

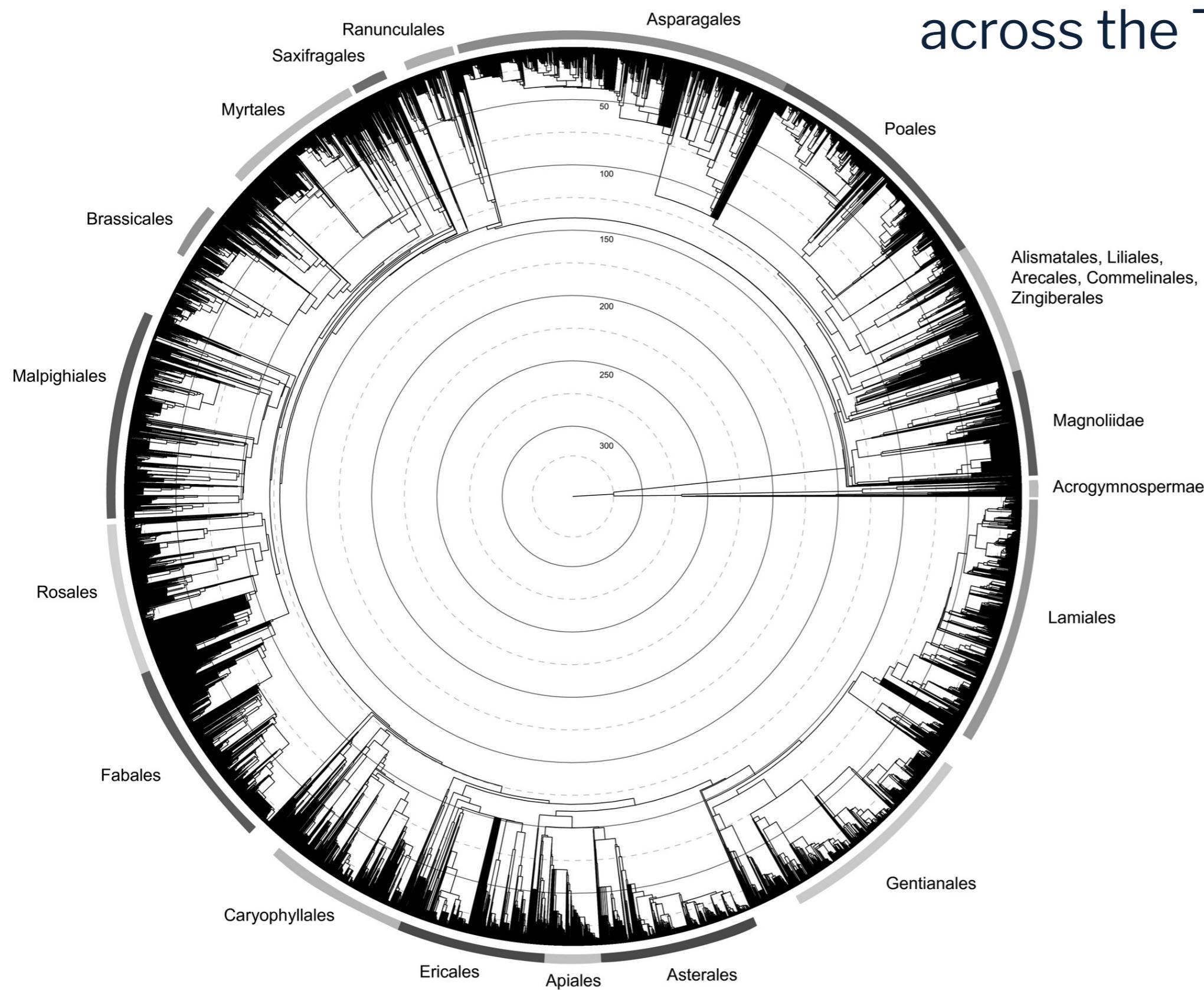
Investigating the dynamics of diversification using molecular phylogenies

Matthew Pennell | University of British Columbia

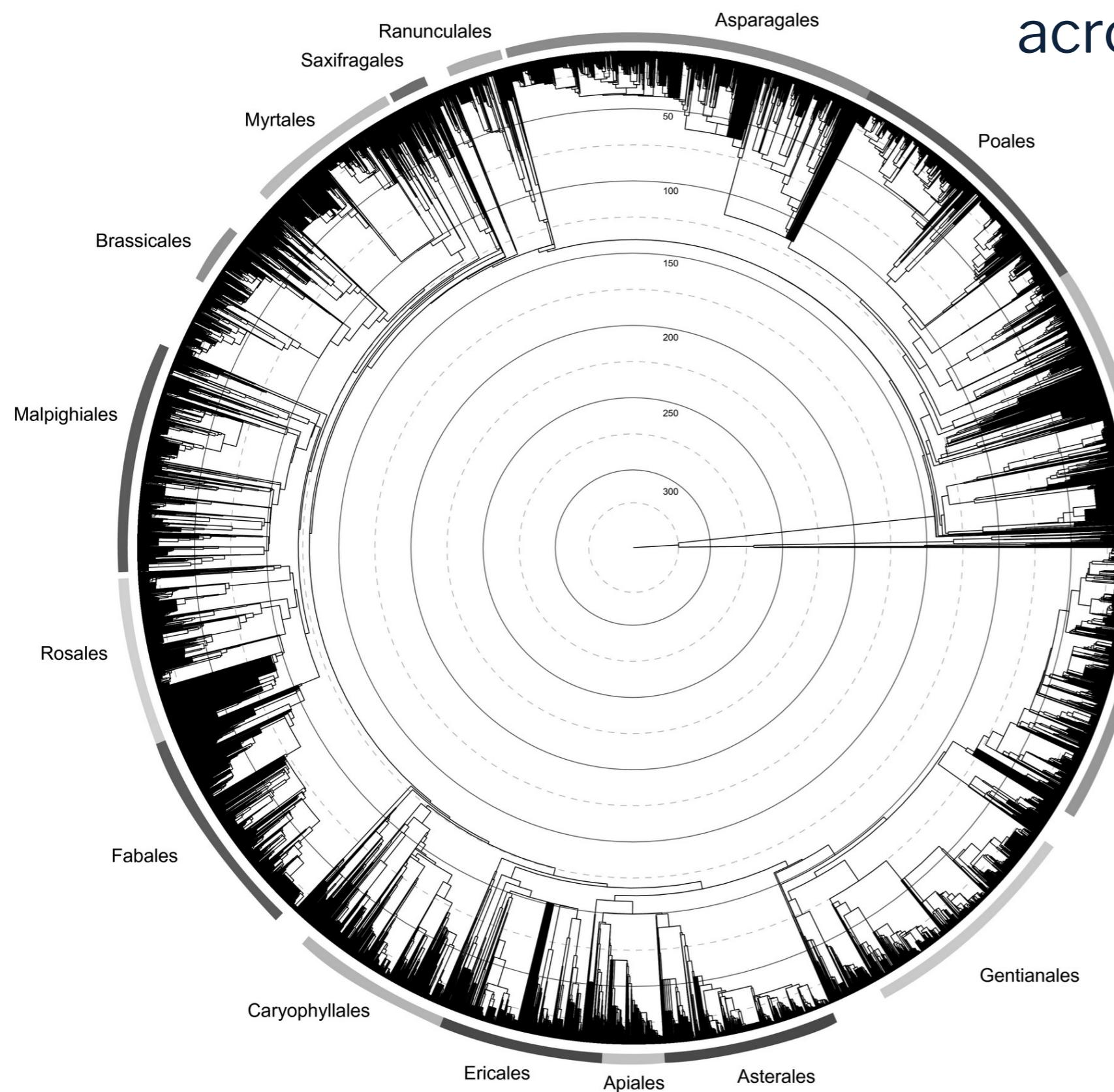
1. The disparity in diversity through time and across the Tree of Life
2. The signature of diversification dynamics in molecular phylogenies
3. Consensus: lots of variation in diversification rates
4. Consensus*: speciation happens where species are not
5. Consensus*: diversification rates appear fastest over short intervals
6. Are we sure we are accurately reconstructing the historical dynamics of diversification?
7. New avenues in the analysis of diversification rates

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Diversity is unevenly distributed across the Tree of Life



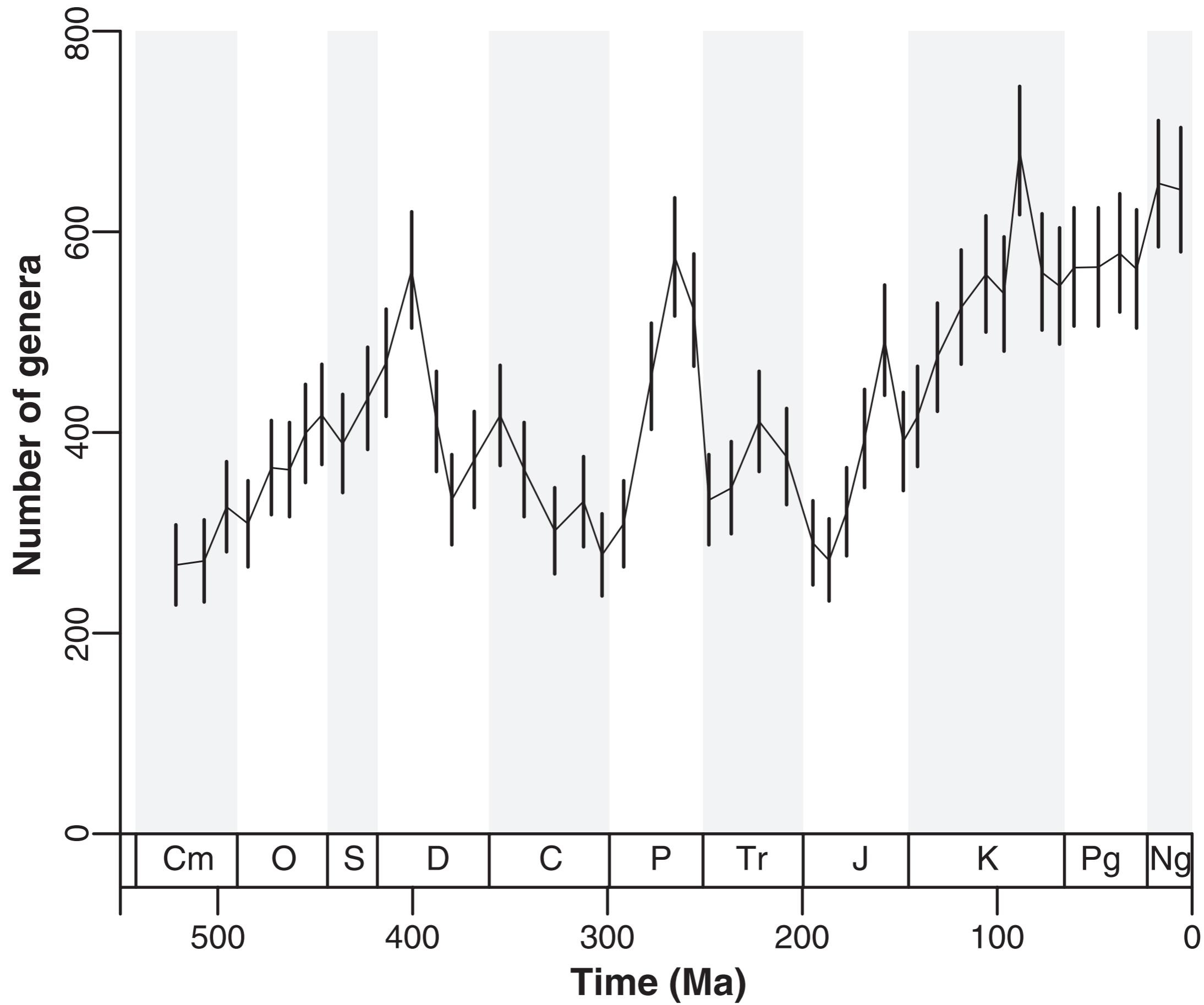
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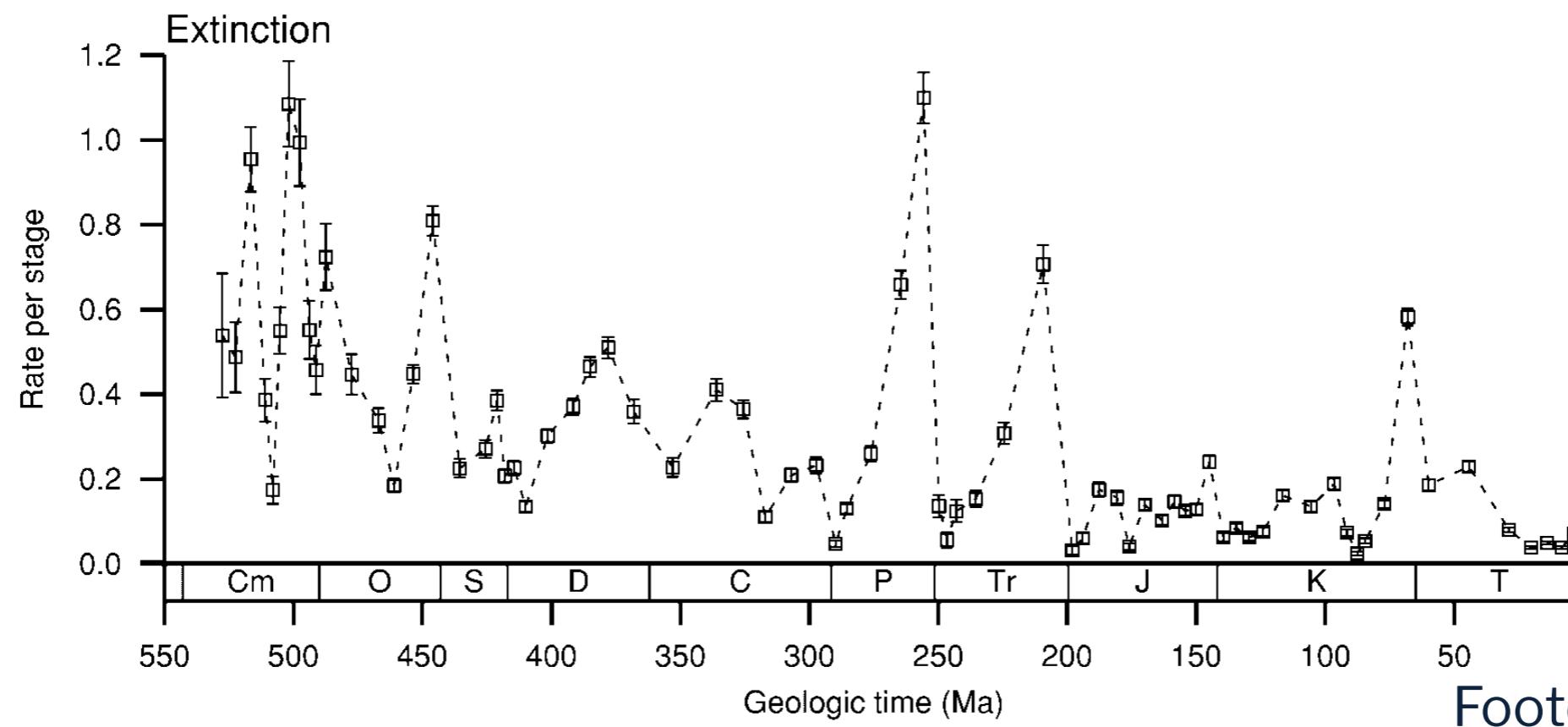
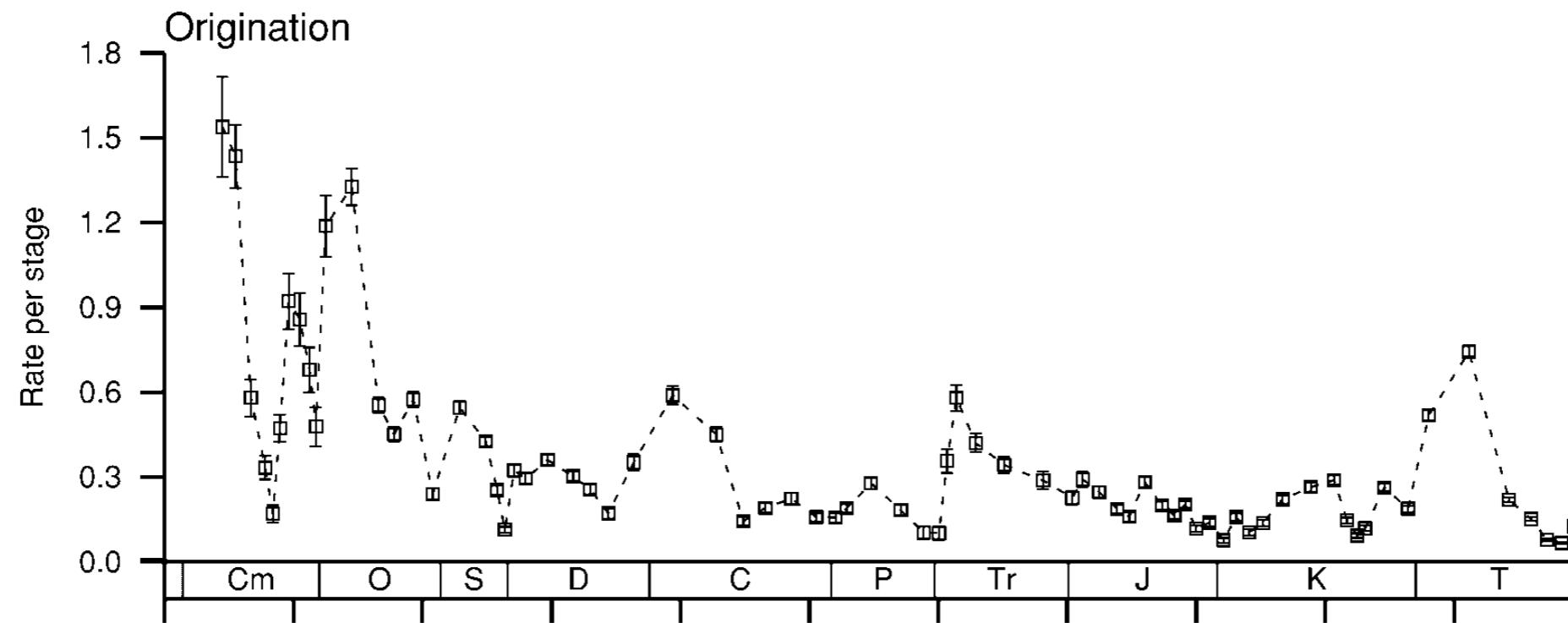
Amborella trichopoda
V.



~400,000 species

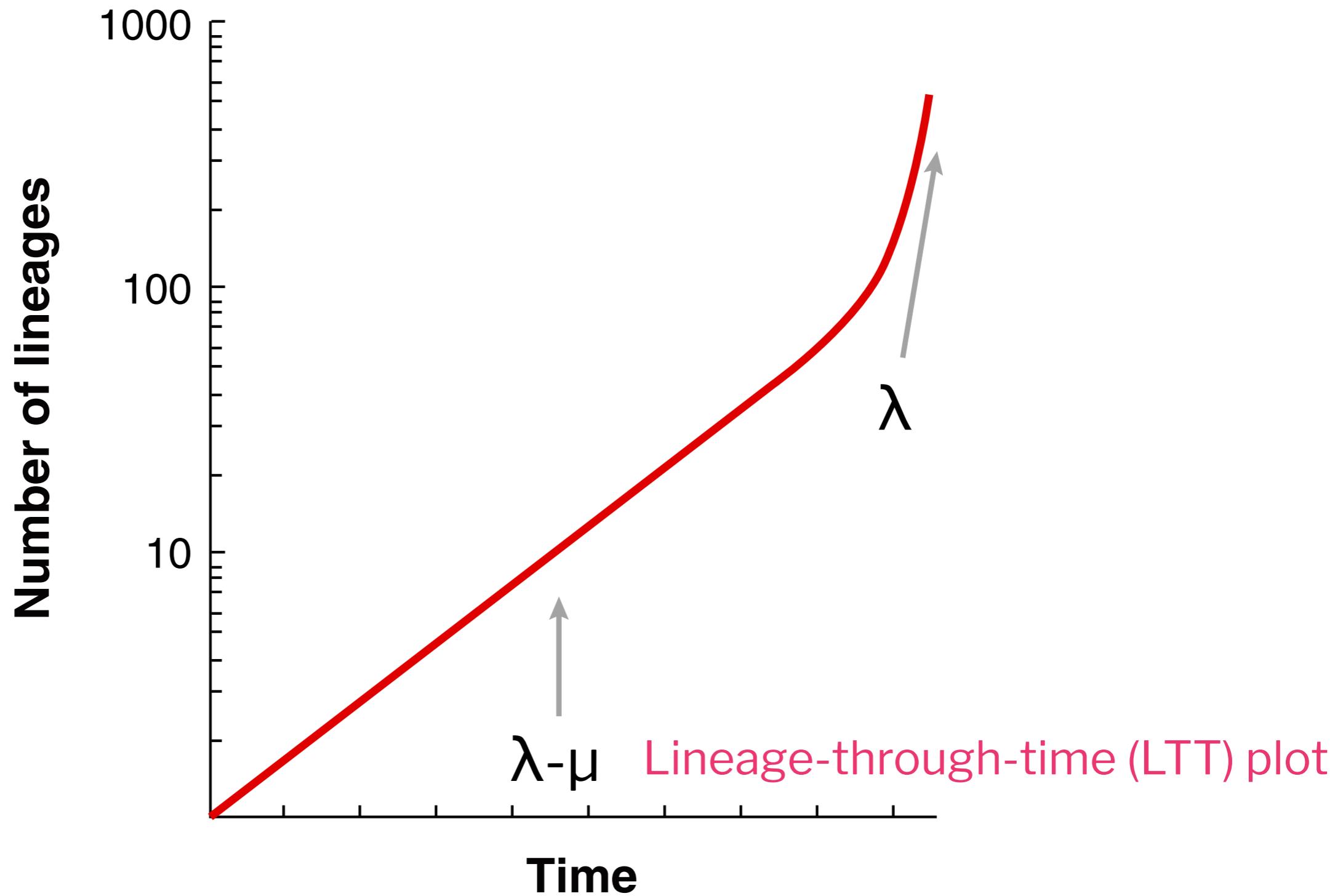


Variation in diversity is a consequence of variation in speciation and extinction rates

