

# Montgomery Slatkin

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Estimation of coalescence probabilities and population divergence times from SNP data. <i>Heredity</i> , <b>2021</b> , 127, 1-9	3.6	
98	Linkage Disequilibrium <b>2021</b> , 31-45		
97	Genome-wide divergence among invasive populations of <i>Aedes aegypti</i> in California. <i>BMC Genomics</i> , <b>2019</b> , 20, 204	4.5	19
96	Transcontinental dispersal of occurred from West African origin via serial founder events. <i>Communications Biology</i> , <b>2019</b> , 2, 473	6.7	9
95	F between archaic and present-day samples. <i>Heredity</i> , <b>2019</b> , 122, 711-718	3.6	2
94	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , <b>2018</b> , 555, 652-656	50.4	138
93	Partial genomic survival of cave bears in living brown bears. <i>Nature Ecology and Evolution</i> , <b>2018</b> , 2, 1563-1570	15.3	82
92	Joint Estimation of Relatedness Coefficients and Allele Frequencies from Ancient Samples. <i>Genetics</i> , <b>2017</b> , 206, 1025-1035	4	4
91	Determination of genetic relatedness from low-coverage human genome sequences using pedigree simulations. <i>Molecular Ecology</i> , <b>2017</b> , 26, 4145-4157	5.7	11
90	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , <b>2017</b> , 358, 655-658	33.3	312
89	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. <i>Current Biology</i> , <b>2017</b> , 27, 3202-3208.e9	6.3	108
88	Distinguishing recent admixture from ancestral population structure. <i>Genome Biology and Evolution</i> , <b>2017</b> ,	3.9	17
87	Excess of genomic defects in a woolly mammoth on Wrangel island. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006601	6	67
86	Ancient DNA and human history. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 6380-7	11.5	103
85	Isolation-by-distance-and-time in a stepping-stone model. <i>Theoretical Population Biology</i> , <b>2016</b> , 108, 24-35	3.2	8
84	Joint Estimation of Contamination, Error and Demography for Nuclear DNA from Ancient Humans. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1005972	6	40
83	Bayesian Inference of Natural Selection from Allele Frequency Time Series. <i>Genetics</i> , <b>2016</b> , 203, 493-511	4	69

82	Statistical methods for analyzing ancient DNA from hominins. <i>Current Opinion in Genetics and Development</i> , <b>2016</b> , 41, 72-76	4.9	9
81	Evolutionary Genomics and Conservation of the Endangered Przewalski Horse. <i>Current Biology</i> , <b>2015</b> , 25, 2577-83	6.3	115
80	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E6889-97	11.5	89
79	A hidden Markov model for investigating recent positive selection through haplotype structure. <i>Theoretical Population Biology</i> , <b>2015</b> , 99, 18-30	1.2	34
78	Using Ancient Samples in Projection Analysis. <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 6, 99-105	3.2	4
77	The effective founder effect in a spatially expanding population. <i>Evolution; International Journal of Organic Evolution</i> , <b>2015</b> , 69, 721-34	3.8	31
76	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , <b>2014</b> , 505, 43-9	50.4	1339
75	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , <b>2014</b> , 514, 445-9	50.4	635
74	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , <b>2014</b> , 513, 409-13	50.4	812
73	Tracing pastoralist migrations to southern Africa with lactase persistence alleles. <i>Current Biology</i> , <b>2014</b> , 24, 875-9	6.3	106
72	A test for ancient selective sweeps and an application to candidate sites in modern humans. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 3344-58	8.3	22
71	The projection of a test genome onto a reference population and applications to humans and archaic hominins. <i>Genetics</i> , <b>2014</b> , 198, 1655-70	4	9
70	A method for estimating the effective number of loci affecting a quantitative character. <i>Theoretical Population Biology</i> , <b>2013</b> , 89, 44-54	1.2	1
69	Higher levels of neanderthal ancestry in East Asians than in Europeans. <i>Genetics</i> , <b>2013</b> , 194, 199-209	4	168
68	Detecting range expansions from genetic data. <i>Evolution; International Journal of Organic Evolution</i> , <b>2013</b> , 67, 3274-89	3.8	83
67	Inferring selection intensity and allele age from multilocus haplotype structure. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 1429-42	3.2	21
66	A sequence-based approach demonstrates that balancing selection in classical human leukocyte antigen (HLA) loci is asymmetric. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 252-61	5.6	16
65	Estimating allele age and selection coefficient from time-serial data. <i>Genetics</i> , <b>2012</b> , 192, 599-607	4	92

