

Yu-Ping Wang

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

96
papers

1,347
citations

19
h-index

33
g-index

103
ext. papers

1,645
ext. citations

4
avg, IF

4.67
L-index

#	Paper	IF	Citations
96	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. <i>Human Molecular Genetics</i> , 2014 , 23, 1923-33	5.6	113
95	Comparative studies of copy number variation detection methods for next-generation sequencing technologies. <i>PLoS ONE</i> , 2013 , 8, e59128	3.7	112
94	Correspondence between fMRI and SNP data by group sparse canonical correlation analysis. <i>Medical Image Analysis</i> , 2014 , 18, 891-902	15.4	90
93	Segmentation of M-FISH Images for Improved Classification of Chromosomes With an Adaptive Fuzzy C-means Clustering Algorithm. <i>IEEE Transactions on Fuzzy Systems</i> , 2012 , 20, 1-8	8.3	85
92	Group sparse canonical correlation analysis for genomic data integration. <i>BMC Bioinformatics</i> , 2013 , 14, 245	3.6	69
91	Chromosome image enhancement using multiscale differential operators. <i>IEEE Transactions on Medical Imaging</i> , 2003 , 22, 685-93	11.7	44
90	A statistical change point model approach for the detection of DNA copy number variations in array CGH data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009 , 6, 529-41	3	36
89	Sparse representation based biomarker selection for schizophrenia with integrated analysis of fMRI and SNPs. <i>NeuroImage</i> , 2014 , 102 Pt 1, 220-8	7.9	35
88	Joint sparse canonical correlation analysis for detecting differential imaging genetics modules. <i>Bioinformatics</i> , 2016 , 32, 3480-3488	7.2	35
87	Sparse models for correlative and integrative analysis of imaging and genetic data. <i>Journal of Neuroscience Methods</i> , 2014 , 237, 69-78	3	34
86	Multiscale curvature-based shape representation using B-spline wavelets. <i>IEEE Transactions on Image Processing</i> , 1999 , 8, 1586-92	8.7	33
85	Image representations using multiscale differential operators. <i>IEEE Transactions on Image Processing</i> , 1999 , 8, 1757-71	8.7	33
84	CNV-TV: a robust method to discover copy number variation from short sequencing reads. <i>BMC Bioinformatics</i> , 2013 , 14, 150	3.6	31
83	Normalization of multicolor fluorescence in situ hybridization (M-FISH) images for improving color karyotyping. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2005 , 64, 101-9	4.6	28
82	Generalized LASSO with under-determined regularization matrices. <i>Signal Processing</i> , 2016 , 127, 239-246	4.4	23
81	Comparison of statistical methods for subnetwork detection in the integration of gene expression and protein interaction network. <i>BMC Bioinformatics</i> , 2017 , 18, 149	3.6	22
80	Adaptive Sparse Multiple Canonical Correlation Analysis With Application to Imaging (Epi)Genomics Study of Schizophrenia. <i>IEEE Transactions on Biomedical Engineering</i> , 2018 , 65, 390-399	5	22

