Hong Yan

List of Publications by Year in descending order

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539 papers 9,906 citations

44069 48 h-index 76900 74 g-index

543 all docs 543 docs citations

543 times ranked

7279 citing authors

#	Article	IF	CITATIONS
1	An adaptive spatial fuzzy clustering algorithm for 3-D MR image segmentation. IEEE Transactions on Medical Imaging, 2003, 22, 1063-1075.	8.9	287
2	Locating and extracting the eye in human face images. Pattern Recognition, 1996, 29, 771-779.	8.1	273
3	An analytic-to-holistic approach for face recognition based on a single frontal view. IEEE Transactions on Pattern Analysis and Machine Intelligence, 1998, 20, 673-686.	13.9	194
4	Missing value imputation for gene expression data: computational techniques to recover missing data from available information. Briefings in Bioinformatics, 2011, 12, 498-513.	6. 5	175
5	A Novel Vessel Segmentation Algorithm for Pathological Retina Images Based on the Divergence of Vector Fields. IEEE Transactions on Medical Imaging, 2008, 27, 237-246.	8.9	168
6	An adaptive logical method for binarization of degraded document images. Pattern Recognition, 2000, 33, 787-807.	8.1	157
7	Interword distance changes represented by sine waves for watermarking text images. IEEE Transactions on Circuits and Systems for Video Technology, 2001, 11, 1237-1245.	8.3	155
8	Recommender systems based on social networks. Journal of Systems and Software, 2015, 99, 109-119.	4.5	152
9	Off-line signature verification based on geometric feature extraction and neural network classification. Pattern Recognition, 1997, 30, 9-17.	8.1	144
10	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
11	Fingerprint classification based on extraction and analysis of singularities and pseudo ridges. Pattern Recognition, 2004, 37, 2233-2243.	8.1	136
12	Blocking Artifacts Suppression in Block-Coded Images Using Overcomplete Wavelet Representation. IEEE Transactions on Circuits and Systems for Video Technology, 2004, 14, 450-461.	8.3	134
13	Handwritten numeral recognition using self-organizing maps and fuzzy rules. Pattern Recognition, 1995, 28, 59-66.	8.1	117
14	A technique of three-level thresholding based on probability partition and fuzzy 3-partition. IEEE Transactions on Fuzzy Systems, 2001, 9, 469-479.	9.8	113
15	Skew Correction of Document Images Using Interline Cross-Correlation. Graphical Models, 1993, 55, 538-543.	0.6	108
16	Current Methods in the Automatic Tissue Segmentation of 3D Magnetic Resonance Brain Images. Current Medical Imaging, 2006, 2, 91-103.	0.8	97
17	Pattern recognition techniques for the emerging field of bioinformatics: A review. Pattern Recognition, 2005, 38, 2055-2073.	8.1	93
18	Microarray missing data imputation based on a set theoretic framework and biological knowledge. Nucleic Acids Research, 2006, 34, 1608-1619.	14.5	92

