

Paul Marjoram

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

6,262
citations

257101

24
h-index

243296

44
g-index

49
all docs

49
docs citations

49
times ranked

9555
citing authors

#	ARTICLE	IF	CITATIONS
1	WhoGEM: an admixture-based prediction machine accurately predicts quantitative functional traits in plants. <i>Genome Biology</i> , 2019, 20, 106.	3.8	9
2	Social effects for locomotion vary between environments in <i>Drosophila melanogaster</i> females. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1765-1775.	1.1	24
3	Conservation of social effects (\hat{r}) between two species of <i>Drosophila</i> despite reversal of sexual dimorphism. <i>Ecology and Evolution</i> , 2017, 7, 10031-10041.	0.8	10
4	Translating natural genetic variation to gene expression in a computational model of the <i>Drosophila</i> gap gene regulatory network. <i>PLoS ONE</i> , 2017, 12, e0184657.	1.1	5
5	Early mutation bursts in colorectal tumors. <i>PLoS ONE</i> , 2017, 12, e0172516.	1.1	1
6	Many private mutations originate from the first few divisions of a human colorectal adenoma. <i>Journal of Pathology</i> , 2015, 237, 355-362.	2.1	30
7	A Bayesian Approach to Social Structure Uncovers Cryptic Regulation of Group Dynamics in <i>Drosophila melanogaster</i> . <i>American Naturalist</i> , 2015, 185, 797-808.	1.0	12
8	A Big Bang model of human colorectal tumor growth. <i>Nature Genetics</i> , 2015, 47, 209-216.	9.4	867
9	al3c: high-performance software for parameter inference using Approximate Bayesian Computation: Table 1.. <i>Bioinformatics</i> , 2015, 31, 3549-3551.	1.8	2
10	Exact likelihood-free Markov chain Monte Carlo for elliptically contoured distributions. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 317-32.	0.2	1
11	Simulation-based Bayesian Analysis of Complex Data. , 2015, 47, 176-183.		1
12	Ancestral inference in tumors: How much can we know?. <i>Journal of Theoretical Biology</i> , 2014, 359, 136-145.	0.8	9
13	Approximation Bayesian computation. <i>OA Genetics</i> , 2013, 1, 853.	0.0	11
14	High DNA Methylation Pattern Intratumoral Diversity Implies Weak Selection in Many Human Colorectal Cancers. <i>PLoS ONE</i> , 2011, 6, e21657.	1.1	18
15	Choice of Summary Statistic Weights in Approximate Bayesian Computation. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.2	17
16	Genome-wide association study of 107 phenotypes in <i>Arabidopsis thaliana</i> inbred lines. <i>Nature</i> , 2010, 465, 627-631.	18.7	1,651
17	Using DNA Methylation Patterns to Infer Tumor Ancestry. <i>PLoS ONE</i> , 2010, 5, e12002.	1.1	10
18	Practical Implications of Coalescent Theory. , 2010, , 63-84.		4

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19	Fast and flexible simulation of DNA sequence data. <i>Genome Research</i> , 2009, 19, 136-142.	2.4	358
20	Critical Role of Nuclear Calcium/Calmodulin-dependent Protein Kinase II β in Cardiomyocyte Survival in Cardiomyopathy. <i>Journal of Biological Chemistry</i> , 2009, 284, 24857-24868.	1.6	56
21	Inferring clonal expansion and cancer stem cell dynamics from DNA methylation patterns in colorectal cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4828-4833.	3.3	134
22	Many colorectal cancers are "flat" clonal expansions. <i>Cell Cycle</i> , 2009, 8, 2187-2193.	1.3	29
23	Approximately Sufficient Statistics and Bayesian Computation. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008, 7, Article26.	0.2	151
24	Exploring Population Genetic Models With Recombination Using Efficient Forward-Time Simulations. <i>Genetics</i> , 2008, 178, 2417-2427.	1.2	48
25	An Arabidopsis Example of Association Mapping in Structured Samples. <i>PLoS Genetics</i> , 2007, 3, e4.	1.5	625
26	Cladistic analysis of genotype data-application to GAW15 Problem 3. <i>BMC Proceedings</i> , 2007, 1, S125.	1.8	2
27	Genome-wide association mapping using mixed-models: application to GAW15 Problem 3. <i>BMC Proceedings</i> , 2007, 1, S164.	1.8	4
28	Towards the Molecular Characterization of Disease: Comparison of Molecular and Histological Analysis of Esophageal Epithelia. <i>Journal of Gastrointestinal Surgery</i> , 2007, 11, 1095-1104.	0.9	5
29	Fast "coalescent" simulation. , 2006, 7, 16.		203
30	Modern computational approaches for analysing molecular genetic variation data. <i>Nature Reviews Genetics</i> , 2006, 7, 759-770.	7.7	172
31	Inferring Population Parameters From Single-Feature Polymorphism Data. <i>Genetics</i> , 2006, 173, 2257-2267.	1.2	7
32	Estimating Recombination Rates From Single-Nucleotide Polymorphisms Using Summary Statistics. <i>Genetics</i> , 2006, 174, 1517-1528.	1.2	28
33	Association Mapping With Single-Feature Polymorphisms. <i>Genetics</i> , 2006, 173, 1125-1133.	1.2	31
34	Fine mapping " 19th century style. <i>BMC Genetics</i> , 2005, 6, S63.	2.7	6
35	Genome-Wide Association Mapping in Arabidopsis Identifies Previously Known Flowering Time and Pathogen Resistance Genes. <i>PLoS Genetics</i> , 2005, 1, e60.	1.5	378
36	The Molecular Signature of Normal Squamous Esophageal Epithelium Identifies the Presence of a Field Effect and Can Discriminate between Patients with Barrett's Esophagus and Patients with Barrett's-Associated Adenocarcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2005, 14, 2113-2117.	1.1	36

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37	Spatial Modeling of Multilocus Data. , 2005, , 471-487.		0
38	Haplotype Structure and Phenotypic Associations in the Chromosomal Regions Surrounding Two Arabidopsis thaliana Flowering Time LociSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY781906, AY785055.. Genetics, 2004, 168, 1627-1638.	1.2	67
39	A multigene expression panel for the molecular diagnosis of Barrett's esophagus and Barrett's adenocarcinoma of the esophagus. Oncogene, 2004, 23, 4780-4788.	2.6	65
40	Estimating the Rate of Gene Conversion on Human Chromosome 21. American Journal of Human Genetics, 2004, 75, 386-397.	2.6	42
41	A survey of current Bayesian gene mapping method. Human Genomics, 2004, 1, 371-4.	1.4	7
42	Application of Bayesian spatial statistical methods to analysis of haplotypes effects and gene mapping. Genetic Epidemiology, 2003, 25, 95-105.	0.6	40
43	Age-related changes of cardiac gene expression following myocardial ischemia/reperfusion. Archives of Biochemistry and Biophysics, 2003, 420, 268-278.	1.4	36
44	Fine-Scale Mapping of Disease Genes with Multiple Mutations via Spatial Clustering Techniques. American Journal of Human Genetics, 2003, 73, 1368-1384.	2.6	91
45	Markov chain Monte Carlo without likelihoods. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15324-15328.	3.3	853
46	Brief episode of ischemia activates protective genetic program in rat heart: a gene chip study. Cardiovascular Research, 2003, 59, 450-459.	1.8	50
47	The Age of a Unique Event Polymorphism. Genetics, 2000, 156, 401-409.	1.2	29
48	The Effects of Rate Variation on Ancestral Inference in the Coalescent. Genetics, 2000, 156, 1427-1436.	1.2	27