Karim Oualkacha

List of Publications by Year
in descending order

37 papers	1,295 citations	1039406 9 h-index	454577 30 g-index
39 all docs	39 docs citations	39 times ranked	4807 citing authors

#	Article	IF	Citations
1	A new GEE method to account for heteroscedasticity using asymmetric least-square regressions. Journal of Applied Statistics, 2022, 49, 3564-3590.	0.6	4
2	Group penalized quantile regression. Statistical Methods and Applications, 2022, 31, 495-529.	0.7	1
3	A novel statistical method for modeling covariate effects in bisulfite sequencing derived measures of DNA methylation. Biometrics, 2021, 77, 424-438.	0.8	3
4	On Path to Informing Hierarchy of Eplet Mismatches as Determinants of Kidney Transplant Loss. Kidney International Reports, 2021, 6, 1567-1579.	0.4	24
5	Block coordinate descent algorithm improves variable selection and estimation in errorâ€inâ€variables regression. Genetic Epidemiology, 2021, 45, 874-890.	0.6	5
6	A flexible copulaâ€based approach for the analysis of secondary phenotypes in ascertained samples. Statistics in Medicine, 2020, 39, 517-543.	0.8	3
7	Simultaneous SNP selection and adjustment for population structure in high dimensional prediction models. PLoS Genetics, 2020, 16, e1008766.	1.5	5
8	Title is missing!. , 2020, 16, e1008766.		0
9	Title is missing!. , 2020, 16, e1008766.		0
10	Title is missing!. , 2020, 16, e1008766.		0
11	Title is missing!. , 2020, 16, e1008766.		0
12	Title is missing!. , 2020, 16, e1008766.		0
13	Title is missing!. , 2020, 16, e1008766.		0
14	The cluster correlation-network support vector machine for high-dimensional binary classification. Journal of Statistical Computation and Simulation, 2019, 89, 1020-1043.	0.7	8
15	Constrained instruments and their application to Mendelian randomization with pleiotropy. Genetic Epidemiology, 2019, 43, 373-401.	0.6	15
16	Multivariate association test for rare variants controlling for cryptic and family relatedness. Canadian Journal of Statistics, 2019, 47, 90-107.	0.6	1
17	Exome-wide rare variant analyses of two bone mineral density phenotypes: the challenges of analyzing rare genetic variation. Scientific Reports, 2018, 8, 220.	1.6	2
18	Principal component of explained variance: An efficient and optimal data dimension reduction framework for association studies. Statistical Methods in Medical Research, 2018, 27, 1331-1350.	0.7	7

#	Article	IF	Citations
19	Investigating potential causal relationships between SNPs, DNA methylation and HDL. BMC Proceedings, 2018, 12, 20.	1.8	3
20	CpG-set association assessment of lipid concentration changes and DNA methylation. BMC Proceedings, 2018, 12, 30.	1.8	2
21	Causal modeling in a multi-omic setting: insights from GAW20. BMC Genetics, 2018, 19, 74.	2.7	9
22	A coordinate descent algorithm for computing penalized smooth quantile regression. Statistics and Computing, 2017, 27, 865-883.	0.8	9
23	A smoothed EM-algorithm for DNA methylation profiles from sequencing-based methods in cell lines or for a single cell type. Statistical Applications in Genetics and Molecular Biology, 2017, 16, 333-347.	0.2	4
24	Performance of an alleleâ€level multiâ€locus HLA genotype imputation tool in hematopoietic stem cell donors from Quebec. Immunity, Inflammation and Disease, 2017, 5, 551-559.	1.3	8
25	Specific expression of novel long non-coding RNAs in high-hyperdiploid childhood acute lymphoblastic leukemia. PLoS ONE, 2017, 12, e0174124.	1.1	24
26	Gene Coexpression Analyses Differentiate Networks Associated with Diverse Cancers Harboring TP53 Missense or Null Mutations. Frontiers in Genetics, 2016, 7, 137.	1.1	23
27	Software Application Profile: RVPedigree: a suite of family-based rare variant association tests for normally and non-normally distributed quantitative traits. International Journal of Epidemiology, 2016, 45, 402-407.	0.9	2
28	A method for analyzing multiple continuous phenotypes in rare variant association studies allowing for flexible correlations in variant effects. European Journal of Human Genetics, 2016, 24, 1344-1351.	1.4	21
29	Joint analysis of multiple blood pressure phenotypes in GAW19 data by using a multivariate rare-variant association test. BMC Proceedings, 2016, 10, 309-313.	1.8	6
30	A rare variant association test in familyâ€based designs and nonâ€normal quantitative traits. Statistics in Medicine, 2016, 35, 905-921.	0.8	7
31	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
32	Pathway analysis for genetic association studies: to do, or not to do? That is the question. BMC Proceedings, 2014, 8, S103.	1.8	2
33	Adjusted Sequence Kernel Association Test for Rare Variants Controlling for Cryptic and Family Relatedness. Genetic Epidemiology, 2013, 37, 366-376.	0.6	50
34	On the estimation of an average rigid body motion. Biometrika, 2012, 99, 585-598.	1.3	6
35	Principal Components of Heritability for High Dimension Quantitative Traits and General Pedigrees. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.2	13
36	A new statistical model for random unit vectors. Journal of Multivariate Analysis, 2009, 100, 70-80.	0.5	8

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37	The Kendall interaction filter for variable interaction screening in high dimensional classification problems. Journal of Applied Statistics, 0, , 1-19.	0.6	5