

A tutorial on how not to over-interpret STRUCTURE and

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Reconstructing Druze population history. <i>Scientific Reports</i> , 2016, 6, 35837.	1.6	18
2	Hybridization in Plants: Old Ideas, New Techniques. <i>Plant Physiology</i> , 2017, 173, 65-78.	2.3	216
3	Population genomics reveals that an anthropophilic population of <i>Aedes aegypti</i> mosquitoes in West Africa recently gave rise to American and Asian populations of this major disease vector. <i>BMC Biology</i> , 2017, 15, 16.	1.7	96
4	A genetic chronology for the Indian Subcontinent points to heavily sex-biased dispersals. <i>BMC Evolutionary Biology</i> , 2017, 17, 88.	3.2	59
5	Admixture on the northern front: population genomics of range expansion in the white-footed mouse (<i>Peromyscus leucopus</i>) and secondary contact with the deer mouse (<i>Peromyscus maniculatus</i>). <i>Heredity</i> , 2017, 119, 447-458.	1.2	27
6	StrAuto: automation and parallelization of STRUCTURE analysis. <i>BMC Bioinformatics</i> , 2017, 18, 192.	1.2	155
7	New gSSR and EST-SSR markers reveal high genetic diversity in the invasive plant <i>Ambrosia artemisiifolia</i> L. and can be transferred to other invasive <i>Ambrosia</i> species. <i>PLoS ONE</i> , 2017, 12, e0176197.	1.1	23
8	Northeast African genomic variation shaped by the continuity of indigenous groups and Eurasian migrations. <i>PLoS Genetics</i> , 2017, 13, e1006976.	1.5	45
9	The genomic ancestry, landscape genetics and invasion history of introduced mice in New Zealand. <i>Royal Society Open Science</i> , 2018, 5, 170879.	1.1	21
10	Assessing the Relationship of Ancient and Modern Populations. <i>Genetics</i> , 2018, 208, 383-398.	1.2	18
11	Paleogenomics of Animal Domestication. <i>Population Genomics</i> , 2018, , 225-272.	0.2	14
12	Computational Tools for Population Genomics. <i>Population Genomics</i> , 2018, , 127-160.	0.2	2
13	Estimating Genetic Relatedness in Admixed Populations. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3203-3220.	0.8	5
14	Latin Americans show wide-spread <i>Converso</i> ancestry and imprint of local Native ancestry on physical appearance. <i>Nature Communications</i> , 2018, 9, 5388.	5.8	123
15	The role of gene flow in rapid and repeated evolution of cave-related traits in Mexican tetra, <i>Astyanax mexicanus</i> . <i>Molecular Ecology</i> , 2018, 27, 4397-4416.	2.0	160
16	Phylogenomics supports incongruence between ecological specialization and taxonomy in a charismatic clade of buck moths. <i>Molecular Ecology</i> , 2018, 27, 4417-4429.	2.0	13
17	Ancient genome-wide analyses infer kinship structure in an Early Medieval Alemannic graveyard. <i>Science Advances</i> , 2018, 4, eaao1262.	4.7	28
18	Fine-scale geographic patterns of gene flow and reproductive character displacement in <i>Drosophila subquinaria</i> and <i>Drosophila recens</i> . <i>Molecular Ecology</i> , 2018, 27, 3655-3670.	2.0	14

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19	Inferring Continuous and Discrete Population Genetic Structure Across Space. <i>Genetics</i> , 2018, 210, 33-52.	1.2	221
20	Population structure of <i>Venturia inaequalis</i> , a causal agent of apple scab, in response to heterogeneous apple tree cultivation. <i>BMC Evolutionary Biology</i> , 2018, 18, 5.	3.2	14
22	Human races are not like dog breeds: refuting a racist analogy. <i>Evolution: Education and Outreach</i> , 2019, 12, .	0.3	12
23	Population analysis reveals genetic structure of an invasive agricultural thrips pest related to invasion of greenhouses and suitable climatic space. <i>Evolutionary Applications</i> , 2019, 12, 1868-1880.	1.5	21
24	Habitat preference differentiates the Holocene range dynamics but not barrier effects on two sympatric, congeneric trees (<i>Tristania</i> , <i>Myrtaceae</i>). <i>Heredity</i> , 2019, 123, 532-548.	1.2	8
25	Genomic clues of the evolutionary history of <i>Bos indicus</i> cattle. <i>Animal Genetics</i> , 2019, 50, 557-568.	0.6	59
26	Genotyping by Sequencing of Cultivated Lentil (<i>Lens culinaris</i> Medik.) Highlights Population Structure in the Mediterranean Gene Pool Associated With Geographic Patterns and Phenotypic Variables. <i>Frontiers in Genetics</i> , 2019, 10, 872.	1.1	35
27	Host plant-related genomic differentiation in the European cherry fruit fly, <i>Rhagoletis cerasi</i> . <i>Molecular Ecology</i> , 2019, 28, 4648-4666.	2.0	10
28	Morphological, phytochemical and molecular analyses define species limits in <i>Eucalyptus magnificata</i> (<i>Myrtaceae</i>) and lead to the discovery of a new rare species. <i>Australian Systematic Botany</i> , 2019, .	0.3	8
29	Limited gene exchange between two sister species of leaf beetles within a hybrid zone in the Alps. <i>Journal of Evolutionary Biology</i> , 2019, 32, 1406-1417.	0.8	6
30	Host plant associations and geography interact to shape diversification in a specialist insect herbivore. <i>Molecular Ecology</i> , 2019, 28, 4197-4211.	2.0	35
31	Reconstructed lost Native American populations from Eastern Brazil are shaped by differential $J_{\text{A}^{\text{a}}}$ /Tupi ancestry. <i>Genome Biology and Evolution</i> , 2019, 11, 2593-2604.	1.1	8
32	CRUMBLER: A tool for the prediction of ancestry in cattle. <i>PLoS ONE</i> , 2019, 14, e0221471.	1.1	7
33	Genomic approaches to identify hybrids and estimate admixture times in European wildcat populations. <i>Scientific Reports</i> , 2019, 9, 11612.	1.6	34
34	Population Genomic Approaches for Weed Science. <i>Plants</i> , 2019, 8, 354.	1.6	14
35	Apparent latent structure within the UK Biobank sample has implications for epidemiological analysis. <i>Nature Communications</i> , 2019, 10, 333.	5.8	240
36	Minor allele frequency thresholds strongly affect population structure inference with genomic data sets. <i>Molecular Ecology Resources</i> , 2019, 19, 639-647.	2.2	255
37	From hybridization to introgression between two closely related sympatric ant species. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 778-788.	0.6	17

