



Fig. 3 | Timetree of 4,705 mammal species. **a**, Times (in Ma) are estimated with MCMCTree²³ using approximate likelihood³⁷. Black bars indicate the 95% highest posterior density credibility interval of node ages, with nodes plotted at the posterior means. Cretaceous–Palaeogene boundary (K-Pg) is indicated.

b, Lineages through time plot (black line) with 95% confidence interval (dotted lines), number of extinct mammal species, mammal genera, and eutherian genera through time (mined from PaleoDB (<https://paleobiodb.org/>)) are shown.

Efficient computing in the genomics era

The species-level MCMC sampling required about 80,000 hours of computing time in a high-performance computing cluster and released approximately⁴⁸ 16.7 tonnes of CO₂. Without the technological improvements used here, these analyses would have required hundreds of years of computing time and emitted more than 1.9 thousand tonnes of CO₂ (Supplementary Information). By using existing tools and combining them in a novel way within the sequential-subtree approach, we have demonstrated that hierarchical Bayesian analysis of species-level timetrees integrating genomes is now feasible. Thus, the methodology developed here can be used to address other contentious cases of species diversification that, so far, have been analysed using limited datasets. By integrating our method with the million and more genomes currently planned for sequencing¹¹, the prospect of obtaining a reliable evolutionary timescale for the entirety of the tree of life now appears within reach.

Online content

Any methods, additional references, Nature Research reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at <https://doi.org/10.1038/s41586-021-04341-1>.

1. Zoonomia Consortium. A comparative genomics multitool for scientific discovery and conservation. *Nature* **587**, 240–245 (2020).
2. Feng, S. et al. Dense sampling of bird diversity increases power of comparative genomics. *Nature* **587**, 252–257 (2020).
3. Harvey, M. G. et al. The evolution of a tropical biodiversity hotspot. *Science* **370**, 1343–1348 (2020).
4. dos Reis, M., Donoghue, P. C. J. & Yang, Z. Bayesian molecular clock dating of species divergences in the genomics era. *Nat. Rev. Genet.* **17**, 71–80 (2016).
5. Meredith, R. W. et al. Impacts of the Cretaceous Terrestrial Revolution and KPg extinction on mammal diversification. *Science* **334**, 521–524 (2011).