

Sebastian Duchene

List of Publications by Citations

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96
papers

4,656
citations

34
h-index

67
g-index

121
ext. papers

7,005
ext. citations

8.9
avg, IF

5.93
L-index

#	Paper	IF	Citations
96	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019 , 15, e1006650	5	1014
95	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. <i>Nature</i> , 2017 , 544, 357-361	50.4	263
94	Molecular-clock methods for estimating evolutionary rates and timescales. <i>Molecular Ecology</i> , 2014 , 23, 5947-65	5.7	187
93	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020 , 6, veaa061	3.7	147
92	Comparative analysis estimates the relative frequencies of co-divergence and cross-species transmission within viral families. <i>PLoS Pathogens</i> , 2017 , 13, e1006215	7.6	143
91	Genome-scale rates of evolutionary change in bacteria. <i>Microbial Genomics</i> , 2016 , 2, e000094	4.4	135
90	Analyses of evolutionary dynamics in viruses are hindered by a time-dependent bias in rate estimates. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014 , 281,	4.4	129
89	17 Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , 2016 , 26, 3407-3412	6.3	118
88	The Performance of the Date-Randomization Test in Phylogenetic Analyses of Time-Structured Virus Data. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1895-906	8.3	117
87	Distinct evolutionary dynamics of horizontal gene transfer in drug resistant and virulent clones of <i>Klebsiella pneumoniae</i> . <i>PLoS Genetics</i> , 2019 , 15, e1008114	6	115
86	The impact of calibration and clock-model choice on molecular estimates of divergence times. <i>Molecular Phylogenetics and Evolution</i> , 2014 , 78, 277-89	4.1	108
85	Population genomics of hypervirulent <i>Klebsiella pneumoniae</i> clonal-group 23 reveals early emergence and rapid global dissemination. <i>Nature Communications</i> , 2018 , 9, 2703	17.4	104
84	Tracking the COVID-19 pandemic in Australia using genomics. <i>Nature Communications</i> , 2020 , 11, 4376	17.4	97
83	Large-Scale Phylogenomic Analysis Reveals the Complex Evolutionary History of Rabies Virus in Multiple Carnivore Hosts. <i>PLoS Pathogens</i> , 2016 , 12, e1006041	7.6	93
82	Mitogenome phylogenetics: the impact of using single regions and partitioning schemes on topology, substitution rate and divergence time estimation. <i>PLoS ONE</i> , 2011 , 6, e27138	3.7	89
81	Bayesian molecular dating: opening up the black box. <i>Biological Reviews</i> , 2018 , 93, 1165-1191	13.5	83
80	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019 , 51, 1035-1043	36.3	67

79	Marine turtle mitogenome phylogenetics and evolution. <i>Molecular Phylogenetics and Evolution</i> , 2012 , 65, 241-50	4.1	64
78	Turnip mosaic potyvirus probably first spread to Eurasian brassica crops from wild orchids about 1000 years ago. <i>PLoS ONE</i> , 2013 , 8, e55336	3.7	64
77	Direct RNA sequencing and early evolution of SARS-CoV-2		61
76	Simulating and detecting autocorrelation of molecular evolutionary rates among lineages. <i>Molecular Ecology Resources</i> , 2015 , 15, 688-96	8.4	60
75	The molecular clock of Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2019 , 15, e1008067	7.6	57
74	Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand. <i>Nature Communications</i> , 2020 , 11, 6351	17.4	57
73	INSECT PHYLOGENOMICS. Comment on "Phylogenomics resolves the timing and pattern of insect evolution". <i>Science</i> , 2015 , 349, 487	33.3	56
72	Geographic and temporal dynamics of a global radiation and diversification in the killer whale. <i>Molecular Ecology</i> , 2015 , 24, 3964-79	5.7	54
71	The paradox of HBV evolution as revealed from a 16th century mummy. <i>PLoS Pathogens</i> , 2018 , 14, e1006750	6.5	53
70	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018 , 9, 5094	17.4	53
69	Analysis of Phylogenomic Tree Space Resolves Relationships Among Marsupial Families. <i>Systematic Biology</i> , 2018 , 67, 400-412	8.4	50
68	Declining transition/transversion ratios through time reveal limitations to the accuracy of nucleotide substitution models. <i>BMC Evolutionary Biology</i> , 2015 , 15, 36	3	49
67	Laboratory and molecular surveillance of paediatric typhoidal Salmonella in Nepal: Antimicrobial resistance and implications for vaccine policy. <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006408	4.8	47
66	Pan-genome Analysis of Ancient and Modern Salmonella enterica Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. <i>Current Biology</i> , 2018 , 28, 2420-2428.e10	6.3	44
65	ClockstaR: choosing the number of relaxed-clock models in molecular phylogenetic analysis. <i>Bioinformatics</i> , 2014 , 30, 1017-9	7.2	44
64	Time-dependent estimates of molecular evolutionary rates: evidence and causes. <i>Molecular Ecology</i> , 2015 , 24, 6007-12	5.7	39
63	The temporal evolution and global spread of Cauliflower mosaic virus, a plant pararetrovirus. <i>PLoS ONE</i> , 2014 , 9, e85641	3.7	38
62	Evaluating the Adequacy of Molecular Clock Models Using Posterior Predictive Simulations. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2986-95	8.3	32

