

Bryan C Carstens

List of Publications by Year in descending order

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Version: 2024-02-01

106
papers

9,067
citations

71102

41
h-index

43889

91
g-index

115
all docs

115
docs citations

115
times ranked

9375
citing authors

#	ARTICLE	IF	CITATIONS
1	How to fail at species delimitation. <i>Molecular Ecology</i> , 2013, 22, 4369-4383.	3.9	896
2	Delimiting Species without Monophyletic Gene Trees. <i>Systematic Biology</i> , 2007, 56, 887-895.	5.6	657
3	Phylogeography's past, present, and future: 10 years after Avise, 2000. <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 291-301.	2.7	535
4	Applications of next-generation sequencing to phylogeography and phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 526-538.	2.7	531
5	Phylogenetic estimation error can decrease the accuracy of species delimitation: a Bayesian implementation of the general mixed Yule-coalescent model. <i>BMC Evolutionary Biology</i> , 2012, 12, 196.	3.2	432
6	STEM: species tree estimation using maximum likelihood for gene trees under coalescence. <i>Bioinformatics</i> , 2009, 25, 971-973.	4.1	419
7	Climate refugia: joint inference from fossil records, species distribution models and phylogeography. <i>New Phytologist</i> , 2014, 204, 37-54.	7.3	361
8	Estimating Species Phylogeny from Gene-Tree Probabilities Despite Incomplete Lineage Sorting: An Example from <i>Melanoplus</i> Grasshoppers. <i>Systematic Biology</i> , 2007, 56, 400-411.	5.6	309
9	INTEGRATING COALESCENT AND ECOLOGICAL NICHE MODELING IN COMPARATIVE PHYLOGEOGRAPHY. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 1439-1454.	2.3	290
10	Distribution modelling and statistical phylogeography: an integrative framework for generating and testing alternative biogeographical hypotheses. <i>Journal of Biogeography</i> , 2007, 34, 1833-1845.	3.0	245
11	SpedeSTEM: a rapid and accurate method for species delimitation. <i>Molecular Ecology Resources</i> , 2011, 11, 473-480.	4.8	223
12	Multilocus Species Delimitation in a Complex of Morphologically Conserved Trapdoor Spiders (<i>Mygalomorphae</i> , <i>Antrodiaetidae</i> , <i>Aliatypus</i>). <i>Systematic Biology</i> , 2013, 62, 805-823.	5.6	221
13	Comparative Gut Microbiota of 59 Neotropical Bird Species. <i>Frontiers in Microbiology</i> , 2015, 6, 1403.	3.5	216
14	INVESTIGATING THE EVOLUTIONARY HISTORY OF THE PACIFIC NORTHWEST MESIC FOREST ECOSYSTEM: HYPOTHESIS TESTING WITHIN A COMPARATIVE PHYLOGEOGRAPHIC FRAMEWORK. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 1639.	2.3	170
15	Shifting distributions and speciation: species divergence during rapid climate change. <i>Molecular Ecology</i> , 2006, 16, 619-627.	3.9	168
16	Species Delimitation Using a Combined Coalescent and Information-Theoretic Approach: An Example from North American <i>Myotis</i> Bats. <i>Systematic Biology</i> , 2010, 59, 400-414.	5.6	167
17	Coupling Genetic and Ecological-Niche Models to Examine How Past Population Distributions Contribute to Divergence. <i>Current Biology</i> , 2007, 17, 940-946.	3.9	148
18	Does gene flow destroy phylogenetic signal? The performance of three methods for estimating species phylogenies in the presence of gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 832-842.	2.7	132

