

Michael DeGiorgio

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

5,730
citations

186265

28
h-index

144013

57
g-index

67
all docs

67
docs citations

67
times ranked

8303
citing authors

#	ARTICLE	IF	CITATIONS
1	Properties and unbiased estimation of F - and D -statistics in samples containing related and inbred individuals. <i>Genetics</i> , 2022, 220, .	2.9	2
2	BalLeRMix +: mixture model approaches for robust joint identification of both positive selection and long-term balancing selection. <i>Bioinformatics</i> , 2022, 38, 861-863.	4.1	3
3	Ancient and modern genomics of the Ohlone Indigenous population of California. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2111533119.	7.1	10
4	A spatially aware likelihood test to detect sweeps from haplotype distributions. <i>PLoS Genetics</i> , 2022, 18, e1010134.	3.5	13
5	The genomic prehistory of the Indigenous peoples of Uruguay. , 2022, 1, .		7
6	The roles of balancing selection and recombination in the evolution of rattlesnake venom. <i>Nature Ecology and Evolution</i> , 2022, 6, 1367-1380.	7.8	13
7	PhyloWGA : chromosome-aware phylogenetic interrogation of whole genome alignments. <i>Bioinformatics</i> , 2021, 37, 1923-1925.	4.1	1
8	Learning Retention Mechanisms and Evolutionary Parameters of Duplicate Genes from Their Expression Data. <i>Molecular Biology and Evolution</i> , 2021, 38, 1209-1224.	8.9	8
9	Of Traits and Trees: Probabilistic Distances under Continuous Trait Models for Dissecting the Interplay among Phylogeny, Model, and Data. <i>Systematic Biology</i> , 2021, 70, 660-680.	5.6	1
10	Understanding the Adaptive Evolutionary Histories of South American Ancient and Present-Day Populations via Genomics. <i>Genes</i> , 2021, 12, 360.	2.4	3
11	Selection and thermostability suggest G-quadruplexes are novel functional elements of the human genome. <i>Genome Research</i> , 2021, 31, 1136-1149.	5.5	20
12	A Likelihood Approach for Uncovering Selective Sweep Signatures from Haplotype Data. <i>Molecular Biology and Evolution</i> , 2020, 37, 3023-3046.	8.9	28
13	Learning the properties of adaptive regions with functional data analysis. <i>PLoS Genetics</i> , 2020, 16, e1008896.	3.5	16
14	Identifying and Classifying Shared Selective Sweeps from Multilocus Data. <i>Genetics</i> , 2020, 215, 143-171.	2.9	14
15	Flexible Mixture Model Approaches That Accommodate Footprint Size Variability for Robust Detection of Balancing Selection. <i>Molecular Biology and Evolution</i> , 2020, 37, 3267-3291.	8.9	23
16	Ampliconic Genes on the Great Ape Y Chromosomes: Rapid Evolution of Copy Number but Conservation of Expression Levels. <i>Genome Biology and Evolution</i> , 2020, 12, 842-859.	2.5	13
17	VolcanoFinder: Genomic scans for adaptive introgression. <i>PLoS Genetics</i> , 2020, 16, e1008867.	3.5	62
18	Maximum Likelihood Estimation of Species Trees from Gene Trees in the Presence of Ancestral Population Structure. <i>Genome Biology and Evolution</i> , 2020, 12, 3977-3995.	2.5	5

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19	VolcanoFinder: Genomic scans for adaptive introgression. , 2020, 16, e1008867.		0
20	VolcanoFinder: Genomic scans for adaptive introgression. , 2020, 16, e1008867.		0
21	VolcanoFinder: Genomic scans for adaptive introgression. , 2020, 16, e1008867.		0
22	VolcanoFinder: Genomic scans for adaptive introgression. , 2020, 16, e1008867.		0
23	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	28.9	126
24	A High-Resolution View of Adaptive Event Dynamics in a Plasmid. Genome Biology and Evolution, 2019, 11, 3022-3034.	2.5	11
25	Localizing and Classifying Adaptive Targets with Trend Filtered Regression. Molecular Biology and Evolution, 2019, 36, 252-270.	8.9	31
26	Detection of Shared Balancing Selection in the Absence of Trans-Species Polymorphism. Molecular Biology and Evolution, 2019, 36, 177-199.	8.9	26
27	High Levels of Copy Number Variation of Ampliconic Genes across Major Human Y Haplogroups. Genome Biology and Evolution, 2018, 10, 1333-1350.	2.5	15
28	Patterns of Genetic Coding Variation in a Native American Population before and after European Contact. American Journal of Human Genetics, 2018, 102, 806-815.	6.2	33
29	Detection and Classification of Hard and Soft Sweeps from Unphased Genotypes by Multilocus Genotype Identity. Genetics, 2018, 210, 1429-1452.	2.9	69
30	Ancient individuals from the North American Northwest Coast reveal 10,000 years of regional genetic continuity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4093-4098.	7.1	100
31	Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation. Molecular Biology and Evolution, 2017, 34, 2704-2715.	8.9	57
32	An Unbiased Estimator of Gene Diversity with Improved Variance for Samples Containing Related and Inbred Individuals of any Ploidy. G3: Genes, Genomes, Genetics, 2017, 7, 671-691.	1.8	26
33	Fast and robust detection of ancestral selective sweeps. Molecular Ecology, 2017, 26, 6871-6891.	3.9	31
34	Admixture and Ancestry Inference from Ancient and Modern Samples through Measures of Population Genetic Drift. Human Biology, 2017, 89, 21.	0.2	30
35	Consistency and inconsistency of consensus methods for inferring species trees from gene trees in the presence of ancestral population structure. Theoretical Population Biology, 2016, 110, 12-24.	1.1	13
36	Reverse Transcription Errors and RNA-DNA Differences at Short Tandem Repeats. Molecular Biology and Evolution, 2016, 33, 2744-2758.	8.9	15

