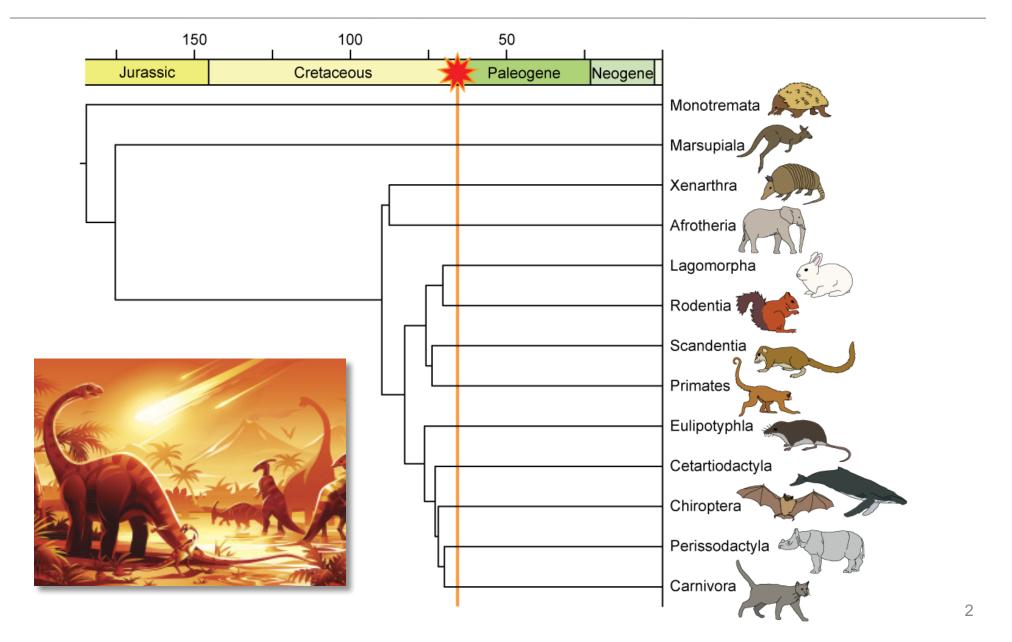
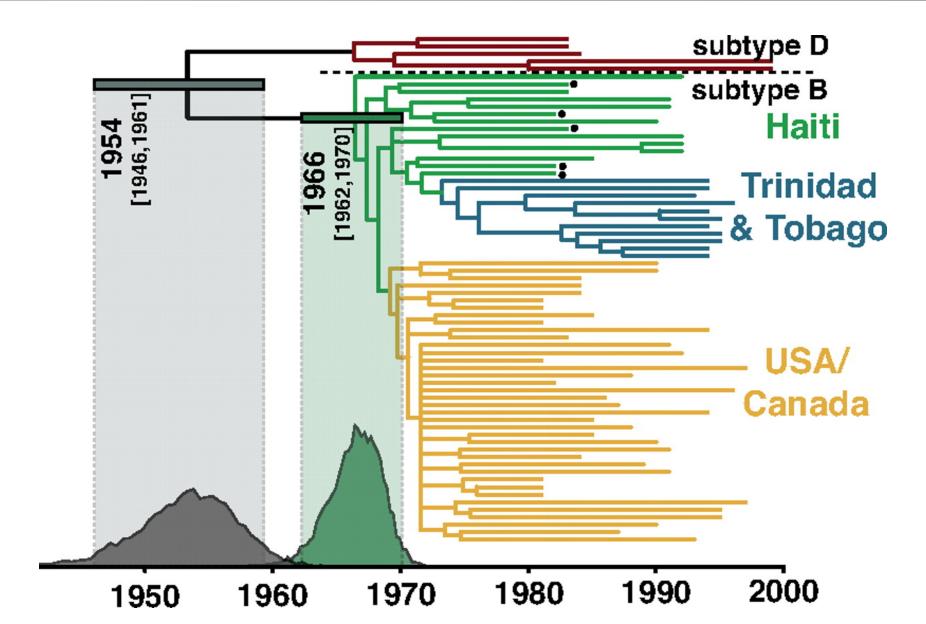
Lecture 1.4: The Molecular Clock