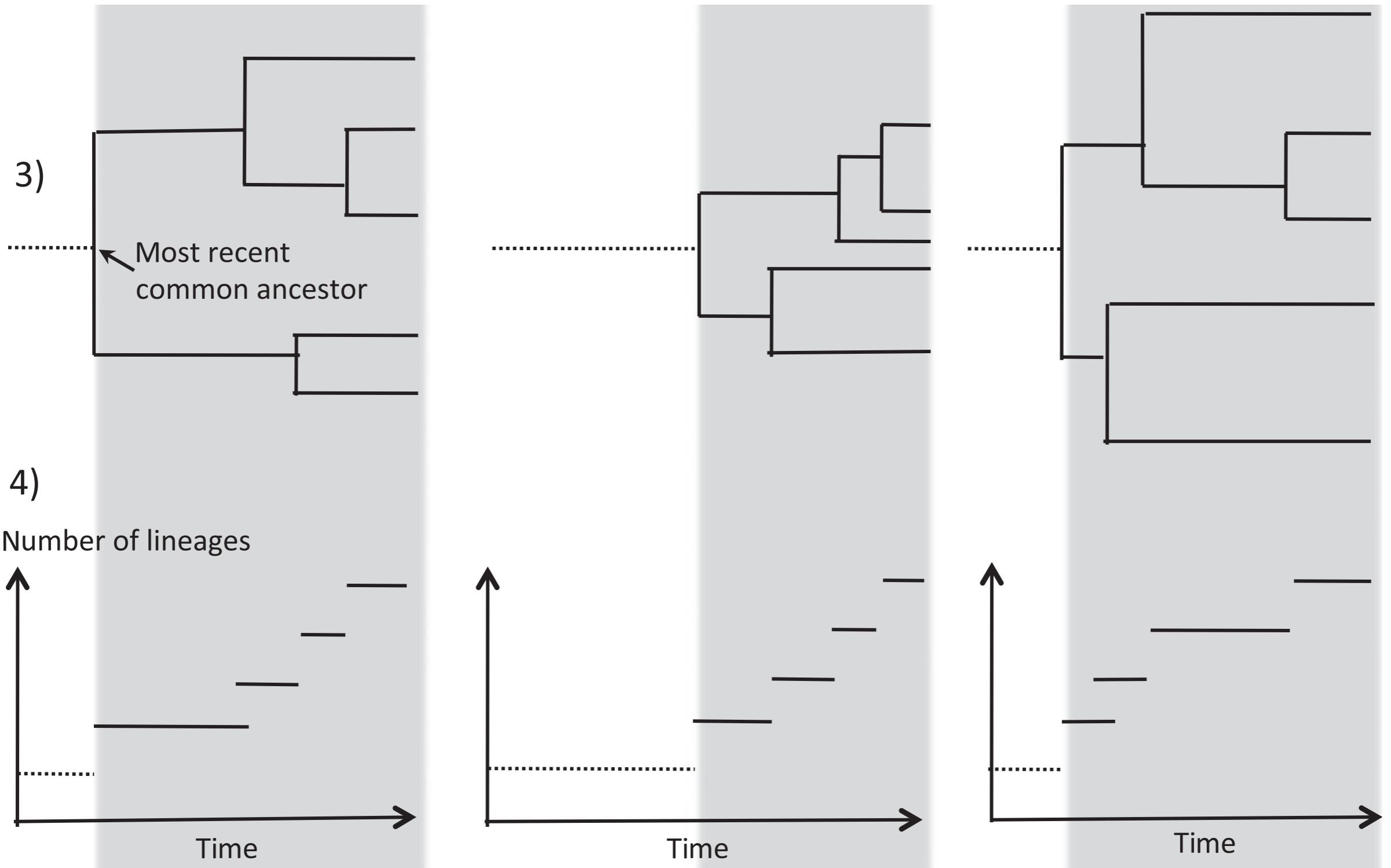


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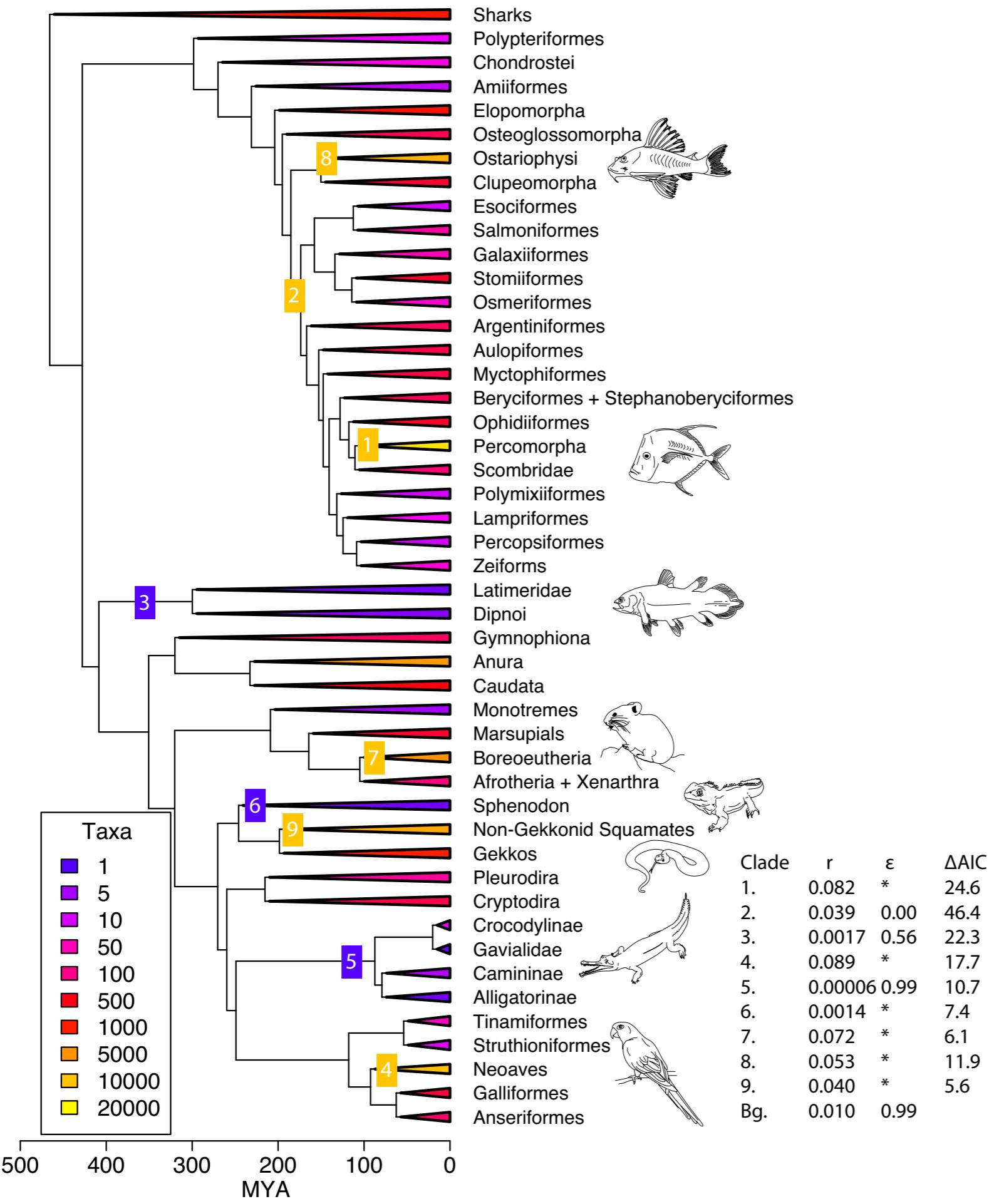
Can estimate speciation (λ) and extinction (μ) from phylogenies of extant taxa only



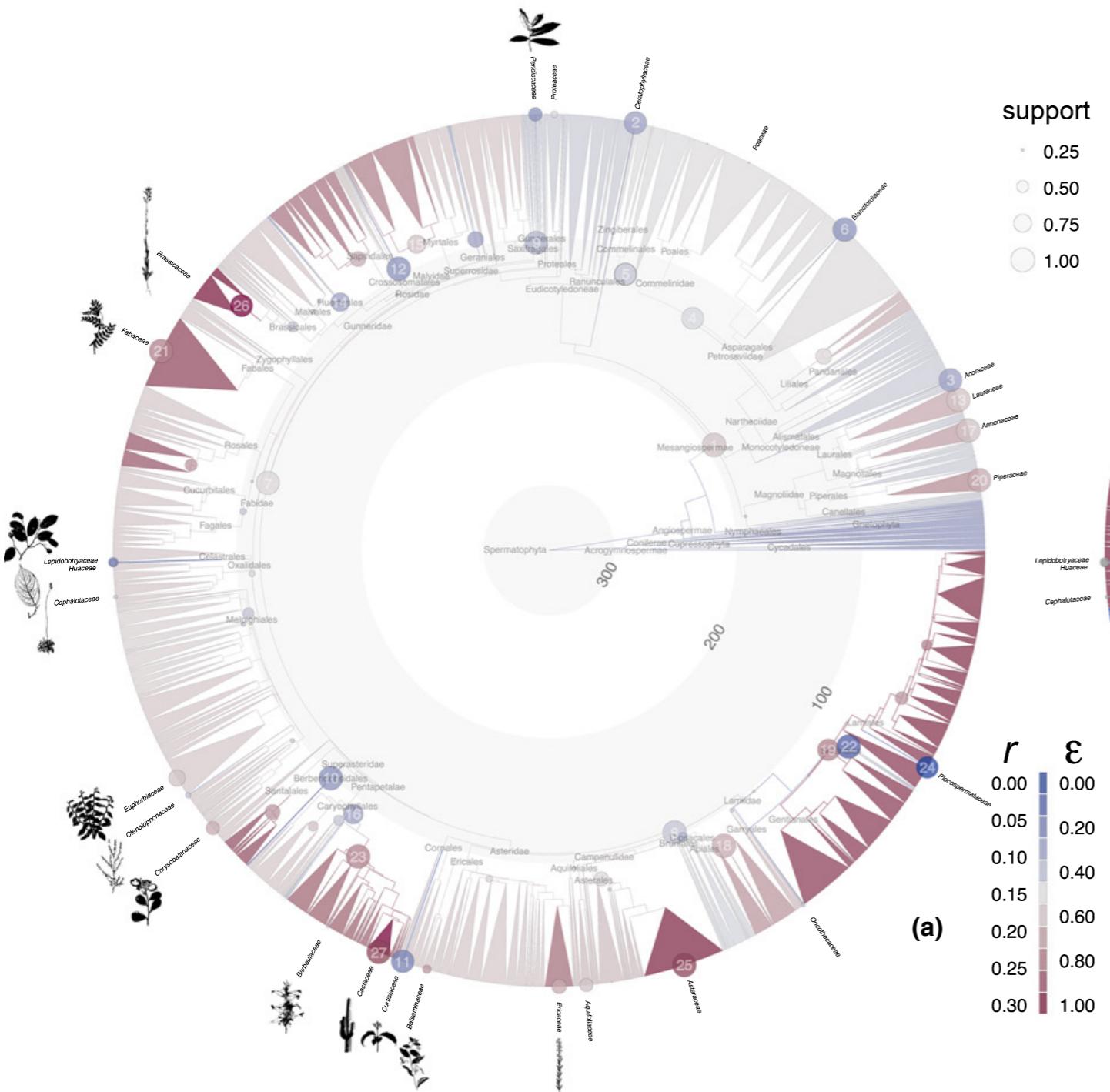
Different processes leave different signatures on phylogenetic trees and LTT plots



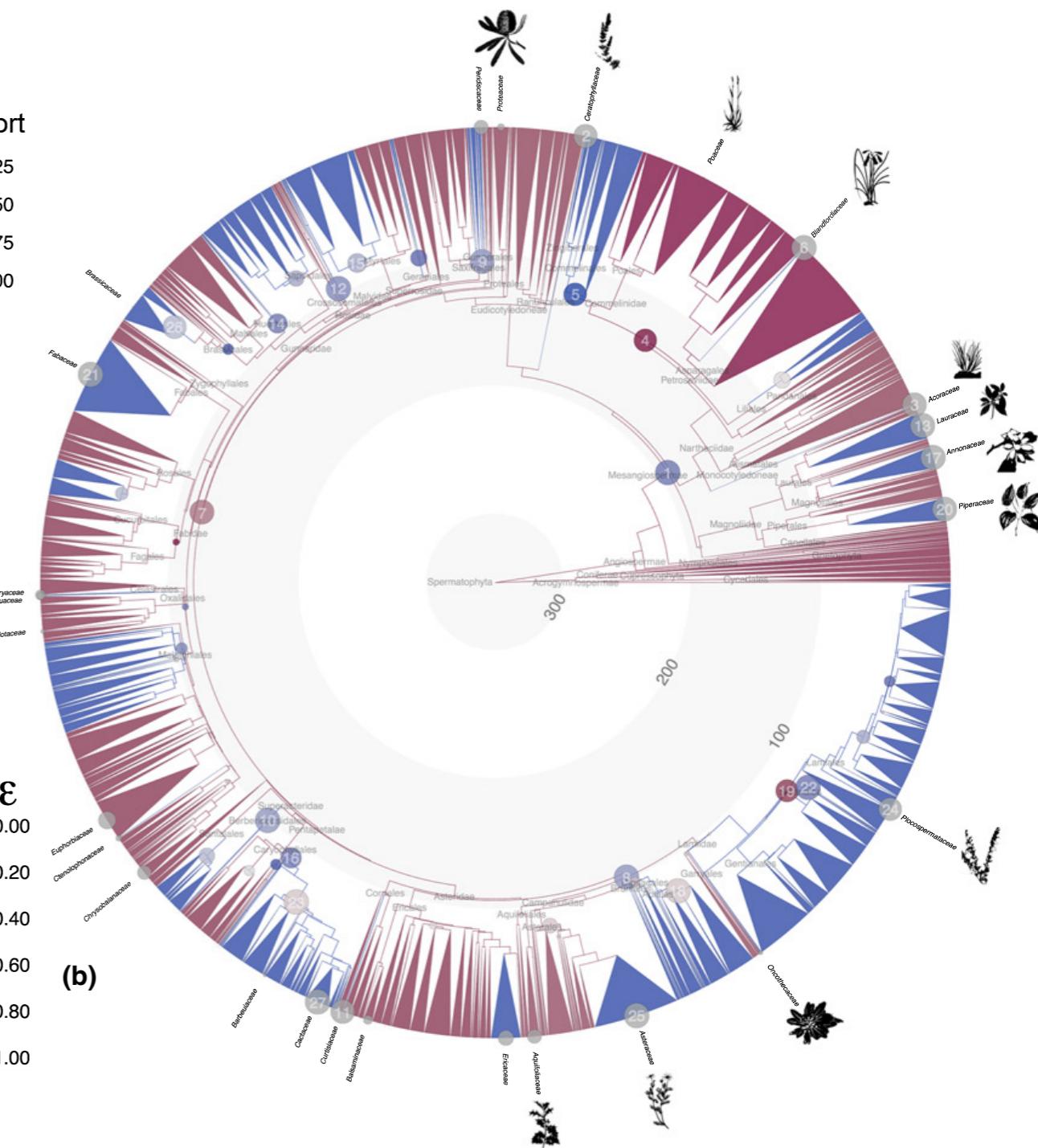
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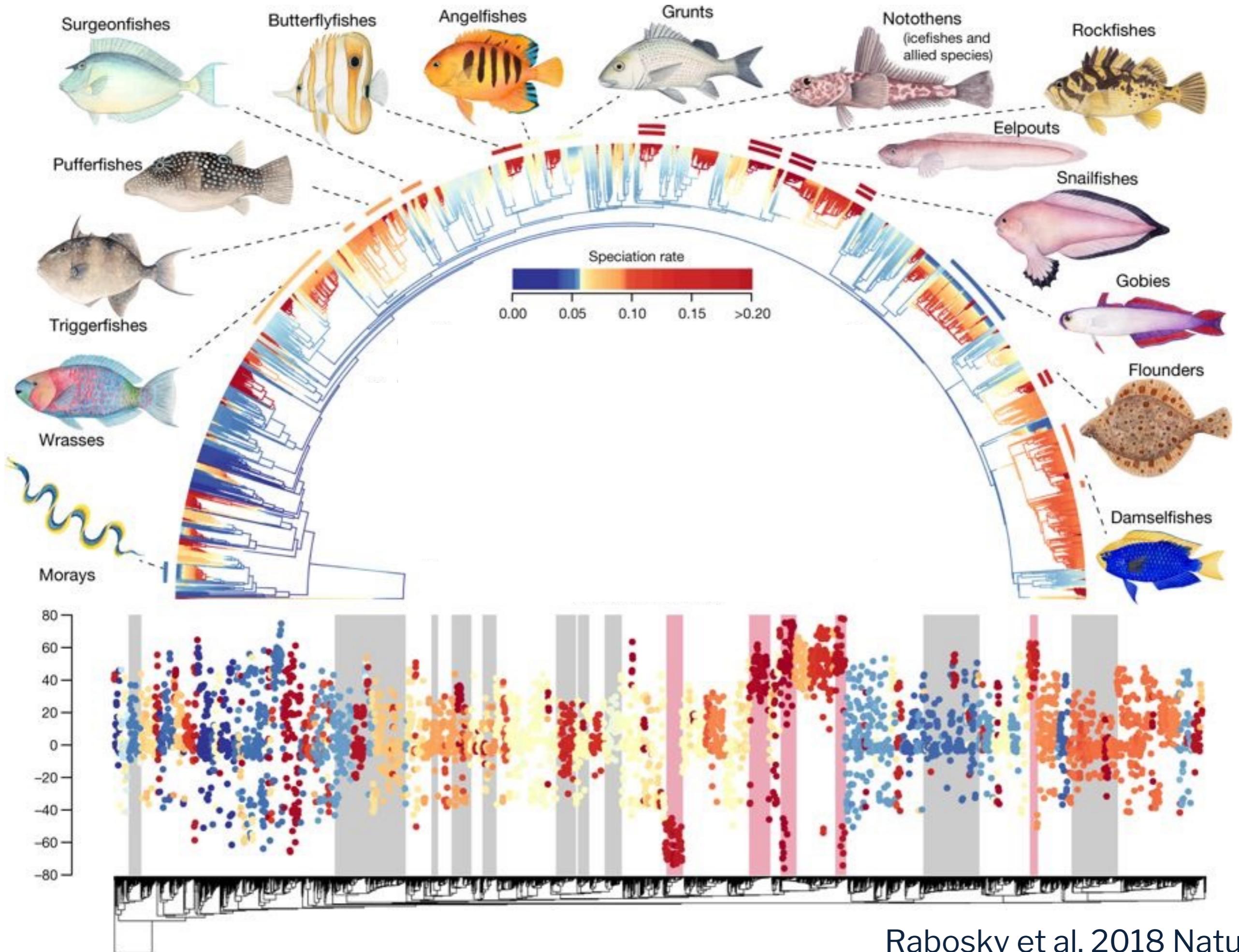


Net diversification rates (r) speciation - extinction

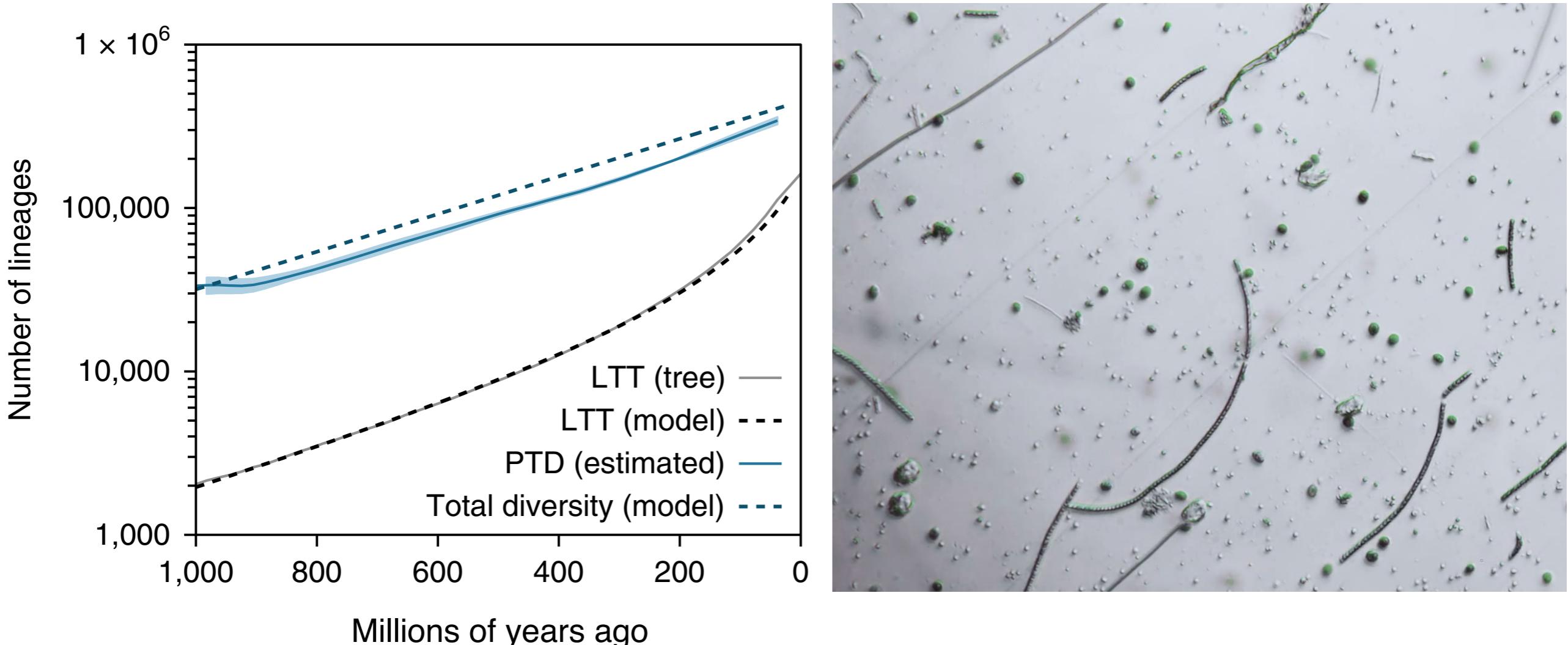


Turnover rates (ϵ) extinction / speciation

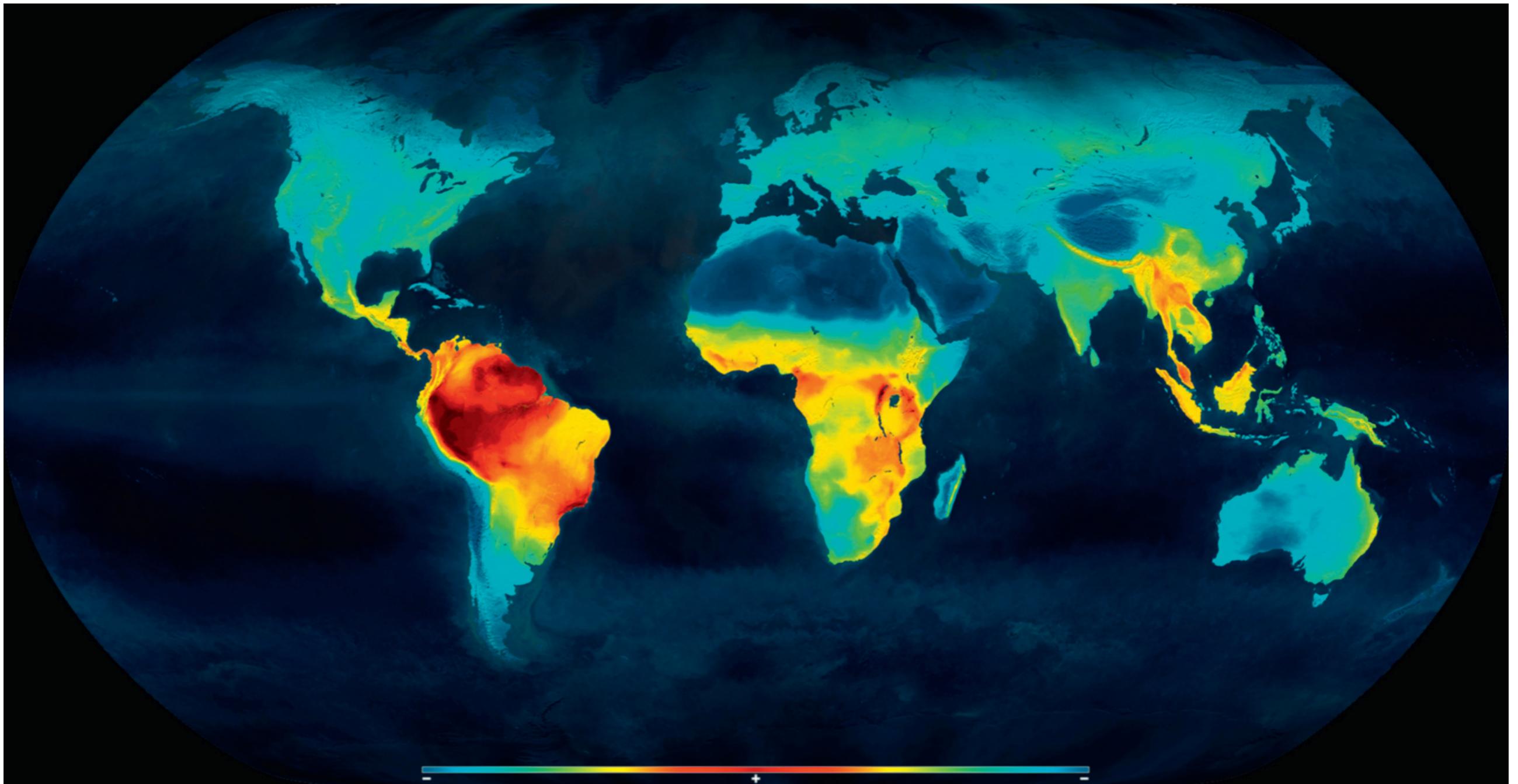




Estimating speciation and extinction rates from a phylogeny of 448,112 bacterial “species”

