

Oscar E Gaggiotti

List of Publications by Year in descending order

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84
papers

10,687
citations

81900

39
h-index

69250

77
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89
all docs

89
docs citations

89
times ranked

13060
citing authors

#	ARTICLE	IF	CITATIONS
1	A Genome-Scan Method to Identify Selected Loci Appropriate for Both Dominant and Codominant Markers: A Bayesian Perspective. <i>Genetics</i> , 2008, 180, 977-993.	2.9	2,366
2	What is a population? An empirical evaluation of some genetic methods for identifying the number of gene pools and their degree of connectivity. <i>Molecular Ecology</i> , 2006, 15, 1419-1439.	3.9	1,266
3	Approximate Bayesian Computation (ABC) in practice. <i>Trends in Ecology and Evolution</i> , 2010, 25, 410-418.	8.7	943
4	Assignment methods: matching biological questions with appropriate techniques. <i>Trends in Ecology and Evolution</i> , 2005, 20, 136-142.	8.7	645
5	Evaluating the performance of a multilocus Bayesian method for the estimation of migration rates. <i>Molecular Ecology</i> , 2007, 16, 1149-1166.	3.9	324
6	A comparison of two indirect methods for estimating average levels of gene flow using microsatellite data. <i>Molecular Ecology</i> , 1999, 8, 1513-1520.	3.9	319
7	Identifying the Environmental Factors That Determine the Genetic Structure of Populations. <i>Genetics</i> , 2006, 174, 875-891.	2.9	295
8	Spatial Inference of Admixture Proportions and Secondary Contact Zones. <i>Molecular Biology and Evolution</i> , 2009, 26, 1963-1973.	8.9	282
9	The goat domestication process inferred from large-scale mitochondrial DNA analysis of wild and domestic individuals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17659-17664.	7.1	279
10	Genome scan methods against more complex models: when and how much should we trust them?. <i>Molecular Ecology</i> , 2014, 23, 2006-2019.	3.9	265
11	Common garden experiments in the genomic era: new perspectives and opportunities. <i>Heredity</i> , 2016, 116, 249-254.	2.6	252
12	Computer simulations: tools for population and evolutionary genetics. <i>Nature Reviews Genetics</i> , 2012, 13, 110-122.	16.3	221
13	DISENTANGLING THE EFFECTS OF EVOLUTIONARY, DEMOGRAPHIC, AND ENVIRONMENTAL FACTORS INFLUENCING GENETIC STRUCTURE OF NATURAL POPULATIONS: ATLANTIC HERRING AS A CASE STUDY. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 2939-2951.	2.3	183
14	A new F _{ST} -based method to uncover local adaptation using environmental variables. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1248-1258.	5.2	164
15	Bringing genetic diversity to the forefront of conservation policy and management. <i>Conservation Genetics Resources</i> , 2013, 5, 593-598.	0.8	145
16	A New Bayesian Method to Identify the Environmental Factors That Influence Recent Migration. <i>Genetics</i> , 2008, 178, 1491-1504.	2.9	141
17	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010, 19, 436-446.	3.9	141
18	Widespread Signals of Convergent Adaptation to High Altitude in Asia and America. <i>American Journal of Human Genetics</i> , 2014, 95, 394-407.	6.2	131

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19	Metapopulation Biology. , 2004, , 3-22.		129
20	Detection of selective sweeps in structured populations: a comparison of recent methods. Molecular Ecology, 2016, 25, 89-103.	3.9	108
21	Differentiation measures for conservation genetics. Evolutionary Applications, 2018, 11, 1139-1148.	3.1	107
22	Emergent patterns of population genetic structure for a coral reef community. Molecular Ecology, 2014, 23, 3064-3079.	3.9	94
23	Quantifying population structure using the F_{ST} model. Molecular Ecology Resources, 2010, 10, 821-830.	4.8	91
24	An Approximate Bayesian Computation Approach to Overcome Biases That Arise When Using Amplified Fragment Length Polymorphism Markers to Study Population Structure. Genetics, 2008, 179, 927-939.	2.9	82
25	Patterns of colonization in a metapopulation of grey seals. Nature, 2002, 416, 424-427.	27.8	81
26	A simple method of removing the effect of a bottleneck and unequal population sizes on pairwise genetic distances. Proceedings of the Royal Society B: Biological Sciences, 2000, 267, 81-87.	2.6	77
27	Detecting adaptive evolution based on association with ecological gradients: Orientation matters!. Heredity, 2015, 115, 22-28.	2.6	76
28	Cultural traditions across a migratory network shape the genetic structure of southern right whales around Australia and New Zealand. Scientific Reports, 2015, 5, 16182.	3.3	72
29	Detecting polygenic selection in marine populations by combining population genomics and quantitative genetics approaches. Environmental Epigenetics, 2016, 62, 603-616.	1.8	67
30	Sample Planning Optimization Tool for conservation and population Genetics ($SPOTG$): a software for choosing the appropriate number of markers and samples. Methods in Ecology and Evolution, 2013, 4, 299-303.	5.2	66
31	Population Genetic Models of Source-Sink Metapopulations. Theoretical Population Biology, 1996, 50, 178-208.	1.1	65
32	Patterns of phenotypic plasticity and local adaptation in the wide elevation range of the alpine plant <i>Arabis alpina</i> . Journal of Ecology, 2018, 106, 1952-1971.	4.0	65
33	Population dynamics and stage structure in a haploid-diploid red seaweed, <i>Gracilaria gracilis</i> . Journal of Ecology, 2001, 89, 436-450.	4.0	64
34	The number of markers and samples needed for detecting bottlenecks under realistic scenarios, with and without recovery: a simulation-based study. Molecular Ecology, 2013, 22, 3444-3450.	3.9	64
35	Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. Evolutionary Applications, 2018, 11, 1176-1193.	3.1	60
36	Combining demographic, environmental and genetic data to test hypotheses about colonization events in metapopulations. Molecular Ecology, 2004, 13, 811-825.	3.9	47

