

Jeremy G Sumner

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

380
citations

949033

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939365

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32
all docs

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docs citations

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times ranked

317
citing authors

#	ARTICLE	IF	CITATIONS
1	A new algebraic approach to genome rearrangement models. <i>Journal of Mathematical Biology</i> , 2022, 84, 49.	0.8	2
2	On equal-input and monotone Markov matrices. <i>Advances in Applied Probability</i> , 2022, 54, 460-492.	0.4	1
3	A symmetry-inclusive algebraic approach to genome rearrangement. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, , 2140015.	0.3	3
4	The Ancient Operational Code is Embedded in the Amino Acid Substitution Matrix and aaRS Phylogenies. <i>Journal of Molecular Evolution</i> , 2020, 88, 136-150.	0.8	9
5	The impracticalities of multiplicatively-closed codon models: a retreat to linear alternatives. <i>Journal of Mathematical Biology</i> , 2020, 81, 549-573.	0.8	0
6	Notes on Markov embedding. <i>Linear Algebra and Its Applications</i> , 2020, 594, 262-299.	0.4	8
7	Systematics and symmetry in molecular phylogenetic modelling: perspectives from physics. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2019, 52, 453001.	0.7	0
8	Lie-Markov Models Derived from Finite Semigroups. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 361-383.	0.9	3
9	Maximum Likelihood Estimates of Rearrangement Distance: Implementing a Representation-Theoretic Approach. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 535-567.	0.9	9
10	Distinguishing Between Convergent Evolution and Violation of the Molecular Clock for Three Taxa. <i>Systematic Biology</i> , 2018, 67, 905-915.	2.7	3
11	Maximum likelihood estimates of pairwise rearrangement distances. <i>Journal of Theoretical Biology</i> , 2017, 423, 31-40.	0.8	15
12	Developing a statistically powerful measure for quartet tree inference using phylogenetic identities and Markov invariants. <i>Journal of Mathematical Biology</i> , 2017, 75, 1619-1654.	0.8	4
13	A representation-theoretic approach to the calculation of evolutionary distance in bacteria. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2017, 50, 335601.	0.7	12
14	Dimensional Reduction for the General Markov Model on Phylogenetic Trees. <i>Bulletin of Mathematical Biology</i> , 2017, 79, 619-634.	0.9	3
15	MULTIPLICATIVELY CLOSED MARKOV MODELS MUST FORM LIE ALGEBRAS. <i>ANZIAM Journal</i> , 2017, 59, 240-246.	0.3	8
16	Matrix group structure and Markov invariants in the strand symmetric phylogenetic substitution model. <i>Journal of Mathematical Biology</i> , 2016, 73, 259-282.	0.8	6
17	A New Hierarchy of Phylogenetic Models Consistent with Heterogeneous Substitution Rates. <i>Systematic Biology</i> , 2015, 64, 638-650.	2.7	31
18	Lie Markov models with purine/pyrimidine symmetry. <i>Journal of Mathematical Biology</i> , 2015, 70, 855-891.	0.8	19

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19	A tensorial approach to the inversion of group-based phylogenetic models. <i>BMC Evolutionary Biology</i> , 2014, 14, 236.	3.2	1
20	Tensor Rank, Invariants, Inequalities, and Applications. <i>SIAM Journal on Matrix Analysis and Applications</i> , 2013, 34, 1014-1045.	0.7	58
21	Lie geometry of 2×2 Markov matrices. <i>Journal of Theoretical Biology</i> , 2013, 327, 88-90.	0.8	4
22	Low-Parameter Phylogenetic Inference Under the General Markov Model. <i>Systematic Biology</i> , 2013, 62, 78-92.	2.7	29
23	Markov Invariants for Phylogenetic Rate Matrices Derived from Embedded Submodels. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 828-836.	1.9	5
24	Is the General Time-Reversible Model Bad for Molecular Phylogenetics?. <i>Systematic Biology</i> , 2012, 61, 1069-1074.	2.7	41
25	The Algebra of the General Markov Model on Phylogenetic Trees and Networks. <i>Bulletin of Mathematical Biology</i> , 2012, 74, 858-880.	0.9	11
26	Lie Markov models. <i>Journal of Theoretical Biology</i> , 2012, 298, 16-31.	0.8	50
27	Phylogenetic estimation with partial likelihood tensors. <i>Journal of Theoretical Biology</i> , 2010, 262, 413-424.	0.8	7
28	Markov invariants and the isotropy subgroup of a quartet tree. <i>Journal of Theoretical Biology</i> , 2009, 258, 302-310.	0.8	16
29	Using the tangle: A consistent construction of phylogenetic distance matrices for quartets. <i>Mathematical Biosciences</i> , 2006, 204, 49-67.	0.9	11
30	Entanglement invariants and phylogenetic branching. <i>Journal of Mathematical Biology</i> , 2005, 51, 18-36.	0.8	11
31	Multiplicatively closed Markov models must form Lie algebras. <i>ANZIAM Journal</i> , 0, 59, 240.	0.0	0