

Inference of Population Splits and Mixtures from Genom

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The genetic prehistory of southern Africa. <i>Nature Communications</i> , 2012, 3, 1143.	5.8	271
2	Ancient Admixture in Human History. <i>Genetics</i> , 2012, 192, 1065-1093.	1.2	2,012
3	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	6.0	1,695
4	Robust Identification of Local Adaptation from Allele Frequencies. <i>Genetics</i> , 2013, 195, 205-220.	1.2	518
5	DNA analysis of an early modern human from Tianyuan Cave, China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2223-2227.	3.3	484
6	Genome-wide data substantiate Holocene gene flow from India to Australia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1803-1808.	3.3	97
7	Inferring Population Histories Using Genome-Wide Allele Frequency Data. <i>Molecular Biology and Evolution</i> , 2013, 30, 654-668.	3.5	34
8	Signatures of natural selection on genetic variants affecting complex human traits. <i>Applied & Translational Genomics</i> , 2013, 2, 78-94.	2.1	23
9	The Missing Link of Jewish European Ancestry: Contrasting the Rhineland and the Khazarian Hypotheses. <i>Genome Biology and Evolution</i> , 2013, 5, 61-74.	1.1	46
10	PHYLOGENOMICS REVEALS EXTENSIVE RETICULATE EVOLUTION IN <i>XIPHOPHORUS</i> FISHES. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2166-2179.	1.1	176
11	Detecting Signatures of Selection Through Haplotype Differentiation Among Hierarchically Structured Populations. <i>Genetics</i> , 2013, 193, 929-941.	1.2	340
12	Understanding the origin of species with genome-scale data: modelling gene flow. <i>Nature Reviews Genetics</i> , 2013, 14, 404-414.	7.7	246
13	Inferring Admixture Histories of Human Populations Using Linkage Disequilibrium. <i>Genetics</i> , 2013, 193, 1233-1254.	1.2	445
14	Efficient Moment-Based Inference of Admixture Parameters and Sources of Gene Flow. <i>Molecular Biology and Evolution</i> , 2013, 30, 1788-1802.	3.5	121
15	Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. <i>Molecular Biology and Evolution</i> , 2013, 30, 1877-1888.	3.5	173
16	High-Throughput Sequencing of a South American Amerindian. <i>PLoS ONE</i> , 2013, 8, e83340.	1.1	9
18	Genome-Wide and Paternal Diversity Reveal a Recent Origin of Human Populations in North Africa. <i>PLoS ONE</i> , 2013, 8, e80293.	1.1	39
19	Standing at the Gateway to Europe - The Genetic Structure of Western Balkan Populations Based on Autosomal and Haploid Markers. <i>PLoS ONE</i> , 2014, 9, e105090.	1.1	54

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20	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. <i>PLoS ONE</i> , 2014, 9, e98076.	1.1	128
21	Computational and Statistical Analyses of Insertional Polymorphic Endogenous Retroviruses in a Non-Model Organism. <i>Computation</i> , 2014, 2, 221-245.	1.0	5
22	Population history and genomic signatures for high-altitude adaptation in Tibetan pigs. <i>BMC Genomics</i> , 2014, 15, 834.	1.2	140
23	iNJclust: Iterative Neighbor-Joining Tree Clustering Framework for Inferring Population Structure. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 903-914.	1.9	10
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25	Genome Sequencing Highlights the Dynamic Early History of Dogs. <i>PLoS Genetics</i> , 2014, 10, e1004016.	1.5	481
26	Speciation and Introgression between <i>Mimulus nasutus</i> and <i>Mimulus guttatus</i> . <i>PLoS Genetics</i> , 2014, 10, e1004410.	1.5	252
27	A Population Genetic Signal of Polygenic Adaptation. <i>PLoS Genetics</i> , 2014, 10, e1004412.	1.5	447
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29	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004254.	1.5	391
30	Reconstructing Austronesian population history in Island Southeast Asia. <i>Nature Communications</i> , 2014, 5, 4689.	5.8	158
31	Genome-Wide SNP Analysis Reveals Population Structure and Demographic History of the Ryukyu Islanders in the Southern Part of the Japanese Archipelago. <i>Molecular Biology and Evolution</i> , 2014, 31, 2929-2940.	3.5	48
32	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5661-9.	3.3	260
33	fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets. <i>Genetics</i> , 2014, 197, 573-589.	1.2	1,429
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37	Variations on a Common STRUCTURE: New Algorithms for a Valuable Model. <i>Genetics</i> , 2014, 197, 809-811.	1.2	13