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37	Identifying consistent allele frequency differences in studies of stratified populations. <i>Methods in Ecology and Evolution</i> , 2017, 8, 1899-1909.	5.2	47
38	The DNA of coral reef biodiversity: predicting and protecting genetic diversity of reef assemblages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160354.	2.6	45
39	Ecology and life history affect different aspects of the population structure of 27 high-alpine plants. <i>Molecular Ecology</i> , 2011, 20, 3144-3155.	3.9	44
40	Mechanisms of Population Extinction. , 2004, , 337-366.		42
41	Combining demography and genetic analysis to assess the population structure of an amphibian in a human-dominated landscape. <i>Conservation Genetics</i> , 2011, 12, 161-173.	1.5	42
42	Effect of life history strategy, environmental variability, and overexploitation on the genetic diversity of pelagic fish populations. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 1999, 56, 1376-1388.	1.4	40
43	Stochastic Migration and Maintenance of Genetic Variation in Sink Populations. <i>American Naturalist</i> , 1996, 147, 919-945.	2.1	39
44	Dispersal and population structure at different spatial scales in the subterranean rodent <i>Ctenomys australis</i> . <i>BMC Genetics</i> , 2010, 11, 9.	2.7	39
45	Metapopulation genetic structure of two coexisting parasitoids of the Glanville fritillary butterfly. <i>Oecologia</i> , 2005, 143, 77-84.	2.0	38
46	Effect of life history strategy, environmental variability, and overexploitation on the genetic diversity of pelagic fish populations. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 1999, 56, 1376-1388.	1.4	36
47	Genetic isolation of a now extinct population of bottlenose dolphins (<i>Tursiops truncatus</i>). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 1611-1616.	2.6	34
48	Conservation Genetic Resources for Effective Species Survival (ConGRESS): Bridging the divide between conservation research and practice. <i>Journal for Nature Conservation</i> , 2013, 21, 433-437.	1.8	32
49	Interactions between environmental factors can hide isolation by distance patterns: a case study of <i>Ctenomys rionegrensis</i> in Uruguay. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 2633-2638.	2.6	30
50	High variance in reproductive success generates a false signature of a genetic bottleneck in populations of constant size: a simulation study. <i>BMC Bioinformatics</i> , 2013, 14, 309.	2.6	29
51	Selection on ancestral genetic variation fuels repeated ecotype formation in bottlenose dolphins. <i>Science Advances</i> , 2021, 7, eabg1245.	10.3	27
52	Changes in selective pressures associated with human population expansion may explain metabolic and immune related pathways enriched for signatures of positive selection. <i>BMC Genomics</i> , 2016, 17, 504.	2.8	24
53	Disentangling the relative merits and disadvantages of parentage analysis and assignment tests for inferring population connectivity. <i>ICES Journal of Marine Science</i> , 2017, 74, 1749-1762.	2.5	24
54	An Ecological Model for the Maintenance of Sex and Geographic Parthenogenesis. <i>Journal of Theoretical Biology</i> , 1994, 167, 201-221.	1.7	23