64	Serial founder effects during range expansion: a spatial analog of genetic drift. <i>Genetics</i> , <b>2012</b> , 191, 171-81	4.1	155
63	Ancient structure in Africa unlikely to explain Neanderthal and non-African genetic similarity. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 2987-95	8.3	73
62	A high-coverage genome sequence from an archaic Denisovan individual. <i>Science</i> , <b>2012</b> , 338, 222-6	33.3	1276
61	Genomic tests of variation in inbreeding among individuals and among chromosomes. <i>Genetics</i> , <b>2012</b> , 192, 1477-82	4	5
60	Using known QTLs to detect directional epistatic interactions. <i>Genetical Research</i> , <b>2012</b> , 94, 39-48	1.1	3
59	Match probabilities in a finite, subdivided population. <i>Theoretical Population Biology</i> , <b>2011</b> , 79, 55-63	1.2	2
58	Testing for ancient admixture between closely related populations. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 2239-52	8.3	689
57	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , <b>2010</b> , 468, 1053-60	50.4	1169
56	Founder mutation(s) in the RSPH9 gene leading to primary ciliary dyskinesia in two inbred Bedouin families. <i>Annals of Human Genetics</i> , <b>2010</b> , 74, 117-25	2.2	12
55	A draft sequence of the Neandertal genome. <i>Science</i> , <b>2010</b> , 328, 710-722	33.3	2599
54	Average probability that a "cold hit" in a DNA database search results in an erroneous attribution. <i>Journal of Forensic Sciences</i> , <b>2009</b> , 54, 22-7	1.8	13
53	Coat color variation at the beginning of horse domestication. <i>Science</i> , <b>2009</b> , 324, 485	33.3	198
52	Epigenetic inheritance and the missing heritability problem. <i>Genetics</i> , <b>2009</b> , 182, 845-50	4	236
51	Linkage disequilibrium--understanding the evolutionary past and mapping the medical future. <i>Nature Reviews Genetics</i> , <b>2008</b> , 9, 477-85	30.1	695
50	A Bayesian method for jointly estimating allele age and selection intensity. <i>Genetical Research</i> , <b>2008</b> , 90, 129-37	1.1	30
49	A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. <i>Cell</i> , <b>2008</b> , 134, 416-26	56.2	405
48	Subdivision in an ancestral species creates asymmetry in gene trees. <i>Molecular Biology and Evolution</i> , <b>2008</b> , 25, 2241-6	8.3	63
47	Exchangeable models of complex inherited diseases. <i>Genetics</i> , <b>2008</b> , 179, 2253-61	4	30

46	Genotype-specific recurrence risks as indicators of the genetic architecture of complex diseases. <i>American Journal of Human Genetics</i> , <b>2008</b> , 83, 120-6	11	8
45	A graphical approach to multi-locus match probability computation: revisiting the product rule. <i>Theoretical Population Biology</i> , <b>2007</b> , 72, 96-110	1.2	6
44	Inbreeding coefficients and coalescence times. <i>Genetical Research</i> , <b>2007</b> , 89, 479-87	1.1	2
43	The joint allele-frequency spectrum in closely related species. <i>Genetics</i> , <b>2007</b> , 177, 387-98	4	22
42	The concordance of gene trees and species trees at two linked loci. <i>Genetics</i> , <b>2006</b> , 172, 1979-84	4	37
41	The beta -globin recombinational hotspot reduces the effects of strong selection around HbC, a recently arisen mutation providing resistance to malaria. <i>American Journal of Human Genetics</i> , <b>2005</b> , 77, 637-42	11	43
40	Seeing ghosts: the effect of unsampled populations on migration rates estimated for sampled populations. <i>Molecular Ecology</i> , <b>2005</b> , 14, 67-73	5.7	116
39	The extent of linkage disequilibrium caused by selection on G6PD in humans. <i>Genetics</i> , <b>2005</b> , 171, 1219-29	7	78
38	A population-genetic test of founder effects and implications for Ashkenazi Jewish diseases. <i>American Journal of Human Genetics</i> , <b>2004</b> , 75, 282-93	11	65
37	Appendix to Paper by Wall and Herbeck. <i>Journal of Molecular Evolution</i> , <b>2003</b> , 56, 689-690	3.1	2
36	A vectorized method of importance sampling with applications to models of mutation and migration. <i>Theoretical Population Biology</i> , <b>2002</b> , 62, 339-48	1.2	9
35	Multiplex relative risk and estimation of the number of loci underlying an inherited disease. <i>American Journal of Human Genetics</i> , <b>2002</b> , 71, 1369-85	11	129
34	Multilocus self-recognition systems in fungi as a cause of trans-species polymorphism. <i>Genetics</i> , <b>2002</b> , 161, 633-41	4	47
33	Natural selection and resistance to HIV. <i>Nature</i> , <b>2001</b> , 411, 545-6	50.4	52
32	Simulating genealogies of selected alleles in a population of variable size. <i>Genetical Research</i> , <b>2001</b> , 78, 49-57	1.1	59
31	The use of intraallelic variability for testing neutrality and estimating population growth rate. <i>Genetics</i> , <b>2001</b> , 158, 865-74	4	40
30	Distinguishing recombination and intragenic gene conversion by linkage disequilibrium patterns. <i>Genetical Research</i> , <b>2000</b> , 75, 61-73	1.1	23
29	Methods for multipoint disease mapping using linkage disequilibrium. <i>Genetic Epidemiology</i> , <b>2000</b> , 19 Suppl 1, S71-7	2.6	18