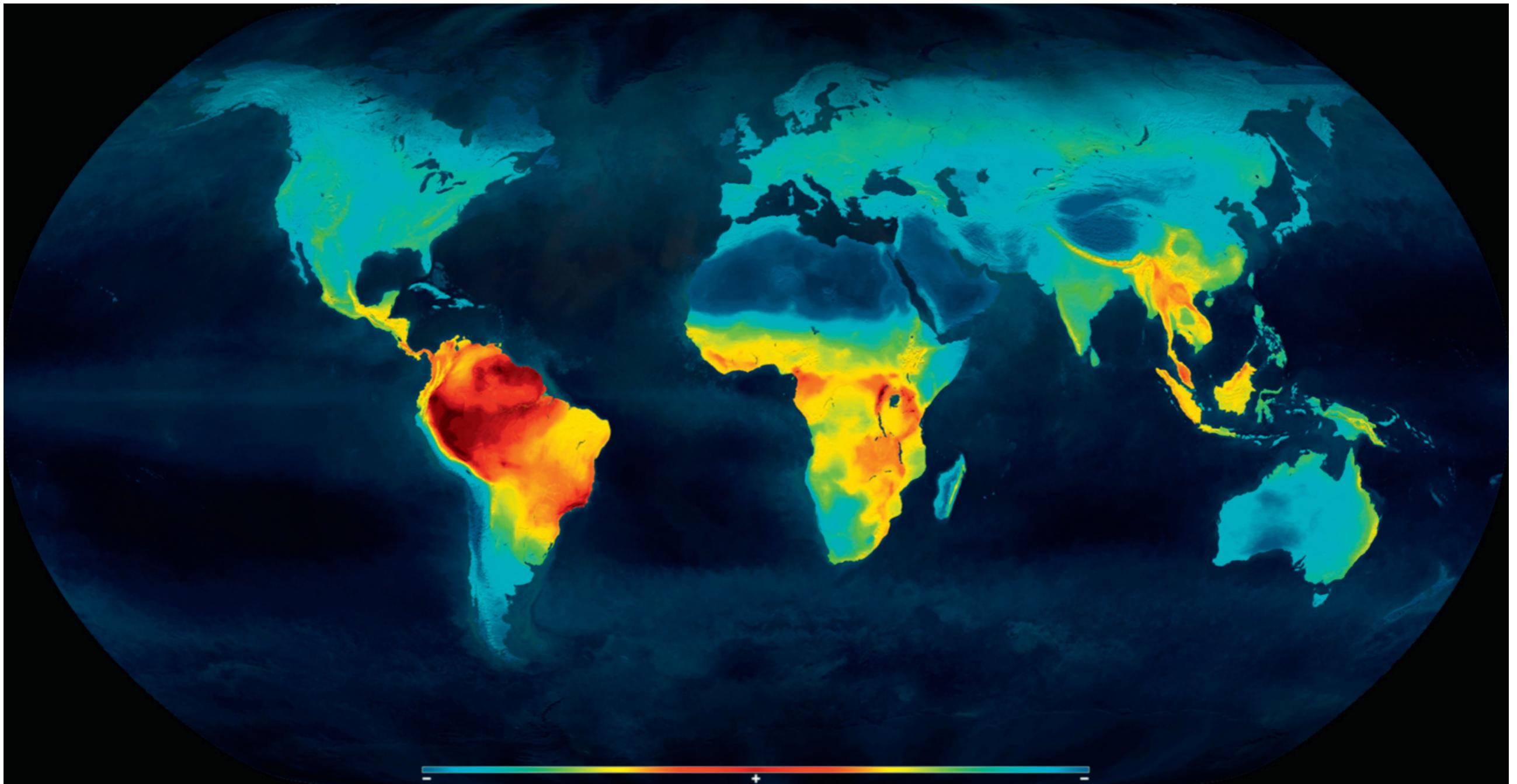


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Mannion et al. 2014 TREE; Data from Jenkins et al. 2013 PNAS

Simple prediction: high species diversity is a result of high diversification rates



Tropical regions have more diversity

Larger areas have more diversity

Middle altitudes have more diversity

Some habitats have more diversity

Tropical regions have more genetic diversity

Unmodified areas have more diversity



Dolph Schluter

Schluter and Pennell 2017 Nature

Tropical regions have more diversity

Larger areas have more diversity

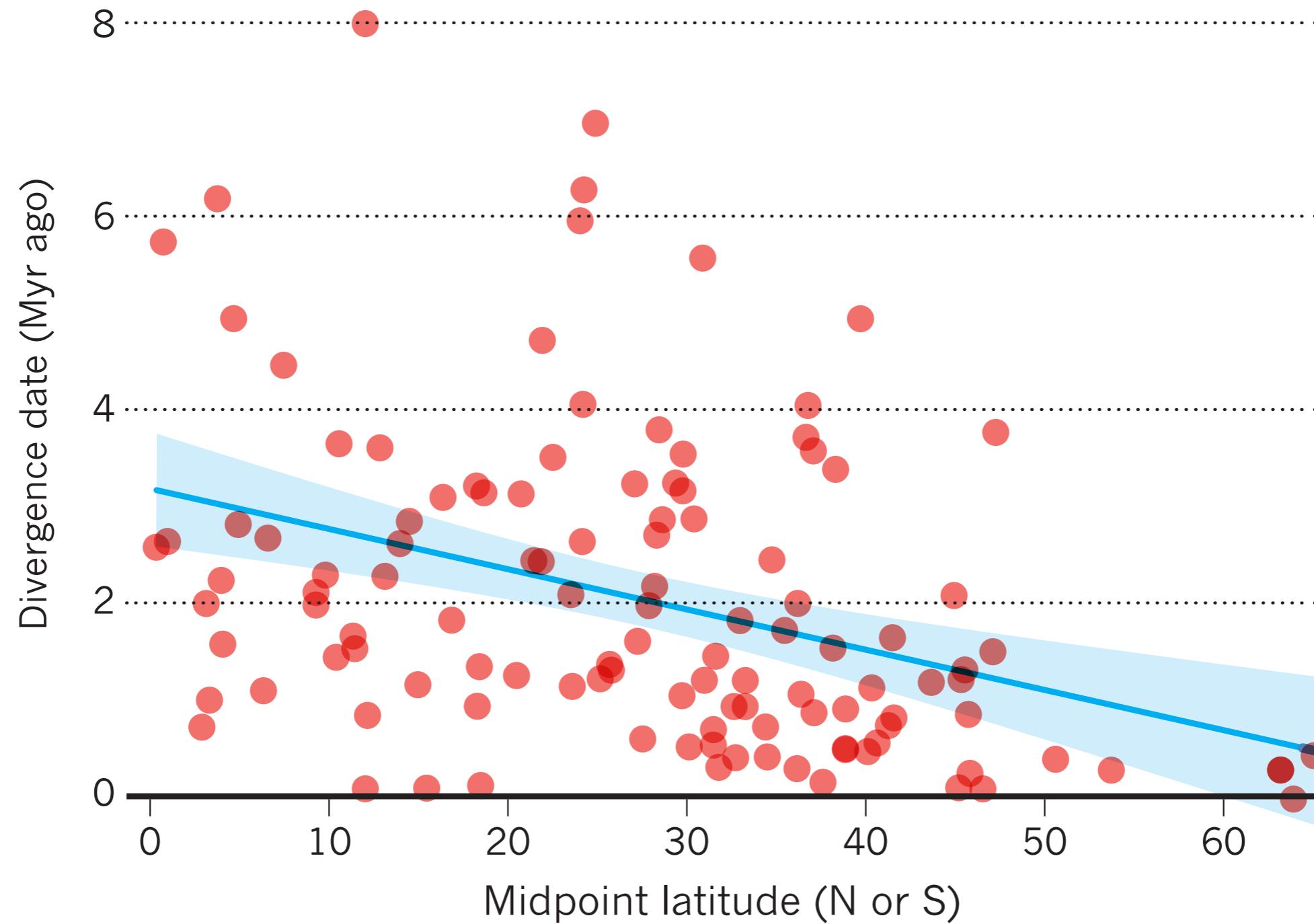
Middle altitudes have more diversity

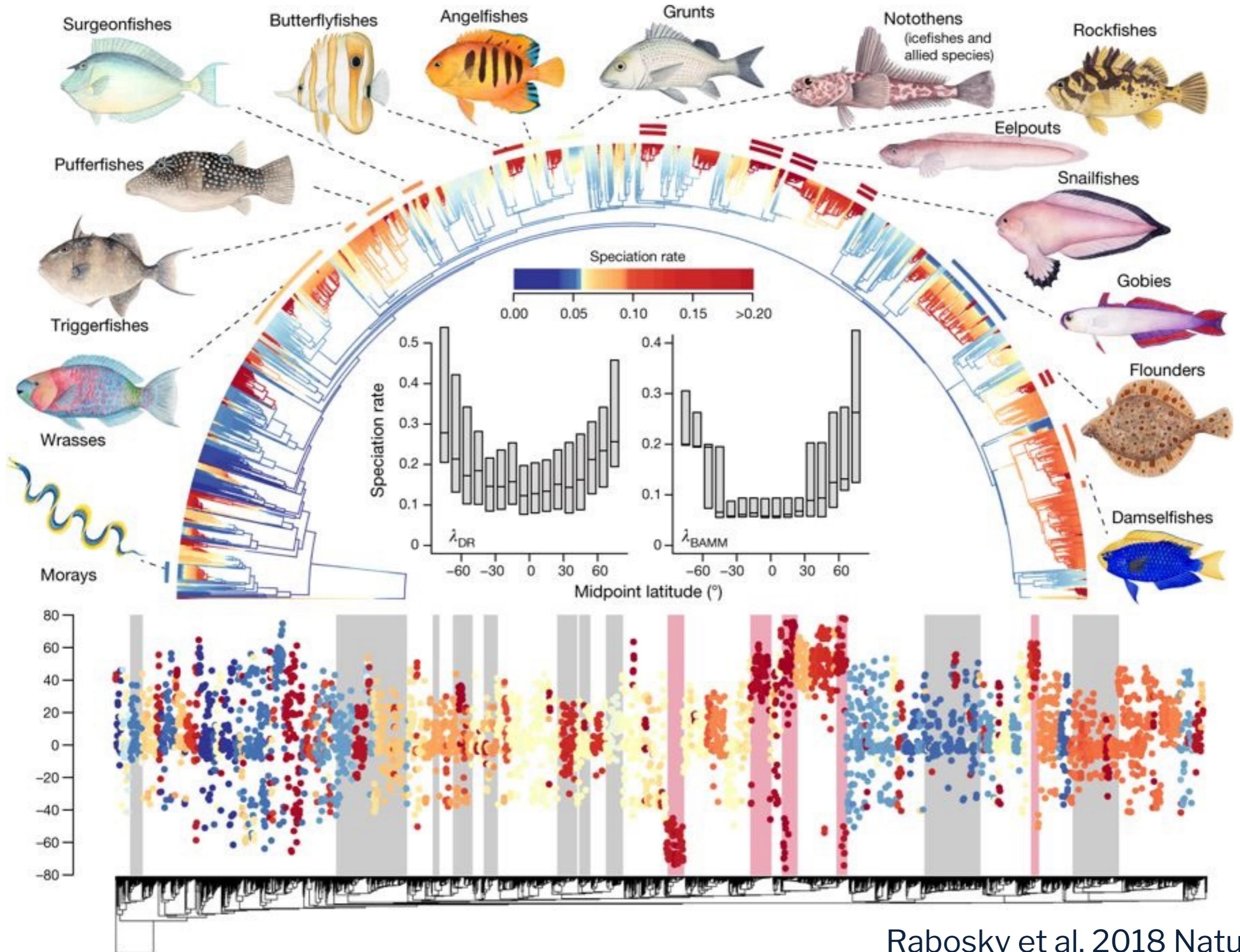
Some habitats have more diversity

Tropical regions have more genetic diversity

Unmodified areas have more diversity

Mammalian species living closer to the poles have diverged more recently than tropical species





Tropical regions have more diversity

Larger areas have more diversity

Middle altitudes have more diversity

Some habitats have more diversity

Tropical regions have more genetic diversity

Unmodified areas have more diversity

Fastest contemporary rates of speciation occur where there are fewer species — “speciation gradients” run in opposite directions to species gradients

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104 time-calibrated phylogenetic trees from the literature
including 25,864 species

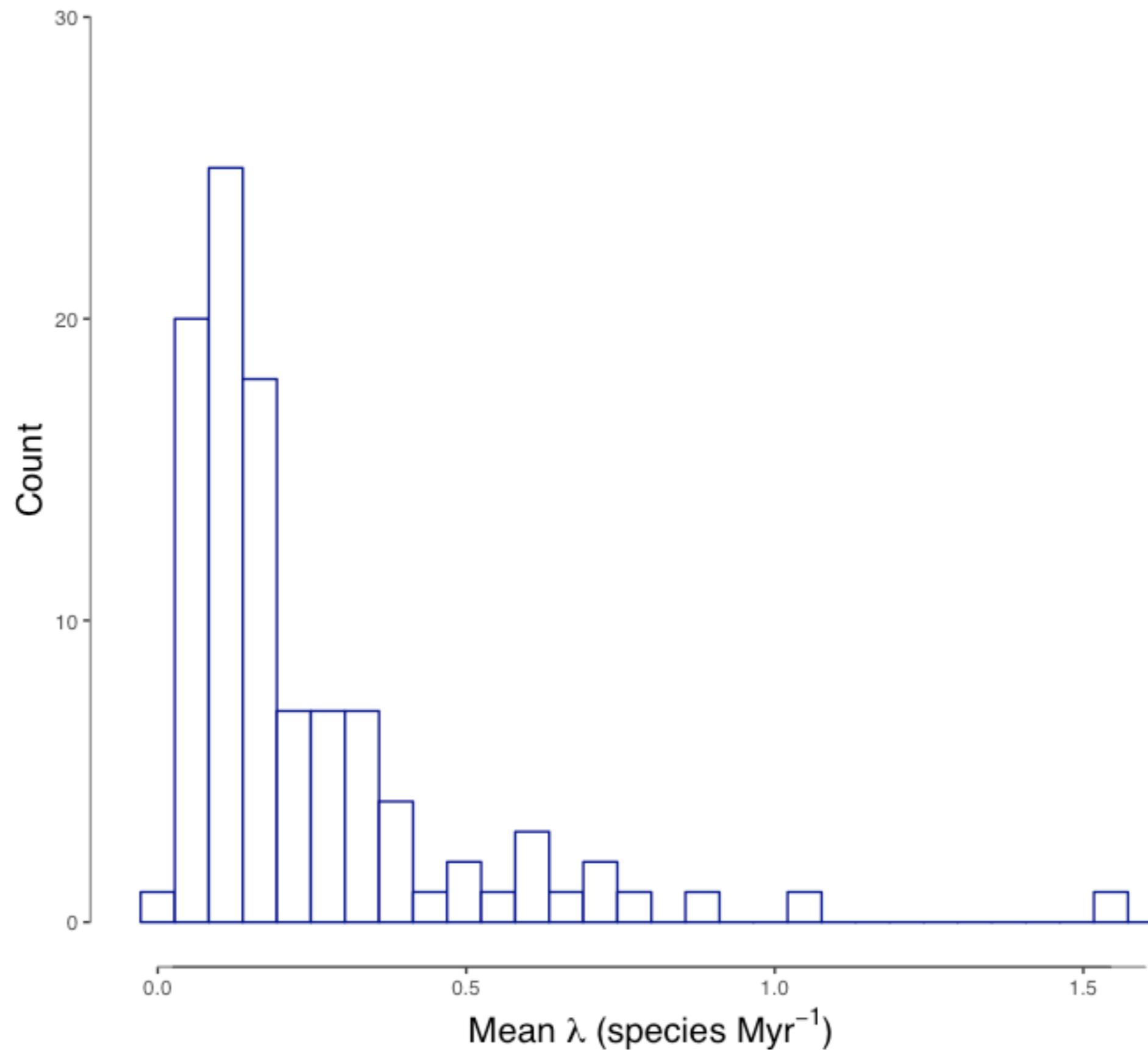
74 fossil time series
including 6,144 genera

