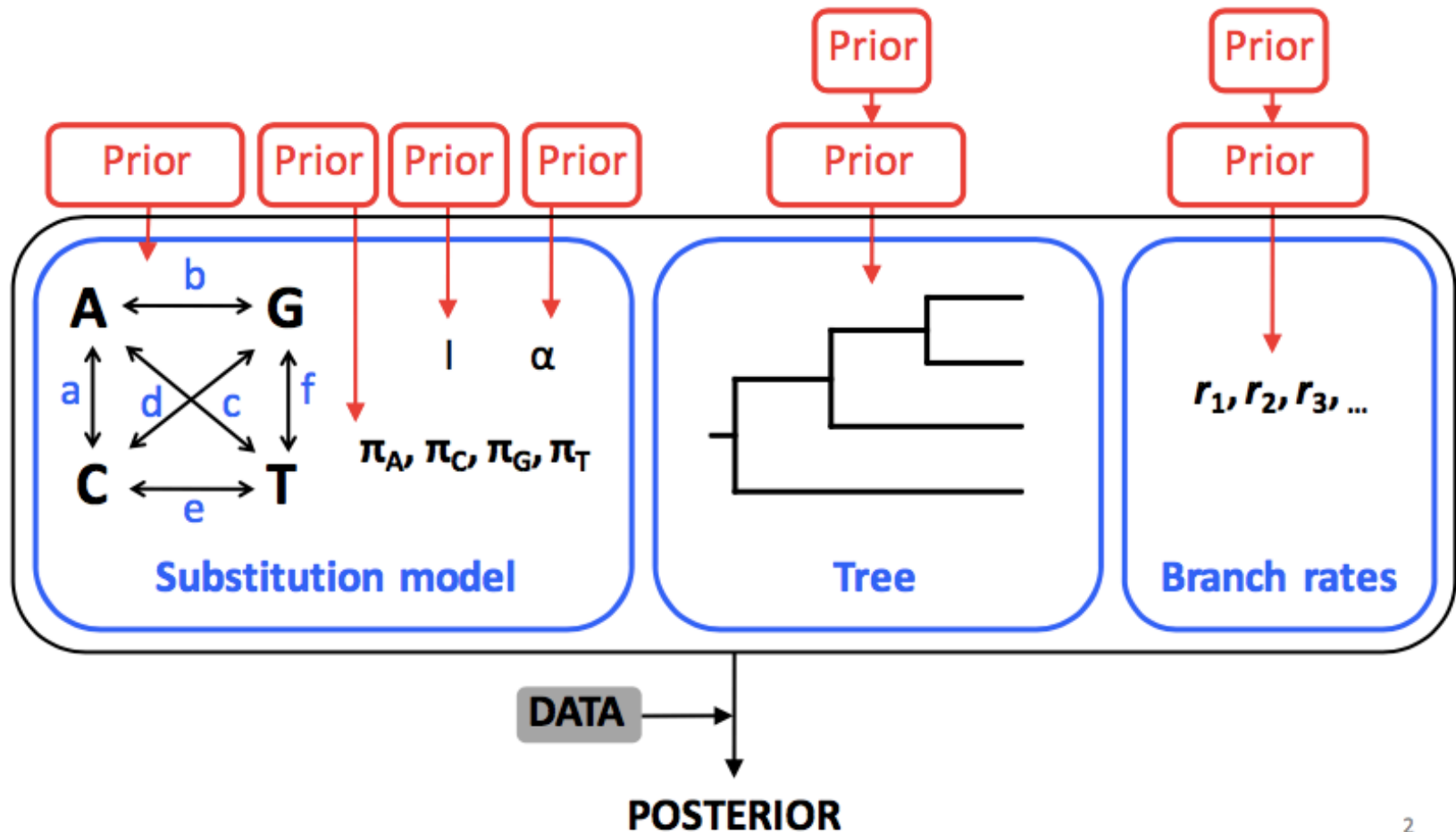


Lecture 2.2:

Priors

The Bayesian hierarchical model



Prior distributions

Priors

- Reflect our prior expectation (and uncertainty) about parameters (without knowledge of the data)
 - Past observations
 - Biological intuition
 - Biological models

Continuous distributions

- Uniform
- Normal

Used to specify prior distributions of various continuous parameters

- Exponential
- Lognormal
- Gamma

Used to specify prior distributions of continuous parameters that cannot take negative values

