Montgomery Slatkin

List of Publications by Citations

99 papers	**16,787** citations	**47** h-index	**103** g-index
103 ext. papers	**20,287** ext. citations	**9.5** avg, IF	**6.7** L-index

#	Paper	IF	Citations
99	A draft sequence of the Neandertal genome. *Science*, **2010**, 328, 710-722	33.3	2599
98	The complete genome sequence of a Neanderthal from the Altai Mountains. *Nature*, **2014**, 505, 43-9	50.4	1339
97	A high-coverage genome sequence from an archaic Denisovan individual. *Science*, **2012**, 338, 222-6	33.3	1276
96	ISOLATION BY DISTANCE IN EQUILIBRIUM AND NON-EQUILIBRIUM POPULATIONS. *Evolution; International Journal of Organic Evolution*, **1993**, 47, 264-279	3.8	1184
95	Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature*, **2010**, 468, 1053-60	50.4	1169
94	Ancient human genomes suggest three ancestral populations for present-day Europeans. *Nature*, **2014**, 513, 409-13	50.4	812
93	Linkage disequilibrium--understanding the evolutionary past and mapping the medical future. *Nature Reviews Genetics*, **2008**, 9, 477-85	30.1	695
92	Testing for ancient admixture between closely related populations. *Molecular Biology and Evolution*, **2011**, 28, 2239-52	8.3	689
91	Genome sequence of a 45,000-year-old modern human from western Siberia. *Nature*, **2014**, 514, 445-9	50.4	635
90	Testing for linkage disequilibrium in genotypic data using the Expectation-Maximization algorithm. *Heredity*, **1996**, 76 (Pt 4), 377-83	3.6	475
89	Inbreeding coefficients and coalescence times. *Genetical Research*, **1991**, 58, 167-75	1.1	451
88	A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. *Cell*, **2008**, 134, 416-26	56.2	405
87	A high-coverage Neandertal genome from Vindija Cave in Croatia. *Science*, **2017**, 358, 655-658	33.3	312
86	Epigenetic inheritance and the missing heritability problem. *Genetics*, **2009**, 182, 845-50	4	236
85	Coat color variation at the beginning of horse domestication. *Science*, **2009**, 324, 485	33.3	198
84	An exact test for neutrality based on the Ewens sampling distribution. *Genetical Research*, **1994**, 64, 71-4	1.1	188
83	NULL MODELS FOR THE NUMBER OF EVOLUTIONARY STEPS IN A CHARACTER ON A PHYLOGENETIC TREE. *Evolution; International Journal of Organic Evolution*, **1991**, 45, 1184-1197	3.8	177

82	Estimating allele age. *Annual Review of Genomics and Human Genetics*, **2000**, 1, 225-49	9.7	171
81	Higher levels of neanderthal ancestry in East Asians than in Europeans. *Genetics*, **2013**, 194, 199-209	4	168
80	SEARCHING FOR EVOLUTIONARY PATTERNS IN THE SHAPE OF A PHYLOGENETIC TREE. *Evolution; International Journal of Organic Evolution*, **1993**, 47, 1171-1181	3.8	167
79	Serial founder effects during range expansion: a spatial analog of genetic drift. *Genetics*, **2012**, 191, 171-81	4	155
78	A correction to the exact test based on the Ewens sampling distribution. *Genetical Research*, **1996**, 68, 259-60	1.1	145
77	Reconstructing the genetic history of late Neanderthals. *Nature*, **2018**, 555, 652-656	50.4	138
76	Multiplex relative risk and estimation of the number of loci underlying an inherited disease. *American Journal of Human Genetics*, **2002**, 71, 1369-85	11	129
75	Genetic hitch-hiking in a subdivided population. *Genetical Research*, **1998**, 71, 155-60	1.1	126
74	Seeing ghosts: the effect of unsampled populations on migration rates estimated for sampled populations. *Molecular Ecology*, **2005**, 14, 67-73	5.7	116
73	Evolutionary Genomics and Conservation of the Endangered Przewalski⬭ Horse. *Current Biology*, **2015**, 25, 2577-83	6.3	115
72	Gene flow and selection in a two-locus system. *Genetics*, **1975**, 81, 787-802	4	115
71	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. *Current Biology*, **2017**, 27, 3202-3208.e9	6.3	108
70	Tracing pastoralist migrations to southern Africa with lactase persistence alleles. *Current Biology*, **2014**, 24, 875-9	6.3	106
69	Ancient DNA and human history. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 6380-7	11.5	103
68	Using maximum likelihood to estimate population size from temporal changes in allele frequencies. *Genetics*, **1999**, 152, 755-61	4	96
67	Estimating allele age and selection coefficient from time-serial data. *Genetics*, **2012**, 192, 599-607	4	92
66	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E6889-97	11.5	89
65	Detecting range expansions from genetic data. *Evolution; International Journal of Organic Evolution*, **2013**, 67, 3274-89	3.8	83

