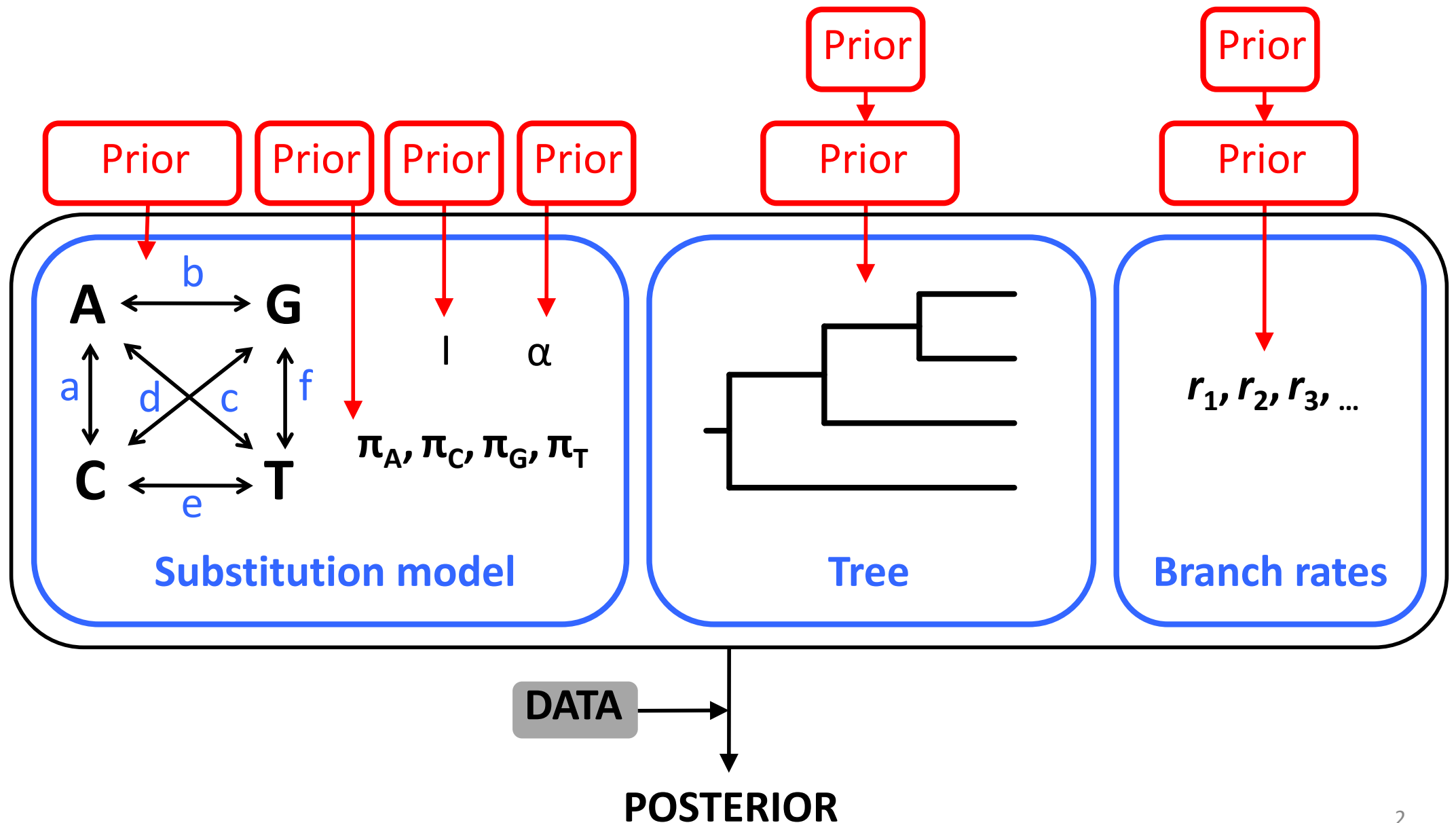Lecture 2.2