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38	Killer whale genomes reveal a complex history of recurrent admixture and vicariance. <i>Molecular Ecology</i> , 2019, 28, 3427-3444.	2.0	46
39	Multispecies hybridization in birds. <i>Avian Research</i> , 2019, 10, .	0.5	27
40	Spatial and temporal genetic diversity of the Texas kangaroo rat, <i>Dipodomys elator</i> (Rodentia): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66.	0.6	6
41	A population genetic assessment of taxonomic species: The case of Lake Malawi cichlid fishes. <i>Molecular Ecology Resources</i> , 2019, 19, 1164-1180.	2.2	7
42	A Likelihood-Free Estimator of Population Structure Bridging Admixture Models and Principal Components Analysis. <i>Genetics</i> , 2019, 212, 1009-1029.	1.2	24
43	Is the incidence of survival in interior Pleistocene refugia (nunataks) underestimated? Phylogeography of the high mountain plant <i>Androsace alpina</i> (Primulaceae) in the European Alps revisited. <i>Ecology and Evolution</i> , 2019, 9, 4078-4086.	0.8	20
44	Codweb: Whole-genome sequencing uncovers extensive reticulations fueling adaptation among Atlantic, Arctic, and Pacific gadids. <i>Science Advances</i> , 2019, 5, eaat8788.	4.7	22
45	The complex geography of domestication of the African rice <i>Oryza glaberrima</i> . <i>PLoS Genetics</i> , 2019, 15, e1007414.	1.5	30
46	Genetic signatures of gene flow and malaria-driven natural selection in sub-Saharan populations of the "endemic Burkitt Lymphoma belt". <i>PLoS Genetics</i> , 2019, 15, e1008027.	1.5	23
47	ddRADâ€seq data reveal significant genomeâ€wide population structure and divergent genomic regions that distinguish the mallard and close relatives in North America. <i>Molecular Ecology</i> , 2019, 28, 2594-2609.	2.0	37
48	Genetic evidence for species cohesion, substructure and hybrids in spruce. <i>Molecular Ecology</i> , 2019, 28, 2029-2045.	2.0	12
49	Identifying hybrids & the genomics of hybridization: Mallards & American black ducks of Eastern North America. <i>Ecology and Evolution</i> , 2019, 9, 3470-3490.	0.8	39
50	When West Meets East: The Origins and Spread of Weedy Rice Between Continental and Island Southeast Asia. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2941-2950.	0.8	8
51	Eukaryote hybrid genomes. <i>PLoS Genetics</i> , 2019, 15, e1008404.	1.5	77
52	Cross-species hybridization and the origin of North African date palms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1651-1658.	3.3	95
53	Potential limits to the benefits of admixture during biological invasion. <i>Molecular Ecology</i> , 2019, 28, 100-113.	2.0	20
54	Phylogenetic Trees and Networks Can Serve as Powerful and Complementary Approaches for Analysis of Genomic Data. <i>Systematic Biology</i> , 2020, 69, 593-601.	2.7	72
55	Is population structure in the genetic biobank era irrelevant, a challenge, or an opportunity?. <i>Human Genetics</i> , 2020, 139, 23-41.	1.8	72

