The coalescent

DOI: 10.1016/0304-4149(82)90011-4
Stochastic Processes and Their Applications, 1982, 13, 235-248

Source: https://exaly.com/paper-pdf/15989906/citation-report.pdf
Version: 2024-04-27

#	Paper	IF	Citations
1951	Mathematical models, problems, and controversies of evolutionary theory. **1984**, 10, 221-274		20
1950	On the genealogy of nested subsamples from a haploid population. **1984**, 16, 471-491		9
1949	Asymptotic line-of-descent distributions. **1984**, 21, 67-75		33
1948	Lines of descent and the coalescent. **1984**, 26, 77-92		70
1947	Line-of-descent and genealogical processes, and their applications in population genetics models. **1984**, 26, 119-64		441
1946	On the genealogy of nested subsamples from a haploid population. **1984**, 16, 471-491		70
1945	Dual processes and an invariance result for exchangeable models in population genetics. **1985**, 23, 103-18		8
1944	Exchangeability and related topics. **1985**, 1-198		398
1943	The genetic divergence of two populations. **1985**, 27, 298-317		21
1942	Partition structures, Polya urns, the Ewens sampling formula, and the ages of alleles. **1986**, 30, 271-88		83
1941	The ages of alleles and a coalescent. **1986**, 18, 1-19		148
1940	The ages of alleles and a coalescent. **1986**, 18, 1-19		74
1939	Dual processes in population genetics. **1986**, 94-105		6
1938	On the divergence of genes in multigene families. **1987**, 31, 178-94		8
1937	The sampling theory of neutral alleles and an urn model in population genetics. **1987**, 25, 123-59		92
1936	The birth process with immigration, and the genealogical structure of large populations. **1987**, 25, 161-8		20
1935	The population genealogy of the infinitely--many neutral alleles model. **1987**, 25, 381-91		27

(1991-1988)

1934	Allelic frequencies given the sample's common ancestral type. **1988**, 33, 126-37		3
1933	The coalescent in two partially isolated diffusion populations. **1988**, 52, 213-22		99
1932	Looking forwards and backwards in a bisexual moran model. **1989**, 26, 880-885		5
1931	A numerical method for calculating moments of coalescent times in finite populations with selection. **1989**, 27, 355-68		7
1930	Genealogical-tree probabilities in the infinitely-many-site model. **1989**, 27, 667-80		37
1929	Looking forwards and backwards in a bisexual moran model. **1989**, 26, 880-885		5
1928	GENE TREES AND ORGANISMAL HISTORIES: A PHYLOGENETIC APPROACH TO POPULATION BIOLOGY. **1989**, 43, 1192-1208		367
1927	Evolution of human mitochondrial DNA: evidence for departure from a pure neutral model of populations at equilibrium. **1990**, 30, 125-39		76
1926	Random permutations and neutral evolution models. *Stochastic Processes and Their Applications*, **1990**, 36, 245-261	1.1	1
1925	Population Biology. **1990**,		1
1924	Genealogy of neutral genes in two partially isolated populations. **1990**, 38, 331-50		55
1923	Mathematical and statistical developments of evolutionary theory: edited by Sabin Lessard, Kluwer Academic Publishers, 1990. Dfl. 195.00/$99.00/£67.00 hbk (xiii + 363 pages) ISBN 0 7923 0595 7. **1991**, 6, 67		
1922	Estimating the frequency of the oldest allele: a bayesian approach. **1991**, 23, 456-475		4
1921	Consistent ordered sampling distributions: characterization and convergence. **1991**, 23, 229-258		23
1920	A multi-dimensional coalescent process applied to multi-allelic selection models and migration models. **1991**, 39, 30-48		60
1919	Consistent ordered sampling distributions: characterization and convergence. **1991**, 23, 229-258		14
1918	Estimating the frequency of the oldest allele: a bayesian approach. **1991**, 23, 456-475		1
1917	Which locus has the oldest allele?. **1991**, 29, 763-77		

1916	A Pólya urn model and the coalescent. **1992**, 29, 1-10	4
1915	Distribution of the number of alleles in multigene families. **1992**, 29, 759-769	2
1914	Do Eve's alleles live on?. **1992**, 60, 221-34	2
1913	Estimating effective population size from samples of sequences: a bootstrap Monte Carlo integration method. **1992**, 60, 209-20	118
1912	USING PHYLOGENETIC TREES TO STUDY SPECIATION AND EXTINCTION. **1992**, 46, 627-640	130
1911	Estimating effective population size from samples of sequences: inefficiency of pairwise and segregating sites as compared to phylogenetic estimates. **1992**, 59, 139-47	168
1910	The mean number of alleles in multigene families. **1992**, 24, 1-19	1
1909	The mean number of alleles in multigene families. **1992**, 24, 1-19	2
1908	A Pólya urn model and the coalescent. **1992**, 29, 1-10	1
1907	Distribution of the number of alleles in multigene families. **1992**, 29, 759-769	
1906	The coalescent in two colonies with symmetric migration. **1993**, 31, 841-51	43
1905	Fleming–Viot Processes in Population Genetics. **1993**, 31, 345-386	106
1904	Measure-valued Markov processes. **1993**, 1-260	207
1903	On the Occasion of the 25th Anniversary of the Neutral Theory. (I). Introductory comments on major papers by Professor Motoo Kimura.. **1993**, 68, 353-394	
1902	Likelihood ratios for the infinite alleles model. **1994**, 31, 595-605	2
1901	The role of molecular genetics in speciation studies. **1994**, 69, 455-77	47
1900	Extinction rates can be estimated from molecular phylogenies. **1994**, 344, 77-82	297
1899	Conservation genetics: beyond the maintenance of marker diversity. **1994**, 3, 423-435	184

(1997-1994)

1898	Likelihood ratios for the infinite alleles model. **1994**, 31, 595-605		7
1897	Human evolution. Y-chromosome clues to human ancestry. **1995**, 5, 1114-5		8
1896	Exchangeable and partially exchangeable random partitions. **1995**, 102, 145-158		264
1895	Comparing Fleming-Viot and Dawson-Watanabe processes. *Stochastic Processes and Their Applications*, **1995**, 60, 171-190	1.1	9
1894	Robustness of the Ewens sampling formula. **1995**, 32, 609-622		2
1893	Robustness of the Ewens sampling formula. **1995**, 32, 609-622		11
1892	The myth of Eve: molecular biology and human origins. **1995**, 270, 1930-6		143
1891	Random discrete distributions invariant under size-biased permutation. **1996**, 28, 525-539		68
1890	A countable representation of the Fleming-Viot measure-valued diffusion. **1996**, 24, 698		75
1889	Random discrete distributions invariant under size-biased permutation. **1996**, 28, 525-539		23
1888	CONDUCTING PHYLOGENETIC COMPARATIVE STUDIES WHEN THE PHYLOGENY IS NOT KNOWN. **1996**, 50, 12-22		116
1887	The asymptotic behavior of an urn model arising in population genetics. *Stochastic Processes and Their Applications*, **1996**, 64, 1-16	1.1	10
1886	Mitochondrial DNA sequence variation and phylogeography of Pimelia darkling beetles on the island of Tenerife (Canary Islands). **1996**, 77 (Pt 6), 589-98		50
1885	Ancestral inference from samples of DNA sequences with recombination. **1996**, 3, 479-502		294
1884	A COMPARISON OF ALTERNATIVE STRATEGIES FOR ESTIMATINGGENE FLOW FROM GENETIC MARKERS. **1997**, 28, 105-128		203
1883	Phylogenetics and the origin of species. **1997**, 94, 7748-55		274
1882	Brownian excursions, critical random graphs and the multiplicative coalescent. **1997**, 25, 812		119
1881	How large was the founding population of Darwin’s finches?. **1997**, 264, 111-118		73

1880	Ancestral Processes with Selection. **1997**, 51, 210-37	189
1879	Evolution of Coalescence Times, Genetic Diversity and Structure during Colonization. **1997**, 51, 148-164	217
1878	Human nature: A critical reader: Edited by Laura Betzig, New York and Oxford: Oxford University Press, 1997. **1997**, 18, 279-283	6
1877	A gene tree for beta-globin sequences from Melanesia. **1997**, 44 Suppl 1, S133-8	23
1876	The history and purview of phylogeography: a personal reflection. **1998**, 7, 371-379	257
1875	Statistical tests of neutrality in the age of weak selection. **1998**, 13, 236-40	64
1874	Ages of mutations on a coalescent tree. **1998**, 153, 41-61	2
1873	Likelihood analysis of disequilibrium mapping, and related problems. **1998**, 62, 459-73	79
1872	Disequilibrium likelihoods for fine-scale mapping of a rare allele. **1998**, 63, 1517-30	52
1871	Maximum likelihood estimation of population divergence times and population phylogenies under the infinite sites model. **1998**, 53, 143-51	44
1870	Segregating sites in Wright's island model. **1998**, 53, 166-74	94
1869	Probability of a segregating pattern in a sample of DNA sequences. **1998**, 54, 1-10	9
1868	Segregating sites in a gene conversion model with mutation. **1998**, 54, 243-56	5
1867	MOLECULAR TRANS-SPECIES POLYMORPHISM. **1998**, 29, 1-21	179
1866	SAMPLING PROPERTIES OF GENEALOGICAL PATHWAYS UNDERLYING POPULATION PEDIGREES. **1998**, 52, 957-966	9
1865	MAXIMUM-LIKELIHOOD ESTIMATION OF POPULATION DIVERGENCE TIMES AND POPULATION PHYLOGENY IN MODELS WITHOUT MUTATION. **1998**, 52, 669-677	34
1864	The age of a mutation in a general coalescent tree. **1998**, 14, 273-295	165
1863	Robustness results for the coalescent. **1998**, 35, 438-447	31

1862	Coalescent results for two-sex population models. **1998**, 30, 513-520	8
1861	A convergence theorem for markov chains arising in population genetics and the coalescent with selfing. **1998**, 30, 493-512	16
1860	Weak convergence to the coalescent in neutral population models. **1999**, 36, 446-460	11
1859	Particle Representations for Measure-Valued Population Models. **1999**, 27, 166	148
1858	More on the X files. **1999**, 96, 2582-4	9
1857	X chromosome evidence for ancient human histories. **1999**, 96, 3320-4	200
1856	Nested clade and phylogeographic analyses of the chub, Leuciscus cephalus (Teleostei, cyprinidae), in Greece: implications for Balkan Peninsula biogeography. **1999**, 13, 566-80	69
1855	Coalescent Random Forests. **1999**, 85, 165-193	44
1854	Evolutionary inference from genomic data. **1999**, 21, 148-156	9
1853	Coalescent estimates of HIV-1 generation time in vivo. **1999**, 96, 2187-91	94
1852	Assessment of linkage disequilibrium by the decay of haplotype sharing, with application to fine-scale genetic mapping. **1999**, 65, 858-75	194
1851	The size distribution of homozygous segments in the human genome. **1999**, 65, 1489-92	37
1850	Some statistical improvements for estimating population size and mutation rate from segregating sites in DNA sequences. **1999**, 55, 235-47	6
1849	The coalescent time in the presence of background fertility selection. **1999**, 55, 260-9	8
1848	Recombination as a point process along sequences. **1999**, 55, 248-59	113
1847	Conditional genealogies and the age of a neutral mutant. **1999**, 56, 183-201	60
1846	The ancestral graph and gene genealogy under frequency-dependent selection. **1999**, 56, 203-14	32
1845	The expected number of alleles in a gene conversion model with mutation. **1999**, 56, 265-77	1

1844	Coalescing into the 21st century: An overview and prospects of coalescent theory. **1999**, 56, 1-10	107
1843	The general coalescent with asynchronous mergers of ancestral lines. **1999**, 36, 1116-1125	130
1842	Coalescents With Multiple Collisions. **1999**, 27, 1870	156
1841	INSIGHT INTO SPECIATION FROM HISTORICAL DEMOGRAPHY IN THE PHYTOPHAGOUS BEETLE GENUS OPHRAELLA. **1999**, 53, 1846-1856	36
1840	A perturbation method for the structured coalescent with strong migration. **2000**, 37, 148-167	5
1839	On the genealogy of a population of biparental individuals. **2000**, 203, 303-15	36
1838	Molecular evolution near a two-locus balanced polymorphism. **2000**, 204, 83-101	35
1837	Ancestral processes in population genetics-the coalescent. **2000**, 204, 629-38	29
1836	Linkage disequilibrium mapping in populations of variable size using the decay of haplotype sharing and a stepwise-mutation model. **2000**, 19 Suppl 1, S99-105	6
1835	Prediction rules for exchangeable sequences related to species sampling. **2000**, 46, 251-256	27
1834	Linkage Disequilibrium Mapping of Disease Susceptibility Genes in Human Populations. **2000**, 68, 23-43	16
1833	Genetic and phylogenetic consequences of island biogeography. **2000**, 54, 387-96	92
1832	The effects of subdivision on the genetic divergence of populations and species. **2000**, 54, 1092-101	163
1831	Chloroplast evolution in the Pinus montezumae complex: a coalescent approach to hybridization. **2000**, 54, 1218-33	61
1830	Perspective: gene divergence, population divergence, and the variance in coalescence time in phylogeographic studies. **2000**, 54, 1839-54	713
1829	Total variation distances and rates of convergence for ancestral coalescent processes in exchangeable population models. **2000**, 32, 983-993	20
1828	SPAM (version 3.2): statistics program for analyzing mixtures. **2000**, 91, 509-10	82
1827	Population bottlenecks and Pleistocene human evolution. **2000**, 17, 2-22	176

1826	Reconstructing genealogies of serial samples under the assumption of a molecular clock using serial-sample UPGMA. **2000**, 17, 1807-15	76
1825	A comparison of estimators of the population recombination rate. **2000**, 17, 156-63	135
1824	SIMCOAL: a general coalescent program for the simulation of molecular data in interconnected populations with arbitrary demography. **2000**, 91, 506-9	167
1823	GENETIC AND PHYLOGENETIC CONSEQUENCES OF ISLAND BIOGEOGRAPHY. **2000**, 54, 387	4
1822	THE EFFECTS OF SUBDIVISION ON THE GENETIC DIVERGENCE OF POPULATIONS AND SPECIES. **2000**, 54, 1092	27
1821	A simple method of removing the effect of a bottleneck and unequal population sizes on pairwise genetic distances. **2000**, 267, 81-7	66
1820	CHLOROPLAST EVOLUTION IN THE PINUS MONTEZUMAE COMPLEX: A COALESCENT APPROACH TO HYBRIDIZATION. **2000**, 54, 1218	5
1819	Simulation of selected genealogies. **2000**, 57, 35-49	31
1818	The number of lines of descent and fixation probabilities of alleles in the pure genetic drift process: analytical approximations. **2000**, 57, 167-75	2
1817	Times on trees, and the age of an allele. **2000**, 57, 109-19	21
1816	The index of dispersion of molecular evolution: slow fluctuations. **2000**, 57, 177-86	8
1815	Inference from gene trees in a subdivided population. **2000**, 57, 79-95	156
1814	A coalescence approach to gene conversion. **2000**, 57, 357-67	18
1813	On the genealogy of a sample of neutral rare alleles. **2000**, 58, 61-75	12
1812	Most recent common ancestor probability distributions in gene genealogies under selection. **2000**, 58, 291-305	22
1811	The neutral theory in an infinite population. **2000**, 261, 11-8	38
1810	Evidence for variable selective pressures at MC1R. **2000**, 66, 1351-61	314
1809	Genetics and the evolutionary process. **2000**, 323, 1155-65	5

1808	Stationary Random Partitions of Positive Integers. **2000**, 44, 60-74	6
1807	PERSPECTIVE: GENE DIVERGENCE, POPULATION DIVERGENCE, AND THE VARIANCE INCOALESCENCE TIME IN PHYLOGEOGRAPHIC STUDIES. **2000**, 54, 1839	579
1806	Genetic hitchhiking. **2000**, 355, 1553-62	368
1805	Linkage disequilibrium mapping: the role of population history, size, and structure. **2001**, 42, 413-37	20
1804	Maximum likelihood estimation of a migration matrix and effective population sizes in n subpopulations by using a coalescent approach. **2001**, 98, 4563-8	1381
1803	The coalescent in an island model of population subdivision with variation among demes. **2001**, 59, 133-44	108
1802	Perfect simulation from population genetic models with selection. **2001**, 59, 263-79	21
1801	Interpreting patterns of diversity in the melanocortin´1 receptor gene. **2001**, 49, 395-396	
1800	Genealogical portraits of speciation in montane grasshoppers (genus Melanoplus) from the sky islands of the Rocky Mountains. **2001**, 268, 319-24	41
1799	Genetic evidence for adaptation-driven incipient speciation of Drosophila melanogaster along a microclimatic contrast in "Evolution Canyon," Israel. **2001**, 98, 13195-200	108
1798	Stochastic models and descriptive statistics for phylogenetic trees, from Yule to today. **2001**, 16, 23	180
1797	Human Evolutionary Genetics. **2001**, 6984-6991	1
1796	A semigroup representation and asymptotic behavior of certain statistics of the fisher-wright-moran coalescent. **2001**, 19, 215-247	6
1795	Population Genetics: Overview. **2001**,	
1794	Coalescent. **2001**, 392-397	1
1793	Coalescence. **2001**,	
1792	Human Populations: Origins and Evolution. **2001**,	
1791	Exploring the demographic history of DNA sequences using the generalized skyline plot. **2001**, 18, 2298-305	194

1790	Estimating mutation rate and generation time from longitudinal samples of DNA sequences. **2001**, 18, 620-6		41
1789	Coalescent theory for seed bank models. **2001**, 38, 285-300		38
1788	Post-data inference of coalescence times and segregating-site distribution in a two-island model with symmetric migration. **2001**, 33, 600-616		
1787	The structured coalescent process with weak migration. **2001**, 38, 1-17		15
1786	On the quantity and quality of single nucleotide polymorphisms in the human genome. *Stochastic Processes and Their Applications*, **2001**, 93, 1-24	1.1	8
1785	Forward and backward diffusion approximations for haploid exchangeable population models. *Stochastic Processes and Their Applications*, **2001**, 95, 133-149	1.1	21
1784	A microbial population-species interface: nested cladistic and coalescent inference with multilocus data. **2001**, 10, 947-64		87
1783	Microsatellite analysis of the inbreeding grass weed Barren Brome (Anisantha sterilis) reveals genetic diversity at the within- and between-farm scales. **2001**, 10, 1035-45		32
1782	Nucleotide sequence variation at two genes of the phenylpropanoid pathway, the FAH1 and F3H genes, in Arabidopsis thaliana. **2001**, 18, 1-9		113
1781	A simulation study of the reliability of recombination detection methods. **2001**, 18, 1929-39		94
1780	Coalescent simulations and statistical tests of neutrality. **2001**, 18, 1134-5; author reply 1136-8		44
1779	Transition between stochastic evolution and deterministic evolution in the presence of selection: general theory and application to virology. **2001**, 65, 151-85		123
1778	Using human immunodeficiency virus type 1 sequences to infer historical features of the acquired immune deficiency syndrome epidemic and human immunodeficiency virus evolution. **2001**, 356, 855-66		54
1777	Statistical phylogeography. **2002**, 11, 2623-35		584
1776	PHYLOGEOGRAPHIC HISTORY OF THE LAND SNAIL CANDIDULA UNIFASCIATA (HELICELLINAE, STYLOMMATOPHORA): FRAGMENTATION, CORRIDOR MIGRATION, AND SECONDARY CONTACT. **2002**, 56, 1776		16
1775	PHYLOGEOGRAPHIC BREAKS WITHOUT GEOGRAPHIC BARRIERS TO GENE FLOW. **2002**, 56, 2383		19
1774	Methods for estimation of demographic parameters from DNA sequence samples. **2002**,		
1773	Experimental phylogeny of neutrally evolving DNA sequences generated by a bifurcate series of nested polymerase chain reactions. **2002**, 19, 170-8		16

1772	Applied Probability in Great Britain. **2002**, 50, 227-239		2
1771	The genealogy of a sequence subject to purifying selection at multiple sites. **2002**, 19, 1376-84		68
1770	Statistical properties of new neutrality tests against population growth. **2002**, 19, 2092-100		1541
1769	A spatially explicit neutral model of beta-diversity in tropical forests. **2002**, 62, 153-68		203
1768	Gene mapping via the ancestral recombination graph. **2002**, 62, 215-29		31
1767	Wright-Fisher revisited: the case of fertility correlation. **2002**, 62, 181-97		19
1766	Recombination in evolutionary genomics. **2002**, 36, 75-97		236
1765	Fine-scale mapping of disease loci via shattered coalescent modeling of genealogies. **2002**, 70, 686-707		106
1764	Estimating Divergence Times from Molecular Data on Phylogenetic and Population Genetic Timescales. **2002**, 33, 707-740		453
1763	Population Genetics of HIV: Parameter Estimation Using Genealogy-based Methods. **2002**, 217-252		5
1762	Ranked Fragmentations. **2002**, 6, 157-175		27
1761	Molecular population genetics. **2002**, 5, 69-73		36
1760	Separating historic events from recurrent processes in cryptic species: phylogeography of mud snails (Hydrobia spp.). **2002**, 11, 1439-51		56
1759	Refuting a controversial case of a human-mediated marine species introduction. **2002**, 5, 577-584		43
1758	The coalescent in population models with time-inhomogeneous environment. *Stochastic Processes and Their Applications*, **2002**, 97, 199-227	1.1	18
1757	Phylogeographic breaks without geographic barriers to gene flow. **2002**, 56, 2383-94		357
1756	Phylogeographic history of the land snail Candidula unifasciata (Helicellinae, Stylommatophora): fragmentation, corridor migration, and secondary contact. **2002**, 56, 1776-88		447
1755	Approximate likelihood methods for estimating local recombination rates. **2002**, 64, 657-680		63

1754	Why do species exist? Insights from sexuals and asexuals. **2003**, 106, 275-82		12
1753	A comparison of two popular statistical methods for estimating the time to most recent common ancestor (TMRCA) from a sample of DNA sequences. **2003**, 82, 7-12		6
1752	On the notion of fitness, or: The selfish ancestor. **2003**, 121, 331-350		8
1751	Reconstructing the demography of prehistoric human populations from molecular data. **2003**, 11, 166-170		3
1750	Linkage disequilibrium assessment via log-linear modeling of SNP haplotype frequencies. **2003**, 25, 106-14		9
1749	A logistic branching process for population genetics. **2003**, 225, 195-203		11
1748	Coalescent processes obtained from supercritical Galton–Watson processes. *Stochastic Processes and Their Applications*, **2003**, 106, 107-139	1.1	101
1747	Incongruent nuclear and mitochondrial phylogeographic patterns in the Timarcha goettingensis species complex (Coleoptera, Chrysomelidae). **2003**, 16, 833-43		38
1746	Bayesian inferences on the recent island colonization history by the bird Zosterops lateralis lateralis. **2003**, 12, 657-74		49
1745	Disjunct distribution of highly diverged mitochondrial lineage clade and population subdivision in a marine bivalve with pelagic larval dispersal. **2003**, 12, 2215-29		122
1744	Evidence for ecological speciation in the sister species Candidula unifasciata (Poiret, 1801) and C. rugosiuscula (Michaud, 1831) (Helicellinae, Gastropoda). **2003**, 79, 611-628		29
1743	The study of structured populations--new hope for a difficult and divided science. **2003**, 4, 535-43		203
1742	Estimating recombination rates from population-genetic data. **2003**, 4, 959-68		163
1741	The evolutionary genomics of pathogen recombination. **2003**, 4, 50-60		158
1740	Calibrating a molecular clock from phylogeographic data: moments and likelihood estimators. **2003**, 57, 2216-25		23
1739	Coalescence in a metapopulation with recurrent local extinction and recolonization. **2003**, 57, 949-61		88
1738	Diversification in sexual and asexual organisms. **2003**, 57, 2166-72		148
1737	Inferences from DNA data: population histories, evolutionary processes and forensic match probabilities. **2003**, 166, 155-188		179

1736	Patterns of human genetic diversity: implications for human evolutionary history and disease. **2003**, 4, 293-340	257
1735	Distinct geographic patterns of genetic diversity are maintained in wild barley (Hordeum vulgare ssp. spontaneum) despite migration. **2003**, 100, 10812-7	83
1734	DIVERSIFICATION IN SEXUAL AND ASEXUAL ORGANISMS. **2003**, 57, 2166	5
1733	A note on distributions of times to coalescence, under time-dependent population size. **2003**, 63, 33-40	41
1732	Ancestral processes for non-neutral models of complex diseases. **2003**, 63, 115-30	12
1731	Exact moment calculations for genetic models with migration, mutation, and drift. **2003**, 63, 231-43	28
1730	Correcting for ascertainment biases when analyzing SNP data: applications to the estimation of linkage disequilibrium. **2003**, 63, 245-55	113
1729	Consistency of estimators of the population-scaled recombination rate. **2003**, 64, 67-79	31
1728	The frequency spectrum of a mutation, and its age, in a general diffusion model. **2003**, 64, 241-51	70
1727	Measurably evolving populations. **2003**, 18, 481-488	300
1726	CALIBRATING A MOLECULAR CLOCK FROM PHYLOGEOGRAPHIC DATA: MOMENTS AND LIKELIHOOD ESTIMATORS. **2003**, 57, 2216	2
1725	Intra-deme molecular diversity in spatially expanding populations. **2003**, 20, 76-86	461
1724	U.S. Human immunodeficiency virus type 1 epidemic: date of origin, population history, and characterization of early strains. **2003**, 77, 6359-66	100
1723	COMMUNITY GENETICS: EXPANDING THE SYNTHESIS OF ECOLOGY AND GENETICS. **2003**, 84, 545-558	97
1722	COALESCENCE IN A METAPOPULATION WITH RECURRENT LOCAL EXTINCTION AND RECOLONIZATION. **2003**, 57, 949	18
1721	Supercritical multitype branching processes: the ancestral types of typical individuals. **2003**, 35, 1090-1110	28
1720	Convergence to the coalescent with simultaneous multiple mergers. **2003**, 40, 839-854	26
1719	Coalescence times for the branching process. **2003**, 35, 1071-1089	25