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19	Molecular subtyping of cancer: current status and moving toward clinical applications. Briefings in Bioinformatics, 2019, 20, 572-584.	6.5	91
20	Cluster Analysis of Gene Expression Data Based on Self-Splitting and Merging Competitive Learning. IEEE Transactions on Information Technology in Biomedicine, 2004, 8, 5-15.	3.2	85
21	Unified formulation of a class of image thresholding techniques. Pattern Recognition, 1996, 29, 2025-2032.	8.1	83
22	Discovering biclusters in gene expression data based on high-dimensional linear geometries. BMC Bioinformatics, 2008, 9, 209.	2.6	82
23	Robust classification using â, "2,1-norm based regression model. Pattern Recognition, 2012, 45, 2708-2718.	8.1	80
24	Coupled Kernel Embedding for Low-Resolution Face Image Recognition. IEEE Transactions on Image Processing, 2012, 21, 3770-3783.	9.8	79
25	HiSCF: leveraging higher-order structures for clustering analysis in biological networks. Bioinformatics, 2021, 37, 542-550.	4.1	76
26	Fast greedy algorithm for active contours. Electronics Letters, 1994, 30, 21-23.	1.0	75
27	Finding Correlated Biclusters from Gene Expression Data. IEEE Transactions on Knowledge and Data Engineering, 2011, 23, 568-584.	5 . 7	75
28	DB-Curve: a novel 2D method of DNA sequence visualization and representation. Chemical Physics Letters, 2003, 367, 170-176.	2.6	74
29	Motion artifact correction in MRI using generalized projections. IEEE Transactions on Medical Imaging, 1991, 10, 40-46.	8.9	72
30	Fast prediction of protein–protein interaction sites based on Extreme Learning Machines. Neurocomputing, 2014, 128, 258-266.	5.9	68
31	Combining Region-of-Interest Extraction and Image Enhancement for Nighttime Vehicle Detection. IEEE Intelligent Systems, 2016, 31, 57-65.	4.0	65
32	Image segmentation based on adaptive cluster prototype estimation. IEEE Transactions on Fuzzy Systems, 2005, 13, 444-453.	9.8	64
33	Gene expression profiling of 1200 pancreatic ductal adenocarcinoma reveals novel subtypes. BMC Cancer, 2018, 18, 603.	2.6	63
34	Skeletonization of ribbon-like shapes based on regularity and singularity analyses. IEEE Transactions on Systems, Man, and Cybernetics, 2001, 31, 401-407.	5.0	62
35	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
36	Autoregressive-Model-Based Missing Value Estimation for DNA Microarray Time Series Data. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 131-137.	3.2	56

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37	Handwritten digit recognition by adaptive-subspace self-organizing map (ASSOM). IEEE Transactions on Neural Networks, 1999, 10, 939-945.	4.2	55
38	Motion artifact suppression: A review of post-processing techniques. Magnetic Resonance Imaging, 1992, 10, 627-635.	1.8	54
39	Attractable snakes based on the greedy algorithm for contour extraction. Pattern Recognition, 2002, 35, 791-806.	8.1	54
40	Robust adaptive spot segmentation of DNA microarray images. Pattern Recognition, 2003, 36, 1251-1254.	8.1	54
41	Stability and style-variation modeling for on-line signature verification. Pattern Recognition, 2003, 36, 2253-2270.	8.1	54
42	A deblocking method for BDCT compressed images based on adaptive projections. IEEE Transactions on Circuits and Systems for Video Technology, 2005, 15, 430-435.	8.3	54
43	Prototype optimization for nearest neighbor classifiers using a two-layer perceptron. Pattern Recognition, 1993, 26, 317-324.	8.1	52
44	Two-stage segmentation of unconstrained handwritten Chinese characters. Pattern Recognition, 2003, 36, 145-156.	8.1	52
45	PromoterExplorer: an effective promoter identification method based on the AdaBoost algorithm. Bioinformatics, 2006, 22, 2722-2728.	4.1	52
46	Singular value decomposition based recommendation using imputed data. Knowledge-Based Systems, 2019, 163, 485-494.	7.1	52
47	Analysis of stroke structures of handwritten Chinese characters. IEEE Transactions on Systems, Man, and Cybernetics, 1999, 29, 47-61.	5.0	51
48	A new geometric biclustering algorithm based on the Hough transform for analysis of large-scale microarray data. Journal of Theoretical Biology, 2008, 251, 264-274.	1.7	51
49	Dermatological disease diagnosis using color-skin images. , 2012, , .		51
50	A Truncated Matrix Decomposition for Hyperspectral Image Super-Resolution. IEEE Transactions on Image Processing, 2020, 29, 8028-8042.	9.8	51
51	An efficient algorithm for smoothing, linearization and detection of structural feature points of binary image contours. Pattern Recognition, 1997, 30, 57-69.	8.1	50
52	Text region extraction in a document image based on the Delaunay tessellation. Pattern Recognition, 2003, 36, 799-809.	8.1	49
53	ID3-derived fuzzy rules and optimized defuzzification for handwritten numeral recognition. IEEE Transactions on Fuzzy Systems, 1996, 4, 24-31.	9.8	48
54	Towards accurate human promoter recognition: a review of currently used sequence features and classification methods. Briefings in Bioinformatics, 2009, 10, 498-508.	6.5	48

