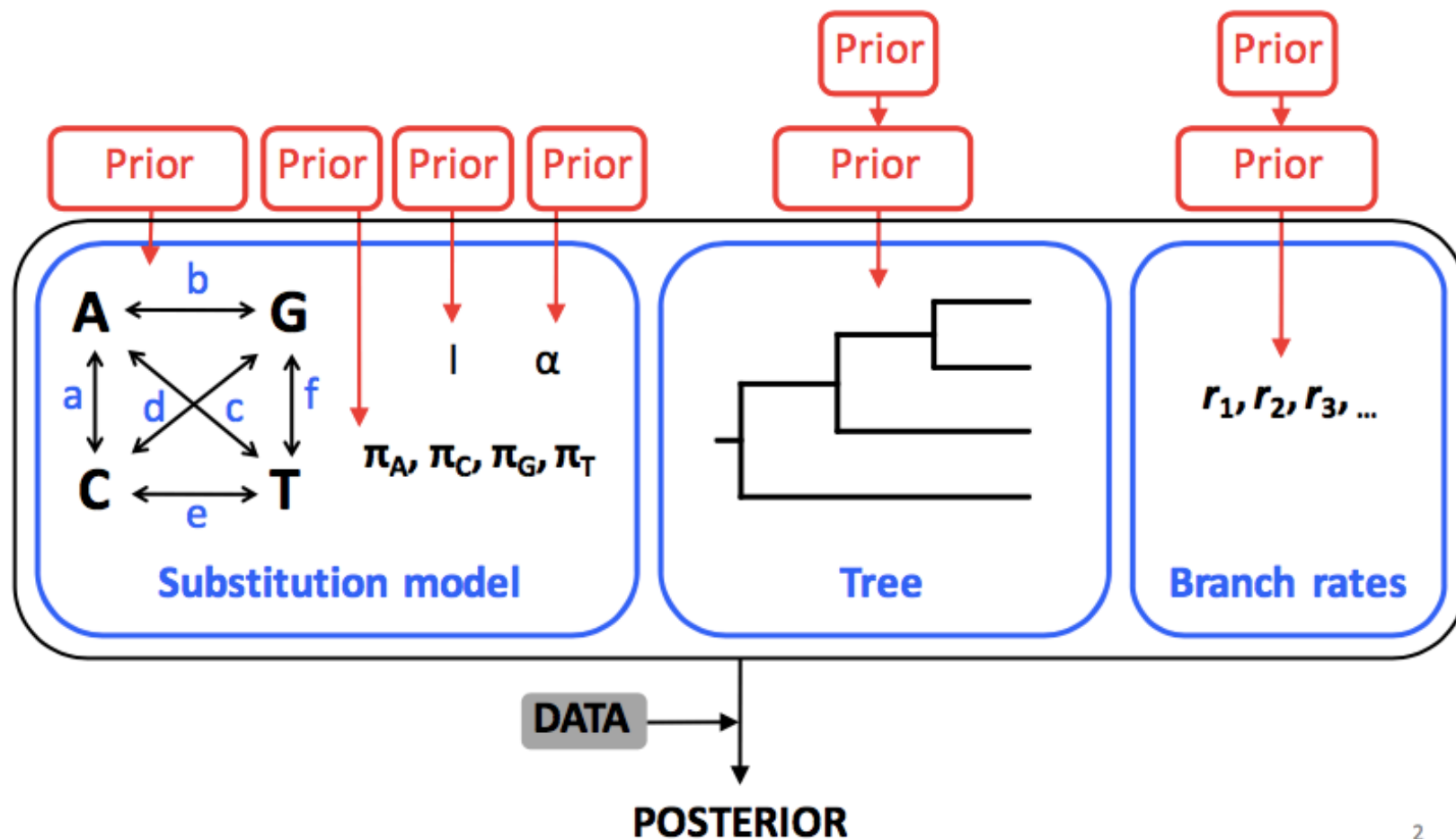# Lecture 2.2:
# Priors

# 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

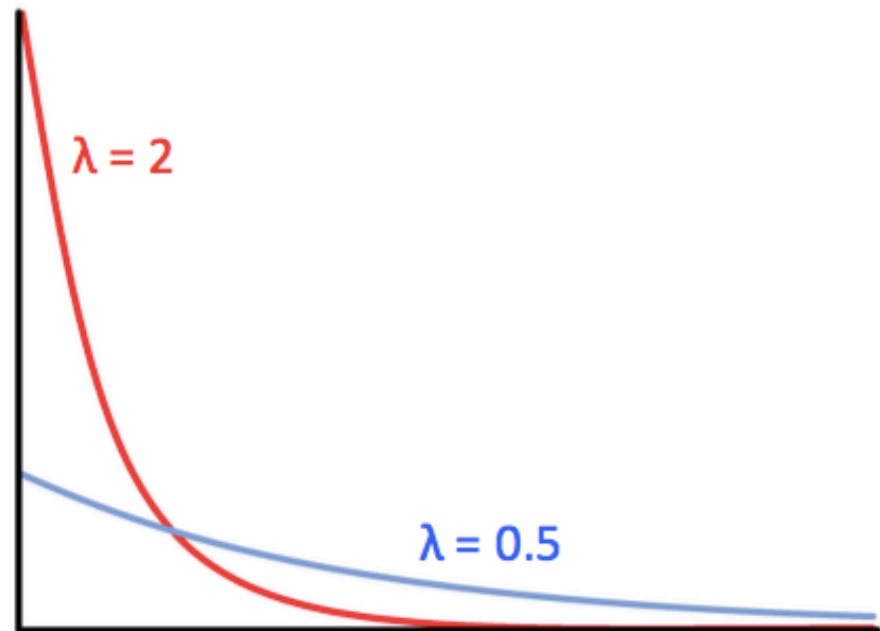→ Used to specify prior distributions of continuous parameters that cannot take negative values

- Beta
- Dirichlet

# Continuous distributions

- Uniform

- Normal

