Assignment 3

Bjørn Christian Weinbach

13th November, 2020

Clear R environment

```
rm(list = ls())
```

Problem 1. Random number generation and Monte Carlo integration.

a) Generate n independent samples from distribution

In this problem the task is to sample n independent samples from the probability distribution

$$p(x) = \frac{2^{\frac{1}{4}}\Gamma\left(\frac{3}{4}\right)}{\pi} \exp\left(-\frac{x^4}{2}\right), \qquad -\infty < x < \infty$$

One might wish to implement a regular Metropolis-Hastings random walk for sampling this distribution, but there is one major disadvantage for using this approach: (Wikipedia contributors 2020)

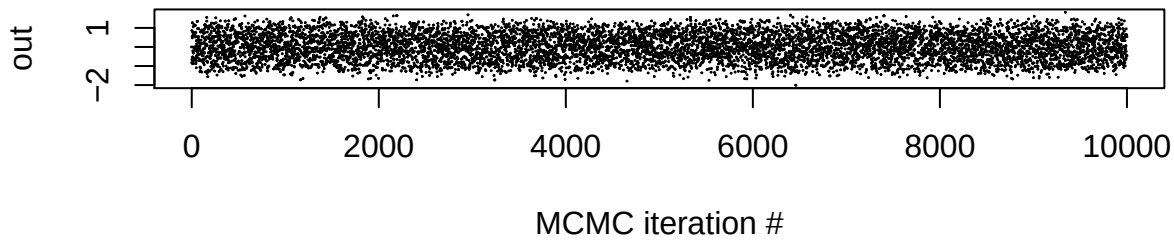
The samples are correlated, even though over the long term they do correctly follow $p(x)$. This is due to the fact that given that you know the current time step, you have a pretty good estimate of what the value of the next one is. In short, the adjacent samples are autocorrelated.

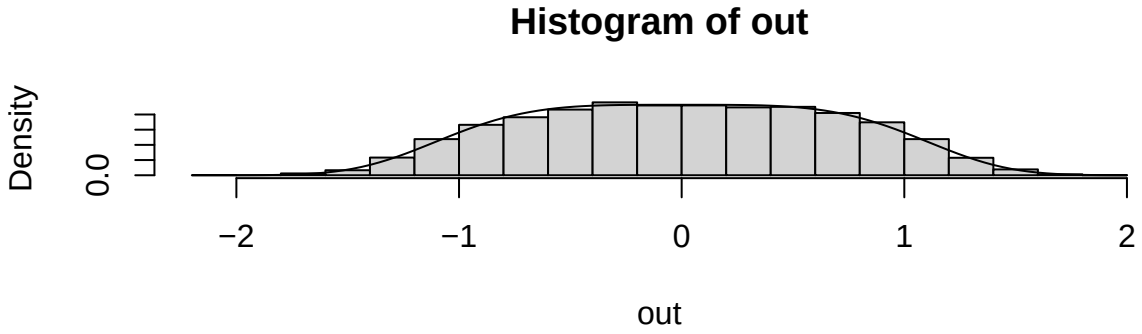
Because of this and the task specifically asking for independent samples. A regular random walk metropolis-hastings approach is not feasible, we then turn to the independent metropolis-hastings approach:

In R:

```
# general 1d independence metropolis hastings
oneD.IRWMH <- function(prob,
                       sigma=1.0,
                       theta1=0.0,
                       Nsamp=10000){
  res <- numeric(Nsamp)
  # allocate memory
  res[1] <- theta1
  # old importance weight
  wt.old <- prob(res[1])/dnorm(res[1], sd=sigma)
  Nacc <- 0
    for(i in 2:Nsamp){
      # proposal (note, independent of past)
      thetaStar <- rnorm(1, sd=sigma)
      # new importance weight
      wt.star <- prob(thetaStar)/dnorm(thetaStar, sd=sigma)
      # accept probability
```

```
      alpha <- min(1.0, wt.star/wt.old)
      # accept/reject
      if(runif(1) < alpha){
        res[i] <- thetaStar
        wt.old <- wt.star
        Nacc <- Nacc+1
      } else {
        res[i] <- res[i-1]
      }
    }
  return(res)
}

# pdf from mandatory pdf
pdf <- function(x) {
  return ((2^0.25*gamma(3/4)/pi) * exp(-x^4 / 2))
}


# sample n samples
n <- 10000
out <- oneD.IRWMH(pdf, theta1 = 0.0, sigma=1, Nsamp = n)

# plot
par(mfrow=c(2,1))
plot(1:length(out),out,pch=20,cex=0.1,xlab="MCMC iteration #")
hist(out, probability = TRUE)
curve(pdf, add = TRUE, -2, 2)
```





b) Generate n independent samples from distribution

Now let's sample from the distribution

$$p(x) = 2x\exp(-x^2), \qquad 0 < x < \infty$$

This function seems to be quite simple to find the CDF for and direct sampling via inverse transform sampling is possible. We get

$$F(x) = \int_0^x p(x) = 1 - e^{-x^2}$$

And by the inverse sampling method, we can calculate

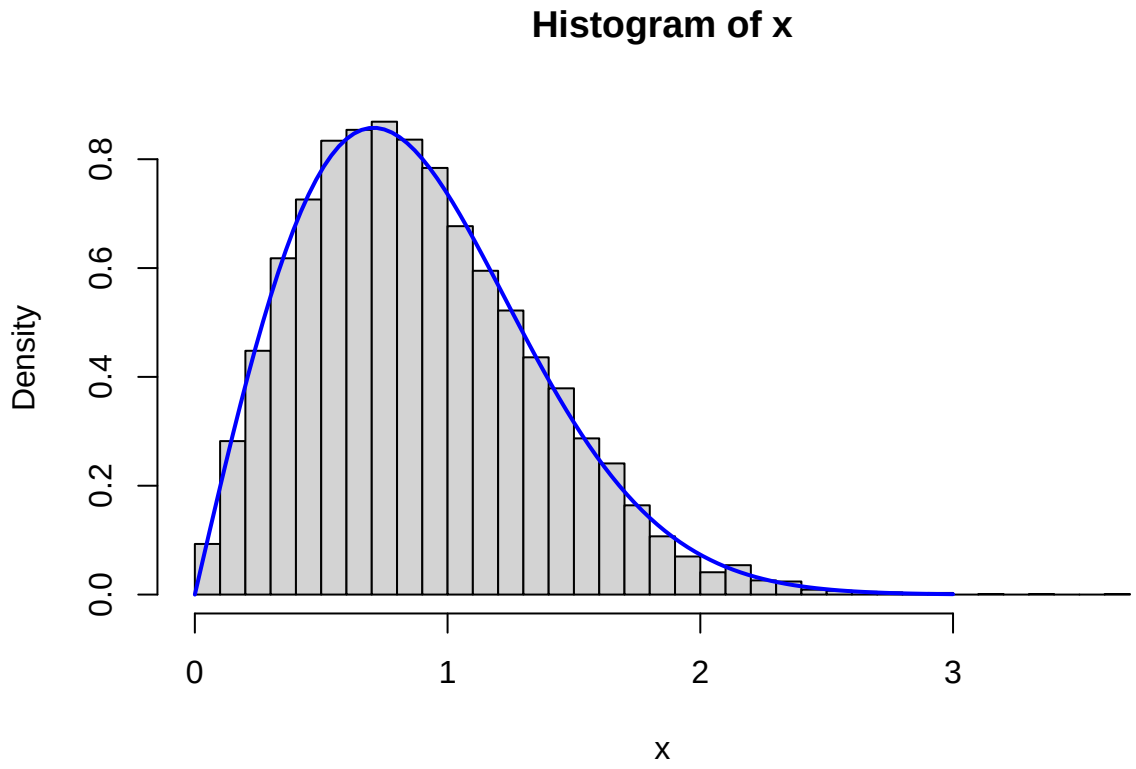
$$X = F^{-1}(U) = \pm\sqrt{-\ln(1-u)}$$

Given the nature of calculating square roots, we get positive and negative X values but since the support of the pdf clearly states that $0 < x < \infty$ we reject the negative values.

in R:

```
# Use inverse sampling method to sample from
# p(x) = 2x exp(-x^2)
inverse_sampling <- function(Nsamples) {
  # Sample n samples from uniform distribution
  u <- runif(Nsamples)
  # Return X = F^-1(U)
```

```r
  return(sqrt(-log(1-u)))
}

# PDF
pdf2 <- function(x) {
  return(2*x * exp(-x^2))
}

x <- inverse_sampling(10000)
hist(x, breaks=40, probability = TRUE)
curve(pdf2, col="blue", lwd=2, 0, 3, add = TRUE)
```



c) Evaluate integral using monte-carlo integration

Now we will consider the integral

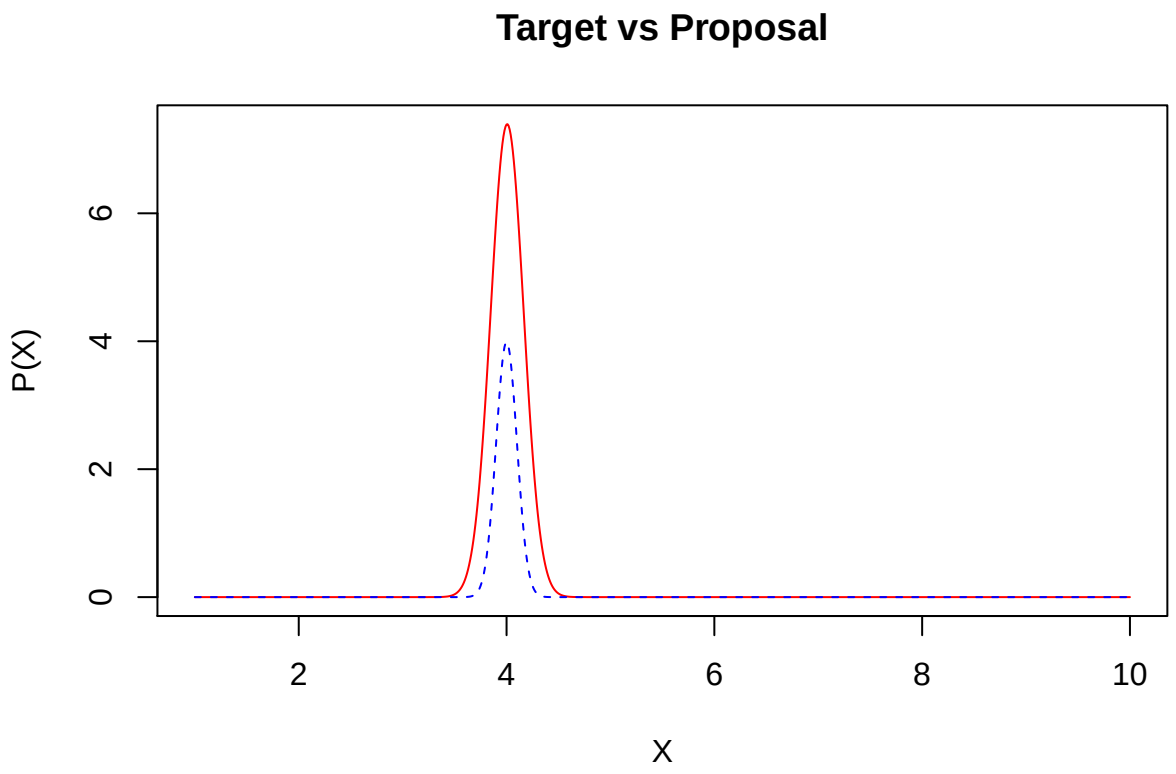
$$\int_0^\infty \exp(\sqrt{x}) \exp(-20(x-4)^2)\, dx$$

Let's evaluate the integral using importance sampling. First let's plot the function $g(x)$ that is being integrated:

In R:

```r
g <- function(x) {
 exp(sqrt(x))*exp(-20*(x-4)^2)
}
```

```r
f <- function(x) {
  dnorm(x, mean=4, sd=0.1)
}

x<-seq(1,10,0.01); y1=g(x); y2=f(x)
plot(x, y1, type="l", pch=19, col="red", xlab="X", ylab="P(X)",
     main="Target vs Proposal")
lines(x, y2, pch=18, col="blue", type="l", lty=2)
legend(1, 95, legend=c("Line 1", "Line 2"),
       col=c("red", "blue"), lty=1:2, cex=0.8)
```



With the function we want to integrate in $g(x)$ in red and the $f(x)$ in dashed blue. We want to calculate $E\left(\frac{g(x)I(x\in A)}{f(x)}\right)$ by sampling X values from f and calculating the empirical mean of $\frac{g(x)I(x\in A)}{f(x)}$ where I is the indicator function for the support.

```r
importance <- function(Nsamp) {
  # Sample from f
  x <- rnorm(Nsamp, 4, 0.1)
  # calculate empirical mean
  return(mean((g(x)*(x>0))/(f(x))))
}

# Estimate of integral using importance sampling
importance(100000)
```

```
## [1] 2.910019
```

```r
# Numerical integration
integrate(g, 0, Inf)$value
```

```
## [1] 2.929669
```

Problem 2. Smile shaped target

a) Sampling using 2 random walk

In this exercise, we shall sample from the distribution

$$\log g(\boldsymbol{\theta}) = -\frac{\theta_1^2}{2} - \frac{(\theta_2 - \theta_1^2)^2}{2}, \qquad \infty < x < \infty$$

To do this, an 2D random walk with multivariate normal proposals as been implemented in R.

In the code below, a 2D random walk with proposal

$$N(\boldsymbol{\theta}, \Sigma)$$

Where

$$\Sigma = \begin{bmatrix} 2, 0 \\ 0, 2 \end{bmatrix}$$

and

$$\boldsymbol{\theta} = \begin{pmatrix} 0 \\ 0 \end{pmatrix}$$

Yielded the greatest effective sample size.

