Hong Yan

List of Publications by Year
in descending order

539	9,906	44069	76900
papers	citations	48	74
		h-index	g-index

543	543	543	7279
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Unsupervised Domain Adaptation via Discriminative Manifold Propagation. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2022, 44, 1653-1669.	13.9	39
2	Identifying Gene Network Rewiring Based on Partial Correlation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 513-521.	3.0	0
3	Correlated Motions and Dynamics in Different Domains of Epidermal Growth Factor Receptor With L858R and T790M Mutations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 383-394.	3.0	12
4	scDEA: differential expression analysis in single-cell RNA-sequencing data via ensemble learning. Briefings in Bioinformatics, 2022, 23, .	6.5	12
5	Patch-Aware Deep Hyperspectral and Multispectral Image Fusion by Unfolding Subspace-Based Optimization Model. IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing, 2022, 15, 1024-1038.	4.9	14
6	Hierarchical scale convolutional neural network for facial expression recognition. Cognitive Neurodynamics, 2022, 16, 847-858.	4.0	9
7	Combined angular margin and cosine margin softmax loss for music classification based on spectrograms. Neural Computing and Applications, 2022, 34, 10337-10353.	5.6	5
8	Dual Quaternions and Dual Quaternion Vectors. Communications on Applied Mathematics and Computation, 2022, 4, 1494-1508.	1.7	19
9	Imputing dropouts for single-cell RNA sequencing based on multi-objective optimization. Bioinformatics, 2022, 38, 3222-3230.	4.1	5
10	Star topology convolution for graph representation learning. Complex & Intelligent Systems, 2022, 8, 5125-5141.	6.5	1
11	Time-Varying Differential Network Analysis for Revealing Network Rewiring over Cancer Progression. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1632-1642.	3.0	4
12	Elastic Net Constraint-Based Tensor Model for High-Order Graph Matching. IEEE Transactions on Cybernetics, 2021, 51, 4062-4074.	9.5	11
13	Multi-deep features fusion for high-resolution remote sensing image scene classification. Neural Computing and Applications, 2021, 33, 2047-2063.	5.6	19
14	Computationally predicting binding affinity in protein–ligand complexes: free energy-based simulations and machine learning-based scoring functions. Briefings in Bioinformatics, 2021, 22, .	6.5	33
15	Joint Transformation Learning via the $L_{2,1}$-Norm Metric for Robust Graph Matching. IEEE Transactions on Cybernetics, 2021, 51, 521-533.	9.5	13
16	Learning Kernel for Conditional Moment-Matching Discrepancy-Based Image Classification. IEEE Transactions on Cybernetics, 2021, 51, 2006-2018.	9.5	9
17	Visualization of Protein-Drug Interactions for the Analysis of Drug Resistance in Lung Cancer. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 1839-1848.	6.3	10
18	Fuzzy SLIC: Fuzzy Simple Linear Iterative Clustering. IEEE Transactions on Circuits and Systems for Video Technology, 2021, 31, 2114-2124.	8.3	20

