Lecture 2.4

Calibrating the Molecular Clock

Calibrating the molecular clock

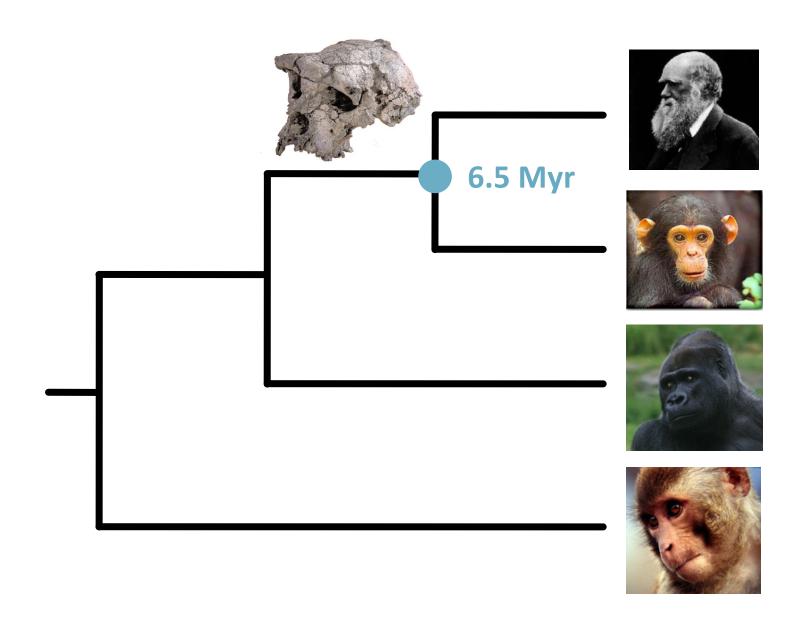
- Rates and times are non-identifiable
- Likelihood only depends on their product
 - Branch lengths in substitutions per site
- To separate rate and time, we need (prior) information about one or the other

Calibrating the molecular clock

- Information about substitution rate
 - Use to fix rate or to specific prior distribution of rate

- Information about node times
 - Fossil record
 - Biogeography
 - Sampling times
 - Documented pedigree

Calibration: Fossil record



Calibration: Fossil record

1. Use fossil data to inform priors on node times

- Minimum age of a node based on oldest fossil assignable to any of its descendent lineages
- Prior distribution of node age specified by user

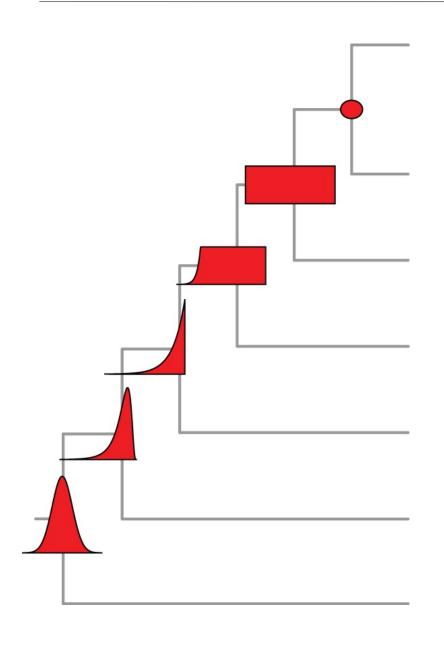
2. Use fossil directly in the analysis

- Model diversification process use fossil occurrence data
- Include fossil taxa in the data matrix (total-evidence dating)

Choosing fossil calibrations

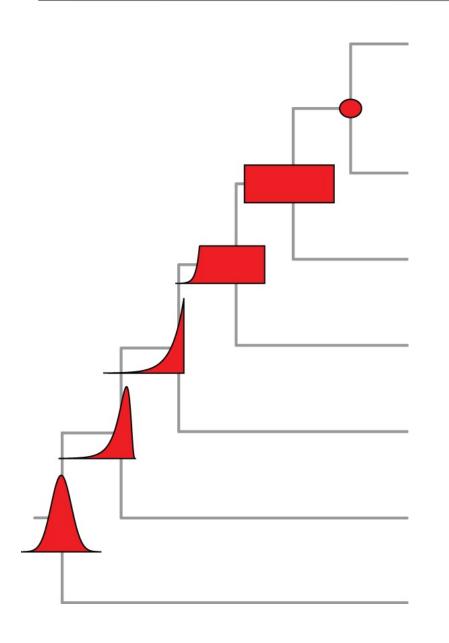
- Museum numbers of specimen that demonstrate all the relevant characters and provenance data
- Apomorphy-based diagnosis or phylogenetic analysis of the specimen
- Explicit statements on the reconciliation of morphological and 3. molecular data sets
- Locality and stratigraphic level from which the calibrating fossil was collected
- Reference to a published radioisotopic age and/or numeric timescale and details of numeric age selection

