

Yu-Ping Wang

List of Publications by Year in descending order

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103
papers

1,884
citations

279487

23
h-index

301761

39
g-index

103
all docs

103
docs citations

103
times ranked

2780
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Comparative Studies of Copy Number Variation Detection Methods for Next-Generation Sequencing Technologies. PLoS ONE, 2013, 8, e59128. | 1.1 | 138 |
| 2 | 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. | 6.5 | 130 |
| 3 | Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. Human Molecular Genetics, 2014, 23, 1923-1933. | 1.4 | 130 |
| 4 | Correspondence between fMRI and SNP data by group sparse canonical correlation analysis. Medical Image Analysis, 2014, 18, 891-902. | 7.0 | 123 |
| 5 | Group sparse canonical correlation analysis for genomic data integration. BMC Bioinformatics, 2013, 14, 245. | 1.2 | 91 |
| 6 | Chromosome image enhancement using multiscale differential operators. IEEE Transactions on Medical Imaging, 2003, 22, 685-693. | 5.4 | 64 |
| 7 | Joint sparse canonical correlation analysis for detecting differential imaging genetics modules. Bioinformatics, 2016, 32, 3480-3488. | 1.8 | 59 |
| 8 | Multiscale curvature-based shape representation using B-spline wavelets. IEEE Transactions on Image Processing, 1999, 8, 1586-1592. | 6.0 | 47 |
| 9 | Image representations using multiscale differential operators. IEEE Transactions on Image Processing, 1999, 8, 1757-1771. | 6.0 | 45 |
| 10 | Sparse models for correlative and integrative analysis of imaging and genetic data. Journal of Neuroscience Methods, 2014, 237, 69-78. | 1.3 | 45 |
| 11 | Sparse representation based biomarker selection for schizophrenia with integrated analysis of fMRI and SNPs. NeuroImage, 2014, 102, 220-228. | 2.1 | 44 |
| 12 | 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, 529-541. | 1.9 | 40 |
| 13 | Generalized LASSO with under-determined regularization matrices. Signal Processing, 2016, 127, 239-246. | 2.1 | 40 |
| 14 | CNV-TV: A robust method to discover copy number variation from short sequencing reads. BMC Bioinformatics, 2013, 14, 150. | 1.2 | 38 |
| 15 | 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, 64A, 101-109. | 1.1 | 37 |
| 16 | Application of deep canonically correlated sparse autoencoder for the classification of schizophrenia. Computer Methods and Programs in Biomedicine, 2020, 183, 105073. | 2.6 | 34 |
| 17 | On individual genome-wide association studies and their meta-analysis. Human Genetics, 2014, 133, 265-279. | 1.8 | 30 |
| 18 | Adaptive sparse multiple canonical correlation analysis with application to imaging (epi)genomics study of schizophrenia. IEEE Transactions on Biomedical Engineering, 2017, 65, 1-1. | 2.5 | 30 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Interpretable Multimodal Fusion Networks Reveal Mechanisms of Brain Cognition. <i>IEEE Transactions on Medical Imaging</i> , 2021, 40, 1474-1483. | 5.4 | 30 |
| 20 | Comparison of statistical methods for subnetwork detection in the integration of gene expression and protein interaction network. <i>BMC Bioinformatics</i> , 2017, 18, 149. | 1.2 | 29 |
| 21 | Cross-Tissue Exploration of Genetic and Epigenetic Effects on Brain Gray Matter in Schizophrenia. <i>Schizophrenia Bulletin</i> , 2018, 44, 443-452. | 2.3 | 29 |
| 22 | FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. <i>Bioinformatics</i> , 2014, 30, 1876-1883. | 1.8 | 27 |
| 23 | Classification of Multicolor Fluorescence In Situ Hybridization (M-FISH) Images With Sparse Representation. <i>IEEE Transactions on Nanobioscience</i> , 2012, 11, 111-118. | 2.2 | 24 |
| 24 | 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, S2. | 0.7 | 24 |
| 25 | Enforcing Co-Expression Within a Brain-Imaging Genomics Regression Framework. <i>IEEE Transactions on Medical Imaging</i> , 2018, 37, 2561-2571. | 5.4 | 24 |
| 26 | Integrative analysis of multiple diverse omics datasets by sparse group multitask regression. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 62. | 1.8 | 23 |
| 27 | 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. | 1.4 | 22 |
| 28 | Common Copy Number Variation Detection From Multiple Sequenced Samples. <i>IEEE Transactions on Biomedical Engineering</i> , 2014, 61, 928-937. | 2.5 | 22 |
| 29 | Identification of a novel <i>FGFRL1</i> MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies. <i>Human Molecular Genetics</i> , 2015, 24, 4710-4727. | 1.4 | 22 |
| 30 | RNA-sequencing study of peripheral blood monocytes in chronic periodontitis. <i>Gene</i> , 2016, 581, 152-160. | 1.0 | 21 |
| 31 | 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 | 21 |
| 32 | Fuzzy Clustering of Raman Spectral Imaging Data with a Wavelet-Based Noise-Reduction Approach. <i>Applied Spectroscopy</i> , 2006, 60, 826-832. | 1.2 | 19 |
| 33 | FDR-Corrected Sparse Canonical Correlation Analysis With Applications to Imaging Genomics. <i>IEEE Transactions on Medical Imaging</i> , 2018, 37, 1761-1774. | 5.4 | 19 |
| 34 | A COMPRESSED SENSING BASED APPROACH FOR SUBTYPING OF LEUKEMIA FROM GENE EXPRESSION DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 631-645. | 0.3 | 18 |
| 35 | 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. | 1.3 | 16 |
| 36 | Identification of Genes for Complex Diseases Using Integrated Analysis of Multiple Types of Genomic Data. <i>PLoS ONE</i> , 2012, 7, e42755. | 1.1 | 15 |

