Lecture 2.2

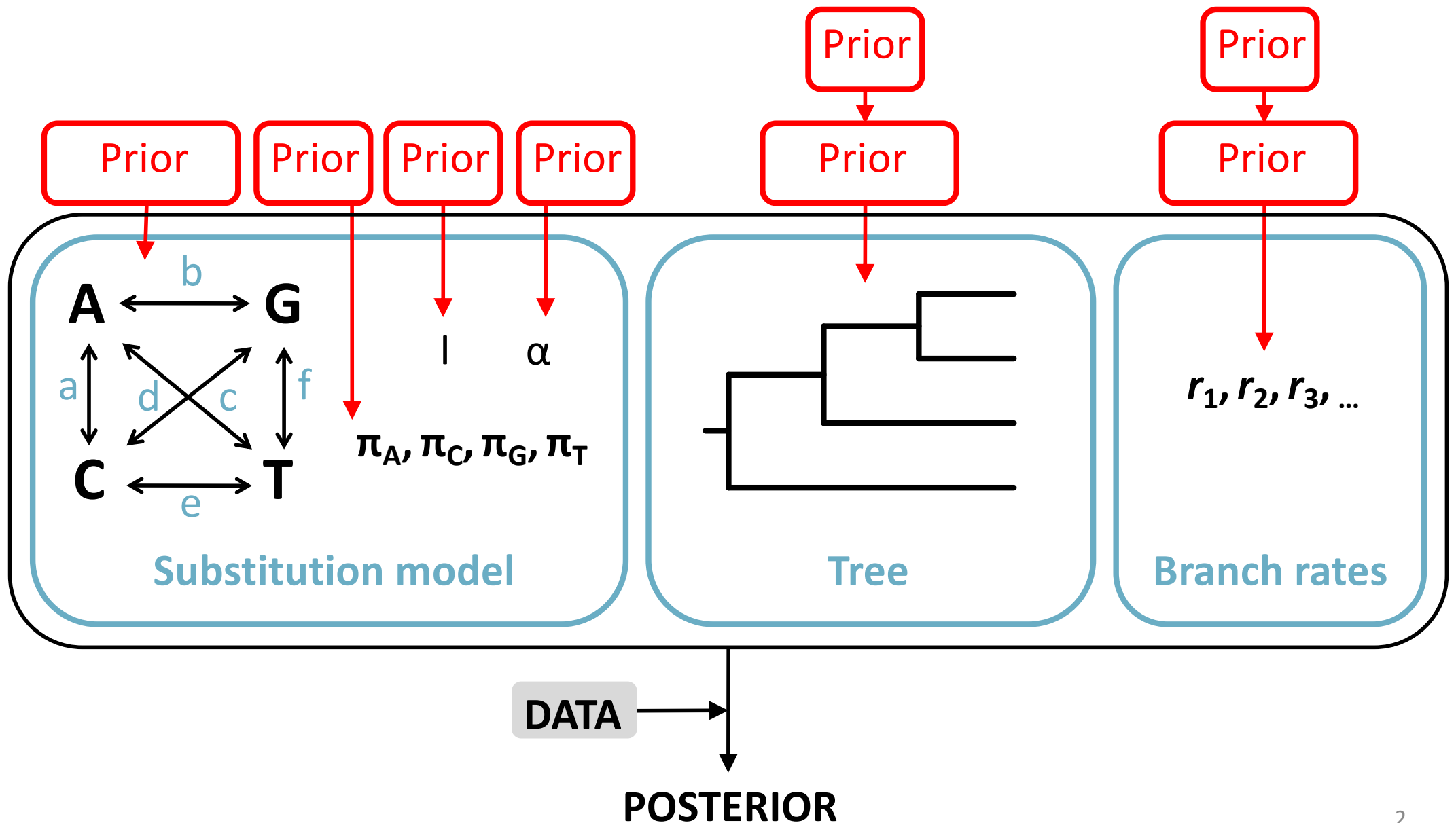# **Models and Priors**

Bayesian hierarchical model

Prior Distributions

Priors

- Reflect our prior expectations (and uncertainty) about values of parameters (without knowledge of the data)