Diversification of mammals

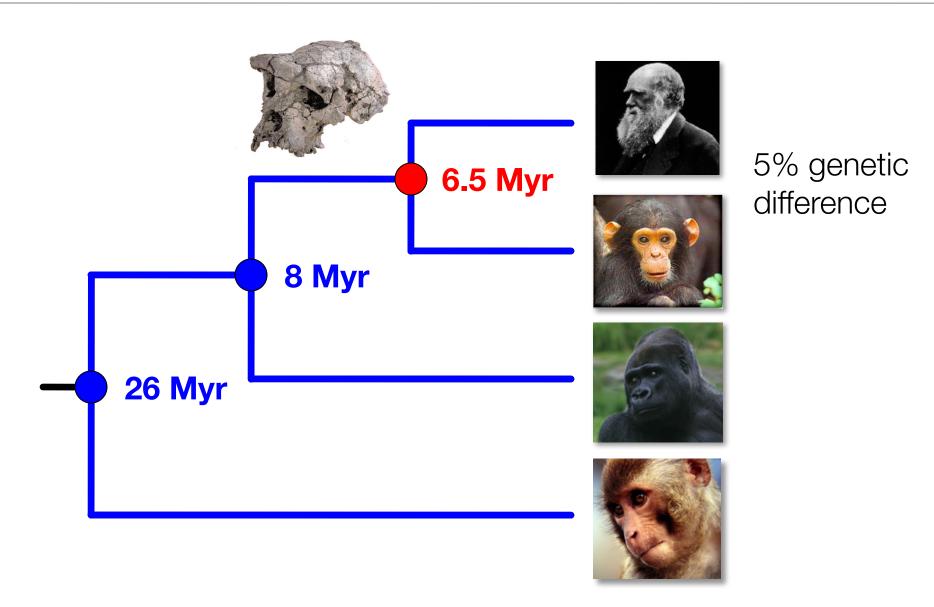


Emergence of HIV/AIDS in the Americas

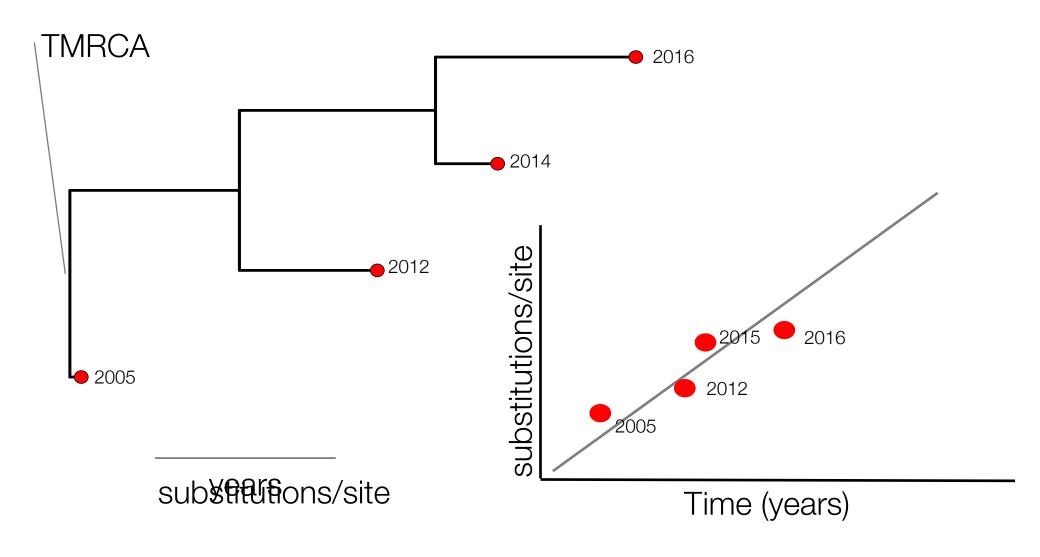


The Molecular Clock

The molecular clock



The molecular clock



The molecular clock

- Zuckerkandl & Pauling (1962)
- Margoliash (1963)
- Doolittle & Blomback (1964)
- Zuckerkandl & Pauling (1965)

Assumed constant rate among species to estimate timing of globin gene duplications