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
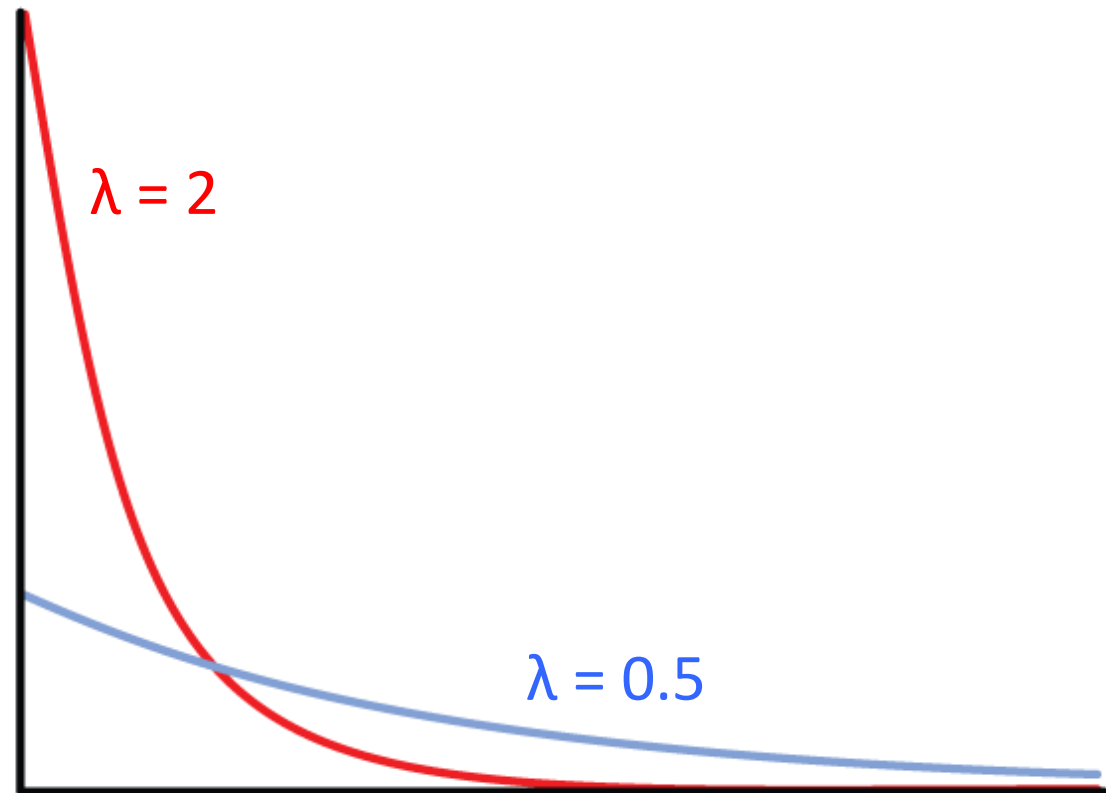
- Beta