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55	Performance evaluation and comparison of PCA Based human face recognition methods for distorted images. International Journal of Machine Learning and Cybernetics, 2011, 2, 245-259.	3.6	47
56	VECTORIZATION OF HAND-DRAWN IMAGE USING PIECEWISE CUBIC BÉZIER CURVES FITTING. Pattern Recognition, 1998, 31, 1747-1755.	8.1	46
57	Off-line signature verification using structural feature correspondence. Pattern Recognition, 2002, 35, 2467-2477.	8.1	46
58	Feature Extraction and Uncorrelated Discriminant Analysis for High-Dimensional Data. IEEE Transactions on Knowledge and Data Engineering, 2008, 20, 601-614.	5.7	46
59	High speed detection of retinal blood vessels in fundus image using phase congruency. Soft Computing, 2011, 15, 1217-1230.	3.6	46
60	Establishment of a morphological atlas of the Caenorhabditis elegans embryo using deep-learning-based 4D segmentation. Nature Communications, 2020, 11, 6254.	12.8	45
61	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
62	Clothing segmentation using foreground and background estimation based on the constrained Delaunay triangulation. Pattern Recognition, 2008, 41, 1581-1592.	8.1	43
63	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
64	POCS-based blocking artifacts suppression using a smoothness constraint set with explicit region modeling. IEEE Transactions on Circuits and Systems for Video Technology, 2005, 15, 795-800.	8.3	41
65	Genome-based expression profiling as a single standardized microarray platform for the diagnosis ofÂendometrial disorder: an array of 126-gene model. Fertility and Sterility, 2010, 94, 114-119.	1.0	41
66	Linking broken character borders with variable sized masks to improve recognition. Pattern Recognition, 1996, 29, 1429-1435.	8.1	40
67	Sign Language Finger Alphabet Recognition from Gabor-PCA Representation of Hand Gestures. , 2007, , .		40
68	Sparse discriminant analysis for breast cancer biomarker identification and classification. Progress in Natural Science: Materials International, 2009, 19, 1635-1641.	4.4	40
69	Incorporating prior information into differential network analysis using non-paranormal graphical models. Bioinformatics, 2017, 33, 2436-2445.	4.1	40
70	Detecting overlapping protein complexes based on a generative model with functional and topological properties. BMC Bioinformatics, 2014, 15, 186.	2.6	39
71	Unsupervised Domain Adaptation via Discriminative Manifold Propagation. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2022, 44, 1653-1669.	13.9	39
72	Artifact reduction in compressed images based on region homogeneity constraints using the projection onto convex sets algorithm. IEEE Transactions on Circuits and Systems for Video Technology, 2002, 12, 891-897.	8.3	38

