

Min Wu

List of Publications by Year in descending order

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107
papers

4,028
citations

172207

29
h-index

133063

59
g-index

111
all docs

111
docs citations

111
times ranked

2624
citing authors

#	ARTICLE	IF	CITATIONS
1	A core-attachment based method to detect protein complexes in PPI networks. BMC Bioinformatics, 2009, 10, 169.	1.2	319
2	Neighborhood Regularized Logistic Matrix Factorization for Drug-Target Interaction Prediction. PLoS Computational Biology, 2016, 12, e1004760.	1.5	289
3	Computational approaches for detecting protein complexes from protein interaction networks: a survey. BMC Genomics, 2010, 11, S3.	1.2	284
4	Machine Remaining Useful Life Prediction via an Attention-Based Deep Learning Approach. IEEE Transactions on Industrial Electronics, 2021, 68, 2521-2531.	5.2	252
5	An Attention-Based Deep Learning Approach for Sleep Stage Classification With Single-Channel EEG. IEEE Transactions on Neural Systems and Rehabilitation Engineering, 2021, 29, 809-818.	2.7	225
6	Drug-Target Interaction Prediction with Graph Regularized Matrix Factorization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 646-656.	1.9	224
7	An overview of state-of-the-art partial discharge analysis techniques for condition monitoring. IEEE Electrical Insulation Magazine, 2015, 31, 22-35.	1.1	206
8	Computational prediction of drug-target interactions using chemogenomic approaches: an empirical survey. Briefings in Bioinformatics, 2019, 20, 1337-1357.	3.2	182
9	Drug-target interaction prediction via class imbalance-aware ensemble learning. BMC Bioinformatics, 2016, 17, 509.	1.2	88
10	Drug-target interaction prediction using ensemble learning and dimensionality reduction. Methods, 2017, 129, 81-88.	1.9	88
11	Inferring Gene-Phenotype Associations via Global Protein Complex Network Propagation. PLoS ONE, 2011, 6, e21502.	1.1	83
12	Predicting human microbe-drug associations via graph convolutional network with conditional random field. Bioinformatics, 2020, 36, 4918-4927.	1.8	82
13	Detecting temporal protein complexes from dynamic protein-protein interaction networks. BMC Bioinformatics, 2014, 15, 335.	1.2	67
14	Contrastive Adversarial Domain Adaptation for Machine Remaining Useful Life Prediction. IEEE Transactions on Industrial Informatics, 2021, 17, 5239-5249.	7.2	65
15	Smartphone Sensor-Based Human Activity Recognition Using Feature Fusion and Maximum Full Posteriori. IEEE Transactions on Instrumentation and Measurement, 2020, 69, 3992-4001.	2.4	63
16	Semantic proximity search on graphs with metagraph-based learning. , 2016, , .		62
17	Dual-dropout graph convolutional network for predicting synthetic lethality in human cancers. Bioinformatics, 2020, 36, 4458-4465.	1.8	58
18	Degradation-Aware Remaining Useful Life Prediction With LSTM Autoencoder. IEEE Transactions on Instrumentation and Measurement, 2021, 70, 1-10.	2.4	56