28	Likelihood analysis of ongoing gene flow and historical association. <i>Evolution; International Journal of Organic Evolution</i> , <b>2000</b> , 54, 44-50	3.8	45
27	Estimating allele age. <i>Annual Review of Genomics and Human Genetics</i> , <b>2000</b> , 1, 225-49	9.7	171
26	Allele age and a test for selection on rare alleles. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2000</b> , 355, 1663-8	5.8	25
25	Balancing selection at closely linked, overdominant loci in a finite population. <i>Genetics</i> , <b>2000</b> , 154, 1367-78	4.8	29
24	A method for estimating the intensity of overdominant selection from the distribution of allele frequencies. <i>Genetics</i> , <b>2000</b> , 156, 2119-26	4	22
23	Discussion: Recent Common Ancestors of all Present-Day Individuals. <i>Advances in Applied Probability</i> , <b>1999</b> , 31, 1027-1035	0.7	6
22	Discussion: Recent Common Ancestors of all Present-Day Individuals. <i>Advances in Applied Probability</i> , <b>1999</b> , 31, 1027-1035	0.7	7
21	Using maximum likelihood to estimate population size from temporal changes in allele frequencies. <i>Genetics</i> , <b>1999</b> , 152, 755-61	4	96
20	Overdominant alleles in a population of variable size. <i>Genetics</i> , <b>1999</b> , 152, 775-81	4	19
19	MAXIMUM-LIKELIHOOD ESTIMATION OF POPULATION DIVERGENCE TIMES AND POPULATION PHYLOGENY IN MODELS WITHOUT MUTATION. <i>Evolution; International Journal of Organic Evolution</i> , <b>1998</b> , 52, 669-677	3.8	34
18	Genetic hitch-hiking in a subdivided population. <i>Genetical Research</i> , <b>1998</b> , 71, 155-60	1.1	126
17	Pathogens & strain diversity: is sex disruptive?. <i>Nature Medicine</i> , <b>1996</b> , 2, 401-3	50.5	
16	Testing for linkage disequilibrium in genotypic data using the Expectation-Maximization algorithm. <i>Heredity</i> , <b>1996</b> , 76 ( Pt 4), 377-83	3.6	475
15	Interaction of selection and recombination in the fixation of negative-epistatic genes. <i>Genetical Research</i> , <b>1996</b> , 67, 257-69	1.1	37
14	A correction to the exact test based on the Ewens sampling distribution. <i>Genetical Research</i> , <b>1996</b> , 68, 259-60	1.1	145
13	Microsatellites: evolution and mutational processes. <i>Novartis Foundation Symposium</i> , <b>1996</b> , 197, 51-67; discussion 67-72		9
12	Gene genealogies within mutant allelic classes. <i>Genetics</i> , <b>1996</b> , 143, 579-87	4	54
11	Epistatic selection opposed by immigration in multiple locus genetic systems. <i>Journal of Evolutionary Biology</i> , <b>1995</b> , 8, 623-633	2.3	13

10	An exact test for neutrality based on the Ewens sampling distribution. <i>Genetical Research</i> , <b>1994</b> , 64, 71-41.1	1.1	188
9	Segregation variance after hybridization of isolated populations. <i>Genetical Research</i> , <b>1994</b> , 64, 51-6	1.1	43
8	ISOLATION BY DISTANCE IN EQUILIBRIUM AND NON-EQUILIBRIUM POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , <b>1993</b> , 47, 264-279	3.8	1184
7	PEAK SHIFTS PRODUCED BY CORRELATED RESPONSE TO SELECTION. <i>Evolution; International Journal of Organic Evolution</i> , <b>1993</b> , 47, 280-290	3.8	63
6	SEARCHING FOR EVOLUTIONARY PATTERNS IN THE SHAPE OF A PHYLOGENETIC TREE. <i>Evolution; International Journal of Organic Evolution</i> , <b>1993</b> , 47, 1171-1181	3.8	167
5	NULL MODELS FOR THE NUMBER OF EVOLUTIONARY STEPS IN A CHARACTER ON A PHYLOGENETIC TREE. <i>Evolution; International Journal of Organic Evolution</i> , <b>1991</b> , 45, 1184-1197	3.8	177
4	Inbreeding coefficients and coalescence times. <i>Genetical Research</i> , <b>1991</b> , 58, 167-75	1.1	451
3	Gene flow and selection in a two-locus system. <i>Genetics</i> , <b>1975</b> , 81, 787-802	4	115
2	On treating the chromosome as the unit of selection. <i>Genetics</i> , <b>1972</b> , 72, 157-68	4	73
1	Joint estimation of contamination, error and demography for nuclear DNA from ancient humans		1