

# Bayesian Analysis #2: MCMC

*NRES 746*

*Fall 2018*

For those wishing to follow along with the R-based demo in class, click [here](#) for the companion R script for this lecture.

## Markov Chain Monte Carlo

Now in many cases, we simply won't have the computational power to partition our parameter space into discrete pixels and completely evaluate the posterior probability for all  $n$ -dimensional pixels in that space. In these cases, we tend to harness ingenious procedures known as *Markov-Chain Monte Carlo* algorithms. This approach uses stochastic jumps in parameter space to (eventually) settle on a posterior distribution. The key to MCMC is the following:

The ratio of successful jump probabilities is proportional to the ratio of the posterior probabilities.

The jump probability can be characterized as:

$$Prob(jump) * Prob(accept)$$

That is: in order to jump, you need to propose a specific jump (according to some probability distribution) and then accept that jump!

The ratio of jump probabilities can be characterized as:

$$\frac{Prob(jump_{b \rightarrow a}) \cdot Prob(accept_a|b)}{Prob(jump_{a \rightarrow b}) \cdot Prob(accept_b|a)}$$

For this procedure to (eventually) sample from the posterior distribution, *this ratio MUST be equal to the ratio of the posterior probabilities*:

$$\frac{Posterior(A)}{Posterior(B)}$$

If this rule is met, then in the long run the chain will spend a lot of time occupying high-probability parts of parameter space, essentially capturing the posterior distribution. With enough jumps, the long-term distribution will match the joint posterior probability distribution.

MCMC is essentially a special type of random number generator that is designed to sample from difficult-to-describe (e.g., multivariate, hierarchical) probability distributions. In many/most cases, the posterior distribution for ecological problems is a very difficult-to-describe probability distribution.

MCMC is kind of magical in that it allows you to sample from probability distributions that are impossible to fully define!

Amazingly, MCMC at its core is not that difficult to describe or implement. Let's look at a simple MCMC algorithm.

## Metropolis-Hastings algorithm

This algorithm is very similar to the simulated annealing algorithm! The main difference: the “temperature” doesn't decrease over time and the parameter  $k$  is set to 1.

The M-H algorithm can be expressed as:

$$Prob(acceptB|A) = \min\left(1, \frac{Posterior(B)}{Posterior(A)} \cdot \frac{Prob(b \rightarrow a)}{Prob(a \rightarrow b)}\right)$$

Note that essentially this is the same as the ‘Metropolis’ simulated annealing algorithm, with the posterior probabilities substituted for the likelihood and the  $k$  parameter set to 1.

**Q:** Does it make sense that this algorithm meets the basic rule of MCMC, that is, that the ratio of jump probabilities to/from any two points in parameter/model space is equal to the ratio of posterior probabilities evaluated at those two points?

## Bivariate normal example

This example is modified from this link by Prof Darren Wilkinson

Remember that MCMC samplers are just a type of random number generator. We can use a Metropolis-Hastings sampler to develop our own random number generator for a fairly simple known distribution. In this example, we use a M-H Sampler to generate random numbers from a standard bivariate normal probability distribution.

We don’t need an MCMC sampler for this simple example. One way to do this would be to use the following code, which draws and visualizes an arbitrary number of independent samples from the bivariate standard normal distribution.

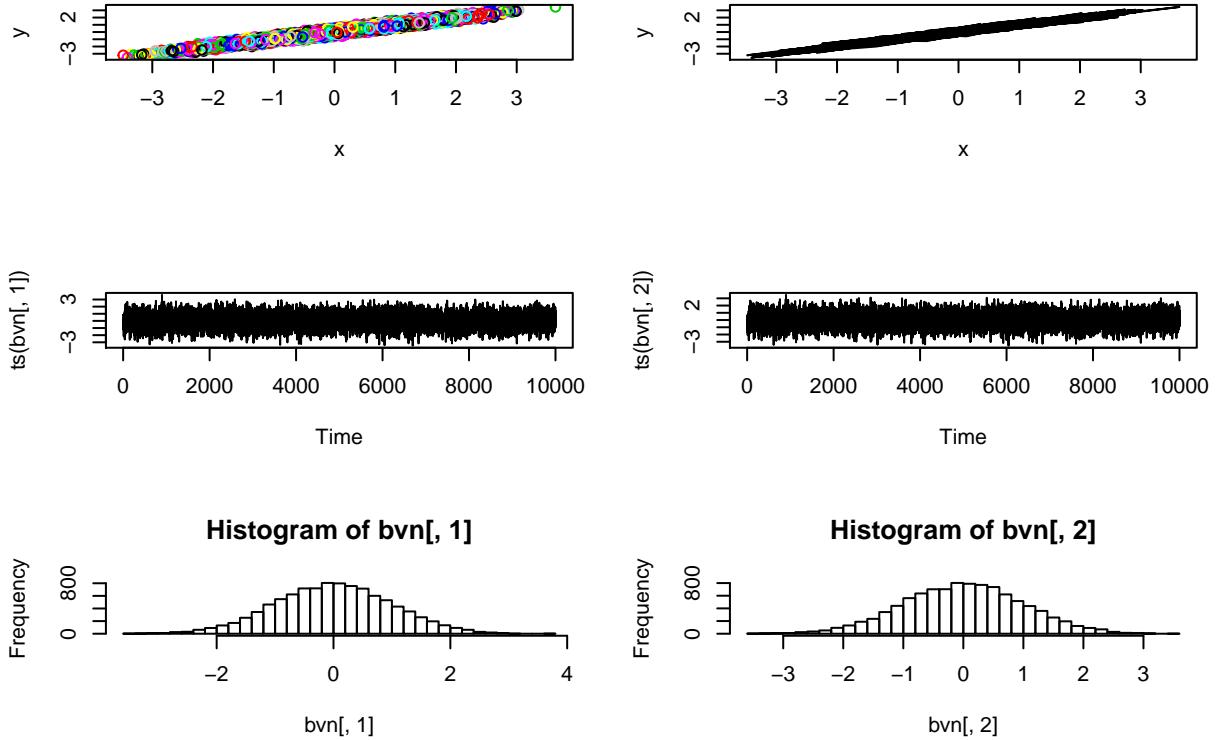
```
#####
# Simple example of MCMC sampling
#####

#####
# first, let's build a function that generates random numbers from a bivariate normal distribution

rbvn<-function (n, rho)    #function for drawing an arbitrary number of independent samples from the biv
{
  x <- rnorm(n, 0, 1)
  y <- rnorm(n, rho * x, sqrt(1 - rho^2))
  cbind(x, y)
}

#####
# Now, plot the random draws from this distribution, make sure this makes sense!

bvn<-rbvn(10000,0.98)
par(mfrow=c(3,2))
plot(bvn,col=1:10000)
plot(bvn,type="l")
plot(ts(bvn[,1]))
plot(ts(bvn[,2]))
hist(bvn[,1],40)
hist(bvn[,2],40)
```



```

par(mfrow=c(1,1))

#####
# Metropolis-Hastings implementation of bivariate normal sampler...

library(mvtnorm)      # load a package that allows us to compute probability densities for mv normal dist

##
## Attaching package: 'mvtnorm'

## The following object is masked from 'package:emdbook':
## 
##     dmvnorm

metropolisHastings <- function (n, rho=0.98){      # a MCMC sampler implementation of a bivariate random walk
  mat <- matrix(ncol = 2, nrow = n)    # matrix for storing the random samples
  x <- 0      # initial values for all parameters
  y <- 0
  prev <- dmvnorm(c(x,y),mean=c(0,0),sigma = matrix(c(1,rho,rho,1),ncol=2))    # probability density of current state
  mat[1, ] <- c(x, y)      # initialize the markov chain
  counter <- 1
  while(counter<=n) {
    newx <- rnorm(1,x,0.5)      # make a jump. Note the symmetrical proposal distribution
    newy <- rnorm(1,y,0.5)

    newprob <- dmvnorm(c(newx,newy),sigma = matrix(c(1,rho,rho,1),ncol=2))    # assess whether the new proposal is better
    ratio <- newprob/prev      # compute the ratio of probabilities at the old (jump from) and proposed states
  }
}
```

```

prob.accept <- min(1,ratio)      # decide the probability of accepting the new jump!
rand <- runif(1)
if(rand<=prob.accept){
  x=newx;y=newy      # set x and y to the new location
  mat[counter,] <- c(x,y)    # store this in the storage array
  counter=counter+1
  prev <- newprob      # get ready for the next iteration
}
}

return(mat)
}

```

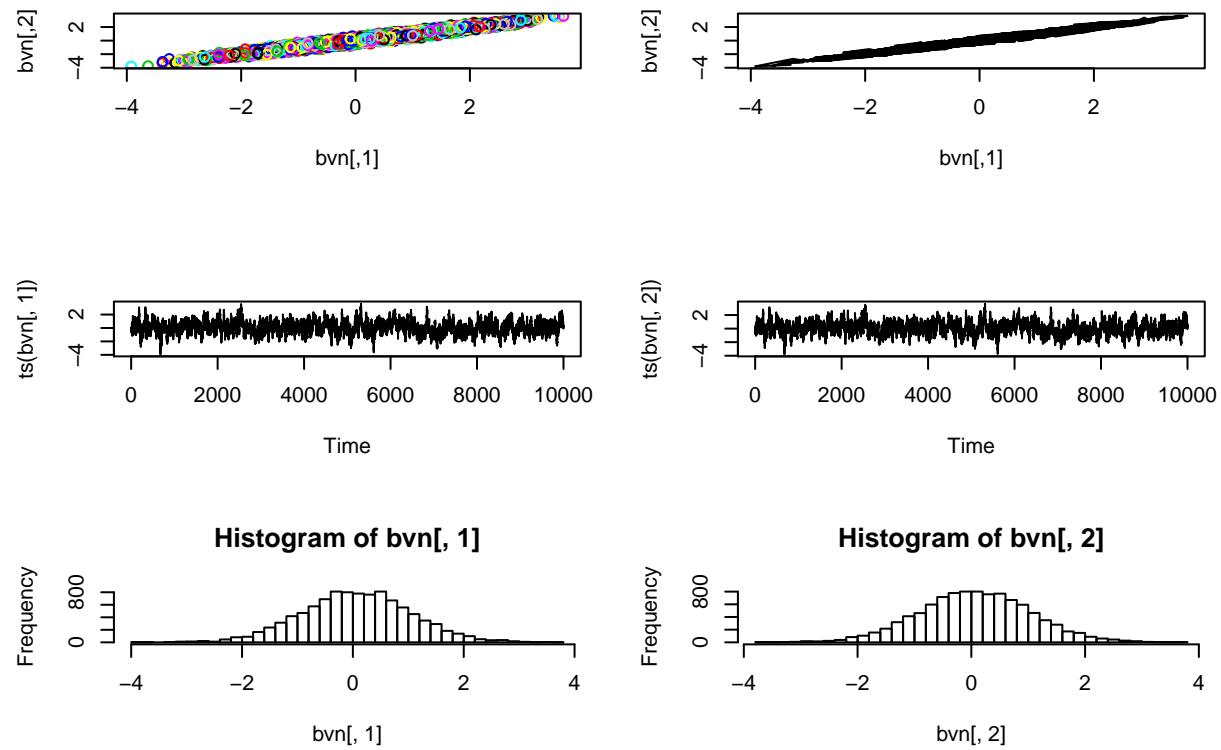
Then we can use the M-H sampler to get random samples from this known distribution...

```

#####
# Test the new M-H sampler

bvn<-metropolisHastings(10000,0.98)
par(mfrow=c(3,2))
plot(bvn,col=1:10000)
plot(bvn,type="l")
plot(ts(bvn[,1]))
plot(ts(bvn[,2]))
hist(bvn[,1],40)
hist(bvn[,2],40)

```



```
par(mfrow=c(1,1))
```

**Q:** Why was it unnecessary to perform an MCMC routine to sample from this (bivariate normal) distribution?

Okay, enough with super simple examples- let's try it for a non-trivial problem, like the Myxomatosis example from the Bolker book!