79	Application of multivariate spectral analyses in micro-Raman imaging to unveil structural/chemical features of the adhesive/dentin interface. <i>Journal of Biomedical Optics</i> , 2008 , 13, 014020	3.5	21
78	Identification of a novel FGFR1 MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies. <i>Human Molecular Genetics</i> , 2015 , 24, 4710-27	5.6	19
77	Cross-Tissue Exploration of Genetic and Epigenetic Effects on Brain Gray Matter in Schizophrenia. <i>Schizophrenia Bulletin</i> , 2018 , 44, 443-452	1.3	19
76	On individual genome-wide association studies and their meta-analysis. <i>Human Genetics</i> , 2014 , 133, 265-79	7.9	19
75	Integrating fMRI and SNP data for biomarker identification for schizophrenia with a sparse representation based variable selection method. <i>BMC Medical Genomics</i> , 2013 , 6 Suppl 3, S2	3.7	19
74	FISH: Fast and accurate diploid genotype imputation via segmental hidden Markov model. <i>Bioinformatics</i> , 2014 , 30, 1876-83	7.2	18
73	Integrative analysis of multiple diverse omics datasets by sparse group multitask regression. <i>Frontiers in Cell and Developmental Biology</i> , 2014 , 2, 62	5.7	17
72	Classification of multicolor fluorescence in situ hybridization (M-FISH) images with sparse representation. <i>IEEE Transactions on Nanobioscience</i> , 2012 , 11, 111-8	3.4	17
71	Application of deep canonically correlated sparse autoencoder for the classification of schizophrenia. <i>Computer Methods and Programs in Biomedicine</i> , 2020 , 183, 105073	6.9	17
70	KCNJ11, ABCC8 and TCF7L2 polymorphisms and the response to sulfonylurea treatment in patients with type 2 diabetes: a bioinformatics assessment. <i>BMC Medical Genetics</i> , 2017 , 18, 64	2.1	16
69	Fuzzy clustering of Raman spectral imaging data with a wavelet-based noise-reduction approach. <i>Applied Spectroscopy</i> , 2006 , 60, 826-32	3.1	16
68	Enforcing Co-Expression Within a Brain-Imaging Genomics Regression Framework. <i>IEEE Transactions on Medical Imaging</i> , 2018 , 37, 2561-2571	11.7	15
67	RNA-sequencing study of peripheral blood monocytes in chronic periodontitis. <i>Gene</i> , 2016 , 581, 152-60	3.8	14
66	Common copy number variation detection from multiple sequenced samples. <i>IEEE Transactions on Biomedical Engineering</i> , 2014 , 61, 928-37	5	13
65	Subtyping glioblastoma by combining miRNA and mRNA expression data using compressed sensing-based approach. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2013 , 2013, 2		12
64	A compressed sensing based approach for subtyping of leukemia from gene expression data. <i>Journal of Bioinformatics and Computational Biology</i> , 2011 , 9, 631-45	1	12
63	Identification of genes for complex diseases using integrated analysis of multiple types of genomic data. <i>PLoS ONE</i> , 2012 , 7, e42755	3.7	12
62	Integrating Imaging Genomic Data in the Quest for Biomarkers of Schizophrenia Disease. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 1480-1491	3	10

61	Integration of SNPs-FMRI-methylation data with sparse multi-CCA for schizophrenia study. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2016 , 2016, 3310-3313	0.9	10
60	A kernel machine method for detecting higher order interactions in multimodal datasets: Application to schizophrenia. <i>Journal of Neuroscience Methods</i> , 2018 , 309, 161-174	3	10
59	FDR-Corrected Sparse Canonical Correlation Analysis With Applications to Imaging Genomics. <i>IEEE Transactions on Medical Imaging</i> , 2018 , 37, 1761-1774	11.7	9
58	A hybrid approach of using wavelets and fuzzy clustering for classifying multispectral fluorescence in situ hybridization images. <i>International Journal of Biomedical Imaging</i> , 2006 , 2006, 54532	5.2	9
57	Improving Separability of Structures with Similar Attributes in 2D Transfer Function Design. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2017 , 23, 1546-1560	4	8
56	An improved sparse representation model with structural information for Multicolour Fluorescence In-Situ Hybridization (M-FISH) image classification. <i>BMC Systems Biology</i> , 2013 , 7 Suppl 4, S5	3.5	8
55	Interaction of Epstein-Barr virus genes with human gastric carcinoma transcriptome. <i>Oncotarget</i> , 2017 , 8, 38399-38412	3.3	8
54	Network-Based Meta-Analyses of Associations of Multiple Gene Expression Profiles with Bone Mineral Density Variations in Women. <i>PLoS ONE</i> , 2016 , 11, e0147475	3.7	8
53	Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 1671-1681	3	8
52	MicroRNA-mRNA interaction analysis to detect potential dysregulation in complex diseases. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015 , 4, 1	1.6	7
51	Aberrant Brain Connectivity in Schizophrenia Detected via a Fast Gaussian Graphical Model. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2019 , 23, 1479-1489	7.2	7
50	Integrative analysis of GWASs, human protein interaction, and gene expression identified gene modules associated with BMDs. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014 , 99, E2392-9	5.6	7
49	On LARS/Homotopy Equivalence Conditions for Over-Determined LASSO. <i>IEEE Signal Processing Letters</i> , 2012 , 19, 894-897	3.2	7
48	Group Sparse Joint Non-negative Matrix Factorization on Orthogonal Subspace for Multi-modal Imaging Genetics Data Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , PP,	3	6
47	Distance canonical correlation analysis with application to an imaging-genetic study. <i>Journal of Medical Imaging</i> , 2019 , 6, 026501	2.6	6
46	A Sparse Model Based Detection of Copy Number Variations From Exome Sequencing Data. <i>IEEE Transactions on Biomedical Engineering</i> , 2016 , 63, 496-505	5	5
45	A patch-based tensor decomposition algorithm for M-FISH image classification. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2017 , 91, 622-632	4.6	5
44	A robust sparse-modeling framework for estimating schizophrenia biomarkers from fMRI. <i>Journal of Neuroscience Methods</i> , 2017 , 276, 46-55	3	5

