

Jagath Chandana Rajapakse

List of Publications by Year in descending order

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Version: 2024-02-01

189
papers

8,890
citations

101535

36
h-index

45310

90
g-index

218
all docs

218
docs citations

218
times ranked

9555
citing authors

#	ARTICLE	IF	CITATIONS
1	Decoding task specific and task general functional architectures of the brain. Human Brain Mapping, 2022, 43, 2801-2816.	3.6	4
2	Combining Neuroimaging and Omics Datasets for Disease Classification Using Graph Neural Networks. Frontiers in Neuroscience, 2022, 16, .	2.8	8
3	Obtaining leaner deep neural networks for decoding brain functional connectome in a single shot. Neurocomputing, 2021, 453, 326-336.	5.9	10
4	Graph embeddings on gene ontology annotations for proteinâ€“protein interaction prediction. BMC Bioinformatics, 2020, 21, 560.	2.6	15
5	Iterative consensus spectral clustering improves detection of subject and group level brain functional modules. Scientific Reports, 2020, 10, 7590.	3.3	17
6	Ambivert degree identifies crucial brain functional hubs and improves detection of Alzheimerâ€™s Disease and Autism Spectrum Disorder. Neurolmage: Clinical, 2020, 25, 102186.	2.7	13
7	Decoding Task States by Spotting Salient Patterns at Time Points and Brain Regions. Lecture Notes in Computer Science, 2020, , 88-97.	1.3	5
8	Fusing gene expressions and transitive protein-protein interactions for inference of gene regulatory networks. BMC Systems Biology, 2019, 13, 37.	3.0	6
9	Functional homogeneity and specificity of topological modules in human proteome. BMC Bioinformatics, 2019, 19, 553.	2.6	2
10	Refining modules to determine functionally significant clusters in molecular networks. BMC Genomics, 2019, 20, 901.	2.8	2
11	Predicting Missing and Spurious Protein-Protein Interactions Using Graph Embeddings on GO Annotation Graph. , 2019, , .		3
12	GO2Vec: transforming GO terms and proteins to vector representations via graph embeddings. BMC Genomics, 2019, 20, 918.	2.8	18
13	A deep neural network approach to predicting clinical outcomes of neuroblastoma patients. BMC Medical Genomics, 2019, 12, 178.	1.5	15
14	Computational Analysis of Proteinâ€“Protein Interactions in Motile T-Cells. Methods in Molecular Biology, 2019, 1930, 149-156.	0.9	3
15	Human Wharton's Jelly Mesenchymal Stem Cells Show Unique Gene Expression Compared with Bone Marrow Mesenchymal Stem Cells Using Single-Cell RNA-Sequencing. Stem Cells and Development, 2019, 28, 196-211.	2.1	52
16	Analysis of correlation-based biomolecular networks from different omics data by fitting stochastic block models. F1000Research, 2019, 8, 465.	1.6	1
17	Analysis of correlation-based biomolecular networks from different omics data by fitting stochastic block models. F1000Research, 2019, 8, 465.	1.6	2
18	Predicting Affective States of Programming Using Keyboard Data and Mouse Behaviors. , 2018, , .		4