In R:

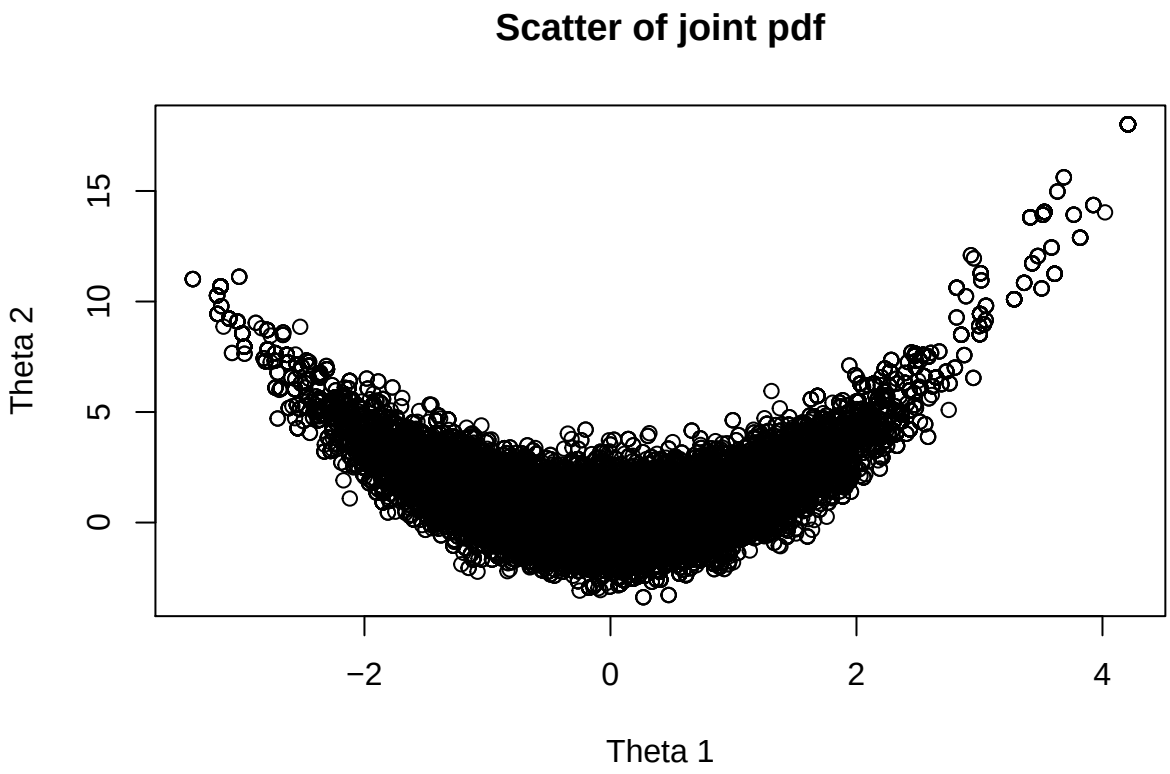
```r
# Load the multivariate normal library
library(mvtnorm)
library(coda)

# Target function from
logg <- function(theta) {
  return(-theta[1]^2/2 - (theta[2] - theta[1]^2)^2 /2)
}

# 2D Random walk using log g
smile_shaped <- function(logg,
                         sigma=diag(2),
                         theta=c(0.0, 0.0),
                         Nsamp=100000){

  # Reserve 2xNsamp matrix with zeros
  res <- matrix(0, Nsamp, 2)

  # Set initial conditions
  res[1,] <- theta

  # Calculate old log-probability
  logold <- logg(theta)
```

```
  # accept counter
  Nacc <- 0

  # Iterate no of samples.
  for(i in 2:Nsamp){
    # Proposal step
    new <- res[i-1,] + rmvnorm(1, theta, sigma)
    # Log-p of proposal step
    lognew <- logg(new)
    # Evaluate step
    logfrac <- exp(min(0.0,lognew-logold))
    # Accept or reject new step
    if(runif(1)<logfrac && is.finite(logfrac)){
      # accept
      res[i,] <- new
      logold <- lognew
      Nacc <- Nacc+1
    } else {
      # reject
      res[i,] <- res[i-1,]
    }
  }
  print(paste("Accept prob: ", Nacc/Nsamp))
  return(res[5000:Nsamp,])
}

# Covariance matrix
sigma <- matrix(c(4.5, 0, 0, 4.5), nrow=2, ncol=2)
m <- smile_shaped(logg=logg, sigma=sigma, c(0.0, 0.0), 50000)
```

```
## [1] "Accept prob:  0.23616"
```

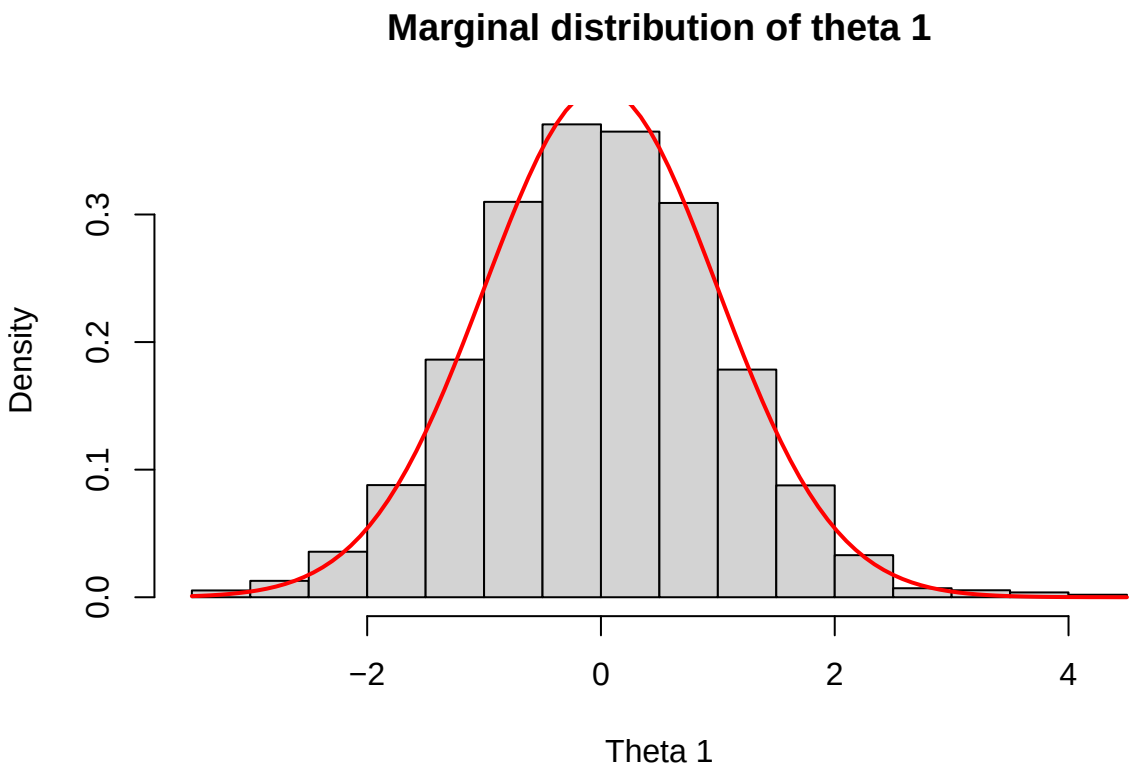
Let's plot the "Smile shaped" distribution:

```
# Plot multivariate distribution
plot(m, xlab="Theta 1", ylab="Theta 2", main="Scatter of joint pdf")
```



Let's also see if the marginal distribution of θ_1 is standard normal:

```
# Plot marginal of theta1 and compare with standard normal
hist(m[,1], xlab="Theta 1", main="Marginal distribution of theta 1",
     probability=TRUE)
curve(dnorm(x, mean=0, sd=1),
      col="red", lwd=2, add=TRUE, yaxt="n")
```



To check if we have explored the distribution well, let's calculate the effective sample size of $theta_1$ and $theta_2$.

```
ESS <- function(x) {
  coda::effectiveSize(x)
}

ESS(m[,1])
```

```
##     var1
## 1962.347
```

```
ESS(m[,2])
```

```
##    var1
## 656.132
```

Problem 3. IMH for simple logistic regression problem

```
# Load the data set
df <- data.frame(read.table("logistic_regression_data.txt"))
x <- df$x
y <- df$y

# function returning a log-posterior kernel for theta
logistic.lp <- function(theta) {
  alpha <- theta[1]
```

```
  beta <- theta[2]
  # log-likelihood
  Eeta <- exp(alpha + beta*x)
  p <- Eeta/(1.0 + Eeta)
  log.like <- sum(dbinom(y, size=1, prob = p, log=TRUE))

  # priors
  log.prior <- dnorm(alpha, sd=10, log=TRUE) + dnorm(beta, sd=10, log=TRUE)

  # log-posterior kernel
  return(log.like+log.prior)
}
```

a) Sample α and β using metropolis-hasting and bayesian inference

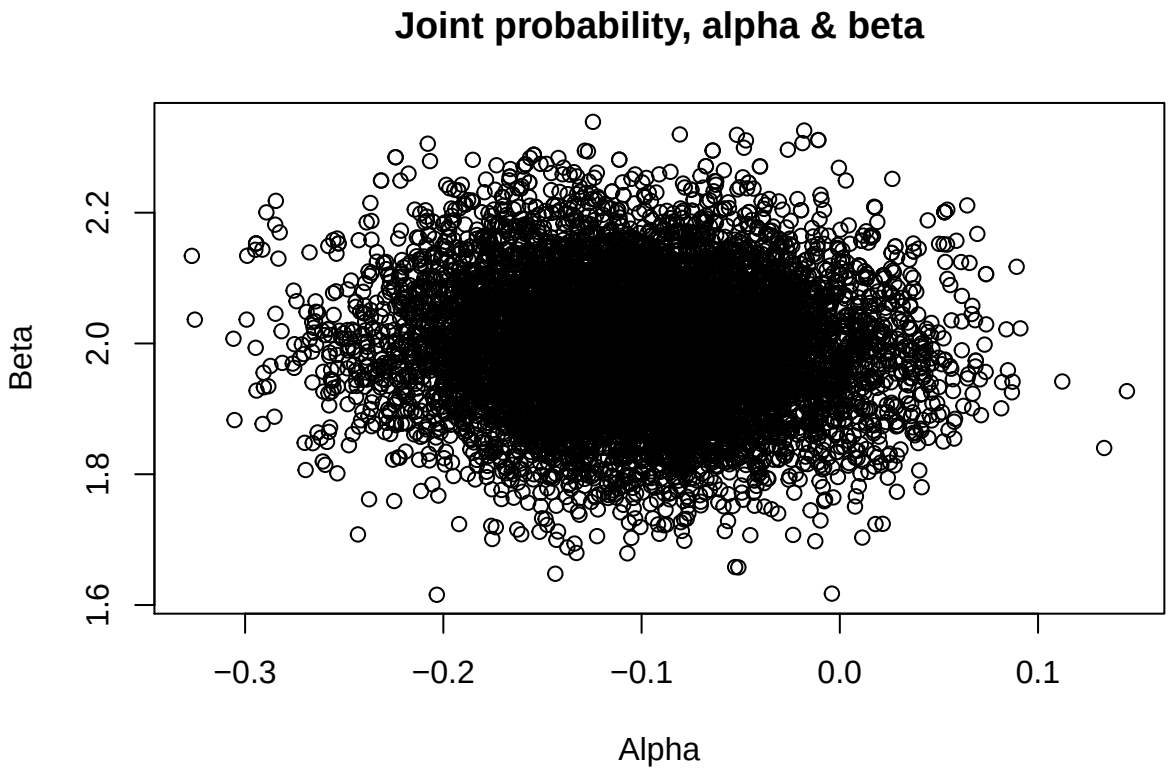
In this task, we will use independent metropolis-hastings sampling for the posterior distribution $p(\boldsymbol{\theta}|\boldsymbol{y})$ using a $N(\hat{\theta}, \delta\hat{\Sigma})$ proposal distribution.

In R:

```
# Independent sampler
IndepMH <- function(lprob, theta=c(0, 0), sigma=diag(2), Nsamp=1000, S=1){
  # Allocate space
  res <- matrix(0, Nsamp, 2)
  # Set initial values
  res[1,] <- theta
  # Old importance
  pold <- lprob(theta) - dmvnorm(theta, mean=theta ,sigma=sigma, log=TRUE)
  # No of accept
  Nacc <- 0
  for (i in 2:Nsamp){
    # Sample theta from multivariate normal with scaled sigma
    new <- rmvnorm(1, theta, S*sigma)
    # Importance of new theta
    pnew <- lprob(new) - dmvnorm(new, mean=theta, sigma=sigma, log=TRUE)
    frac <- exp(min(0.0, pnew-pold))
    if(runif(1)<frac && is.finite(frac)){
      # Accept
      res[i,] <- new
      pold <- pnew
      Nacc <- Nacc+1
    } else {
      # Reject
      res[i,] <- res[(i-1),]
    }
  }
  print(paste0("accept rate : ",Nacc/Nsamp))
  return(res[1000:Nsamp,])
}

sigma <- matrix(c(0.00653,-0.00058,-0.00058,0.01689),2,2)

m <- IndepMH(logistic.lp, c(-0.102, 1.993), sigma, 10000, 0.6)
```

```
## [1] "accept rate : 0.984"
```

```
plot(m, xlab = "Alpha", ylab="Beta", main="Joint probability, alpha & beta")
```



Calculate ESS

```
ESS(m[,1])
```

```
##     var1
## 8693.267
```

```
ESS(m[,2])
```

```
##     var1
## 8165.144
```

b/c) Plot quantiles of data and find $x*$ such that $P(m(x*) > 0.8) = 0.99$

To solve this problem, we calculate $m(x*)$ the median and quantiles for $x \in [-5, 5]$ where α and β has been estimated based on the dataset provided in the mandatory assignment.