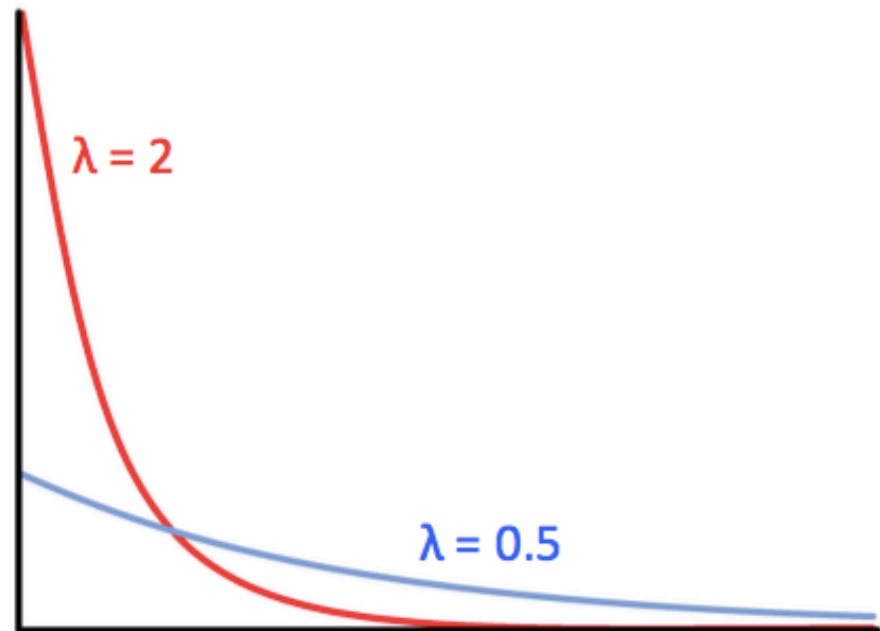
- Beta
- Dirichlet

Continuous distributions

- Uniform
- Normal
- **Exponential**
- Lognormal
- Gamma
- Beta
- Dirichlet

Parameters

- λ = rate of decay



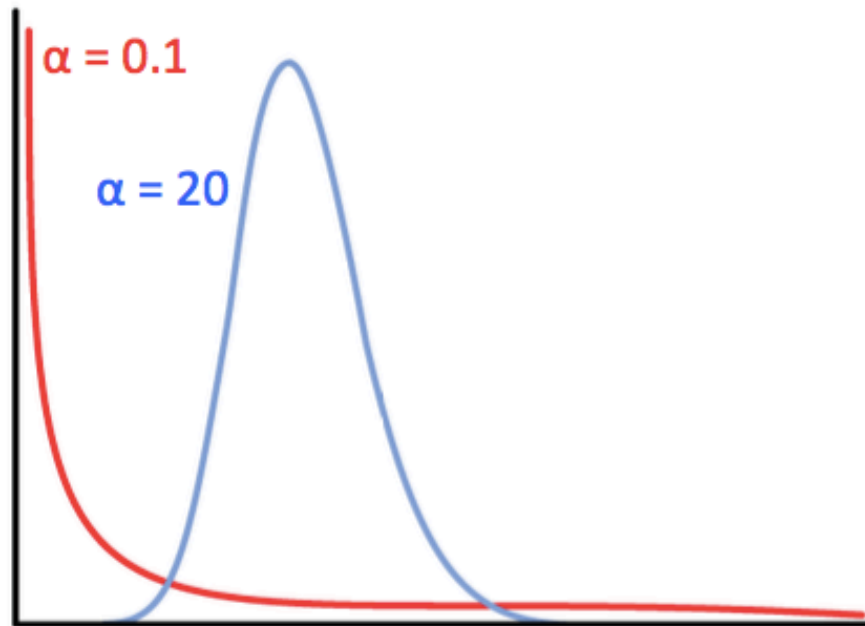
Continuous distributions

- Uniform
- Normal
- Exponential
- Lognormal
- **Gamma**
- Beta
- Dirichlet

Parameters

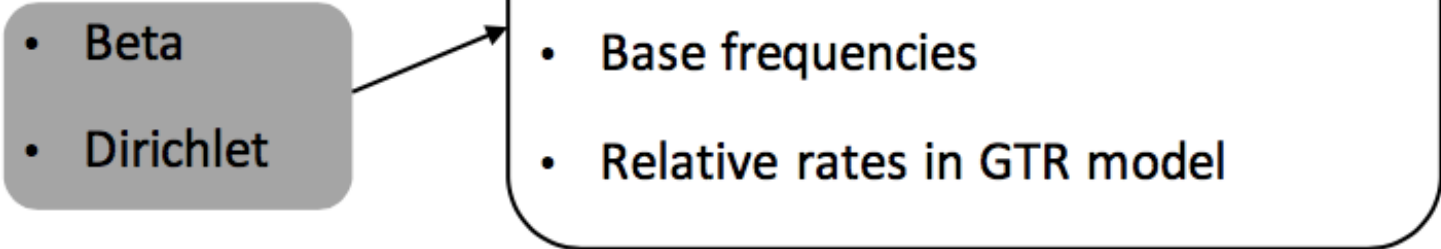
- α = shape
- β = inverse scale

Scaled gamma:
 $\alpha = \beta$



Continuous distributions

- Uniform
- Normal
- Exponential
- Lognormal
- Gamma
- Beta
- Dirichlet



Used to specify the prior distributions of simplex parameters

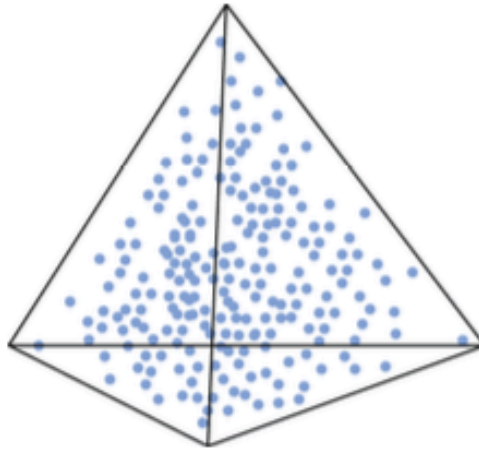
- Base frequencies
- Relative rates in GTR model

Continuous distributions

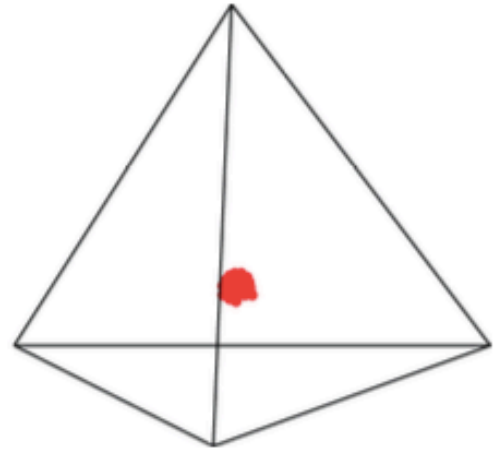
- Uniform
- Normal
- Exponential
- Lognormal
- Gamma
- Beta
- **Dirichlet**

Parameters

- $\alpha_1, \alpha_2, \dots$ = shape parameters



$$\alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = 1$$



$$\alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = 300$$