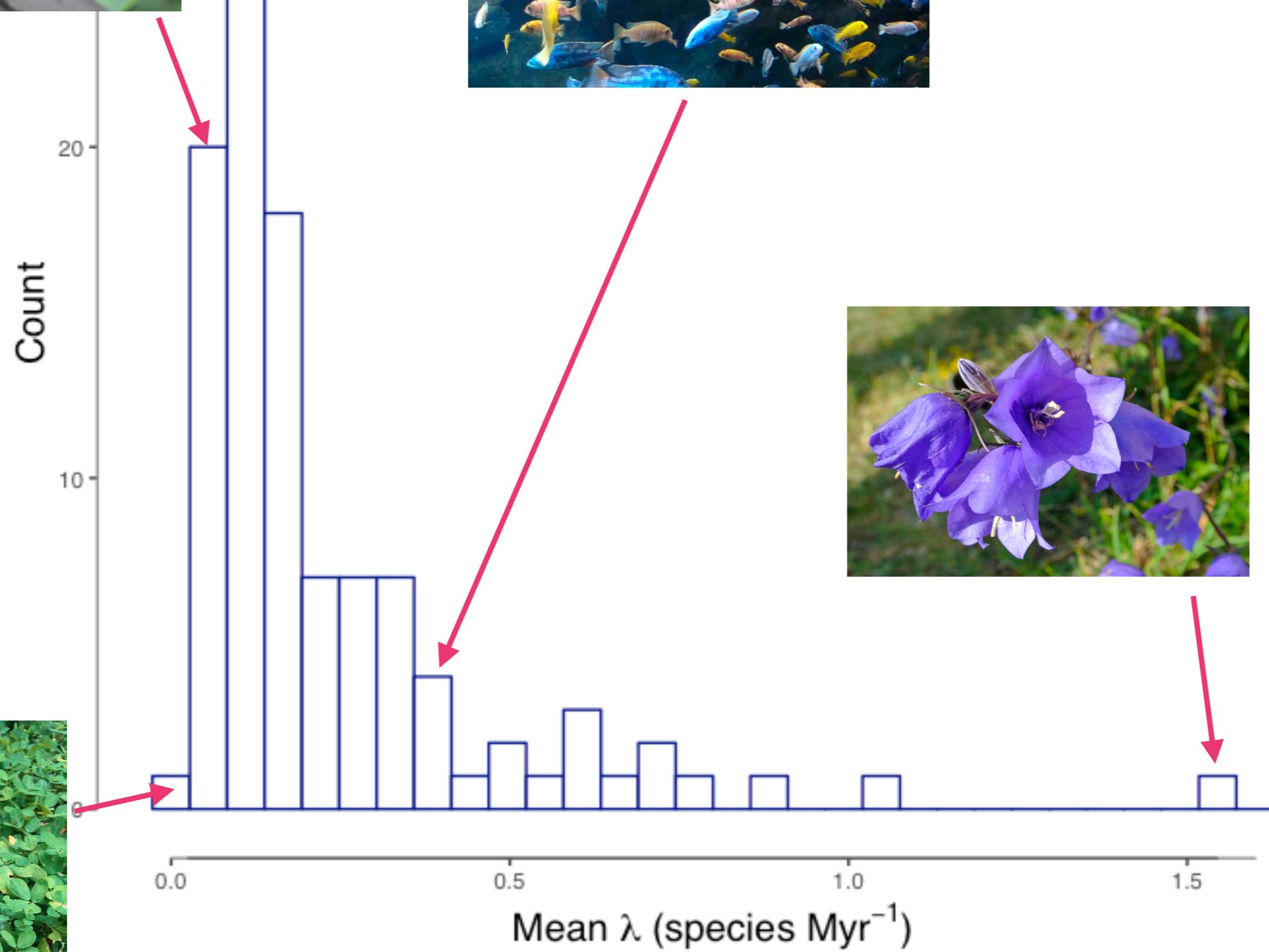


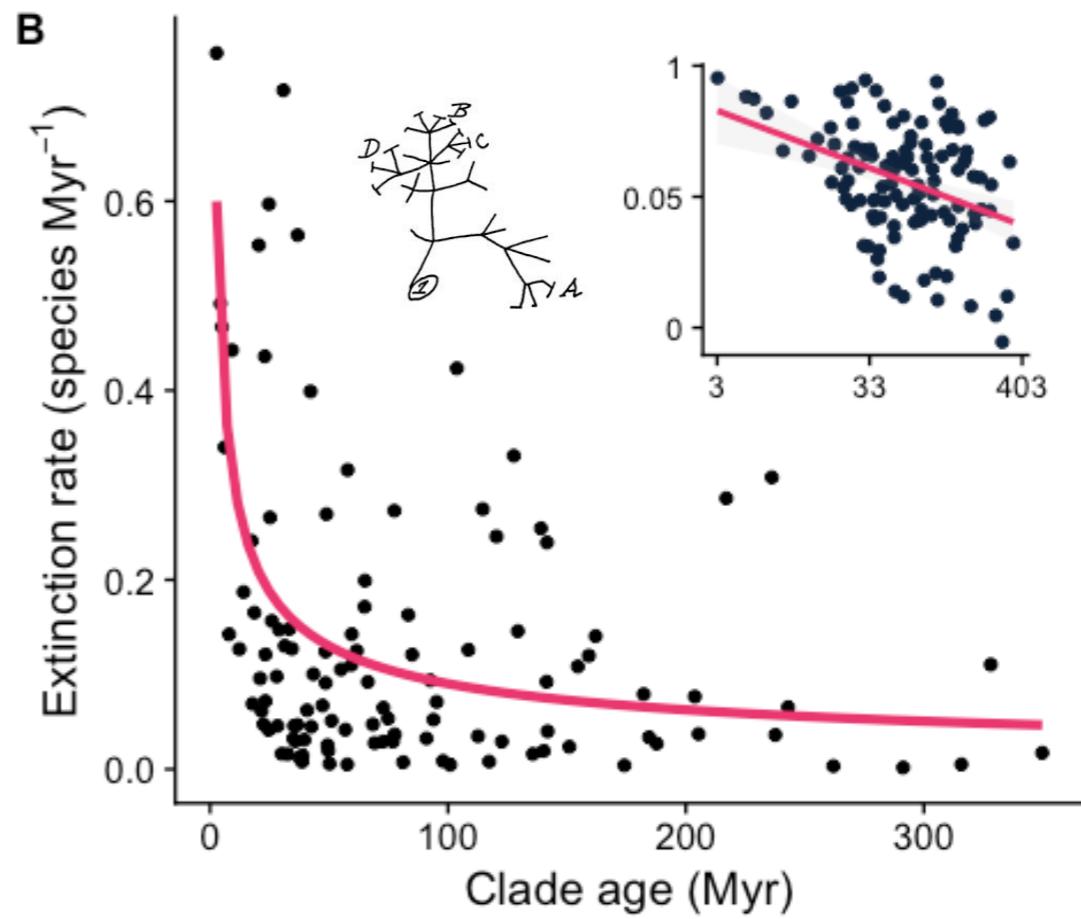
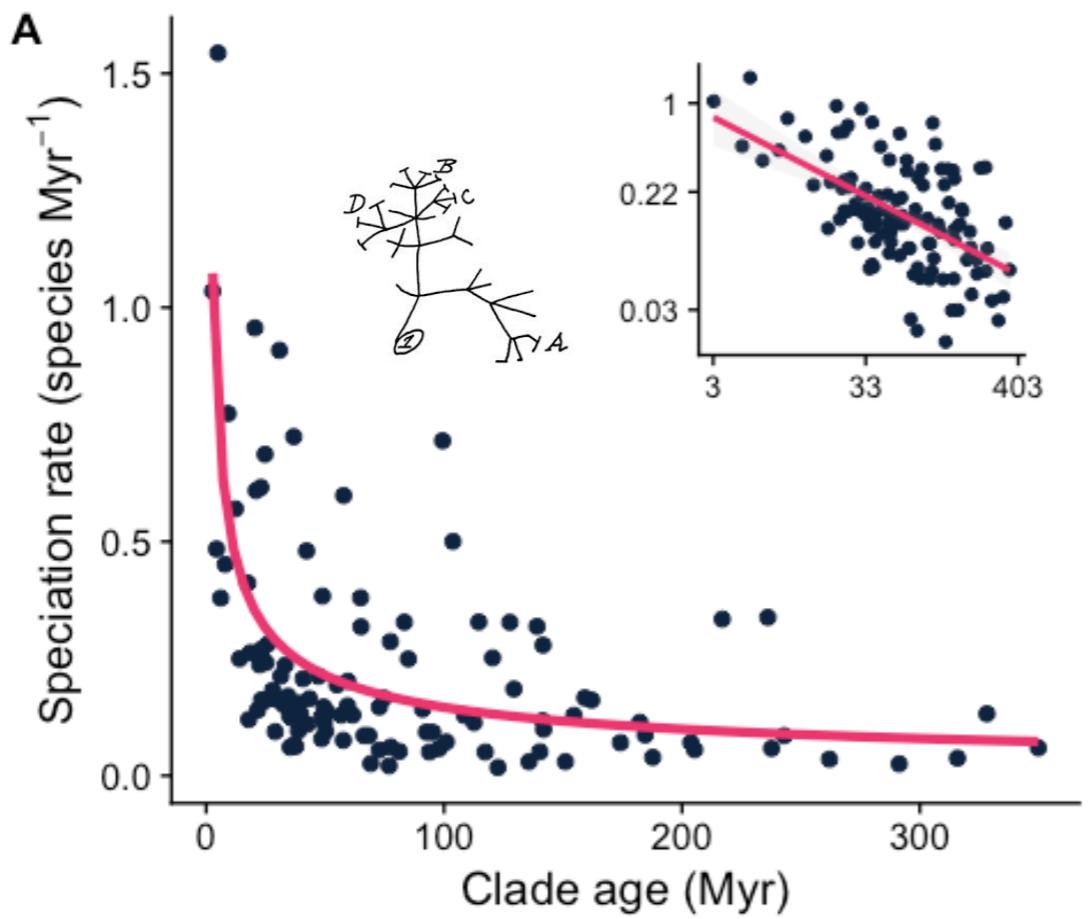
Francisco Henao Diaz Mauro Sugawara

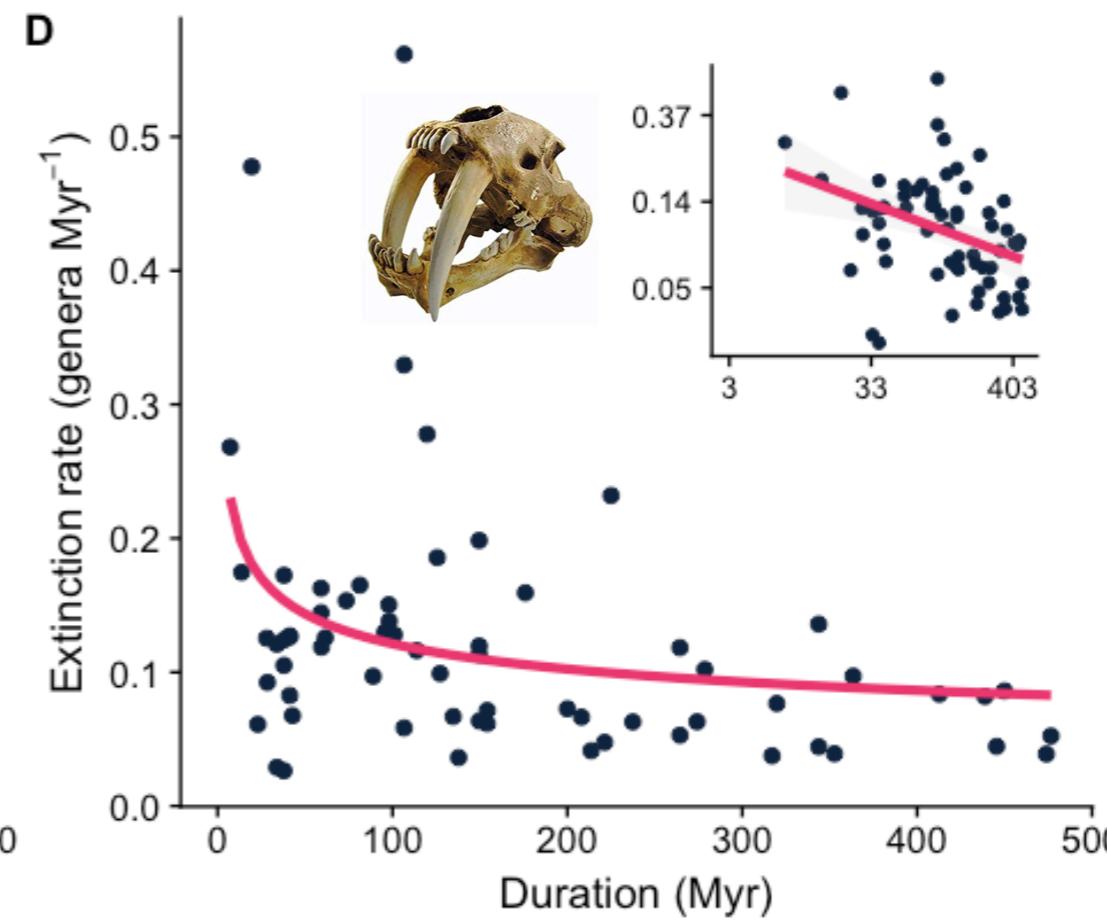
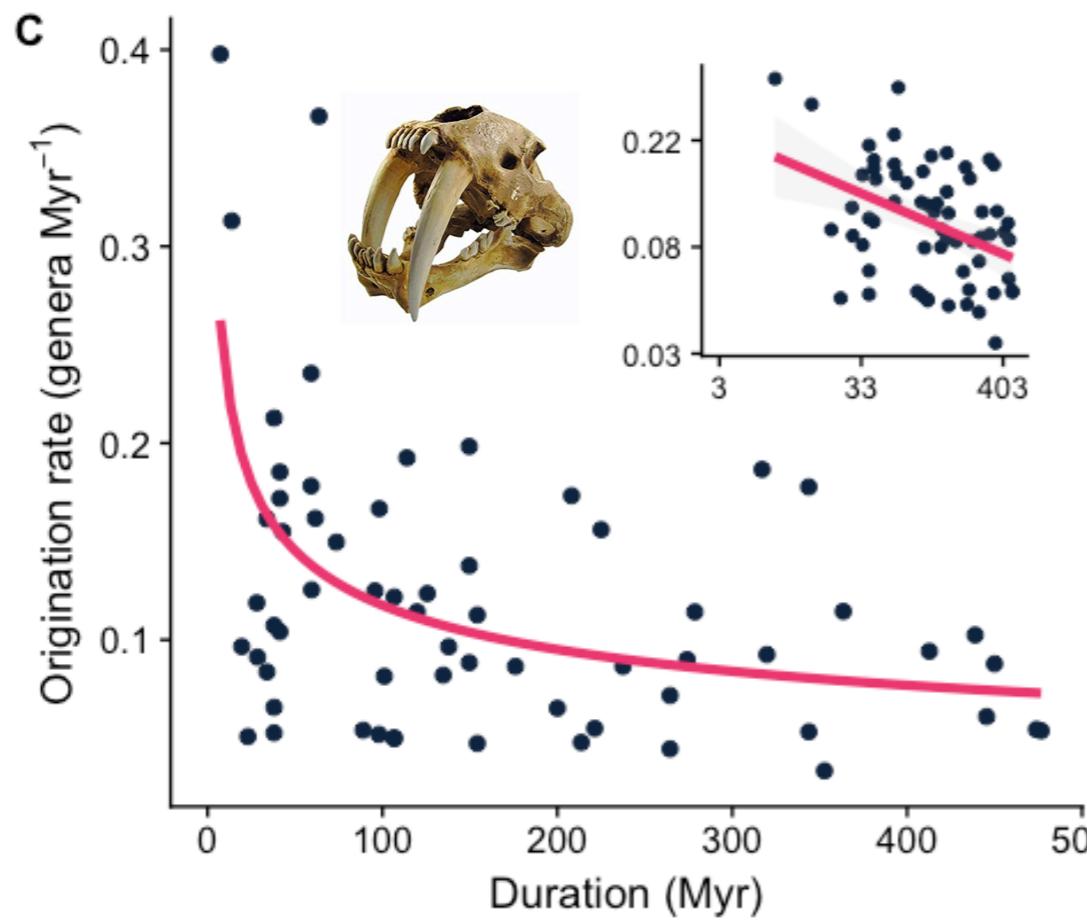
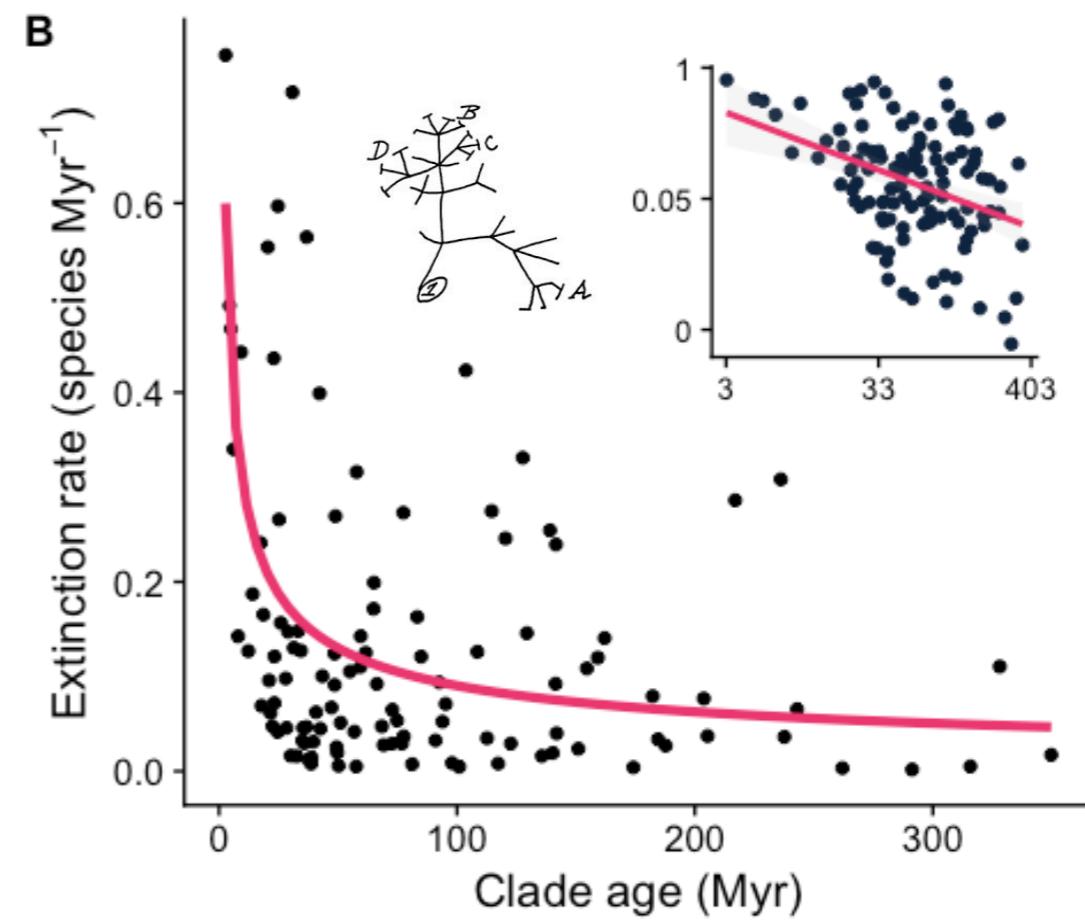
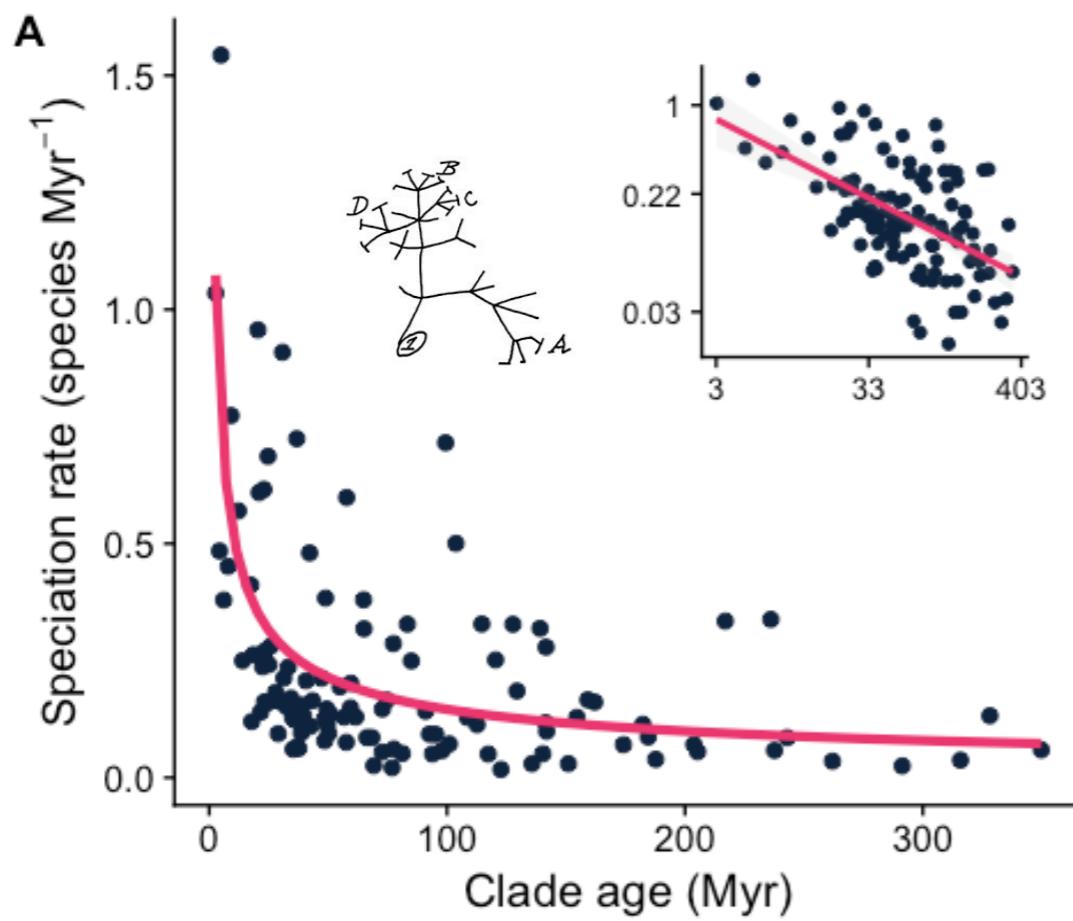
Eliot Miller