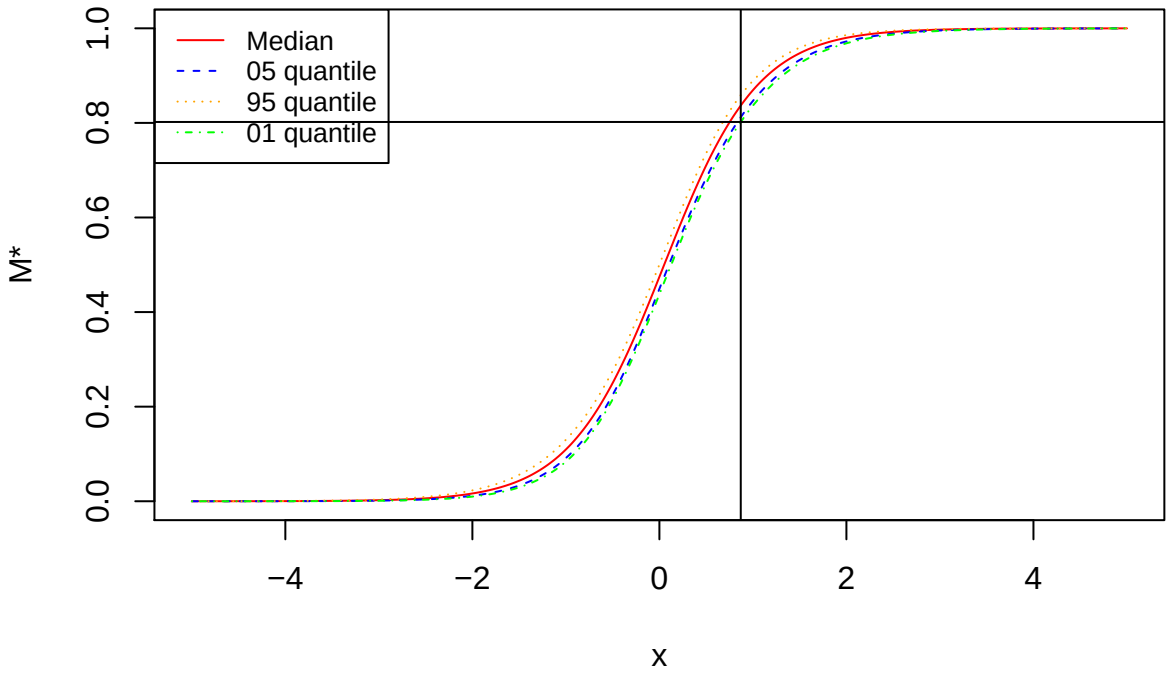
We use the following algorithm to solve this problem:

1. Given data, estimate α, β using independent metropolis hastings
2. Select sequence of $x*$ we want to explore
3. Iterate through each value of $x*$
4. Calculate median and 01th, 05th and 95th quantiles and return these as a vector
5. Store vector as row in matrix
6. Repeat steps 4-5 for each value in $x*$

When this algorithm terminates, we have a 2D matrix of medians and quantiles for all $x*$. We use this for plotting and finding the $x*$ where $P(m(x*) > 0.8) = 0.99$

In R:

```
# Plotdist is function for calculating values for plotting
plotdist <- function (x) {
  # Calculate m(x*)
  mstar <- exp(m[,1] + m[,2]*x) / (1 + exp(m[,1] + m[,2]*x))
  # calulcate median given x*
  med <- median(mstar)
  # Caltulate quantiles given x*
  quant05 <- quantile(mstar, 0.05)
  quant95 <- quantile(mstar, 0.95)
  quant01 <- quantile(mstar, 0.01)
  # return vector of calculations
  return(c(med, quant05, quant95, quant01))
}

# sequence of x* values
x <- seq(-5, 5, 0.01)
# plot
plotmat <- matrix(0, length(x), 4)
# set index
i <- 0
# Loop through all x* values in sequence
for (val in x) {
  # increment index for each value in xÆ
  i <- i+1
  plotmat[i,] <- plotdist(val)
}

# First value larger than 0.8 (for plotting horizontal)
horizontal <- plotmat[, 4][plotmat[, 4] > 0.8][1]

# First x-value of m-value with 99% probability of being larger than 0.8
vertical <- x[Position(function(x) x > 0.8, plotmat[, 4])]

# Plot all medians and quantiles conditional on x*
plot(x, plotmat[, 1], type="l", col="red", ylab="M*")
lines(x, plotmat[, 2], type="l", col="blue", lty=2)
lines(x, plotmat[, 3], type="l", col="orange", lty=3)
lines(x, plotmat[, 4], type="l", col="green", lty=4)
# Add vertical line for x values
abline(v = vertical, col="black")
# add horizontal line for m values
abline(h = horizontal, col="black")
legend("topleft", legend=c("Median", "05 quantile", "95 quantile", "01 quantile"),
       col=c("red", "blue", "orange", "green"), lty=1:4, cex=0.8)
```




```
# X* where P(M(X*) > 0.8) = 0.99
print(vertical)
```

```
## [1] 0.87
```

Problem 4. Gibbs sampler for simple linear regression model

a) Find conditional posteriors.

The posterior for τ is given as

$$\pi(\tau|\alpha,\beta,\boldsymbol{y}) \sim \text{gamma}\left(\frac{n}{2}+1, \frac{1}{\frac{1}{2}\sum_{i=1}^{n}(y_i-\alpha-\beta x_i)^2+1}\right)$$

To calculate the posterior of α we see by inspection that the posterior log-density kernel is possibly on the form $\log\pi(\alpha|\beta,\tau,\boldsymbol{y}) = a + b\alpha + c\alpha^2$ which tells us the posterior distribution is normal and that the constant a is unimportant.

Let's calculate $\log\pi(\alpha|\beta,\tau,\boldsymbol{y})$.

From the log-density kernel in the assignment description, we get

$$\log\pi(\alpha|\beta,\tau,\boldsymbol{y}) = c'_\alpha - \frac{\tau}{2}\sum_{i=1}^{n}(y_i-\alpha-\beta x_i)^2 - \frac{\alpha^2}{200}.$$

Where c'_α is a unimportant constant containing all values not dependent on α. By squaring the term in the sum and adding unimportant values to c'_α we now get.

$$\log \pi(\alpha|\beta,\tau,\boldsymbol{y}) = c'_\alpha - \frac{\tau}{2}(n\alpha^2 + \alpha\sum_{i=1}^{n}(2\beta x_i - 2y_i)) - \frac{\alpha^2}{200}$$

By multiplying the τ term and reshuffling we get

$$\log \pi(\alpha|\beta,\tau,\boldsymbol{y}) = c_\alpha - \tau\sum_{i=1}^{n}(\beta x_i - y_i)\alpha - \left(\frac{\tau n}{2} + \frac{1}{200}\right)\alpha^2$$

And we have

$$b_\alpha = -\tau\sum_{i=1}^{n}(\beta x_i - y_i)$$

and

$$c_\alpha = -\left(\frac{\tau n}{2} + \frac{1}{200}\right)$$

and the posterior (from the lecture notes) is

$$\pi(\alpha|\beta,\tau,\boldsymbol{y}) \sim N\left(-\frac{b_\alpha}{2c_\alpha}, -\frac{1}{2c_\alpha}\right)$$

And we do the same for $\pi(\beta|\alpha,\tau,\boldsymbol{y})$

From the log-density kernel in the assignment description, we get

$$\log \pi(\beta|\alpha,\tau,\boldsymbol{y}) = c'_\beta - \frac{\tau}{2}\sum_{i=1}^{n}(y_i - \alpha - \beta x_i)^2 - \frac{\beta^2}{200}.$$

Where c'_β is a unimportant constant containing all values not dependent on β. By squaring the term in the sum and adding unimportant values to c'_β we now get.

$$\log \pi(\beta|\alpha,\tau,\boldsymbol{y}) = c'_\beta - \frac{\tau}{2}\sum_{i=1}^{n}\left(2\alpha\beta x_i + \beta^2 x_i^2 - 2\beta x_i y_i\right) - \frac{\beta^2}{200}$$

By multiplying the τ term and reshuffling we get

$$\log \pi(\beta|\alpha,\tau,\boldsymbol{y}) = c'_\beta - \tau\left(\sum_{i=1}^{n}\alpha x_i - \sum_{i=1}^{n}x_i y_i\right)\beta - \left(\frac{\tau}{2}\sum_{i=1}^{n}x_i^2 + \frac{1}{200}\right)\beta^2$$

And we have

$$b_\beta = -\tau\left(\sum_{i=1}^{n}\alpha x_i - \sum_{i=1}^{n}x_i y_i\right)$$

and

$$c_\beta = -\left(\frac{\tau}{2}\sum_{i=1}^{n}x_i^2 + \frac{1}{200}\right)$$

and the posterior (from the lecture notes) is

$$\pi(\beta|\alpha,\tau,\boldsymbol{y}) \sim N\left(-\frac{b_\beta}{2c_\beta}, -\frac{1}{2c_\beta}\right)$$

b) Gibbs sampler with three blocks

Load the data

```
# Load regression data
df <- data.frame(read.table(file="linear_regression_data.txt"))
x <- df$x
y <- df$y
```

Let's implement the gibbs sampler

```
gibbs <- function(x, y, theta=c(1.0, -1.2, 1.0), Nsamp=10000) {
  # Result matrix (State stored thrice each iteration)
  res <- matrix(0.0, 3*Nsamp+1, 3)
  # Set state 1 to initial values
  res[1, ] <- theta
  # Set gamma shape parameter
  gammashape <- length(x)/2 + 1
  # Set counter
  k <- 2
  # Iterate...
  for(i in 1:Nsamp){

      # Block 1. Alpha
      balpha <- -theta[3]*sum(theta[2]*x - y)
      calpha <- -theta[3]*length(y)*0.5 - 1/200
      theta[1] <- rnorm(1, -balpha/(2*calpha), -1/(2*calpha))
      # store state
      res[k, ] <- theta
      k <- k+1

      # Block 2. Beta
      bbeta <- -theta[3]*(sum(x*theta[1]) - sum(x*y))
      cbeta <- -theta[3]*0.5*sum(x^2) - 1/200
      theta[2] <- rnorm(1, -bbeta/(2*cbeta), -1/(2*cbeta))
      # store state
      res[k, ] <- theta
      k <- k+1

       # Block 3. Tau
      gammascale <- 1/(0.5*sum((y - theta[1] - theta[2]*x)^2)) + 1
      theta[3] <- rgamma(1, gammashape, scale = gammascale)
      # store state
      res[k, ] <- theta
      k <- k+1
  }
  # Return results minus burn in
  return(res[500:k-1,])
}

# Get samples to matrix
m <- gibbs(x, y)
```

```r
# Calculate column means
colMeans(m)
```

```
## [1]  1.088701 -1.207007 52.035515
```

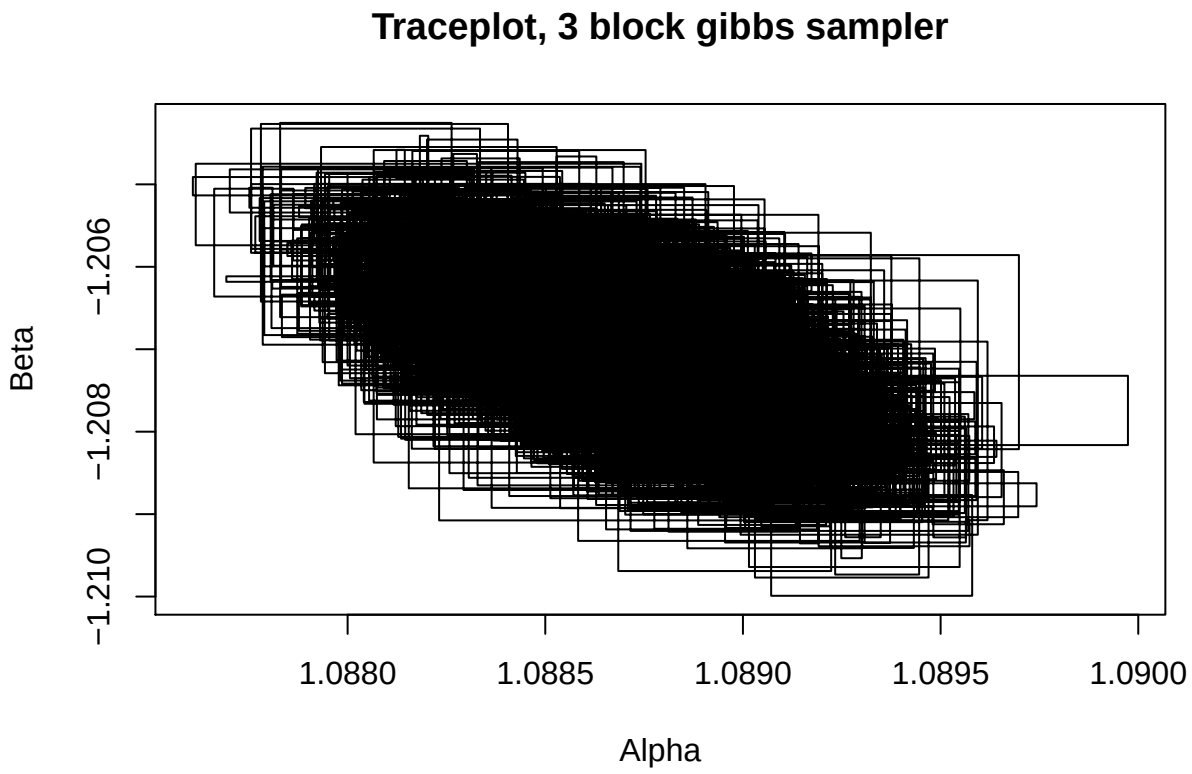
```r
# Compre with one simple linear regression
lm(y~x, data=df)
```

```
##
## Call:
## lm(formula = y ~ x, data = df)
##
## Coefficients:
## (Intercept)            x
##       1.089       -1.207
```

c) Check if samples have converged

Our means seem pretty good, let's plot trace plots of alpha and beta.

```r
# Traceplot alpha vs beta
plot(m[,1], m[,2], type="l", xlab="Alpha", ylab="Beta",
     main="Traceplot, 3 block gibbs sampler")
```



Also, let's calculate all the effective sample sizes for each variable

```r
ESS(m[,1])
```

```
##     var1
```

```
## 4945.713
```

```
ESS(m[,2])
```

```
##     var1
## 4889.256
```

```
ESS(m[,3])
```

```
##    var1
## 10027.6
```

We see that we have a pretty good sample size. Now let's investigate whether we can improve this by reducing the no of blocks and making blocks less dependent.

d) Improve gibbs sampler

Let's combine the blocks for α and β from two normal distribution to one block of a multinormal distribution. With a posterior distribution $\pi(\alpha, \beta|\tau, \boldsymbol{y}) \sim N(\boldsymbol{\mu}, \boldsymbol{\Sigma})$

where

$$\boldsymbol{\Sigma} = -\boldsymbol{c}^{-1}$$

and

$$\boldsymbol{\mu} = -\boldsymbol{c}^{-1}\boldsymbol{b}$$

and $\boldsymbol{c}$ and $\boldsymbol{b}$ is given in the assignment.

