Xiaolong Wang

List of Publications by Year
in descending order

108 papers	4,264 citations	186265 28 h-index	114465 63 g-index
110 all docs	110 docs citations	110 times ranked	2667 citing authors

#	Article	IF	Citations
1	Fast and Robust Online Handwritten Chinese Character Recognition With Deep Spatial and Contextual Information Fusion Network. IEEE Transactions on Multimedia, 2023, 25, 2140-2152.	7.2	6
2	Transfer learning and GRU-CRF augmentation for Covid-19 fake news detection. Computer Science and Information Systems, 2022, 19, 639-658.	1.0	6
3	Jointly modeling transfer learning of industrial chain information and deep learning for stock prediction. Expert Systems With Applications, 2022, 191, 116257.	7.6	22
4	Augmentation and heterogeneous graph neural network for AAAI2021-COVID-19 fake news detection. International Journal of Machine Learning and Cybernetics, 2022, 13, 2033-2043.	3.6	18
5	TB-BCG: Topic-Based BART Counterfeit Generator for Fake News Detection. Mathematics, 2022, 10, 585.	2.2	3
6	Multi-channel fusion LSTM for medical event prediction using EHRs. Journal of Biomedical Informatics, 2022, 127, 104011.	4.3	13
7	A stock time series forecasting approach incorporating candlestick patterns and sequence similarity. Expert Systems With Applications, 2022, 205, 117595.	7.6	12
8	Construction of stock portfolios based on k-means clustering of continuous trend features. Knowledge-Based Systems, 2022, 252, 109358.	7.1	14
9	A hybrid framework based on extreme learning machine, discrete wavelet transform, and autoencoder with feature penalty for stock prediction. Expert Systems With Applications, 2022, 207, 118006.	7.6	11
10	RFPR-IDP: reduce the false positive rates for intrinsically disordered protein and region prediction by incorporating both fully ordered proteins and disordered proteins. Briefings in Bioinformatics, 2021, 22, 2000-2011.	6.5	20
11	A Hybrid Method Based on Extreme Learning Machine and Wavelet Transform Denoising for Stock Prediction. Entropy, 2021, 23, 440.	2.2	25
12	Novel Graph-Based Model With Biaffine Attention for Family History Extraction From Clinical Text: Modeling Study. JMIR Medical Informatics, 2021, 9, e23587.	2.6	0
13	A Novel Time-Sensitive Composite Similarity Model for Multivariate Time-Series Correlation Analysis. Entropy, 2021, 23, 731.	2.2	2
14	CapsTM: capsule network for Chinese medical text matching. BMC Medical Informatics and Decision Making, 2021, 21, 94.	3.0	3
15	Statistical analysis of the community lockdown for COVID-19 pandemic. Applied Intelligence, 2021, , 1-18.	5.3	2
16	PFC: A Novel Perceptual Features-Based Framework for Time Series Classification. Entropy, 2021, 23, 1059.	2.2	6
17	A BERT-Based Generation Model to Transform Medical Texts to SQL Queries for Electronic Medical Records: Model Development and Validation. JMIR Medical Informatics, 2021, 9, e32698.	2.6	5
18	Improving deep learning method for biomedical named entity recognition by using entity definition information. BMC Bioinformatics, 2021, 22, 600.	2.6	4

