Hulin Wu

List of Publications by Year
in descending order

44	1,939	471509	289244
papers	citations	17	40
		h-index	g-index

44	44	44	2153
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	On Identifiability of Nonlinear ODE Models and Applications in Viral Dynamics. SIAM Review, 2011, 53, 3-39.	9.5	412
2	RegNetwork: an integrated database of transcriptional and post-transcriptional regulatory networks in human and mouse. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav095.	3.0	338
3	Hierarchical Bayesian Methods for Estimation of Parameters in a Longitudinal HIV Dynamic System. Biometrics, 2006, 62, 413-423.	1.4	188
4	Parameter Estimation for Differential Equation Models Using a Framework of Measurement Error in Regression Models. Journal of the American Statistical Association, 2008, 103, 1570-1583.	3.1	151
5	Sieve estimation of constant and time-varying coefficients in nonlinear ordinary differential equation models by considering both numerical error and measurement error. Annals of Statistics, 2010, 38, 2351-2387.	2.6	83
6	A study of generalizability of recurrent neural network-based predictive models for heart failure onset risk using a large and heterogeneous EHR data set. Journal of Biomedical Informatics, 2018, 84, 11-16.	4.3	80
7	High-Dimensional ODEs Coupled With Mixed-Effects Modeling Techniques for Dynamic Gene Regulatory Network Identification. Journal of the American Statistical Association, 2011, 106, 1242-1258.	3.1	64
8	Sparse Additive Ordinary Differential Equations for Dynamic Gene Regulatory Network Modeling. Journal of the American Statistical Association, 2014, 109, 700-716.	3.1	64
9	Statistical methods for HIV dynamic studies in AIDS clinical trials. Statistical Methods in Medical Research, 2005, 14, 171-192.	1.5	62
10	Efficient Local Estimation for Time-Varying Coefficients in Deterministic Dynamic Models With Applications to HIV-1 Dynamics. Journal of the American Statistical Association, 2008, 103, 369-384.	3.1	61
11	Semiparametric Time-Varying Coefficients Regression Model for Longitudinal Data. Scandinavian Journal of Statistics, 2005, 32, 21-47.	1.4	51
12	More powerful significant testing for time course gene expression data using functional principal component analysis approaches. BMC Bioinformatics, 2013, 14, 6.	2.6	49
13	Designing acceptance sampling schemes for life testing with mixed censoring. Naval Research Logistics, 2004, 51, 597-612.	2.2	44
14	Systematic identification of transcriptional and post-transcriptional regulations in human respiratory epithelial cells during influenza A virus infection. BMC Bioinformatics, 2014, 15, 336.	2.6	35
15	A content-based dataset recommendation system for researchersâ€"a case study on Gene Expression Omnibus (GEO) repository. Database: the Journal of Biological Databases and Curation, 2020, 2020, 1.	3.0	34
16	A content-based literature recommendation system for datasets to improve data reusability â€" A case study on Gene Expression Omnibus (GEO) datasets. Journal of Biomedical Informatics, 2020, 104, 103399.	4.3	28
17	Numerical Discretizationâ€Based Estimation Methods for Ordinary Differential Equation Models via Penalized Spline Smoothing with Applications in Biomedical Research. Biometrics, 2012, 68, 344-352.	1.4	27
18	Restructured GEO: restructuring Gene Expression Omnibus metadata for genome dynamics analysis. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	17