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56	Single nucleotide polymorphism-based species phylogeny of greater fritillary butterflies (Lepidoptera): Tj ETQq0 0.0 rgBT /Overlock 10 2020, 45, 269-280.	1.7	16
57	Genetic assignment of individuals to source populations using network estimation tools. <i>Methods in Ecology and Evolution</i> , 2020, 11, 333-344.	2.2	5
58	Relationship of Icelandic cattle with Northern and Western European cattle breeds, admixture and population structure. <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2020, 69, 25-38.	0.2	6
59	Human Genomic Diversity Where the Mediterranean Joins the Atlantic. <i>Molecular Biology and Evolution</i> , 2020, 37, 1041-1055.	3.5	11
60	Evidence of linked selection on the Z chromosome of hybridizing hummingbirds*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 725-739.	1.1	18
61	Genome variation and population structure among 1142 mosquitoes of the African malaria vector species <i>Anopheles gambiae</i> and <i>Anopheles coluzzii</i> . <i>Genome Research</i> , 2020, 30, 1533-1546.	2.4	81
62	The shaping of immunological responses through natural selection after the Roma Diaspora. <i>Scientific Reports</i> , 2020, 10, 16134.	1.6	2
63	Comparative assessment of range-wide patterns of genetic diversity and structure with SNPs and microsatellites: A case study with Iberian amphibians. <i>Ecology and Evolution</i> , 2020, 10, 10353-10363.	0.8	23
64	Historical isolation facilitates species radiation by sexual selection: Insights from <i>Chorthippus</i> grasshoppers. <i>Molecular Ecology</i> , 2020, 29, 4985-5002.	2.0	18
65	Secondary contact and genomic admixture between rhesus and long-tailed macaques in the Indochina Peninsula. <i>Journal of Evolutionary Biology</i> , 2020, 33, 1164-1179.	0.8	13
66	The Genetic Population Structure of Robinson Crusoe Island, Chile. <i>Frontiers in Genetics</i> , 2020, 11, 669.	1.1	0
67	Variation under domestication in animal models: the case of the Mexican axolotl. <i>BMC Genomics</i> , 2020, 21, 827.	1.2	1
68	Sampling schemes and drift can bias admixture proportions inferred by <i>structure</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 1769-1785.	2.2	17
69	Genetic diversity in Iranian indigenous sheep vis-à-vis selected exogenous sheep breeds and wild mouflon. <i>Animal Genetics</i> , 2020, 51, 772-787.	0.6	11
70	Unsupervised detection of ancestry tracks with the GHap <i>r</i> package. <i>Methods in Ecology and Evolution</i> , 2020, 11, 1448-1454.	2.2	6
71	Comparing Genomic Signatures of Selection Between the Abbassa Strain and Eight Wild Populations of Nile Tilapia (<i>Oreochromis niloticus</i>) in Egypt. <i>Frontiers in Genetics</i> , 2020, 11, 567969.	1.1	8
72	Introgression across evolutionary scales suggests reticulation contributes to Amazonian tree diversity. <i>Molecular Ecology</i> , 2020, 29, 4170-4185.	2.0	23
73	Quantifying and contextualizing the impact of bioRxiv preprints through automated social media audience segmentation. <i>PLoS Biology</i> , 2020, 18, e3000860.	2.6	35

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74	Evidence for the Pleistocene Arc Hypothesis from genome-wide SNPs in a Neotropical dry forest specialist, the Rufous-fronted Thornbird (Furnariidae: <i>Phacellodomus rufifrons</i>). <i>Molecular Ecology</i> , 2020, 29, 4457-4472.	2.0	15
75	The role of agro-ecological factors and transboundary transhumance in shaping the genetic diversity in four indigenous cattle populations of Benin. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 622-640.	0.8	9
76	Range-wide population genetics study informs on conservation translocations and reintroductions for the endangered Murray hardyhead (<i>Craterocephalus fluviatilis</i>). <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2020, 30, 1959-1974.	0.9	3
77	Concordant geographic and genetic structure revealed by genotyping-by-sequencing in a New Zealand marine isopod. <i>Ecology and Evolution</i> , 2020, 10, 13624-13639.	0.8	7
78	Evaluation of the Ion AmpliSeq, PhenoTrivium Panel: MPS-Based Assay for Ancestry and Phenotype Predictions Challenged by Casework Samples. <i>Genes</i> , 2020, 11, 1398.	1.0	19
79	Rapid colour shift by reproductive character displacement in <i>Cupido</i> butterflies. <i>Molecular Ecology</i> , 2020, 29, 4942-4955.	2.0	10
80	Genomic footprints of an old affair: Single nucleotide polymorphism data reveal historical hybridization and the subsequent evolution of reproductive barriers in two recently diverged grasshoppers with partly overlapping distributions. <i>Molecular Ecology</i> , 2020, 29, 2254-2268.	2.0	17
81	Cadaveric blood cards: Assessing DNA quality and quantity and the utility of STRs for the individual estimation of trihybrid ancestry and admixture proportions. <i>Forensic Science International (Online)</i> , 2020, 2, 114-122.	0.6	2
82	Ancient Hybridization with an Unknown Population Facilitated High-Altitude Adaptation of Canids. <i>Molecular Biology and Evolution</i> , 2020, 37, 2616-2629.	3.5	46
83	Recent introgression between Taiga Bean Goose and Tundra Bean Goose results in a largely homogeneous landscape of genetic differentiation. <i>Heredity</i> , 2020, 125, 73-84.	1.2	13
84	Genome-wide SNP analysis reveals an increase in adaptive genetic variation through selective breeding of coral. <i>Molecular Ecology</i> , 2020, 29, 2176-2188.	2.0	46
85	The Genomic History of the Bronze Age Southern Levant. <i>Cell</i> , 2020, 181, 1146-1157.e11.	13.5	51
86	Estimation of Genomic Breed Composition for Purebred and Crossbred Animals Using Sparsely Regularized Admixture Models. <i>Frontiers in Genetics</i> , 2020, 11, 576.	1.1	8
87	Genetic Structure of Smallmouth Bass in the Lake Michigan and Upper Mississippi River Drainages Relates to Habitat, Distance, and Drainage Boundaries. <i>Transactions of the American Fisheries Society</i> , 2020, 149, 383-397.	0.6	8
88	Opening the door to greater phylogeographic inference in Southeast Asia: Comparative genomic study of five codistributed rainforest bird species using target capture and historical DNA. <i>Ecology and Evolution</i> , 2020, 10, 3222-3247.	0.8	10
89	The spatiotemporal spread of human migrations during the European Holocene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8989-9000.	3.3	52
90	Ecosystem size predicts the probability of speciation in migratory freshwater fish. <i>Molecular Ecology</i> , 2020, 29, 3071-3083.	2.0	6
91	Native American gene flow into Polynesia predating Easter Island settlement. <i>Nature</i> , 2020, 583, 572-577.	13.7	64