Image modified from Paul Lewis's slides

Discrete distributions

- Bernoulli distribution
- Binomial
- Multinomial
- Poisson

Default priors

	<i>BEAST</i>	<i>MrBayes</i>
Rate matrix parameters	Gamma(0.05,10)	Dirichlet(1,1,1,1,1,1)
Base frequencies	Uniform(0,1)	Dirichlet(1,1,1,1)
Shape parameter (α)	Exponential(0.5)	Exponential(2)
Proportion invariable	Uniform(0,1)	Uniform(0,1)

Uninformative priors

- Flat or uniform prior
- Jeffreys prior
 - Invariant to reparameterisation
 - Only works well for models with a single parameter
- Reference priors
 - Maximise expected distance between prior and posterior
 - Allows data to have maximum effect on the posterior

Bayesian relaxed clocks and priors

Relaxed clocks

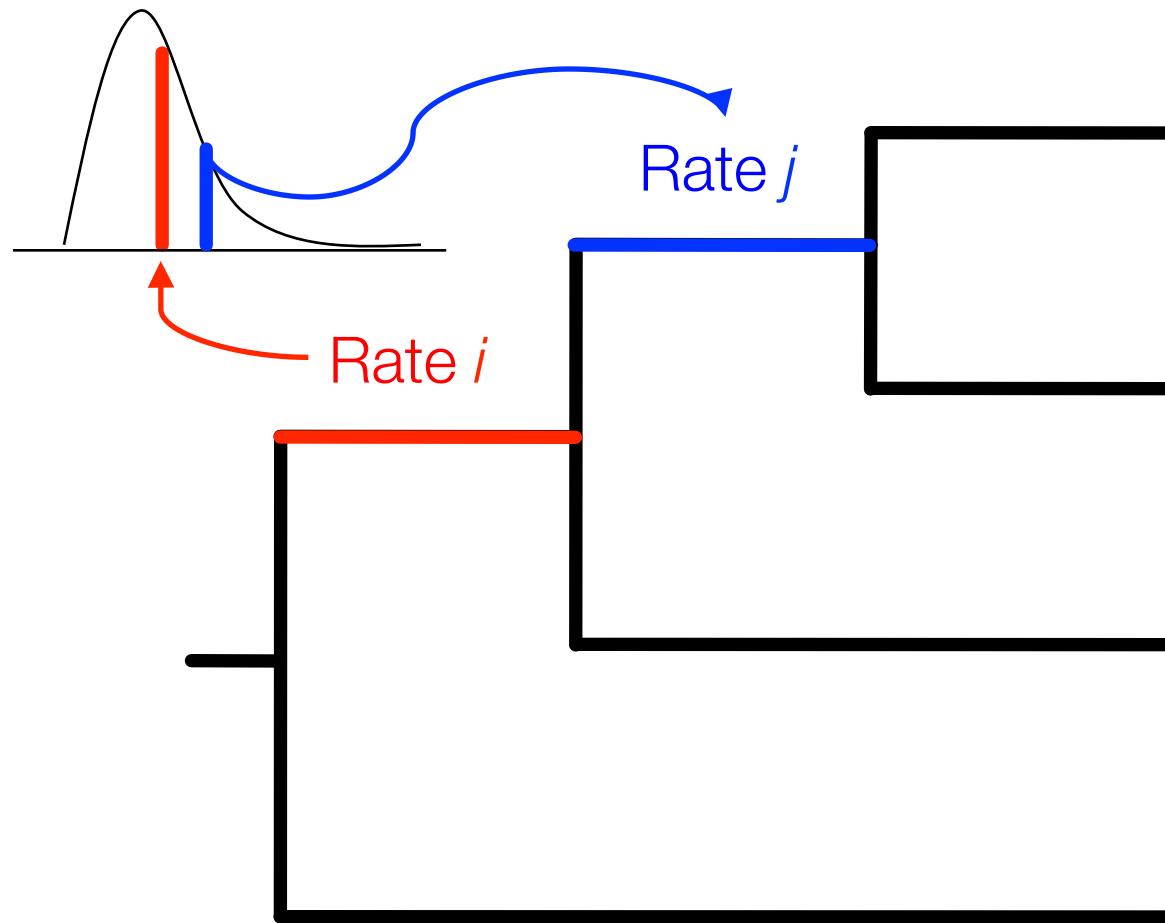
- We know that life-history characteristics:
 - Have effects on rates of molecular evolution
 - Are usually heritable to some degree
- Treat molecular rate as a heritable trait
- Relaxed clocks generally assume that closely related species share similar rates