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19	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 May 2009–31 July 2009. <i>Molecular Ecology Resources</i> , 2009, 9, 1460-1466.	4.8	128
20	Sampling locality is more detectable than taxonomy or ecology in the gut microbiota of the brood-parasitic Brown-headed Cowbird (<i>Molothrus ater</i>). <i>PeerJ</i> , 2014, 2, e321.	2.0	126
21	The evolution of phylogeographic data sets. <i>Molecular Ecology</i> , 2015, 24, 1164-1171.	3.9	119
22	Species Delimitation with Gene Flow. <i>Systematic Biology</i> , 2017, 66, syw117.	5.6	118
23	A road map for molecular ecology. <i>Molecular Ecology</i> , 2013, 22, 2605-2626.	3.9	100
24	ESTIMATING A GEOGRAPHICALLY EXPLICIT MODEL OF POPULATION DIVERGENCE. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 477-493.	2.3	92
25	Predicting plant conservation priorities on a global scale. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13027-13032.	7.1	92
26	Accounting for coalescent stochasticity in testing phylogeographical hypotheses: modelling Pleistocene population structure in the Idaho giant salamander <i>Dicamptodon aterrimus</i> . <i>Molecular Ecology</i> , 2004, 14, 255-265.	3.9	89
27	Testing Nested Phylogenetic and Phylogeographic Hypotheses in the <i>Plethodon vandykei</i> Species Group. <i>Systematic Biology</i> , 2004, 53, 781-792.	5.6	85
28	Poor Fit to the Multispecies Coalescent is Widely Detectable in Empirical Data. <i>Systematic Biology</i> , 2014, 63, 322-333.	5.6	78
29	Deep Phylogeographic Structure and Environmental Differentiation in the Carnivorous Plant <i>Sarracenia alata</i> . <i>Systematic Biology</i> , 2012, 61, 763-777.	5.6	69
30	An information-theoretical approach to phylogeography. <i>Molecular Ecology</i> , 2009, 18, 4270-4282.	3.9	66
31	Exploring population genetic structure in three species of Lesser Antillean bats. <i>Molecular Ecology</i> , 2004, 13, 2557-2566.	3.9	64
32	Recurrent connections between Amazon and Atlantic forests shaped diversity in Caatinga four-eyed frogs. <i>Journal of Biogeography</i> , 2016, 43, 1045-1056.	3.0	64
33	Process-based species delimitation leads to identification of more biologically relevant species*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 216-229.	2.3	63
34	PHRAPL: Phylogeographic Inference Using Approximate Likelihoods. <i>Systematic Biology</i> , 2017, 66, 1045-1053.	5.6	59
35	Model selection as a tool for phylogeographic inference: an example from the willow <i>Salix melanopsis</i> . <i>Molecular Ecology</i> , 2013, 22, 4014-4028.	3.9	58
36	The Carnivorous Pale Pitcher Plant Harbors Diverse, Distinct, and Time-Dependent Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1851-1860.	3.1	56

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37	The carnivorous plant described as <i>Sarracenia alata</i> contains two cryptic species. <i>Biological Journal of the Linnean Society</i> , 2013, 109, 737-746.	1.6	56
38	Model choice for phylogeographic inference using a large set of models. <i>Molecular Ecology</i> , 2014, 23, 3028-3043.	3.9	55
39	PRGmatic: an efficient pipeline for collating genome-enriched second-generation sequencing data using a provisional reference genome™. <i>Molecular Ecology Resources</i> , 2011, 11, 743-748. ^{4.8}		52
40	Speciation with Gene Flow in North American <i>Myotis</i> Bats. <i>Systematic Biology</i> , 2017, 66, syw100.	5.6	50
41	Geographical range size and latitude predict population genetic structure in a global survey. <i>Biology Letters</i> , 2018, 14, 20170566.	2.3	50
42	Demographic model selection using random forests and the site frequency spectrum. <i>Molecular Ecology</i> , 2017, 26, 4562-4573.	3.9	49
43	Testing hypotheses of speciation timing in <i>Dicamptodon copei</i> and <i>Dicamptodon aterrimus</i> (Caudata: Tj ETQq1 1 0.784314 rrgBT /Over 2.7 48	2.7	48
44	Identifying cryptic diversity with predictive phylogeography. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161529.	2.6	45
45	Insights into the Biogeography of the Pacific Northwest of North America: Evidence from the Phylogeography of <i>Salix melanopsis</i> . <i>Systematic Botany</i> , 2007, 32, 129-139.	0.5	44
46	Phylogeographic model selection leads to insight into the evolutionary history of four-eyed frogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8010-8017.	7.1	43
47	Diversification rates have no effect on the convergent evolution of foraging strategies in the most speciose genus of bats, <i>Myotis</i> *. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 2263-2280.	2.3	40
48	Title is missing!. <i>Journal of Mammalian Evolution</i> , 2002, 9, 23-53.	1.8	38
49	Phylogeographic concordance factors quantify phylogeographic congruence among co-distributed species in the <i>Sarracenia alata</i> pitcher plant system. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1105-1119.	2.3	37
50	Evidence that <i>Myotis lucifugus</i> Subspecies are Five Nonsister Species, Despite Gene Flow. <i>Systematic Biology</i> , 2018, 67, 756-769.	5.6	37
51	The Promises and Pitfalls of Next-Generation Sequencing Data in Phylogeography. <i>Systematic Biology</i> , 2012, 61, 713-715.	5.6	36
52	Assessing model fit in phylogeographical investigations: an example from the North American sandbar willow <i>Salix melanopsis</i> . <i>Journal of Biogeography</i> , 2013, 40, 131-141.	3.0	35
53	Do ecological communities disperse across biogeographic barriers as a unit?. <i>Molecular Ecology</i> , 2017, 26, 3533-3545.	3.9	35
54	The Microbial Phylogeography of the Carnivorous Plant <i>Sarracenia alata</i> . <i>Microbial Ecology</i> , 2011, 61, 750-758.	2.8	34