  - Past observations

  - Personal beliefs

  - Use of a biological model

Continuous distributions

- Uniform

- Normal

Used to specify prior distributions of various continuous parameters

- Exponential

- Lognormal

- Gamma

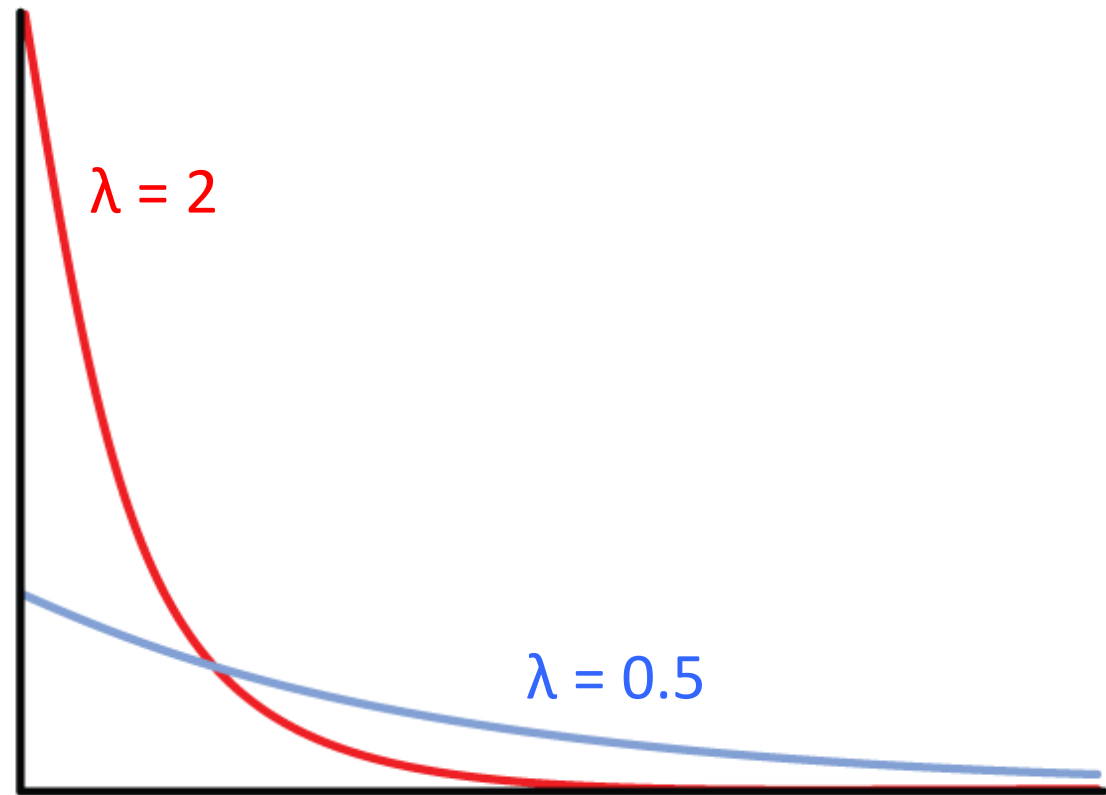Used to specify prior distributions of continuous parameters that cannot take negative values