43	A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model. <i>Scientific Reports</i> , 2019 , 9, 10863	4.9	5
42	Segmentation of M-FISH Images for improved classification of chromosomes with an adaptive fuzzy c-means clustering algorithm 2011 ,		5
41	Interpretable Multimodal Fusion Networks Reveal Mechanisms of Brain Cognition. <i>IEEE Transactions on Medical Imaging</i> , 2021 , 40, 1474-1483	11.7	5
40	Predicting schizophrenia by fusing networks from SNPs, DNA methylation and fMRI data. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2016 , 2016, 1447-1450	0.9	4
39	Imposing Uniqueness to Achieve Sparsity. <i>Signal Processing</i> , 2016 , 12, 1-8	4.4	4
38	A promoter polymorphism rs2075824 within IMPA2 gene affecting the transcription activity: possible relationship with schizophrenia. <i>Journal of Cellular and Molecular Medicine</i> , 2017 , 21, 658-664	5.6	4
37	Detection of chromosomal abnormalities with multi-color fluorescence in situ hybridization (M-FISH) imaging and multi-spectral wavelet analysis. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2008 , 2008, 1222-5	0.9	4
36	A Comparison of Fuzzy Clustering Approaches for Quantification of Microarray Gene Expression. <i>Journal of Signal Processing Systems</i> , 2008 , 50, 305-320	1.4	4
35	Classification of multi-spectral florescence in situ hybridization images with fuzzy clustering and multiscale feature selection 2006 ,		4
34	Influence Function of Multiple Kernel Canonical Analysis to Identify Outliers in Imaging Genetics Data 2016 ,		4
33	Identifying outliers using multiple kernel canonical correlation analysis with application to imaging genetics. <i>Computational Statistics and Data Analysis</i> , 2018 , 125, 70-85	1.6	3
32	Segmentation of Multicolor Fluorescence In-Situ Hybridization (M-FISH) image using an improved Fuzzy C-means clustering algorithm while incorporating both spatial and spectral information 2015 ,		3
31	Subtyping of Gliomaby Combining Gene Expression and CNVs Data Based on a Compressive Sensing Approach. <i>Advancements in Genetic Engineering</i> , 2012 , 1, 101		3
30	Integration of gene expression and gene copy number variations with independent component analysis. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2008 , 2008, 5700-3	0.9	3
29	Multi-modal Brain Connectivity Study Using Deep Collaborative Learning. <i>Lecture Notes in Computer Science</i> , 2018 , 66-73	0.9	3
28	Robust Kernel Canonical Correlation Analysis to Detect Gene-Gene Interaction for Imaging Genetics Data 2016 ,		3
27	A Sparse Regression Method for Group-Wise Feature Selection with False Discovery Rate Control. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 1066-1078	3	2
26	Robust kernel canonical correlation analysis to detect gene-gene co-associations: A case study in genetics. <i>Journal of Bioinformatics and Computational Biology</i> , 2019 , 17, 1950028	1	2

