Michael A Charleston

List of Publications by Year
in descending order

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	Methods of analysing patterns of multimorbidity using network analysis: a scoping review.. Zeitschrift Fur Gesundheitswissenschaften, 2023, 31, 1217-1223.	0.8	5
2	Hunting alters viral transmission and evolution in a large carnivore. Nature Ecology and Evolution, 2022, 6, 174-182.	3.4	5
3	Unattained geometric configurations of secondary structure elements in protein structural space. Journal of Structural Biology, 2022, 214, 107870.	1.3	1
4	Fluralaner as a novel treatment for sarcoptic mange in the bare-nosed wombat (Vombatus ursinus): safety, pharmacokinetics, efficacy and practicable use. Parasites and Vectors, 2021, 14, 18.	1.0	10
5	Long‐Term Spatiotemporal Dynamics and Factors Associated with Trends in Bare‐Nosed Wombats. Journal of Wildlife Management, 2021, 85, 449-461.	0.7	11
6	Optimising predictive modelling of Ross River virus using meteorological variables. PLoS Neglected Tropical Diseases, 2021, 15, e0009252.	1.3	5
7	Methods of analyzing patterns of multimorbidity using network analysis: a scoping review protocol. JBI Evidence Synthesis, 2021, 19, 2857-2862.	0.6	3
8	MrIML: Multi‐response interpretable machine learning to model genomic landscapes. Molecular Ecology Resources, 2021, 21, 2766-2781.	2.2	12
9	The forecasting of dynamical Ross River virus outbreaks: Victoria, Australia. Epidemics, 2020, 30, 100377.	1.5	26
10	Benchmarking Methods of Protein Structure Alignment. Journal of Molecular Evolution, 2020, 88, 575-597.	0.8	4
11	Emerging phylogenetic structure of the SARS-CoV-2 pandemic. Virus Evolution, 2020, 6, veaa082.	2.2	21
12	Mainstreaming Microbes across Biomes. BioScience, 2020, 70, 589-596.	2.2	11
13	Bioacoustics Data Analysis – A Taxonomy, Survey and Open Challenges. IEEE Access, 2020, 8, 57684-57708.	2.6	20
14	Molecular Phylogenetics. , 2019, , 700-711.		0
15	Macronutrient intakes and the lifespan-fecundity trade-off: a geometric framework agent-based model. Journal of the Royal Society Interface, 2019, 16, 20180733.	1.5	15
16	Establishing a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia. Briefings in Bioinformatics, 2019, 20, 384-389.	3.2	11
17	Draft Genome Sequences of Three Sub-Antarctic Rhodococcus spp., Including Two Novel Psychrophilic Genomospecies. Genome Announcements, 2017, 5, .	0.8	4
18	Draft Genome Sequences of Two Novel Sub-Antarctic <i>Williamsia</i> Species. Genome Announcements, 2017, 5, .	0.8	2

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19	Collective foraging in spatially complex nutritional environments. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160238.	1.8	41
20	Mitochondrial genome sequencing reveals potential origins of the scabies mite Sarcoptes scabiei infesting two iconic Australian marsupials. BMC Evolutionary Biology, 2017, 17, 233.	3.2	22
21	Draft Genome Sequence of Subantarctic *Rhodococcus* sp. Strain 1139. Genome Announcements, 2017, 5, .	0.8	2
22	Adaptive collective foraging in groups with conflicting nutritional needs. Royal Society Open Science, 2016, 3, 150638.	1.1	11
23	Australian spiny mountain crayfish and their temnocephalan ectosymbionts: an ancient association on the edge of coextinction?. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20160585.	1.2	13
24	The emergence of sarcoptic mange in Australian wildlife: an unresolved debate. Parasites and Vectors, 2016, 9, 316.	1.0	45
25	Towards sub-quadratic time and space complexity solutions for the dated tree reconciliation problem. Algorithms for Molecular Biology, 2016, 11, 15.	0.3	5
26	Biological Network Edit Distance. Journal of Computational Biology, 2016, 23, 776-788.	0.8	1
27	RASCAL: A Randomized Approach for Coevolutionary Analysis. Journal of Computational Biology, 2016, 23, 218-227.	0.8	8
28	Mining autograding data in computer science education. , 2016, , .		11
29	Fungal identification using a Bayesian classifier and the Warcup training set of internal transcribed spacer sequences. Mycologia, 2016, 108, 1-5.	0.8	178
30	Wing patterning genes and coevolution of MÃ¼llerian mimicry in *Heliconius* butterflies: Support from phylogeography, cophylogeny, and divergence times. Evolution; International Journal of Organic Evolution, 2015, 69, 3082-3096.	1.1	19
31	How to test bioinformatics software?. Biophysical Reviews, 2015, 7, 343-352.	1.5	16
32	Simple, rapid and accurate genotyping-by-sequencing from aligned whole genomes with ArrayMaker. Bioinformatics, 2015, 31, 599-601.	1.8	1
33	Nutritional ecology beyond the individual: a conceptual framework for integrating nutrition and social interactions. Ecology Letters, 2015, 18, 273-286.	3.0	92
34	A time and space complexity reduction for coevolutionary analysis of trees generated under both a Yule and Uniform model. Computational Biology and Chemistry, 2015, 57, 61-71.	1.1	4
35	Evolving Nutritional Strategies in the Presence of Competition: A Geometric Agent-Based Model. PLoS Computational Biology, 2015, 11, e1004111.	1.5	28
36	Node Handprinting: A Scalable and Accurate Algorithm for Aligning Multiple Biological Networks. Journal of Computational Biology, 2015, 22, 687-697.	0.8	2

