



Predicting small ancestors using contemporary genomes of large mammals

Bruce Rannala

Department of Evolution and Ecology, Univ. California at Davis -- Davis, USA
Correspondence to Bruce Rannala (brannala@ucdavis.edu)
doi: [10.24072/pci.evolbiol.100042](https://doi.org/10.24072/pci.evolbiol.100042)

Published: 05th Nov. 2017

Cite as: Rannala B. 2017. Predicting small ancestors using contemporary genomes of large mammals. *Peer Community in Evolutionary Biology*, 100042 doi: [10.24072/pci.evolbiol.100042](https://doi.org/10.24072/pci.evolbiol.100042)

Open Access

A recommendation – based on reviews by Bruce Rannala and an anonymous reviewer – of

Figuet E, Ballenghien M, Lartillot N, Galtier N. 2017. Reconstruction of body mass evolution in the Cetartiodactyla and mammals using phylogenomic data. *bioRxiv*, 139147, ver. 3 of 4th December 2017. doi: [10.1101/139147](https://doi.org/10.1101/139147)

Copyright: This work is licensed under the Creative Commons Attribution-NoDerivatives 4.0 International License. To view a copy of this license, visit <http://creativecommons.org/licenses/by-nd/4.0/>

Recent methodological developments and increased genome sequencing efforts have introduced the tantalizing possibility of inferring ancestral phenotypes using DNA from contemporary species. One intriguing application of this idea is to exploit the apparent correlation between substitution rates and body size to infer ancestral species' body sizes using the inferred patterns of substitution rate variation among species lineages based on genomes of extant species [1]. The recommended paper by Figuet et al. [2] examines the utility of such approaches by analyzing the Cetartiodactyla, a clade of large mammals that have mostly well resolved phylogenetic relationships and a reasonably good fossil record. This combination of genomic data and fossils allows a direct comparison between body size predictions obtained from the genomic data and empirical evidence from the fossil record. If predictions seem good in groups such as the Cetartiodactyla, where there is independent evidence from the fossil record, this would increase the credibility of predictions made for species with less abundant fossils. Figuet et al. [2] analyze transcriptome data for 41 species and report a significant effect of body mass on overall substitution rate, synonymous vs. non-synonymous rates, and the dynamics of GC-content, thus allowing a prediction of small ancestral body size in this group despite the fact that the extant species that were analyzed are nearly all large. A comparative method based solely on morphology and phylogenetic relationships would be very unlikely to make such a prediction. There are many sources of uncertainty in the variables and parameters

associated with these types of approaches: phylogenetic uncertainty (topology and branch lengths), uncertainty about inferred substitution rates, and so on. Although the authors do not account for all these sources of uncertainty the fact that their predicted body sizes appear sensible is encouraging and undoubtedly the methods will become more statistically sophisticated over time.

References

- [1] Romiguier J, Ranwez V, Douzery EJP and Galtier N. 2013. Genomic evidence for large, long-lived ancestors to placental mammals. *Molecular Biology and Evolution* 30: 5–13. doi: 10.1093/molbev/mss211
- [2] Figuet E, Ballenghien M, Lartillot N and Galtier N. 2017. Reconstruction of body mass evolution in the Cetartiodactyla and mammals using phylogenomic data. *bioRxiv*, 139147, ver. 3 of 4th December. doi: 10.1101/139147

Appendix

Reviews by Bruce Rannala and an anonymous reviewer: <http://dx.doi.org/10.24072/pci.evolbiol.100042>