

Turki Turki

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

526
citations

840119

11
h-index

794141

19
g-index

64
all docs

64
docs citations

64
times ranked

564
citing authors

#	ARTICLE	IF	CITATIONS
1	A link prediction approach to cancer drug sensitivity prediction. BMC Systems Biology, 2017, 11, 94.	3.0	47
2	Transfer Learning Approaches to Improve Drug Sensitivity Prediction in Multiple Myeloma Patients. IEEE Access, 2017, 5, 7381-7393.	2.6	46
3	A 3D Atrous Convolutional Long Short-Term Memory Network for Background Subtraction. IEEE Access, 2018, 6, 43450-43459.	2.6	46
4	A new advanced in silico drug discovery method for novel coronavirus (SARS-CoV-2) with tensor decomposition-based unsupervised feature extraction. PLoS ONE, 2020, 15, e0238907.	1.1	38
5	Boosting support vector machines for cancer discrimination tasks. Computers in Biology and Medicine, 2018, 101, 236-249.	3.9	35
6	A transfer learning approach via procrustes analysis and mean shift for cancer drug sensitivity prediction. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840014.	0.3	34
7	DLGraph: Malware Detection Using Deep Learning and Graph Embedding. , 2018, , .		25
8	Clinical intelligence: New machine learning techniques for predicting clinical drug response. Computers in Biology and Medicine, 2019, 107, 302-322.	3.9	22
9	Weighted Gene Co-Expression Network Analysis Reveals Dysregulation of Mitochondrial Oxidative Phosphorylation in Eating Disorders. Genes, 2018, 9, 325.	1.0	14
10	SCGRNs: Novel supervised inference of single-cell gene regulatory networks of complex diseases. Computers in Biology and Medicine, 2020, 118, 103656.	3.9	14
11	Learning approaches to improve prediction of drug sensitivity in breast cancer patients. , 2016, 2016, 3314-3320.		13
12	Tensor Decomposition-Based Unsupervised Feature Extraction Applied to Single-Cell Gene Expression Analysis. Frontiers in Genetics, 2019, 10, 864.	1.1	13
13	An empirical study of machine learning algorithms for cancer identification. , 2018, , .		12
14	Machine learning algorithms for predicting drugsâ€™tissues relationships. Expert Systems With Applications, 2019, 127, 167-186.	4.4	12
15	Automatic Classification of Melanoma Skin Cancer with Deep Convolutional Neural Networks. AI, 2022, 3, 512-525.	2.1	12
16	Discriminating the single-cell gene regulatory networks of human pancreatic islets: A novel deep learning application. Computers in Biology and Medicine, 2021, 132, 104257.	3.9	11
17	Inferring Gene Regulatory Networks by Combining Supervised and Unsupervised Methods. , 2016, , .		10
18	Novel Hate Speech Detection Using Word Cloud Visualization and Ensemble Learning Coupled with Count Vectorizer. Applied Sciences (Switzerland), 2022, 12, 6611.	1.3	10

#	ARTICLE	IF	CITATIONS
19	Tensor-Decomposition-Based Unsupervised Feature Extraction in Single-Cell Multiomics Data Analysis. <i>Genes</i> , 2021, 12, 1442.	1.0	8
20	MaxSSmap: a GPU program for mapping divergent short reads to genomes with the maximum scoring subsequence. <i>BMC Genomics</i> , 2014, 15, 969.	1.2	7
21	A New Approach to Link Prediction in Gene Regulatory Networks. <i>Lecture Notes in Computer Science</i> , 2015, , 404-415.	1.0	7
22	MapReduce Algorithms for Inferring Gene Regulatory Networks from Time-Series Microarray Data Using an Information-Theoretic Approach. <i>BioMed Research International</i> , 2017, 2017, 1-8.	0.9	7
23	Generative Adversarial Networks for Stochastic Video Prediction With Action Control. <i>IEEE Access</i> , 2020, 8, 63336-63348.	2.6	6
24	Neurological Disorder Drug Discovery from Gene Expression with Tensor Decomposition. <i>Current Pharmaceutical Design</i> , 2020, 25, 4589-4599.	0.9	6
25	Improved Deep Convolutional Neural Networks via Boosting for Predicting the Quality of In Vitro Bovine Embryos. <i>Electronics (Switzerland)</i> , 2022, 11, 1363.	1.8	6
26	A greedy-based oversampling approach to improve the prediction of mortality in MERS patients. , 2016, , .		5
27	Application of Tensor Decomposition to Gene Expression of Infection of Mouse Hepatitis Virus Can Identify Critical Human Genes and Effective Drugs for SARS-CoV-2 Infection. <i>IEEE Journal on Selected Topics in Signal Processing</i> , 2021, 15, 746-758.	7.3	5
28	Mathematical formulation and application of kernel tensor decomposition based unsupervised feature extraction. <i>Knowledge-Based Systems</i> , 2021, 217, 106834.	4.0	4
29	Novel method for the prediction of drug-drug Interaction based on gene expression profiles. <i>European Journal of Pharmaceutical Sciences</i> , 2021, 160, 105742.	1.9	4
30	Novel feature selection method via kernel tensor decomposition for improved multi-omics data analysis. <i>BMC Medical Genomics</i> , 2022, 15, 37.	0.7	4
31	Reverse Engineering Gene Regulatory Networks Using Graph Mining. <i>Lecture Notes in Computer Science</i> , 2018, , 335-349.	1.0	3
32	Universal Nature of Drug Treatment Responses in Drug-Tissue-Wide Model-Animal Experiments Using Tensor Decomposition-Based Unsupervised Feature Extraction. <i>Frontiers in Genetics</i> , 2020, 11, 695.	1.1	3
33	Tensor-Decomposition-Based Unsupervised Feature Extraction Applied to Prostate Cancer Multiomics Data. <i>Genes</i> , 2020, 11, 1493.	1.0	3
34	Unsupervised tensor decomposition-based method to extract candidate transcription factors as histone modification bookmarks in post-mitotic transcriptional reactivation. <i>PLoS ONE</i> , 2021, 16, e0251032.	1.1	3
35	Weighted Maximum Variance Dimensionality Reduction. <i>Lecture Notes in Computer Science</i> , 2014, , 11-20.	1.0	3
36	Top-k Parametrized Boost. <i>Lecture Notes in Computer Science</i> , 2014, , 91-98.	1.0	3

#	ARTICLE	IF	CITATIONS
37	A Learning Framework to Improve Unsupervised Gene Network Inference. Lecture Notes in Computer Science, 2016, , 28-42.	1.0	3
38	Reverse Engineering Gene Regulatory Networks Using Sampling and Boosting Techniques. Lecture Notes in Computer Science, 2017, , 63-77.	1.0	1
39	Reverse Engineering Regulatory Networks in Cells Using a Dynamic Bayesian Network and Mutual Information Scoring Function. , 2017, , .		1
40	Effects of Collagenâ€™Glycosaminoglycan Mesh on Gene Expression as Determined by Using Principal Component Analysis-Based Unsupervised Feature Extraction. Polymers, 2021, 13, 4117.	2.0	1
41	An Omnibus Test for Differential Distribution Analysis of Continuous Microbiome Data. IEEE Access, 2021, 9, 100029-100039.	2.6	0
42	End-to-End Deep Learning for Detecting Metastatic Breast Cancer in Axillary Lymph Node from Digital Pathology Images. Lecture Notes in Computer Science, 2021, , 343-353.	1.0	0
43	Integrated Analysis of Tissue-Specific Gene Expression in Diabetes by Tensor Decomposition Can Identify Possible Associated Diseases. Genes, 2022, 13, 1097.	1.0	0