# Toward Extracting All Phylogenetic Information from M

## Citation Report

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 1 | Trees, Fast and Accurate. Science, 2010, 327, 1334-1335. | 6.0 | 5 |
| 2 | TASI Lectures on Complex Structures. , 2011, , . | | 6 |
| 3 | On the Inference of Large Phylogenies with Long Branches: How Long Is Too Long?. Bulletin of Mathematical Biology, 2011, 73, 1627-1644. | 0.9 | 11 |
| 4 | Algebraic Methods in Mathematical Biology. Bulletin of Mathematical Biology, 2011, 73, 701-705. | 0.9 | 0 |
| 5 | Polytomy identification in microbial phylogenetic reconstruction. BMC Systems Biology, 2011, 5, S2. | 3.0 | 15 |
| 6 | Estimating phylogenetic trees from pairwise likelihoods and posterior probabilities of substitution counts. Journal of Theoretical Biology, 2011, 280, 159-166. | 0.8 | 2 |
| 7 | DACTAL: divide-and-conquer trees (almost) without alignments. Bioinformatics, 2012, 28, i274-i282. | 1.8 | 41 |
| 8 | Combinatorics of distance-based tree inference. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16443-16448. | 3.3 | 13 |
| 9 | Estimating Optimal Species Trees from Incomplete Gene Trees Under Deep Coalescence. Journal of Computational Biology, 2012, 19, 591-605. | 0.8 | 36 |
| 10 | Global alignment of molecular sequences via ancestral state reconstruction. Stochastic Processes and Their Applications, 2012, 122, 3852-3874. | 0.4 | 10 |
| 11 | PHYRN: A Robust Method for Phylogenetic Analysis of Highly Divergent Sequences. PLoS ONE, 2012, 7, e34261. | 1.1 | 15 |
| 12 | Novel algorithm for phylogenetic analysis of proteins: application to analysis of the evolution of H5N1 influenza viruses. Journal of Mathematical Chemistry, 2013, 51, 2238-2255. | 0.7 | 10 |
| 13 | Phylogenetic Tree Reconstruction: Geometric Approaches. , 2013, , 307-342. | | 3 |
| 14 | Models and Algorithms for Genome Evolution. Computational Biology, 2013, , . | 0.1 | 7 |
| 15 | Robust Estimation of Latent Tree Graphical Models: Inferring Hidden States With Inexact Parameters. IEEE Transactions on Information Theory, 2013, 59, 4357-4373. | 1.5 | 10 |
| 16 | Evolutionary inference via the Poisson Indel Process. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1160-1166. | 3.3 | 34 |
| 17 | <scp>SIDIER</scp>: substitution and indel distances to infer evolutionary relationships. Methods in Ecology and Evolution, 2013, 4, 1195-1200. | 2.2 | 25 |
| 18 | New sample complexity bounds for phylogenetic inference from multiple loci. , 2014, , . | | 2 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 19 | Phylogenetic relationships among Porodaedalea pini from Poland and related Porodaedalea species. Open Life Sciences, 2014, 9, 614-627. | 0.6 | 2 |
| 20 | ASTRID: Accurate Species TRees from Internode Distances. BMC Genomics, 2015, 16, S3. | 1.2 | 143 |
| 21 | Data Requirement for Phylogenetic Inference from Multiple Loci: A New Distance Method. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 422-432. | 1.9 | 36 |
| 22 | Species Trees from Gene Trees Despite a High Rate of Lateral Genetic Transfer: A Tight Bound (Extended) Tj ETQq1 1 0.784314 rgBT /Ov | | 8 |
| 23 | 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, . | 0.6 | 5 |
| 24 | A Poissonian Model of Indel Rate Variation for Phylogenetic Tree Inference. Systematic Biology, 2017, 66, 698-714. | 2.7 | 4 |
| 26 | Phase transition in the sample complexity of likelihood-based phylogeny inference. Probability Theory and Related Fields, 2017, 169, 3-62. | 0.9 | 14 |
| 27 | Î±-Acetoxyarone synthesis via iodine-catalyzed and tert-butyl hydroperoxide-mediateded self-intermolecular oxidative coupling of aryl ketones. Beilstein Journal of Organic Chemistry, 2017, 13, 1079-1084. | 1.3 | 13 |
| 28 | A Two-State Model of Tree Evolution and Its Applications to Alu Retrotransposition. Systematic Biology, 2018, 67, 475-489. | 2.7 | 5 |
| 29 | On the Variance of Internode Distance Under the Multispecies Coalescent. Lecture Notes in Computer Science, 2018, , 196-206. | 1.0 | 1 |
| 30 | Optimal sequence length requirements for phylogenetic tree reconstruction with indels. , 2019, , . | | 4 |
| 31 | Hands-on Introduction to Sequence-Length Requirements in Phylogenetics. Computational Biology, 2019, , 47-86. | 0.1 | 4 |
| 32 | Constrained incremental tree building: new absolute fast converging phylogeny estimation methods with improved scalability and accuracy. Algorithms for Molecular Biology, 2019, 14, 2. | 0.3 | 9 |
| 33 | Broadcasting on Random Directed Acyclic Graphs. IEEE Transactions on Information Theory, 2020, 66, 780-812. | 1.5 | 6 |
| 34 | Indel-K2P: a modified Kimura 2 Parameters (K2P) model to incorporate insertion and deletion (Indel) information in phylogenetic analysis. Cyber-Physical Systems, 2022, 8, 32-44. | 1.6 | 21 |
| 35 | Reconstruction on 2D Regular Grids. , 2021, , . | | 1 |
| 37 | Large-Scale Multiple Sequence Alignment and Phylogeny Estimation. Computational Biology, 2013, , 85-146. | 0.1 | 14 |
| 38 | Reconstruction on Trees: Exponential Moment Bounds for Linear Estimators. Electronic Communications in Probability, 2011, 16, . | 0.1 | 2 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 39 | Evolutionary Distances in the Twilight Zoneâ€"A Rational Kernel Approach. PLoS ONE, 2010, 5, e15788. | 1.1 | 13 |
| 40 | First Large-Scale DNA Barcoding Assessment of Reptiles in the Biodiversity Hotspot of Madagascar, Based on Newly Designed COI Primers. PLoS ONE, 2012, 7, e34506. | 1.1 | 171 |
| 41 | Fast and accurate estimation of the covariance between pairwise maximum likelihood distances. PeerJ, 2014, 2, e583. | 0.9 | 1 |
| 45 | Broadcasting on Two-Dimensional Regular Grids. IEEE Transactions on Information Theory, 2022, , 1-1. | 1.5 | 1 |
| 46 | A deep learning approach to real-time HIV outbreak detection using genetic data. PLoS Computational Biology, 2022, 18, e1010598. | 1.5 | 3 |
| 47 | Species tree estimation under joint modeling of coalescence and duplication: Sample complexity of quartet methods. Annals of Applied Probability, 2022, 32, . | 0.6 | 2 |