64	Partial genomic survival of cave bears in living brown bears. *Nature Ecology and Evolution*, **2018**, 2, 1563-1570	15.7	82
63	The extent of linkage disequilibrium caused by selection on G6PD in humans. *Genetics*, **2005**, 171, 1219-29	4	78
62	Ancient structure in Africa unlikely to explain Neanderthal and non-African genetic similarity. *Molecular Biology and Evolution*, **2012**, 29, 2987-95	8.3	73
61	On treating the chromosome as the unit of selection. *Genetics*, **1972**, 72, 157-68	4	73
60	Bayesian Inference of Natural Selection from Allele Frequency Time Series. *Genetics*, **2016**, 203, 493-511	4	69
59	Excess of genomic defects in a woolly mammoth on Wrangel island. *PLoS Genetics*, **2017**, 13, e1006601	6	67
58	A population-genetic test of founder effects and implications for Ashkenazi Jewish diseases. *American Journal of Human Genetics*, **2004**, 75, 282-93	11	65
57	Subdivision in an ancestral species creates asymmetry in gene trees. *Molecular Biology and Evolution*, **2008**, 25, 2241-6	8.3	63
56	PEAK SHIFTS PRODUCED BY CORRELATED RESPONSE TO SELECTION. *Evolution; International Journal of Organic Evolution*, **1993**, 47, 280-290	3.8	63
55	Simulating genealogies of selected alleles in a population of variable size. *Genetical Research*, **2001**, 78, 49-57	1.1	59
54	Gene genealogies within mutant allelic classes. *Genetics*, **1996**, 143, 579-87	4	54
53	Natural selection and resistance to HIV. *Nature*, **2001**, 411, 545-6	50.4	52
52	Multilocus self-recognition systems in fungi as a cause of trans-species polymorphism. *Genetics*, **2002**, 161, 633-41	4	47
51	Likelihood analysis of ongoing gene flow and historical association. *Evolution; International Journal of Organic Evolution*, **2000**, 54, 44-50	3.8	45
50	The beta -globin recombinational hotspot reduces the effects of strong selection around HbC, a recently arisen mutation providing resistance to malaria. *American Journal of Human Genetics*, **2005**, 77, 637-42	11	43
49	Segregation variance after hybridization of isolated populations. *Genetical Research*, **1994**, 64, 51-6	1.1	43
48	The use of intraallelic variability for testing neutrality and estimating population growth rate. *Genetics*, **2001**, 158, 865-74	4	40
47	Joint Estimation of Contamination, Error and Demography for Nuclear DNA from Ancient Humans. *PLoS Genetics*, **2016**, 12, e1005972	6	40

46	The concordance of gene trees and species trees at two linked loci. *Genetics*, **2006**, 172, 1979-84	4	37
45	Interaction of selection and recombination in the fixation of negative-epistatic genes. *Genetical Research*, **1996**, 67, 257-69	1.1	37
44	A hidden Markov model for investigating recent positive selection through haplotype structure. *Theoretical Population Biology*, **2015**, 99, 18-30	1.2	34
43	MAXIMUM-LIKELIHOOD ESTIMATION OF POPULATION DIVERGENCE TIMES AND POPULATION PHYLOGENY IN MODELS WITHOUT MUTATION. *Evolution; International Journal of Organic Evolution*, **1998**, 52, 669-677	3.8	34
42	The effective founder effect in a spatially expanding population. *Evolution; International Journal of Organic Evolution*, **2015**, 69, 721-34	3.8	31
41	A Bayesian method for jointly estimating allele age and selection intensity. *Genetical Research*, **2008**, 90, 129-37	1.1	30
40	Exchangeable models of complex inherited diseases. *Genetics*, **2008**, 179, 2253-61	4	30
39	Balancing selection at closely linked, overdominant loci in a finite population. *Genetics*, **2000**, 154, 1367-78	4	29
38	Allele age and a test for selection on rare alleles. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2000**, 355, 1663-8	5.8	25
37	Distinguishing recombination and intragenic gene conversion by linkage disequilibrium patterns. *Genetical Research*, **2000**, 75, 61-73	1.1	23
36	A test for ancient selective sweeps and an application to candidate sites in modern humans. *Molecular Biology and Evolution*, **2014**, 31, 3344-58	8.3	22
35	The joint allele-frequency spectrum in closely related species. *Genetics*, **2007**, 177, 387-98	4	22
34	A method for estimating the intensity of overdominant selection from the distribution of allele frequencies. *Genetics*, **2000**, 156, 2119-26	4	22
33	Inferring selection intensity and allele age from multilocus haplotype structure. *G3: Genes, Genomes, Genetics*, **2013**, 3, 1429-42	3.2	21
32	Genome-wide divergence among invasive populations of Aedes aegypti in California. *BMC Genomics*, **2019**, 20, 204	4.5	19
31	Overdominant alleles in a population of variable size. *Genetics*, **1999**, 152, 775-81	4	19
30	Methods for multipoint disease mapping using linkage disequilibrium. *Genetic Epidemiology*, **2000**, 19 Suppl 1, S71-7	2.6	18
29	Distinguishing recent admixture from ancestral population structure. *Genome Biology and Evolution*, **2017**,	3.9	17

