Diversification rates

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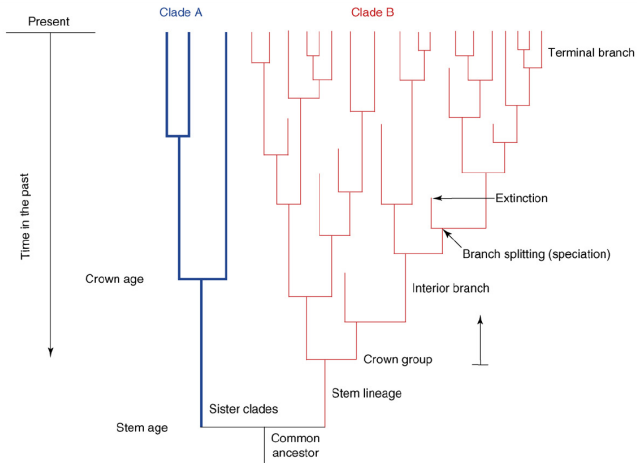Can we estimate rates of speciation and extinction from phylogenies of sampled extant tips?

Models for tree shapes:

Yule or 'Pure Birth' model: lineages have a constant probability of speciation.λ.

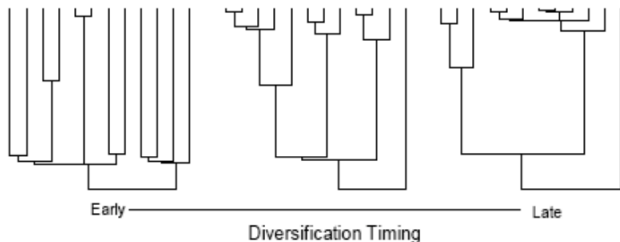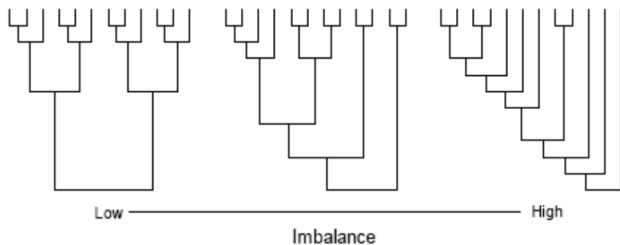Birth-Death: Lineages have a constant probabilities λ of speciation, or μ extinction.

Diversification rate: ρ, equals the $\lambda - \mu$
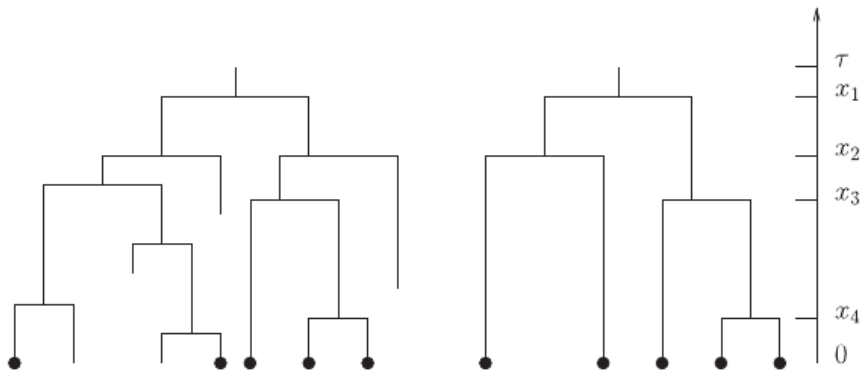
Relative extinction rate or 'turnover rate': μ/λ

(Ricklefs, TREE, 2007)

Tree shapes are the same for Yule and Birth Death processes, but waiting times are not.

Low ——————————————————— High
Imbalance

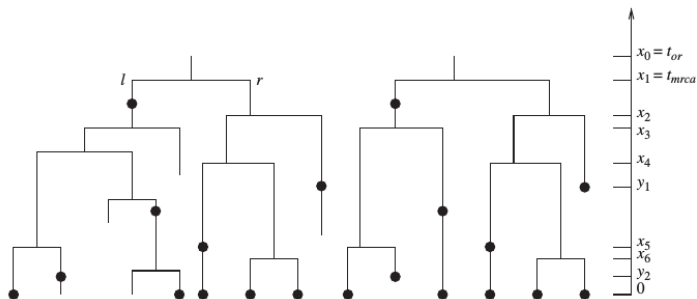Early ——————————————————— Late
Diversification Timing

