

Xiang Wan

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

8,735
citations

643344

15
h-index

299063

42
g-index

50
all docs

50
docs citations

50
times ranked

11283
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimating the sample mean and standard deviation from the sample size, median, range and/or interquartile range. BMC Medical Research Methodology, 2014, 14, 135.	1.4	5,713
2	Optimally estimating the sample mean from the sample size, median, mid-range, and/or mid-quartile range. Statistical Methods in Medical Research, 2018, 27, 1785-1805.	0.7	1,687
3	BOOST: A Fast Approach to Detecting Gene-Gene Interactions in Genome-wide Case-Control Studies. American Journal of Human Genetics, 2010, 87, 325-340.	2.6	452
4	Predictive rule inference for epistatic interaction detection in genome-wide association studies. Bioinformatics, 2010, 26, 30-37.	1.8	156
5	GBOOST: a GPU-based tool for detecting gene-gene interactions in genome-wide case control studies. Bioinformatics, 2011, 27, 1309-1310.	1.8	137
6	MegaSNPHunter: a learning approach to detect disease predisposition SNPs and high level interactions in genome wide association study. BMC Bioinformatics, 2009, 10, 13.	1.2	86
7	A unified framework for cross-population trait prediction by leveraging the genetic correlation of polygenic traits. American Journal of Human Genetics, 2021, 108, 632-655.	2.6	73
8	NBLDA: negative binomial linear discriminant analysis for RNA-Seq data. BMC Bioinformatics, 2016, 17, 369.	1.2	33
9	Piecewise-constant and low-rank approximation for identification of recurrent copy number variations. Bioinformatics, 2014, 30, 1943-1949.	1.8	29
10	Comparison of Holmium Laser Enucleation and Plasmakinetic Resection of Prostate: A Randomized Trial with 72-Month Follow-Up. Journal of Endourology, 2018, 32, 139-143.	1.1	28
11	Detecting two-locus associations allowing for interactions in genome-wide association studies. Bioinformatics, 2010, 26, 2517-2525.	1.8	23
12	EPS: an empirical Bayes approach to integrating pleiotropy and tissue-specific information for prioritizing risk genes. Bioinformatics, 2016, 32, 1856-1864.	1.8	19
13	The complete compositional epistasis detection in genome-wide association studies. BMC Genetics, 2013, 14, 7.	2.7	18
14	LSMM: a statistical approach to integrating functional annotations with genome-wide association studies. Bioinformatics, 2018, 34, 2788-2796.	1.8	18
15	Learning to improve medical decision making from imbalanced data without a priori cost. BMC Medical Informatics and Decision Making, 2014, 14, 111.	1.5	17
16	Hypoxia-preconditioned adipose-derived stem cells combined with scaffold promote urethral reconstruction by upregulation of angiogenesis and glycolysis. Stem Cell Research and Therapy, 2020, 11, 535.	2.4	17
17	Stochastic modelling of infectious diseases for heterogeneous populations. Infectious Diseases of Poverty, 2016, 5, 107.	1.5	16
18	XPPX: improving polygenic prediction by cross-population and cross-phenotype analysis. Bioinformatics, 2022, 38, 1947-1955.	1.8	16

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19	Inferring Epidemic Network Topology from Surveillance Data. PLoS ONE, 2014, 9, e100661.	1.1	15
20	Machine Learning Algorithms for Risk Prediction of Severe Hand-Foot-Mouth Disease in Children. Scientific Reports, 2017, 7, 5368.	1.6	15
21	A Comparative study of two types of organ-sparing surgeries for early stage penile cancer: Wide local excision vs partial penectomy. European Journal of Surgical Oncology, 2018, 44, 1425-1431.	0.5	14
22	CISA: Combined NMR Resonance Connectivity Information Determination and Sequential Assignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 336-348.	1.9	13
23	Sharing and Reusing Gene Expression Profiling Data in Neuroscience. Neuroinformatics, 2007, 5, 161-175.	1.5	13
24	Targeting High Value Customers While Under Resource Constraint: Partial Order Constrained Optimization with Genetic Algorithm. Journal of Interactive Marketing, 2015, 29, 27-37.	4.3	13
25	A novel fluorescent probe for the early detection of prostate cancer based on endogenous zinc sensing. Prostate, 2019, 79, 1406-1413.	1.2	13
26	IGESS: a statistical approach to integrating individual-level genotype data and summary statistics in genome-wide association studies. Bioinformatics, 2017, 33, 2882-2889.	1.8	12
27	Classifying next-generation sequencing data using a zero-inflated Poisson model. Bioinformatics, 2018, 34, 1329-1335.	1.8	12
28	A framework for optimising the cost and performance of concept testing. Journal of Marketing Management, 2012, 28, 1000-1013.	1.2	10
29	Leveraging the local genetic structure for trans-ancestry association mapping. American Journal of Human Genetics, 2022, 109, 1317-1337.	2.6	10
30	GD-RDA: A New Regularized Discriminant Analysis for High-Dimensional Data. Journal of Computational Biology, 2017, 24, 1099-1111.	0.8	7
31	The choice of null distributions for detecting gene-gene interactions in genome-wide association studies. BMC Bioinformatics, 2011, 12, S26.	1.2	6
32	Identifying disease-associated SNP clusters via contiguous outlier detection. Bioinformatics, 2011, 27, 2578-2585.	1.8	6
33	LLR: a latent low-rank approach to colocalizing genetic risk variants in multiple GWAS. Bioinformatics, 2017, 33, 3878-3886.	1.8	6
34	HISTOGRAM-BASED SCORING SCHEMES FOR PROTEIN NMR RESONANCE ASSIGNMENT. Journal of Bioinformatics and Computational Biology, 2004, 02, 747-764.	0.3	5
35	Surgical treatment of advanced penile cancer. Journal of Cancer Research and Clinical Oncology, 2017, 143, 1865-1870.	1.2	5
36	Effect of Sulforaphane on Bladder Compliance in a Rat Model of Partial Bladder Outlet Obstruction. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-7.	1.9	5

#	ARTICLE	IF	CITATIONS
37	An extracellular matrix-mimicking, bilayered, heterogeneous, porous, nanofibrous scaffold for anterior urethroplasty in a rabbit model. <i>Biomedical Materials (Bristol)</i> , 2020, 15, 065008.	1.7	5
38	GASA: A GRAPH-BASED AUTOMATED NMR BACKBONE RESONANCE SEQUENTIAL ASSIGNMENT PROGRAM. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 313-333.	0.3	3
39	Comments on "An empirical comparison of several recent epistatic interaction detection methods". <i>Bioinformatics</i> , 2012, 28, 145-146.	1.8	3
40	A hidden two-locus disease association pattern in genome-wide association studies. <i>BMC Bioinformatics</i> , 2011, 12, 156.	1.2	2
41	HapBoost: A Fast Approach to Boosting Haplotype Association Analyses in Genome-Wide Association Studies. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 207-212.	1.9	2
42	Posttraumatic Arterial Priapism Treated with Superselective Embolization: Our Clinical Experience and a Review of the Literature. <i>Advances in Therapy</i> , 2019, 36, 684-690.	1.3	1
43	Optimally estimating the sample mean from the sample size, median, mid-range, and/or mid-quartile range. , 0, .		1
44	Primary Hyperaldosteronism Induced by Aldosterone-Producing Adenoma Co-Existing with A Left Suprarenal Accessory Spleen: Two Case Reports and A Review of The Literature. <i>Urology Journal</i> , 2019, 16, 318-321.	0.3	0