Sebastien Roch

List of Publications by Year
in descending order

44 papers	1,592 citations	516710 16 h-index	330143 37 g-index
46 all docs	46 docs citations	46 times ranked	1498 citing authors

#	Article	IF	Citations
1	Upstream reciprocity and the evolution of gratitude. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 605-610.	2.6	236
2	Likelihood-based tree reconstruction on a concatenation of aligned sequence data sets can be statistically inconsistent. Theoretical Population Biology, 2015, 100, 56-62.	1.1	218
3	On the Robustness to Gene Tree Estimation Error (or lack thereof) of Coalescent-Based Species Tree Methods. Systematic Biology, 2015, 64, 663-676.	5.6	161
4	Incomplete Lineage Sorting: Consistent Phylogeny Estimation from Multiple Loci. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 166-171.	3.0	146
5	A Short Proof that Phylogenetic Tree Reconstruction by Maximum Likelihood Is Hard. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 92-94.	3.0	108
6	An approximation algorithm for Stackelberg network pricing. Networks, 2005, 46, 57-67.	2.7	77
7	Submodularity of Influence in Social Networks: From Local to Global. SIAM Journal on Computing, 2010, 39, 2176-2188.	1.0	77
8	Long-Branch Attraction in Species Tree Estimation: Inconsistency of Partitioned Likelihood and Topology-Based Summary Methods. Systematic Biology, 2019, 68, 281-297.	5.6	77
9	Toward Extracting All Phylogenetic Information from Matrices of Evolutionary Distances. Science, 2010, 327, 1376-1379.	12.6	48
10	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
11	Learning nonsingular phylogenies and hidden Markov models. Annals of Applied Probability, 2006, 16, 583.	1.3	35
12	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
13	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
14	Geometry of the Sample Frequency Spectrum and the Perils of Demographic Inference. Genetics, 2018, 210, 665-682.	2.9	29
15	The Kesten-Stigum Reconstruction Bound Is Tight for Roughly Symmetric Binary Channels. , 2006, , .		28
16	A smoothing heuristic for a bilevel pricing problem. European Journal of Operational Research, 2006, 174, 1396-1413.	5.7	24
17	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. Journal of Computational Biology, 2021, 28, 452-468.	1.6	23
18	Species Tree Estimation Using ASTRAL: How Many Genes Are Enough?. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1738-1747.	3.0	19

#	Article	IF	Citations
19	Phylogenies without Branch Bounds: Contracting the Short, Pruning the Deep. SIAM Journal on Discrete Mathematics, 2011, 25, 872-893.	0.8	16
20	Alignment-free phylogenetic reconstruction: Sample complexity via a branching process analysis. Annals of Applied Probability, 2013, 23, .	1.3	14
21	Phase transition in the sample complexity of likelihood-based phylogeny inference. Probability Theory and Related Fields, 2017, 169, 3-62.	1.8	14
22	Phase transition on the convergence rate of parameter estimation under an Ornstein–Uhlenbeck diffusion on a tree. Journal of Mathematical Biology, 2017, 74, 355-385.	1.9	13
23	Phylogenies without Branch Bounds: Contracting the Short, Pruning the Deep. Lecture Notes in Computer Science, 2009, , 451-465.	1.3	13
24	Network delay inference from additive metrics. Random Structures and Algorithms, 2010, 37, 176-203.	1.1	12
25	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
26	Sequence Length Requirement of Distance-Based Phylogeny Reconstruction: Breaking the Polynomial Barrier. , 2008, , .		10
27	Global alignment of molecular sequences via ancestral state reconstruction. Stochastic Processes and Their Applications, 2012, 122, 3852-3874.	0.9	10
28	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
29	Species Trees from Gene Trees Despite a High Rate of Lateral Genetic Transfer: A Tight Bound (Extended) Tj ETQq1 1 0.784314 rgBT /O		8
30	Slow emergence of cooperation for win-stay lose-shift on trees. Machine Learning, 2007, 67, 7-22.	5.4	6
31	Phylogenetic mixtures: Concentration of measure in the large-tree limit. Annals of Applied Probability, 2012, 22, .	1.3	6
32	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
33	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. Lecture Notes in Computer Science, 2020, , 120-135.	1.3	6
34	AN ANALYTICAL COMPARISON OF MULTILOCUS METHODS UNDER THE MULTISPECIES COALESCENT: THE THREE-TAXON CASE. , 2012, , .		5
35	Distance-based species tree estimation under the coalescent: Information-theoretic trade-off between number of loci and sequence length. Annals of Applied Probability, 2017, 27, .	1.3	5
36	Hands-on Introduction to Sequence-Length Requirements in Phylogenetics. Computational Biology, 2019, , 47-86.	0.2	4

#	Article	IF	Citations
37	Generalized least squares can overcome the critical threshold in respondent-driven sampling. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10299-10304.	7.1	2
38	Statistically consistent and computationally efficient inference of ancestral DNA sequences in the TKF91 model under dense taxon sampling. Bulletin of Mathematical Biology, 2020, 82, 21.	1.9	2
39	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
40	On the Variance of Internode Distance Under the Multispecies Coalescent. Lecture Notes in Computer Science, 2018, , 196-206.	1.3	1
41	Impossibility of Consistent Distance Estimation from Sequence Lengths Under the TKF91 Model. Bulletin of Mathematical Biology, 2020, 82, 123.	1.9	1
42	Sufficient condition for root reconstruction by parsimony on binary trees with general weights. Electronic Communications in Probability, 2021, 26, .	0.4	1
43	A stochastic Farris transform for genetic data under the multispecies coalescent with applications to data requirements. Journal of Mathematical Biology, 2022, 84, 36.	1.9	1
44	On learning thresholds of parities and unions of rectangles in random walk models. Random Structures and Algorithms, 2007, 31, 406-417.	1.1	0