Calibration Priors



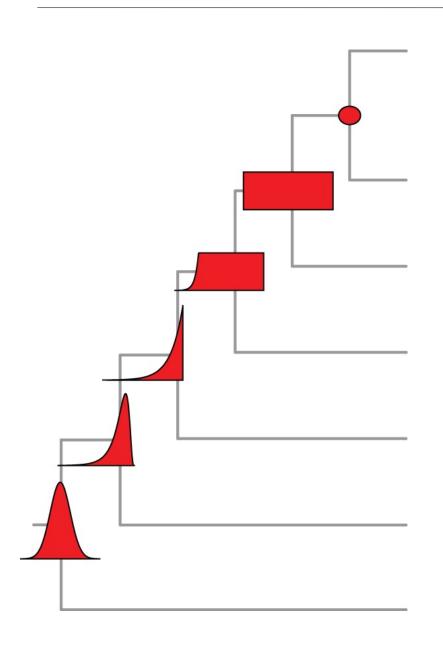
Point calibration

 Ignores uncertainty due to preservational biases, isotopic dating errors, etc.



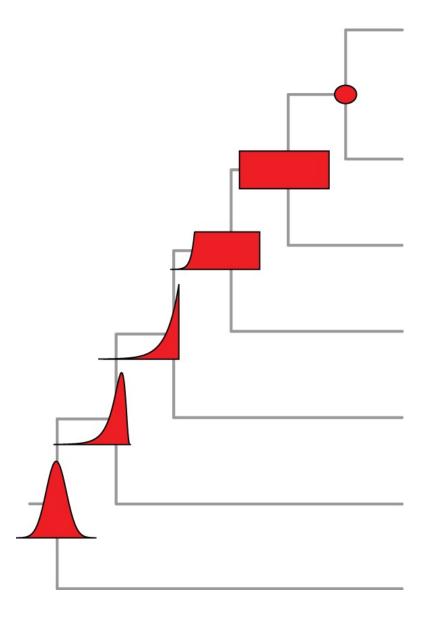
Uniform prior

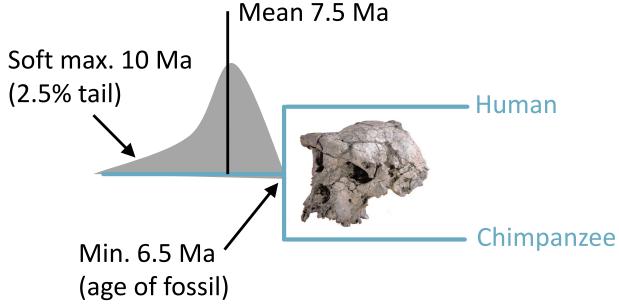
- Combination of hard minimum and maximum bounds
- Does not effectively use information at hand
- Difficult to choose useful maximum bounds



Exponential prior

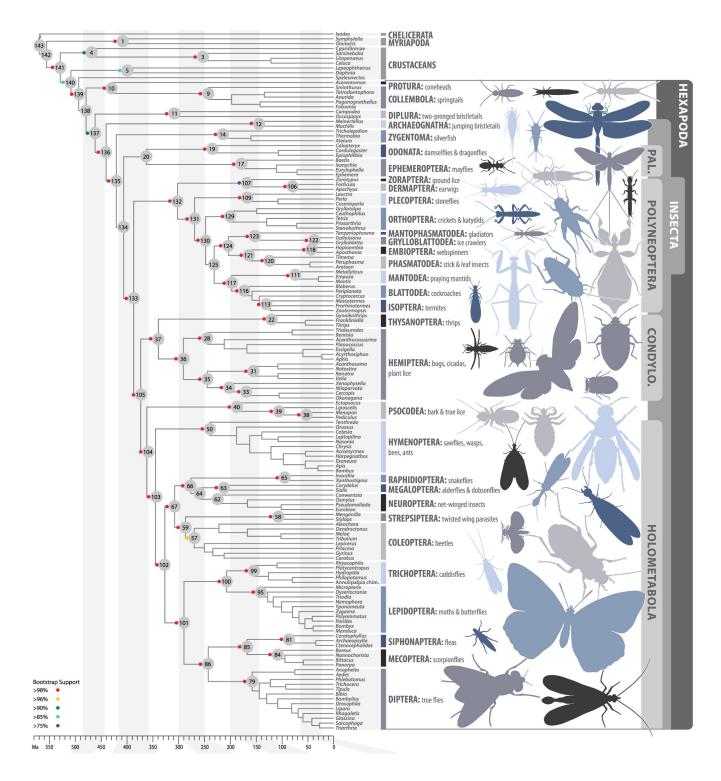
- Need 2 values: minimum and mean
- Strong assumption about relationship of fossil taxon to internal node





