Qing Lu

List of Publications by Year
in descending order

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56 papers	660 citations	759233 12 h-index	642732 23 g-index
57 all docs	57 docs citations	57 times ranked	1490 citing authors

#	Article	IF	Citations
1	Expectile Neural Networks for Genetic Data Analysis of Complex Diseases. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 352-359.	3.0	2
2	Genome-wide Association Meta-analysis of Childhood and Adolescent Internalizing Symptoms. Journal of the American Academy of Child and Adolescent Psychiatry, 2022, 61, 934-945.	0.5	26
3	Explainable deep transfer learning model for disease risk prediction using high-dimensional genomic data. PLoS Computational Biology, 2022, 18, e1010328.	3.2	7
4	Setâ€based genetic association and interaction tests for survival outcomes based on weighted V statistics. Genetic Epidemiology, 2021, 45, 46-63.	1.3	2
5	Applying probability calibration to ensemble methods to predict 2-year mortality in patients with DLBCL. BMC Medical Informatics and Decision Making, 2021, 21, 14.	3.0	5
6	Polygenic Risk for Insomnia in Adolescents of Diverse Ancestry. Frontiers in Genetics, 2021, 12, 654717.	2.3	4
7	Genetic association study of childhood aggression across raters, instruments, and age. Translational Psychiatry, 2021, 11, 413.	4.8	31
8	A goodness-of-fit test based on neural network sieve estimators. Statistics and Probability Letters, 2021, 174, 109100.	0.7	5
9	Probability calibration-based prediction of recurrence rate in patients with diffuse large B-cell lymphoma. BioData Mining, 2021, 14, 38.	4.0	3
10	Multiâ€marker genetic association and interaction tests with intervalâ€censored survival outcomes. Genetic Epidemiology, 2021, 45, 860-873.	1.3	0
11	A conditional autoregressive model for genetic association analysis accounting for genetic heterogeneity. Statistics in Medicine, 2021, 41, 517.	1.6	1
12	A multi-locus predictiveness curve and its summary assessment for genetic risk prediction. Statistical Methods in Medical Research, 2020, 29, 44-56.	1.5	0
13	Multiplier method estimates of the population of men who have sex with men: the effect of privacy protection. Journal of Public Health, 2020, 42, 429-434.	1.8	2
14	The postnatal presence of human chorionic gonadotropin in preterm infants and its potential inverse association with retinopathy of prematurity. Pediatric Research, 2020, 87, 558-563.	2.3	6
15	Multi-kernel linear mixed model with adaptive lasso for prediction analysis on high-dimensional multi-omics data. Bioinformatics, 2020, 36, 1785-1794.	4.1	25
16	Multikernel linear mixed model with adaptive lasso for complex phenotype prediction. Statistics in Medicine, 2020, 39, 1311-1327.	1.6	9
17	Considering Genetic Heterogeneity in the Association Analysis Finds Genes Associated With Nicotine Dependence. Frontiers in Genetics, 2019, 10, 448.	2.3	4
18	An integrative U method for joint analysis of multi-level omic data. BMC Genetics, 2019, 20, 40.	2.7	2

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19	Sleep quality mediating the association of personality traits and quality of life among underground workers and surface workers of Chinese coal mine: A multi-group SEM with latent response variable mediation analysis. Psychiatry Research, 2019, 272, 196-205.	3.3	7
20	Statistical Methods and Software for Substance Use and Dependence Genetic Research. Current Genomics, 2019, 20, 172-183.	1.6	0
21	An ensemble-based likelihood ratio approach for family-based genomic risk prediction. Journal of Zhejiang University: Science B, 2018, 19, 935-947.	2.8	0
22	Detecting Rare Mutations with Heterogeneous Effects Using a Family-Based Genetic Random Field Method. Genetics, 2018, 210, 463-476.	2.9	4
23	Joint analysis of genetic and epigenetic data using a conditional autoregressive model. BMC Genetics, 2018, 19, 71.	2.7	1
24	Genetic risk prediction using a spatial autoregressive model with adaptive lasso. Statistics in Medicine, 2018, 37, 3764-3775.	1.6	4
25	A generalized association test based on U statistics. Bioinformatics, 2017, 33, 1963-1971.	4.1	11
26	Genome-Wide Association Studies of a Broad Spectrum of Antisocial Behavior. JAMA Psychiatry, 2017, 74, 1242.	11.0	174
27	A functional Uâ€statistic method for association analysis of sequencing data. Genetic Epidemiology, 2017, 41, 636-643.	1.3	5
28	Risk Prediction Modeling on Family-Based Sequencing Data Using a Random Field Method. Genetics, 2017, 207, 63-73.	2.9	8
29	Detecting Gene-Gene Interactions Associated with Multiple Complex Traits with U-Statistics. Current Genomics, 2016, 17, 403-415.	1.6	2
30	Testing Allele Transmission of an SNP Set Using a Familyâ€Based Generalized Genetic Random Field Method. Genetic Epidemiology, 2016, 40, 341-351.	1.3	4
31	A Clustered Multiclass Likelihoodâ€Ratio Ensemble Method for Familyâ€Based Association Analysis Accounting for Phenotypic Heterogeneity. Genetic Epidemiology, 2016, 40, 512-519.	1.3	3
32	A weighted U statistic for association analyses considering genetic heterogeneity. Statistics in Medicine, 2016, 35, 2802-2814.	1.6	7
33	Uncovering Local Trends in Genetic Effects of Multiple Phenotypes via Functional Linear Models. Genetic Epidemiology, 2016, 40, 210-221.	1.3	10
34	A Three-Way Interaction among Maternal and Fetal Variants Contributing to Congenital Heart Defects. Annals of Human Genetics, 2016, 80, 20-31.	0.8	9
35	Genome-wide joint analysis of single-nucleotide variant sets and gene expression for hypertension and related phenotypes. BMC Proceedings, 2016, 10, 125-129.	1.6	3
36	Risk Prediction Modeling of Sequencing Data Using a Forward Random Field Method. Scientific Reports, 2016, 6, 21120.	3.3	7