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92	Impacts of the Toba eruption and montane forest expansion on diversification in Sumatran parachuting frogs (<i>Rhacophorus</i>). <i>Molecular Ecology</i> , 2020, 29, 2994-3009.	2.0	4
93	Confidently identifying the correct K value using the $\hat{\Gamma}$ method: When does $\hat{\Gamma} = \hat{\Gamma}^2$?. <i>Molecular Ecology</i> , 2020, 29, 862-869.	2.0	67
94	Serendipitous In Situ Conservation of Faba Bean Landraces in Tunisia: A Case Study. <i>Genes</i> , 2020, 11, 236.	1.0	7
95	Assessing connectivity despite high diversity in island populations of a malaria mosquito. <i>Evolutionary Applications</i> , 2020, 13, 417-431.	1.5	11
96	Spatio-temporal dynamics of <i>Plasmodium falciparum</i> transmission within a spatial unit on the Colombian Pacific Coast. <i>Scientific Reports</i> , 2020, 10, 3756.	1.6	23
97	The genetic history of France. <i>European Journal of Human Genetics</i> , 2020, 28, 853-865.	1.4	15
98	Analysis of evolutionary relationships provides new clues to the origins of weedy rice. <i>Ecology and Evolution</i> , 2020, 10, 891-900.	0.8	8
99	Evaluation of model fit of inferred admixture proportions. <i>Molecular Ecology Resources</i> , 2020, 20, 936-949.	2.2	43
100	A genetically unique Chinese cattle population shows evidence of common ancestry with wild species when analysed with a reduced ascertainment bias SNP panel. <i>PLoS ONE</i> , 2020, 15, e0231162.	1.1	8
101	Widespread genetic connectivity of feral pigeons across the Northeastern megacity. <i>Evolutionary Applications</i> , 2021, 14, 150-162.	1.5	25
102	Urbanization reduces gene flow but not genetic diversity of stream salamander populations in the New York City metropolitan area. <i>Evolutionary Applications</i> , 2021, 14, 99-116.	1.5	21
103	Biased assessment of ongoing admixture using STRUCTURE in the absence of reference samples. <i>Molecular Ecology Resources</i> , 2021, 21, 677-689.	2.2	5
104	A Primer on the Population Genetic Analysis of Ancient Genomes. , 2021, , 1-15.		0
105	Genomic Adaptations to Salinity Resist Gene Flow in the Evolution of Floridian Watersnakes. <i>Molecular Biology and Evolution</i> , 2021, 38, 745-760.	3.5	11
106	Hybridization and cryptic speciation in the Iberian endemic plant genus <i>Phalacrocarpum</i> (Asteraceae-Anthemideae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 156, 107024.	1.2	6
107	Genetic diversity and structure of <i>Taxus baccata</i> from the Cantabrian-Atlantic area in northern Spain: A guide for conservation and management actions. <i>Forest Ecology and Management</i> , 2021, 482, 118844.	1.4	8
108	Does the genetic diversity among pubescent white oaks in southern Italy, Sicily and Sardinia islands support the current taxonomic classification?. <i>European Journal of Forest Research</i> , 2021, 140, 355-371.	1.1	20
109	Almond diversity and homozygosity define structure, kinship, inbreeding, and linkage disequilibrium in cultivated germplasm, and reveal genomic associations with nut and seed weight. <i>Horticulture Research</i> , 2021, 8, 15.	2.9	16