1718	Coalescence times and F ST values in subdivided populations with symmetric structure. **2003**, 35, 665-690	6
1717	Coalescence times and F ST values in subdivided populations with symmetric structure. **2003**, 35, 665-690	2
1716	Supercritical multitype branching processes: the ancestral types of typical individuals. **2003**, 35, 1090-1110	6
1715	The coalescent process in a population with stochastically varying size. **2003**, 40, 33-48	32
1714	Coalescence times for the branching process. **2003**, 35, 1071-1089	9
1713	Convergence to the coalescent with simultaneous multiple mergers. **2003**, 40, 839-854	25
1712	Solving the Fisher-Wright and coalescence problems with a discrete Markov chain analysis. **2004**, 36, 1175-1197	1
1711	Recent trends in population genetics: more data! More math! Simple models?. **2004**, 95, 397-405	45
1710	The effect of selection on genealogies. **2004**, 166, 1115-31	71
1709	Influence of spatial and temporal heterogeneities on the estimation of demographic parameters in a continuous population using individual microsatellite data. **2004**, 166, 1081-92	75
1708	Reconstituting the frequency spectrum of ascertained single-nucleotide polymorphism data. **2004**, 168, 2373-82	117
1707	Using temporally spaced sequences to simultaneously estimate migration rates, mutation rate and population sizes in measurably evolving populations. **2004**, 168, 2407-20	35
1706	Impact of Ice Ages on the genetic structure of trees and shrubs. **2004**, 359, 197-207	95
1705	Pattern of polymorphism after strong artificial selection in a domestication event. **2004**, 101, 10667-72	246
1704	Studying the effect of environmental change on biotic evolution: past genetic contributions, current work and future directions. **2004**, 362, 2795-820	12
1703	Optimal selection of SNP markers for disease association studies. **2004**, 58, 190-202	55
1702	The analysis of variation of mtDNA hypervariable region 1 suggests that Eastern and Western Pygmies diverged before the Bantu expansion. **2004**, 163, 212-26	66
1701	POPULATION STRUCTURE AND EFFECTIVE SIZE IN CRITICALLY ENDANGERED CAPE FEAR SHINERS NOTROPIS MEKISTOCHOLAS. **2004**, 3, 89-102	11

1700	Mathematics is biology’s next microscope, only better; biology is mathematics’ next physics, only better. **2004**, 2, e439	136
1699	Metapopulation models for historical inference. **2004**, 13, 865-75	57
1698	Genetic structure, phylogeography and demography of two ground-beetle species endemic to the Tenerife laurel forest (Canary Islands). **2004**, 13, 3153-67	34
1697	Phylogeography and intraspecific genetic variation of prochilodontid fishes endemic to rivers of northern South America. **2004**, 64, 186-201	46
1696	The Bayesian revolution in genetics. **2004**, 5, 251-61	328
1695	Cladogenesis, coalescence and the evolution of the three domains of life. **2004**, 20, 182-7	76
1694	Beyond FST: Analysis of population genetic data for conservation. **2004**, 5, 585-602	279
1693	Beyond FST: Analysis of population genetic data for conservation. **2004**, 5, 585-602	203
1692	Extreme isolation by distance in a montane frog Rana cascadae. **2004**, 5, 827-835	40
1691	Comparative genomics: methods and applications. **2004**, 91, 405-21	13
1690	Microgeographic heterogeneity in spatial distribution and mtDNA variability of gray mouse lemurs (Microcebus murinus, Primates: Cheirogaleidae). **2004**, 56, 393	24
1689	The two-locus ancestral graph in a subdivided population: convergence as the number of demes grows in the island model. **2004**, 48, 275-92	20
1688	Random covering of an interval and a variation of Kingman’s coalescent. **2004**, 25, 277-292	3
1687	Evaluating associations of haplotypes with traits. **2004**, 27, 348-64	270
1686	A separation-of-timescales approach to the coalescent in a continuous population. **2004**, 168, 2227-44	56
1685	Multilocus methods for estimating population sizes, migration rates and divergence time, with applications to the divergence of Drosophila pseudoobscura and D. persimilis. **2004**, 167, 747-60	1137
1684	Environmental Microbiology. **2004**,	2
1683	Coalescent process with fluctuating population size and its effective size. **2004**, 65, 39-48	13

1682	Brownian models and coalescent structures. **2004**, 65, 249-61	8
1681	The role of marriage rules in the structure of genetic relatedness. **2004**, 66, 13-24	2
1680	The many-demes limit for selection and drift in a subdivided population. **2004**, 66, 83-91	31
1679	Ancestral inference on gene trees under selection. **2004**, 66, 219-32	72
1678	The time back to the most recent common ancestor in exchangeable population models. **2004**, 36, 78-97	12
1677	References. **2004**, 599-682	
1676	Little loss of information due to unknown phase for fine-scale linkage-disequilibrium mapping with single-nucleotide-polymorphism genotype data. **2004**, 74, 945-53	62
1675	Estimating the rate of gene conversion on human chromosome 21. **2004**, 75, 386-97	41
1674	Quasi-stationary distributions of a pair of Markov chains related to time evolution of a DNA locus. **2004**, 36, 57-77	5
1673	Quasi-stationary distributions of a pair of Markov chains related to time evolution of a DNA locus. **2004**, 36, 57-77	2
1672	The time back to the most recent common ancestor in exchangeable population models. **2004**, 36, 78-97	6
1671	Importance sampling on coalescent histories. I. **2004**, 36, 417-433	9
1670	Using PEBBLE for the evolutionary analysis of serially sampled molecular sequences. **2004**, Chapter 6, Unit 6.8	1
1669	Inferring Process from Pattern in Fungal Population Genetics. **2004**, 29-58	19
1668	Importance sampling on coalescent histories. I. **2004**, 36, 417-433	60
1667	Population genetic analysis of ascertained SNP data. **2004**, 1, 218-24	95
1666	Demographic estimates from Y chromosome microsatellite polymorphisms: analysis of a worldwide sample. **2004**, 1, 345-54	14
1665	Genome-wide scans for loci under selection in humans. **2005**, 2, 113-25	37

1664	Minimal clade size and external branch length under the neutral coalescent. **2005**, 37, 647-662		10
1663	Minimal clade size and external branch length under the neutral coalescent. **2005**, 37, 647-662		25
1662	Effects of Habitat Fragmentation on Effective Population Size in the Endangered Rio Grande Silvery Minnow. **2005**, 19, 1138-1148		88
1661	The Isthmus of Panama: a major physical barrier to gene flow in a highly mobile pantropical seabird. **2005**, 18, 1000-8		51
1660	Northwestern song sparrow populations show genetic effects of sequential colonization. **2005**, 14, 1421-34		61
1659	Intra-population diversity between citrus viroid II variants described as agents of cachexia disease. **2005**, 146, 449-458		5
1658	HISTORICAL DEMOGRAPHY, SELECTION, AND COALESCENCE OF MITOCHONDRIAL AND NUCLEAR GENES IN PROCHILODUS SPECIES OF NORTHERN SOUTH AMERICA. **2005**, 59, 599-610		25
1657	Estimation of individual admixture: analytical and study design considerations. **2005**, 28, 289-301		477
1656	Phylogeography of the calanoid copepods Calanus helgolandicus and C. euxinus suggests Pleistocene divergences between Atlantic, Mediterranean, and Black Sea populations. **2005**, 147, 1353-1365		45
1655	Different epidemic potentials of the HIV-1B and C subtypes. **2005**, 60, 598-605		43
1654	A coalescent model for the effect of advantageous mutations on the genealogy of a population. *Stochastic Processes and Their Applications*, **2005**, 115, 1628-1657	1.1	64
1653	Microbial forensics: the next forensic challenge. **2005**, 119, 317-30		63
1652	Phylogeographic breaks in low-dispersal species: the emergence of concordance across gene trees. **2005**, 124, 179-86		97
1651	Conservation genetics and Pacific fisheries bycatch: Mitochondrial differentiation and population assignment in black-footed albatrosses (Phoebastria nigripes). **2005**, 6, 289-295		23
1650	Fine mapping--19th century style. **2005**, 6 Suppl 1, S63		6
1649	Population Divergence Times and Historical Demography in red Knots and Dunlins. **2005**, 107, 497-513		38
1648	The branching process with logistic growth. **2005**, 15, 1506		61
1647	Random partitions approximating the coalescence of lineages during a selective sweep. **2005**, 15, 1591		33

1646	Binary sequential representations of random partitions. **2005**, 11, 847	3
1645	Modeling human genetic history. **2005**,	1
1644	Maximum-likelihood estimation of coalescence times in genealogical trees. **2005**, 171, 2073-84	7
1643	A statistical characterization of consistent patterns of human immunodeficiency virus evolution within infected patients. **2005**, 22, 456-68	38
1642	Simulation algorithms for integrals of a class of sampling distributions arising in population genetics. **2005**, 75, 731-749	
1641	On the number of New World founders: a population genetic portrait of the peopling of the Americas. **2005**, 3, e193	263
1640	A test of founder effect speciation using multiple loci in the auklets (Aethia spp.). **2005**, 171, 1885-94	16
1639	Genetically indistinguishable SNPs and their influence on inferring the location of disease-associated variants. **2005**, 15, 1503-10	22
1638	SNAP: workbench management tool for evolutionary population genetic analysis. **2005**, 21, 402-4	119
1637	Fitting background-selection predictions to levels of nucleotide variation and divergence along the human autosomes. **2005**, 15, 1211-21	37
1636	On the genealogy of populations: trees, branches and offspring. **2005**, 2005, P07011-P07011	14
1635	Serial SimCoal: a population genetics model for data from multiple populations and points in time. **2005**, 21, 1733-4	178
1634	Estimation of effective population sizes from data on genetic markers. **2005**, 360, 1395-409	267
1633	Population Genetics. **2005**,	
1632	How old is the most recent ancestor of two copies of an allele?. **2005**, 169, 1093-104	6
1631	The structured ancestral selection graph and the many-demes limit. **2005**, 169, 1117-31	12
1630	On the meaning and existence of an effective population size. **2005**, 169, 1061-70	111
1629	Phylodynamic analysis of human immunodeficiency virus type 1 in distinct brain compartments provides a model for the neuropathogenesis of AIDS. **2005**, 79, 11343-52	83

1628	Gene genealogy and properties of test statistics of neutrality under population growth. **2005**, 169, 1687-97	13
1627	HISTORICAL DEMOGRAPHY, SELECTION, AND COALESCENCE OF MITOCHONDRIAL AND NUCLEAR GENES IN PROCHILODUS SPECIES OF NORTHERN SOUTH AMERICA. **2005**, 59, 599	
1626	Finding associations in dense genetic maps: a genetic algorithm approach. **2005**, 60, 97-108	13
1625	simuPOP: a forward-time population genetics simulation environment. **2005**, 21, 3686-7	232
1624	Potential importance of error catastrophe to the development of antiviral strategies for hantaviruses. **2005**, 107, 195-205	21
1623	Ewens' sampling formula and related formulae: combinatorial proofs, extensions to variable population size and applications to ages of alleles. **2005**, 68, 167-77	24
1622	Genetic structure of sylvatic, peridomestic and domestic populations of Triatoma dimidiata (Hemiptera: Reduviidae) from an endemic zone of Boyaca, Colombia. **2005**, 93, 23-9	44
1621	Population Divergence Times and Historical Demography in red Knots and Dunlins. **2005**, 107, 497	39
1620	Backward simulation of ancestors of sampled individuals. **2005**, 67, 75-83	18
1619	Stepwise mutation likelihood computation by sequential importance sampling in subdivided population models. **2005**, 68, 41-53	36
1618	Lumpability and Commutativity of Markov Processes. **2006**, 24, 685-702	21
1617	Perfect simulation from nonneutral population genetic models: variable population size and population subdivision. **2006**, 174, 1397-406	7
1616	Inference about recombination from haplotype data: lower bounds and recombination hotspots. **2006**, 13, 501-21	13
1615	Counting all possible ancestral configurations of sample sequences in population genetics. **2006**, 3, 239-51	12
1614	A coalescence-guided hierarchical Bayesian method for haplotype inference. **2006**, 79, 313-22	25
1613	A new method for detecting human recombination hotspots and its applications to the HapMap ENCODE data. **2006**, 79, 628-39	20
1612	Single Nucleotide Polymorphisms and Their Applications. **2006**, 311-349	3
1611	The coalescence time of sampled genes in the structured coalescent model. **2006**, 70, 289-99	3

(2006-2006)

1610	Corridors for migration between large subdivided populations, and the structured coalescent. **2006** , 70, 412-20	6
1609	Accuracy of coalescent likelihood estimates: do we need more sites, more sequences, or more loci?. **2006**, 23, 691-700	232
1608	Insights into recombination from population genetic variation. **2006**, 16, 565-72	24
1607	Recent advances in assessing gene flow between diverging populations and species. **2006**, 16, 592-6	155
1606	Genealogical theory for random mating populations with two sexes. **2006**, 202, 133-55	4
1605	Using statistical phylogeography to infer population history: Case studies on Pimelia darkling beetles from the Canary Islands. **2006**, 66, 477-497	7
1604	On the number of segregating sites for populations with large family sizes. **2006**, 38, 750-767	9
1603	The mean, variance and limiting distribution of two statistics sensitive to phylogenetic tree balance. **2006**, 16, 2195	52
1602	Evolutionary Genetics, Statistics in. **2006**,	
1601	Coalescent lineage distributions. **2006**, 38, 405-429	9
1600	Structured coalescent with nonconservative migration. **2006**, 43, 351-362	4
1599	Estimating Population Parameters using the Structured Serial Coalescent with Bayesian MCMC Inference when some Demes are Hidden. **2006**, 2, 117693430600200	7
1598	Coalescent lineage distributions. **2006**, 38, 405-429	7
1597	Course 11 Evolution in fluctuating populations. **2006**, 489-545	4
1596	On the number of segregating sites for populations with large family sizes. **2006**, 38, 750-767	21
1595	Assessment of the historical population size of an endangered bird, the black-faced spoonbill (Platalea minor) by analysis of mitochondrial DNA diversity. **2006**, 9, 1-10	20
1594	Population structure of an island malaria vector. **2006**, 20, 393-401	4
1593	Genetics of recent habitat contraction and reduction in population size: does isolation by distance matter?. **2006**, 15, 3601-15	68

1592	Reconstructing human origins in the genomic era. **2006**, 7, 669-80		179
1591	Modern computational approaches for analysing molecular genetic variation data. **2006**, 7, 759-70		156
1590	Different aspects of a random fragmentation model. *Stochastic Processes and Their Applications*, **2006**, 116, 345-369	1.1	4
1589	The process of most recent common ancestors in an evolving coalescent. *Stochastic Processes and Their Applications*, **2006**, 116, 1836-1859	1.1	24
1588	Genetic structure and historical demography of the shanny Lipophrys pholis in the Portuguese coast based on mitochondrial DNA analysis. **2006**, 39, 288-92		9
1587	Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. **2006**, 22, 341-5		646
1586	Mean fixation time estimates in constant size populations. **2006**, 47, 1042-1053		
1585	Consistency of estimators of population scaled parameters using composite likelihood. **2006**, 53, 821-41		31
1584	Genomic insights into positive selection. **2006**, 22, 437-46		315
1583	A model-based approach to selection of tag SNPs. **2006**, 7, 303		20
1582	Genetic structure of the Aleuts and Circumpolar populations based on mitochondrial DNA sequences: a synthesis. **2006**, 129, 446-64		42
1581	Evolution of the most recent common ancestor of a population with no selection. **2006**, 2006, P05002-P05002		10
1580	Mitochondrial DNA replacement versus nuclear DNA persistence. **2006**, 2006, P10013-P10013		3
1579	Widespread discordance of gene trees with species tree in Drosophila: evidence for incomplete lineage sorting. **2006**, 2, e173		265
1578	Coherent permutations with descent statistic and the boundary problem for the graph of zigzag diagrams. **2006**,		14
1577	Evolution of the human immunodeficiency virus envelope gene is dominated by purifying selection. **2006**, 174, 1441-53		58
1576	Inferring phylogeny despite incomplete lineage sorting. **2006**, 55, 21-30		792
1575	A likelihood approach to analysis of network data. **2006**, 103, 7566-70		48

1574	Modified Hudson-Kreitman-Aguade test and two-dimensional evaluation of neutrality tests. **2006**, 173, 1725-33	28
1573	Inferring population parameters from single-feature polymorphism data. **2006**, 173, 2257-67	7
1572	Molecular diversity after a range expansion in heterogeneous environments. **2006**, 174, 2009-20	63
1571	Conditional coalescent trees with two mutation rates and their application to genomic instability. **2006**, 172, 1809-20	1
1570	Relaxed phylogenetics and dating with confidence. **2006**, 4, e88	4483
1569	The molecular genetic basis of plant adaptation. **2006**, 93, 953-62	37
1568	Serial NetEvolve: a flexible utility for generating serially-sampled sequences along a tree or recombinant network. **2006**, 22, 2313-4	6
1567	Continuous Time Markov Processes on Graphs. **2006**, 24, 953-972	2
1566	A simple and robust statistical test for detecting the presence of recombination. **2006**, 172, 2665-81	939
1565	Coalescent processes when the distribution of offspring number among individuals is highly skewed. **2006**, 172, 2621-33	162
1564	Association mapping with single-feature polymorphisms. **2006**, 173, 1125-33	28
1563	Statistical evaluation of alternative models of human evolution. **2007**, 104, 17614-9	409
1562	Inference of bacterial microevolution using multilocus sequence data. **2007**, 175, 1251-66	550
1561	Neutral evolution of multiple quantitative characters: a genealogical approach. **2007**, 176, 455-66	24
1560	Forward-time simulations of human populations with complex diseases. **2007**, 3, e47	42
1559	GENOME: a rapid coalescent-based whole genome simulator. **2007**, 23, 1565-7	97
1558	SimulFold: simultaneously inferring RNA structures including pseudoknots, alignments, and trees using a Bayesian MCMC framework. **2007**, 3, e149	57
1557	On Wright–Fisher diffusion and its relatives. **2007**, 2007, P11006-P11006	12

1556	Confounding factors in HGT detection: statistical error, coalescent effects, and multiple solutions. **2007**, 14, 517-35	70
1555	Effect of selection on ancestry: an exactly soluble case and its phenomenological generalization. **2007**, 76, 041104	70
1554	An exact sampling formula for the Wright-Fisher model and a solution to a conjecture about the finite-island model. **2007**, 177, 1249-54	10
1553	On the choice of genetic distance in spatial-genetic studies. **2007**, 177, 427-34	2
1552	Integration within the Felsenstein equation for improved Markov chain Monte Carlo methods in population genetics. **2007**, 104, 2785-90	789
1551	Comparing likelihood and Bayesian coalescent estimation of population parameters. **2007**, 175, 155-65	73
1550	Incorporating experimental design and error into coalescent/mutation models of population history. **2007**, 176, 2335-42	5
1549	Cooperation is less likely to evolve in a finite population with a highly skewed distribution of family size. **2007**, 274, 1861-5	6
1548	Sliding MinPD: building evolutionary networks of serial samples via an automated recombination detection approach. **2007**, 23, 2993-3000	6
1547	On recombination-induced multiple and simultaneous coalescent events. **2007**, 177, 2151-60	13
1546	Estimating species phylogeny from gene-tree probabilities despite incomplete lineage sorting: an example from Melanoplus grasshoppers. **2007**, 56, 400-11	278
1545	HAPLOPOOL: improving haplotype frequency estimation through DNA pools and phylogenetic modeling. **2007**, 23, 3048-55	18
1544	Population genetic inference using a fixed number of segregating sites: a reassessment. **2007**, 89, 231-44	9
1543	Identity and coalescence in structured populations: a commentary on 'Inbreeding coefficients and coalescence times' by Montgomery Slatkin. **2007**, 89, 475-7	1
1542	Inconsistency of phylogenetic estimates from concatenated data under coalescence. **2007**, 56, 17-24	708
1541	Bayesian logistic regression using a perfect phylogeny. **2007**, 8, 32-52	14
1540	Mlcoalsim: Multilocus Coalescent Simulations. **2007**, 3, 117693430700300	11
1539	Mammalian meiotic recombination hot spots. **2007**, 41, 369-99	82

1538	Coalescent theory for a completely random mating monoecious population. **2007**, 205, 315-24		2
1537	Gaussian approximations for phylogenetic branch length statistics under stochastic models of biodiversity. **2007**, 209, 108-23		8
1536	Fast Plug-in Method for Parzen Probability Density Estimator Applied to Genetic Neutrality Study. **2007**,		0
1535	Two Variance Results in Population Genetics Theory. **2007**, 14, 93-110		2
1534	A step toward barcoding life: a model-based, decision-theoretic method to assign genes to preexisting species groups. **2007**, 56, 44-56		73
1533	How to compute the effective size of spatiotemporally structured populations using separation of time scales. **2007**, 71, 174-81		3
1532	On the length distribution of external branches in coalescence trees: genetic diversity within species. **2007**, 72, 245-52		25
1531	Climate change, genetics or human choice: why were the shells of mankind's earliest ornament larger in the pleistocene than in the holocene?. **2007**, 2, e614		22
1530	A Fleming–Viot process and Bayesian nonparametrics. **2007**, 17,		10
1529	Exchangeable partitions derived from Markovian coalescents. **2007**, 17,		21
1528	Random orderings of the integers and card shuffling. *Stochastic Processes and Their Applications*, **2007**, 117, 708-719	1.1	6
1527	Asymptotic results concerning the total branch length of the Bolthausen–Sznitman coalescent. *Stochastic Processes and Their Applications*, **2007**, 117, 1404-1421	1.1	40
1526	Coalescent random walks on graphs. **2007**, 202, 144-154		2
1525	The evolution of genetic structure in the marine pathogen, Vibrio vulnificus. **2007**, 7, 685-93		48
1524	Prediction of group patterns in social mammals based on a coalescent model. **2007**, 249, 262-70		7
1523	The effect of family structure on the likelihood for kin-biased distribution: an empirical study of brown trout populations. **2007**, 71, 98-110		8
1522	Neutral theory: a historical perspective. **2007**, 20, 2075-91		129
1521	Microbial diversity--insights from population genetics. **2008**, 10, 251-64		28

1520	Estimating the number of founder lineages from haplotypes of closely linked SNPs. **2007**, 16, 2237-45		9
1519	Distribution modelling and statistical phylogeography: an integrative framework for generating and testing alternative biogeographical hypotheses. **2007**, 34, 1833-1845		215
1518	HOW DID LIFE BECOME SO DIVERSE? THE DYNAMICS OF DIVERSIFICATION ACCORDING TO THE FOSSIL RECORD AND MOLECULAR PHYLOGENETICS. **2007**, 50, 23-40		139
1517	Testing the role of interspecific competition in the evolutionary origin of elevational zonation: an example with Buarremon brush-finches (Aves, Emberizidae) in the neotropical mountains. **2007**, 61, 1120-36		35
1516	Integrating coalescent and ecological niche modeling in comparative phylogeography. **2007**, 61, 1439-54		259
1515	Population size changes reshape genomic patterns of diversity. **2007**, 61, 3001-6		129
1514	Estimating genealogies from linked marker data: a Bayesian approach. **2007**, 8, 411		8
1513	Recodon: coalescent simulation of coding DNA sequences with recombination, migration and demography. **2007**, 8, 458		40
1512	Fixation probability for a beneficial allele and a mutant strategy in a linear game under weak selection in a finite island model. **2007**, 72, 409-25		17
1511	MtDNA population structure and gene flow in lingcod (Ophiodon elongatus): limited connectivity despite long-lived pelagic larvae. **2007**, 150, 1301-1311		25
1510	Implications of life history for genetic structure and migration rates of southern African coastal invertebrates: planktonic, abbreviated and direct development. **2007**, 152, 697-711		81
1509	Distributions of Random Partitions and Their Applications. **2007**, 9, 163-193		7
1508	Gibbs Distributions for Random Partitions Generated by a Fragmentation Process. **2007**, 127, 381-418		25
1507	Coalescent size versus coalescent time with strong selection. **2007**, 69, 2249-59		6
1506	Evolutionary game dynamics in a finite asymmetric two-deme population and emergence of cooperation. **2008**, 255, 137-51		11
1505	Asymptotic regimes for the occupancy scheme of multiplicative cascades. *Stochastic Processes and Their Applications*, **2008**, 118, 1586-1605	1.1	6
1504	The prior probabilities of phylogenetic trees. **2008**, 23, 455-473		15
1503	Computational methods for complex stochastic systems: a review of some alternatives to MCMC. **2008**, 18, 151-171		61

1502	Computing likelihoods for coalescents with multiple collisions in the infinitely many sites model. **2008**, 57, 435-65	43
1501	New analytic results for speciation times in neutral models. **2008**, 70, 1082-97	46
1500	Mathematische Modelle in der Populationsgenetik. **2008**, 20, 282-287	3
1499	Fully Bayesian tests of neutrality using genealogical summary statistics. **2008**, 9, 68	21
1498	Species polyphyly and mtDNA introgression among three Serrasalmus sister-species. **2008**, 46, 375-81	9
1497	Trypanosoma brucei gambiense Type 1 populations from human patients are clonal and display geographical genetic differentiation. **2008**, 8, 847-54	45
1496	Estimating species trees using multiple-allele DNA sequence data. **2008**, 62, 2080-91	177
1495	A genealogical approach to quantifying lineage divergence. **2008**, 62, 2411-22	192
1494	The genomic and epidemiological dynamics of human influenza A virus. **2008**, 453, 615-9	685
1493	Evolutionary history of the critically endangered Cozumel dwarf carnivores inferred from mitochondrial DNA analyses. **2008**, 276, 176-186	15
1492	Multilocus analysis of variation using a large empirical data set: phenylpropanoid pathway genes in Arabidopsis thaliana. **2008**, 17, 1211-23	27
1491	Interspecific hybridization and restricted trans-Pacific gene flow in the Tropical Eastern Pacific Pocillopora. **2008**, 17, 1304-12	52
1490	Mid-Holocene decline in African buffalos inferred from Bayesian coalescent-based analyses of microsatellites and mitochondrial DNA. **2008**, 17, 4845-58	45
1489	Phylogeographic structure and regional history of Lemniscomys striatus (Rodentia: Muridae) in tropical Africa. **2008**, 35, 2074-2089	52
1488	Bayesian inference of population size history from multiple loci. **2008**, 8, 289	526
1487	Gene surfing in expanding populations. **2008**, 73, 158-70	244
1486	The distribution of the coalescence time and the number of pairwise nucleotide differences in the "isolation with migration" model. **2008**, 73, 277-88	30
1485	Summary statistics of neutral mutations in longitudinal DNA samples. **2008**, 74, 56-67	2

