Yu-Ping Wang

List of Publications by Year in Descending Order

96	1,347	19	33
papers	citations	h-index	g-index
103	1,645	4	4.67
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
96	Interpretable Multimodal Fusion Networks Reveal Mechanisms of Brain Cognition. *IEEE Transactions on Medical Imaging*, **2021**, 40, 1474-1483	11.7	5
95	A Latent Gaussian Copula Model for Mixed Data Analysis in Brain Imaging Genetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2021**, 18, 1350-1360	3	1
94	Multi-Paradigm fMRI Fusion via Sparse Tensor Decomposition in Brain Functional Connectivity Study. *IEEE Journal of Biomedical and Health Informatics*, **2021**, 25, 1712-1723	7.2	0
93	Group Sparse Joint Non-negative Matrix Factorization on Orthogonal Subspace for Multi-modal Imaging Genetics Data Analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2020**, PP,	3	6
92	Canonical Correlation Analysis of Imaging Genetics Data Based on Statistical Independence and Structural Sparsity. *IEEE Journal of Biomedical and Health Informatics*, **2020**, 24, 2621-2629	7.2	0
91	Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2020**, 17, 1671-1681	3	8
90	Application of deep canonically correlated sparse autoencoder for the classification of schizophrenia. *Computer Methods and Programs in Biomedicine*, **2020**, 183, 105073	6.9	17
89	Detection of False-Positive Deletions from the Database of Genomic Variants. *BioMed Research International*, **2019**, 2019, 8420547	3	
88	Aberrant Brain Connectivity in Schizophrenia Detected via a Fast Gaussian Graphical Model. *IEEE Journal of Biomedical and Health Informatics*, **2019**, 23, 1479-1489	7.2	7
87	A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model. *Scientific Reports*, **2019**, 9, 10863	4.9	5
86	Robust kernel canonical correlation analysis to detect gene-gene co-associations: A case study in genetics. *Journal of Bioinformatics and Computational Biology*, **2019**, 17, 1950028	1	2
85	Distance canonical correlation analysis with application to an imaging-genetic study. *Journal of Medical Imaging*, **2019**, 6, 026501	2.6	6
84	Identifying outliers using multiple kernel canonical correlation analysis with application to imaging genetics. *Computational Statistics and Data Analysis*, **2018**, 125, 70-85	1.6	3
83	A Sparse Regression Method for Group-Wise Feature Selection with False Discovery Rate Control. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2018**, 15, 1066-1078	3	2
82	Joint Detection of Associations between DNA Methylation and Gene Expression from Multiple Cancers. *IEEE Journal of Biomedical and Health Informatics*, **2018**, 22, 1960-1969	7.2	1
81	FDR-Corrected Sparse Canonical Correlation Analysis With Applications to Imaging Genomics. *IEEE Transactions on Medical Imaging*, **2018**, 37, 1761-1774	11.7	9
80	Cross-Tissue Exploration of Genetic and Epigenetic Effects on Brain Gray Matter in Schizophrenia. *Schizophrenia Bulletin*, **2018**, 44, 443-452	1.3	19

79	Enforcing Co-Expression Within a Brain-Imaging Genomics Regression Framework. *IEEE Transactions on Medical Imaging*, **2018**, 37, 2561-2571	11.7	15
78	Integrating Imaging Genomic Data in the Quest for Biomarkers of Schizophrenia Disease. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2018**, 15, 1480-1491	3	10
77	Adaptive Sparse Multiple Canonical Correlation Analysis With Application to Imaging (Epi)Genomics Study of Schizophrenia. *IEEE Transactions on Biomedical Engineering*, **2018**, 65, 390-399	5	22
76	Multi-modal Brain Connectivity Study Using Deep Collaborative Learning. *Lecture Notes in Computer Science*, **2018**, 66-73	0.9	3
75	A kernel machine method for detecting higher order interactions in multimodal datasets: Application to schizophrenia. *Journal of Neuroscience Methods*, **2018**, 309, 161-174	3	10
74	Classifying Schizophrenia Subjects by Fusing Networks From Single-Nucleotide Polymorphisms, DNA Methylation, and Functional Magnetic Resonance Imaging Data **2018**, 61-83		
73	High dimensional latent Gaussian copula model for mixed data in imaging genetics **2018**,		2
72	Improving Separability of Structures with Similar Attributes in 2D Transfer Function Design. *IEEE Transactions on Visualization and Computer Graphics*, **2017**, 23, 1546-1560	4	8
71	A patch-based tensor decomposition algorithm for M-FISH image classification. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2017**, 91, 622-632	4.6	5
70	Comparison of statistical methods for subnetwork detection in the integration of gene expression and protein interaction network. *BMC Bioinformatics*, **2017**, 18, 149	3.6	22
69	A robust sparse-modeling framework for estimating schizophrenia biomarkers from fMRI. *Journal of Neuroscience Methods*, **2017**, 276, 46-55	3	5
68	Coupled Dimensionality-Reduction Model for Imaging Genomics. *Lecture Notes in Computer Science*, **2017**, 241-248	0.9	
67	KCNJ11, ABCC8 and TCF7L2 polymorphisms and the response to sulfonylurea treatment in patients with type 2 diabetes: a bioinformatics assessment. *BMC Medical Genetics*, **2017**, 18, 64	2.1	16
66	Integration of multiple genomic imaging data for the study of schizophrenia using joint nonnegative matrix factorization **2017**,		1
65	A promoter polymorphism rs2075824 within IMPA2 gene affecting the transcription activity: possible relationship with schizophrenia. *Journal of Cellular and Molecular Medicine*, **2017**, 21, 658-664	5.6	4
64	ENFORCING CO-EXPRESSION IN MULTIMODAL REGRESSION FRAMEWORK. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2017**, 22, 105-116	1.3	2
63	Interaction of Epstein-Barr virus genes with human gastric carcinoma transcriptome. *Oncotarget*, **2017**, 8, 38399-38412	3.3	8
62	Segmentation of multicolor fluorescence hybridization images using an improved fuzzy C-means clustering algorithm by incorporating both spatial and spectral information. *Journal of Medical Imaging*, **2017**, 4, 044001	2.6	1