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37	A Sub-quadratic Time and Space Complexity Solution for the Dated Tree Reconciliation Problem for Select Tree Topologies. Lecture Notes in Computer Science, 2015, , 93-107.	1.0	1
38	Node Fingerprinting: An Efficient Heuristic for Aligning Biological Networks. Journal of Computational Biology, 2014, 21, 760-770.	0.8	6
39	Modelling nutrition across organizational levels: From individuals to superorganisms. Journal of Insect Physiology, 2014, 69, 2-11.	0.9	42
40	An improved node mapping algorithm for the cophylogeny reconstruction problem. Coevolution, 2014, 2, 1-17.	1.2	13
41	Event-Based Cophylogenetic Comparative Analysis. , 2014, , 465-480.		13
42	Introducing TreeCollapse: a novel greedy algorithm to solve the cophylogeny reconstruction problem. BMC Bioinformatics, 2014, 15, S14.	1.2	14
43	Active subnetwork recovery with a mechanism-dependent scoring function; with application to angiogenesis and organogenesis studies. BMC Bioinformatics, 2013, 14, 59.	1.2	4
44	A SIMPLE MODEL EXPLAINS THE DYNAMICS OF PREFERENTIAL HOST SWITCHING AMONG MAMMAL RNA VIRUSES. Evolution; International Journal of Organic Evolution, 2013, 67, 980-990.	1.1	22
45	Phylogenetic Codivergence Supports Coevolution of Mimetic Heliconius Butterflies. PLoS ONE, 2012, 7, e36464.	1.1	41
46	Network modelling of gene regulation. Biophysical Reviews, 2011, 3, 1-13.	1.5	4
47	Evolution of endogenous retroviruses in the Suidae: evidence for different viral subpopulations in African and Eurasian host species. BMC Evolutionary Biology, 2011, 11, 139.	3.2	9
48	VERIFICATION OF PHYLOGENETIC INFERENCE PROGRAMS USING METAMORPHIC TESTING. Journal of Bioinformatics and Computational Biology, 2011, 09, 729-747.	0.3	10
49	Phylogenetic estimation with partial likelihood tensors. Journal of Theoretical Biology, 2010, 262, 413-424.	0.8	7
50	Hierarchical kernel mixture models for the prediction of AIDS disease progression using HIV structural gp120 profiles. BMC Genomics, 2010, 11, S22.	1.2	7
51	Modelling nutritional interactions: from individuals to communities. Trends in Ecology and Evolution, 2010, 25, 53-60.	4.2	111
52	Insights into the Evolutionary History of an Emerging Livestock Pathogen: Porcine Circovirus 2. Journal of Virology, 2009, 83, 12813-12821.	1.5	208
53	A model selection approach to discover age-dependent gene expression patterns using quantile regression models. BMC Genomics, 2009, 10, S16.	1.2	14
54	Intercalated discs: multiple proteins perform multiple functions in non-failing and failing human hearts. Biophysical Reviews, 2009, 1, 43-49.	1.5	49