- **Exponential**
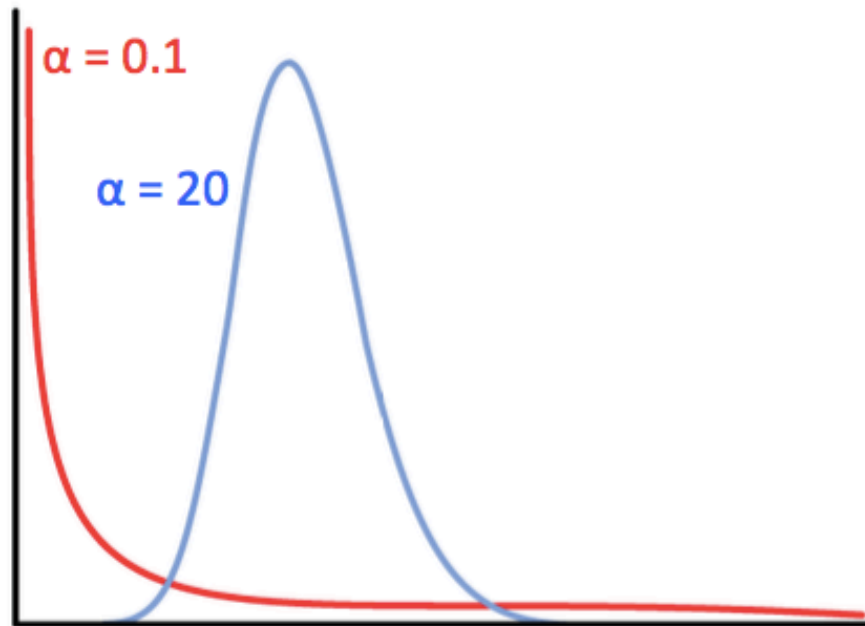
- Lognormal

- Gamma

- Beta

- Dirichlet

Parameters
- $\lambda$ = rate of decay

# Continuous distributions

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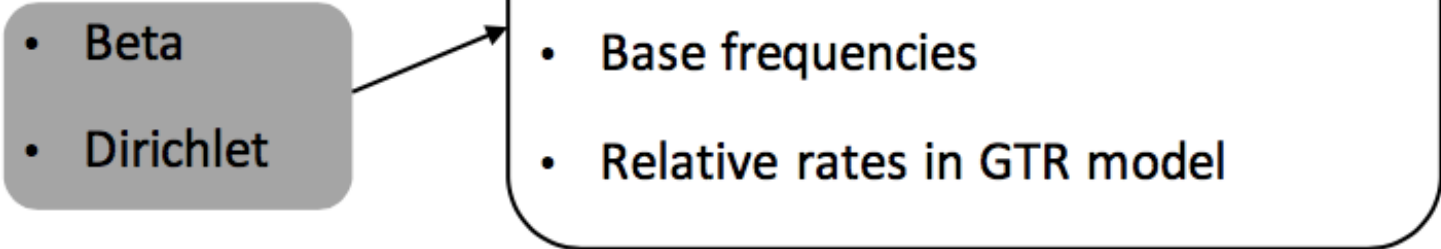- Exponential
- Lognormal
- **Gamma**
- Beta
- Dirichlet