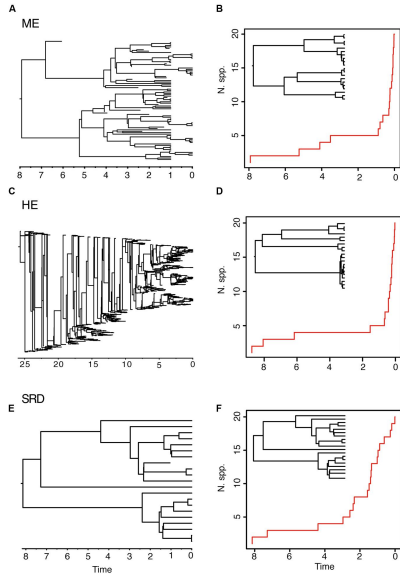# Sampled birth-death process tree prior

Stadler, J. Theoretical Biology. 2009

Sampling through time in birth-death trees

Stadler (2010) J. Theoretical Biology

Different birth–death models can generate reconstructed phylogenies with similar realized tree shapes.

(Sanmartin and Meseguer, Frontiers in Genetics, 2016)

'Pull of the present': diversification appears to increase close to the present because lineages that arose more recently are less likely to have gone extinct. (Nee et al. PNAS, 1993)

Diversification rates often appear to decrease (Etitenne and Rosindel, Syst Bio, 2012)
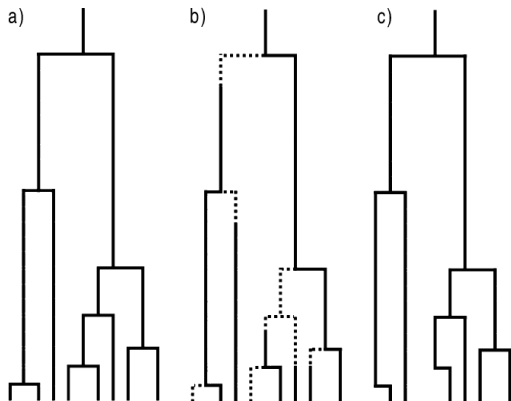

FIGURE 1. The pure birth model a) with and b) without protracted speciation. Dotted lines indicate an incipient species and solid lines are good species. c) Phylogeny of the protracted pure birth process of panel b: only those lineages that have completed speciation before the present will show up in the phylogeny. Note that the branching points are at the times that the incipient species are produced, not at the times that they become good species.

Can we estimate diversification rates?

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Yes. Different diversification rates result in different expectations for tree shape, which are testable.

Can we map shifts in diversification rates across the tree?

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Yes, but 'trickle-down effect' likely to be problematic, and large sample sizes are needed

Rate shifts within clades can increase support for inference of rate shifts in more inclusive clades.
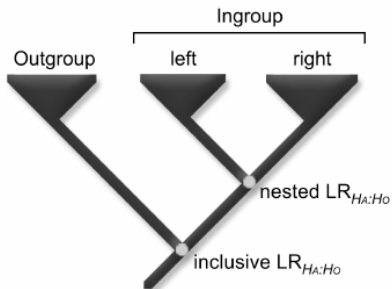

(Moore et al. Phylogenetic Supertrees, 2004)

Summary: Some General Advice for Exploring Diversification Rates

1. Expectations under SBP models are diffuse to a degree that defies intuition

   this makes it difficult to detect departures from stochastic expectations

2. When using methods that entail SBP models for estimation it's critical to:

   carefully assess model fit/adequacy

   carefully assess our ability to reliably estimate under the assumed model

3. It's important to accommodate various sources of phylogenetic uncertainty

   inferences based on point estimates are unlikely to be reliable

4. The statistical behavior of many recent methods is poorly characterized

   power analyses may be useful for assessing the ability of methods to make the desired inferences from your data

5. Make an effort to understand–and assess–the (implicit) assumptions

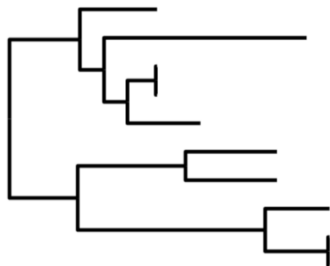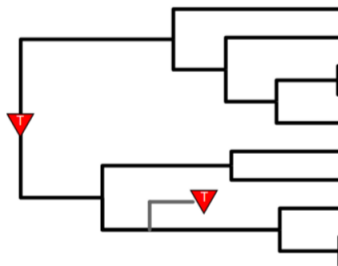   the assumptions are often cryptic, critical and frequently violated in real data
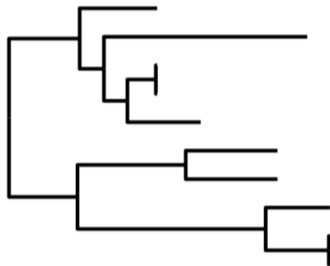
From Brian Moore

Branch lengths

Branch lengths = SUBSTITION RATE X TIME

figure from Tracy Heath

Branch lengths = SUBSTITION RATE X TIME

Branch lengths = TIME

figure from Tracy Heath