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19	HiSCF: leveraging higher-order structures for clustering analysis in biological networks. Bioinformatics, 2021, 37, 542-550.	4.1	76
20	A Joint Graphical Model for Inferring Gene Networks Across Multiple Subpopulations and Data Types. IEEE Transactions on Cybernetics, 2021, 51, 1043-1055.	9.5	10
21	Improved Deep Classwise Hashing With Centers Similarity Learning for Image Retrieval. , 2021, , .		2
22	Geometrical Features of Epidermal Growth Factor Receptor-Related Dimers Reveal the Mechanisms of Drug Resistance in Lung Cancer Patients. IEEE Access, 2021, 9, 5704-5715.	4.2	1
23	A Deep Learning Based Light-Weight Face Mask Detector With Residual Context Attention and Gaussian Heatmap to Fight Against COVID-19. IEEE Access, 2021, 9, 96964-96974.	4.2	31
24	Saliency Detection Using Deep Features and Affinity-Based Robust Background Subtraction. IEEE Transactions on Multimedia, 2021, 23, 2902-2916.	7.2	19
25	Proteo-chemometrics interaction fingerprints of protein–ligand complexes predict binding affinity. Bioinformatics, 2021, 37, 2570-2579.	4.1	6
26	Exploiting higher-order patterns for community detection in attributed graphs. Integrated Computer-Aided Engineering, 2021, 28, 207-218.	4.6	24
27	WDNE: an integrative graphical model for inferring differential networks from multi-platform gene expression data with missing values. Briefings in Bioinformatics, 2021, 22, .	6.5	2
28	An Efficient Randomized Algorithm for Computing the Approximate Tucker Decomposition. Journal of Scientific Computing, 2021, 88, 1.	2.3	11
29	Genotype-determined EGFR-RTK heterodimerization and its effects on drug resistance in lung Cancer treatment revealed by molecular dynamics simulations. BMC Molecular and Cell Biology, 2021, 22, 34.	2.0	6
30	Differential network analysis by simultaneously considering changes in gene interactions and gene expression. Bioinformatics, 2021, 37, 4414-4423.	4.1	10
31	An Efficient Parallel Processor for Dense Tensor Computation. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2021, 29, 1335-1347.	3.1	1
32	Semantic Hierarchy Preserving Deep Hashing for Large-Scale Image Retrieval. , 2021, , .		1
33	Mechanism of Actions of Dexamethasone Against COVID-19 Predicted by Alpha Shape Analysis of Binding Sites. Current Bioinformatics, 2021, 16, 682-690.	1.5	1
34	Deep center-based dual-constrained hashing for discriminative face image retrieval. Pattern Recognition, 2021, 117, 107976.	8.1	14
35	A Novel Regularized Model for Third-Order Tensor Completion. IEEE Transactions on Signal Processing, 2021, 69, 3473-3483.	5.3	7
36	Structure-based protein–ligand interaction fingerprints for binding affinity prediction. Computational and Structural Biotechnology Journal, 2021, 19, 6291-6300.	4.1	14

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37	Co-Clustering to Reveal Salient Facial Features for Expression Recognition. IEEE Transactions on Affective Computing, 2020, 11, 348-360.	8.3	25
38	Generalized Conditional Domain Adaptation: A Causal Perspective With Low-Rank Translators. IEEE Transactions on Cybernetics, 2020, 50, 821-834.	9.5	19
39	MCNF: A Novel Method for Cancer Subtyping by Integrating Multi-Omics and Clinical Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1682-1690.	3.0	10
40	Deep Class-Wise Hashing: Semantics-Preserving Hashing via Class-Wise Loss. IEEE Transactions on Neural Networks and Learning Systems, 2020, 31, 1681-1695.	11.3	22
41	Image Correspondence With CUR Decomposition-Based Graph Completion and Matching. IEEE Transactions on Circuits and Systems for Video Technology, 2020, 30, 3054-3067.	8.3	8
42	Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2162-2169.	3.0	2
43	Discriminative Residual Analysis for Image Set Classification With Posture and Age Variations. IEEE Transactions on Image Processing, 2020, 29, 2875-2888.	9.8	12
44	Generalized Tensor Regression for Hyperspectral Image Classification. IEEE Transactions on Geoscience and Remote Sensing, 2020, 58, 1244-1258.	6.3	36
45	Hypergraph Clustering Using a New Laplacian Tensor with Applications in Image Processing. SIAM Journal on Imaging Sciences, 2020, 13, 1157-1178.	2.2	13
46	A Truncated Matrix Decomposition for Hyperspectral Image Super-Resolution. IEEE Transactions on Image Processing, 2020, 29, 8028-8042.	9.8	51
47	Contour and region harmonic features for sub-local facial expression recognition. Journal of Visual Communication and Image Representation, 2020, 73, 102949.	2.8	13
48	Establishment of a morphological atlas of the Caenorhabditis elegans embryo using deep-learning-based 4D segmentation. Nature Communications, 2020, 11, 6254.	12.8	45
49	Predicting the impacts of mutations on protein-ligand binding affinity based on molecular dynamics simulations and machine learning methods. Computational and Structural Biotechnology Journal, 2020, 18, 439-454.	4.1	43
50	Saliency detection via multiple-morphological and superpixel based fast fuzzy C-mean clustering network. Expert Systems With Applications, 2020, 161, 113654.	7.6	14
51	scTSSR: gene expression recovery for single-cell RNA sequencing using two-side sparse self-representation. Bioinformatics, 2020, 36, 3131-3138.	4.1	22
52	Joint reconstruction of multiple gene networks by simultaneously capturing inter-tumor and intra-tumor heterogeneity. Bioinformatics, 2020, 36, 2755-2762.	4.1	4
53	Learning Multiple Parameters for Kernel Collaborative Representation Classification. IEEE Transactions on Neural Networks and Learning Systems, 2020, 31, 5068-5078.	11.3	12
54	Stability Analysis at Key Positions of EGFR Related to Non-small Cell Lung Cancer. Current Bioinformatics, 2020, 15, 260-267.	1.5	5

