

# Bayesian phylogenetic inference

## **Comparative Genomic Analyses**

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# Bayesian inference

Bayesian inference: way to reason about probabilities.

- ▶ nothing more than a probability analysis
- ▶ a mathematical formalization of a decision process
- ▶ constitutes a different interpretation of probability

Thomas Bayes (1702-1761)



# Bayesian inference

Bayesian approach to probability has some unique aspects.

- ▶ prior beliefs
- ▶ information from the data
- ▶ the idea of updated probability

# Bayesian inference

The Bayes' theorem or Bayes' rule is the fundamental formula of Bayesian inference.

$$p(\theta|D) \propto p(\theta)p(D|\theta)$$

- ▶  $p(\theta)$ : **prior distribution**
- ▶  $p(D|\theta)$ : **likelihood**
- ▶  $p(\theta|D)$ : **posterior distribution**, which specifies the the probability after the prior has been updated with the available data

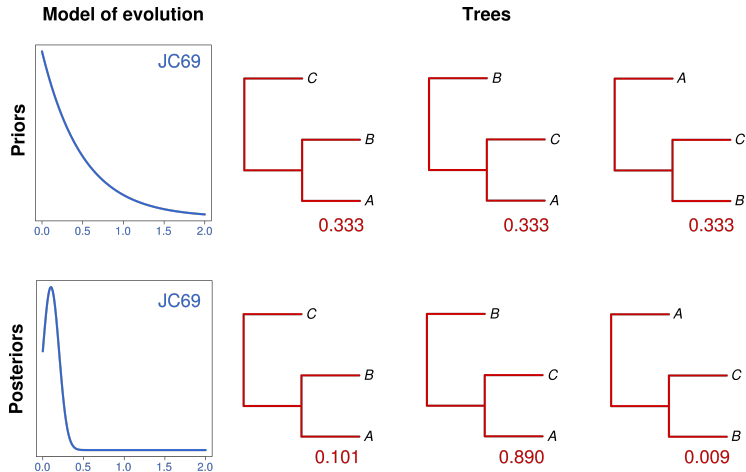
# Bayesian phylogenetic inference

The Bayes' theorem translates quite straightforwardly to tree inference problems.

$$p(\tau, \theta | D) \propto p(\tau, \theta) p(D | \tau, \theta)$$

- ▶  $D$  is the molecular sequence alignment
- ▶  $\tau$  and  $\theta$  represent the tree and the model of evolution parameters

# Bayesian phylogenetic inference



# Bayesian phylogenetic inference

Estimating the posterior distribution in a phylogenetic context can be difficult.

- ▶ impossible to derive the posterior probability distribution analytically
- ▶ concentrated in a small part of a vast parameter space

# Markov chain Monte Carlo

Estimate the posterior distribution using Markov chain Monte Carlo (MCMC) sampling

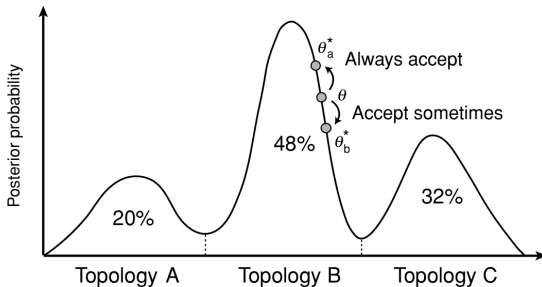
- ▶ set up a Markov chain that converges onto the posterior probability distribution
- ▶ MCMC represents random samples from the posterior



# Markov chain Monte Carlo

Metropolis-Hastings algorithm is an MCMC method

- ▶ make small random changes on the parameter values
- ▶ accept or reject those changes according to the appropriate probabilities



# Markov chain Monte Carlo

An MCMC run is a random sample of the posterior distribution.

- ▶ the amount of time it spends sampling a particular region is proportional to the posterior probability of that region given that it converged to the target distribution
- ▶ convergence needs to be monitored

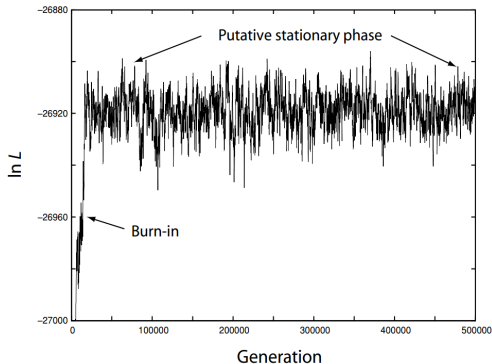
# Markov chain Monte Carlo

## Burn-in:

- ▶ early phase of the run
- ▶ heavily influenced by the starting points
- ▶ likelihood increases very rapidly

## Stationary phase:

- ▶ the chain approaches its stationary distribution
- ▶ the likelihood values reach a plateau



# Summarizing the posterior distribution

The model parameters and the tree are summarized differently:

- ▶ model parameters are usually continuous and can be summarized as any usual statistical quantity: means, median, the credibility interval
- ▶ trees are more difficult to summarize
- ▶ **posterior clade probabilities**: the sum of the posterior probabilities of all trees that contain that clade

# Summarizing the posterior distribution

## Exercise

Bayesian phylogenetic inference in a sequence alignment with five species returned the posterior probabilities (P.p.) of 3 topologies.

| Topology                              | P.p. |
|---------------------------------------|------|
| ((Human,Dog),(Chicken,Lizard)),Frog   | 0.76 |
| ((((Human,Dog),Chicken),Lizard),Frog) | 0.17 |
| ((Human,Dog),Chicken),(Lizard,Frog))  | 0.07 |

What is the posterior probability of the following clades: (Chicken,Frog), (Chicken lizard), ((Human,Dog),Chicken) and (Human,Dog)?

# Bayesian *versus* maximum likelihood trees

## Maximum-Likelihood trees

- ▶  $p(D|\tau, \theta)$
- ▶ Maximum likelihood tree
- ▶ ignores pre-existing information
- ▶ bootstrapping
- ▶ resample characters

## Bayesian trees

- ▶  $p(\tau, \theta|D)$
- ▶ Maximum a-posteriori tree
- ▶ considers pre-existing information
- ▶ MCMC
- ▶ resample parameters

# Literature

**The Phylogenetic Handbook** by Lemey, Salemi and Vandamme (2009)  
Cambridge University Press

- ▶ Chapter 7: sections 7.1, 7.2 and 7.3, 7.4, 7.6, 7.7 and 7.9