronic health records and polygenic risk scores for predicting disease risk. Nature Reviews Genetics, 2020, 21, 493-502.	16.3	78
97	Integrated analysis of genetic and proteomic data identifies biomarkers associated with adverse events following smallpox vaccination. Genes and Immunity, 2009, 10, 112-119.	4.1	77
98	Multifactor dimensionality reduction for graphics processing units enables genome-wide testing of epistasis in sporadic ALS. Bioinformatics, 2010, 26, 694-695.	4.1	76
99	E-cadherin expression in primary and metastatic thoracic neoplasms and in Barrett's oesophagus. British Journal of Cancer, 1995, 71, 166-172.	6.4	75
100	Single nucleotide polymorphisms in ANKK1 and the dopamine D2 receptor gene affect cognitive outcome shortly after traumatic brain injury: A replication and extension study. Brain Injury, 2008, 22, 705-714.	1.2	75
101	Obesity Is Mediated by Differential Aryl Hydrocarbon Receptor Signaling in Mice Fed a Western Diet. Environmental Health Perspectives, 2012, 120, 1252-1259.	6.0	74
102	Polymorphisms in the Brain-Derived Neurotrophic Factor Gene Influence Memory and Processing Speed One Month after Brain Injury. Journal of Neurotrauma, 2012, 29, 1111-1118.	3.4	72
103	Where are we now?. , 2018, , .		72
104	COMT Val158Met Genotype and Individual Differences in Executive Function in Healthy Adults. Journal of the International Neuropsychological Society, 2011, 17, 174-180.	1.8	70
105	A Pilot Characterization of the Human Chronobiome. Scientific Reports, 2017, 7, 17141.	3.3	70
106	An information-gain approach to detecting three-way epistatic interactions in genetic association studies. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 630-636.	4.4	69
107	Longitudinal assessment of cognitive changes associated with adjuvant treatment for breast cancer: the impact of APOE and smoking. Psycho-Oncology, 2014, 23, 1382-1390.	2.3	69
108	MnSOD polymorphism and breast cancer in a population-based caseâ€“control study. Cancer Letters, 2003, 199, 27-33.	7.2	68

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109	Genetic Basis for Adverse Events after Smallpox Vaccination. Journal of Infectious Diseases, 2008, 198, 16-22.	4.0	67
110	Optimization of gene set annotations via entropy minimization over variable clusters (EMVC). Bioinformatics, 2014, 30, 1698-1706.	4.1	65
111	Ideal discrimination of discrete clinical endpoints using multilocus genotypes. In Silico Biology, 2004, 4, 183-94.	0.9	63
112	Î²2-Adrenergic receptor genotype and preterm delivery. American Journal of Obstetrics and Gynecology, 2002, 187, 1294-1298.	1.3	62
113	A Robust Multifactor Dimensionality Reduction Method for Detecting Gene-Gene Interactions with Application to the Genetic Analysis of Bladder Cancer Susceptibility. Annals of Human Genetics, 2011, 75, 20-28.	0.8	62
114	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.	4.4	61
115	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.	4.3	61
116	Genetic programming neural networks: A powerful bioinformatics tool for human genetics. Applied Soft Computing Journal, 2007, 7, 471-479.	7.2	60
117	Design and Implementation of the International Genetics and Translational Research in Transplantation Network. Transplantation, 2015, 99, 2401-2412.	1.0	60
118	Effect of cardiopulmonary bypass on urea cycle intermediates and nitric oxide levels after congenital heart surgery. Journal of Pediatrics, 2003, 142, 26-30.	1.8	59
119	Role of genetic heterogeneity and epistasis in bladder cancer susceptibility and outcome: a learning classifier system approach. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 603-612.	4.4	59
120	Gene expression signatures for autoimmune disease in peripheral blood mononuclear cells. Arthritis Research, 2004, 6, 120.	2.0	58
121	Association of Homozygous Wild-Type Glutathione S-Transferase M1 Genotype with Increased Breast Cancer Risk. Cancer Research, 2004, 64, 1233-1236.	0.9	57
122	A novel survival multifactor dimensionality reduction method for detecting geneâ€“gene interactions with application to bladder cancer prognosis. Human Genetics, 2011, 129, 101-110.	3.8	57
123	Transcriptome-guided amyloid imaging genetic analysis via a novel structured sparse learning algorithm. Bioinformatics, 2014, 30, i564-i571.	4.1	57
124	Feature Selection using a Random Forests Classifier for the Integrated Analysis of Multiple Data Types. , 2006, , .		55
125	Entropy-based information gain approaches to detect and to characterize gene-gene and gene-environment interactions/correlations of complex diseases. Genetic Epidemiology, 2011, 35, 706-721.	1.3	54
126	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.	4.4	54

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127	Effect of Genetic Variants, Especially CYP2C9 and VKORC1, on the Pharmacology of Warfarin. Seminars in Thrombosis and Hemostasis, 2012, 38, 893-904.	2.7	53
128	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
129	Intestinal differentiation andp53 gene alterations in barrett's esophagus and esophageal adenocarcinoma. International Journal of Cancer, 1994, 56, 487-493.	5.1	52
130	Detecting, Characterizing, and Interpreting Nonlinear Geneâ€“Gene Interactions Using Multifactor Dimensionality Reduction. Advances in Genetics, 2010, 72, 101-116.	1.8	52
131	Single-cell multi-omics analysis of human pancreatic islets reveals novel cellular states in type 1 diabetes. Nature Metabolism, 2022, 4, 284-299.	11.9	52
132	Integrated analysis of genetic, genomic and proteomic data. Expert Review of Proteomics, 2004, 1, 67-75.	3.0	51
133	Routine discovery of complex genetic models using genetic algorithms. Applied Soft Computing Journal, 2004, 4, 79-86.	7.2	51
134	Transcriptional Profiling in Coronary Artery Disease. Circulation, 2006, 114, 1811-1820.	1.6	51
135	Symbolic Modeling of Epistasis. Human Heredity, 2007, 63, 120-133.	0.8	51
136	Geneâ€“gene interactions in folate and adenosine biosynthesis pathways affect methotrexate efficacy and tolerability in rheumatoid arthritis. Pharmacogenetics and Genomics, 2009, 19, 935-944.	1.5	51
137	Detecting gene-gene interactions using a permutation-based random forest method. BioData Mining, 2016, 9, 14.	4.0	51
138	Investigating the parameter space of evolutionary algorithms. BioData Mining, 2018, 11, 2.	4.0	51
139	An analysis pipeline with statistical and visualization-guided knowledge discovery for Michigan-style learning classifier systems. IEEE Computational Intelligence Magazine, 2012, 7, 35-45.	3.2	50
140	The ENCODE Project and Perspectives on Pathways. Genetic Epidemiology, 2014, 38, 275-280.	1.3	47
141	STatistical Inference Relief (STIR) feature selection. Bioinformatics, 2019, 35, 1358-1365.	4.1	47
142	Examination of polymorphic glutathione S-transferase (GST) genes, tobacco smoking and prostate cancer risk among Men of African Descent: A case-control study. BMC Cancer, 2009, 9, 397.	2.6	46
143	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.	4.4	46
144	Detecting Pathway-Based Gene-Gene and Gene-Environment Interactions in Pancreatic Cancer. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1470-1479.	2.5	45

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145	Role for proteinâ€“protein interaction databases in human genetics. Expert Review of Proteomics, 2009, 6, 647-659.	3.0	45
146	Sucrase-isomaltase gene expression in Barrett's esophagus and adenocarcinoma. Gastroenterology, 1993, 105, 837-844.	1.3	44
147	Gender-specific correlations of plasminogen activator inhibitor-1 and tissue plasminogen activator levels with cardiovascular disease-related traits. Journal of Thrombosis and Haemostasis, 2007, 5, 313-320.	3.8	44
148	Systems genetics for drug target discovery. Trends in Pharmacological Sciences, 2011, 32, 623-630.	8.7	44
149	Adapting bioinformatics curricula for big data. Briefings in Bioinformatics, 2016, 17, 43-50.	6.5	44
150	Alterations of K-ras, p53, and erbB-2/neu in human lung adenocarcinomas. Journal of Thoracic and Cardiovascular Surgery, 1994, 107, 590-595.	0.8	43
151	Cytokine Expression Patterns Associated with Systemic Adverse Events following Smallpox Immunization. Journal of Infectious Diseases, 2006, 194, 444-453.	4.0	43
152	A Dietary-Wide Association Study (DWAS) of Environmental Metal Exposure in US Children and Adults. PLoS ONE, 2014, 9, e104768.	2.5	43
153	Robustness, Evolvability, and the Logic of Genetic Regulation. Artificial Life, 2014, 20, 111-126.	1.3	43
154	Genome-Wide Association Study for Circulating Tissue Plasminogen Activator Levels and Functional Follow-Up Implicates Endothelial STXBP5 and STX2. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1093-1101.	2.4	43
155	A Probabilistic and Multi-Objective Analysis of Lexicase Selection and Îµ-Lexicase Selection. Evolutionary Computation, 2019, 27, 377-402.	3.0	43
156	Diabetic Nephropathy Is Associated With Gene Expression Levels of Oxidative Phosphorylation and Related Pathways. Diabetes, 2006, 55, 1826-1831.	0.6	42
157	Interaction among variant vascular endothelial growth factor (VEGF) and its receptor in relation to prostate cancer risk. Prostate, 2010, 70, 341-352.	2.3	42
158	Fetal exposures and perinatal influences on the stool microbiota of premature infants. Journal of Maternal-Fetal and Neonatal Medicine, 2016, 29, 99-105.	1.5	42
159	Model selection for metabolomics: predicting diagnosis of coronary artery disease using automated machine learning. Bioinformatics, 2020, 36, 1772-1778.	4.1	42
160	Cardiovascular Disease Risk Factors in Ghana during the Rural-to-Urban Transition: A Cross-Sectional Study. PLoS ONE, 2016, 11, e0162753.	2.5	41
161	Distinct patterns of DNA methylation in conventional adenomas involving the right and left colon. Modern Pathology, 2014, 27, 145-155.	5.5	40
162	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. Nature Communications, 2017, 8, 1167.	12.8	40