Parameters
- $\alpha$ = shape
- $\beta$ = inverse scale

**Scaled gamma:**
**$\alpha=\beta$**



$\alpha = 0.1$

$\alpha = 20$

# Continuous distributions

- Uniform

- Normal

- Exponential

- Lognormal

- Gamma

- Beta

- Dirichlet

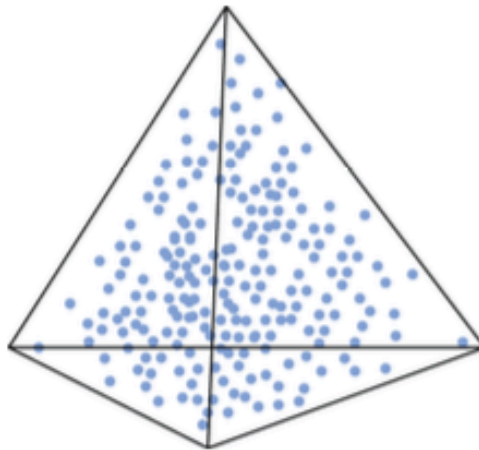Used to specify the prior distributions of simplex parameters

- Base frequencies

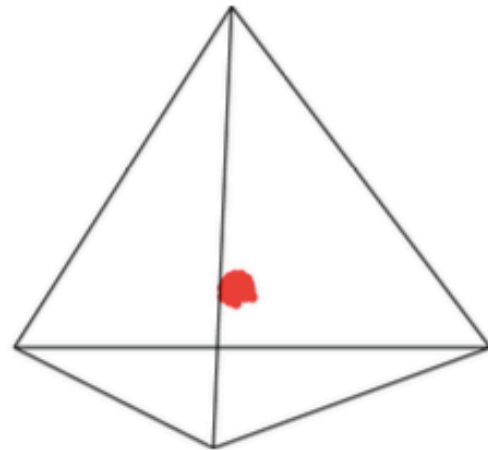- Relative rates in GTR model

# Continuous distributions

- Uniform

- Normal

- Exponential

- Lognormal

- Gamma

- Beta

- **Dirichlet**

Parameters
- $\alpha_1$ , $\alpha_2$ , ... = 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

| | BEAST | MrBayes |
|---|---|---|
| **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 of 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
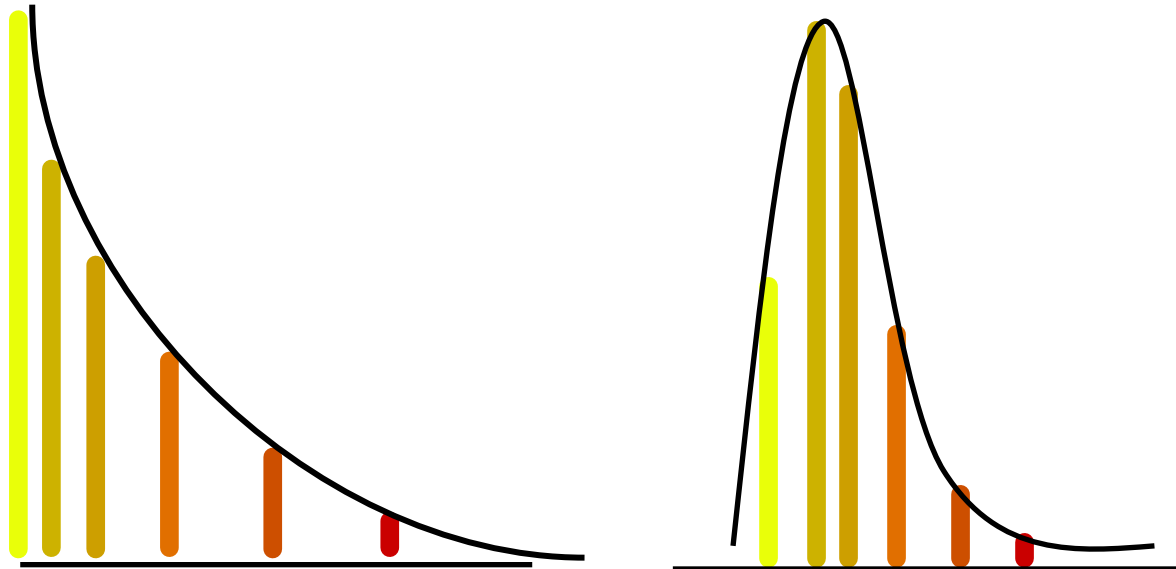
# Autocorrelated relaxed clock



