Seunggeun Lee

List of Publications by Year
in descending order

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Version: 2024-02-01

50 papers	7,042 citations	279798 23 h-index	189892 50 g-index
72 all docs	72 docs citations	72 times ranked	12509 citing authors

#	Article	IF	Citations
1	Rare-Variant Association Testing for Sequencing Data with the Sequence Kernel Association Test. American Journal of Human Genetics, 2011, 89, 82-93.	6.2	2,060
2	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341.	21.4	896
3	Optimal Unified Approach for Rare-Variant Association Testing with Application to Small-Sample Case-Control Whole-Exome Sequencing Studies. American Journal of Human Genetics, 2012, 91, 224-237.	6.2	880
4	Optimal tests for rare variant effects in sequencing association studies. Biostatistics, 2012, 13, 762-775.	1.5	581
5	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	21.4	547
6	Sequence Kernel Association Tests for the Combined Effect of Rare and Common Variants. American Journal of Human Genetics, 2013, 92, 841-853.	6.2	393
7	General Framework for Meta-analysis of Rare Variants in Sequencing Association Studies. American Journal of Human Genetics, 2013, 93, 42-53.	6.2	211
8	Exploring and visualizing large-scale genetic associations by using PheWeb. Nature Genetics, 2020, 52, 550-552.	21.4	129
9	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. Nature Genetics, 2020, 52, 634-639.	21.4	124
10	A Fast and Accurate Algorithm to Test for Binary Phenotypes and Its Application to PheWAS. American Journal of Human Genetics, 2017, 101, 37-49.	6.2	116
11	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
12	Update on the State of the Science for Analytical Methods for Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 762-770.	3.4	79
13	Convergence and prediction of principal component scores in high-dimensional settings. Annals of Statistics, 2010, 38, 3605-3629.	2.6	60
14	Kernel Machine SNPâ€Set Testing Under Multiple Candidate Kernels. Genetic Epidemiology, 2013, 37, 267-275.	1.3	60
15	A Fast and Accurate Method for Genome-Wide Time-to-Event Data Analysis and Its Application to UK Biobank. American Journal of Human Genetics, 2020, 107, 222-233.	6.2	57
16	UK Biobank Whole-Exome Sequence Binary Phenome Analysis with Robust Region-Based Rare-Variant Test. American Journal of Human Genetics, 2020, 106, 3-12.	6.2	56
17	GEEâ€Based SNP Set Association Test for Continuous and Discrete Traits in Familyâ€Based Association Studies. Genetic Epidemiology, 2013, 37, 778-786.	1.3	55
18	Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. Nature Communications, 2019, 10, 1847.	12.8	55