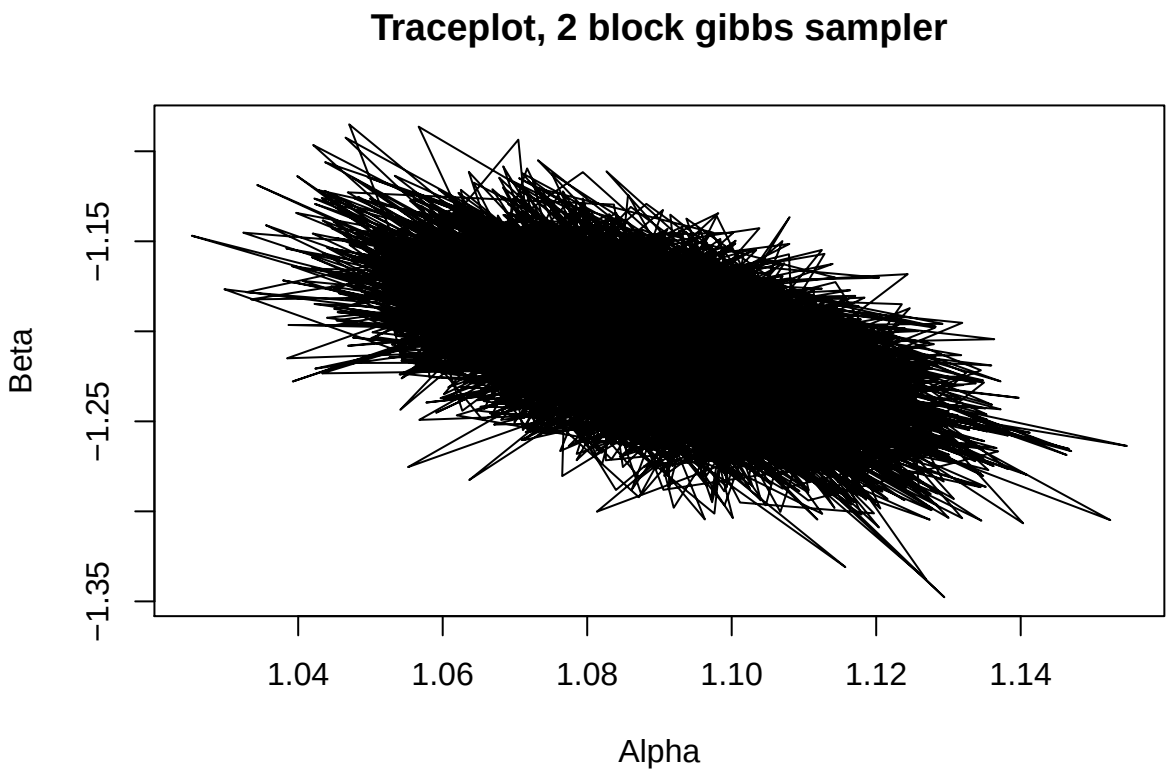
Let's alter the function for gibbs sampling to have two blocks instead.

```
gibbs_multi <- function(x, y, theta=c(1.0, -1.2, 1.0), Nsamp=10000) {
  # Result matrix (State stored thrice each iteration)
  res <- matrix(0.0, 2*Nsamp+1, 3)
  # Set state 1 to initial values
  res[1, ] <- theta
  # Set gamma shape parameter
  gammashape <- length(x)/2 + 1
  # Set counter
  k <- 2

  # Calculations that can be done once for improvment of performance
  # Sum of x
  sumx <- sum(x)
  # Sum of x^2
  sumx2 <- sum(x^2)
  # Sum of y
  sumy <- sum(y)
  # Sum of xy
  sumyx <- sum(x*y)
  # No of datapoints
  n <- length(x)

  # Iterate...
  for(i in 1:Nsamp){

    # Block 1. [alpha, beta]
```

```
    # C from assignment description
    c <- matrix(c(-n*theta[3] - 0.01, -theta[3]*sumx,
                  -theta[3]*sumx, -theta[3]*sumx2 - 0.01), nrow=2, ncol=2)
    # b from assignment description
    b <- c(theta[3]*sumy, theta[3]*sumyx)

    theta[1:2] <- rmvnorm(1, -solve(c)%*%b, -solve(c))
    res[k, ] <- theta
    k <- k+1

     # Block 2. Tau
    gammascale <- 1/(0.5*sum((y - theta[1] - theta[2]*x)^2)) + 1
    theta[3] <- rgamma(1, gammashape, scale = gammascale)
    # store state
    res[k, ] <- theta
    k <- k+1
  }
  # Return results minus burn in
  return(res[500:k-1,])
}

m2 <- gibbs_multi(x, y)
colMeans(m2)
```

```
## [1]  1.088831 -1.207511 52.150151
```

```
plot(m2[,1], m2[,2], type = "l", main="Traceplot, 2 block gibbs sampler",
     xlab="Alpha", ylab="Beta")
```



Now, is this gibbs sampler better than our first implementation? Let's check the effective sample size:

```
ESS(m2[,1])
```

```
##     var1
## 10553.17
```

```
ESS(m2[,2])
```

```
##     var1
## 9752.093
```

```
ESS(m2[,3])
```

```
##     var1
## 11210.11
```

Which makes sense, we sampled *beta* and *alpha* with normal distributions dependent on the values of one another, in this case we sample both from a multinormal distribution according to the given covariance matrix where each pair of samples are independent from one another.

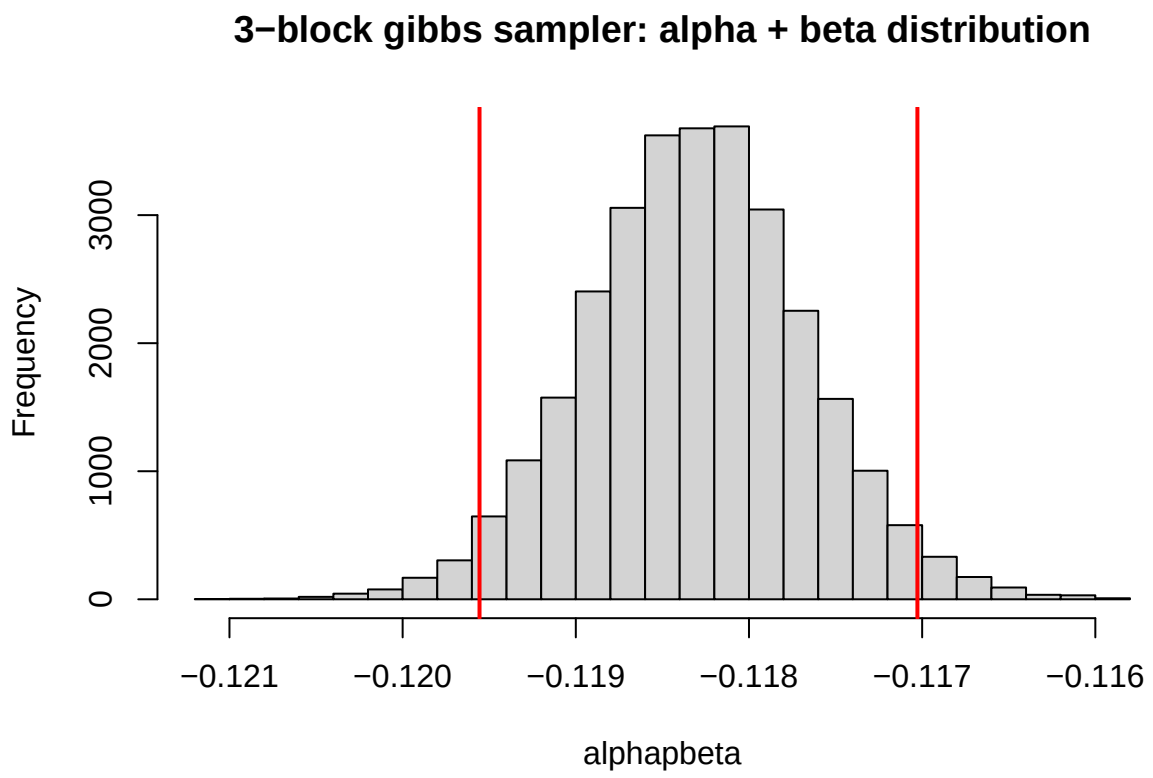
Fewer blocks and striving for independence among blocks will, according to the lectures, give better samples.

e) Investigate whether $\alpha + \beta = 0$

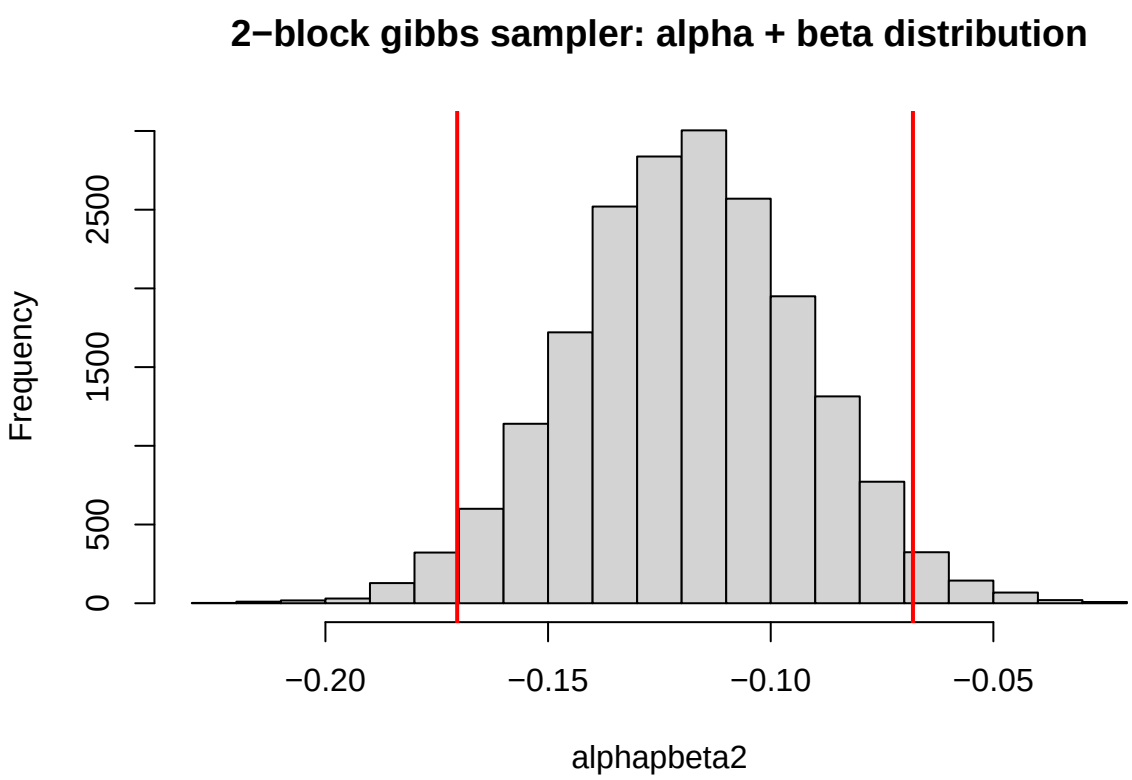
To do a simple "hypothesis test" using quantiles and our samples. for every sample, calculate $\alpha + \beta$ and store the values, calculate the 95% quantile confidence interval and plot the histogram with the interval.

This could be done more appropriately by using a more analytical approach for our calculations but we resort to this simple case.

```
alphapbeta <- m[,1] + m[,2]
hist(alphapbeta, breaks=25,
     main = "3-block gibbs sampler: alpha + beta distribution")
abline(v = quantile(alphapbeta, 0.975), col="red", lwd="2")
abline(v = quantile(alphapbeta, 1-0.975), col="red", lwd="2")
```




```
alphapbeta2 <- m2[,1] + m2[,2]
hist(alphapbeta2, breaks=25,
     main = "2-block gibbs sampler: alpha + beta distribution")
abline(v = quantile(alphapbeta2, 0.975), col="red", lwd="2")
abline(v = quantile(alphapbeta2, 1-0.975), col="red", lwd="2")
```



In the first distribution, we accept (with a significance of 5%), that $\alpha + \beta \neq 0$.

In the second distribution, we fail to reject the null-hypothesis that
$\alpha + \beta = 0$.

