

Michael A Charleston

List of Publications by Year in descending order

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84
papers

4,052
citations

257357

24
h-index

123376

61
g-index

86
all docs

86
docs citations

86
times ranked

5577
citing authors

#	ARTICLE	IF	CITATIONS
1	The Epidemic Behavior of the Hepatitis C Virus. <i>Science</i> , 2001, 292, 2323-2325.	6.0	405
2	From Gene to Organismal Phylogeny: Reconciled Trees and the Gene Tree/Species Tree Problem. <i>Molecular Phylogenetics and Evolution</i> , 1997, 7, 231-240.	1.2	384
3	Trees within trees: phylogeny and historical associations. <i>Trends in Ecology and Evolution</i> , 1998, 13, 356-359.	4.2	261
4	Preferential Host Switching by Primate Lentiviruses Can Account for Phylogenetic Similarity with the Primate Phylogeny. <i>Systematic Biology</i> , 2002, 51, 528-535.	2.7	239
5	Jungles: a new solution to the host/parasite phylogeny reconciliation problem. <i>Mathematical Biosciences</i> , 1998, 149, 191-223.	0.9	229
6	Hantavirus Evolution in Relation to Its Rodent and Insectivore Hosts: No Evidence for Codivergence. <i>Molecular Biology and Evolution</i> , 2008, 26, 143-153.	3.5	209
7	Insights into the Evolutionary History of an Emerging Livestock Pathogen: Porcine Circovirus 2. <i>Journal of Virology</i> , 2009, 83, 12813-12821.	1.5	208
8	Host Switch Leads to Emergence of Plasmodium vivax Malaria in Humans. <i>Molecular Biology and Evolution</i> , 2005, 22, 1686-1693.	3.5	199
9	Fungal identification using a Bayesian classifier and the Warcup training set of internal transcribed spacer sequences. <i>Mycologia</i> , 2016, 108, 1-5.	0.8	178
10	Mathematical Elegance with Biochemical Realism: The Covarion Model of Molecular Evolution. <i>Journal of Molecular Evolution</i> , 2001, 53, 711-723.	0.8	173
11	A covariotide model explains apparent phylogenetic structure of oxygenic photosynthetic lineages. <i>Molecular Biology and Evolution</i> , 1998, 15, 1183-1188.	3.5	135
12	Differential variability analysis of gene expression and its application to human diseases. <i>Bioinformatics</i> , 2008, 24, i390-i398.	1.8	128
13	Modelling nutritional interactions: from individuals to communities. <i>Trends in Ecology and Evolution</i> , 2010, 25, 53-60.	4.2	111
14	A Cophylogenetic Perspective of RNA-Virus Evolution. <i>Molecular Biology and Evolution</i> , 2003, 21, 45-57.	3.5	102
15	Nutritional ecology beyond the individual: a conceptual framework for integrating nutrition and social interactions. <i>Ecology Letters</i> , 2015, 18, 273-286.	3.0	92
16	Traversing the tangle: Algorithms and applications for cophylogenetic studies. <i>Journal of Biomedical Informatics</i> , 2006, 39, 62-71.	2.5	77
17	On the Computational Complexity of the Reticulate Cophylogeny Reconstruction Problem. <i>Journal of Computational Biology</i> , 2009, 16, 105-117.	0.8	57
18	Intercalated discs: multiple proteins perform multiple functions in non-failing and failing human hearts. <i>Biophysical Reviews</i> , 2009, 1, 43-49.	1.5	49