- Beta

- Dirichlet

Continuous distributions

- Uniform

- Normal

- **Exponential**

- Lognormal

- Gamma

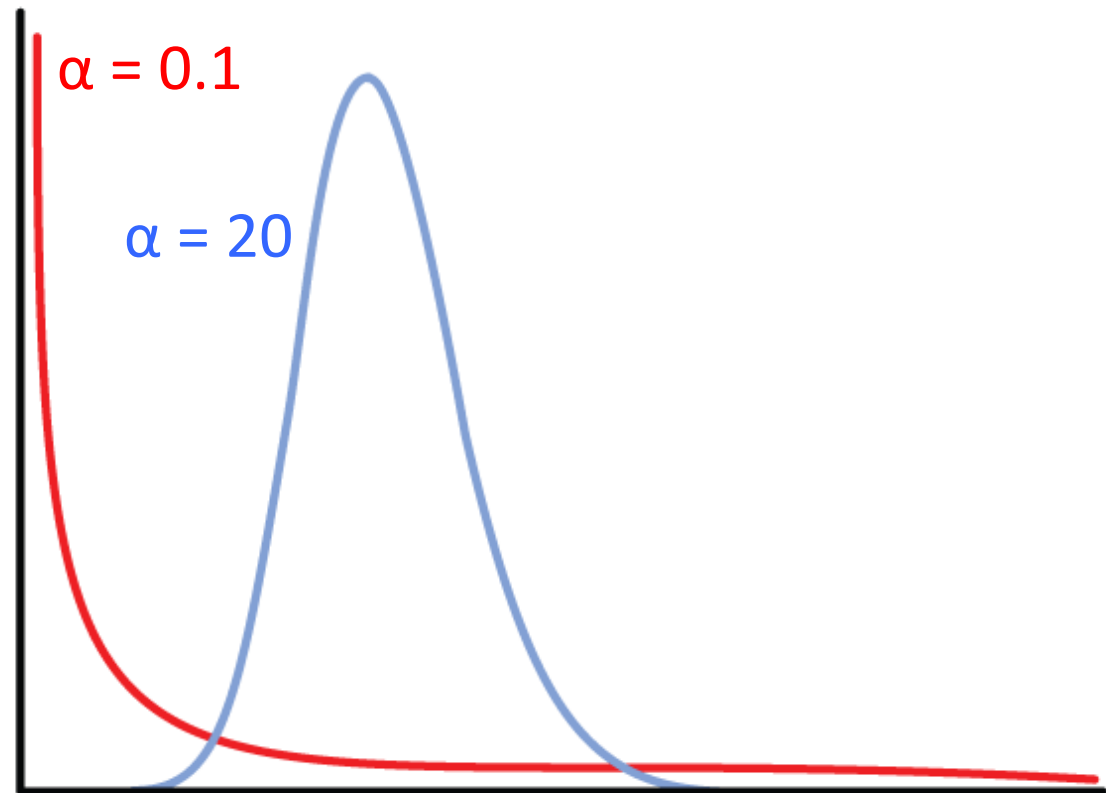- Beta

- Dirichlet

Parameters
- λ = rate of decay

λ = 2

λ = 0.5

Continuous distributions

- Uniform

- Normal

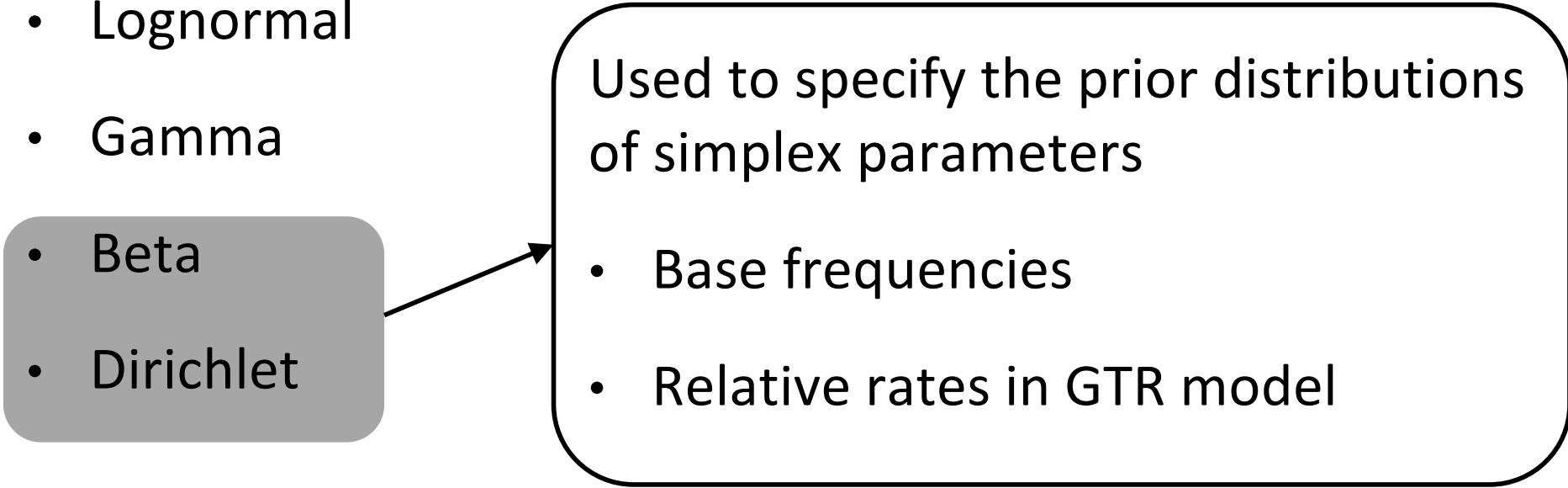- Exponential

- Lognormal

- **Gamma**

- Beta

- Dirichlet

Parameters
- α = shape