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55	Patterns of Offspring Size at Birth in Clonal and Sexual Strains of Poeciliopsis (Poeciliidae). <i>Copeia</i> , 1993, 1993, 1003.	1.3	20
56	Incorporating non-equilibrium dynamics into demographic history inferences of a migratory marine species. <i>Heredity</i> , 2019, 122, 53-68.	2.6	20
57	The evolution of a highly speciose group in a changing environment: are we witnessing speciation in the Iberian wetlands?. <i>Molecular Ecology</i> , 2012, 21, 3266-3282.	3.9	19
58	Speciation in the deep: genomics and morphology reveal a new species of beaked whale <i>Mesoplodon eueu</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211213.	2.6	18
59	Making inferences about speciation using sophisticated statistical genetics methods: look before you leap. <i>Molecular Ecology</i> , 2011, 20, 2229-2232.	3.9	17
60	Genetic Diversity and Connectivity of Southern Right Whales (<i>Eubalaena australis</i>) Found in the Brazil and Chile-Peru Wintering Grounds and the South Georgia (Islas Georgias del Sur) Feeding Ground. <i>Journal of Heredity</i> , 2020, 111, 263-276.	2.4	17
61	Perturbation drives changing metapopulation dynamics in a top marine predator. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200318.	2.6	16
62	Metapopulations of Marine Species with Larval Dispersal: A Counterpoint to Ilkka's Glanville Fritillary Metapopulations. <i>Annales Zoologici Fennici</i> , 2017, 54, 97-112.	0.6	13
63	Invalid arguments against ABC: Reply to A.R. Templeton. <i>Trends in Ecology and Evolution</i> , 2010, 25, 490-491.	8.7	12
64	Influence of environmental heterogeneity on the distribution and persistence of a subterranean rodent in a highly unstable landscape. <i>Genetica</i> , 2016, 144, 711-722.	1.1	12
65	Fine-scale population structure and connectivity of bottlenose dolphins, <i>Tursiops truncatus</i> , in European waters and implications for conservation. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2019, 29, 197-211.	2.0	12
66	Common garden experiments to study local adaptation need to account for population structure. <i>Journal of Ecology</i> , 2022, 110, 1005-1009.	4.0	12
67	High genetic structure of the Cozumel Harvest mice, a critically endangered island endemic: conservation implications. <i>Conservation Genetics</i> , 2014, 15, 1393-1402.	1.5	11
68	Deep learning and satellite imagery predict genetic diversity and differentiation. <i>Methods in Ecology and Evolution</i> , 2022, 13, 711-721.	5.2	8
69	Multilocus Genotype Methods for the Study of Metapopulation Processes. , 2004, , 367-386.		6
70	colonise: a computer program to study colonization processes in metapopulations. <i>Molecular Ecology Notes</i> , 2005, 5, 705-707.	1.7	6
71	Bayesian statistical treatment of the fluorescence of AFLP bands leads to accurate genetic structure inference. <i>Molecular Ecology</i> , 2010, 19, 4586-4588.	3.9	6
72	Demographic history and genetic diversity in West Indian <i>Coereba flaveola</i> populations. <i>Genetica</i> , 2012, 140, 137-148.	1.1	6

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73	Genetic Structure in Heterogeneous Environments. , 2004, , 229-243.		5
74	Preface to the special issue: advances in the analysis of spatial genetic data. Molecular Ecology Resources, 2010, 10, 757-759.	4.8	5
75	Landscape, colonization, and life history: their effects on genetic diversity in four sympatric species inhabiting a dendritic system. Canadian Journal of Fisheries and Aquatic Sciences, 2019, 76, 2288-2302.	1.4	5
76	Accounting for stochasticity in demographic compensation along the elevational range of an alpine plant. Ecology Letters, 2020, 23, 870-880.	6.4	5
77	Effect of Stage-specific Vital Rates on Population Growth Rates and Effective Population Sizes in an Endangered Iteroparous Plant. Conservation Biology, 2012, 26, 208-217.	4.7	4
78	Estimating contemporary migration rates: effect and joint inference of inbreeding, null alleles and mistyping. Journal of Ecology, 2017, 105, 49-62.	4.0	4
79	Making use of the social network in conservation genomics: Integrating kinship and network analyses to understand connectivity. Molecular Ecology Resources, 2019, 19, 307-309.	4.8	3
80	Going back to Darwin's works. Trends in Plant Science, 2006, 11, 471-472.	8.8	1
81	Evolutionary population genetics: Were the Vikings immune to HIV?. Heredity, 2006, 96, 280-281.	2.6	1
82	Variation in $\delta^{13}C$ and $\delta^{15}N$ values of mothers and their calves across southern right whale nursery grounds: The effects of nutritional stress?. Marine Mammal Science, 0, , .	1.8	1
83	The Effect of Overlapping Generations and Population Structure on Gene-Frequency Clines. , 1997, , 355-369.		1
84	Information-based summary statistics for spatial genetic structure inference. Molecular Ecology Resources, 2022, 22, 2183-2195.	4.8	0