- Dirichlet

Continuous distributions

- Uniform

- Normal

- **Exponential**

- Lognormal

- Gamma

- Beta

- Dirichlet

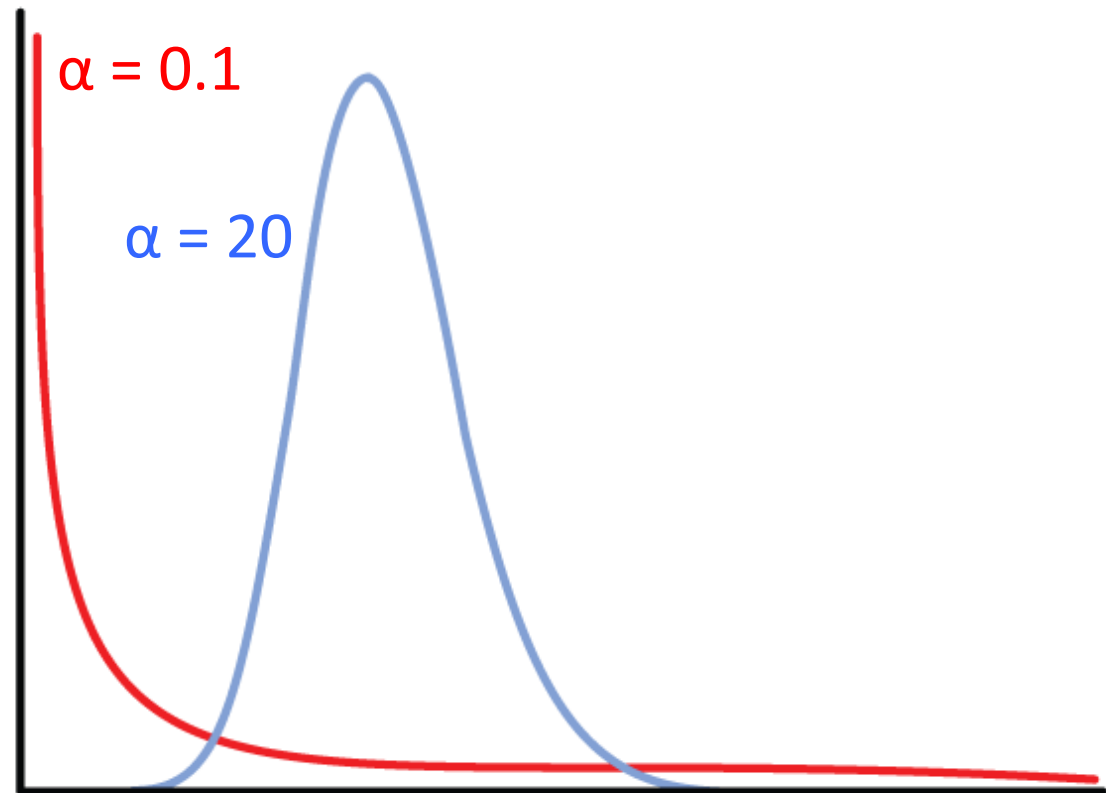Parameters
- λ = rate of decay

λ = 2

λ = 0.5

Continuous distributions

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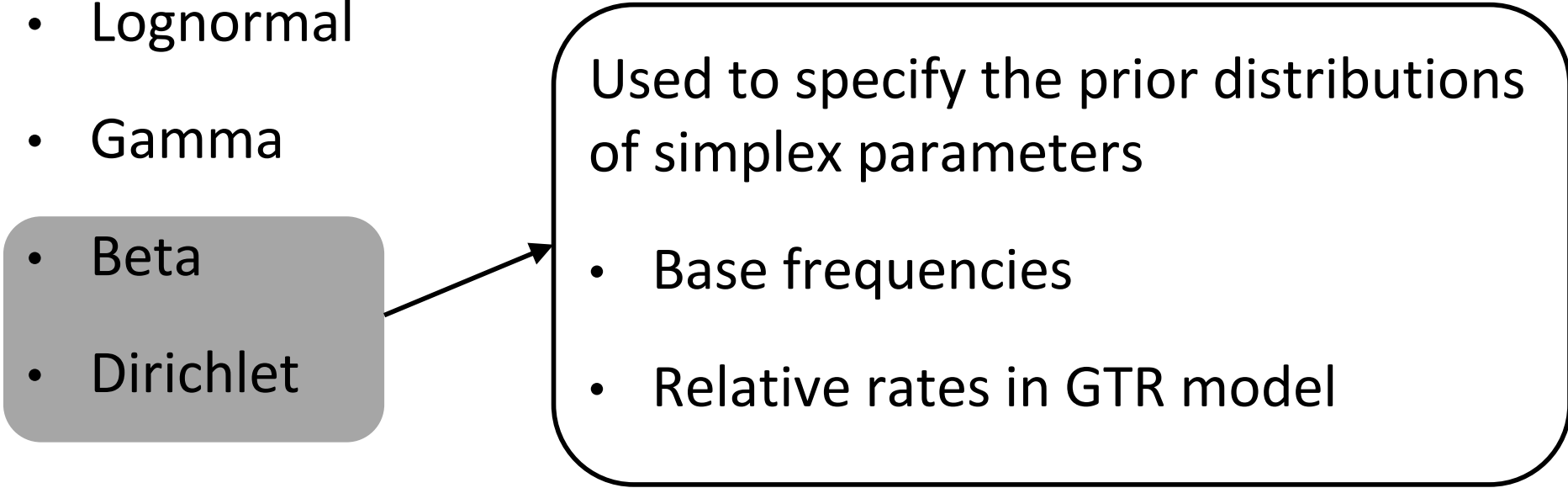- Exponential
- Lognormal
- **Gamma**
- Beta
- Dirichlet