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19	Nodal degree distributions of resting-state functional brain modules. , 2018, , .		3
20	Profiling heterogeneity of Alzheimer's disease using white-matter impairment factors. Neurolmage: Clinical, 2018, 20, 1222-1232.	2.7	12
21	Gene Ontology Enrichment Improves Performances of Functional Similarity of Genes. Scientific Reports, 2018, 8, 12100.	3.3	22
22	Predicting clinical outcome of neuroblastoma patients using an integrative network-based approach. Biology Direct, 2018, 13, 12.	4.6	13
23	Automated fluorescence intensity and gradient analysis enables detection of rare fluorescent mutant cells deep within the tissue of RaDR mice. Scientific Reports, 2018, 8, 12108.	3.3	7
24	Fitting networks models for functional brain connectivity. , 2017, , .		4
25	Detecting functional modules of the brain using eigen value decomposition of the signless Laplacian. , 2017, , .		0
26	MultiDCoX: Multi-factor analysis of differential co-expression. BMC Bioinformatics, 2017, 18, 576.	2.6	5
27	Mixed spectrum analysis in spatial context: Application to fMRI. , 2016, , .		0
28	Locality regularized sparse subspace clustering with application to cortex parcellation on resting fMRI. , 2016, , .		0
29	Quantification of liver fibrosis via second harmonic imaging of the Glisson's capsule from liver surface. Journal of Biophotonics, 2016, 9, 351-363.	2.3	46
30	Mixed Spectrum Analysis on fMRI Time-Series. IEEE Transactions on Medical Imaging, 2016, 35, 1555-1564.	8.9	14
31	Gene and sample selection using T-score with sample selection. Journal of Biomedical Informatics, 2016, 59, 31-41.	4.3	21
32	Aging exacerbates damage and delays repair of alveolar epithelia following influenza viral pneumonia. Respiratory Research, 2014, 15, 116.	3.6	29
33	Rosa26-GFP Direct Repeat (RaDR-GFP) Mice Reveal Tissue- and Age-Dependence of Homologous Recombination in Mammals In Vivo. PLoS Genetics, 2014, 10, e1004299.	3.5	44
34	Extracting rate changes in transcriptional regulation from MEDLINE abstracts. BMC Bioinformatics, 2014, 15, S4.	2.6	2
35	Identification of a new export signal in <i>Plasmodium yoelii</i> : identification of a new exportome. Cellular Microbiology, 2014, 16, 673-686.	2.1	14
36	qFibrosis: A fully-quantitative innovative method incorporating histological features to facilitate accurate fibrosis scoring in animal model and chronic hepatitis B patients. Journal of Hepatology, 2014, 61, 260-269.	3.7	127

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37	CUDAGRAN: Parallel Speedup of Inferring Large Gene Regulatory Networks from Expression Data Using Random Forest. Lecture Notes in Computer Science, 2014, , 85-97.	1.3	0
38	Multiclass Gene Selection Using Pareto-Fronts. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 87-97.	3.0	23
39	Neutrophils infected with highly virulent influenza H3N2 virus exhibit augmented early cell death and rapid induction of type I interferon signaling pathways. Genomics, 2013, 101, 101-112.	2.9	32
40	Spatiotemporal quantification of cell dynamics in the lung following influenza virus infection. Journal of Biomedical Optics, 2013, 18, 046001.	2.6	15
41	Inferring Gene Regulatory Networks from Time-Series Expressions Using Random Forests Ensemble. Lecture Notes in Computer Science, 2013, , 13-22.	1.3	21
42	Inferring Time-Delayed Gene Regulatory Networks Using Cross-Correlation and Sparse Regression. Lecture Notes in Computer Science, 2013, , 64-75.	1.3	10
43	Simultaneous Sample and Gene Selection Using T-score and Approximate Support Vectors. Lecture Notes in Computer Science, 2013, , 79-90.	1.3	0
44	Serum Proteome and Cytokine Analysis in a Longitudinal Cohort of Adults with Primary Dengue Infection Reveals Predictive Markers of DHF. PLoS Neglected Tropical Diseases, 2012, 6, e1887.	3.0	89
45	Improving signal-to-noise ratio of structured light microscopy based on photon reassignment. Biomedical Optics Express, 2012, 3, 206.	2.9	5
46	Differential pulmonary transcriptomic profiles in murine lungs infected with low and highly virulent influenza H3N2 viruses reveal dysregulation of TREM1 signaling, cytokines, and chemokines. Functional and Integrative Genomics, 2012, 12, 105-117.	3.5	37
47	Levodopa and the feedback process on setâ€shifting in parkinson's disease. Human Brain Mapping, 2012, 33, 27-39.	3.6	17
48	Scale-space analysis of event-related fMRI data using higher harmonics. , 2011, , .		0
49	Toward Better Understanding of Protein Secondary Structure: Extracting Prediction Rules. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 858-864.	3.0	9
50	Stability of building gene regulatory networks with sparse autoregressive models. BMC Bioinformatics, 2011, 12, S17.	2.6	20
51	Correlation of cell membrane dynamics and cell motility. BMC Bioinformatics, 2011, 12, S19.	2.6	11
52	Features for cells and nuclei classification. , 2011, 2011, 6601-4.		5
53	Automated scoring of liver fibrosis through combined features from different collagen groups. , 2011, 2011, 4503-6.		2
54	Staging tissues with conditional random fields. , 2011, 2011, 5128-31.		11