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19	The emergence of sarcoptic mange in Australian wildlife: an unresolved debate. <i>Parasites and Vectors</i> , 2016, 9, 316.	1.0	45
20	Modelling nutrition across organizational levels: From individuals to superorganisms. <i>Journal of Insect Physiology</i> , 2014, 69, 2-11.	0.9	42
21	The Effects of Sequence Length, Tree Topology, and Number of Taxa on the Performance of Phylogenetic Methods. <i>Journal of Computational Biology</i> , 1994, 1, 133-151.	0.8	41
22	Phylogenetic Codivergence Supports Coevolution of Mimetic <i>Heliconius</i> Butterflies. <i>PLoS ONE</i> , 2012, 7, e36464.	1.1	41
23	Collective foraging in spatially complex nutritional environments. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160238.	1.8	41
24	Evolving Nutritional Strategies in the Presence of Competition: A Geometric Agent-Based Model. <i>PLoS Computational Biology</i> , 2015, 11, e1004111.	1.5	28
25	The forecasting of dynamical Ross River virus outbreaks: Victoria, Australia. <i>Epidemics</i> , 2020, 30, 100377.	1.5	26
26	Recent Results in Cophylogeny Mapping. <i>Advances in Parasitology</i> , 2003, 54, 303-330.	1.4	25
27	Markov invariants, plethysms, and phylogenetics. <i>Journal of Theoretical Biology</i> , 2008, 253, 601-615.	0.8	24
28	EVOLUTION: Is the "Big Bang" in Animal Evolution Real?. <i>Science</i> , 2005, 310, 1910-1911.	6.0	22
29	A SIMPLE MODEL EXPLAINS THE DYNAMICS OF PREFERENTIAL HOST SWITCHING AMONG MAMMAL RNA VIRUSES. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 980-990.	1.1	22
30	Mitochondrial genome sequencing reveals potential origins of the scabies mite <i>Sarcoptes scabiei</i> infesting two iconic Australian marsupials. <i>BMC Evolutionary Biology</i> , 2017, 17, 233.	3.2	22
31	Emerging phylogenetic structure of the SARS-CoV-2 pandemic. <i>Virus Evolution</i> , 2020, 6, veaa082.	2.2	21
32	Bioacoustics Data Analysis – A Taxonomy, Survey and Open Challenges. <i>IEEE Access</i> , 2020, 8, 57684-57708.	2.6	20
33	Wing patterning genes and coevolution of Müllerian mimicry in <i>Heliconius</i> butterflies: Support from phylogeography, cophylogeny, and divergence times. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 3082-3096.	1.1	19
34	Hadamard conjugation: A versatile tool for modelling nucleotide sequence evolution. <i>New Zealand Journal of Botany</i> , 1993, 31, 231-237.	0.8	16
35	How to test bioinformatics software?. <i>Biophysical Reviews</i> , 2015, 7, 343-352.	1.5	16
36	Macronutrient intakes and the lifespan-fecundity trade-off: a geometric framework agent-based model. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20180733.	1.5	15

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37	HIV-1 gp120 N-linked glycosylation differs between plasma and leukocyte compartments. <i>Virology Journal</i> , 2008, 5, 14.	1.4	14
38	A model selection approach to discover age-dependent gene expression patterns using quantile regression models. <i>BMC Genomics</i> , 2009, 10, S16.	1.2	14
39	Introducing TreeCollapse: a novel greedy algorithm to solve the cophylogeny reconstruction problem. <i>BMC Bioinformatics</i> , 2014, 15, S14.	1.2	14
40	Five surprising properties of parsimoniously colored trees. <i>Bulletin of Mathematical Biology</i> , 1995, 57, 367-375.	0.9	13
41	An improved node mapping algorithm for the cophylogeny reconstruction problem. <i>Coevolution</i> , 2014, 2, 1-17.	1.2	13
42	Event-Based Cophylogenetic Comparative Analysis. , 2014, , 465-480.		13
43	Australian spiny mountain crayfish and their temnocephalan ectosymbionts: an ancient association on the edge of coextinction?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160585.	1.2	13
44	Tracing the origin and co-phylogeny of the caliciviruses. <i>Journal of General Virology</i> , 2006, 87, 1229-1235.	1.3	12
45	MrIML: Multi-response interpretable machine learning to model genomic landscapes. <i>Molecular Ecology Resources</i> , 2021, 21, 2766-2781.	2.2	12
46	Neighbor-Joining Uses the Optimal Weight for Net Divergence. <i>Molecular Phylogenetics and Evolution</i> , 1993, 2, 6-12.	1.2	11
47	Adaptive collective foraging in groups with conflicting nutritional needs. <i>Royal Society Open Science</i> , 2016, 3, 150638.	1.1	11
48	Mining autograding data in computer science education. , 2016, , .		11
49	Establishing a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia. <i>Briefings in Bioinformatics</i> , 2019, 20, 384-389.	3.2	11
50	Mainstreaming Microbes across Biomes. <i>BioScience</i> , 2020, 70, 589-596.	2.2	11
51	Long-Term Spatiotemporal Dynamics and Factors Associated with Trends in Bare-Nosed Wombats. <i>Journal of Wildlife Management</i> , 2021, 85, 449-461.	0.7	11
52	VERIFICATION OF PHYLOGENETIC INFERENCE PROGRAMS USING METAMORPHIC TESTING. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 729-747.	0.3	10
53	Fluralaner as a novel treatment for sarcoptic mange in the bare-nosed wombat (<i>Vombatus ursinus</i>): safety, pharmacokinetics, efficacy and practicable use. <i>Parasites and Vectors</i> , 2021, 14, 18.	1.0	10
54	Evolution of endogenous retroviruses in the Suidae: evidence for different viral subpopulations in African and Eurasian host species. <i>BMC Evolutionary Biology</i> , 2011, 11, 139.	3.2	9