Rate *j*

Rate *i*

# Uncorrelated relaxed clock



Rate *j*

Rate *i*
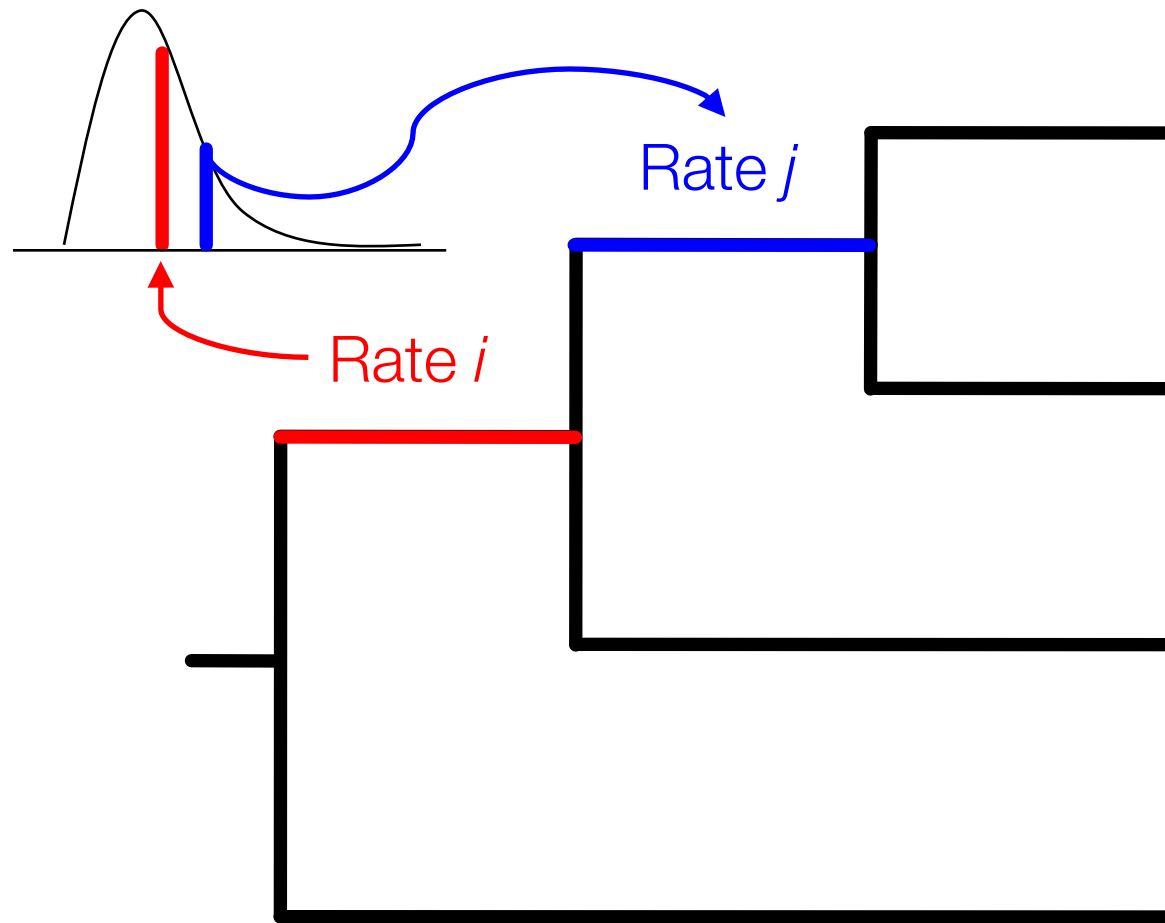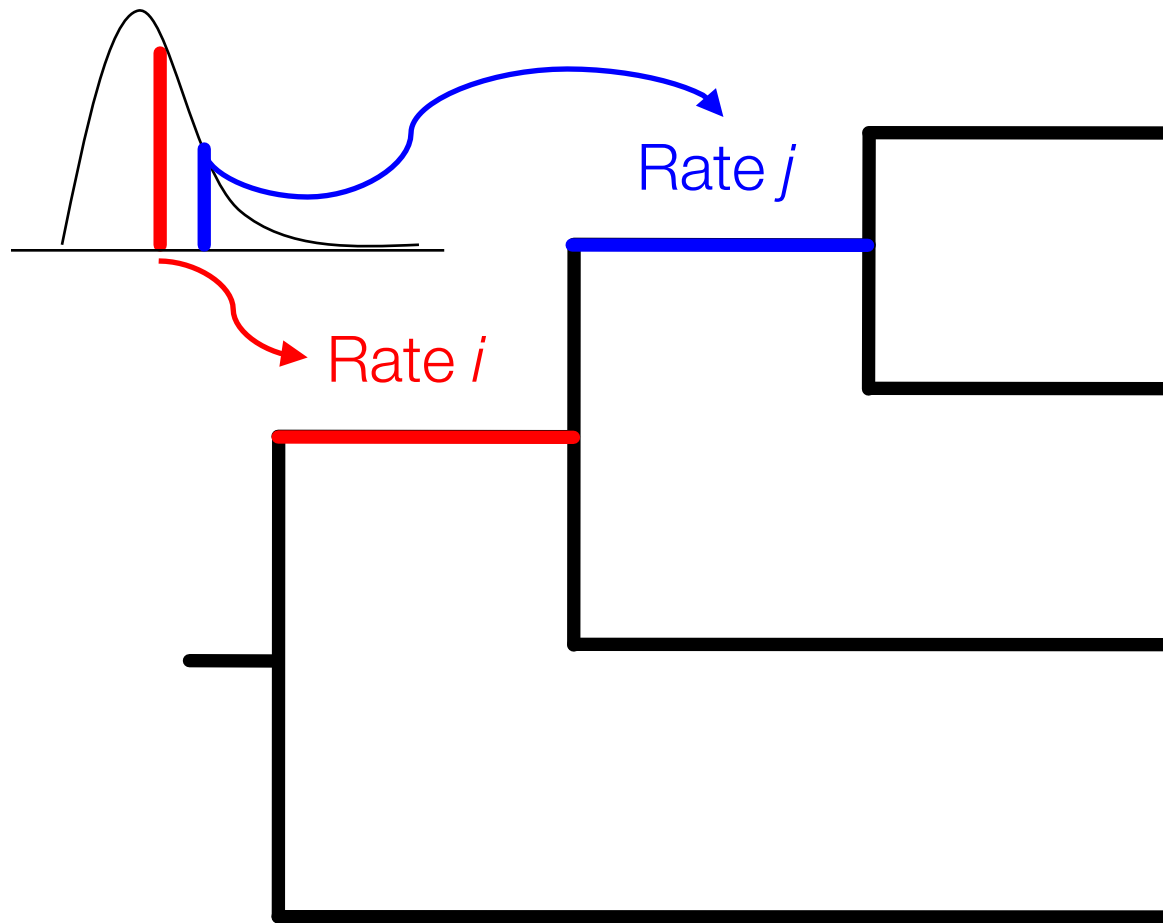
# Uncorrelated relaxed clock