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55	Superpixel Based Hierarchical Segmentation for Color Image. IEICE Transactions on Information and Systems, 2020, E103.D, 2246-2249.	0.7	3
56	Joint Learning of Multiple Differential Networks With Latent Variables. IEEE Transactions on Cybernetics, 2019, 49, 3494-3506.	9.5	10
57	Parametric Models for Understanding Atomic Trajectories in Different Domains of Lung Cancer Causing Protein. IEEE Access, 2019, 7, 67551-67563.	4.2	12
58	Multimodal Co-clustering Analysis of Big Data Based on Matrix and Tensor Decomposition. , 2019, , 95-124.		0
59	Superpixel Tensor Pooling for Visual Tracking Using Multiple Midlevel Visual Cues Fusion. IEEE Access, 2019, 7, 147462-147469.	4.2	1
60	Improve L2-normalized Softmax with Exponential Moving Average. , 2019, , .		0
61	New Insights to Hydrogen Bonds to Provide Stability in the EGFR Related to Non-small Cell Lung Cancer. , 2019, , .		0
62	DiffNetFDR: differential network analysis with false discovery rate control. Bioinformatics, 2019, 35, 3184-3186.	4.1	14
63	EnImpute: imputing dropout events in single-cell RNA-sequencing data via ensemble learning. Bioinformatics, 2019, 35, 4827-4829.	4.1	29
64	Multiscale co-clustering for tensor data based on canonical polyadic decomposition and slice-wise factorization. Information Sciences, 2019, 503, 72-91.	6.9	4
65	A unified formulation of a class of graph matching techniques. Pattern Recognition, 2019, 95, 223-234.	8.1	0
66	3DMMS: robust 3D Membrane Morphological Segmentation of C. elegans embryo. BMC Bioinformatics, 2019, 20, 176.	2.6	15
67	Stability Investigation Using Hydrogen Bonds for Different Mutations and Drug Resistance in Non-Small Cell Lung Cancer Patients. , 2019, , .		0
68	Computational Analysis of Structural Dynamics of EGFR and its Mutants. , 2019, , .		5
69	An Efficient Application Specific Instruction Set Processor (ASIP) for Tensor Computation. , 2019, , .		3
70	Manifold Extraction in Fluorescent Stack via Deep Learning. , 2019, , .		0
71	Hyperspectral Image Classification Via Tensor Ridge Regression. , 2019, , .		0
72	Singular value decomposition based recommendation using imputed data. Knowledge-Based Systems, 2019, 163, 485-494.	7.1	52