1484	A coalescent process with simultaneous multiple mergers for approximating the gene genealogies of many marine organisms. **2008**, 74, 104-14	59
1483	To what extent does genealogical ancestry imply genetic ancestry?. **2008**, 74, 182-90	15
1482	Phylogenetic inference using whole genomes. **2008**, 9, 217-31	138
1481	Human Populations: Origins and Evolution. **2008**,	
1480	Statistical power analysis of neutrality tests under demographic expansions, contractions and bottlenecks with recombination. **2008**, 179, 555-67	208
1479	Resolving Species Phylogenies of Recent Evolutionary Radiations1. **2008**, 95, 224-231	37
1478	Lineages-through-time plots of neutral models for speciation. **2008**, 216, 163-71	28
1477	Population Dynamics and Random Genealogies. **2008**, 24, 45-163	53
1476	Fast and flexible simulation of DNA sequence data. **2009**, 19, 136-42	267
1475	Generating Linkage Disequilibrium Patterns in Data Simulations Using genomeSIMLA. **2008**, 24-35	29
1474	The effect of ancient DNA damage on inferences of demographic histories. **2008**, 25, 2181-7	41
1473	Chloroplast DNA phylogeography in long-lived Huon pine, a Tasmanian rain forest conifer. **2008**, 38, 1576-1589	8
1472	Forward-time simulations of non-random mating populations using simuPOP. **2008**, 24, 1408-9	49
1471	An accurate model for genetic hitchhiking. **2008**, 178, 439-51	9
1470	Linkage disequilibrium under skewed offspring distribution among individuals in a population. **2008**, 178, 1517-32	26
1469	Correlating hydrographic events and divergence times of speckled dace (Rhinichthys: Teleostei: Cyprinidae) in the Colorado River drainage. **2008**, 301-317	10
1468	The impact of founder events on chromosomal variability in multiply mating species. **2008**, 25, 1728-36	32
1467	Conditional gene genealogies under strong purifying selection. **2008**, 25, 2615-26	10

1466	Experimental estimation of mutation rates in a wheat population with a gene genealogy approach. **2008**, 179, 2195-211	23
1465	Exploring population genetic models with recombination using efficient forward-time simulations. **2008**, 178, 2417-27	38
1464	Inferring genomic flux in bacteria. **2009**, 19, 306-17	26
1463	The perils of plenty: what are we going to do with all these genes?. **2008**, 363, 3893-902	64
1462	Bayesian inference of fine-scale recombination rates using population genomic data. **2008**, 363, 3921-30	36
1461	Temporal and spatial dynamics of human immunodeficiency virus type 1 circulating recombinant forms 08_BC and 07_BC in Asia. **2008**, 82, 9206-15	121
1460	Characterization of reticulate networks based on the coalescent with recombination. **2008**, 25, 2517-20	19
1459	The promise of composite likelihood methods for addressing computationally intensive challenges. **2008**, 60, 637-54	1
1458	Universal tree structures in directed polymers and models of evolving populations. **2008**, 78, 061102	16
1457	The pattern of genetic hitchhiking under recurrent mutation. **2008**, 13,	11
1456	Expected coalescence time for a nonuniform allocation process. **2008**, 40, 1002-1032	1
1455	Asymptotic behavior of a Feller evolution family involved in the Fisher-Wright model. **2008**, 40, 734-758	0
1454	Asymptotic results on the length of coalescent trees. **2008**, 18,	30
1453	Duality and Asymptotics for a Class of Nonneutral Discrete Moran Models. **2009**, 46, 866-893	4
1452	Phylogenetic analysis in the anomaly zone. **2009**, 58, 452-60	88
1451	Accommodating the effect of ancient DNA damage on inferences of demographic histories. **2009**, 26, 245-8	77
1450	STEM: species tree estimation using maximum likelihood for gene trees under coalescence. **2009**, 25, 971-3	357
1449	A Duality Approach to the Genealogies of Discrete Nonneutral Wright-Fisher Models. **2009**, 2009, 1-22	5

1448	Identifying hybridization events in the presence of coalescence via model selection. **2009**, 58, 478-88	142
1447	Coalescence times and FST under a skewed offspring distribution among individuals in a population. **2009**, 181, 615-29	43
1446	Estimating species phylogenies using coalescence times among sequences. **2009**, 58, 468-77	342
1445	The genealogical consequences of fecundity variance polymorphism. **2009**, 182, 813-37	9
1444	What is the danger of the anomaly zone for empirical phylogenetics?. **2009**, 58, 527-36	82
1443	Closed-form two-locus sampling distributions: accuracy and universality. **2009**, 183, 1087-103	15
1442	Maximum likelihood estimates of species trees: how accuracy of phylogenetic inference depends upon the divergence history and sampling design. **2009**, 58, 501-8	91
1441	Polymorphism data can reveal the origin of species abundance statistics. **2009**, 5, e1000359	1
1440	Coalescent Theory: An Introduction. **2009**, 58, 162-165	3
1439	RNAmutants: a web server to explore the mutational landscape of RNA secondary structures. **2009**, 37, W281-6	13
1438	Phylogenomics of primates and their ancestral populations. **2009**, 19, 1929-41	35
1437	Joint estimation of gene conversion rates and mean conversion tract lengths from population SNP data. **2009**, 25, i231-9	15
1436	Phylodynamics of infectious disease epidemics. **2009**, 183, 1421-30	151
1435	Invited commentary: Evaluating vaccination programs using genetic sequence data. **2009**, 170, 1464-6; discussion 1467-8	5
1434	Inference of historical changes in migration rate from the lengths of migrant tracts. **2009**, 181, 711-9	138
1433	Detecting hybrid speciation in the presence of incomplete lineage sorting using gene tree incongruence: a model. **2009**, 75, 35-45	165
1432	Duality, ancestral and diffusion processes in models with selection. **2009**, 75, 164-75	21
1431	Fixation probability with multiple alleles and projected average allelic effect on selection. **2009**, 75, 266-77	8

1430	The genealogy, site frequency spectrum and ages of two nested mutant alleles. **2009**, 75, 260-5	7
1429	A coalescent dual process in a Moran model with genic selection. **2009**, 75, 320-30	34
1428	The conditional ancestral selection graph with strong balancing selection. **2009**, 75, 355-64	9
1427	Structured coalescent processes from a modified Moran model with large offspring numbers. **2009**, 76, 92-104	13
1426	Accurate and fast methods to estimate the population mutation rate from error prone sequences. **2009**, 10, 247	12
1425	The global pattern of gene identity variation reveals a history of long-range migrations, bottlenecks, and local mate exchange: implications for biological race. **2009**, 139, 35-46	73
1424	Association mapping by generalized linear regression with density-based haplotype clustering. **2009**, 33, 16-26	6
1423	A gene conversion hotspot in the human growth hormone (GH1) gene promoter. **2009**, 30, 239-47	12
1422	Directional gene flow patterns in disjunct populations of the black ratsnake (Pantheropis obsoletus) and the Blanding� turtle (Emydoidea blandingii). **2009**, 10, 407-417	19
1421	Multilocus phylogeography and phylogenetics using sequence-based markers. **2009**, 135, 439-55	247
1420	Population genetic models of duplicated genes. **2009**, 137, 19-37	51
1419	Limit theorems for sequences of random trees. **2009**, 18, 302-315	8
1418	The mutation process in colored coalescent theory. **2009**, 71, 1873-89	3
1417	Bayesian multilocus association mapping on ordinal and censored traits and its application to the analysis of genetic variation among Oryza sativa L. germplasms. **2009**, 118, 865-80	21
1416	Diffusion approximations for one-locus multi-allele kin selection, mutation and random drift in group-structured populations: a unifying approach to selection models in population genetics. **2009**, 59, 659-96	15
1415	Genetic population structure and distribution of a fungal polypore, Datronia caperata (Polyporaceae), in mangrove forests of Central America. **2009**, 36, 266-279	16
1414	Statistical inferences in phylogeography. **2009**, 18, 1034-47	219
1413	Using phylochronology to reveal cryptic population histories: review and synthesis of 29 ancient DNA studies. **2009**, 18, 1310-30	89

1412	A comparison of homologous recombination rates in bacteria and archaea. **2009**, 3, 199-208		394
1411	Genetics in geographically structured populations: defining, estimating and interpreting F(ST). **2009**, 10, 639-50		805
1410	Variable progress toward ecological speciation in parapatry: stickleback across eight lake-stream transitions. **2009**, 63, 1740-53		162
1409	Contrasting patterns of genetic structure in Caryocar (Caryocaraceae) congeners from flooded and upland Amazonian forests. **2009**, 98, 278-290		14
1408	GENETIC AND MORPHOLOGICAL ANALYSES OF THE SOUTHERN BULL KELP DURVILLAEA ANTARCTICA (PHAEOPHYCEAE: DURVILLAEALES) IN NEW ZEALAND REVEAL CRYPTIC SPECIES(1). **2009**, 45, 436-43		59
1407	Stochastic coalescence with homogeneous-like interaction rates. *Stochastic Processes and Their Applications*, **2009**, 119, 45-73	1.1	4
1406	Speciation of a tropical fungal species pair following transoceanic dispersal. **2009**, 51, 413-26		7
1405	Strategy abundance in 2x2 games for arbitrary mutation rates. **2009**, 257, 340-4		70
1404	Mutation-selection equilibrium in games with multiple strategies. **2009**, 258, 614-22		101
1403	On incomplete sampling under birth-death models and connections to the sampling-based coalescent. **2009**, 261, 58-66		250
1402	Genealogical trees from genetic distances. **2009**, 69, 455-463		3
1401	A genome-wide survey of the prevalence and evolutionary forces acting on human nonsense SNPs. **2009**, 84, 224-34		58
1400	Coalescent genealogy samplers: windows into population history. **2009**, 24, 86-93		214
1399	Modeling the past: a resource for the future. **2009**, 24, 125-126		1
1398	A statistical approach for distinguishing hybridization and incomplete lineage sorting. **2009**, 174, E54-70		302
1397	Mitochondrial DNA: Interpretation. **2009**,		
1396	Assessment of Population Structure and Its Effects on Genome-Wide Association Studies. **2009**, 38, 2843-2855		1
1395	Haplotype Structure. **2009**, 25-79		2

1394	IBDSim: a computer program to simulate genotypic data under isolation by distance. **2009**, 9, 107-9	43
1393	Molecular Estimation of Dispersal for Ecology and Population Genetics. **2009**, 40, 193-216	203
1392	Phylogeography. **2009**,	
1391	Phylogeography and disjunct distribution in Lychnophora ericoides (Asteraceae), an endangered cerrado shrub species. **2009**, 104, 655-64	50
1390	On the Height and Length of the Ancestral Recombination Graph. **2009**, 46, 669-689	3
1389	On the Height and Length of the Ancestral Recombination Graph. **2009**, 46, 669-689	1
1388	Population genetic analysis of an Eastern U.S. wheat powdery mildew population reveals geographic subdivision and recent common ancestry with U.K. and Israeli populations. **2009**, 99, 840-9	20
1387	References. **2009**, 295-327	
1386	On the use of bootstrapped topologies in coalescent-based Bayesian MCMC inference: a comparison of estimation and computational efficiencies. **2009**, 5, 97-105	2
1385	AN ASYMPTOTIC SAMPLING FORMULA FOR THE COALESCENT WITH RECOMBINATION. **2010**, 20, 1005-1028	16
1384	Time reversal of some stationary jump diffusion processes from population genetics. **2010**, 42, 1147-1171	1
1383	The □coalescent speed of coming down from infinity. **2010**, 38,	26
1382	Intermediate range migration in the two-dimensional stepping stone model. **2010**, 20,	2
1381	The diversity of a distributed genome in bacterial populations. **2010**, 20,	23
1380	Time reversal of some stationary jump diffusion processes from population genetics. **2010**, 42, 1147-1171	0
1379	Convergence time to the Ewens sampling formula in the infinite alleles Moran model. **2010**, 60, 189-206	2
1378	Maximum tree: a consistent estimator of the species tree. **2010**, 60, 95-106	51
1377	Probabilistic analysis of a genealogical model of animal group patterns. **2010**, 60, 451-68	2

1376	Population genetics, ecology and the size of populations. **2010**, 60, 469-72		7
1375	An application of the central limit theorem to coalescence times in the structured coalescent model with strong migration. **2010**, 61, 695-714		3
1374	Genetic structure across the GBR: evidence from short-lived gobies. **2010**, 157, 945-953		8
1373	A limit theorem for trees of alleles in branching processes with rare neutral mutations. *Stochastic Processes and Their Applications*, **2010**, 120, 678-697	1.1	14
1372	Asymptotic results for coalescent processes without proper frequencies and applications to the two-parameter PoissonDirichlet coalescent. *Stochastic Processes and Their Applications*, **2010**, 120, 2159-2173	1.1	25
1371	Sampling-through-time in birth-death trees. **2010**, 267, 396-404		239
1370	The use of approximate Bayesian computation in conservation genetics and its application in a case study on yellow-eyed penguins. **2010**, 11, 421-433		23
1369	Multi-site adaptation in the presence of infrequent recombination. **2010**, 77, 189-204		28
1368	A coalescent dual process in a Moran model with genic selection, and the lambda coalescent limit. **2010**, 78, 77-92		25
1367	Internalin profiling and multilocus sequence typing suggest four Listeria innocua subgroups with different evolutionary distances from Listeria monocytogenes. **2010**, 10, 97		18
1366	Gene flow and demographic history of the mangrove crab Neosarmatium meinerti: A case study from the western Indian Ocean. **2010**, 86, 179-188		30
1365	Non-homogeneous infinitely many sites discrete-time model with exact coalescent. **2010**, 33, 713-732		2
1364	ABC: a useful Bayesian tool for the analysis of population data. **2010**, 10, 826-33		43
1363	Models of RNA virus evolution and their roles in vaccine design. **2010**, 6 Suppl 2, S5		17
1362	Conservation implications of drastic reductions in the smallest and most isolated populations of giant pandas. **2010**, 24, 1299-306		43
1361	Mathematics of kin- and group-selection: formally equivalent?. **2010**, 64, 316-23		47
1360	In defence of model-based inference in phylogeography. **2010**, 19, 436-446		127
1359	Reconstructing routes of invasion using genetic data: why, how and so what?. **2010**, 19, 4113-30		431

1358	Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure. **2010**, 19, 4648-60	91
1357	Inferring introduction routes of invasive species using approximate Bayesian computation on microsatellite data. **2010**, 104, 88-99	129
1356	Particle Markov chain Monte Carlo methods. **2010**, 72, 269-342	912
1355	Coalescent theory for a Monoecious Random Mating Population with a Varying Size. **2010**, 47, 41-57	1
1354	Recurrence Equations for the Probability Distribution of Sample Configurations in Exact Population Genetics Models. **2010**, 47, 732-751	4
1353	Genome simulation approaches for synthesizing in silico datasets for human genomics. **2010**, 72, 1-24	11
1352	A continuous-state coalescent and the impact of weak selection on the structure of gene genealogies. **2010**, 27, 1162-72	43
1351	Inference of homologous recombination in bacteria using whole-genome sequences. **2010**, 186, 1435-49	118
1350	Evolutionary genetics of human enterovirus 71: origin, population dynamics, natural selection, and seasonal periodicity of the VP1 gene. **2010**, 84, 3339-50	182
1349	A principled approach to deriving approximate conditional sampling distributions in population genetics models with recombination. **2010**, 186, 321-38	24
1348	Some consequences of demographic stochasticity in population genetics. **2010**, 185, 1345-54	37
1347	Bayesian estimation of divergence times from large sequence alignments. **2010**, 27, 1768-81	36
1346	Topologies of the conditional ancestral trees and full-likelihood-based inference in the general coalescent tree framework. **2010**, 185, 1355-68	2
1345	HIV classification using the coalescent theory. **2010**, 26, 1409-15	8
1344	The Coalescent of Bacterial Populations. **2010**, 1-18	4
1343	Sequence-Based Analysis of Bacterial Population Structures. **2010**, 37-60	5
1342	Coalescent simulation of intracodon recombination. **2010**, 184, 429-37	55
1341	The total branch length of sample genealogies in populations of variable size. **2010**, 186, 601-11	8

1340	MSMS: a coalescent simulation program including recombination, demographic structure and selection at a single locus. **2010**, 26, 2064-5	274
1339	How robust are "isolation with migration" analyses to violations of the im model? A simulation study. **2010**, 27, 297-310	200
1338	Inferring the dynamics of diversification: a coalescent approach. **2010**, 8, e1000493	153
1337	SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. **2010**, 26, 2993-4	96
1336	Global migration dynamics underlie evolution and persistence of human influenza A (H3N2). **2010**, 6, e1000918	123
1335	BUCKy: gene tree/species tree reconciliation with Bayesian concordance analysis. **2010**, 26, 2910-1	312
1334	Inference of population history by coupling exploratory and model-driven phylogeographic analyses. **2010**, 11, 1190-227	28
1333	Sampling trees from evolutionary models. **2010**, 59, 465-76	61
1332	Population Genetics: Overview. **2010**,	0
1331	USING POPULATION GENOMICS TO DETECT SELECTION IN NATURAL POPULATIONS: KEY CONCEPTS AND METHODOLOGICAL CONSIDERATIONS. **2010**, 171, 1059-1071	136
1330	DendroPy: a Python library for phylogenetic computing. **2010**, 26, 1569-71	1053
1329	The Distribution of Family Sizes Under a Time-Homogeneous Birth and Death Process. **2010**, 39, 1761-1775	
1328	The Distribution of F st for the Island Model in the Large Population, Weak Mutation Limit. **2010**, 28, 577-601	3
1327	Use of phylogenetics in the molecular epidemiology and evolutionary studies of viral infections. **2010**, 47, 5-49	48
1326	Population Genetic Principles and Human Populations. **2010**, 487-506	
1325	DnaSAM: Software to perform neutrality testing for large datasets with complex null models. **2010**, 10, 542-5	24
1324	Combining contemporary and ancient DNA in population genetic and phylogeographical studies. **2010**, 10, 760-72	45
1323	Practical Implications of Coalescent Theory. **2010**, 63-84	1

1322	Exact computation of coalescent likelihood for panmictic and subdivided populations under the infinite sites model. **2010**, 7, 611-8	8
1321	Genetic variation of Anastrepha suspensa (Diptera: Tephritidae) in Florida and the Caribbean using microsatellite DNA markers. **2010**, 103, 2214-22	11
1320	Population structure in the endangered cyprinid fish Pararasbora moltrechti in Taiwan, based on mitochondrial and microsatellite DNAs. **2011**, 28, 642-51	14
1319	Some Mathematical Models in Evolutionary Genetics. **2011**, 67-89	4
1318	Coalescence: the Sharing of Ancestry of Alleles. **2011**,	2
1317	Ginkgo: spatially-explicit simulator of complex phylogeographic histories. **2011**, 11, 364-9	3
1316	Skyline-plot methods for estimating demographic history from nucleotide sequences. **2011**, 11, 423-34	308
1315	Analysing recombination in nucleotide sequences. **2011**, 11, 943-55	85
1314	Evolution and population genetics of exotic and re-emerging pathogens: novel tools and approaches. **2011**, 49, 249-67	78
1313	Likelihood-free estimation of model evidence. **2011**, 6,	60
1312	Coalescence theory for a general class of structured populations with fast migration. **2011**, 43, 1027-1047	7
1311	Phylodynamics and molecular evolution of influenza A virus nucleoprotein genes in Taiwan between 1979 and 2009. **2011**, 6, e23454	5
1310	Multiple independent lineages of HIV-1 persist in breast milk and plasma. **2011**, 25, 143-52	16
1309	Bayesian population genomic inference of crossing over and gene conversion. **2011**, 189, 607-19	3
1308	Dates of HIV infection can be estimated for seroprevalent patients by coalescent analysis of serial next-generation sequencing data. **2011**, 25, 2019-26	25
1307	Towards modelling persistence of woodland birds: the role of genetics. **2011**, 111, 19-39	35
1306	Deep intra-island divergence of a montane forest endemic: phylogeography of the Puerto Rican frog Eleutherodactylus portoricensis (Anura: Eleutherodactylidae). **2011**, 38, 2311-2325	10
1305	Genealogical lineage sorting leads to significant, but incorrect Bayesian multilocus inference of population structure. **2011**, 20, 1108-21	25

1304	The performance of phylogenetic algorithms in estimating haplotype genealogies with migration. **2011**, 20, 1952-63	251
1303	A review of ecological models for brown trout: towards a new demogenetic model. **2011**, 20, 167-198	30
1302	Calibrating divergence times on species trees versus gene trees: implications for speciation history of Aphelocoma jays. **2011**, 65, 184-202	200
1301	The influence of partial panmixia on neutral models of spatial variation. **2011**, 79, 19-38	11
1300	Analytical results on the neutral non-equilibrium allele frequency spectrum based on diffusion theory. **2011**, 79, 184-91	27
1299	The effect of recurrent mutation on the frequency spectrum of a segregating site and the age of an allele. **2011**, 80, 158-73	23
1298	Estimation of parameters in large offspring number models and ratios of coalescence times. **2011**, 80, 16-28	16
1297	Generalized population models and the nature of genetic drift. **2011**, 80, 80-99	44
1296	Time to the MRCA of a sample in a Wright-Fisher model with variable population size. **2011**, 80, 265-71	1
1295	Phylogenetic and epidemic modeling of rapidly evolving infectious diseases. **2011**, 11, 1825-41	51
1294	The structure of population genetic diversity in Vallisneria americana in the Chesapeake Bay: implications for restoration. **2011**, 12, 1269-1285	15
1293	The tree length of an evolving coalescent. **2011**, 151, 529-557	14
1292	The distribution of Fst and other genetic statistics for a class of population structure models. **2011**, 62, 203-89	3
1291	Strategy abundance in evolutionary many-player games with multiple strategies. **2011**, 283, 180-91	23
1290	On the Robustness of the Extension of the One-Third Law of Evolution to the Multi-Player Game. **2011**, 1, 408-418	26
1289	Effective Game Matrix and Inclusive Payoff in Group-Structured Populations. **2011**, 1, 301-318	15
1288	Experiments with the site frequency spectrum. **2011**, 73, 829-72	7
1287	Fast and accurate methods for phylogenomic analyses. **2011**, 12 Suppl 9, S4	28

1286	Estimating hybridization in the presence of coalescence using phylogenetic intraspecific sampling. **2011**, 11, 291	43
1285	A multilocus phylogeny of the Sulidae (Aves: Pelecaniformes). **2011**, 58, 181-91	35
1284	Integrating statistical genetic and geospatial methods brings new power to phylogeography. **2011**, 59, 523-37	153
1283	Evidence for the equal resilience of Triodia spp. (Poaceae), from different functional groups, to frequent fire dating back to the late Pleistocene. **2011**, 107, 558-64	7
1282	Taylor's power law and fluctuation scaling explained by a central-limit-like convergence. **2011**, 83, 066115	40
1281	Inference of population mutation rate and detection of segregating sites from next-generation sequence data. **2011**, 189, 595-605	7
1280	Concave-Convex Adaptive Rejection Sampling. **2011**, 20, 670-691	16
1279	A method for accurate inference of population size from serially sampled genealogies distorted by selection. **2011**, 28, 3171-81	3
1278	Inferring epidemiological parameters on the basis of allele frequencies. **2011**, 188, 663-72	22
1277	AIP mutation in pituitary adenomas in the 18th century and today. **2011**, 364, 43-50	122
1276	Evaluation of a bayesian coalescent method of species delimitation. **2011**, 60, 747-61	195
1275	The accuracy of species tree estimation under simulation: a comparison of methods. **2011**, 60, 126-37	190
1274	Recovering population parameters from a single gene genealogy: an unbiased estimator of the growth rate. **2011**, 28, 1617-31	19
1273	GEOECODYNAMICS AND THE KALAHARI EPEIROGENY: LINKING ITS GENOMIC RECORD, TREE OF LIFE AND PALIMPSEST INTO A UNIFIED NARRATIVE OF LANDSCAPE EVOLUTION. **2011**, 114, 489-514	42
1272	Multiple incursions and putative species revealed using a mitochondrial and nuclear phylogenetic approach to the Trogoderma variabile (Coleoptera: Dermestidae) trapping program in Australia. **2011**, 101, 333-43	8
1271	Joint inference of microsatellite mutation models, population history and genealogies using transdimensional Markov Chain Monte Carlo. **2011**, 188, 151-64	43
1270	Coalescence-time distributions in a serial founder model of human evolutionary history. **2011**, 189, 579-93	29
1269	Joint inference of population assignment and demographic history. **2011**, 189, 561-77	15

1268	Population Genetics Models with Skewed Fertilities: A Forward and Backward Analysis. **2011**, 27, 521-554	21
1267	Inference from samples of DNA sequences using a two-locus model. **2011**, 18, 109-27	14
1266	An autosomal analysis gives no genetic evidence for complex speciation of humans and chimpanzees. **2012**, 29, 145-56	19
1265	Fixation probability in a two-locus model by the ancestral recombination-selection graph. **2012**, 190, 691-707	8
1264	Resistance and relatedness on an evolutionary graph. **2012**, 9, 511-7	3
1263	Inferring pandemic growth rates from sequence data. **2012**, 9, 1797-808	30
1262	Rates of coalescence for common epidemiological models at equilibrium. **2012**, 9, 997-1007	28
1261	Detection of dispersed short tandem repeats using reversible jump Markov chain Monte Carlo. **2012**, 40, e147	
1260	Alignment-free population genomics: an efficient estimator of sequence diversity. **2012**, 2, 883-9	4
1259	Gene genealogies within a fixed pedigree, and the robustness of Kingman's coalescent. **2012**, 190, 1433-45	57
1258	Extending coalescent theory to autotetraploids. **2012**, 192, 195-204	33
1257	Linkage disequilibrium under recurrent bottlenecks. **2012**, 190, 217-29	15
1256	Local adaptation along smooth ecological gradients causes phylogeographic breaks and phenotypic clustering. **2012**, 180, 35-49	47
1255	Coalescent-based DNA barcoding: multilocus analysis and robustness. **2012**, 19, 271-8	7
1254	Phylodynamics and movement of Phycodnaviruses among aquatic environments. **2012**, 6, 237-47	15
1253	FTEC: a coalescent simulator for modeling faster than exponential growth. **2012**, 28, 1282-3	12
1252	The structure of genealogies in the presence of purifying selection: a fitness-class coalescent. **2012**, 190, 753-79	38
1251	Dynamics of neutral and selected alleles when the offspring distribution is skewed. **2012**, 191, 1331-44	33

1250	Glaciation effects on the phylogeographic structure of Oligoryzomys longicaudatus (Rodentia: Sigmodontinae) in the southern Andes. **2012**, 7, e32206	25
1249	Stochastic equations, flows and measure-valued processes. **2012**, 40,	74
1248	Species delimitation and global biosecurity. **2012**, 8, 1-37	120
1247	Drift-barrier hypothesis and mutation-rate evolution. **2012**, 109, 18488-92	240
1246	Reconstructing the demographic history of the human lineage using whole-genome sequences from human and three great apes. **2012**, 4, 1133-45	18
1245	Phylodynamic inference of infectious diseases caused by HIV, enterovirus 71 and the 2009 swine-origin human influenza virus. **2012**, 7, 403-412	
1244	Tracing the origin and history of HIV-1 subtype B' epidemic by near full-length genome analyses. **2012**, 26, 877-84	66
1243	Basic Concepts and Models. **2012**, 1-29	
1242	Dynamics of the evolving Bolthausen-Sznitman coalecent. **2012**, 17,	11
1241	Tree-valued Fleming–Viot dynamics with mutation and selection. **2012**, 22,	26
1240	CLOSED-FORM ASYMPTOTIC SAMPLING DISTRIBUTIONS UNDER THE COALESCENT WITH RECOMBINATION FOR AN ARBITRARY NUMBER OF LOCI. **2012**, 44, 391-407	9
1239	Genealogies of regular exchangeable coalescents with applications to sampling. **2012**, 48,	2
1238	Molecular biogeography and phylogeography of the freshwater fauna of the Indo-Australian Archipelago. 316-347	5
1237	Closed-Form Asymptotic Sampling Distributions under the Coalescent with Recombination for an Arbitrary Number of Loci. **2012**, 44, 391-407	5
1236	Approximate Sampling Formulae for General Finite-Alleles Models of Mutation. **2012**, 44, 408-428	5
1235	Impact of fertility transmission and other sociodemographic factors on reproductive success and coalescent trees. **2012**, 94, 121-31	6
1234	Smaller population size at the MRCA time for stationary branching processes. **2012**, 40,	11
1233	Almost sure asymptotics for the number of types for simple Xi-coalescents. **2012**, 17,	2

