Chen-An Tsai

List of Publications by Year
in descending order

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	Gene Set Correlation Analysis and Visualization Using Gene Expression Data. Current Bioinformatics, 2021, 16, 406-421.	1.5	2
2	Development of predictive signatures for treatment selection in precision medicine with survival outcomes. Pharmaceutical Statistics, 2018, 17, 105-116.	1.3	7
3	An Exhaustive Scan Method for SNP Main Effects and SNPâ€‰Ã—â€‰SNP Interactions Over Highly Homozygous Genomes. Journal of Computational Biology, 2017, 24, 1254-1264.	1.6	3
4	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
5	Gene set analysis using sufficient dimension reduction. BMC Bioinformatics, 2016, 17, 74.	2.6	7
6	MAVTgsa: An R Package for Gene Set (Enrichment) Analysis. BioMed Research International, 2014, 2014, 1-11.	1.9	5
7	An approximate approach to sample size determination in bioequivalence testing with multiple pharmacokinetic responses. Statistics in Medicine, 2014, 33, 3300-3317.	1.6	6
8	Asymptomatic ratio for seasonal H1N1 influenza infection among schoolchildren in Taiwan. BMC Infectious Diseases, 2014, 14, 80.	2.9	33
9	Random forests-based differential analysis of gene sets for gene expression data. Gene, 2013, 518, 179-186.	2.2	21
10	Identifying Gene Set Association Enrichment Using the Coefficient of Intrinsic Dependence. PLoS ONE, 2013, 8, e58851.	2.5	5
11	Recursive Feature Selection with Significant Variables of Support Vectors. Computational and Mathematical Methods in Medicine, 2012, 2012, 1-12.	1.3	3
12	Association of response to hepatitis B vaccination and survival in dialysis patients. BMC Nephrology, 2012, 13, 97.	1.8	20
13	Serological response and persistence in schoolchildren with high baseline seropositive rate after receiving 2009 pandemic influenza A(H1N1) vaccine. Vaccine, 2011, 29, 617-623.	3.8	9
14	Comparison of hepatitis B surface antibody decay rates after vaccination between hemodialysis and peritoneal dialysis patients. Vaccine, 2011, 29, 3738-3741.	3.8	12
15	Factors associated with infection by 2009 pandemic H1N1 influenza virus during different phases of the epidemic. International Journal of Infectious Diseases, 2011, 15, e695-e701.	3.3	6
16	Sarcosine Therapy for Obsessive Compulsive Disorder. Journal of Clinical Psychopharmacology, 2011, 31, 369-374.	1.4	34
17	Serological Evidence of Subclinical Transmission of the 2009 Pandemic H1N1 Influenza Virus Outside of Mexico. PLoS ONE, 2011, 6, e14555.	2.5	16
18	Development of biomarker classifiers from high-dimensional data. Briefings in Bioinformatics, 2009, 10, 537-546.	6.5	54

#	ARTICLE	IF	CITATIONS
19	Multivariate analysis of variance test for gene set analysis. Bioinformatics, 2009, 25, 897-903.	4.1	92
20	Effect of p53 genotype on gene expression profiles in murine liver. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2008, 640, 54-73.	1.0	3
21	Multispectra CWT-Based Algorithm (MCWT) in Mass Spectra for Peak Extraction. Journal of Biopharmaceutical Statistics, 2008, 18, 869-882.	0.8	2
22	Significance analysis of groups of genes in expression profiling studies. Bioinformatics, 2007, 23, 2104-2112.	4.1	28
23	An Integrated Tree-Based Classification Approach to Prognostic Grouping with Application to Localized Melanoma Patients. Journal of Biopharmaceutical Statistics, 2007, 17, 445-460.	0.8	12
24	Incorporating the number of true null hypotheses to improve power in multiple testing: application to gene microarray data. Journal of Statistical Computation and Simulation, 2007, 77, 757-767.	1.2	5
25	Kernel estimation for adjusted -values in multiple testing. Computational Statistics and Data Analysis, 2007, 51, 3885-3897.	1.2	5
26	Reproducibility of microarray data: a further analysis of microarray quality control (MAQC) data. BMC Bioinformatics, 2007, 8, 412.	2.6	121
27	Gene selection with multiple ordering criteria. BMC Bioinformatics, 2007, 8, 74.	2.6	29
28	Database Composition Can Affect the Structure–Activity Relationship Prediction. Journal of Toxicology and Environmental Health - Part A: Current Issues, 2006, 69, 1527-1540.	2.3	3
29	Alterations in gene expression profiles and the DNA-damage response in ionizing radiation-exposed TK6 cells. Environmental and Molecular Mutagenesis, 2005, 45, 188-205.	2.2	48
30	Sample size for gene expression microarray experiments. Bioinformatics, 2005, 21, 1502-1508.	4.1	63
31	Multi-class clustering and prediction in the analysis of microarray data. Mathematical Biosciences, 2005, 193, 79-100.	1.9	32
32	Gene Selection for Sample Classifications in Microarray Experiments. DNA and Cell Biology, 2004, 23, 607-614.	1.9	28
33	Analysis of variance components in gene expression data. Bioinformatics, 2004, 20, 1436-1446.	4.1	78
34	Significance Analysis of ROC Indices for Comparing Diagnostic Markers: Applications to Gene Microarray Data. Journal of Biopharmaceutical Statistics, 2004, 14, 985-1003.	0.8	13
35	A Generalized Additive Model For Microarray Gene Expression Data Analysis. Journal of Biopharmaceutical Statistics, 2004, 14, 553-573.	0.8	6
36	Estimation of False Discovery Rates in Multiple Testing: Application to Gene Microarray Data. Biometrics, 2003, 59, 1071-1081.	1.4	138

#	Article	IF	Citations
37	Testing for differentially expressed genes with microarray data. Nucleic Acids Research, 2003, 31, 52e-52.	14.5	62
38	Quality assessment of gene expression data. , 0, , .		0