Jung-Ying Tzeng

List of Publications by Year
in descending order

53	3,300	687363 13	182427 51
papers	citations	h-index	g-index

57	57	57	7887
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Phylogeny-guided microbiome OTU-specific association test (POST). Microbiome, 2022, 10, .	11.1	2
2	Gene-set integrative analysis of multi-omics data using tensor-based association test. Bioinformatics, 2021, 37, 2259-2265.	4.1	6
3	An Integrative Co-localization (INCO) Analysis for SNV and CNV Genomic Features With an Application to Taiwan Biobank Data. Frontiers in Genetics, 2021, 12, 709555.	2.3	2
4	SEAGLE: A Scalable Exact Algorithm for Large-Scale Set-Based Gene-Environment Interaction Tests in Biobank Data. Frontiers in Genetics, 2021, 12, 710055.	2.3	2
5	Copy number variation (CNV) identification and association study on 3,928 Alzheimer's disease whole genome sequencing data from the Alzheimer's Disease Sequencing Project (ADSP).. Alzheimer's and Dementia, 2021, 17 Suppl 3, e052721.	0.8	0
6	Association test using Copy Number Profile Curves (CONCUR) enhances power in rare copy number variant analysis. PLoS Computational Biology, 2020, 16, e1007797.	3.2	6
7	The association between neuraxial anesthesia and the development of childhood asthma â€“ a secondary analysis of the newborn epigenetics study cohort. Current Medical Research and Opinion, 2020, 36, 1025-1032.	1.9	4
8	Robust kernel association testing (RobKAT). Genetic Epidemiology, 2020, 44, 272-282.	1.3	2
9	Effective SNP ranking improves the performance of eQTL mapping. Genetic Epidemiology, 2020, 44, 611-619.	1.3	2
10	Identifying individual risk rare variants using protein structure guided local tests (POINT). PLoS Computational Biology, 2019, 15, e1006722.	3.2	11
11	Efficient Signal Inclusion With Genomic Applications. Journal of the American Statistical Association, 2019, 114, 1787-1799.	3.1	4
12	Genetic loci determining total immunoglobulin E levels from birth through adulthood. Allergy: European Journal of Allergy and Clinical Immunology, 2019, 74, 621-625.	5.7	2
13	Reference equations for spirometry in healthyÂAsian children aged 5 to 18 years inÂTaiwan. World Allergy Organization Journal, 2019, 12, 100074.	3.5	26
14	Cadmium exposure increases the risk of juvenile obesity: a human and zebrafish comparative study. International Journal of Obesity, 2018, 42, 1285-1295.	3.4	54
15	Reexamining Dis/Similarity-Based Tests for Rare-Variant Association with Case-Control Samples. Genetics, 2018, 209, 105-113.	2.9	0
16	Rejoinder to â€œA Note on Testing and Estimation in Marker-set Association Study Using Semiparametric Quantile Regression Kernel Machineâ€• Biometrics, 2018, 74, 767-768.	1.4	1
17	On the substructure controls in rare variant analysis: Principal components or variance components?. Genetic Epidemiology, 2018, 42, 276-287.	1.3	10
18	Inference on phenotypeâ€specific effects of genes using multivariate kernel machine regression. Genetic Epidemiology, 2018, 42, 64-79.	1.3	1

