Markov Chain Monte Carlo Simulation

Dec 8, 2022

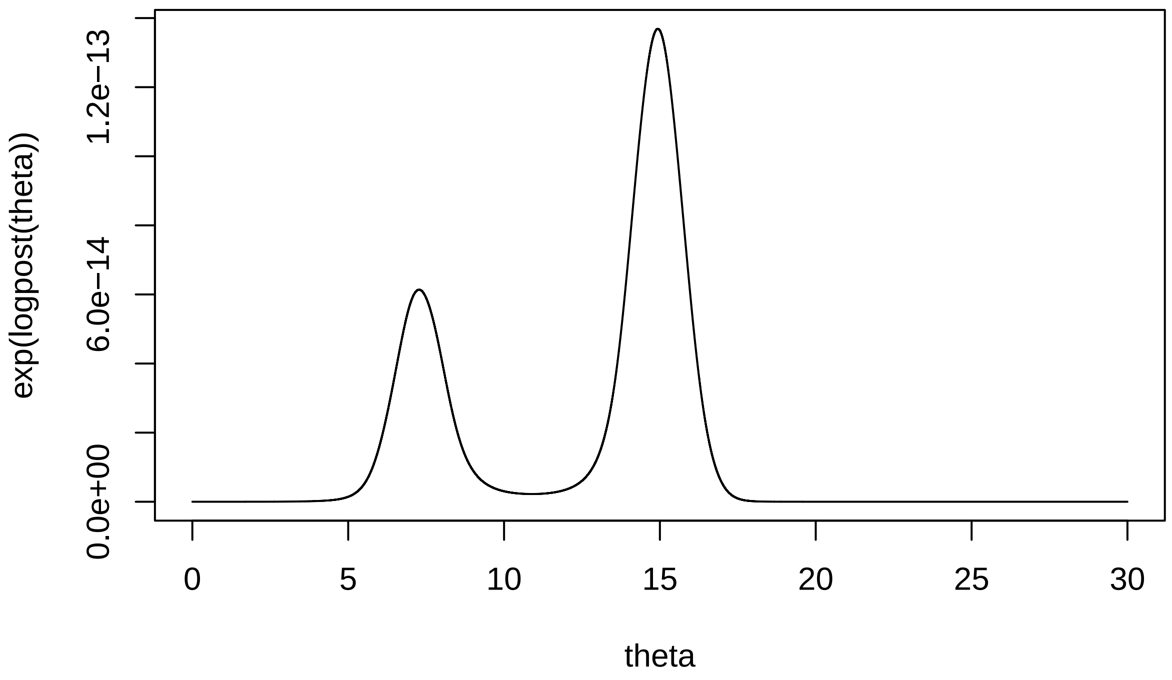
We can generate Markov Chain Monte Carlo Samples to approximate any posterior distribution without having to know its normalizing constant.

Here, we approximate the bimodal Cauchy Distribution with arbitrarily set values

```
set.seed(10)

# We will find the log posterior
logpost = function(theta){
  y <- c(3, 6, 7, 8, 15, 14, 16, 17)
  log_likelihood <- 0

  for (i in 1:length(y)){
    log_likelihood = log_likelihood + log((1 / (pi * (1 + (y[i] - theta)^2))))
  }

  return(log_likelihood)
}
```

Cauchy Distribution

```
theta <- seq(0, 30, by = 0.0001)
plot(theta, exp(logpost(theta)), type = 'l')
```