### Myxomatosis revisited (again!)

```
#####
# MCMC implementation of the Myxomatosis example from the Bolker book
#####

library(emdbook)

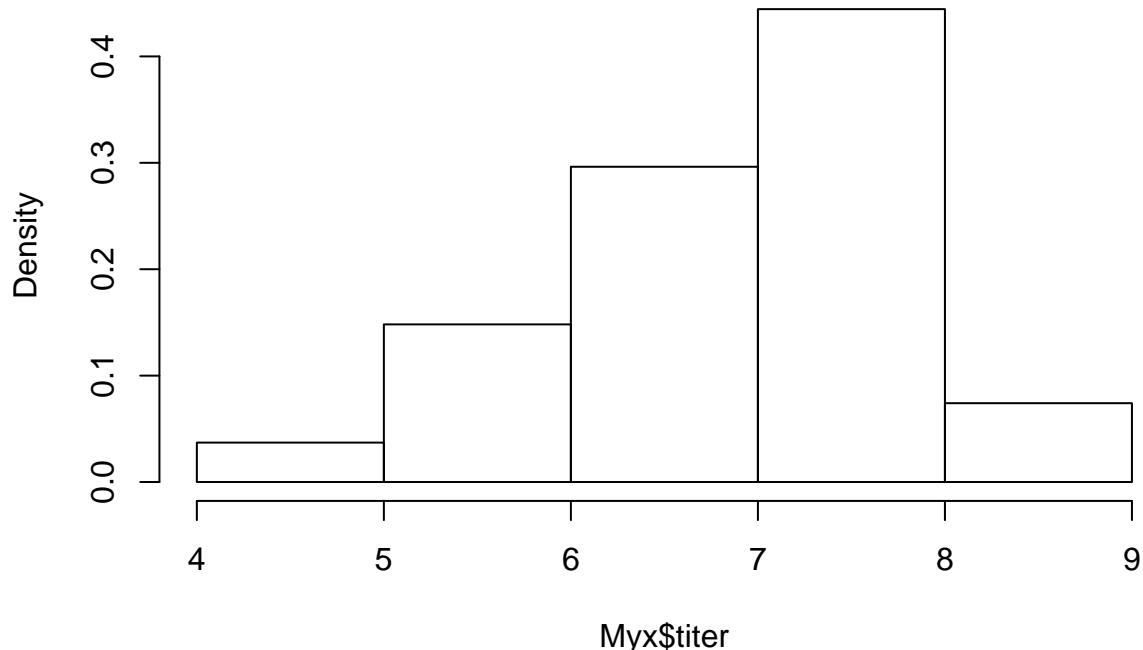
MyxDat <- MyxoTiter_sum
Myx <- subset(MyxDat, grade==1)
head(Myx)
```

Recall that we are modeling the distribution of measured titers (virus loads) for Australian rabbits. Bolker chose to use a Gamma distribution. Here is the empirical distribution:

```
#####
# Visualize the Myxomatosis data for the 100th time!

hist(Myx$titer,freq=FALSE)
```

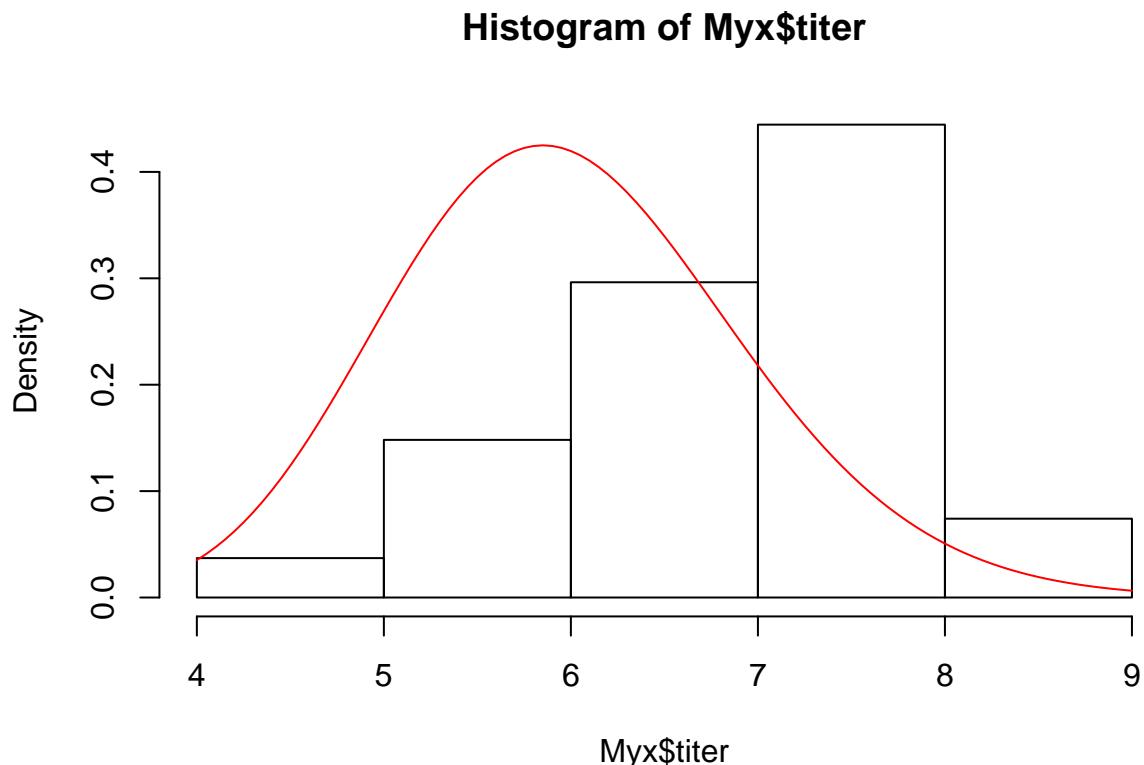
**Histogram of Myx\$titer**



We need to estimate the gamma rate and shape parameters that best fit this empirical distribution. Here is one example of a Gamma fit to this distribution:

```
#####
# ... and overlay a proposed data-generating model (gamma distribution)

hist(Myx$titer,freq=FALSE)
curve(dgamma(x,shape=40,scale=0.15),add=T,col="red")
```



Recall that the 2-D (log) likelihood surface looks something like this:

```
#####
# define 2-D parameter space!
#####

shapevec <- seq(3,100,by=0.1)
scalevec <- seq(0.01,0.5,by=0.001)

#####
# define the likelihood surface across this grid within parameter space
#####

GammaLogLikelihoodFunction <- function(params){
  sum(dgamma(Myx$titer,shape=params['shape'],scale=params['scale'],log=T))
}
surface2D <- matrix(nrow=length(shapevec),ncol=length(scalevec)) # initialize storage variable

newparams <- c(shape=50,scale=0.2)
```

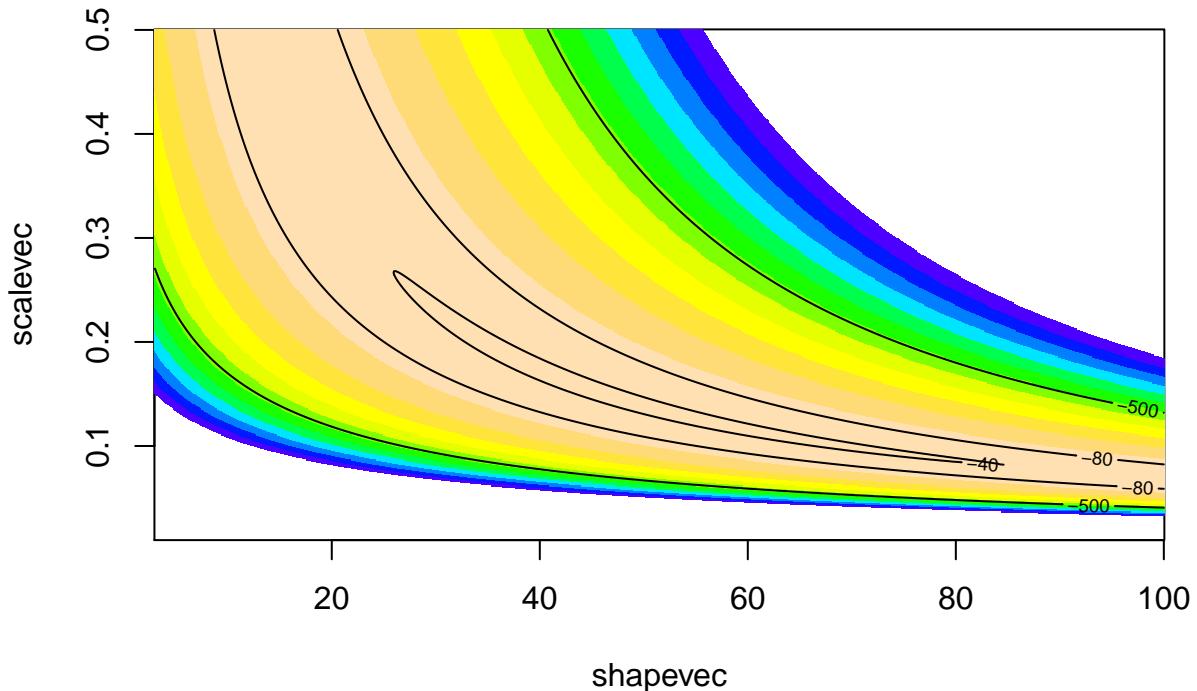
```

for(i in 1:length(shapevec)){
  newparams['shape'] <- shapevec[i]
  for(j in 1:length(scalevec)){
    newparams['scale'] <- scalevec[j]
    surface2D[i,j] <- GammaLogLikelihoodFunction(newparams)
  }
}

#####
# Visualize the likelihood surface
#####

image(x=shapevec,y=scalevec,z=surface2D,zlim=c(-1000,-30),col=topo.colors(12))
contour(x=shapevec,y=scalevec,z=surface2D,levels=c(-30,-40,-80,-500),add=T)

```



Here is an implementation of the M-H algorithm to find the joint posterior distribution!

First, we need a likelihood function (our old friend!)- this time, we will return real probabilities- NOT log-transformed probabilities

```

#####
# Write a non-log-transformed likelihood function

GammaLikelihoodFunction <- function(params){
  prod(dgamma(Myx$titer,shape=params['shape'],scale=params['scale'],log=F))
}
```

```

params <- c(shape=40,scale=0.15)
params

## shape scale
## 40.00 0.15
GammaLikelihoodFunction(params)

## [1] 2.906766e-22

```

Then, we need a prior distribution for our parameters! Let's assign relatively flat priors for both of our parameters. In this case, let's assign a  $\text{gamma}(\text{shape} = 0.01, \text{scale} = 100)$  for the shape parameter (mean of 1 and very large variance) and a  $\text{gamma}(\text{shape} = 0.1, \text{scale} = 10)$  distribution (mean of 1 and slightly lower variance) for the scale parameter:

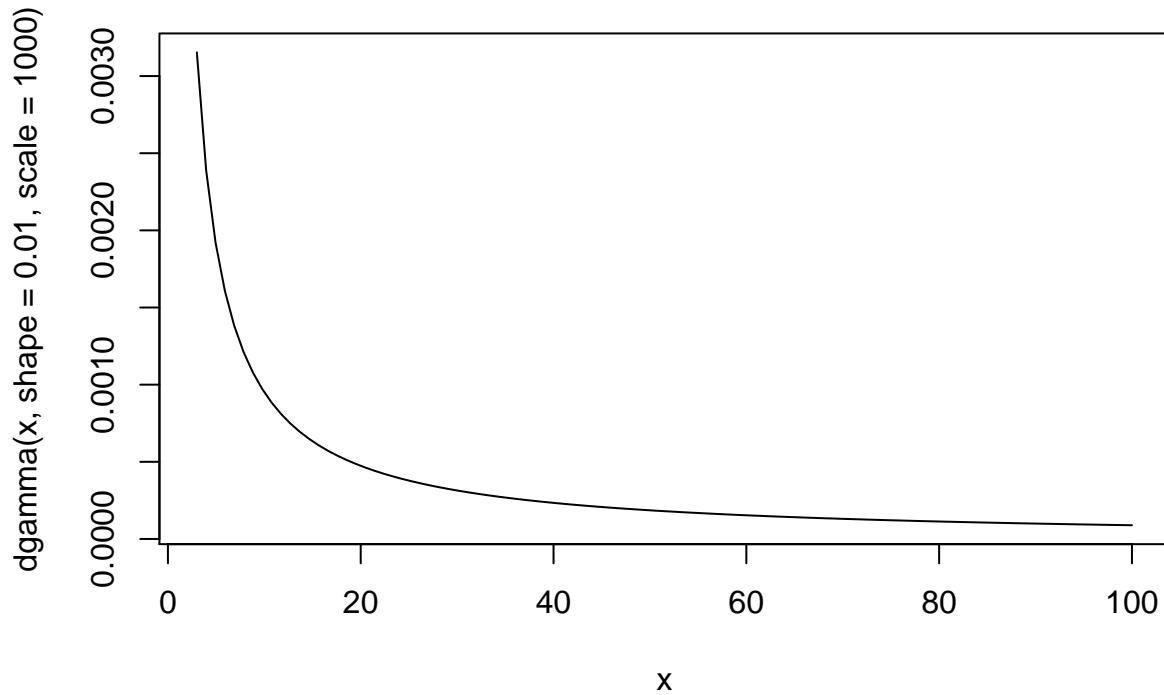
```

#####
# Function for returning the prior probability density for any point in parameter space

GammaPriorFunction <- function(params){
  prior <- c(shape=NA,scale=NA)
  prior['shape'] <- dgamma(params['shape'],shape=0.01,scale=100)
  prior['scale'] <- dgamma(params['scale'],shape=0.001,scale=1000)
  # prior['shape'] <- dunif(params['shape'],3,100)           # alternative: could use uniform prior!
  # prior['scale'] <- dunif(params['scale'],0.01,0.5)
  return(prod(prior))
}

curve(dgamma(x,shape=0.01,scale=1000),3,100)

```



```

params <- c(shape=40,scale=0.15)
params

## shape scale
## 40.00 0.15
GammaPriorFunction(params)

## [1] 1.104038e-06

```

Note that we are also assuming (fairly standard assumption) that the shape and scale are *independent* in the prior (multiplicative probabilities for the joint prior).