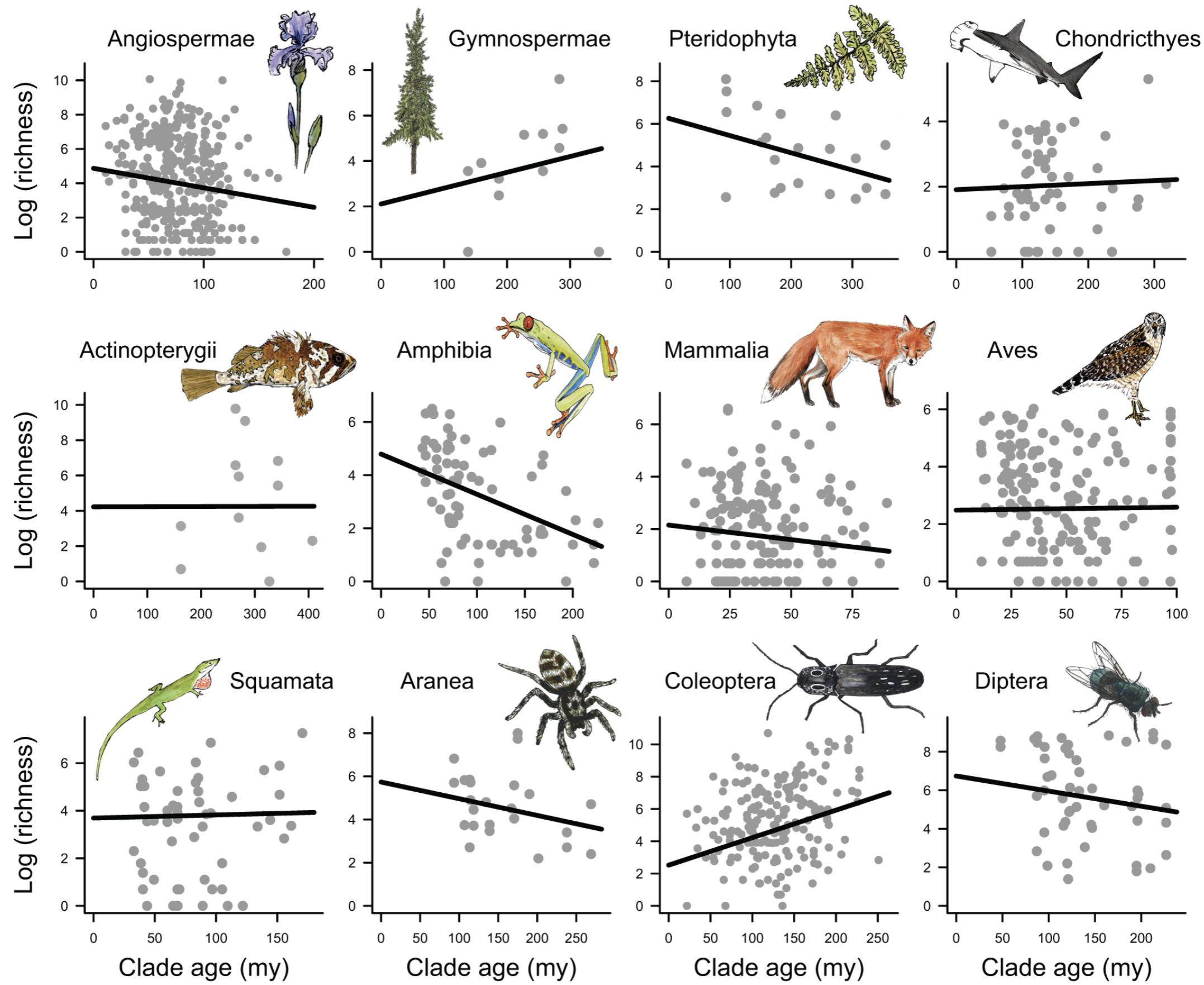
Luke Harmon

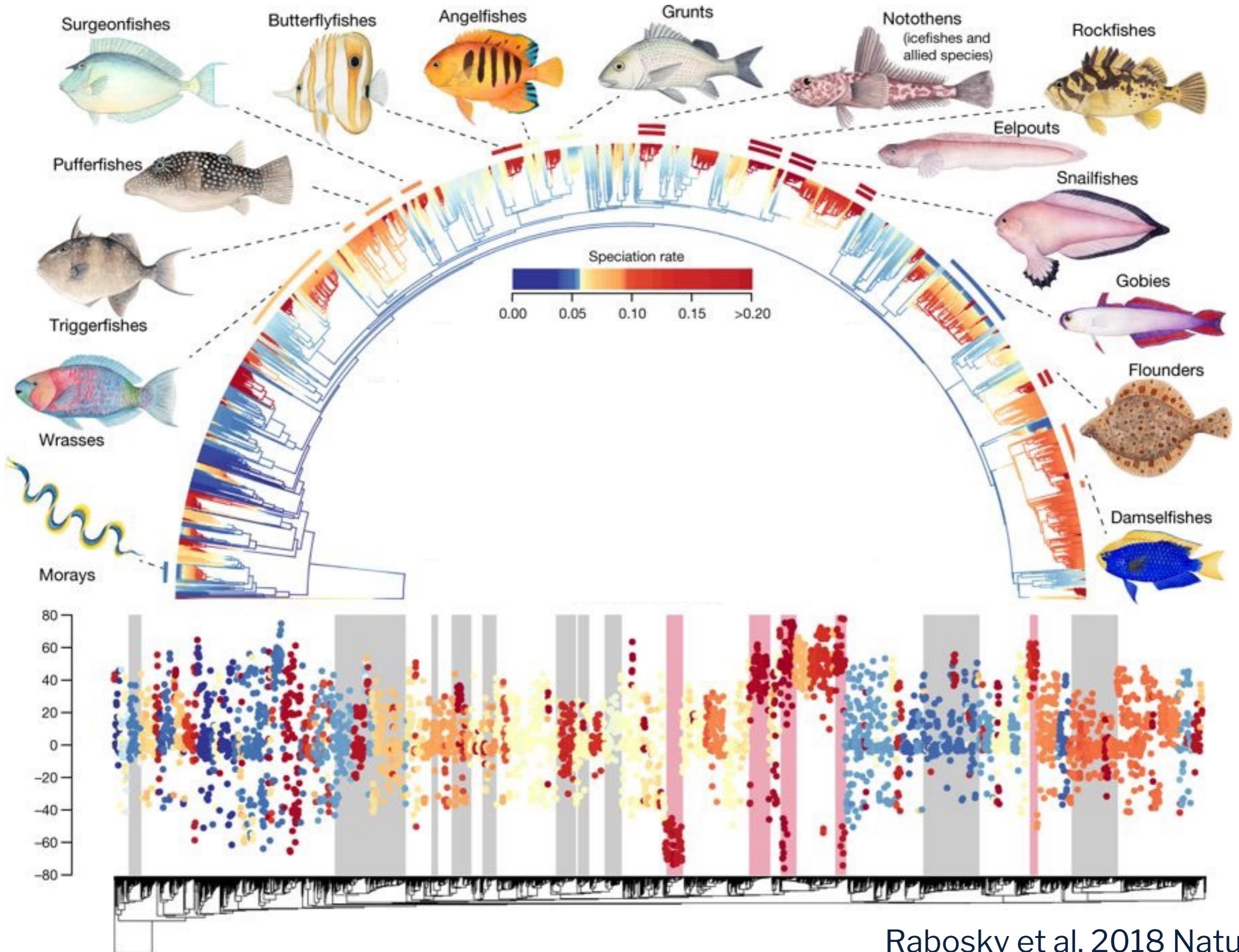


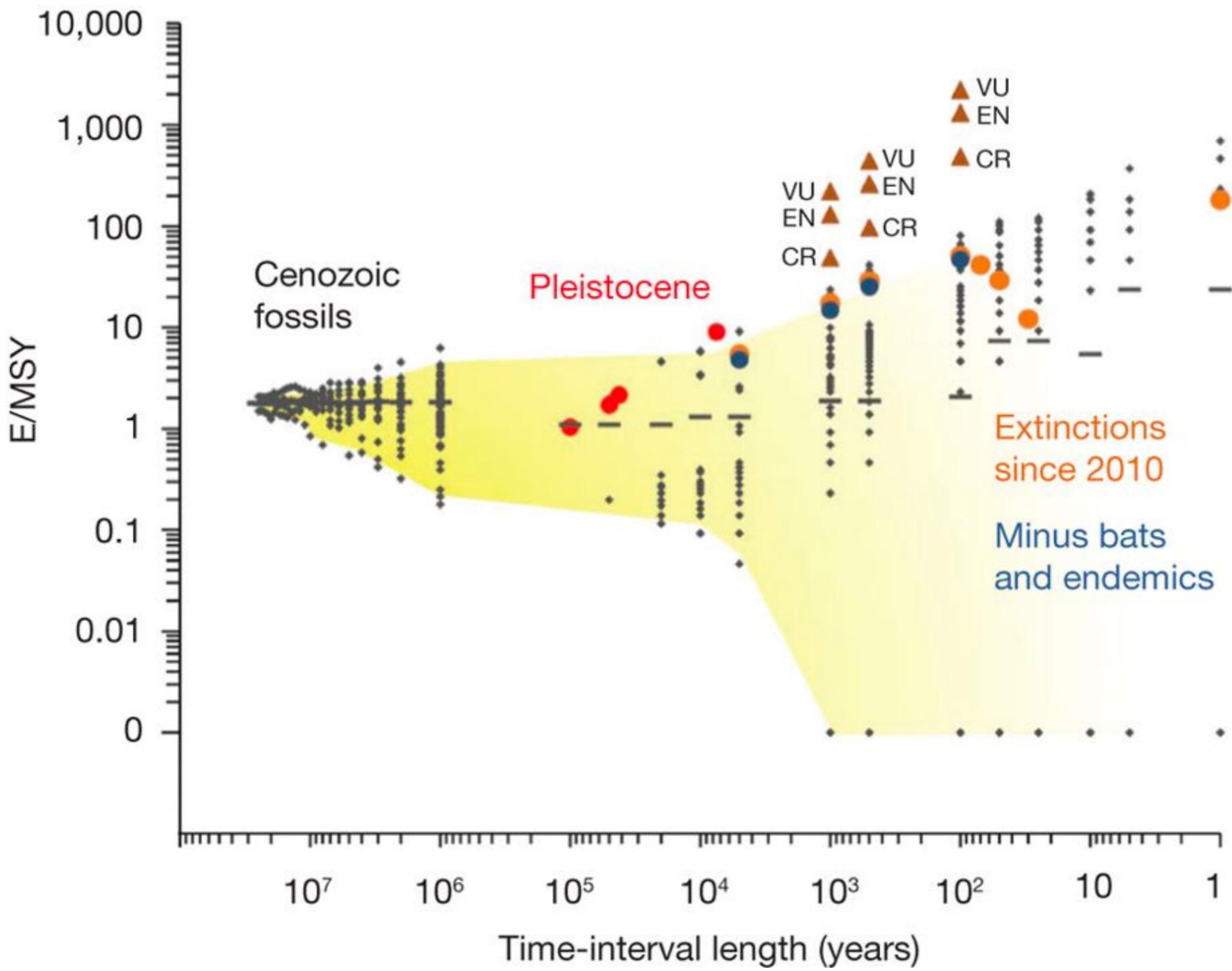








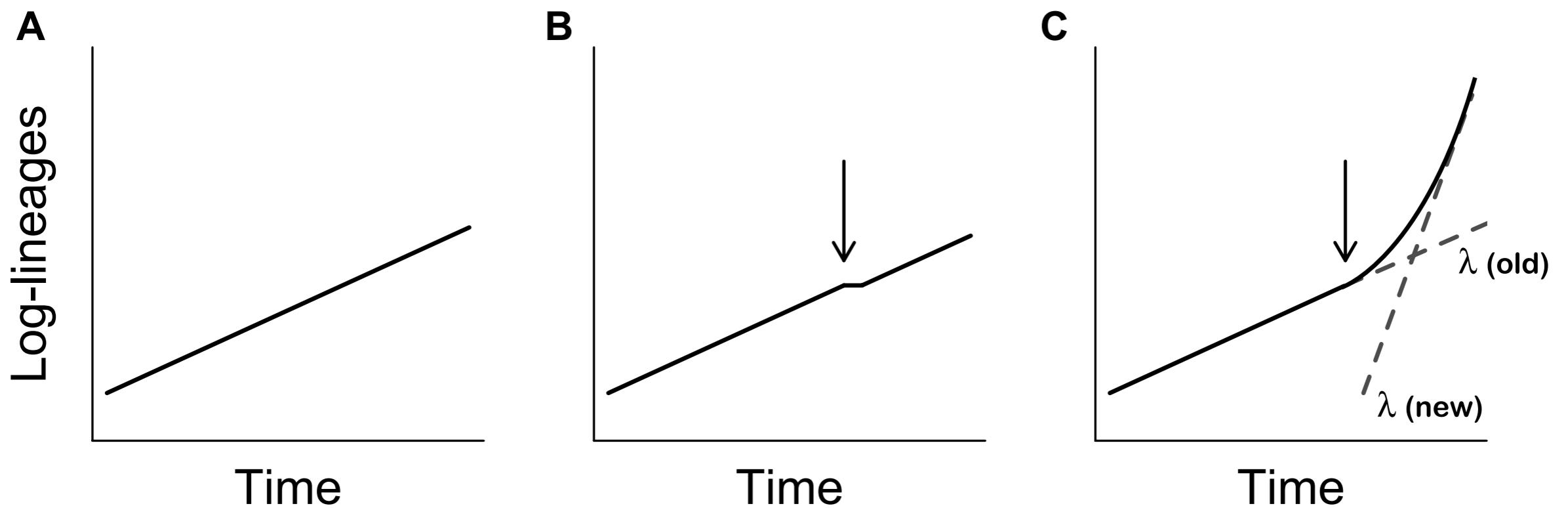




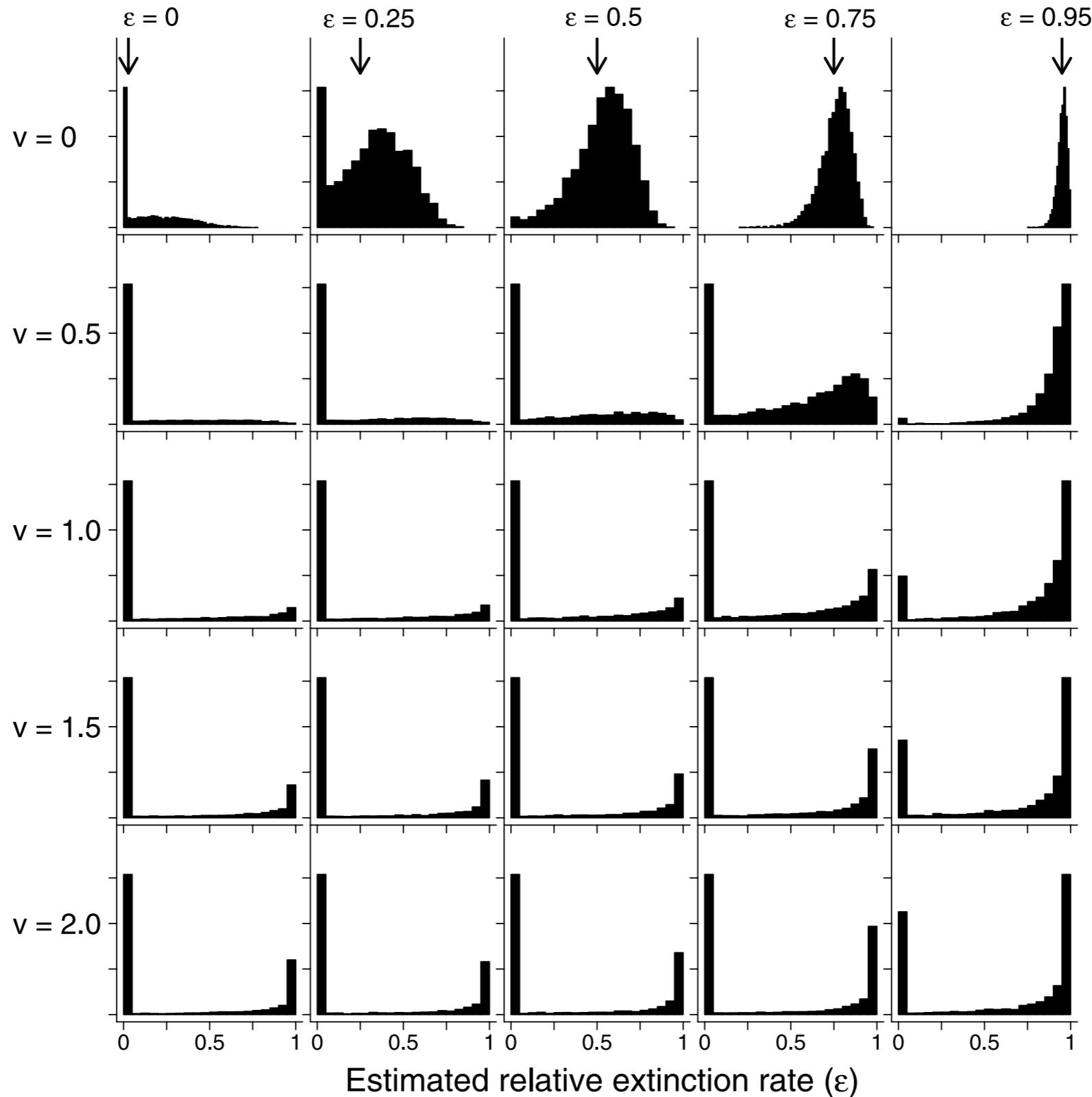
Fastest rates of speciation are
happening in young radiations –
consistent pattern across scales
but explanation not entirely clear

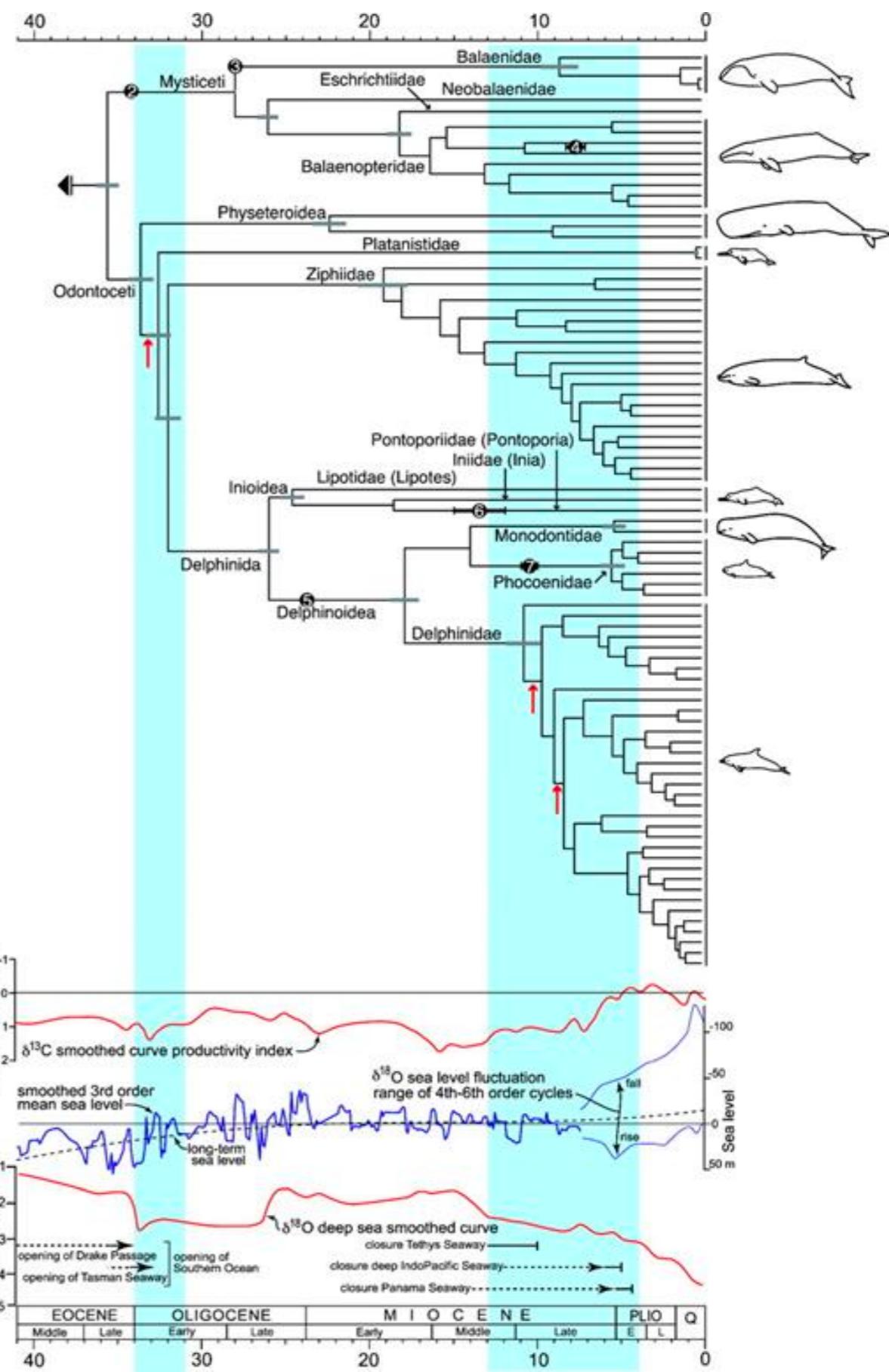
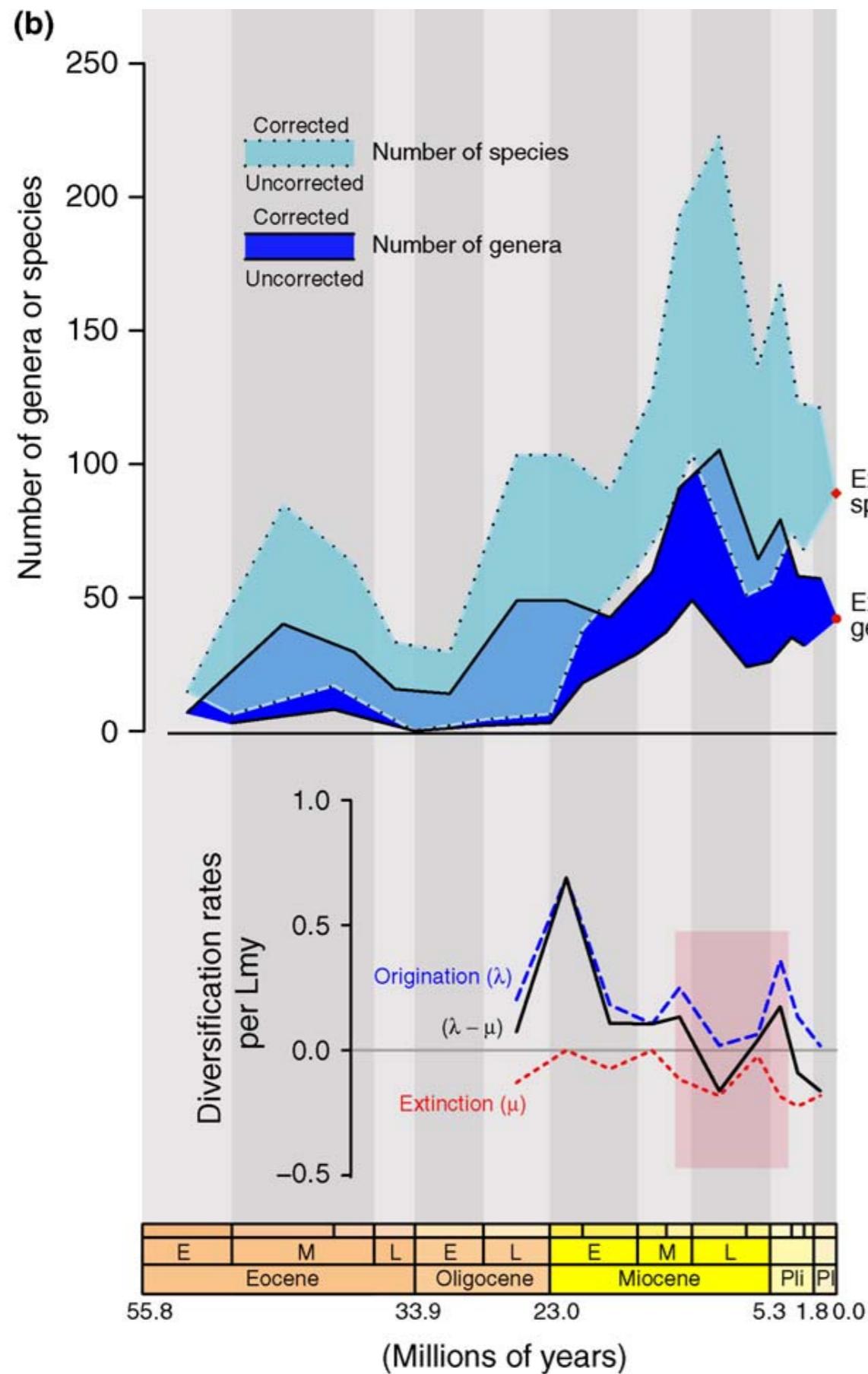
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Different processes can generate similar looking LTT plots



Extinction rates are poorly estimated from phylogenies if model assumptions are violated



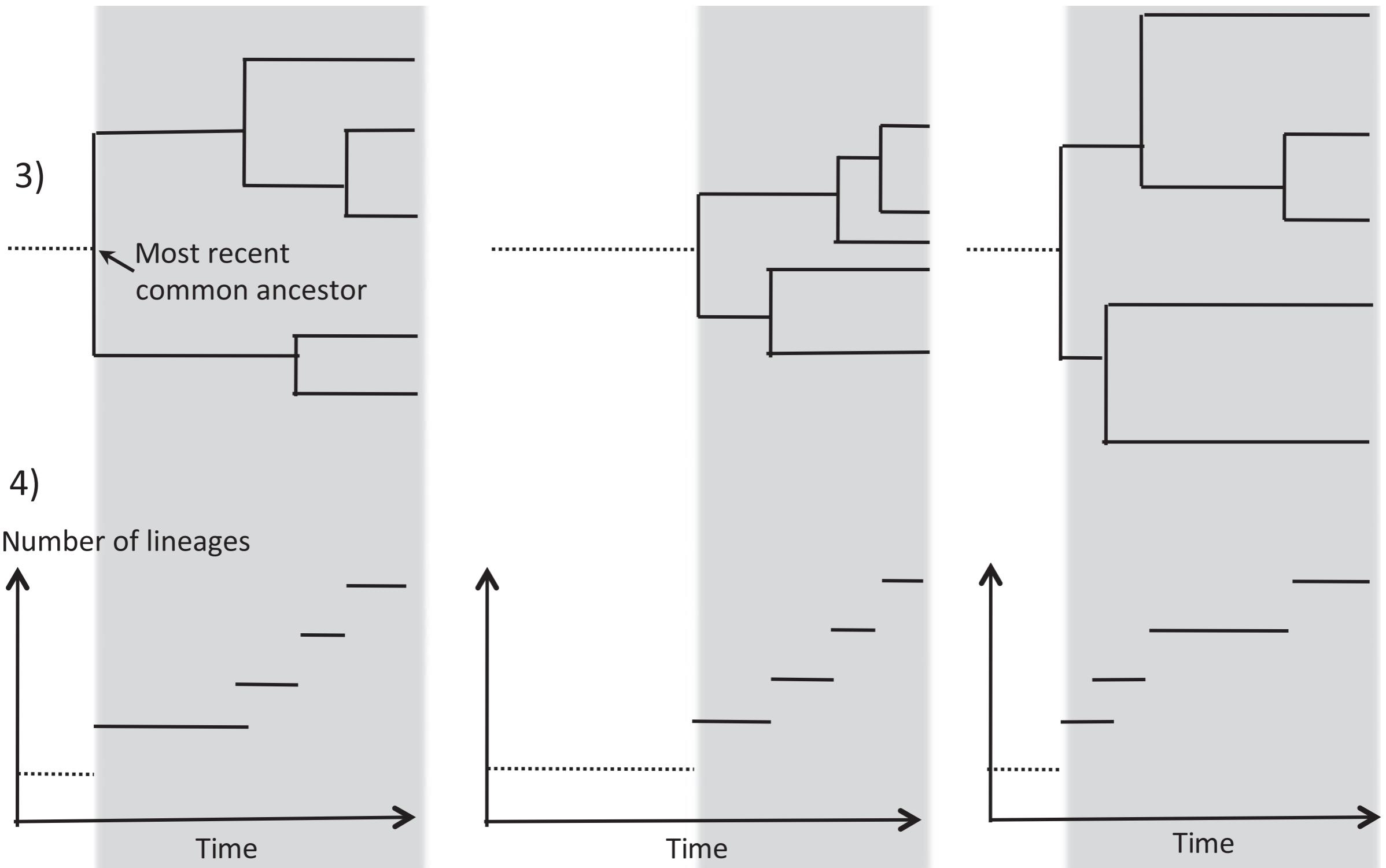


Can we determine which evolutionary scenarios
we can actually distinguish using only phylogenies
of extant lineages?