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110	Dispersal syndromes drive the formation of biogeographical regions, illustrated by the case of Wallace's Line. <i>Global Ecology and Biogeography</i> , 2021, 30, 685-696.	2.7	15
111	Implications of genetic heterogeneity for plant translocation during ecological restoration. <i>Ecology and Evolution</i> , 2021, 11, 1100-1110.	0.8	2
113	Comparative Performance of Popular Methods for Hybrid Detection using Genomic Data. <i>Systematic Biology</i> , 2021, 70, 891-907.	2.7	29
114	Structure and ancestry patterns of Ethiopians in genome-wide autosomal DNA. <i>Human Molecular Genetics</i> , 2021, 30, R42-R48.	1.4	3
115	Genetic population structure of a top predatory fish (northern pike, <i>Esox lucius</i>) covaries with anthropogenic alteration of freshwater ecosystems. <i>Freshwater Biology</i> , 2021, 66, 884-901.	1.2	5
117	Model-based genotype and ancestry estimation for potential hybrids with mixed ploidy. <i>Molecular Ecology Resources</i> , 2021, 21, 1434-1451.	2.2	35
119	The conservation management implications of isolation by distance and high genetic diversity in Great Spotted Kiwi (<i>Apteryx haastii</i>). <i>Emu</i> , 2021, 121, 10-22.	0.2	8
120	The History of Lentil (<i>Lens culinaris</i> subsp. <i>culinaris</i>) Domestication and Spread as Revealed by Genotyping-by-Sequencing of Wild and Landrace Accessions. <i>Frontiers in Plant Science</i> , 2021, 12, 628439.	1.7	25
121	Assessing the genetic background and genomic relatedness of red cattle populations originating from Northern Europe. <i>Genetics Selection Evolution</i> , 2021, 53, 23.	1.2	15
122	The choices we make and the impacts they have: Machine learning and species delimitation in North American box turtles (<i>Terrapene</i> spp.). <i>Molecular Ecology Resources</i> , 2021, 21, 2801-2817.	2.2	8
123	Genetic Differentiation and Demographic Trajectory of the Insular Formosan and Ori's Flying Foxes. <i>Journal of Heredity</i> , 2021, 112, 192-203.	1.0	1
124	Whole-genome resequencing reveals persistence of forest-associated mammals in Late Pleistocene refugia along North America's North Pacific Coast. <i>Journal of Biogeography</i> , 2021, 48, 1153-1169.	1.4	7
125	Changes in the fine-scale genetic structure of Finland through the 20th century. <i>PLoS Genetics</i> , 2021, 17, e1009347.	1.5	8
127	Tracing the origins of hybrids through history: monstrous cultivars and Napoleon's exiled paper daisies (Asteraceae; Gnaphalieae). <i>Botanical Journal of the Linnean Society</i> , 2021, 197, 277-289.	0.8	1
128	Evidence for ephemeral ring species formation during the diversification history of western fence lizards (<i>Sceloporus occidentalis</i>). <i>Molecular Ecology</i> , 2022, 31, 620-631.	2.0	17
129	HLA-DQB1 6672G>C (rs113332494) is associated with clozapine-induced neutropenia and agranulocytosis in individuals of European ancestry. <i>Translational Psychiatry</i> , 2021, 11, 214.	2.4	12
130	On the Unfounded Enthusiasm for Soft Selective Sweeps III: The Supervised Machine Learning Algorithm That Isn't. <i>Genes</i> , 2021, 12, 527.	1.0	2
132	Population genetic considerations for using biobanks as international resources in the pandemic era and beyond. <i>BMC Genomics</i> , 2021, 22, 351.	1.2	11

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133	Spatial population genetics in heavily managed species: Separating patterns of historical translocation from contemporary gene flow in white-tailed deer. <i>Evolutionary Applications</i> , 2021, 14, 1673-1689.	1.5	14
134	Ancient and modern stickleback genomes reveal the demographic constraints on adaptation. <i>Current Biology</i> , 2021, 31, 2027-2036.e8.	1.8	33
135	The genomic history of the Aegean palatial civilizations. <i>Cell</i> , 2021, 184, 2565-2586.e21.	13.5	43
136	Comment on "Population genetics reveal <i>Myotis keenii</i> (Keen's myotis) and <i>Myotis evotis</i> (long-eared myotis) to be a single species". <i>Canadian Journal of Zoology</i> , 2021, 99, 415-422.	0.4	5
138	Four times out of Europe: Serial invasions of the winter moth, <i>Operophtera brumata</i> , to North America. <i>Molecular Ecology</i> , 2021, 30, 3439-3452.	2.0	3
139	Genetic Admixture in the Culturally Unique Peranakan Chinese Population in Southeast Asia. <i>Molecular Biology and Evolution</i> , 2021, 38, 4463-4474.	3.5	8
140	An overview of current population genomics methods for the analysis of whole-genome resequencing data in eukaryotes. <i>Molecular Ecology</i> , 2021, 30, 6036-6071.	2.0	38
141	Evidence of the interplay of genetics and culture in Ethiopia. <i>Nature Communications</i> , 2021, 12, 3581.	5.8	25
142	Highly Replicated Evolution of Parapatric Ecotypes. <i>Molecular Biology and Evolution</i> , 2021, 38, 4805-4821.	3.5	17
143	Cooperative Communication with Humans Evolved to Emerge Early in Domestic Dogs. <i>Current Biology</i> , 2021, 31, 3137-3144.e11.	1.8	22
144	Dispersal in a house sparrow metapopulation: An integrative case study of genetic assignment calibrated with ecological data and pedigree information. <i>Molecular Ecology</i> , 2021, 30, 4740-4756.	2.0	10
145	LINADMIX: evaluating the effect of ancient admixture events on modern populations. <i>Bioinformatics</i> , 2021, 37, 4744-4755.	1.8	1
146	Genomic time-series data show that gene flow maintains high genetic diversity despite substantial genetic drift in a butterfly species. <i>Molecular Ecology</i> , 2021, 30, 4991-5008.	2.0	13
147	Evidence for genetic isolation and local adaptation in the field cricket <i>Gryllus campestris</i> . <i>Journal of Evolutionary Biology</i> , 2021, 34, 1624-1636.	0.8	6
148	Taxonomic Uncertainty and the Anomaly Zone: Phylogenomics Disentangle a Rapid Radiation to Resolve Contentious Species (<i>Gila robusta</i> Complex) in the Colorado River. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	9
149	Population structure of the brown-banded bamboo shark, <i>Chiloscyllium punctatum</i> and its relation to fisheries management in the Indo-Malay region. <i>Fisheries Research</i> , 2021, 240, 105972.	0.9	6
150	Demographic modeling informs functional connectivity and management interventions in Graham's beardtongue. <i>Conservation Genetics</i> , 2021, 22, 993.	0.8	1
151	Ancestral Spectrum Analysis With Population-Specific Variants. <i>Frontiers in Genetics</i> , 2021, 12, 724638.	1.1	3