Parameters
- α = shape
- β = inverse scale

**Scaled gamma:
α=β**

α = 0.1

α = 20

Continuous distributions

- Uniform

- Normal

- Exponential

- Lognormal

- Gamma

- Beta

- Dirichlet

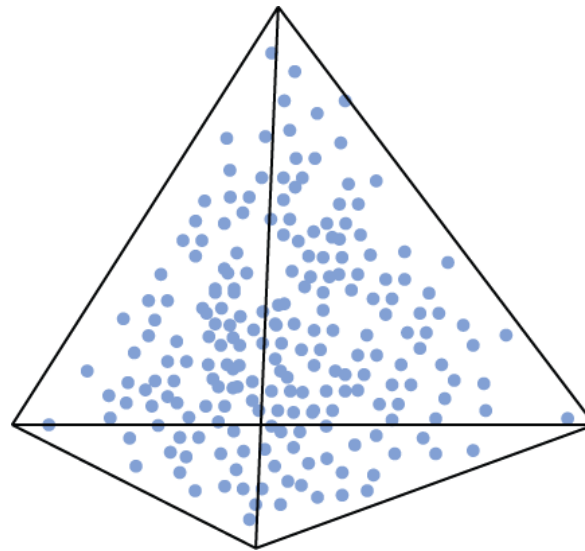Used to specify the prior distributions of simplex parameters