1232	An overview of population genetic data simulation. **2012**, 19, 42-54	44
1231	Testing hypotheses for genealogical discordance in a rainforest lizard. **2012**, 21, 5059-72	26
1230	Application of the Apn2/MAT locus to improve the systematics of the Colletotrichum gloeosporioides complex: an example from coffee (Coffea spp.) hosts. **2012**, 104, 396-409	103
1229	A coupled phylogeographical and species distribution modelling approach recovers the demographical history of a Neotropical seasonally dry forest tree species. **2012**, 21, 5845-63	82
1228	Calibrated tree priors for relaxed phylogenetics and divergence time estimation. **2012**, 61, 138-49	204
1227	Phylogeographic ancestral inference using the coalescent model on haplotype trees. **2012**, 19, 745-55	11
1226	How genealogies are affected by the speed of evolution. **2012**, 92, 255-271	8
1225	Hierarchical factor modeling of proteomics data. **2012**,	2
1224	Population biology of fungal plant pathogens. **2012**, 835, 333-63	1
1223	Strict consistency between genetic and topographic landscapes of the brown tree frog (Buergeria robusta) in Taiwan. **2012**, 62, 251-62	19
1222	Exploring diversity in cryptorhynchine weevils (Coleoptera) using distance-, character- and tree-based species delineation. **2012**, 63, 1-14	43
1221	A multigene species tree for Western Mediterranean painted frogs (Discoglossus). **2012**, 64, 690-6	22
1220	Coalescent-based species delimitation in an integrative taxonomy. **2012**, 27, 480-8	564
1219	Length distributions of identity by descent reveal fine-scale demographic history. **2012**, 91, 809-22	165
1218	High-Dimensional Longitudinal Genomic Data: An analysis used for monitoring viral infections. **2012**, 29, 108-123	9
1217	Sea level, topography and island diversity: phylogeography of the Puerto Rican Red-eyed Coqu� Eleutherodactylus antillensis. **2012**, 21, 6033-52	12
1216	Spatial and temporal patterns of genetic variation in the widespread antitropical deep-sea coral Paragorgia arborea. **2012**, 21, 6053-67	42
1215	Multiple merger gene genealogies in two species: Monophyly, paraphyly, and polyphyly for two examples of Lambda coalescents. **2012**, 82, 117-30	8

1214	Effect of epistasis and linkage on fixation probability in three-locus models: an ancestral recombination-selection graph approach. **2012**, 82, 131-45	4
1213	The distribution of the coalescence time and the number of pairwise nucleotide differences in a model of population divergence or speciation with an initial period of gene flow. **2012**, 82, 92-108	21
1212	Epistasis can increase multivariate trait diversity in haploid non-recombining populations. **2012**, 82, 209-21	3
1211	Viral Genomics: Implications for the Understanding and Control of Emerging Viral Diseases. **2012**, 91-114	1
1210	References. **2012**, 395-432	
1209	Transition probabilities for general birth-death processes with applications in ecology, genetics, and evolution. **2012**, 65, 553-80	52
1208	Heterogeneity in genetic diversity among non-coding loci fails to fit neutral coalescent models of population history. **2012**, 7, e31972	23
1207	Analytical framework for identifying and differentiating recent hitchhiking and severe bottleneck effects from multi-locus DNA sequence data. **2012**, 7, e37588	1
1206	Phylogeographic pattern of the striped snakehead, Channa striata in Sundaland: ancient river connectivity, geographical and anthropogenic signatures [corrected]. **2012**, 7, e52089	27
1205	APPROXIMATE SAMPLING FORMULAS FOR GENERAL FINITE-ALLELES MODELS OF MUTATION. **2012**, 44, 408-428	10
1204	Recent explosive human population growth has resulted in an excess of rare genetic variants. **2012**, 336, 740-3	387
1203	Molecular phylogenetics: principles and practice. **2012**, 13, 303-14	403
1202	Phylogeography of Tibouchina papyrus (Pohl) Toledo (Melastomataceae), an endangered tree species from rocky savannas, suggests bidirectional expansion due to climate cooling in the Pleistocene. **2012**, 2, 1024-35	23
1201	Intense harvesting of eastern wolves facilitated hybridization with coyotes. **2012**, 2, 19-33	43
1200	Ultraconserved elements are novel phylogenomic markers that resolve placental mammal phylogeny when combined with species-tree analysis. **2012**, 22, 746-54	279
1199	Phylogenetic analysis of ancient DNA using BEAST. **2012**, 840, 229-41	
1198	Global divergence of spatial coalescents. **2012**, 152, 625-679	7
1197	Computer simulations: tools for population and evolutionary genetics. **2012**, 13, 110-22	162

1196	Coalescent-based species tree inference from gene tree topologies under incomplete lineage sorting by maximum likelihood. **2012**, 66, 763-775	110
1195	The value of repetitive sequences in chloroplast DNA for phylogeographic inference: a comment on Vachon & Freeland 2011. **2012**, 12, 581-5; discussion 586-9	14
1194	Neutral communities in fragmented landscapes. **2012**, 121, 1737-1748	14
1193	How mutation affects evolutionary games on graphs. **2012**, 299, 97-105	62
1192	Phylogenetic evidence based on Trypanosoma cruzi nuclear gene sequences and information entropy suggest that inter-strain intragenic recombination is a basic mechanism underlying the allele diversity of hybrid strains. **2012**, 12, 1064-71	18
1191	The mapping of epistatic effects onto a genealogical tree in haploid populations. **2012**, 81, 32-44	3
1190	The joint allele frequency spectrum of multiple populations: a coalescent theory approach. **2012**, 81, 179-95	37
1189	Sequence diversity under the multispecies coalescent with Yule process and constant population size. **2012**, 81, 97-101	4
1188	A universal scaling law determines time reversibility and steady state of substitutions under selection. **2012**, 82, 66-76	6
1187	ABGD, Automatic Barcode Gap Discovery for primary species delimitation. **2012**, 21, 1864-77	1708
1186	Estimating population divergence time and phylogeny from single-nucleotide polymorphisms data with outgroup ascertainment bias. **2012**, 21, 974-86	10
1185	Common misconceptions in molecular ecology: echoes of the modern synthesis. **2012**, 21, 4171-89	109
1184	Constructing summary statistics for approximate Bayesian computation: semi-automatic approximate Bayesian computation. **2012**, 74, 419-474	293
1183	Sampling HIV intrahost genealogies based on a model of acute stage CTL response. **2012**, 74, 509-35	3
1182	Phylogeography of a species complex of lowland Neotropical rain forest trees (Carapa, Meliaceae). **2013**, 40, 676-692	29
1181	Probability that a Sequence is Lost Without Trace Under the Neutral Wright–Fisher Model with Recombination. **2013**, 15, 919-933	
1180	Reconstructing past changes in locus-specific recombination rates. **2013**, 14, 11	3
1179	Coalescent theory has many new branches. **2013**, 87, 1-4	15

1178	A continuous method for gene flow. **2013**, 194, 687-96	3
1177	Effects of missing data on species tree estimation under the coalescent. **2013**, 69, 1057-62	57
1176	Mathematics, genetics and evolution. **2013**, 1, 9-31	4
1175	Tree-valued resampling dynamics Martingale problems and applications. **2013**, 155, 789-838	19
1174	Primate molecular phylogenetics in a genomic era. **2013**, 66, 565-8	15
1173	Multi-locus species tree for the Amazonian peacock basses (Cichlidae: Cichla): emergent phylogenetic signal despite limited nuclear variation. **2013**, 69, 479-90	12
1172	Comparative species divergence across eight triplets of spiny lizards (Sceloporus) using genomic sequence data. **2013**, 5, 2410-9	26
1171	Genotype imputation in a coalescent model with infinitely-many-sites mutation. **2013**, 87, 62-74	4
1170	Detecting recent changes in the demographic parameters of drosophilid populations from western and central Africa. **2013**, 345, 297-305	4
1169	Protein evolution along phylogenetic histories under structurally constrained substitution models. **2013**, 29, 3020-8	32
1168	Population genomics of rapid adaptation by soft selective sweeps. **2013**, 28, 659-69	324
1167	Multilocus species delimitation in a complex of morphologically conserved trapdoor spiders (mygalomorphae, antrodiaetidae, aliatypus). **2013**, 62, 805-23	182
1166	Dispersal at a snail's pace: historical processes affect contemporary genetic structure in the exploited wavy top snail (Megastraea undosa). **2013**, 104, 327-40	11
1165	Human genetic data reveal contrasting demographic patterns between sedentary and nomadic populations that predate the emergence of farming. **2013**, 30, 2629-44	28
1164	Parsimonious inference of hybridization in the presence of incomplete lineage sorting. **2013**, 62, 738-51	75
1163	Birth-death models and coalescent point processes: the shape and probability of reconstructed phylogenies. **2013**, 90, 113-28	61
1162	Looking for trees in the forest: summary tree from posterior samples. **2013**, 13, 221	91
1161	The common ancestor process revisited. **2013**, 75, 2003-27	5

1160	Permanental Partition Models and Markovian Gibbs Structures. **2013**, 153, 698-726		5
1159	Bayesian Hierarchical Modeling of the HIV Evolutionary Response to Therapy. **2013**, 108, 1230-1242		1
1158	Climate change influenced female population sizes through time across the Indonesian archipelago. **2013**, 85, 135-52		17
1157	The coalescent in boundary-limited range expansions. **2013**, 67, 1307-20		16
1156	Global lack of flyway structure in a cosmopolitan bird revealed by a genome wide survey of single nucleotide polymorphisms. **2013**, 22, 41-55		48
1155	The effect of fluctuating selection on the genealogy at a linked site. **2013**, 87, 34-50		3
1154	The ancestral selection graph under strong directional selection. **2013**, 87, 25-33		11
1153	Yule-generated trees constrained by node imbalance. **2013**, 246, 139-47		4
1152	Exact enumeration of cherries and pitchforks in ranked trees under the coalescent model. **2013**, 242, 195-200		16
1151	Muller's ratchet clicks in finite time. *Stochastic Processes and Their Applications*, **2013**, 123, 2370-2397	1.1	1
1150	On spatial coalescents with multiple mergers in two dimensions. **2013**, 87, 90-104		5
1149	On the length of an external branch in the Beta-coalescent. *Stochastic Processes and Their Applications*, **2013**, 123, 1691-1715	1.1	14
1148	Publisher's note: Article removed. **2013**, 83, 20		2
1147	Estimating trace-suspect match probabilities for singleton Y-STR haplotypes using coalescent theory. **2013**, 7, 264-71		27
1146	On the extended Moran model and its relation to coalescents with multiple collisions. **2013**, 87, 5-14		22
1145	Fluctuations in fitness distributions and the effects of weak linked selection on sequence evolution. **2013**, 85, 86-102		17
1144	The odd couple: contrasting phylogeographic patterns in two sympatric sibling species of woodlouse-hunter spiders in the Canary Islands. **2013**, 51, 29-37		9
1143	Paleo-drainage basin connectivity predicts evolutionary relationships across three Southeast Asian biodiversity hotspots. **2013**, 62, 398-410		53

1142	Demographic history and the low genetic diversity in Dipteryx alata (Fabaceae) from Brazilian Neotropical savannas. **2013**, 111, 97-105	42
1141	Meiotic gene-conversion rate and tract length variation in the human genome. **2013**,	15
1140	Functional extinction of birds drives rapid evolutionary changes in seed size. **2013**, 340, 1086-90	418
1139	Combined analyses of kinship and FST suggest potential drivers of chaotic genetic patchiness in high gene-flow populations. **2013**, 22, 3476-94	110
1138	An ancestral recombination graph for diploid populations with skewed offspring distribution. **2013**, 193, 255-90	30
1137	Phylogeography of the shrimp Palaemon floridanus (Crustacea: Caridea: Palaemonidae): a partial test of meta-population genetic structure in the wider Caribbean. **2013**, 34, 381-393	13
1136	Species tree phylogeny and character evolution in the genus Centipeda (Asteraceae): evidence from DNA sequences from coding and non-coding loci from the plastid and nuclear genomes. **2013**, 68, 239-50	9
1135	Analysis of DNA sequence variation within marine species using Beta-coalescents. **2013**, 87, 15-24	35
1134	M�odos de an�isis gen�icos, espaciales y de conectividad en gen�ica del paisaje. **2013**, 84, 1031-1054	6
1133	How the dynamics and structure of sexual contact networks shape pathogen phylogenies. **2013**, 9, e1003105	35
1132	Coalescent tree imbalance and a simple test for selective sweeps based on microsatellite variation. **2013**, 9, e1003060	19
1131	Molecular epidemiology of community-associated methicillin-resistant Staphylococcus aureus in the genomic era: a cross-sectional study. **2013**, 3, 1902	33
1130	Age-dependent transition from cell-level to population-level control in murine intestinal homeostasis revealed by coalescence analysis. **2013**, 9, e1003326	11
1129	Current Approaches in Spatial Genetics. **2013**, 217-229	
1128	Markov chain Monte Carlo sampling of gene genealogies conditional on unphased SNP genotype data. **2013**, 12, 559-81	3
1127	A stochastic simulator of birth-death master equations with application to phylodynamics. **2013**, 30, 1480-93	43
1126	Asymptotic distributions of coalescence times and ancestral lineage numbers for populations with temporally varying size. **2013**, 194, 721-36	15
1125	Inference of historical migration rates via haplotype sharing. **2013**, 29, i180-8	45

1124	Intercoalescence time distribution of incomplete gene genealogies in temporally varying populations, and applications in population genetic inference. **2013**, 77, 158-73	5
1123	A Note on Distinguishing Random Trees Populations. **2013**, 42, 239-251	
1122	Gaussian process-based Bayesian nonparametric inference of population size trajectories from gene genealogies. **2013**, 69, 8-18	27
1121	Statistical properties of the site-frequency spectrum associated with lambda-coalescents. **2013**, 195, 1037-53	29
1120	The effect of quenched disorder in neutral theories. **2013**, 2013, P04032	14
1119	Latent protein trees. **2013**, 7,	2
1118	Conditional formulae for Gibbs-type exchangeable random partitions. **2013**, 23,	18
1117	General fragmentation trees. **2013**, 18,	5
1116	The genealogy of branching Brownian motion with absorption. **2013**, 41,	42
1115	Asymptotic theory with hierarchical autocorrelation: Ornstein�Uhlenbeck tree models. **2013**, 41,	26
1114	Path-properties of the tree-valued Fleming�Viot process. **2013**, 18,	3
1113	Bayesian non-parametrics and the probabilistic approach to modelling. **2013**, 371, 20110553	50
1112	Defining Predictive Probability Functions for Species Sampling Models. **2013**, 28, 209-222	30
1111	On the external branches of coalescents with multiple collisions. **2013**, 18,	5
1110	Using ancestral information to detect and localize quantitative trait loci in genome-wide association studies. **2013**, 14, 200	15
1109	Genealogies in simple models of evolution. **2013**, 2013, P01006	18
1108	A Construction of a �Coalescent via the Pruning of Binary Trees. **2013**, 50, 772-790	
1107	Ancestral Graph with Bias in Gene Conversion. **2013**, 50, 239-255	

1106	Duality Between the Two-Locus Wright–Fisher Diffusion Model and the Ancestral Process with Recombination. **2013**, 50, 256-271	1
1105	Stochastic coalescence in logarithmic time. **2013**, 23,	
1104	The coalescent point process of branching trees. **2013**, 23,	17
1103	A Construction of a β-Coalescent via the Pruning of Binary Trees. **2013**, 50, 772-790	6
1102	The effect of single recombination events on coalescent tree height and shape. **2013**, 8, e60123	9
1101	The power to detect recent fragmentation events using genetic differentiation methods. **2013**, 8, e63981	18
1100	Effect of Landscape Structure on Species Diversity. **2013**, 8, e66495	23
1099	Contrasting genetic structure among populations of two amphidromous fish species (Sicydiinae) in the Central West Pacific. **2013**, 8, e75465	20
1098	The effect of multiple paternity on genetic diversity of small populations during and after colonisation. **2013**, 8, e75587	16
1097	Non-invasive ancient DNA protocol for fluid-preserved specimens and phylogenetic systematics of the genus Orestias (Teleostei: Cyprinodontidae). **2013**, 3640, 373-94	16
1096	Ancestral Graph with Bias in Gene Conversion. **2013**, 50, 239-255	4
1095	Duality Between the Two-Locus Wright–Fisher Diffusion Model and the Ancestral Process with Recombination. **2013**, 50, 256-271	2
1094	On Asymptotics of the Beta Coalescents. **2014**, 46, 496-515	4
1093	Marginal likelihood estimate comparisons to obtain optimal species delimitations in Silene sect. Cryptoneurae (Caryophyllaceae). **2014**, 9, e106990	26
1092	A framework including recombination for analyzing the dynamics of within-host HIV genetic diversity. **2014**, 9, e87655	1
1091	Comparative population genomics of the Borrelia burgdorferi species complex reveals high degree of genetic isolation among species and underscores benefits and constraints to studying intra-specific epidemiological processes. **2014**, 9, e94384	19
1090	Interpretation of Mitochondrial DNA Evidence. **2014**, 1-10	
1089	An efficient estimator of the mutation parameter and analysis of polymorphism from the 1000 genomes project. **2014**, 5, 561-75	2

1088	Minimal Clade Size in the Bolthausen-Sznitman Coalescent. **2014**, 51, 657-668	7
1087	Evolutionary Genetics, Statistics in. **2014**,	
1086	Population Genetics. **2014**,	
1085	Inference of the properties of the recombination process from whole bacterial genomes. **2014**, 196, 253-65	29
1084	ASTRAL: genome-scale coalescent-based species tree estimation. **2014**, 30, i541-8	684
1083	Phylogeographic patterns of two tiger beetle species at both sides of the strait of Gibraltar (Coleoptera: Cicindelini). **2014**, 50, 399-406	3
1082	Distortion of genealogical properties when the sample is very large. **2014**, 111, 2385-90	43
1081	Models of nucleotide substitution. **2014**, 1-34	1
1080	Genome-wide inference of ancestral recombination graphs. **2014**, 10, e1004342	200
1079	A new general analytical approach for modeling patterns of genetic differentiation and effective size of subdivided populations over time. **2014**, 258, 113-33	13
1078	Inference of epidemiological dynamics based on simulated phylogenies using birth-death and coalescent models. **2014**, 10, e1003913	30
1077	Using an epidemiological model for phylogenetic inference reveals density dependence in HIV transmission. **2014**, 31, 6-17	43
1076	How to infer relative fitness from a sample of genomic sequences. **2014**, 197, 913-23	12
1075	Soft selective sweeps in complex demographic scenarios. **2014**, 198, 669-84	53
1074	Population genetics inference for longitudinally-sampled mutants under strong selection. **2014**, 198, 1237-50	21
1073	Range-wide genetic structure of maritime pine predates the last glacial maximum: evidence from nuclear DNA. **2014**, 151, 1-13	8
1072	Quartet inference from SNP data under the coalescent model. **2014**, 30, 3317-24	585
1071	Paleoclimate Shaped Bluefish Structure in the Northern Hemisphere. **2014**, 39, 578-586	8

1070	Microsatellite data show recent demographic expansions in sedentary but not in nomadic human populations in Africa and Eurasia. **2014**, 22, 1201-7	15
1069	Detecting past changes of effective population size. **2014**, 7, 663-81	44
1068	Neutral null models for diversity in serial transfer evolution experiments. **2014**, 68, 2727-36	1
1067	Contemporary pollen-mediated gene immigration reflects the historical isolation of a rare, animal-pollinated shrub in a fragmented landscape. **2014**, 112, 172-81	28
1066	Recovering species demographic history from multi-model inference: the case of a Neotropical savanna tree species. **2014**, 14, 213	21
1065	Hypothesis testing of meiotic recombination rates from population genetic data. **2014**, 15, 122	
1064	Sampling through time and phylodynamic inference with coalescent and birth-death models. **2014**, 11, 20140945	27
1063	Bayesian inference of infectious disease transmission from whole-genome sequence data. **2014**, 31, 1869-79	138
1062	The influence of sampling design on species tree inference: a new relationship for the New World chickadees (Aves: Poecile). **2014**, 68, 501-13	27
1061	Gene tree rooting methods give distributions that mimic the coalescent process. **2014**, 70, 63-9	7
1060	Metadata beyond the sequence enables the phylodynamic inference of bovine viral diarrhea virus type 1a isolates from Western Canada. **2014**, 28, 367-74	16
1059	Genetic markers reveal a gradient of hybridization between cape hakes (Merluccius capensis and Merluccius paradoxus) in their sympatric geographic distribution. **2014**, 86, 69-75	7
1058	Quasi-Monte Carlo method in population genetics parameter estimation. **2014**, 103, 33-38	
1057	Pareto genealogies arising from a Poisson branching evolution model with selection. **2014**, 68, 727-61	11
1056	Measures of success in a class of evolutionary models with fixed population size and structure. **2014**, 68, 109-43	50
1055	Critical assessment of coalescent simulators in modeling recombination hotspots in genomic sequences. **2014**, 15, 3	14
1054	Contrasting spatial genetic structure in Annona crassiflora populations from fragmented and pristine savannas. **2014**, 300, 1719-1727	13
1053	Time to most recent common ancestor for stationary continuous state branching processes with immigration. **2014**, 9, 239-260	0

1052	Quasi equilibrium, variance effective size and fixation index for populations with substructure. **2014**, 69, 1057-128	9
1051	DNA barcode-based delineation of putative species: efficient start for taxonomic workflows. **2014**, 14, 706-15	198
1050	Coalescence 2.0: a multiple branching of recent theoretical developments and their applications. **2014**, 23, 2637-52	57
1049	Single-cell genomics reveals hundreds of coexisting subpopulations in wild Prochlorococcus. **2014**, 344, 416-20	361
1048	Storytelling and story testing in domestication. **2014**, 111, 6159-64	80
1047	Is diagnosability an indicator of speciation? Response to "Why one century of phenetics is enough". **2014**, 63, 833-7	18
1046	Phylogeography and ecological niche modelling, coupled with the fossil pollen record, unravel the demographic history of a Neotropical swamp palm through the Quaternary. **2014**, 41, 673-686	45
1045	Can novel genetic analyses help to identify low-dispersal marine invasive species?. **2014**, 4, 2848-66	17
1044	The largest strongly connected component in the cyclical pedigree model of Wakeley et al. **2014**, 98, 28-37	
1043	Comparative phylogeography of mutualists and the effect of the host on the genetic structure of its partners. **2014**, 113, 1021-1035	23
1042	Investigating population history using temporal genetic differentiation. **2014**, 31, 2516-27	34
1041	A new method for modeling coalescent processes with recombination. **2014**, 15, 273	10
1040	Molecular-clock methods for estimating evolutionary rates and timescales. **2014**, 23, 5947-65	187
1039	The impact of accelerating faster than exponential population growth on genetic variation. **2014**, 196, 819-28	11
1038	Discord between morphological and phylogenetic species boundaries: incomplete lineage sorting and recombination results in fuzzy species boundaries in an asexual fungal pathogen. **2014**, 14, 38	62
1037	A path integral formulation of the Wright-Fisher process with genic selection. **2014**, 92, 30-5	4
1036	Molecular phylogenetic analysis of the Papionina using concatenation and species tree methods. **2014**, 66, 18-28	13
1035	Within a sample from a population, the distribution of the number of descendants of a subsample's most recent common ancestor. **2014**, 92, 51-4	3

1034	An Introduction to Population Genetics: Theory and Applications.By Rasmus Nielsen and Montgomery Slatkin.. **2014**, 63, 843-844	
1033	The Irish potato famine pathogen Phytophthora infestans originated in central Mexico rather than the Andes. **2014**, 111, 8791-6	130
1032	Demography-adjusted tests of neutrality based on genome-wide SNP data. **2014**, 95, 1-12	13
1031	Applying spatial analysis of genetic and environmental data to predict connection corridors to the New World screwworm populations in South America. **2014**, 138 Suppl, S34-41	7
1030	Efficient computation in the IM model. **2014**, 68, 1423-51	15
1029	The evolving beta coalescent. **2014**, 19,	6
1028	The cut-and-paste process. **2014**, 42,	17
1027	From flows of $Lambda$-Fleming-Viot processes to lookdown processes via flows of partitions. **2014**, 19,	3
1026	DESCARTES’ RULE OF SIGNS AND THE IDENTIFIABILITY OF POPULATION DEMOGRAPHIC MODELS FROM GENOMIC VARIATION DATA. **2014**, 42, 2469-2493	44
1025	Markov jump processes in modeling coalescent with recombination. **2014**, 42,	1
1024	▯coalescents: a survey. **2014**, 51, 23-40	2
1023	Disk covering methods improve phylogenomic analyses. **2014**, 15 Suppl 6, S7	21
1022	The Total External Branch Length of Beta-Coalescents▯ **2014**, 23, 1010-1027	11
1021	Minimal Clade Size in the Bolthausen-Sznitman Coalescent. **2014**, 51, 657-668	3
1020	Identifiability of a Coalescent-Based Population Tree Model. **2014**, 51, 921-929	
1019	On Asymptotics of the Beta Coalescents. **2014**, 46, 496-515	4
1018	Computational Inference Beyond Kingman’s Coalescent. **2015**, 52, 519-537	10
1017	The Coalescent in Peripatric Metapopulations. **2015**, 52, 538-557	