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163	Bioinformatics Challenges in Genome-Wide Association Studies (GWAS). Methods in Molecular Biology, 2014, 1168, 63-81.	0.9	40
164	Petri net modeling of high-order genetic systems using grammatical evolution. BioSystems, 2003, 72, 177-186.	2.0	39
165	A role for CETP TaqIB polymorphism in determining susceptibility to atrial fibrillation: a nested case control study. BMC Medical Genetics, 2006, 7, 39.	2.1	39
166	Evaporative cooling feature selection for genotypic data involving interactions. Bioinformatics, 2007, 23, 2113-2120.	4.1	39
167	Analysis of Geneâ€Gene Interactions. Current Protocols in Human Genetics, 2011, 70, Unit1.14.	3.5	39
168	Vi<scp>SEN</scp>: Methodology and Software for Visualization of Statistical Epistasis Networks. Genetic Epidemiology, 2013, 37, 283-285.	1.3	39
169	Problems with genome-wide association studies. Science, 2007, 316, 1840-2.	12.6	39
170	Ant Colony Optimization for Genome-Wide Genetic Analysis. Lecture Notes in Computer Science, 2008, , 37-47.	1.3	38
171	The application of michigan-style learning classifiersystems to address genetic heterogeneity and epistasisin association studies. , 2010, , .		37
172	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.	4.4	37
173	Accelerating epistasis analysis in human genetics with consumer graphics hardware. BMC Research Notes, 2009, 2, 149.	1.4	36
174	Measuring the microbiome: perspectives on advances in DNA-based techniques for exploring microbial life. Briefings in Bioinformatics, 2012, 13, 420-429.	6.5	36
175	Expression of tumor suppressive micro<scp>RNA</scp>â€34a is associated with a reduced risk of bladder cancer recurrence. International Journal of Cancer, 2015, 137, 1158-1166.	5.1	36
176	Multidimensional genetic programming for multiclass classification. Swarm and Evolutionary Computation, 2019, 44, 260-272.	8.1	36
177	A Novel Structure-Aware Sparse Learning Algorithm for Brain Imaging Genetics. Lecture Notes in Computer Science, 2014, 17, 329-336.	1.3	36
178	ABCB1 and GST polymorphisms associated with TP53 status in breast cancer. Pharmacogenetics and Genomics, 2007, 17, 127-136.	1.5	35
179	Ability of epistatic interactions of cytokine singleâ€nucleotide polymorphisms to predict susceptibility to disease subsets in systemic sclerosis patients. Arthritis and Rheumatism, 2008, 59, 974-983.	6.7	35
180	ENABLING PERSONAL GENOMICS WITH AN EXPLICIT TEST OF EPISTASIS. , 2009, , 327-336.		35

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181	Layers of epistasis: genomeâ€wide regulatory networks and network approaches to genomeâ€wide association studies. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 513-526.	6.6	35
182	Epistasis Analysis Using Multifactor Dimensionality Reduction. Methods in Molecular Biology, 2015, 1253, 301-314.	0.9	35
183	Gene Expression Profiles in Human Autoimmune Disease. Current Pharmaceutical Design, 2003, 9, 1905-1917.	1.9	34
184	Identification of a two-loci epistatic interaction associated with susceptibility to rheumatoid arthritis through reverse engineering and multifactor dimensionality reduction. Genomics, 2007, 90, 6-13.	2.9	34
185	SLC39A2 and FSIP1 polymorphisms as potential modifiers of arsenic-related bladder cancer. Human Genetics, 2012, 131, 453-461.	3.8	34
186	Multifactor dimensionality reduction reveals a three-locus epistatic interaction associated with susceptibility to pulmonary tuberculosis. BioData Mining, 2013, 6, 4.	4.0	34
187	Analysis of Geneâ€Gene Interactions. Current Protocols in Human Genetics, 2017, 95, 1.14.1-1.14.10.	3.5	34
188	Ion channels and schizophrenia: a gene set-based analytic approach to GWAS data for biological hypothesis testing. Human Genetics, 2012, 131, 373-391.	3.8	33
189	International Analysis of Electronic Health Records of Children and Youth Hospitalized With COVID-19 Infection in 6 Countries. JAMA Network Open, 2021, 4, e2112596.	5.9	33
190	The gender-specific role of polymorphisms from the fibrinolytic, renin-angiotensin, and bradykinin systems in determining plasma t-PA and PAI-1 levels. Thrombosis and Haemostasis, 2006, 96, 471-477.	3.4	33
191	The multiscale backbone of the human phenotype network based on biological pathways. BioData Mining, 2014, 7, 1.	4.0	32
192	Genetic pathwayâ€based hierarchical clustering analysis of older adults with cognitive complaints and amnestic mild cognitive impairment using clinical and neuroimaging phenotypes. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 1060-1069.	1.7	31
193	Gene Expression Differences in Skin Fibroblasts in Identical Twins Discordant for Type 1 Diabetes. Diabetes, 2012, 61, 739-744.	0.6	31
194	Embracing Complex Associations in Common Traits: Critical Considerations for Precision Medicine. Trends in Genetics, 2016, 32, 470-484.	6.7	31
195	Connecting the dots between genes, biochemistry, and disease susceptibility: systems biology modeling in human genetics. Molecular Genetics and Metabolism, 2005, 84, 104-111.	1.1	30
196	Epistatic effects of polymorphisms in genes from the renin-angiotensin, bradykinin, and fibrinolytic systems on plasma t-PA and PAI-1 levels. Genomics, 2007, 89, 362-369.	2.9	30
197	CLCNKB-T481S and essential hypertension in a Ghanaian population. Journal of Hypertension, 2009, 27, 298-304.	0.5	30
198	Instance-linked attribute tracking and feedback for michigan-style supervised learning classifier systems. , 2012, , .		30

#	Article	IF	Citations
199	Predicting the difficulty of pure, strict, epistatic models: metrics for simulated model selection. BioData Mining, 2012, 5, 15.	4.0	30
200	Evolutionary dynamics on multiple scales: a quantitative analysis of the interplay between genotype, phenotype, and fitness in linear genetic programming. Genetic Programming and Evolvable Machines, 2012, 13, 305-337.	2.2	30
201	A call for biological data mining approaches in epidemiology. BioData Mining, 2016, 9, 1.	4.0	30
202	Diagnostic biomarkers to differentiate sepsis from cytokine release syndrome in critically ill children. Blood Advances, 2020, 4, 5174-5183.	5.2	30
203	Microarray analysis of cytoplasmic versus whole cell RNA reveals a considerable number of missed and false positive mRNAs. Rna, 2009, 15, 1917-1928.	3.5	29
204	Cancer heterogeneity: origins and implications for genetic association studies. Trends in Genetics, 2012, 28, 538-543.	6.7	28
205	Diverse convergent evidence in the genetic analysis of complex disease: coordinating omic, informatic, and experimental evidence to better identify and validate risk factors. BioData Mining, 2014, 7, 10.	4.0	28
206	EBIC: an evolutionary-based parallel biclustering algorithm for pattern discovery. Bioinformatics, 2018, 34, 3719-3726.	4.1	28
207	Preparing next-generation scientists for biomedical big data: artificial intelligence approaches. Personalized Medicine, 2019, 16, 247-257.	1.5	28
208	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.	3.5	28
209	A comparison of combinatorial partitioning and linear regression for the detection of epistatic effects of the ACE I/D and PAIâ€1 4G/5G polymorphisms on plasma PAIâ€1 levels. Clinical Genetics, 2002, 62, 74-79.	2.0	27
210	Correlation Between Genetic Variations in Hox Clusters and Hirschsprung's Disease. Annals of Human Genetics, 2007, 71, 526-536.	0.8	27
211	Personalized Medicine. Annals of Surgery, 2009, 250, 524-530.	4.2	27
212	Genetic polymorphisms modify bladder cancer recurrence and survival in a <scp>USA</scp> populationâ€based prognostic study. BJU International, 2015, 115, 238-247.	2.5	27
213	Genome-Wide Genetic Analysis Using Genetic Programming: The Critical Need for Expert Knowledge. , 2007, , 11-28.		27
214	The relationship between plasma tâ€PA and PAIâ€1 levels is dependent on epistatic effects of the ACE I/D and PAIâ€1 4G/5G polymorphisms. Clinical Genetics, 2002, 62, 53-59.	2.0	26
215	A Simple and Computationally Efficient Sampling Approach to Covariate Adjustment for Multifactor Dimensionality Reduction Analysis of Epistasis. Human Heredity, 2010, 70, 219-225.	0.8	26
216	Interaction among apoptosis-associated sequence variants and joint effects on aggressive prostate cancer. BMC Medical Genomics, 2012, 5, 11.	1.5	26