#	Article	IF	Citations
19	Modeling Genome-Wide Dynamic Regulatory Network in Mouse Lungs with Influenza Infection Using High-Dimensional Ordinary Differential Equations. PLoS ONE, 2014, 9, e95276.	2.5	16
20	Machine learning prediction of the adverse outcome for nontraumatic subarachnoid hemorrhage patients. Annals of Clinical and Translational Neurology, 2020, 7, 2178-2185.	3.7	14
21	Dynamic transcriptional signatures and network responses for clinical symptoms in influenza-infected human subjects using systems biology approaches. Journal of Pharmacokinetics and Pharmacodynamics, 2014, 41, 509-521.	1.8	12
22	Correlation-based iterative clustering methods for time course data: The identification of temporal gene response modules for influenza infection in humans. Infectious Disease Modelling, 2016, 1, 28-39.	1.9	12
23	Vasopressor treatment and mortality following nontraumatic subarachnoid hemorrhage: a nationwide electronic health record analysis. Neurosurgical Focus, 2020, 48, E4.	2.3	12
24	Ion-Current-Based Temporal Proteomic Profiling of Influenza-A-Virus-Infected Mouse Lungs Revealed Underlying Mechanisms of Altered Integrity of the Lung Microvascular Barrier. Journal of Proteome Research, 2016, 15, 540-553.	3.7	11
25	Controllability and stability analysis of large transcriptomic dynamic systems for host response to influenza infection in human. Infectious Disease Modelling, 2016, 1, 52-70.	1.9	9
26	A big data pipeline: Identifying dynamic gene regulatory networks from time-course <i>Gene Expression Omnibus</i> data with applications to influenza infection. Statistical Methods in Medical Research, 2018, 27, 1930-1955.	1.5	9
27	A novel approach for propensity score matching and stratification for multiple treatments: Application to an electronic health record<scp>–derived</scp> study. Statistics in Medicine, 2020, 39, 2308-2323.	1.6	9
28	High-dimensional linear state space models for dynamic microbial interaction networks. PLoS ONE, 2017, 12, e0187822.	2.5	9
29	Diversity in Compartmental Dynamics of Gene Regulatory Networks: The Immune Response in Primary Influenza A Infection in Mice. PLoS ONE, 2015, 10, e0138110.	2.5	8
30	Variable selection for sparse high-dimensional nonlinear regression models by combining nonnegative garrote and sure independence screening. Statistica Sinica, 2014, 24, 1365-1387.	0.3	8
31	A novel group of genes that cause endocrine resistance in breast cancer identified by dynamic gene expression analysis. Oncotarget, 2022, 13, 600-613.	1.8	4
32	Estimation of Smooth Time-Varying Parameters in State Space Models. Journal of Computational and Graphical Statistics, 2007, 16, 813-832.	1.7	3
33	Modelling of hypoxia gene expression for three different cancer cell lines. International Journal of Computational Biology and Drug Design, 2020, 13, 124.	0.3	3
34	Parameter estimation for a type of nonlinear stochastic models observed with error. Computational Statistics and Data Analysis, 2014, 79, 113-119.	1.2	2
35	An informatics research platform to make public gene expression time-course datasets reusable for more scientific discoveries. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	2
36	Mental Health Severity Detection from Psychological Forum Data using Domain-Specific Unlabelled Data. AMIA Summits on Translational Science Proceedings, 2020, 2020, 487-496.	0.4	2

#	Article	IF	Citations
37	Characterization of Symptoms and Symptom Clusters for Type 2 Diabetes Using a Large Nationwide Electronic Health Record Database. Diabetes Spectrum, 2022, 35, 159-170.	1.0	2
38	ImmuneData: an integrated data discovery system for immunology data repositories. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	2
39	Independence screening for high dimensional nonlinear additive ODE models with applications to dynamic gene regulatory networks. Statistics in Medicine, 2018, 37, 2630-2644.	1.6	1
40	Investigation of temporal and spatial heterogeneities of the immune responses to Bordetella pertussis infection in the lung and spleen of mice via analysis and modeling of dynamic microarray gene expression data. Infectious Disease Modelling, 2019, 4, 215-226.	1.9	1
41	HIV Dynamics Modeling and Prediction of Clinical Outcomes in AIDS Clinical Research. , 0, , 81-96.		0
42	Capillary extraction by detecting polarity in circular profiles. IET Image Processing, 2016, 10, 339-348.	2.5	0
43	Modelling of hypoxia gene expression for three different cancer cell lines. International Journal of Computational Biology and Drug Design, 2020, 13, 124.	0.3	0
44	Identifiability analysis of linear ordinary differential equation systems with a single trajectory. Applied Mathematics and Computation, 2022, 430, 127260.	2.2	0