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19	A Powerful Test for SNP Effects on Multivariate Binary Outcomes Using Kernel Machine Regression. Statistics in Biosciences, 2018, 10, 117-138.	1.2	7
20	Rare Variants Association Analysis in Large-Scale Sequencing Studies at the Single Locus Level. PLoS Computational Biology, 2016, 12, e1004993.	3.2	11
21	Testing and Estimation in Marker-Set Association Study Using Semiparametric Quantile Regression Kernel Machine. Biometrics, 2016, 72, 364-371.	1.4	8
22	Acrossâ€Platform Imputation of DNA Methylation Levels Incorporating Nonlocal Information Using Penalized Functional Regression. Genetic Epidemiology, 2016, 40, 333-340.	1.3	10
23	Detection of Geneâ€“Gene Interactions Using Multistage Sparse and Low-Rank Regression. Biometrics, 2016, 72, 85-94.	1.4	12
24	A Penalized Likelihood Approach for Investigating Geneâ€“Drug Interactions in Pharmacogenetic Studies. Biometrics, 2015, 71, 529-537.	1.4	0
25	A Fast Multipleâ€Kernel Method With Applications to Detect Geneâ€Environment Interaction. Genetic Epidemiology, 2015, 39, 456-468.	1.3	10
26	A New Method for Detecting Associations with Rare Copy-Number Variants. PLoS Genetics, 2015, 11, e1005403.	3.5	14
27	Assessing Gene-Environment Interactions for Common and Rare Variants with Binary Traits Using Gene-Trait Similarity Regression. Genetics, 2015, 199, 695-710.	2.9	27
28	Proper Use of Allele-Specific Expression Improves Statistical Power forcis-eQTL Mapping with RNA-Seq Data. Journal of the American Statistical Association, 2015, 110, 962-974.	3.1	52
29	Complete Effectâ€Profile Assessment in Association Studies With Multiple Genetic and Multiple Environmental Factors. Genetic Epidemiology, 2015, 39, 122-133.	1.3	8
30	Module-Based Association Analysis for Omics Data with Network Structure. PLoS ONE, 2015, 10, e0122309.	2.5	5
31	Pathway-Guided Identification of Gene-Gene Interactions. Annals of Human Genetics, 2014, 78, 478-491.	0.8	4
32	Heritability and genomics of gene expression in peripheral blood. Nature Genetics, 2014, 46, 430-437.	21.4	370
33	Integrative gene set analysis of multi-platform data with sample heterogeneity. Bioinformatics, 2014, 30, 1501-1507.	4.1	10
34	Gene-level pharmacogenetic analysis on survival outcomes using gene-trait similarity regression. Annals of Applied Statistics, 2014, 8, 1232-1255.	1.1	9
35	Analysis of Gene-Gene Interactions Using Gene-Trait Similarity Regression. Human Heredity, 2014, 78, 17-26.	0.8	4
36	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067

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37	Statistical Considerations in Biosimilar Assessment Using Biosimilarity Index. Journal of Bioequivalence & Bioavailability, 2013, 05, 209-214.	0.1	5
38	Establishment of reference standards in biosimilar studies. GaBI Journal, 2013, 2, 173-177.	0.3	3
39	Combining an Evolution-guided Clustering Algorithm and Haplotype-based LRT in Family Association Studies. BMC Genetics, 2011, 12, 48.	2.7	3
40	Studying Gene and Gene-Environment Effects of Uncommon and Common Variants on Continuous Traits: A Marker-Set Approach Using Gene-Trait Similarity Regression. American Journal of Human Genetics, 2011, 89, 277-288.	6.2	74
41	On the Aggregation of Multimarker Information for Marker-Set and Sequencing Data Analysis: Genotype Collapsing vs. Similarity Collapsing. Frontiers in Genetics, 2011, 2, 110.	2.3	10
42	Evaluating haplotype effects in caseâ€control studies via penalizedâ€likelihood approaches: prospective or retrospective analysis?. Genetic Epidemiology, 2010, 34, 892-911.	1.3	4
43	A comprehensive approach to haplotype-specific analysis by penalized likelihood. European Journal of Human Genetics, 2010, 18, 95-103.	2.8	12
44	Haplotype-Based Pharmacogenetic Analysis for Longitudinal Quantitative Traits in the Presence of Dropout. Journal of Biopharmaceutical Statistics, 2010, 20, 334-350.	0.8	3
45	Geneâ€Trait Similarity Regression for Multimarkerâ€Based Association Analysis. Biometrics, 2009, 65, 822-832.	1.4	45
46	A Regressionâ€based Association Test for Caseâ€control Studies that Uses Inferred Ancestral Haplotype Similarity. Annals of Human Genetics, 2009, 73, 520-526.	0.8	6
47	Haplotype-Based Association Analysis via Variance-Components Score Test. American Journal of Human Genetics, 2007, 81, 927-938.	6.2	69
48	Regression-Based Association Analysis with Clustered Haplotypes through Use of Genotypes. American Journal of Human Genetics, 2006, 78, 231-242.	6.2	79
49	A two-stage design for multiple testing in large-scale association studies. Journal of Human Genetics, 2006, 51, 523-532.	2.3	9
50	Evolutionaryâ€based grouping of haplotypes in association analysis. Genetic Epidemiology, 2005, 28, 220-231.	1.3	44
51	On the Identification of Disease Mutations by the Analysis of Haplotype Similarity and Goodness of Fit. American Journal of Human Genetics, 2003, 72, 891-902.	6.2	127
52	Outlier Detection and False Discovery Rates for Whole-Genome DNA Matching. Journal of the American Statistical Association, 2003, 98, 236-246.	3.1	27
53	Comparing the performance of two indices for spatial model selection: application to two mortality data. Statistics in Medicine, 2000, 19, 1915-1930.	1.6	14