61	A regularized clustering approach to brain parcellation from functional MRI data **2017**,		1
60	Imaging Genetics: Information Fusion and Association Techniques Between Biomedical Images and Genetic Factors. *Health Information Science*, **2017**, 103-114	0.1	
59	A Sparse Model Based Detection of Copy Number Variations From Exome Sequencing Data. *IEEE Transactions on Biomedical Engineering*, **2016**, 63, 496-505	5	5
58	On efficient meta-filtering of big data. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2016**, 2016, 2958-2961	0.9	
57	Integration of SNPs-FMRI-methylation data with sparse multi-CCA for schizophrenia study. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2016**, 2016, 3310-3313	0.9	10
56	Predicting schizophrenia by fusing networks from SNPs, DNA methylation and fMRI data. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2016**, 2016, 1447-1450	0.9	4
55	Generalized LASSO with under-determined regularization matrices. *Signal Processing*, **2016**, 127, 239-246	4.4	23
54	RNA-sequencing study of peripheral blood monocytes in chronic periodontitis. *Gene*, **2016**, 581, 152-60	3.8	14
53	Imposing Uniqueness to Achieve Sparsity. *Signal Processing*, **2016**, 12, 1-8	4.4	4
52	Network-Based Meta-Analyses of Associations of Multiple Gene Expression Profiles with Bone Mineral Density Variations in Women. *PLoS ONE*, **2016**, 11, e0147475	3.7	8
51	Robust Kernel Canonical Correlation Analysis to Detect Gene-Gene Interaction for Imaging Genetics Data **2016**,		3
50	Influence Function of Multiple Kernel Canonical Analysis to Identify Outliers in Imaging Genetics Data **2016**,		4
49	The Next Generation Sequencing and Applications in Clinical Research. *Translational Bioinformatics*, **2016**, 83-113		
48	Joint sparse canonical correlation analysis for detecting differential imaging genetics modules. *Bioinformatics*, **2016**, 32, 3480-3488	7.2	35
47	Identification of a novel FGFRL1 MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies. *Human Molecular Genetics*, **2015**, 24, 4710-27	5.6	19
46	MicroRNA-mRNA interaction analysis to detect potential dysregulation in complex diseases. *Network Modeling Analysis in Health Informatics and Bioinformatics*, **2015**, 4, 1	1.6	7
45	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	
44	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

#	Citation		
43	On individual genome-wide association studies and their meta-analysis. *Human Genetics*, **2014**, 133, 265-79	6.3	19
42	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. *Human Molecular Genetics*, **2014**, 23, 1923-33	5.6	113
41	Common copy number variation detection from multiple sequenced samples. *IEEE Transactions on Biomedical Engineering*, **2014**, 61, 928-37	5	13
40	Sparse models for correlative and integrative analysis of imaging and genetic data. *Journal of Neuroscience Methods*, **2014**, 237, 69-78	3	34
39	Sparse representation based biomarker selection for schizophrenia with integrated analysis of fMRI and SNPs. *NeuroImage*, **2014**, 102 Pt 1, 220-8	7.9	35
38	Correspondence between fMRI and SNP data by group sparse canonical correlation analysis. *Medical Image Analysis*, **2014**, 18, 891-902	15.4	90
37	Integrative analysis of multiple diverse omics datasets by sparse group multitask regression. *Frontiers in Cell and Developmental Biology*, **2014**, 2, 62	5.7	17
36	Detection and Reconstruction of an Implicit Boundary Surface by Adaptively Expanding A Small Surface Patch in a 3D Image. *IEEE Transactions on Visualization and Computer Graphics*, **2014**, 20, 1490-506	4	2
35	Integrative analysis of GWASs, human protein interaction, and gene expression identified gene modules associated with BMDs. *Journal of Clinical Endocrinology and Metabolism*, **2014**, 99, E2392-9	5.6	7
34	FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. *Bioinformatics*, **2014**, 30, 1876-83	7.2	18
33	Population clustering based on copy number variations detected from next generation sequencing data. *Journal of Bioinformatics and Computational Biology*, **2014**, 12, 1450021	1	
32	CNV-TV: a robust method to discover copy number variation from short sequencing reads. *BMC Bioinformatics*, **2013**, 14, 150	3.6	31
31	Subtyping glioblastoma by combining miRNA and mRNA expression data using compressed sensing-based approach. *Eurasip Journal on Bioinformatics and Systems Biology*, **2013**, 2013, 2		12
30	An improved sparse representation model with structural information for Multicolour Fluorescence In-Situ Hybridization (M-FISH) image classification. *BMC Systems Biology*, **2013**, 7 Suppl 4, S5	3.5	8
29	Group sparse canonical correlation analysis for genomic data integration. *BMC Bioinformatics*, **2013**, 14, 245	3.6	69
28	Integrating fMRI and SNP data for biomarker identification for schizophrenia with a sparse representation based variable selection method. *BMC Medical Genomics*, **2013**, 6 Suppl 3, S2	3.7	19
27	Comparative studies of copy number variation detection methods for next-generation sequencing technologies. *PLoS ONE*, **2013**, 8, e59128	3.7	112
26	Segmentation of M-FISH Images for Improved Classification of Chromosomes With an Adaptive Fuzzy C-means Clustering Algorithm. *IEEE Transactions on Fuzzy Systems*, **2012**, 20, 1-8	8.3	85