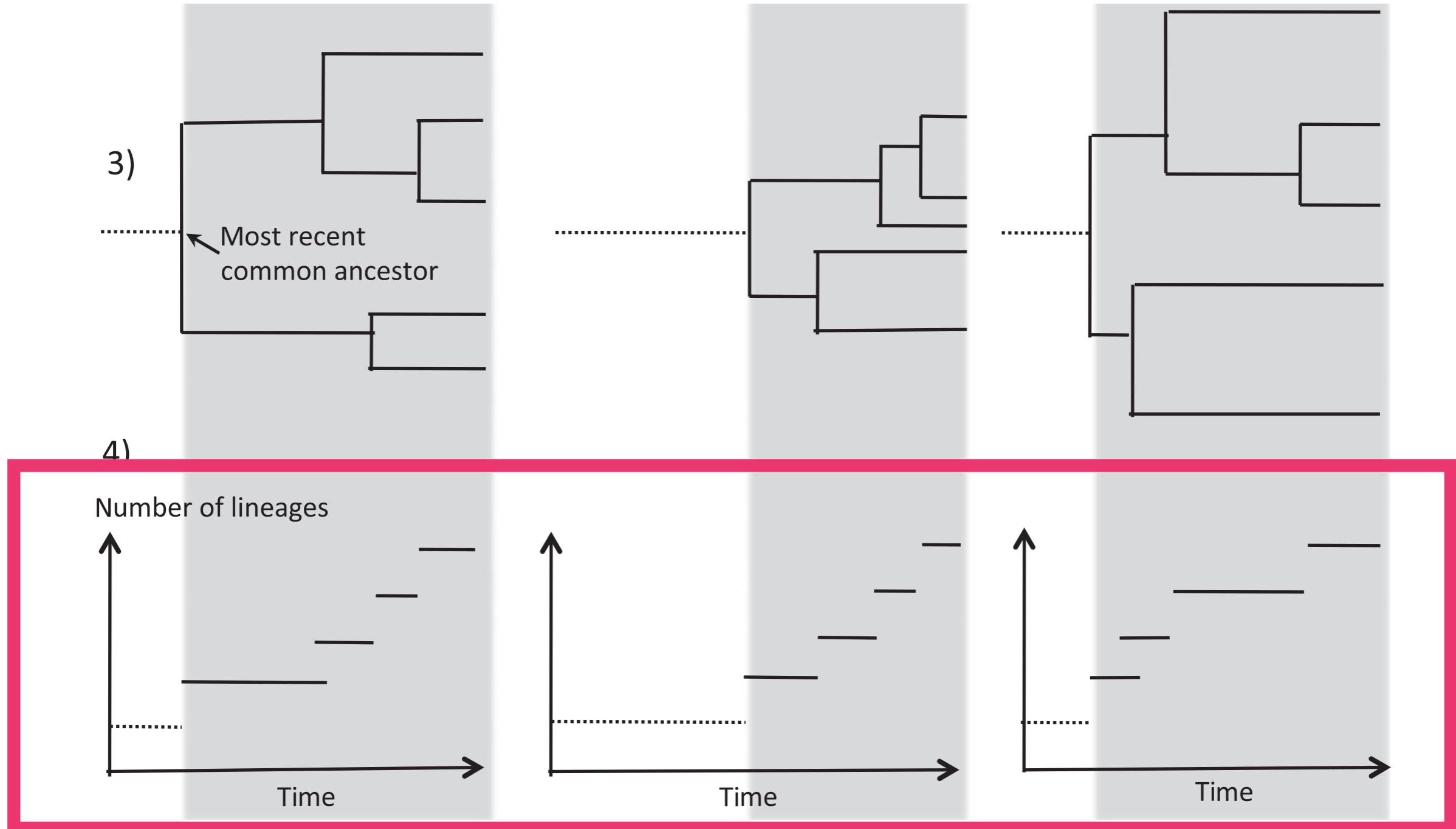


Stilianos Louca

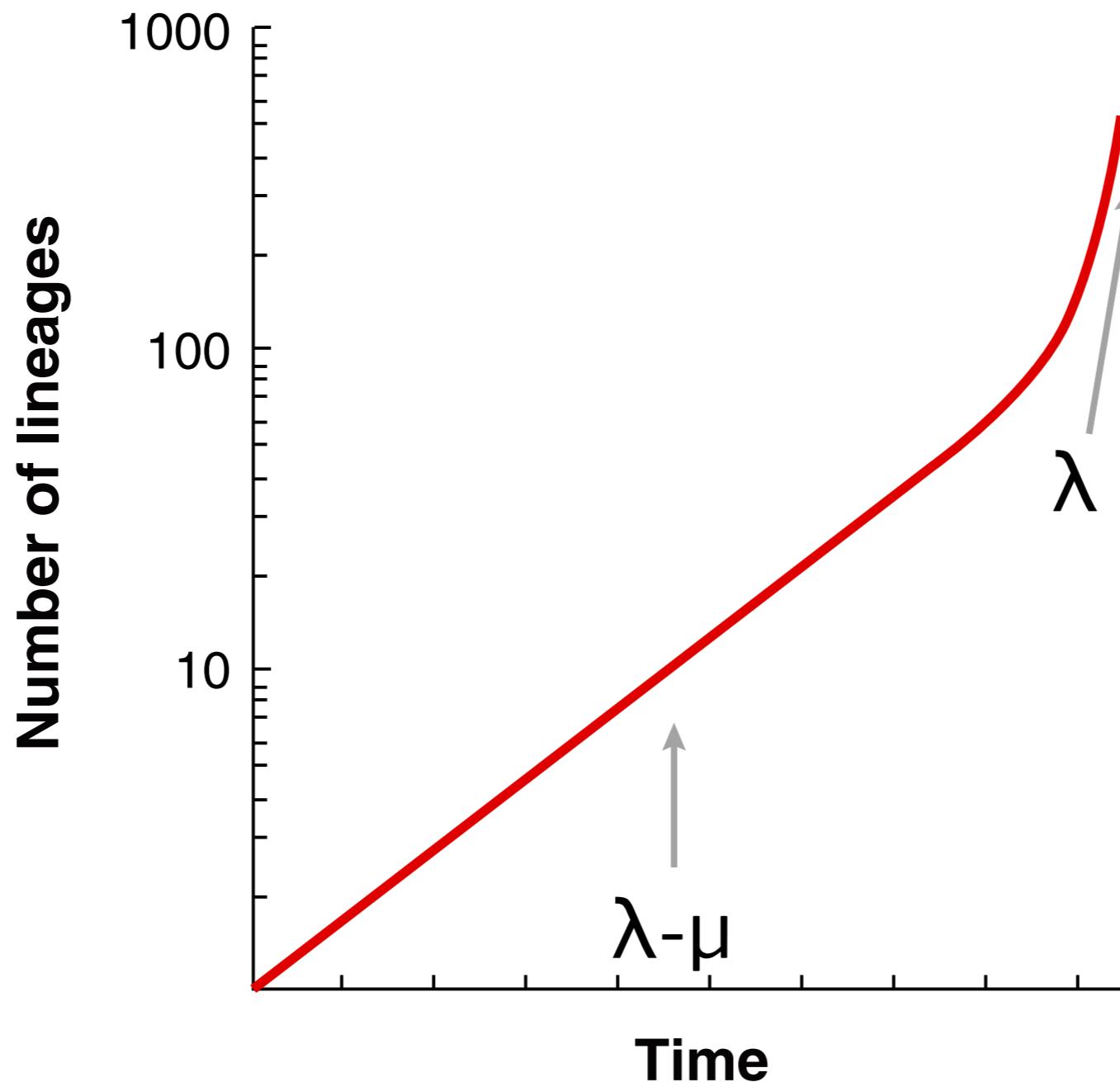
Likelihood = $\Pr(\text{Data} \mid \text{Model of evolution})$



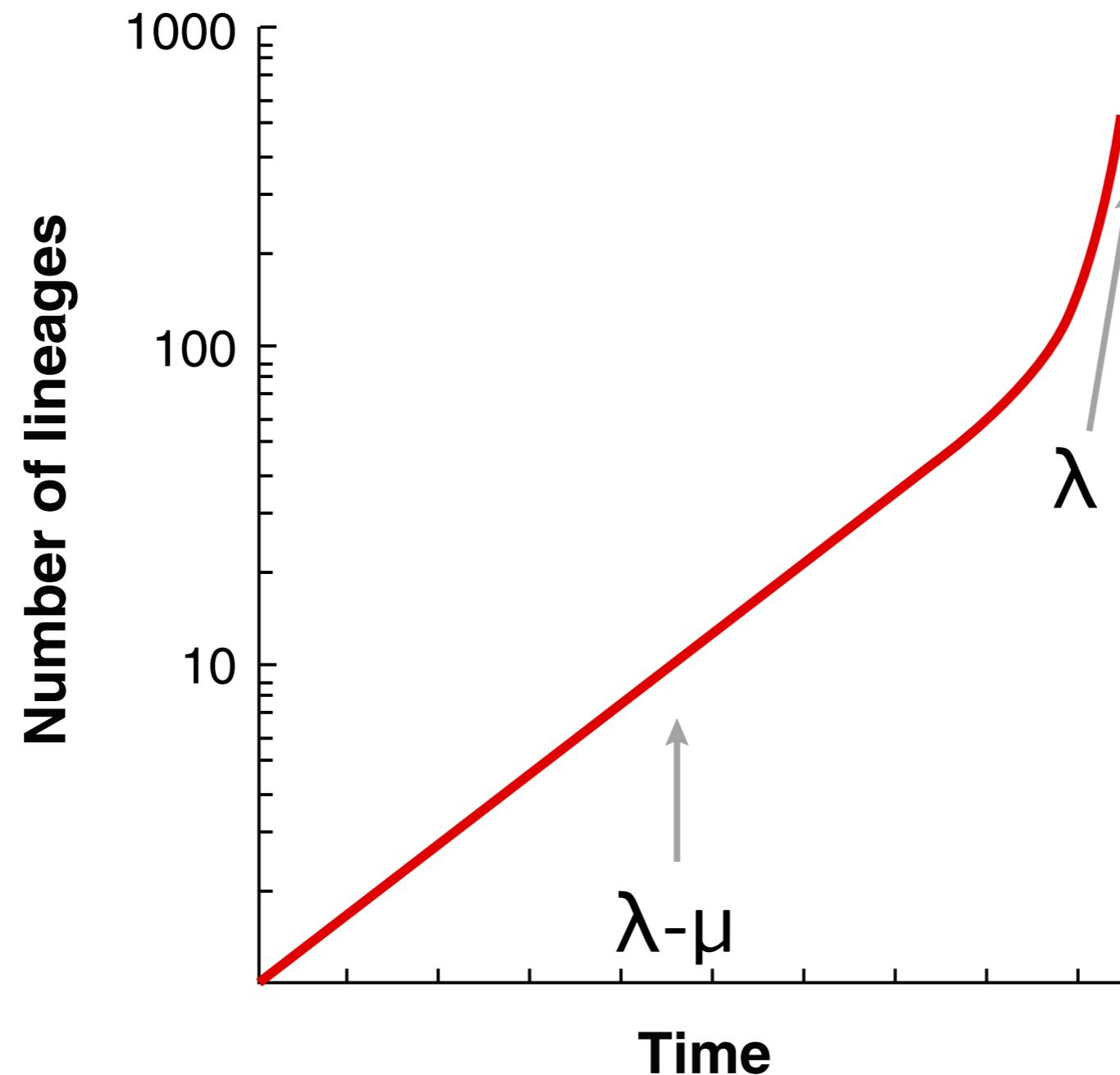
For a homogenous speciation-extinction process, all of the information about the rates are contained in the lineages-through-time (LTT) plot



The likelihood of a model can be written in terms of its “deterministic” lineage-through-time plot (dLTT)



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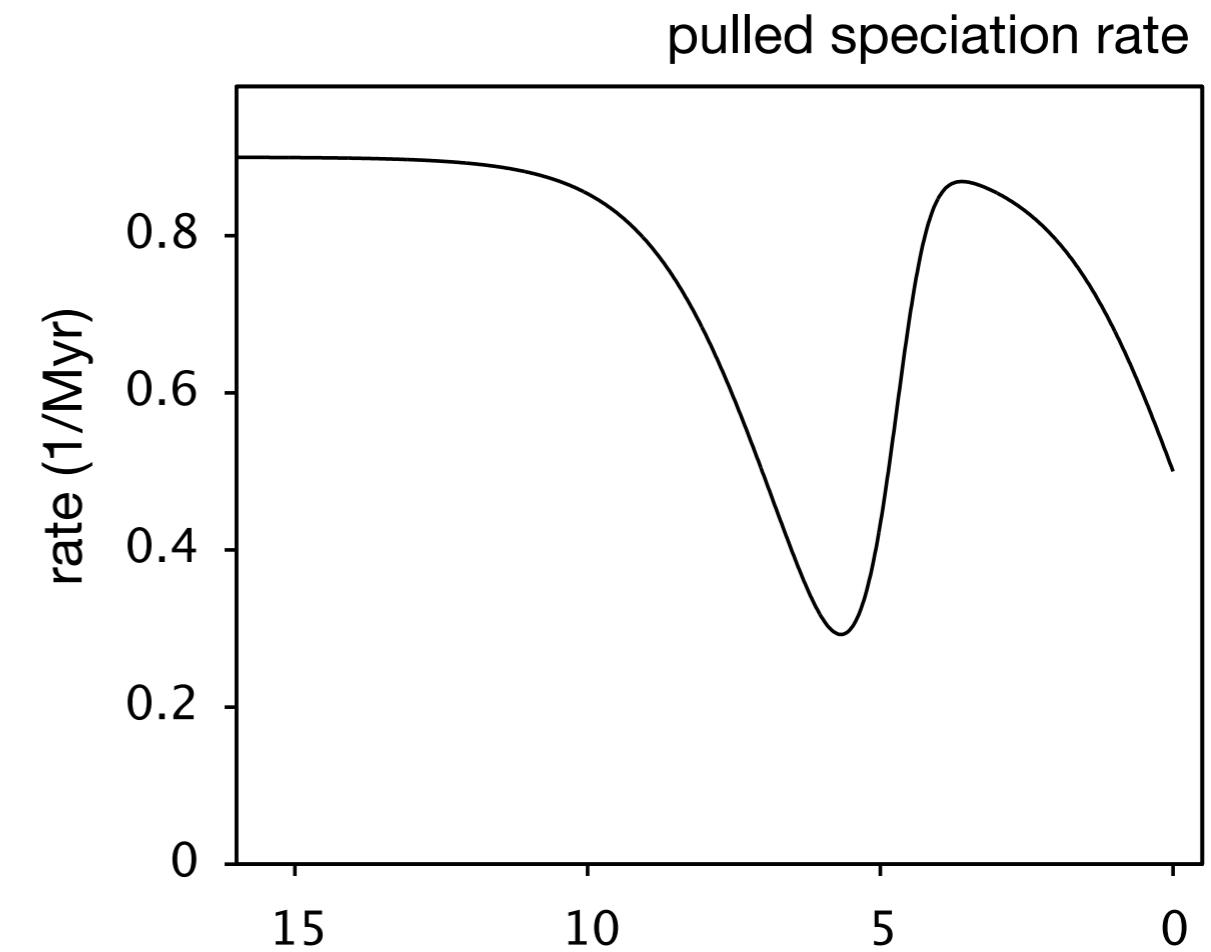
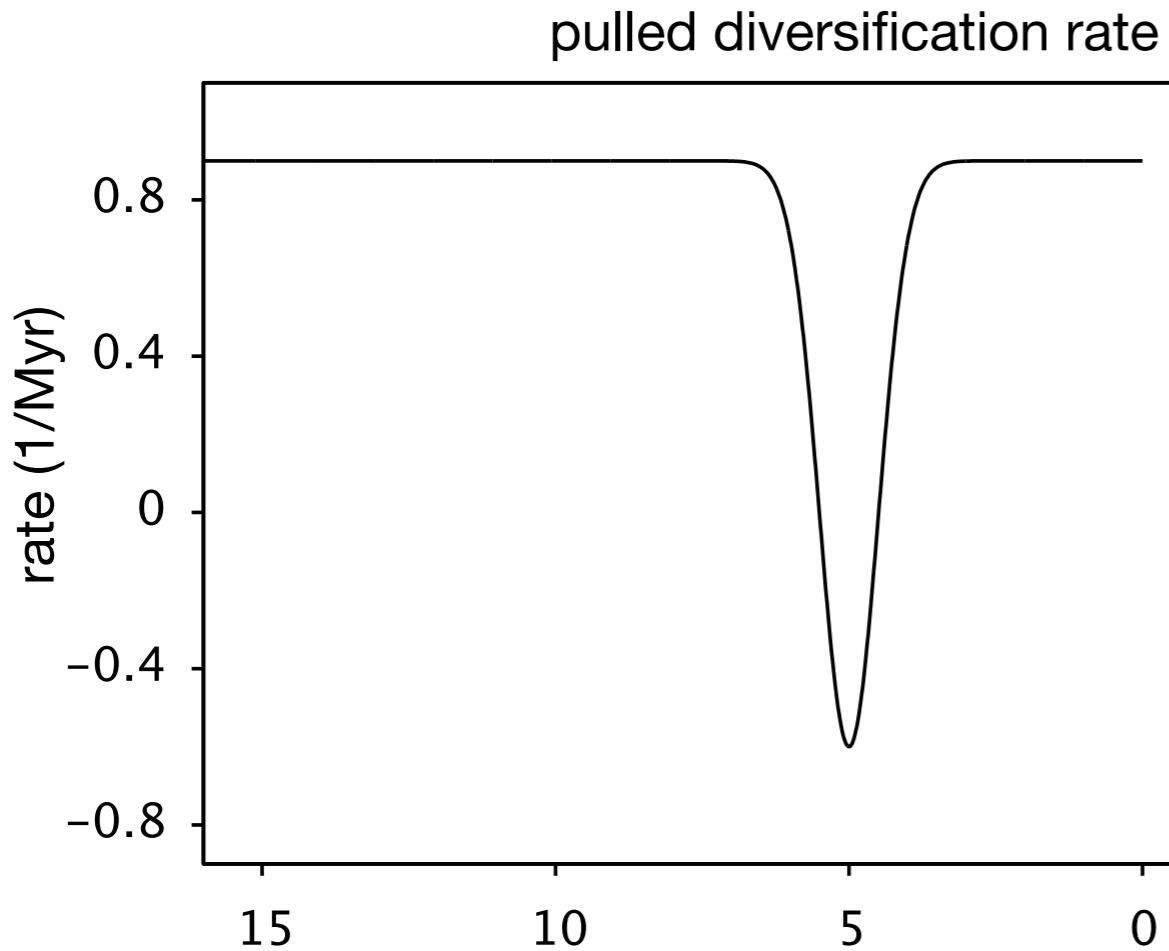


All models with the same dLTT have the exact same likelihood

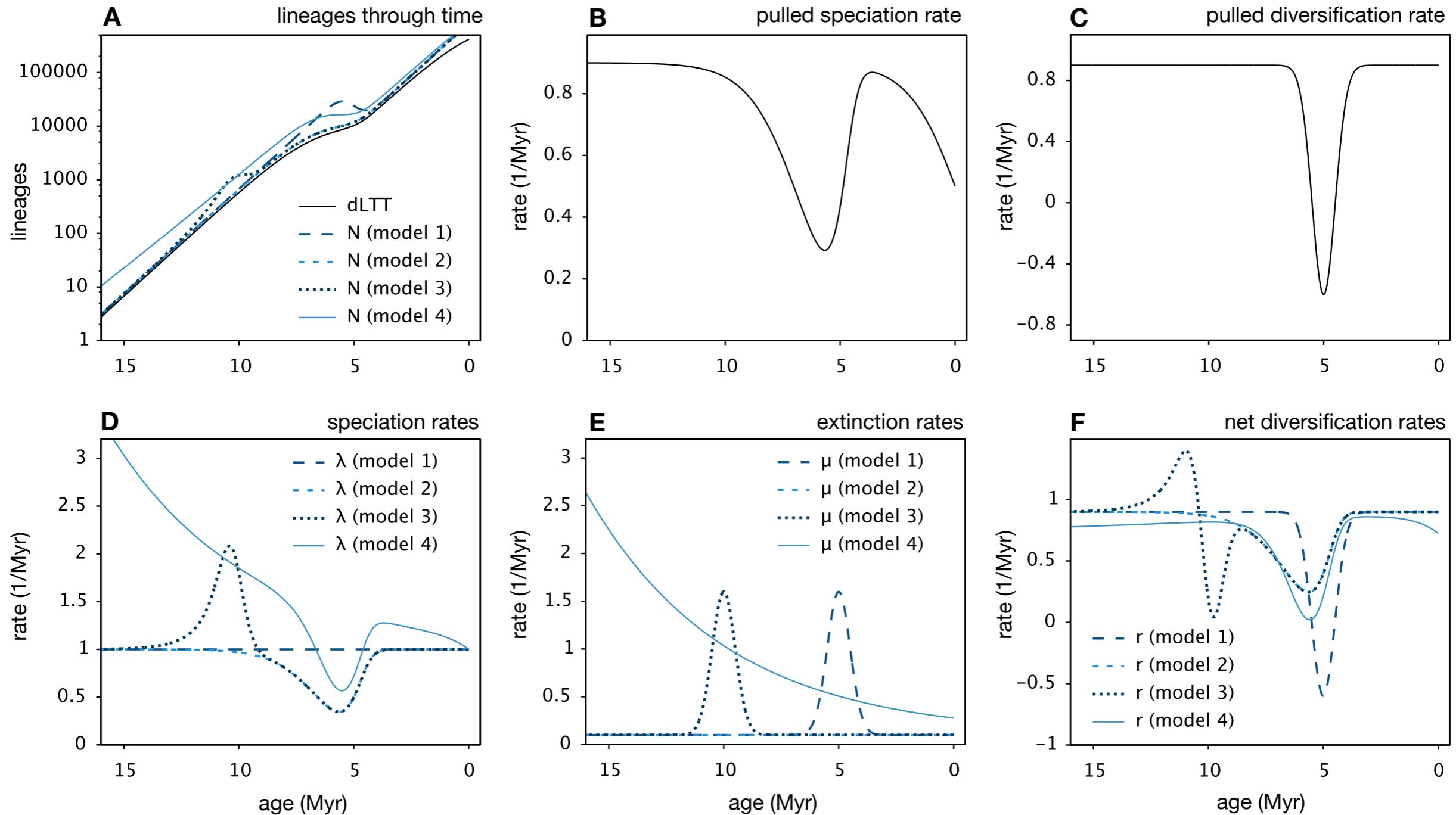
The dLTT can be transformed into other curves parameterized in terms of speciation and extinction rates