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55	Tree-structured algorithm for long weak motif discovery. Bioinformatics, 2011, 27, 2641-2647.	4.1	14
56	Intensity normalization of two-photon microscopy images for liver fibrosis analysis. , 2011, , .		0
57	Estimation of the population of neutrophils induced to differentiate from the MPRO mouse promyelocytic cell line. , 2011, 2011, 6001-4.		0
58	Integration of Epigenetic Data in Bayesian Network Modeling of Gene Regulatory Network. Lecture Notes in Computer Science, 2011, , 87-96.	1.3	7
59	Stability of Inferring Gene Regulatory Structure with Dynamic Bayesian Networks. Lecture Notes in Computer Science, 2011, , 237-246.	1.3	0
60	DISCRIMINATIVE FRAMEWORK OF NEURAL ACTIVATION ANALYSIS WITH fMRI. , 2011, , 483-500.		0
61	Gene and sample selection for cancer classification with support vectors based t-statistic. Neurocomputing, 2010, 73, 2353-2362.	5.9	42
62	RecMotif: a novel fast algorithm for weak motif discovery. BMC Bioinformatics, 2010, 11, S8.	2.6	14
63	Building gene networks with time-delayed regulations. Pattern Recognition Letters, 2010, 31, 2133-2137.	4.2	12
64	A Cell Profiling Framework for Modeling Drug Responses from HCS Imaging. Journal of Biomolecular Screening, 2010, 15, 858-868.	2.6	13
65	Toward surface quantification of liver fibrosis progression. Journal of Biomedical Optics, 2010, 15, 056007.	2.6	25
66	Gene regulatory networks with variable-order dynamic Bayesian networks. , 2010, , .		4
67	ListMotif: A time and memory efficient algorithm for weak motif discovery. , 2010, , .		1
68	Complex ICA-R. , 2010, , .		2
69	Pulse-modulated second harmonic imaging microscope quantitatively demonstrates marked increase of collagen in tumor after chemotherapy. Journal of Biomedical Optics, 2010, 15, 056016.	2.6	11
70	SVM-RFE With MRMR Filter for Gene Selection. IEEE Transactions on Nanobioscience, 2010, 9, 31-37.	3.3	267
71	Evolutionary approach to ICA-R. , 2010, , .		1
72	Support vectors based correlation coefficient for gene and sample selection in cancer classification. , 2010, , .		1

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73	Quantification of Cytoskeletal Protein Localization from High-Content Images. Lecture Notes in Computer Science, 2010, , 289-300.	1.3	2
74	Identifying Cells in Histopathological Images. Lecture Notes in Computer Science, 2010, , 244-252.	1.3	6
75	Fibro-C-Index: comprehensive, morphology-based quantification of liver fibrosis using second harmonic generation and two-photon microscopy. Journal of Biomedical Optics, 2009, 14, 044013.	2.6	73
76	Sub-population analysis based on temporal features of high content images. BMC Bioinformatics, 2009, 10, S4.	2.6	3
77	Detecting robust time-delayed regulation in Mycobacterium tuberculosis. BMC Genomics, 2009, 10, S28.	2.8	6
78	Segmentation of Clustered Nuclei With Shape Markers and Marking Function. IEEE Transactions on Biomedical Engineering, 2009, 56, 741-748.	4.2	264
79	Comparative genomic workflow. IEEE Engineering in Medicine and Biology Magazine, 2009, 28, 19-24.	0.8	2
80	Computational techniques and pattern recognition [Introduction to the special issue. IEEE Engineering in Medicine and Biology Magazine, 2009, 28, 16-18.	0.8	0
81	Time Efficient DT-MRI Acquisition Parameters for Robust Estimation of Fiber Tracts. Journal of Signal Processing Systems, 2009, 54, 25-31.	2.1	0
82	Di-codon usage for classification of genes. BioSystems, 2009, 98, 1-6.	2.0	5
83	Gene Classification Using Codon Usage and Support Vector Machines. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 134-143.	3.0	33
84	Di-codon Usage for Gene Classification. Lecture Notes in Computer Science, 2009, , 211-221.	1.3	5
85	Joint Tracking of Cell Morphology and Motion. Lecture Notes in Computer Science, 2009, , 36-45.	1.3	1
86	F-score with Pareto Front Analysis for Multiclass Gene Selection. Lecture Notes in Computer Science, 2009, , 56-67.	1.3	3
87	Probabilistic Framework for Brain Connectivity From Functional MR Images. IEEE Transactions on Medical Imaging, 2008, 27, 825-833.	8.9	10
88	Fuzzy approach to incorporate hemodynamic variability and contextual information for detection of brain activation. Neurocomputing, 2008, 71, 3184-3192.	5.9	6
89	Extracting decision rules in prediction of protein secondary structure. , 2008, , .		0
90	Extracting EEG rhythms using ICA-R. , 2008, , .		7

