

Huann-Sheng Chen

List of Publications by Year in descending order

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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 | Data-driven choice of a model selection method in joinpoint regression. <i>Journal of Applied Statistics</i> , 2023, 50, 1992-2013. | 0.6 | 5 |
| 2 | 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 |
| 3 | On the application, reporting, and sharing of in silico simulations for genetic studies. <i>Genetic Epidemiology</i> , 2021, 45, 131-141. | 0.6 | 4 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 8 | CP*Trends: An Online Tool for Comparing Cohort and Period Trends Across Cancer Sites. <i>American Journal of Epidemiology</i> , 2019, 188, 1361-1370. | 1.6 | 3 |
| 9 | Genetic Simulation Resources and the GSR Certification Program. <i>Bioinformatics</i> , 2019, 35, 709-710. | 1.8 | 6 |
| 10 | 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 |
| 11 | Early estimates of SEER cancer incidence, 2014. <i>Cancer</i> , 2017, 123, 2524-2534. | 2.0 | 39 |
| 12 | Improved confidence interval for average annual percent change in trend analysis. <i>Statistics in Medicine</i> , 2017, 36, 3059-3074. | 0.8 | 59 |
| 13 | Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. <i>PLoS Genetics</i> , 2017, 13, e1006945. | 1.5 | 3 |
| 14 | Bottom-up GGM algorithm for constructing multilayered hierarchical gene regulatory networks that govern biological pathways or processes. <i>BMC Bioinformatics</i> , 2016, 17, 132. | 1.2 | 19 |
| 15 | Preliminary estimates of SEER cancer incidence for 2013. <i>Cancer</i> , 2016, 122, 1579-1587. | 2.0 | 10 |
| 16 | Genetic Data Simulators and their Applications: An Overview. <i>Genetic Epidemiology</i> , 2015, 39, 2-10. | 0.6 | 26 |
| 17 | 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 |
| 18 | Genetic Simulation Tools for Post-Genome Wide Association Studies of Complex Diseases. <i>Genetic Epidemiology</i> , 2015, 39, 11-19. | 0.6 | 22 |

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|----|--|-----|-----------|
| 19 | Clustering of trend data using joinpoint regression models. <i>Statistics in Medicine</i> , 2014, 33, 4087-4103. | 0.8 | 30 |
| 20 | Developments and challenges in statistical methods in cancer surveillance. <i>Statistics and Its Interface</i> , 2014, 7, 135-151. | 0.2 | 5 |
| 21 | A combined p-value test for multiple hypothesis testing. <i>Journal of Statistical Planning and Inference</i> , 2013, 143, 764-770. | 0.4 | 17 |
| 22 | Genetic Simulation Resources: a website for the registration and discovery of genetic data simulators. <i>Bioinformatics</i> , 2013, 29, 1101-1102. | 1.8 | 29 |
| 23 | A Powerful Method for Combining p -Values in Genomic Studies. <i>Genetic Epidemiology</i> , 2013, 37, 814-819. | 0.6 | 5 |
| 24 | Evaluation of Gene Association Methods for Coexpression Network Construction and Biological Knowledge Discovery. <i>PLoS ONE</i> , 2012, 7, e50411. | 1.1 | 100 |
| 25 | Predicting US and state level cancer counts for the current calendar year. <i>Cancer</i> , 2012, 118, 1091-1099. | 2.0 | 44 |
| 26 | Predicting US and state level cancer counts for the current calendar year. <i>Cancer</i> , 2012, 118, 1100-1109. | 2.0 | 48 |
| 27 | Entropy-based information gain approaches to detect and to characterize gene-gene and gene-environment interactions/correlations of complex diseases. <i>Genetic Epidemiology</i> , 2011, 35, 706-721. | 0.6 | 54 |
| 28 | 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 |
| 29 | 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 |
| 30 | Association Between Two Unlinked Loci at 8q24 and Prostate Cancer Risk Among European Americans. <i>Journal of the National Cancer Institute</i> , 2007, 99, 1525-1533. | 3.0 | 126 |
| 31 | Genome-wide association tests by using block information in family data. <i>BMC Proceedings</i> , 2007, 1, S149. | 1.8 | 1 |
| 32 | A new association test using haplotype similarity. <i>Genetic Epidemiology</i> , 2007, 31, 577-593. | 0.6 | 21 |
| 33 | Multiple testing in the genomics era: Findings from Genetic Analysis Workshop 15, Group 15. <i>Genetic Epidemiology</i> , 2007, 31, S124-S131. | 0.6 | 14 |
| 34 | Haplotype sharing transmission/disequilibrium tests that allow for genotyping errors. <i>Genetic Epidemiology</i> , 2005, 28, 341-351. | 0.6 | 11 |
| 35 | Metabolic Profiling of the Sink-to-Source Transition in Developing Leaves of Quaking Aspen. <i>Plant Physiology</i> , 2004, 136, 3364-3375. | 2.3 | 81 |
| 36 | Joint analysis of two microarray gene-expression data sets to select lung adenocarcinoma marker genes. <i>BMC Bioinformatics</i> , 2004, 5, 81. | 1.2 | 228 |

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|----|--|-----|-----------|
| 37 | Reply to Knapp and Becker. American Journal of Human Genetics, 2004, 74, 591-593. | 2.6 | 8 |
| 38 | Transmission/Disequilibrium Test Based on Haplotype Sharing for Tightly Linked Markers. American Journal of Human Genetics, 2003, 73, 566-579. | 2.6 | 73 |
| 39 | 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 |
| 40 | Estimation of the exponential mean under type I censored sampling. Journal of Statistical Planning and Inference, 1992, 33, 187-196. | 0.4 | 3 |