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

# Lognormal uncorrelated relaxed clock

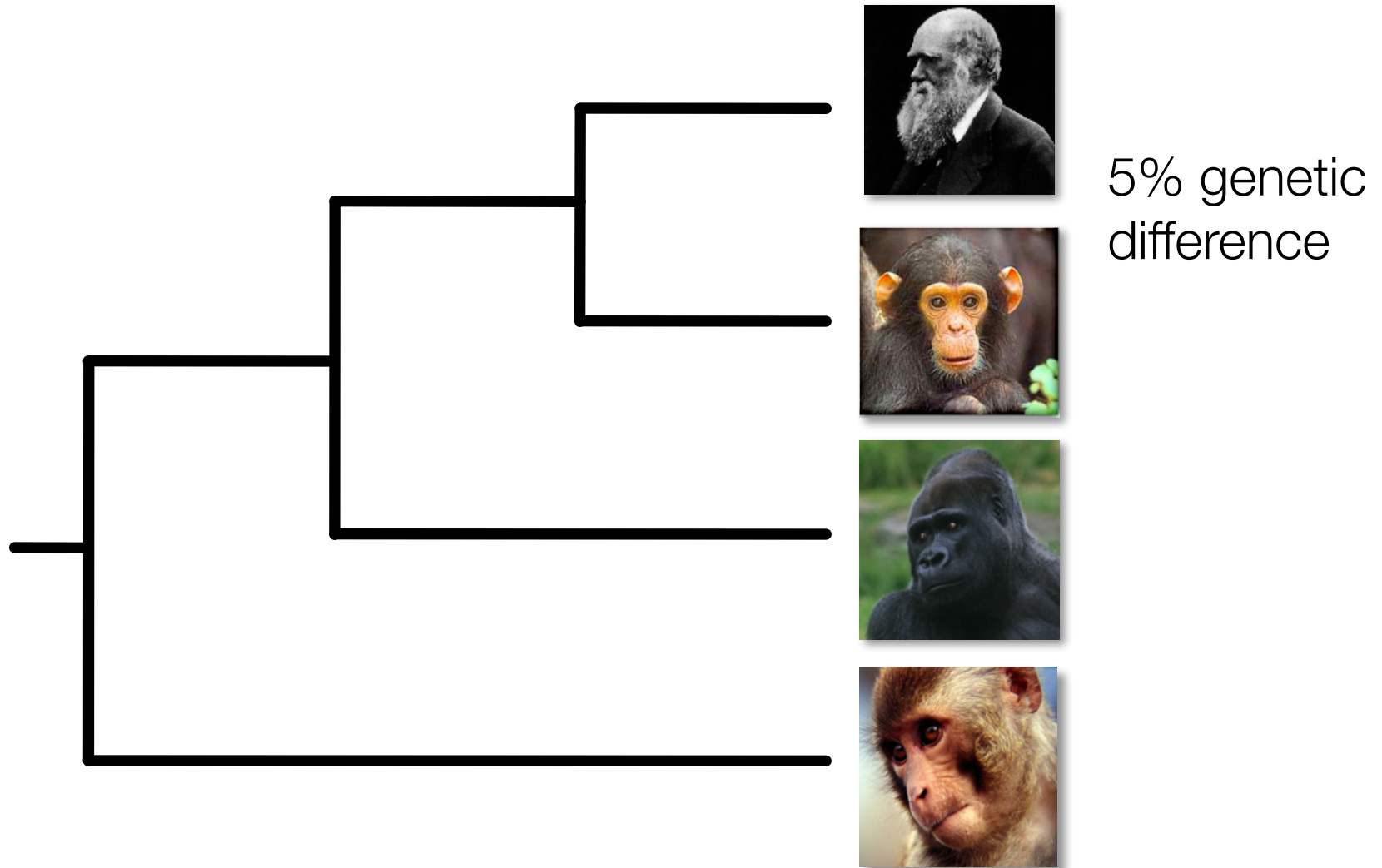- In the uncorrelated lognormal relaxed clock, two statistics can be obtained:

  1. **Coefficient of variation of rates**
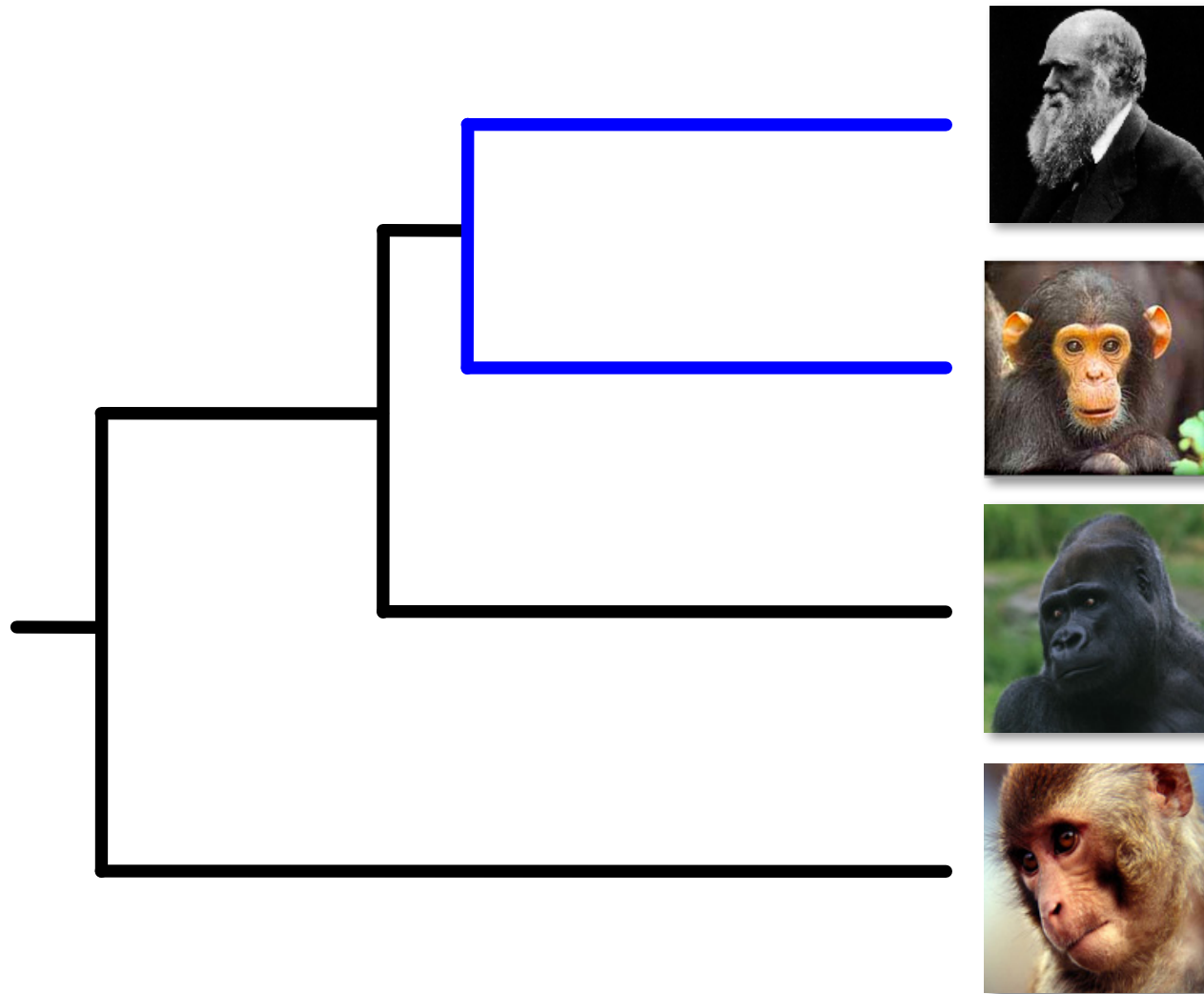     Measures the rate variation among branches
     A value of 0 indicates clocklike evolution
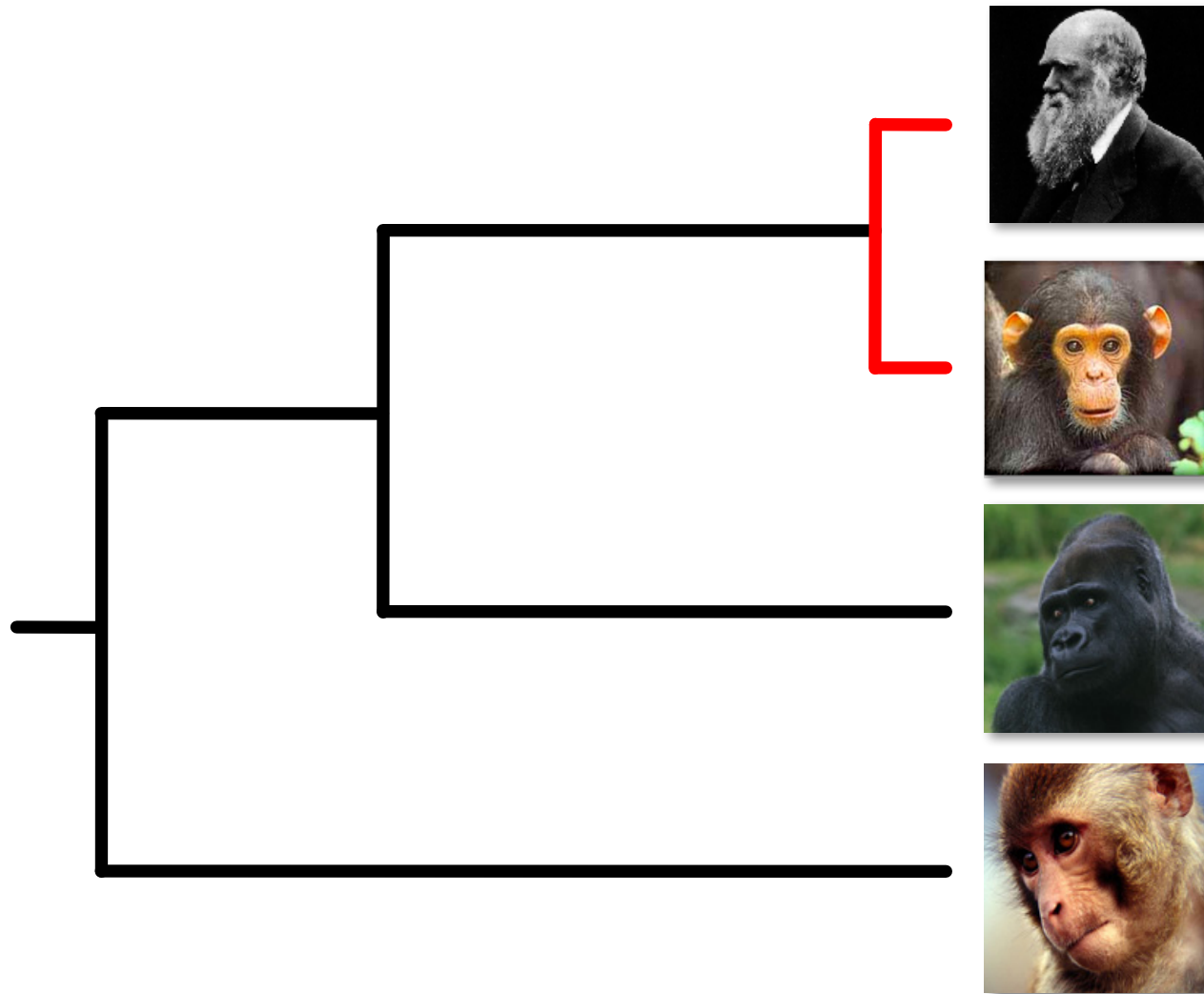
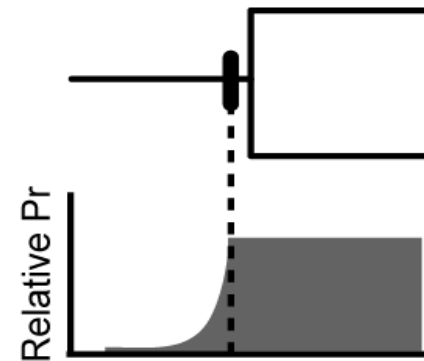  2. **Covariance of rates**
     Measures autocorrelation of rates between adjacent branches