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19	A hybrid method of recurrent neural network and graph neural network for next-period prescription prediction. International Journal of Machine Learning and Cybernetics, 2020, 11, 2849-2856.	3.6	32
20	Gated Semantic Difference Based Sentence Semantic Equivalence Identification. IEEE/ACM Transactions on Audio Speech and Language Processing, 2020, 28, 2770-2780.	5.8	3
21	A Labeling Method for Financial Time Series Prediction Based on Trends. Entropy, 2020, 22, 1162.	2.2	36
22	Distributed representation and one-hot representation fusion with gated network for clinical semantic textual similarity. BMC Medical Informatics and Decision Making, 2020, 20, 72.	3.0	23
23	Learning to Generate Diverse Questions from Keywords. , 2020, , .		0
24	KEoG: A knowledge-aware edge-oriented graph neural network for document-level relation extraction. , 2020, , .		2
25	Cohort selection for clinical trials using hierarchical neural network. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1203-1208.	4.4	21
26	Identification of Intrinsically Disordered Proteins and Regions by Length-Dependent Predictors Based on Conditional Random Fields. Molecular Therapy - Nucleic Acids, 2019, 17, 396-404.	5.1	13
27	Extracting entities with attributes in clinical text via joint deep learning. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1584-1591.	4.4	14
28	Dynamic Working Memory for Context-Aware Response Generation. IEEE/ACM Transactions on Audio Speech and Language Processing, 2019, 27, 1419-1431.	5.8	5
29	A fine-grained Chinese word segmentation and part-of-speech tagging corpus for clinical text. BMC Medical Informatics and Decision Making, 2019, 19, 66.	3.0	14
30	Entity recognition in Chinese clinical text using attention-based CNN-LSTM-CRF. BMC Medical Informatics and Decision Making, 2019, 19, 74.	3.0	35
31	Temporal indexing of medical entity in Chinese clinical notes. BMC Medical Informatics and Decision Making, 2019, 19, 17.	3.0	5
32	Family history information extraction via deep joint learning. BMC Medical Informatics and Decision Making, 2019, 19, 277.	3.0	18
33	A comprehensive review and comparison of existing computational methods for intrinsically disordered protein and region prediction. Briefings in Bioinformatics, 2019, 20, 330-346.	6.5	129
34	Protein Remote Homology Detection and Fold Recognition Based on Sequence-Order Frequency Matrix. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 292-300.	3.0	21
35	De-identification of Clinical Text via Bi-LSTM-CRF with Neural Language Models. AMIA ... Annual Symposium proceedings, 2019, 2019, 857-863.	0.2	2
36	Learning to recognize opinion targets using recurrent neural networks. Pattern Recognition Letters, 2018, 106, 41-46.	4.2	3

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37	A comprehensive review and comparison of different computational methods for protein remote homology detection. Briefings in Bioinformatics, 2018, 19, 231-244.	6.5	106
38	Structural regularity exploration in multidimensional networks via Bayesian inference. Neural Computing and Applications, 2018, 29, 413-424.	5.6	9
39	IDPâ€"CRF: Intrinsically Disordered Protein/Region Identification Based on Conditional Random Fields. International Journal of Molecular Sciences, 2018, 19, 2483.	4.1	19
40	Recognizing Continuous and Discontinuous Adverse Drug Reaction Mentions from Social Media Using LSTM-CRF. Wireless Communications and Mobile Computing, 2018, 2018, 1-8.	1.2	23
41	Chinese Clinical Entity Recognition via Attention-Based CNN-LSTM-CRF. , 2018, , .		7
42	Answer Selection in Community Question Answering via Attentive Neural Networks. IEEE Signal Processing Letters, 2017, 24, 505-509.	3.6	40
43	Entity disambiguation with decomposable neural networks. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2017, 7, e1215.	6.8	2
44	Incorporating loose-structured knowledge into conversation modeling via recall-gate LSTM. , 2017, , .		31
45	Entity recognition from clinical texts via recurrent neural network. BMC Medical Informatics and Decision Making, 2017, 17, 67.	3.0	135
46	Pse-Analysis: a python package for DNA/RNA and protein/peptide sequence analysis based on pseudo components and kernel methods. Oncotarget, 2017, 8, 13338-13343.	1.8	119
47	Optimizing ranking for response prediction via triplet-wise learning from historical feedback. International Journal of Machine Learning and Cybernetics, 2017, 8, 1777-1793.	3.6	5
48	SOFM-Top: Protein Remote Homology Detection and Fold Recognition Based on Sequence-Order Frequency Matrix. Lecture Notes in Computer Science, 2017, , 469-480.	1.3	0
49	Distant Supervision for Relation Extraction with Ranking-Based Methods. Entropy, 2016, 18, 204.	2.2	7
50	iRSpot-DACC: a computational predictor for recombination hot/cold spots identification based on dinucleotide-based auto-cross covariance. Scientific Reports, 2016, 6, 33483.	3.3	29
51	iMiRNA-SSF: Improving the Identification of MicroRNA Precursors by Combining Negative Sets with Different Distributions. Scientific Reports, 2016, 6, 19062.	3.3	65
52	iMiRNA-PseDPC: microRNA precursor identification with a pseudo distance-pair composition approach. Journal of Biomolecular Structure and Dynamics, 2016, 34, 223-235.	3.5	120
53	repRNA: a web server for generating various feature vectors of RNA sequences. Molecular Genetics and Genomics, 2016, 291, 473-481.	2.1	122
54	A comparison of conditional random fields and structured support vector machines for chemical entity recognition in biomedical literature. Journal of Cheminformatics, 2015, 7, S8.	6.1	26

