Bayesian Phylogenetics

Mark Holder (with **big** thanks to Paul Lewis)

Outline

- Intro
 - What is Bayesian Analysis?
 - Why be a Bayesian?
- What is required to do a Bayesian Analysis? (Priors)
- How can the required calculations be done? (MCMC)
- Prospects and Warnings

Simple Example:

Vesicouretural Reflux (VUR) - valves between the ureters and bladder do not shut fully.

- leads to urinary tract infections
- if not corrected, can cause serious kidney damage
- effective diagnostic tests are available, but they are expensive and invasive

- $\approx 1\%$ of children will have VUR
- $\approx 80\%$ of children with VUR will see a doctor about an infection
- $\approx 2\%$ of all children will see doctor about an infection

Should a child with 1 infection be screened for VUR?

1% of the population has VUR Pr(V) = 0.01

 $\frac{Q}{X}$ = 0.1% of the population

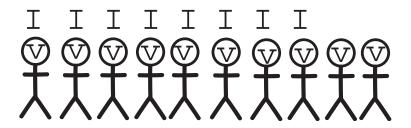
80% of kids with VUR get an infection Pr(I|V) = 0.8

Pr(I | V) is a *conditional* probability

So, 0.8% of the population has VUR and will get an infection

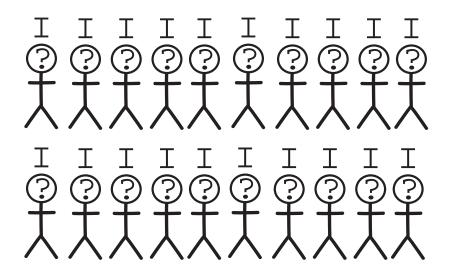
$$Pr(V)Pr(I|V) = 0.01 \times 0.8 = 0.008$$

 $Pr(I,V) = 0.008$

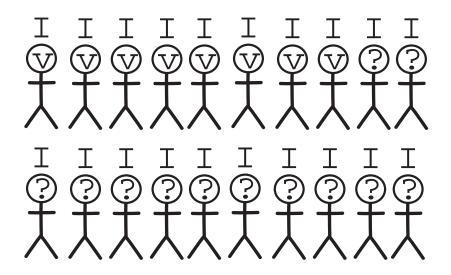


Pr(I,V) is a **joint** probability

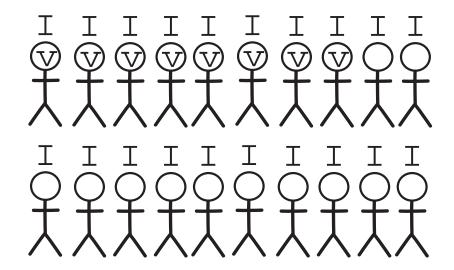
2% of the population gets an infection Pr(I) = 0.02



We just calculted that 0.8% of kids have VUR and get an infection



The other 0.12% must not have VUR



So, 40% of kids with infections have VUR Pr(V|I) = 0.4

$$Pr(V|I) = \frac{Pr(V)Pr(I|V)}{Pr(I)}$$

$$Pr(V|I) = \frac{0.01 \times 0.8}{0.02}$$
$$= 0.40$$

Pr(I) is higher for females.

$$Pr(I|\mathbf{Q}) = 0.03$$
 $Pr(I|\mathbf{Q}) = 0.01$

$$Pr(V|I, \mathbf{Q}) = \frac{0.01 \times 0.8}{0.03}$$
 $Pr(V|I, \mathbf{C}) = \frac{0.01 \times 0.8}{0.01}$

$$Pr(V|I, \mathbf{Q}) = 0.267$$
 $Pr(V|I, \mathbf{Q}) = 0.8$

$$Pr(V|I, \mathbf{C}) = \frac{0.01 \times 0.8}{0.01}$$

$$Pr(V|I, \mathbf{C}) = 0.8$$

Bayes' Rule

$$Pr(A|B) = \frac{Pr(A)Pr(B|A)}{Pr(B)}$$

$$Pr(\text{Hypothesis}|\text{Data}) = \frac{Pr(\text{Hypothesis})Pr(\text{Data}|\text{Hypothesis})}{Pr(\text{Data})}$$

$$Pr(\text{Tree}|\text{Data}) = \frac{Pr(\text{Tree})Pr(\text{Data}|\text{Tree})}{\mathbf{Pr}(\mathbf{Data})}$$

