

Reevaluation of SNP heritability in complex human traits

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Determining Genetic Component of a Disease. , 0, , 91-115.		11
2	The impact of rare and low-frequency genetic variants in common disease. <i>Genome Biology</i> , 2017, 18, 77.	3.8	277
3	Genome-wide association studies of cancer: current insights and future perspectives. <i>Nature Reviews Cancer</i> , 2017, 17, 692-704.	12.8	285
4	Blood Pressure Genome-Wide Association Studies, Missing Heritability, and Omnigenics. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	4
5	Concepts, estimation and interpretation of SNP-based heritability. <i>Nature Genetics</i> , 2017, 49, 1304-1310.	9.4	378
6	Polygenicity and Epistasis Underlie Fitness-Proximal Traits in the <i>Caenorhabditis elegans</i> Multiparental Experimental Evolution (CeMEE) Panel. <i>Genetics</i> , 2017, 207, 1663-1685.	1.2	81
7	Childhood behaviour problems show the greatest gap between DNA-based and twin heritability. <i>Translational Psychiatry</i> , 2017, 7, 1284.	2.4	46
8	Collaborative phenotype inference from comorbid substance use disorders and genotypes. , 2017, 2017, 392-397.		1
9	Contribution of rare and low-frequency whole-genome sequence variants to complex traits variation in dairy cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 60.	1.2	15
10	Estimated allele substitution effects underlying genomic evaluation models depend on the scaling of allele counts. <i>Genetics Selection Evolution</i> , 2017, 49, 79.	1.2	9
11	Genetics of biologically based psychological differences. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170162.	1.8	19
12	Genome-wide association studies in Crohn's disease: Past, present and future. <i>Clinical and Translational Immunology</i> , 2018, 7, e1001.	1.7	80
13	Environment dominates over host genetics in shaping human gut microbiota. <i>Nature</i> , 2018, 555, 210-215.	18.7	1,958
14	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	9.4	304
15	Narrow-sense heritability estimation of complex traits using identity-by-descent information. <i>Heredity</i> , 2018, 121, 616-630.	1.2	20
16	Power Analysis for Genetic Association Test (PAGEANT) provides insights to challenges for rare variant association studies. <i>Bioinformatics</i> , 2018, 34, 1506-1513.	1.8	18
17	Using partitioned heritability methods to explore genetic architecture. <i>Nature Reviews Genetics</i> , 2018, 19, 185-185.	7.7	9
18	Obesity genetics: insights from the Pakistani population. <i>Obesity Reviews</i> , 2018, 19, 364-380.	3.1	20

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19	A network approach to exploring the functional basis of gene-gene epistatic interactions in disease susceptibility. <i>Bioinformatics</i> , 2018, 34, 1741-1749.	1.8	11
20	Genetic Correlation Profile of Schizophrenia Mirrors Epidemiological Results and Suggests Link Between Polygenic and Rare Variant (22q11.2) Cases of Schizophrenia. <i>Schizophrenia Bulletin</i> , 2018, 44, 1350-1361.	2.3	26
21	Obligatory and facilitative allelic variation in the DNA methylome within common disease-associated loci. <i>Nature Communications</i> , 2018, 9, 8.	5.8	107
22	Inferring Causal Relationships Between Risk Factors and Outcomes from Genome-Wide Association Study Data. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 303-327.	2.5	163
23	Genetic and Environmental Contributions to the Covariation Between Cardiometabolic Traits. <i>Journal of the American Heart Association</i> , 2018, 7, .	1.6	1
24	Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits. <i>Nature Genetics</i> , 2018, 50, 737-745.	9.4	205
25	Statistical genetics and its application to neuroimmunology. <i>Clinical and Experimental Neuroimmunology</i> , 2018, 9, 7-12.	0.5	3
26	Population structure in genetic studies: Confounding factors and mixed models. <i>PLoS Genetics</i> , 2018, 14, e1007309.	1.5	164
27	Prediction of treatment response in rheumatoid arthritis patients using genome-wide SNP data. <i>Genetic Epidemiology</i> , 2018, 42, 754-771.	0.6	15
28	Detecting the dominance component of heritability in isolated and outbred human populations. <i>Scientific Reports</i> , 2018, 8, 18048.	1.6	3
29	Inferring phenotypes from substance use via collaborative matrix completion. <i>BMC Systems Biology</i> , 2018, 12, 104.	3.0	0
30	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, 5052.	5.8	75
31	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. <i>Nature Communications</i> , 2018, 9, 5269.	5.8	331
32	Methods and results from the genome-wide association group at GAW20. <i>BMC Genetics</i> , 2018, 19, 79.	2.7	0
33	Understanding the potential bias of variance components estimators when using genomic models. <i>Genetics Selection Evolution</i> , 2018, 50, 41.	1.2	7
34	Reliability of genomic predictions of complex human phenotypes. <i>BMC Proceedings</i> , 2018, 12, 51.	1.8	7
35	Heritability and genetic associations of triglyceride and HDL-C levels using pedigree-based and empirical kinships. <i>BMC Proceedings</i> , 2018, 12, 34.	1.8	5
36	Genomic inference using diffusion models and the allele frequency spectrum. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 140-147.	1.5	25