Then, we need a function that can compute the ratio of posterior probabilities for any given jump in parameter space. Because we are dealing with a *ratio* of posterior probabilities, *we do NOT need to compute the normalization constant*.

Without the need for a normalization constant, we just need to compute the ratio of weighted likelihoods (that is, the likelihood weighted by the prior)

```

#####
# Function for computing the ratio of posterior densities between any two points in parameter space

PosteriorRatio <- function(oldguess,newguess){
  oldLik <- max(1e-90,GammaLikelihoodFunction(oldguess))    # compute likelihood and prior density at old
  oldPrior <- max(1e-90,GammaPriorFunction(oldguess))
  newLik <- GammaLikelihoodFunction(newguess)                  # compute likelihood and prior density at new
  newPrior <- GammaPriorFunction(newguess)
  return((newLik*newPrior)/(oldLik*oldPrior))                 # compute ratio of weighted likelihoods
}
```

```

}

oldguess <- params
newguess <- c(shape=39,scale=0.15)

PosteriorRatio(oldguess,newguess)

```

```
## [1] 0.01436301
```

Then we need a function for making new guesses, or jumps in parameter space:

```
#####
# Define proposal distribution for jumps in parameter space (use normal distribution)!
```

```

# function for making new guesses
newGuess <- function(oldguess){
  sdshapejump <- 4
  sdscalejump <- 0.07
  jump <- c(shape=rnorm(1,mean=0,sd=sdshapejump),scale=rnorm(1,0,sdscalejump))
  newguess <- abs(oldguess + jump)
  return(newguess)
}
# set a new "guess" near to the original guess

newGuess(oldguess=params)
```

```
##      shape      scale
## 34.4175949  0.1543069
newGuess(oldguess=params)
```

```
##      shape      scale
## 34.8642978  0.2411021
newGuess(oldguess=params)
```

```
##      shape      scale
## 39.03659117  0.05989554
```

Now we are ready to implement the Metropolis-Hastings MCMC algorithm:

We need a starting point:

```
#####
# Set a starting point in parameter spacer

startingvals <- c(shape=75,scale=0.28)    # starting point for the algorithm
```

Let's play with the different functions we have so far...

```
#####
# Try our new functions

newguess <- newGuess(startingvals)    # take a jump in parameter space
newguess

##      shape      scale
## 72.1504449  0.2399536
```

```
PosteriorRatio(startingvals,newguess)    # difference in posterior ratio
```

```
## [1] 3.972783e-195
```

Now let's look at the Metropolis-Hastings routine:

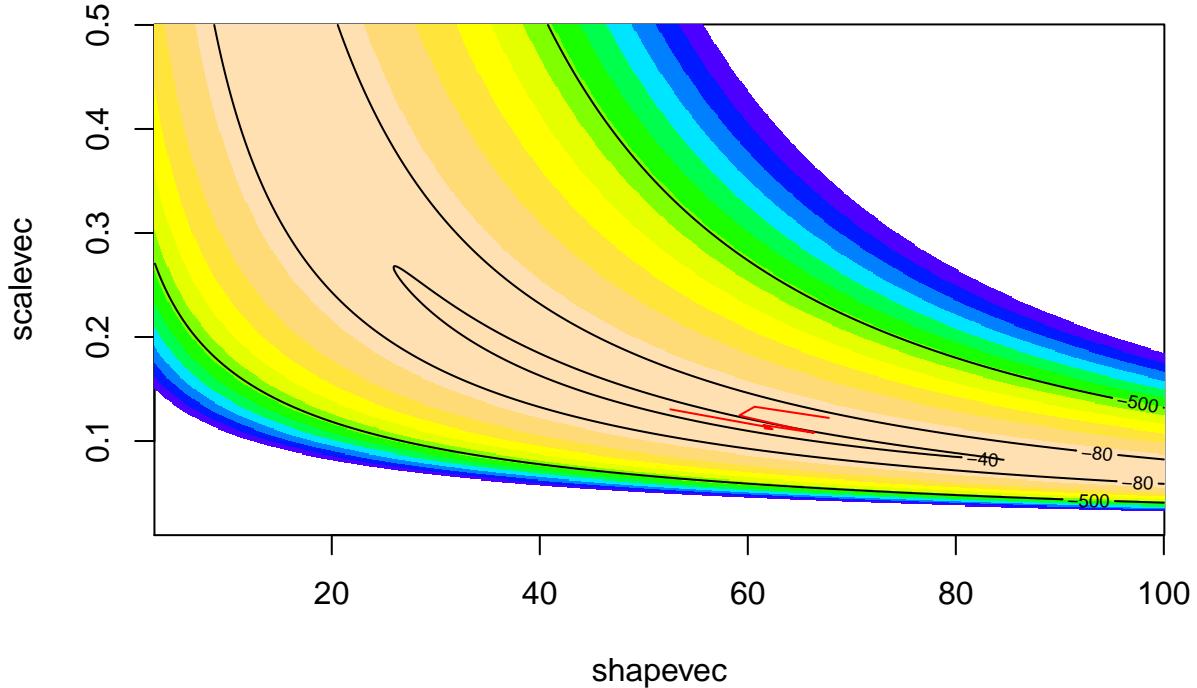
```
#####
# Visualize the Metropolis-Hastings routine:
```

```
chain.length <- 10
oldguess <- startingvals
guesses <- matrix(0,nrow=chain.length,ncol=2)
colnames(guesses) <- names(startingvals)

counter <- 1
while(counter <= chain.length){
  newguess <- newGuess(oldguess)
  post.rat <- PosteriorRatio(oldguess,newguess)
  prob.accept <- min(1,post.rat)
  rand <- runif(1)
  if(rand<=prob.accept){
    oldguess <- newguess
    guesses[counter,] <- newguess
    counter=counter+1
  }
}
```

```
# visualize!
```

```
image(x=shapevec,y=scalevec,z=surface2D,zlim=c(-1000,-30),col=topo.colors(12))
contour(x=shapevec,y=scalevec,z=surface2D,levels=c(-30,-40,-80,-500),add=T)
lines(guesses,col="red")
```



Let's run it for longer...

```
#####
# Get more MCMC samples

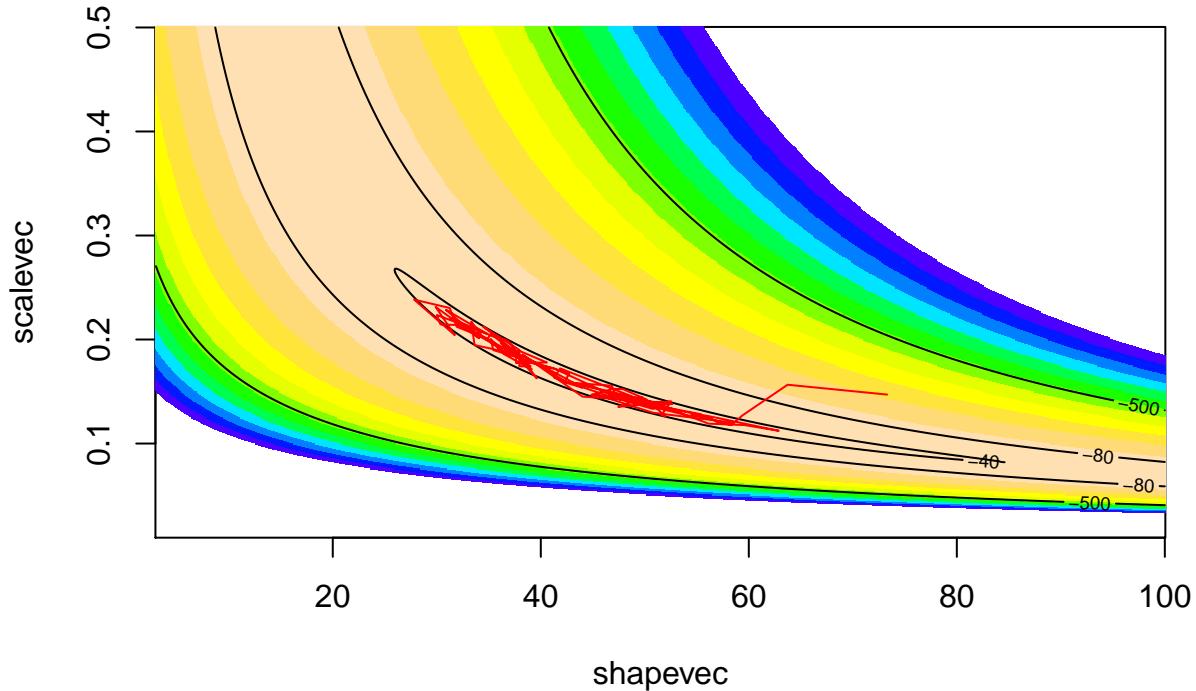
chain.length <- 100
oldguess <- startingvals
guesses <- matrix(0,nrow=chain.length,ncol=2)
colnames(guesses) <- names(startingvals)

counter <- 1
while(counter <= chain.length){
  newguess <- newGuess(oldguess)
  post.rat <- PosteriorRatio(oldguess,newguess)
  prob.accept <- min(1,post.rat)
  rand <- runif(1)
  if(rand<=prob.accept){
    oldguess <- newguess
    guesses[counter,] <- newguess
    counter=counter+1
  }
}

# visualize!

image(x=shapevec,y=scalevec,z=surface2D,zlim=c(-1000,-30),col=topo.colors(12))
contour(x=shapevec,y=scalevec,z=surface2D,levels=c(-30,-40,-80,-500),add=T)
```

```
lines(guesses,col="red")
```