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152	Ecomorphs are not species: the case of locally adapted populations of red crossbills. <i>Journal of Avian Biology</i> , 2021, 52, .	0.6	3
154	Relative performance of cluster algorithms and validation indices in maize genome-wide structure patterns. <i>Euphytica</i> , 2021, 217, 1.	0.6	2
155	Population structure of North Pacific gray whales in light of trans-Pacific movements. <i>Marine Mammal Science</i> , 2022, 38, 433-468.	0.9	4
157	Genetic and Ecogeographic Controls on Species Cohesion in Australia's Most Diverse Lizard Radiation. <i>American Naturalist</i> , 2022, 199, E57-E75.	1.0	6
158	The impact of estimator choice: Disagreement in clustering solutions across <i>K</i> estimators for Bayesian analysis of population genetic structure across a wide range of empirical data sets. <i>Molecular Ecology Resources</i> , 2022, 22, 1135-1148.	2.2	3
159	Ancient DNA from Guam and the peopling of the Pacific. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
172	A cautionary note on the use of unsupervised machine learning algorithms to characterise malaria parasite population structure from genetic distance matrices. <i>PLoS Genetics</i> , 2020, 16, e1009037.	1.5	5
173	A variant-centric perspective on geographic patterns of human allele frequency variation. <i>ELife</i> , 2020, 9, .	2.8	33
174	Yangtze River, an insignificant genetic boundary in tufted deer (<i>Elaphodus cephalophus</i>): the evidence from a first population genetics study. <i>PeerJ</i> , 2016, 4, e2654.	0.9	10
175	How much genetic variation is stored in the endangered and fragmented shrub <i>Tetraena mongolica</i> Maxim?. <i>PeerJ</i> , 2018, 6, e5645.	0.9	7
176	Whole genome resequencing data enables a targeted SNP panel for conservation and aquaculture of <i>Oreochromis</i> cichlid fishes. <i>Aquaculture</i> , 2022, 548, 737637.	1.7	8
177	Detecting Selection in Multiple Populations by Modeling Ancestral Admixture Components. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	24
178	Genetic structure in Louisiana Iris species reveals patterns of recent and historical admixture. <i>American Journal of Botany</i> , 2021, 108, 2257-2268.	0.8	4
179	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021, 598, 634-640.	13.7	142
186	Species limits and phylogeographic structure in two genera of solitary African mole-rats <i>Georchus</i> and <i>Heliophobius</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 167, 107337.	1.2	7
187	Homoploid hybrids, allopolyploids, and high ploidy levels characterize the evolutionary history of a western North American quillwort (<i>Isoetes</i>) complex. <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107332.	1.2	12
192	Sometimes hidden but always there: the assumptions underlying genetic inference of demographic histories. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20190719.	1.8	12
193	A Primer on the Population Genetic Analysis of Ancient Genomes. , 2021, , 371-385.		0

#	ARTICLE	IF	CITATIONS
194	Hybridization and range expansion in tamarisk beetles (<i>Diorhabda</i> spp.) introduced to North America for classical biological control. <i>Evolutionary Applications</i> , 2022, 15, 60-77.	1.5	6
195	Reevaluating Genetic Diversity and Structure of <i>Helianthus verticillatus</i> (Asteraceae) after the Discovery of New Populations. <i>Castanea</i> , 2022, 86, .	0.2	1
196	Genetic European Ancestry and Incident Diabetes in Black Individuals: Insights From the SPRINT Trial. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003468.	1.6	3
197	Review of the Forensic Applicability of Biostatistical Methods for Inferring Ancestry from Autosomal Genetic Markers. <i>Genes</i> , 2022, 13, 141.	1.0	5
198	A deep learning framework for characterization of genotype data. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	12
199	Physical geography, isolation by distance and environmental variables shape genomic variation of wild barley (<i>Hordeum vulgare</i> L. ssp. <i>spontaneum</i>) in the Southern Levant. <i>Heredity</i> , 2022, 128, 107-119.	1.2	10
200	Struct-f4: a Rcpp package for ancestry profile and population structure inference from f_4 -statistics. <i>Bioinformatics</i> , 2022, 38, 2070-2071.	1.8	4
201	DNA barcodes and microsatellites: How they complement for species identification in the complex genus <i>Tamarix</i> (Tamaricaceae). <i>Journal of Systematics and Evolution</i> , 2022, 60, 1140-1157.	1.6	5
202	Merging genotyping-by-sequencing data from two ex situ collections provides insights on the pea evolutionary history. <i>Horticulture Research</i> , 2022, , .	2.9	3
203	Global flyway evolution in red knots <i>Calidris canutus</i> and genetic evidence for a Nearctic refugium. <i>Molecular Ecology</i> , 2022, 31, 2124-2139.	2.0	7
204	Ghost Lineages Highly Influence the Interpretation of Introgression Tests. <i>Systematic Biology</i> , 2022, 71, 1147-1158.	2.7	49
205	Resilience to Historical Human Manipulations in the Genomic Variation of Italian Wild Boar Populations. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	6
207	Indian genetic heritage in Southeast Asian populations. <i>PLoS Genetics</i> , 2022, 18, e1010036.	1.5	19
208	Candidate-species delimitation in <i>Desmognathus</i> salamanders reveals gene flow across lineage boundaries, confounding phylogenetic estimation and clarifying hybrid zones. <i>Ecology and Evolution</i> , 2022, 12, e8574.	0.8	18
209	Genome-wide analysis suggests multiple domestication events of Chinese local pigs. <i>Animal Genetics</i> , 2022, 53, 293-306.	0.6	5
210	Genomic Screening to Identify Food Trees Potentially Dispersed by Precolonial Indigenous Peoples. <i>Genes</i> , 2022, 13, 476.	1.0	5
212	Genomic signatures of adaptive divergence in lacustrine copepods. <i>Freshwater Biology</i> , 2022, 67, 1045-1062.	1.2	3
213	Reproductive homing and fine-scaled genetic structuring of anadromous Baltic Sea perch (<i>Perca</i> Tj ETQq1 1 0,784314 rgBT /Overl	1.0	4

