

Sebastien Roch

List of Publications by Year in descending order

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44
papers

1,592
citations

516710

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37
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all docs

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docs citations

46
times ranked

1498
citing authors

#	ARTICLE	IF	CITATIONS
1	A stochastic Farris transform for genetic data under the multispecies coalescent with applications to data requirements. <i>Journal of Mathematical Biology</i> , 2022, 84, 36.	1.9	1
2	Sufficient condition for root reconstruction by parsimony on binary trees with general weights. <i>Electronic Communications in Probability</i> , 2021, 26, .	0.4	1
3	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. <i>Journal of Computational Biology</i> , 2021, 28, 452-468.	1.6	23
4	Impossibility of Consistent Distance Estimation from Sequence Lengths Under the TKF91 Model. <i>Bulletin of Mathematical Biology</i> , 2020, 82, 123.	1.9	1
5	Statistically consistent and computationally efficient inference of ancestral DNA sequences in the TKF91 model under dense taxon sampling. <i>Bulletin of Mathematical Biology</i> , 2020, 82, 21.	1.9	2
6	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. <i>Lecture Notes in Computer Science</i> , 2020, , 120-135.	1.3	6
7	Hands-on Introduction to Sequence-Length Requirements in Phylogenetics. <i>Computational Biology</i> , 2019, , 47-86.	0.2	4
8	Long-Branch Attraction in Species Tree Estimation: Inconsistency of Partitioned Likelihood and Topology-Based Summary Methods. <i>Systematic Biology</i> , 2019, 68, 281-297.	5.6	77
9	Species Tree Estimation Using ASTRAL: How Many Genes Are Enough?. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1738-1747.	3.0	19
10	Generalized least squares can overcome the critical threshold in respondent-driven sampling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10299-10304.	7.1	2
11	On the Variance of Internode Distance Under the Multispecies Coalescent. <i>Lecture Notes in Computer Science</i> , 2018, , 196-206.	1.3	1
12	Geometry of the Sample Frequency Spectrum and the Perils of Demographic Inference. <i>Genetics</i> , 2018, 210, 665-682.	2.9	29
13	Phase transition on the convergence rate of parameter estimation under an Ornstein-Uhlenbeck diffusion on a tree. <i>Journal of Mathematical Biology</i> , 2017, 74, 355-385.	1.9	13
14	Distance-based species tree estimation under the coalescent: Information-theoretic trade-off between number of loci and sequence length. <i>Annals of Applied Probability</i> , 2017, 27, .	1.3	5
15	Phase transition in the sample complexity of likelihood-based phylogeny inference. <i>Probability Theory and Related Fields</i> , 2017, 169, 3-62.	1.8	14
16	Species Trees from Gene Trees Despite a High Rate of Lateral Genetic Transfer: A Tight Bound (Extended) <i>Tj ETQq0 0 0 rgBT /Qverlock 10</i>		
17	Likelihood-based tree reconstruction on a concatenation of aligned sequence data sets can be statistically inconsistent. <i>Theoretical Population Biology</i> , 2015, 100, 56-62.	1.1	218
18	On the Robustness to Gene Tree Estimation Error (or lack thereof) of Coalescent-Based Species Tree Methods. <i>Systematic Biology</i> , 2015, 64, 663-676.	5.6	161

#	ARTICLE	IF	CITATIONS
19	Data Requirement for Phylogenetic Inference from Multiple Loci: A New Distance Method. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 422-432.	3.0	36
20	Identifiability and inference of non-parametric rates-across-sites models on large-scale phylogenies. Journal of Mathematical Biology, 2013, 67, 767-797.	1.9	6
21	Robust Estimation of Latent Tree Graphical Models: Inferring Hidden States With Inexact Parameters. IEEE Transactions on Information Theory, 2013, 59, 4357-4373.	2.4	10
22	Recovering the Treelike Trend of Evolution Despite Extensive Lateral Genetic Transfer: A Probabilistic Analysis. Journal of Computational Biology, 2013, 20, 93-112.	1.6	31
23	Alignment-free phylogenetic reconstruction: Sample complexity via a branching process analysis. Annals of Applied Probability, 2013, 23, .	1.3	14
24	An analytical comparison of multilocus methods under the multispecies coalescent: the three-taxon case. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 297-306.	0.7	2
25	AN ANALYTICAL COMPARISON OF MULTILOCUS METHODS UNDER THE MULTISPECIES COALESCENT: THE THREE-TAXON CASE. , 2012, , .		5
26	Phylogenetic mixtures: Concentration of measure in the large-tree limit. Annals of Applied Probability, 2012, 22, .	1.3	6
27	Global alignment of molecular sequences via ancestral state reconstruction. Stochastic Processes and Their Applications, 2012, 122, 3852-3874.	0.9	10
28	Phylogenies without Branch Bounds: Contracting the Short, Pruning the Deep. SIAM Journal on Discrete Mathematics, 2011, 25, 872-893.	0.8	16
29	Evolutionary trees and the Ising model on the Bethe lattice: a proof of Steel's conjecture. Probability Theory and Related Fields, 2011, 149, 149-189.	1.8	35
30	On the Inference of Large Phylogenies with Long Branches: How Long Is Too Long?. Bulletin of Mathematical Biology, 2011, 73, 1627-1644.	1.9	11
31	Network delay inference from additive metrics. Random Structures and Algorithms, 2010, 37, 176-203.	1.1	12
32	Toward Extracting All Phylogenetic Information from Matrices of Evolutionary Distances. Science, 2010, 327, 1376-1379.	12.6	48
33	Submodularity of Influence in Social Networks: From Local to Global. SIAM Journal on Computing, 2010, 39, 2176-2188.	1.0	77
34	Incomplete Lineage Sorting: Consistent Phylogeny Estimation from Multiple Loci. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 166-171.	3.0	146
35	Phylogenies without Branch Bounds: Contracting the Short, Pruning the Deep. Lecture Notes in Computer Science, 2009, , 451-465.	1.3	13
36	Sequence Length Requirement of Distance-Based Phylogeny Reconstruction: Breaking the Polynomial Barrier. , 2008, , .		10

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37	Upstream reciprocity and the evolution of gratitude. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 605-610.	2.6	236
38	On learning thresholds of parities and unions of rectangles in random walk models. <i>Random Structures and Algorithms</i> , 2007, 31, 406-417.	1.1	0
39	Slow emergence of cooperation for win-stay lose-shift on trees. <i>Machine Learning</i> , 2007, 67, 7-22.	5.4	6
40	The Kesten-Stigum Reconstruction Bound Is Tight for Roughly Symmetric Binary Channels. , 2006, , .		28
41	A Short Proof that Phylogenetic Tree Reconstruction by Maximum Likelihood Is Hard. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 92-94.	3.0	108
42	Learning nonsingular phylogenies and hidden Markov models. <i>Annals of Applied Probability</i> , 2006, 16, 583.	1.3	35
43	A smoothing heuristic for a bilevel pricing problem. <i>European Journal of Operational Research</i> , 2006, 174, 1396-1413.	5.7	24
44	An approximation algorithm for Stackelberg network pricing. <i>Networks</i> , 2005, 46, 57-67.	2.7	77