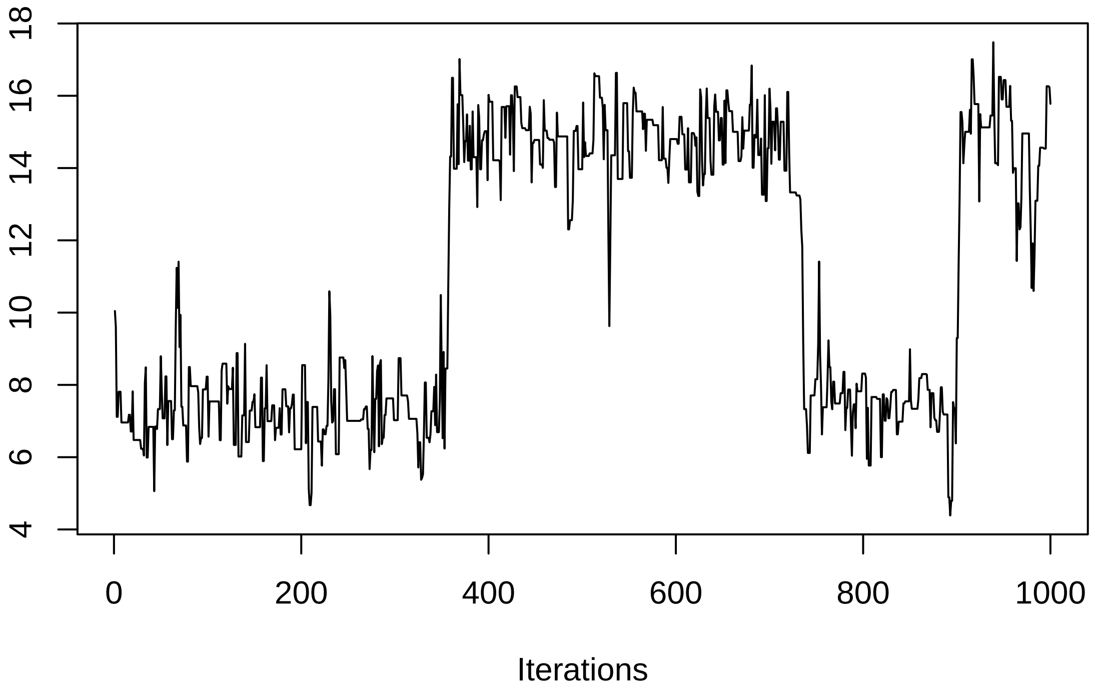


```r
metropolis <- function(logpost, current, C, iter){
  S <- rep(0, iter)
  theta_t <- current

  for(j in 1:iter){
    # Proposal Distribution
    theta_p <- runif(1, theta_t - C, theta_t + C)

    ## Log-rejection ratio for symmetric proposal
    logr <- log(min(1, exp(logpost(theta_p)) / exp(logpost(theta_t))))

    # Reject/Accept proposal state
        if (log(runif(1,0,1)) < logr){
      theta_t <- theta_p
        }

    # Save in our S
    S[j] <- theta_t
    }
  return(S)
}
```

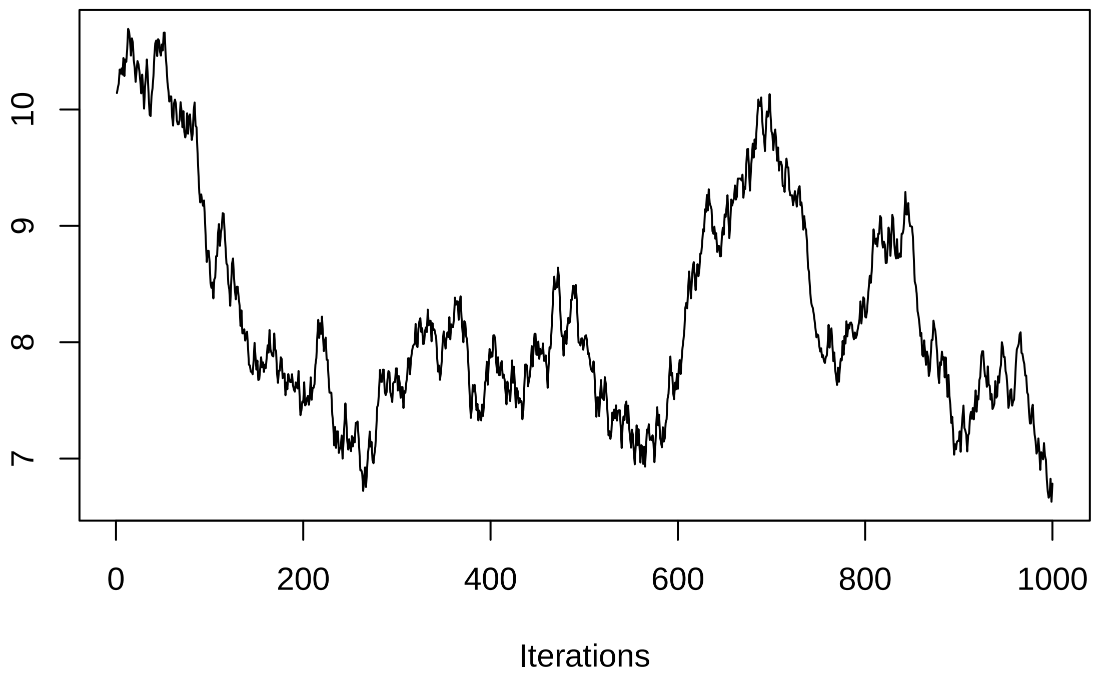
Metropolis-Hastings Function Implementation