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91	Protein localization on cellular images with Markov random fields. , 2008, , .		0
92	Support Vector Based T-Score for Gene Ranking. Lecture Notes in Computer Science, 2008, , 144-153.	1.3	7
93	Fusion of Gene Regulatory and Protein Interaction Networks Using Skip-Chain Models. Lecture Notes in Computer Science, 2008, , 214-224.	1.3	4
94	Comparison of Human and Mouse Pseudogenes. , 2007, , .		0
95	One-Versus-One and One-Versus-All Multiclass SVM-RFE for Gene Selection in Cancer Classification. , 2007, , 47-56.		35
96	Amino Acid Features for Prediction of Protein-Protein Interface Residues with Support Vector Machines. , 2007, , 187-196.		2
97	SVM-RFE with Relevancy and Redundancy Criteria for Gene Selection. Lecture Notes in Computer Science, 2007, , 242-252.	1.3	19
98	Prediction of Protein Secondary Structure with two-stage multi-class SVMs. International Journal of Data Mining and Bioinformatics, 2007, 1, 248.	0.1	31
99	Guest Editors' Introduction to the Special Section: Computational Intelligence Approaches in Computational Biology and Bioinformatics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 161-162.	3.0	1
100	Learning effective brain connectivity with dynamic Bayesian networks. NeuroImage, 2007, 37, 749-760.	4.2	122
101	Grid-Enabled BLASTZ: Application to Comparative Genomics. Journal of Signal Processing Systems, 2007, 48, 301-309.	1.0	1
102	Power spectral based detection of brain activation from fMR images. Neural Computing and Applications, 2007, 16, 551-557.	5.6	1
103	Modeling hemodynamic variability with fuzzy features for detecting brain activation from fMR time-series. Neural Computing and Applications, 2007, 16, 541-549.	5.6	0
104	Validation of Gene Regulatory Networks from Protein-Protein Interaction Data: Application to Cell-Cycle Regulation. Lecture Notes in Computer Science, 2007, , 300-310.	1.3	3
105	Time-Frequency Method Based Activation Detection in Functional MRI Time-Series. Lecture Notes in Computer Science, 2007, , 368-377.	1.3	0
106	Human Brain Anatomical Connectivity Analysis Using Sequential Sampling and Resampling. Lecture Notes in Computer Science, 2007, , 391-400.	1.3	0
107	FPGA Neurocomputers. , 2006, , 1-36.		7
108	Determination of the Relative Importance of Gene Function or Taxonomic Grouping to Codon Usage Bias Using Cluster Analysis and SVMs. , 2006, , .		1

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109	Learning functional structure from fMR images. NeuroImage, 2006, 31, 1601-1613.	4.2	74
110	Contextual modeling of functional MR images with conditional random fields. IEEE Transactions on Medical Imaging, 2006, 25, 804-812.	8.9	29
111	Protein-Protein Interface Residue Prediction with SVM Using Evolutionary Profiles and Accessible Surface Areas. , 2006, , .		7
112	Two-stage support vector regression approach for predicting accessible surface areas of amino acids. Proteins: Structure, Function and Bioinformatics, 2006, 63, 542-550.	2.6	46
113	Editorial for special issue on “Soft Computing for Bioinformatics and Medical Informatics” Soft Computing, 2006, 10, 285-286.	3.6	0
114	Input encoding method for identifying transcription start sites in RNA polymerase II promoters by neural networks. Soft Computing, 2006, 10, 331-337.	3.6	0
115	NURBS-based visualization of age-related diversity in cortical morphology. Journal of Visualization, 2006, 9, 9-11.	1.8	1
116	Exploratory analysis of brain connectivity with ICA. IEEE Engineering in Medicine and Biology Magazine, 2006, 25, 102-111.	0.8	27
117	ICA with Reference. Neurocomputing, 2006, 69, 2244-2257.	5.9	167
118	Extraction of Fuzzy Features for Detecting Brain Activation from Functional MR Time-Series. Lecture Notes in Computer Science, 2006, , 983-992.	1.3	1
119	Multiple SVM-RFE for Gene Selection in Cancer Classification With Expression Data. IEEE Transactions on Nanobioscience, 2005, 4, 228-234.	3.3	357
120	Prediction of protein relative solvent accessibility with a two-stage SVM approach. Proteins: Structure, Function and Bioinformatics, 2005, 59, 30-37.	2.6	56
121	Markov Encoding for Detecting Signals in Genomic Sequences. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 131-142.	3.0	57
122	Segmentation of subcortical brain structures using fuzzy templates. NeuroImage, 2005, 28, 915-924.	4.2	58
123	Phonological processing in Chinese-English bilingual biculturals: An fMRI study. NeuroImage, 2005, 28, 579-587.	4.2	43
124	Proteomic Cancer Classification with Mass Spectrometry Data. Molecular Diagnosis and Therapy, 2005, 5, 281-292.	3.3	32
125	Approach and Applications of Constrained ICA. IEEE Transactions on Neural Networks, 2005, 16, 203-212.	4.2	259
126	Syntactic Approach to Predict Membrane Spanning Regions of Transmembrane Proteins. Lecture Notes in Computer Science, 2005, , 95-104.	1.3	0

