

Masao Ueki

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

322
citations

1040056

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1058476

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docs citations

16
times ranked

553
citing authors

#	ARTICLE	IF	CITATIONS
1	Smooth-threshold multivariate genetic prediction incorporating gene-environment interactions. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	0
2	Clustering by phenotype and genome-wide association study in autism. <i>Translational Psychiatry</i> , 2020, 10, 290.	4.8	29
3	Machine learning for effectively avoiding overfitting is a crucial strategy for the genetic prediction of polygenic psychiatric phenotypes. <i>Translational Psychiatry</i> , 2020, 10, 294.	4.8	11
4	Machine learning to reveal hidden risk combinations for the trajectory of posttraumatic stress disorder symptoms. <i>Scientific Reports</i> , 2020, 10, 21726.	3.3	3
5	Improved metabolomic data-based prediction of depressive symptoms using nonlinear machine learning with feature selection. <i>Translational Psychiatry</i> , 2020, 10, 157.	4.8	24
6	3.5KJPNv2: an allele frequency panel of 3552 Japanese individuals including the X chromosome. <i>Human Genome Variation</i> , 2019, 6, 28.	0.7	115
7	Quick assessment for systematic test statistic inflation/deflation due to null model misspecifications in genome-wide environment interaction studies. <i>PLoS ONE</i> , 2019, 14, e0219825.	2.5	5
8	ENHANCING POWER OF SCORE TESTS FOR REGRESSION MODELS VIA FISHER TRANSFORMATION. <i>Journal of the Japanese Society of Computational Statistics</i> , 2018, 30, 37-53.	0.2	1
9	Potential identification of vitamin B6 responsiveness in autism spectrum disorder utilizing phenotype variables and machine learning methods. <i>Scientific Reports</i> , 2018, 8, 14840.	3.3	18
10	Detecting genetic association through shortest paths in a bidirected graph. <i>Genetic Epidemiology</i> , 2017, 41, 481-497.	1.3	5
11	Smooth-Threshold Multivariate Genetic Prediction with Unbiased Model Selection. <i>Genetic Epidemiology</i> , 2016, 40, 233-243.	1.3	10
12	On the choice of degrees of freedom for testing gene-gene interactions. <i>Statistics in Medicine</i> , 2014, 33, 4934-4948.	1.6	4
13	Multiple choice from competing regression models under multicollinearity based on standardized update. <i>Computational Statistics and Data Analysis</i> , 2013, 63, 31-41.	1.2	11
14	Ultrahigh-dimensional variable selection method for whole-genome gene-gene interaction analysis. <i>BMC Bioinformatics</i> , 2012, 13, 72.	2.6	33
15	A note on automatic variable selection using smooth-threshold estimating equations. <i>Biometrika</i> , 2009, 96, 1005-1011.	2.4	53
16	Beta-negative binomial nonlinear spatio-temporal random effects modeling of COVID-19 case counts in Japan. <i>Journal of Applied Statistics</i> , 0, , 1-14.	1.3	0