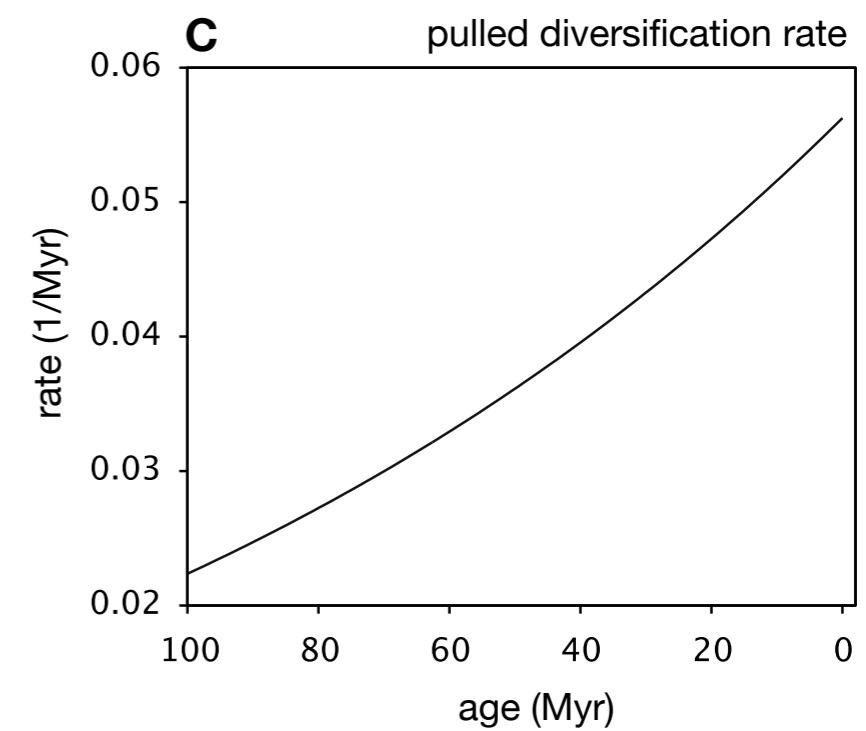
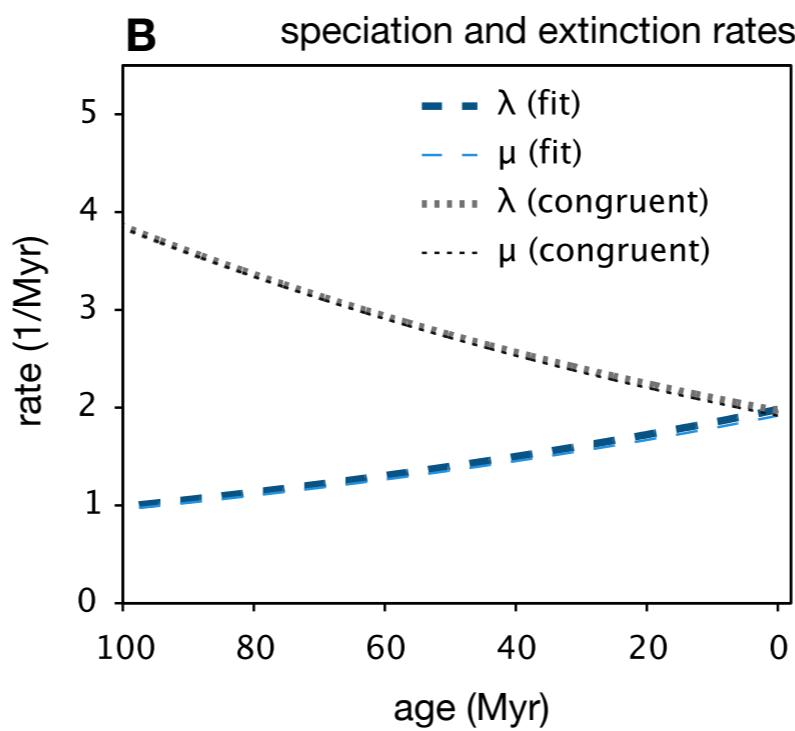
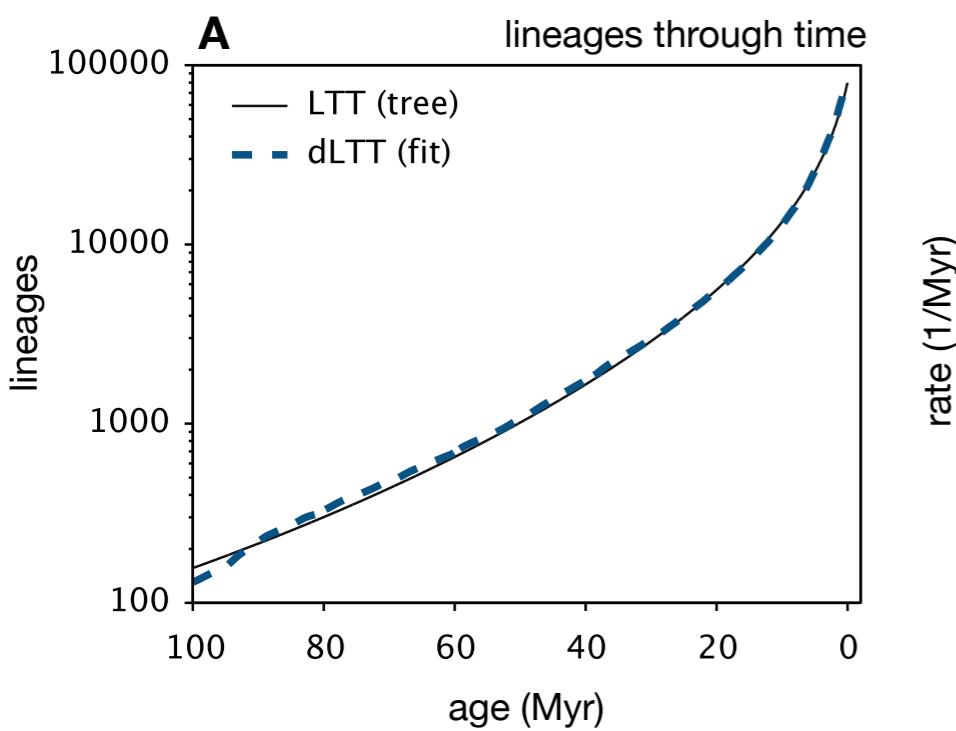
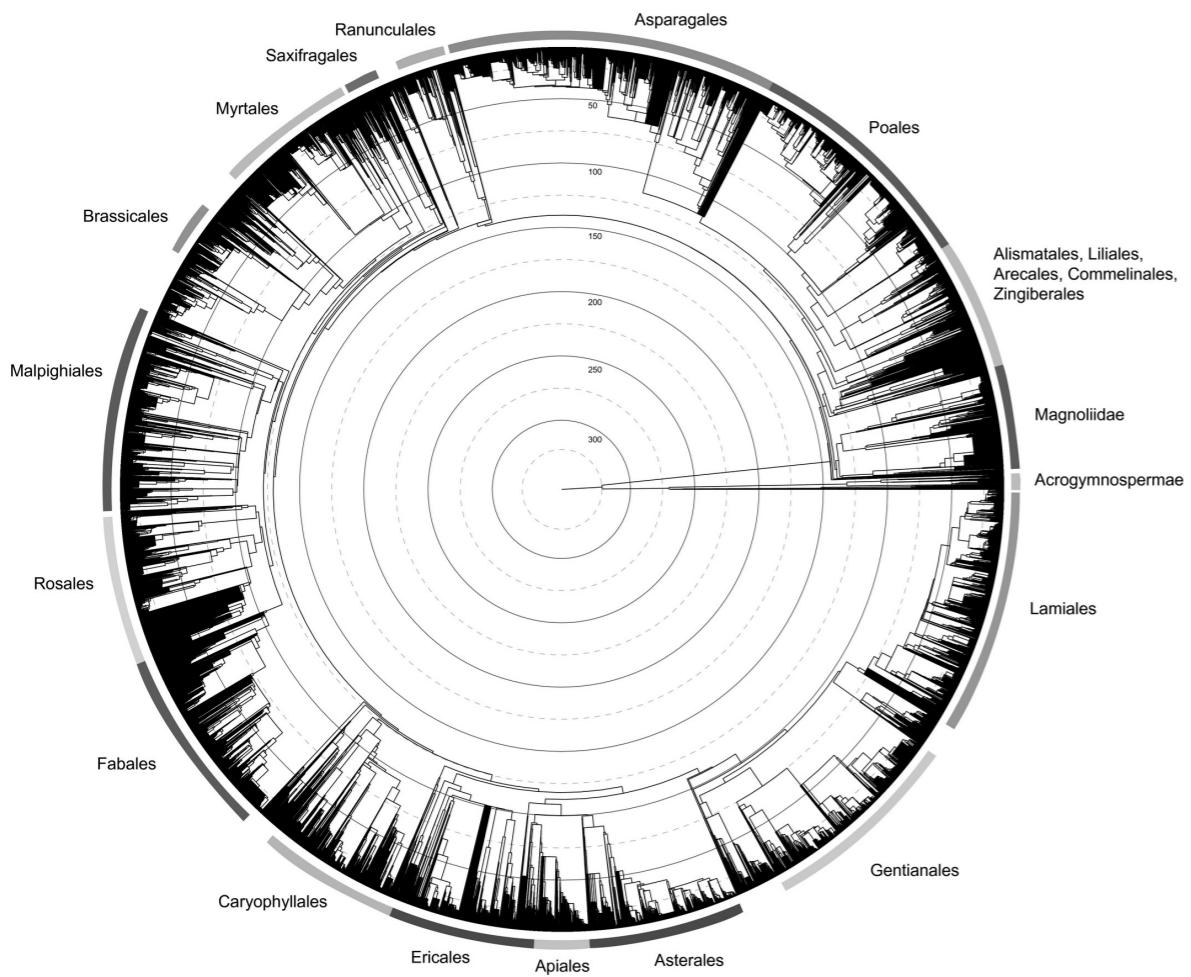
$$r_p = \lambda - \mu + \frac{1}{\lambda} \frac{d\lambda}{dt}$$

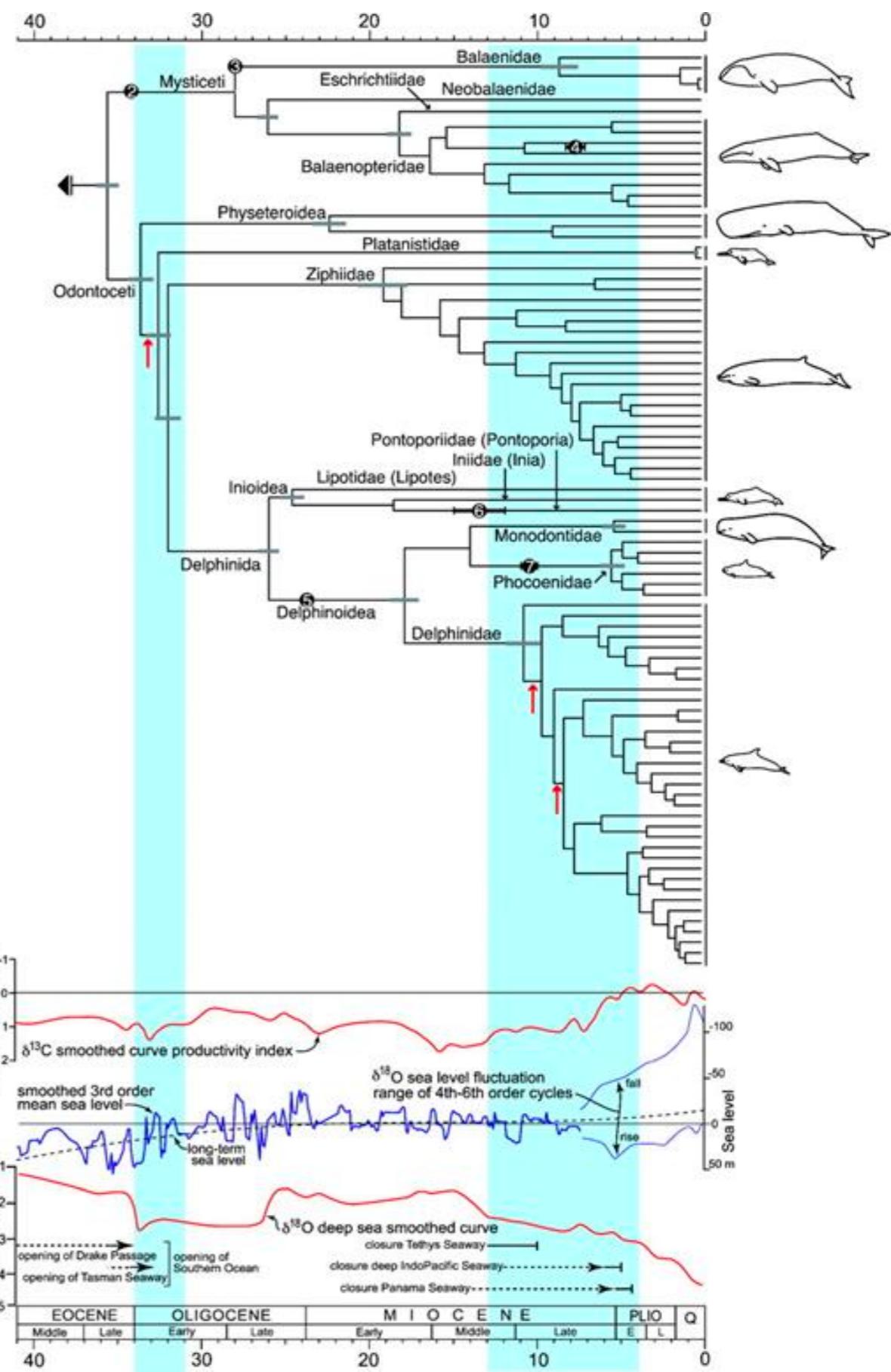
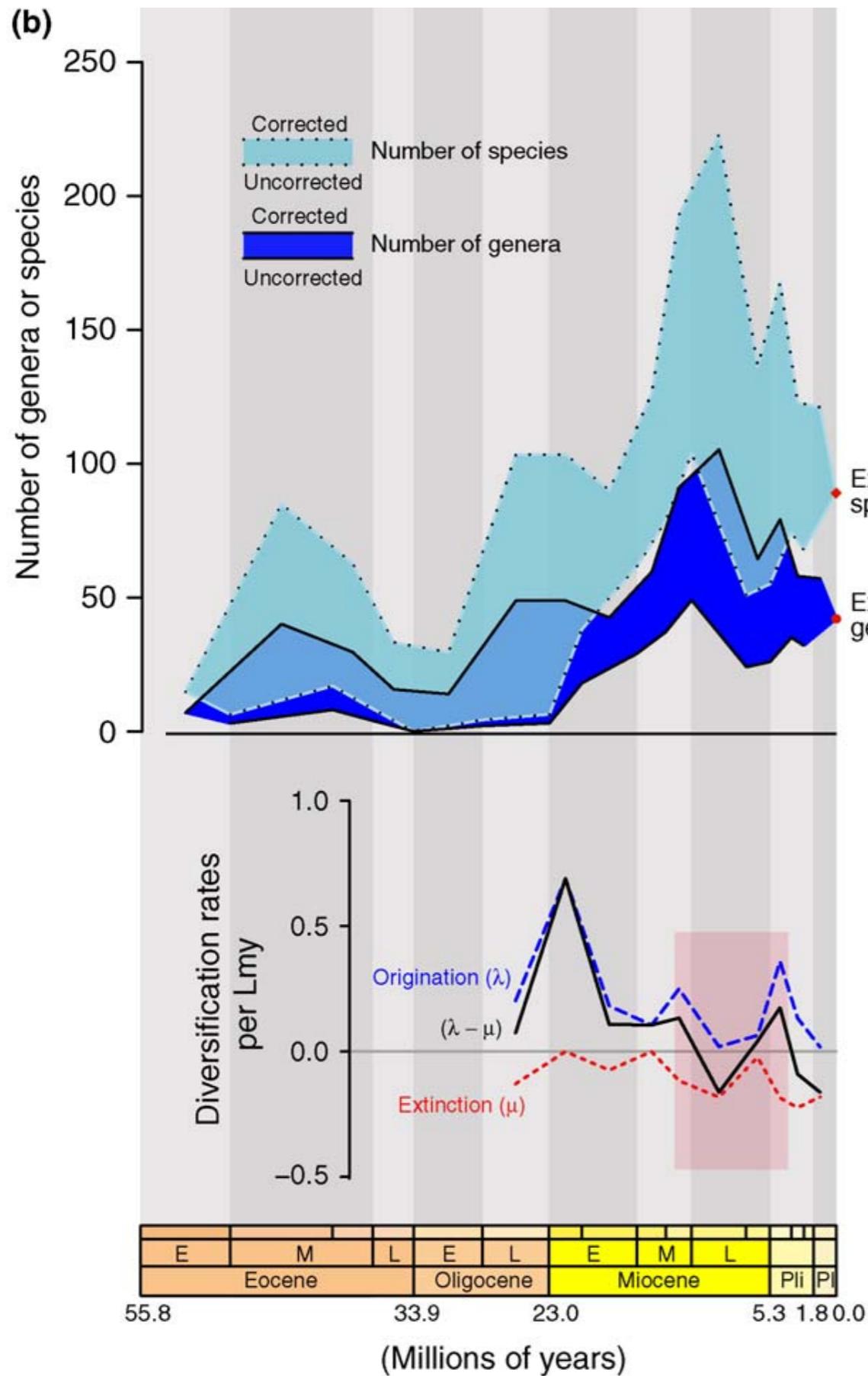
$$\lambda_p = P(\tau)\lambda$$

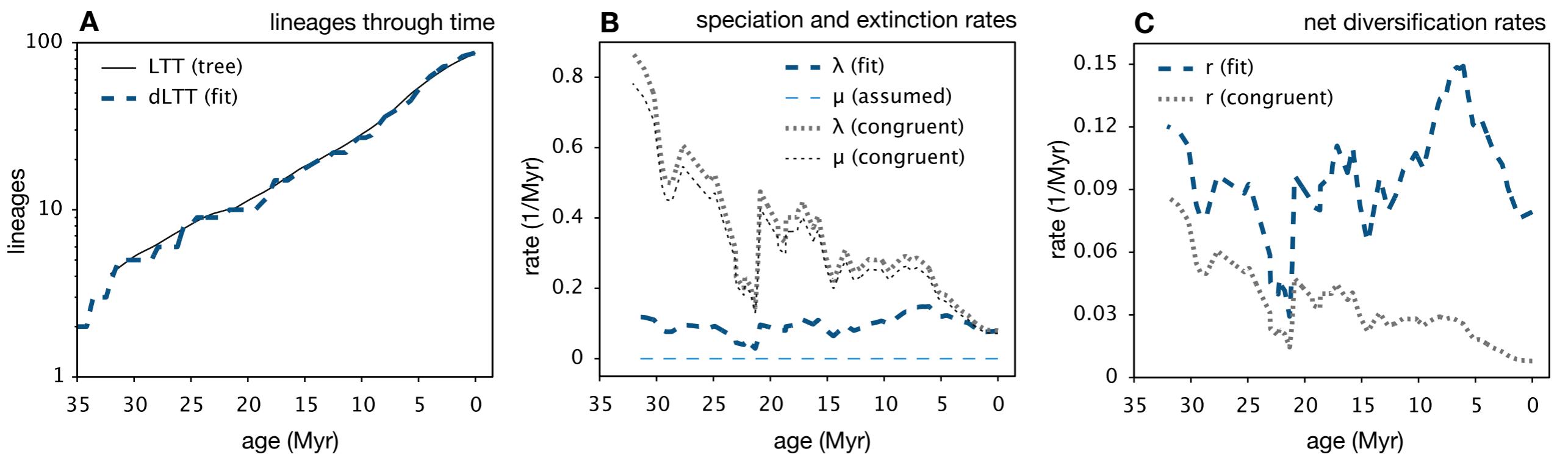


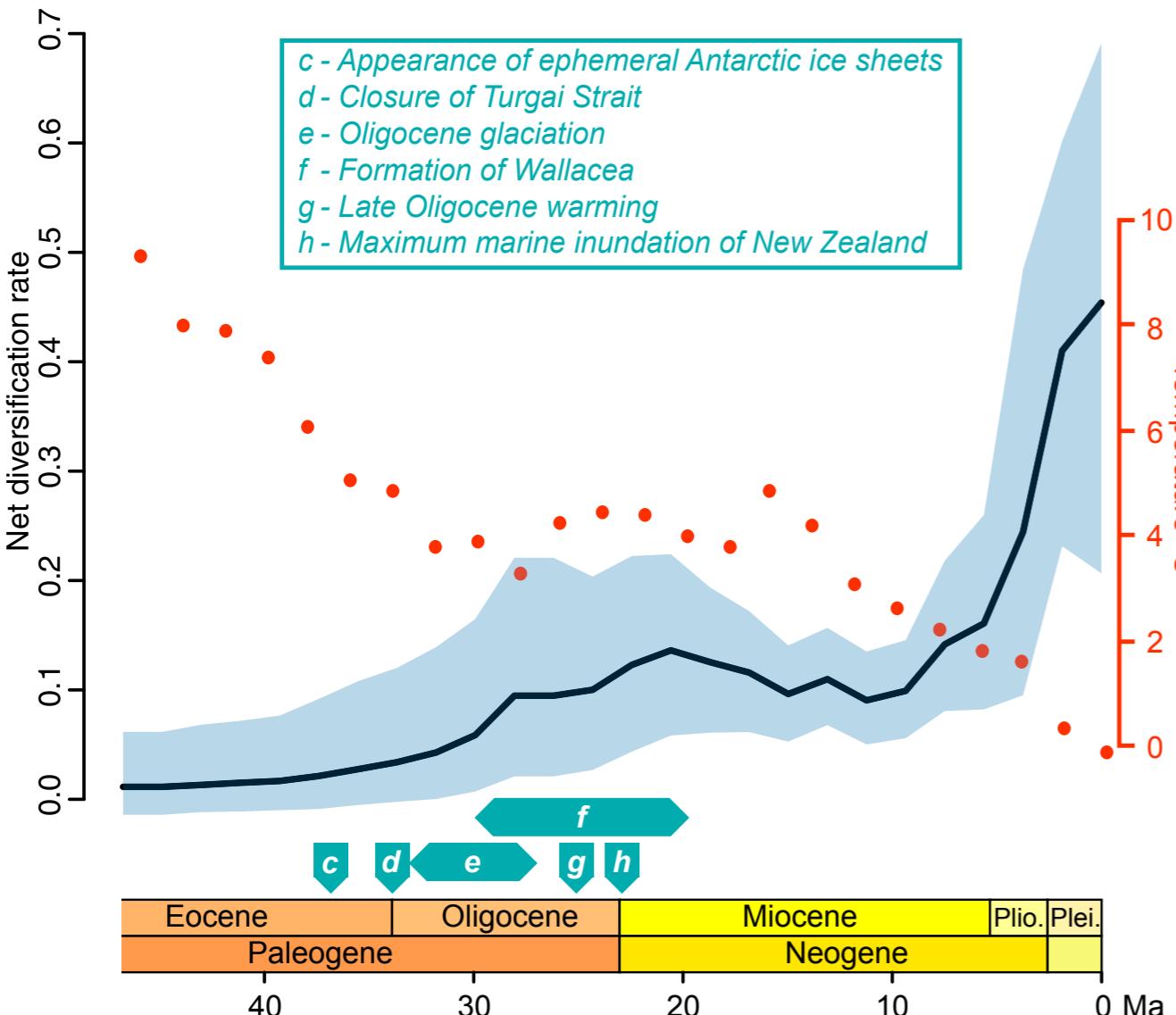
There are an **infinite number of ways** that speciation and extinction can vary through time which result in the **same dLTT and therefore same likelihood**