How about for even longer??

```
#####
# And more...

chain.length <- 1000
oldguess <- startingvals
guesses <- matrix(0,nrow=chain.length,ncol=2)
colnames(guesses) <- names(startingvals)

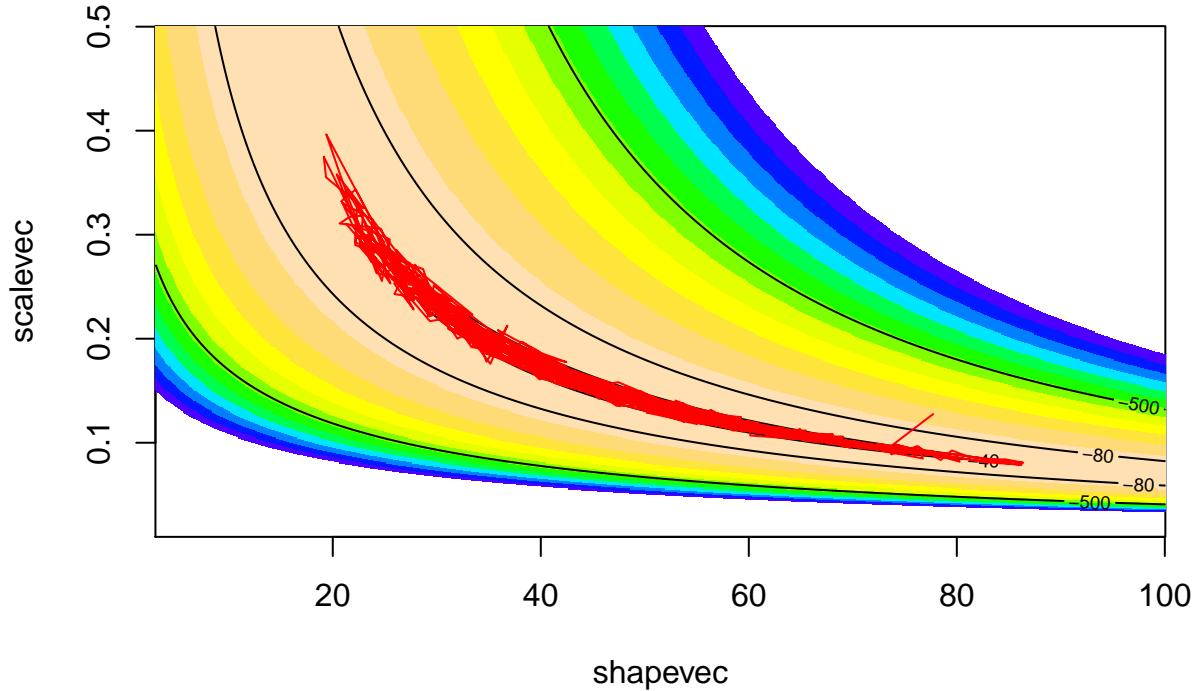
counter <- 1
while(counter <= chain.length){
  newguess <- newGuess(oldguess)
  post.rat <- PosteriorRatio(oldguess,newguess)
  prob.accept <- min(1,post.rat)
  rand <- runif(1)
  if(rand<=prob.accept){
    oldguess <- newguess
    guesses[counter,] <- newguess
    counter=counter+1
  }
}

# visualize!
```

```

image(x=shapevec,y=scalevec,z=surface2D,zlim=c(-1000,-30),col=topo.colors(12))
contour(x=shapevec,y=scalevec,z=surface2D,levels=c(-30,-40,-80,-500),add=T)
lines(guesses,col="red")

```



This looks better! The search algorithm is finding the high-likelihood parts of parameter space pretty well!  
Now, let's look at the chain for the "shape" parameter

```

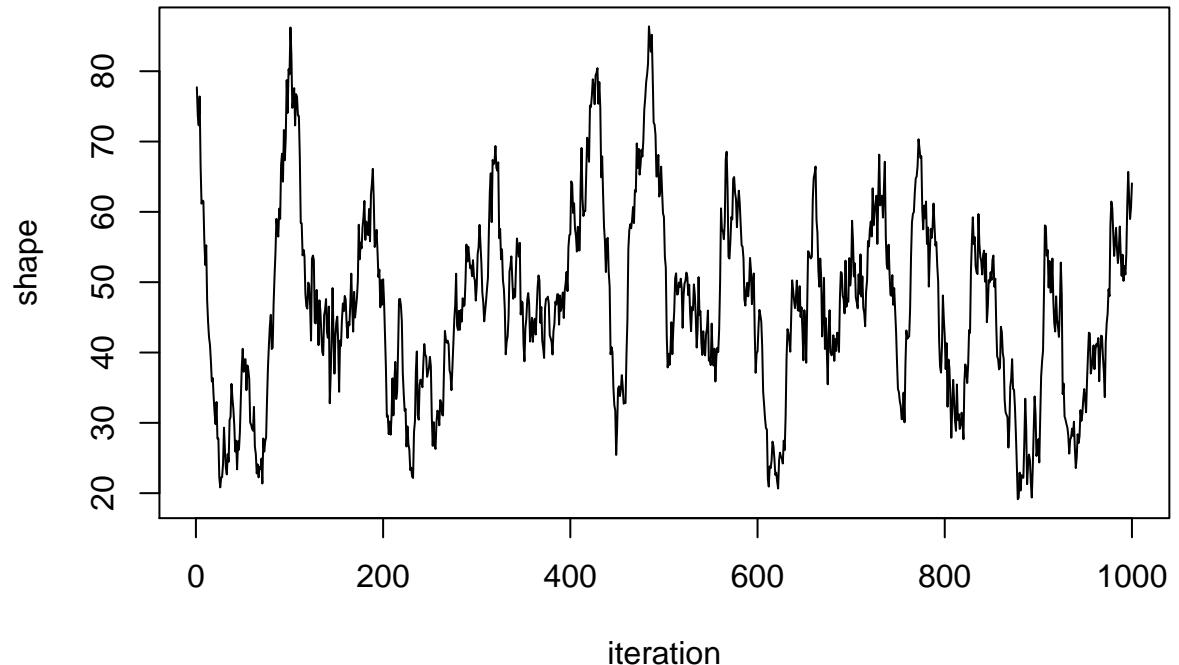
#####
# Evaluate "traceplot" for the MCMC samples...
#####

##### Shape parameter

plot(1:chain.length,guesses[, 'shape'],type="l",main="shape parameter",xlab="iteration",ylab="shape")

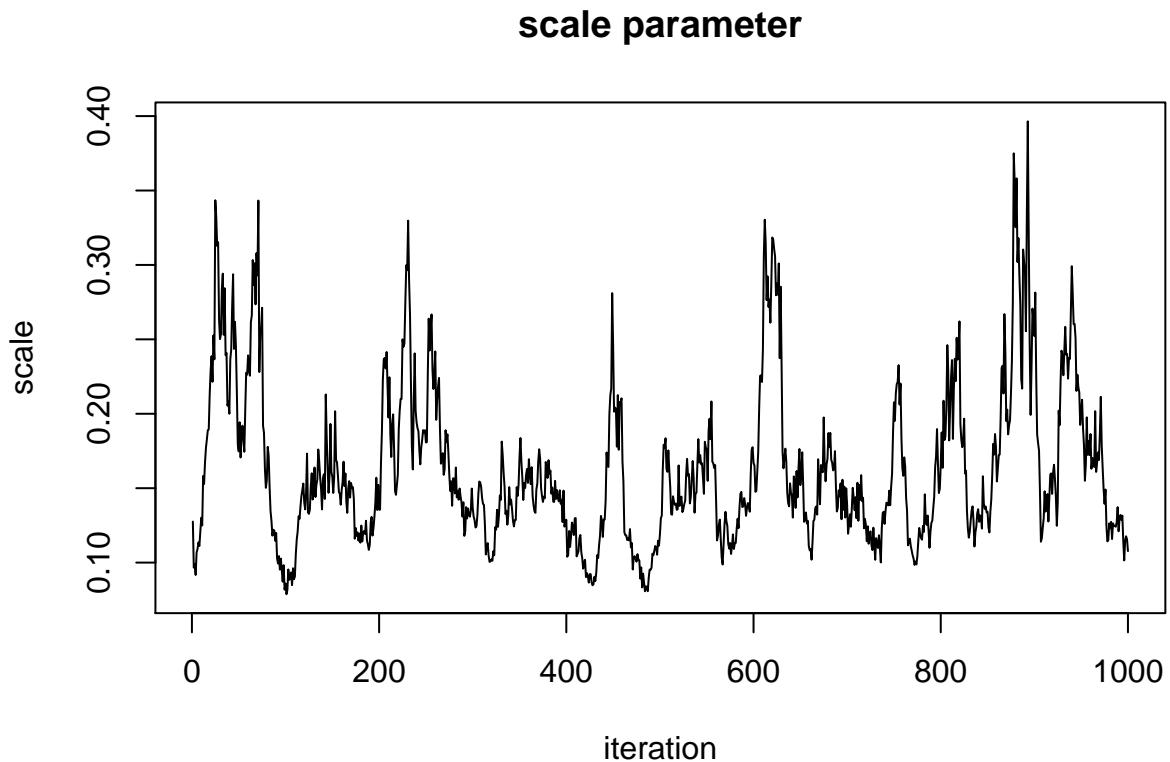
```

## shape parameter



And for the scale parameter...

```
##### Scale parameter  
plot(1:chain.length,guesses[, 'scale'],type="l",main="scale parameter",xlab="iteration",ylab="scale")
```



Can we say that these chains have converged on the posterior distribution for the shape parameter??

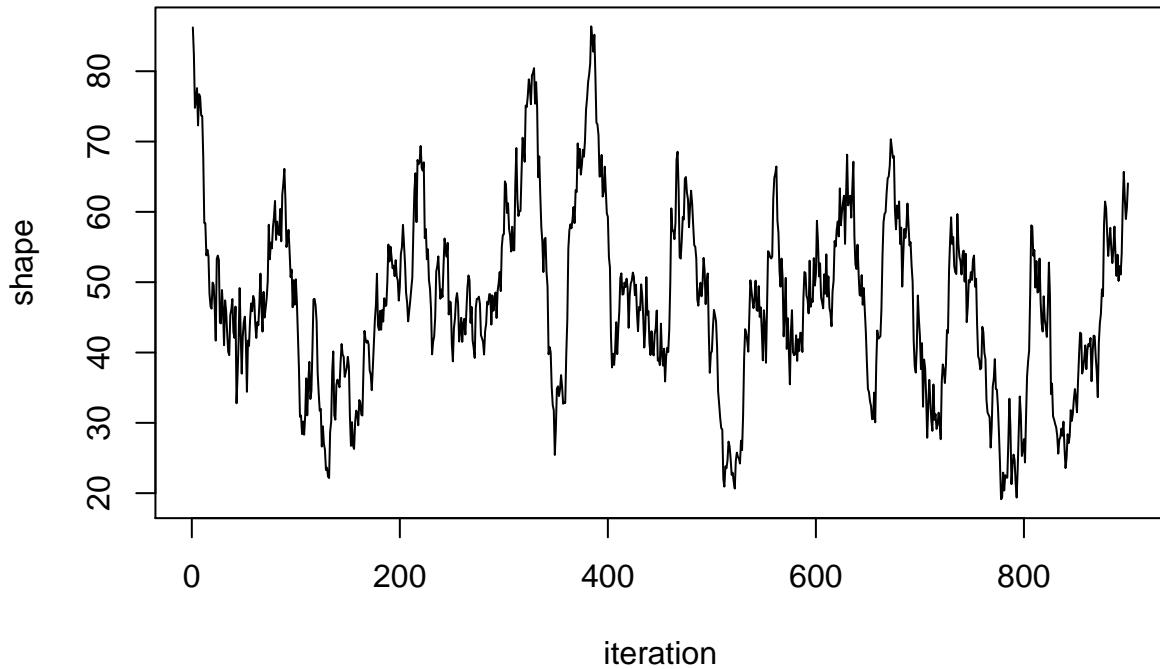
First of all, the beginning of the chain “remembers” the starting value, and is therefore not a stationary distribution. We need to remove the first part of the chain, called the ‘burn-in’.

```
#####
# Remove "burn-in" (allow MCMC routine some time to get to the posterior)

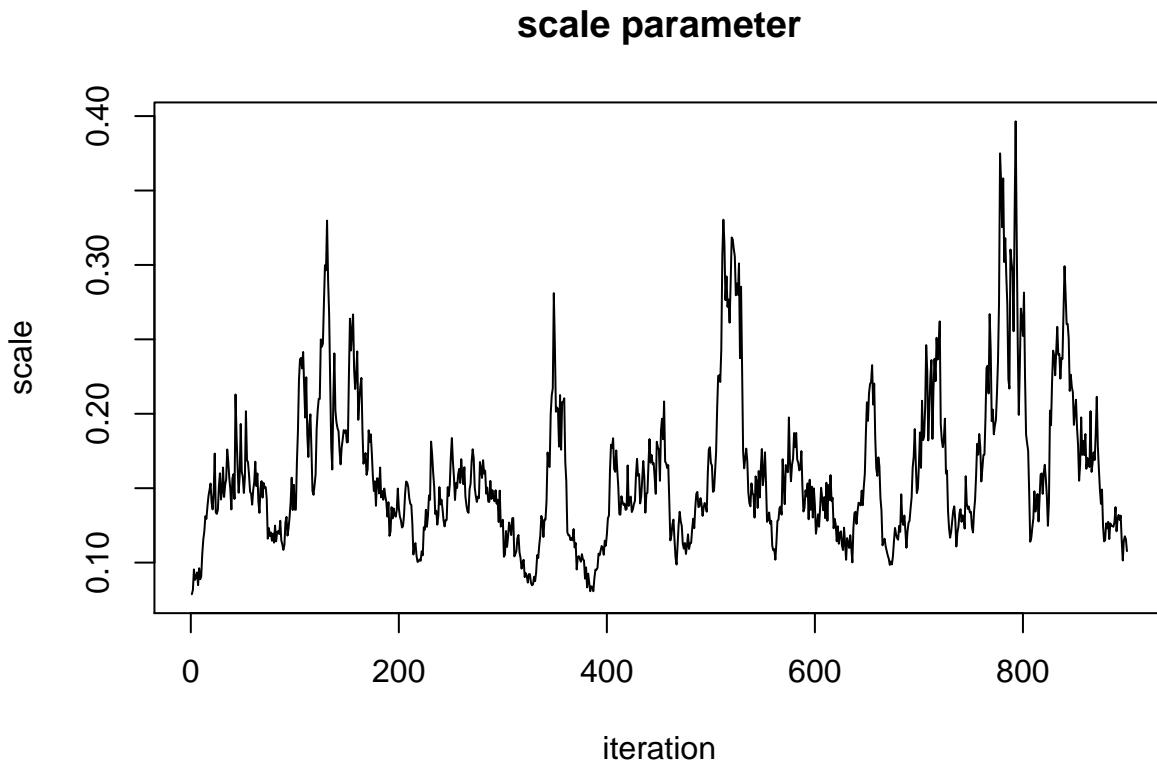
burn.in <- 100
MCMCsamples <- guesses[-c(1:burn.in),]

chain.length=chain.length-burn.in
plot(1:chain.length,MCMCsamples[, 'shape'],type="l",main="shape parameter",xlab="iteration",ylab="shape")
```