61	Understanding dengue virus evolution to support epidemic surveillance and counter-measure development. <i>Infection, Genetics and Evolution</i> , 2018 , 62, 279-295	4.5	29
60	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020 , 37, 3363-3379	8.3	27
59	New Statistical Criteria Detect Phylogenetic Bias Caused by Compositional Heterogeneity. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1529-1534	8.3	26
58	Benign Rabbit Caliciviruses Exhibit Evolutionary Dynamics Similar to Those of Their Virulent Relatives. <i>Journal of Virology</i> , 2016 , 90, 9317-29	6.6	26
57	Phylogenetic uncertainty can bias the number of evolutionary transitions estimated from ancestral state reconstruction methods. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2015 , 324, 517-24	1.8	26
56	Using multiple relaxed-clock models to estimate evolutionary timescales from DNA sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2014 , 77, 65-70	4.1	25
55	Tree imbalance causes a bias in phylogenetic estimation of evolutionary timescales using heterochronous sequences. <i>Molecular Ecology Resources</i> , 2015 , 15, 785-94	8.4	25
54	Temporal signal and the phylodynamic threshold of SARS-CoV-2		24
53	PhyloMAd: efficient assessment of phylogenomic model adequacy. <i>Bioinformatics</i> , 2018 , 34, 2300-2301	7.2	22
52	Initial Evidence for Adaptive Selection on the NADH Subunit Two of Freshwater Dolphins by Analyses of Mitochondrial Genomes. <i>PLoS ONE</i> , 2015 , 10, e0123543	3.7	22
51	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Lineage from the Indian Subcontinent. <i>MBio</i> , 2019 , 10,	7.8	22
50	The Asian Lineage of Zika Virus: Transmission and Evolution in Asia and the Americas. <i>Virologica Sinica</i> , 2019 , 34, 1-8	6.4	21
49	Can Sequence Phylogenies Safely Infer the Origin of the Global Virome?. <i>MBio</i> , 2019 , 10,	7.8	21
48	Continental synchronicity of human influenza virus epidemics despite climatic variation. <i>PLoS Pathogens</i> , 2018 , 14, e1006780	7.6	21
47	Phylogeography, genetic diversity and population structure of common bottlenose dolphins in the Wider Caribbean inferred from analyses of mitochondrial DNA control region sequences and microsatellite loci: conservation and management implications. <i>Animal Conservation</i> , 2012 , 15, 95-112	3.2	21
46	Estimating evolutionary rates using time-structured data: a general comparison of phylogenetic methods. <i>Bioinformatics</i> , 2016 , 32, 3375-3379	7.2	20
45	Linking Branch Lengths across Sets of Loci Provides the Highest Statistical Support for Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1202-1210	8.3	20
44	Substitution Model Adequacy and Assessing the Reliability of Estimates of Virus Evolutionary Rates and Time Scales. <i>Molecular Biology and Evolution</i> , 2016 , 33, 255-67	8.3	19

43	Genomic Epidemiology of the First Wave of SARS-CoV-2 in Italy. <i>Viruses</i> , 2020 , 12,	6.2	19
42	A comparison of methods for estimating substitution rates from ancient DNA sequence data. <i>BMC Evolutionary Biology</i> , 2018 , 18, 70	3	17
41	Genomics-informed responses in the elimination of COVID-19 in Victoria, Australia: an observational, genomic epidemiological study. <i>Lancet Public Health, The</i> , 2021 , 6, e547-e556	22.4	17
40	Phylogeography and sex-biased dispersal across riverine manatee populations (<i>Trichechus inunguis</i> and <i>Trichechus manatus</i>) in South America. <i>PLoS ONE</i> , 2012 , 7, e52468	3.7	16
39	Mammalian genome evolution is governed by multiple pacemakers. <i>Bioinformatics</i> , 2015 , 31, 2061-5	7.2	13
38	Inferring demographic parameters in bacterial genomic data using Bayesian and hybrid phylogenetic methods. <i>BMC Evolutionary Biology</i> , 2018 , 18, 95	3	13
37	Tracing Ancient Human Migrations into Sahul Using Hepatitis B Virus Genomes. <i>Molecular Biology and Evolution</i> , 2019 , 36, 942-954	8.3	12
36	BEAST 2.5: An Advanced Software Platform for Bayesian Evolutionary Analysis		12
35	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , 2016 , 16, 115	3	12
34	The first wave of the COVID-19 epidemic in Spain was associated with early introductions and fast spread of a dominating genetic variant. <i>Nature Genetics</i> , 2021 , 53, 1405-1414	36.3	12
33	Estimating the number and assignment of clock models in analyses of multigene datasets. <i>Bioinformatics</i> , 2016 , 32, 1281-5	7.2	10
32	Phylogenetic Model Adequacy Using Posterior Predictive Simulations. <i>Systematic Biology</i> , 2019 , 68, 358-364	8.4	10
31	Millennia of genomic stability within the invasive Para C Lineage of <i>Salmonella enterica</i>		9
30	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations		9
29	Differences in Performance among Test Statistics for Assessing Phylogenomic Model Adequacy. <i>Genome Biology and Evolution</i> , 2018 , 10, 1375-1388	3.9	9
28	Evolution, Expression, and Function of Nonneuronal Ligand-Gated Chloride Channels in <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 2003-12	3.2	8
27	The emergence of SARS-CoV-2 variants of concern is driven by acceleration of the substitution rate.. <i>Molecular Biology and Evolution</i> , 2022 ,	8.3	8
26	Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand		8