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19	An efficient resampling method for calibrating single and gene-based rare variant association analysis in caseâ€“control studies. Biostatistics, 2016, 17, 1-15.	1.5	46
20	Unified Sequence-Based Association Tests Allowing for Multiple Functional Annotations and Meta-analysis of Noncoding Variation in Metabochip Data. American Journal of Human Genetics, 2017, 101, 340-352.	6.2	45
21	Multiâ€SKAT: General framework to test for rareâ€variant association with multiple phenotypes. Genetic Epidemiology, 2019, 43, 4-23.	1.3	40
22	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
23	On cross-ancestry cancer polygenic risk scores. PLoS Genetics, 2021, 17, e1009670.	3.5	32
24	Association analysis of rare variants near the APOE region with CSF and neuroimaging biomarkers of Alzheimerâ€™s disease. BMC Medical Genomics, 2017, 10, 29.	1.5	28
25	Efficient mixed model approach for large-scale genome-wide association studies of ordinal categorical phenotypes. American Journal of Human Genetics, 2021, 108, 825-839.	6.2	25
26	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. Nature Communications, 2020, 11, 4093.	12.8	24
27	Fast and robust ancestry prediction using principal component analysis. Bioinformatics, 2020, 36, 3439-3446.	4.1	21
28	A Fast and Accurate Method for Genome-wide Scale Phenome-wide G Ã— E Analysis and Its Application to UK Biobank. American Journal of Human Genetics, 2019, 105, 1182-1192.	6.2	20
29	Convergence of sample eigenvalues, eigenvectors, and principal component scores for ultra-high dimensional data. Biometrika, 2014, 101, 484-490.	2.4	18
30	Improving power for rareâ€variant tests by integrating external controls. Genetic Epidemiology, 2017, 41, 610-619.	1.3	18
31	A Novel Random Effect Model for GWAS Meta-Analysis and Its Application to Trans-Ethnic Meta-Analysis. Biometrics, 2016, 72, 945-954.	1.4	17
32	Knowledge-driven binning approach for rare variant association analysis: application to neuroimaging biomarkers in Alzheimerâ€™s disease. BMC Medical Informatics and Decision Making, 2017, 17, 61.	3.0	16
33	Set-Based Tests for the Geneâ€“Environment Interaction in Longitudinal Studies. Journal of the American Statistical Association, 2017, 112, 966-978.	3.1	14
34	Setâ€based tests for genetic association in longitudinal studies. Biometrics, 2015, 71, 606-615.	1.4	13
35	Evaluating the Calibration and Power of Three Gene-Based Association Tests of Rare Variants for the X Chromosome. Genetic Epidemiology, 2015, 39, 499-508.	1.3	12
36	Rare variant testing across methods and thresholds using the multi-kernel sequence kernel association test (MK-SKAT). Statistics and Its Interface, 2015, 8, 495-505.	0.3	11

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37	Novel score test to increase power in association test by integrating external controls. Genetic Epidemiology, 2021, 45, 293-304.	1.3	10
38	Metaâ€MultiSKAT: Multiple phenotype metaâ€analysis for regionâ€based association test. Genetic Epidemiology, 2019, 43, 800-814.	1.3	9
39	Applying Novel Methods for Assessing Individual- and Neighborhood-Level Social and Psychosocial Environment Interactions with Genetic Factors in the Prediction of Depressive Symptoms in the Multi-Ethnic Study of Atherosclerosis. Behavior Genetics, 2016, 46, 89-99.	2.1	8
40	Robust Tests for Additive Gene-Environment Interaction in Case-Control Studies Using Gene-Environment Independence. American Journal of Epidemiology, 2018, 187, 366-377.	3.4	8
41	A powerful subset-based method identifies gene set associations and improves interpretation in UK Biobank. American Journal of Human Genetics, 2021, 108, 669-681.	6.2	8
42	Robust metaâ€analysis of biobankâ€based genomeâ€wide association studies with unbalanced binary phenotypes. Genetic Epidemiology, 2019, 43, 462-476.	1.3	7
43	Asymptotic properties of principal component analysis and shrinkage-bias adjustment under the generalized spiked population model. Journal of Multivariate Analysis, 2019, 173, 145-164.	1.0	6
44	Subset-Based Analysis Using Gene-Environment Interactions for Discovery of Genetic Associations across Multiple Studies or Phenotypes. Human Heredity, 2018, 83, 283-314.	0.8	5
45	NETMAGE: A human disease phenotype map generator for the network-based visualization of phenome-wide association study results. GigaScience, 2022, 11, .	6.4	5
46	Rareâ€variant association tests in longitudinal studies, with an application to the Multiâ€Ethnic Study of Atherosclerosis (MESA). Genetic Epidemiology, 2017, 41, 801-810.	1.3	3
47	Understanding the Patterns of Serological Testing for COVID-19 Pre- and Post-Vaccination Rollout in Michigan. Journal of Clinical Medicine, 2021, 10, 4341.	2.4	3
48	Scalable and Robust Regression Methods for Phenome-Wide Association Analysis on Large-Scale Biobank Data. Frontiers in Genetics, 2021, 12, 682638.	2.3	2
49	Integrating external controls in caseâ€“control studies improves power for rareâ€variant tests. Genetic Epidemiology, 2022, 46, 145-158.	1.3	2
50	Trans-ethnic meta-analysis of rare variants in sequencing association studies. Biostatistics, 2021, 22, 706-722.	1.5	1