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37	A time transect of exomes from a Native American population before and after European contact. <i>Nature Communications</i> , 2016, 7, 13175.	12.8	134
38	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	27.8	360
39	Empty Niches after Extinctions Increase Population Sizes of Modern Corals. <i>Current Biology</i> , 2016, 26, 3190-3194.	3.9	79
40	Detecting recent selective sweeps while controlling for mutation rate and background selection. <i>Molecular Ecology</i> , 2016, 25, 142-156.	3.9	157
41	S<sc>weep</sc>F<sc>inder</sc>2: increased sensitivity, robustness and flexibility. <i>Bioinformatics</i> , 2016, 32, 1895-1897.	4.1	238
42	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	12.6	449
43	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , 2015, 25, 459-466.	5.5	348
44	Computational and Statistical Analyses of Insertional Polymorphic Endogenous Retroviruses in a Non-Model Organism. <i>Computation</i> , 2014, 2, 221-245.	2.0	5
45	A Model-Based Approach for Identifying Signatures of Ancient Balancing Selection in Genetic Data. <i>PLoS Genetics</i> , 2014, 10, e1004561.	3.5	159
46	<i>bammds</i> : a tool for assessing the ancestry of low-depth whole-genome data using multidimensional scaling (MDS). <i>Bioinformatics</i> , 2014, 30, 2962-2964.	4.1	40
47	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	27.8	500
48	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , 2014, 507, 225-228.	27.8	328
49	Robustness to Divergence Time Underestimation When Inferring Species Trees from Estimated Gene Trees. <i>Systematic Biology</i> , 2014, 63, 66-82.	5.6	54
50	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	27.8	821
51	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	3.9	73
52	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. <i>American Journal of Human Genetics</i> , 2014, 95, 584-589.	6.2	119
53	An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines. <i>BMC Evolutionary Biology</i> , 2014, 14, 67.	3.2	21
54	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255832.	12.6	264

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55	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. <i>American Journal of Human Genetics</i> , 2013, 93, 1072-1086.	6.2	124
56	Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. <i>Molecular Biology and Evolution</i> , 2013, 30, 1877-1888.	8.9	173
57	Geographic Sampling Scheme as a Determinant of the Major Axis of Genetic Variation in Principal Components Analysis. <i>Molecular Biology and Evolution</i> , 2013, 30, 480-488.	8.9	20
58	Coalescence-Time Distributions in a Serial Founder Model of Human Evolutionary History. <i>Genetics</i> , 2011, 189, 579-593.	2.9	41
59	Unbiased Estimation of Gene Diversity in Samples Containing Related Individuals: Exact Variance and Arbitrary Ploidy. <i>Genetics</i> , 2010, 186, 1367-1387.	2.9	8
60	Fast and Consistent Estimation of Species Trees Using Supermatrix Rooted Triples. <i>Molecular Biology and Evolution</i> , 2010, 27, 552-569.	8.9	61
61	Properties of Consensus Methods for Inferring Species Trees from Gene Trees. <i>Systematic Biology</i> , 2009, 58, 35-54.	5.6	135
62	Explaining worldwide patterns of human genetic variation using a coalescent-based serial founder model of migration outward from Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16057-16062.	7.1	161
63	An Unbiased Estimator of Gene Diversity in Samples Containing Related Individuals. <i>Molecular Biology and Evolution</i> , 2008, 26, 501-512.	8.9	26