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38	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. <i>Nature Communications</i> , 2018, 9, 3707.	5.8	86
39	Another Round of "Clue" to Uncover the Mystery of Complex Traits. <i>Genes</i> , 2018, 9, 61.	1.0	7
40	The personal and clinical utility of polygenic risk scores. <i>Nature Reviews Genetics</i> , 2018, 19, 581-590.	7.7	1,102
41	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018, 102, 1185-1194.	2.6	119
42	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. <i>Drug and Alcohol Dependence</i> , 2018, 188, 94-101.	1.6	10
43	Estimating SNP-Based Heritability and Genetic Correlation in Case-Control Studies Directly and with Summary Statistics. <i>American Journal of Human Genetics</i> , 2018, 103, 89-99.	2.6	102
44	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. <i>Nature Genetics</i> , 2018, 50, 1041-1047.	9.4	154
45	Using whole genome scores to compare three clinical phenotyping methods in complex diseases. <i>Scientific Reports</i> , 2018, 8, 11360.	1.6	9
46	Prediction of Complex Traits: Robust Alternatives to Best Linear Unbiased Prediction. <i>Frontiers in Genetics</i> , 2018, 9, 195.	1.1	29
47	Analysis of Gene Expression Variance in Schizophrenia Using Structural Equation Modeling. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 192.	1.4	20
48	Bias in Mendelian randomization due to assortative mating. <i>Genetic Epidemiology</i> , 2018, 42, 608-620.	0.6	81
49	A Statistical Framework for Mapping Risk Genes from De Novo Mutations in Whole-Genome-Sequencing Studies. <i>American Journal of Human Genetics</i> , 2018, 102, 1031-1047.	2.6	26
50	A systematic review of genome-wide research on psychotic experiences and negative symptom traits: new revelations and implications for psychiatry. <i>Human Molecular Genetics</i> , 2018, 27, R136-R152.	1.4	27
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53	Estimation of complex effect-size distributions using summary-level statistics from genome-wide association studies across 32 complex traits. <i>Nature Genetics</i> , 2018, 50, 1318-1326.	9.4	225
54	Using genetic data to strengthen causal inference in observational research. <i>Nature Reviews Genetics</i> , 2018, 19, 566-580.	7.7	298

