

Chen-An Tsai

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

1,011
citations

516710

16
h-index

434195

31
g-index

39
all docs

39
docs citations

39
times ranked

1457
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimation of False Discovery Rates in Multiple Testing: Application to Gene Microarray Data. <i>Biometrics</i> , 2003, 59, 1071-1081.	1.4	138
2	Reproducibility of microarray data: a further analysis of microarray quality control (MAQC) data. <i>BMC Bioinformatics</i> , 2007, 8, 412.	2.6	121
3	Multivariate analysis of variance test for gene set analysis. <i>Bioinformatics</i> , 2009, 25, 897-903.	4.1	92
4	Analysis of variance components in gene expression data. <i>Bioinformatics</i> , 2004, 20, 1436-1446.	4.1	78
5	Sample size for gene expression microarray experiments. <i>Bioinformatics</i> , 2005, 21, 1502-1508.	4.1	63
6	Testing for differentially expressed genes with microarray data. <i>Nucleic Acids Research</i> , 2003, 31, 52e-52.	14.5	62
7	Development of biomarker classifiers from high-dimensional data. <i>Briefings in Bioinformatics</i> , 2009, 10, 537-546.	6.5	54
8	Alterations in gene expression profiles and the DNA-damage response in ionizing radiation-exposed TK6 cells. <i>Environmental and Molecular Mutagenesis</i> , 2005, 45, 188-205.	2.2	48
9	Sarcosine Therapy for Obsessive Compulsive Disorder. <i>Journal of Clinical Psychopharmacology</i> , 2011, 31, 369-374.	1.4	34
10	Asymptomatic ratio for seasonal H1N1 influenza infection among schoolchildren in Taiwan. <i>BMC Infectious Diseases</i> , 2014, 14, 80.	2.9	33
11	Multi-class clustering and prediction in the analysis of microarray data. <i>Mathematical Biosciences</i> , 2005, 193, 79-100.	1.9	32
12	Gene selection with multiple ordering criteria. <i>BMC Bioinformatics</i> , 2007, 8, 74.	2.6	29
13	Gene Selection for Sample Classifications in Microarray Experiments. <i>DNA and Cell Biology</i> , 2004, 23, 607-614.	1.9	28
14	Significance analysis of groups of genes in expression profiling studies. <i>Bioinformatics</i> , 2007, 23, 2104-2112.	4.1	28
15	Random forests-based differential analysis of gene sets for gene expression data. <i>Gene</i> , 2013, 518, 179-186.	2.2	21
16	Association of response to hepatitis B vaccination and survival in dialysis patients. <i>BMC Nephrology</i> , 2012, 13, 97.	1.8	20
17	Serological Evidence of Subclinical Transmission of the 2009 Pandemic H1N1 Influenza Virus Outside of Mexico. <i>PLoS ONE</i> , 2011, 6, e14555.	2.5	16
18	Significance Analysis of ROC Indices for Comparing Diagnostic Markers: Applications to Gene Microarray Data. <i>Journal of Biopharmaceutical Statistics</i> , 2004, 14, 985-1003.	0.8	13

#	ARTICLE	IF	CITATIONS
19	An Integrated Tree-Based Classification Approach to Prognostic Grouping with Application to Localized Melanoma Patients. <i>Journal of Biopharmaceutical Statistics</i> , 2007, 17, 445-460.	0.8	12
20	Comparison of hepatitis B surface antibody decay rates after vaccination between hemodialysis and peritoneal dialysis patients. <i>Vaccine</i> , 2011, 29, 3738-3741.	3.8	12
21	Serological response and persistence in schoolchildren with high baseline seropositive rate after receiving 2009 pandemic influenza A(H1N1) vaccine. <i>Vaccine</i> , 2011, 29, 617-623.	3.8	9
22	Gene set analysis using sufficient dimension reduction. <i>BMC Bioinformatics</i> , 2016, 17, 74.	2.6	7
23	Development of predictive signatures for treatment selection in precision medicine with survival outcomes. <i>Pharmaceutical Statistics</i> , 2018, 17, 105-116.	1.3	7
24	A Generalized Additive Model For Microarray Gene Expression Data Analysis. <i>Journal of Biopharmaceutical Statistics</i> , 2004, 14, 553-573.	0.8	6
25	Factors associated with infection by 2009 pandemic H1N1 influenza virus during different phases of the epidemic. <i>International Journal of Infectious Diseases</i> , 2011, 15, e695-e701.	3.3	6
26	An approximate approach to sample size determination in bioequivalence testing with multiple pharmacokinetic responses. <i>Statistics in Medicine</i> , 2014, 33, 3300-3317.	1.6	6
27	Incorporating the number of true null hypotheses to improve power in multiple testing: application to gene microarray data. <i>Journal of Statistical Computation and Simulation</i> , 2007, 77, 757-767.	1.2	5
28	Kernel estimation for adjusted α -values in multiple testing. <i>Computational Statistics and Data Analysis</i> , 2007, 51, 3885-3897.	1.2	5
29	Identifying Gene Set Association Enrichment Using the Coefficient of Intrinsic Dependence. <i>PLoS ONE</i> , 2013, 8, e58851.	2.5	5
30	MAVTgsa: An R Package for Gene Set (Enrichment) Analysis. <i>BioMed Research International</i> , 2014, 2014, 1-11.	1.9	5
31	Database Composition Can Affect the Structure-Activity Relationship Prediction. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2006, 69, 1527-1540.	2.3	3
32	Effect of p53 genotype on gene expression profiles in murine liver. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 640, 54-73.	1.0	3
33	Recursive Feature Selection with Significant Variables of Support Vectors. <i>Computational and Mathematical Methods in Medicine</i> , 2012, 2012, 1-12.	1.3	3
34	An Exhaustive Scan Method for SNP Main Effects and SNP-SNP Interactions Over Highly Homozygous Genomes. <i>Journal of Computational Biology</i> , 2017, 24, 1254-1264.	1.6	3
35	Multispectra CWT-Based Algorithm (MCWT) in Mass Spectra for Peak Extraction. <i>Journal of Biopharmaceutical Statistics</i> , 2008, 18, 869-882.	0.8	2
36	Gene Set Correlation Analysis and Visualization Using Gene Expression Data. <i>Current Bioinformatics</i> , 2021, 16, 406-421.	1.5	2

#	ARTICLE	IF	CITATIONS
37	Quality assessment of gene expression data. , 0, , .		0
38	Addressing Loss of Efficiency Due to Misclassification Error in Enriched Clinical Trials for the Evaluation of Targeted Therapies Based on the Cox Proportional Hazards Model. PLoS ONE, 2016, 11, e0153525.	2.5	0