- Base frequencies

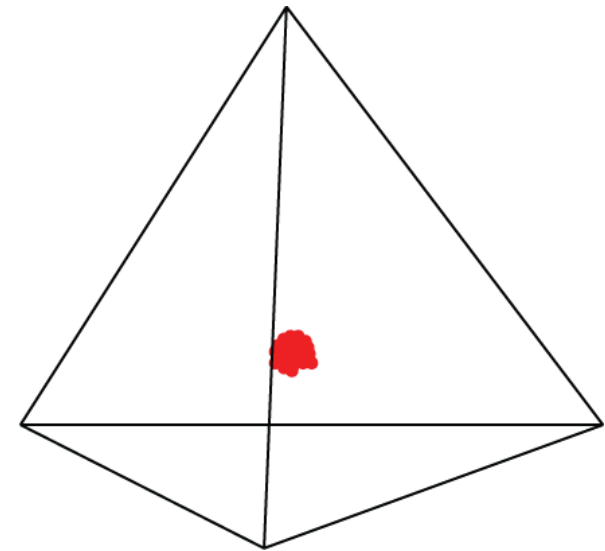- Relative rates in GTR model

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**
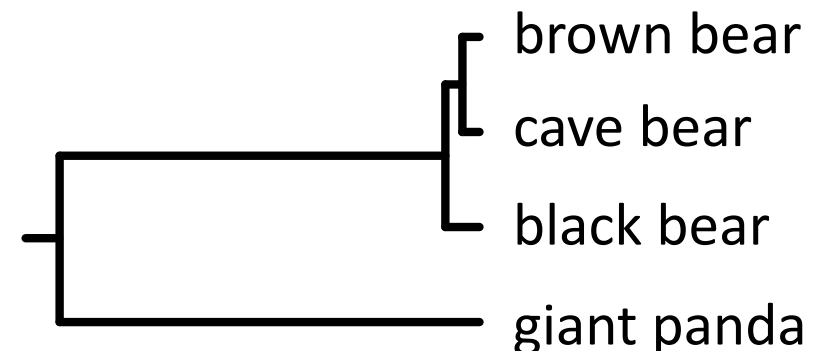