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56	Leveraging GWAS for complex traits to detect signatures of natural selection in humans. Current Opinion in Genetics and Development, 2018, 53, 9-14.	1.5	22
57	Heritability of Regional Brain Volumes in Large-Scale Neuroimaging and Genetic Studies. Cerebral Cortex, 2019, 29, 2904-2914.	1.6	36
58	A global overview of pleiotropy and genetic architecture in complex traits. Nature Genetics, 2019, 51, 1339-1348.	9.4	774
59	Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. American Journal of Human Genetics, 2019, 105, 456-476.	2.6	175
60	Genome-wide association studies of severe P. falciparum malaria susceptibility: progress, pitfalls and prospects. BMC Medical Genomics, 2019, 12, 120.	0.7	28
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66	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. Nature Communications, 2019, 10, 4558.	5.8	363
67	Genome-Wide Association Studies. , 2019, , .		7
68	Contribution of Common Genetic Variants to Familial Aggregation of Disease and Implications for Sequencing Studies. PLoS Genetics, 2019, 15, e1008490.	1.5	8
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70	Complex Phenotypes: Mechanisms Underlying Variation in Human Stature. Current Osteoporosis Reports, 2019, 17, 301-323.	1.5	11
72	Early progression to active tuberculosis is a highly heritable trait driven by 3q23 in Peruvians. Nature Communications, 2019, 10, 3765.	5.8	43
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74	Contribution of genetics to visceral adiposity and its relation to cardiovascular and metabolic disease. Nature Medicine, 2019, 25, 1390-1395.	15.2	172

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77	Genetic and phenotypic landscape of the major histocompatibility complex region in the Japanese population. <i>Nature Genetics</i> , 2019, 51, 470-480.	9.4	75
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79	Heritability analysis of nontraditional glycemic biomarkers in the Atherosclerosis Risk in Communities Study. <i>Genetic Epidemiology</i> , 2019, 43, 776-785.	0.6	8
80	Genetic correlations of polygenic disease traits: from theory to practice. <i>Nature Reviews Genetics</i> , 2019, 20, 567-581.	7.7	236
81	Estimation of metabolic syndrome heritability in three large populations including full pedigree and genomic information. <i>Human Genetics</i> , 2019, 138, 739-748.	1.8	4
82	Bivariate causal mixture model quantifies polygenic overlap between complex traits beyond genetic correlation. <i>Nature Communications</i> , 2019, 10, 2417.	5.8	190
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84	The Genetic Basis of Child and Adolescent Anxiety. , 2019, , 17-46.		9
85	Sequence imputation from low density single nucleotide polymorphism panel in a black poplar breeding population. <i>BMC Genomics</i> , 2019, 20, 302.	1.2	6
86	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. <i>Nature Communications</i> , 2019, 10, 2154.	5.8	172
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88	Reliable heritability estimation using sparse regularization in ultrahigh dimensional genome-wide association studies. <i>BMC Bioinformatics</i> , 2019, 20, 219.	1.2	7
89	Genes with High Network Connectivity Are Enriched for Disease Heritability. <i>American Journal of Human Genetics</i> , 2019, 104, 896-913.	2.6	46
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92	Evaluation of an <i>HMG2</i> variant for pleiotropic effects on height and metabolic traits in ponies. <i>Journal of Veterinary Internal Medicine</i> , 2019, 33, 942-952.	0.6	31

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94	Adjustment for index event bias in genome-wide association studies of subsequent events. Nature Communications, 2019, 10, 1561.	5.8	87
95	Meta-analysis of genome-wide association studies provides insights into genetic control of tomato flavor. Nature Communications, 2019, 10, 1534.	5.8	91
96	Do polygenic risk and stressful life events predict pharmacological treatment response in obsessive compulsive disorder? A geneâ€environment interaction approach. Translational Psychiatry, 2019, 9, 70.	2.4	19
97	Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. Nature Communications, 2019, 10, 790.	5.8	98
98	Transcriptome-Wide Association Supplements Genome-Wide Association in <i>Zea mays</i> . G3: Genes, Genomes, Genetics, 2019, 9, 3023-3033.	0.8	64
99	Insights into malaria susceptibility using genome-wide data on 17,000 individuals from Africa, Asia and Oceania. Nature Communications, 2019, 10, 5732.	5.8	126
100	Identification of four novel associations for B-cell acute lymphoblastic leukaemia risk. Nature Communications, 2019, 10, 5348.	5.8	58
101	Comprehensive identification of pleiotropic loci for body fat distribution using the NHGRIâ€EBI Catalog of published genomeâ€wide association studies. Obesity Reviews, 2019, 20, 385-406.	3.1	10
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108	Exploring the role of genetic confounding in the association between maternal and offspring body mass index: evidence from three birth cohorts. International Journal of Epidemiology, 2020, 49, 233-243.	0.9	18
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110	Genome-Wide Meta-Analyses of FTND and TTFC Phenotypes. Nicotine and Tobacco Research, 2020, 22, 900-909.	1.4	17