Problem 5. Simple linear regression analysis, bootstrap approach

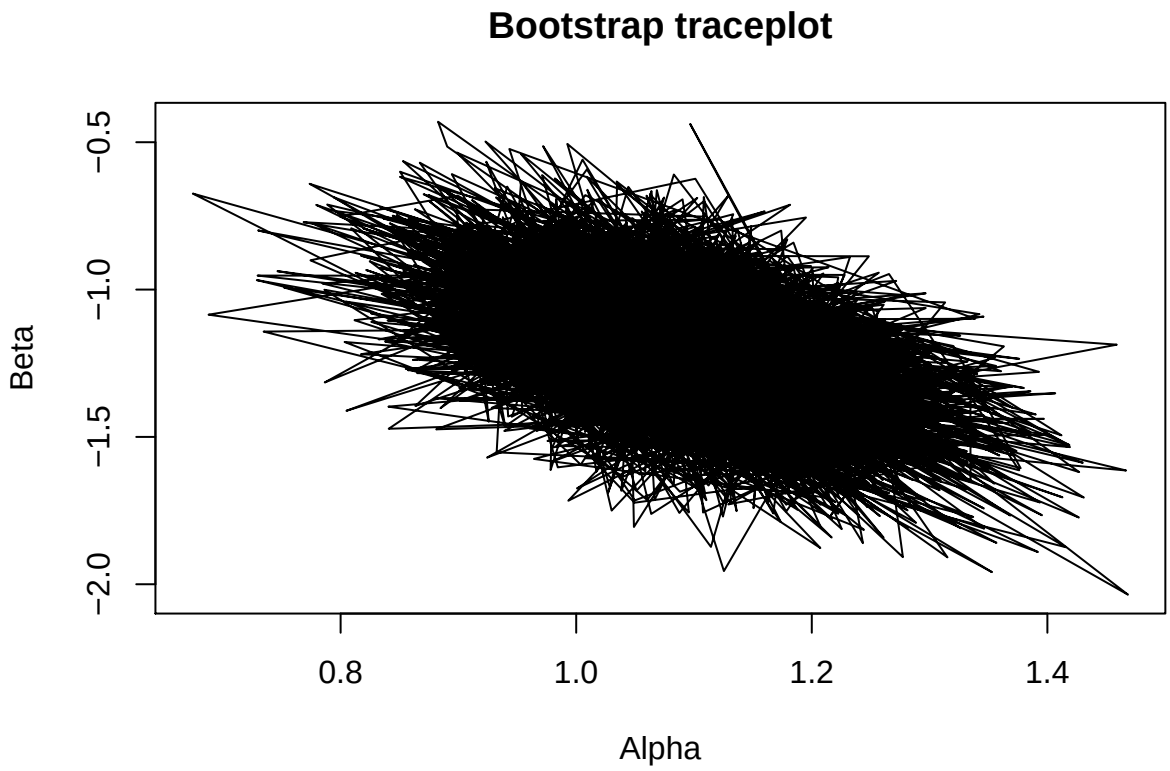
Now, let's address the same linear regression problem as problem 4 but instead of using bayesian inference, we consider a classical approach using bootstrapping.

In our case, our statistic will be the simple linear regression on bootstrapped datasets such that we get α and β pairs for each bootstrapped datasets and we can investigate their distribution.

Let's implement this in R:

```
# Import bootstrap library
library(boot)

# Our statistic (simple linear regression y ~ alpha + beta x)
slr <- function(data,i) {
  lm(data[i, 1]~data[i, 2],data = df)$coefficients
}

# Run bootstrap on our data
boot.obj <- boot(data = df, statistic = slr, R = 5000)

# Traceplot bootstrap estimate to compare with our bayesian approach
```

```r
plot(boot.obj$t[,1], boot.obj$t[,2], main="Bootstrap traceplot", type="l",
     xlab="Alpha", ylab="Beta")
```

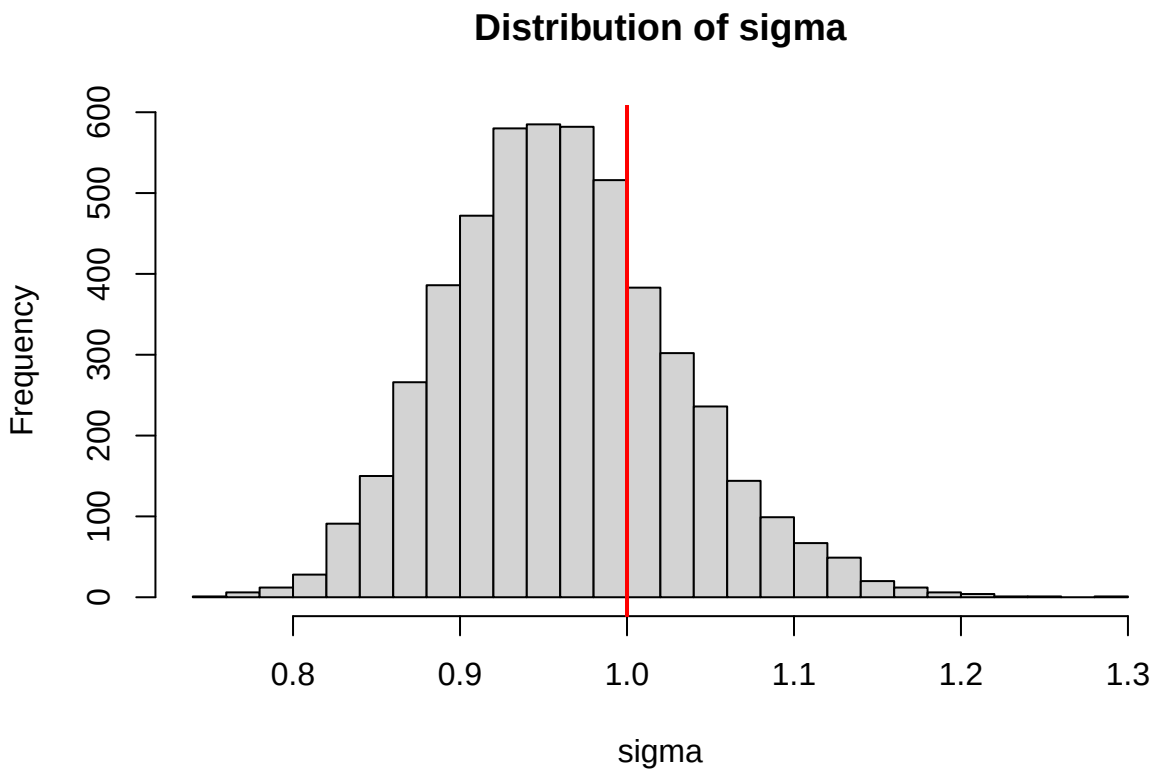


We see that out bootstrapped joint distribution is very similar to the bayesian joint distribution that we calculated in problem 4.

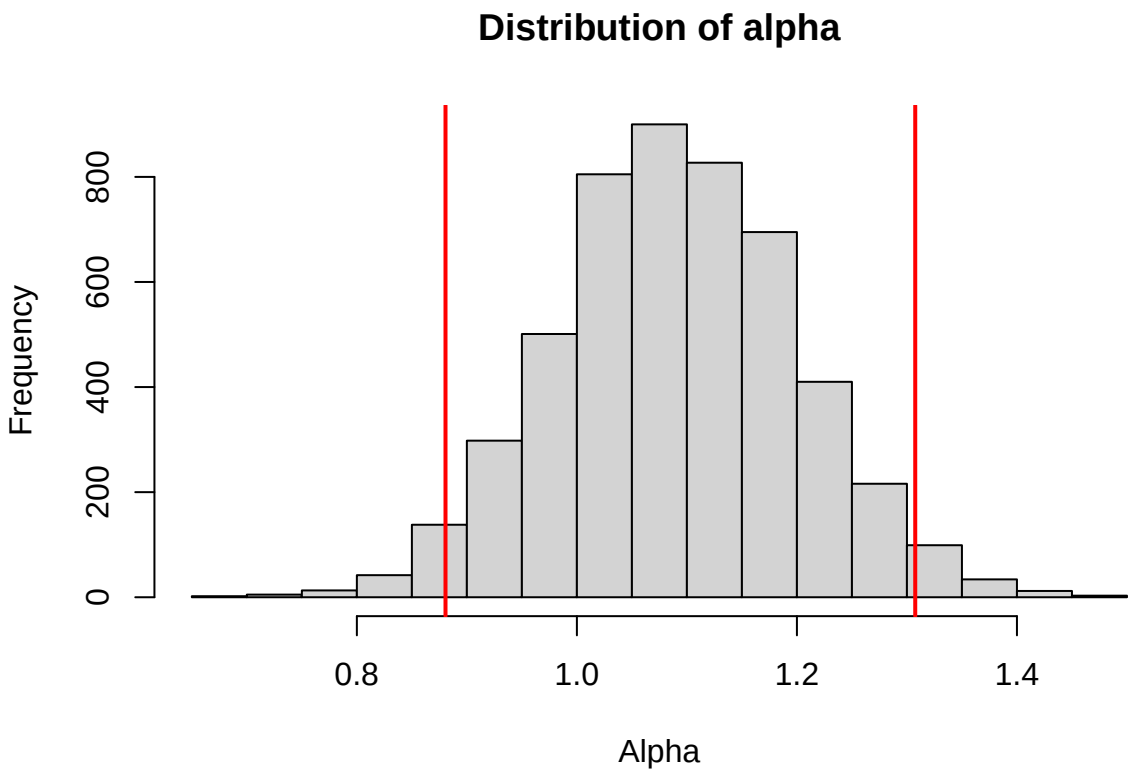
Now, let's go through each of the following cases

1. $\sigma = 1/\sqrt{\tau}$ is strictly smaller than 1.0
2. α is equal to 0
3. $\alpha + \beta$ is equal to 0

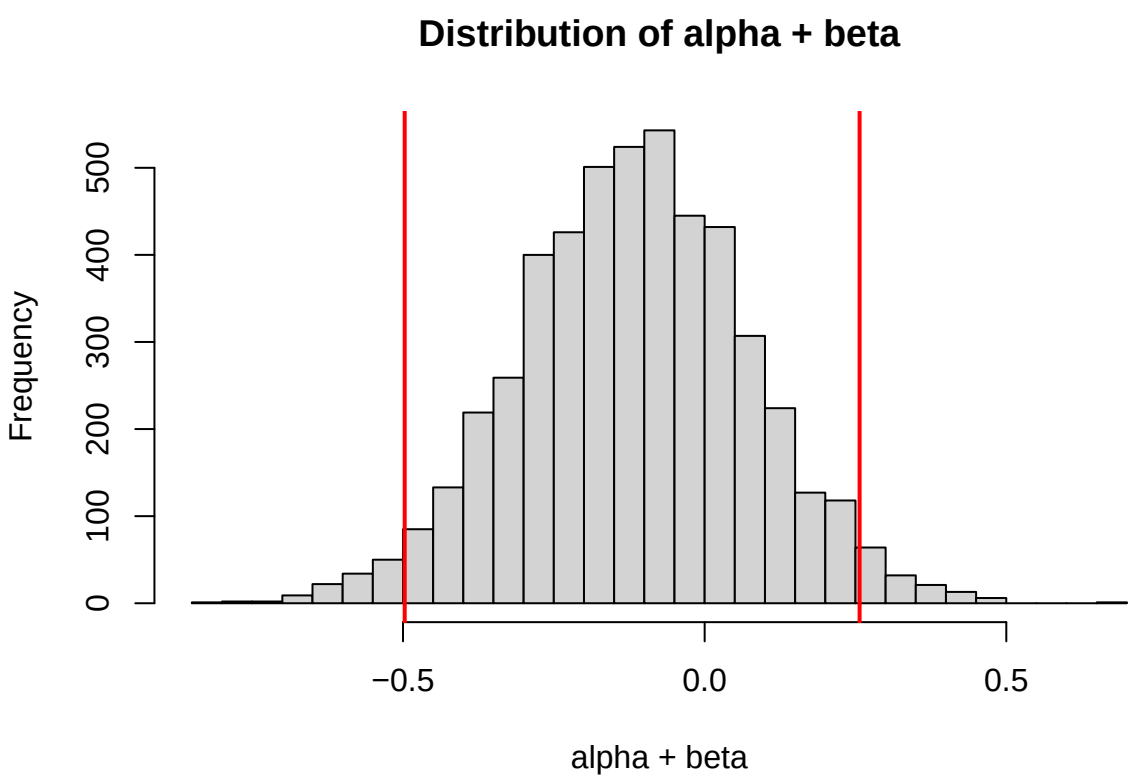
```r
# Set gamma shape parameter
gammashape <- length(x)/2 + 1

# Calculate sigma for every alpha-beta pair
sigma <- 1/sqrt(
  rgamma(5000, shape = gammashape,
  scale = 1/(1/2 * sum((y - mean(boot.obj$t[,1]) -
                        mean(boot.obj$t[,2])*x)^2) + 1))
)

# Claim 1
hist(sigma, breaks=25, main="Distribution of sigma")
abline(v = 1, col="red", lwd="2")
```




```r
# Claim 2
hist(boot.obj$t[,1], breaks=25, main="Distribution of alpha", xlab="Alpha")
abline(v = quantile(boot.obj$t[,1], 0.975), col="red", lwd="2")
abline(v = quantile(boot.obj$t[,1], 1-0.975), col="red", lwd="2")
```




```
# Claim 3
hist(boot.obj$t[,1] + boot.obj$t[,2], breaks=25,
     main="Distribution of alpha + beta", xlab="alpha + beta")
abline(v = quantile(boot.obj$t[,1] + boot.obj$t[,2], 0.975),
       col="red", lwd="2")
abline(v = quantile(boot.obj$t[,1] + boot.obj$t[,2], 1-0.975),
       col="red", lwd="2")
```



Using our quantile confidence intervals, we reject claim 1 as it is clear that *tau* is greater than 1 on several occasions. claim 2 is also rejected, our 95% confidence interval does not include $\alpha = 0$. Claim 3 holds in our since the confidence interval for $\alpha + \beta$ contains 0.