1016	On the total length of external branches for beta-coalescents. **2015**, 47, 693-714	2
1015	Amphibian molecular ecology and how it has informed conservation. **2015**, 24, 5084-109	33
1014	Molecular operational taxonomic units as approximations of species in the light of evolutionary models and empirical data from Fungi. **2015**, 24, 5770-7	50
1013	Evolutionary processes driving spatial patterns of intraspecific genetic diversity in river ecosystems. **2015**, 24, 4586-604	54
1012	The internal branch lengths of the Kingman coalescent. **2015**, 25,	11
1011	The segregated $Lambda$-coalescent. **2015**, 43,	1
1010	Some large deviations in Kingman's coalescent. **2015**, 20,	1
1009	The fragmentation process of an infinite recursive tree and Ornstein-Uhlenbeck type processes. **2015**, 20,	6
1008	A mixing tree-valued process arising under neutral evolution with recombination. **2015**, 20,	
1007	Diffusion limits at small times for $Lambda$-coalescents with a Kingman component. **2015**, 20,	1
1006	TRACTABLE DIFFUSION AND COALESCENT PROCESSES FOR WEAKLY CORRELATED LOCI. **2015**, 20,	3
1005	Lipschitz partition processes. **2015**, 21,	1
1004	Time-varying network models. **2015**, 21,	6
1003	The Coalescent in Peripatric Metapopulations. **2015**, 52, 538-557	10
1002	How well can the exponential-growth coalescent approximate constant-rate birth-death population dynamics?. **2015**, 282, 20150420	19
1001	A comparative study of SVDquartets and other coalescent-based species tree estimation methods. **2015**, 16 Suppl 10, S2	95
1000	On the total length of external branches for beta-coalescents. **2015**, 47, 693-714	1
999	A spectral decomposition for the Bolthausen-Sznitman coalescent and the Kingman coalescent. **2015**, 20,	1

998	Strong Migration Limit for Games in Structured Populations: Applications to Dominance Hierarchy and Set Structure. **2015**, 6, 318-346	5
997	Delineating species with DNA barcodes: a case of taxon dependent method performance in moths. **2015**, 10, e0122481	77
996	Analyses of Twelve New Whole Genome Sequences of Cassava Brown Streak Viruses and Ugandan Cassava Brown Streak Viruses from East Africa: Diversity, Supercomputing and Evidence for Further Speciation. **2015**, 10, e0139321	45
995	Independent Demographic Responses to Climate Change among Temperate and Tropical Milksnakes (Colubridae: Genus Lampropeltis). **2015**, 10, e0128543	8
994	Evolutionary Genetics, Statistics in. **2015**, 1-6	
993	Relaxed random walk model coupled with ecological niche modeling unravel the dispersal dynamics of a Neotropical savanna tree species in the deeper Quaternary. **2015**, 6, 653	30
992	Computational Inference Beyond Kingman's Coalescent. **2015**, 52, 519-537	7
991	Fundamental limits on the accuracy of demographic inference based on the sample frequency spectrum. **2015**, 112, 7677-82	51
990	Parallel Epidemics of Community-Associated Methicillin-Resistant Staphylococcus aureus USA300 Infection in North and South America. **2015**, 212, 1874-82	75
989	An Operator Semigroup in Mathematical Genetics. **2015**,	0
988	Can the site-frequency spectrum distinguish exponential population growth from multiple-merger coalescents?. **2015**, 199, 841-56	45
987	Inferring Learning Strategies from Cultural Frequency Data. **2015**, 85-101	2
986	Inferring phylogenies of evolving sequences without multiple sequence alignment. **2014**, 4, 6504	43
985	Statistical Physics Methods Provide the Exact Solution to a Long-Standing Problem of Genetics. **2015**, 114, 238101	3
984	Genetic Variability Under the Seedbank Coalescent. **2015**, 200, 921-34	19
983	Bayesian Nonparametric Inference of Population Size Changes from Sequential Genealogies. **2015**, 201, 281-304	22
982	Evolution. **2015**, 673-696	
981	Can one hear the shape of a population history?. **2015**, 100C, 26-38	17

980	Modeling the genealogy of a cultural trait. **2015**, 101, 1-8	6
979	Inference of sex-specific expansion patterns in human populations from Y-chromosome polymorphism. **2015**, 157, 217-25	6
978	Practice-Oriented Controversies and Borrowed Epistemic Credibility In Current Evolutionary Biology: Phylogeography As A Case Study. **2015**, 23, 310-334	
977	Genetic data simulators and their applications: an overview. **2015**, 39, 2-10	19
976	Pitman Yor Diffusion Trees for Bayesian Hierarchical Clustering. **2015**, 37, 271-89	8
975	A coalescent-based method for population tree inference with haplotypes. **2015**, 31, 691-8	8
974	On the eigenvalue effective size of structured populations. **2015**, 71, 595-646	5
973	Asymptotics of Symmetric Compound Poisson Population Models. **2015**, 24, 216-253	5
972	ClonalFrameML: efficient inference of recombination in whole bacterial genomes. **2015**, 11, e1004041	458
971	An efficient Bayesian inference framework for coalescent-based nonparametric phylodynamics. **2015**, 31, 3282-9	19
970	The effect of inbreeding constraints and offspring distribution on time to the most recent common ancestor. **2015**, 382, 74-80	5
969	Genetic diversity, paraphyly and incomplete lineage sorting of mtDNA, ITS2 and microsatellite flanking region in closely related Heliopora species (Octocorallia). **2015**, 93, 161-71	19
968	Evolution of cooperation in a multidimensional phenotype space. **2015**, 102, 60-75	5
967	Metapopulation inbreeding dynamics, effective size and subpopulation differentiation--A general analytical approach for diploid organisms. **2015**, 102, 40-59	10
966	Putative floral brood-site mimicry, loss of autonomous selfing, and reduced vegetative growth are significantly correlated with increased diversification in Asarum (Aristolochiaceae). **2015**, 89, 194-204	8
965	Clustering and Feature Allocation. **2015**, 145-174	1
964	Backbones of evolutionary history test biodiversity theory for microbes. **2015**, 112, 8356-61	29
963	Plastid DNA Homogeneity in Celtis australis L. (Cannabaceae) and Nerium oleander L. (Apocynaceae) throughout the Mediterranean Basin. **2015**, 176, 421-432	7

962	Identifiability of the unrooted species tree topology under the coalescent model with time-reversible substitution processes, site-specific rate variation, and invariable sites. **2015**, 374, 35-47	156
961	Closed form modeling of evolutionary rates by exponential Brownian functionals. **2015**, 71, 1387-409	1
960	Calibrated birth-death phylogenetic time-tree priors for bayesian inference. **2015**, 64, 369-83	34
959	Phylogeographic Analyses of American Black Bears (Ursus americanus) Suggest Four Glacial Refugia and Complex Patterns of Postglacial Admixture. **2015**, 32, 2338-50	66
958	Multi-model inference in comparative phylogeography: an integrative approach based on multiple lines of evidence. **2015**, 6, 31	20
957	Inferring epidemiological dynamics with Bayesian coalescent inference: the merits of deterministic and stochastic models. **2015**, 199, 595-607	16
956	Problems and Cautions With Sequence Mismatch Analysis and Bayesian Skyline Plots to Infer Historical Demography. **2015**, 106, 333-46	148
955	Species delimitation and relationships: The dance of the seven veils. **2015**, 64, 3-16	96
954	Molecular phylogeny and divergence time estimation of Cosmodela (Coleoptera: Carabidae: Cicindelinae) tiger beetle species from Southeast Asia. **2015**, 44, 437-445	15
953	Viral meningitis epidemics and a single, recent, recombinant and anthroponotic origin of swine vesicular disease virus. **2015**, 2015, 289-303	10
952	Multiple genetic lineages challenge the monospecific status of the West African endemic frog family Odontobatrachidae. **2015**, 15, 67	6
951	Mathematical Ecology. **2015**, 157-295	0
950	Relaxed Observance of Traditional Marriage Rules Allows Social Connectivity without Loss of Genetic Diversity. **2015**, 32, 2254-62	13
949	Phylodynamic Inference with Kernel ABC and Its Application to HIV Epidemiology. **2015**, 32, 2483-95	30
948	Revisiting the time until fixation of a neutral mutant in a finite population - A coalescent theory approach. **2015**, 380, 98-102	5
947	Migration and horizontal gene transfer divide microbial genomes into multiple niches. **2015**, 6, 8924	70
946	One species in eight: DNA barcodes from type specimens resolve a taxonomic quagmire. **2015**, 15, 967-84	49
945	Cancer evolution: mathematical models and computational inference. **2015**, 64, e1-25	181

944	An overview of SNP interactions in genome-wide association studies. **2015**, 14, 143-55	67
943	Is the extremely rare Iberian endemic plant species Castrilanthemum debeauxii (Compositae, Anthemideae) a 'living fossil'? Evidence from a multi-locus species tree reconstruction. **2015**, 82 Pt A, 118-30	23
942	An analytical framework in the general coalescent tree setting for analyzing polymorphisms created by two mutations. **2015**, 70, 913-56	7
941	Finding the best resolution for the Kingman-Tajima coalescent: theory and applications. **2015**, 70, 1207-47	9
940	Can Theory Improve the Scope of Quantitative Metazoan Metabarcoding?. **2016**, 8, 1	7
939	Site recurrence for coalescing random walk. **2016**, 21,	4
938	Reflections on the Field of Human Genetics: A Call for Increased Disease Genetics Theory. **2016**, 7, 106	1
937	Convergence to the structured coalescent process. **2016**, 53, 502-517	2
936	Rejoinder: The Ubiquitous Ewens Sampling Formula. **2016**, 31,	7
935	SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent. **2016**, 12, e1005130	64
934	The Structure of Genetic Diversity in Eelgrass (Zostera marina L.) along the North Pacific and Bering Sea Coasts of Alaska. **2016**, 11, e0152701	11
933	Coalescent Simulation and Paleodistribution Modeling for Tabebuia rosealba Do Not Support South American Dry Forest Refugia Hypothesis. **2016**, 11, e0159314	18
932	Interspecific Hybridization in Pilot Whales and Asymmetric Genetic Introgression in Northern Globicephala melas under the Scenario of Global Warming. **2016**, 11, e0160080	10
931	Genetic demographic networks: Mathematical model and applications. **2016**, 111, 75-86	
930	Understanding Past Population Dynamics: Bayesian Coalescent-Based Modeling with Covariates. **2016**, 65, 1041-1056	32
929	Evolutionary Patterns and Processes: Lessons from Ancient DNA. **2017**, 66, e1-e29	53
928	Bayesian analyses of Yemeni mitochondrial genomes suggest multiple migration events with Africa and Western Eurasia. **2016**, 159, 382-93	16
927	Inference of Super-exponential Human Population Growth via Efficient Computation of the Site Frequency Spectrum for Generalized Models. **2016**, 202, 235-45	24

926	Current hypotheses to explain genetic chaos under the sea. **2016**, 62, 551-566	47
925	Fumio Tajima and the Origin of Modern Population Genetics. **2016**, 204, 389-390	
924	A Matter of Time □Understanding the Limits of the Power of Molecular Data for Delimiting Species Boundaries. **2016**, 29, 479-492	30
923	Random walk Green kernels in the neutral Moran model conditioned on survivors at a random time to origin. **2016**, 23, 164-200	1
922	Challenges in Species Tree Estimation Under the Multispecies Coalescent Model. **2016**, 204, 1353-1368	89
921	Statistical Inference in the Wright-Fisher Model Using Allele Frequency Data. **2017**, 66, e30-e46	25
920	An algorithm for computing the gene tree probability under the multispecies coalescent and its application in the inference of population tree. **2016**, 32, i225-i233	9
919	A new coalescent for seed-bank models. **2016**, 26,	24
918	Species differentiation in the genus Chara (Charophyceae): considerable phenotypic plasticity occurs within homogenous genetic groups. **2016**, 51, 282-293	21
917	The contrasting nature of woody plant species in different neotropical forest biomes reflects differences in ecological stability. **2016**, 210, 25-37	62
916	Genetic drift in populations governed by a Galton-Watson branching process. **2016**, 109, 63-74	7
915	Fixation probability in a two-locus intersexual selection model. **2016**, 109, 75-87	2
914	The site-frequency spectrum associated with □coalescents. **2016**, 110, 36-50	17
913	Genetic and morphological studies of Trichosirocalus species introduced to North America, Australia and New Zealand for the biological control of thistles. **2016**, 106, 99-113	4
912	Demographic inference under the coalescent in a spatial continuum. **2016**, 111, 43-50	9
911	Incipient speciation with gene flow on a continental island: Species delimitation of the Hainan Hwamei (Leucodioptron canorum owstoni, Passeriformes, Aves). **2016**, 102, 62-73	6
910	References. **2016**, 447-486	
909	The Site Frequency Spectrum for General Coalescents. **2016**, 202, 1549-61	18

908	Motoo Kimura and James Crow on the Infinitely Many Alleles Model. **2016**, 202, 1243-5	3
907	Demographic inference under a spatially continuous coalescent model. **2016**, 117, 94-9	5
906	Helicobacter pylori: Genetics, Recombination, Population Structure, and Human Migrations. **2016**, 3-27	6
905	Coalescent inferences in conservation genetics: should the exception become the rule?. **2016**, 12,	9
904	The transmission process: A combinatorial stochastic process for the evolution of transmission trees over networks. **2016**, 410, 137-170	5
903	Reversible polymorphism-aware phylogenetic models and their application to tree inference. **2016**, 407, 362-370	34
902	Hypothesis tests for phylogenetic quartets, with applications to coalescent-based species tree inference. **2016**, 408, 179-186	7
901	A coalescent dual process for a Wright-Fisher diffusion with recombination and its application to haplotype partitioning. **2016**, 112, 126-138	2
900	Images of a finite set under iterations of two random dependent mappings. **2016**, 26,	3
899	Does asymmetric gene flow among matrilines maintain the evolutionary potential of the European eel?. **2016**, 6, 5305-20	6
898	On Hille-type approximation of degenerate semigroups of operators. **2016**, 511, 31-53	3
897	On the importance of skewed offspring distributions and background selection in virus population genetics. **2016**, 117, 393-399	29
896	Evolutionary Biology. **2016**,	3
895	Maximum Likelihood Implementation of an Isolation-with-Migration Model for Three Species. **2017**, 66, 379-398	28
894	Differential influences of local subpopulations on regional diversity and differentiation for greater sage-grouse (Centrocercus urophasianus). **2016**, 25, 4424-37	4
893	Trends in the Mechanistic and Dynamic Modeling of Infectious Diseases. **2016**, 3, 212-222	18
892	Multilocus inference of species trees and DNA barcoding. **2016**, 371,	48
891	New insights on the history of canids in Oceania based on mitochondrial and nuclear data. **2016**, 144, 553-565	41

890	The non-equilibrium allele frequency spectrum in a Poisson random field framework. **2016**, 111, 51-64	3
889	Statistical mechanics of ecological systems: Neutral theory and beyond. **2016**, 88,	76
888	Population Growth Combined with Wide Offspring Distributions can Increase Fixation Rate and Reduce Genetic Diversity. **2016**, 78, 1477-92	1
887	Phylogeographic model selection leads to insight into the evolutionary history of four-eyed frogs. **2016**, 113, 8010-7	33
886	Selective Sweeps. **2016**, 23-32	0
885	The Ubiquitous Ewens Sampling Formula. **2016**, 31,	45
884	The Impact of the Tree Prior on Molecular Dating of Data Sets Containing a Mixture of Inter- and Intraspecies Sampling. **2017**, 66, 413-425	51
883	Bayesian Phylogenetic Methods. **2016**, 137-140	
882	Molecular Epidemiology and Evolution Concepts in Microbial Forensics. **2016**, 561-582	
881	Evolutionary Medicine IV. Evolution and Emergence of Novel Pathogens. **2016**, 77-82	
880	Reconstructing contact network parameters from viral phylogenies. **2016**, 2, vew029	7
879	Demographical history and palaeodistribution modelling show range shift towards Amazon Basin for a Neotropical tree species in the LGM. **2016**, 16, 213	15
878	Inferring the Dynamics of Effective Population Size Using Autosomal Genomes. **2016**, 6, 20079	1
877	A performance study of the impact of recombination on species tree analysis. **2016**, 17, 785	7
876	Stochastic analysis of the extra clustering model for animal grouping. **2016**, 73, 123-59	1
875	Coalescent models for developmental biology and the spatio-temporal dynamics of growing tissues. **2016**, 13,	8
874	Does Gene Tree Discordance Explain the Mismatch between Macroevolutionary Models and Empirical Patterns of Tree Shape and Branching Times?. **2016**, 65, 628-39	12
873	Ancient split of major genetic lineages of European Black Pine: evidence from chloroplast DNA. **2016**, 12, 1	10

872	Mutational pattern of a sample from a critical branching population. **2016**, 73, 627-64	3
871	Asymptotics of the Minimal Clade Size and Related Functionals of Certain Beta-Coalescents. **2016**, 142, 127-148	6
870	Nonlinear effects in evolution - an ab initio study: A model in which the classical theory of evolution occurs as a special case. **2016**, 401, 94-108	1
869	Neutral Models of Genetic Drift and Mutation. **2016**, 119-123	1
868	Erratum. **2016**, 65, 943	
867	ARGON: fast, whole-genome simulation of the discrete time Wright-fisher process. **2016**, 32, 3032-4	17
866	Spatially explicit summary statistics for historical population genetic inference. **2016**, 7, 418-427	10
865	Exchangeable Markov Processes on ([k]^{mathbb N}) with Cadlag Sample Paths. **2016**, 29, 206-230	
864	Who lives where? Molecular and morphometric analyses clarify which Unio species (Unionida, Mollusca) inhabit the southwestern Palearctic. **2016**, 16, 597-611	47
863	Phylogenomic analyses resolve an ancient trichotomy at the base of Ischyropsalidoidea (Arachnida, Opiliones) despite high levels of gene tree conflict and unequal minority resolution frequencies. **2016**, 95, 171-82	16
862	Examining the sensitivity of molecular species delimitations to the choice of mitochondrial marker. **2016**, 16, 467-480	8
861	Transmission dynamics of HIV-1 subtype B in the Basque Country, Spain. **2016**, 40, 91-97	9
860	Using ancient DNA and coalescent-based methods to infer extinction. **2016**, 12, 20150822	10
859	The uniqueness of hierarchically extended backward solutions of the WrightFisher model. **2016**, 41, 447-483	2
858	Efficient Strategies for Calculating Blockwise Likelihoods Under the Coalescent. **2016**, 202, 775-86	40
857	Molecular approaches to trematode systematics: 'best practice' and implications for future study. **2016**, 93, 295-306	99
856	Coexistence of crypticBrachionus calyciflorus(Rotifera) species: roles of environmental variables. **2016**, 38, 478-489	18
855	Richard Hudson and Norman Kaplan on the Coalescent Process. **2016**, 202, 865-6	2

854	Paradigm Shifts in the Phylogeographic Analysis of Seaweeds. **2016**, 23-62	7
853	Nuclear phylogenomics of the palm subfamily Arecoideae (Arecaceae). **2016**, 97, 32-42	22
852	A Naturally Occurring Domestic Cat APOBEC3 Variant Confers Resistance to Feline Immunodeficiency Virus Infection. **2016**, 90, 474-85	14
851	Spread of pedigree versus genetic ancestry in spatially distributed populations. **2016**, 108, 1-12	11
850	Ancestries of a recombining diploid population. **2016**, 72, 363-408	1
849	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. **2016**, 94, 447-62	230
848	A Nonparametric Bayesian Model for Nested Clustering. **2016**, 1362, 129-41	
847	Molecular data from contemporary and historical collections reveal a complex story of cryptic diversification in the Varanus (Polydaedalus) niloticus Species Group. **2016**, 94, 591-604	18
846	The distribution of branch lengths in phylogenetic trees. **2016**, 94, 136-45	4
845	Efficient computation of the joint sample frequency spectra for multiple populations. **2017**, 26, 182-194	40
844	The origin of Chinese domestic horses revealed with novel mtDNA variants. **2017**, 88, 19-26	9
843	A large historical refugium explains spatial patterns of genetic diversity in a Neotropical savanna tree species. **2017**, 119, 239-252	19
842	Hierarchical evolving Dirichlet processes for modeling nonlinear evolutionary traces in temporal data. **2017**, 31, 32-64	7
841	The problem of estimating recent genetic connectivity in a changing world. **2017**, 31, 126-135	34
840	Species tree estimation using Neighbor Joining. **2017**, 414, 5-7	11
839	Recursions for the exchangeable partition function of the seedbank coalescent. **2017**, 114, 95-106	
838	Using multi-locus sequence data for addressing species boundaries in commonly accepted lichen-forming fungal species. **2017**, 17, 351-363	18
837	Resolving evolutionary relationships in closely related nonmodel organisms: a case study using chromosomally distinct members of a black fly species complex. **2017**, 42, 489-508	7

836	Population structure and coalescence in pedigrees: Comparisons to the structured coalescent and a framework for inference. **2017**, 115, 1-12	7
835	Modeling Spatial Covariance Using the Limiting Distribution of Spatio-Temporal Random Walks. **2017**, 112, 497-507	11
834	Bayesian species identification under the multispecies coalescent provides significant improvements to DNA barcoding analyses. **2017**, 26, 3028-3036	48
833	A population genetics perspective on the determinants of intra-tumor heterogeneity. **2017**, 1867, 109-126	29
832	Inference of Gene Flow in the Process of Speciation: An Efficient Maximum-Likelihood Method for the Isolation-with-Initial-Migration Model. **2017**, 205, 1597-1618	16
831	Demographic stability and high historical connectivity explain the diversity of a savanna tree species in the Quaternary. **2017**, 119, 645-657	15
830	Inferring Demographic History Using Two-Locus Statistics. **2017**, 206, 1037-1048	17
829	Accuracy of Demographic Inferences from the Site Frequency Spectrum: The Case of the Yoruba Population. **2017**, 206, 439-449	46
828	Generalized Markov branching trees. **2017**, 49, 108-133	2
827	A permutation approach for inferring species networks from gene trees in polyploid complexes by minimising deep coalescences. **2017**, 8, 835-849	12
826	A null model for microbial diversification. **2017**, 114, E5414-E5423	5
825	Signatures of adaptive molecular evolution in American pikas (Ochotona princeps). **2017**, 98, 1156-1167	6
824	Molecular systematics of threadfin breams and relatives (Teleostei, Nemipteridae). **2017**, 46, 536-551	7
823	The Bacterial Sequential Markov Coalescent. **2017**, 206, 333-343	17
822	Molecular Population Genetics. **2017**, 205, 1003-1035	55
821	The impact of GC bias on phylogenetic accuracy using targeted enrichment phylogenomic data. **2017**, 111, 149-157	35
820	On the computational complexity of the maximum parsimony reconciliation problem in the duplication-loss-coalescence model. **2017**, 12, 6	4
819	Inferring Ancestral Recombination Graphs from Bacterial Genomic Data. **2017**, 205, 857-870	26

818	A hidden Markov model for latent temporal clustering with application to ideological alignment in the U.S. Supreme Court. **2017**, 110, 19-36	1
817	Genetics and the conservation of natural populations: allozymes to genomes. **2017**, 26, 420-430	141
816	Different kinds of genetic markers permit inference of Paleolithic and Neolithic expansions in humans. **2017**, 25, 360-365	4
815	WrightFisher-like models with constant population size on average. **2017**, 10, 1750078	1
814	Ancient genetic bottleneck and Plio-Pleistocene climatic changes imprinted the phylobiogeography of European Black Pine populations. **2017**, 136, 767-786	3
813	Genetic and linguistic histories in Central Asia inferred using approximate Bayesian computations. **2017**, 284,	7
812	Inferring Demographic History Using Genomic Data. **2017**, 511-537	9
811	Speciation below ground: Tempo and mode of diversification in a radiation of endogean ground beetles. **2017**, 26, 6053-6070	9
810	Forward and backward evolutionary processes and allele frequency spectrum in a cancer cell population. **2017**, 117, 43-50	13
809	Rigorous results for a population model with selection II: genealogy of the population. **2017**, 22,	11
808	Scalable Parallelization of a Markov Coalescent Genealogy Sampler. **2017**,	
807	Recombination-Driven Genome Evolution and Stability of Bacterial Species. **2017**, 207, 281-295	30
806	Using Genomic Location and Coalescent Simulation to Investigate Gene Tree Discordance in Medicago L. **2017**, 66, 934-949	8
805	Neutron clustering in Monte Carlo iterated-source calculations. **2017**, 49, 1211-1218	8
804	Recovering geography from a matrix of genetic distances. **2017**, 118, 48003	3
803	Inferring incomplete lineage sorting, duplications, transfers and losses with reconciliations. **2017**, 432, 1-13	25
802	Limit theorems for pure death processes coming down from infinity. **2017**, 54, 720-731	2
801	The comb representation of compact ultrametric spaces. **2017**, 9, 22-38	5

800	Molecular phylogenetic analyses reveal the importance of taxon sampling in cryptic diversity: Liolaemus nigroviridis and L. monticola (Liolaeminae) as focal species. **2017**, 90,	2
799	phylodyn: an R package for phylodynamic simulation and inference. **2017**, 17, 96-100	29
798	Different Lineage of Porcine Deltacoronavirus in Thailand, Vietnam and Lao PDR in 2015. **2017**, 64, 3-10	60
797	GeneEvolve: a fast and memory efficient forward-time simulator of realistic whole-genome sequence and SNP data. **2017**, 33, 294-296	10
796	Population expansion, current and past gene flow in Gould's petrel: implications for conservation. **2017**, 18, 105-115	4
795	Resampling: An improvement of importance sampling in varying population size models. **2017**, 114, 70-87	1
794	On the Moments of the Absorption Time of Kingman's Coalescent. **2017**, 19, 349-355	
793	Expected pairwise congruence among gene trees under the coalescent model. **2017**, 106, 144-150	3
792	Different historical backgrounds determine contrasting phylogeographical patterns in two co-distributed Erica species (Ericaceae) across the Strait of Gibraltar. **2017**, 185, 359-375	8
791	Identifying spatially concordant evolutionary significant units across multiple species through DNA barcodes: Application to the conservation genetics of the freshwater fishes of Java and Bali. **2017**, 12, 170-187	19
790	Effects of the Ordering of Natural Selection and Population Regulation Mechanisms on Wright-Fisher Models. **2017**, 7, 2095-2106	5
789	Second order behavior of the block counting process of beta coalescents. **2017**, 22,	1
788	Towards rapid population genetics forward-in-time simulations. **2017**,	1
787	Computational Methods in Microbial Population Genomics. **2017**, 3-29	2
786	Probabilistic models for the (sub)tree(s) of life. **2017**, 31,	9
785	Dirichlet approximation of equilibrium distributions in Cannings models with mutation. **2017**, 49, 927-959	5
784	A phase transition in excursions from infinity of the "fast" fragmentation-coalescence process. **2017**, 45,	2
783	World Dispersals and Genetic Diversity of Mankind. **2017**, 65-83	0