### shape parameter



```
plot(1:chain.length,MCMCsamples[, 'scale'],type="l",main="scale parameter",xlab="iteration",ylab="scale")
```



But it still doesn't look all that great. Let's run it for even longer, and see if we get something that looks more like a proper random number generator (white noise)...

```
#####
# Try again- run for much longer

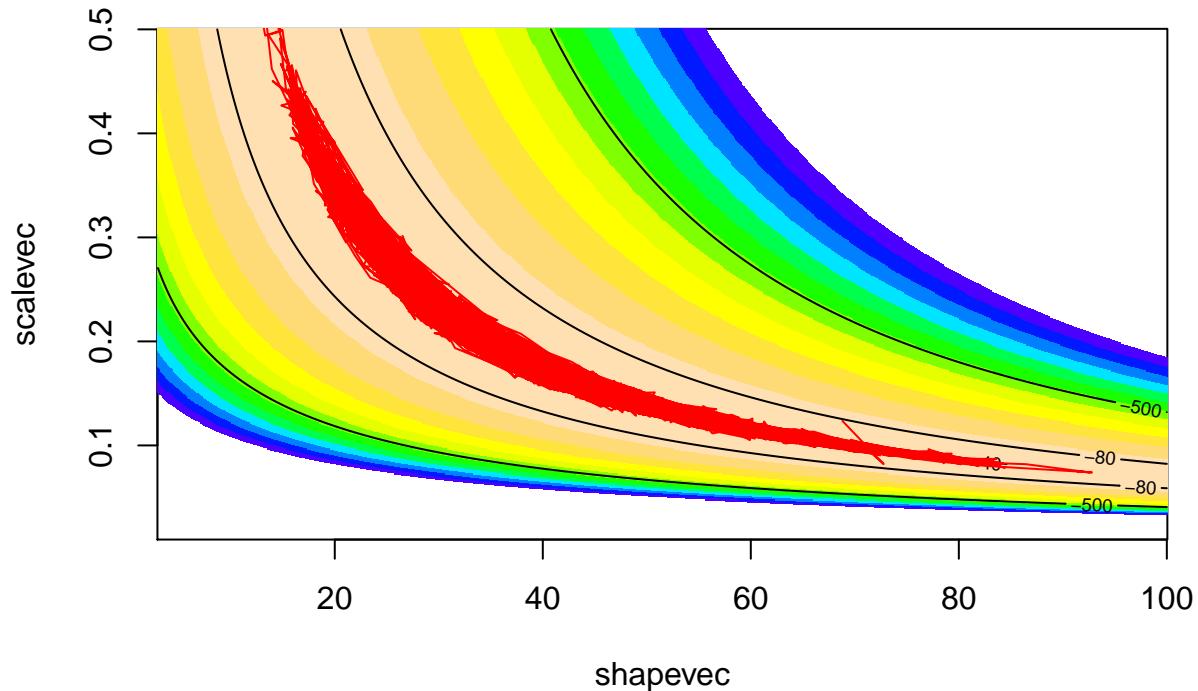
chain.length <- 20000
oldguess <- startingvals
guesses <- matrix(0,nrow=chain.length,ncol=2)
colnames(guesses) <- names(startingvals)

counter <- 1
while(counter <= chain.length){
  newguess <- newGuess(oldguess)
  post.rat <- PosteriorRatio(oldguess,newguess)
  prob.accept <- min(1,post.rat)
  rand <- runif(1)
  if(rand<=prob.accept){
    oldguess <- newguess
    guesses[counter,] <- newguess
    counter=counter+1
  }
}

# visualize!

image(x=shapevec,y=scalevec,z=surface2D,zlim=c(-1000,-30),col=topo.colors(12))
```

```
contour(x=shapevec,y=scalevec,z=surface2D,levels=c(-30,-40,-80,-500),add=T)
lines(guesses,col="red")
```



Let's first remove the first 5000 samples as a burn-in

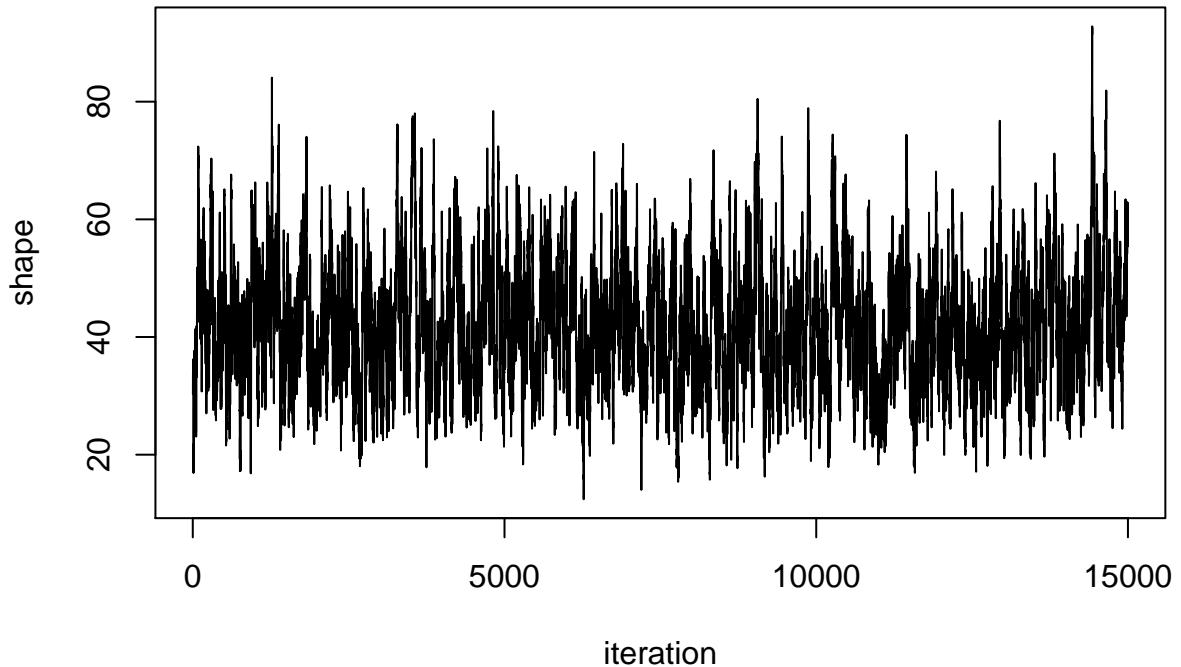
```
#####
# Use longer "burn-in"

burn.in <- 5000
MCMCsamples <- guesses[-c(1:burn.in),]
chain.length=chain.length-burn.in
```

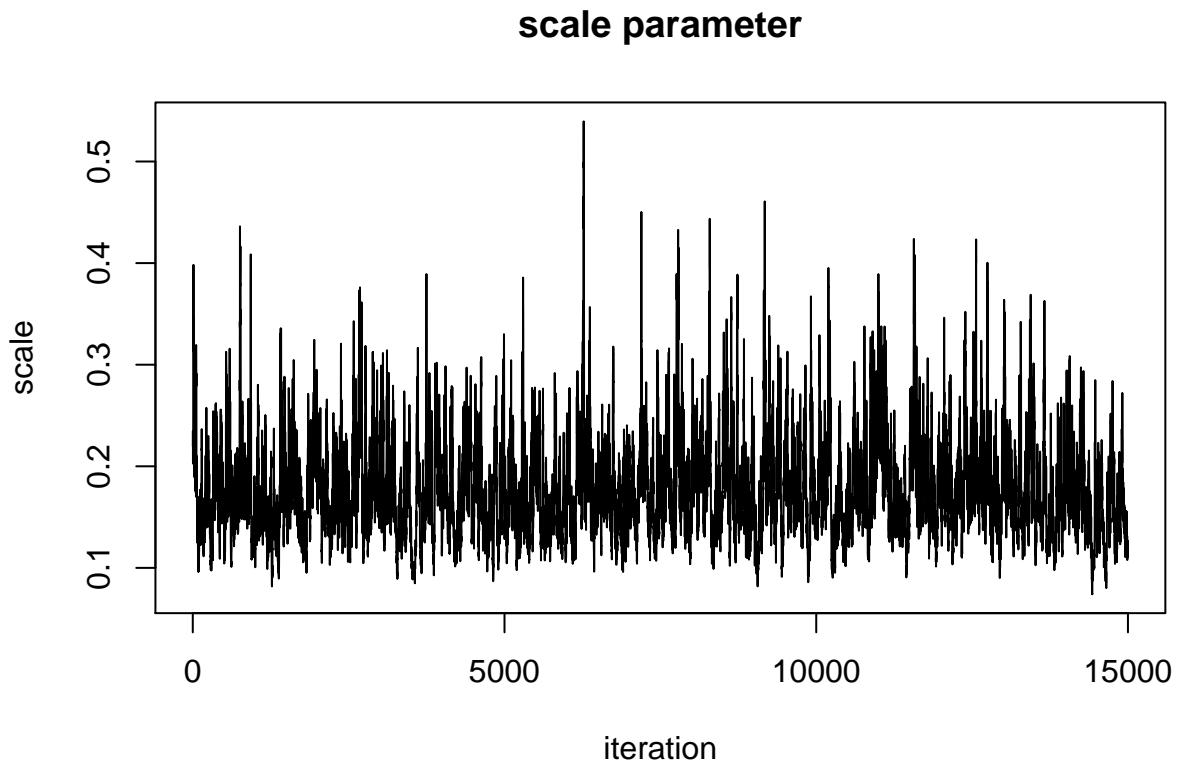
Now, let's look at the chains again

```
plot(1:chain.length,MCMCsamples[, 'shape'],type="l",main="shape parameter",xlab="iteration",ylab="shape")
```