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73	Dominant spectral component analysis for transcriptional regulations using microarray time-series data. Bioinformatics, 2004, 20, 742-749.	4.1	38
74	A faster converging snake algorithm to locate object boundaries. IEEE Transactions on Image Processing, 2006, 15, 1182-1191.	9.8	37
75	Biclustering Analysis for Pattern Discovery: Current Techniques, Comparative Studies and Applications. Current Bioinformatics, 2012, 7, 43-55.	1.5	37
76	Tensor Decomposition of Gait Dynamics in Parkinson's Disease. IEEE Transactions on Biomedical Engineering, 2018, 65, 1820-1827.	4.2	36
77	Generalized Tensor Regression for Hyperspectral Image Classification. IEEE Transactions on Geoscience and Remote Sensing, 2020, 58, 1244-1258.	6.3	36
78	A nonlinear neural network model of mixture of local principal component analysis: application to handwritten digits recognition. Pattern Recognition, 2001, 34, 203-214.	8.1	35
79	Personalized prediction of EGFR mutation-induced drug resistance in lung cancer. Scientific Reports, 2013, 3, 2855.	3.3	34
80	Studies of spectral properties of short genes using the wavelet subspace Hilbert–Huang transform (WSHHT). Physica A: Statistical Mechanics and Its Applications, 2008, 387, 4223-4247.	2.6	33
81	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
82	Color image segmentation using fuzzy integral and mountain clustering. Fuzzy Sets and Systems, 1999, 107, 121-130.	2.7	32
83	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
84	An improved algorithm for 2-D translational motion artifact correction. IEEE Transactions on Medical Imaging, 1991, 10, 548-553.	8.9	31
85	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
86	Alpha shape and Delaunay triangulation in studies of protein-related interactions. Briefings in Bioinformatics, 2014, 15, 54-64.	6.5	30
87	Handwritten digit recognition using an optimized nearest neighbor classifier. Pattern Recognition Letters, 1994, 15, 207-211.	4.2	29
88	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
89	Exon prediction using empirical mode decomposition and Fourier transform of structural profiles of DNA sequences. Pattern Recognition, 2012, 45, 947-955.	8.1	29
90	Differential network analysis from cross-platform gene expression data. Scientific Reports, 2016, 6, 34112.	3.3	29

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91	Deciphering mechanisms of acquired T790M mutation after EGFR inhibitors for NSCLC by computational simulations. Scientific Reports, 2017, 7, 6595.	3.3	29
92	EnImpute: imputing dropout events in single-cell RNA-sequencing data via ensemble learning. Bioinformatics, 2019, 35, 4827-4829.	4.1	29
93	A curve bend function based method to characterize contour shapes. Pattern Recognition, 1997, 30, 1661-1671.	8.1	28
94	Reconstruction of broken handwritten digits based on structural morphological features. Pattern Recognition, 2001, 34, 235-254.	8.1	28
95	Spectral estimation in unevenly sampled space of periodically expressed microarray time series data. BMC Bioinformatics, 2007, 8, 137.	2.6	28
96	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
97	A computer simulation study on the input function sampling schedules in tracer kinetic modeling with positron emission tomography (PET). Computer Methods and Programs in Biomedicine, 1994, 45, 175-186.	4.7	27
98	Recognition of handwritten digits based on contour information. Pattern Recognition, 1998, 31, 235-255.	8.1	27
99	Recovery of upper body poses in static images based on joints detection. Pattern Recognition Letters, 2009, 30, 503-512.	4.2	27
100	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
101	Fat tissue and fat suppression. Magnetic Resonance Imaging, 1993, 11, 385-393.	1.8	26
102	Statistical power of Fisher test for the detection of short periodic gene expression profiles. Pattern Recognition, 2009, 42, 549-556.	8.1	26
103	The theoretic framework of local weighted approximation for microarray missing value estimation. Pattern Recognition, 2010, 43, 2993-3002.	8.1	26
104	A nonlinear model for fractal image coding. IEEE Transactions on Image Processing, 1997, 6, 373-382.	9.8	25
105	Structural primitive extraction and coding for handwritten numeral recognition. Pattern Recognition, 1998, 31, 493-509.	8.1	25
106	Gene expression data clustering and visualization based on a binary hierarchical clustering framework. Journal of Visual Languages and Computing, 2003, 14, 341-362.	1.8	25
107	Eukaryotic promoter prediction based on relative entropy and positional information. Physical Review E, 2007, 75, 041908.	2.1	25
108	OMWSA: detection of DNA repeats using moving window spectral analysis. Bioinformatics, 2007, 23, 631-633.	4.1	25