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19	Repeat Buyer Prediction for E-Commerce. , 2016, , .		52
20	A graph regularized generalized matrix factorization model for predicting links in biomedical bipartite networks. <i>Bioinformatics</i> , 2020, 36, 3474-3481.	1.8	51
21	A joint classification-regression method for multi-stage remaining useful life prediction. <i>Journal of Manufacturing Systems</i> , 2021, 58, 109-119.	7.6	48
22	Adaptive Cost-Sensitive Online Classification. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2019, 31, 214-228.	4.0	46
23	Recent advances in network-based methods for disease gene prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	42
24	Discovery of Protein Complexes with Core-Attachment Structures from Tandem Affinity Purification (TAP) Data. <i>Journal of Computational Biology</i> , 2012, 19, 1027-1042.	0.8	36
25	KDnet-RUL: A Knowledge Distillation Framework to Compress Deep Neural Networks for Machine Remaining Useful Life Prediction. <i>IEEE Transactions on Industrial Electronics</i> , 2022, 69, 2022-2032.	5.2	36
26	Adversarial Multiple-Target Domain Adaptation for Fault Classification. <i>IEEE Transactions on Instrumentation and Measurement</i> , 2021, 70, 1-11.	2.4	35
27	Attention-based sequence to sequence model for machine remaining useful life prediction. <i>Neurocomputing</i> , 2021, 466, 58-68.	3.5	35
28	Conditional Contrastive Domain Generalization for Fault Diagnosis. <i>IEEE Transactions on Instrumentation and Measurement</i> , 2022, 71, 1-12.	2.4	35
29	Construction of co-complex score matrix for protein complex prediction from AP-MS data. <i>Bioinformatics</i> , 2011, 27, i159-i166.	1.8	34
30	Ensembling graph attention networks for human microbe-drug association prediction. <i>Bioinformatics</i> , 2020, 36, i779-i786.	1.8	34
31	SL ² MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 748-757.	1.9	32
32	An Attention Based CNN-LSTM Approach for Sleep-Wake Detection With Heterogeneous Sensors. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 3270-3277.	3.9	31
33	KG4SL: knowledge graph neural network for synthetic lethality prediction in human cancers. <i>Bioinformatics</i> , 2021, 37, i418-i425.	1.8	31
34	Integrating node embeddings and biological annotations for genes to predict disease-gene associations. <i>BMC Systems Biology</i> , 2018, 12, 138.	3.0	29
35	CtIP Silencing as a Novel Mechanism of Tamoxifen Resistance in Breast Cancer. <i>Molecular Cancer Research</i> , 2007, 5, 1285-1295.	1.5	28
36	Bi-LSTM-Based Two-Stream Network for Machine Remaining Useful Life Prediction. <i>IEEE Transactions on Instrumentation and Measurement</i> , 2022, 71, 1-10.	2.4	28

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37	Pre-training graph neural networks for link prediction in biomedical networks. <i>Bioinformatics</i> , 2022, 38, 2254-2262.	1.8	26
38	Graph contextualized attention network for predicting synthetic lethality in human cancers. <i>Bioinformatics</i> , 2021, 37, 2432-2440.	1.8	25
39	In Silico Prediction of Synthetic Lethality by Meta-Analysis of Genetic Interactions, Functions, and Pathways in Yeast and Human Cancer. <i>Cancer Informatics</i> , 2014, 13s3, CIN.S14026.	0.9	24
40	Predicting essential genes and synthetic lethality via influence propagation in signaling pathways of cancer cell fates. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1541002.	0.3	24
41	Predicting synthetic lethal interactions in human cancers using graph regularized self-representative matrix factorization. <i>BMC Bioinformatics</i> , 2019, 20, 657.	1.2	24
42	An Attention-Based Deep Sequential GRU Model for Sensor Drift Compensation. <i>IEEE Sensors Journal</i> , 2021, 21, 7908-7917.	2.4	24
43	Computational Prediction of Drug-Target Interactions via Ensemble Learning. <i>Methods in Molecular Biology</i> , 2019, 1903, 239-254.	0.4	23
44	Syn-Lethality: An Integrative Knowledge Base of Synthetic Lethality towards Discovery of Selective Anticancer Therapies. <i>BioMed Research International</i> , 2014, 2014, 1-7.	0.9	22
45	Contextualized Graph Attention Network for Recommendation with Item Knowledge Graph. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2021, , 1-1.	4.0	21
46	Prediction of Synthetic Lethal Interactions in Human Cancers Using Multi-View Graph Auto-Encoder. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 4041-4051.	3.9	19
47	Learning User Dependencies for Recommendation. , 2017, , .		19
48	Identifying protein complexes from heterogeneous biological data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2023-2033.	1.5	18
49	Disease gene classification with metagraph representations. <i>Methods</i> , 2017, 131, 83-92.	1.9	18
50	mg2vec: Learning Relationship-Preserving Heterogeneous Graph Representations via Metagraph Embedding. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2022, 34, 1317-1329.	4.0	18
51	A two-layer integration framework for protein complex detection. <i>BMC Bioinformatics</i> , 2016, 17, 100.	1.2	17
52	Metagraph-Based Learning on Heterogeneous Graphs. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2021, 33, 154-168.	4.0	17
53	Node-based learning of differential networks from multi-platform gene expression data. <i>Methods</i> , 2017, 129, 41-49.	1.9	16
54	Characterising Alzheimer's Disease With EEG-Based Energy Landscape Analysis. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 992-1000.	3.9	16