Lognormal prior

- Need 3 values: minimum, mean, and stdev
- Perhaps the most appropriate for fossils 11



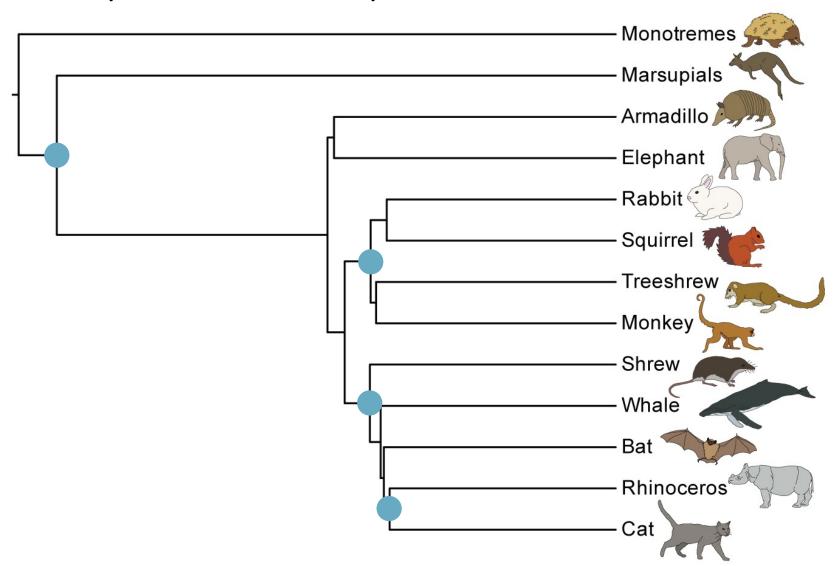
- Misof et al. (2014)
- Lognormal priors for ages of 20 nodes
- Arbitrary values:

