## Brian C O'meara

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Retiring "Cradles―and "Museums―of Biodiversity. American Naturalist, 2022, 199, 194-205.	2.1	22
2	A flexible method for estimating tip diversification rates across a range of speciation and extinction scenarios. Evolution; International Journal of Organic Evolution, 2022, 76, 1420-1433.	2.3	26
3	A Spatially Explicit Model of Stabilizing Selection for Improving Phylogenetic Inference. Molecular Biology and Evolution, 2021, 38, 1641-1652.	8.9	1
4	The ecological and genomic basis of explosive adaptive radiation. Nature, 2020, 586, 75-79.	27.8	146
5	Unlocking a signal of introgression from codons in Lachancea kluyveri using a mutation-selection model. BMC Evolutionary Biology, 2020, 20, 109.	3.2	5
6	The evolution of a tropical biodiversity hotspot. Science, 2020, 370, 1343-1348.	12.6	179
7	Phylotastic: Improving Access to Tree-of-Life Knowledge With Flexible, on-the-Fly Delivery of Trees. Evolutionary Bioinformatics, 2020, 16, 117693431989938.	1.2	2
8	On the Matrix Condition of Phylogenetic Tree. Evolutionary Bioinformatics, 2020, 16, 117693432090172.	1.2	3
9	Leaf reflectance spectra capture the evolutionary history of seed plants. New Phytologist, 2020, 228, 485-493.	7.3	72
10	Gene expression of functionally-related genes coevolves across fungal species: detecting coevolution of gene expression using phylogenetic comparative methods. BMC Genomics, 2020, 21, 370.	2.8	10
11	Diversity and skepticism are vital for comparative biology: aÂresponse to Donoghue and Edwards (2019). American Journal of Botany, 2019, 106, 613-617.	1.7	15
12	Reef fish functional traits evolve fastest at trophic extremes. Nature Ecology and Evolution, 2019, 3, 191-199.	7.8	23
13	Population Genetics Based Phylogenetics Under Stabilizing Selection for an Optimal Amino Acid Sequence: A Nested Modeling Approach. Molecular Biology and Evolution, 2019, 36, 834-851.	8.9	11
14	Can we build it? Yes we can, but should we use it? AssessingÂthe quality and value of a very large phylogeny ofÂcampanulid angiosperms. American Journal of Botany, 2018, 105, 417-432.	1.7	45
15	Hidden state models improve state-dependent diversification approaches, including biogeographical models. Evolution; International Journal of Organic Evolution, 2018, 72, 2308-2324.	2.3	145
16	<i>AnnotationBustR</i> : an R package to extract subsequences from GenBank annotations. PeerJ, 2018, 6, e5179.	2.0	9
17	Species Delimitation with Gene Flow. Systematic Biology, 2017, 66, syw117.	5.6	118
18	Speciation with Gene Flow in North American <i>Myotis</i> Bats. Systematic Biology, 2017, 66, syw100.	5.6	50

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19	PHRAPL: Phylogeographic Inference Using Approximate Likelihoods. Systematic Biology, 2017, 66, 1045-1053.	5.6	59
20	Objective choice of phylogeographic models. Molecular Phylogenetics and Evolution, 2017, 116, 136-140.	2.7	13
21	The ontogeny of personality traits in the desert funnelâ€web spider, <i>Agelenopsis lisa</i> (Araneae:) Tj ETQq1	1 0.78431 1.1	4 ggBT /Over
22	Non-equilibrium dynamics and floral trait interactions shape extant angiosperm diversity. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20152304.	2.6	79
23	Past, future, and present of stateâ€dependent models of diversification. American Journal of Botany, 2016, 103, 792-795.	1.7	39
24	Detecting Hidden Diversification Shifts in Models of Trait-Dependent Speciation and Extinction. Systematic Biology, 2016, 65, 583-601.	5.6	447
25	Zanne et al. reply. Nature, 2015, 521, E6-E7.	27.8	3
26	Extinction can be estimated from moderately sized molecular phylogenies. Evolution; International Journal of Organic Evolution, 2015, 69, 1036-1043.	2.3	92
27	Heterogeneous Rates of Molecular Evolution and Diversification Could Explain the Triassic Age Estimate for Angiosperms. Systematic Biology, 2015, 64, 869-878.	5.6	108
28	Evolutionary models for the retention of adult–adult social play in primates: The roles of diet and other factors associated with resource acquisition. Adaptive Behavior, 2015, 23, 381-391.	1.9	10
29	The Xeromphalina campanella/kauffmanii complex: species delineation and biogeographical patterns of speciation. Mycologia, 2015, 107, 1270-1284.	1.9	16
30	Repeated evolution of tricellular (and bicellular) pollen. American Journal of Botany, 2014, 101, 559-571.	1.7	53
31	Functional distinctiveness of major plant lineages. Journal of Ecology, 2014, 102, 345-356.	4.0	108
32	Investigating the performance of AIC in selecting phylogenetic models. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 459-75.	0.6	10
33	Three keys to the radiation of angiosperms into freezing environments. Nature, 2014, 506, 89-92.	27.8	1,284
34	Reol: R interface to the E ncyclopedia of L ife. Ecology and Evolution, 2014, 4, 2577-2583.	1.9	5
35	Associations Between Eating Occasion Characteristics and Age, Gender, Presence of Children and BMI Among U.S. Adults. Journal of the American College of Nutrition, 2014, 33, 315-327.	1.8	14
36	Modelling Stabilizing Selection: The Attraction of Ornstein–Uhlenbeck Models. , 2014, , 381-393.		16