#	Article	IF	Citations
217	Meta-analysis of Randomized Controlled Trials of Genotype-Guided vs Standard Dosing of Warfarin. Chest, 2015, 148, 701-710.	0.8	26
218	Multiple Threshold Spatially Uniform ReliefF for the Genetic Analysis of Complex Human Diseases. Lecture Notes in Computer Science, 2013, , 1-10.	1.3	26
219	Genome-Wide Analysis of Epistasis Using Multifactor Dimensionality Reduction. , 2007, , 17-30.		26
220	Profiles of Gene Expression in Human Autoimmune Disease. Cell Biochemistry and Biophysics, 2004, 40, 081-096.	1.8	25
221	Coâ€localization of differentially expressed genes and shared susceptibility loci in human autoimmunity. Genetic Epidemiology, 2004, 27, 162-172.	1.3	25
222	Confronting complexity in lateâ€onset Alzheimer disease: application of twoâ€stage analysis approach addressing heterogeneity and epistasis. Genetic Epidemiology, 2008, 32, 187-203.	1.3	25
223	Continuous correction of differential path length factor in near-infrared spectroscopy. Journal of Biomedical Optics, 2013, 18, 056001.	2.6	25
224	Genetic Programming Neural Networks as a Bioinformatics Tool for Human Genetics. Lecture Notes in Computer Science, 2004, , 438-448.	1.3	25
225	Artificial intelligence programming with LabVIEW: genetic algorithms for instrumentation control and optimization. Computer Methods and Programs in Biomedicine, 1995, 47, 73-79.	4.7	24
226	Reporting of model validation procedures in human studies of genetic interactions. Nutrition, 2004, 20, 69-73.	2.4	24
227	Dissecting trait heterogeneity: a comparison of three clustering methods applied to genotypic data. BMC Bioinformatics, 2006, 7, 204.	2.6	24
228	Selective repression of retinoic acid target genes by RIP140 during induced tumor cell differentiation of pluripotent human embryonal carcinoma cells. Molecular Cancer, 2007, 6, 57.	19.2	24
229	No association between variant DNA repair genes and prostate cancer risk among men of African descent. Prostate, 2010, 70, 113-119.	2.3	24
230	The Informative Extremes: Using Both Nearest and Farthest Individuals Can Improve Relief Algorithms in the Domain of Human Genetics. Lecture Notes in Computer Science, 2010, , 182-193.	1.3	24
231	Using Expert Knowledge to Guide Covering and Mutation in a Michigan Style Learning Classifier System to Detect Epistasis and Heterogeneity. Lecture Notes in Computer Science, 2012, , 266-275.	1.3	24
232	Hippocampal transcriptome-guided genetic analysis of correlated episodic memory phenotypes in Alzheimer's disease. Frontiers in Genetics, 2015, 6, 117.	2.3	23
233	Tissue-specific network-based genome wide study of amygdala imaging phenotypes to identify functional interaction modules. Bioinformatics, 2017, 33, 3250-3257.	4.1	23
234	Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 771-777.	3.4	23

#	Article	IF	Citations
235	Learning feature spaces for regression with genetic programming. Genetic Programming and Evolvable Machines, 2020, 21, 433-467.	2.2	23
236	Metabolomics Insights in Early Childhood Caries. Journal of Dental Research, 2021, 100, 615-622.	5.2	23
237	Development and Evaluation of an Open-Ended Computational Evolution System for the Genetic Analysis of Susceptibility to Common Human Diseases. , 2008, , 129-140.		23
238	Additive Functions in Boolean Models of Gene Regulatory Network Modules. PLoS ONE, 2011, 6, e25110.	2.5	22
239	Principal component gene set enrichment (PCGSE). BioData Mining, 2015, 8, 25.	4.0	22
240	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	1.3	22
241	Collective feature selection to identify crucial epistatic variants. BioData Mining, 2018, 11, 5.	4.0	22
242	Mapping Patient Trajectories using Longitudinal Extraction and Deep Learning in the MIMIC-III Critical Care Database. , 2018, , .		22
243	Genetic interactions model among Eotaxin gene polymorphisms in asthma. Journal of Human Genetics, 2008, 53, 867-875.	2.3	21
244	Maleâ€“female differences in the genetic regulation of t-PA and PAI-1 levels in a Ghanaian population. Human Genetics, 2008, 124, 479-488.	3.8	21
245	Plasminogen Activator Inhibitorâ€1 and Diagnosis of the Metabolic Syndrome in a West African Population. Journal of the American Heart Association, 2016, 5, .	3.7	21
246	SNCA and mTOR Pathway Single Nucleotide Polymorphisms Interact to Modulate the Age at Onset of Parkinson's Disease. Movement Disorders, 2019, 34, 1333-1344.	3.9	21
247	Optimal Use of Expert Knowledge in Ant Colony Optimization for the Analysis of Epistasis in Human Disease. Lecture Notes in Computer Science, 2009, , 92-103.	1.3	21
248	Bioinformatics. Journal of Cellular Physiology, 2007, 213, 365-369.	4.1	20
249	Genomic mining for complex disease traits with â€œrandom chemistryâ€• Genetic Programming and Evolvable Machines, 2007, 8, 395-411.	2.2	20
250	Exploiting graphics processing units for computational biology and bioinformatics. Interdisciplinary Sciences, Computational Life Sciences, 2010, 2, 213-220.	3.6	20
251	Identifying significant geneâ€environment interactions using a combination of screening testing and hierarchical false discovery rate control. Genetic Epidemiology, 2016, 40, 544-557.	1.3	20
252	H3K27ac acetylome signatures reveal the epigenomic reorganization in remodeled non-failing human hearts. Clinical Epigenetics, 2020, 12, 106.	4.1	20

#	Article	IF	Citations
253	Ideas for how informaticians can get involved with COVID-19 research. BioData Mining, 2020, 13, 3.	4.0	20
254	The gender-specific role of polymorphisms from the fibrinolytic, renin-angiotensin, and bradykinin systems in determining plasma t-PA and PAI-1 levels. Thrombosis and Haemostasis, 2006, 96, 471-7.	3.4	20
255	Evolving hard problems: Generating human genetics datasets with a complex etiology. BioData Mining, 2011, 4, 21.	4.0	19
256	The Association of the Metabolic Syndrome with PAI-1 and t-PA Levels. Cardiology Research and Practice, 2011, 2011, 1-8.	1.1	19
257	Characterizing gene-gene interactions in a statistical epistasis network of twelve candidate genes for obesity. BioData Mining, 2015, 8, 45.	4.0	19
258	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. Npj Genomic Medicine, 2016, 1, .	3.8	19
259	Toward the automated analysis of complex diseases in genome-wide association studies using genetic programming. , 2017, , .		19
260	Conservation machine learning: a case study of random forests. Scientific Reports, 2021, 11, 3629.	3.3	19
261	From genotypes to genometypes: putting the genome back in genome-wide association studies. European Journal of Human Genetics, 2009, 17, 1205-1206.	2.8	18
262	HSD3B and Gene-Gene Interactions in a Pathway-Based Analysis of Genetic Susceptibility to Bladder Cancer. PLoS ONE, 2012, 7, e51301.	2.5	18
263	Epistasis, Complexity, and Multifactor Dimensionality Reduction. Methods in Molecular Biology, 2013, 1019, 465-477.	0.9	18
264	Differential Gene Expression in Diabetic Nephropathy in Individuals With Type 1 Diabetes. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E876-E882.	3.6	18
265	Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. Genetics, 2016, 202, 457-470.	2.9	18
266	Druggability of Coronary Artery Disease Risk Loci. Circulation Genomic and Precision Medicine, 2018, 11, e001977.	3.6	18
267	The Role of Genetic Ancestry as a Risk Factor for Primary Open-angle Glaucoma in African Americans. , 2021, 62, 28.		18
268	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.	6.2	18
269	A comparison of methods for interpreting random forest models of genetic association in the presence of non-additive interactions. BioData Mining, 2021, 14, 9.	4.0	18
270	Symbolic Discriminant Analysis for Mining Gene Expression Patterns. Lecture Notes in Computer Science, 2001, , 372-381.	1.3	18

#	Article	IF	Citations
271	Plasma biomarkers associated with adverse outcomes in patients with calcific aortic stenosis. European Journal of Heart Failure, 2021, 23, 2021-2032.	7.1	18
272	Robustness, Evolvability, and Accessibility in Linear Genetic Programming. Lecture Notes in Computer Science, 2011, , 13-24.	1.3	17
273	Evidence for epistatic interactions in antiepileptic drug resistance. Journal of Human Genetics, 2011, 56, 71-76.	2.3	17
274	SNP characteristics predict replication success in association studies. Human Genetics, 2014, 133, 1477-1486.	3.8	17
275	Identifying gene-gene interactions that are highly associated with Body Mass Index using Quantitative Multifactor Dimensionality Reduction (QMDR). BioData Mining, 2015, 8, 41.	4.0	17
276	Variant Set Enrichment: an R package to identify disease-associated functional genomic regions. BioData Mining, 2017, 10, 9.	4.0	17
277	runibic: a Bioconductor package for parallel row-based biclustering of gene expression data. Bioinformatics, 2018, 34, 4302-4304.	4.1	17
278	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.	4.4	17
279	An Expert Knowledge-Guided Mutation Operator for Genome-Wide Genetic Analysis Using Genetic Programming. Lecture Notes in Computer Science, 2007, , 30-40.	1.3	17
280	Bootstrapping, permutation testing and the method of surrogate data. Physics in Medicine and Biology, 1999, 44, L11-L12.	3.0	16
281	Effect of time of day on intraindividual variability in ambulatory blood pressure. American Journal of Hypertension, 2000, 13, 1203-1209.	2.0	16
282	The effects of polymorphisms in genes from the reninâ€“angiotensin, bradykinin, and fibrinolytic systems on plasma t-PA and PAI-1 levels are dependent on environmental context. Human Genetics, 2007, 122, 275-281.	3.8	16
283	Genetic Variation in the Autonomic Nervous System Affects Mortality: A Study of 1,095 Trauma Patients. Journal of the American College of Surgeons, 2009, 208, 663-668.	0.5	16
284	The Effects of Recombination on Phenotypic Exploration and Robustness in Evolution. Artificial Life, 2014, 20, 457-470.	1.3	16
285	Evolutionary computation: the next major transition of artificial intelligence?. BioData Mining, 2017, 10, 26.	4.0	16
286	Considerations for automated machine learning in clinical metabolic profiling: Altered homocysteine plasma concentration associated with metformin exposure. , 2018, , .		16
287	Regional imaging genetic enrichment analysis. Bioinformatics, 2020, 36, 2554-2560.	4.1	16
288	The Cosmos Collaborative: A Vendor-Facilitated Electronic Health Record Data Aggregation Platform. ACI Open, 2021, 05, e36-e46.	0.5	16