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73	Hydrogen bond analysis of the EGFR-ErbB3 heterodimer related to non-small cell lung cancer and drug resistance. Journal of Theoretical Biology, 2019, 464, 63-71.	1.7	17
74	Feature Selection Based on Tensor Decomposition and Object Proposal for Night-Time Multiclass Vehicle Detection. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2019, 49, 71-80.	9.3	28
75	EmDL: Extracting miRNA-Drug Interactions from Literature. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1722-1728.	3.0	11
76	Molecular subtyping of cancer: current status and moving toward clinical applications. Briefings in Bioinformatics, 2019, 20, 572-584.	6.5	91
77	DrPOCS: Drug Repositioning Based on Projection Onto Convex Sets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 154-162.	3.0	16
78	Establishment of Signaling Interactions with Cellular Resolution for Every Cell Cycle of Embryogenesis. Genetics, 2018, 209, 37-49.	2.9	19
79	DiffGraph: an R package for identifying gene network rewiring using differential graphical models. Bioinformatics, 2018, 34, 1571-1573.	4.1	13
80	Prediction of sensitivity to gefitinib/erlotinib for EGFR mutations in NSCLC based on structural interaction fingerprints and multilinear principal component analysis. BMC Bioinformatics, 2018, 19, 88.	2.6	20
81	Tensor Decomposition of Gait Dynamics in Parkinson's Disease. IEEE Transactions on Biomedical Engineering, 2018, 65, 1820-1827.	4.2	36
82	Bayes Saliency-Based Object Proposal Generator for Nighttime Traffic Images. IEEE Transactions on Intelligent Transportation Systems, 2018, 19, 814-825.	8.0	23
83	Some inequalities for the Hadamard product of tensors. Linear and Multilinear Algebra, 2018, 66, 1199-1214.	1.0	13
84	A quadratic penalty method for hypergraph matching. Journal of Global Optimization, 2018, 70, 237-259.	1.8	6
85	Spatial-dependence recurrence sample entropy. Physica A: Statistical Mechanics and Its Applications, 2018, 494, 581-590.	2.6	23
86	Computing the p-Spectral Radii of Uniform Hypergraphs with Applications. Journal of Scientific Computing, 2018, 75, 1-25.	2.3	13
87	Accurate Cell Segmentation Based on Biological Morphology Features. , 2018, , .		3
88	Tagrec-CMTF: Coupled Matrix and Tensor Factorization for Tag Recommendation. IEEE Access, 2018, 6, 64142-64152.	4.2	5
89	Constructing Dynamic Topic Models Based on Variational Autoencoder and Factor Graph. IEEE Access, 2018, 6, 53102-53111.	4.2	3
90	Gene expression profiling of 1200 pancreatic ductal adenocarcinoma reveals novel subtypes. BMC Cancer, 2018, 18, 603.	2.6	63

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91	Analysis of the Relative Movements Between EGFR and Drug Inhibitors Based on Molecular Dynamics Simulation. Current Bioinformatics, 2018, 13, 299-309.	1.5	4
92	Cascade feature selection and coarse-to-fine mechanism for nighttime multiclass vehicle detection. Journal of Electronic Imaging, 2018, 27, 1.	0.9	2
93	Inference of cellular level signaling networks using single-cell gene expression data in <i>Caenorhabditis elegans</i> reveals mechanisms of cell fate specification. Bioinformatics, 2017, 33, 1528-1535.	4.1	6
94	An Eigen-Binding Site Based Method for the Analysis of Anti-EGFR Drug Resistance in Lung Cancer Treatment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1187-1194.	3.0	10
95	Sliced Inverse Regression With Adaptive Spectral Sparsity for Dimension Reduction. IEEE Transactions on Cybernetics, 2017, 47, 759-771.	9.5	4
96	Incorporating prior information into differential network analysis using non-paranormal graphical models. Bioinformatics, 2017, 33, 2436-2445.	4.1	40
97	Coclustering of Multidimensional Big Data: A Useful Tool for Genomic, Financial, and Other Data Analysis. IEEE Systems, Man, and Cybernetics Magazine, 2017, 3, 23-30.	1.4	15
98	mTD: A database of microRNAs affecting therapeutic effects of drugs. Journal of Genetics and Genomics, 2017, 44, 269-271.	3.9	17
99	Node-based differential network analysis in genomics. Computational Biology and Chemistry, 2017, 69, 194-201.	2.3	10
100	An online spatio-temporal tensor learning model for visual tracking and its applications to facial expression recognition. Expert Systems With Applications, 2017, 90, 427-438.	7.6	17
101	Deciphering mechanisms of acquired T790M mutation after EGFR inhibitors for NSCLC by computational simulations. Scientific Reports, 2017, 7, 6595.	3.3	29
102	Identifying differential networks based on multi-platform gene expression data. Molecular BioSystems, 2017, 13, 183-192.	2.9	14
103	Nighttime Vehicle Detection Based on Bio-Inspired Image Enhancement and Weighted Score-Level Feature Fusion. IEEE Transactions on Intelligent Transportation Systems, 2017, 18, 927-936.	8.0	59
104	Tensor learningusing N-mode SVD for dynamic background modelling and subtraction. , 2017, , .		0
105	Detection of correlated co-clusters in tensor data based on the slice-wise factorization. , 2017, , .		1
106	Predicting new indications of compounds with a network pharmacology approach: Liuwei Dihuang Wan as a case study. Oncotarget, 2017, 8, 93957-93968.	1.8	10
107	Analysis of drug resistance in non-small-cell lung cancer based on singular value decomposition. , 2016, , .		0
108	Identifying protein complexes via multi-network clustering. , 2016, , .		1

