

# David Bryant

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

15,254  
citations

516561

16  
h-index

454834

30  
g-index

34  
all docs

34  
docs citations

34  
times ranked

21080  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Application of Phylogenetic Networks in Evolutionary Studies. <i>Molecular Biology and Evolution</i> , 2006, 23, 254-267.   | 3.5  | 7,402     |
| 2  | <scp>popart</scp>: full-featured software for haplotype network construction. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1110-1116.   | 2.2  | 4,199     |
| 3  | Neighbor-Net: An Agglomerative Method for the Construction of Phylogenetic Networks. <i>Molecular Biology and Evolution</i> , 2003, 21, 255-265.  | 3.5  | 1,675     |
| 4  | Inferring Species Trees Directly from Biallelic Genetic Markers: Bypassing Gene Trees in a Full Coalescent Analysis. <i>Molecular Biology and Evolution</i> , 2012, 29, 1917-1932.          | 3.5  | 828       |
| 5  | Endosymbiotic origin and differential loss of eukaryotic genes. <i>Nature</i> , 2015, 524, 427-432.   | 13.7 | 251       |
| 6  | Origins of major archaeal clades correspond to gene acquisitions from bacteria. <i>Nature</i> , 2015, 517, 77-80.   | 13.7 | 238       |
| 7  | A classification of consensus methods for phylogenetics. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 2003, , 163-183.                                   | 0.0  | 173       |
| 8  | Investigating the Global Dispersal of Chickens in Prehistory Using Ancient Mitochondrial DNA Signatures. <i>PLoS ONE</i> , 2012, 7, e39171.   | 1.1  | 111       |
| 9  | Continuous and tractable models for the variation of evolutionary rates. <i>Mathematical Biosciences</i> , 2006, 199, 216-233.  | 0.9  | 52        |
| 10 | Species delimitation and phylogeny of a New Zealand plant species radiation. <i>BMC Evolutionary Biology</i> , 2009, 9, 111.  | 3.2  | 47        |
| 11 | Flexible methods for estimating genetic distances from single nucleotide polymorphisms. <i>Methods in Ecology and Evolution</i> , 2015, 6, 938-948.   | 2.2  | 38        |
| 12 | Can We “Future-Proof” Consensus Trees?. <i>Systematic Biology</i> , 2017, 66, 611-619.  | 2.7  | 30        |
| 13 | How disturbance and dispersal influence intraspecific structure. <i>Journal of Ecology</i> , 2018, 106, 1298-1306.  | 1.9  | 24        |
| 14 | Monte Carlo Strategies for Selecting Parameter Values in Simulation Experiments. <i>Systematic Biology</i> , 2015, 64, 741-751.   | 2.7  | 21        |
| 15 | Bayesian Inference of Species Trees using Diffusion Models. <i>Systematic Biology</i> , 2021, 70, 145-161.  | 2.7  | 21        |
| 16 | Hyperconvexity and tight-span theory for diversities. <i>Advances in Mathematics</i> , 2012, 231, 3172-3198.  | 0.5  | 19        |
| 17 | The dimensionality of niche space allows bounded and unbounded processes to jointly influence diversification. <i>Nature Communications</i> , 2018, 9, 4258.                                | 5.8  | 16        |
| 18 | The probability of monophyly of a sample of gene lineages on a species tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8002-8009. | 3.3  | 15        |

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|----|---|-----|-----------|
| 19 | Hunting for Trees in Binary Character Sets: Efficient Algorithms for Extraction, Enumeration, and Optimization. <i>Journal of Computational Biology</i> , 1996, 3, 275-288. | 0.8 | 14        |
| 20 | Efficient Recycled Algorithms for Quantitative Trait Models on Phylogenies. <i>Genome Biology and Evolution</i> , 2016, 8, 1338-1350.                                       | 1.1 | 13        |
| 21 | A Universal Separable Diversity. <i>Analysis and Geometry in Metric Spaces</i> , 2017, 5, 138-151.  | 0.2 | 6         |
| 22 | Microbial Phylogenetic Context Using Phylogenetic Outlines. <i>Genome Biology and Evolution</i> , 2021, 13, .   | 1.1 | 6         |
| 23 | Statistical flaws undermine pre-Columbian chicken debate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3584.        | 3.3 | 5         |
| 24 | V-Spline: An Adaptive Smoothing Spline for Trajectory Reconstruction. <i>Sensors</i> , 2021, 21, 3215.  | 2.1 | 5         |
| 25 | Failure to Recover Major Events of Gene Flux in Real Biological Data Due to Method Misapplication. <i>Genome Biology and Evolution</i> , 2018, 10, 1198-1209.               | 1.1 | 4         |
| 26 | Discrete coalescent trees. <i>Journal of Mathematical Biology</i> , 2021, 83, 60.   | 0.8 | 4         |
| 27 | Constant Distortion Embeddings of Symmetric Diversities. <i>Analysis and Geometry in Metric Spaces</i> , 2016, 4, .   | 0.2 | 3         |
| 28 | The link between segregation and phylogenetic diversity. <i>Journal of Mathematical Biology</i> , 2012, 64, 149-162.  | 0.8 | 2         |
| 29 | An $O(n \log n)$ Time Algorithm for Computing the Path-Length Distance Between Trees. <i>Algorithmica</i> , 2019, 81, 3692-3706.  | 1.0 | 1         |
| 30 | Negative-Type Diversities, a Multi-dimensional Analogue of Negative-Type Metrics. <i>Journal of Geometric Analysis</i> , 2021, 31, 1703-1720.                               | 0.5 | 1         |
| 31 | FRAËSSÄ% LIMITS FOR RELATIONAL METRIC STRUCTURES. <i>Journal of Symbolic Logic</i> , 0, , 1-22.   | 0.4 | 1         |
| 32 | â€Bureaucraticâ€™ set systems, and their role in phylogenetics. <i>Applied Mathematics Letters</i> , 2012, 25, 1148-1152.   | 1.5 | 0         |
| 33 | Forty Years of Model-Based Phylogeography. <i>Computational Biology</i> , 2013, , 17-28.  | 0.1 | 0         |