

Weichuan Yu

List of Publications by Year in descending order

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87
papers

3,377
citations

279798

23
h-index

149698

56
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93
all docs

93
docs citations

93
times ranked

4635
citing authors

#	ARTICLE	IF	CITATIONS
1	Moving Object Detection by Detecting Contiguous Outliers in the Low-Rank Representation. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2013, 35, 597-610.	13.9	623
2	BOOST: A Fast Approach to Detecting Gene-Gene Interactions in Genome-wide Case-Control Studies. American Journal of Human Genetics, 2010, 87, 325-340.	6.2	452
3	Stable feature selection for biomarker discovery. Computational Biology and Chemistry, 2010, 34, 215-225.	2.3	251
4	Comparison of public peak detection algorithms for MALDI mass spectrometry data analysis. BMC Bioinformatics, 2009, 10, 4.	2.6	220
5	SNPHarvester: a filtering-based approach for detecting epistatic interactions in genome-wide association studies. Bioinformatics, 2009, 25, 504-511.	4.1	182
6	GBOOST: a GPU-based tool for detecting gene-gene interactions in genome-wide case control studies. Bioinformatics, 2011, 27, 1309-1310.	4.1	137
7	Combinative multi-scale level set framework for echocardiographic image segmentation. Medical Image Analysis, 2003, 7, 529-537.	11.6	121
8	Progression of diabetic kidney disease and trajectory of kidney function decline in Chinese patients with Type 2 diabetes. Kidney International, 2019, 95, 178-187.	5.2	105
9	Low-Rank Modeling and Its Applications in Image Analysis. ACM Computing Surveys, 2015, 47, 1-33.	23.0	102
10	Protein inference: a review. Briefings in Bioinformatics, 2012, 13, 586-614.	6.5	96
11	MegaSNPHunter: a learning approach to detect disease predisposition SNPs and high level interactions in genome wide association study. BMC Bioinformatics, 2009, 10, 13.	2.6	86
12	Technical, bioinformatical and statistical aspects of liquid chromatography-mass spectrometry (LC-MS) and capillary electrophoresis-mass spectrometry (CE-MS) based clinical proteomics: A critical assessment. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2009, 877, 1250-1258.	2.3	80
13	Towards pointwise motion tracking in echocardiographic image sequences - Comparing the reliability of different features for speckle tracking. Medical Image Analysis, 2006, 10, 495-508.	11.6	58
14	Apical constriction is driven by a pulsatile apical myosin network in delaminating Drosophila neuroblasts. Development (Cambridge), 2017, 144, 2153-2164.	2.5	47
15	Detecting and aligning peaks in mass spectrometry data with applications to MALDI. Computational Biology and Chemistry, 2006, 30, 27-38.	2.3	45
16	Identifying main effects and epistatic interactions from large-scale SNP data via adaptive group Lasso. BMC Bioinformatics, 2010, 11, S18.	2.6	33
17	Motif-All: discovering all phosphorylation motifs. BMC Bioinformatics, 2011, 12, S22.	2.6	32
18	Using MicroPET Imaging in Quantitative Verification of the Acupuncture Effect in Ischemia Stroke Treatment. Scientific Reports, 2013, 3, 1070.	3.3	31