782	Epidemiology and Evolution of Fungal Pathogens in Plants and Animals. **2017**, 71-98	3
781	Phylogenetic and divergence time analysis of the Chelonoidis chilensis complex (Testudines: Testudinidae). **2017**, 4320, 487	1
780	Genomic divergence and cohesion in a species of pelagic freshwater bacteria. **2017**, 18, 794	8
779	Principal component analysis and the locus of the Fr�het mean in the space of phylogenetic trees. **2017**, 104, 901-922	17
778	Composite likelihood method for inferring local pedigrees. **2017**, 13, e1006963	15
777	Bayesian estimation of scaled mutation rate under the coalescent: a sequential Monte Carlo approach. **2017**, 18, 541	1
776	Biased phylodynamic inferences from analysing clusters of viral sequences. **2017**, 3, vex020	20
775	Modeling the Growth and Decline of Pathogen Effective Population Size Provides Insight into Epidemic Dynamics and Drivers of Antimicrobial Resistance. **2018**, 67, 719-728	38
774	SARS-CoV related Betacoronavirus and diverse Alphacoronavirus members found in western old-world. **2018**, 517, 88-97	44
773	Disentangling genetic structure for genetic monitoring of complex populations. **2018**, 11, 1149-1161	8
772	Ranked Tree Shapes, Nonrandom Extinctions, and the Loss of Phylogenetic Diversity. **2018**, 67, 1025-1040	6
771	Likelihood ratio development for mixed Y-STR profiles. **2018**, 35, 82-96	13
770	Unravelling the genetic differentiation among varieties of the Neotropical savanna tree Hancornia speciosa Gomes. **2018**, 122, 973-984	5
769	Genomic analyses identify multiple Asian origins and deeply diverged mitochondrial clades in inbred brown rats (). **2018**, 11, 718-726	8
768	Fluctuations uncover a distinct class of traveling waves. **2018**, 115, E3645-E3654	35
767	Origin, Genetic Diversity, and Population History of a Marine Population (Chanidae: Chanos chanos) in an Enclosed Lagoon in French Polynesia. **2018**, 72, 223-231	1
766	Neutral Theory: From Complex Population History to Natural Selection and Sociocultural Phenomena in Human Populations. **2018**, 35, 1304-1307	
765	Single and simultaneous binary mergers in Wright-Fisher genealogies. **2018**, 121, 60-71	3

764	Demographical expansion of Handroanthus ochraceus in the Cerrado during the Quaternary: implications for the genetic diversity of Neotropical trees. **2018**, 123, 561-577	9
763	A representation of exchangeable hierarchies by sampling from random real trees. **2018**, 172, 1-29	2
762	Bayesian non-parametric inference for $Lambda$-coalescents: Posterior consistency and a parametric method. **2018**, 24,	2
761	Ancient genomic variation underlies repeated ecological adaptation in young stickleback populations. **2018**, 2, 9-21	79
760	Combining allele frequency and tree-based approaches improves phylogeographic inference from natural history collections. **2018**, 27, 1012-1024	6
759	Phylodynamics of classical swine fever virus with emphasis on Ecuadorian strains. **2018**, 65, 782-790	8
758	Generative inference for cultural evolution. **2018**, 373,	24
757	Exploring Approximate Bayesian Computation for inferring recent demographic history with genomic markers in nonmodel species. **2018**, 18, 525-540	14
756	Mutation in populations governed by a Galton-Watson branching process. **2018**, 120, 52-61	1
755	Dynamics of widespread foot-and-mouth disease virus serotypes A, O and Asia-1 in southern Asia: A Bayesian phylogenetic perspective. **2018**, 65, 696-710	9
754	Is salinity an obstacle for biological invasions?. **2018**, 24, 2708-2720	21
753	Coalescent Processes with Skewed Offspring Distributions and Nonequilibrium Demography. **2018**, 208, 323-338	23
752	Evolutionary history of Mexican domesticated and wild Meleagris gallopavo. **2018**, 50, 19	6
751	Combinatorial L�y processes. **2018**, 28,	2
750	TreeTime: Maximum-likelihood phylodynamic analysis. **2018**, 4, vex042	392
749	Genealogical Properties of Subsamples in Highly Fecund Populations. **2018**, 172, 175-207	3
748	The road to evolutionary success: insights from the demographic history of an Amazonian palm. **2018**, 121, 183-195	18
747	A Review on Methods for Detecting SNP Interactions in High-Dimensional Genomic Data. **2018**, 15, 599-612	27

746	A non-zero variance of Tajima's estimator for two sequences even for infinitely many unlinked loci. **2018**, 122, 22-29		11
745	Phylogeny of the manta and devilrays (Chondrichthyes: mobulidae), with an updated taxonomic arrangement for the family. **2018**, 182, 50-75		68
744	Detecting hybridization by likelihood calculation of gene tree extra lineages given explicit models. **2018**, 9, 121-133		6
743	On the block counting process and the fixation line of the Bolthausen–Sznitman coalescent. *Stochastic Processes and Their Applications*, **2018**, 128, 939-962	1.1	2
742	An efficient algorithm for generating the internal branches of a Kingman coalescent. **2018**, 122, 57-66		1
741	Wright-Fisher diffusion bridges. **2018**, 122, 67-77		4
740	Microbial sequence typing in the genomic era. **2018**, 63, 346-359		31
739	Clustering and classification problems in genetics through U-statistics. **2018**, 88, 1882-1902		2
738	The role of climatic cycles and trans-Saharan migration corridors in species diversification: Biogeography of Psammophis schokari group in North Africa. **2018**, 118, 64-74		22
737	Weak atomic convergence of finite voter models toward Fleming–Viot processes. *Stochastic Processes and Their Applications*, **2018**, 128, 2463-2488	1.1	1
736	Effects of the Pleistocene on the mitochondrial population genetic structure and demographic history of the silky shark (Carcharhinus falciformis) in the western Atlantic Ocean. **2018**, 28, 213-227		21
735	Lines of Descent Under Selection. **2018**, 172, 156-174		2
734	Congruent phylogeographic patterns in a young radiation of live-bearing marine snakes: Pleistocene vicariance and the conservation implications of cryptic genetic diversity. **2018**, 24, 325-340		7
733	Bayesian molecular dating: opening up the black box. **2018**, 93, 1165-1191		83
732	Temporal patterns and processes of genetic differentiation of the Brachionus calyciflorus (Rotifera) complex in a subtropical shallow lake. **2018**, 807, 313-331		15
731	Resolving taxonomic turbulence and uncovering cryptic diversity in the musk turtles (Sternotherus) using robust demographic modeling. **2018**, 120, 1-15		12
730	On the genealogy and coalescence times of Bienaymé–Galton–Watson branching processes. **2018**, 34, 1-24		6
729	On the joint distribution of tree height and tree length under the coalescent. **2018**, 122, 46-56		4

728	The sequential loss of allelic diversity. **2018**, 50, 13-29	0
727	Bridging trees for posterior inference on ancestral recombination graphs. **2018**, 474, 20180568	2
726	Testing Hypotheses of Diversification in Panamanian Frogs and Freshwater Fishes Using Hierarchical Approximate Bayesian Computation with Model Averaging. **2018**, 10, 120	3
725	Linearization of the Kingman Coalescent. **2018**, 6, 82	2
724	Coalescent theory. **2018**, 1-3	
723	Extreme value statistics of mutation accumulation in renewing cell populations. **2018**, 98,	2
722	The IICR and the non-stationary structured coalescent: towards demographic inference with arbitrary changes in population structure. **2018**, 121, 663-678	16
721	Advancing Understanding of Amphibian Evolution, Ecology, Behavior, and Conservation with Massively Parallel Sequencing. **2018**, 211-254	8
720	Demographic histories and genetic diversity across pinnipeds are shaped by human exploitation, ecology and life-history. **2018**, 9, 4836	29
719	The Wright-Fisher site frequency spectrum as a perturbation of the coalescent's. **2018**, 124, 81-92	
718	The Site Frequency/Dosage Spectrum of Autopolyploid Populations. **2018**, 9, 480	2
717	Coalescent results for diploid exchangeable population models. **2018**, 23,	7
716	FastNet: Fast and Accurate Statistical Inference of Phylogenetic Networks Using Large-Scale Genomic Sequence Data. **2018**, 242-259	4
715	Genomics of Extinction. **2018**, 393-418	1
714	Utility of molecular-assisted alpha taxonomy of the genus Cystophora (Fucales, Phaeophyceae) from New Zealand and Australia. **2018**, 57, 374-384	2
713	Large-deviation properties of the extended Moran model. **2018**, 98,	1
712	Selection Mapping Identifies Loci Underpinning Autumn Dormancy in Alfalfa (). **2018**, 8, 461-468	4
711	Evolution of populations expanding on curved surfaces (a). **2018**, 123, 58005	8

710	Selecting among Alternative Scenarios of Human Evolution by Simulated Genetic Gradients. **2018**, 9,	3
709	Bayesian inference of ancestral dates on bacterial phylogenetic trees. **2018**, 46, e134	71
708	Coagulation and universal scaling limits for critical Galton□Watson processes. **2018**, 50, 504-542	0
707	Inference of species phylogenies from bi-allelic markers using pseudo-likelihood. **2018**, 34, i376-i385	18
706	Selection-Like Biases Emerge in Population Models with Recurrent Jackpot Events. **2018**, 210, 1053-1073	13
705	Rerooting Trees Increases Opportunities for Concurrent Computation and Results in Markedly Improved Performance for Phylogenetic Inference. **2018**,	2
704	Molecular evolution methods to study HIV-1 epidemics. **2018**, 13, 399-404	1
703	Plant Species Complexes as Models to Understand Speciation and Evolution: A Review of South American Studies. **2018**, 37, 54-80	32
702	Divergence Estimation in the Presence of Incomplete Lineage Sorting and Migration. **2019**, 68, 19-31	15
701	Which Model(s) Explain Biodiversity?. **2018**, 39-61	
700	Population genomics of bacterial host adaptation. **2018**, 19, 549-565	105
699	Multispecies coalescent analysis confirms standing phylogenetic instability in Hexapoda. **2018**, 31, 1623-1631	6
698	Comparative Co-Evolution Analysis Between the HA and NA Genes of Influenza A Virus. **2018**, 9, 1178122X18788328	10
697	Inference of population history using coalescent HMMs: review and outlook. **2018**, 53, 70-76	24
696	Locus-aware decomposition of gene trees with respect to polytomous species trees. **2018**, 13, 11	1
695	Exploring the Ecology of Deep-Sea Hydrothermal Vents in a Metacommunity Framework. **2018**, 5,	33
694	Bayesian inference of selection in the Wright-Fisher diffusion model. **2018**, 17,	1
693	Bayesian nonparametric inference beyond the Gibbs-type framework. **2018**, 45, 1062-1091	6

692	Fine-tuning of Approximate Bayesian Computation for human population genomics. **2018**, 53, 60-69		2
691	Disentangling the drivers of diversification in an imperiled group of freshwater fishes (Cyprinodontiformes: Goodeidae). **2018**, 18, 116		13
690	Parapatric genetic divergence among deep evolutionary lineages in the Mediterranean green crab, Carcinus aestuarii (Brachyura, Portunoidea, Carcinidae), accounts for a sharp phylogeographic break in the Eastern Mediterranean. **2018**, 18, 53		5
689	Genealogies and ages of cultural traits: An application of the theory of duality to the research on cultural evolution. **2018**, 123, 18-27		4
688	Immigrant and native? The case of the swamp foxtail Cenchrus purpurascens in Australia. **2018**, 24, 1169-1181		2
687	Geometry of the Sample Frequency Spectrum and the Perils of Demographic Inference. **2018**, 210, 665-682		15
686	Demographic and genetic approaches to study dispersal in wild animal populations: A methodological review. **2018**, 27, 3976-4010		62
685	The third moments of the site frequency spectrum. **2018**, 120, 16-28		4
684	Tuberculosis outbreak investigation using phylodynamic analysis. **2018**, 25, 47-53		13
683	Multi-locus data distinguishes between population growth and multiple merger coalescents. **2018**, 17,		10
682	Analysis of 3800-year-old Yersinia pestis genomes suggests Bronze Age origin for bubonic plague. **2018**, 9, 2234		72
681	What is Speciation Genomics? The roles of ecology, gene flow, and genomic architecture in the formation of species. **2018**, 124, 561-583		55
680	Phylogeography and species distribution modelling reveal the effects of the Pleistocene ice ages on an intertidal limpet from the south-eastern Pacific. **2018**, 45, 1751-1767		8
679	Ancient genomes reveal a high diversity of Mycobacterium leprae in medieval Europe. **2018**, 14, e1006997		70
678	Identifiability and Reconstructibility of Species Phylogenies Under a Modified Coalescent. **2019**, 81, 408-430		11
677	Coalescence times for three genes provide sufficient information to distinguish population structure from population size changes. **2019**, 78, 189-224		5
676	Random Recursive Trees and Preferential Attachment Trees are Random Split Trees. **2019**, 28, 81-99		8
675	The split-and-drift random graph, a null model for speciation. *Stochastic Processes and Their Applications*, **2019**, 129, 2010-2048	1.1	2

674	Applications of the Coalescent for the Evolutionary Analysis of Genetic Data. **2019**, 746-758	1
673	Linkage Disequilibrium, Recombination and Haplotype Structure. **2019**, 51-86	
672	Haplotype Estimation and Genotype Imputation. **2019**, 87-114	6
671	Mathematical Models in Population Genetics. **2019**, 115-20	0
670	Coalescent Theory. **2019**, 145-30	4
669	Paleomicrobiology: Diagnosis and Evolution of Ancient Pathogens. **2019**, 73, 639-666	20
668	TreeMerge: a new method for improving the scalability of species tree estimation methods. **2019**, 35, i417-i426	8
667	The influence of heterogeneous codon frequencies along sequences on the estimation of molecular adaptation. **2020**, 36, 430-436	1
666	Population Genomics and Phylogeography. **2019**, 237-265	1
665	Addressing the diversity of complex through integrative taxonomy. **2019**, 10, 9	5
664	The transition distribution of a sample from a Wright-Fisher diffusion with general small mutation rates. **2019**, 79, 2315-2342	1
663	The multifurcating skyline plot. **2019**, 5, vez031	7
662	Evolutionary games on isothermal graphs. **2019**, 10, 5107	12
661	From Coalescing Random Walks on a Torus to Kingman's Coalescent. **2019**, 177, 1172-1206	
660	"Any news?" Special issue in honor of Marcus Feldman's 75th birthday. **2019**, 129, 1-3	0
659	Chance, Variation and Shared Ancestry: Population Genetics After the Synthesis. **2019**, 52, 537-567	
658	The effect of undetected recombination on genealogy sampling and inference under an isolation-with-migration model. **2019**, 19, 1593-1609	3
657	Phylogeography of sand-burrowing amphipods (Haustoriidae) supports an ancient suture zone in the Gulf of Mexico. **2019**, 46, 2532-2547	6

656	A Service-Oriented Platform for Approximate Bayesian Computation in Population Genetics. **2019**, 26, 266-279	1
655	Consensus of All Solutions for Intractable Phylogenetic Tree Inference. **2021**, 18, 149-161	1
654	Influence of the tree prior and sampling scale on Bayesian phylogenetic estimates of the origin times of language families. **2019**, 4, 108-123	5
653	Comparison of Markov Chain Monte Carlo Software for the Evolutionary Analysis of Y-Chromosomal Microsatellite Data. **2019**, 17, 1082-1090	
652	Assessing biases in phylodynamic inferences in the presence of super-spreaders. **2019**, 50, 74	0
651	Phylogeography of the second plague pandemic revealed through analysis of historical Yersinia pestis genomes. **2019**, 10, 4470	55
650	An integrative taxonomic and phylogenetic approach reveals a complex of cryptic species in the □peppermint□shrimpLysmata wurdemanni sensu stricto. **2019**, 185, 1018-1038	4
649	Phylogeographic assessment of mtDNA paraphyly and the evolution of unisexuality in Calligrapha (Coleoptera: Chrysomelidae). **2019**, 57, 561-579	2
648	A Survey on Bayesian Nonparametric Learning. **2019**, 52, 1-36	7
647	Exact limits of inference in coalescent models. **2019**, 125, 75-93	3
646	New Divide-and-Conquer Techniques for Large-Scale Phylogenetic Estimation. **2019**, 3-21	
645	An invariants-based method for efficient identification of hybrid species from large-scale genomic data. **2019**, 19, 112	28
644	Joint Estimation of Pedigrees and Effective Population Size Using Markov Chain Monte Carlo. **2019**, 212, 855-868	3
643	Three prospective agents instead of one? Cryptic diversity of the biological control agent Psylliodes chalcomera. **2019**, 136, 103998	2
642	Phylogeographic and evolutionary history analyses of the warty crab Eriphia verrucosa (Decapoda, Brachyura, Eriphiidae) unveil genetic imprints of a late Pleistocene vicariant event across the Gibraltar Strait, erased by postglacial expansion and admixture among refugial lineages. **2019**, 19, 105	7
641	Estimating Epidemic Incidence and Prevalence from Genomic Data. **2019**, 36, 1804-1816	17
640	Highly polymorphic mitochondrial DNA and deceiving haplotypic differentiation: implications for assessing population genetic differentiation and connectivity. **2019**, 19, 92	5
639	Oceanographic barriers, divergence, and admixture: Phylogeography and taxonomy of two putative subspecies of short-finned pilot whale. **2019**, 28, 2886-2902	6

638	SANTA-SIM: simulating viral sequence evolution dynamics under selection and recombination. **2019** , 5, vez003	15
637	An average-case sublinear forward algorithm for the haploid Li and Stephens model. **2019**, 14, 11	1
636	Inferring Demography and Selection in Organisms Characterized by Skewed Offspring Distributions. **2019**, 211, 1019-1028	16
635	The origins and dispersal history of the trichaline net-winged beetles in Southeast Asia, Wallacea, New Guinea and Australia. **2019**, 185, 1079-1094	16
634	Robust model selection between population growth and multiple merger coalescents. **2019**, 311, 1-12	9
633	Fractional coalescent. **2019**, 116, 6244-6249	13
632	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. **2019**, 15, e1006650	1014
631	Detection of Quantitative Trait Loci From Genome-Wide Association Studies. **2019**, 40, 287-353	
630	The nested Kingman coalescent: Speed of coming down from infinity. **2019**, 29,	5
629	On the stationary distribution of the block counting process for population models with mutation and selection. **2019**, 474, 1049-1081	0
628	Ancient pathogen genomics as an´emerging tool for infectious disease´research. **2019**, 20, 323-340	76
627	Incomplete estimates of genetic diversity within species: Implications for DNA barcoding. **2019**, 9, 2996-3010	31
626	The height of the latest common ancestor of two randomly chosen leaves from a (sub-)critical Galton–Watson tree. **2019**, 106, 28-36	
625	Cooperative hierarchical Dirichlet processes: Superposition vs. maximization. **2019**, 271, 43-73	2
624	A Computational Approach for Modeling the Allele Frequency Spectrum of Populations with Arbitrarily Varying Size. **2019**, 17, 635-644	1
623	Bayesian Estimation of Population Size Changes by Sampling Tajima's Trees. **2019**, 213, 967-986	3
622	A spatio-temporal point process model for particle growth. **2019**, 56, 23-38	
621	Recovering the Brownian coalescent point process from the Kingman coalescent by conditional sampling. **2019**, 25,	1

620	An ancestral process with selection in an ecological community. **2019**, 466, 128-144	0
619	A Backward View of Genetic Drift: Coalescence. **2019**, 129-153	
618	A mathematical formalism for natural selection with arbitrary spatial and genetic structure. **2019**, 78, 1147-1210	12
617	The stationary distribution of a sample from the Wright-Fisher diffusion model with general small mutation rates. **2019**, 78, 1211-1224	3
616	Signatures of selection in the human antibody repertoire: Selective sweeps, competing subclones, and neutral drift. **2019**, 116, 1261-1266	38
615	Extreme Lewontin's Paradox in Ubiquitous Marine Phytoplankton Species. **2019**, 36, 4-14	17
614	Metapop: An individual-based model for simulating the evolution of tree populations in spatially and temporally heterogeneous landscapes. **2019**, 19, 296-305	2
613	Diversification of the widespread neotropical frog Physalaemus cuvieri in response to Neogene-Quaternary geological events and climate dynamics. **2019**, 132, 67-80	19
612	Distribution theory for hierarchical processes. **2019**, 47,	26
611	A Bayesian approach to Mendelian randomisation with dependent instruments. **2019**, 38, 985-1001	3
610	The Influence of Protein Stability on Sequence Evolution: Applications to Phylogenetic Inference. **2019**, 1851, 215-231	6
609	Identifiability of Phylogenetic Parameters from k-mer Data Under the Coalescent. **2019**, 81, 431-451	1
608	A new combinatorial representation of the additive coalescent. **2019**, 54, 340-370	1
607	Efficiently inferring the demographic history of many populations with allele count data. **2020**, 115, 1472-1487	33
606	First-order effect of frequency-dependent selection on fixation probability in an age-structured population with application to a public goods game. **2020**, 133, 80-96	5
605	Coagulation-transport equations and the nested coalescents. **2020**, 176, 77-147	3
604	Fossil Calibration of Mitochondrial Phylogenetic Relationships of North American Pine Martens, Martes, Suggests an Older Divergence of M. americana and M. caurina than Previously Hypothesized. **2020**, 27, 535-548	2
603	Evolutionary dynamics of Ceratonova species (Cnidaria: Myxozoa) reveal different host adaptation strategies. **2020**, 78, 104081	3

602	Genealogical distances under low levels of selection. **2020**, 131, 2-11	
601	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. **2020**, 29, 1596-1610	33
600	Sequential Monte Carlo with transformations. **2020**, 30, 663-676	3
599	Genome-wide sequence information reveals recurrent hybridization among diploid wheat wild relatives. **2020**, 102, 493-506	26
598	A practical introduction to sequentially Markovian coalescent methods for estimating demographic history from genomic data. **2020**, 10, 579-589	22
597	Genetic variability and demographic history of Anguilla mossambica (Peters, 1852) from continental Africa and Madagascar. **2020**, 96, 1251-1259	1
596	Local fluctuations of genetic processes defined on two time scales, with applications to effective size estimation. **2020**, 131, 79-99	1
595	Phylogeographic pattern and population structure of the Persian stone loach, Oxynoemacheilus persa (Heckel 1847) (family: Nemacheilidae) in southern Iran with implications for conservation. **2020**, 103, 77-88	3
594	Molecular phylogeny of sturgeon mimiviruses and Bayesian hierarchical modeling of their effect on wild Lake Sturgeon (Acipenser fulvescens) in Central Canada. **2020**, 84, 104491	1
593	Phylogenetics and Systematics in a Nutshell. **2020**, 81-112	1
592	Considering Genomic Scans for Selection as Coalescent Model Choice. **2020**, 12, 871-877	1
591	Phylogenetic and phylodynamic analyses of SARS-CoV-2. **2020**, 287, 198098	56
590	Machine learning based imputation techniques for estimating phylogenetic trees from incomplete distance matrices. **2020**, 21, 497	8
589	Molecular Clocks without Rocks: New Solutions for Old Problems. **2020**, 36, 845-856	15
588	Inference of population admixture network from local gene genealogies: a coalescent-based maximum likelihood approach. **2020**, 36, i326-i334	2
587	Integrative taxonomic investigation of Petaurus breviceps (Marsupialia: Petauridae) reveals three distinct species. **2020**,	13
586	How to choose sets of ancestry informative markers: A supervised feature selection approach. **2020**, 46, 102259	7
585	Testing for population decline using maximal linkage disequilibrium blocks. **2020**, 134, 171-181	1

584	Mitochondrial DNA diversity: Insight into population diversity, structure and demographic history of Penaeus monodon along the entire coastal region of India. **2020**, 51, 4649-4680	1
583	Sampling and summarizing transmission trees with multi-strain infections. **2020**, 36, i362-i370	0
582	Applied phyloepidemiology: Detecting drivers of pathogen transmission from genomic signatures using density measures. **2020**, 13, 1513-1525	2
581	Investigation of spp. in brazilian mammals with emphasis on rodents and bats from the Atlantic Forest. **2020**, 13, 80-89	6
580	Effects of niche overlap on coexistence, fixation and invasion in a population of two interacting species. **2020**, 7, 192181	4
579	Variola virus genome sequenced from an eighteenth-century museum specimen supports the recent origin of smallpox. **2020**, 375, 20190572	7
578	Evolutionary Genomics of High Fecundity. **2020**, 54, 213-236	4
577	Foliose species of New Zealand red algae: diversity in the genus Tsengia (Tsengiaceae, Halymeniales), including T. northlandica sp. nov.. **2020**, 59, 437-448	3
576	A test of Generalized Bayesian dating: A new linguistic dating method. **2020**, 15, e0236522	2
575	Mitochondrial genomics reveals the evolutionary history of the porpoises (Phocoenidae) across the speciation continuum. **2020**, 10, 15190	7
574	Continual Learning for Infinite Hierarchical Change-Point Detection. **2020**,	1
573	Determinants of dengue virus dispersal in the Americas. **2020**, 6, veaa074	1
572	Horseshoe-based Bayesian nonparametric estimation of effective population size trajectories. **2020**, 76, 677-690	10
571	Phylogenetic tree building in the genomic age. **2020**, 21, 428-444	76
570	Measuring the external branches of a Kingman tree: A discrete approach. **2020**, 134, 92-105	1
569	ipcoal: an interactive Python package for simulating and analyzing genealogies and sequences on a species tree or network. **2020**, 36, 4193-4196	3
568	Coalescent Models of Demographic History: Application to Plant Domestication. **2020**, 1	
567	Introductions and early spread of SARS-CoV-2 in the New York City area. **2020**, 369, 297-301	244

566	Maximum Likelihood Estimation of Species Trees from Gene Trees in the Presence of Ancestral Population Structure. **2020**, 12, 3977-3995	3
565	Current State and Perspectives in Population Genomics of the Common Bean. **2020**, 9,	8
564	Developments in coalescent theory from single loci to chromosomes. **2020**, 133, 56-64	1
563	Coalescence modeling of intrainfection populations allows estimation of infection parameters in wild populations. **2020**, 117, 4273-4280	4
562	The genetic legacy of extreme exploitation in a polar vertebrate. **2020**, 10, 5089	4
561	Using a coalescent approach to assess gene flow and effective population size of Acrocomia aculeata (Jacq.) Lodd. Ex Mart. in the Brazilian Atlantic Forest. **2020**, 16, 1	4
560	Scale-invariant topology and bursty branching of evolutionary trees emerge from niche construction. **2020**, 117, 7879-7887	7
559	Space is the Place: Effects of Continuous Spatial Structure on Analysis of Population Genetic Data. **2020**, 215, 193-214	26
558	A Simulation Study to Examine the Information Content in Phylogenomic Data Sets under the Multispecies Coalescent Model. **2020**, 37, 3211-3224	4
557	On the minimum value of the Colless index and the bifurcating trees that achieve it. **2020**, 80, 1993-2054	7
556	Insights from a general, full-likelihood Bayesian approach to inferring shared evolutionary events from genomic data: Inferring shared demographic events is challenging. **2020**, 74, 2184-2206	3
555	Correction to: The performance of coalescent-based species tree estimation methods under models of missing data. **2020**, 21, 133	1
554	Statistical tools for seed bank detection. **2020**, 132, 1-15	3
553	STELAR: a statistically consistent coalescent-based species tree estimation method by maximizing triplet consistency. **2020**, 21, 136	8
552	Emerging Frontiers in the Study of Molecular Evolution. **2020**, 88, 211-226	3
551	A comparative approach for species delimitation based on multiple methods of multi-locus DNA sequence analysis: A case study of the genus Giraffa (Mammalia, Cetartiodactyla). **2020**, 15, e0217956	14
550	From Summary Statistics to Gene Trees: Methods for Inferring Positive Selection. **2020**, 36, 243-258	8
549	Evaluation of haplotype callers for next-generation sequencing of viruses. **2020**, 82, 104277	20