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55	On the Computational Complexity of the Reticulate Cophylogeny Reconstruction Problem. Journal of Computational Biology, 2009, 16, 105-117.	0.8	57
56	Markov invariants, plethysms, and phylogenetics. Journal of Theoretical Biology, 2008, 253, 601-615.	0.8	24
57	Hantavirus Evolution in Relation to Its Rodent and Insectivore Hosts: No Evidence for Codivergence. Molecular Biology and Evolution, 2008, 26, 143-153.	3.5	209
58	HIV-1 gp120 N-linked glycosylation differs between plasma and leukocyte compartments. Virology Journal, 2008, 5, 14.	1.4	14
59	Differential variability analysis of gene expression and its application to human diseases. Bioinformatics, 2008, 24, i390-i398.	1.8	128
60	INFERRING DIFFERENTIAL LEUKOCYTE ACTIVITY FROM ANTIBODY MICROARRAYS USING A LATENT VARIABLE MODEL. , 2008, , .		2
61	Inferring differential leukocyte activity from antibody microarrays using a latent variable model. Genome Informatics, 2008, 21, 126-37.	0.4	3
62	Lability of Antiretroviral Drug Resistance Mutations - Correlates with Immunological and Virological Responses. Current HIV Research, 2007, 5, 430-439.	0.2	2
63	Traversing the tangle: Algorithms and applications for cophylogenetic studies. Journal of Biomedical Informatics, 2006, 39, 62-71.	2.5	77
64	Tracing the origin and co-phylogeny of the caliciviruses. Journal of General Virology, 2006, 87, 1229-1235.	1.3	12
65	A cophylogenetic perspective on host-pathogen evolution. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 2006, , 145-160.	0.0	1
66	Host Switch Leads to Emergence of Plasmodium vivax Malaria in Humans. Molecular Biology and Evolution, 2005, 22, 1686-1693.	3.5	199
67	EVOLUTION: Is the "Big Bang" in Animal Evolution Real?. Science, 2005, 310, 1910-1911.	6.0	22
68	A Cophylogenetic Perspective of RNA-Virus Evolution. Molecular Biology and Evolution, 2003, 21, 45-57.	3.5	102
69	Recent Results in Cophylogeny Mapping. Advances in Parasitology, 2003, 54, 303-330.	1.4	25
70	Principles of cophylogenetic maps. , 2002, , 122-147.		7
71	Preferential Host Switching by Primate Lentiviruses Can Account for Phylogenetic Similarity with the Primate Phylogeny. Systematic Biology, 2002, 51, 528-535.	2.7	239
72	The Epidemic Behavior of the Hepatitis C Virus. Science, 2001, 292, 2323-2325.	6.0	405

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73	Hitch-Hiking: A Parallel Heuristic Search Strategy, Applied to the Phylogeny Problem. Journal of Computational Biology, 2001, 8, 79-91.	0.8	8
74	Mathematical Elegance with Biochemical Realism: The Covarion Model of Molecular Evolution. Journal of Molecular Evolution, 2001, 53, 711-723.	0.8	173
75	Lack of Evidence for Cospeciation Between Retroelements and Their Hosts. Journal of Molecular Evolution, 2000, 50, 194-201.	0.8	5
76	Comments on Allard and Carpenter (1996), or the â€œAquatic Apeâ€•Hypothesis Revisited. Cladistics, 1999, 15, 73-74.	1.5	7
77	Trees within trees: phylogeny and historical associations. Trends in Ecology and Evolution, 1998, 13, 356-359.	4.2	261
78	Jungles: a new solution to the host/parasite phylogeny reconciliation problem. Mathematical Biosciences, 1998, 149, 191-223.	0.9	229
79	A covariotide model explains apparent phylogenetic structure of oxygenic photosynthetic lineages. Molecular Biology and Evolution, 1998, 15, 1183-1188.	3.5	135
80	From Gene to Organismal Phylogeny: Reconciled Trees and the Gene Tree/Species Tree Problem. Molecular Phylogenetics and Evolution, 1997, 7, 231-240.	1.2	384
81	Five surprising properties of parsimoniously colored trees. Bulletin of Mathematical Biology, 1995, 57, 367-375.	0.9	13
82	The Effects of Sequence Length, Tree Topology, and Number of Taxa on the Performance of Phylogenetic Methods. Journal of Computational Biology, 1994, 1, 133-151.	0.8	41
83	Neighbor-Joining Uses the Optimal Weight for Net Divergence. Molecular Phylogenetics and Evolution, 1993, 2, 6-12.	1.2	11
84	Hadamard conjugation: A versatile tool for modelling nucleotide sequence evolution. New Zealand Journal of Botany, 1993, 31, 231-237.	0.8	16