Proportional relationship between genetic distance and time since divergence

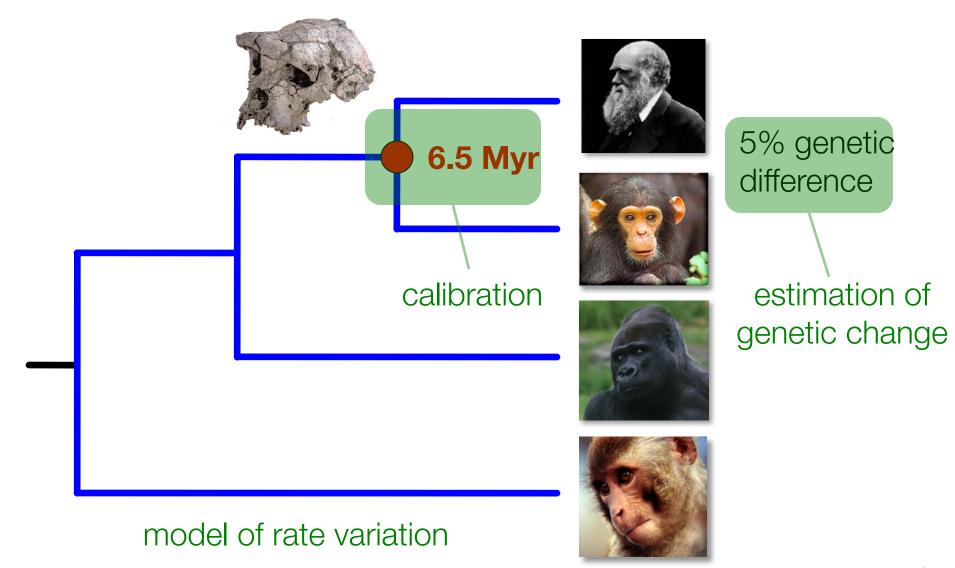




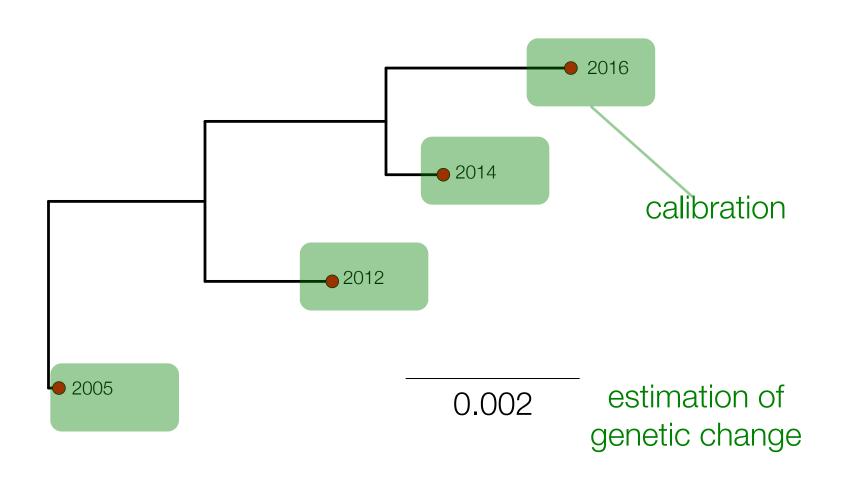
Examined correlation between time and genetic divergence in mammalian fibrinopeptides

Introduced the term 'molecular evolutionary clock'

Sources of error



Sources of error



model of rate variation

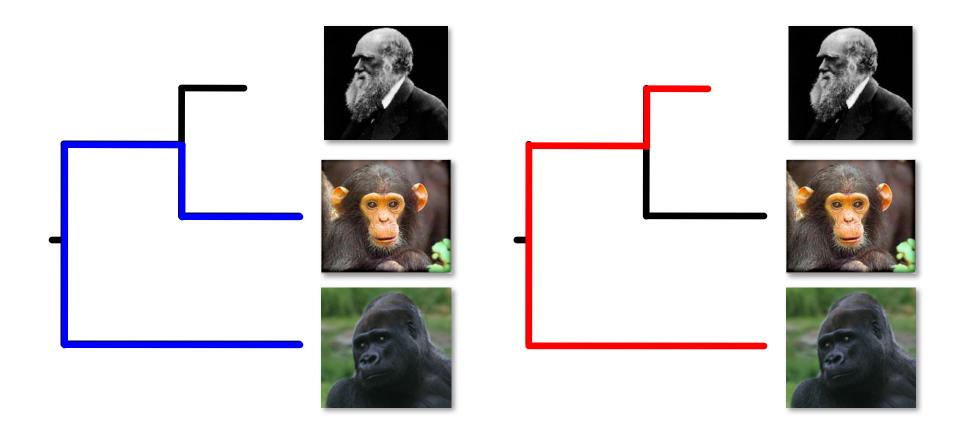
Departures from the clock

- Rates vary among lineages
 - Differences in mutation rates
 - Differences in strength and direction of selection
 - Differences in population size



Testing for clocklike evolution

Relative-rates test (Fitch, 1976)



Why keep the molecular clock?