Problem 6. Bayesian inference for the SEIR model.

Let's once again take a look at the SEIR model. We are tasked with estimating the reproduction number R and the social distancing factor S based on the dataset $y_t{}_{i=1}^{T}$ of counts of the number of hospitalized persons (out of a population of 1 million) recorded every day between 31st March, 2020 and 18th July, 2020.

We model the data using independent Poisson distributions

$$y_y \sim \text{Poisson}(\lambda(t, \boldsymbol{\theta})), \qquad t = 1, \ldots, N$$

where $\lambda(t, \boldsymbol{\theta})$ is taken to be the combined (SEIR-model implied) number of persons in the hospital states HH, HC and CC (i.e. 1000000(HH +HC +CC)) for the days t we have data for.

a) Obtain MCMC samples targeting $p(\boldsymbol{\theta}|\boldsymbol{y})$

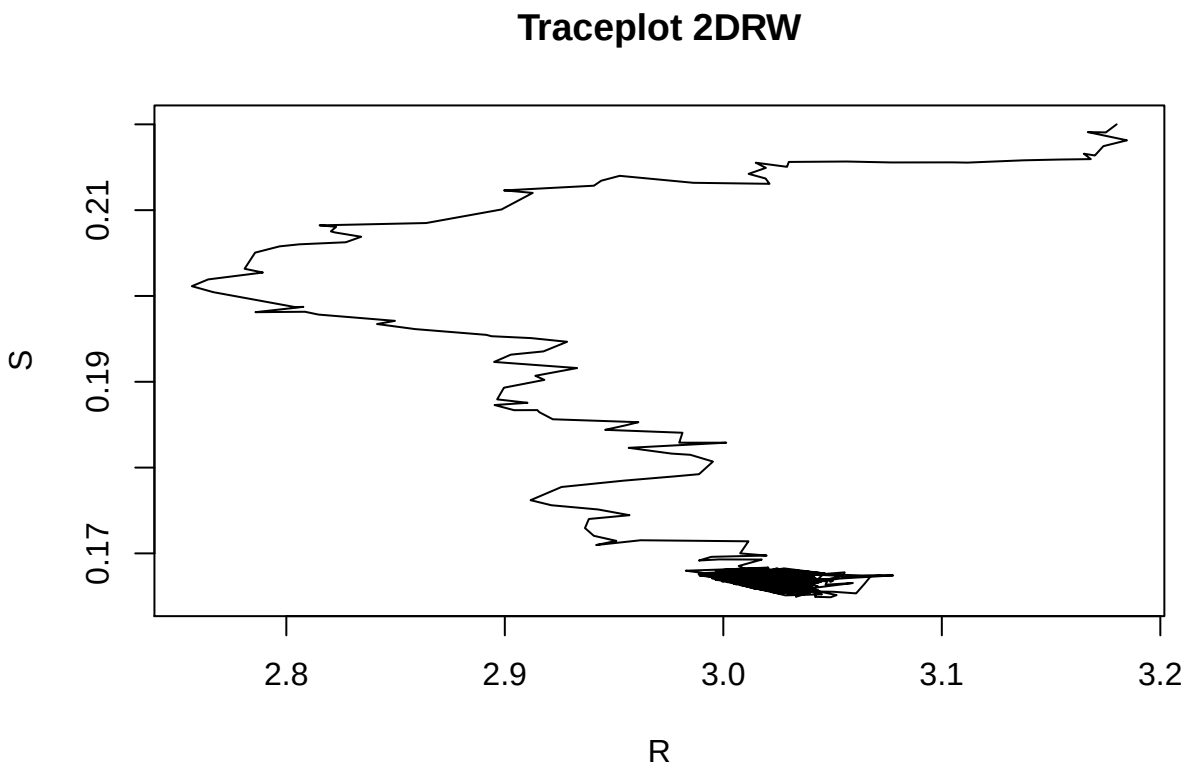
Let's run a 2D random walk on the posterior and see if we are able to converge on some value. We choose the mean vector that we found in assignment 2 problem 4 c for tuning the theta variable, the code and covariance matrix is borrowed from the tip in the assignment text.

```
source("seir_mcmc_funs.R")

twoD_RWMH_poisson <- function(lprob, # log-probability density kernel
                      Sigma=diag(2), # default proposal covariance = identity matrix
```

```
                      theta1=c(3.18,0.22), # default initial configuration
                      n=1000){

  # Cholesky factorization (used for effective sampling)
  L = t(chol(Sigma))

  output <- matrix(0.0,n,2)
  output[1,] <- theta1
  # store old lprob
  pastVal <- lprob(theta1)
  # accept counter
  Nacc <- 0
  # main iteration loop
  for(i in 2:n){
    # proposal
    thetaStar <- output[(i-1),] + L%*%rnorm(2)
    currVal <- lprob(thetaStar)
    # accept prob
    alpha <- exp(min(0.0,currVal-pastVal))
    # accept/reject
    if(runif(1)<alpha && is.finite(alpha)){
      # accept
      output[i,] <- thetaStar
      pastVal <- currVal
      Nacc <- Nacc+1
    } else {
      output[i,] <- output[(i-1),]
    }
  } # main iteration loop

   print(paste0("RWMH done, accept rate : ",Nacc/(n-1)))
  return(round(output,5))

}

# Tune model with mean vector from assignment 2
m <- twoD_RWMH_poisson(seir.lp, theta1=c(3.18,0.22),
                       Sigma=matrix(c(0.0003,0,0,0.0000005),2,2),
                       n=1000)
```

```
## [1] "RWMH done, accept rate : 0.46046046046046"
```

```
plot(m[,1], m[,2], type="l", xlab="R", ylab="S", main="Traceplot 2DRW")
```

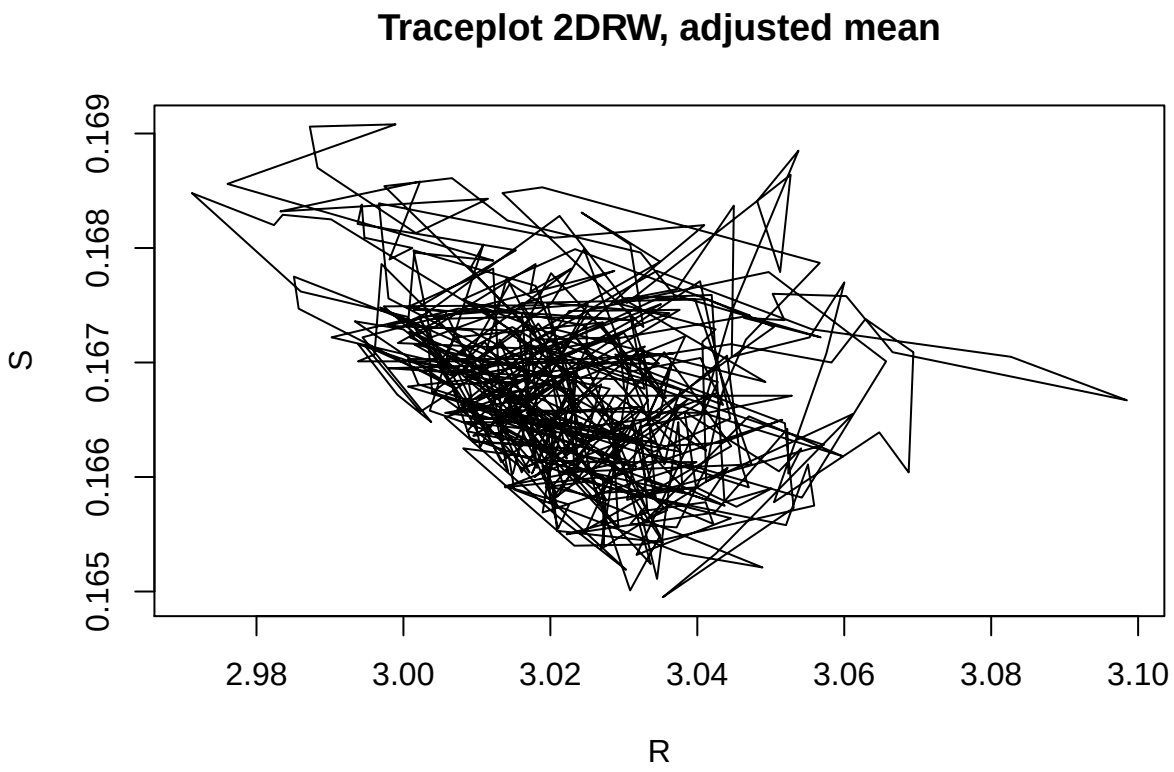


From our traceplot, we see that the random walk takes us from the mean of the posterior and it converges down on $3.0 < R < 3.05$ and $S \approx 0.17$. Let's start our random walk with a mean vector closer to these values and run the code again.

```
# Tune model with mean vector from assignment 2
m <- twoD_RWMH_poisson(seir.lp, theta1=c(3.02,0.167),
                       Sigma=matrix(c(0.0003,0,0,0.0000005),2,2),
                       n=1000)
```

```
## [1] "RWMH done, accept rate : 0.485485485485485"
```

```
plot(m[,1], m[,2], type="l", xlab="R", ylab="S",
     main="Traceplot 2DRW, adjusted mean")
```




```
ESS(m[,1])
```

```
##     var1
## 73.00817
```

```
ESS(m[,2])
```

```
##     var1
## 68.03008
```

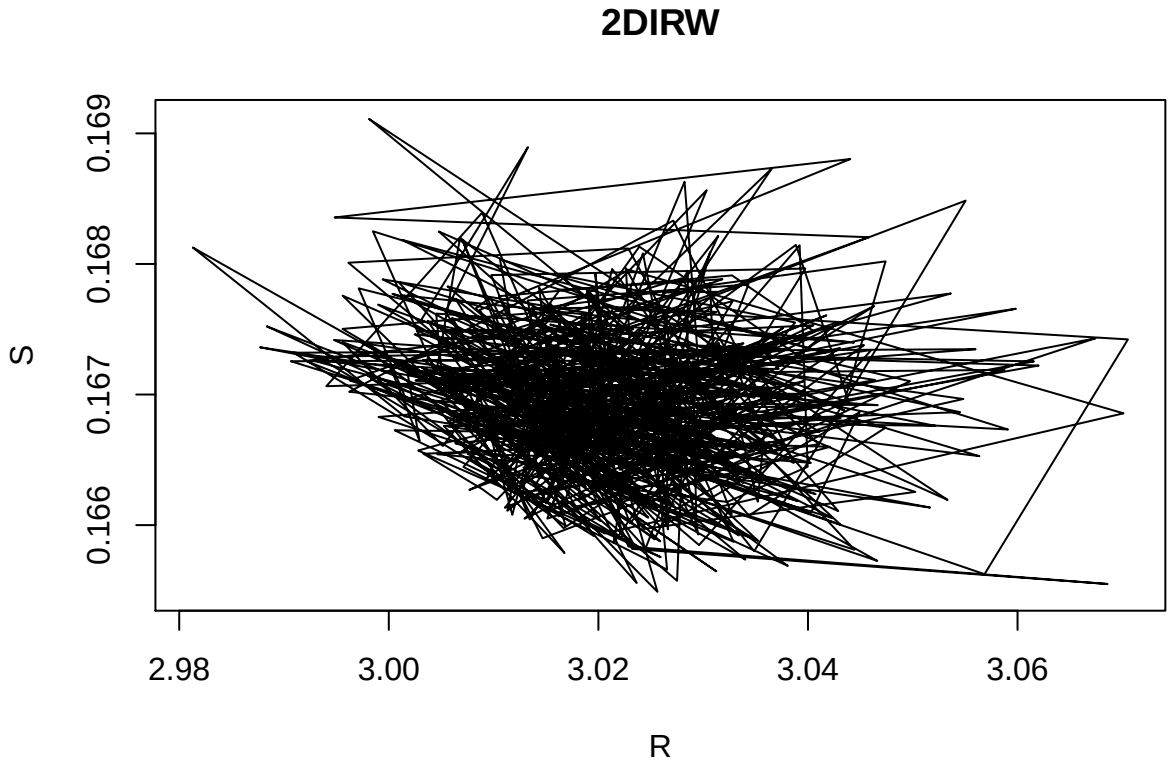
Still, our sample size is relatively small, let's use our independent random walk implementation instead.

```
# Independent sampler
IndepMH <- function(lprob, theta=c(0, 0), sigma=diag(2), Nsamp=1000, S=1){
  # Allocate space
  res <- matrix(0, Nsamp, 2)
  # Set initial values
  res[1,] <- theta
  # Old importance
  pold <- lprob(theta) - dmvnorm(theta, mean=theta ,sigma=sigma, log=TRUE)
  # No of accept
  Nacc <- 0
  for (i in 2:Nsamp){
    # Sample theta from multivariate normal with scaled sigma
    new <- rmvnorm(1, theta, S*sigma)
    # Importance of new theta
    pnew <- lprob(new) - dmvnorm(new, mean=theta, sigma=sigma, log=TRUE)
    frac <- exp(min(0.0, pnew-pold))
```

```
    if(runif(1)<frac && is.finite(frac)){
      # Accept
      res[i,] <- new
      pold <- pnew
      Nacc <- Nacc+1
    } else {
      # Reject
      res[i,] <- res[(i-1),]
    }
  }
  print(paste0("accept rate : ",Nacc/Nsamp))
  return(res)
}


m <- IndepMH(seir.lp, theta=c(3.019, 0.167),
             sigma=matrix(c(0.0003,0,0,0.0000005),2,2),
             Nsamp=1000, S=0.8)
```

```
## [1] "accept rate : 0.606"
```

```
plot(m[,1], m[,2], type="l", main="2DIRW", xlab="R", ylab="S")
```




```
ESS(m[,1])
```

```
##     var1
## 413.5558
```

```r
ESS(m[,2])
```