#	Article	IF	Citations
289	A CELLULAR AUTOMATA APPROACH TO DETECTING INTERACTIONS AMONG SINGLE-NUCLEOTIDE POLYMORPHISMS IN COMPLEX MULTIFACTORIAL DISEASES. , 2001, , .		16
290	Application of Genetic Algorithms to the Discovery of Complex Models for Simulation Studies in Human Genetics. , 2002, 2002, 1150-1155.		16
291	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
292	Activation of cryptic 3' splice sites within introns of cellular genes following gene entrapment. Nucleic Acids Research, 2004, 32, 2912-2924.	14.5	15
293	Specific Polymorphic Variation in the Mitochondrial Genome and Increased In-Hospital Mortality After Severe Trauma. Annals of Surgery, 2007, 246, 406-414.	4.2	15
294	Indoor and outdoor air pollution and lung cancer in New Hampshire and Vermont. Toxicological and Environmental Chemistry, 2012, 94, 605-615.	1.2	15
295	The influence of assortativity on the robustness of signal-integration logic in gene regulatory networks. Journal of Theoretical Biology, 2012, 296, 21-32.	1.7	15
296	Complex and dynamic population structures: synthesis, open questions, and future directions. Soft Computing, 2013, 17, 1109-1120.	3.6	15
297	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.	3.8	15
298	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.	4.4	15
299	Embedding covariate adjustments in tree-based automated machine learning for biomedical big data analyses. BMC Bioinformatics, 2020, 21, 430.	2.6	15
300	Epistasis Analysis Using Information Theory. Methods in Molecular Biology, 2015, 1253, 257-268.	0.9	15
301	PMLB v1.0: an open-source dataset collection for benchmarking machine learning methods. Bioinformatics, 2022, 38, 878-880.	4.1	15
302	Exploratory visual analysis of pharmacogenomic results. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 296-307.	0.7	15
303	Sensible initialization using expert knowledge for genome-wide analysis of epistasis using genetic programming. , 2009, 2009, 1289-1296.		14
304	Ecogeographic genetic epidemiology. Genetic Epidemiology, 2009, 33, 281-289.	1.3	14
305	Risk estimation using probability machines. BioData Mining, 2014, 7, 2.	4.0	14
306	Meta-dimensional data integration identifies critical pathways for susceptibility, tumorigenesis and progression of endometrial cancer. Oncotarget, 2016, 7, 55249-55263.	1.8	14

#	Article	IF	Citations
307	DNAp: A Pipeline for DNA-seq Data Analysis. Scientific Reports, 2018, 8, 6793.	3.3	14
308	Semantic variation operators for multidimensional genetic programming. , 2019, , .		14
309	GN-SCCA: GraphNet Based Sparse Canonical Correlation Analysis for Brain Imaging Genetics. Lecture Notes in Computer Science, 2015, 9250, 275-284.	1.3	14
310	Using Machine Learning on Home Health Care Assessments to Predict Fall Risk. Studies in Health Technology and Informatics, 2019, 264, 684-688.	0.3	14
311	Filling the gap between biology and computer science. BioData Mining, 2008, 1, 1.	4.0	13
312	Genetic Architecture of Tissue-Type Plasminogen Activator and Plasminogen Activator Inhibitor-1. Seminars in Thrombosis and Hemostasis, 2008, 34, 562-568.	2.7	13
313	Mining the diseasome. BioData Mining, 2011, 4, 25.	4.0	13
314	The limits of p-values for biological data mining. BioData Mining, 2013, 6, 10.	4.0	13
315	An Extended Michigan-Style Learning Classifier System for Flexible Supervised Learning, Classification, and Data Mining. Lecture Notes in Computer Science, 2014, , 211-221.	1.3	13
316	A System-Level Pathway-Phenotype Association Analysis Using Synthetic Feature Random Forest. Genetic Epidemiology, 2014, 38, 209-219.	1.3	13
317	gammaMAXT: a fast multiple-testing correction algorithm. BioData Mining, 2015, 8, 36.	4.0	13
318	Studying the Genetics of Complex Disease With Ancestryâ€Specific Human Phenotype Networks: The Case of Type 2 Diabetes in East Asian Populations. Genetic Epidemiology, 2016, 40, 293-303.	1.3	13
319	Two-dimensional enrichment analysis for mining high-level imaging genetic associations. Brain Informatics, 2017, 4, 27-37.	3.0	13
320	Analysis validation has been neglected in the Age of Reproducibility. PLoS Biology, 2018, 16, e3000070.	5.6	13
321	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.	4.4	13
322	treeheatr: an R package for interpretable decision tree visualizations. Bioinformatics, 2021, 37, 282-284.	4.1	13
323	Evaluating recommender systems for AI-driven biomedical informatics. Bioinformatics, 2021, 37, 250-256.	4.1	13
324	TPOT-NN: augmenting tree-based automated machine learning with neural network estimators. Genetic Programming and Evolvable Machines, 2021, 22, 207-227.	2.2	13

#	Article	IF	Citations
325	Why Is the Electronic Health Record So Challenging for Research and Clinical Care?. Methods of Information in Medicine, 2021, 60, 032-048.	1.2	13
326	Epistasis Analysis Using ReliefF. Methods in Molecular Biology, 2015, 1253, 315-325.	0.9	13
327	A System for Accessible Artificial Intelligence. Genetic and Evolutionary Computation, 2018, , 121-134.	1.0	13
328	EXPLORATORY VISUAL ANALYSIS OF PHARMACOGENOMIC RESULTS. , 2004, , .		13
329	USING THE BIPARTITE HUMAN PHENOTYPE NETWORK TO REVEAL PLEIOTROPY AND EPISTASIS BEYOND THE GENE. , 2013, , .		13
330	ODAL: A one-shot distributed algorithm to perform logistic regressions on electronic health records data from multiple clinical sites. , 2018, , .		13
331	Multi-task learning based structured sparse canonical correlation analysis for brain imaging genetics. Medical Image Analysis, 2022, 76, 102297.	11.6	13
332	The role of the apolipoprotein E polymorphism in the prediction of coronary artery disease age of onset. Clinical Genetics, 1997, 51, 22-25.	2.0	12
333	Interleukin-1 gene complex single nucleotide polymorphisms in systemic sclerosis: A further step ahead. Human Immunology, 2008, 69, 187-192.	2.4	12
334	HUMAN MICROBIOME VISUALIZATION USING 3D TECHNOLOGY. , 2010, , 154-164.		12
335	Interaction between allelic variations in vitamin D receptor and retinoid X receptor genes on metabolic traits. BMC Genetics, 2014, 15, 37.	2.7	12
336	Grid-based stochastic search for hierarchical gene-gene interactions in population-based genetic studies of common human diseases. BioData Mining, 2017, 10, 19.	4.0	12
337	Scalable biclustering â€" the future of big data exploration?. GigaScience, 2019, 8, .	6.4	12
338	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.	3.4	12
339	How to increase our belief in discovered statistical interactions via large-scale association studies?. Human Genetics, 2019, 138, 293-305.	3.8	12
340	Genetic Variation in Complement Component 2 of the Classical Complement Pathway is Associated With Increased Mortality and Infection: A Study of 627 Patients With Trauma. Journal of Trauma, 2009, 66, 1265-1272.	2.3	11
341	Genes in the insulin and insulin-like growth factor pathway and odds of metachronous colorectal neoplasia. Human Genetics, 2011, 129, 503-512.	3.8	11
342	Gene ontology analysis of pairwise genetic associations in two genome-wide studies of sporadic ALS. BioData Mining, 2012, 5, 9.	4.0	11