Making traceplots to deterine how our Metropolis-Hastings MCMC samples look:

```
library(coda)

# Traceplot for S1
coda::traceplot(as.mcmc(S1))
```

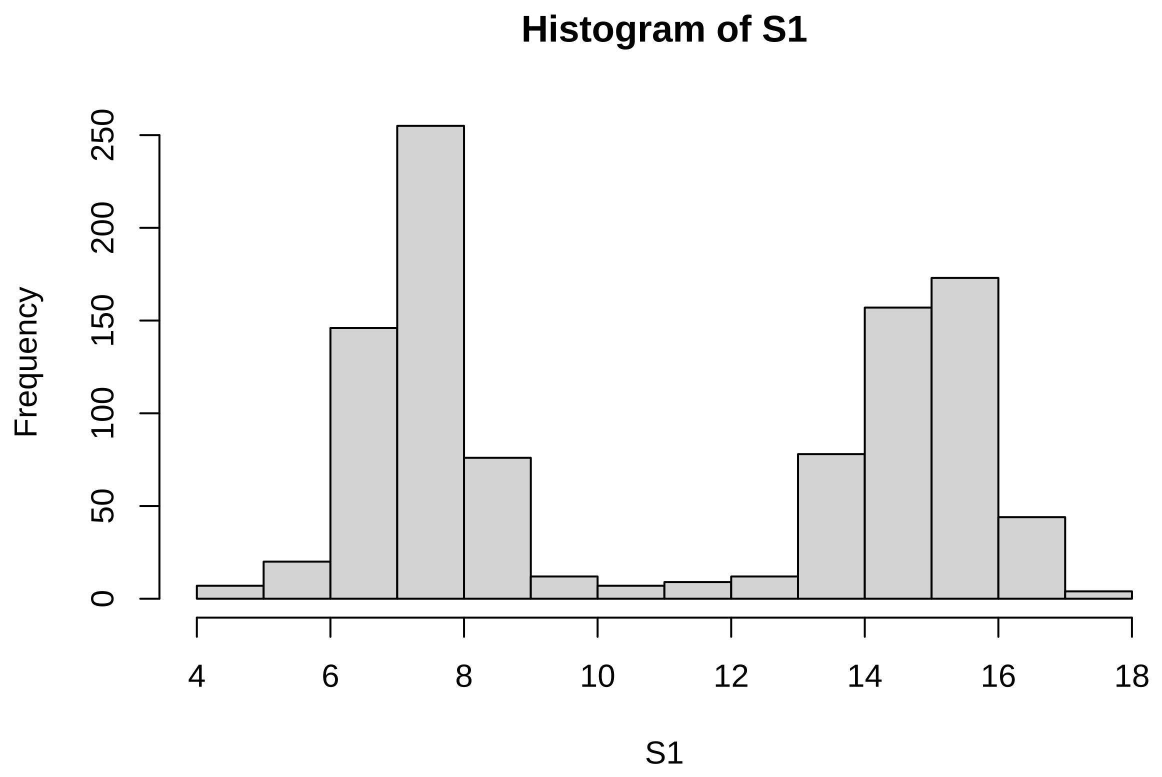


```
# Traceplot for S2
coda::traceplot(as.mcmc(S2))
```