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109	Feature selection based on co-clustering for effective facial expression recognition. , 2016, , .		6
110	Singular vector decomposition based hybrid pattern search â€" An efficient co-clustering method. , 2016, , .		1
111	Protein complex detection based on partially shared multi-view clustering. BMC Bioinformatics, 2016, 17, 371.	2.6	10
112	Comparative analysis of housekeeping and tissue-specific driver nodes in human protein interaction networks. BMC Bioinformatics, 2016, 17, 358.	2.6	14
113	Differential network analysis from cross-platform gene expression data. Scientific Reports, 2016, 6, 34112.	3.3	29
114	Gabor phase representation on human face recognition for distorted images. , 2016, , .		2
115	Identifying EGFR mutation-induced drug resistance based on alpha shape model analysis of the dynamics. Proteome Science, 2016, 14, 12.	1.7	13
116	Analysis of the relationship between lung cancer drug response level and atom connectivity dynamics based on trimmed Delaunay triangulation. Chemical Physics Letters, 2016, 652, 117-122.	2.6	7
117	A two-layer integration framework for protein complex detection. BMC Bioinformatics, 2016, 17, 100.	2.6	17
118	Regularized logistic regression with network-based pairwise interaction for biomarker identification in breast cancer. BMC Bioinformatics, 2016, 17, 108.	2.6	18
119	Fruit classification based on weighted score-level feature fusion. Journal of Electronic Imaging, 2016, 25, 013009.	0.9	12
120	Text-Independent Phoneme Segmentation Combining EGG and Speech Data. IEEE/ACM Transactions on Audio Speech and Language Processing, 2016, 24, 1029-1037.	5.8	14
121	Combining Region-of-Interest Extraction and Image Enhancement for Nighttime Vehicle Detection. IEEE Intelligent Systems, 2016, 31, 57-65.	4.0	65
122	Selectivity profile of afatinib for EGFR-mutated non-small-cell lung cancer. Molecular BioSystems, 2016, 12, 1552-1563.	2.9	6
123	A study on the discriminating characteristics of Gabor phase-face and an improved method for face recognition. International Journal of Machine Learning and Cybernetics, 2016, 7, 1115-1130.	3.6	5
124	An integrative C. elegans proteinâ€"protein interaction network with reliability assessment based on a probabilistic graphical model. Molecular BioSystems, 2016, 12, 85-92.	2.9	12
125	A Probabilistic Relaxation Labeling (PRL) Based Method for C. elegans Cell Tracking in Microscopic Image Sequences. IEEE Journal on Selected Topics in Signal Processing, 2016, 10, 185-192.	10.8	6
126	Identifying Multi-Dimensional Co-Clusters in Tensors Based on Hyperplane Detection in Singular Vector Spaces. PLoS ONE, 2016, 11, e0162293.	2.5	13

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127	Computational Evaluation of EGFR Dynamic Characteristics in Mutation-Induced Drug Resistance Prediction. , 2015, , .		2
128	Systemsâ€level quantification of division timing reveals a common genetic architecture controlling asynchrony and fate asymmetry. Molecular Systems Biology, 2015, 11, 814.	7.2	27
129	Engineering education in China. , 2015, , .		1
130	Local Topology Preserved Tensor Models for Graph Matching. , 2015, , .		3
131	Gene regulatory effects inference for cell fate determination based on single-cell resolution data. , 2015, , .		1
132	Support System Using Microsoft Kinect and Mobile Phone for Daily Activity of Visually Impaired. , 2015, , 425-440.		5
133	Adaptive Cockroach Colony Optimization for Rod-Like Robot Navigation. Journal of Bionic Engineering, 2015, 12, 324-337.	5.0	11
134	EGFR Mutant Structural Database: computationally predicted 3D structures and the corresponding binding free energies with gefitinib and erlotinib. BMC Bioinformatics, 2015, 16, 85.	2.6	32
135	Decoding the EGFR mutation-induced drug resistance in lung cancer treatment by local surface geometric properties. Computers in Biology and Medicine, 2015, 63, 293-300.	7.0	11
136	Sample Weighting: An Inherent Approach for Outlier Suppressing Discriminant Analysis. IEEE Transactions on Knowledge and Data Engineering, 2015, 27, 3070-3083.	5.7	14
137	C. elegans cell matching and tracking in a 4D imageing system. , 2015, , .		1
138	Mining of proteinâ€"protein interfacial residues from massive protein sequential and spatial data. Fuzzy Sets and Systems, 2015, 258, 101-116.	2.7	5
139	Recommender systems based on social networks. Journal of Systems and Software, 2015, 99, 109-119.	4.5	152
140	Contribution of EGFR and ErbB-3 Heterodimerization to the EGFR Mutation-Induced Gefitinib- and Erlotinib-Resistance in Non-Small-Cell Lung Carcinoma Treatments. PLoS ONE, 2015, 10, e0128360.	2.5	23
141	Bicluster Analysis for Coherent Pattern Discovery. , 2015, , 1665-1674.		1
142	Chapter 2: Identification of Genes and their Regulatory Regions Based on Multiple Physical and Structural Properties of a DNA Sequence. Science, Engineering, and Biology Informatics, 2014, , 33-65.	0.1	0
143	A Bicluster-Based Bayesian Principal Component Analysis Method for Microarray Missing Value Estimation. IEEE Journal of Biomedical and Health Informatics, 2014, 18, 863-871.	6.3	24
144	Alpha shape and Delaunay triangulation in studies of protein-related interactions. Briefings in Bioinformatics, 2014, 15, 54-64.	6.5	30