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19	Establishment of Dimethyl Labeling-based Quantitative Acetylproteomics in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1010-1027.	3.8	31
20	Piecewise-constant and low-rank approximation for identification of recurrent copy number variations. <i>Bioinformatics</i> , 2014, 30, 1943-1949.	4.1	29
21	A Recombination Hotspot in a Schizophrenia-Associated Region of GABRB2. <i>PLoS ONE</i> , 2010, 5, e9547.	2.5	28
22	PIPI: PTM-Invariant Peptide Identification Using Coding Method. <i>Journal of Proteome Research</i> , 2016, 15, 4423-4435.	3.7	28
23	Semi-supervised protein subcellular localization. <i>BMC Bioinformatics</i> , 2009, 10, S47.	2.6	26
24	Multiple Peak Alignment in Sequential Data Analysis: A Scale-Space-Based Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 208-219.	3.0	24
25	Active Contours with Group Similarity. , 2013, , .		24
26	Data imbalance in CRISPR off-target prediction. <i>Briefings in Bioinformatics</i> , 2020, 21, 1448-1454.	6.5	24
27	Detecting two-locus associations allowing for interactions in genome-wide association studies. <i>Bioinformatics</i> , 2010, 26, 2517-2525.	4.1	23
28	Multisample aCGH Data Analysis via Total Variation and Spectral Regularization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 230-235.	3.0	23
29	On Feature Motion Decorrelation in Ultrasound Speckle Tracking. <i>IEEE Transactions on Medical Imaging</i> , 2013, 32, 435-448.	8.9	22
30	Controlling the joint local false discovery rate is more powerful than meta-analysis methods in joint analysis of summary statistics from multiple genome-wide association studies. <i>Bioinformatics</i> , 2017, 33, 500-507.	4.1	21
31	Exhaustively Identifying Cross-Linked Peptides with a Linear Computational Complexity. <i>Journal of Proteome Research</i> , 2017, 16, 3942-3952.	3.7	21
32	Development of in Planta Chemical Cross-Linking-Based Quantitative Interactomics in <i>Arabidopsis</i> . <i>Journal of Proteome Research</i> , 2018, 17, 3195-3213.	3.7	20
33	The complete compositional epistasis detection in genome-wide association studies. <i>BMC Genetics</i> , 2013, 14, 7.	2.7	18
34	<i>In planta</i> chemical cross-linking and mass spectrometry analysis of protein structure and interaction in <i>Arabidopsis</i> . <i>Proteomics</i> , 2016, 16, 1915-1927.	2.2	18
35	Development of genome-wide polygenic risk scores for lipid traits and clinical applications for dyslipidemia, subclinical atherosclerosis, and diabetes cardiovascular complications among East Asians. <i>Genome Medicine</i> , 2021, 13, 29.	8.2	18
36	Power estimation and sample size determination for replication studies of genome-wide association studies. <i>BMC Genomics</i> , 2016, 17, 3.	2.8	17

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37	ECL: an exhaustive search tool for the identification of cross-linked peptides using whole database. BMC Bioinformatics, 2016, 17, 217.	2.6	16
38	Xolik: finding cross-linked peptides with maximum paired scores in linear time. Bioinformatics, 2019, 35, 251-257.	4.1	16
39	Multiple motion analysis: in spatial or in spectral domain?. Computer Vision and Image Understanding, 2003, 90, 129-152.	4.7	14
40	A Partial Set Covering Model for Protein Mixture Identification Using Mass Spectrometry Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 368-380.	3.0	13
41	PBOOST: a GPU-based tool for parallel permutation tests in genome-wide association studies. Bioinformatics, 2015, 31, 1460-1462.	4.1	11
42	A network approach to exploring the functional basis of gene-gene epistatic interactions in disease susceptibility. Bioinformatics, 2018, 34, 1741-1749.	4.1	11
43	Three dimensional orientation signatures with conic kernel filtering for multiple motion analysis. Image and Vision Computing, 2003, 21, 447-458.	4.5	10
44	Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. Journal of Computational Biology, 2010, 17, 221-235.	1.6	10
45	Score regularization for peptide identification. BMC Bioinformatics, 2011, 12, S2.	2.6	9
46	Low-rank modeling and its applications in medical image analysis. Proceedings of SPIE, 2013, , .	0.8	9
47	Statistical Methods in Proteomics. , 2006, , 623-638.		9
48	Oriented structure of the occlusion distortion: is it reliable?. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2002, 24, 1286-1290.	13.9	8
49	Peak bagging for peptide mass fingerprinting. Bioinformatics, 2008, 24, 1293-1299.	4.1	8
50	A Regularized Method for Peptide Quantification. Journal of Proteome Research, 2010, 9, 2705-2712.	3.7	8
51	Rotated wedge averaging method for junction characterization. , 0, , .		7
52	Automatic mitral leaflet tracking in echocardiography by outlier detection in the low-rank representation. , 2012, , .		7
53	Region-based interaction detection in genome-wide case-control studies. BMC Medical Genomics, 2019, 12, 133.	1.5	7
54	Improving peptide identification with single-stage mass spectrum peaks. Bioinformatics, 2009, 25, 2969-2974.	4.1	6