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55	DNA binding protein identification by combining pseudo amino acid composition and profile-based protein representation. Scientific Reports, 2015, 5, 15479.	3.3	92
56	PseDNAâ€Pro: DNAâ€Binding Protein Identification by Combining Chouâ€™s PseAAC and Physicochemical Distance Transformation. Molecular Informatics, 2015, 34, 8-17.	2.5	152
57	Bias Modeling for Distantly Supervised Relation Extraction. Mathematical Problems in Engineering, 2015, 2015, 1-10.	1.1	2
58	Evaluating tag quality for blogger modelling via topic models. , 2015, , .		1
59	Automatic de-identification of electronic medical records using token-level and character-level conditional random fields. Journal of Biomedical Informatics, 2015, 58, S47-S52.	4.3	58
60	repDNA: a Python package to generate various modes of feature vectors for DNA sequences by incorporating user-defined physicochemical properties and sequence-order effects. Bioinformatics, 2015, 31, 1307-1309.	4.1	242
61	Pse-in-One: a web server for generating various modes of pseudo components of DNA, RNA, and protein sequences. Nucleic Acids Research, 2015, 43, W65-W71.	14.5	664
62	N-gram distribution and unification gain problem and its optimal solution. International Journal of Systems Science, 2015, 46, 1327-1336.	5.5	0
63	Protein remote homology detection by combining Chouâ€™s distance-pair pseudo amino acid composition and principal component analysis. Molecular Genetics and Genomics, 2015, 290, 1919-1931.	2.1	62
64	Deep Belief Network-Based Approaches for Link Prediction in Signed Social Networks. Entropy, 2015, 17, 2140-2169.	2.2	48
65	Application of learning to rank to protein remote homology detection. Bioinformatics, 2015, 31, 3492-3498.	4.1	85
66	Identification of microRNA precursor with the degenerate K-tuple or Kmer strategy. Journal of Theoretical Biology, 2015, 385, 153-159.	1.7	159
67	Identification of Real MicroRNA Precursors with a Pseudo Structure Status Composition Approach. PLoS ONE, 2015, 10, e0121501.	2.5	193
68	Recognizing Disjoint Clinical Concepts in Clinical Text Using Machine Learning-based Methods. AMIA ... Annual Symposium proceedings, 2015, 2015, 1184-93.	0.2	6
69	Protein Binding Site Prediction by Combining Hidden Markov Support Vector Machine and Profile-Based Propensities. Scientific World Journal, The, 2014, 2014, 1-6.	2.1	9
70	Evaluating Word Representation Features in Biomedical Named Entity Recognition Tasks. BioMed Research International, 2014, 2014, 1-6.	1.9	94
71	enDNA-Prot: Identification of DNA-Binding Proteins by Applying Ensemble Learning. BioMed Research International, 2014, 2014, 1-10.	1.9	32
72	Combining evolutionary information extracted from frequency profiles with sequence-based kernels for protein remote homology detection. Bioinformatics, 2014, 30, 472-479.	4.1	266