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55	SynLethDB 2.0: a web-based knowledge graph database on synthetic lethality for novel anticancer drug discovery. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	16
56	Modeling perceived stress via HRV and accelerometer sensor streams. , 2015, 2015, 1625-8.		15
57	A Novel Real-Time Deep Learning Approach for Indoor Localization Based on RF Environment Identification. , 2020, 4, 1-4.		15
58	Benchmarking Human Protein Complexes to Investigate Drug-Related Systems and Evaluate Predicted Protein Complexes. PLoS ONE, 2013, 8, e53197.	1.1	14
59	Contrastive adversarial knowledge distillation for deep model compression in time-series regression tasks. Neurocomputing, 2022, 485, 242-251.	3.5	14
60	Adversarial Transfer Learning for Machine Remaining Useful Life Prediction. , 2020, , .		13
61	Privacy-Preserving Cross-Environment Human Activity Recognition. IEEE Transactions on Cybernetics, 2023, 53, 1765-1775.	6.2	13
62	Integrating diverse biological and computational sources for reliable protein-protein interactions. BMC Bioinformatics, 2010, 11, S8.	1.2	12
63	PLW: Probabilistic Local Walks for detecting protein complexes from protein interaction networks. BMC Genomics, 2013, 14, S15.	1.2	12
64	Matrix factorization for biomedical link prediction and scRNA-seq data imputation: an empirical survey. Briefings in Bioinformatics, 2022, 23, .	3.2	12
65	Protein Complex Detection via Effective Integration of Base Clustering Solutions and Co-Complex Affinity Scores. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 733-739.	1.9	11
66	Cost-Sensitive Online Classification with Adaptive Regularization and Its Applications. , 2015, , .		10
67	A Novel Ensemble Deep Learning Approach for Sleep-Wake Detection Using Heart Rate Variability and Acceleration. IEEE Transactions on Emerging Topics in Computational Intelligence, 2021, 5, 803-812.	3.4	9
68	Automatic detection of retinopathy with optical coherence tomography images via a semi-supervised deep learning method. Biomedical Optics Express, 2021, 12, 2684.	1.5	9
69	Deep Learning for Building Occupancy Estimation Using Environmental Sensors. Studies in Computational Intelligence, 2020, , 335-357.	0.7	9
70	Self-Supervised Autoregressive Domain Adaptation for Time Series Data. IEEE Transactions on Neural Networks and Learning Systems, 2024, 35, 1341-1351.	7.2	9
71	Heterogeneous graph attention networks for drug virus association prediction. Methods, 2021, 198, 11-11.	1.9	8
72	Epigenetic functions enriched in transcription factors binding to mouse recombination hotspots. Proteome Science, 2012, 10, S11.	0.7	6