- β = inverse scale

Scaled gamma: $\alpha=\beta$

$\alpha = 0.1$

$\alpha = 20$

Continuous distributions

- Uniform

- Normal

- Exponential

- Lognormal

- Gamma

- Beta

- Dirichlet

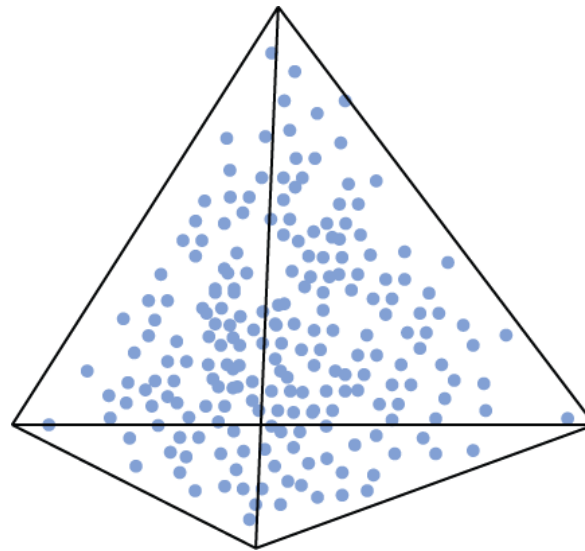Used to specify the prior distributions of simplex parameters

- Base frequencies

- Relative rates in GTR model
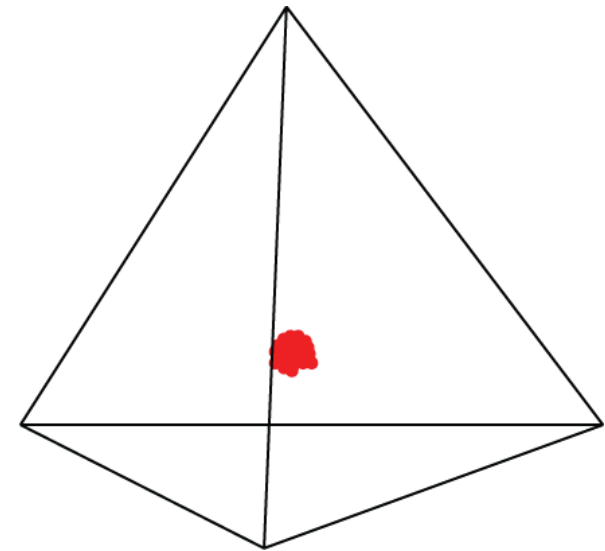
Continuous distributions