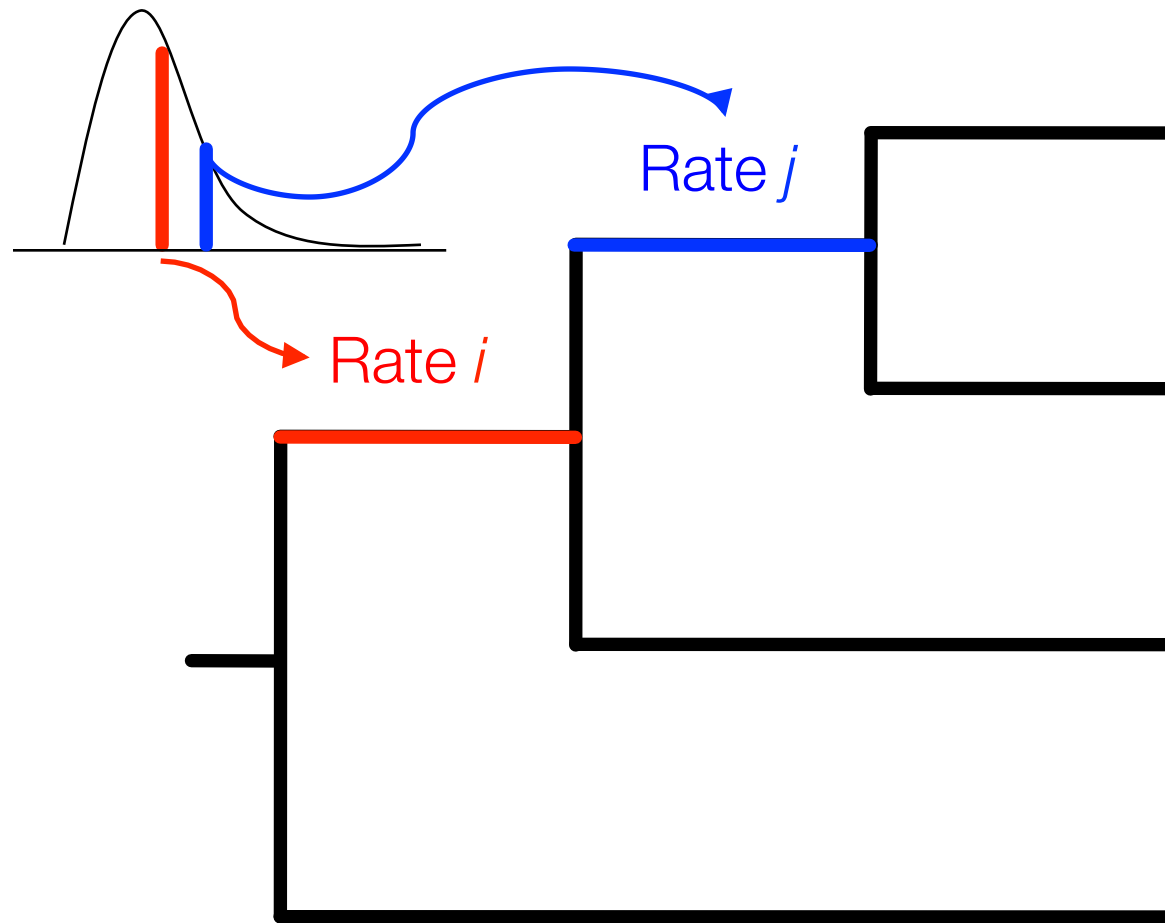
Bayesian relaxed clocks

- Allow a different rate in each branch
- Statistical models of rates among branches
- Rates can be autocorrelated or uncorrelated
 - **Autocorrelated:** rates in neighbouring branches are related
 - **Uncorrelated:** rates identically and independently distributed among branches

Autocorrelated relaxed clock

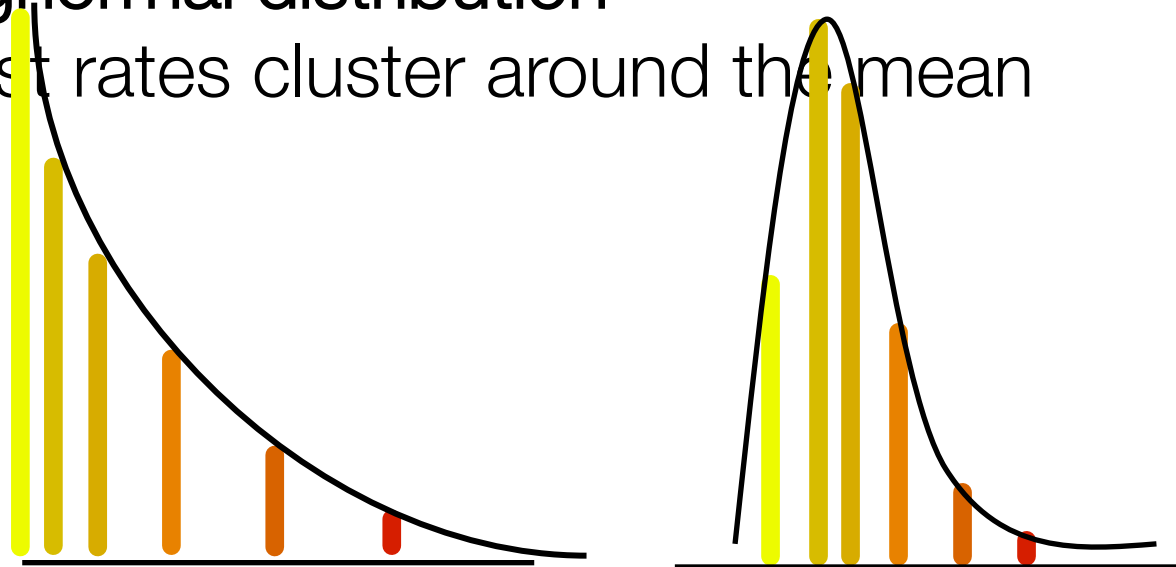


Uncorrelated relaxed clock



Uncorrelated relaxed clock

- Models available in BEAST
 - Exponential distribution
Most rates are quite low
 - Lognormal distribution
Most rates cluster around the mean