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73	LDsplit: screening for cis-regulatory motifs stimulating meiotic recombination hotspots by analysis of DNA sequence polymorphisms. BMC Bioinformatics, 2014, 15, 48.	1.2	6
74	Multi-View Collaborative Network Embedding. ACM Transactions on Knowledge Discovery From Data, 2021, 15, 1-18.	2.5	6
75	Deep learning with long short-term memory networks for classification of dementia related travel patterns. , 2020, 2020, 5563-5566.		6
76	Disease Gene Classification with Metagraph Representations. Methods in Molecular Biology, 2018, 1807, 211-224.	0.4	6
77	Meta-analysis of Genomic and Proteomic Features to Predict Synthetic Lethality of Yeast and Human Cancer. , 2013, , .		5
78	Online Collaborative Filtering with Implicit Feedback. Lecture Notes in Computer Science, 2019, , 433-448.	1.0	5
79	Mahalanobis Distance Based Adversarial Network for Anomaly Detection. , 2020, , .		5
80	Significance of activation functions in developing an online classifier for semiconductor defect detection. Knowledge-Based Systems, 2022, 248, 108818.	4.0	5
81	Feature selection and domain adaptation for cross-machine product quality prediction. Journal of Intelligent Manufacturing, 2023, 34, 1573-1584.	4.4	4
82	Predicting Synthetic Lethality in Human Cancers via Multi-Graph Ensemble Neural Network. , 2021, 2021, 1731-1734.		4
83	Prediction of Trans-regulators of Recombination Hotspots in Mouse Genome. , 2011, , .		3
84	A Deep Learning Approach for Sleep-Wake Detection from HRV and Accelerometer Data. , 2019, , .		3
85	Predicting Surface Roughness and Flank Wear in Turning Processes. , 2020, , .		3
86	<scp>Cross-domain</scp> retinopathy classification with optical coherence tomography images via a novel deep domain adaptation method. Journal of Biophotonics, 2021, 14, e202100096.	1.1	3
87	Integration of genomic and epigenomic features to predict meiotic recombination hotspots in human and mouse. , 2012, , .		2
88	Active learning for accurate analysis of streaming partial discharge data. , 2015, , .		2
89	LDsplitDB: a database for studies of meiotic recombination hotspots in MHC using human genomic data. BMC Medical Genomics, 2018, 11, 27.	0.7	2
90	Adaptive Grid-Based k-median Clustering of Streaming Data with Accuracy Guarantee. Lecture Notes in Computer Science, 2015, , 75-91.	1.0	2

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91	Predicting Drugs for COVID-19/SARS-CoV-2 via Heterogeneous Graph Attention Networks. , 2020, , .		2
92	Semi-Supervised Deep Adversarial Forest for Cross-Environment Localization. IEEE Transactions on Vehicular Technology, 2022, 71, 10215-10219.	3.9	2
93	NetPipe. , 2012, , .		1
94	Syn-Lethality: An integrative knowledge base of synthetic lethality towards discovery of selective anticancer therapies. , 2013, , .		1
95	Data-driven prediction of cancer cell fates with a nonlinear model of signaling pathways. , 2014, , .		1
96	A Novel Classifier - Weighted Features Cost-Sensitive SVM. , 2016, , .		1
97	Active Learning for On-Line Partial Discharge Monitoring in Noisy Environments. , 2016, , .		1
98	Mobile Robot Routing with Energy Consumption Optimization. , 2019, , .		1
99	Conv-inheritance: A hardware-efficient method to compress convolutional neural networks for edge applications. Neurocomputing, 2022, 487, 172-180.	3.5	1
100	Multi-feature Fused Bidirectional Long Short-term Memory for Remaining Useful Life Prediction. , 2021, , .		1
101	Semantic Labeling to Identify Reliable Interactions in the Protein Interaction Network. , 2008, , .		0
102	The Algorithm of Abstract Extraction Based on Semantics. Applied Mechanics and Materials, 2013, 303-306, 1506-1509.	0.2	0
103	Design and Implementation of College English Online Courseware Based on the Method of "Goal-Directed" Interaction Design. Applied Mechanics and Materials, 0, 380-384, 2058-2062.	0.2	0
104	Finding trans-regulatory genes and protein complexes modulating meiotic recombination hotspots of human, mouse and yeast. BMC Systems Biology, 2014, 8, 107.	3.0	0
105	Power-Law Modeling of Cancer Cell Fates Driven by Signaling Data to Reveal Drug Effects. PLoS ONE, 2016, 11, e0165049.	1.1	0
106	Design and Implementation of Multimedia Online Courseware Based on XML/XSLT and JavaScript. Communications in Computer and Information Science, 2011, , 456-462.	0.4	0
107	Matrix Factorization for Drug-Target Interaction Prediction. , 2017, , 83-106.		0