ANU Seminar

EVOLUTION, ECOLOGY, & GENETICS RESEARCH SCHOOL OF BIOLOGY

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Solid Dates, Different Rates: Divergence time estimation in the face of extreme rate heterogeneity



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Dating events in the Tree of Life requires nucleotide substitution models that can accommodate heterogeneity of rates of molecular evolution both within the genome (e.g., among different loci and/or codon positions) and among lineages in the phylogeny. Recent developments in modeling nucleotide substitution, including models that permit locus-specific parameters and the decoupling of nucleotide substitution rates between descendant lineages, may be powerful tools to improve the accuracy of molecular divergence dates. However, the performance of these models in empirical data sets remains little studied, especially in data sets with extreme rate heterogeneity. I present two case studies that evaluate the ability of currently available nucleotide substitution models to accommodate rate heterogeneity among loci and codon positions in blue-tailed skinks (Plestiodon), and overall rates of molecular evolution between toothed and baleen whales.

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