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Title: The fossilized birth-death process for coherent calibration of divergence-time estimates

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Source: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA Volume: 111 Issue: 29 Pages: E2957-E2966 DOI: 10.1073/pnas.1319091111 Published: JUL 22 2014 **Times Cited in Web of Science Core Collection: 89 Total Times Cited: 92** Usage Count (Last 180 days): 10 Usage Count (Since 2013): 65 **Cited Reference Count: 85** Abstract: Time-calibrated species phylogenies are critical for addressing a wide range of questions in evolutionary biology, such as those that elucidate historical biogeography or uncover patterns of coevolution and diversification. Because molecular sequence data are not informative on absolute time, external data-most commonly, fossil age estimates-are required to calibrate estimates of species divergence dates. For Bayesian divergence time methods, the common practice for calibration using fossil information involves placing arbitrarily chosen parametric distributions on internal nodes, often disregarding most of the information in the fossil record. We introduce the "fossilized birth-death" (FBD) process-a model for calibrating divergence time estimates in a Bayesian framework, explicitly acknowledging that extant species and fossils are part of the same macroevolutionary process. Under this model, absolute node age estimates are calibrated by a single diversification model and arbitrary calibration densities are not necessary. Moreover, the FBD model allows for inclusion of all available fossils. We performed analyses of simulated data and show that node age estimation under the FBD model results in robust and accurate estimates of species divergence times with realistic measures of statistical uncertainty, overcoming major limitations of standard divergence time estimation methods. We used this model to estimate the speciation times for a dataset composed of all living bears, indicating that the genus Ursus diversified in the Late Miocene to Middle Pliocene. Accession Number: WOS:000339310700007 PubMed ID: 25009181 Language: English Document Type: Article Author Keywords: phylogenetics; Bayesian divergence time estimation; relaxed clock; MCMC; time tree KeyWords Plus: BAYESIAN PHYLOGENETIC INFERENCE; RECONSTRUCTED EVOLUTIONARY PROCESS; MAXIMUM-LIKELIHOOD; MOLECULAR CLOCK; DNA-SEQUENCES; SUBSTITUTION RATES; RELAXED PHYLOGENETICS; TREES; MODELS; RADIATION Addresses: [Heath, Tracy A.; Huelsenbeck, John P.] Univ Calif Berkeley, Dept Integrat Biol, Berkeley, CA 94720 USA. [Heath, Tracy A.] Univ Kansas, Dept Ecol & Evolutionary Biol, Lawrence, KS 66045 USA [Huelsenbeck, John P.] King Abdulaziz Univ, Dept Biol Sci, Fac Sci, Jeddah 21589, Saudi Arabia. [Stadler, Tanja] ETH, Dept Environm Syst Sci, CH-8092 Zurich, Switzerland. [Stadler, Tanja] ETH, Dept Biosyst Sci & Engn, CH-4058 Basel, Switzerland. Reprint Address: Stadler, T (reprint author), ETH, Dept Environm Syst Sci, CH-8092 Zurich, Switzerland. E-mail Addresses: tanja.stadler@bsse.ethz.ch Author Identifiers: Author **ResearcherID** Number **ORCID** Number Stadler, Tanja 0000-0001-6431-535X J-4742-2013 Fac Sci, KAU, Biol Sci Dept L-4228-2013 Publisher: NATL ACAD SCIENCES Publisher Address: 2101 CONSTITUTION AVE NW, WASHINGTON, DC 20418 USA Web of Science Categories: Multidisciplinary Sciences Research Areas: Science & Technology - Other Topics **IDS Number: AL7JS** ISSN: 0027-8424 29-char Source Abbrev .: P NATL ACAD SCI USA ISO Source Abbrev.: Proc. Natl. Acad. Sci. U. S. A.

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