

# Yi-Hau Chen

## List of Publications by Year in descending order

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87  
papers

1,357  
citations

411340

20  
h-index

425179

34  
g-index

94  
all docs

94  
docs citations

94  
times ranked

1454  
citing authors

#	ARTICLE	IF	CITATIONS
1	Overlapping group screening for detection of gene-environment interactions with application to TCGA high-dimensional survival genomic data. BMC Bioinformatics, 2022, 23, .	1.2	1
2	Distribution-free regression model selection with a nested spatial correlation structure. Spatial Statistics, 2021, 41, 100476.	0.9	1
3	Implementing horizontal-to-vertical Fourier spectral ratios and spatial correlation in a ground-motion prediction equation to predict site effects. Earthquake Spectra, 2021, 37, 827-856.	1.6	10
4	A novel cross-validation strategy for artificial neural networks using distributed-lag environmental factors. PLoS ONE, 2021, 16, e0244094.	1.1	2
5	Study Protocol for radiation exposure and cancer risk assessment- The Taiwan Nuclear Power Plants and Epidemiology Cohort Study (TNPECS). Journal of Epidemiology, 2021, , .	1.1	0
6	Extensions of the distributed lag non-linear model (DLNM) to account for cumulative mortality. Environmental Science and Pollution Research, 2021, 28, 38679-38688.	2.7	6
7	Quantile function regression analysis for interval censored data, with application to salary survey data. Japanese Journal of Statistics and Data Science, 2021, 4, 999-1018.	0.7	3
8	The Association between Migraine and Depression based on miRNA Biomarkers and Cohort Studies. Current Medicinal Chemistry, 2021, 28, 5648-5656.	1.2	11
9	Network-adjusted Kendall's Tau Measure for Feature Screening with Application to High-dimensional Survival Genomic Data. Bioinformatics, 2021, 37, 2150-2156.	1.8	4
10	microRNA Biomarkers in Clinical Study. Biomolecules, 2021, 11, 1810.	1.8	1
11	Discrete-time survival data with longitudinal covariates. Statistics in Medicine, 2020, 39, 4372-4385.	0.8	3
12	&lt;p&gt;Exploring Diversity of COVID-19 Based on Substitution Distance&lt;/p&gt;. Infection and Drug Resistance, 2020, Volume 13, 3887-3894.	1.1	6
13	Semiparametric copula-based analysis for treatment effects in the presence of treatment switching. Statistics in Medicine, 2020, 39, 2936-2948.	0.8	0
14	Joint analysis of panel count and interval-censored data using distribution-free frailty analysis. Biometrical Journal, 2020, 62, 1164-1175.	0.6	3
15	Interaction screening by Kendall's partial correlation for ultrahigh-dimensional data with survival trait. Bioinformatics, 2020, 36, 2763-2769.	1.8	7
16	The Association between Depression and Gastroesophageal Reflux based on Phylogenetic Analysis of miRNA Biomarkers. Current Medicinal Chemistry, 2020, 27, 6536-6547.	1.2	17
17	Assessing wage status transition and stagnation using quantile transition regression. Annals of Applied Statistics, 2020, 14, .	0.5	0
18	A Novel Regression Analysis Method for Randomly Truncated Strong-Motion Data. Earthquake Spectra, 2019, 35, 977-1001.	1.6	9

#	ARTICLE	IF	CITATIONS
19	Regularized approach for data missing not at random. <i>Statistical Methods in Medical Research</i> , 2019, 28, 134-150.	0.7	7
20	Sample size determination for semiparametric analysis of current status data. <i>Statistical Methods in Medical Research</i> , 2019, 28, 2247-2257.	0.7	1
21	Pseudo and Conditional Score Approach to Joint Analysis of Current Count and Current Status Data. <i>Biometrics</i> , 2018, 74, 1223-1231.	0.8	4
22	Analysis of Survival Data with Dependent Censoring. <i>SpringerBriefs in Statistics</i> , 2018, , .	0.3	38
23	Model Selection for Semiparametric Marginal Mean Regression Accounting for Within-Cluster Subsampling Variability and Informative Cluster Size. <i>Biometrics</i> , 2018, 74, 934-943.	0.8	2
24	Joint model selection of marginal mean regression and correlation structure for longitudinal data with missing outcome and covariates. <i>Biometrical Journal</i> , 2018, 60, 20-33.	0.6	2
25	Overlapping group screening for detection of gene-gene interactions: application to gene expression profiles with survival trait. <i>BMC Bioinformatics</i> , 2018, 19, 335.	1.2	4
26	Introduction to Survival Analysis. <i>SpringerBriefs in Statistics</i> , 2018, , 9-26.	0.3	0
27	Copula Models for Dependent Censoring. <i>SpringerBriefs in Statistics</i> , 2018, , 27-40.	0.3	0
28	Gene Selection and Survival Prediction Under Dependent Censoring. <i>SpringerBriefs in Statistics</i> , 2018, , 57-70.	0.3	0
29	Optimization of Lookup Table Size in Table-Bound Design of Function Computation. , 2018, , .		4
30	Hierarchical Multipartite Function Evaluation. <i>IEEE Transactions on Computers</i> , 2017, 66, 89-99.	2.4	22
31	Joint Regression Analysis of Marginal Quantile and Quantile Association: Application to Longitudinal Body Mass Index in Adolescents. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2017, 66, 1075-1090.	0.5	2
32	Composite marginal quantile regression analysis for longitudinal adolescent body mass index data. <i>Statistics in Medicine</i> , 2017, 36, 3380-3397.	0.8	4
33	Regression analysis for bivariate gap time with missing first gap time data. <i>Lifetime Data Analysis</i> , 2017, 23, 83-101.	0.4	0
34	Subdistribution Regression for Recurrent Events Under Competing Risks: with Application to Shunt Thrombosis Study in Dialysis Patients. <i>Statistics in Biosciences</i> , 2017, 9, 339-356.	0.6	3
35	Estimating links of a network from time to event data. <i>Annals of Applied Statistics</i> , 2017, 11, .	0.5	0
36	A knowledge-based T2-statistic to perform pathway analysis for quantitative proteomic data. <i>PLoS Computational Biology</i> , 2017, 13, e1005601.	1.5	1