- Uniform

- Normal

- Exponential

- Lognormal

- Gamma

- Beta

- **Dirichlet**

Parameters
- α_1 , α_2 , ... = shape parameters

$\alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = 1$ $\alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = 300$

Discrete distributions

- Bernoulli distribution

- Binomial

- Multinomial

- Poisson

Default priors

	BEAST2	*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(1)	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 posterior

Tree Prior

Tree prior

1. Use a **flat prior** (*MrBayes*)

    - All trees have equal probability

    - Also need a prior for branch lengths or node times

2. Use a **biological model** (*BEAST* and *MrBayes*)

    - Among species: speciation model
    - Within species: coalescent model

   } **Priors on rooted trees**

Speciation model

- Tree shape described by a stochastic branching process

- **Yule process**
  - The root lineage splits into two
  - Lineages split at a constant rate
  - Simulates speciation process

- **Birth-death process**
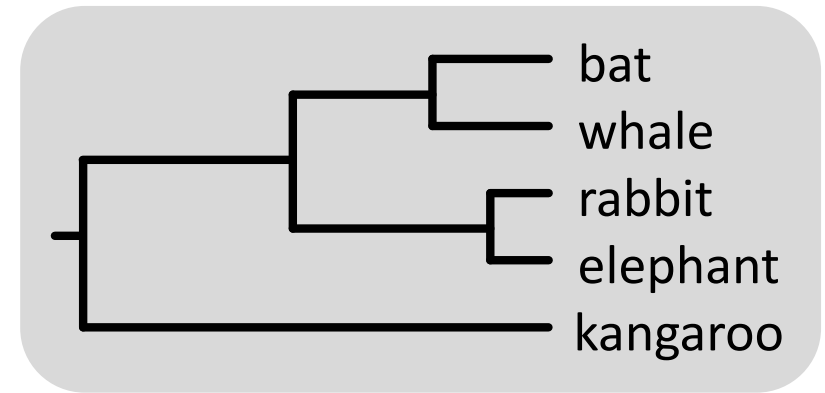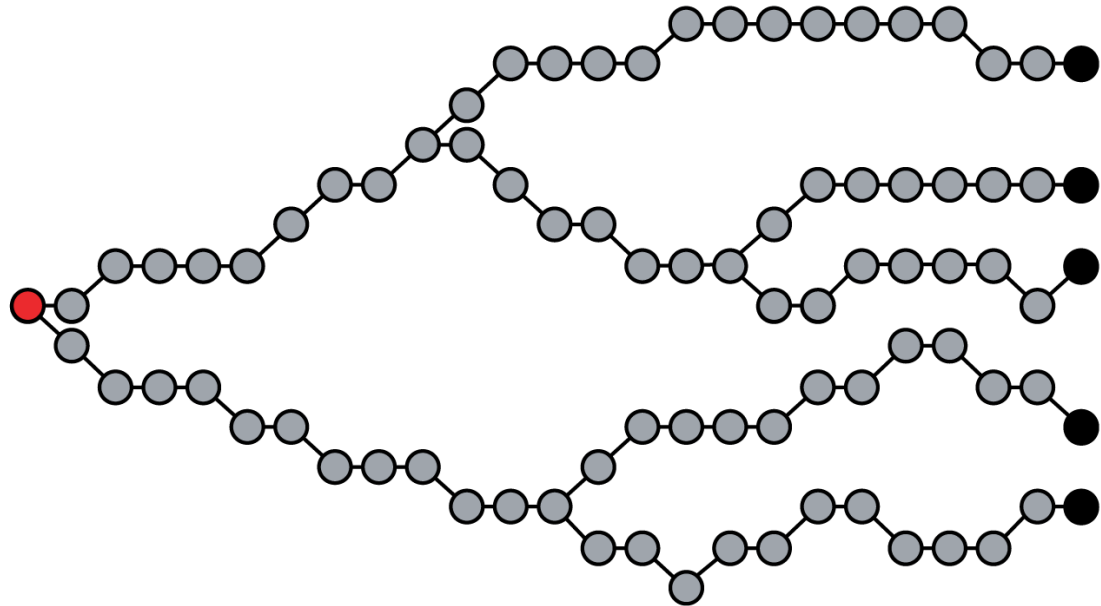 - Allow lineages to go extinct
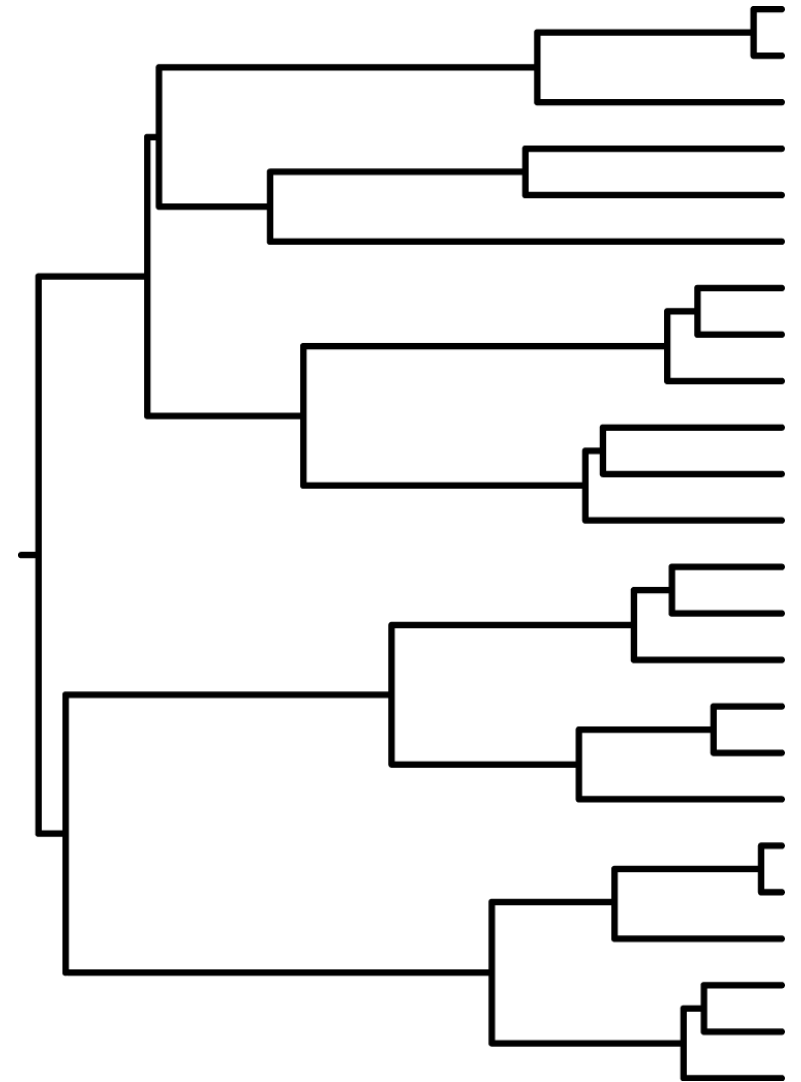
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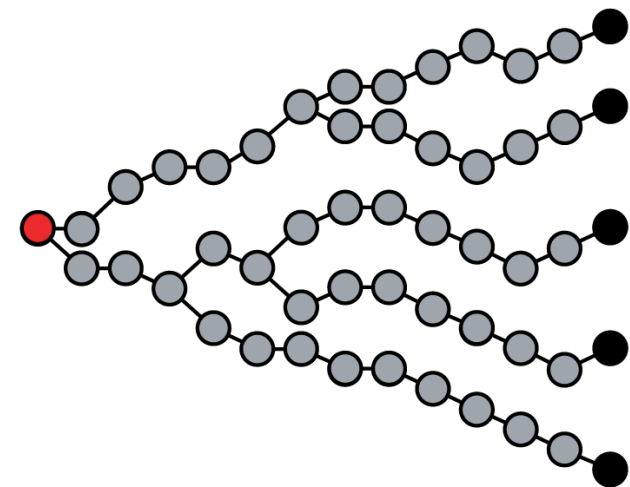 - Allow lineages to go extinct
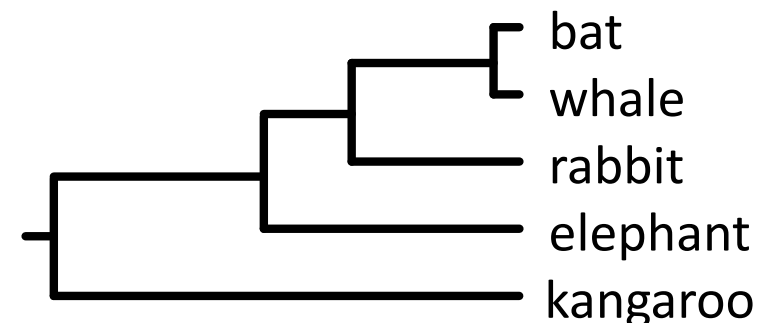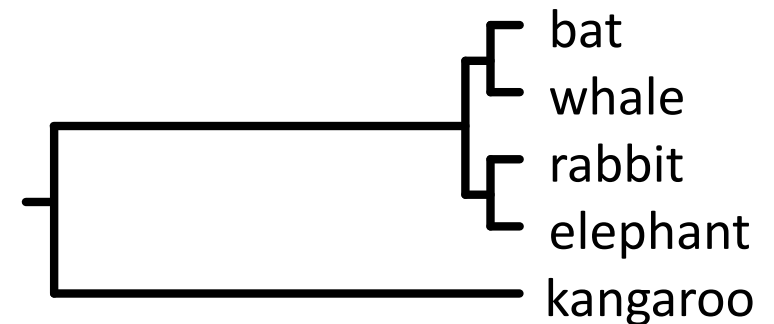
Coalescent model

