

Power and type I error rate of false discovery rate approaches

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Data mining. Genetic Epidemiology, 2005, 29, S103-S109.	0.6	7
2	Polymorphisms of CUL5 Are Associated with CD4+ T Cell Loss in HIV-1 Infected Individuals. PLoS Genetics, 2007, 3, e19.	1.5	47
3	Exploring design-related bias in clinical studies on receptor genetic polymorphism of hypertension. Journal of Clinical Epidemiology, 2007, 60, 1.e1-1.e11.	2.4	12
4	Sample size calculation with dependence adjustment for FDR-control in microarray studies. Statistics in Medicine, 2007, 26, 4219-4237.	0.8	33
5	Genome-wide significance for dense SNP and resequencing data. Genetic Epidemiology, 2008, 32, 179-185.	0.6	187
6	Polymorphisms in the interleukin 13 and GATA binding protein 3 genes and the development of eczema during childhood. British Journal of Dermatology, 2008, 158, 1315-1322.	1.4	42
7	Gene expression patterns within cell lines are predictive of chemosensitivity. BMC Genomics, 2008, 9, 74.	1.2	15
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9	How to Interpret a Genome-wide Association Study. JAMA - Journal of the American Medical Association, 2008, 299, 1335.	3.8	786
10	GOEAST: a web-based software toolkit for Gene Ontology enrichment analysis. Nucleic Acids Research, 2008, 36, W358-W363.	6.5	569
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12	A HapMap harvest of insights into the genetics of common disease. Journal of Clinical Investigation, 2008, 118, 1590-1605.	3.9	788
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16	Criteria for the selection of single nucleotide polymorphisms in pathway pharmacogenetics: TNF inhibitors as a case study. Drug Discovery Today, 2009, 14, 837-844.	3.2	9
17	Association mapping of straighthead disorder induced by arsenic in <i>Oryza sativa</i> . Plant Breeding, 2009, 128, 551-558.	1.0	31
18	Search for Cancer Risk Factors with Microarray-Based Genome-Wide Association Studies. Technology in Cancer Research and Treatment, 2010, 9, 107-121.	0.8	7

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19	Genome Wide Association Studies. , 2010, , 159-175.		0
20	Genome-Wide Association Scan of Dupuytren's Disease. Journal of Hand Surgery, 2011, 36, 755-756.	0.7	4
21	A conceptual framework for pharmacodynamic genome-wide association studies in pharmacogenomics. Drug Discovery Today, 2011, 16, 884-890.	3.2	19
22	Breeding for disease resistance in poultry: opportunities with challenges. World's Poultry Science Journal, 2011, 67, 687-696.	1.4	19
23	Genetic Effects of <i>FTO</i> and <i>MC4R</i> Polymorphisms on Body Mass in Constitutional Types. Evidence-based Complementary and Alternative Medicine, 2011, 2011, 1-7.	0.5	30
24	Sample Size Growth with an Increasing Number of Comparisons. Journal of Probability and Statistics, 2012, 2012, 1-10.	0.3	1
25	Genome-Wide Association Analysis of Meat Quality Traits in a Porcine Large White \times Minzhu Intercross Population. International Journal of Biological Sciences, 2012, 8, 580-595.	2.6	85
26	Genome-wide Association Study of Porcine Hematological Parameters in a Large White \times Minzhu F2 Resource Population. International Journal of Biological Sciences, 2012, 8, 870-881.	2.6	35
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28	Single nucleotide polymorphism in genome-wide association of human population: A tool for broad spectrum service. Egyptian Journal of Medical Human Genetics, 2013, 14, 123-134.	0.5	55
29	Genome-Wide Association Study of Meat Quality Traits in a White Duroc \times Erhualian F2 Intercross and Chinese Sutai Pigs. PLoS ONE, 2013, 8, e64047.	1.1	63
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31	A genome-wide SNP scan in a porcine Large White \times Minzhu intercross population reveals a locus influencing muscle mass on chromosome 2. Animal Science Journal, 2014, 85, 969-975.	0.6	3
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33	A genome-wide association study of limb bone length using a Large White \times Minzhu intercross population. Genetics Selection Evolution, 2014, 46, 56.	1.2	31
34	The thresholds for statistical and clinical significance – a five-step procedure for evaluation of intervention effects in randomised clinical trials. BMC Medical Research Methodology, 2014, 14, 34.	1.4	132
35	Identification and visualization of stimulus-specific transcriptional activity in cardiac hypertrophy in mice. International Journal of Cardiovascular Imaging, 2014, 30, 211-219.	0.7	0
36	Genome-wide association studies for hematological traits in Chinese Sutai pigs. BMC Genetics, 2014, 15, 41.	2.7	40

