

phytools 2.0

An updated R ecosystem for phylogenetic comparative methods (and other things)

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Abstract

Modern phylogenetic comparative methods are not new. Perhaps the most important article in the development of the phylogenetic approach to comparative biology (Felsenstein 1985) was first authored nearly 40 years ago, and was even the subject of a recent retrospective (Huey et al. 2019). Nonetheless, it's fair to say that phylogenetic comparative methods have seen a relatively impressive expansion and diversification over the past two decades (e.g., Butler and King 2004; Felsenstein 2005; O'Meara et al. 2006; Maddison et al. 2007; Hohenlohe and Arnold 2008; Revell and Collar 2009; Morlon et al. 2010; Stadler 2011; Etienne and Haegeman 2012; Goldberg and Igić 2012; Beaulieu et al. 2013; Rabosky 2014; Uyeda and Harmon 2014; Beaulieu and O'Meara 2016; Revell 2021, and many others; reviewed in Garamszegi 2014; Harmon 2019; Revell and Harmon 2022). This has included the development of new approaches for studying the generating processes of trees (that is, speciation and extinction), the relationship between phenotypic traits and species diversification, and a range of approaches for investigating heterogeneity in the evolutionary process across the branches and clades of the tree of life. Phylogenetic comparative methods have also begun to be applied outside their traditional domain of evolutionary research. In particular, phylogenies and the comparative method have made recent appearances in studies on infectious disease epidemiology, virology, sociolinguistics, biological anthropology, molecular genomics, and community ecology, among other disciplines (e.g., Moura et al. 2016; Baele et al. 2018; Bentz et al. 2018; Beale et al. 2019; Bushman et al. 2019; Sánchez-Busó et al. 2019; Valles-Colomer et al. 2019; Freitas et al. 2020; Jezovit et al. 2020; Blinkhorn and Grove 2021; McLaughlin et al. 2022; Pepke and Eisenberg 2022; Pozzi et al. 2022; Compton et al. 2023; Mifsud et al. 2023; Van Borm et al. 2023, and many others).

Baele, G., S. Dellicour, M. A. Suchard, P. Lemey, and B. Vrancken. 2018. Recent advances in computational phylodynamics. *Curr. Opin. Virol.* 31:24–32. Elsevier BV.

Beale, M. A., M. Marks, S. K. Sahi, L. C. Tantalo, A. V. Nori, P. French, S. A. Lukehart, C. M. Marra, and N. R. Thomson. 2019. Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages. *Nat. Commun.* 10:3255. Springer Science; Business Media LLC.

Beaulieu, J. M., and B. C. O'Meara. 2016. Detecting hidden diversification shifts in models of Trait-Dependent speciation and extinction. *Syst. Biol.* 65:583–601.

Beaulieu, J. M., B. C. O'Meara, and M. J. Donoghue. 2013. Identifying hidden rate changes in the evolution of a binary morphological character: The evolution of plant habit in campanulid angiosperms. *Syst. Biol.* 62:725–737.

Bentz, C., D. Dediu, A. Verkerk, and G. Jäger. 2018. The evolution of language families is shaped by the environment beyond neutral drift. *Nat. Hum. Behav.* 2:816–821. Springer Science; Business Media LLC.

Blinkhorn, J., and M. Grove. 2021. Explanations of variability in middle stone age stone tool assemblage composition and raw material use in eastern africa. *Archaeol. Anthropol. Sci.* 13. Springer Science; Business Media LLC.

Bushman, F. D., K. McCormick, and S. Sherrill-Mix. 2019. Virus structures constrain transmission modes. *Nat. Microbiol.* 4:1778–1780. Springer Science; Business Media LLC.

Butler, M. A., and A. A. King. 2004. Phylogenetic comparative analysis: A modeling approach for adaptive