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112	Genome-wide heritability analysis of severe malaria resistance reveals evidence of polygenic inheritance. <i>Human Molecular Genetics</i> , 2020, 29, 168-176.	1.4	8
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114	Heritability estimates for 361 blood metabolites across 40 genome-wide association studies. <i>Nature Communications</i> , 2020, 11, 39.	5.8	64
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116	Alterations in stomatal response to fluctuating light increase biomass and yield of rice under drought conditions. <i>Plant Journal</i> , 2020, 104, 1334-1347.	2.8	26
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122	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. <i>Nature Communications</i> , 2020, 11, 3865.	5.8	129
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125	Efficient variance components analysis across millions of genomes. <i>Nature Communications</i> , 2020, 11, 4020.	5.8	31
126	The search for sexually antagonistic genes: Practical insights from studies of local adaptation and statistical genomics. <i>Evolution Letters</i> , 2020, 4, 398-415.	1.6	45
127	A framework for pathway knowledge driven prioritization in genome-wide association studies. <i>Genetic Epidemiology</i> , 2020, 44, 841-853.	0.6	2
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131	Models of Personality Structure. , 2020, , 115-128.		0
132	The Five-Factor Model of Personality: Consensus and Controversy. , 2020, , 129-141.		2
133	Temperament and Brain Networks of Attention. , 2020, , 155-168.		2
134	Personality in Nonhuman Animals. , 2020, , 235-246.		0
135	Genetics of Personality. , 2020, , 247-258.		0
136	Approach–Avoidance Theories of Personality. , 2020, , 259-272.		1
137	Cognitive Processes and Models. , 2020, , 295-315.		0
138	Basic Needs, Goals and Motivation. , 2020, , 330-338.		1
139	Personality and the Self. , 2020, , 339-351.		6
140	Social Relations and Social Support. , 2020, , 386-399.		0
141	Personality and Politics. , 2020, , 413-424.		1
142	Personality at Work. , 2020, , 427-438.		2
144	Personality in Clinical Psychology. , 2020, , 451-462.		0
146	Conceptual and Historical Perspectives. , 2020, , 13-30.		3
147	Personality and the Unconscious. , 2020, , 69-80.		0
148	Personality and Emotion. , 2020, , 81-100.		8
149	Personality Assessment Methods. , 2020, , 103-114.		0

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151	Development of Personality across the Life Span. , 2020, , 169-182.		3
152	Personality Traits and Mental Disorders. , 2020, , 183-192.		0
153	Attachment Theory. , 2020, , 208-220.		0
154	Evolutionary Personality Psychology. , 2020, , 223-234.		4
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156	Self-Regulation and Control in Personality Functioning. , 2020, , 316-329.		0
157	Traits and Dynamic Processes. , 2020, , 352-363.		0
158	Anxiety, Depression and Cognitive Dysfunction. , 2020, , 364-374.		0
159	Personality in Cross-Cultural Perspective. , 2020, , 400-412.		1
160	Personality, Preferences and Socioeconomic Behavior. , 2020, , 477-494.		2
162	States and Situations, Traits and Environments. , 2020, , 56-68.		1
163	Narrative Identity in the Social World. , 2020, , 377-385.		0
164	Personality and Crime. , 2020, , 463-476.		0
165	Models of Physical Health and Personality. , 2020, , 193-207.		2
167	Beyond SNP heritability: Polygenicity and discoverability of phenotypes estimated with a univariate Gaussian mixture model. PLoS Genetics, 2020, 16, e1008612.	1.5	120
168	Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics. American Journal of Human Genetics, 2020, 107, 46-59.	2.6	30
169	Fine-tuning of Genome-Wide Polygenic Risk Scores and Prediction of Gestational Diabetes in South Asian Women. Scientific Reports, 2020, 10, 8941.	1.6	25