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55	The choice of null distributions for detecting gene-gene interactions in genome-wide association studies. BMC Bioinformatics, 2011, 12, S26.	2.6	6
56	Identifying disease-associated SNP clusters via contiguous outlier detection. Bioinformatics, 2011, 27, 2578-2585.	4.1	6
57	Bioinformatic Analysis of Data Generated from MALDI Mass Spectrometry for Biomarker Discovery. Topics in Current Chemistry, 2012, 331, 193-209.	4.0	6
58	Ultrasound bio-microscopic image segmentation for evaluation of zebrafish cardiac function. IEEE Transactions on Ultrasonics, Ferroelectrics, and Frequency Control, 2013, 60, 718-726.	3.0	6
59	FPGA Implementation of the Coupled Filtering Method and the Affine Warping Method. IEEE Transactions on Nanobioscience, 2017, 16, 314-325.	3.3	6
60	Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. Lecture Notes in Computer Science, 2009, , 16-30.	1.3	6
61	Using skew Gabor filter in source signal separation and local spectral orientation analysis. Image and Vision Computing, 2005, 23, 377-392.	4.5	5
62	A new protocol of analyzing isotope-coded affinity tag data from high-resolution LC-MS spectrometry. Computational Biology and Chemistry, 2007, 31, 215-221.	2.3	5
63	Isotopically Dimethyl Labeling-Based Quantitative Proteomic Analysis of Phosphoproteomes of Soybean Cultivars. Biomolecules, 2021, 11, 1218.	4.0	5
64	MALDI-MS Data Analysis for Disease Biomarker Discovery. , 2006, 328, 199-216.		4
65	Comments on "An empirical comparison of several recent epistatic interaction detection methods". Bioinformatics, 2012, 28, 145-146.	4.1	3
66	A Combinatorial Perspective of the Protein Inference Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1542-1547.	3.0	3
67	What is the probability of replicating a statistically significant association in genome-wide association studies?. Briefings in Bioinformatics, 2017, 18, bbw091.	6.5	3
68	3D-orientation signatures with conic kernel filtering for multiple motion analysis. , 0, , .		2
69	A hidden two-locus disease association pattern in genome-wide association studies. BMC Bioinformatics, 2011, 12, 156.	2.6	2
70	Guest Editors' Introduction to the Special Issue on "New Trends in Signal Processing and Biomedical Engineering". Computers and Electrical Engineering, 2012, 38, 1-2.	4.8	2
71	HapBoost: A Fast Approach to Boosting Haplotype Association Analyses in Genome-Wide Association Studies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 207-212.	3.0	2
72	Low-Rank Adaptive Clutter Filtering for Robust Ultrasound Vector Flow Imaging. , 2018, , .		2

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73	Using MicroPET Imaging in Quantitative Verification of Acupuncture Effect in Ischemia Stroke Treatment. Nature Precedings, 2010, , .	0.1	1
74	A coupled filtering method to solve feature-motion decorrelation in speckle tracking. , 2010, , .		1
75	SyncPro : A synchronized visualization tool for differential analysis of proteomics data sets. , 2010, , .		1
76	Peptide Reranking with Protein-Peptide Correspondence and Precursor Peak Intensity Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1212-1219.	3.0	1
77	Jointly determining significance levels of primary and replication studies by controlling the false discovery rate in two-stage genome-wide association studies. Statistical Methods in Medical Research, 2018, 27, 2795-2808.	1.5	1
78	LEFT VENTRICULAR BOUNDARY SEGMENTATION FROM ECHOCARDIOGRAPHY. , 2005, , 89-108.		1
79	Using skew gabor filter in source signal separation and local spectral multi-orientation analysis. , 0, , .		0
80	Aligning Peaks Across Multiple Mass Spectrometry Data Sets Using A Scale-Space Based Approach. , 0, , .		0
81	Bayesian Mass Spectra Peak Alignment from Mass Charge Ratios. Cancer Informatics, 2008, 6, 117693510800600.	1.9	0
82	Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. Nature Precedings, 2008, , .	0.1	0
83	Accurate segmentation of ultrasound images using the motion cue. , 2010, , .		0
84	A brief review of signal processing issues in mass spectrometry-based proteomics studies. , 2011, , .		0
85	FPGA implementation of the coupled filtering method. , 2016, , .		0
86	Understanding the Limit of Open Search in the Identification of Peptides With Post-translational Modifications â€” A Simulation-Based Study. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2884-2890.	3.0	0
87	Bayesian mass spectra peak alignment from mass charge ratios. Cancer Informatics, 2008, 6, 217-41.	1.9	0