

Oscar E Gaggiotti

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

10,687
citations

81743

39
h-index

69108

77
g-index

89
all docs

89
docs citations

89
times ranked

13060
citing authors

#	ARTICLE	IF	CITATIONS
1	Common garden experiments to study local adaptation need to account for population structure. <i>Journal of Ecology</i> , 2022, 110, 1005-1009.	1.9	12
2	Information-based summary statistics for spatial genetic structure inference. <i>Molecular Ecology Resources</i> , 2022, 22, 2183-2195.	2.2	0
3	Deep learning and satellite imagery predict genetic diversity and differentiation. <i>Methods in Ecology and Evolution</i> , 2022, 13, 711-721.	2.2	8
4	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.	1.2	18
5	Selection on ancestral genetic variation fuels repeated ecotype formation in bottlenose dolphins. <i>Science Advances</i> , 2021, 7, eabg1245.	4.7	27
6	Perturbation drives changing metapopulation dynamics in a top marine predator. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200318.	1.2	16
7	Accounting for stochasticity in demographic compensation along the elevational range of an alpine plant. <i>Ecology Letters</i> , 2020, 23, 870-880.	3.0	5
8	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.	1.0	17
9	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.	0.9	12
10	Making use of the social network in conservation genomics: Integrating kinship and network analyses to understand connectivity. <i>Molecular Ecology Resources</i> , 2019, 19, 307-309.	2.2	3
11	Landscape, colonization, and life history: their effects on genetic diversity in four sympatric species inhabiting a dendritic system. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2019, 76, 2288-2302.	0.7	5
12	Incorporating non-equilibrium dynamics into demographic history inferences of a migratory marine species. <i>Heredity</i> , 2019, 122, 53-68.	1.2	20
13	Patterns of phenotypic plasticity and local adaptation in the wide elevation range of the alpine plant <i>Arabis alpina</i> . <i>Journal of Ecology</i> , 2018, 106, 1952-1971.	1.9	65
14	Differentiation measures for conservation genetics. <i>Evolutionary Applications</i> , 2018, 11, 1139-1148.	1.5	107
15	Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. <i>Evolutionary Applications</i> , 2018, 11, 1176-1193.	1.5	60
16	Estimating contemporary migration rates: effect and joint inference of inbreeding, null alleles and mistyping. <i>Journal of Ecology</i> , 2017, 105, 49-62.	1.9	4
17	Identifying consistent allele frequency differences in studies of stratified populations. <i>Methods in Ecology and Evolution</i> , 2017, 8, 1899-1909.	2.2	47
18	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.	1.2	24

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19	Metapopulations of Marine Species with Larval Dispersal: A Counterpoint to Ilkka's Glanville Fritillary Metapopulations. <i>Annales Zoologici Fennici</i> , 2017, 54, 97-112.	0.2	13
20	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.	1.2	24
21	Detection of selective sweeps in structured populations: a comparison of recent methods. <i>Molecular Ecology</i> , 2016, 25, 89-103.	2.0	108
22	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.	1.2	45
23	Detecting polygenic selection in marine populations by combining population genomics and quantitative genetics approaches. <i>Environmental Epigenetics</i> , 2016, 62, 603-616.	0.9	67
24	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.	0.5	12
25	Common garden experiments in the genomic era: new perspectives and opportunities. <i>Heredity</i> , 2016, 116, 249-254.	1.2	252
26	A new F_{ST} -based method to uncover local adaptation using environmental variables. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1248-1258.	2.2	164
27	Cultural traditions across a migratory network shape the genetic structure of southern right whales around Australia and New Zealand. <i>Scientific Reports</i> , 2015, 5, 16182.	1.6	72
28	Detecting adaptive evolution based on association with ecological gradients: Orientation matters!. <i>Heredity</i> , 2015, 115, 22-28.	1.2	76
29	Genome scan methods against more complex models: when and how much should we trust them?. <i>Molecular Ecology</i> , 2014, 23, 2006-2019.	2.0	265
30	High genetic structure of the Cozumel Harvest mice, a critically endangered island endemic: conservation implications. <i>Conservation Genetics</i> , 2014, 15, 1393-1402.	0.8	11
31	Emergent patterns of population genetic structure for a coral reef community. <i>Molecular Ecology</i> , 2014, 23, 3064-3079.	2.0	94
32	Widespread Signals of Convergent Adaptation to High Altitude in Asia and America. <i>American Journal of Human Genetics</i> , 2014, 95, 394-407.	2.6	131
33	The number of markers and samples needed for detecting bottlenecks under realistic scenarios, with and without recovery: a simulation-based study. <i>Molecular Ecology</i> , 2013, 22, 3444-3450.	2.0	64
34	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.	0.8	32
35	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.	1.2	29
36	Bringing genetic diversity to the forefront of conservation policy and management. <i>Conservation Genetics Resources</i> , 2013, 5, 593-598.	0.4	145