#	Article	IF	Citations
343	Epiregulin (EREG) and human V-ATPase (TCIRG1): genetic variation, ethnicity and pulmonary tuberculosis susceptibility in Guinea-Bissau and The Gambia. Genes and Immunity, 2014, 15, 370-377.	4.1	11
344	Phenotypic Robustness and the Assortativity Signature of Human Transcription Factor Networks. PLoS Computational Biology, 2014, 10, e1003780.	3.2	11
345	Influence networks based on coexpression improve drug target discovery for the development of novel cancer therapeutics. BMC Systems Biology, 2014, 8, 12.	3.0	11
346	Functional dyadicity and heterophilicity of gene-gene interactions in statistical epistasis networks. BioData Mining, 2015, 8, 43.	4.0	11
347	Considerations for higher efficiency and productivity in research activities. BioData Mining, 2016, 9, 35.	4.0	11
348	Identifying geneâ€“gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. Human Genetics, 2017, 136, 165-178.	3.8	11
349	The phenomics and genetics of addictive and affective comorbidity in opioid use disorder. Drug and Alcohol Dependence, 2021, 221, 108602.	3.2	11
350	Environmental Sensing of Expert Knowledge in a Computational Evolution System for Complex Problem Solving in Human Genetics. Genetic and Evolutionary Computation, 2010, , 19-36.	1.0	11
351	Genetic programming approaches to learning fair classifiers. , 2020, , .		11
352	Cardiovascular Risk Associated with Interactions among Polymorphisms in Genes from the Renin-Angiotensin, Bradykinin, and Fibrinolytic Systems. PLoS ONE, 2010, 5, e12757.	2.5	11
353	Hybrid grammar-based approach to nonlinear dynamical system identification from biological time series. Physical Review E, 2006, 73, 021912.	2.1	10
354	Fast genome-wide epistasis analysis using ant colony optimization for multifactor dimensionality reduction analysis on graphics processing units. , 2010, , .		10
355	Toward robust network based complex systems: from evolutionary cellular automata to biological models. Intelligenza Artificiale, 2011, 5, 37-47.	1.6	10
356	No-boundary thinking in bioinformatics research. BioData Mining, 2013, 6, 19.	4.0	10
357	The influence of assortativity on the robustness and evolvability of gene regulatory networks upon gene birth. Journal of Theoretical Biology, 2013, 330, 26-36.	1.7	10
358	Preterm Birth Genome Project (PGP) â€“ validation of resources for preterm birth genome-wide studies. Journal of Perinatal Medicine, 2013, 41, 45-9.	1.4	10
359	Predicting targeted drug combinations based on Pareto optimal patterns of coexpression network connectivity. Genome Medicine, 2014, 6, 33.	8.2	10
360	The future of genomic medicine education in Africa. Genome Medicine, 2015, 7, 47.	8.2	10

#	Article	IF	Citations
361	Heuristic Identification of Biological Architectures for Simulating Complex Hierarchical Genetic Interactions. Genetic Epidemiology, 2015, 39, 25-34.	1.3	10
362	Differential Response to High Glucose in Skin Fibroblasts of Monozygotic Twins Discordant for Type 1 Diabetes. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E883-E889.	3.6	10
363	Multi-class computational evolution: development, benchmark evaluation and application to RNA-Seq biomarker discovery. BioData Mining, 2017, 10, 13.	4.0	10
364	Transfer learning with chest X-rays for ER patient classification. Scientific Reports, 2020, 10, 20900.	3.3	10
365	Genetic Analysis of Prostate Cancer Using Computational Evolution, Pareto-Optimization and Post-processing. Genetic and Evolutionary Computation, 2013, , 87-101.	1.0	10
366	SGP-DT: Semantic Genetic Programming Based on Dynamic Targets. Lecture Notes in Computer Science, 2020, , 167-183.	1.3	10
367	Using the bipartite human phenotype network to reveal pleiotropy and epistasis beyond the gene. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 188-99.	0.7	10
368	A population-based study in Ghana to investigate inter-individual variation in plasma t-PA and PAI-1. Ethnicity and Disease, 2007, 17, 492-7.	2.3	10
369	Visual analysis of statistical results from microarray studies of human breast cancer. Oncology Reports, 2006, 15 Spec no., 1043-7.	2.6	9
370	A classification and characterization of two-locus, pure, strict, epistatic models for simulation and detection. BioData Mining, 2014, 7, 8.	4.0	9
371	Structured sparse CCA for brain imaging genetics via graph OSCAR. BMC Systems Biology, 2016, 10, 68.	3.0	9
372	THE TRAINING OF NEXT GENERATION DATA SCIENTISTS IN BIOMEDICINE. , 2017, 22, 640-645.		9
373	Genetic Programming Representations for Multi-dimensional Feature Learning in Biomedical Classification. Lecture Notes in Computer Science, 2017, , 158-173.	1.3	9
374	A General Feature Engineering Wrapper for Machine Learning Using $$epsilon $$ -Lexicase Survival. Lecture Notes in Computer Science, 2017, , 80-95.	1.3	9
375	Eleven quick tips for architecting biomedical informatics workflows with cloud computing. PLoS Computational Biology, 2018, 14, e1005994.	3.2	9
376	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.	4.4	9
377	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.	4.4	9
378	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.	3.0	9

#	Article	IF	Citations
379	Sensible Initialization of a Computational Evolution System Using Expert Knowledge for Epistasis Analysis in Human Genetics. Adaptation, Learning, and Optimization, 2010, , 215-226.	0.6	9
380	Robustness and Evolvability of Recombination in Linear Genetic Programming. Lecture Notes in Computer Science, 2013, , 97-108.	1.3	9
381	The promise of automated machine learning for the genetic analysis of complex traits. Human Genetics, 2022, 141, 1529-1544.	3.8	9
382	Interpretation of machine learning predictions for patient outcomes in electronic health records. AMIA ... Annual Symposium proceedings, 2019, 2019, 572-581.	0.2	9
383	Shared Genetic Architecture and Causal Relationship Between Asthma and Cardiovascular Diseases: A Large-Scale Cross-Trait Analysis. Frontiers in Genetics, 2021, 12, 775591.	2.3	9
384	A cellular automata approach to detecting interactions among single-nucleotide polymorphisms in complex multifactorial diseases. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2002, , 53-64.	0.7	9
385	Cross Validation Consistency for the Assessment of Genetic Programming Results in Microarray Studies. Lecture Notes in Computer Science, 2003, , 99-106.	1.3	8
386	Genome-wide association studies for the identification of biomarkers in metabolic diseases. Expert Opinion on Medical Diagnostics, 2010, 4, 39-51.	1.6	8
387	STATISTICAL EPISTASIS NETWORKS REDUCE THE COMPUTATIONAL COMPLEXITY OF SEARCHING THREE-LOCUS GENETIC MODELS. , 2012, , .		8
388	Sex, Adiposity, and Hypertension Status Modify the Inverse Effect of Marine Food Intake on Blood Pressure in Alaska Native (Yupâ€™ik) People. Journal of Nutrition, 2015, 145, 931-938.	2.9	8
389	Phenotype validation in electronic health records based genetic association studies. Genetic Epidemiology, 2017, 41, 790-800.	1.3	8
390	Ensemble representation learning. , 2017, , .		8
391	Leveraging epigenomics and contactomics data to investigate SNP pairs in GWAS. Human Genetics, 2018, 137, 413-425.	3.8	8
392	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.	0.8	8
393	The Application of Pittsburgh-Style Learning Classifier Systems to Address Genetic Heterogeneity and Epistasis in Association Studies. , 2010, , 404-413.		8
394	Genetics of Plasminogen Activator Inhibitor-1 (PAI-1) in a Ghanaian Population. PLoS ONE, 2015, 10, e0136379.	2.5	8
395	Statistical epistasis networks reduce the computational complexity of searching three-locus genetic models. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 397-408.	0.7	8
396	Common single nucleotide polymorphisms in the promoter region of the human factor XI gene. Journal of Thrombosis and Haemostasis, 2003, 1, 1854-1856.	3.8	7

#	Article	IF	Citations
397	Human-Computer Interaction in a Computational Evolution System for the Genetic Analysis of Cancer. Genetic and Evolutionary Computation, 2011, , 153-171.	1.0	7
398	Key genes for modulating information flow play a temporal role as breast tumor coexpression networks are dynamically rewired by letrozole. BMC Medical Genomics, 2013, 6, S2.	1.5	7
399	Functional genomics annotation of a statistical epistasis network associated with bladder cancer susceptibility. BioData Mining, 2014, 7, 5.	4.0	7
400	The genetic interacting landscape of 63 candidate genes in Major Depressive Disorder: an explorative study. BioData Mining, 2014, 7, 19.	4.0	7
401	Retooling Fitness for Noisy Problems in a Supervised Michigan-style Learning Classifier System. , 2015, , .		7
402	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	4.0	7
403	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.	1.6	7
404	Comparing drug safety of hepatitis C therapies using post-market data. BMC Medical Informatics and Decision Making, 2019, 19, 147.	3.0	7
405	OMNIREP: originating meaning by coevolving encodings and representations. Memetic Computing, 2019, 11, 251-261.	4.0	7
406	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.	3.6	7
407	EBIC: an open source software for high-dimensional and big data analyses. Bioinformatics, 2019, 35, 3181-3183.	4.1	7
408	Does Complexity Matter? Artificial Evolution, Computational Evolution and the Genetic Analysis of Epistasis in Common Human Diseases.. Genetic and Evolutionary Computation, 2009, , 1-19.	1.0	7
409	Exploratory Visual Analysis of statistical results from microarray experiments comparing high and low grade glioma. Cancer Informatics, 2007, 5, 19-24.	1.9	7
410	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
411	TargetTox: A Feature Selection Pipeline for Identifying Predictive Targets Associated with Drug Toxicity. Journal of Chemical Information and Modeling, 2021, 61, 5386-5394.	5.4	7
412	AddGBoost: A gradient boosting-style algorithm based on strong learners. Machine Learning With Applications, 2022, 7, 100243.	4.4	7
413	An Improved Grammatical Evolution Strategy for Hierarchical Petri Net Modeling of Complex Genetic Systems. Lecture Notes in Computer Science, 2004, , 63-72.	1.3	6
414	Application of HapMap data to the evaluation of 8 candidate genes for pediatric slow transit constipation. Journal of Pediatric Surgery, 2007, 42, 666-671.	1.6	6