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171	Estimation of non-null SNP effect size distributions enables the detection of enriched genes underlying complex traits. <i>PLoS Genetics</i> , 2020, 16, e1008855.	1.5	9
172	Quantifying Differences in Heritability among Psoriatic Arthritis (PsA), Cutaneous Psoriasis (PsC) and Psoriasis vulgaris (PsV). <i>Scientific Reports</i> , 2020, 10, 4925.	1.6	20
173	Genetic influence on ageing-related changes in resting-state brain functional networks in healthy adults: A systematic review. <i>Neuroscience and Biobehavioral Reviews</i> , 2020, 113, 98-110.	2.9	23
174	Evaluating and improving heritability models using summary statistics. <i>Nature Genetics</i> , 2020, 52, 458-462.	9.4	128
175	No Evidence of Persistence or Inheritance of Mitochondrial DNA Copy Number in Holocaust Survivors and Their Descendants. <i>Frontiers in Genetics</i> , 2020, 11, 87.	1.1	5
176	Statistical methods for SNP heritability estimation and partition: A review. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1557-1568.	1.9	41
177	Polygenic Architecture of Human Neuroanatomical Diversity. <i>Cerebral Cortex</i> , 2020, 30, 2307-2320.	1.6	16
178	Genomic dissection of maternal, additive and non-additive genetic effects for growth and carcass traits in Nile tilapia. <i>Genetics Selection Evolution</i> , 2020, 52, 1.	1.2	78
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181	Statistical Methods in Genome-Wide Association Studies. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 265-288.	2.8	6
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183	The contribution of rare genetic variants to the pathogenesis of polycystic ovary syndrome. <i>Current Opinion in Endocrine and Metabolic Research</i> , 2020, 12, 26-32.	0.6	21
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185	Population phenomena inflate genetic associations of complex social traits. <i>Science Advances</i> , 2020, 6, eaay0328.	4.7	110
186	Dissecting the heritable risk of breast cancer: From statistical methods to susceptibility genes. <i>Seminars in Cancer Biology</i> , 2021, 72, 175-184.	4.3	10
187	Risk in Relatives, Heritability, SNP-Based Heritability, and Genetic Correlations in Psychiatric Disorders: A Review. <i>Biological Psychiatry</i> , 2021, 89, 11-19.	0.7	59

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189	Computational Tools for Causal Inference in Genetics. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2021, 11, a039248.	2.9	3
190	The genetic architecture of human complex phenotypes is modulated by linkage disequilibrium and heterozygosity. <i>Genetics</i> , 2021, 217, .	1.2	10
191	OUP accepted manuscript. <i>Human Molecular Genetics</i> , 2021, 30, 1521-1534.	1.4	32
192	An Academic Clinician's Road Map to Hypertension Genomics. <i>Hypertension</i> , 2021, 77, 284-295.	1.3	9
193	A GWAS in Latin Americans identifies novel face shape loci, implicating VPS13B and a Denisovan introgressed region in facial variation. <i>Science Advances</i> , 2021, 7, .	4.7	32
195	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021, 12, 1164.	5.8	50
197	Boosting heritability: estimating the genetic component of phenotypic variation with multiple sample splitting. <i>BMC Bioinformatics</i> , 2021, 22, 164.	1.2	7
198	Motivating and Discouraging Factors for Bipolar Patient Participation in Genomic Research. <i>Public Health Genomics</i> , 2021, 24, 89-98.	0.6	2
199	Incorporating European GWAS findings improve polygenic risk prediction accuracy of breast cancer among East Asians. <i>Genetic Epidemiology</i> , 2021, 45, 471-484.	0.6	7
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