

Hai-Hui Huang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5528712/publications.pdf>

Version: 2024-02-01

24
papers

480
citations

932766

10
h-index

839053

18
g-index

24
all docs

24
docs citations

24
times ranked

553
citing authors

#	ARTICLE	IF	CITATIONS
1	FUZZY DECISION MAKING METHOD BASED ON COCOSO WITH CRITIC FOR FINANCIAL RISK EVALUATION. Technological and Economic Development of Economy, 2020, 26, 695-724.	2.3	108
2	A method to identify trace sulfated IgG N-glycans as biomarkers for rheumatoid arthritis. Nature Communications, 2017, 8, 631.	5.8	85
3	Feature Selection and Cancer Classification via Sparse Logistic Regression with the Hybrid L1/2 +2 Regularization. PLoS ONE, 2016, 11, e0149675.	1.1	55
4	Improved Classification of Blood-Brain-Barrier Drugs Using Deep Learning. Scientific Reports, 2019, 9, 8802.	1.6	46
5	Hybrid L1/2+L2 method for gene selection in the Cox proportional hazards model. Computer Methods and Programs in Biomedicine, 2018, 164, 65-73.	2.6	34
6	Orthopair fuzzy decision-making framework for integrating mobile edge caching scheme preferences. International Journal of Intelligent Systems, 2021, 36, 2229-2266.	3.3	24
7	An integrative analysis system of gene expression using self-paced learning and SCAD-Net. Expert Systems With Applications, 2019, 135, 102-112.	4.4	21
8	SLNL: A novel method for gene selection and phenotype classification. International Journal of Intelligent Systems, 2022, 37, 6283-6304.	3.3	21
9	Clinical Drug Response Prediction by Using a Lq Penalized Network-Constrained Logistic Regression Method. Cellular Physiology and Biochemistry, 2018, 51, 2073-2084.	1.1	12
10	Identification of 13 blood-based gene expression signatures to accurately distinguish tuberculosis from other pulmonary diseases and healthy controls. Bio-Medical Materials and Engineering, 2015, 26, S1837-S1843.	0.4	11
11	Network-Based Logistic Classification with an Enhanced L1/2 Solver Reveals Biomarker and Subnetwork Signatures for Diagnosing Lung Cancer. BioMed Research International, 2015, 2015, 1-7.	0.9	11
12	SPLSN: An efficient tool for survival analysis and biomarker selection. International Journal of Intelligent Systems, 2021, 36, 5845-5865.	3.3	11
13	A novel Cox proportional hazards model for high - dimensional genomic data in cancer prognosis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	1.9	10
14	Cancer classification and biomarker selection via a penalized logsum network-based logistic regression model. Technology and Health Care, 2021, 29, 287-295.	0.5	8
15	Molecular pathway identification using a new L1/2 solver and biological network-constrained model. International Journal of Data Mining and Bioinformatics, 2017, 17, 189.	0.1	7
16	Reply to "Trace N-glycans including sulphated species may originate from various plasma glycoproteins and not necessarily IgG". Nature Communications, 2018, 9, 2915.	5.8	4
17	Protein-protein interaction network construction for cancer using a new L1/2-penalized Net-SVM model. Genetics and Molecular Research, 2016, 15, .	0.3	4
18	When CCN meets MCGDM: optimal cache replacement policy achieved by PRSRV with Pythagorean fuzzy set pair analysis. Artificial Intelligence Review, 0, , 1.	9.7	3

#	ARTICLE	IF	CITATIONS
19	Robust sparse accelerated failure time model for survival analysis. <i>Technology and Health Care</i> , 2018, 26, 55-63.	0.5	2
20	Low-rank and sparse matrix decomposition based on $S_{1/2}$ and $L_{1/2}$ regularizations in dynamic MRI. , 2016, , .		1
21	Integrating molecular interactions and gene expression to identify biomarkers to predict response to tumor necrosis factor inhibitor therapies in rheumatoid arthritis patients. <i>Technology and Health Care</i> , 2022, , 1-7.	0.5	1
22	Integrating molecular interactions and gene expression to identify biomarkers and network modules of chronic obstructive pulmonary disease. <i>Technology and Health Care</i> , 2022, , 1-8.	0.5	1
23	Image Super-Resolution Reconstruction via $L_{1/2}$ and $S_{1/2}$ Regularizations. , 2016, , .		0
24	A Genotype-Based Ensemble Classifier System for Non-Small-Cell Lung Cancer. <i>IEEE Access</i> , 2020, 8, 128509-128518.	2.6	0