#	Article	IF	Citations
415	Environmental noise improves epistasis models of genetic data discovered using a computational evolution system. , 2009, , .		6
416	Computational genetics analysis of grey matter density in Alzheimerâ€™s disease. BioData Mining, 2014, 7, 17.	4.0	6
417	A BIPARTITE NETWORK APPROACH TO INFERRING INTERACTIONS BETWEEN ENVIRONMENTAL EXPOSURES AND HUMAN DISEASES. , 2014, , .		6
418	Lumping versus splitting: the need for biological data mining in precision medicine. BioData Mining, 2015, 8, 16.	4.0	6
419	SPARCoC: A New Framework for Molecular Pattern Discovery and Cancer Gene Identification. PLoS ONE, 2015, 10, e0117135.	2.5	6
420	Big data - a 21st century science Maginot Line? No-boundary thinking: shifting from the big data paradigm. BioData Mining, 2015, 8, 7.	4.0	6
421	Spectral gene set enrichment (SGSE). BMC Bioinformatics, 2015, 16, 70.	2.6	6
422	An Independent Filter for Gene Set Testing Based on Spectral Enrichment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1076-1086.	3.0	6
423	The tip of the iceberg: challenges of accessing hospital electronic health record data for biological data mining. BioData Mining, 2016, 9, 29.	4.0	6
424	Complex systems analysis of bladder cancer susceptibility reveals a role for decarboxylase activity in two genome-wide association studies. BioData Mining, 2016, 9, 40.	4.0	6
425	Evolutionary triangulation: informing genetic association studies with evolutionary evidence. BioData Mining, 2016, 9, 12.	4.0	6
426	Improving machine learning reproducibility in genetic association studies with proportional instance cross validation (PICV). BioData Mining, 2018, 11, 6.	4.0	6
427	Evolutionary Computation in Microarray Data Analysis. , 2002, , 23-35.		6
428	Image Feature Learning with Genetic Programming. Lecture Notes in Computer Science, 2020, , 63-78.	1.3	6
429	Benchmarking Manifold Learning Methods on a Large Collection of Datasets. Lecture Notes in Computer Science, 2020, , 135-150.	1.3	6
430	Genome-Wide Analysis of Epistasis Using Multifactor Dimensionality Reduction. , 0, , 2140-2153.		6
431	Using expert knowledge in initialization for genome-wide analysis of epistasis using genetic programming. , 2008, , .		5
432	SMAD4â€dependent polysome RNA recruitment in human pancreatic cancer cells. Molecular Carcinogenesis, 2012, 51, 771-782.	2.7	5

#	Article	IF	Citations
433	The role of visualization and 3-D printing in biological data mining. BioData Mining, 2015, 8, 22.	4.0	5
434	A Systems Genetics Approach to Dyslipidemia in Children and Adolescents. OMICS A Journal of Integrative Biology, 2015, 19, 248-259.	2.0	5
435	Continuous Endpoint Data Mining with ExSTraCS. , 2015, , .		5
436	The golden era of biomedical informatics has begun. BioData Mining, 2016, 9, 15.	4.0	5
437	To know the objective is not (necessarily) to know the objective function. BioData Mining, 2018, 11, 21.	4.0	5
438	EBIC. , 2018, , .		5
439	Solution and Fitness Evolution (SAFE): Coevolving Solutions and Their Objective Functions. Lecture Notes in Computer Science, 2019, , 146-161.	1.3	5
440	Prevalence and Characterization of Yoga Mentions in the Electronic Health Record. Journal of the American Board of Family Medicine, 2019, 32, 790-800.	1.5	5
441	Global identifiability of latent class models with applications to diagnostic test accuracy studies: A GrÃ¶bner basis approach. Biometrics, 2020, 76, 98-108.	1.4	5
442	Case contamination in electronic health records based caseâ€control studies. Biometrics, 2021, 77, 67-77.	1.4	5
443	Novel EDGE encoding method enhances ability to identify genetic interactions. PLoS Genetics, 2021, 17, e1009534.	3.5	5
444	Cellular Automata and Genetic Algorithms for Parallel Problem Solving in Human Genetics. Lecture Notes in Computer Science, 2002, , 821-830.	1.3	5
445	Solving Complex Problems in Human Genetics Using Genetic Programming: The Importance of Theorist-Practitionercomputer Interaction. , 2008, , 69-85.		5
446	Exploiting Expert Knowledge of Protein-Protein Interactions in a Computational Evolution System for Detecting Epistasis. Genetic and Evolutionary Computation, 2011, , 195-210.	1.0	5
447	Exploring Interestingness in a Computational Evolution System for the Genome-Wide Genetic Analysis of Alzheimerâ€™s Disease. Genetic and Evolutionary Computation, 2014, , 31-45.	1.0	5
448	Genome-Wide Epistasis and Pleiotropy Characterized by the Bipartite Human Phenotype Network. Methods in Molecular Biology, 2015, 1253, 269-283.	0.9	5
449	Network-Guided Sparse Learning for Predicting Cognitive Outcomes from MRI Measures. Lecture Notes in Computer Science, 2013, 8159, 202-210.	1.3	5
450	A SCREENING-TESTING APPROACH FOR DETECTING GENE-ENVIRONMENT INTERACTIONS USING SEQUENTIAL PENALIZED AND UNPENALIZED MULTIPLE LOGISTIC REGRESSION. , 2014, , .		5

#	Article	IF	Citations
451	Robust-ODAL: Learning from heterogeneous health systems without sharing patient-level data. , 2019, , .		5
452	Estimating prevalence of human traits among populations from polygenic risk scores. Human Genomics, 2021, 15, 70.	2.9	5
453	Automating Predictive Toxicology Using ComptoxAI. Chemical Research in Toxicology, 2022, 35, 1370-1382.	3.3	5
454	Predictors of interindividual variation in ambulatory blood pressure and their time or activity dependence. American Journal of Hypertension, 2000, 13, 52-60.	2.0	4
455	Improved Power of Sib-Pair Linkage Analysis Using Measures of Complex Trait Dynamics. Human Heredity, 2001, 52, 113-115.	0.8	4
456	Bases, Bits and Disease: Bases, bits and disease: a mathematical theory of human genetics. European Journal of Human Genetics, 2008, 16, 143-144.	2.8	4
457	Analysis of Geneâ€Gene Interactions. Current Protocols in Human Genetics, 2008, 59, Unit 1.14.	3.5	4
458	Solving complex problems in human genetics using GP. ACM SIGEVOlution, 2008, 3, 2-8.	0.5	4
459	Genetic Population Structure Analysis in New Hampshire Reveals Eastern European Ancestry. PLoS ONE, 2009, 4, e6928.	2.5	4
460	The disconnect between classical biostatistics and the biological data mining community. BioData Mining, 2013, 6, 12.	4.0	4
461	Big Data analysis on autopilot?. BioData Mining, 2013, 6, 22.	4.0	4
462	Bioinformatics: What the Clinical Laboratorian Needs to Know and Prepare For. Clinical Chemistry, 2013, 59, 1301-1305.	3.2	4
463	Identification of Novel Genetic Models of Glaucoma Using the â€œEMERGENTâ€•Genetic Programming-Based Artificial Intelligence System. Genetic and Evolutionary Computation, 2015, , 17-35.	1.0	4
464	Pareto Inspired Multi-objective Rule Fitness for Noise-Adaptive Rule-Based Machine Learning. Lecture Notes in Computer Science, 2016, , 514-524.	1.3	4
465	A global test for geneâ€gene interactions based on random matrix theory. Genetic Epidemiology, 2016, 40, 689-701.	1.3	4
466	Gene Set Enrichment Analyses: lessons learned from the heart failure phenotype. BioData Mining, 2017, 10, 18.	4.0	4
467	A heuristic method for simulating open-data of arbitrary complexity that can be used to compare and evaluate machine learning methods. , 2018, , .		4
468	Mining Regional Imaging Genetic Associations via Voxel-wise Enrichment Analysis. , 2019, 2019, .		4

#	Article	IF	Citations
469	Genetic Effects on the Correlation Structure of CVD Risk Factors: Exome-Wide Data From a Ghanaian Population. Global Heart, 2017, 12, 133.	2.3	4
470	Genetic programming theory and practice: a fifteen-year trajectory. Genetic Programming and Evolvable Machines, 2020, 21, 169-179.	2.2	4
471	Embracing study heterogeneity for finding genetic interactions in largeâ€scale research consortia. Genetic Epidemiology, 2020, 44, 52-66.	1.3	4
472	Conservation machine learning. BioData Mining, 2020, 13, 9.	4.0	4
473	How Computational Experiments Can Improve Our Understanding of the Genetic Architecture of Common Human Diseases. Artificial Life, 2020, 26, 23-37.	1.3	4
474	Symbolic-regression boosting. Genetic Programming and Evolvable Machines, 2021, 22, 357-381.	2.2	4
475	Harnessing electronic health records to study emerging environmental disasters: a proof of concept with perfluoroalkyl substances (PFAS). Npj Digital Medicine, 2021, 4, 122.	10.9	4
476	Systems Biology Modeling in Human Genetics Using Petri Nets and Grammatical Evolution. Lecture Notes in Computer Science, 2004, , 392-401.	1.3	4
477	Inferring Human Phenotype Networks from Genome-Wide Genetic Associations. Lecture Notes in Computer Science, 2013, , 23-34.	1.3	4
478	Image feature learning with a genetic programming autoencoder. , 2020, , .		4
479	SGP-DT. , 2020, , .		4
480	Epistatic Interactions in Genetic Regulation of t-PA and PAI-1 Levels in a Ghanaian Population. PLoS ONE, 2011, 6, e16639.	2.5	4
481	Translational Bioinformatics: Biobanks in the Precision Medicine Era. , 2019, , .		4
482	A screening-testing approach for detecting gene-environment interactions using sequential penalized and unpenalized multiple logistic regression. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 183-94.	0.7	4
483	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
484	Mask functions for the symbolic modeling of epistasis using genetic programming. , 2008, , .		3
485	LÃ©vy-Flight Genetic Programming: Towards a New Mutation Paradigm. Lecture Notes in Computer Science, 2012, , 38-49.	1.3	3
486	Optimal Use of Biological Expert Knowledge from Literature Mining in Ant Colony Optimization for Analysis of Epistasis in Human Disease. Lecture Notes in Computer Science, 2013, , 129-140.	1.3	3