 The behaviour of most real sequences does not satisfy the assumption of a strict molecular clock

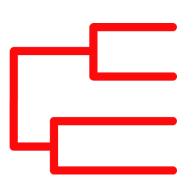
Bromham & Penny (2003):

The molecular clock is an irreplaceable source of information in evolutionary biology and it would be foolish to abandon it altogether

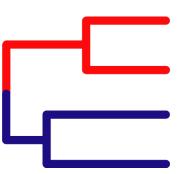
Relaxed Molecular Clocks

Molecular-clock models

Strict or 'global' molecular clock

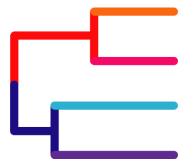


Local molecular clock

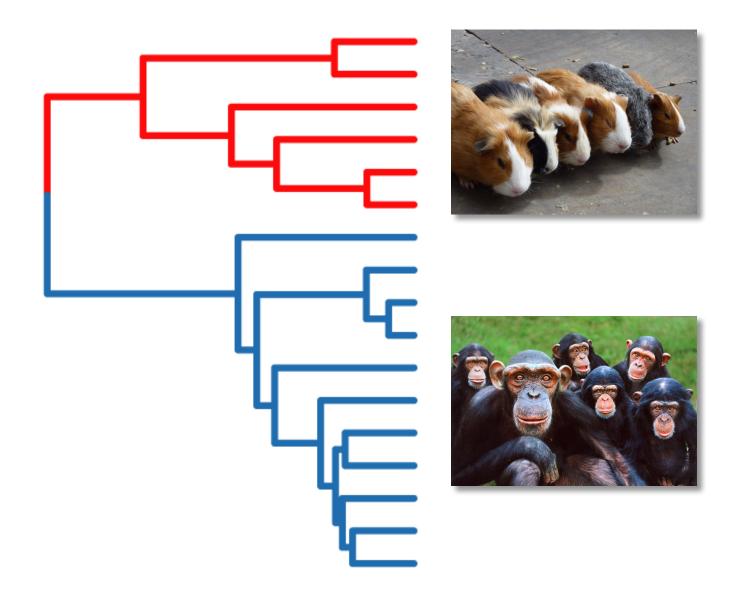


Relaxed molecular clock

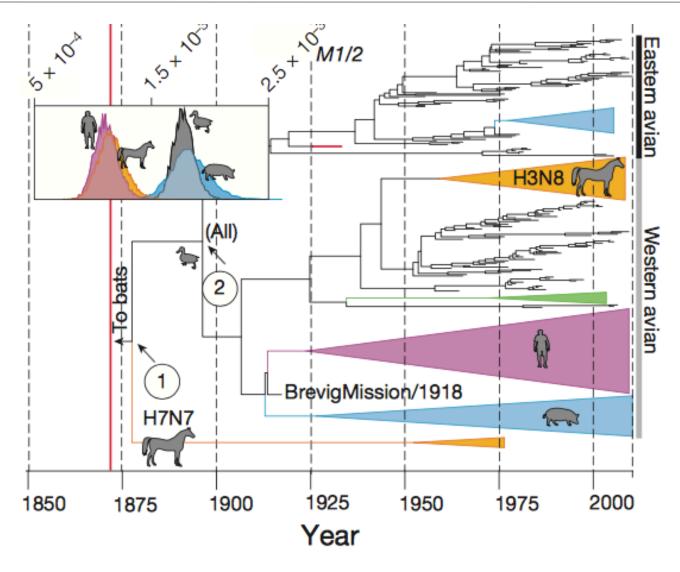




Local molecular clock



Host-specific clock



From: Worobey et al. 2014 Nature

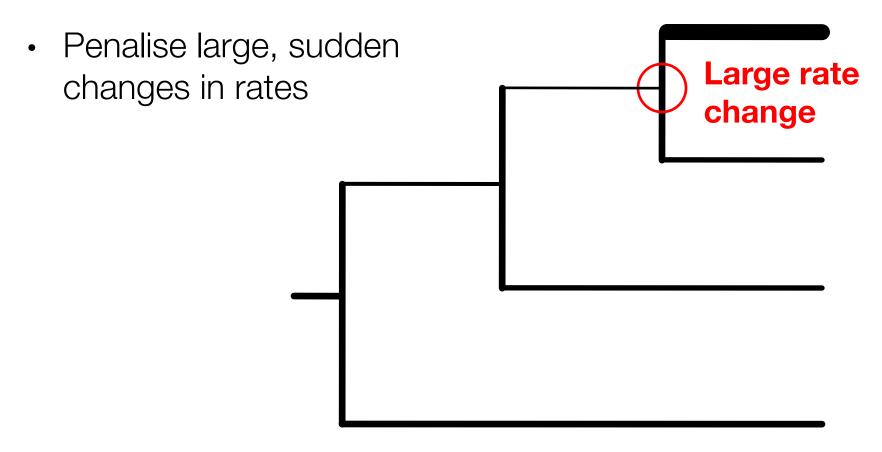
Relaxed clocks

- We know that life-history characteristics:
 - Have effects on rates of molecular evolution
 - Are usually heritable to some degree
- Treat molecular rate as a heritable trait
- Relaxed clocks generally assume that closely related species share similar rates