We can ignore Pr(Data)

(2nd half of this lecture)

$$Pr(\text{Tree}|\text{Data}) \propto \mathbf{Pr}(\mathbf{Tree})Pr(\text{Data}|\text{Tree})$$

Pr(Tree) is the *prior* probability of the tree.

$$Pr(\text{Tree}|\text{Data}) \propto Pr(\text{Tree}) \mathbf{Pr}(\mathbf{Data}|\mathbf{Tree})$$

Pr(Tree) is the *prior* probability of the tree.

Pr(**Data**|**Tree**) is the likelihood of the tree.

 $Pr(\text{Tree}|\text{Data}) \propto Pr(\text{Tree})L(\text{Tree})$

$\mathbf{Pr}(\mathbf{Tree}|\mathbf{Data}) \propto Pr(\mathbf{Tree})L(\mathbf{Tree})$

Pr(Tree) is the *prior* probability of the tree.

L(Tree) is the likelihood of the tree.

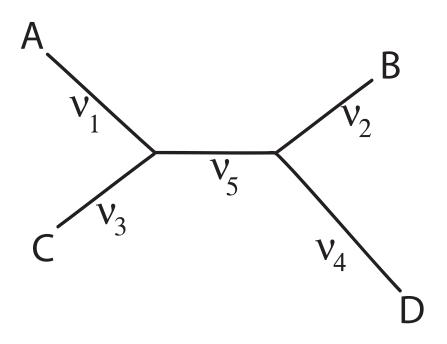
 $\mathbf{Pr}(\mathbf{Tree}|\mathbf{Data})$ is the *posterior* probability of the tree.

The posterior probability is a great way to evaluate trees:

- Ranks trees
- Intuitive measure of confidence
- Is the ideal "weight" for a tree in secondary analyses
- Closely tied to the likelihood

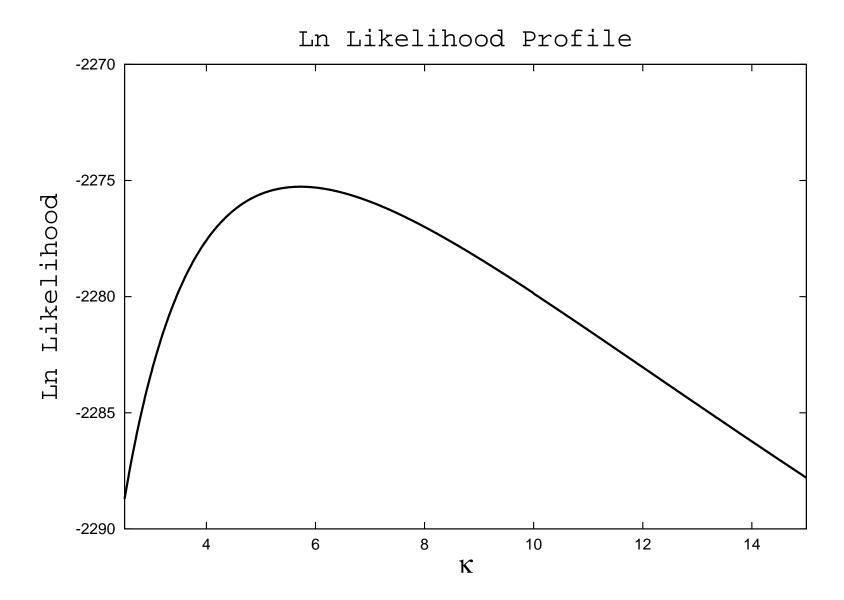
Our models don't give us L(Tree)