25	The Recovery, Interpretation and Use of Ancient Pathogen Genomes. <i>Current Biology</i> , 2020 , 30, R1215-R1231	8
24	Genome Analysis of Coxsackievirus A4 Isolates From Hand, Foot, and Mouth Disease Cases in Shandong, China. <i>Frontiers in Microbiology</i> , 2019 , 10, 1001	5-7 7
23	Estimating evolutionary rates in giant viruses using ancient genomes. <i>Virus Evolution</i> , 2018 , 4, vey006	3-7 6
22	SNPPar: identifying convergent evolution and other homoplasies from microbial whole-genome alignments	6
21	Dating the emergence of human pathogens. <i>Science</i> , 2020 , 368, 1310-1311	33-3 5
20	The emergence of SARS-CoV-2 variants of concern is driven by acceleration of the evolutionary rate	5
19	Evolutionary stasis of viruses?. <i>Nature Reviews Microbiology</i> , 2019 , 17, 329	22-2 4
18	Evolutionary dynamics of multidrug resistant Salmonella enterica serovar 4,[5],12:i:- in Australia. <i>Nature Communications</i> , 2021 , 12, 4786	17-4 4
17	Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya. <i>ELife</i> , 2021 , 10,	8-9 4
16	Limited Sustained Local Transmission of HIV-1 CRF01_AE in New South Wales, Australia. <i>Viruses</i> , 2019 , 11,	6-2 3
15	The impact of public health interventions in the Nordic countries during the first year of SARS-CoV-2 transmission and evolution. <i>Eurosurveillance</i> , 2021 , 26,	19-8 3
14	The impacts of drift and selection on genomic evolution in insects. <i>PeerJ</i> , 2017 , 5, e3241	3-1 3
13	Development of Phylodynamic Methods for Bacterial Pathogens. <i>Trends in Microbiology</i> , 2021 , 29, 788-797	7-4 3
12	Linking Branch Lengths Across Loci Provides the Best Fit for Phylogenetic Inference	2
11	Genome-scale rates of evolutionary change in bacteria	2
10	The first wave of the Spanish COVID-19 epidemic was associated with early introductions and fast spread of a dominating genetic variant	2
9	Exploring the evolution and epidemiology of European CC1-MRSA-IV: tracking a multidrug-resistant community-associated meticillin-resistant clone. <i>Microbial Genomics</i> , 2021 , 7,	4-4 2
8	SNPPar: identifying convergent evolution and other homoplasies from microbial whole-genome alignments. <i>Microbial Genomics</i> , 2021 , 7,	4-4 2

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| 7 | Estimating Evolutionary Rates and Timescales from Time-Stamped Data 2020 , 157-174 | 1 |
| 6 | Evolution and global transmission of a multidrug-resistant, community-associated MRSA lineage from the Indian subcontinent | 1 |
| 5 | Laboratory and Molecular Surveillance of Paediatric Typhoidal Salmonella in Nepal: Antimicrobial Resistance and Implications for Vaccine Policy | 1 |
| 4 | Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya | 1 |
| 3 | Infectious disease phylodynamics with occurrence data. <i>Methods in Ecology and Evolution</i> , 2021 , 12, 1498-1507 | 1 |
| 2 | The International Virus Bioinformatics Meeting 2022. <i>Viruses</i> , 2022 , 14, 973 | 6.2 0 |
| 1 | Assessment of Coronavirus Disease 2019 Intervention Strategies in the Nordic Countries Using Genomic Epidemiology.. <i>Open Forum Infectious Diseases</i> , 2022 , 9, ofab665 | 1 |