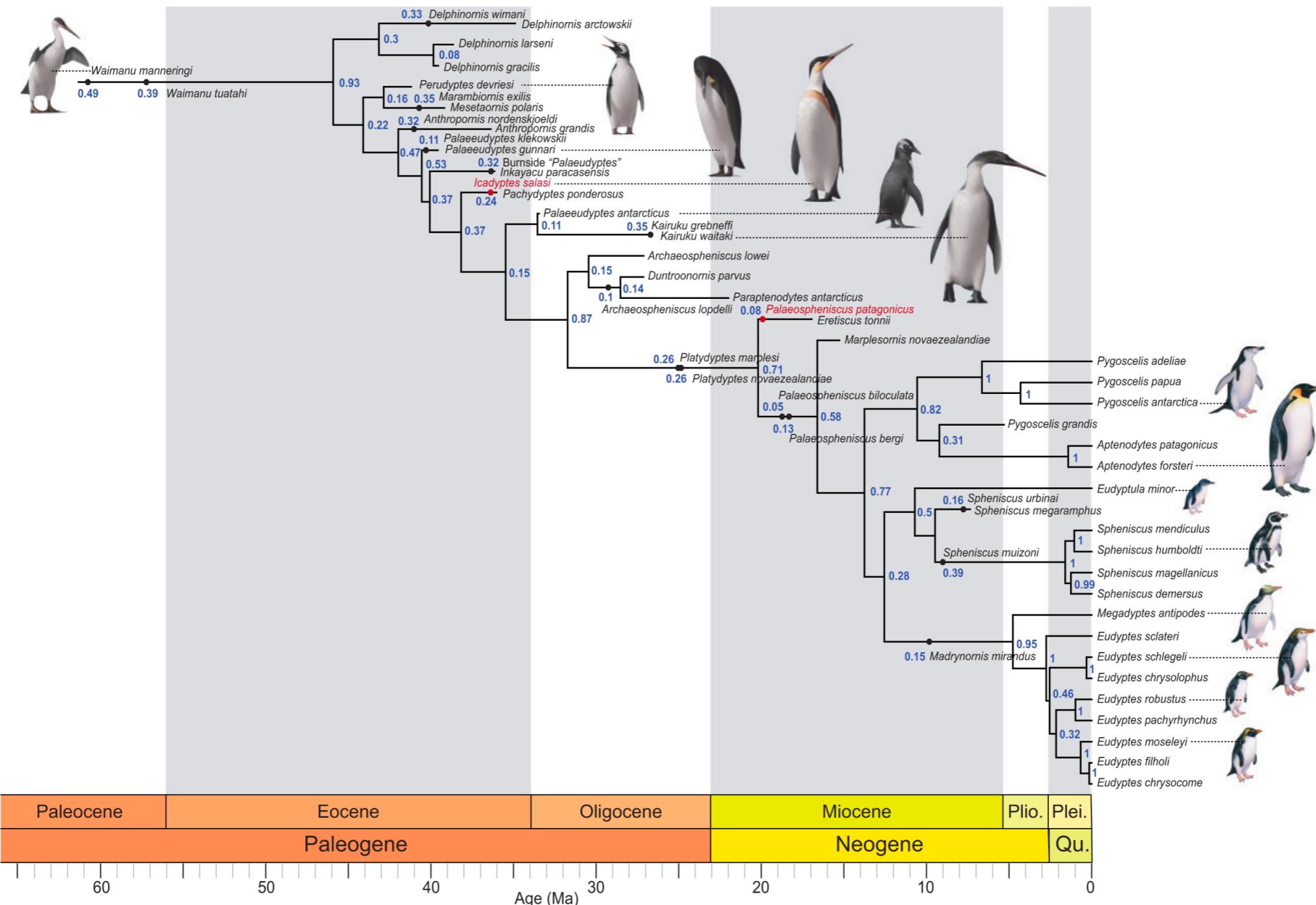




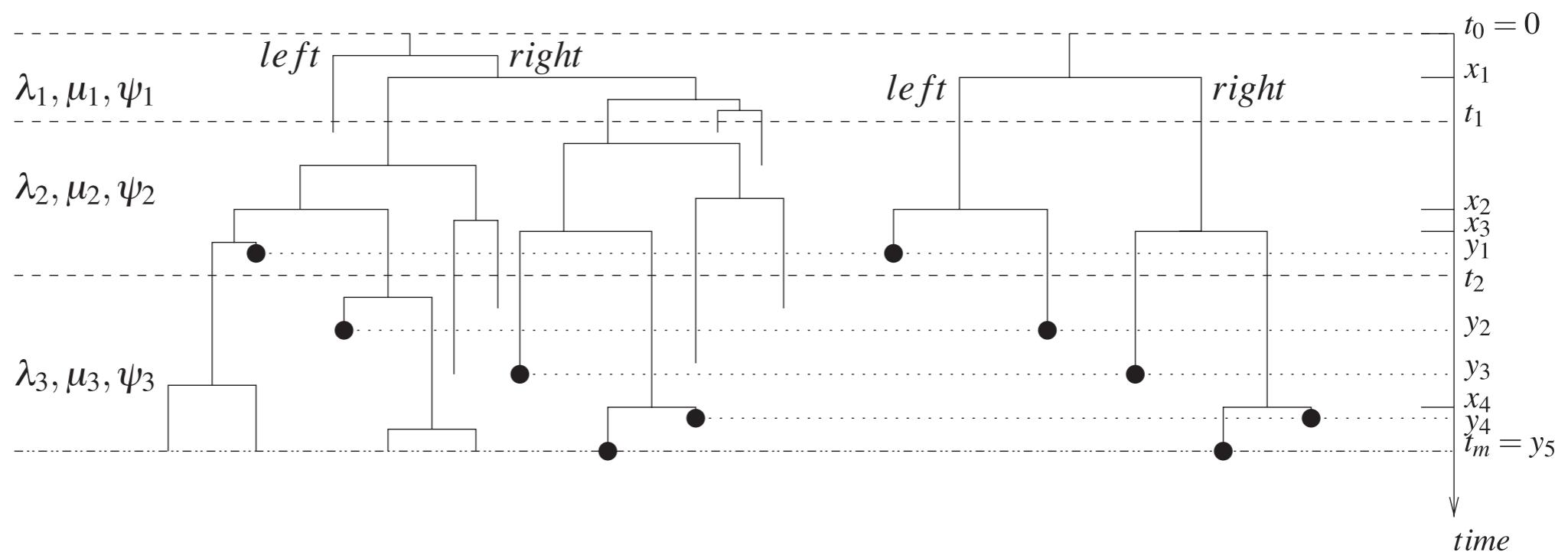
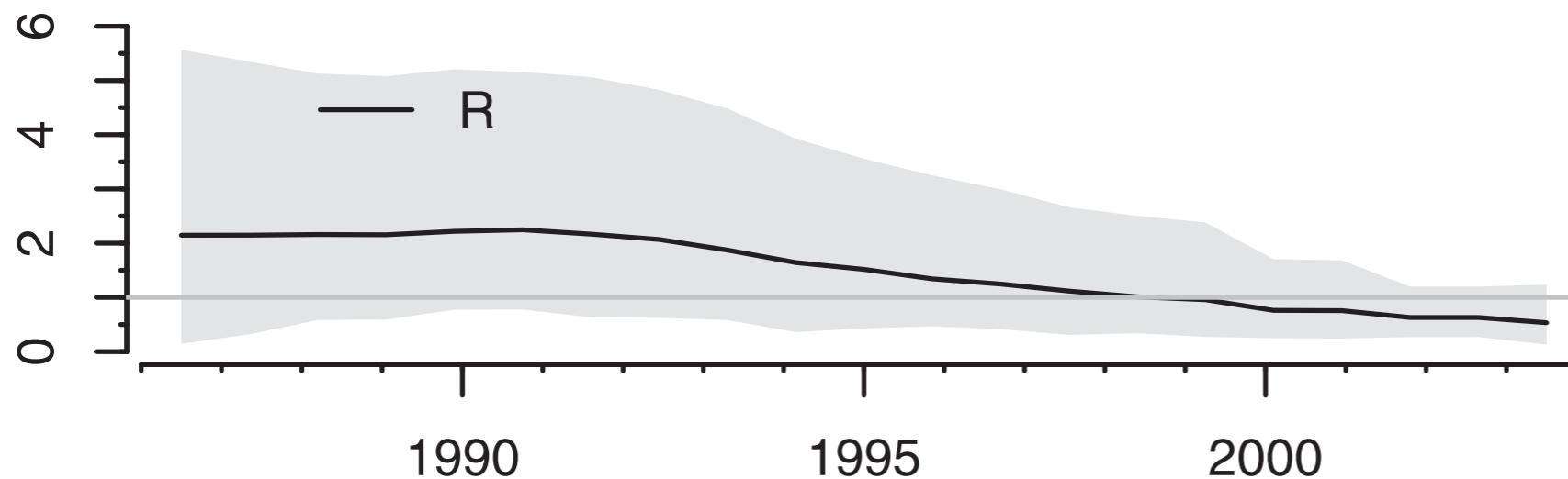


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Integrate molecular and fossil data into a single phylogeny



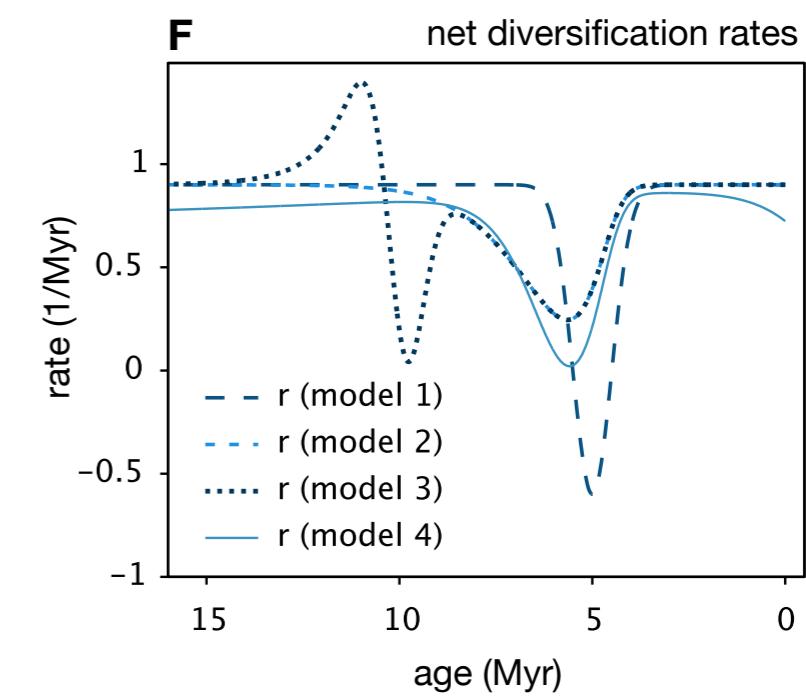
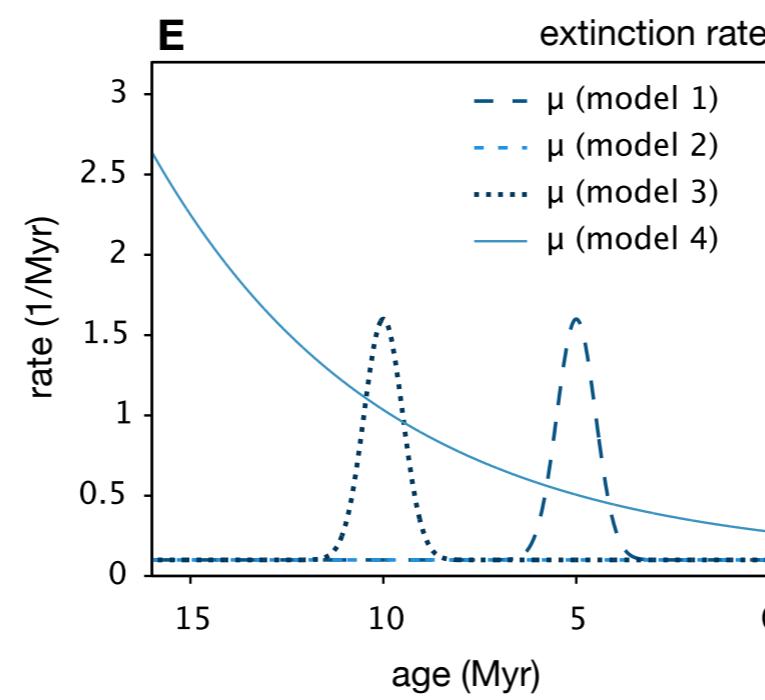
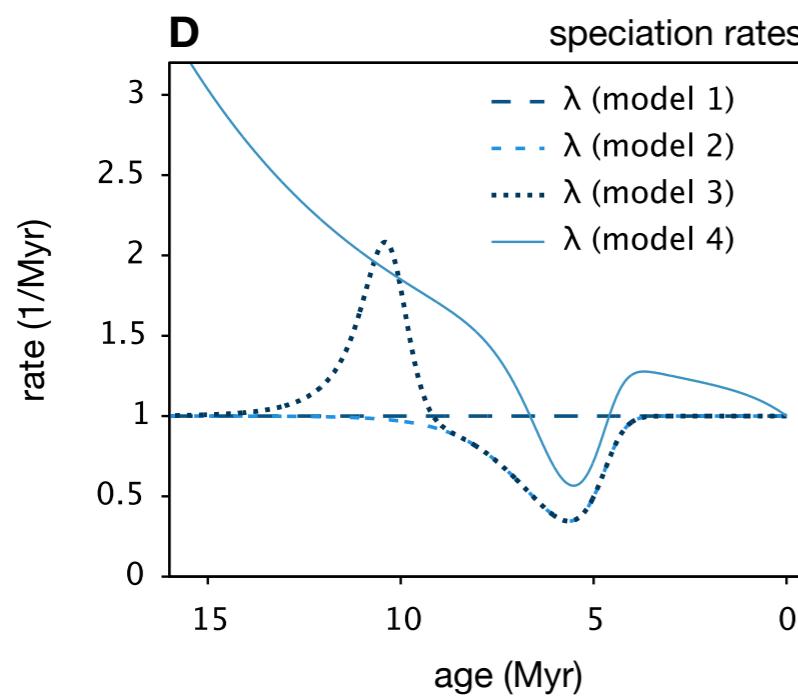
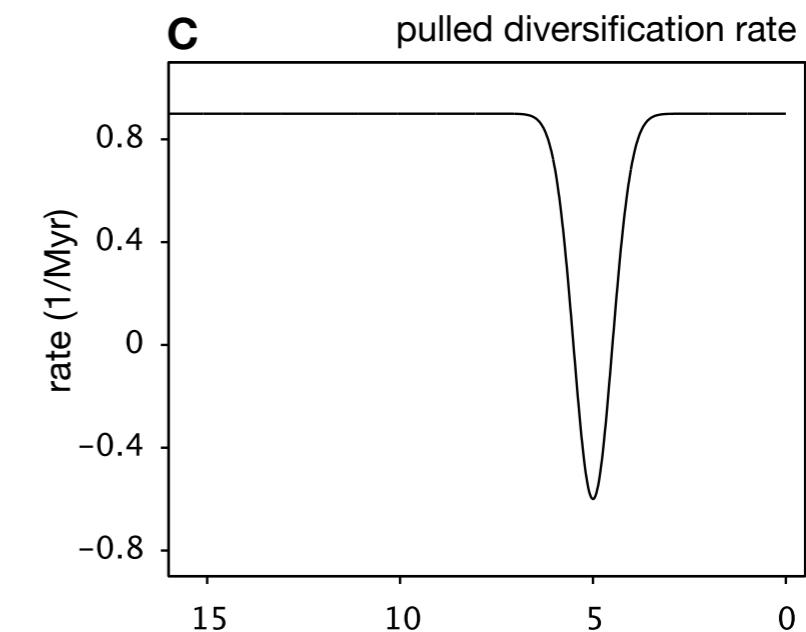
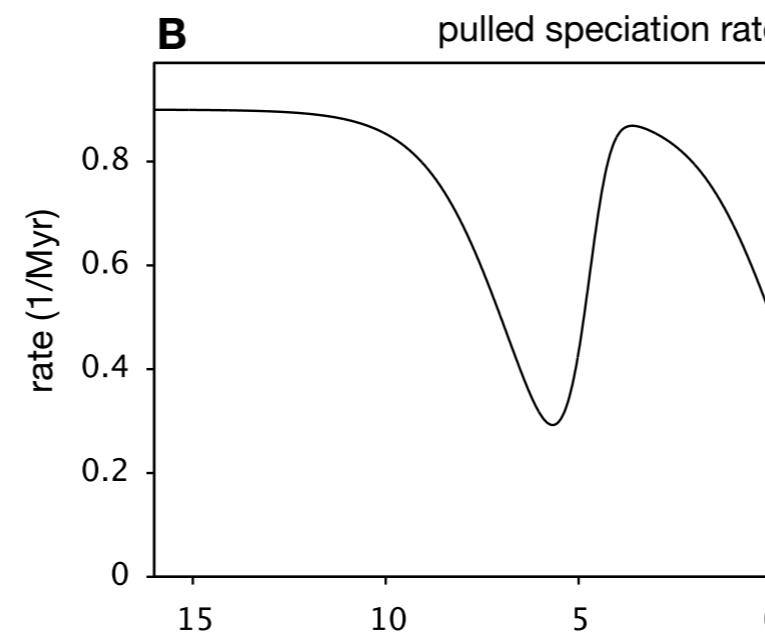
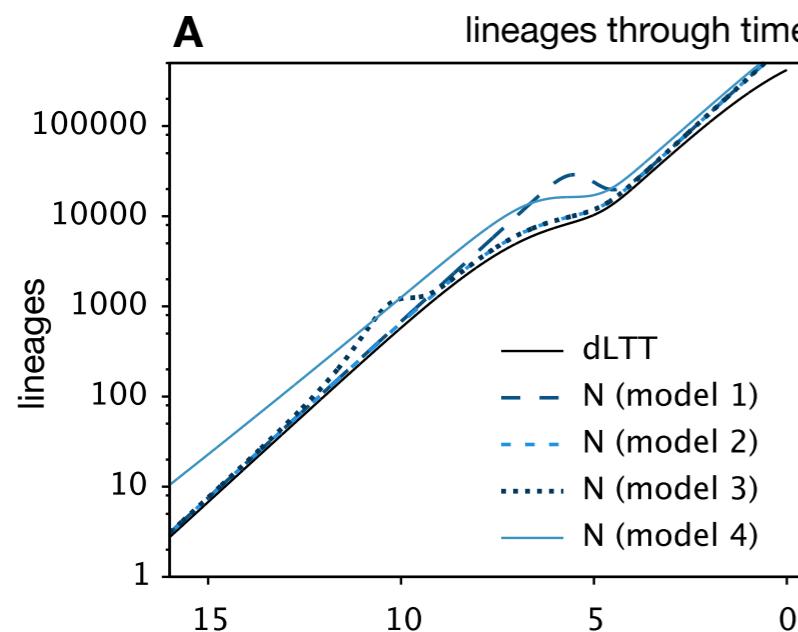
Viral phylodynamics also makes use of temporal sampling to infer “diversification rates”



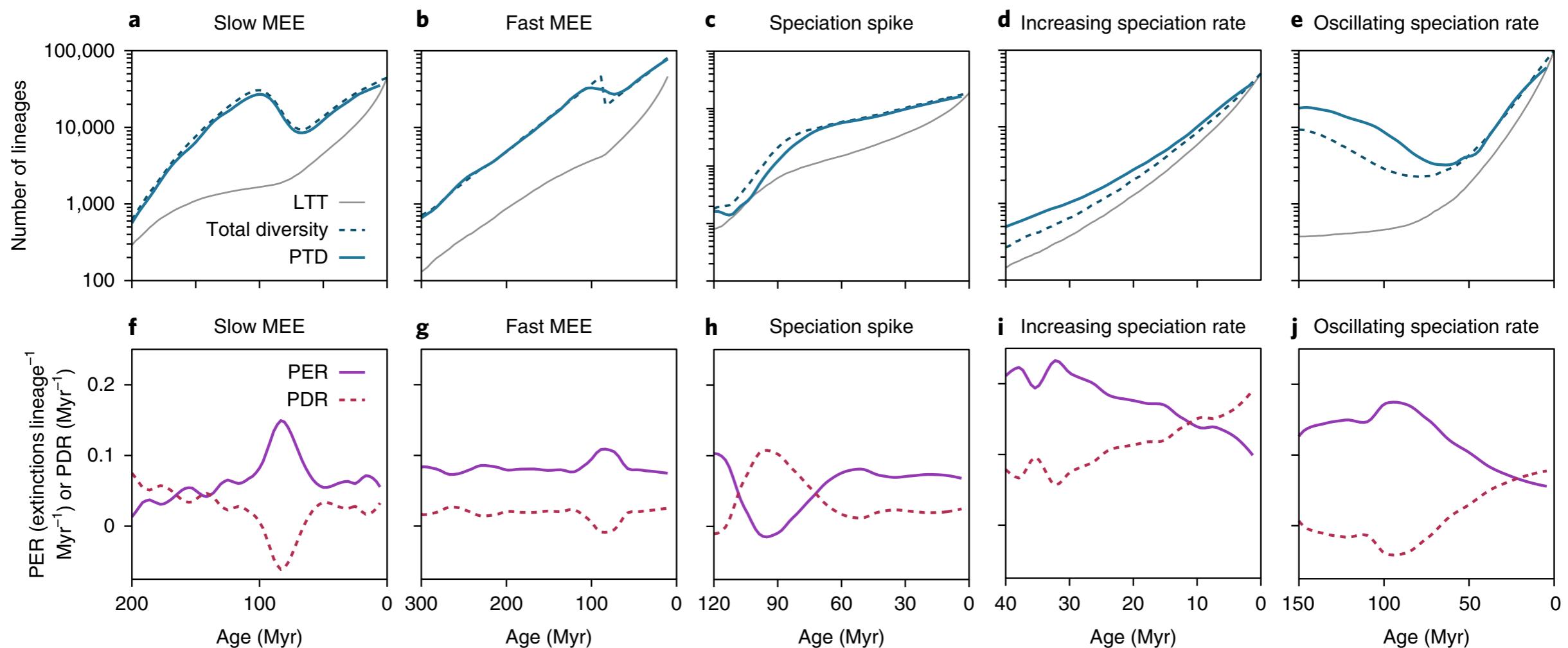


BEAST

Bayesian evolutionary analysis by sampling trees



Characterize the dynamics of composite “identifiable” parameters such as: $r_p = \lambda - \mu + \frac{1}{\lambda} \frac{d\lambda}{dt}$



Have a great course

pennell@zoology.ubc.ca