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127	FULLY AUTOMATED PEELING TECHNIQUE FOR T1-WEIGHTED, HIGH-QUALITY MR HEAD SCANS. International Journal of Image and Graphics, 2004, 04, 141-156.	1.5	5
128	Graphical approach to weak motif recognition. Genome Informatics, 2004, 15, 52-62.	0.4	8
129	Eliminating indeterminacy in ICA. Neurocomputing, 2003, 50, 271-290.	5.9	47
130	NURBS snakes. Image and Vision Computing, 2003, 21, 551-562.	4.5	25
131	NURBS-Based Segmentation of the Brain in Medical Images. International Journal of Pattern Recognition and Artificial Intelligence, 2003, 17, 995-1009.	1.2	7
132	General Framework for Two-stage Approaches to Protein Secondary Structure Prediction. Asia Pacific Biotech News, 2003, 07, 122-128.	0.0	0
133	9th International Conference on Neural Information Processing [front matter]. , 2002, , .		0
134	Splice site detection with neural networks/Markov model hybrids. , 2002, , .		1
135	Optimal approach to sequence-to-sequence prediction: applications in bioinformatics. , 2002, , .		0
136	Segmentation of pathological features in MRI brain datasets. , 2002, , .		4
137	Proton Spectroscopic Imaging Shows Abnormalities in Glial and Neuronal Cell Pools in Frontal Lobe Epilepsy. Epilepsia, 2001, 42, 1507-1514.	5.1	48
138	Bayesian approach to segmentation of statistical parametric maps. IEEE Transactions on Biomedical Engineering, 2001, 48, 1186-1194.	4.2	43
139	Spatiotemporal Analysis of Functional Images Using the Fixed Effect Model. Lecture Notes in Computer Science, 2001, , 190-196.	1.3	0
140	Random-grid stereologic volumetry of MR head scans. Journal of Magnetic Resonance Imaging, 2000, 12, 833-841.	3.4	5
141	Efficient Sampling in 3-D Stereologic Volumetry. Critical Reviews in Biomedical Engineering, 2000, 28, 493-498.	0.9	1
142	Probabilistic Fusion of Hemodynamic Parameter Maps. Critical Reviews in Biomedical Engineering, 2000, 28, 363-369.	0.9	1
143	MR image segmentation and tissue metabolite contrast in ¹ H spectroscopic imaging of normal and aging brain. Magnetic Resonance in Medicine, 1999, 41, 841-845.	3.0	58
144	Development of the human corpus callosum during childhood and adolescence: A longitudinal MRI study. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 1999, 23, 571-588.	4.8	338