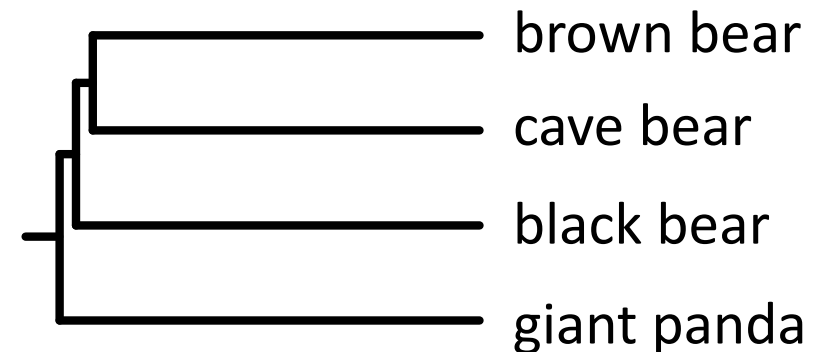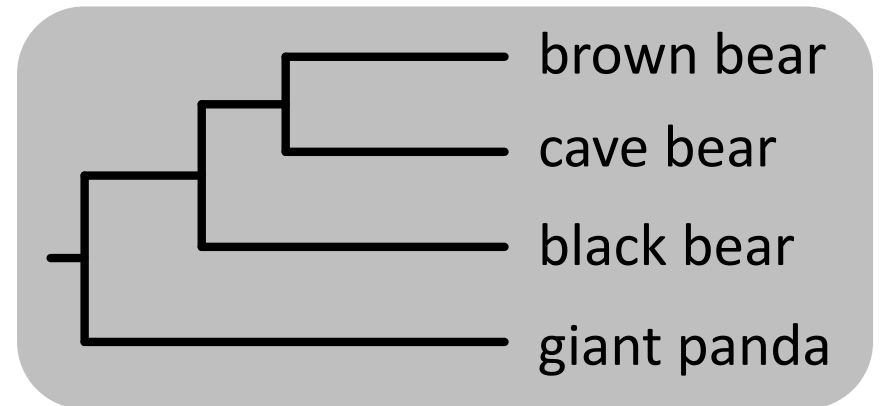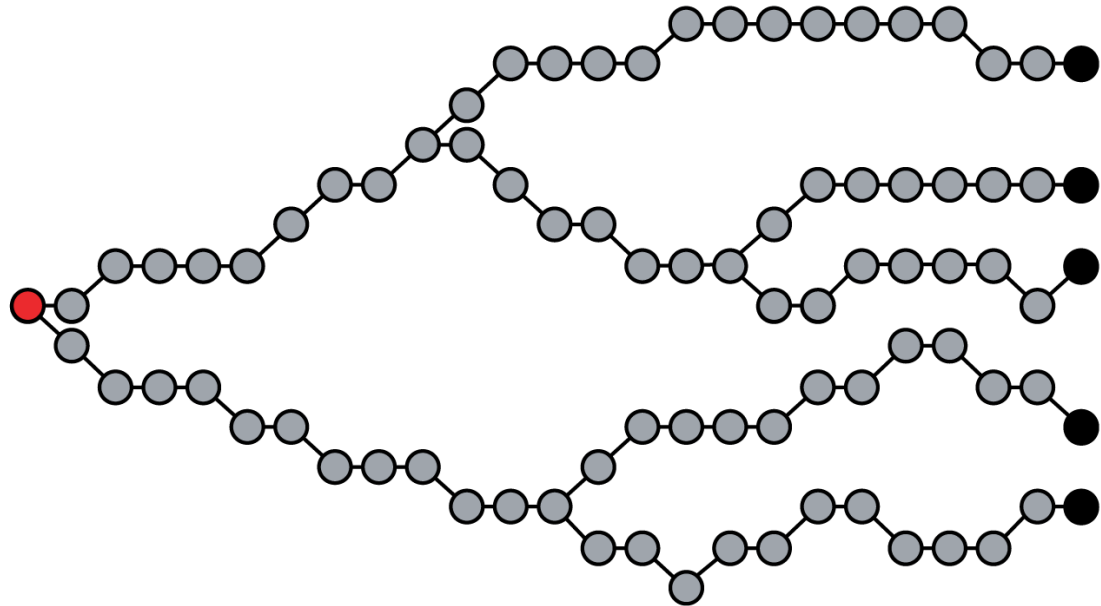
  - Allow lineages to go extinct
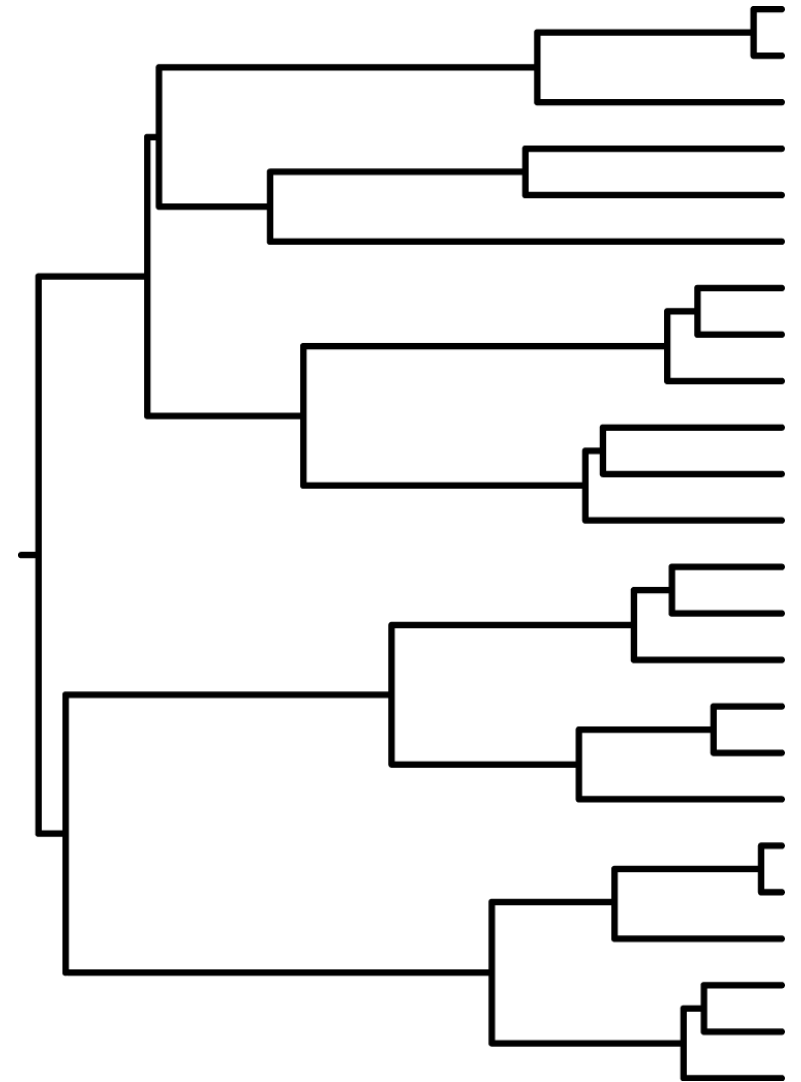
Speciation model