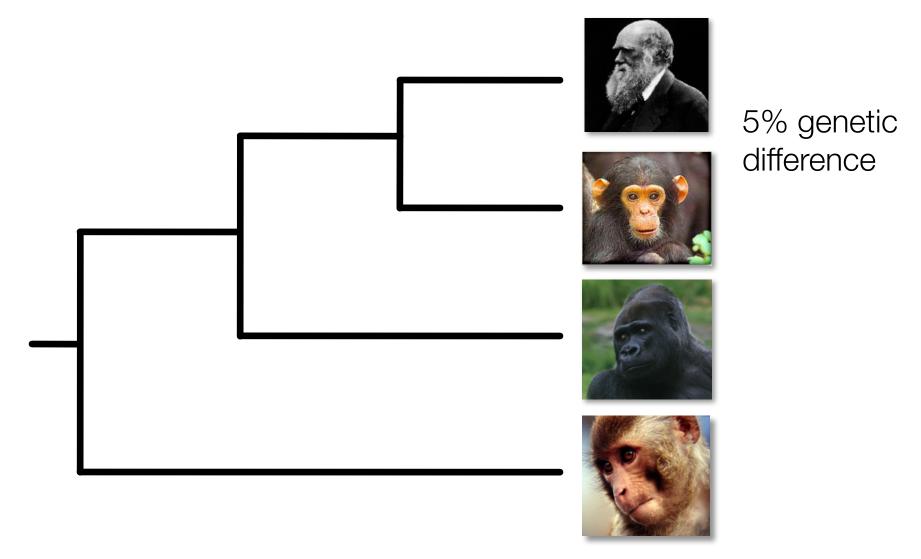
Likelihood-based relaxed clocks

Allow a different rate in each branch

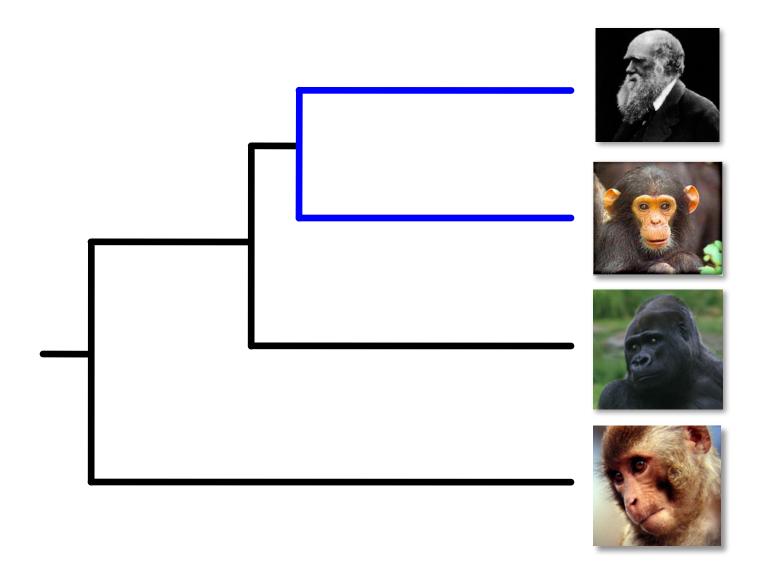


Calibrating the Molecular Clock

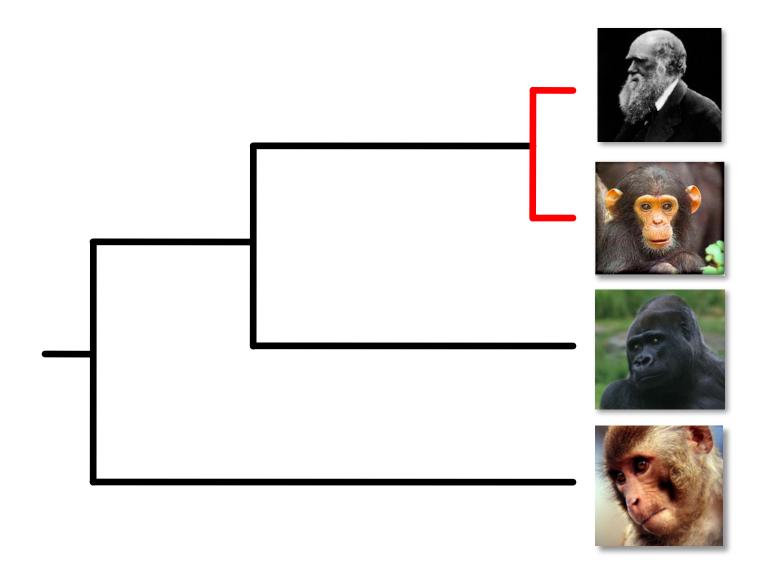
Calibrating the molecular clock



Calibrating the molecular clock

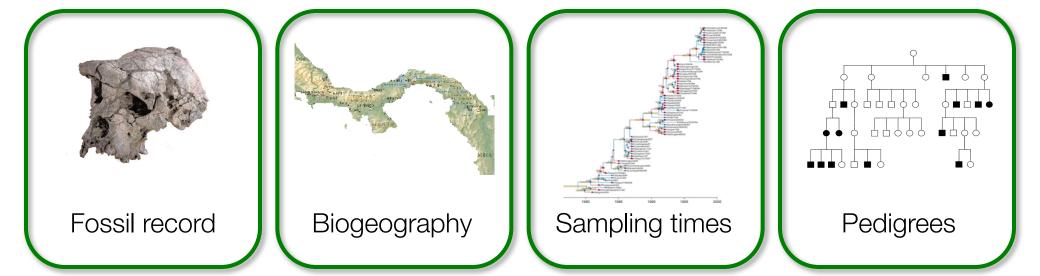


Calibrating the molecular clock