Constant size

Exponential growth

Choosing a tree prior

- Test whether inferences are robust to the choice of tree prior

- Mixed data sets: multiple sequences from each species

  - Birth-death prior generally works well

- Compare tree priors using Bayesian model selection

Bayesian Model Selection

Bayesian model selection

- Bayesian model selection is usually based on the marginal probability of the data, conditioned on the model:

$$\textbf{Pr(D|M)}$$

- This is a weighted average of the likelihood

- Weights are given by the prior distribution

Marginal likelihood of the model

Bayesian model selection

- Compare marginal likelihoods of competing models

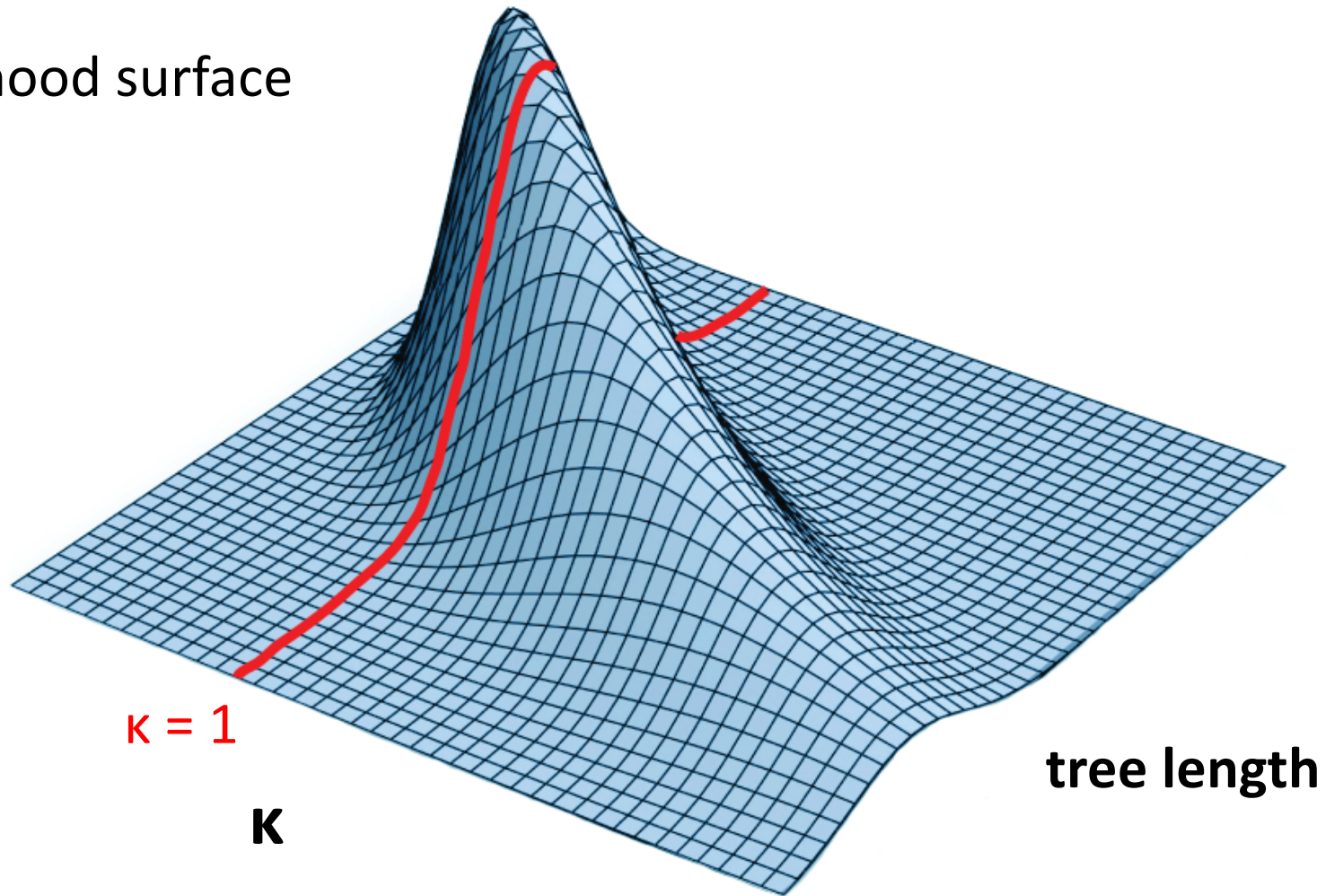- Ratio of marginal likelihoods is the **Bayes factor**

$$\mathbf{BF} = \frac{\mathbf{Pr(D|M_1)}}{\mathbf{Pr(D|M_2)}}$$

$$\mathbf{logBF = logPr(D|M_1) - logPr(D|M_2)}$$

- Models do not need to be nested

- Do not need to correct for number of parameters

Bayesian model selection

Likelihood surface

κ = 1

κ

tree length

Bayesian model selection

- Interpreting the Bayes factor

BF	log*BF*	Evidence against M_2
1 – 3	0 – 1	Not worth mentioning
3 – 20	1 – 3	Positive
20 – 150	3 – 5	Strong
> 150	> 5	Very strong

Kass & Raftery (1995) *J Am Stat Assoc*

Useful references