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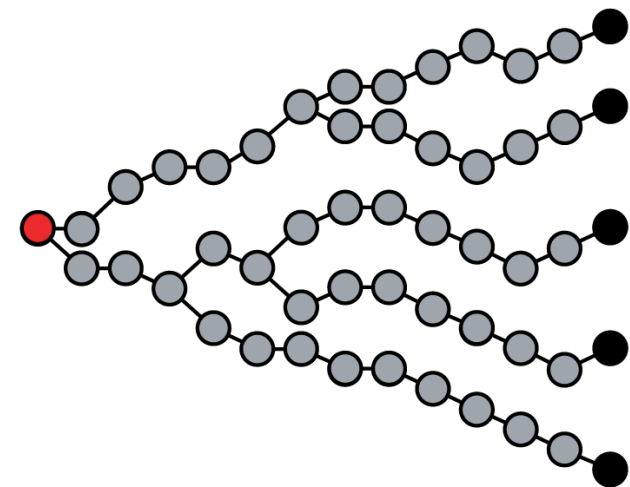
  - Allow lineages to go extinct

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:

$$Pr(D|M)$$

- 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

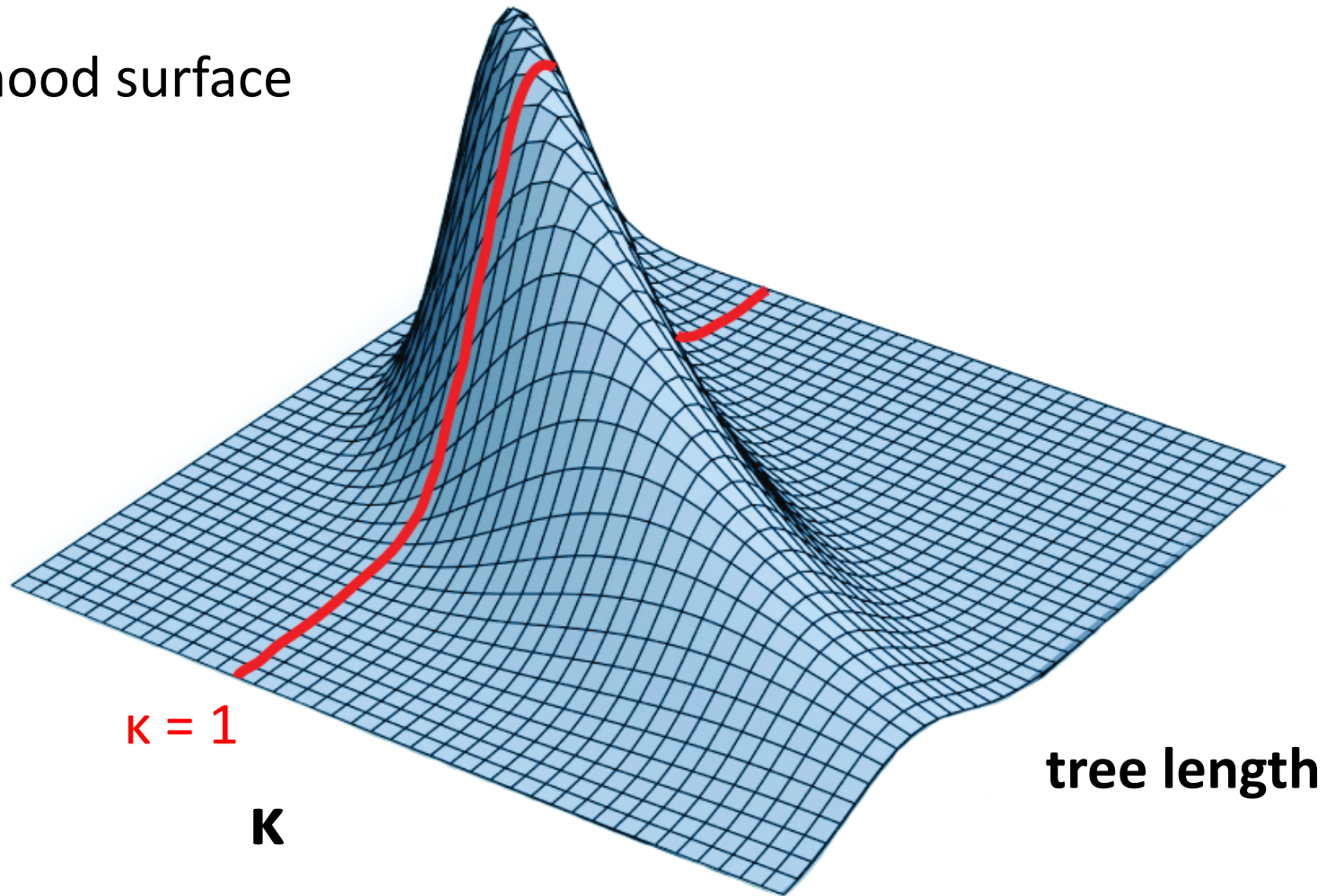- Ratio of marginal likelihoods is the **Bayes factor**

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

$$logBF = logPr(D|M_1) - logPr(D|M_2)$$

- 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

- **The impact of the tree prior on molecular dating of data sets containing a mixture of inter- and intraspecies sampling**
Ritchie, Lo, & Ho (2017) *Syst Biol*, 66: 413–425.