#	Article	IF	Citations
487	Message prioritization of epidemic forwarding in delay-tolerant networks. , 2014, , .		3
488	Delay-tolerant networks and network coding: Comparative studies on simulated and real-device experiments. Computer Networks, 2015, 83, 349-362.	5.1	3
489	Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. PLoS Genetics, 2017, 13, e1006945.	3.5	3
490	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.	4.4	3
491	Attribute tracking. , 2018, , .		3
492	Exploration of a diversity of computational and statistical measures of association for genome-wide genetic studies. BioData Mining, 2019, 12, 14.	4.0	3
493	Why mind-body medicine is poised to set a new standard for clinical research. Journal of Clinical Epidemiology, 2019, 116, 167-170.	5.0	3
494	Testing the assumptions of parametric linear models: the need for biological data mining in disciplines such as human genetics. BioData Mining, 2019, 12, 6.	4.0	3
495	Automated discovery of test statistics using genetic programming. Genetic Programming and Evolvable Machines, 2019, 20, 127-137.	2.2	3
496	Ten important roles for academic leaders to promote equity, diversity, and inclusion in data science. BioData Mining, 2021, 14, 22.	4.0	3
497	Towards effective GP multi-class classification based on dynamic targets. , 2021, , .		3
498	Artificial Immune Systems for Epistasis Analysis in Human Genetics. Lecture Notes in Computer Science, 2010, , 194-204.	1.3	3
499	The Role of Mutations in Whole Genome Duplication. Lecture Notes in Computer Science, 2012, , 122-133.	1.3	3
500	Supervising Random Forest Using Attribute Interaction Networks. Lecture Notes in Computer Science, 2013, , 104-116.	1.3	3
501	TRAINING THE NEXT GENERATION OF QUANTITATIVE BIOLOGISTS IN THE ERA OF BIG DATA. , 2014, , .		3
502	Evolution of Active Categorical Image Classification via Saccadic Eye Movement. Lecture Notes in Computer Science, 2016, , 581-590.	1.3	3
503	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.	0.7	3
504	Detection of linear and nonlinear dependencies in time series using the method of surrogate data in S-PLUS. Computer Methods and Programs in Biomedicine, 2000, 63, 117-121.	4.7	2

#	Article	IF	Citations
505	Linear dynamic features of ambulatory blood pressure in a population-based study. Blood Pressure Monitoring, 2004, 9, 259-267.	0.8	2
506	Multifactor dimensionality reduction analysis identifies specific nucleotide patterns promoting genetic polymorphisms. BioData Mining, 2009, 2, 2.	4.0	2
507	Identification of SNPs associated with variola virus virulence. BioData Mining, 2013, 6, 3.	4.0	2
508	A multi-core parallelization strategy for statistical significance testing in learning classifier systems. Evolutionary Intelligence, 2013, 6, 127-134.	3.6	2
509	Effect of Genetic Variants, Especially CYP2C9 and VKORC1, on the Pharmacology of Warfarin. Seminars in Thrombosis and Hemostasis, 2013, 39, 112-112.	2.7	2
510	BUILDING THE NEXT GENERATION OF QUANTITATIVE BIOLOGISTS. , 2013, , .		2
511	Editorial (Thematic Issue: Pharmacogenetics and Molecular Medicine: â€œSo Close and Yet So Farâ€). Current Molecular Medicine, 2014, 14, 803-804.	1.3	2
512	Combining functional genomics strategies identifies modular heterogeneity of breast cancer intrinsic subtypes. BioData Mining, 2014, 7, 27.	4.0	2
513	Delay-tolerant networks with network coding: How well can we simulate real devices?. , 2014, , .		2
514	GENOME-WIDE GENETIC INTERACTION ANALYSIS OF GLAUCOMA USING EXPERT KNOWLEDGE DERIVED FROM HUMAN PHENOTYPE NETWORKS. , 2014, , .		2
515	Testing multiple hypotheses through IMP weighted FDR based on a genetic functional network with application to a new zebrafish transcriptome study. BioData Mining, 2015, 8, 17.	4.0	2
516	Bicliques in Graphs with Correlated Edges: From Artificial to Biological Networks. Lecture Notes in Computer Science, 2016, , 138-155.	1.3	2
517	On metaâ€•and megaâ€analyses for geneâ€“environment interactions. Genetic Epidemiology, 2017, 41, 876-886.	1.3	2
518	Leveraging putative enhancer-promoter interactions to investigate two-way epistasis in Type 2 Diabetes GWAS. , 2018, , .		2
519	How computational thought experiments can improve our understanding of the genetic architecture of common human diseases. , 2018, , .		2
520	A multidimensional genetic programming approach for identifying epsistatic gene interactions. , 2018, , .		2
521	EBIC. , 2019, , .		2
522	Anticancer Therapy at the End of Life: Lessons From a Community Cancer Institute. Journal of Palliative Care, 2021, 36, 87-92.	1.0	2

#	Article	IF	Citations
523	Lossless integration of multiple electronic health records for identifying pleiotropy using summary statistics. Nature Communications, 2021, 12, 168.	12.8	2
524	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.	2.3	2
525	EBIC.JL. , 2021, , .		2
526	A Model Free Method to Generate Human Genetics Datasets with Complex Gene-Disease Relationships. Lecture Notes in Computer Science, 2010, , 74-85.	1.3	2
527	An Analysis of New Expert Knowledge Scaling Methods for Biologically Inspired Computing. Lecture Notes in Computer Science, 2011, , 286-293.	1.3	2
528	Cell-Based Metrics Improve the Detection of Gene-Gene Interactions Using Multifactor Dimensionality Reduction. Lecture Notes in Computer Science, 2013, , 200-211.	1.3	2
529	Data Science Approaches to Pharmacogenetics. Current Molecular Medicine, 2014, 14, 805-813.	1.3	2
530	Population Exploration on Genotype Networks in Genetic Programming. Lecture Notes in Computer Science, 2014, , 424-433.	1.3	2
531	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
532	Genome-wide genetic interaction analysis of glaucoma using expert knowledge derived from human phenotype networks. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 207-18.	0.7	2
533	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
534	Gene-Interaction-Sensitive enrichment analysis in congenital heart disease. BioData Mining, 2022, 15, 4.	4.0	2
535	Basic Statistics. Current Protocols in Human Genetics, 2003, 37, Appendix 3M.	3.5	1
536	Analysis of Geneâ€Gene Interactions. Current Protocols in Human Genetics, 2003, 39, Unit 1.14.	3.5	1
537	Development and evaluation of an open-ended computational evolution system for the creation of digital organisms with complex genetic architecture. , 2009, , .		1
538	Nature-inspired algorithms for the genetic analysis of epistasis in common human diseases: Theoretical assessment of wrapper vs. filter approaches. , 2009, , .		1
539	Artificial Evolution Methods in the Biological and Biomedical Sciences. Journal of Artificial Evolution and Applications, 2009, 2009, 1-1.	1.8	1
540	O3-06-01: Association analysis of candidate SNPs on hippocampal volume and shape in mild cognitive impairment and older adults with cognitive complaints. , 2010, 6, S137-S138.		1

#	Article	IF	Citations
541	Mining beyond the exome. BioData Mining, 2011, 4, 14.	4.0	1
542	Data mining and the evolution of biological complexity. BioData Mining, 2011, 4, 7.	4.0	1
543	Random artificial incorporation of noise in a learning classifier system environment. , 2011, , .		1
544	Coevolution of rules and topology in cellular automata. , 2013, , .		1
545	Dissecting the obesity disease landscape: Identifying gene-gene interactions that are highly associated with body mass index. , 2014, , .		1
546	Learning Classifier Systems: The Rise of Genetics-Based Machine Learning in Biomedical Data Mining. , 2014, , 265-311.		1
547	Critical properties of cellular automata with evolving network topologies. , 2015, , .		1
548	Two-Dimensional Enrichment Analysis for Mining High-Level Imaging Genetic Associations. Lecture Notes in Computer Science, 2015, 9250, 115-124.	1.3	1
549	AN INTEGRATED NETWORK APPROACH TO IDENTIFYING BIOLOGICAL PATHWAYS AND ENVIRONMENTAL EXPOSURE INTERACTIONS IN COMPLEX DISEASES. , 2016, , .		1
550	Evolutionarily derived networks to inform disease pathways. Genetic Epidemiology, 2017, 41, 866-875.	1.3	1
551	NO-BOUNDARY THINKING IN BIOINFORMATICS. , 2017, 22, 646-648.		1
552	GPU Accelerated Browser for Neuroimaging Genomics. Neuroinformatics, 2018, 16, 393-402.	2.8	1
553	Evolutionary computation. , 2018, , .		1
554	Solution and Fitness Evolution (SAFE): A Study of Multiobjective Problems. , 2019, , .		1
555	Strategies for improving performance of evolutionary biclustering algorithm EBIC. , 2019, , .		1
556	A comparison of two workflows for regulome and transcriptomeâ€based prioritization of genetic variants associated with myocardial mass. Genetic Epidemiology, 2019, 43, 717-726.	1.3	1
557	Gamorithm. IEEE Transactions on Games, 2020, 12, 115-118.	1.4	1
558	Translational Bioinformatics: Integrating Electronic Health Record and Omics Data. , 2020, , .		1