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73	iDNA-Prot|dis: Identifying DNA-Binding Proteins by Incorporating Amino Acid Distance-Pairs and Reduced Alphabet Profile into the General Pseudo Amino Acid Composition. PLoS ONE, 2014, 9, e106691.	2.5	242
74	A support vector machine based MSM model for financial short-term volatility forecasting. Neural Computing and Applications, 2013, 22, 21-28.	5.6	22
75	Exploring social features for answer quality prediction in CQA portals. , 2013, , .		3
76	Protein Remote Homology Detection by Combining Chouâ€™s Pseudo Amino Acid Composition and Profileâ€Based Protein Representation. Molecular Informatics, 2013, 32, 775-782.	2.5	103
77	Sequence memoizer based model for Biomedical Named Entity Recognition. , 2012, , .		0
78	Features for link prediction in social networks: A comprehensive study. , 2012, , .		10
79	Using Amino Acid Physicochemical Distance Transformation for Fast Protein Remote Homology Detection. PLoS ONE, 2012, 7, e46633.	2.5	94
80	Biomedical named entity recognition using generalized expectation criteria. International Journal of Machine Learning and Cybernetics, 2011, 2, 235-243.	3.6	5
81	Multi-class Relationship Extraction from Biomedical Literature Using Maximum Entropy. , 2010, , .		0
82	Ranknet based English stressed syllable detection. , 2010, , .		0
83	CogQTaxo: Modeling human cognitive process with a three-dimensional question taxonomy. , 2010, , .		0
84	A Block Segmentation Based Approach for Web Information Extraction. , 2010, , .		1
85	Study on feature selection in finance text categorization. , 2009, , .		3
86	STRank: A SiteRank algorithm using semantic relevance and time frequency. , 2009, , .		5
87	Foxinfo1.0: A Chinese Topic-Oriented Search Engine. , 2009, , .		0
88	An interactive semantic knowledge base unifying Wikipedia and HowNet. , 2009, , .		2
89	An Ontology-Based NLP Approach to Semantic Annotation of Annual Report. , 2009, , .		0
90	Extracting Chinese question-answer pairs from online forums. , 2009, , .		13

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91	Extracting Event Temporal Information Based on Web. , 2009, , .		2
92	A discriminative method for protein remote homology detection and fold recognition combining Top-n-grams and latent semantic analysis. BMC Bioinformatics, 2008, 9, 510.	2.6	129
93	Semantic Chunk Annotation for questions using Maximum Entropy. Conference Proceedings IEEE International Conference on Systems, Man, and Cybernetics, 2008, , .	0.0	0
94	Chinese Unknown Word Recognition Using Improved Conditional Random Fields. , 2008, , .		2
95	Chinese chunking and its application on similarity computation. , 2008, , .		0
96	Genre identification of Chinese finance text using machine learning method. Conference Proceedings IEEE International Conference on Systems, Man, and Cybernetics, 2008, , .	0.0	1
97	Model fusion of conditional random fields. , 2007, , .		0
98	A Dynamic SOM Algorithm for Clustering Large-Scale Document Collection. , 2007, , .		0
99	Automatic text summarization based on textual cohesion. Journal of Electronics, 2007, 24, 338-346.	0.2	3
100	A Maximum Entropy chunking model with N-fold template correction. Journal of Electronics, 2007, 24, 690-695.	0.2	0
101	Research of Pinyin-To-Character conversion based on Maximum Entropy model. Journal of Electronics, 2006, 23, 864-869.	0.2	1
102	Combining feature scaling estimation with SVM classifier design using GA approach. Journal of Electronics, 2005, 22, 550-557.	0.2	0
103	COMBINING MULTIPLE CLASSIFIERS BASED ON A STATISTICAL METHOD FOR HANDWRITTEN CHINESE CHARACTER RECOGNITION. International Journal of Pattern Recognition and Artificial Intelligence, 2005, 19, 1027-1040.	1.2	6
104	Mining Pinyin-to-Character Conversion Rules From Large-Scale Corpus: A Rough Set Approach. IEEE Transactions on Systems, Man, and Cybernetics, 2004, 34, 834-844.	5.0	11
105	AN APPROACH TO NATURAL STROKE EXTRACTION FOR OFF-LINE LOOSELY-CONSTRAINED HANDWRITTEN CHINESE CHARACTERS. International Journal of Pattern Recognition and Artificial Intelligence, 2003, 17, 1483-1513.	1.2	1
106	Combining trigram and automatic weight distribution in Chinese spelling error correction. Journal of Computer Science and Technology, 2002, 17, 915-923.	1.5	9
107	A new linguistic decoding method for online handwritten Chinese character recognition. Journal of Computer Science and Technology, 2000, 15, 597-603.	1.5	1
108	Scaling Gaussian RBF kernel width to improve SVM classification. , 0, , .		15