

Yalu Wen

List of Publications by Year in descending order

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Version: 2024-02-01

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	Project FIT: A School, Community and Social Marketing Intervention Improves Healthy Eating Among Low-Income Elementary School Children. <i>Journal of Community Health</i> , 2015, 40, 815-826.	3.8	32
2	Detection of differentially methylated regions in whole genome bisulfite sequencing data using local Getis-Ord statistics. <i>Bioinformatics</i> , 2016, 32, 3396-3404.	4.1	27
3	Multi-kernel linear mixed model with adaptive lasso for prediction analysis on high-dimensional multi-omics data. <i>Bioinformatics</i> , 2020, 36, 1785-1794.	4.1	25
4	Effects of Changes in Lunch-Time Competitive Foods, Nutrition Practices, and Nutrition Policies on Low-Income Middle-School Children's Diets. <i>Childhood Obesity</i> , 2013, 9, 509-523.	1.5	24
5	The Michigan <i>Healthy School Action Tools</i> Process Generates Improvements in School Nutrition Policies and Practices, and Student Dietary Intake. <i>Health Promotion Practice</i> , 2015, 16, 401-410.	1.6	14
6	Hybridization modeling of oligonucleotide SNP arrays for accurate DNA copy number estimation. <i>Nucleic Acids Research</i> , 2009, 37, e117-e117.	14.5	12
7	Multikernel linear mixed model with adaptive lasso for complex phenotype prediction. <i>Statistics in Medicine</i> , 2020, 39, 1311-1327.	1.6	9
8	Risk Prediction Modeling on Family-Based Sequencing Data Using a Random Field Method. <i>Genetics</i> , 2017, 207, 63-73.	2.9	8
9	Risk prediction models for oral clefts allowing for phenotypic heterogeneity. <i>Frontiers in Genetics</i> , 2015, 6, 264.	2.3	7
10	A social marketing approach to promoting healthful eating and physical activity in low-income and ethnically diverse schools. <i>Health Education Journal</i> , 2015, 74, 351-363.	1.2	7
11	Risk Prediction Modeling of Sequencing Data Using a Forward Random Field Method. <i>Scientific Reports</i> , 2016, 6, 21120.	3.3	7
12	Explainable deep transfer learning model for disease risk prediction using high-dimensional genomic data. <i>PLoS Computational Biology</i> , 2022, 18, e1010328.	3.2	7
13	A Multiclass Likelihood Ratio Approach for Genetic Risk Prediction Allowing for Phenotypic Heterogeneity. <i>Genetic Epidemiology</i> , 2013, 37, 715-725.	1.3	6
14	The prognostic landscape of interactive biological processes presents treatment responses in cancer. <i>EBioMedicine</i> , 2019, 41, 120-133.	6.1	6
15	An Imputation Approach for Oligonucleotide Microarrays. <i>PLoS ONE</i> , 2013, 8, e58677.	2.5	4
16	Genetic risk prediction using a spatial autoregressive model with adaptive lasso. <i>Statistics in Medicine</i> , 2018, 37, 3764-3775.	1.6	4
17	A Bayesian linear mixed model for prediction of complex traits. <i>Bioinformatics</i> , 2021, 36, 5415-5423.	4.1	4
18	A Clustered Multiclass Likelihood Ratio Ensemble Method for Family-Based Association Analysis Accounting for Phenotypic Heterogeneity. <i>Genetic Epidemiology</i> , 2016, 40, 512-519.	1.3	3

#	ARTICLE	IF	CITATIONS
19	A penalized linear mixed model with generalized method of moments for prediction analysis on high-dimensional multi-omics data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	3
20	Catching the Genomic Wave in Oligonucleotide Single-Nucleotide Polymorphism Arrays by Modeling Sequence Binding. <i>Journal of Computational Biology</i> , 2013, 20, 514-523.	1.6	2
21	Detecting Gene-Gene Interactions Associated with Multiple Complex Traits with U-Statistics. <i>Current Genomics</i> , 2016, 17, 403-415.	1.6	2
22	A Bivariate Mann-Whitney Approach for Unraveling Genetic Variants and Interactions Contributing to Comorbidity. <i>Genetic Epidemiology</i> , 2013, 37, 248-255.	1.3	1
23	A U-statistics for integrative analysis of multilayer omics data. <i>Bioinformatics</i> , 2020, 36, 2365-2374.	4.1	1
24	A conditional autoregressive model for genetic association analysis accounting for genetic heterogeneity. <i>Statistics in Medicine</i> , 2021, 41, 517.	1.6	1
25	MA-SNP -- A New Genotype Calling Method for Oligonucleotide SNP Arrays Modeling the Batch Effect with a Normal Mixture Model. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.6	0
26	A Single-Array-Based Method for Detecting Copy Number Variants Using Affymetrix High Density SNP Arrays and its Application to Breast Cancer. <i>Cancer Informatics</i> , 2014, 13s4, CIN.S15203.	1.9	0
27	A multi-locus predictiveness curve and its summary assessment for genetic risk prediction. <i>Statistical Methods in Medical Research</i> , 2020, 29, 44-56.	1.5	0
28	Some Critical Data Quality Control Issues of Oligoarrays. <i>Computational Biology</i> , 2010, , 39-59.	0.2	0