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145	Segmentation of MR images with intensity inhomogeneities. Image and Vision Computing, 1998, 16, 165-180.	4.5	129
146	Modeling hemodynamic response for analysis of functional MRI time-series. , 1998, 6, 283-300.		185
147	Regional glucose metabolic abnormalities are not the result of atrophy in Alzheimer's disease. Neurology, 1998, 50, 1585-1593.	1.1	300
148	Statistical approach to segmentation of single-channel cerebral MR images. IEEE Transactions on Medical Imaging, 1997, 16, 176-186.	8.9	567
149	Quantitative magnetic resonance imaging of the corpus callosum in childhood onset schizophrenia. Psychiatry Research - Neuroimaging, 1997, 68, 77-86.	1.8	64
150	Sexual dimorphism of the developing human brain. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 1997, 21, 1185-1201.	4.8	443
151	Regional MRI measurements of the corpus callosum: a methodological and developmental study. Brain and Development, 1996, 18, 379-388.	1.1	90
152	Quantitative Brain Magnetic Resonance Imaging in Attention-Deficit Hyperactivity Disorder. Archives of General Psychiatry, 1996, 53, 607.	12.3	965
153	Brain Anatomic Magnetic Resonance Imaging in Childhood-Onset Schizophrenia. Archives of General Psychiatry, 1996, 53, 617.	12.3	193
154	Temporal lobe morphology in childhood-onset schizophrenia [published erratum appears in Am J Psychiatry 1996 Jun;153(6):851]. American Journal of Psychiatry, 1996, 153, 355-361.	7.2	104
155	Quantitative Magnetic Resonance Imaging of Human Brain Development: Ages 4â€“18. Cerebral Cortex, 1996, 6, 551-559.	2.9	952
156	A quantitative MRI study of the corpus callosum in children and adolescents. Developmental Brain Research, 1996, 91, 274-280.	1.7	275
157	Quantitative MRI of the temporal lobe, amygdala, and hippocampus in normal human development: Ages 4-18 years. Journal of Comparative Neurology, 1996, 366, 223-230.	1.6	676
158	A technique for single-channel MR brain tissue segmentation: Application to a pediatric sample. Magnetic Resonance Imaging, 1996, 14, 1053-1065.	1.8	41
159	Cerebral Magnetic Resonance Image Segmentation Using Data Fusion. Journal of Computer Assisted Tomography, 1996, 20, 206-218.	0.9	33
160	<title>Multimodality fusion of physiological images using regularization theory and deformable models</title>. , 1994, , .		0
161	<title>Regularization approach to multisensor reconstruction</title>. , 1993, , .		0
162	<title>Hierarchical neural architecture for visual pattern recognition and reconstruction</title>. , 1990, 1246, 288.		1

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163	Fuzzy region integration approach for subcortical structure segmentation. , 0, , .		0
164	Neural network modeling of neuronal-vascular coupling. , 0, , .		0
165	Functional MR image registration using a genetic algorithm. , 0, , .		2
166	Random-grid stereology applied to MR head scans. , 0, , .		0
167	Emerging segmentation of neuroanatomical structures in magnetic resonance images. , 0, , .		1
168	Independent component analysis and beyond in brain imaging: EEG, MEG, fMRI, and PET. , 0, , .		13
169	Cerebral and hippocampal volumetry in early Alzheimer's disease. , 0, , .		2
170	Neural networks in FPGAs. , 0, , .		18
171	Genetic approach to biosequence alignment (GABA). , 0, , .		1
172	Ovarian cancer classification with missing data. , 0, , .		14
173	Wavelet analyses of event-related fMRI experiments. , 0, , .		1
174	NURBS-based detection of age-related variability of the human brain surface. , 0, , .		0
175	Bayesian tissue segmentation of multispectral brain images. , 0, , .		0
176	Non independent strategies for blind source separation in functional MRI. , 0, , .		0
177	Prediction of protein secondary structure using Bayesian method and support vector machines. , 0, , .		1
178	Soft computing approach to brain structure segmentation. , 0, , .		0
179	Tissue segmentation of MR images using first order polynomial modeling. , 0, , .		0
180	Subspace blind extraction by less-complete ICA. , 0, , .		0

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181	Denoising of functional MRI using ICA. , 0, , .		3
182	Curvature-based rational surface model for the detection of age and gender-related diversity in cortical morphology. , 0, , .		1
183	Tissue segmentation of multi-channel brain images with inhomogeneity correction. , 0, , .		0
184	Color channel encoding with NMF for face recognition. , 0, , .		46
185	Extraction of event-related potentials from EEG signals using ICA with reference. , 0, , .		6
186	Comparative genomic study of parkinson's disease candidate genes. , 0, , .		0
187	Feature Selection for Ensemble Learning and Its Application. , 0, , 135-155.		4
188	Feature Characterization and Testing of Bidirectional Promoters in the Human Genome—Significance and Applications in Human Genome Research. , 0, , 321-338.		0
189	Evolutionary Granular Kernel Trees for Protein Subcellular Location Prediction. , 0, , 229-239.		0