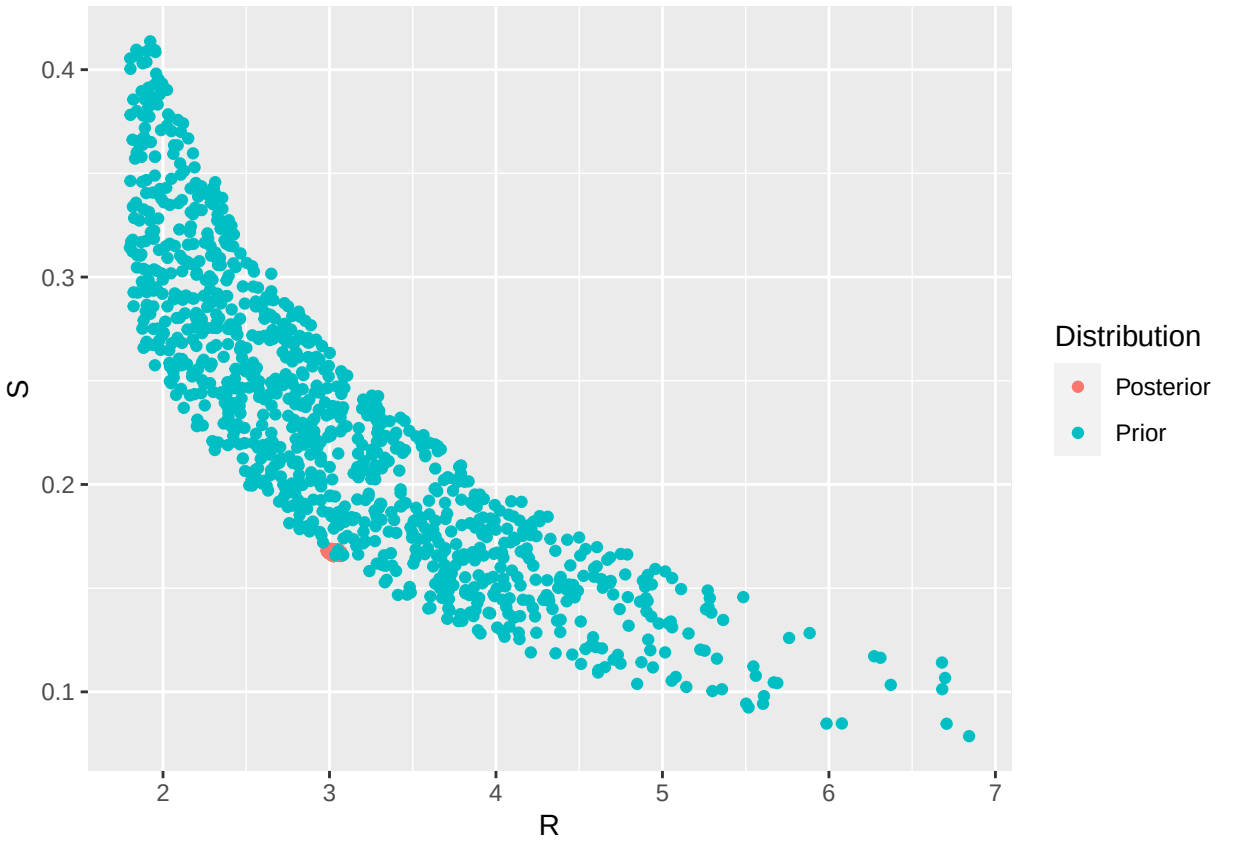
```
##     var1
## 321.7022
```

Finally we have a ESS of above 200 for 1000 samples. We see that our distribution is quite well explored using independent random walk.

b) Comparing prior and posterior

Let's sample from the prior distribution and posterior distribution and plot both in a colored scatterplot to see how our bayesian analysis has updated our belief in R and S.

```r
library(ggplot2)

#
# inverse transform algorithm
# (borrowed from mandatory 2 to sample R)
#
rltrunc_normal <- function(n,l,mu,sigma){
  Fl <- pnorm(q=l,mean=mu,sd=sigma)
  return(qnorm(p=(Fl + runif(n)*(1.0-Fl)),mean=mu,sd=sigma))
}

#
# simulate random variates from joint distribution
# (borrowed from mandatory to sample prior)
#
rRS <- function(n){
  R <- rltrunc_normal(n,1.8,2.2,1.5)
  S <- runif(n,min=0.5/R,0.8/R)
  return(cbind(R,S))
}

# Sample 1000 priors
m2 <- rRS(1000)

# Create vectors for dataframe
R <- c(m[,1], m2[,1])
S <- c(m[,2], m2[,2])
Distribution <- c(replicate(length(m[,1]), "Posterior"),
                  replicate(length(m2[,1]), "Prior"))

# Create dataframe
df <- data.frame(R, S, Distribution)

ggplot(df, aes(R, S)) + geom_point(aes(colour = Distribution))
```



It's safe to say that our posterior distribution provides us with much information on the R and S values during the period of 21st March, 2020 to 18th July, 2020.

c) Redo assignment 2 problem 4f)

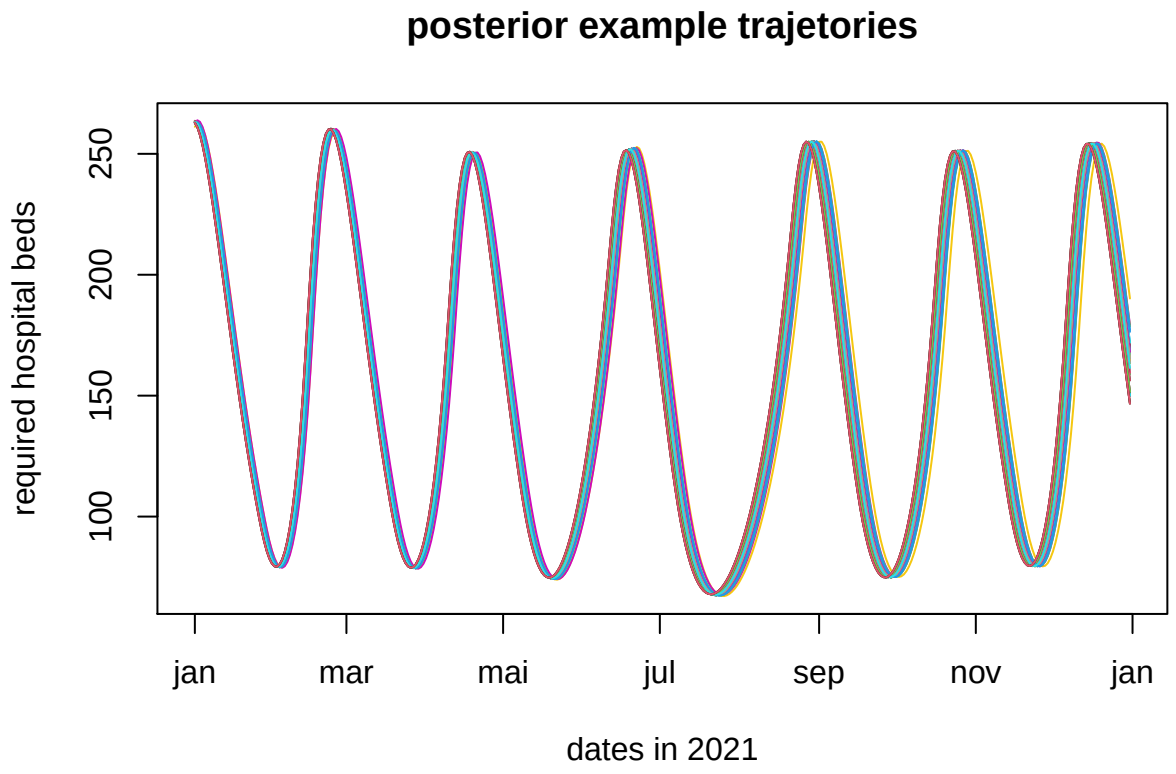
To do this, i reuse the code from mandatory 2 solution since the visualizations were better than what i previously obtained in my solution.

The changes to the code below is that instead of sampling R and S from $p(\boldsymbol{\theta})$ we sample from $p(\boldsymbol{\theta}|\boldsymbol{y})$ which we have stored in a matrix above.

Also, instead of saving the plots as their own pdf they are displayed inside the notebook.

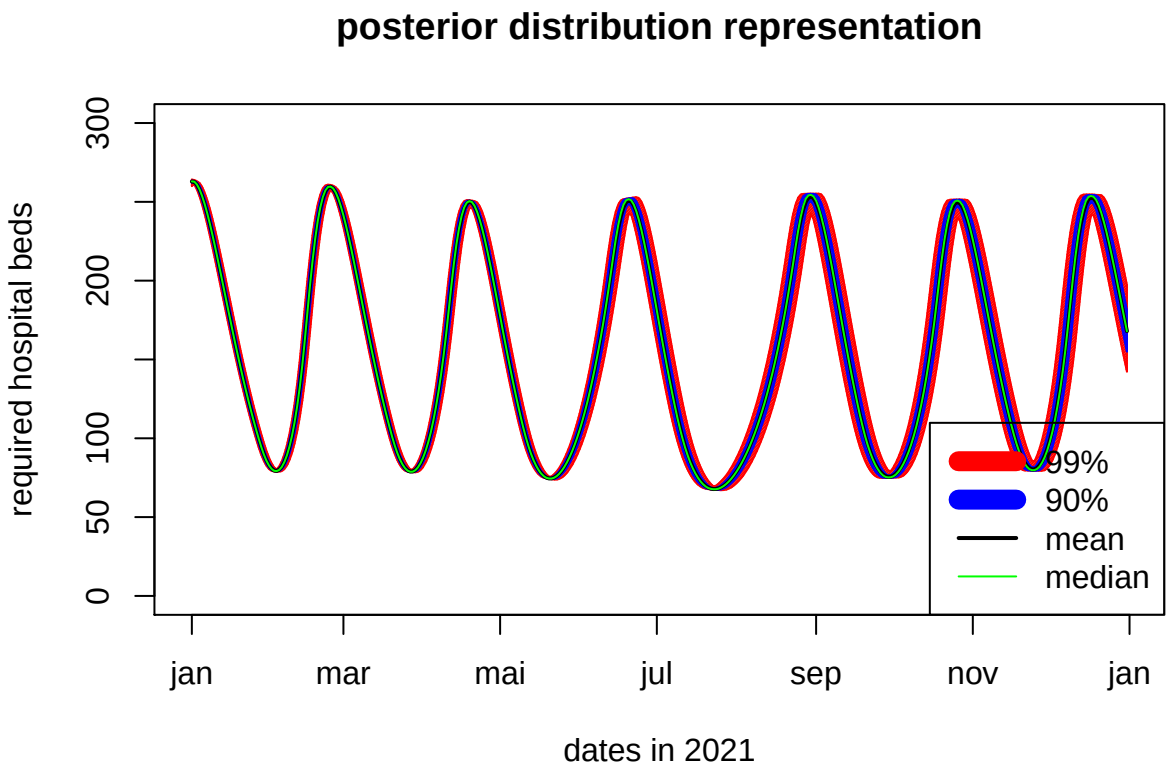
```
nsim <- 500 # total number of simulations

# CODE BELOW FROM MANDATORY 2 SOLUTION

# run simulations
M <- numeric(nsim)
H <- matrix(0.0,nsim,365) # prepare for next point
for(i in 1:nsim){
  # CHANGE (choose R and S from our posterior samples)
  ff <- seir_sim(R0max = m[i, 1], soc_dist_Rfac = m[i, 2])
  t1 <- which(ff$dates=="2021-01-01")
  t2 <- which(ff$dates=="2021-12-31")
  H[i,] <- rowSums(1000000*ff$ode[t1:t2,c("HH","HC","CC")])
  M[i] <- max(H[i,])
}
```

```r
# make a data frame to facilitate plotting with dates
df <- data.frame(t(H),dates=ff$dates[t1:t2])

# in the upper plot, simply show some of the trajectories:
plot(df$dates,df$X1,type="l",
     xlab="dates in 2021",
     ylab="required hospital beds",
     main="posterior example trajetories")
for(i in 2:50) lines(df$dates,df[,i],col=i)
```




```r
# compute daily statistics for plotting
daily.stats <- matrix(0.0,365,6)
for(t in 1:365){
  daily.stats[t,1] <- mean(H[,t])
  daily.stats[t,2] <- median(H[,t])
  daily.stats[t,3:6] <- quantile(H[,t],probs=c(0.005,0.1,0.9,0.995))
}

df2 <- data.frame(daily.stats,ff$dates[t1:t2])
colnames(df2) <- c("mean","median","q05","q10","q90","q995","dates")

plot(df2$dates,df2$mean,ylim=c(0,300),col=0,
     xlab="dates in 2021",
     ylab="required hospital beds",
     main="posterior distribution representation") # simply sets up plot window
polygon(c(df2$dates,rev(df2$dates)),c(df2$q05,rev(df2$q995)),
```