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55	Hitch-Hiking: A Parallel Heuristic Search Strategy, Applied to the Phylogeny Problem. <i>Journal of Computational Biology</i> , 2001, 8, 79-91.	0.8	8
56	RASCAL: A Randomized Approach for Coevolutionary Analysis. <i>Journal of Computational Biology</i> , 2016, 23, 218-227.	0.8	8
57	Comments on Allard and Carpenter (1996), or the "Aquatic Ape" Hypothesis Revisited. <i>Cladistics</i> , 1999, 15, 73-74.	1.5	7
58	Principles of cophylogenetic maps. , 2002, , 122-147.		7
59	Phylogenetic estimation with partial likelihood tensors. <i>Journal of Theoretical Biology</i> , 2010, 262, 413-424.	0.8	7
60	Hierarchical kernel mixture models for the prediction of AIDS disease progression using HIV structural gp120 profiles. <i>BMC Genomics</i> , 2010, 11, S22.	1.2	7
61	Node Fingerprinting: An Efficient Heuristic for Aligning Biological Networks. <i>Journal of Computational Biology</i> , 2014, 21, 760-770.	0.8	6
62	Lack of Evidence for Cospeciation Between Retroelements and Their Hosts. <i>Journal of Molecular Evolution</i> , 2000, 50, 194-201.	0.8	5
63	Towards sub-quadratic time and space complexity solutions for the dated tree reconciliation problem. <i>Algorithms for Molecular Biology</i> , 2016, 11, 15.	0.3	5
64	Optimising predictive modelling of Ross River virus using meteorological variables. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009252.	1.3	5
65	Hunting alters viral transmission and evolution in a large carnivore. <i>Nature Ecology and Evolution</i> , 2022, 6, 174-182.	3.4	5
66	Methods of analysing patterns of multimorbidity using network analysis: a scoping review.. <i>Zeitschrift Fur Gesundheitswissenschaften</i> , 2023, 31, 1217-1223.	0.8	5
67	Network modelling of gene regulation. <i>Biophysical Reviews</i> , 2011, 3, 1-13.	1.5	4
68	Active subnetwork recovery with a mechanism-dependent scoring function; with application to angiogenesis and organogenesis studies. <i>BMC Bioinformatics</i> , 2013, 14, 59.	1.2	4
69	A time and space complexity reduction for coevolutionary analysis of trees generated under both a Yule and Uniform model. <i>Computational Biology and Chemistry</i> , 2015, 57, 61-71.	1.1	4
70	Draft Genome Sequences of Three Sub-Antarctic <i>Rhodococcus</i> spp., Including Two Novel Psychrophilic Genomespecies. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
71	Benchmarking Methods of Protein Structure Alignment. <i>Journal of Molecular Evolution</i> , 2020, 88, 575-597.	0.8	4
72	Methods of analyzing patterns of multimorbidity using network analysis: a scoping review protocol. <i>JBI Evidence Synthesis</i> , 2021, 19, 2857-2862.	0.6	3

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73	Inferring differential leukocyte activity from antibody microarrays using a latent variable model. <i>Genome Informatics</i> , 2008, 21, 126-37.	0.4	3
74	Lability of Antiretroviral Drug Resistance Mutations - Correlates with Immunological and Virological Responses. <i>Current HIV Research</i> , 2007, 5, 430-439.	0.2	2
75	Node Handprinting: A Scalable and Accurate Algorithm for Aligning Multiple Biological Networks. <i>Journal of Computational Biology</i> , 2015, 22, 687-697.	0.8	2
76	Draft Genome Sequences of Two Novel Sub-Antarctic <i>Williamsia</i> Species. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
77	Draft Genome Sequence of Subantarctic <i>Rhodococcus</i> sp. Strain 1139. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
78	INFERRING DIFFERENTIAL LEUKOCYTE ACTIVITY FROM ANTIBODY MICROARRAYS USING A LATENT VARIABLE MODEL. , 2008, , .		2
79	Simple, rapid and accurate genotyping-by-sequencing from aligned whole genomes with ArrayMaker. <i>Bioinformatics</i> , 2015, 31, 599-601.	1.8	1
80	Biological Network Edit Distance. <i>Journal of Computational Biology</i> , 2016, 23, 776-788.	0.8	1
81	A Sub-quadratic Time and Space Complexity Solution for the Dated Tree Reconciliation Problem for Select Tree Topologies. <i>Lecture Notes in Computer Science</i> , 2015, , 93-107.	1.0	1
82	A cophylogenetic perspective on host-pathogen evolution. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 2006, , 145-160.	0.0	1
83	Unattained geometric configurations of secondary structure elements in protein structural space. <i>Journal of Structural Biology</i> , 2022, 214, 107870.	1.3	1
84	Molecular Phylogenetics. , 2019, , 700-711.		0