Innappropriate parameteirzation of fossilized birth-death models causes incorrect estimates of topology and node ages

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Today

OUTLINE

- ► Overview: The Fossilized-Birth Death Process
- ► Our Research Question
- ► Methods
- ► Results

► A probabilistic model for estimating divergence times

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Is this an inherent property of 'total-evidence' approaches, or is this related to model misspecification?

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 - ► 25 extant tips with nucleotide sequence data
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- Simulate different values for λ, μ, ψ

- ► Empirical Data
 - ▶ Bear data set of Heath et al. 2014.

- ► Estimation
 - ► Estimate a tree for each dataset using both sampled ancestor and non-sampled ancestor models in BEAST2

RESULTS