

Hulin Wu

List of Publications by Year in descending order

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44
papers

1,939
citations

471509

17
h-index

289244

40
g-index

44
all docs

44
docs citations

44
times ranked

2153
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of Symptoms and Symptom Clusters for Type 2 Diabetes Using a Large Nationwide Electronic Health Record Database. <i>Diabetes Spectrum</i> , 2022, 35, 159-170.	1.0	2
2	ImmuneData: an integrated data discovery system for immunology data repositories. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	2
3	A novel group of genes that cause endocrine resistance in breast cancer identified by dynamic gene expression analysis. <i>Oncotarget</i> , 2022, 13, 600-613.	1.8	4
4	Identifiability analysis of linear ordinary differential equation systems with a single trajectory. <i>Applied Mathematics and Computation</i> , 2022, 430, 127260.	2.2	0
5	Machine learning prediction of the adverse outcome for nontraumatic subarachnoid hemorrhage patients. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 2178-2185.	3.7	14
6	A content-based dataset recommendation system for researchers—a case study on Gene Expression Omnibus (GEO) repository. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, 1.	3.0	34
7	Modelling of hypoxia gene expression for three different cancer cell lines. <i>International Journal of Computational Biology and Drug Design</i> , 2020, 13, 124.	0.3	3
8	A content-based literature recommendation system for datasets to improve data reusability — A case study on Gene Expression Omnibus (GEO) datasets. <i>Journal of Biomedical Informatics</i> , 2020, 104, 103399.	4.3	28
9	A novel approach for propensity score matching and stratification for multiple treatments: Application to an electronic health record-derived study. <i>Statistics in Medicine</i> , 2020, 39, 2308-2323.	1.6	9
10	Vasopressor treatment and mortality following nontraumatic subarachnoid hemorrhage: a nationwide electronic health record analysis. <i>Neurosurgical Focus</i> , 2020, 48, E4.	2.3	12
11	An informatics research platform to make public gene expression time-course datasets reusable for more scientific discoveries. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	2
12	Modelling of hypoxia gene expression for three different cancer cell lines. <i>International Journal of Computational Biology and Drug Design</i> , 2020, 13, 124.	0.3	0
13	Mental Health Severity Detection from Psychological Forum Data using Domain-Specific Unlabelled Data. <i>AMIA Summits on Translational Science Proceedings</i> , 2020, 2020, 487-496.	0.4	2
14	Investigation of temporal and spatial heterogeneities of the immune responses to <i>Bordetella pertussis</i> infection in the lung and spleen of mice via analysis and modeling of dynamic microarray gene expression data. <i>Infectious Disease Modelling</i> , 2019, 4, 215-226.	1.9	1
15	Restructured GEO: restructuring Gene Expression Omnibus metadata for genome dynamics analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	17
16	Independence screening for high dimensional nonlinear additive ODE models with applications to dynamic gene regulatory networks. <i>Statistics in Medicine</i> , 2018, 37, 2630-2644.	1.6	1
17	A big data pipeline: Identifying dynamic gene regulatory networks from time-course Gene Expression Omnibus data with applications to influenza infection. <i>Statistical Methods in Medical Research</i> , 2018, 27, 1930-1955.	1.5	9
18	A study of generalizability of recurrent neural network-based predictive models for heart failure onset risk using a large and heterogeneous EHR data set. <i>Journal of Biomedical Informatics</i> , 2018, 84, 11-16.	4.3	80

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19	High-dimensional linear state space models for dynamic microbial interaction networks. PLoS ONE, 2017, 12, e0187822.	2.5	9
20	Capillary extraction by detecting polarity in circular profiles. IET Image Processing, 2016, 10, 339-348.	2.5	0
21	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
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	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
24	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
25	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
26	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
27	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
28	Sparse Additive Ordinary Differential Equations for Dynamic Gene Regulatory Network Modeling. Journal of the American Statistical Association, 2014, 109, 700-716.	3.1	64
29	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
30	Parameter estimation for a type of nonlinear stochastic models observed with error. Computational Statistics and Data Analysis, 2014, 79, 113-119.	1.2	2
31	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
32	More powerful significant testing for time course gene expression data using functional principal component analysis approaches. BMC Bioinformatics, 2013, 14, 6.	2.6	49
33	Numerical Discretization-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
34	On Identifiability of Nonlinear ODE Models and Applications in Viral Dynamics. SIAM Review, 2011, 53, 3-39.	9.5	412
35	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
36	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

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37	Parameter Estimation for Differential Equation Models Using a Framework of Measurement Error in Regression Models. <i>Journal of the American Statistical Association</i> , 2008, 103, 1570-1583.	3.1	151
38	Efficient Local Estimation for Time-Varying Coefficients in Deterministic Dynamic Models With Applications to HIV-1 Dynamics. <i>Journal of the American Statistical Association</i> , 2008, 103, 369-384.	3.1	61
39	Estimation of Smooth Time-Varying Parameters in State Space Models. <i>Journal of Computational and Graphical Statistics</i> , 2007, 16, 813-832.	1.7	3
40	Hierarchical Bayesian Methods for Estimation of Parameters in a Longitudinal HIV Dynamic System. <i>Biometrics</i> , 2006, 62, 413-423.	1.4	188
41	Semiparametric Time-Varying Coefficients Regression Model for Longitudinal Data. <i>Scandinavian Journal of Statistics</i> , 2005, 32, 21-47.	1.4	51
42	Statistical methods for HIV dynamic studies in AIDS clinical trials. <i>Statistical Methods in Medical Research</i> , 2005, 14, 171-192.	1.5	62
43	Designing acceptance sampling schemes for life testing with mixed censoring. <i>Naval Research Logistics</i> , 2004, 51, 597-612.	2.2	44
44	HIV Dynamics Modeling and Prediction of Clinical Outcomes in AIDS Clinical Research. , 0, , 81-96.		0