Mean = 2

St. dev. = 0.5

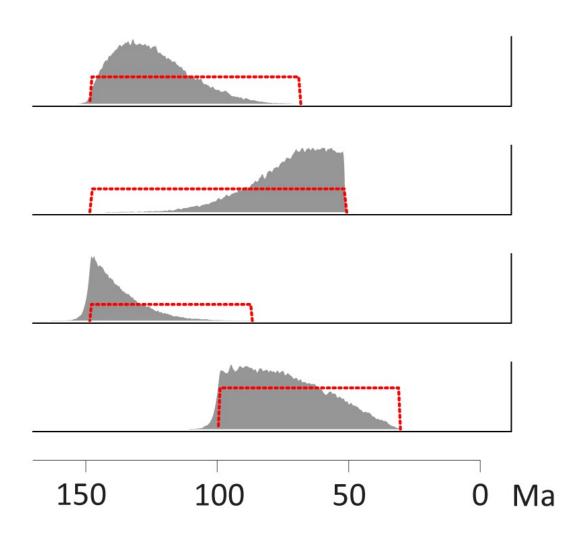
Multiple calibrations

Use multiple calibrations if possible



Multiple calibrations

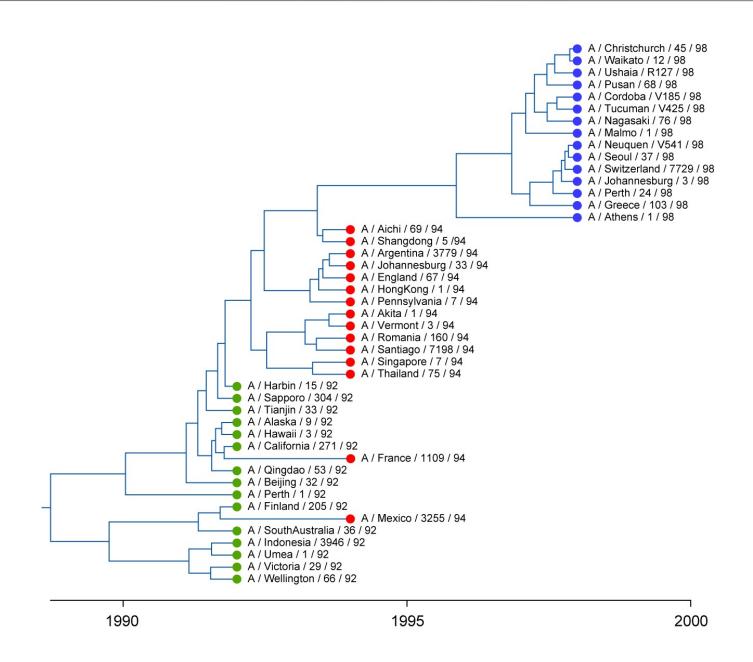
- Priors on node ages are the joint product of the tree prior and the userspecified calibration priors
- These priors can interact
- Marginal priors can differ from user-specified priors



Calibration: Biogeography

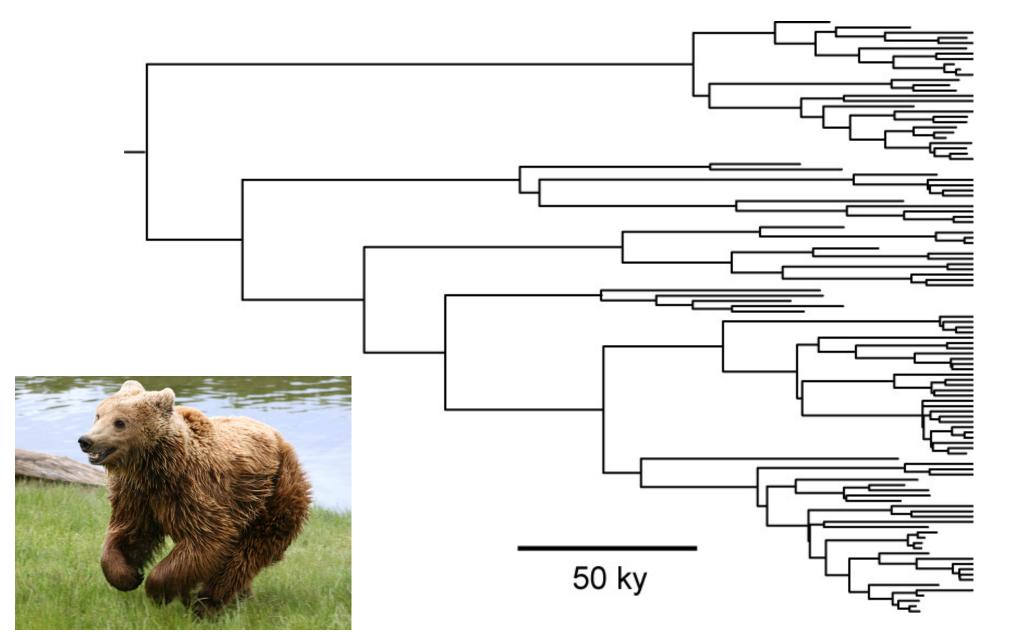
Time Vicariance Geodispersal Biological dispersal