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38	Genome-wide association analyses for meat quality traits in Chinese Erhualian pigs and a Western Duroc×(Landrace ×Yorkshire) commercial population. <i>Genetics Selection Evolution</i> , 2015, 47, 44.	1.2	70
39	Multi-breed genome-wide association study reveals novel loci associated with the weight of internal organs. <i>Genetics Selection Evolution</i> , 2015, 47, 87.	1.2	10
40	Genome-wide association analysis reveals genetic loci and candidate genes for meat quality traits in Chinese Laiwu pigs. <i>Mammalian Genome</i> , 2015, 26, 181-190.	1.0	45
41	Association mapping of oil content and fatty acid components in soybean. <i>Euphytica</i> , 2015, 203, 83-96.	0.6	37
42	A GWA study reveals genetic loci for body conformation traits in Chinese Laiwu pigs and its implications for human BMI. <i>Mammalian Genome</i> , 2016, 27, 610-621.	1.0	26
43	Possible introgression of the VRTN mutation increasing vertebral number, carcass length and teat number from Chinese pigs into European pigs. <i>Scientific Reports</i> , 2016, 6, 19240.	1.6	58
44	Multi-breed genome-wide association study reveals heterogeneous loci associated with loin eye area in pigs. <i>Journal of Applied Genetics</i> , 2016, 57, 511-518.	1.0	10
45	An imputation-based genome-wide association study on traits related to male reproduction in a White Duroc×Erhualian F ₂ population. <i>Animal Science Journal</i> , 2016, 87, 646-654.	0.6	7
46	A genome-wide association study reveals candidate genes for the supernumerary nipple phenotype in sheep (<i>Ovis aries</i>). <i>Animal Genetics</i> , 2017, 48, 570-579.	0.6	33
47	Genome-wide association study identifies 22 new loci for body dimension and body weight traits in a White Duroc×Erhualian F2 intercross population. <i>Asian-Australasian Journal of Animal Sciences</i> , 2017, 30, 1066-1073.	2.4	13
48	Microarray expression profiling and co-expression network analysis of circulating lncRNAs and mRNAs associated with neurotoxicity induced by BPA. <i>Environmental Science and Pollution Research</i> , 2018, 25, 15006-15018.	2.7	15
49	Re-assessment of multiple testing strategies for more efficient genome-wide association studies. <i>European Journal of Human Genetics</i> , 2018, 26, 1038-1048.	1.4	9
50	Genome-wide association study reveals genetic loci and candidate genes for average daily gain in Duroc pigs. <i>Asian-Australasian Journal of Animal Sciences</i> , 2018, 31, 480-488.	2.4	20
51	Genetic Architecture of Feeding Behavior and Feed Efficiency in a Duroc Pig Population. <i>Frontiers in Genetics</i> , 2018, 9, 220.	1.1	105
52	Single-Locus and Multi-Locus Genome-Wide Association Studies for Intramuscular Fat in Duroc Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 619.	1.1	47
53	Genome-wide detection of genetic loci and candidate genes for teat number and body conformation traits at birth in Chinese Sushan pigs. <i>Animal Genetics</i> , 2019, 50, 753-756.	0.6	13
54	Muscle glycogen level and occurrence of acid meat in commercial hybrid pigs are regulated by two low-frequency causal variants with large effects and multiple common variants with small effects. <i>Genetics Selection Evolution</i> , 2019, 51, 46.	1.2	11

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55	Analysis of Hematological Traits in Polled Yak by Genome-Wide Association Studies Using Individual SNPs and Haplotypes. <i>Genes</i> , 2019, 10, 463.	1.0	17
56	Whole-Genome Resequencing Identifies KIT New Alleles That Affect Coat Color Phenotypes in Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 218.	1.1	17
57	Genetic variations in plant architecture traits in cotton (<i>Gossypium hirsutum</i>) revealed by a genome-wide association study. <i>Crop Journal</i> , 2019, 7, 209-216.	2.3	16
58	Genome-wide association study for growth and fatness traits in Chinese Sujiang pigs. <i>Animal Genetics</i> , 2020, 51, 314-318.	0.6	19
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60	Aggressive prostate cancer phenotype and genome-wide association studies: where are we now?. <i>Pharmacogenomics</i> , 2020, 21, 487-503.	0.6	4
61	Genome-wide detection of CNV regions and their potential association with growth and fatness traits in Duroc pigs. <i>BMC Genomics</i> , 2021, 22, 332.	1.2	25
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65	Impact of Variation at the FTO Locus on Milk Fat Yield in Holstein Dairy Cattle. <i>PLoS ONE</i> , 2013, 8, e63406.	1.1	23
66	Genome-wide association analysis reveals genetic loci and candidate genes for feeding behavior and eating efficiency in Duroc boars. <i>PLoS ONE</i> , 2017, 12, e0183244.	1.1	34
67	Genome-wide association analysis reveals genetic loci and candidate genes associated with intramuscular fat in Duroc pigs. <i>Frontiers of Agricultural Science and Engineering</i> , 2017, 4, 335.	0.9	5
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72	Identification of genes associated with carotenoids accumulation in scallop (<i>Patinopecten</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T5	1.7	10
73	POWER BOOSTING FOR ORDERED MULTIPLE HYPOTHESES WITH APPLICATION TO GENOME-WIDE ASSOCIATION STUDIES. , 2022, 1, 1-17.		0
74	Genome-Wide Association Study and FST Analysis Reveal Four Quantitative Trait Loci and Six Candidate Genes for Meat Color in Pigs. <i>Frontiers in Genetics</i> , 2022, 13, 768710.	1.1	4

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75	Genetic Factors Underlying Single Fiber Quality in A-Genome Donor Asian Cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 19 Tf 50 742	1.1	9
76	Identification and validation of a regulatory mutation upstream of the BMP2 gene associated with carcass length in pigs. <i>Genetics Selection Evolution</i> , 2021, 53, 94.	1.2	21
87	An imputation-based genome-wide association study for growth and fatness traits in Sujiang pigs. <i>Animal</i> , 2022, 16, 100591.	1.3	3
88	Genome-Wide Association Study Identified a Quantitative Trait Locus and Two Candidate Genes on <i>Sus scrofa</i> Chromosome 2 Affecting Vulvar Traits of Suhuai Pigs. <i>Genes</i> , 2022, 13, 1294.	1.0	1
89	Genome-Wide Association Study for Body Conformation Traits and Fitness in Czech Holsteins. <i>Animals</i> , 2022, 12, 3522.	1.0	2
90	Brain structure and allelic associations in Alzheimer's disease. <i>CNS Neuroscience and Therapeutics</i> , 2023, 29, 1034-1048.	1.9	2
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