

Celine Scornavacca

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

3,809
citations

257450

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233421

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docs citations

54
times ranked

6017
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep Ancestral Introgression Shapes Evolutionary History of Dragonflies and Damselflies. <i>Systematic Biology</i> , 2022, 71, 526-546.	5.6	32
2	NetRAX: accurate and fast maximum likelihood phylogenetic network inference. <i>Bioinformatics</i> , 2022, 38, 3725-3733.	4.1	13
3	The Multilocus Multispecies Coalescent: A Flexible New Model of Gene Family Evolution. <i>Systematic Biology</i> , 2021, 70, 822-837.	5.6	9
4	High-quality carnivoran genomes from roadkill samples enable comparative species delineation in aardwolf and bat-eared fox. <i>ELife</i> , 2021, 10, .	6.0	15
5	Island songbirds as windows into evolution in small populations. <i>Current Biology</i> , 2021, 31, 1303-1310.e4.	3.9	56
6	On the inference of complex phylogenetic networks by Markov Chain Monte-Carlo. <i>PLoS Computational Biology</i> , 2021, 17, e1008380.	3.2	12
7	Whole Genome Shotgun Phylogenomics Resolves the Pattern and Timing of Swallowtail Butterfly Evolution. <i>Systematic Biology</i> , 2020, 69, 38-60.	5.6	65
8	ASTRAL-Pro: Quartet-Based Species-Tree Inference despite Paralogy. <i>Molecular Biology and Evolution</i> , 2020, 37, 3292-3307.	8.9	116
9	Generation of Binary Tree-Child phylogenetic networks. <i>PLoS Computational Biology</i> , 2019, 15, e1007347.	3.2	7
10	Pervasive hybridizations in the history of wheat relatives. <i>Science Advances</i> , 2019, 5, eaav9188.	10.3	79
11	On the Weighted Quartet Consensus problem. <i>Theoretical Computer Science</i> , 2019, 769, 1-17.	0.9	18
12	OrthoMaM v10: Scaling-Up Orthologous Coding Sequence and Exon Alignments with More than One Hundred Mammalian Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 861-862.	8.9	64
13	Improved Maximum Parsimony Models for Phylogenetic Networks. <i>Systematic Biology</i> , 2018, 67, 518-542.	5.6	10
14	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. <i>Nucleic Acids Research</i> , 2018, 46, D718-D725.	14.5	90
15	RecPhyloXML: a format for reconciled gene trees. <i>Bioinformatics</i> , 2018, 34, 3646-3652.	4.1	22
16	Incomplete Lineage Sorting in Mammalian Phylogenomics. <i>Systematic Biology</i> , 2017, 66, syw082.	5.6	88
17	Reconstructing Phylogenetic Level-1 Networks from Nondense Binet and Trinet Sets. <i>Algorithmica</i> , 2017, 77, 173-200.	1.3	23
18	DeCoSTAR: Reconstructing the Ancestral Organization of Genes or Genomes Using Reconciled Phylogenies. <i>Genome Biology and Evolution</i> , 2017, 9, 1312-1319.	2.5	32

#	ARTICLE	IF	CITATIONS
19	Rearrangement moves on rooted phylogenetic networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005611.	3.2	15
20	ecceTERA: comprehensive gene tree-species tree reconciliation using parsimony. <i>Bioinformatics</i> , 2016, 32, 2056-2058.	4.1	98
21	ANISEED 2015: a digital framework for the comparative developmental biology of ascidians. <i>Nucleic Acids Research</i> , 2016, 44, D808-D818.	14.5	68
22	Do Branch Lengths Help to Locate a Tree in a Phylogenetic Network?. <i>Bulletin of Mathematical Biology</i> , 2016, 78, 1773-1795.	1.9	8
23	Fast and accurate branch lengths estimation for phylogenomic trees. <i>BMC Bioinformatics</i> , 2016, 17, 23.	2.6	23
24	On Computing the Maximum Parsimony Score of a Phylogenetic Network. <i>SIAM Journal on Discrete Mathematics</i> , 2015, 29, 559-585.	0.8	17
25	Joint amalgamation of most parsimonious reconciled gene trees. <i>Bioinformatics</i> , 2015, 31, 841-848.	4.1	44
26	Reconstructible Phylogenetic Networks: Do Not Distinguish the Indistinguishable. <i>PLoS Computational Biology</i> , 2015, 11, e1004135.	3.2	65
27	Constructing Minimal Phylogenetic Networks from Softwired Clusters is Fixed Parameter Tractable. <i>Algorithmica</i> , 2014, 68, 886-915.	1.3	16
28	A practical approximation algorithm for solving massive instances of hybridization number for binary and nonbinary trees. <i>BMC Bioinformatics</i> , 2014, 15, 127.	2.6	9
29	OrthoMaM v8: A Database of Orthologous Exons and Coding Sequences for Comparative Genomics in Mammals. <i>Molecular Biology and Evolution</i> , 2014, 31, 1923-1928.	8.9	77
30	REPRESENTING A SET OF RECONCILIATIONS IN A COMPACT WAY. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1250025.	0.8	41
31	Bio++: Efficient Extensible Libraries and Tools for Computational Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2013, 30, 1745-1750.	8.9	163
32	A First Step Toward Computing All Hybridization Networks For Two Rooted Binary Phylogenetic Trees. <i>Journal of Computational Biology</i> , 2012, 19, 1227-1242.	1.6	7
33	Cycle Killer...Qu'est-ce que c'est? On the Comparative Approximability of Hybridization Number and Directed Feedback Vertex Set. <i>SIAM Journal on Discrete Mathematics</i> , 2012, 26, 1635-1656.	0.8	18
34	Fast computation of minimum hybridization networks. <i>Bioinformatics</i> , 2012, 28, 191-197.	4.1	56
35	Dendroscope 3: An Interactive Tool for Rooted Phylogenetic Trees and Networks. <i>Systematic Biology</i> , 2012, 61, 1061-1067.	5.6	1,438
36	A Practical Approximation Algorithm for Solving Massive Instances of Hybridization Number. <i>Lecture Notes in Computer Science</i> , 2012, , 430-440.	1.3	1

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37	Multigenic phylogeny and analysis of tree incongruences in Triticeae (Poaceae). BMC Evolutionary Biology, 2011, 11, 181.	3.2	72
38	A Survey of Combinatorial Methods for Phylogenetic Networks. Genome Biology and Evolution, 2011, 3, 23-35.	2.5	165
39	Tanglegrams for rooted phylogenetic trees and networks. Bioinformatics, 2011, 27, i248-i256.	4.1	86
40	An Efficient Algorithm for Gene/Species Trees Parsimonious Reconciliation with Losses, Duplications and Transfers. Lecture Notes in Computer Science, 2010, , 93-108.	1.3	78
41	From Gene Trees to Species Trees through a Supertree Approach. Lecture Notes in Computer Science, 2009, , 702-714.	1.3	9
42	PhySIC_IST: cleaning source trees to infer more informative supertrees. BMC Bioinformatics, 2008, 9, 413.	2.6	42
43	Exploring the Solution Space of Sorting by Reversals, with Experiments and an Application to Evolution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 348-356.	3.0	36
44	PhySIC: A Veto Supertree Method with Desirable Properties. Systematic Biology, 2007, 56, 798-817.	5.6	49
45	The Solution Space of Sorting by Reversals. , 2007, , 293-304.		13
46	A bird's white-eye view on avian sex chromosome evolution. , 0, 1, .		13