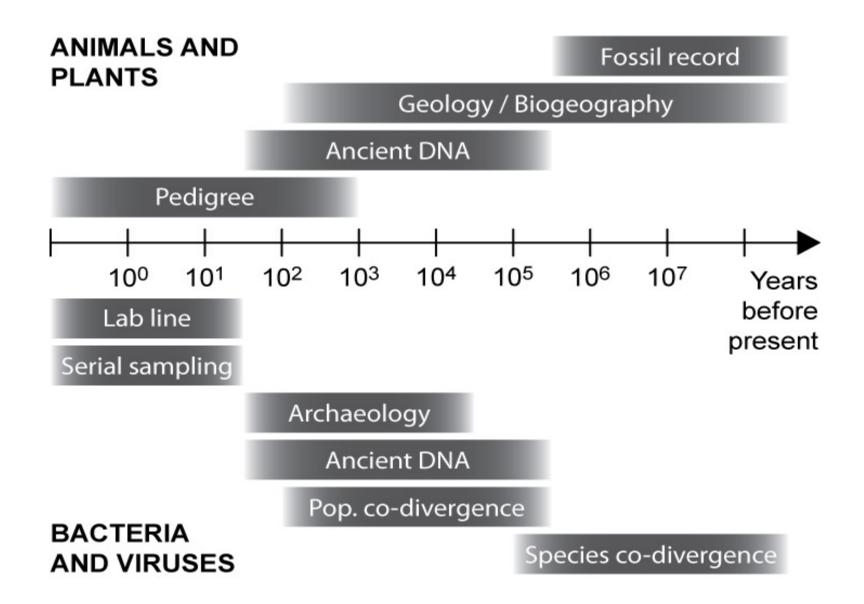
Calibration: Sampling times



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Calibration: Sampling times





Choosing calibrations

- Use multiple calibrations if possible
- The age estimates for poorly supported clades should be interpreted carefully
- Careful selection of clock models can improve the estimates

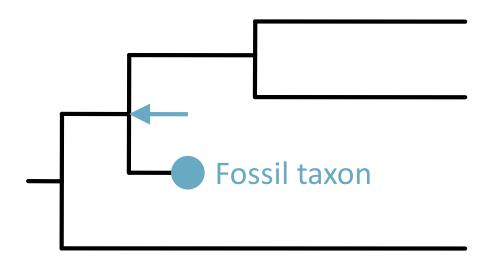
Total-Evidence Dating

Total-evidence dating

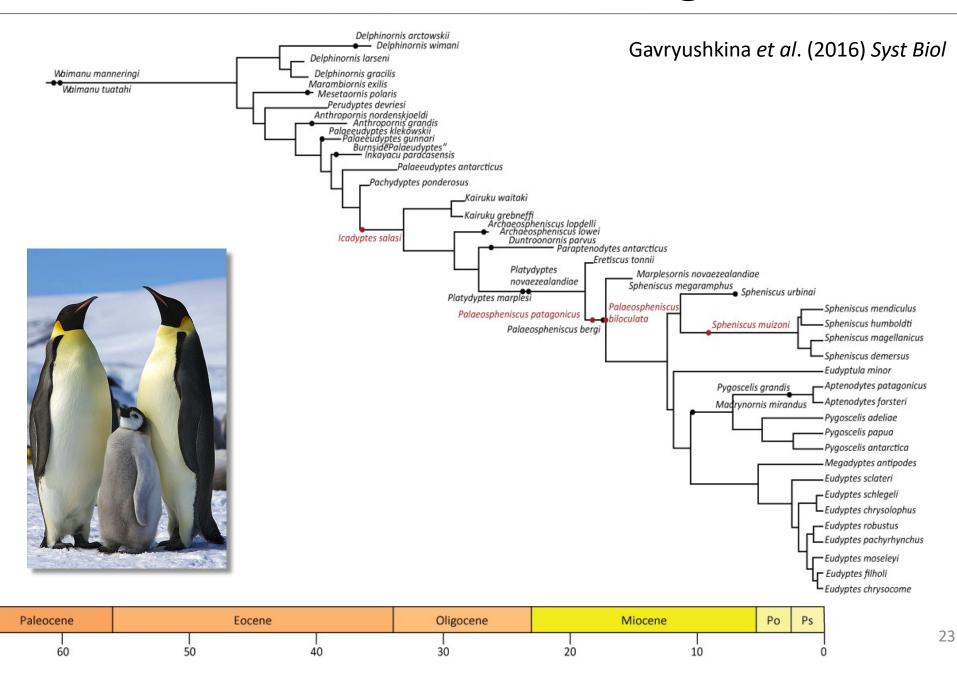
- Combined morphological and molecular data set
- Fossil taxa included
 - Phylogenetic placement estimated using morphological data
 - Age acts as a calibration by constraining the age of parent node
- Birth-death tree prior

Total-evidence dating

- Avoids the need to construct priors for ages of internal nodes
- Can include fossil taxa with uncertain phylogenetic position
- Can provide sufficient calibration without the need to include maximum age constraints



Total-evidence dating



Useful references

- Calibration uncertainty in molecular dating analyses: there is no substitution for the prior evaluation of time priors
 Warnock et al. (2014) Proceedings of the Royal Society B, 282: 20141013.
- Accounting for uncertainty in phylogenetic estimation of evolutionary divergence times
 Ho & Phillips (2009) Systematic Biology, 58: 367–380.
- Best practices for justifying fossil calibrations
 Parham et al. (2012) Systematic Biology, 61: 346–359.
- Biogeographic calibrations for the molecular clock Ho et al. (2015) Biology Letters, 11: 20150194.