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109	Co-Clustering to Reveal Salient Facial Features for Expression Recognition. IEEE Transactions on Affective Computing, 2020, 11, 348-360.	8.3	25
110	Data truncation artifact reduction in MR imaging using a multilayer neural network. IEEE Transactions on Medical Imaging, 1993, 12, 73-77.	8.9	24
111	SEPARATION OF SINGLE-TOUCHING HANDWRITTEN NUMERAL STRINGS BASED ON STRUCTURAL FEATURES. Pattern Recognition, 1998, 31, 1835-1847.	8.1	24
112	Convergence Condition and Efficient Implementation of the Fuzzy Curve-Tracing (FCT) Algorithm. IEEE Transactions on Systems, Man, and Cybernetics, 2004, 34, 210-221.	5.0	24
113	Detection of Tandem Repeats in DNA Sequences Based on Parametric Spectral Estimation. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 747-755.	3.2	24
114	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
115	Exploiting higher-order patterns for community detection in attributed graphs. Integrated Computer-Aided Engineering, 2021, 28, 207-218.	4.6	24
116	Bayes Saliency-Based Object Proposal Generator for Nighttime Traffic Images. IEEE Transactions on Intelligent Transportation Systems, 2018, 19, 814-825.	8.0	23
117	Spatial-dependence recurrence sample entropy. Physica A: Statistical Mechanics and Its Applications, 2018, 494, 581-590.	2.6	23
118	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
119	Face Recognition Using the Weighted Fractal Neighbor Distance. IEEE Transactions on Systems, Man and Cybernetics, Part C: Applications and Reviews, 2005, 35, 576-582.	2.9	22
120	A probabilistic relaxation labeling framework for reducing the noise effect in geometric biclustering of gene expression data. Pattern Recognition, 2009, 42, 2578-2588.	8.1	22
121	Framelet Kernels With Applications to Support Vector Regression and Regularization Networks. IEEE Transactions on Systems, Man, and Cybernetics, 2010, 40, 1128-1144.	5.0	22
122	Analysis of surface structures of hydrogen bonding in protein–ligand interactions using the alpha shape model. Chemical Physics Letters, 2012, 545, 125-131.	2.6	22
123	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
124	scTSSR: gene expression recovery for single-cell RNA sequencing using two-side sparse self-representation. Bioinformatics, 2020, 36, 3131-3138.	4.1	22
125	Character and line extraction from color map images using a multi-layer neural network. Pattern Recognition Letters, 1994, 15, 97-103.	4.2	21
126	An adaptive split-and-merge method for binary image contour data compression. Pattern Recognition Letters, 2001, 22, 299-307.	4.2	21