548	From the Triangle to the Rhombus: Exploration, Systematization, and Material for a Genealogical Theory. **2021**, 46, 363-379	
547	Consistency of SVDQuartets and Maximum Likelihood for Coalescent-Based Species Tree Estimation. **2021**, 70, 33-48	7
546	The impact of genetic diversity statistics on model selection between coalescents. **2021**, 156, 107055	3
545	Multiple Merger Genealogies in Outbreaks of Mycobacterium tuberculosis. **2021**, 38, 290-306	2
544	Phylogeographic Approaches to Characterize the Emergence of Plant Pathogens. **2021**, 111, 68-77	1
543	Another stripe on the tiger makes no difference? Unexpected diversity in the widespread tiger tarantula Davus pentaloris (Araneae: Theraphosidae: Theraphosinae). **2021**, 192, 75-104	1
542	Assessing Uncertainty in the Rooting of the SARS-CoV-2 Phylogeny. **2021**, 38, 1537-1543	19
541	Plitvice Lakes National park harbors ancient, yet endangered diversity of trout (genus Salmo). **2021** , 37, 20-37	3
540	Bayesian Inference of Species Trees using Diffusion Models. **2021**, 70, 145-161	4
539	Asymptotic expansions and precise deviations in the Kingman coalescent. **2021**, 26,	
538	Molecular epidemiology of foodborne pathogens. **2021**, 47-62	0
537	Visualizing population structure with variational autoencoders. **2021**, 11,	10
536	Sweeps in time: leveraging the joint distribution of branch lengths.	0
535	Moment-based approximations for the Wright-Fisher model of population dynamics under natural selection at two linked loci.	0
534	Positive Selection in Human Populations: Practical Aspects and Current Knowledge. **2021**, 29-65	1
533	Model design for non-parametric phylodynamic inference and applications to pathogen surveillance. **2021**,	0
532	Cancer phylogenetics using single-cell RNA-seq data.	3
531	Coalescent Models. **2021**, 3-30	

530	Comparing Methods for Species Tree Estimation with Gene Duplication and Loss. **2021**, 106-117	0
529	Geospatial distributions reflect temperatures of linguistic features. **2021**, 7,	3
528	Challenges in estimating virus divergence times in short epidemic timescales with special reference to the evolution of SARS-CoV-2 pandemic. **2021**, 44, e20200254	1
527	Fixation probabilities in evolutionary dynamics under weak selection. **2021**, 82, 14	10
526	FASTRAL: Improving scalability of phylogenomic analysis. **2021**,	1
525	Fixation probabilities in graph-structured populations under weak selection. **2021**, 17, e1008695	5
524	Comparative genomics of MRSA strains from human and canine origins reveals similar virulence gene repertoire. **2021**, 11, 4724	5
523	The use of statistical phylogenetics in virology. **2021**, 11, 42-56	
522	Comparing Methods for Species Tree Estimation With Gene Duplication and Loss.	
521	Dissecting Incongruence between Concatenation- and Quartet-Based Approaches in Phylogenomic Data. **2021**, 70, 997-1014	2
520	A unified genealogy of modern and ancient genomes.	4
519	The genomic revolution and species delimitation in birds (and other organisms): Why phenotypes should not be overlooked. **2021**, 138,	6
518	Reconstructing the Lineage Histories and Differentiation Trajectories of Individual Cancer Cells in Myeloproliferative Neoplasms. **2021**, 28, 514-523.e9	42
517	Theoretical Advances in Species–Area Relationship Research. **2021**, 155-318	
516	The effect of variability in payoffs on average abundance in two-player linear games under symmetric mutation. **2021**, 513, 110569	2
515	Phylogeny of cercosporoid fungi (Mycosphaerellaceae, Mycosphaerellales) from Hawaii and New York reveals novel species within the Cercospora beticola complex. **2021**, 20, 261-287	2
514	Large-scale inference of correlation among mixed-type biological traits with phylogenetic multivariate probit models. **2021**, 15,	4
513	Traces of Late Bronze and Early Iron Age Mongolian Horse Mitochondrial Lineages in Modern Populations. **2021**, 12,	0

512	Minimal clustering and species delimitation based on multi-locus alignments vs SNPs: the case of the Seriphium plumosum L. complex (Gnaphalieae: Asteraceae).	
511	The SpeciesArea Relationships of Ecological Neutral Theory. **2021**, 259-288	1
510	Ultraconserved Elements Improve the Resolution of Difficult Nodes within the Rapid Radiation of Neotropical Sigmodontine Rodents (Cricetidae: Sigmodontinae). **2021**, 70, 1090-1100	2
509	An instantaneous coalescent method insensitive to population structure. **2021**, 48, 219-224	1
508	Phylogeographic analysis of Thyrsites atun (Perciformes: Gempylidae) reveals connectivity between fish from South Africa and Chile. **2021**, 17, 401-413	1
507	RF-Net 2: Fast Inference of Virus Reassortment and Hybridization Networks.	
506	Circumpolar phylogeography and demographic history of beluga whales reflect past climatic fluctuations. **2021**, 30, 2543-2559	3
505	Nonparametric coalescent inference of mutation spectrum history and demography. **2021**, 118,	5
504	References. **2021**, 668-722	
503	The germline mutational process in rhesus macaque and its implications for phylogenetic dating. **2021**, 10,	6
502	A phylogenetic approach for weighting genetic sequences. **2021**, 22, 285	0
501	The minimal observable clade size of exchangeable coalescents. **2021**, 35,	1
500	Diversity and selection of SARS-CoV-2 minority variants in the early New York City outbreak.	1
499	Robust detection of natural selection using a probabilistic model of tree imbalance.	
498	Inferring Population Size Histories using Coalescent Hidden Markov Models with TMRCA and Total Branch Length as Hidden States.	0
497	GSpace: an exact coalescence simulator of recombining genomes under isolation by distance. **2021**,	1
496	Universality of evolutionary dynamics with arbitrary demography.	0
495	A marginal habitat, but not a sink: Ecological genetics reveal a diversification hotspot for marine invertebrates in the brackish Baltic Sea.	

494	Population genetics of polymorphism and divergence in rapidly evolving populations.	
493	Identifying loci under selection via explicit demographic models. **2021**, 21, 2719-2737	2
492	wQFM: Highly Accurate Genome-scale Species Tree Estimation from Weighted Quartets. **2021**,	2
491	fastsimcoal2: demographic inference under complex evolutionary scenarios. **2021**,	14
490	An efficient coalescent epoch model for Bayesian phylogenetic inference.	0
489	Bayesian-Weighted Triplet and Quartet Methods for Species Tree Inference. **2021**, 83, 93	4
488	Epidemiological dynamics of SARS-CoV-2 VOC Gamma in Rio de Janeiro, Brazil.	2
487	Generalizing Bayesian phylogenetics to infer shared evolutionary events.	
486	Addressing alpine plant phylogeography using integrative distributional, demographic and coalescent modeling.. **2022**, 132, 5-19	1
485	Coalescence: The Sharing of Ancestry of Alleles. 2, 1-7	
484	A New Likelihood-based Test for Natural Selection.	0
483	Bayesian inference of clonal expansions in a dated phylogeny.	0
482	Tracking the transition to agriculture in Southern Europe through ancient DNA analysis of dental calculus. **2021**, 118,	2
481	The infinite alleles model revisited: a Gibbs sampling approach.	
480	Multispecies coalescent and its applications to infer species phylogenies and cross-species gene flow.. **2021**, 8, nwab127	2
479	Phylogenomics reveals multiple introductions and early spread of SARS-CoV-2 into Peru. **2021**, 93, 5961-5968	6
478	Opportunities and challenges of macrogenetic studies. **2021**, 22, 791-807	6
477	Site Pattern Probabilities Under the Multispecies Coalescent and a Relaxed Molecular Clock: Theory and Applications.	

476	Strong neutral sweeps occurring during a population contraction.	0
475	Principles of seed banks and the emergence of complexity from dormancy. **2021**, 12, 4807	9
474	ProteinEvolverABC: Coestimation of Recombination and Substitution Rates in Protein Sequences by approximate Bayesian computation. **2021**,	0
473	Inference of gene flow in the process of speciation: Efficient maximum-likelihood implementation of a generalised isolation-with-migration model. **2021**, 140, 1-15	0
472	Genealogical structure changes as range expansions transition from pushed to pulled. **2021**, 118,	1
471	Multispecies Coalescent: Theory and Applications in Phylogenetics. **2021**, 52,	2
470	Sweeps in time: leveraging the joint distribution of branch lengths. **2021**, 219,	0
469	DISCO: Species Tree Inference using Multi-Copy gene family Tree Decomposition. **2021**,	2
468	Variational inference using approximate likelihood under the coalescent with recombination. **2021**, 31, 2107-2119	0
467	A geometric representation of fragmentation processes on stable trees. **2021**, 49,	0
466	Divergence in the Aquilegia ecalcarata complex is correlated with geography and climate oscillations: Evidence from plastid genome data. **2021**, 30, 5796-5813	2
465	Sweepstake reproductive success and collective dispersal produce chaotic genetic patchiness in a broadcast spawner. **2021**, 7, eabj4713	3
464	Efficient ancestry and mutation simulation with msprime 1.0.	0
463	Exact site frequency spectra of neutrally evolving tumors: A transition between power laws reveals a signature of cell viability. **2021**, 142, 67-90	1
462	The role of Sahara highlands in the diversification and desert colonization of the Bosc's fringe-toed lizard. **2021**, 48, 2891	0
461	From the Strait of Gibraltar to northern Europe: Pleistocene refugia and biogeographic history of heather (Calluna vulgaris, Ericaceae).	1
460	The distribution of waiting distances in ancestral recombination graphs. **2021**, 141, 34-43	0
459	Autosomal, sex-linked and mitochondrial loci resolve evolutionary relationships among wrens in the genus Campylorhynchus. **2021**, 163, 107242	1

458	Simulations of Human Dispersal and Genetic Diversity. **2021**, 231-256	
457	Stochastic Model for the Spread of the COVID-19 Virus. **2021**, 12, 24-31	2
456	Estimation of Species Trees.	1
455	Interpreting genetic variability: the effects of shared evolutionary history. **1996**, 197, 25-40; discussion 40-50	7
454	Basics of Population Genetics: Quantifying Neutral and Adaptive Genetic Variation for Landscape Genetic Studies. 35-57	3
453	Landscapes and Plant Population Genetics. 181-198	1
452	The Multispecies Coalescent. **2019**, 219-246	8
451	Identifiability Issues in Phylogeny-Based Detection of Horizontal Gene Transfer. **2006**, 215-229	4
450	Evolutionary Phylogenetic Networks: Models and Issues. **2010**, 125-158	48
449	A Population Genomics Lexicon. **2020**, 2090, 3-17	3
448	Coalescent Simulation with msprime. **2020**, 2090, 191-230	4
447	Advances in Urn Models during the Past Two Decades. **1997**, 203-257	46
446	Recent Results for the Stepping Stone Model. **1987**, 73-83	5
445	Phylogenetic Analysis on the Edge: The Application of Cladistic Techniques at the Population Level. **1994**, 154-174	2
444	Patterns of Polymorphism and Between Species Divergence in the Enzymes of Central Metabolism. **1994**, 18-28	3
443	Beanbag Genetics and After. **1993**, 7-29	6
442	Applications of Metropolis-Hastings Genealogy Sampling. **1997**, 183-192	3
441	The Structured Coalescent. **1997**, 231-255	23

440	An Ancestral Recombination Graph. **1997**, 257-270	119
439	Human Demography and the Time Since Mitochondrial Eve. **1997**, 107-131	7
438	Coalescent Theory and Its Applications in Population Genetics. **1999**, 45-79	8
437	Origin and Evolution of Human Immunodeficiency Viruses. **2015**, 587-611	3
436	A Not-So-Long Introduction to Computational Molecular Evolution. **2019**, 1910, 71-117	3
435	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. **2020**, 120-135	5
434	Dual Random Fragmentation and Coagulation and an Application to the Genealogy of Yule Processes. **2004**, 295-308	6
433	The role of molecular genetics in speciation studies. **1998**, 131-156	18
432	Inference Methods for Multiple Merger Coalescents. **2016**, 347-371	3
431	Coestimation of Gene Trees and Reconciliations Under a Duplication-Loss-Coalescence Model. **2017**, 196-210	7
430	Inferring Local Genealogies on Closely Related Genomes. **2017**, 10562, 213-231	1
429	Exact Computation of Coalescent Likelihood under the Infinite Sites Model. **2009**, 209-220	2
428	A Genealogical Description of the Infinitely-Many Neutral Alleles Model. **1987**, 27-35	2
427	Homogenenous Multitype Fragmentations. **2008**, 161-183	5
426	Population Genetics Theory - The Past and the Future. **1990**, 177-227	72
425	Integration of Evolutionary Theory into Cancer Biology and Caspase Signaling. **2019**, 131-155	1
424	Human Evolutionary Genetics. **2015**, 289-296	1
423	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. **2021**, 28, 452-468	8

422	Molecular Evolution. **2014**,	146
421	Maximum likelihood estimation of population growth rates based on the coalescent. **1998**, 149, 429-34	486
420	Inference of population history using a likelihood approach. **1998**, 149, 1539-46	113
419	Simultaneous estimation of all the parameters of a stepwise mutation model. **1998**, 150, 487-97	32
418	Genealogical inference from microsatellite data. **1998**, 150, 499-510	203
417	The ancestry of a sample of sequences subject to recombination. **1999**, 151, 1217-28	37
416	Gustave Malécot, 1911-1998. Population genetics founding father. **1999**, 152, 477-84	8
415	Maximum-likelihood estimation of migration rates and effective population numbers in two populations using a coalescent approach. **1999**, 152, 763-73	764
414	Gene genealogies in geographically structured populations. **1999**, 152, 797-806	15
413	Estimation of past demographic parameters from the distribution of pairwise differences when the mutation rates vary among sites: application to human mitochondrial DNA. **1999**, 152, 1079-89	1146
412	Pattern of nucleotide substitution and rate heterogeneity in the hypervariable regions I and II of human mtDNA. **1999**, 152, 1103-10	182
411	Nonequilibrium migration in human history. **1999**, 153, 1863-71	182
410	The probability of duplicate gene preservation by subfunctionalization. **2000**, 154, 459-73	1145
409	Estimation of population parameters and recombination rates from single nucleotide polymorphisms. **2000**, 154, 931-42	243
408	The coalescent with gene conversion. **2000**, 155, 451-62	93
407	Detecting bottlenecks and selective sweeps from DNA sequence polymorphism. **2000**, 155, 981-7	136
406	Consequences of recombination on traditional phylogenetic analysis. **2000**, 156, 879-91	415
405	Maximum likelihood estimation of recombination rates from population data. **2000**, 156, 1393-401	151

404	Origins of the coalescent. 1974-1982. **2000**, 156, 1461-3	132
403	Distinguishing migration from isolation: a Markov chain Monte Carlo approach. **2001**, 158, 885-96	1031
402	DNA variation at the rp49 gene region of Drosophila simulans: evolutionary inferences from an unusual haplotype structure. **2001**, 158, 1147-55	94
401	Estimation of admixture proportions: a likelihood-based approach using Markov chain Monte Carlo. **2001**, 158, 1347-62	93
400	Mutations as missing data: inferences on the ages and distributions of nonsynonymous and synonymous mutations. **2001**, 159, 401-11	17
399	Gene genealogies in a metapopulation. **2001**, 159, 893-905	209
398	Estimating recombination rates from population genetic data. **2001**, 159, 1299-318	222
397	Estimating the total number of alleles using a sample coverage method. **2001**, 159, 1365-73	21
396	Inferring population history from microsatellite and enzyme data in serially introduced cane toads, Bufo marinus. **2001**, 159, 1671-87	120
395	Recombination, balancing selection and phylogenies in MHC and self-incompatibility genes. **2001**, 159, 1833-44	56
394	A coalescent-based method for detecting and estimating recombination from gene sequences. **2002**, 160, 1231-41	530
393	Estimation of effective population size of HIV-1 within a host: a pseudomaximum-likelihood approach. **2002**, 160, 1283-93	55
392	Frequentist estimation of coalescence times from nucleotide sequence data using a tree-based partition. **2002**, 161, 447-59	65
391	Recombination and gene conversion in a 170-kb genomic region of Arabidopsis thaliana. **2002**, 161, 1269-78	56
390	Estimating mutation parameters, population history and genealogy simultaneously from temporally spaced sequence data. **2002**, 161, 1307-20	744
389	The matrix coalescent and an application to human single-nucleotide polymorphisms. **2002**, 161, 1641-50	39
388	A genealogical interpretation of linkage disequilibrium. **2002**, 162, 987-91	137
387	Genetic effective size is three orders of magnitude smaller than adult census size in an abundant, Estuarine-dependent marine fish (Sciaenops ocellatus). **2002**, 162, 1329-39	160

386	A coalescent model of recombination hotspots. **2003**, 164, 407-17	16
385	The extent of linkage disequilibrium and haplotype sharing around a polymorphic site. **2003**, 165, 437-44	17
384	Modeling linkage disequilibrium and identifying recombination hotspots using single-nucleotide polymorphism data. **2003**, 165, 2213-33	652
383	Influence of Spatial and Temporal Heterogeneities on the Estimation of Demographic Parameters in a Continuous Population Using Individual Microsatellite Data. **2004**, 166, 1081-1092	5
382	The Effect of Selection on Genealogies. **2004**, 166, 1115-1131	14
381	The limits of theoretical population genetics. **2005**, 169, 1-7	32
380	Molecular epidemiological study on Infectious Pancreatic Necrosis Virus isolates from aquafarms in Scotland over three decades. **2018**, 99, 1567-1581	10
379	Genealogical typing of Neisseria meningitidis. **2009**, 155, 3176-3186	31
378	On the importance of skewed offspring distributions and background selection in viral population genetics.	3
377	Population structure and coalescence in pedigrees: comparisons to the structured coalescent and a framework for inference.	2
376	Recombination-driven genome evolution and stability of bacterial species.	1
375	Taming the Late Quaternary phylogeography of the Eurasiatic wild ass through ancient and modern DNA.	1
374	Composite Likelihood Method for Inferring Local Pedigrees.	1
373	Signatures of Selection in the Human Antibody Repertoire: Selective Sweeps, Competing Subclones, and Neutral Drift.	5
372	TreeTime: maximum likelihood phylodynamic analysis.	2
371	Multiple merger genealogies in outbreaks ofMycobacterium tuberculosis.	2
370	Evolution, geographic spreading, and demographic distribution of Enterovirus D68.	1
369	Hospital outbreak of carbapenem-resistant Enterobacteriales associated with an OXA-48 plasmid carried mostly byEscherichia coliST399.	5

368	Joint nonparametric coalescent inference of mutation spectrum history and demography.	3
367	Assessing uncertainty in the rooting of the SARS-CoV-2 phylogeny.	9
366	The germline mutational process in rhesus macaque and its implications for phylogenetic dating.	3
365	Numerical simulation of the two-locus Wright-Fisher stochastic differential equation with application to approximating transition probability densities.	1
364	Phylogenomics reveals multiple introductions and early spread of SARS-CoV-2 into Peru.	7
363	Exact decoding of the sequentially Markov coalescent.	1
362	Relative time constraints improve molecular dating.	4
361	Simulating trajectories and phylogenies from population dynamics models with TiPS.	2
360	PipeMaster: inferring population divergence and demographic history with approximate Bayesian computation and supervised machine-learning in R.	2
359	Genealogical structure changes as range expansions transition from pushed to pulled.	1
358	Modeling the growth and decline of pathogen effective population size provides insight into epidemic dynamics and drivers of antimicrobial resistance.	0
357	A Likelihood-Free Inference Framework for Population Genetic Data using Exchangeable Neural Networks.	23
356	Efficiently inferring the demographic history of many populations with allele count data.	14
355	Recent demographic histories and genetic diversity across pinnipeds are shaped by anthropogenic interactions and mediated by ecology and life-history.	2
354	Phase-type distributions in population genetics.	1
353	Bayesian inference of ancestral dates on bacterial phylogenetic trees.	0
352	Modern wolves trace their origin to a late Pleistocene expansion from Beringia.	2
351	Genetic draft and valley crossing.	1

350	Why panmictic bacteria are rare.	10
349	Inferring demography and selection in organisms characterized by skewed offspring distributions.	1
348	The global diversity of the major parasitic nematodeHaemonchus contortusis shaped by human intervention and climate.	3
347	BEAST 2.5: An Advanced Software Platform for Bayesian Evolutionary Analysis.	12
346	Consistency of SVDQuartets and Maximum Likelihood for Coalescent-based Species Tree Estimation.	1
345	A conservative approach for species delimitation based on multi-locus DNA sequences: a case study of the genus Giraffa (Mammalia, Cetartiodactyla).	1
344	Space is the Place: Effects of Continuous Spatial Structure on Analysis of Population Genetic Data.	4
343	Insights from a general, full-likelihood Bayesian approach to inferring shared evolutionary events from genomic data: Inferring shared demographic events is challenging.	1
342	Coalescent models at small effective population sizes and population declines are positively misleading.	2
341	Machine learning based imputation techniques for estimating phylogenetic trees from incomplete distance matrices.	1
340	Locally adaptive Bayesian birth-death model successfully detects slow and rapid rate shifts.	3
339	Trans-specific Mhc polymorphism and the origin of species in primates. **1993**, 22, 57-64	43
338	Scalable Statistical Introgression Mapping Using Approximate Coalescent-Based Inference. **2019**,	1
337	Population Genetics and Inference of Ecosystem History. **2006**, 417-432	4
336	Power laws for family sizes in a duplication model. **2005**, 33,	11
335	Beta-coalescents and continuous stable random trees. **2007**, 35,	59
334	Small-time behavior of beta coalescents. **2008**, 44,	47
333	Coalescence in a random background. **2004**, 14,	36

332	The asymptotic distribution of the length of Beta-coalescent trees. **2012**, 22,	21
331	Mutations on a random binary tree with measured boundary. **2018**, 28,	1
330	Trees within trees: simple nested coalescents. **2018**, 23,	8
329	Random self-similar trees: A mathematical theory of Horton laws. **2020**, 17,	5
328	Statistical Inference for the Evolutionary History of Cancer Genomes. **2020**, 35,	2
327	A transition function expansion for a diffusion model with selection. **2000**, 10,	20
326	Genealogical processes for Fleming-Viot models with selection and recombination. **1999**, 9,	80
325	The representation of composition structures. **1997**, 25,	32
324	Standard stochastic coalescence with sum kernels. **2006**, 11,	1
323	Coalescent processes derived from some compound Poisson population models. **2011**, 16,	6
322	Brownian Excursion Conditioned on Its Local Time. **1998**, 3,	14
321	Time-Space Analysis of the Cluster-Formation in Interacting Diffusions. **1996**, 1,	11
320	Alpha-Stable Branching and Beta-Coalescents. **2005**, 10,	59
319	Representation Theorems for Interacting Moran Models, Interacting Fisher-Wrighter Diffusions and Applications. **2005**, 10,	14
318	Fragmentation of Ordered Partitions and Intervals. **2006**, 11,	5
317	On the Number of Collisions in $Lambda$-Coalescents. **2007**, 12,	26
316	Asymptotics of the Allele Frequency Spectrum Associated with the Bolthausen-Sznitman Coalescent. **2008**, 13,	25
315	Coalescent processes in subdivided populations subject to recurrent mass extinctions. **2009**, 14,	13

314	A New Model for Evolution in a Spatial Continuum. **2010**, 15,	38
313	On the Total External Length of the Kingman Coalescent. **2011**, 16,	21
312	The Entrance Boundary of the Multiplicative Coalescent. **1998**, 3,	18
311	Two Coalescents Derived from the Ranges of Stable Subordinators. **2000**, 5,	14
310	Coalescents with Simultaneous Multiple Collisions. **2000**, 5,	72
309	Post-data inference of coalescence times and segregating-site distribution in a two-island model with symmetric migration. **2001**, 33, 600-616	1
308	A convergence theorem for markov chains arising in population genetics and the coalescent with selfing. **1998**, 30, 493-512	56
307	Coalescent results for two-sex population models. **1998**, 30, 513-520	20
306	Solving the Fisher-Wright and coalescence problems with a discrete Markov chain analysis. **2004**, 36, 1175-1197	2
305	Expected coalescence time for a nonuniform allocation process. **2008**, 40, 1002-1032	4
304	Coalescence theory for a general class of structured populations with fast migration. **2011**, 43, 1027-1047	6
303	A perturbation method for the structured coalescent with strong migration. **2000**, 37, 148-167	8
302	Robustness results for the coalescent. **1998**, 35, 438-447	47
301	Weak convergence to the coalescent in neutral population models. **1999**, 36, 446-460	12
300	The general coalescent with asynchronous mergers of ancestral lines. **1999**, 36, 1116-1125	170
299	The coalescent process in a population with stochastically varying size. **2003**, 40, 33-48	21
298	Structured coalescent with nonconservative migration. **2006**, 43, 351-362	5
297	Duality and Asymptotics for a Class of Nonneutral Discrete Moran Models. **2009**, 46, 866-893	4

296	Coalescent theory for a Monoecious Random Mating Population with a Varying Size. **2010**, 47, 41-57	2
295	Recurrence Equations for the Probability Distribution of Sample Configurations in Exact Population Genetics Models. **2010**, 47, 732-751	4
294	□-coalescents: a survey. **2014**, 51, 23-40	4
293	Identifiability of a Coalescent-Based Population Tree Model. **2014**, 51, 921-929	1
292	The structured coalescent process with weak migration. **2001**, 38, 1-17	7
291	Coalescent theory for seed bank models. **2001**, 38, 285-300	31
290	Quantifying and Mitigating the Effect of Preferential Sampling on Phylodynamic Inference. **2016**, 12, e1004789	25
289	Efficient Coalescent Simulation and Genealogical Analysis for Large Sample Sizes. **2016**, 12, e1004842	287
288	Bayesian phylogeography of influenza A/H3N2 for the 2014-15 season in the United States using three frameworks of ancestral state reconstruction. **2017**, 13, e1005389	19
287	Estimating effective population size changes from preferentially sampled genetic sequences. **2020**, 16, e1007774	6
286	Locally adaptive Bayesian birth-death model successfully detects slow and rapid rate shifts. **2020**, 16, e1007999	4
285	New Routes to Phylogeography: A Bayesian Structured Coalescent Approximation. **2015**, 11, e1005421	133
284	High-resolution molecular epidemiology and evolutionary history of HIV-1 subtypes in Albania. **2008**, 3, e1390	55
283	Coalescent-based genome analyses resolve the early branches of the euarchontoglires. **2013**, 8, e60019	28
282	A bayesian approach to genome/linguistic relationships in native South Americans. **2013**, 8, e64099	8
281	Long-distance dispersal by sea-drifted seeds has maintained the global distribution of Ipomoea pes-caprae subsp. brasiliensis (Convolvulaceae). **2014**, 9, e91836	32
280	Back to BaySICS: a user-friendly program for Bayesian Statistical Inference from Coalescent Simulations. **2014**, 9, e98011	9
279	High Species Richness of Scinax Treefrogs (Hylidae) in a Threatened Amazonian Landscape Revealed by an Integrative Approach. **2016**, 11, e0165679	28