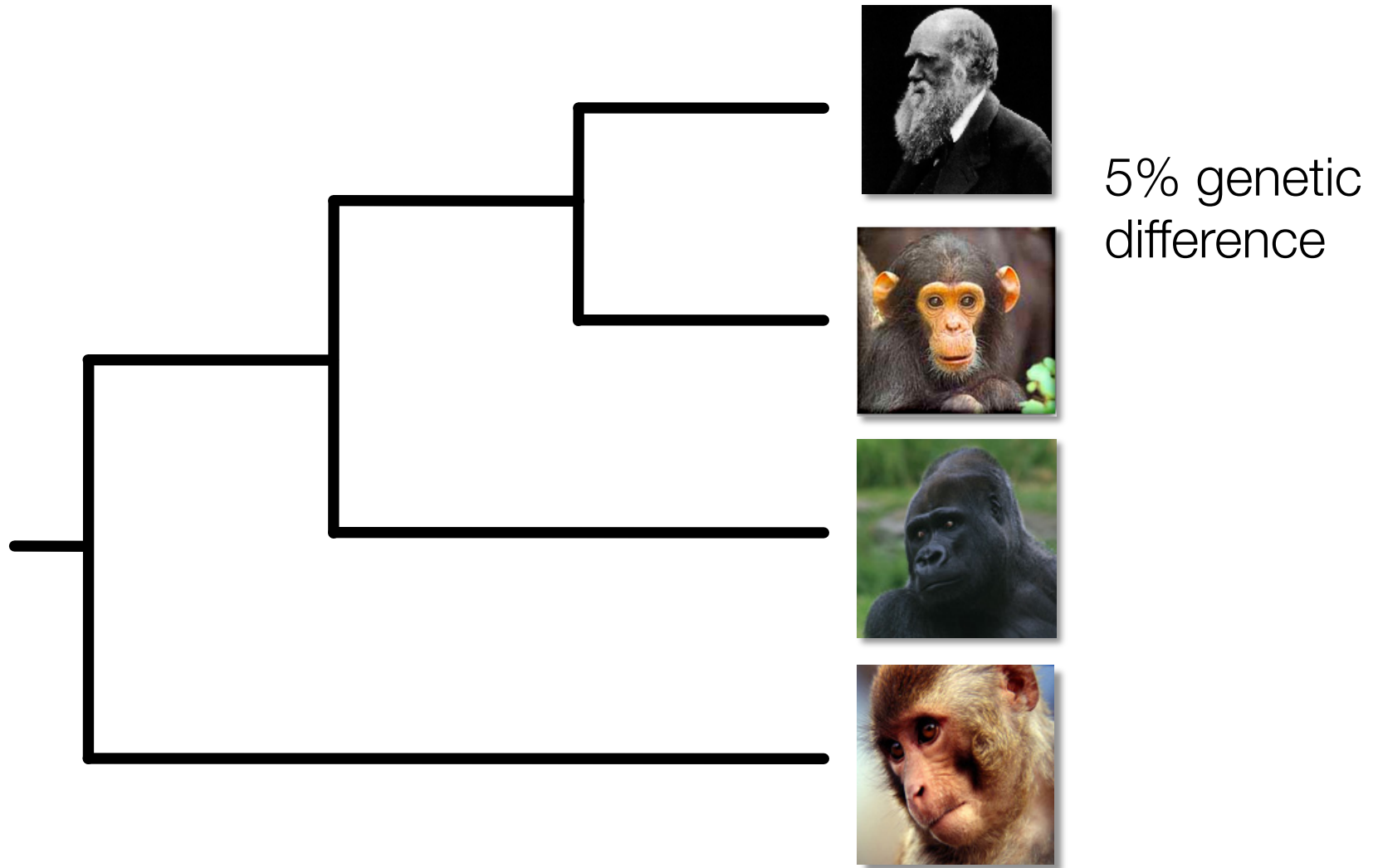
Lognormal uncorrelated relaxed clock

- In the uncorrelated lognormal relaxed clock, two statistics can be obtained:
 1. **Coefficient of variation of rates**

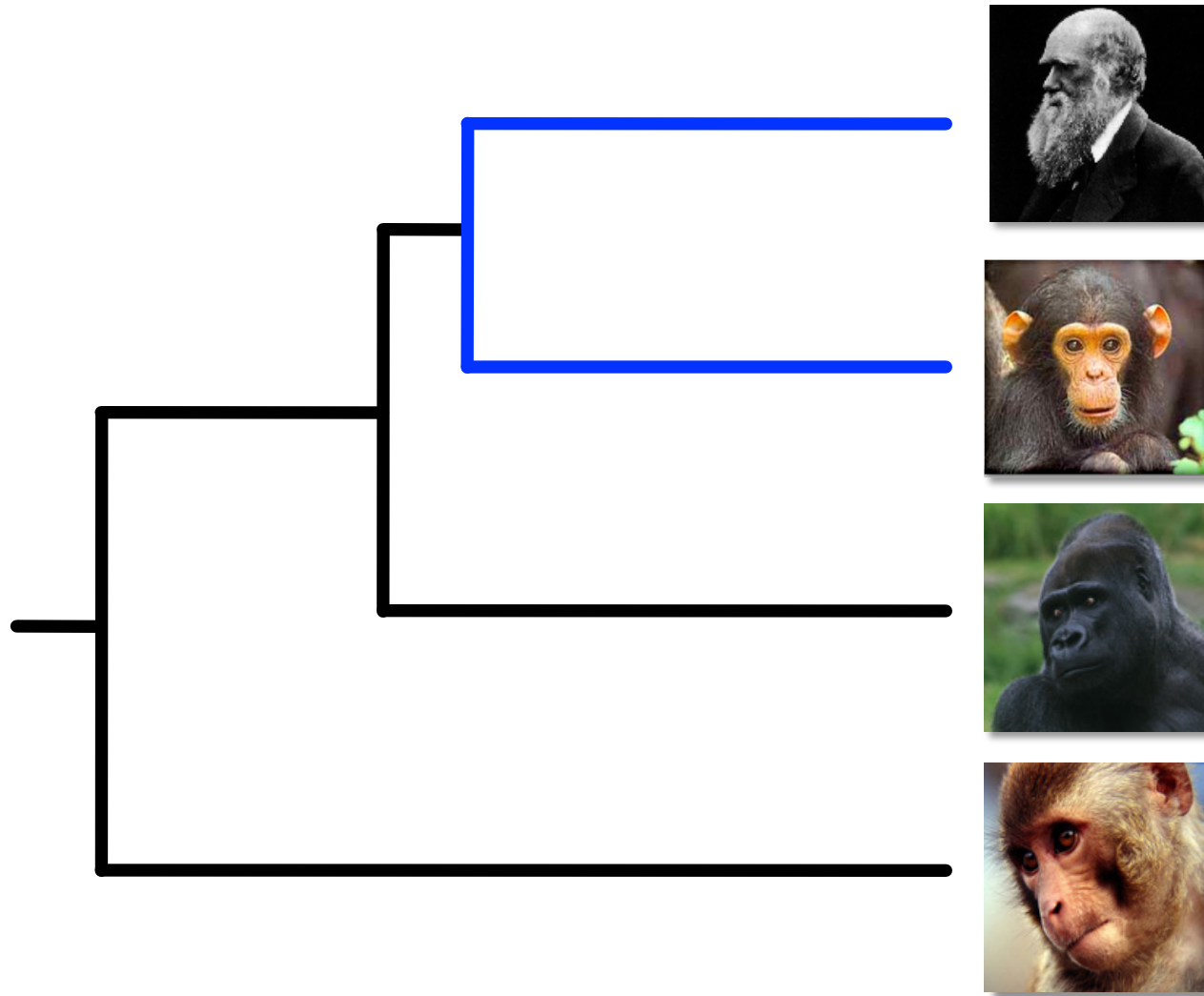
Measures the rate variation among branches
A value of 0 indicates clocklike evolution
 2. **Covariance of rates**