### shape parameter



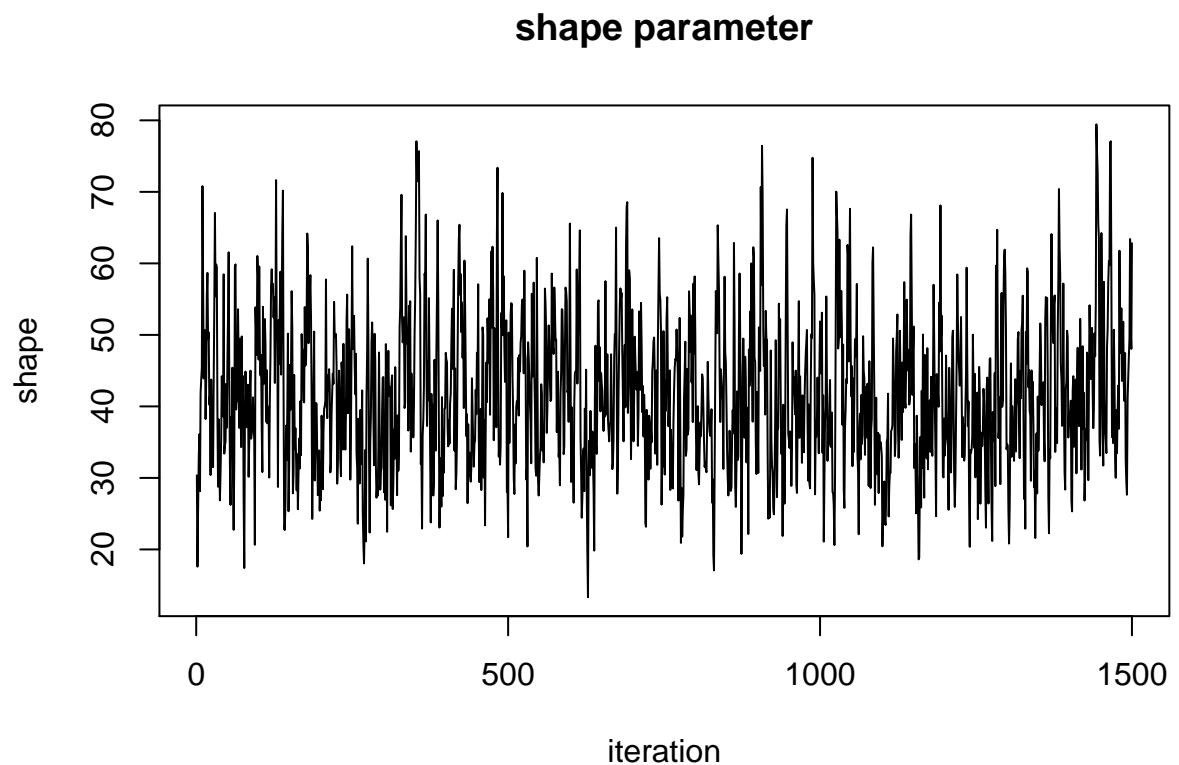
```
plot(1:chain.length,MCMCsamples[, 'scale'],type="l",main="scale parameter",xlab="iteration",ylab="scale")
```



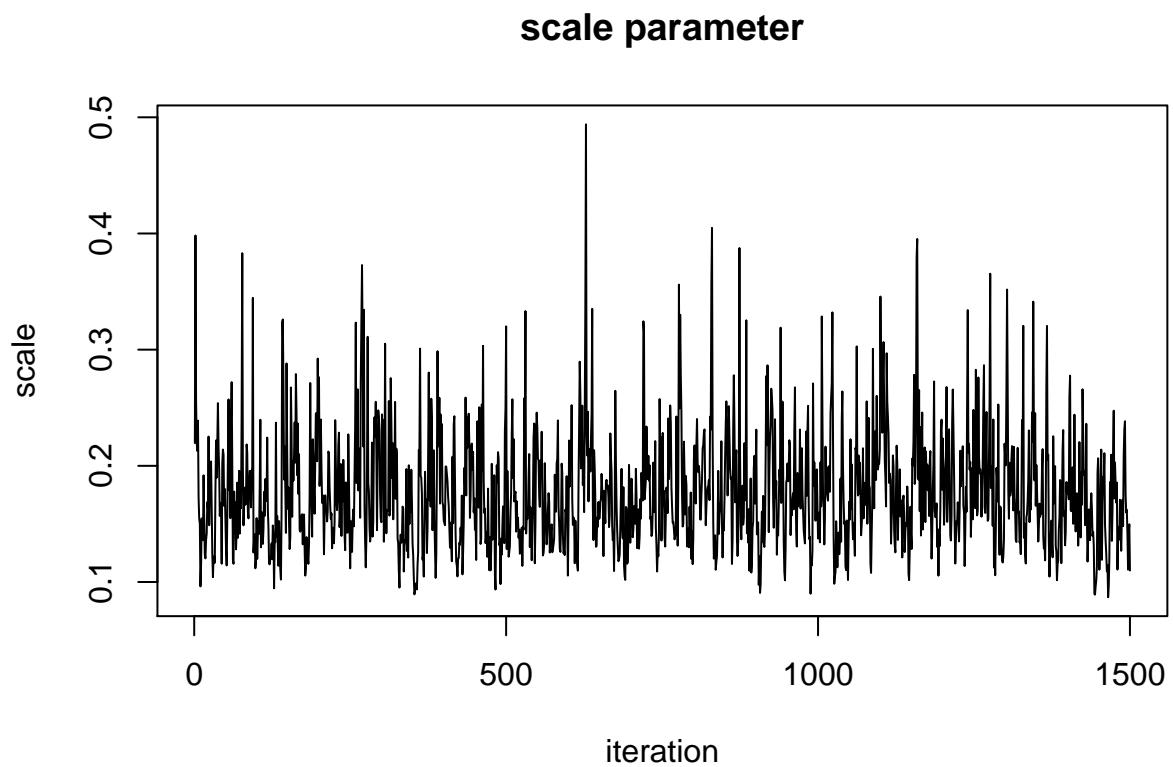
When evaluating these trace plots, we are hoping to see a “stationary distribution” that looks like white noise. This trace plot looks like it might have a little autocorrelation. One way to “fix” this is to thin the MCMC samples:

```
#####
# "thin" the MCMC samples

thinnedMCMC <- MCMCsamples[seq(1,chain.length,by=10),]
plot(1:nrow(thinnedMCMC),thinnedMCMC[, 'shape'],type="l",main="shape parameter",xlab="iteration",ylab="s")
```



```
plot(1:nrow(thinnedMCMC),thinnedMCMC[, 'scale'],type="l",main="scale parameter",xlab="iteration",ylab="s
```

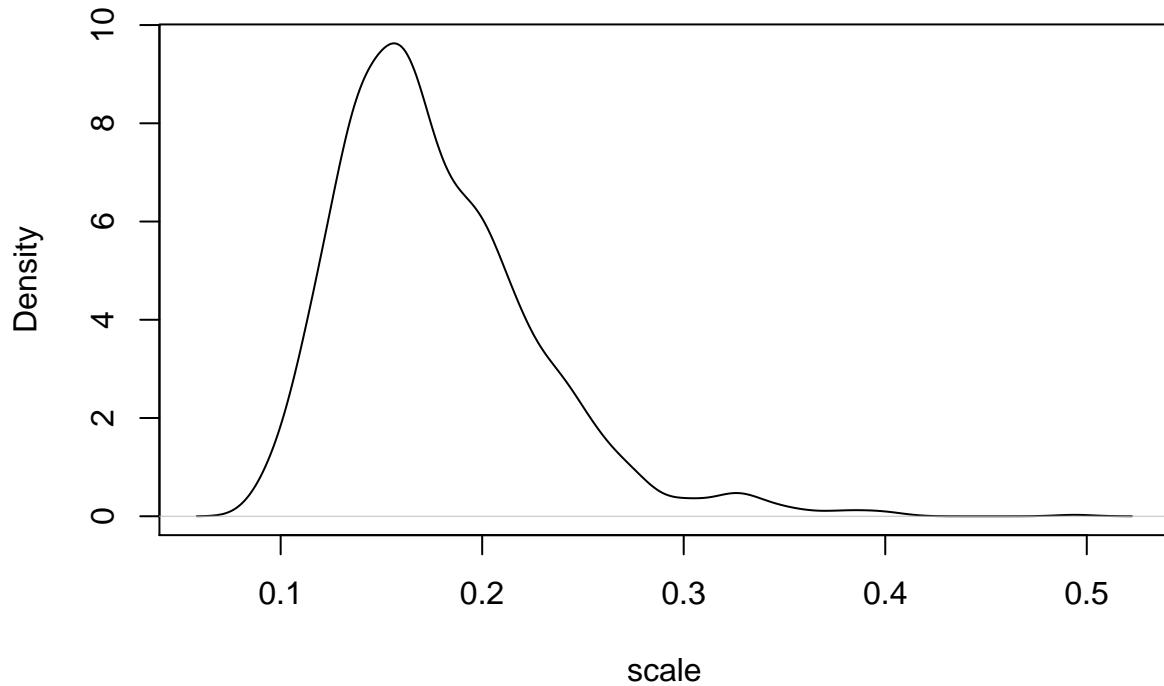


Now we can examine our posterior distribution!

```
# Visualize the posterior!
```

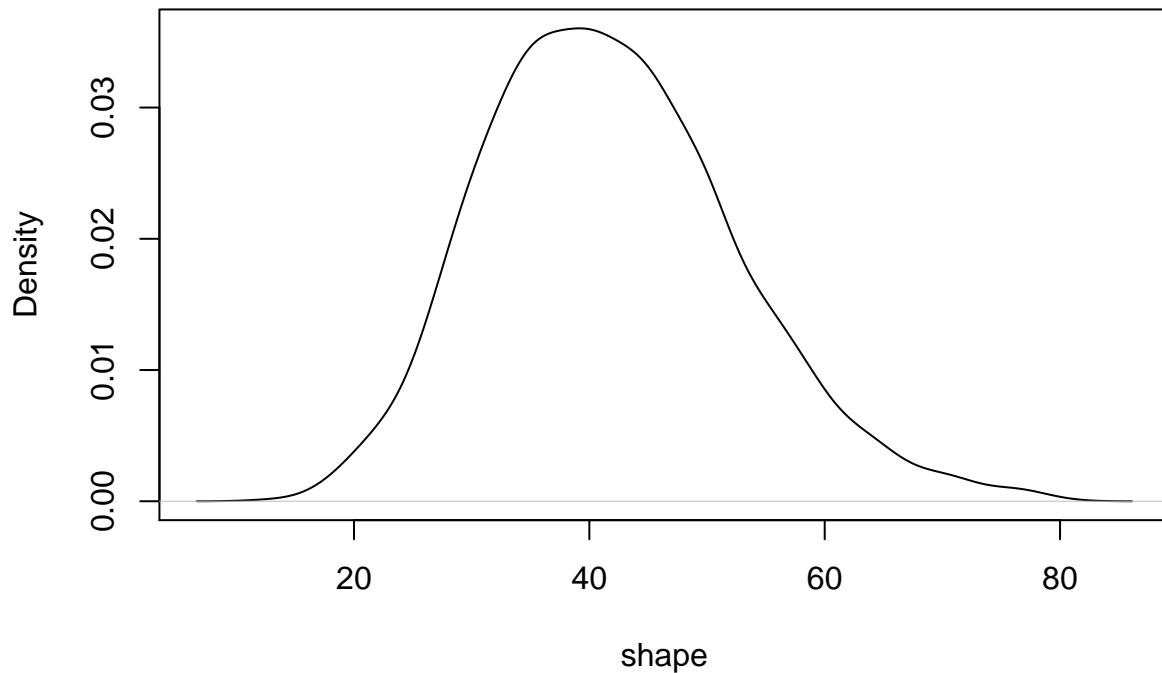
```
plot(density(thinnedMCMC[, 'scale']), main="scale parameter", xlab="scale")
```

