Yalu Wen

List of Publications by Year
in descending order

28 papers	218 citations	1307594 7 h-index	1125743 13 g-index
30 all docs	30 docs citations	30 times ranked	353 citing authors

#	Article	IF	Citations
1	A penalized linear mixed model with generalized method of moments for prediction analysis on high-dimensional multi-omics data. Briefings in Bioinformatics, 2022, 23, .	6.5	3
2	Explainable deep transfer learning model for disease risk prediction using high-dimensional genomic data. PLoS Computational Biology, 2022, 18, e1010328.	3.2	7
3	A Bayesian linear mixed model for prediction of complex traits. Bioinformatics, 2021, 36, 5415-5423.	4.1	4
4	A conditional autoregressive model for genetic association analysis accounting for genetic heterogeneity. Statistics in Medicine, 2021, 41, 517.	1.6	1
5	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
6	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
7	Multikernel linear mixed model with adaptive lasso for complex phenotype prediction. Statistics in Medicine, 2020, 39, 1311-1327.	1.6	9
8	A U-statistics for integrative analysis of multilayer omics data. Bioinformatics, 2020, 36, 2365-2374.	4.1	1
9	The prognostic landscape of interactive biological processes presents treatment responses in cancer. EBioMedicine, 2019, 41, 120-133.	6.1	6
10	Genetic risk prediction using a spatial autoregressive model with adaptive lasso. Statistics in Medicine, 2018, 37, 3764-3775.	1.6	4
11	Risk Prediction Modeling on Family-Based Sequencing Data Using a Random Field Method. Genetics, 2017, 207, 63-73.	2.9	8
12	Detecting Gene-Gene Interactions Associated with Multiple Complex Traits with U-Statistics. Current Genomics, 2016, 17, 403-415.	1.6	2
13	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
14	Detection of differentially methylated regions in whole genome bisulfite sequencing data using local Getis-Ord statistics. Bioinformatics, 2016, 32, 3396-3404.	4.1	27
15	Risk Prediction Modeling of Sequencing Data Using a Forward Random Field Method. Scientific Reports, 2016, 6, 21120.	3.3	7
16	Risk prediction models for oral clefts allowing for phenotypic heterogeneity. Frontiers in Genetics, 2015, 6, 264.	2.3	7
17	A social marketing approach to promoting healthful eating and physical activity in low-income and ethnically diverse schools. Health Education Journal, 2015, 74, 351-363.	1.2	7
18	The Michigan *Healthy School Action Tools* Process Generates Improvements in School Nutrition Policies and Practices, and Student Dietary Intake. Health Promotion Practice, 2015, 16, 401-410.	1.6	14

#	ARTICLE	IF	CITATIONS
19	Project FIT: A School, Community and Social Marketing Intervention Improves Healthy Eating Among Low-Income Elementary School Children. Journal of Community Health, 2015, 40, 815-826.	3.8	32
20	A Single-Array-Based Method for Detecting Copy Number Variants Using Affymetrix High Density SNP Arrays and its Application to Breast Cancer. Cancer Informatics, 2014, 13s4, CIN.S15203.	1.9	0
21	A Multiclass Likelihood Ratio Approach for Genetic Risk Prediction Allowing for Phenotypic Heterogeneity. Genetic Epidemiology, 2013, 37, 715-725.	1.3	6
22	Effects of Changes in Lunch-Time Competitive Foods, Nutrition Practices, and Nutrition Policies on Low-Income Middle-School Children's Diets. Childhood Obesity, 2013, 9, 509-523.	1.5	24
23	A Bivariate Mannâ€Whitney Approach for Unraveling Genetic Variants and Interactions Contributing to Comorbidity. Genetic Epidemiology, 2013, 37, 248-255.	1.3	1
24	Catching the Genomic Wave in Oligonucleotide Single-Nucleotide Polymorphism Arrays by Modeling Sequence Binding. Journal of Computational Biology, 2013, 20, 514-523.	1.6	2
25	An Imputation Approach for Oligonucleotide Microarrays. PLoS ONE, 2013, 8, e58677.	2.5	4
26	MA-SNP -- A New Genotype Calling Method for Oligonucleotide SNP Arrays Modeling the Batch Effect with a Normal Mixture Model. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.6	0
27	Some Critical Data Quality Control Issues ofÂOligoarrays. Computational Biology, 2010, , 39-59.	0.2	0
28	Hybridization modeling of oligonucleotide SNP arrays for accurate DNA copy number estimation. Nucleic Acids Research, 2009, 37, e117-e117.	14.5	12