

# Huann-Sheng Chen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5222453/publications.pdf>

Version: 2024-02-01

40  
papers

1,227  
citations

516215

16  
h-index

377514

34  
g-index

41  
all docs

41  
docs citations

41  
times ranked

1931  
citing authors

#	ARTICLE	IF	CITATIONS
1	Joint analysis of two microarray gene-expression data sets to select lung adenocarcinoma marker genes. BMC Bioinformatics, 2004, 5, 81.	1.2	228
2	Association Between Two Unlinked Loci at 8q24 and Prostate Cancer Risk Among European Americans. Journal of the National Cancer Institute, 2007, 99, 1525-1533.	3.0	126
3	Evaluation of Gene Association Methods for Coexpression Network Construction and Biological Knowledge Discovery. PLoS ONE, 2012, 7, e50411.	1.1	100
4	Metabolic Profiling of the Sink-to-Source Transition in Developing Leaves of Quaking Aspen. Plant Physiology, 2004, 136, 3364-3375.	2.3	81
5	Transmission/Disequilibrium Test Based on Haplotype Sharing for Tightly Linked Markers. American Journal of Human Genetics, 2003, 73, 566-579.	2.6	73
6	Improved confidence interval for average annual percent change in trend analysis. Statistics in Medicine, 2017, 36, 3059-3074.	0.8	59
7	Entropy-based information gain approaches to detect and to characterize gene-gene and gene-environment interactions/correlations of complex diseases. Genetic Epidemiology, 2011, 35, 706-721.	0.6	54
8	Predicting US and state level cancer counts for the current calendar year. Cancer, 2012, 118, 1100-1109.	2.0	48
9	Predicting US and state level cancer counts for the current calendar year. Cancer, 2012, 118, 1091-1099.	2.0	44
10	Early estimates of SEER cancer incidence, 2014. Cancer, 2017, 123, 2524-2534.	2.0	39
11	Clustering of trend data using joinpoint regression models. Statistics in Medicine, 2014, 33, 4087-4103.	0.8	30
12	Genetic Simulation Resources: a website for the registration and discovery of genetic data simulators. Bioinformatics, 2013, 29, 1101-1102.	1.8	29
13	Genetic Data Simulators and their Applications: An Overview. Genetic Epidemiology, 2015, 39, 2-10.	0.6	26
14	Genetic Simulation Tools for Post-Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	0.6	22
15	A new association test using haplotype similarity. Genetic Epidemiology, 2007, 31, 577-593.	0.6	21
16	Bottom-up GGM algorithm for constructing multilayered hierarchical gene regulatory networks that govern biological pathways or processes. BMC Bioinformatics, 2016, 17, 132.	1.2	19
17	A combined p-value test for multiple hypothesis testing. Journal of Statistical Planning and Inference, 2013, 143, 764-770.	0.4	17
18	Multiple testing in the genomics era: Findings from Genetic Analysis Workshop 15, Group 15. Genetic Epidemiology, 2007, 31, S124-S131.	0.6	14

#	ARTICLE	IF	CITATIONS
19	TF-finder: A software package for identifying transcription factors involved in biological processes using microarray data and existing knowledge base. <i>BMC Bioinformatics</i> , 2010, 11, 425.	1.2	13
20	Early estimates of <sc>SEER</sc> cancer incidence for 2012: Approaches, opportunities, and cautions for obtaining preliminary estimates of cancer incidence. <i>Cancer</i> , 2015, 121, 2053-2062.	2.0	13
21	Twenty years since Joinpoint 1.0: Two major enhancements, their justification, and impact. <i>Statistics in Medicine</i> , 2022, 41, 3102-3130.	0.8	13
22	The Joinpoint-Jump and Joinpoint-Comparability Ratio Model for Trend Analysis with Applications to Coding Changes in Health Statistics. <i>Journal of Official Statistics</i> , 2020, 36, 49-62.	0.1	12
23	Haplotype sharing transmission/disequilibrium tests that allow for genotyping errors. <i>Genetic Epidemiology</i> , 2005, 28, 341-351.	0.6	11
24	Preliminary estimates of SEER cancer incidence for 2013. <i>Cancer</i> , 2016, 122, 1579-1587.	2.0	10
25	Early estimates of cancer incidence for 2015: Expanding to include estimates for white and black races. <i>Cancer</i> , 2018, 124, 2192-2204.	2.0	9
26	Updated Methodology for Projecting U.S.- and State-Level Cancer Counts for the Current Calendar Year: Part II: Evaluation of Incidence and Mortality Projection Methods. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1993-2000.	1.1	9
27	Reply to Knapp and Becker. <i>American Journal of Human Genetics</i> , 2004, 74, 591-593.	2.6	8
28	Genetic Simulation Resources and the GSR Certification Program. <i>Bioinformatics</i> , 2019, 35, 709-710.	1.8	6
29	Updated Methodology for Projecting U.S.- and State-Level Cancer Counts for the Current Calendar Year: Part I: Spatio-temporal Modeling for Cancer Incidence. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1620-1626.	1.1	6
30	A Powerful Method for Combining <i>P</i>-Values in Genomic Studies. <i>Genetic Epidemiology</i> , 2013, 37, 814-819.	0.6	5
31	Developments and challenges in statistical methods in cancer surveillance. <i>Statistics and Its Interface</i> , 2014, 7, 135-151.	0.2	5
32	Data-driven choice of a model selection method in joinpoint regression. <i>Journal of Applied Statistics</i> , 2023, 50, 1992-2013.	0.6	5
33	A combinatorial approach for detecting gene-gene interaction using multiple traits of Genetic Analysis Workshop 16 rheumatoid arthritis data. <i>BMC Proceedings</i> , 2009, 3, S43.	1.8	4
34	Regional differences in tobacco smoking and lung cancer in Portugal in 2018: a population-based analysis using nationwide incidence and mortality data. <i>BMJ Open</i> , 2020, 10, e038937.	0.8	4
35	On the application, reporting, and sharing of in silico simulations for genetic studies. <i>Genetic Epidemiology</i> , 2021, 45, 131-141.	0.6	4
36	Estimation of the exponential mean under type I censored sampling. <i>Journal of Statistical Planning and Inference</i> , 1992, 33, 187-196.	0.4	3

#	ARTICLE	IF	CITATIONS
37	Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. PLoS Genetics, 2017, 13, e1006945.	1.5	3
38	CP*Trends: An Online Tool for Comparing Cohort and Period Trends Across Cancer Sites. American Journal of Epidemiology, 2019, 188, 1361-1370.	1.6	3
39	Genome-wide association tests by using block information in family data. BMC Proceedings, 2007, 1, S149.	1.8	1
40	Efficient L1 estimation and related inferences in linear regression with unknown form of heteroscedasticity. Journal of Nonparametric Statistics, 2002, 14, 607-622.	0.4	0