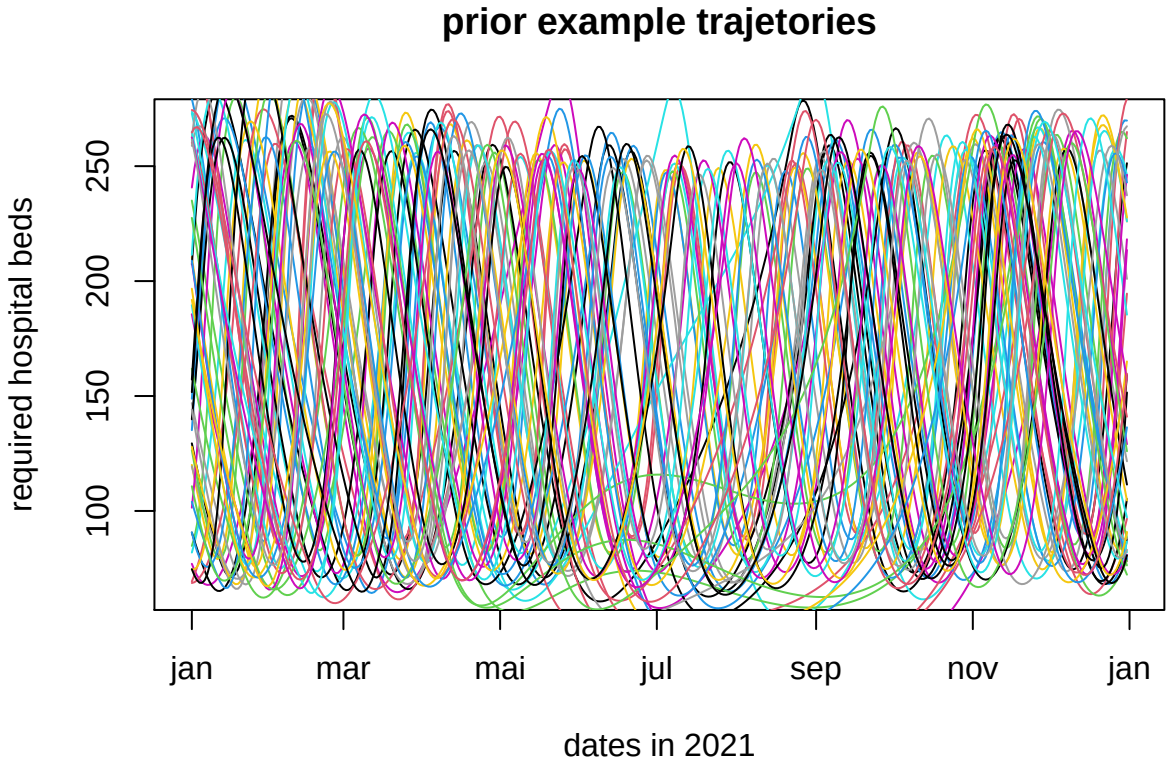
```
        col="red",density=100)
polygon(c(df2$dates,rev(df2$dates)),c(df2$q10,rev(df2$q90)),
        col="blue",density=100)
lines(df2$dates,df2$mean,lwd=2)
lines(df2$dates,df2$median,col="green")
legend("bottomright",lty=c(1,1,1,1),lwd=c(10,10,2,1),
       legend=c("99%","90%","mean","median"),
       col=c("red","blue","black","green"),)
```



Now, let's plot this again using the prior distribution for R and S.

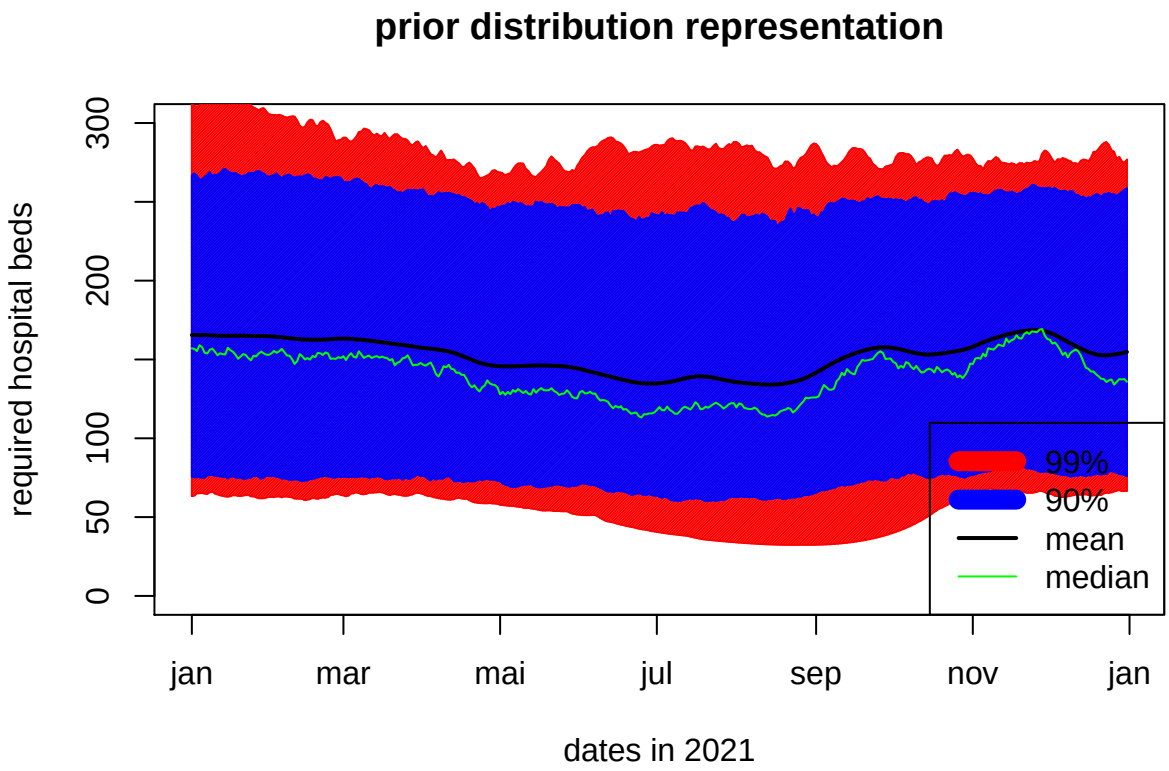
```
nsim <- 500 # total number of simulations

# CODE BELOW FROM MANDATORY 2 SOLUTION

# run simulations
M <- numeric(nsim)
H <- matrix(0.0,nsim,365) # prepare for next point
for(i in 1:nsim){
  # CHANGE (choose R and S from our prior samples)
  ff <- seir_sim(R0max = m2[i, 1], soc_dist_Rfac = m2[i, 2])
  t1 <- which(ff$dates=="2021-01-01")
  t2 <- which(ff$dates=="2021-12-31")
  H[i,] <- rowSums(1000000*ff$ode[t1:t2,c("HH","HC","CC")])
  M[i] <- max(H[i,])
}
```

```r
# make a data frame to facilitate plotting with dates
df <- data.frame(t(H),dates=ff$dates[t1:t2])

# in the upper plot, simply show some of the trajectories:
plot(df$dates,df$X1,type="l",
     xlab="dates in 2021",
     ylab="required hospital beds",
     main="prior example trajetories")
for(i in 2:50) lines(df$dates,df[,i],col=i)
```




```r
# compute daily statistics for plotting
daily.stats <- matrix(0.0,365,6)
for(t in 1:365){
  daily.stats[t,1] <- mean(H[,t])
  daily.stats[t,2] <- median(H[,t])
  daily.stats[t,3:6] <- quantile(H[,t],probs=c(0.005,0.1,0.9,0.995))
}

df2 <- data.frame(daily.stats,ff$dates[t1:t2])
colnames(df2) <- c("mean","median","q05","q10","q90","q995","dates")

plot(df2$dates,df2$mean,ylim=c(0,300),col=0,
     xlab="dates in 2021",
     ylab="required hospital beds",
     main="prior distribution representation") # simply sets up plot window
polygon(c(df2$dates,rev(df2$dates)),c(df2$q05,rev(df2$q995)),
```

```
        col="red",density=100)
polygon(c(df2$dates,rev(df2$dates)),c(df2$q10,rev(df2$q90)),
        col="blue",density=100)
lines(df2$dates,df2$mean,lwd=2)
lines(df2$dates,df2$median,col="green")
legend("bottomright",lty=c(1,1,1,1),lwd=c(10,10,2,1),
       legend=c("99%","90%","mean","median"),
       col=c("red","blue","black","green"),)
```



As expected, with the prior distribution chosen we get a much larger uncertainty. With the data we can update our beliefs of what the R and S values are and we simulate 2021 hospitalizations using these new, updated, values.

d) Calculate total beds in december, january and february

Lets simulate total number of needed hospital beds in december, january and february. We will simulate 500 samples of (R, S) form $p(\boldsymbol{\theta})$ and the $p(\boldsymbol{\theta}|\boldsymbol{y})$ to see if our

```
nsim <- 500 # total number of simulations

des <- matrix(0.0,nsim,31)
jan <- matrix(0.0,nsim,31)
feb <- matrix(0.0,nsim,28)

for(i in 1:nsim){
  # CHANGE (choose R and S from our prior samples)
  ff <- seir_sim(R0max = m2[i, 1], soc_dist_Rfac = m2[i, 2])
```

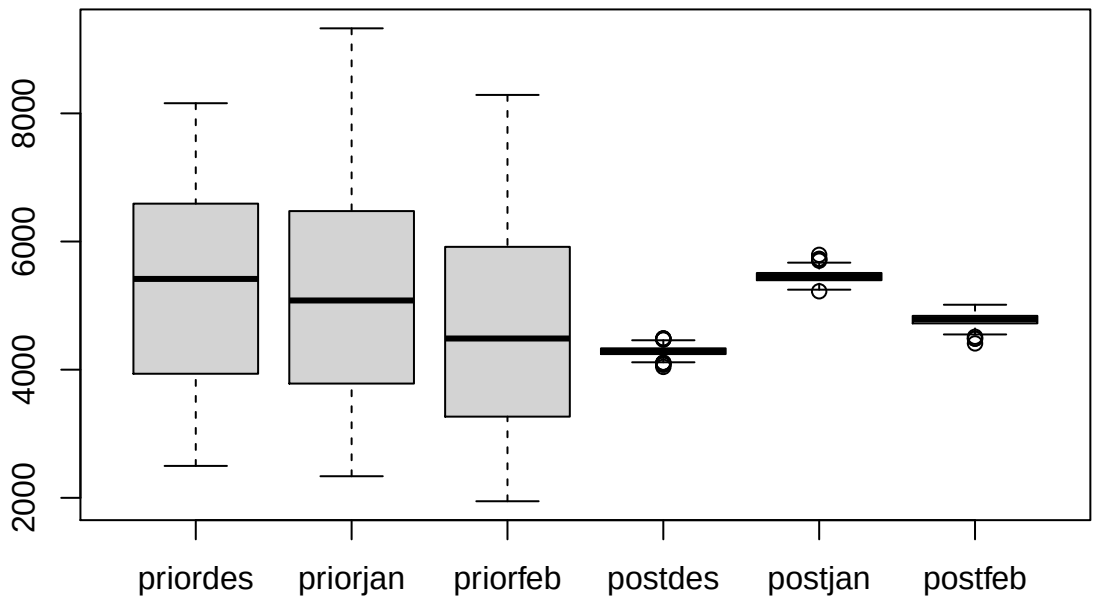
```
  t1 <- which(ff$dates=="2020-12-01")
  t2 <- which(ff$dates=="2020-12-31")
  des[i,] <- rowSums(1000000*ff$ode[t1:t2,c("HH","HC","CC")])

  t1 <- which(ff$dates=="2021-01-01")
  t2 <- which(ff$dates=="2021-01-31")
  jan[i,] <- rowSums(1000000*ff$ode[t1:t2,c("HH","HC","CC")])

  t1 <- which(ff$dates=="2021-02-01")
  t2 <- which(ff$dates=="2021-02-28")
  feb[i,] <- rowSums(1000000*ff$ode[t1:t2,c("HH","HC","CC")])
}

# Calculate total no of hospital beds for all simulations
priordes <- rowSums(des)
priorjan <- rowSums(jan)
priorfeb <- rowSums(feb)
```

Do the same for posterior

```
des <- matrix(0.0,nsim,31)
jan <- matrix(0.0,nsim,31)
feb <- matrix(0.0,nsim,28)

for(i in 1:nsim){
  # CHANGE (choose R and S from our posterior samples)
  ff <- seir_sim(R0max = m[i, 1], soc_dist_Rfac = m[i, 2])
  t1 <- which(ff$dates=="2020-12-01")
  t2 <- which(ff$dates=="2020-12-31")
  des[i,] <- rowSums(1000000*ff$ode[t1:t2,c("HH","HC","CC")])

  t1 <- which(ff$dates=="2021-01-01")
  t2 <- which(ff$dates=="2021-01-31")
  jan[i,] <- rowSums(1000000*ff$ode[t1:t2,c("HH","HC","CC")])

  t1 <- which(ff$dates=="2021-02-01")
  t2 <- which(ff$dates=="2021-02-28")
  feb[i,] <- rowSums(1000000*ff$ode[t1:t2,c("HH","HC","CC")])
}

# Calculate total no of hospital beds for all simulations
postdes <- rowSums(des)
postjan <- rowSums(jan)
postfeb <- rowSums(feb)
```

Plot the different scenarios:

```
df <- data.frame(priordes, priorjan, priorfeb, postdes, postjan, postfeb)
boxplot(df)
```



In summary, given our knowledge of how diseases reproduce and how social distancing affect the spread of the disease, we expect that the number of hospital beds needed for the months of december, january and february is between 4000 and 6000 and in the wors case as high as 8000.

If the spread of the disease and the reproduction number is similar to what was observed during the period form 21st March, 2020 to 18th July, 2020, we can with much more confidence say that the number of needed beds is about 4284, 5460 and 4772 for december, january and febuary respectively.

This is, as stated above, under the assumption that the conditions are similar to the time frame above.

Bibliography

Wikipedia contributors. 2020. “Metropolis-Hastings Algorithm — Wikipedia, the Free Encyclopedia.” https://en.wikipedia.org/w/index.php?title=Metropolis%E2%80%93Hastings_algorithm&oldid=983825650.