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37	The impact of genetic structure on sequencing analysis. BMC Proceedings, 2016, 10, 171-174.	1.6	1
38	Risk prediction models for oral clefts allowing for phenotypic heterogeneity. Frontiers in Genetics, 2015, 6, 264.	2.3	7
39	A Powerful Nonparametric Statistical Framework for Family-Based Association Analyses. Genetics, 2015, 200, 69-78.	2.9	2
40	Analysis pipeline for the epistasis search Ã¢â‚¬â€œ statistical versus biological filtering. Frontiers in Genetics, 2014, 5, 106.	2.3	57
41	GWGGI: software for genome-wide gene-gene interaction analysis. BMC Genetics, 2014, 15, 101.	2.7	7
42	A Generalized Genetic Random Field Method for the Genetic Association Analysis of Sequencing Data. Genetic Epidemiology, 2014, 38, 242-253.	1.3	13
43	Modeling and testing for joint association using a genetic random field model. Biometrics, 2014, 70, 471-479.	1.4	13
44	A non-parametric approach for detecting gene-gene interactions associated with age-at-onset outcomes. BMC Genetics, 2014, 15, 79.	2.7	3
45	Comparison of Frozen and Unfrozen Blood Spots for Gene Expression Studies. Journal of Pediatrics, 2014, 164, 189-191.e1.	1.8	10
46	A WeightedU-Statistic for Genetic Association Analyses of Sequencing Data. Genetic Epidemiology, 2014, 38, 699-708.	1.3	10
47	Functional Analysis of Variance for Association Studies. PLoS ONE, 2014, 9, e105074.	2.5	24
48	Bridge: a GUI package for genetic risk prediction. BMC Genetics, 2013, 14, 122.	2.7	0
49	A Likelihood Ratioâ€Based Mannâ€Whitney Approach Finds Novel Replicable Joint Gene Action for Type 2 Diabetes. Genetic Epidemiology, 2012, 36, 583-593.	1.3	15
50	Detecting genetic interactions for quantitative traits with U-statistics. Genetic Epidemiology, 2011, 35, n/a-n/a.	1.3	22
51	A clustered optimal ROC curve method for family-based genetic risk prediction. Statistics and Its Interface, 2011, 4, 373-380.	0.3	1
52	Using the Optimal Robust Receiver Operating Characteristic (ROC) Curve for Predictive Genetic Tests. Biometrics, 2010, 66, 586-593.	1.4	12
53	Bagging Optimal ROC Curve Method for Predictive Genetic Tests, with an Application for Rheumatoid Arthritis. Journal of Biopharmaceutical Statistics, 2010, 20, 401-414.	0.8	5
54	The effect of multiple genetic variants in predicting the risk of type 2 diabetes. BMC Proceedings, 2009, 3, S49.	1.6	13

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55	Using the Optimal Receiver Operating Characteristic Curve to Design a Predictive Genetic Test, Exemplified with Type 2 Diabetes. American Journal of Human Genetics, 2008, 82, 641-651.	6.2	52
56	Neuralâ€network transformation models for counting processes. Statistical Analysis and Data Mining, 0, , .	2.8	0