#	Article	IF	Citations
559	An Automated Functional Annotation Pipeline That Rapidly Prioritizes Clinically Relevant Genes for Autism Spectrum Disorder. International Journal of Molecular Sciences, 2020, 21, 9029.	4.1	1
560	Empowering the data science scientist. BioData Mining, 2021, 14, 8.	4.0	1
561	Socio-cognitive Evolution Strategies. Lecture Notes in Computer Science, 2021, , 329-342.	1.3	1
562	Epistasis Analysis Using Artificial Intelligence. Methods in Molecular Biology, 2015, 1253, 327-346.	0.9	1
563	A semantic genetic programming framework based on dynamic targets. Genetic Programming and Evolvable Machines, 2021, 22, 463-493.	2.2	1
564	An Open-Ended Computational Evolution Strategy for Evolving Parsimonious Solutions to Human Genetics Problems. Lecture Notes in Computer Science, 2011, , 313-320.	1.3	1
565	Ten simple rules for writing a paper about scientific software. PLoS Computational Biology, 2020, 16, e1008390.	3.2	1
566	Mask Functions for the Symbolic Modeling of Epistasis Using Genetic Programming. , 2008, 2008, 339-346.		1
567	Systems genetics of alcoholism. Alcohol Research, 2008, 31, 14-25.	1.0	1
568	Comparing Different Adverse Effects Among Multiple Drugs Using FAERS Data. Studies in Health Technology and Informatics, 2017, 245, 1268.	0.3	1
569	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.	2.9	1
570	Quantitative Trait Linkage Analysis. , 0, , 237-253.		0
571	Towards human-human-computer interaction for biologically-inspired problem-solving in human genetics. , 2007, , .		0
572	Exploratory Visual Analysis of Statistical Results from Microarray Experiments Comparing High and Low Grade Glioma. Cancer Informatics, 2007, 5, 117693510700500.	1.9	0
573	Analysis of Complex Datasets. , 0, , 207-222.		0
574	The spatial dimension in biological data mining. BioData Mining, 2011, 4, 6.	4.0	0
575	The central role of biological data mining in connecting diverse disciplines. BioData Mining, 2013, 6, 14.	4.0	0
576	A simple multi-core parallelization strategy for learning classifier system evaluation. , 2013, , .		0

#	Article	IF	Citations
577	Bipartite networks to study the genotype-to-phenotype relationship in cellular automata models. , 2013, , .		0
578	Testing multiple hypotheses through IMP weighted FDR based on a genetic functional network with application to a new zebrafish transcriptome study. , 2014, , .		0
579	O brave new world that has such machines in it. BioData Mining, 2014, 7, 26.	4.0	0
580	Innovation is often unnerving: the door into summer. BioData Mining, 2014, 7, 12.	4.0	0
581	First complex, then simple. BioData Mining, 2014, 7, 13.	4.0	0
582	The Critical Need for Computational Methods and Software for Simulating Complex Genetic and Genomic Data. Genetic Epidemiology, 2015, 39, 1-1.	1.3	0
583	Prediction of relevant biomedical documents: a human microbiome case study. BioData Mining, 2015, 8, 28.	4.0	0
584	Pareto Inspired Multi-objective Rule Fitness for Adaptive Rule-based Machine Learning. , 2016, , .		0
585	Artificial intelligence: more human with human. BioData Mining, 2017, 10, 34.	4.0	0
586	Reading Between the Genes: Computational Models to Discover Function from Noncoding DNA. , 2018, , .		0
587	Comparing adverse effects of Hepatitis C drugs using FAERS data. , 2018, , .		0
588	Retrieving Impressions from Semantic Memory Modeled with Associative Pulsing Neural Networks. , 2018, , .		0
589	Grammatical Evolution Strategies for Bioinformatics and Systems Genomics. , 2018, , 395-405.		0
590	Bootstrapped Sparse Canonical Correlation Analysis. , 2018, , 101-117.		0
591	Integration of Molecular and Cellular Pathogenesis. , 2018, , 243-249.		0
592	Gene-Gene Interactions: An Essential Component to Modeling Complexity for Precision Medicine. , 2019, , 171-177.		0
593	Discovering test statistics using genetic programming. , 2019, , .		0
594	WellExplorer: an integrative resource linking hydraulic fracturing chemicals with hormonal pathways and geographic location. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	0

#	Article	IF	Citations
595	Integration of molecular and cellular pathogenesis - a bioinformatics approach. , 2020, , 201-207.		0
596	Ten important roles for academic leaders in data science. BioData Mining, 2020, 13, 18.	4.0	0
597	1 Personalized medicine. , 2020, , 1-14.		0
598	REGENS: an open source Python package for simulating realistic autosomal genotypes. Journal of Open Source Software, 2021, 6, 2743.	4.6	0
599	The Translational Machine: A novel machineâ€learning approach to illuminate complex genetic architectures. Genetic Epidemiology, 2021, 45, 485-536.	1.3	0
600	Rapid prototyping of evolution-driven biclustering methods in Julia. , 2021, , .		0
601	Integration of Molecular and Cellular Pathogenesis: A Bioinformatics Approach. , 2009, , 219-224.		0
602	Sexual Recombination in Self-Organizing Interaction Networks. Lecture Notes in Computer Science, 2010, , 41-50.	1.3	0
603	Integration of Molecular and Cellular Pathogenesis. , 2010, , 153-158.		0
604	Employing Publically Available Biological Expert Knowledge from Protein-Protein Interaction Information. Lecture Notes in Computer Science, 2010, , 395-406.	1.3	0
605	Validating a Threshold-Based Boolean Model of Regulatory Networks on a Biological Organism. Lecture Notes in Computer Science, 2011, , 59-68.	1.3	0
606	Addressing the Challenges of Detecting Epistasis in Genome-Wide Association Studies of Common Human Diseases Using Biological Expert Knowledge. , 2011, , 128-147.		0
607	MICROBIOME STUDIES: ANALYTICAL TOOLS AND TECHNIQUES. , 2011, , .		0
608	Artificial Immune Systems Perform Valuable Work When Detecting Epistasis in Human Genetic Datasets. Lecture Notes in Computer Science, 2012, , 189-200.	1.3	0
609	Models of Gene Regulation: Integrating Modern Knowledge into the Random Boolean Network Framework. , 2014, , 43-57.		0
610	Translational Epidemiology, Biostatistics and Informatics. , 2014, , 633-657.		0
611	SESSION INTRODUCTION: CHARACTERIZING THE IMPORTANCE OF ENVIRONMENTAL EXPOSURES, INTERACTIONS BETWEEN THE ENVIRONMENT AND GENETIC ARCHITECTURE, AND GENETIC INTERACTIONS: NEW METHODS FOR UNDERSTANDING THE ETIOLOGY OF COMPLEX TRAITS AND DISEASE. , 2014, , .		0
612	EVE: Cloud-Based Annotation of Human Genetic Variants. Lecture Notes in Computer Science, 2017, , 83-95.	1.3	0

#	Article	IF	Citations
613	Improving the Reproducibility of Genetic Association Results Using Genotype Resampling Methods. Lecture Notes in Computer Science, 2017, , 96-108.	1.3	0
614	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
615	Workshop during the Pacific Symposium of Biocomputing, Jan 3-7, 2019: Reading between the genes: interpreting non-coding DNA in high-throughput. , 2018, , .		0
616	Translational informatics of population health: How large biomolecular and clinical datasets unite. , 2018, , .		0
617	New Pathways in Coevolutionary Computation. Genetic and Evolutionary Computation, 2020, , 295-305.	1.0	0
618	Coevolving Artistic Images Using OMNIREP. Lecture Notes in Computer Science, 2020, , 165-178.	1.3	0
619	Large scale biomedical data analysis with tree-based automated machine learning. , 2020, , .		0
620	Addressing the Challenges of Detecting Epistasis in Genome-Wide Association Studies of Common Human Diseases Using Biological Expert Knowledge. , 0, , 725-744.		0
621	Solving Complex Problems in Human Genetics Using Nature-Inspired Algorithms Requires Strategies which Exploit Domain-Specific Knowledge. , 0, , 1867-1881.		0
622	Automated discovery of test statistics using genetic programming. Genetic Programming and Evolvable Machines, 2019, 20, 127-137.	2.2	0
623	Human Intrigue: Meta-analysis approaches for big questions with big data while shaking up the peer review process. , 2021, , .		0
624	Solving Complex Problems in Human Genetics using Nature-Inspired Algorithms Requires Strategies which Exploit Domain-Specific Knowledge. , 0, , 166-180.		0
625	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, .	3.3	0
626	Novel digital approaches to the assessment of problematic opioid use. BioData Mining, 2022, 15, .	4.0	0