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145	Retina based biometric authentication using phase congruency. International Journal of Machine Learning and Cybernetics, 2014, 5, 933-945.	3.6	8
146	Design Exploration of Geometric Biclustering for Microarray Data Analysis in Data Mining. IEEE Transactions on Parallel and Distributed Systems, 2014, 25, 2540-2550.	5.6	9
147	Detecting overlapping protein complexes based on a generative model with functional and topological properties. BMC Bioinformatics, 2014, 15, 186.	2.6	39
148	Dimensionality reduction and topographic mapping of binary tensors. Pattern Analysis and Applications, 2014, 17, 497-515.	4.6	6
149	A Machine Learning Approach to Improve Contactless Heart Rate Monitoring Using a Webcam. IEEE Journal of Biomedical and Health Informatics, 2014, 18, 1153-1160.	6.3	144
150	GPU-based biclustering for microarray data analysis in neurocomputing. Neurocomputing, 2014, 134, 239-246.	5.9	11
151	Fast prediction of protein–protein interaction sites based on Extreme Learning Machines. Neurocomputing, 2014, 128, 258-266.	5.9	68
152	An FPGA based scalable architecture of a stochastic state point process filter (SSPPF) to track the nonlinear dynamics underlying neural spiking. Microelectronics Journal, 2014, 45, 690-701.	2.0	7
153	Genome-wide nucleosome detection based on the dinucleotide position frequencies. International Journal of Data Mining and Bioinformatics, 2014, 10, 285.	0.1	0
154	Recognizing Bangladeshi Currency for Visually Impaired. Communications in Computer and Information Science, 2014, , 129-135.	0.5	6
155	Identification of DNA-Binding and Protein-Binding Proteins Using Enhanced Graph Wavelet Features. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1017-1031.	3.0	3
156	Autoregressive and Iterative Hidden Markov Models for Periodicity Detection and Solenoid Structure Recognition in Protein Sequences. IEEE Journal of Biomedical and Health Informatics, 2013, 17, 436-441.	6.3	6
157	A graph spectrum based geometric biclustering algorithm. Journal of Theoretical Biology, 2013, 317, 200-211.	1.7	8
158	Bangla text processing and recognition based on Fuzzy unsupervised Feature Extraction and SVM. , 2013, , .		2
159	Noise filtering and occurrence identification of mouse ultrasonic vocalization call. , 2013, , .		1
160	Prediction of anti-EGFR drug resistance base on binding free energy and hydrogen bond analysis. , 2013, , .		5
161	An efficient searching algorithm based on local shape complementarity of hydrogen bonds and relaxation labeling for protein-ligand docking. , 2013, , .		0
162	Prediction of Protein-Protein Interactions Based on Molecular Interface Features and the Support Vector Machine. Current Bioinformatics, 2013, 8, 3-8.	1.5	1