# Calibrating the molecular clock
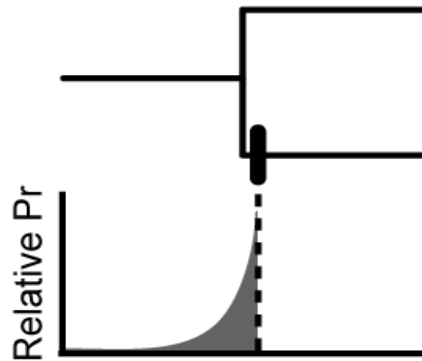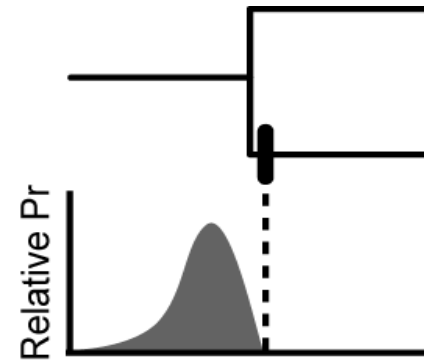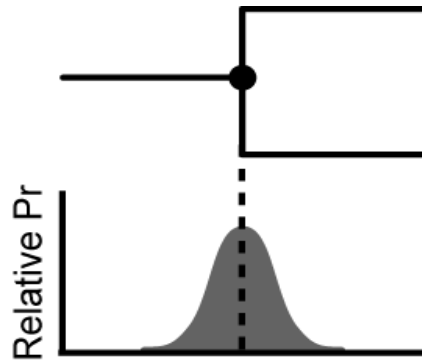