### scale parameter



```
plot(density(thinnedMCMC[, 'shape']), main="shape parameter", xlab="shape")
```

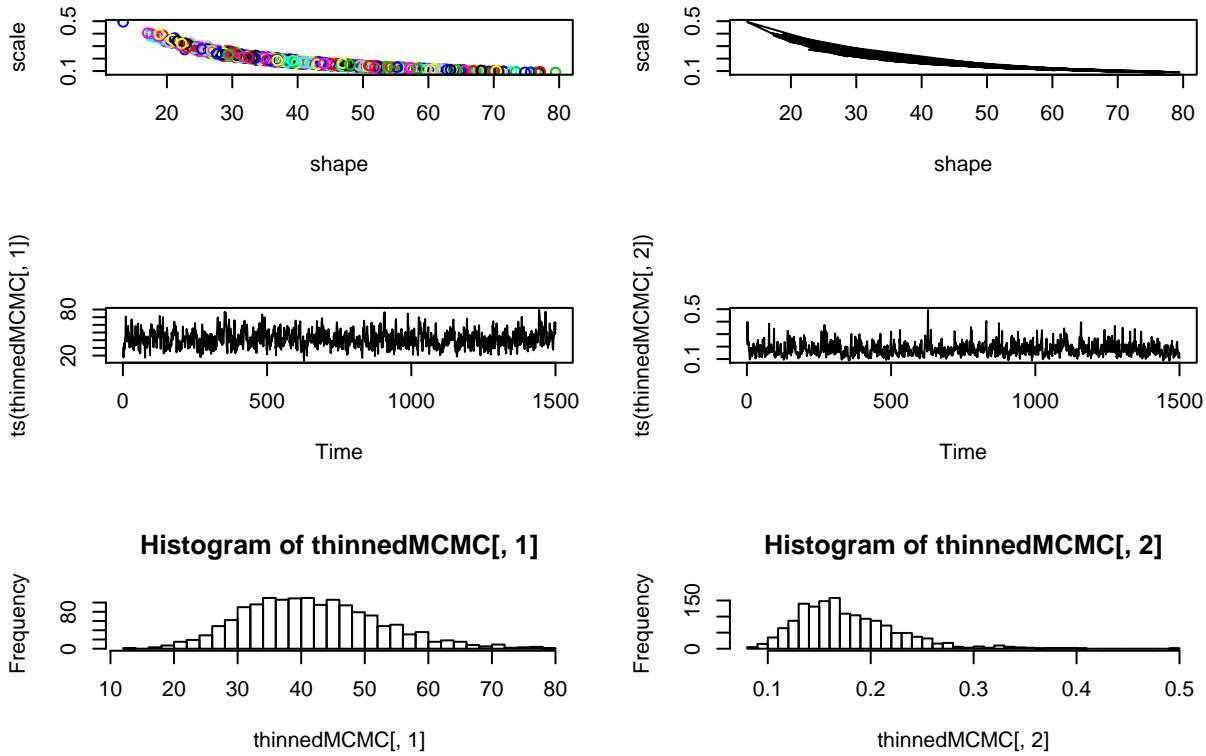
## shape parameter



And we can visualize as before.

```
#####
# More visual posterior checks...

par(mfrow=c(3,2))
plot(thinnedMCMC,col=1:10000)
plot(thinnedMCMC,type="l")
plot(ts(thinnedMCMC[,1]))
plot(ts(thinnedMCMC[,2]))
hist(thinnedMCMC[,1],40)
hist(thinnedMCMC[,2],40)
```



```
par(mfrow=c(1,1))
```

Hopefully it is clear that the Metropolis-Hastings MCMC method could be modified to fit arbitrary numbers of free parameters for arbitrary models. However, the M-H algorithm by itself is not necessarily the most easily generalizable to a host of different model types. That award tends to go to the **Gibbs sampler**. In lab we will play around with Gibbs samplers, mostly using a remarkable modeling language called **BUGS** (**B**ayesian **I**nference **U**sing **G**ibbs **S**ampling).

NOTE: BUGS implementations (e.g., JAGS) actually tend to use a combination of M-H and Gibbs sampling!

## Gibbs sampler

The Gibbs sampler is amazingly straightforward and powerful. Basically, the algorithm successively samples from the *full conditional* probability distribution – that is, the posterior distribution for arbitrary parameter  $i$  conditional on known values for all other parameters in the model.

In many cases, we can't work out the full posterior distribution for our model directly, but we **CAN** work out the conditional posterior distribution analytically if all parameters except for the parameter in question were known with certainty. This is especially true if we use conjugate priors for our model specification (what BUGS/JAGS tries to do!). Even if not, the full conditional is often analytically tractable. Nonetheless, even if it's not analytically tractable, we can use a univariate M-H procedure as a “brute force” last resort!

**Q:** Why is a Gibbs sampler usually much more efficient than a pure M-H sampler?

## Bivariate normal example

Again, remember that MCMC samplers are just a type of random number generator. We can use a Gibbs sampler to develop our own random number generator for a fairly simple known distribution. In this example (same as before), we use a Gibbs Sampler to generate random numbers from a standard bivariate normal probability distribution. Notice that the Gibbs sampler is in many ways more simple and straightforward than the M-H algorithm.

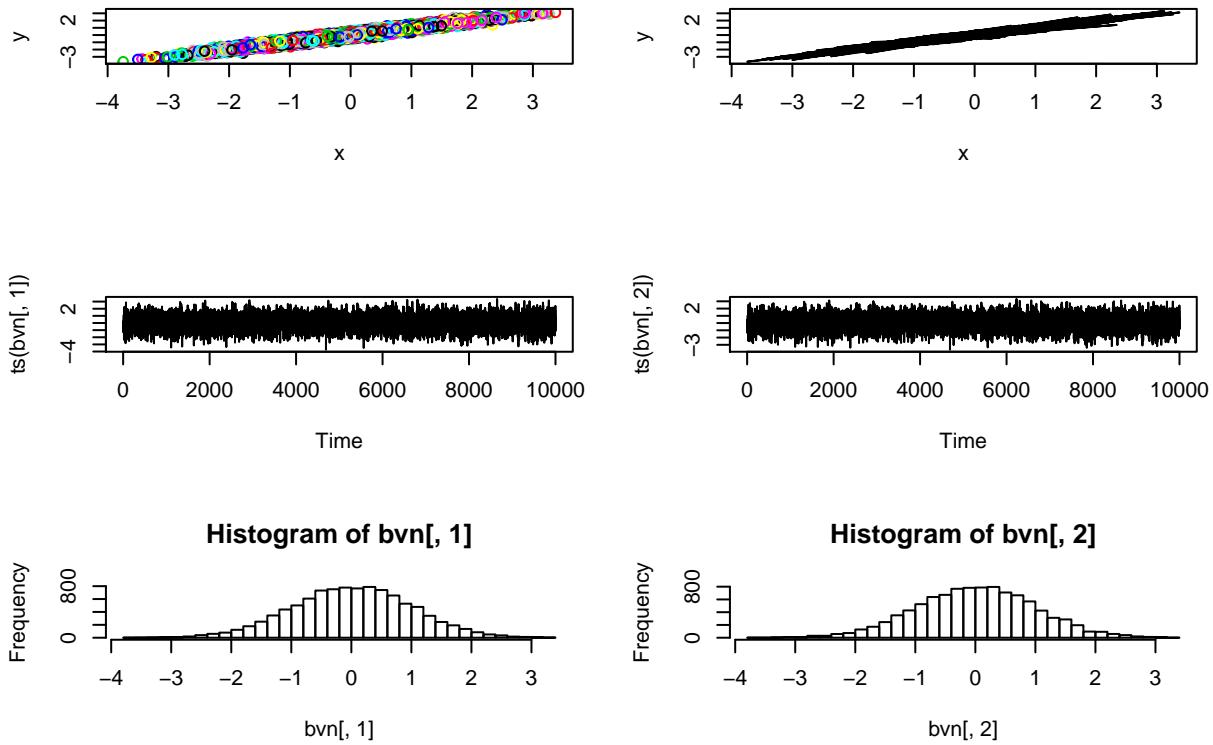
We don't need a Gibbs Sampler for this simple example. One way to do this would be to use the following code, which draws and visualizes an arbitrary number of independent samples from the bivariate standard normal distribution.

```
#####
# Simple example of a Gibbs sampler
#####

#####
# first, recall our simple bivariate normal sampler

rbvn<-function (n, rho){ #function for drawing an arbitrary number of independent samples from the biv
  x <- rnorm(n, 0, 1)
  y <- rnorm(n, rho * x, sqrt(1 - rho^2))
  cbind(x, y)
}

bvn<-rbvn(10000,0.98)
par(mfrow=c(3,2))
plot(bvn,col=1:10000)
plot(bvn,type="l")
plot(ts(bvn[,1]))
plot(ts(bvn[,2]))
hist(bvn[,1],40)
hist(bvn[,2],40)
```



```
par(mfrow=c(1,1))

#####
# Now construct a Gibbs sampler alternative

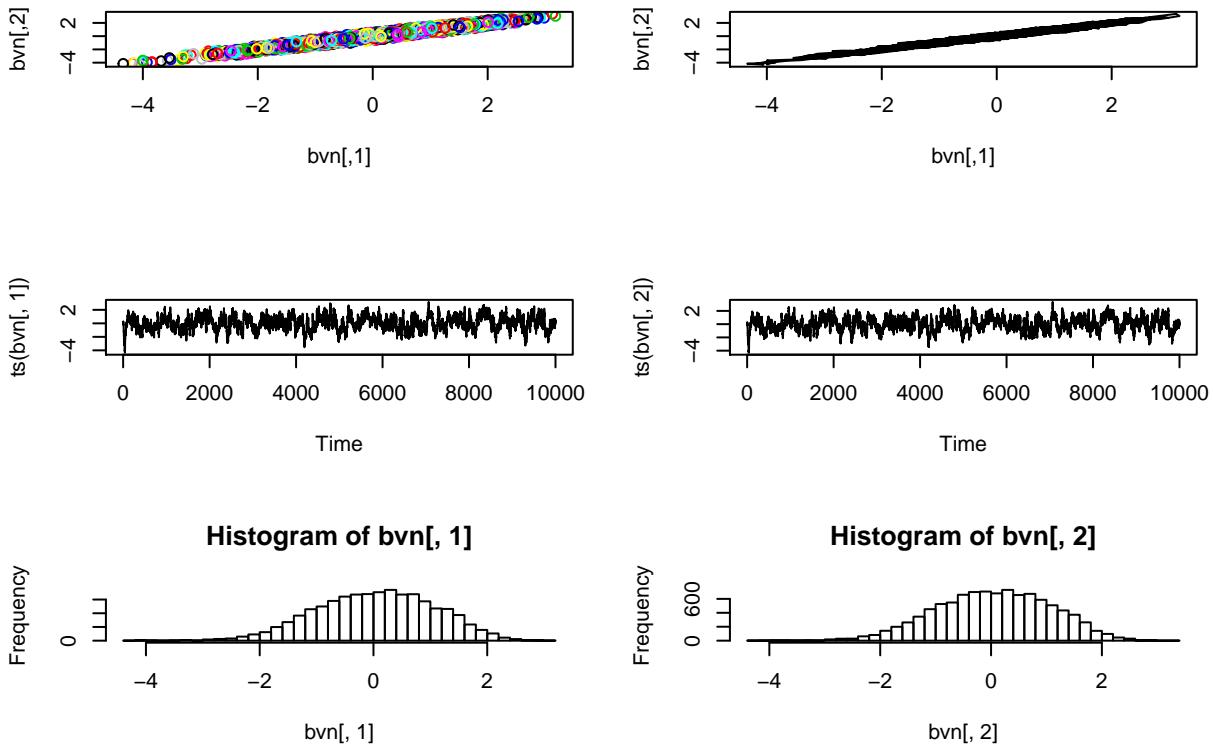
gibbs<-function (n, rho){      # a gibbs sampler implementation of a bivariate random number generator
  mat <- matrix(ncol = 2, nrow = n)    # matrix for storing the random samples
  x <- 0
  y <- 0
  mat[1, ] <- c(x, y)          # initialize the markov chain
  for (i in 2:n) {
    x <- rnorm(1, rho * y, sqrt(1 - rho^2))      # sample from x conditional on y
    y <- rnorm(1, rho * x, sqrt(1 - rho^2))      # sample from y conditional on x
    mat[i, ] <- c(x, y)
  }
  mat
}
```

Then we can use the Gibbs sampler to get random samples from this known distribution...

```
#####
# Test the Gibbs sampler

bvn<-gibbs(10000,0.98)
par(mfrow=c(3,2))
plot(bvn,col=1:10000)
plot(bvn,type="l")
```

```
plot(ts(bvn[,1]))
plot(ts(bvn[,2]))
hist(bvn[,1],40)
hist(bvn[,2],40)
```



```
par(mfrow=c(1,1))
```

There is quite a bit of apparent autocorrelation in the samples of the markov chain here. Gibbs samplers frequently have this issue!

## Back to Myxomatosis!

### Aside: the BUGS language

Finally, let's build a Gibbs sampler for our favorite Myxomatosis example! To do this, we will use the BUGS language, as implemented in JAGS, to help us!

The BUGS language looks similar to R, but there are several key differences:

- First of all, BUGS is a compiled language, so the order of operations in your code doesn't really matter
- BUGS is not vectorized- you need to use FOR loops for just about everything!
- Several probability distributions are parameterized very differently in BUGS. Notably, the normal distribution is parameterized with a mean and a precision ( $1/Variance$ ).