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55	Genetic diversity in migratory bats: Results from RADseq data for three tree bat species at an Ohio windfarm. <i>PeerJ</i> , 2016, 4, e1647.	2.0	33
56	Conservation genetic inferences in the carnivorous pitcher plant <i>Sarracenia alata</i> (Sarraceniaceae). <i>Conservation Genetics</i> , 2010, 11, 2027-2038.	1.5	32
57	Historical Species Distribution Models Predict Species Limits in Western <i>Plethodon</i> Salamanders. <i>Systematic Biology</i> , 2015, 64, 909-925.	5.6	31
58	Rapid and accurate species tree estimation for phylogeographic investigations using replicated subsampling. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 888-898.	2.7	29
59	A global analysis of bats using automated comparative phylogeography uncovers a surprising impact of Pleistocene glaciation. <i>Journal of Biogeography</i> , 2018, 45, 1795-1805.	3.0	26
60	Comparative phylogeography of mutualists and the effect of the host on the genetic structure of its partners. <i>Biological Journal of the Linnean Society</i> , 2014, 113, 1021-1035.	1.6	23
61	Diversification of North American natricine snakes. <i>Biological Journal of the Linnean Society</i> , 2015, 116, 1-12.	1.6	23
62	X Chromosome Inactivation and Xist Evolution in a Rodent Lacking LINE-1 Activity. <i>PLoS ONE</i> , 2009, 4, e6252.	2.5	23
63	Posterior predictive checks of coalescent models: P2C2M, an R package. <i>Molecular Ecology Resources</i> , 2016, 16, 193-205.	4.8	21
64	Using Next Generation RAD Sequencing to Isolate Multispecies Microsatellites for <i>Pilosocereus</i> (Cactaceae). <i>PLoS ONE</i> , 2015, 10, e0142602.	2.5	19
65	From inland to the coast: Spatial and environmental signatures on the genetic diversity in the colonization of the South Atlantic Coastal Plain. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2017, 28, 47-57.	2.7	18
66	Predicting migration routes for three species of migratory bats using species distribution models. <i>PeerJ</i> , 2021, 9, e11177.	2.0	17
67	Comparing range evolution in two western <i>Plethodon</i> salamanders: glacial refugia, competition, ecological niches, and spatial sorting. <i>Journal of Biogeography</i> , 2016, 43, 2237-2249.	3.0	16
68	Anonymous nuclear markers reveal taxonomic incongruence and long-term disjunction in a cactus species complex with continental-island distribution in South America. <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 11-19.	2.7	16
69	Variable nuclear markers for <i>Melanoplus oregonensis</i> identified from the screening of a genomic library. <i>Molecular Ecology Notes</i> , 2006, 6, 683-685.	1.7	15
70	Testing monophyly without well-supported gene trees: Evidence from multi-locus nuclear data conflicts with existing taxonomy in the snake tribe <i>Thamnophiini</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 425-431.	2.7	15
71	Phylogeographic model selection using convolutional neural networks. <i>Molecular Ecology Resources</i> , 2021, 21, 2661-2675.	4.8	14
72	Objective choice of phylogeographic models. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 136-140.	2.7	13