278	Coalescence computations for large samples drawn from populations of time-varying sizes. **2017**, 12, e0170701	3
277	BEASTling: A software tool for linguistic phylogenetics using BEAST 2. **2017**, 12, e0180908	8
276	High genetic diversity of ancient horses from the Ukok Plateau. **2020**, 15, e0241997	2
275	On the size of the block of 1 for □-coalescents with dust. **2017**, 4, 407-425	3
274	Models Beyond the Dirichlet Process.	2
273	On the exponential functional of Markov Additive Processes, and applications to multi-type self-similar fragmentation processes and trees. **2018**, 15, 1257	7
272	Survey, monitoring and assessment of marine communities conducted by new technology. **2020**, 73, 53-63	1
271	Geography and life history traits account for the accumulation of cryptic diversity among Indo-West Pacific coral reef fishes. **2017**, 583, 179-193	13
270	A molecular phylogeny of the spiny lobster highlights a separately evolving lineage from the Southwest Indian Ocean. **2017**, 5, e3356	12
269	Contrasting gene flow at different spatial scales revealed by genotyping-by-sequencing in , a massively colour polymorphic New Zealand marine isopod. **2018**, 6, e5462	12
268	Natural history and molecular evolution of demersal Mediterranean sharks and skates inferred by comparative phylogeographic and demographic analyses. **2018**, 6, e5560	5
267	First steps towards assessing the evolutionary history and phylogeography of a widely distributed Neotropical grassland bird (Motacillidae:). **2018**, 6, e5886	8
266	The choice of tree prior and molecular clock does not substantially affect phylogenetic inferences of diversification rates. **2019**, 7, e6334	16
265	Molecular taxonomy of endemic coastal isopods from the Hawaiian Islands: re-description of and description of seven novel cryptic species. **2019**, 7, e7531	2
264	Nucleotide variation and balancing selection at the Ckma gene in Atlantic cod: analysis with multiple merger coalescent models. **2015**, 3, e786	26
263	Trans-species polymorphism at antimicrobial innate immunity cathelicidin genes of Atlantic cod and related species. **2015**, 3, e976	14
262	Old and ancient trees are life history lottery winners and act as evolutionary buffers against long-term environmental change.	1
261	Revisiting Shao and Sokal's [Formula: see text] index of phylogenetic balance. **2021**, 83, 52	3

260	Adaptive preferential sampling in phylodynamics with an application to SARS-CoV-2. 1-29	0
259	Quantifying the scale of genetic diversity extinction in the Anthropocene.	0
258	A coalescent model of ancestry for a rare allele. **2000**, 156, 375-84	2
257	A Fleming-Viot Process and Bayesian Nonparametrics.	
256	A population model for $Lambda$-coalescents with neutral mutations. **2007**, 12,	1
255	Coalescent methods for fine-scale disease-gene mapping. **2007**, 376, 123-40	1
254	Asymptotic behavior of a Feller evolution family involved in the Fisher-Wright model. **2008**, 40, 734-758	1
253	Generalised Stable Fleming-Viot Processes as Flickering Random Measures. **2009**, 14,	
252	Measure-valued Processes, Self-similarity and Flickering Random Measures. **2009**, 175-196	1
251	On the Speed of Coming Down from Infinity for Xi-Coalescent Processes. **2010**, 15,	6
250	A Contemporary View of Population Genetics in Evolution. **2011**, 281-290	
249	Stability on {0, 1, 2, }S: Birth-Death Chains and Particle Systems. **2011**, 311-329	
248	Stochastische Modelle in der Populationsgenetik. **2011**, 347-370	
247	????????????????. **2011**, 27, 141-152	
246	The Ancestry of Genetic Segments. **2012**, 2012, 1-8	
245	Genetics, Geography, and Human Variation. 99-142	
244	Forty Years of Model-Based Phylogeography. **2013**, 17-28	
243	Epidemiological Diffusion and Discrete Branching Models for Malware Propagation in Computer Networks. **2014**, 139-179	

242 [illegible] **2014**, 26, 43-50 8

241 Introductory comments on major papers by Professor Motoo Kimura. **1993**, 68, 353-394

240 Molecular Population Genetics in Drosophila Pseudoobscura: Three Future Directions. **1994**, 29-45

239 Molecular Population Genetics of a Phenotypically Monomorphic Protein in Drosophila. **1997**, 133-148

238 Phylogeny reconstruction: overview. **2014**, 70-101

237 Comparison of phylogenetic methods and tests on trees. **2014**, 153-181

236 Molecular clock and estimation of species divergence times. **2014**, 361-389

235 Models of amino acid and codon substitution. **2014**, 35-69

234 Maximum likelihood methods. **2014**, 102-152

233 Bayesian theory. **2014**, 182-213

232 Simulating molecular evolution. **2014**, 418-441 0

231 Neutral and adaptive protein evolution. **2014**, 390-417

230 Appendices. **2014**, 442-449

229 Bayesian phylogenetics. **2014**, 263-307

228 Coalescent theory and species trees. **2014**, 308-360

227 Bayesian computation (MCMC). **2014**, 214-262

226 [illegible] **2015**, 27, 133-140 5

225 Genetic Background. **2015**, 3-18

224	ARGON: Fast, Whole-Genome Simulation of the Discrete Time Wright-Fisher Process.	0
223	A Glance at Recombination Hotspots in the Domestic Cat. **2016**, 11, e0148710	
222	Reversible Polymorphism-Aware Phylogenetic Models and their Application to Tree Inference.	
221	Efficient Maximum-Likelihood Inference For The Isolation-With-Initial-Migration Model With Potentially Asymmetric Gene Flow.	
220	Coalescent inferences in conservation genetics: should the exception become the rule?.	0
219	Bayesian inference of ancestral recombination graphs for bacterial populations.	
218	Effects of the Ordering of Natural Selection and Population Regulation Mechanisms on Wright-Fisher Models.	
217	A non-zero variance of Tajima's estimator for two sequences even for infinitely many unlinked loci.	
216	Accuracy of demographic inferences from site frequency spectrum: the case of the yoruba population.	
215	Estimation of sub-epidemic dynamics by means of Sequential Monte Carlo Approximate Bayesian Computation: an application to the Swiss HIV Cohort Study.	1
214	Joint inference of demography and mutation rates from polymorphism data and pedigrees.	
213	The Bacterial Sequential Markov Coalescent.	
212	Introduction. **2017**, 1-15	
211	Wright–Fisher and Moran models. **2017**, 203-218	0
210	Coagulation and diffusion: A probabilistic perspective on the Smoluchowski PDE. **2017**, 14,	
209	Continuous Approximations. **2017**, 77-101	
208	The Wright–Fisher Model. **2017**, 17-43	
207	The third moments of the site frequency spectrum.	3

206	Inferring demographic history using two-locus statistics.	0
205	Scaling limits of coalescent processes near time zero. **2017**, 53,	
204	Fast and accurate statistical inference of phylogenetic networks using large-scale genomic sequence data.	1
203	Estimating epidemic incidence and prevalence from genomic data.	
202	Coalescent Processes with Skewed Offspring Distributions and non-Equilibrium Demography.	1
201	Ancient genomic variation underlies repeated ecological adaptation in young stickleback populations.	4
200	Genealogical properties of subsamples in highly fecund populations.	
199	The Validity of the Coalescent Approximation for Large Samples.	
198	Divergence estimation in the presence of incomplete lineage sorting and migration.	
197	Neither pulled nor pushed: Genetic drift and front wandering uncover a new class of reaction-diffusion waves.	
196	Population networks from DNA sequences: methodological developments.	
195	The Fractional Coalescent.	
194	Time-conditional properties of branches in coalescent gene trees.	1
193	Multispecies coalescent analysis unravels the non-monophyly and controversial relationships of Hexapoda.	
192	Ranked tree shapes, non-random extinctions and the loss of phylogenetic diversity.	
191	Geometry of the sample frequency spectrum and the perils of demographic inference.	0
190	A Note on the Small-Time Behaviour of the Largest Block Size of Beta n-Coalescents. **2018**, 219-234	1
189	Exploring Approximate Bayesian Computation for inferring recent demographic history with genomic markers in non-model species.	

188	A spectral decomposition for the block counting process and the fixation line of the beta(3,1)-coalescent. **2018**, 23,	
187	Inference of Species Phylogenies from Bi-allelic Markers Using Pseudo-likelihood.	1
186	The Wright-Fisher Site Frequency Spectrum as a Perturbation of the Coalescent's.	0
185	An average-case sublinear exact Li and Stephens forward algorithm.	
184	The IICR and the non-stationary structured coalescent: demographic inference with arbitrary changes in population structure.	1
183	The multifurcating skyline plot.	
182	SANTA-SIM: Simulating Viral Sequence Evolution Dynamics Under Selection and Recombination.	
181	Bayesian coalescent inference of in-host evolution using Next Generation Sequencing.	
180	Evolution of populations expanding on curved surfaces.	
179	An Efficient Computational Approach for Constructing the Allele Frequency Spectrum of Populations with Arbitrary Complex History.	
178	Genealogical distances under low levels of selection.	
177	Analysing Emergent Dynamics of Evolving Computation in 2D Cellular Automata. **2019**, 3-40	0
176	Genetische Drift und Mutation. **2019**, 13-29	
175	The genealogy of Galton-Watson trees. **2019**, 24,	3
174	External branch lengths of $Lambda $-coalescents without´a´dust component. **2019**, 24,	
173	Multiple-serotype models of dengue virus transmission: simulation study and perspectives for the application of inference in epidemiological surveillance.	0
172	Population divergence time estimation using individual lineage label switching.	
171	STELAR: A statistically consistent coalescent-based species tree estimation method by maximizing triplet consistency.	

170	Bayesian Estimation of Population Size Changes by Sampling Tajima’s Trees.	
169	Bayesian nonparametric analysis of Kingman’s coalescent. **2019**, 55,	
168	Estimation of Speciation Times Under the Multispecies Coalescent.	0
167	Genome-wide sequence information reveals recurrent hybridization among diploid wheat wild relatives.	
166	Distinguishing coalescent models - which statistics matter most?.	2
165	Bacterial Population Genomics. **2019**, 997-1020	3
164	Testing for population decline using maximal linkage disequilibrium blocks.	
163	Maximum likelihood estimation of species trees from gene trees in the presence of ancestral population structure.	
162	Statistical inference for the evolutionary history of cancer genomes.	1
161	How to choose sets of ancestry informative markers: A supervised feature selection approach.	
160	Fine human genetic map based on UK10K data set.	
159	Polynomial-Time Statistical Estimation of Species Trees under Gene Duplication and Loss.	2
158	SharpTNI: Counting and Sampling Parsimonious Transmission Networks under a Weak Bottleneck.	2
157	Evaluation of haplotype callers for next-generation sequencing of viruses.	
156	The eternal multiplicative coalescent encoding via excursions of Lévy-type processes. **2019**, 25,	
155	A Metric Space of Ranked Tree Shapes and Ranked Genealogies.	
154	Demographic history and genomics of local adaptation in blue tit populations.	
153	ipcoal: An interactive Python package for simulating and analyzing genealogies and sequences on a species tree or network.	1

152	TiTUS: Sampling and Summarizing Transmission Trees with Multi-strain Infections.	1
151	Speeding up Inference of Homologous Recombination in Bacteria.	
150	Inference of Population Admixture Network from Local Gene Genealogies: a Coalescent-based Maximum Likelihood Approach.	
149	Trees within trees II: Nested fragmentations. **2020**, 56,	3
148	Phantom histories of misspecified pasts.	
147	Pervasive selection biases inferences of the species tree.	0
146	Visualizing Population Structure with Variational Autoencoders.	1
145	Variational Inference Using Approximate Likelihood Under the Coalescent With Recombination.	
144	Exchangeable coalescents, ultrametric spaces, nested interval-partitions: A unifying approach. **2021**, 31,	
143	The magical Ewens sampling formula.	1
142	wQFM: Statistically Consistent Genome-scale Species Tree Estimation from Weighted Quartets.	0
141	The distribution of waiting distances in ancestral recombination graphs and its applications.	0
140	A novel coalescent method insensitive to population structure.	
139	Phylogenetic Novelty Scores: a New Approach for Weighting Genetic Sequences.	
138	A discrete approach to the external branches of a Kingman coalescent tree. Theoretical results and practical applications.	
137	Kingman's coalescent with erosion. **2020**, 25,	2
136	Bacterial Microevolution and the Pangenome. **2020**, 129-149	1
135	Towards a Phylogenetic Measure to Quantify HIV Incidence. **2020**, 34-50	

134	Estimating Evolutionary Rates and Timescales from Time-Stamped Data. **2020**, 157-174	1
133	Asymptotic genealogies of interacting particle systems with an application to sequential Monte Carlo. **2020**, 48,	3
132	Trophic guild and forest type explain phyllostomid bat abundance variation from human habitat disturbance.	
131	Scalable Species Tree Inference with External Constraints.	
130	Discrete coalescent trees. **2021**, 83, 60	1
129	Identifying loci under selection via explicit demographic models.	0
128	CoaTran: Coalescent tree simulation along a transmission network.	0
127	Identifiability of speciation times under the multispecies coalescent.	0
126	Molecular Markers in Anthropological Genetic Studies. 141-186	5
125	Application of a Markovian ancestral model to the temporal and spatial dynamics of cultural evolution on a population network. **2021**, 143, 14-29	1
124	Remembering Richard Lewontin (1929–2021). **2021**, 16, 257	0
123	Fragmentations with self-similar branching speeds. **2021**, 53, 1149-1189	
122	A scalable analytical approach from bacterial genomes to epidemiology.	0
121	Phylogenomic approaches to detecting and characterizing introgression. **2021**,	3
120	Nucleotide usage biases distort inferences of the species tree.. **2022**,	1
119	Markov genealogy processes.. **2021**, 143, 77-77	
118	Asymptotic genealogies for a class of generalized Wright–Fisher models. **2022**, 17-43	1
117	Zig-zag sampling for discrete structures and non-reversible phylogenetic MCMC. 1-000	2

116	The effect of mainland dynamics on data and parameter estimates in island biogeography.	0
115	Robust detection of natural selection using a probabilistic model of tree imbalance.. **2022**,	
114	Early Human Colonization, Climate Change and Megafaunal Extinction in Madagascar: The Contribution of Genetics in a Framework of Reciprocal Causations. **2022**, 9,	0
113	The bounded coalescent model: conditioning a genealogy on a minimum root date.	
112	Correspondence Between Genomic- and Genealogical/Coalescent-Based Inference of Homozygosity by Descent in Large French-Canadian Genealogies.. **2021**, 12, 808829	0
111	Old and ancient trees are life history lottery winners and vital evolutionary resources for long-term adaptive capacity.. **2022**,	1
110	□coalescents arising in a population with dormancy. **2022**, 27,	0
109	RF-Net 2: Fast Inference of Virus Reassortment and Hybridization Networks.. **2022**,	0
108	Bayesian inference of clonal expansions in a dated phylogeny. **2021**,	0
107	A unified genealogy of modern and ancient genomes.. **2022**, 375, eabi8264	1
106	Evolutionary dynamics of SARS-CoV-2 circulating in Yogyakarta and Central Java, Indonesia: sequence analysis covering furin cleavage site (FCS) region of the spike protein.. **2022**, 1	0
105	Methods Combining Genomic and Epidemiological Data in the Reconstruction of Transmission Trees: A Systematic Review.. **2022**, 11,	
104	Population divergence time estimation using individual lineage label switching.. **2022**,	1
103	An Efficient Coalescent Epoch Model for Bayesian Phylogenetic Inference.. **2022**,	1
102	Strong neutral sweeps occurring during a population contraction.. **2022**,	0
101	The symmetric coalescent and Wright□Fisher models with bottlenecks. **2022**, 32,	
100	The stochastic Fisher-KPP Equation with seed bank and on/off branching coalescing Brownian motion. 1	0
99	Graph-based algorithms for phase-type distributions.	0

98	Novel Low Pathogenic Avian Influenza H6N1 in Backyard Chicken in Easter Island (Rapa Nui), Chilean Polynesia.. **2022**, 14,	0
97	A dynamic ancestral graph model and GPU-based simulation of a community based on metagenomic sampling.. **2022**,	
96	The coalescent tree of a Markov branching process with generalised logistic growth.. **2022**, 84, 33	0
95	Coalescence in branching processes with age dependent structure in population. 1-14	
94	Approximations to the expectations and variances of ratios of tree properties under the coalescent.	
93	Population genetics of polymorphism and divergence in rapidly evolving populations.. **2022**,	
92	Variances and covariances of linear summary statistics of segregating sites.. **2022**,	0
91	Site Pattern Probabilities Under the Multispecies Coalescent and a Relaxed Molecular Clock: Theory and Applications.. **2022**, 111078	0
90	Accounting for spatial sampling patterns in Bayesian phylogeography.. **2021**, 118,	1
89	Efficient ancestry and mutation simulation with msprime 1.0.. **2021**,	8
88	Identification of natural selection in genomic data with deep convolutional neural network. **2021**, 14, 51	1
87	Covariance of pairwise differences on a multi-species coalescent tree and implications for .. **2022**, 377, 20200415	2
86	Interpreting the pervasive observation of U-shaped Site Frequency Spectra.	2
85	Hospital outbreak of carbapenem-resistant Enterobacterales associated with a plasmid carried mostly by ST399.. **2022**, 8,	0
84	Lack of Statistical Rigor in DNA Barcoding Likely Invalidates the Presence of a True Species' Barcode Gap. **2022**, 10,	0
83	Generative Moment Matching Networks for Genotype Simulation.	
82	Data_Sheet_1.pdf. **2018**,	
81	Data_Sheet_2.zip. **2018**,	

80	Selection on the gametophyte: Modeling alternation of generations in plants.. **2022**, 10, e11472	1
79	Evolutionary Game Dynamics in a Finite Continental Island Population Model and Emergence of Cooperation. 1	
78	Enumeration of binary trees compatible with a perfect phylogeny.. **2022**, 84, 54	
77	Eukaryogenesis: The Rise of an Emergent Superorganism. **2022**, 13,	0
76	Classes of explicit phylogenetic networks and their biological and mathematical significance.. **2022**, 84, 47	0
75	Phylogenetics in Space: How Continuous Spatial Structure Impacts Tree Inference.. **2022**, 107505	
74	Statistical Challenges in Tracking the Evolution of SARS-CoV-2. **2022**, 37,	1
73	Sweepstakes reproductive success via pervasive and recurrent selective sweeps.	1
72	The Occurrence Birth-Death Process for combined-evidence analysis in macroevolution and epidemiology.	0
71	An environmental gradient dominates ecological and genetic differentiation of marine invertebrates between the North and Baltic Sea. **2022**, 12,	0
70	Graph-based algorithms for Laplace transformed coalescence time distributions.	
69	Bayesian Inference of Dependent Population Dynamics in Coalescent Models.	
68	Epidemiological Inference From Pathogen Genomes: A Review of Phylodynamic Models and Applications.	0
67	General selection models: Bernstein duality and minimal ancestral structures. **2022**, 32,	1
66	SVDquintets: a New Tool for Species Tree Inference.	
65	Asymptotic behaviour of sampling and transition probabilities in coalescent models under selection and parent dependent mutations. **2022**, 27,	
64	Evolution, geographic spreading, and demographic distribution of Enterovirus D68. **2022**, 18, e1010515	0
63	The Viral Susceptibility of the Haloferax Species. **2022**, 14, 1344	0

62	PhaseTypeR: phase-type distributions in R with reward transformations and a view towards population genetics.	0
61	The bounded coalescent model: Conditioning a genealogy on a minimum root date. **2022**, 548, 111186	0
60	Comparative genetic research on Microtus mystacinus (de´Filippi, 1865) distributed in Asia and Europe inferred´from mitochondrial (CYTB and COXI) and´nuclear´(IRBP) gene regions. **2022**, 1-16	1
59	Rapid evolution allows coexistence of highly divergent lineages within the same niche.	1
58	Distinguishing imported cases from locally acquired cases within a geographically limited genomic sample of an infectious disease.	
57	Generalizing Bayesian phylogenetics to infer shared evolutionary events. **2022**, 119,	1
56	Game-theoretical approach for opinion dynamics on social networks. **2022**, 32, 073117	
55	Vaccination shapes evolutionary trajectories of SARS-CoV-2.	0
54	DNA barcoding of commercially relevant marine fish species in Tunisian waters. 1-8	0
53	Preface. **2014**, vii-viii	
52	Copyright Page. **2014**, iv-iv	
51	Foreword. **2014**, v-vi	
50	Detection of HIV-1 Transmission Clusters from Dried Blood Spots within a Universal Test-and-Treat Trial in East Africa. **2022**, 14, 1673	
49	Forest Genetics Research in the Mediterranean Basin: Bibliometric Analysis, Knowledge Gaps, and Perspectives.	0
48	A scalable analytical approach from bacterial genomes to epidemiology. **2022**, 377,	0
47	LinguaPhylo: a probabilistic model specification language for reproducible phylogenetic analyses.	
46	Equivalence of mean-field avalanches and branching diffusions: From the Brownian force model to the super-Brownian motion.	0
45	Estimating Waiting Distances Between Genealogy Changes under a Multi-Species Extension of the Sequentially Markov Coalescent.	

44	Haplotype-based inference of recent effective population size in modern and ancient DNA samples.	
43	VGsim: Scalable viral genealogy simulator for global pandemic. **2022**, 18, e1010409	0
42	Phylogeography and taxonomy of Coleonyx elegans Gray 1845 (Squamata: Eublepharidae) in Mesoamerica: The Isthmus of Tehuantepec as an environmental barrier. **2023**, 178, 107632	0
41	Generative Moment Matching Networks for Genotype Simulation. **2022**,	0
40	Genetic diversity loss in the Anthropocene. **2022**, 377, 1431-1435	1
39	An adjacent-swap Markov chain on coalescent trees. 1-18	0
38	Graph-based algorithms for Laplace transformed coalescence time distributions. **2022**, 18, e1010532	1
37	Robust inference of population size histories from genomic sequencing data. **2022**, 18, e1010419	0
36	Average abundancy of cooperation in multi-player games with random payoffs. **2022**, 85,	0
35	Exploring Conflicts in Whole Genome Phylogenetics: A Case Study within Manakins (Aves: Pipridae).	0
34	Data Integration in Bayesian Phylogenetics. **2023**, 10,	0
33	Simultaneous Inference of Past Demography and Selection from the Ancestral Recombination Graph under the Beta Coalescent.	0
32	Coalescent simulations indicate that the São Francisco River is a biogeographic barrier for six vertebrates in a seasonally dry South American forest. 10,	0
31	On the genetic consequences of habitat contraction: edge effects and habitat loss.	0
30	OTU Delimitation with Earthworm DNA Barcodes: A Comparison of Methods. **2022**, 14, 866	0
29	Graph-based algorithms for phase-type distributions. **2022**, 32,	0
28	Instantaneous support propagation for Fleming–Viot processes. **2022**,	0
27	The spread of Carpophilus truncatus is on the razor's edge between an outbreak and a pest invasion. **2022**, 12,	0

26	Molecular source attribution. **2022**, 18, e1010649	0
25	Distinguishing imported cases from locally acquired cases within a geographically limited genomic sample of an infectious disease.	0
24	Quantitative fate mapping: A general framework for analyzing progenitor state dynamics via retrospective lineage barcoding. **2022**, 185, 4604-4620.e32	0
23	Testing for Phylogenetic Signal in Single-Cell RNA-Seq Data.	0
22	On the origin and structure of haplotype blocks.	1
21	Bayesian Molecular Dating Analyses Combined with Mutational Profiling Suggest an Independent Origin and Evolution of SARS-CoV-2 Omicron BA.1 and BA.2 Sub-Lineages. **2022**, 14, 2764	0
20	Species tree estimation under joint modeling of coalescence and duplication: Sample complexity of quartet methods. **2022**, 32,	0
19	TiPS : Rapidly simulating trajectories and phylogenies from compartmental models.	0
18	Spatial evolution of human cultures inferred through Bayesian phylogenetic analysis. **2023**, 20,	1
17	Assessing Species Boundaries in the Freshwater Snail Family Physidae Using Coalescent-Based Delimitation Methods. **2022**, 65,	0
16	Agent-based modeling and phylogenetic analysis suggests that COVID-19 will remain a low-severity albeit highly transmissible disease.	0
15	Fitting stochastic epidemic models to gene genealogies using linear noise approximation. **2023**, 17,	0
14	High turnover ofde novotranscripts inDrosophila melanogaster.	0
13	Sweepstakes reproductive success via pervasive and recurrent selective sweeps. 12,	0
12	Large-scale behaviour and hydrodynamic limit of beta coalescents. **2023**, 33,	0
11	Estimating single cell clonal dynamics in human blood using coalescent theory.	0
10	Sweepstakes reproduction facilitates rapid adaptation in highly fecund populations.	0
9	A spatial approach to jointly estimate Wright's neighborhood size and long-term effective population size.	0

8	Estimating the Lambda measure in multiple-merger coalescents.	0
7	NeogeneQuaternary tectonic, eustatic and climatic events shaped the evolution of a South American treefrog. **2023**, 50, 987-999	0
6	adaPop: Bayesian inference of dependent population dynamics in coalescent models. **2023**, 19, e1010897	0
5	Statistical genetics in and out of quasi-linkage equilibrium. **2023**, 86, 052601	0
4	Interpreting the pervasive observation of U-shaped Site Frequency Spectra. **2023**, 19, e1010677	0
3	Kinship Demography Inferring the expectation, variance and distribution of the number of collaterals of a dynamical process in a structured population.	0
2	Next-generation inference of past population history by integrating diverse types of genomic markers.	0
1	The phylogenetic structure and coalescent species delimitation of an endemic trapdoor spider genus, Stasimopus (Araneae, Mygalomorphae, Stasimopidae) in the Karoo region of South Africa. **2023**, 107798	0