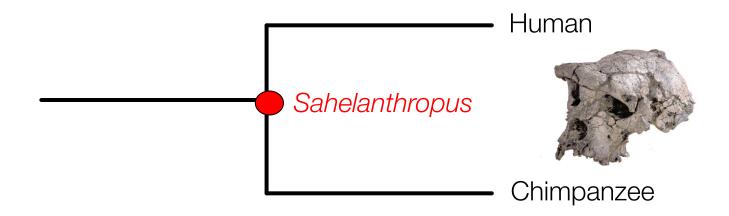
Calibrating information

- Information about the rate
 - Substitution rate obtained from an independent study
- Information about time



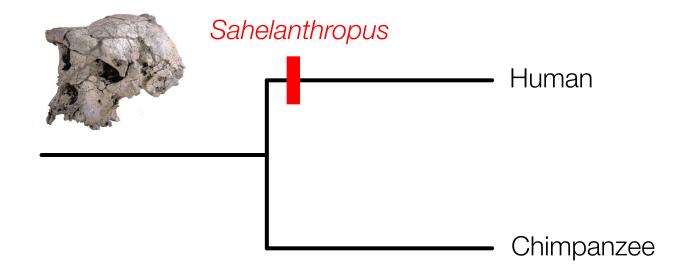
Point calibrations

- Traditional approach
- Artificial precision: ignores the uncertainty arising from preservational biases, isotopic dating errors, etc.