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73	Predicting amphibian intraspecific diversity with machine learning: Challenges and prospects for integrating traits, geography, and genetic data. <i>Molecular Ecology Resources</i> , 2021, 21, 2818-2831.	4.8	13
74	Genomic data from the Brazilian sibilator frog reveal contrasting pleistocene dynamics and regionalism in two South American dry biomes. <i>Journal of Biogeography</i> , 2021, 48, 1112-1123.	3.0	13
75	Analysis of biodiversity data suggests that mammal species are hidden in predictable places. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2103400119.	7.1	13
76	Integrating life history traits into predictive phylogeography. <i>Molecular Ecology</i> , 2019, 28, 2062-2073.	3.9	11
77	Population genetic structure and demographic history of the lone star tick, <i>Amblyomma americanum</i> (Ixodida: Ixodidae): New evidence supporting old records. <i>Molecular Ecology</i> , 2020, 29, 2810-2823.	3.9	11
78	Using trace elements to identify the geographic origin of migratory bats. <i>PeerJ</i> , 2020, 8, e10082.	2.0	11
79	Biogeographic barriers drive co-diversification within associated eukaryotes of the <i>Sarracenia alata</i> pitcher plant system. <i>PeerJ</i> , 2016, 4, e1576.	2.0	11
80	phylogatR: Phylogeographic data aggregation and repurposing. <i>Molecular Ecology Resources</i> , 2022, 22, 2830-2842.	4.8	11
81	Testing for the presence of cryptic diversity in tail-dropper slugs (<i>Prophysaon</i>) using molecular data. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 518-532.	1.6	10
82	Complex interplay of ancient vicariance and recent patterns of geographical speciation in north-western North American temperate rainforests explains the phylogeny of jumping slugs (<i>Hemphillia</i> spp.). <i>Biological Journal of the Linnean Society</i> , 2019, 127, 876-889.	1.6	10
83	Does habitat stability structure intraspecific genetic diversity? It's complicated.... <i>Frontiers of Biogeography</i> , 2020, 12, .	1.8	10
84	P2C2M.GMYC: An R package for assessing the utility of the Generalized Mixed Yule Coalescent model. <i>Methods in Ecology and Evolution</i> , 2021, 12, 487-493.	5.2	10
85	Combining allele frequency and tree-based approaches improves phylogeographic inference from natural history collections. <i>Molecular Ecology</i> , 2018, 27, 1012-1024.	3.9	9
86	Navigating the unknown: model selection in phylogeography. <i>Molecular Ecology</i> , 2010, 19, 4581-4582.	3.9	8
87	A role of asynchrony of seasons in explaining genetic differentiation in a Neotropical toad. <i>Heredity</i> , 2021, 127, 363-372.	2.6	7
88	Genetic diversity of North American vertebrates in protected areas. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 388-399.	1.6	7
89	Assessing model adequacy leads to more robust phylogeographic inference. <i>Trends in Ecology and Evolution</i> , 2022, 37, 402-410.	8.7	7
90	Testing population genetic structure using parametric bootstrapping and MIGRATE-N. <i>Genetica</i> , 2005, 124, 71-75.	1.1	6

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91	Statistical hybrid detection and the inference of ancestral distribution areas in Tolpis (Asteraceae). <i>Biological Journal of the Linnean Society</i> , 2017, 121, 133-149.	1.6	6
92	The <i>Sarracenia alata</i> pitcher plant system and obligate arthropod inquilines should be considered an evolutionary community. <i>Journal of Biogeography</i> , 2019, 46, 485-496.	3.0	6
93	The Phylogeographic Shortfall in Hexapods: A Lot of Leg Work Remaining. <i>Insect Systematics and Diversity</i> , 2021, 5, .	1.7	6
94	Evaluating the adaptive evolutionary convergence of carnivorous plant taxa through functional genomics. <i>PeerJ</i> , 2018, 6, e4322.	2.0	6
95	Identifying model violations under the multispecies coalescent model using P2C2M.SNAPP. <i>PeerJ</i> , 2020, 8, e8271.	2.0	6
96	Comparative and predictive phylogeography in the South American diagonal of open formations: Unravelling the biological and environmental influences on multitaxon demography. <i>Molecular Ecology</i> , 2022, 31, 331-342.	3.9	6
97	Community trees: Identifying codiversification in the Páramo dipteran community. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1080-1093.	2.3	5
98	Comment on "Population genetics reveal <i>Myotis keenii</i> (<i>Keen's myotis</i>) and <i>Myotis evotis</i> (long-eared myotis) to be a single species" Canadian <i>Journal of Zoology</i> , 2021, 99, 415-422.	1.0	5
99	Genomic evidence of an ancient inland temperate rainforest in the Pacific Northwest of North America. <i>Molecular Ecology</i> , 2022, , .	3.9	4
100	The role of multiple Pleistocene refugia in promoting diversification in the Pacific Northwest. <i>Molecular Ecology</i> , 2022, 31, 4402-4416.	3.9	4
101	Phylogeny of Leafhopper Subgenus <i>Errhomus</i> (<i>Erronus</i>) (Hemiptera: Cicadellidae) Based on Mitochondrial DNA Sequences. <i>Annals of the Entomological Society of America</i> , 2005, 98, 165-172.	2.5	3
102	Anonymous nuclear markers data supporting species tree phylogeny and divergence time estimates in a cactus species complex in South America. <i>Data in Brief</i> , 2016, 6, 456-460.	1.0	3
103	Comparative phylogeography of two Northern Rocky Mountain endemics: the widespread <i>Anguispira kochi occidentalis</i> and the narrow-range <i>Anguispira nimapuna</i> (Gastropoda: Discidae). <i>Biological Journal of the Linnean Society</i> , 2021, 133, 817-834.	1.6	2
104	Identifying traits that enable lizard adaptation to different habitats. <i>Journal of Biogeography</i> , 2022, 49, 104-116.	3.0	2
105	Genomic Resources for the North American Water Vole (<i>Microtus richardsoni</i>) and the Montane Vole (<i>Microtus montanus</i>). <i>GigaByte</i> , 0, 2021, 1-13.	0.0	1
106	Giant tree frogs exemplify the promise of integrating multiple types of data in phylogeographic investigations. <i>Molecular Ecology</i> , 0, , .	3.9	1