#	ARTICLE	IF	CITATIONS
215	The first steps toward a global pandemic: Reconstructing the demographic history of parasite host switches in its native range. <i>Molecular Ecology</i> , 2022, 31, 1358-1374.	2.0	6
216	A multiple predictive tool approach for phenotypic and biogeographical ancestry inferences. <i>Journal of the Canadian Society of Forensic Science</i> , 0, , 1-29.	0.7	0
217	Hybridization Dynamics and Extensive Introgression in the <i>Daphnia longispina</i> Species Complex: New Insights from a High-Quality <i>Daphnia galeata</i> Reference Genome. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	11
218	CLARITY: comparing heterogeneous data using dissimilarity. <i>Royal Society Open Science</i> , 2021, 8, 202182.	1.1	0
219	Genome-Wide Sequence-Based Genotyping Supports a Nonhybrid Origin of <i>Castanea alabamensis</i> . <i>Systematic Botany</i> , 2021, 46, 973-984.	0.2	3
220	Population expansion, divergence, and persistence in Western Fence Lizards (<i>Sceloporus occidentalis</i>) at the northern extreme of their distributional range. <i>Scientific Reports</i> , 2022, 12, 6310.	1.6	2
221	Human genetic admixture through the lens of population genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200410.	1.8	15
222	Re-situations of scientific knowledge: a case study of a skirmish over clusters vs clines in human population genomics. <i>History and Philosophy of the Life Sciences</i> , 2022, 44, 16.	0.6	1
223	Genomic consequences of a century of inbreeding and isolation in the Danish wild boar population. <i>Evolutionary Applications</i> , 2022, 15, 954-966.	1.5	0
225	Getting genetic ancestry right for science and society. <i>Science</i> , 2022, 376, 250-252.	6.0	93
245	Whole genome sequencing and the application of a SNP panel reveal primary evolutionary lineages and genomic variation in the lion (<i>Panthera leo</i>). <i>BMC Genomics</i> , 2022, 23, 321.	1.2	5
246	Population Genetics and Phylogeography of Galapagos Fur Seals. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	1
247	What Is Race? Four Philosophers, Six Views. <i>Philosophical Papers</i> , 2022, 51, 115-145.	0.2	2
248	Spatial genetic structure and limited gene flow in fragmented populations of the threatened Malleefowl (<i>Leipoa ocellata</i>). <i>Ecological Genetics and Genomics</i> , 2022, 24, 100127.	0.3	1
249	Visualizing population substructures using multidimensional scaling and data smoothing. , 2021, , .		1
250	There's gold in them thar hills! Morphology and molecules delimit species in. <i>Australian Systematic Botany</i> , 2022, 35, 120-185.	0.3	4
251	Genomic evidence of speciation by fusion in a recent radiation of grasshoppers. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 2618-2633.	1.1	3
252	Genomic Insights Into the Demographic History of the Southern Chinese. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	13