Measures autocorrelation of rates between adjacent branches

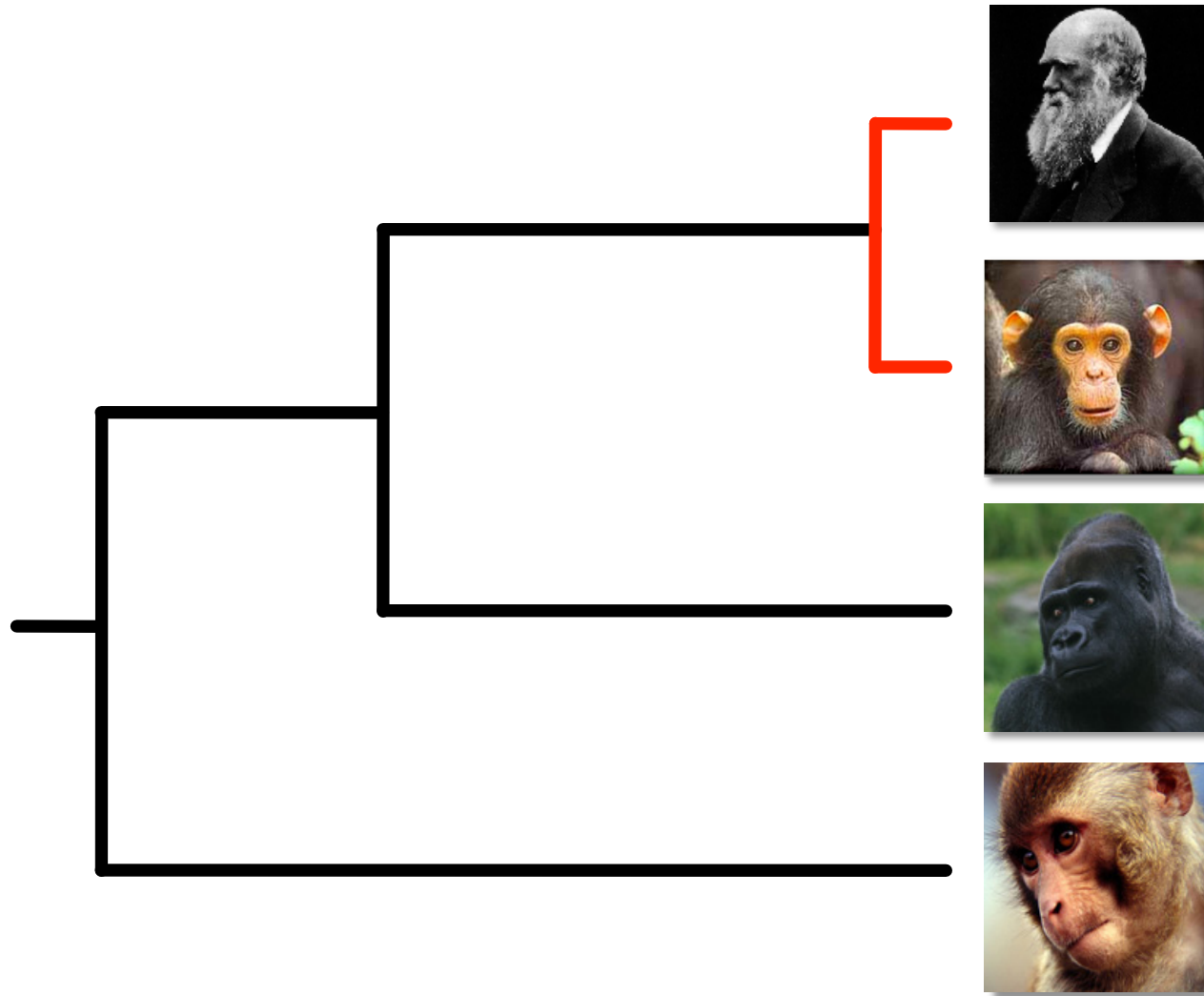
Calibrating the molecular clock



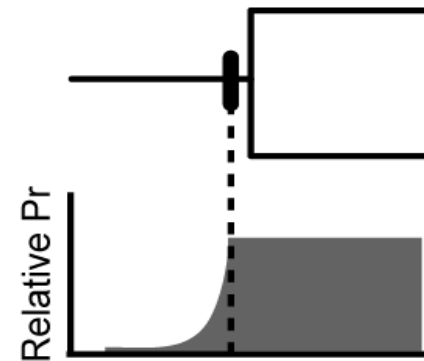
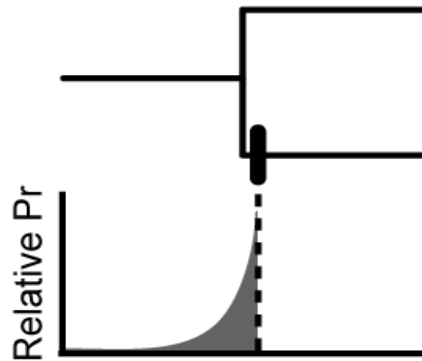
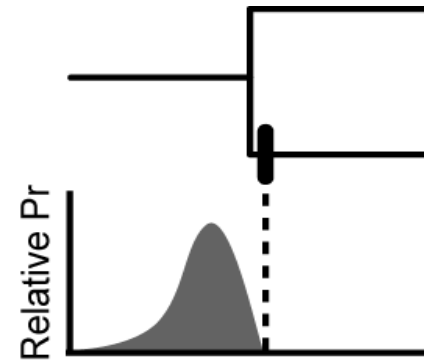
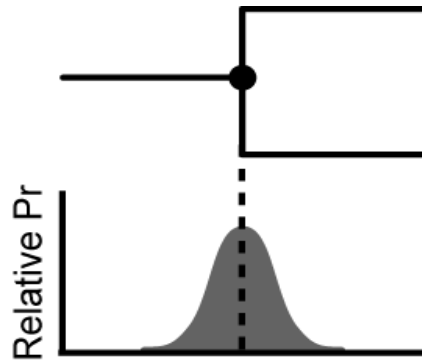