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163	Boolean genetic network model for the control of C. elegans early embryonic cell cycles. BioMedical Engineering OnLine, 2013, 12, S1.	2.7	17
164	A Flexible and Customizable Architecture for the Relaxation Labeling Algorithm. IEEE Transactions on Circuits and Systems II: Express Briefs, 2013, 60, 106-110.	3.0	2
165	Personalized prediction of EGFR mutation-induced drug resistance in lung cancer. Scientific Reports, 2013, 3, 2855.	3.3	34
166	A novel cell nuclei segmentation method for 3D C. elegans embryonic time-lapse images. BMC Bioinformatics, 2013, 14, 328.	2.6	13
167	A Survey on Structural Analysis of Nucleosome Core Particles. Current Bioinformatics, 2013, 8, 112-132.	1.5	0
168	Transcriptional Protein-Protein Cooperativity in POU/HMG/DNA Complexes Revealed by Normal Mode Analysis. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-10.	1.3	1
169	Prediction of Protein-Protein Interactions Based on Molecular Interface Features and the Support Vector Machine. Current Bioinformatics, 2013, 8, 3-8.	1.5	3
170	A Hierarchical Multilevel Image Thresholding Method Based on the Maximum Fuzzy Entropy Principle. , 2013, , 241-272.		0
171	Image Processing and Reconstruction of Cultured Neuron Skeletons. Studies in Computational Intelligence, 2013, , 43-78.	0.9	0
172	Biclustering Analysis for Pattern Discovery: Current Techniques, Comparative Studies and Applications. Current Bioinformatics, 2012, 7, 43-55.	1.5	37
173	Measurement of retinal arteriolar diameters from auto scale phase congruency with fuzzy weighting and L1 Regularization. , 2012, 2012, 1434-7.		0
174	Selection and mapping of DNA structural features for short gene recognition. International Journal of Data Mining and Bioinformatics, 2012, 6, 675.	0.1	1
175	Transcriptional cooperativity in molecular dynamics based on normal mode analysis. , 2012, , .		0
176	Biomarker Identification and Cancer Classification Based on Microarray Data Using Laplace Naive Bayes Model with Mean Shrinkage. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1649-1662.	3.0	44
177	The relationship between geometric patterns of hydrogen bonds and periodic dinucleotides in nucleosome structures. Journal of Theoretical Biology, 2012, 313, 136-141.	1.7	4
178	A hierarchical multilevel thresholding method for edge information extraction using fuzzy entropy. International Journal of Machine Learning and Cybernetics, 2012, 3, 297-305.	3.6	13
179	Analysis of surface structures of hydrogen bonding in proteinâ€"ligand interactions using the alpha shape model. Chemical Physics Letters, 2012, 545, 125-131.	2.6	22
180	Analysis of DNA deformation patterns in nucleosome core particles based on isometric feature mapping and continuous wavelet transform. Chemical Physics Letters, 2012, 547, 73-81.	2.6	3

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181	A graph spectrum framework for optimizing the combination process of geometric biclustering. , 2012, , .		0
182	Fundus phase congruency based biometrics system. , 2012, , .		0
183	Dermatological disease diagnosis using color-skin images. , 2012, , .		51
184	Hypergraph based geometric biclustering algorithm. Pattern Recognition Letters, 2012, 33, 1656-1665.	4.2	11
185	Hybrid method for the analysis of time series gene expression data. Knowledge-Based Systems, 2012, 35, 14-20.	7.1	4
186	Analysis of ligand binding sites using alpha shapes. , 2012, , .		0
187	Coupled Kernel Embedding for Low-Resolution Face Image Recognition. IEEE Transactions on Image Processing, 2012, 21, 3770-3783.	9.8	79
188	PRLâ€dock: Proteinâ€ligand docking based on hydrogen bond matching and probabilistic relaxation labeling. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2137-2153.	2.6	29
189	Noise reduction in microarray gene expression data based on spectral analysis. International Journal of Machine Learning and Cybernetics, 2012, 3, 51-57.	3.6	19
190	Exon prediction using empirical mode decomposition and Fourier transform of structural profiles of DNA sequences. Pattern Recognition, 2012, 45, 947-955.	8.1	29
191	Robust classification using â„"2,1-norm based regression model. Pattern Recognition, 2012, 45, 2708-2718.	8.1	80
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193	Blood cell image segmentation based on the Hough transform and fuzzy curve tracing. , 2011, , .		20
194	Finding Correlated Biclusters from Gene Expression Data. IEEE Transactions on Knowledge and Data Engineering, 2011, 23, 568-584.	5.7	75
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