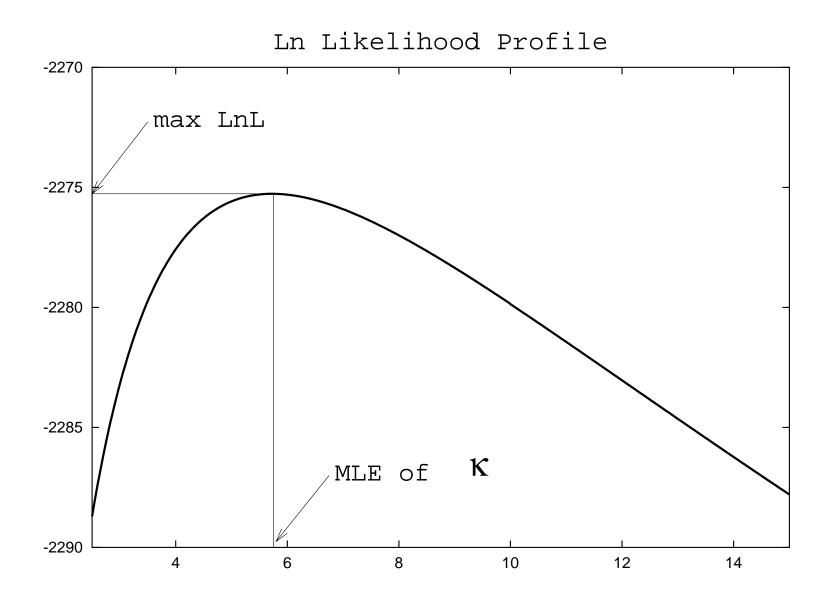
They give us things like $L(\text{Tree}, \kappa, \alpha, \nu_1, \nu_2, \nu_3, \nu_4, \nu_5)$



"Nuisance Parameters"

Aspects of the evolutionary model that we don't care about, but are in the likelihood equation.





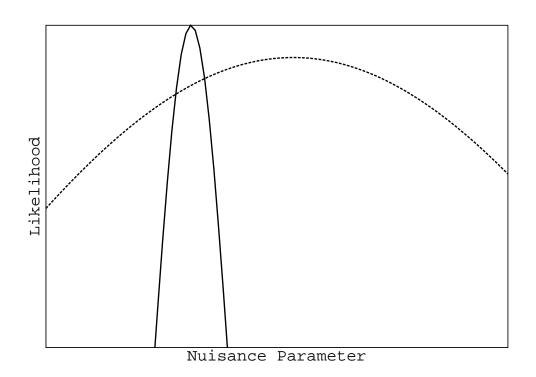
Marginalizing over (integrating out) nuisance parameters

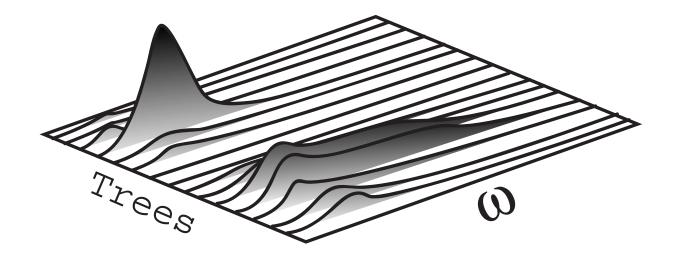
$$L(\text{Tree}) = \int L(\text{Tree}, \kappa) Pr(\kappa) d\kappa$$

- Removes the nuisance parameter
- Takes the entire likelihood function into account

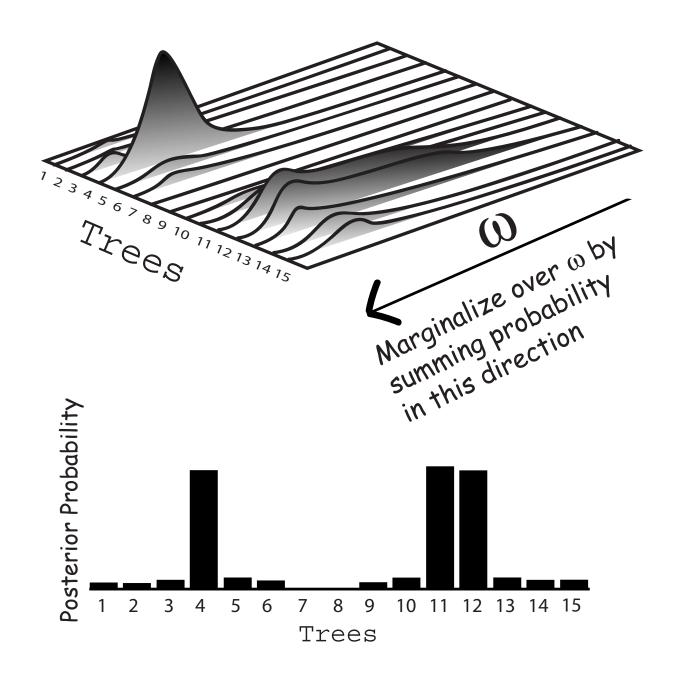
- Avoids estimation errors
- Requires a prior for the parameter

