

# Olivier Gascuel

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

48,982  
citations

117625

34  
h-index

88630

70  
g-index

82  
all docs

82  
docs citations

82  
times ranked

55291  
citing authors

#	ARTICLE	IF	CITATIONS
1	A tutorial on the balanced minimum evolution problem. <i>European Journal of Operational Research</i> , 2022, 300, 1-19.	5.7	4
2	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal. <i>Virus Evolution</i> , 2022, 8, veac029.	4.9	5
3	Gotree/Goalign: toolkit and Go API to facilitate the development of phylogenetic workflows. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab075.	3.2	50
4	Cuban history of CRF19 recombinant subtype of HIV-1. <i>PLoS Pathogens</i> , 2021, 17, e1009786.	4.7	3
5	Using machine learning and big data to explore the drug resistance landscape in HIV. <i>PLoS Computational Biology</i> , 2021, 17, e1008873.	3.2	8
6	Drug resistance mutations in HIV: new bioinformatics approaches and challenges. <i>Current Opinion in Virology</i> , 2021, 51, 56-64.	5.4	23
7	A Darwinian Uncertainty Principle. <i>Systematic Biology</i> , 2020, 69, 521-529.	5.6	12
8	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	7.1	68
9	A Fast Likelihood Method to Reconstruct and Visualize Ancestral Scenarios. <i>Molecular Biology and Evolution</i> , 2019, 36, 2069-2085.	8.9	153
10	NGPhylogeny.fr: new generation phylogenetic services for non-specialists. <i>Nucleic Acids Research</i> , 2019, 47, W260-W265.	14.5	489
11	Distribution and asymptotic behavior of the phylogenetic transfer distance. <i>Journal of Mathematical Biology</i> , 2019, 79, 485-508.	1.9	2
12	Generalized Bootstrap Supports for Phylogenetic Analyses of Protein Sequences Incorporating Alignment Uncertainty. <i>Systematic Biology</i> , 2018, 67, 997-1009.	5.6	12
13	Improving pairwise comparison of protein sequences with domain co-occurrence. <i>PLoS Computational Biology</i> , 2018, 14, e1005889.	3.2	7
14	SMS: Smart Model Selection in PhyML. <i>Molecular Biology and Evolution</i> , 2017, 34, 2422-2424.	8.9	1,572
15	The Role of Phylogenetics as a Tool to Predict the Spread of Resistance. <i>Journal of Infectious Diseases</i> , 2017, 216, S820-S823.	4.0	10
16	The combinatorics of overlapping genes. <i>Journal of Theoretical Biology</i> , 2017, 415, 90-101.	1.7	29
17	Inferring epidemiological parameters from phylogenies using regression-ABC: A comparative study. <i>PLoS Computational Biology</i> , 2017, 13, e1005416.	3.2	39
18	In-depth analysis of HIV-1 drug resistance mutations in HIV-infected individuals failing first-line regimens in West and Central Africa. <i>Aids</i> , 2016, 30, 2577-2589.	2.2	24

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19	Concomitant emergence of the antisense protein gene of HIV-1 and of the pandemic. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11537-11542.	7.1	64
20	A $\tilde{\sigma}$ Stochastic Safety Radius <sup>TM</sup> for Distance-Based Tree Reconstruction. Algorithmica, 2016, 74, 1386-1403.	1.3	10
21	Fast Dating Using Least-Squares Criteria and Algorithms. Systematic Biology, 2016, 65, 82-97.	5.6	336
22	A phylotype-based analysis highlights the role of drug-naive HIV-positive individuals in the transmission of antiretroviral resistance in the UK. Aids, 2015, 29, 1917-1925.	2.2	41
23	TCS: a web server for multiple sequence alignment evaluation and phylogenetic reconstruction: Figure 1.. Nucleic Acids Research, 2015, 43, W3-W6.	14.5	44
24	Mathematical and Computational Evolutionary Biology (2013). Systematic Biology, 2015, 64, 1-2.	5.6	52
25	FastME 2.0: A Comprehensive, Accurate, and Fast Distance-Based Phylogeny Inference Program: Table 1.. Molecular Biology and Evolution, 2015, 32, 2798-2800.	8.9	1,103
26	Deep Conservation of Human Protein Tandem Repeats within the Eukaryotes. Molecular Biology and Evolution, 2014, 31, 1132-1148.	8.9	62
27	Predicting the Ancestral Character Changes in a Tree is Typically Easier than Predicting the Root State. Systematic Biology, 2014, 63, 421-435.	5.6	31
28	Identification of Divergent Protein Domains by Combining HMM-HMM Comparisons and Co-Occurrence Detection. PLoS ONE, 2014, 9, e95275.	2.5	6
29	Sexually-Transmitted/Founder HIV-1 Cannot Be Directly Predicted from Plasma or PBMC-Derived Viral Quasispecies in the Transmitting Partner. PLoS ONE, 2013, 8, e69144.	2.5	18
30	Branch Lengths on Birth-Death Trees and the Expected Loss of Phylogenetic Diversity. Systematic Biology, 2012, 61, 195-203.	5.6	67
31	Modeling Protein Evolution with Several Amino Acid Replacement Matrices Depending on Site Rates. Molecular Biology and Evolution, 2012, 29, 2921-2936.	8.9	201
32	Combinatorics of distance-based tree inference. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16443-16448.	7.1	13
33	The Origin and Evolutionary History of HIV-1 Subtype C in Senegal. PLoS ONE, 2012, 7, e33579.	2.5	20
34	EuPathDomains: The divergent domain database for eukaryotic pathogens. Infection, Genetics and Evolution, 2011, 11, 698-707.	2.3	8
35	Survey of Branch Support Methods Demonstrates Accuracy, Power, and Robustness of Fast Likelihood-based Approximation Schemes. Systematic Biology, 2011, 60, 685-699.	5.6	912
36	Robustness of Phylogenetic Inference Based on Minimum Evolution. Bulletin of Mathematical Biology, 2010, 72, 1820-1839.	1.9	15

