

ASSESSING THE QUALITY OF CALIBRATION POINTS FOR PROKARYOTES. L. M. Jones¹ and F. U. Battistuzzi¹, ¹Oakland University Department of Biological Sciences.

Introduction: Reconstructing the history of life on Earth and correlating that history with geological events is an essential goal in astrobiology, as it provides us with a framework for the possibility of life on other planets. Given the almost exclusive reliance of pre-Cambrian timelines of life on molecular data, it is essential to use accurate and reliable molecular dating methods. However, the use of differing calibration points and differing methodologies often leads to discordant timetrees. Our working hypothesis is that discrepancies among molecular timetrees are caused by incorrect assumptions and parameters and that the change or removal of these biasing factors will reconcile molecular timetrees from different studies¹.

The advent of fourth generation molecular clocks, which reduce algorithmic uncertainties by eliminating most prior assumptions, allows us to compare divergence times from previous studies and identify possible calibration points that are highly constraining. Recently, Battistuzzi et al² used a calibration-free approach (RelTime) to compare divergence nodes in a timetree of metazoan diversification produced by Erwin et al³. They found two highly constraining calibration points, the removal of which significantly improved linearity between the original approach and the calibration-free approach.

In this study, we have used a timetree of prokaryote species from Battistuzzi and Hedges⁴, which was produced using ML and Bayesian methods, and analyzed the tree with RelTime. The results show a high linear concordance with the original data, indicating the absence of any highly constraining calibration points. This suggests that calibration points used to calibrate prokaryote trees are reliable. Further work will involve comparison of the confidence intervals of node divergence times produced by the two methods, as well as the prior-free analysis of additional timetrees. With a focus on prokaryotes, we hope to reveal more details about the long history of microbial life on Earth.

References: [1] Warnock et al. (2015) *Proc R Soc B*, 282, 20141013. [2] Battistuzzi et al. (2015) *Mol Biol Evol*, 32 (7), 1907-1912. [3] Erwin et al. (2011) *Science*, 334, 1091-1097. [4] Battistuzzi F. U. and Hedges S. B. (2009) *Mol Biol Evol*, 26 (2), 335-343.