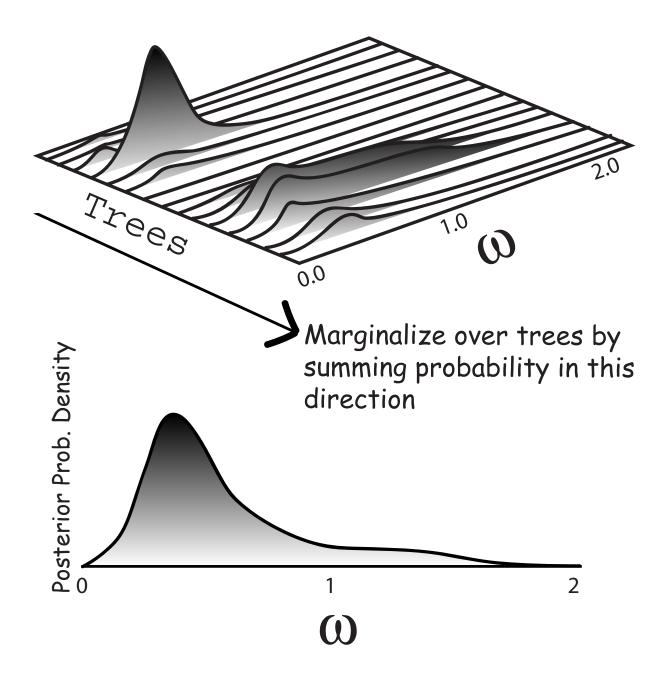
When there is substantial uncertainty in a parameter's value, marginalizing can give qualitatively different answers than using the MLE.





Joint posterior probability density for trees and $\boldsymbol{\omega}$





The Bayesian Perspective

Pros	Cons	
Posterior probability	Is it robust?	
is the ideal measure		
of support		
Focus of inference is		
flexible		
Marginalizes over	Requires a prior	
nuisance parameters		

Priors

- Probability distributions
- Specified *before* analyzing the data
- Needed for
 - Hypotheses (trees)
 - Parameters