5% genetic difference
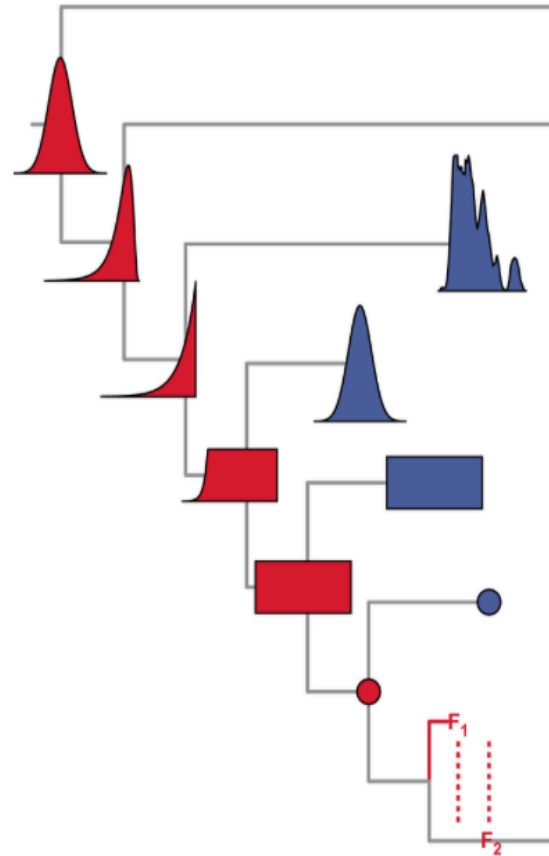
# Calibrating the molecular clock

# 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**