25	Classification of multicolor fluorescence in situ hybridization (M-FISH) images with sparse representation. *IEEE Transactions on Nanobioscience*, **2012**, 11, 111-8	3.4	17
24	On LARS/Homotopy Equivalence Conditions for Over-Determined LASSO. *IEEE Signal Processing Letters*, **2012**, 19, 894-897	3.2	7
23	Classification of multicolor fluorescence in-situ hybridization (M-FISH) image using structure based sparse representation model **2012**,		1
22	Subtyping of Gliomaby Combining Gene Expression and CNVs Data Based on a Compressive Sensing Approach. *Advancements in Genetic Engineering*, **2012**, 1, 101		3
21	Classification of multicolor fluorescencein-situhybridization (M-FISH) image using regularized multinomial logistic regression **2012**,		1
20	Detection of common copy number variation with application to population clustering from next generation sequencing data. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2012**, 2012, 1246-9	0.9	2
19	Identification of genes for complex diseases using integrated analysis of multiple types of genomic data. *PLoS ONE*, **2012**, 7, e42755	3.7	12
18	A compressed sensing based approach for subtyping of leukemia from gene expression data. *Journal of Bioinformatics and Computational Biology*, **2011**, 9, 631-45	1	12
17	Segmentation of M-FISH Images for improved classification of chromosomes with an adaptive fuzzy c-means clustering algorithm **2011**,		5
16	A statistical change point model approach for the detection of DNA copy number variations in array CGH data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2009**, 6, 529-41	3	36
15	Detection of chromosomal abnormalities with multi-color fluorescence in situ hybridization (M-FISH) imaging and multi-spectral wavelet analysis. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2008**, 2008, 1222-5	0.9	4
14	Application of multivariate spectral analyses in micro-Raman imaging to unveil structural/chemical features of the adhesive/dentin interface. *Journal of Biomedical Optics*, **2008**, 13, 014020	3.5	21
13	Integration of gene expression and gene copy number variations with independent component analysis. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2008**, 2008, 5700-3	0.9	3
12	Data Processing and Analysis **2008**, 165-X		
11	A Comparison of Fuzzy Clustering Approaches for Quantification of Microarray Gene Expression. *Journal of Signal Processing Systems*, **2008**, 50, 305-320	1.4	4
10	A wavelet approach for the identification of axonal synaptic varicosities from microscope images. *IEEE Transactions on Information Technology in Biomedicine*, **2007**, 11, 296-304		1
9	A hybrid approach of using wavelets and fuzzy clustering for classifying multispectral florescence in situ hybridization images. *International Journal of Biomedical Imaging*, **2006**, 2006, 54532	5.2	9
8	Classification of multi-spectral florescence in situ hybridization images with fuzzy clustering and multiscale feature selection **2006**,		4

LIST OF PUBLICATIONS

7	Fuzzy clustering of Raman spectral imaging data with a wavelet-based noise-reduction approach. *Applied Spectroscopy*, **2006**, 60, 826-32	3.1	16
6	Normalization of multicolor fluorescence in situ hybridization (M-FISH) images for improving color karyotyping. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2005**, 64, 101-9	4.6	28
5	Chromosome image enhancement using multiscale differential operators. *IEEE Transactions on Medical Imaging*, **2003**, 22, 685-93	11.7	44
4	Multiscale curvature-based shape representation using B-spline wavelets. *IEEE Transactions on Image Processing*, **1999**, 8, 1586-92	8.7	33
3	Image representations using multiscale differential operators. *IEEE Transactions on Image Processing*, **1999**, 8, 1757-71	8.7	33
2	Initialization and inner product computations of wavelet transform by interpolatory subdivision scheme. *IEEE Transactions on Signal Processing*, **1999**, 47, 876-880	4.8	1
1	A differential wavelet-based noise reduction approach to improve clustering of hyperspectral Raman imaging data		1