Probability Distributions

Reflect the action of random forces

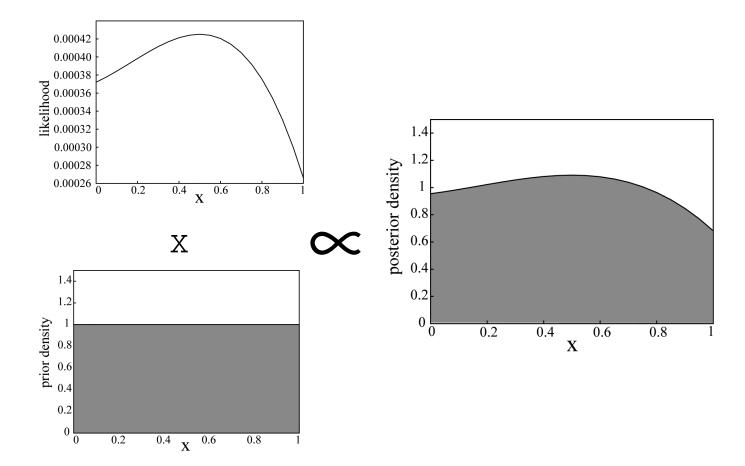
Probability Distributions

Reflect the action of random forces

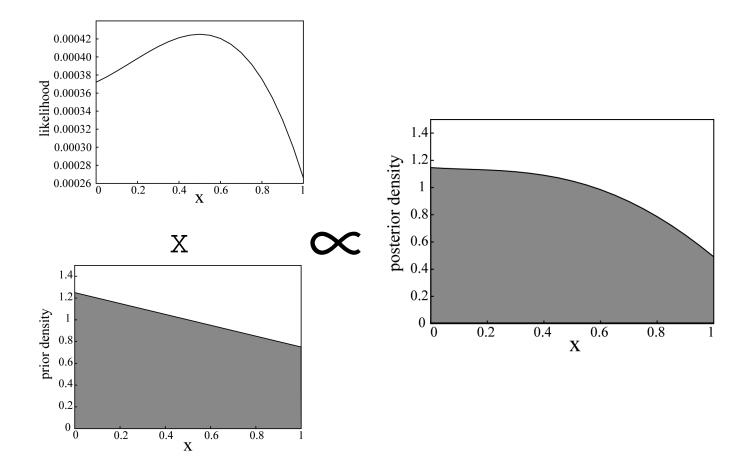
OR

(if you're a Bayesian)