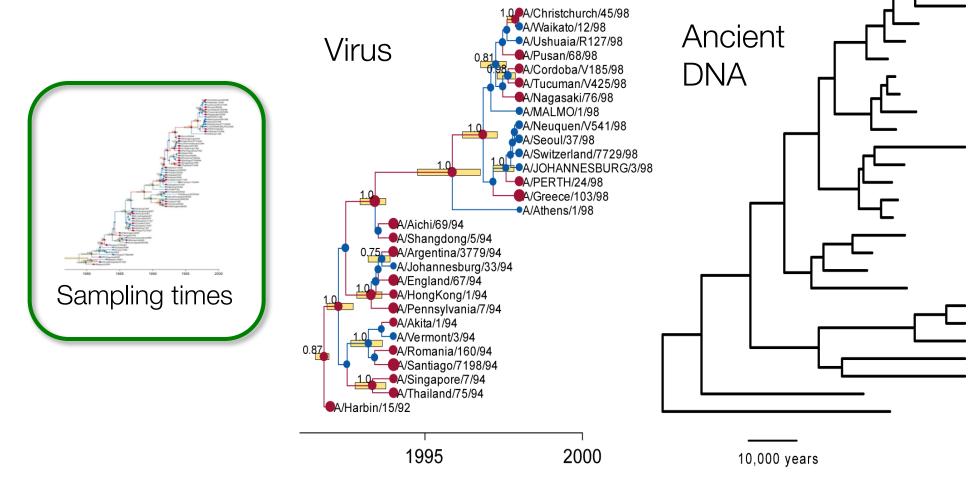
Hard calibration bounds

Minimum or maximum age constraints

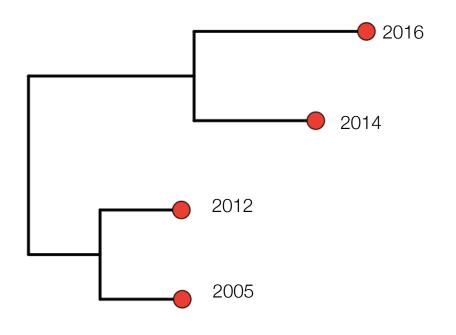


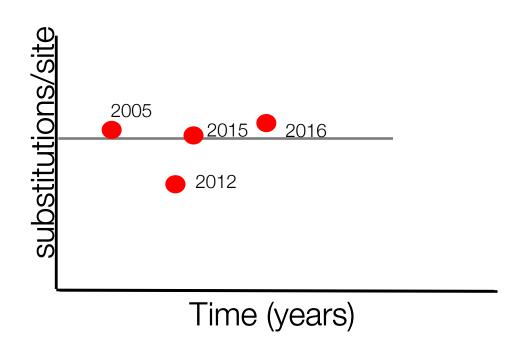
- Discards potentially useful information
- Inadequate information for estimating divergence times

Calibration: Sampling times

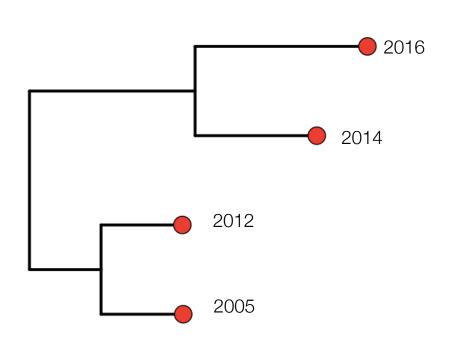


Validating estimates: Root-to-tip regression



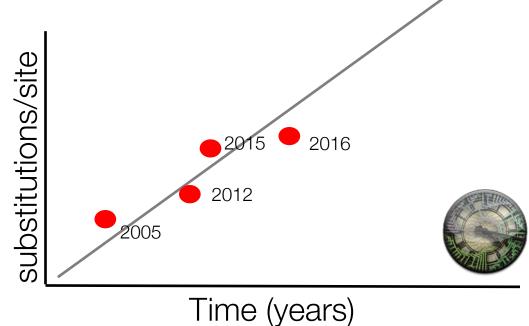


Validating estimates: Root-to-tip regression

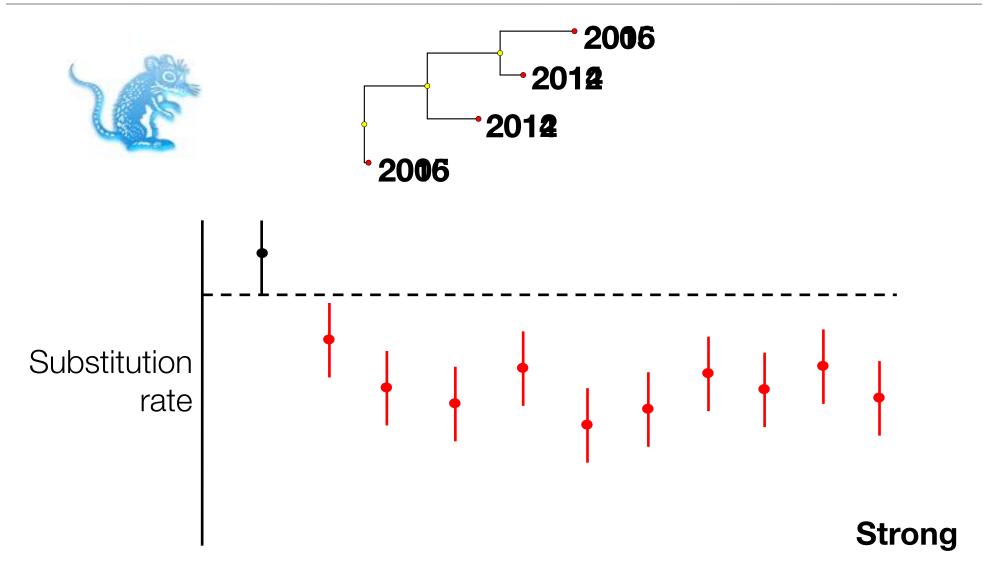


- High R²
- Positive rate
- P-value (controversial)