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127	AN EMPIRICAL STUDY ON THE CHARACTERISTICS OF GABOR REPRESENTATIONS FOR FACE RECOGNITION. International Journal of Pattern Recognition and Artificial Intelligence, 2009, 23, 401-431.	1.2	21
128	Handwritten numeral recognition using a small number of fuzzy rules with optimized defuzzification parameters. Neural Networks, 1995, 8, 821-827.	5.9	20
129	Document image mosaicing. , 0, , .		20
130	Fuzzy curve-tracing algorithm. IEEE Transactions on Systems, Man, and Cybernetics, 2001, 31, 768-780.	5.0	20
131	Robust topology-adaptive snakes for image segmentation. Image and Vision Computing, 2002, 20, 147-164.	4.5	20
132	A discriminatory function for prediction of protein–DNA interactions based on alpha shape modeling. Bioinformatics, 2010, 26, 2541-2548.	4.1	20
133	Blood cell image segmentation based on the Hough transform and fuzzy curve tracing. , $2011, , .$		20
134	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
135	Fuzzy SLIC: Fuzzy Simple Linear Iterative Clustering. IEEE Transactions on Circuits and Systems for Video Technology, 2021, 31, 2114-2124.	8.3	20
136	Fat suppression with an improved selective presaturation pulse. Magnetic Resonance Imaging, 1992, 10, 49-53.	1.8	19
137	An improved algorithm for rotational motion artifact suppression in MRI. IEEE Transactions on Medical Imaging, 1998, 17, 310-317.	8.9	19
138	SCS: Signal, Context, and Structure Features for Genome-Wide Human Promoter Recognition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 550-562.	3.0	19
139	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
140	Establishment of Signaling Interactions with Cellular Resolution for Every Cell Cycle of Embryogenesis. Genetics, 2018, 209, 37-49.	2.9	19
141	Generalized Conditional Domain Adaptation: A Causal Perspective With Low-Rank Translators. IEEE Transactions on Cybernetics, 2020, 50, 821-834.	9.5	19
142	Multi-deep features fusion for high-resolution remote sensing image scene classification. Neural Computing and Applications, 2021, 33, 2047-2063.	5.6	19
143	Saliency Detection Using Deep Features and Affinity-Based Robust Background Subtraction. IEEE Transactions on Multimedia, 2021, 23, 2902-2916.	7.2	19
144	Dual Quaternions and Dual Quaternion Vectors. Communications on Applied Mathematics and Computation, 2022, 4, 1494-1508.	1.7	19

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145	A modified Gerchberg-Saxton algorithm for one-dimensional motion artifact correction in MRI. IEEE Transactions on Signal Processing, 1991, 39, 1428-1433.	5. 3	18
146	Extracting strokes from static line images based on selective searching. Pattern Recognition, 1999, 32, 935-946.	8.1	18
147	Image analysis for digital media applications. IEEE Computer Graphics and Applications, 2001, 21, 18-26.	1.2	18
148	Object recognition based on fractal neighbor distance. Signal Processing, 2001, 81, 2105-2129.	3.7	18
149	Clustering of temporal gene expression data by regularized spline regression and an energy based similarity measure. Pattern Recognition, 2010, 43, 3969-3976.	8.1	18
150	Rapid feature extraction for Bangla handwritten digit recognition. , 2011, , .		18
151	Regularized logistic regression with network-based pairwise interaction for biomarker identification in breast cancer. BMC Bioinformatics, 2016, 17, 108.	2.6	18
152	Shape skeletonization by identifying discrete local symmetries. Pattern Recognition, 2001, 34, 1895-1905.	8.1	17
153	The fractal neighbor distance measure. Pattern Recognition, 2002, 35, 1371-1387.	8.1	17
154	PCA based face recognition and testing criteria. , 2009, , .		17
155	Prediction of DNA-binding protein based on statistical and geometric features and support vector machines. Proteome Science, 2011, 9, S1.	1.7	17
156			
	Boolean genetic network model for the control of C. elegans early embryonic cell cycles. BioMedical Engineering OnLine, 2013, 12, S1.	2.7	17
157		2.7	17
157 158	Engineering OnLine, 2013, 12, S1.		
	Engineering OnLine, 2013, 12, S1. A two-layer integration framework for protein complex detection. BMC Bioinformatics, 2016, 17, 100. mTD: A database of microRNAs affecting therapeutic effects of drugs. Journal of Genetics and	2.6	17
158	Engineering OnLine, 2013, 12, S1. A two-layer integration framework for protein complex detection. BMC Bioinformatics, 2016, 17, 100. mTD: A database of microRNAs affecting therapeutic effects of drugs. Journal of Genetics and Genomics, 2017, 44, 269-271. An online spatio-temporal tensor learning model for visual tracking and its applications to facial	2.6 3.9	17
158 159	Engineering OnLine, 2013, 12, S1. A two-layer integration framework for protein complex detection. BMC Bioinformatics, 2016, 17, 100. mTD: A database of microRNAs affecting therapeutic effects of drugs. Journal of Genetics and Genomics, 2017, 44, 269-271. 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. Hydrogen bond analysis of the EGFR-ErbB3 heterodimer related to non-small cell lung cancer and	2.6 3.9 7.6	17 17 17