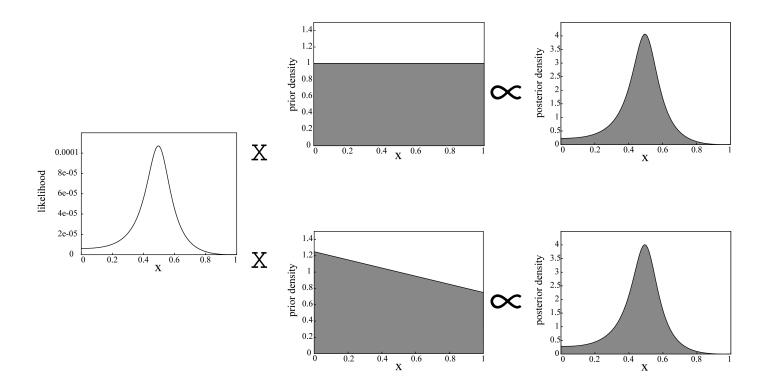
Reflect your uncertainty



slide courtesy of Derrick Zwickl

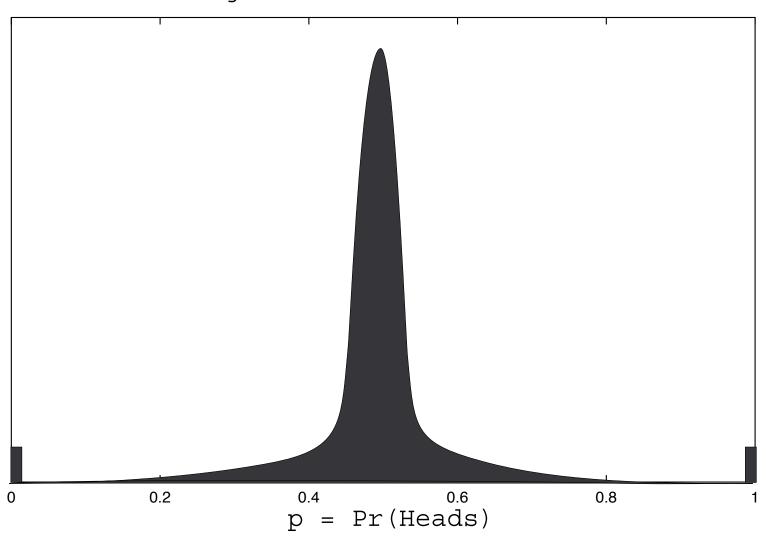


slide courtesy of Derrick Zwickl

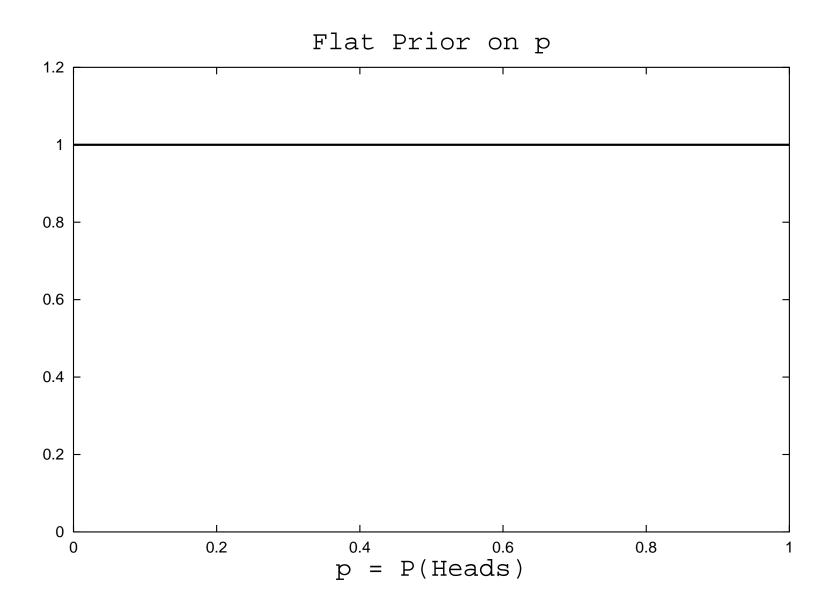


• What values are most likely?

Subjective Prior on Pr(Heads)



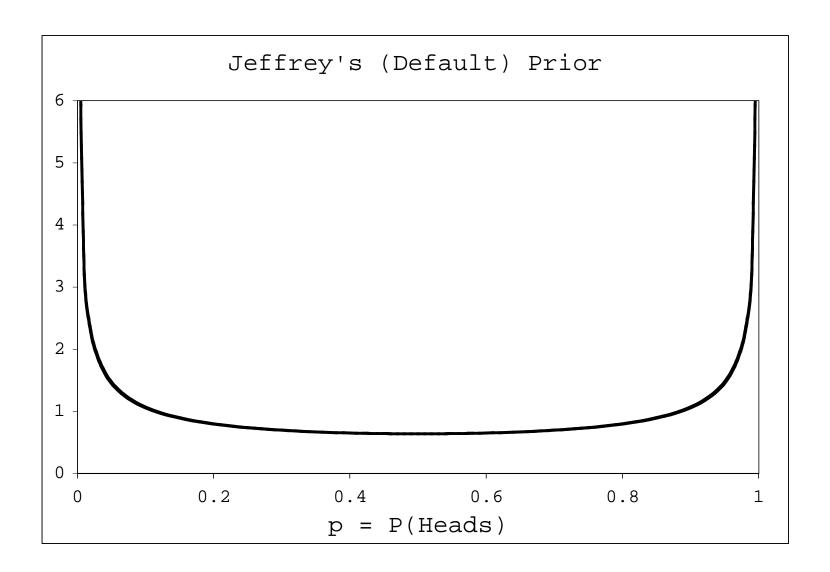
- What values are most likely?
- How do you express ignorance?
 - vague distributions



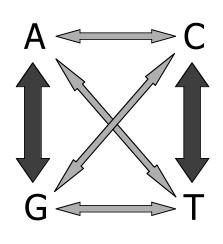
"Non-informative" priors

- Misleading term
- Used by many Bayesians to mean "prior that is expected to have the smallest effect on the posterior"
- Not always a uniform prior

- What values are most likely?
- How do you express ignorance?
 - vague distributions
 - How easily can the likelihood discriminate between parameter values?



Example: The Kimura model



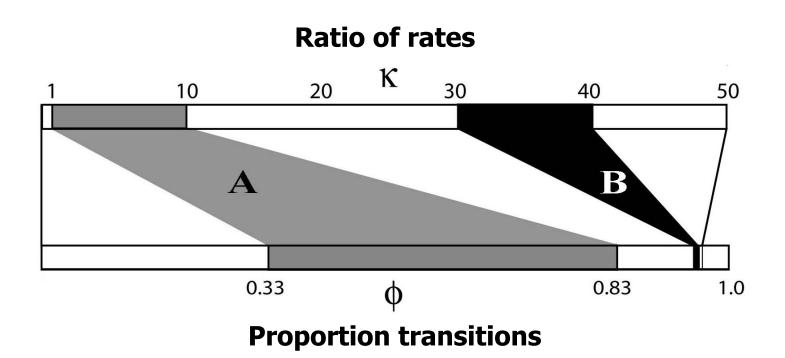
Ratio of rates $(0, \infty)$

$$\kappa = \frac{r_{ti}}{r_{tv}}$$

Proportion transitions (0,1)