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37	Accounting for Solvent Accessibility and Secondary Structure in Protein Phylogenetics Is Clearly Beneficial. <i>Systematic Biology</i> , 2010, 59, 277-287.	5.6	107
38	New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. <i>Systematic Biology</i> , 2010, 59, 307-321.	5.6	15,166
39	SeaView Version 4: A Multiplatform Graphical User Interface for Sequence Alignment and Phylogenetic Tree Building. <i>Molecular Biology and Evolution</i> , 2010, 27, 221-224.	8.9	5,075
40	Inferring ancestral sequences in taxon-rich phylogenies. <i>Mathematical Biosciences</i> , 2010, 227, 125-135.	1.9	20
41	Consistency of Topological Moves Based on the Balanced Minimum Evolution Principle of Phylogenetic Inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 110-117.	3.0	27
42	An Improved General Amino Acid Replacement Matrix. <i>Molecular Biology and Evolution</i> , 2008, 25, 1307-1320.	8.9	2,748
43	Phylogenetic mixture models for proteins. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 3965-3976.	4.0	202
44	Empirical profile mixture models for phylogenetic reconstruction. <i>Bioinformatics</i> , 2008, 24, 2317-2323.	4.1	292
45	Duplication and Inversion History of a Tandemly Repeated Genes Family. <i>Journal of Computational Biology</i> , 2007, 14, 462-478.	1.6	26
46	Genomics, biogeography, and the diversification of placental mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14395-14400.	7.1	158
47	Identification of novel peptide hormones in the human proteome by hidden Markov model screening. <i>Genome Research</i> , 2007, 17, 320-327.	5.5	231
48	SDM: A Fast Distance-Based Approach for (Super)Tree Building in Phylogenomics. <i>Systematic Biology</i> , 2006, 55, 740-755.	5.6	69
49	Neighbor-Joining Revealed. <i>Molecular Biology and Evolution</i> , 2006, 23, 1997-2000.	8.9	252
50	Approximate Likelihood-Ratio Test for Branches: A Fast, Accurate, and Powerful Alternative. <i>Systematic Biology</i> , 2006, 55, 539-552.	5.6	2,426
51	An exact and polynomial distance-based algorithm to reconstruct single copy tandem duplication trees. <i>Journal of Discrete Algorithms</i> , 2005, 3, 362-374.	0.7	4
52	Topological Rearrangements and Local Search Method for Tandem Duplication Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 15-28.	3.0	16
53	Performance Analysis of Hierarchical Clustering Algorithms. <i>Journal of Classification</i> , 2004, 21, 3-18.	2.2	21
54	On the consistency of the minimum evolution principle of phylogenetic inference. <i>Discrete Applied Mathematics</i> , 2003, 127, 63-77.	0.9	17

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55	A Simple, Fast, and Accurate Algorithm to Estimate Large Phylogenies by Maximum Likelihood. <i>Systematic Biology</i> , 2003, 52, 696-704.	5.6	15,438
56	Theoretical Foundation of the Balanced Minimum Evolution Method of Phylogenetic Inference and Its Relationship to Weighted Least-Squares Tree Fitting. <i>Molecular Biology and Evolution</i> , 2003, 21, 587-598.	8.9	201
57	The Combinatorics of Tandem Duplication Trees. <i>Systematic Biology</i> , 2003, 52, 110-118.	5.6	23
58	Improvement of Distance-Based Phylogenetic Methods by a Local Maximum Likelihood Approach Using Triplets. <i>Molecular Biology and Evolution</i> , 2002, 19, 1952-1963.	8.9	63
59	Reconstructing the Duplication History of Tandemly Repeated Genes. <i>Molecular Biology and Evolution</i> , 2002, 19, 278-288.	8.9	71
60	Efficient Biased Estimation of Evolutionary Distances When Substitution Rates Vary Across Sites. <i>Molecular Biology and Evolution</i> , 2002, 19, 534-543.	8.9	40
61	Fast and Accurate Phylogeny Reconstruction Algorithms Based on the Minimum-Evolution Principle. <i>Journal of Computational Biology</i> , 2002, 9, 687-705.	1.6	417
62	Quartet-Based Phylogenetic Inference: Improvements and Limits. <i>Molecular Biology and Evolution</i> , 2001, 18, 1103-1116.	8.9	93
63	Strengths and Limitations of the Minimum Evolution Principle. <i>Systematic Biology</i> , 2001, 50, 621-627.	5.6	45
64	Data Model and Classification by Trees: The Minimum Variance Reduction (MVR) Method. <i>Journal of Classification</i> , 2000, 17, 67-99.	2.2	22
65	On the Optimization Principle in Phylogenetic Analysis and the Minimum-Evolution Criterion. <i>Molecular Biology and Evolution</i> , 2000, 17, 401-405.	8.9	64
66	Twelve Numerical, Symbolic and Hybrid Supervised Classification Methods. <i>International Journal of Pattern Recognition and Artificial Intelligence</i> , 1998, 12, 517-571.	1.2	10
67	A reduction algorithm for approximating a (nonmetric) dissimilarity by a tree distance. <i>Journal of Classification</i> , 1996, 13, 129-155.	2.2	20
68	Distribution-free performance bounds with the resubstitution error estimate. <i>Pattern Recognition Letters</i> , 1992, 13, 757-764.	4.2	14
69	Protein export in prokaryotes and eukaryotes: Indications of a difference in the mechanism of exportation. <i>Journal of Molecular Evolution</i> , 1986, 24, 130-142.	1.8	46