#	ARTICLE	IF	CITATIONS
253	Complex population structure and haplotype patterns in the Western European honey bee from sequencing a large panel of haploid drones. <i>Molecular Ecology Resources</i> , 2022, 22, 3068-3086.	2.2	9
254	Population structure and inbreeding in wild house mice (<i>Mus musculus</i>) at different geographic scales. <i>Heredity</i> , 2022, 129, 183-194.	1.2	12
255	Including diverse and admixed populations in genetic epidemiology research. <i>Genetic Epidemiology</i> , 2022, 46, 347-371.	0.6	11
256	Genomic resolution of cryptic species diversity in chipmunks. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 2004-2019.	1.1	2
257	Selection signature analyses and genome-wide association reveal genomic hotspot regions that reflect differences between breeds of horse with contrasting risk of degenerative suspensory ligament desmitis. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
258	Complex population history affects admixture analyses in nine-spined sticklebacks. <i>Molecular Ecology</i> , 2022, 31, 5386-5401.	2.0	14
259	Contemporary genetic structure of Xantus's Hummingbird (<i>Basilinna xantusii</i>) in the Baja California peninsula. <i>Ibis</i> , 2023, 165, 270-287.	1.0	0
260	A single introduction of wild rabbits triggered the biological invasion of Australia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	12
261	W Chromosome Evolution by Repeated Recycling in the Frog <i>Glandirana rugosa</i> . <i>Dna</i> , 2022, 2, 172-184.	0.4	4
262	Principal Component Analyses (PCA)-based findings in population genetic studies are highly biased and must be reevaluated. <i>Scientific Reports</i> , 2022, 12, .	1.6	48
263	The Biological Hierarchy, Time, and Temporal Omics in Evolutionary Biology: A Perspective. <i>Integrative and Comparative Biology</i> , 2022, 62, 1872-1886.	0.9	4
265	Genomic insights into rapid speciation within the world's largest tree genus <i>Syzygium</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	13
266	A central limit theorem concerning uncertainty in estimates of individual admixture. <i>Theoretical Population Biology</i> , 2022, 148, 28-39.	0.5	1
267	Theoretical analysis of principal components in an umbrella model of intraspecific evolution. <i>Theoretical Population Biology</i> , 2022, 148, 11-21.	0.5	2
268	Integrative QTL mapping and selection signatures in Groningen White Headed cattle inferred from whole-genome sequences. <i>PLoS ONE</i> , 2022, 17, e0276309.	1.1	3
269	A roadmap to robust Discriminant Analysis of Principal Components (DAPC). <i>Molecular Ecology Resources</i> , 0, , .	2.2	1
270	Subspecies at crossroads: the evolutionary significance of genomic and phenotypic variation in a wide-ranging Australian lizard (<i>Ctenotus pantherinus</i>). <i>Zoological Journal of the Linnean Society</i> , 2023, 197, 768-786.	1.0	3
271	Population genomic insights into invasion success in a polyphagous agricultural pest, <i>Halyomorpha halys</i> . <i>Molecular Ecology</i> , 2023, 32, 138-151.	2.0	12

#	ARTICLE	IF	CITATIONS
272	Pervasive Introgression During Rapid Diversification of the European Mountain Genus <i>Soldanella</i> (L.) (Primulaceae). <i>Systematic Biology</i> , 2023, 72, 491-504.	2.7	5
273	Unexpected genetic integrity boosts hope for the conservation of the red-legged partridge (<i>Alectoris</i>) Tj ETQq1 1 0,784314 rgBT /Ove	0.6	1
275	The influence of genetic structure on phenotypic diversity in the Australian mango (<i>Mangifera indica</i>) gene pool. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
277	Cultural and demic co-diffusion of Tubo Empire on Tibetan Plateau. <i>IScience</i> , 2022, 25, 105636.	1.9	6
280	Genomic Consequences of and Demographic Response to Pervasive Hybridization Over Time in Climate-Sensitive Pikas. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4
281	Low population genetic structure is consistent with high habitat connectivity in a commercially important fish species (<i>Lutjanus jocu</i>). <i>Marine Biology</i> , 2023, 170, .	0.7	4
282	Common protein-coding variants influence the racing phenotype in galloping racehorse breeds. <i>Communications Biology</i> , 2022, 5, .	2.0	4
283	Population Subdivision in the Gopher Frog (<i>Rana capito</i>) across the Fragmented Longleaf Pine-Wiregrass Savanna of the Southeastern USA. <i>Diversity</i> , 2023, 15, 93.	0.7	1
284	Phylogeography within the <i>Peromyscus maniculatus</i> species group: Understanding past distribution of genetic diversity and areas of refugia in western North America. <i>Molecular Phylogenetics and Evolution</i> , 2023, 180, 107701.	1.2	1
285	Visualizing Population Structures by Multidimensional Scaling of Smoothed PCA-Transformed Data. <i>IEEE Access</i> , 2023, 11, 13594-13604.	2.6	1
286	Range-wide whole-genome resequencing of the brown bear reveals drivers of intraspecies divergence. <i>Communications Biology</i> , 2023, 6, .	2.0	4
287	The population genetics of speciation by cascade reinforcement. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	1
288	Deep reticulation: the long legacy of hybridization in vascular plant evolution. <i>Plant Journal</i> , 2023, 114, 743-766.	2.8	23
289	Population genomics and phylogeography of four Australasian waterfowl. <i>Emu</i> , 0, , 1-13.	0.2	0
290	Climate-induced range shifts drive adaptive response via spatio-temporal sieving of alleles. <i>Nature Communications</i> , 2023, 14, .	5.8	7
291	Kazakh national dog breed Tazy: What do we know?. <i>PLoS ONE</i> , 2023, 18, e0282041.	1.1	3
292	Global, regional, and cryptic population structure in a high gene-flow transatlantic fish. <i>PLoS ONE</i> , 2023, 18, e0283351.	1.1	3
293	Genetic consequence of widespread plantations of <i>Cryptomeria japonica</i> var. <i>sinensis</i> in Southern China: implications for afforestation strategies under climate change. <i>Tree Genetics and Genomes</i> , 2023, 19, .	0.6	0

#	ARTICLE	IF	CITATIONS
329	Ancient Wheat Genomes Illuminate Domestication, Dispersal, and Diversity. Compendium of Plant Genomes, 2024, , 113-134.	0.3	0