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|----|---|-----|-----------|
| 37 | 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. | 1.4 | 15 |
| 38 | 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. | 1.9 | 13 |
| 39 | Integration of SNPs-FMRI-methylation data with sparse multi-CCA for schizophrenia study. , 2016, 2016, 3310-3313. | | 12 |
| 40 | A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model. <i>Scientific Reports</i> , 2019, 9, 10863. | 1.6 | 12 |
| 41 | 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. | 1.9 | 12 |
| 42 | 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. | 1.1 | 12 |
| 43 | 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. | 2.9 | 11 |
| 44 | Interaction of Epstein-Barr virus genes with human gastric carcinoma transcriptome. <i>Oncotarget</i> , 2017, 8, 38399-38412. | 0.8 | 11 |
| 45 | 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, 1-11. | 3.0 | 10 |
| 46 | 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-E2399. | 1.8 | 10 |
| 47 | MicroRNA-mRNA interaction analysis to detect potential dysregulation in complex diseases. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015, 4, 1. | 1.2 | 10 |
| 48 | A robust sparse-modeling framework for estimating schizophrenia biomarkers from fMRI. <i>Journal of Neuroscience Methods</i> , 2017, 276, 46-55. | 1.3 | 10 |
| 49 | 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. | 3.9 | 10 |
| 50 | 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> , 2022, 19, 479-490. | 1.9 | 10 |
| 51 | On LARS/Homotopy Equivalence Conditions for Over-Determined LASSO. <i>IEEE Signal Processing Letters</i> , 2012, 19, 894-897. | 2.1 | 8 |
| 52 | 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, S5. | 3.0 | 8 |
| 53 | Identifying outliers using multiple kernel canonical correlation analysis with application to imaging genetics. <i>Computational Statistics and Data Analysis</i> , 2018, 125, 70-85. | 0.7 | 8 |
| 54 | Distance canonical correlation analysis with application to an imaging-genetic study. <i>Journal of Medical Imaging</i> , 2019, 6, 1. | 0.8 | 8 |

