## The choice of prior distributions can potentially turn a good model bad!



## Bayes' rule

Prior probability density

$f(\theta \mid D)=\frac{f(D \mid \theta) f(\theta)}{\int f(D \mid \theta) f(\theta) d \theta}$


Marginal probability of the data

Posterior probability density

## Marginal <br> $p(D)=\int_{\theta} p(D \mid \theta) p(\theta) d \theta$

## $\underset{\text { Likelihood }}{\text { Marginal }}>p(D)=\int_{\theta} p(D \mid \theta) p(\theta) d \theta$

We always condition on model used (but this is often not made explicit in notation used)

$$
p(D \mid M)=\int_{\theta} p(D \mid \theta, M) p(\theta \mid M) d \theta
$$

## Likelihood surface when K80 is the true model

| sequence length | $=500$ sites |
| :--- | :--- |
| true edge length | $=0.15$ |
| true kappa | $=\mathbf{5 . 0}$ |



## Likelihood surface when <br> JC is the true model

sequence length $=500$ sites true edge length $=0.15$ true kappa
$=1.0$

$\qquad$


## Estimating the marginal likelihood




## Estimating the marginal likelihood



Unnormalized posterior $\longrightarrow p(D \mid \theta) p(\theta)$

## Estimating the marginal likelihood






Steppingstone method
$\frac{\beta_{1}}{\beta_{0}}=\left(\frac{\beta_{0.00002}}{\beta_{0}}\right)\left(\frac{\beta_{0.00222}}{\beta_{0.00002}}\right)\left(\frac{\beta_{0.03319}}{\beta_{0.00222}}\right)\left(\frac{\beta_{0.22591}}{\beta_{0.03319}}\right)\left(\frac{\beta_{1}}{\beta_{0.22591}}\right)$ $0.000061=(0.816537)(0.167866)(0.289389)(0.172237)(0.008923)$

$0.000025=$ true value

## How many "stepping stones" (i.e. ratios) are needed?

Newton and Raftery 1994

Xie et al. 2011; Fan et al. 2011

Lartillot and Philippe 2006


## Bayesian Information Criterion (BIC)



## $\mathrm{BIC} \approx-\log (\mathrm{marginal}$ likelihood)



## Akaike Information Criterion (AIC)

Calculate AIC for each model:

$$
\operatorname{AIC}=-2 \max (\log L)+2 K
$$

Model with smallest AIC is best

Twice expected (relative) K-L divergence from model A to true model

(K-L stands for Kullback-Leibler)

## Recall from likelihood lecture...

First 32 nucleotides of the $\psi \eta$-globin gene of gorilla:

## GAAGTCCTTGAGAAATAAACTGCACACACTGG

$\log L=12 \log \left(\pi_{A}\right)+7 \log \left(\pi_{C}\right)+7 \log \left(\pi_{G}\right)+6 \log \left(\pi_{T}\right)$
Find maximum logL under F81 (unconstrained) model:

$$
\begin{aligned}
\log L & =12 \log \left(\pi_{A}\right)+7 \log \left(\pi_{C}\right)+7 \log \left(\pi_{G}\right)+6 \log \left(\pi_{T}\right) \\
& =12 \log (0.375)+7 \log (0.219)+7 \log (0.219)+6 \log (0.187) \\
& =-43.1
\end{aligned}
$$

Find maximum logL under JC69 (constrained) model:

$$
\begin{aligned}
& \log L=12 \log \left(\pi_{A}\right)+7 \log \left(\pi_{C}\right)+7 \log \left(\pi_{G}\right)+6 \log \left(\pi_{T}\right) \\
& =12 \log (0.25)+7 \log (0.25)+7 \log (0.25)+6 \log (0.25) \\
& =-44.4
\end{aligned}
$$

## Akaike Information Criterion (AIC)

## Calculate AIC for each model:

$$
\begin{aligned}
A I C & =2 K-2 \log \left(L_{\max }\right) \\
A I C_{\text {free }} & =2(3)-2(-43.1)=96.6 \\
A I C_{\text {equal }} & =2(0)-2(-44.4)=88.8
\end{aligned}
$$

The constrained model ("equal") is a better choice than the unconstrained model ("free") according to AIC

## Bayesian Information Criterion (BIC)

Calculate BIC for each model:

$$
\begin{aligned}
B I C & =K \log (n)-2 \log \left(L_{\max }\right) \\
B I C_{\text {free }} & =3 \log (32)-2(-43.1)=96.6 \\
B I C_{\text {equal }} & =0 \log (32)-2(-44.4)=88.8
\end{aligned}
$$

The constrained model ("equal") is a better choice than the unconstrained model ("free") according to BIC too