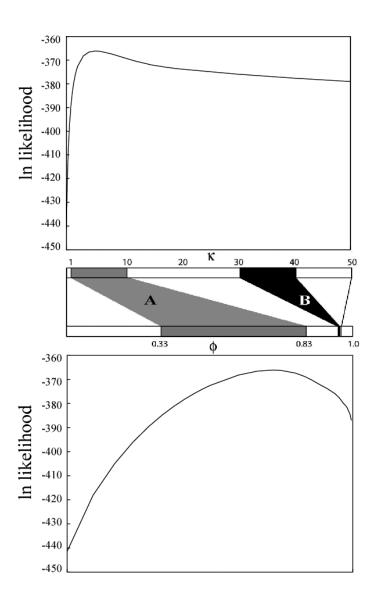
$$\phi = \frac{r_{ti}}{r_{ti} + 2r_{tv}}$$

 κ and φ map onto the predictions of K80 very differently

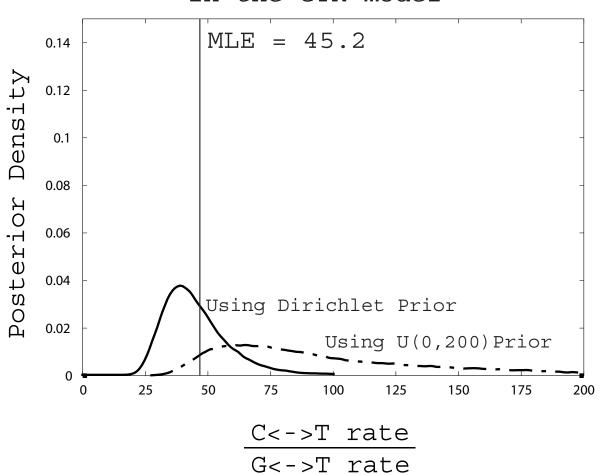


$K80: \kappa$ and ϕ

- The likelihood surface is tied to the model predictions
- The ML estimates are equivalent
- The curve shapes (and integrals) are quite different