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|----|---|-----|-----------|
| 55 | Classification of multi-spectral florescence in situ hybridization images with fuzzy clustering and multiscale feature selection. , 2006, , . | | 7 |
| 56 | Segmentation of M-FISH Images for improved classification of chromosomes with an adaptive fuzzy c-means clustering algorithm. , 2011, , . | | 7 |
| 57 | Multi-Paradigm fMRI Fusion via Sparse Tensor Decomposition in Brain Functional Connectivity Study. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 1712-1723. | 3.9 | 7 |
| 58 | 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. | 1.1 | 6 |
| 59 | Detection of chromosomal abnormalities with multi-color fluorescence in situ hybridization (M-FISH) imaging and multi-spectral wavelet analysis. , 2008, 2008, 1222-5. | | 5 |
| 60 | Predicting schizophrenia by fusing networks from SNPs, DNA methylation and fMRI data. , 2016, 2016, 1447-1450. | | 5 |
| 61 | Imposing uniqueness to achieve sparsity. Signal Processing, 2016, 123, 1-8. | 2.1 | 5 |
| 62 | A Sparse Model Based Detection of Copy Number Variations From Exome Sequencing Data. IEEE Transactions on Biomedical Engineering, 2016, 63, 496-505. | 2.5 | 5 |
| 63 | A promoter polymorphism rs2075824 within <scp>IMPA</scp>2 gene affecting the transcription activity: possible relationship with schizophrenia. Journal of Cellular and Molecular Medicine, 2017, 21, 658-664. | 1.6 | 5 |
| 64 | 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. | 1.9 | 5 |
| 65 | Joint Detection of Associations Between DNA Methylation and Gene Expression From Multiple Cancers. IEEE Journal of Biomedical and Health Informatics, 2018, 22, 1960-1969. | 3.9 | 5 |
| 66 | A Comparison of Fuzzy Clustering Approaches for Quantification of Microarray Gene Expression. Journal of Signal Processing Systems, 2008, 50, 305-320. | 1.4 | 4 |
| 67 | Subtyping of Glioma by Combining Gene Expression and CNVs Data Based on a Compressive Sensing Approach. Advancements in Genetic Engineering, 2012, 01, 101. | 0.1 | 4 |
| 68 | 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, , . | | 4 |
| 69 | Influence Function of Multiple Kernel Canonical Analysis to Identify Outliers in Imaging Genetics Data. , 2016, , . | | 4 |
| 70 | 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. | 1.9 | 4 |
| 71 | M-fish image registration and classification. , 0, , . | | 3 |
| 72 | Integration of gene expression and gene copy number variations with independent component analysis. , 2008, 2008, 5700-3. | | 3 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 73 | Detection of common copy number variation with application to population clustering from next generation sequencing data. , 2012, 2012, 1246-9. | | 3 |
| 74 | Classification of multicolor fluorescence in-situ hybridization (M-FISH) image using structure based sparse representation model. , 2012, , . | | 3 |
| 75 | 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, 1490-1506. | 2.9 | 3 |
| 76 | Robust Kernel Canonical Correlation Analysis to Detect Gene-Gene Interaction for Imaging Genetics Data. , 2016, , . | | 3 |
| 77 | Multi-modal Brain Connectivity Study Using Deep Collaborative Learning. Lecture Notes in Computer Science, 2018, , 66-73. | 1.0 | 3 |
| 78 | From Gaussian scale-space to B-spline scale-space. , 1999, , . | | 2 |
| 79 | A Differential Wavelet-Based Noise Reduction Approach to Improve the Clustering of Hyperspectral Raman Imaging Data. , 0, , . | | 2 |
| 80 | Genomic Imaging: A Modern Environment for TCM Research. , 2009, , . | | 2 |
| 81 | Integration of multiple genomic imaging data for the study of schizophrenia using joint nonnegative matrix factorization. , 2017, , . | | 2 |
| 82 | ENFORCING CO-EXPRESSION IN MULTIMODAL REGRESSION FRAMEWORK. , 2017, 22, 105-116. | | 2 |
| 83 | High dimensional latent Gaussian copula model for mixed data in imaging genetics. , 2018, , . | | 2 |
| 84 | 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. | 0.3 | 2 |
| 85 | 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. | 3.9 | 2 |
| 86 | Initialization and inner product computations of wavelet transform by interpolatory subdivision scheme. IEEE Transactions on Signal Processing, 1999, 47, 876-880. | 3.2 | 1 |
| 87 | A Wavelet Approach for the Identification of Axonal Synaptic Varicosities from Microscope Images. IEEE Transactions on Information Technology in Biomedicine, 2007, 11, 296-304. | 3.6 | 1 |
| 88 | Classification of multicolor fluorescence in-situ hybridization (M-FISH) image using regularized multinomial logistic regression. , 2012, , . | | 1 |
| 89 | Segmentation of multicolor fluorescence in situ hybridization images using an improved fuzzy C-means clustering algorithm by incorporating both spatial and spectral information. Journal of Medical Imaging, 2017, 4, 1. | 0.8 | 1 |
| 90 | A regularized clustering approach to brain parcellation from functional MRI data. , 2017, , . | | 1 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 91 | Accurate Quantification of Gene Expression using Fuzzy Clustering Approaches. , 2007, , . | | 0 |
| 92 | Data Processing and Analysis. , 2008, , 165-X. | | 0 |
| 93 | Classifying six glioma subtypes from combined gene expression and CNVs data based on compressive sensing approach. , 2011, , . | | 0 |
| 94 | Modeling exome sequencing data with generalized Gaussian distribution with application to copy number variation detection. , 2013, , . | | 0 |
| 95 | Classification of multicolor fluorescence in-situ hybridization (M-FISH) image using structure based sparse representation model with different constrains. , 2013, , . | | 0 |
| 96 | Population clustering based on copy number variations detected from next generation sequencing data. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450021. | 0.3 | 0 |
| 97 | An optimal method to segment piecewise poisson distributed signals with application to sequencing data. , 2015, 2015, 6465-8. | | 0 |
| 98 | The Next Generation Sequencing and Applications in Clinical Research. Translational Bioinformatics, 2016, , 83-113. | 0.0 | 0 |
| 99 | On efficient meta-filtering of big data. , 2016, 2016, 2958-2961. | | 0 |
| 100 | Coupled Dimensionality-Reduction Model forÂImaging Genomics. Lecture Notes in Computer Science, 2017, , 241-248. | 1.0 | 0 |
| 101 | Classifying Schizophrenia Subjects by Fusing Networks From Single-Nucleotide Polymorphisms, DNA Methylation, and Functional Magnetic Resonance Imaging Data. , 2018, , 61-83. | | 0 |
| 102 | Detection of False-Positive Deletions from the Database of Genomic Variants. BioMed Research International, 2019, 2019, 1-8. | 0.9 | 0 |
| 103 | Imaging Genetics: Information Fusion and Association Techniques Between Biomedical Images and Genetic Factors. Health Information Science, 2017, , 103-114. | 0.3 | 0 |