Calibrating the molecular clock



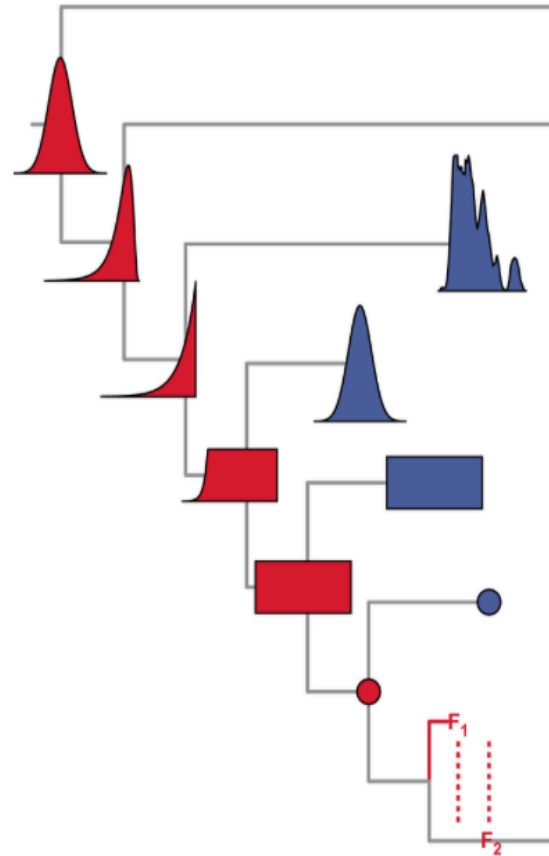
Calibrating the molecular clock



Parametric prior distributions



Parametric prior distributions



From: Ho and Duchene 2014 *Molecular Ecology*

Go to Practical 2: Markov
Chain Monte Carlo