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37	Sample Planning Optimization Tool for conservation and population Genetics (<scp>SPOTG</scp>): a software for choosing the appropriate number of markers and samples. <i>Methods in Ecology and Evolution</i> , 2013, 4, 299-303.	2.2	66
38	Demographic history and genetic diversity in West Indian <i>Coereba flaveola</i> populations. <i>Genetica</i> , 2012, 140, 137-148.	0.5	6
39	Effect of Stage-specific Vital Rates on Population Growth Rates and Effective Population Sizes in an Endangered Iteroparous Plant. <i>Conservation Biology</i> , 2012, 26, 208-217.	2.4	4
40	Computer simulations: tools for population and evolutionary genetics. <i>Nature Reviews Genetics</i> , 2012, 13, 110-122.	7.7	221
41	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.	2.0	19
42	Making inferences about speciation using sophisticated statistical genetics methods: look before you leap. <i>Molecular Ecology</i> , 2011, 20, 2229-2232.	2.0	17
43	Ecology and life history affect different aspects of the population structure of 27 high-alpine plants. <i>Molecular Ecology</i> , 2011, 20, 3144-3155.	2.0	44
44	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.	0.8	42
45	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
46	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010, 19, 436-446.	2.0	141
47	Bayesian statistical treatment of the fluorescence of AFLP bands leads to accurate genetic structure inference. <i>Molecular Ecology</i> , 2010, 19, 4586-4588.	2.0	6
48	Approximate Bayesian Computation (ABC) in practice. <i>Trends in Ecology and Evolution</i> , 2010, 25, 410-418.	4.2	943
49	Invalid arguments against ABC: Reply to A.R. Templeton. <i>Trends in Ecology and Evolution</i> , 2010, 25, 490-491.	4.2	12
50	Quantifying population structure using the F_{ST} model. <i>Molecular Ecology Resources</i> , 2010, 10, 821-830.	2.2	91
51	Preface to the special issue: advances in the analysis of spatial genetic data. <i>Molecular Ecology Resources</i> , 2010, 10, 757-759.	2.2	5
52	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.	1.1	183
53	Spatial Inference of Admixture Proportions and Secondary Contact Zones. <i>Molecular Biology and Evolution</i> , 2009, 26, 1963-1973.	3.5	282
54	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.	1.2	2,366

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55	An Approximate Bayesian Computation Approach to Overcome Biases That Arise When Using Amplified Fragment Length Polymorphism Markers to Study Population Structure. <i>Genetics</i> , 2008, 179, 927-939.	1.2	82
56	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.	3.3	279
57	A New Bayesian Method to Identify the Environmental Factors That Influence Recent Migration. <i>Genetics</i> , 2008, 178, 1491-1504.	1.2	141
58	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.	1.2	30
59	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.	1.2	34
60	Evaluating the performance of a multilocus Bayesian method for the estimation of migration rates. <i>Molecular Ecology</i> , 2007, 16, 1149-1166.	2.0	324
61	Identifying the Environmental Factors That Determine the Genetic Structure of Populations. <i>Genetics</i> , 2006, 174, 875-891.	1.2	295
62	Going back to Darwin's works. <i>Trends in Plant Science</i> , 2006, 11, 471-472.	4.3	1
63	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.	2.0	1,266
64	Evolutionary population genetics: Were the Vikings immune to HIV?. <i>Heredity</i> , 2006, 96, 280-281.	1.2	1
65	colonise: a computer program to study colonization processes in metapopulations. <i>Molecular Ecology Notes</i> , 2005, 5, 705-707.	1.7	6
66	Metapopulation genetic structure of two coexisting parasitoids of the Glanville fritillary butterfly. <i>Oecologia</i> , 2005, 143, 77-84.	0.9	38
67	Assignment methods: matching biological questions with appropriate techniques. <i>Trends in Ecology and Evolution</i> , 2005, 20, 136-142.	4.2	645
68	Genetic Structure in Heterogeneous Environments. , 2004, , 229-243.		5
69	Mechanisms of Population Extinction. , 2004, , 337-366.		42
70	Multilocus Genotype Methods for the Study of Metapopulation Processes. , 2004, , 367-386.		6
71	Metapopulation Biology. , 2004, , 3-22.		129
72	Combining demographic, environmental and genetic data to test hypotheses about colonization events in metapopulations. <i>Molecular Ecology</i> , 2004, 13, 811-825.	2.0	47

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73	Patterns of colonization in a metapopulation of grey seals. <i>Nature</i> , 2002, 416, 424-427.	13.7	81
74	Population dynamics and stage structure in a haploid-diploid red seaweed, <i>Gracilaria gracilis</i> . <i>Journal of Ecology</i> , 2001, 89, 436-450.	1.9	64
75	A simple method of removing the effect of a bottleneck and unequal population sizes on pairwise genetic distances. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 81-87.	1.2	77
76	A comparison of two indirect methods for estimating average levels of gene flow using microsatellite data. <i>Molecular Ecology</i> , 1999, 8, 1513-1520.	2.0	319
77	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.	0.7	40
78	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.	0.7	36
79	The Effect of Overlapping Generations and Population Structure on Gene-Frequency Clines. , 1997, , 355-369.		1
80	Population Genetic Models of Source-Sink Metapopulations. <i>Theoretical Population Biology</i> , 1996, 50, 178-208.	0.5	65
81	Stochastic Migration and Maintenance of Genetic Variation in Sink Populations. <i>American Naturalist</i> , 1996, 147, 919-945.	1.0	39
82	An Ecological Model for the Maintenance of Sex and Geographic Parthenogenesis. <i>Journal of Theoretical Biology</i> , 1994, 167, 201-221.	0.8	23
83	Patterns of Offspring Size at Birth in Clonal and Sexual Strains of <i>Poeciliopsis</i> (Poeciliidae). <i>Copeia</i> , 1993, 1993, 1003.	1.4	20
84	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?. <i>Marine Mammal Science</i> , 0, , .	0.9	1