28	A sequence-based approach demonstrates that balancing selection in classical human leukocyte antigen (HLA) loci is asymmetric. *Human Molecular Genetics*, **2013**, 22, 252-61	5.6	16
27	Average probability that a "cold hit" in a DNA database search results in an erroneous attribution. *Journal of Forensic Sciences*, **2009**, 54, 22-7	1.8	13
26	Epistatic selection opposed by immigration in multiple locus genetic systems. *Journal of Evolutionary Biology*, **1995**, 8, 623-633	2.3	13
25	Founder mutation(s) in the RSPH9 gene leading to primary ciliary dyskinesia in two inbred Bedouin families. *Annals of Human Genetics*, **2010**, 74, 117-25	2.2	12
24	Determination of genetic relatedness from low-coverage human genome sequences using pedigree simulations. *Molecular Ecology*, **2017**, 26, 4145-4157	5.7	11
23	The projection of a test genome onto a reference population and applications to humans and archaic hominins. *Genetics*, **2014**, 198, 1655-70	4	9
22	A vectorized method of importance sampling with applications to models of mutation and migration. *Theoretical Population Biology*, **2002**, 62, 339-48	1.2	9
21	Microsatellites: evolution and mutational processes. *Novartis Foundation Symposium*, **1996**, 197, 51-67; discussion 67-72		9
20	Statistical methods for analyzing ancient DNA from hominins. *Current Opinion in Genetics and Development*, **2016**, 41, 72-76	4.9	9
19	Transcontinental dispersal of occurred from West African origin via serial founder events. *Communications Biology*, **2019**, 2, 473	6.7	9
18	Isolation-by-distance-and-time in a stepping-stone model. *Theoretical Population Biology*, **2016**, 108, 24-35	1.2	8
17	Genotype-specific recurrence risks as indicators of the genetic architecture of complex diseases. *American Journal of Human Genetics*, **2008**, 83, 120-6	11	8
16	Discussion: Recent Common Ancestors of all Present-Day Individuals. *Advances in Applied Probability*, **1999**, 31, 1027-1035	0.7	7
15	A graphical approach to multi-locus match probability computation: revisiting the product rule. *Theoretical Population Biology*, **2007**, 72, 96-110	1.2	6
14	Discussion: Recent Common Ancestors of all Present-Day Individuals. *Advances in Applied Probability*, **1999**, 31, 1027-1035	0.7	6
13	Genomic tests of variation in inbreeding among individuals and among chromosomes. *Genetics*, **2012**, 192, 1477-82	4	5
12	Joint Estimation of Relatedness Coefficients and Allele Frequencies from Ancient Samples. *Genetics*, **2017**, 206, 1025-1035	4	4
11	Using Ancient Samples in Projection Analysis. *G3: Genes, Genomes, Genetics*, **2015**, 6, 99-105	3.2	4

List of Publications

10	Using known QTLs to detect directional epistatic interactions. *Genetical Research*, **2012**, 94, 39-48	1.1	3
9	Match probabilities in a finite, subdivided population. *Theoretical Population Biology*, **2011**, 79, 55-63	1.2	2
8	Inbreeding coefficients and coalescence times. *Genetical Research*, **2007**, 89, 479-87	1.1	2
7	Appendix to Paper by Wall and Herbeck. *Journal of Molecular Evolution*, **2003**, 56, 689-690	3.1	2
6	F between archaic and present-day samples. *Heredity*, **2019**, 122, 711-718	3.6	2
5	A method for estimating the effective number of loci affecting a quantitative character. *Theoretical Population Biology*, **2013**, 89, 44-54	1.2	1
4	Joint estimation of contamination, error and demography for nuclear DNA from ancient humans		1
3	Pathogens & strain diversity: is sex disruptive?. *Nature Medicine*, **1996**, 2, 401-3	50.5	
2	Estimation of coalescence probabilities and population divergence times from SNP data. *Heredity*, **2021**, 127, 1-9	3.6	
1	Linkage Disequilibrium **2021**, 31-45		