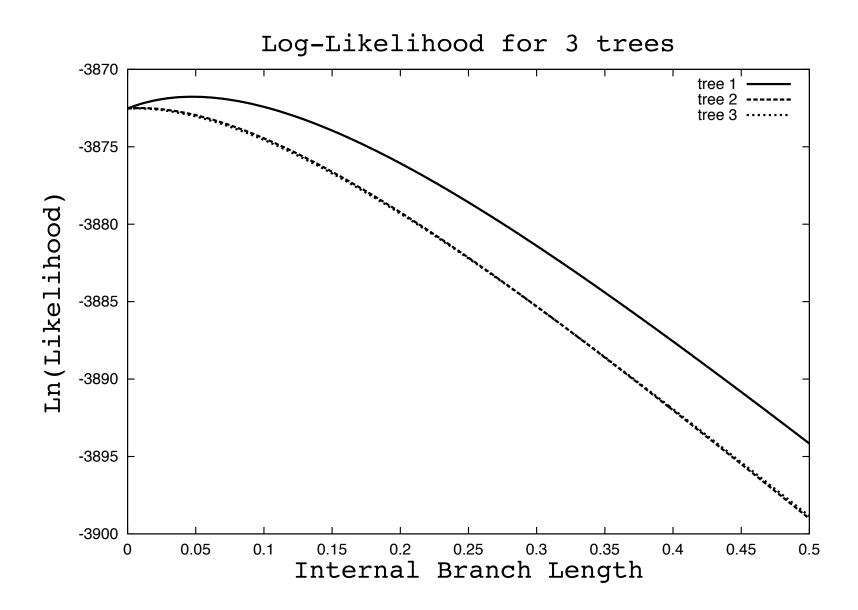
Effects of the Prior in the GTR model



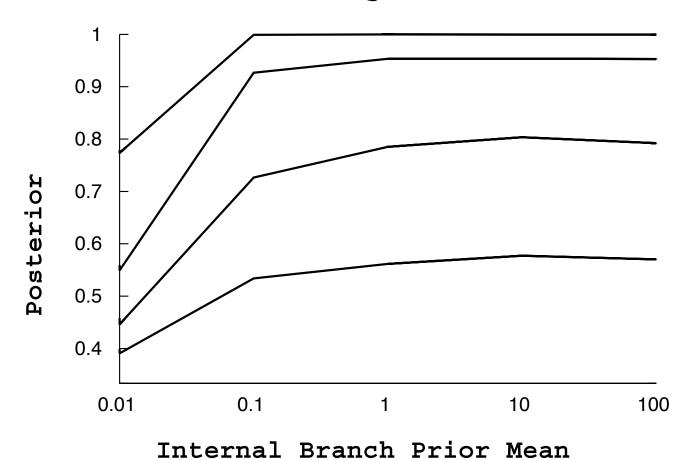
Minimizing the effect of priors

- Flat \neq non-informative
- Familiar model parameterizations may perform poorly in a Bayesian analysis with flat priors.

- What values are most likely?
- How do you express ignorance? (minimally informative priors)
- Are some errors better than others?



The *Tree's* Posterior vs the *Branch Length's* Prior Mean



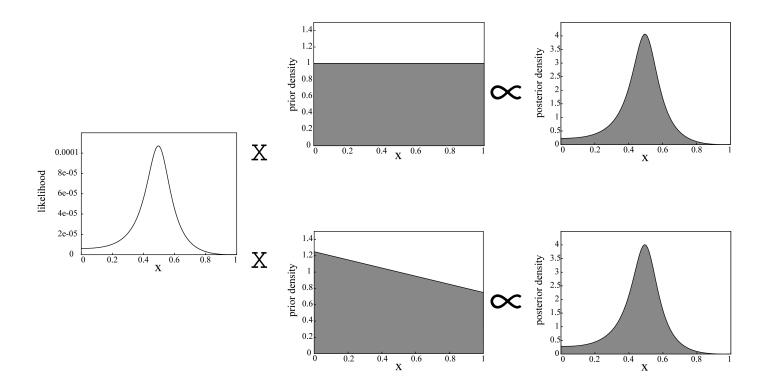
We might make analyses more conservative by

- Favoring short internal branch lengths
- Placing some prior probability on "star" trees (Lewis *et al.*)

We need to worry about sensitivity of our conclusions to all "inputs"

- Data
- Model
- Priors

Often priors will be the *least* of our concerns



The prior can be a benefit (not just a necessity) of Bayesian analysis

- Incorporate previous information
- Make the analysis more conservative

But...

It can be hard to say "I don't know"

Priors can strongly affect the analysis if...

- The prior strongly favors some parameter values, OR
- The data (via the likelihood) are not very informative (little data or complex model)

Because Bayesian inference relies on marginalization, the priors for *all* parameters can affect the posterior probabilities of the hypotheses of interest.

How do we calculate a posterior probability?

$$Pr(\text{Tree}|\text{Data}) = \frac{Pr(\text{Tree})L(\text{Tree})}{\mathbf{Pr}(\mathbf{Data})}$$

In particular, how do we calculate Pr(Data)?

Pr(Data) is the marginal probability of the data, so

$$Pr(Data) = \sum_{i} Pr(Tree_i) L(Tree_i)$$

But this is a sum over all trees (there are *lots* of trees).

Recall that even $L(\text{Tree}_i)$ involves multiple integrals.

$$Pr(D) = \sum \int \int \int \int \int Posterior Probability Density$$

$$L(\text{Tree}_i, \kappa, \alpha, \nu_1, \nu_2, \nu_3, \nu_4, \nu_5) Pr(\text{Tree}_i) Pr(\kappa) Pr(\alpha) Pr(\nu_1) Pr(\nu_2) \cdots$$

Markov chain Monte Carlo

- Simulates a walk through parameter/tree space.
- Lets us estimate posterior probabilities for any aspect of the model
- Relies on the *ratio* of posterior densities between two points

$$R = \frac{Pr(\text{Point}_2|\text{Data})}{Pr(\text{Point}_1|\text{Data})}$$

$$R = \frac{\frac{Pr(\text{Point}_2)L(\text{Point}_2)}{Pr(\text{Data})}}{\frac{Pr(\text{Point}_1)L(\text{Point}_1)}{Pr(\text{Data})}}$$

$$R = \frac{Pr \left(\text{Point}_2 \right) L \left(\text{Point}_2 \right)}{Pr \left(\text{Point}_1 \right) L \left(\text{Point}_1 \right)}$$