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39	Whole genome sequencing of Turkish genomes reveals functional private alleles and impact of genetic interactions with Europe, Asia and Africa. <i>BMC Genomics</i> , 2014, 15, 963.	1.2	46
40	Deciphering the Genetic Blueprint behind Holstein Milk Proteins and Production. <i>Genome Biology and Evolution</i> , 2014, 6, 1366-1374.	1.1	37
41	Genetic landscape of populations along the Silk Road: admixture and migration patterns. <i>BMC Genetics</i> , 2014, 15, 131.	2.7	24
42	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	13.7	500
43	A Genetic Atlas of Human Admixture History. <i>Science</i> , 2014, 343, 747-751.	6.0	691
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47	Divergent population structure and climate associations of a chromosomal inversion polymorphism across the <i><scp>M</scp>imulus guttatus</i> species complex. <i>Molecular Ecology</i> , 2014, 23, 2844-2860.	2.0	60
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49	Lactase Persistence Alleles Reveal Partial East African Ancestry of Southern African Khoe Pastoralists. <i>Current Biology</i> , 2014, 24, 852-858.	1.8	111
50	The impact of whole-genome sequencing on the reconstruction of human population history. <i>Nature Reviews Genetics</i> , 2014, 15, 149-162.	7.7	147
51	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	13.7	821
52	Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014, 346, 1113-1118.	6.0	287
53	Genetic structure of the four wild tomato species in the <i><scp>S</scp>olanum peruvianum</i>s.l. species complex. <i>Genome</i> , 2014, 57, 169-180.	0.9	18
54	A worldwide survey of genome sequence variation provides insight into the evolutionary history of the honeybee <i>Apis mellifera</i> . <i>Nature Genetics</i> , 2014, 46, 1081-1088.	9.4	273
55	Toward a new history and geography of human genes informed by ancient DNA. <i>Trends in Genetics</i> , 2014, 30, 377-389.	2.9	227

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57	So, you want to use next-generation sequencing in marine systems? Insight from the Pan-Pacific Advanced Studies Institute. <i>Bulletin of Marine Science</i> , 2014, 90, 79-122.	0.4	53
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61	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255-1262.	6.0	264
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63	Admixture and the organization of genetic diversity in a butterfly species complex revealed through common and rare genetic variants. <i>Molecular Ecology</i> , 2014, 23, 4555-4573.	2.0	169
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73	Merino and Merino-derived sheep breeds: a genome-wide intercontinental study. <i>Genetics Selection Evolution</i> , 2015, 47, 64.	1.2	97

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89	Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. Molecular Biology and Evolution, 2015, 32, 600-612.	3.5	55
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102	A Genomic Portrait of Haplotype Diversity and Signatures of Selection in Indigenous Southern African Populations. <i>PLoS Genetics</i> , 2015, 11, e1005052.	1.5	42
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111	Genetic structure in village dogs reveals a Central Asian domestication origin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13639-13644.	3.3	192
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117	Inference Under a Wright-Fisher Model Using an Accurate Beta Approximation. <i>Genetics</i> , 2015, 201, 1133-1141.	1.2	21
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130	Phylogeographic Analysis of <i>Blastomyces dermatitidis</i> and <i>Blastomyces gilchristii</i> Reveals an Association with North American Freshwater Drainage Basins. <i>PLoS ONE</i> , 2016, 11, e0159396.	1.1	34
131	Use of Population Genetics to Assess the Ecology, Evolution, and Population Structure of <i>Coccidioides</i> . <i>Emerging Infectious Diseases</i> , 2016, 22, 1022-1030.	2.0	58
132	Whole-Genome Sequencing of Native Sheep Provides Insights into Rapid Adaptations to Extreme Environments. <i>Molecular Biology and Evolution</i> , 2016, 33, 2576-2592.	3.5	271
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134	A genomic perspective on hybridization and speciation. <i>Molecular Ecology</i> , 2016, 25, 2337-2360.	2.0	458
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141	Evolutionary Patterns and Processes: Lessons from Ancient DNA. <i>Systematic Biology</i> , 2017, 66, syw059.	2.7	73
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151	Statistical Inference in the Wright-Fisher Model Using Allele Frequency Data. <i>Systematic Biology</i> , 2016, 66, syw056.	2.7	46
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1308	Genomic analyses reveal range-wide devastation of sea otter populations. <i>Molecular Ecology</i> , 2023, 32, 281-298.	2.0	12
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1759	Frequencies of variants in genes associated with dyslipidemias identified in Costa Rican genomes. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
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1768	Domestication and lowland adaptation of coastal preceramic maize from Paredones, Peru. <i>ELife</i> , 0, 12, .	2.8	4
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