- evolution. *Am. Nat.* 164:683–695.
- Compton, Z., V. Harris, W. Mellon, S. Rupp, D. Mallo, S. E. Kapsetaki, M. Wilmot, R. Kennington, K. Noble, C. Baciú, L. Ramirez, A. Peraza, B. Martins, S. Sudhakar, S. Aksoy, G. Furukawa, O. Vincze, M. Giraudeau, E. G. Duke, S. Spiro, E. Flach, H. Davidson, A. Zehnder, T. A. Graham, B. Troan, T. M. Harrison, M. Tollis, J. D. Schiffman, A. Aktipis, L. M. Abegglen, C. C. Maley, and A. M. Boddy. 2023. Cancer prevalence across vertebrates. *bioRxiv*org.
- Etienne, R. S., and B. Haegeman. 2012. A conceptual and statistical framework for adaptive radiations with a key role for diversity dependence. *Am. Nat.* 180:E75–89.
- Felsenstein, J. 1985. Phylogenies and the comparative method. *Am. Nat.* 125:1–15.
- Felsenstein, J. 2005. Using the quantitative genetic threshold model for inferences between and within species. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 360:1427–1434.
- Freitas, A. R., A. P. Tedim, C. Novais, V. F. Lanza, and L. Peixe. 2020. Comparative genomics of global *optrA*-carrying *enterococcus faecalis* uncovers a common chromosomal hotspot for *optrA* acquisition within a diversity of core and accessory genomes. *Microb. Genom.* 6. Microbiology Society.
- Garamszegi, L. Z. 2014. Modern phylogenetic comparative methods and their application in evolutionary biology: Concepts and practice. Springer.
- Goldberg, E. E., and B. Igić. 2012. Tempo and mode in plant breeding system evolution. *Evolution* 66:3701–3709. Wiley Online Library.
- Harmon, L. J. 2019. Phylogenetic comparative methods: Learning from trees. *Ecoevorxiv*.
- Hohenlohe, P. A., and S. J. Arnold. 2008. MIPoD: A hypothesis-testing framework for microevolutionary inference from patterns of divergence. *Am. Nat.* 171:366–385.
- Huey, R. B., T. Garland Jr, and M. Turelli. 2019. Revisiting a key innovation in evolutionary biology: Felsenstein’s “phylogenies and the comparative method.” *Am. Nat.* 193:755–772. The University of Chicago Press Chicago, IL.
- Jezovit, J. A., R. Rooke, J. Schneider, and J. D. Levine. 2020. Behavioral and environmental contributions to drosophilid social networks. *Proc. Natl. Acad. Sci. U. S. A.* 117:11573–11583. Proceedings of the National Academy of Sciences.
- Maddison, W. P., P. E. Midford, and S. P. Otto. 2007. Estimating a binary character’s effect on speciation and extinction. *Syst. Biol.* 56:701–710. *sysbio.oxfordjournals.org*.
- McLaughlin, A., V. Montoya, R. L. Miller, G. J. Mordecai, Canadian COVID-19 Genomics Network (CanCOGen) Consortium, M. Worobey, A. F. Y. Poon, and J. B. Joy. 2022. Genomic epidemiology of the first two waves of SARS-CoV-2 in Canada. *Elife* 11. eLife Sciences Publications, Ltd.
- Mifsud, J. C. O., V. A. Costa, M. E. Petrone, E. M. Marzinelli, E. C. Holmes, and E. Harvey. 2023. Transcriptome mining extends the host range of the flaviviridae to non-bilaterians. *Virus Evol.* 9:veac124. Oxford University Press (OUP).
- Morlon, H., M. D. Potts, and J. B. Plotkin. 2010. Inferring the dynamics of diversification: A coalescent approach. *PLoS Biol.* 8.
- Moura, A., A. Criscuolo, H. Pouseele, M. M. Maury, A. Leclercq, C. Tarr, J. T. Björkman, T. Dallman, A. Reimer, V. Enouf, E. Larssonneur, H. Carleton, H. Bracq-Dieye, L. S. Katz, L. Jones, M. Touchon, M. Tourdjman, M. Walker, S. Stroika, T. Cantinelli, V. Chenal-Francisque, Z. Kucerova, E. P. C. Rocha, C. Nadon, K. Grant, E. M. Nielsen, B. Pot, P. Gerner-Smidt, M. Lecuit, and S. Brisse. 2016. Whole genome-based population biology and epidemiological surveillance of *listeria monocytogenes*. *Nat. Microbiol.* 2:16185.
- O’Meara, B. C., C. Ané, M. J. Sanderson, and P. C. Wainwright. 2006. Testing for different rates of continuous trait evolution using likelihood. *Evolution* 60:922–933.
- Pepke, M. L., and D. T. A. Eisenberg. 2022. On the comparative biology of mammalian telomeres: Telomere length co-evolves with body mass, lifespan and cancer risk. *Mol. Ecol.* 31:6286–6296. Wiley.
- Pozzi, L., M. Voskamp, and P. M. Kappeler. 2022. The effects of body size, activity, and phylogeny on primate sleeping ecology. *Am. J. Biol. Anthropol.* 179:598–608. Wiley.
- Rabosky, D. L. 2014. Automatic detection of key innovations, rate shifts, and diversity-dependence on phylogenetic trees. *PLoS One* 9:e89543. Public Library of Science.
- Revell, L. J. 2021. A variable-rate quantitative trait evolution model using penalized-likelihood. *PeerJ* 9:e11997. PeerJ.
- Revell, L. J., and D. C. Collar. 2009. Phylogenetic analysis of the evolutionary correlation using likelihood.

- Evolution 63:1090–1100.
- Revell, L. J., and L. J. Harmon. 2022. Phylogenetic comparative methods in R. Princeton University Press, Princeton, NJ.
- Sánchez-Busó, L., D. Golparian, J. Corander, Y. H. Grad, M. Ohnishi, R. Flemming, J. Parkhill, S. D. Bentley, M. Unemo, and S. R. Harris. 2019. The impact of antimicrobials on gonococcal evolution. *Nat. Microbiol.* 4:1941–1950. Springer Science; Business Media LLC.
- Stadler, T. 2011. Inferring speciation and extinction processes from extant species data. *Proc. Natl. Acad. Sci. U. S. A.* 108:16145–16146. National Acad Sciences.
- Uyeda, J. C., and L. J. Harmon. 2014. A novel Bayesian method for inferring and interpreting the dynamics of adaptive landscapes from phylogenetic comparative data. *Syst. Biol.* 63:902–918.
- Valles-Colomer, M., G. Falony, Y. Darzi, E. F. Tigchelaar, J. Wang, R. Y. Tito, C. Schiweck, A. Kurilshikov, M. Joossens, C. Wijmenga, S. Claes, L. Van Oudenhove, A. Zhernakova, S. Vieira-Silva, and J. Raes. 2019. The neuroactive potential of the human gut microbiota in quality of life and depression. *Nat. Microbiol.* 4:623–632. Springer Science; Business Media LLC.
- Van Borm, S., G. Boseret, S. Dellicour, M. Steensels, V. Roupie, F. Vandenbussche, E. Mathijs, A. Vilain, M. Driesen, M. Dispas, A. W. Delcloo, P. Lemey, I. Mertens, M. Gilbert, B. Lambrecht, and T. van den Berg. 2023. Combined phylogeographic analyses and epidemiologic contact tracing to characterize atypically pathogenic avian influenza (H3N1) epidemic, belgium, 2019. *Emerg. Infect. Dis.* 29:351–359. Centers for Disease Control; Prevention (CDC).