Here is the myxomatosis example, as implemented in the BUGS language:

NOTE: this code looks a little like R, but don't be confused- this is not R!

```

model {

#####
# LIKELIHOOD
#####
for(obs in 1:n.observations){
  titer[obs] ~ dgamma(shape,rate)
}

#####
# PRIORS
#####
shape ~ dgamma(0.001,0.001)
scale ~ dgamma(0.01,0.01)
rate <- 1/scale  # convert the scale parameter to a "rate" for BUGS
}

```

We can use the “cat” function in R to write out this model to a text file in your working directory:

```

#####
# Myxomatosis example in BUGS modeling language

#####
# Write the BUGS model to file

cat("
model {

#####
# LIKELIHOOD
#####
for(obs in 1:n.observations){
  titer[obs] ~ dgamma(shape,rate)
}

#####
# PRIORS
#####
shape ~ dgamma(0.001,0.001)
scale ~ dgamma(0.01,0.01)
rate <- 1/scale
}

", file="BUGSmodel.txt")

```

Now that we have the BUGS model packaged as a text file, we “package” the data into a single list object that contains all the relevant data referenced in the BUGS code:

```

#####
# Encapsulate the data into a single "list" object

myx.data.for.bugs <- list(
  titer = Myx$titer,
  n.observations = length(Myx$titer)
)
```

```
myx.data.for.bugs
```

```
## $titer
## [1] 5.207 5.734 6.613 5.997 6.612 6.810 5.930 6.501 7.182 7.292 7.819
## [12] 7.489 6.918 6.808 6.235 6.916 4.196 7.682 8.189 7.707 7.597 7.112
## [23] 7.354 7.158 7.466 7.927 8.499
##
## $n.observations
## [1] 27
```

Then we need to define the initial values for all parameters. It is convenient to define this as a function, so that each MCMC chain can be initialized with different starting values. This will become clear later!

```
#####
# Function for generating random initial values for all free parameters
```

```
init.vals.for.bugs <- function(){
  init.list <- list(
    shape=runif(1,20,100),
    scale=runif(1,0.05,0.3)
  )
  return(init.list)
}
```

```
init.vals.for.bugs()
```

```
## $shape
## [1] 46.97861
##
## $scale
## [1] 0.1962645
```

```
init.vals.for.bugs()
```

```
## $shape
## [1] 36.49894
##
## $scale
## [1] 0.2905416
```

```
init.vals.for.bugs()
```

```
## $shape
## [1] 29.31525
##
## $scale
## [1] 0.2834338
```

Now we can call JAGS!

```
#####
# Run JAGS!!!!
#####
```

```
library(R2jags)
```

```
## Loading required package: rjags
```



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*****	56%
*****	58%
*****	60%
*****	62%
*****	64%
*****	66%
*****	68%
*****	70%
*****	72%

```

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|
| ****| 98%
|
| ****| 100%

```

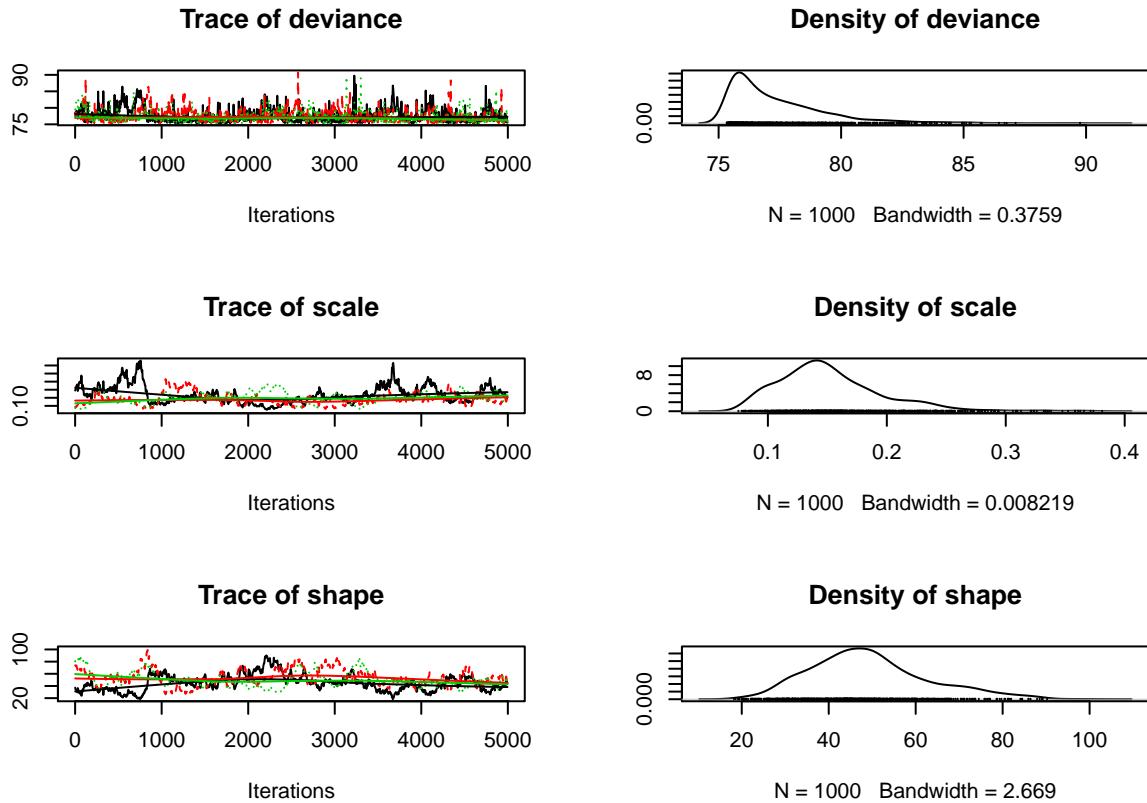
```
jagsfit.mcmc <- as.mcmc(jags.fit) # convert to "MCMC" object (coda package)

summary(jagsfit.mcmc)

## 
## Iterations = 1:4996
## Thinning interval = 5
## Number of chains = 3
## Sample size per chain = 1000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean        SD  Naive SE Time-series SE
## deviance 77.3505  2.00868 0.0366733      0.136426
## scale     0.1519   0.04439 0.0008104      0.006158
## shape     49.2844 13.54732 0.2473391      2.035749
##
## 2. Quantiles for each variable:
##
##           2.5%       25%       50%       75%       97.5%
## deviance 75.38343 75.8713 76.7336 78.2276 82.6929
## scale     0.08599  0.1221  0.1451  0.1736  0.2538
## shape     27.02071 39.9048 47.8913 56.6369 80.2778

```

```
plot(jagsfit.mcmc)
```



### Assessing convergence

This is probably a good time to talk about convergence of MCMC chains on the stationary posterior distribution. The above plots don't look great. We want to see white noise, and we want to see chains that look similar to one another.

The first check is just visual- we look for the following to assess convergence:

- The chains for each parameter, when viewed as a “trace plot” should look like white noise, or similar.
- Multiple chains with different starting conditions should look the same!!

One way we might be able to do a better job here is to run the chains longer and discard the initial samples as a *burn in*!

We can also try to reduce serial autocorrelation by thinning our chain- here we retain only 1 out of every 20 samples.

```
#####
# Run the chains for longer!

jags.fit <- jags(data=myx.data.for.bugs, inits=init.vals.for.bugs, parameters.to.save=params.to.store, n.i

## Compiling model graph
## Resolving undeclared variables
## Allocating nodes
## Graph information:
```

```

##      Observed stochastic nodes: 27
##      Unobserved stochastic nodes: 2
##      Total graph size: 37
##
## Initializing model
##
##  

| | 0%  

| ++++++ | 10%  

| +++++++ | 20%  

| ++++++++ | 30%  

| +++++++ | 40%  

| +++++++ | 50%  

| +++++++ | 60%  

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| +++++++ | 80%  

| +++++++ | 90%  

| +++++++ | 100%  

##  

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| * | 2%  

| ** | 5%  

| **** | 8%  

| ***** | 10%  

| ***** | 12%  

| ***** | 15%  

| ***** | 18%  

| ***** | 20%  

| ***** | 22%  

| ***** | 25%  

| ***** | 28%

```

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*****	75%
*****	78%
*****	80%
*****	82%
*****	85%
*****	88%
*****	90%
*****	92%
*****	95%

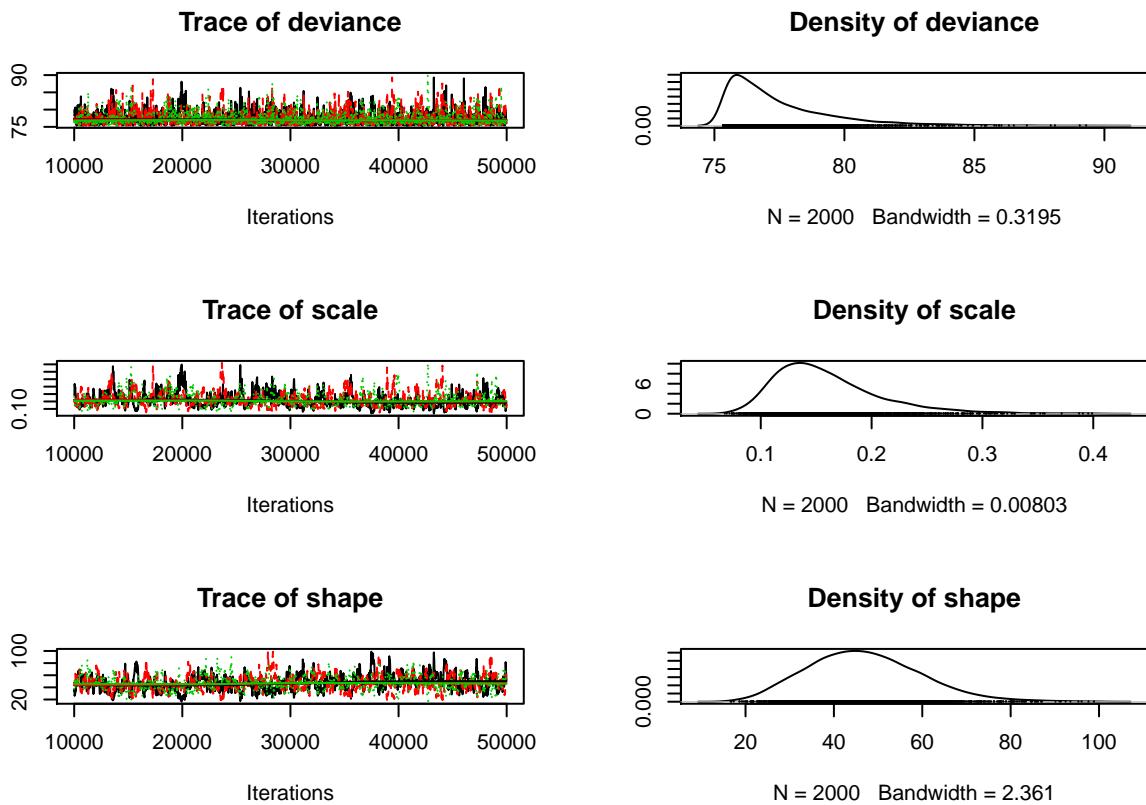
```

| *
| **** | 98%
|
| *****| 100%
jagsfit.mcmc <- as.mcmc(jags.fit) # convert to "MCMC" object (coda package)

summary(jagsfit.mcmc)

##
## Iterations = 10001:49981
## Thinning interval = 20
## Number of chains = 3
## Sample size per chain = 2000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean      SD  Naive SE Time-series SE
## deviance 77.4270 2.04505 0.0264015      0.064220
## scale     0.1598 0.04823 0.0006226      0.002522
## shape     46.9281 12.75558 0.1646738      0.648651
##
## 2. Quantiles for each variable:
##
##           2.5%     25%     50%     75%   97.5%
## deviance 75.38271 75.9444 76.7844 78.2451 83.0197
## scale     0.09269 0.1256 0.1504 0.1834 0.2796
## shape     25.13005 37.8354 46.1196 54.8379 74.2652
plot(jagsfit.mcmc)

```



Just visually, this looks better. Now we can use some more quantitative convergence metrics.

### The Gelman-R Rubin diagnostic

One simple and intuitive convergence diagnostic is the *Gelman-Rubin diagnostic*, which assesses whether chains are more different from one another than they should be on the basis of simple Monte Carlo error:

```
#####
# Run convergence diagnostics
gelman.diag(jagsfit.mcmc)

## Potential scale reduction factors:
##
##          Point est. Upper C.I.
## deviance     1.00     1.00
## scale        1.00     1.01
## shape        1.01     1.03
##
## Multivariate psrf
##
## 1.01
```

In general, values of 1.1 or higher are considered poorly converged (sometimes the less stringent criterion of 1.2 is used). If so, you should try running longer chains!

So this model looks pretty good!!

## Useful links for MCMC

Darren Winkinson's research blog

Where do the full conditionals come from in Gibbs sampling?

-go to next lecture-