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37	Hidden Markov Models for Studying the Evolution of Binary Morphological Characters. , 2014, , 395-408.		17
38	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. BMC Bioinformatics, 2013, 14, 158.	2.6	33
39	Phylogenetic relationships and character evolution analysis of Saxifragales using a supermatrix approach. American Journal of Botany, 2013, 100, 916-929.	1.7	92
40	Identifying Hidden Rate Changes in the Evolution of a Binary Morphological Character: The Evolution of Plant Habit in Campanulid Angiosperms. Systematic Biology, 2013, 62, 725-737.	5.6	306
41	Mitochondrial genome primers for Lake Malawi cichlids. Molecular Ecology Resources, 2013, 13, 347-353.	4.8	15
42	treePL: divergence time estimation using penalized likelihood for large phylogenies. Bioinformatics, 2012, 28, 2689-2690.	4.1	558
43	Evolutionary Inferences from Phylogenies: A Review of Methods. Annual Review of Ecology, Evolution, and Systematics, 2012, 43, 267-285.	8.3	200
44	Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis. BMC Research Notes, 2012, 5, 574.	1.4	42
45	MODELING STABILIZING SELECTION: EXPANDING THE ORNSTEIN-UHLENBECK MODEL OF ADAPTIVE EVOLUTION. Evolution; International Journal of Organic Evolution, 2012, 66, 2369-2383.	2.3	537
46	RBrownie: an R package for testing hypotheses about rates of evolutionary change. Methods in Ecology and Evolution, 2011, 2, 660-662.	5.2	11
47	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. Frontiers in Plant Science, 2011, 2, 34.	3.6	396
48	Developmental evolution of flowering plant pollen tube cell walls: callose synthase (CalS) gene expression patterns. EvoDevo, 2011, 2, 14.	3.2	38
49	Habitat use affects morphological diversification in dragon lizards. Journal of Evolutionary Biology, 2010, 23, 1033-1049.	1.7	79
50	New Heuristic Methods for Joint Species Delimitation and Species Tree Inference. Systematic Biology, 2010, 59, 59-73.	5.6	241
51	Morphogenera, monophyly, and macroevolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, E97-8; author reply E99-100.	7.1	4
52	PISCIVORY LIMITS DIVERSIFICATION OF FEEDING MORPHOLOGY IN CENTRARCHID FISHES. Evolution; International Journal of Organic Evolution, 2009, 63, 1557-1573.	2.3	139
53	Five Drosophila Genomes Reveal Nonneutral Evolution and the Signature of Host Specialization in the Chemoreceptor Superfamily. Genetics, 2007, 177, 1395-1416.	2.9	179
54	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. Evolution; International Journal of Organic Evolution, 2006, 60, 922.	2.3	183

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55	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. Evolution; International Journal of Organic Evolution, 2006, 60, 922-933.	2.3	516
56	Testing for different rates of continuous trait evolution using likelihood. Evolution; International Journal of Organic Evolution, 2006, 60, 922-33.	2.3	153
57	Prospects for Building the Tree of Life from Large Sequence Databases. Science, 2004, 306, 1172-1174.	12.6	233
58	<i>MonoPhy</i> : a simple R package to find and visualize monophyly issues. PeerJ Computer Science, 0, 2, e56.	4.5	22