Masao Ueki

List of Publications by Year
in descending order

16	322	1040056	1058476
papers	citations	9	14
		h-index	g-index

16	16	16	553
all docs	docs citations	times ranked	citing authors

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