The rate estimate is phylogenetically non-independent

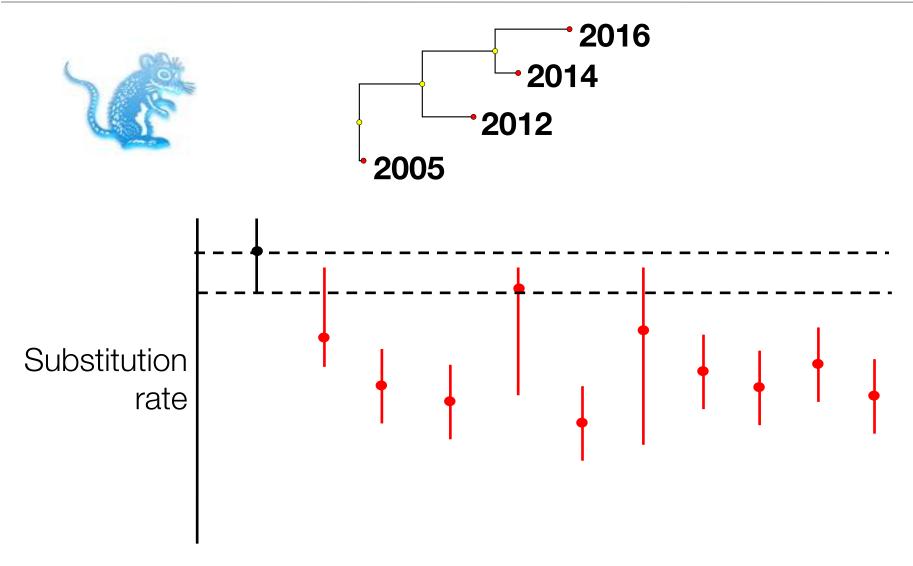


The date-randomisation test



From: Duchene et al. 2015 Mol Biol Evo

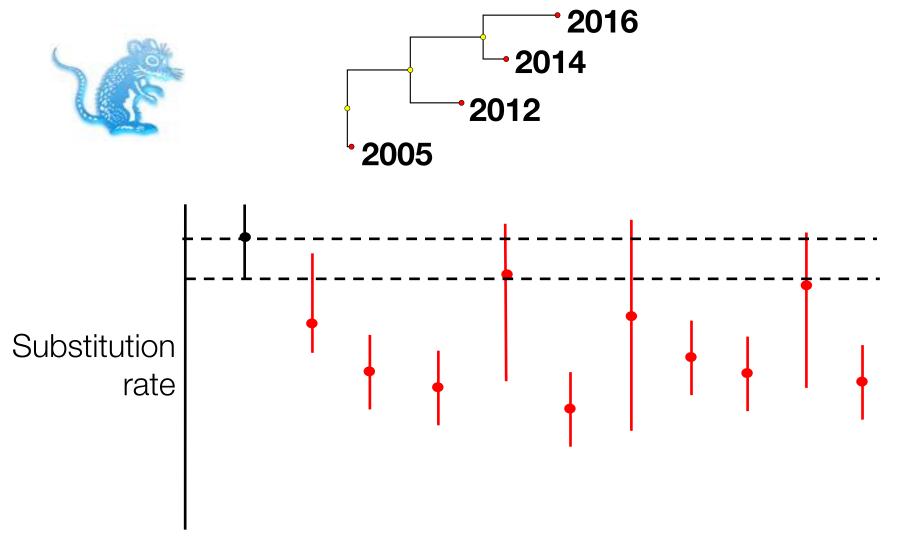
The date-randomisation test



From: Duchene et al. 2015 Mol Biol Evo

Medium

The date-randomisation test



From: Duchene et al. 2015 Mol Biol Evo

Weak

Some useful references

- Ho, Simon YW, and Sebastián Duchêne. "Molecular-clock methods for estimating evolutionary rates and timescales." Molecular Ecology 23.24 (2014): 5947-5965.
- Rieux, Adrien, and François Balloux. "Inferences from tip-calibrated phylogenies: a review and a practical guide." Molecular ecology 25.9 (2016): 1911-1924.
- Duchêne, Sebastián, et al. "The performance of the daterandomisation test in phylogenetic analyses of time-structured virus data." Molecular biology and evolution (2015).

Go to Practical 1d: Assessing temporal structure in *TempEst*

Note: TempEst for mac sometimes doeworking. Please download the Linux version, and run the .jar file.