25	ENFORCING CO-EXPRESSION IN MULTIMODAL REGRESSION FRAMEWORK. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2017 , 22, 105-116	1.3	2
24	Detection and Reconstruction of an Implicit Boundary Surface by Adaptively Expanding A Small Surface Patch in a 3D Image. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2014 , 20, 1490-506	4	2
23	Detection of common copy number variation with application to population clustering from next generation sequencing data. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2012 , 2012, 1246-9	0.9	2
22	High dimensional latent Gaussian copula model for mixed data in imaging genetics 2018 ,		2
21	Joint Detection of Associations between DNA Methylation and Gene Expression from Multiple Cancers. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2018 , 22, 1960-1969	7.2	1
20	Integration of multiple genomic imaging data for the study of schizophrenia using joint nonnegative matrix factorization 2017 ,		1
19	Classification of multicolor fluorescence in-situ hybridization (M-FISH) image using structure based sparse representation model 2012 ,		1
18	Classification of multicolor fluorescence in-situ hybridization (M-FISH) image using regularized multinomial logistic regression 2012 ,		1
17	A wavelet approach for the identification of axonal synaptic varicosities from microscope images. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2007 , 11, 296-304		1
16	A differential wavelet-based noise reduction approach to improve clustering of hyperspectral Raman imaging data		1
15	Initialization and inner product computations of wavelet transform by interpolatory subdivision scheme. <i>IEEE Transactions on Signal Processing</i> , 1999 , 47, 876-880	4.8	1
14	Segmentation of multicolor fluorescence hybridization images using an improved fuzzy C-means clustering algorithm by incorporating both spatial and spectral information. <i>Journal of Medical Imaging</i> , 2017 , 4, 044001	2.6	1
13	A regularized clustering approach to brain parcellation from functional MRI data 2017 ,		1
12	A Latent Gaussian Copula Model for Mixed Data Analysis in Brain Imaging Genetics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 1350-1360	3	1
11	Canonical Correlation Analysis of Imaging Genetics Data Based on Statistical Independence and Structural Sparsity. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020 , 24, 2621-2629	7.2	0
10	Multi-Paradigm fMRI Fusion via Sparse Tensor Decomposition in Brain Functional Connectivity Study. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , 25, 1712-1723	7.2	0
9	Detection of False-Positive Deletions from the Database of Genomic Variants. <i>BioMed Research International</i> , 2019 , 2019, 8420547	3	
8	On efficient meta-filtering of big data. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2016 , 2016, 2958-2961	0.9	

- 7 Coupled Dimensionality-Reduction Model for Imaging Genomics. *Lecture Notes in Computer Science*, **2017**, 241-248 0.9
- 6 An optimal method to segment piecewise poisson distributed signals with application to sequencing data. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2015**, 2015, 6465-8 0.9
- 5 Population clustering based on copy number variations detected from next generation sequencing data. *Journal of Bioinformatics and Computational Biology*, **2014**, 12, 1450021 1
- 4 Data Processing and Analysis **2008**, 165-X
- 3 Imaging Genetics: Information Fusion and Association Techniques Between Biomedical Images and Genetic Factors. *Health Information Science*, **2017**, 103-114 0.1
- 2 The Next Generation Sequencing and Applications in Clinical Research. *Translational Bioinformatics*, **2016**, 83-113
- 1 Classifying Schizophrenia Subjects by Fusing Networks From Single-Nucleotide Polymorphisms, DNA Methylation, and Functional Magnetic Resonance Imaging Data **2018**, 61-83