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37	Semiparametric regression analysis of recurrent gap times in the presence of competing risks. <i>Statistica Sinica</i> , 2017, , .	0.2	0
38	Gene selection for survival data under dependent censoring: A copula-based approach. <i>Statistical Methods in Medical Research</i> , 2016, 25, 2840-2857.	0.7	55
39	Optimal linear combination of biomarkers for multi-category diagnosis. <i>Statistics in Medicine</i> , 2016, 35, 202-213.	0.8	7
40	Joint analysis of current count and current status data. <i>Journal of Multivariate Analysis</i> , 2016, 143, 153-164.	0.5	4
41	Constrained Maximum Likelihood Estimation for Model Calibration Using Summary-Level Information From External Big Data Sources. <i>Journal of the American Statistical Association</i> , 2016, 111, 107-117.	1.8	87
42	Dissecting multiple imputation from a multi-phase inference perspective: what happens when God's, imputer's and analyst's models are uncongenial?. <i>Statistica Sinica</i> , 2016, , .	0.2	12
43	Model selection for marginal regression analysis of longitudinal data with missing observations and covariate measurement error. <i>Biostatistics</i> , 2015, 16, 740-753.	0.9	6
44	Semiparametric analysis of incomplete current status outcome data under transformation models. <i>Biometrics</i> , 2014, 70, 335-345.	0.8	4
45	Adjustment for Missing Confounders in Studies Based on Observational Databases: 2-Stage Calibration Combining Propensity Scores From Primary and Validation Data. <i>American Journal of Epidemiology</i> , 2014, 180, 308-317.	1.6	33
46	Testing goodness-of-fit for the proportional hazards model based on nested case-control data. <i>Biometrics</i> , 2014, 70, 845-851.	0.8	4
47	A class of semiparametric transformation models for survival data with a cured proportion. <i>Lifetime Data Analysis</i> , 2014, 20, 369-386.	0.4	8
48	The Logistic Regression Model for Gene-Environment Interactions Using Both Case-Parent Trios and Unrelated Case-Controls. <i>Annals of Human Genetics</i> , 2014, 78, 299-305.	0.3	1
49	A functional inference approach for interval-censored data with covariate measurement error. <i>Statistica Sinica</i> , 2014, , .	0.2	0
50	Model selection of generalized estimating equations with multiply imputed longitudinal data. <i>Biometrical Journal</i> , 2013, 55, 899-911.	0.6	28
51	A method for analyzing clustered interval-censored data based on Cox's model. <i>Statistics in Medicine</i> , 2013, 32, 822-832.	0.8	19
52	Using shared genetic controls in studies of gene-environment interactions. <i>Biometrika</i> , 2013, 100, 319-338.	1.3	4
53	Assessing age-at-onset risk factors with incomplete covariate current status data under proportional odds models. <i>Statistics in Medicine</i> , 2013, 32, 2001-2012.	0.8	6
54	A FRAILTY MODEL APPROACH FOR REGRESSION ANALYSIS OF BIVARIATE INTERVAL-CENSORED SURVIVAL DATA. <i>Statistica Sinica</i> , 2013, , .	0.2	1