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163	DrPOCS: Drug Repositioning Based on Projection Onto Convex Sets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 154-162.	3.0	16
164	Signature verification using fractal transformation. , 0, , .		15
165	Separation of touching handwritten multi-numeral strings based on morphological structural features. Pattern Recognition, 2001, 34, 587-599.	8.1	15
166	Modeling and animation of human expressions using NURBS curves based on facial anatomy. Signal Processing: Image Communication, 2002, 17, 457-465.	3.2	15
167	Spectral Estimation Techniques for DNA Sequence and Microarray Data Analysis. Current Bioinformatics, 2007, 2, 145-156.	1.5	15
168	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
169	3DMMS: robust 3D Membrane Morphological Segmentation of C. elegans embryo. BMC Bioinformatics, 2019, 20, 176.	2.6	15
170	Handwritten signature verification based on neural 'gas' based vector quantization., 0,,.		14
171	Newspaper document analysis featuring connected line segmentation. , 0, , .		14
172	Identification of Elite Swimmers' Race Patterns Using Cluster Analysis. International Journal of Sports Science and Coaching, 2007, 2, 293-303.	1.4	14
173	HoughFeature, a novel method for assessing drug effects in three-color cDNA microarray experiments. BMC Bioinformatics, 2007, 8, 256.	2.6	14
174	Structural property of regulatory elements in human promoters. Physical Review E, 2008, 77, 041908.	2.1	14
175	Relationship between periodic dinucleotides and the nucleosome structure revealed by alpha shape modeling. Chemical Physics Letters, 2010, 489, 225-228.	2.6	14
176	Sample Weighting: An Inherent Approach for Outlier Suppressing Discriminant Analysis. IEEE Transactions on Knowledge and Data Engineering, 2015, 27, 3070-3083.	5.7	14
177	Comparative analysis of housekeeping and tissue-specific driver nodes in human protein interaction networks. BMC Bioinformatics, 2016, 17, 358.	2.6	14
178	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
179	Identifying differential networks based on multi-platform gene expression data. Molecular BioSystems, 2017, 13, 183-192.	2.9	14
180	DiffNetFDR: differential network analysis with false discovery rate control. Bioinformatics, 2019, 35, 3184-3186.	4.1	14

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181	Saliency detection via multiple-morphological and superpixel based fast fuzzy C-mean clustering network. Expert Systems With Applications, 2020, 161, 113654.	7.6	14
182	Deep center-based dual-constrained hashing for discriminative face image retrieval. Pattern Recognition, 2021, 117, 107976.	8.1	14
183	Structure-based protein–ligand interaction fingerprints for binding affinity prediction. Computational and Structural Biotechnology Journal, 2021, 19, 6291-6300.	4.1	14
184	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
185	Slice profile improvement for a clinical MRI system. Magnetic Resonance Imaging, 1990, 8, 767-770.	1.8	13
186	Stroke extraction as pre-processing step to improve thinning results of Chinese characters. Pattern Recognition Letters, 2000, 21, 817-825.	4.2	13
187	An Improved Position Weight Matrix method based on an entropy measure for the recognition of prokaryotic promoters. International Journal of Data Mining and Bioinformatics, 2011, 5, 22.	0.1	13
188	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
189	A novel cell nuclei segmentation method for 3D C. elegans embryonic time-lapse images. BMC Bioinformatics, 2013, 14, 328.	2.6	13
190	Identifying EGFR mutation-induced drug resistance based on alpha shape model analysis of the dynamics. Proteome Science, 2016, 14, 12.	1.7	13
191	DiffGraph: an R package for identifying gene network rewiring using differential graphical models. Bioinformatics, 2018, 34, 1571-1573.	4.1	13
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