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List of Publications by Year in descending order

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Version: 2024-02-01

794141 840119 43 526 11 19 citations h-index g-index papers 64 64 64 564 docs citations citing authors all docs times ranked

#	Article	IF	Citations
1	Novel feature selection method via kernel tensor decomposition for improved multi-omics data analysis. BMC Medical Genomics, 2022, 15, 37.	0.7	4
2	Improved Deep Convolutional Neural Networks via Boosting for Predicting the Quality of In Vitro Bovine Embryos. Electronics (Switzerland), 2022, 11, 1363.	1.8	6
3	Automatic Classification of Melanoma Skin Cancer with Deep Convolutional Neural Networks. Al, 2022, 3, 512-525.	2.1	12
4	Integrated Analysis of Tissue-Specific Gene Expression in Diabetes by Tensor Decomposition Can Identify Possible Associated Diseases. Genes, 2022, 13, 1097.	1.0	0
5	Novel Hate Speech Detection Using Word Cloud Visualization and Ensemble Learning Coupled with Count Vectorizer. Applied Sciences (Switzerland), 2022, 12, 6611.	1.3	10
6	An Omnibus Test for Differential Distribution Analysis of Continuous Microbiome Data. IEEE Access, 2021, 9, 100029-100039.	2.6	0
7	Application of Tensor Decomposition to Gene Expression of Infection of Mouse Hepatitis Virus Can Identify Critical Human Genes and Efffective Drugs for SARS-CoV-2 Infection. IEEE Journal on Selected Topics in Signal Processing, 2021, 15, 746-758.	7.3	5
8	Mathematical formulation and application of kernel tensor decomposition based unsupervised feature extraction. Knowledge-Based Systems, 2021, 217, 106834.	4.0	4
9	Unsupervised tensor decomposition-based method to extract candidate transcription factors as histone modification bookmarks in post-mitotic transcriptional reactivation. PLoS ONE, 2021, 16, e0251032.	1.1	3
10	Novel method for the prediction of drug-drug Interaction based on gene expression profiles. European Journal of Pharmaceutical Sciences, 2021, 160, 105742.	1.9	4
11	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
12	Tensor-Decomposition-Based Unsupervised Feature Extraction in Single-Cell Multiomics Data Analysis. Genes, 2021, 12, 1442.	1.0	8
13	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
14	Effects of Collagen–Glycosaminoglycan Mesh on Gene Expression as Determined by Using Principal Component Analysis-Based Unsupervised Feature Extraction. Polymers, 2021, 13, 4117.	2.0	1
15	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
16	Universal Nature of Drug Treatment Responses in Drug-Tissue-Wide Model-Animal Experiments Using Tensor Decomposition-Based Unsupervised Feature Extraction. Frontiers in Genetics, 2020, 11, 695.	1.1	3
17	Tensor-Decomposition-Based Unsupervised Feature Extraction Applied to Prostate Cancer Multiomics Data. Genes, 2020, 11, 1493.	1.0	3
18	SCGRNs: Novel supervised inference of single-cell gene regulatory networks of complex diseases. Computers in Biology and Medicine, 2020, 118, 103656.	3.9	14

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19	Generative Adversarial Networks for Stochastic Video Prediction With Action Control. IEEE Access, 2020, 8, 63336-63348.	2.6	6
20	Neurological Disorder Drug Discovery from Gene Expression with Tensor Decomposition. Current Pharmaceutical Design, 2020, 25, 4589-4599.	0.9	6
21	Tensor Decomposition-Based Unsupervised Feature Extraction Applied to Single-Cell Gene Expression Analysis. Frontiers in Genetics, 2019, 10, 864.	1.1	13
22	Machine learning algorithms for predicting drugs–tissues relationships. Expert Systems With Applications, 2019, 127, 167-186.	4.4	12
23	Clinical intelligence: New machine learning techniques for predicting clinical drug response. Computers in Biology and Medicine, 2019, 107, 302-322.	3.9	22
24	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
25	DLGraph: Malware Detection Using Deep Learning and Graph Embedding. , 2018, , .		25
26	A 3D Atrous Convolutional Long Short-Term Memory Network for Background Subtraction. IEEE Access, 2018, 6, 43450-43459.	2.6	46
27	An empirical study of machine learning algorithms for cancer identification. , 2018, , .		12
28	Reverse Engineering Gene Regulatory Networks Using Graph Mining. Lecture Notes in Computer Science, 2018, , 335-349.	1.0	3
29	Weighted Gene Co-Expression Network Analysis Reveals Dysregulation of Mitochondrial Oxidative Phosphorylation in Eating Disorders. Genes, 2018, 9, 325.	1.0	14
30	Boosting support vector machines for cancer discrimination tasks. Computers in Biology and Medicine, 2018, 101, 236-249.	3.9	35
31	Transfer Learning Approaches to Improve Drug Sensitivity Prediction in Multiple Myeloma Patients. IEEE Access, 2017, 5, 7381-7393.	2.6	46
32	Reverse Engineering Gene Regulatory Networks Using Sampling and Boosting Techniques. Lecture Notes in Computer Science, 2017, , 63-77.	1.0	1
33	Reverse Engineering Regulatory Networks in Cells Using a Dynamic Bayesian Network and Mutual Information Scoring Function., 2017,,.		1
34	A link prediction approach to cancer drug sensitivity prediction. BMC Systems Biology, 2017, 11, 94.	3.0	47
35	MapReduce Algorithms for Inferring Gene Regulatory Networks from Time-Series Microarray Data Using an Information-Theoretic Approach. BioMed Research International, 2017, 2017, 1-8.	0.9	7
36	Inferring Gene Regulatory Networks by Combining Supervised and Unsupervised Methods. , 2016, , .		10

Turki Turki

#	Article	IF	CITATIONS
37	Learning approaches to improve prediction of drug sensitivity in breast cancer patients. , 2016, 2016, 3314-3320.		13
38	A greedy-based oversampling approach to improve the prediction of mortality in MERS patients. , 2016, , .		5
39	A Learning Framework to Improve Unsupervised Gene Network Inference. Lecture Notes in Computer Science, 2016, , 28-42.	1.0	3
40	A New Approach to Link Prediction in Gene Regulatory Networks. Lecture Notes in Computer Science, 2015, , 404-415.	1.0	7
41	MaxSSmap: a GPU program for mapping divergent short reads to genomes with the maximum scoring subsequence. BMC Genomics, 2014, 15, 969.	1.2	7
42	Weighted Maximum Variance Dimensionality Reduction. Lecture Notes in Computer Science, 2014, , 11-20.	1.0	3
43	Top-k Parametrized Boost. Lecture Notes in Computer Science, 2014, , 91-98.	1.0	3