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55	Assessing Dose-Region Profile of Drug Efficacy: A Multiregional Trial Strategy. <i>Journal of Biopharmaceutical Statistics</i> , 2012, 22, 894-902.	0.4	1
56	Survival Prediction Based on Compound Covariate under Cox Proportional Hazard Models. <i>PLoS ONE</i> , 2012, 7, e47627.	1.1	26
57	Model Selection for Generalized Estimating Equations Accommodating Dropout Missingness. <i>Biometrics</i> , 2012, 68, 1046-1054.	0.8	42
58	Conditional Score Approach to Errors-in-Variable Current Status Data Under the Proportional Odds Model. <i>Scandinavian Journal of Statistics</i> , 2012, 39, 635-644.	0.9	6
59	Maximum likelihood analysis of semicompeting risks data with semiparametric regression models. <i>Lifetime Data Analysis</i> , 2012, 18, 36-57.	0.4	38
60	Nonparametric maximum likelihood analysis of clustered current status data with the gamma-frailty Cox model. <i>Computational Statistics and Data Analysis</i> , 2011, 55, 1053-1060.	0.7	19
61	Semiparametric Marginal Regression Analysis for Dependent Competing Risks Under an Assumed Copula. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2010, 72, 235-251.	1.1	64
62	Association Analysis under Population Stratification: A Two-Stage Procedure Utilizing Population- and Family-Based Analyses. <i>Human Heredity</i> , 2010, 69, 160-170.	0.4	6
63	Analysis of Case-Control Association Studies: SNPs, Imputation and Haplotypes. <i>Statistical Science</i> , 2009, 24, 489-502.	1.6	19
64	Shrinkage Estimators for Robust and Efficient Inference in Haplotype-Based Case-Control Studies. <i>Journal of the American Statistical Association</i> , 2009, 104, 220-233.	1.8	56
65	Weighted Breslow-type and maximum likelihood estimation in semiparametric transformation models. <i>Biometrika</i> , 2009, 96, 591-600.	1.3	36
66	A Bayesian Approach to Evaluating Regional Treatment Effect in a Multiregional Trial. <i>Journal of Biopharmaceutical Statistics</i> , 2009, 19, 900-915.	0.4	10
67	Two-stage analysis for gene-environment interaction utilizing both case-only and family-based analysis. <i>Genetic Epidemiology</i> , 2009, 33, 95-104.	0.6	9
68	Case-cohort analysis with semiparametric transformation models. <i>Journal of Statistical Planning and Inference</i> , 2009, 139, 3706-3717.	0.4	16
69	Associations of Physician Volume and Weekend Admissions With Ischemic Stroke Outcome in Taiwan. <i>Medical Care</i> , 2009, 47, 1018-1025.	1.1	71
70	Simple association analysis combining data from trios/sibships and unrelated controls. <i>Genetic Epidemiology</i> , 2008, 32, 520-527.	0.6	23
71	Retrospective analysis of haplotype-based case-control studies under a flexible model for gene-environment association. <i>Biostatistics</i> , 2008, 9, 81-99.	0.9	22
72	Maximum likelihood inference on a mixed conditionally and marginally specified regression model for genetic epidemiologic studies with two-phase sampling. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2007, 69, 123-142.	1.1	12

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73	A semiparametric pseudo-score method for analysis of two-phase studies with continuous phase-I covariates. <i>Lifetime Data Analysis</i> , 2007, 13, 607-622.	0.4	5
74	HLA typing associated with hepatitis B E antigen seroconversion in children with chronic hepatitis B virus infection: A long-term prospective sibling cohort study in Taiwan. <i>Journal of Pediatrics</i> , 2006, 148, 647-651.e1.	0.9	18
75	Bone Mineral Density in Long-Term Chinese Heart Transplant Recipients: A Cross-Sectional Study. <i>Transplantation Proceedings</i> , 2006, 38, 2141-2144.	0.3	12
76	Multinomial logistic regression approach to haplotype association analysis in population-based case-control studies. <i>BMC Genetics</i> , 2006, 7, 43.	2.7	9
77	The Path Effect in Ground-Motion Variability: An Application of the Variance-Components Technique. <i>Bulletin of the Seismological Society of America</i> , 2006, 96, 1170-1176.	1.1	18
78	Computationally efficient Monte Carlo EM algorithms for generalized linear mixed models. <i>Journal of Statistical Computation and Simulation</i> , 2006, 76, 817-828.	0.7	2
79	New approach to association testing in case-parent designs under informative parental missingness. <i>Genetic Epidemiology</i> , 2004, 27, 131-140.	0.6	29
80	A Pseudoscore Estimator for Regression Problems With Two-Phase Sampling. <i>Journal of the American Statistical Association</i> , 2003, 98, 158-168.	1.8	113
81	SAMPLE SIZE AND OPTIMAL DESIGNS IN STRATIFIED COMPARATIVE TRIALS TO ESTABLISH THE EQUIVALENCE OF TREATMENT EFFECTS AMONG TWO ETHNIC GROUPS. <i>Journal of Biopharmaceutical Statistics</i> , 2002, 12, 553-566.	0.4	1
82	A New Method for Estimation of the Attenuation Relationship with Variance Components. <i>Bulletin of the Seismological Society of America</i> , 2002, 92, 1984-1991.	1.1	70
83	Cox regression in cohort studies with validation sampling. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2002, 64, 51-62.	1.1	31
84	A unified approach to regression analysis under double-sampling designs. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2000, 62, 449-460.	1.1	54
85	Miscellanea. A robust imputation method for surrogate outcome data. <i>Biometrika</i> , 2000, 87, 711-716.	1.3	17
86	Incomplete covariates data in generalized linear models. <i>Journal of Statistical Planning and Inference</i> , 1999, 79, 247-258.	0.4	4
87	Classes of life distributions and renewal counting process. <i>Journal of Applied Probability</i> , 1994, 31, 1110-1115.	0.4	38