Determinig Early Life's Evolutionary Rate. A.C. Brown[1] and F. U.Battistuzzi[1]. [1]Oakland University, Department of Biological Sciences, Rochester, MI 48309.

A chronological framework of life is fundamental to reconstruct the major steps of life's evolution on Earth; from an astrobiological perspective, this can be used to determine the pace of the origin of unique biological processes on Earth and how they relate to the habitability of a planet. However, while the estimation of timetrees in phylogenetic studies has increased due to improved understanding of evolutionary mechanisms, many questions remain on their accuracy. Questions regarding basic assumptions, such as the variation in evolutionary rates among branches of a phylogeny, need to be further investigated to reduce biases derived during the time estimation process. Here we investigate one of the assumptions, the fit of branch-specific evolutionary rates to auto-correlated (AR) and uncorrelated (UR) rate models. Through our large-scale simulation study of prokaryote class and phylum phylogenies, we compare the simulated distributions of ancestor-descendant rate changes to empirical data to determine their fit. We find variable rates among branches but no significant clustering among groups sharing the same common ancestor, even for closely related lineages that would be expected to share similar rates of evolution. Additionally, we find that the empirical data follows neither the AR or UR model, but rather a combination of the two patterns. These results suggested caution when applying these assumptions in divergence time estimations and encourage the use of molecular clock methods that implement fewer assumptions to derive timeline estimations.