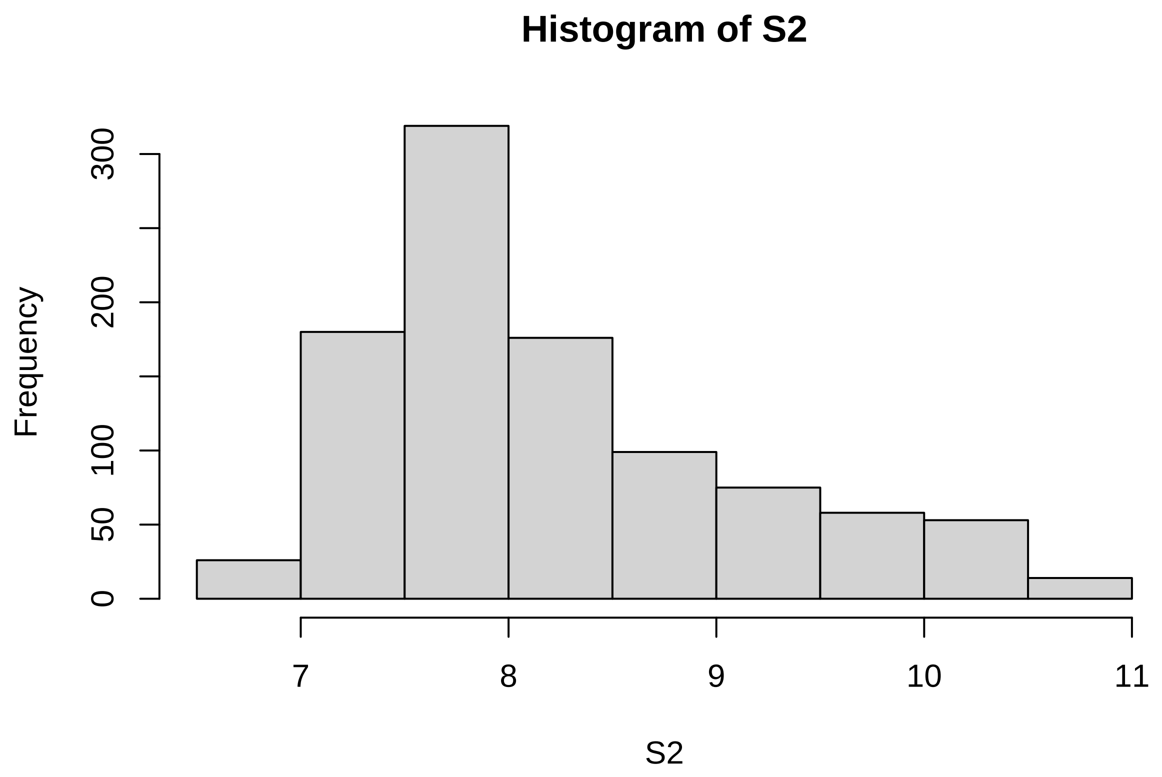


By inspecting the traceplot for S1 (C = 3) and S2 (C = 0.2), we can see that our C = 3 is a better approximation of our posterior because we lead to a stationary distribution at either of the two areas where we have the highest height in our Cauchy distribution. However, S2 constantly changes and is still not stationary even after the 1000th iteration. Thus, S1 is the better approximator.

```
hist(S1)
```


Histogram of S1
Frequency
S1
0
50
100
150
200
250
4
6
8
10
12
14
16
18

```
hist(S2)
```



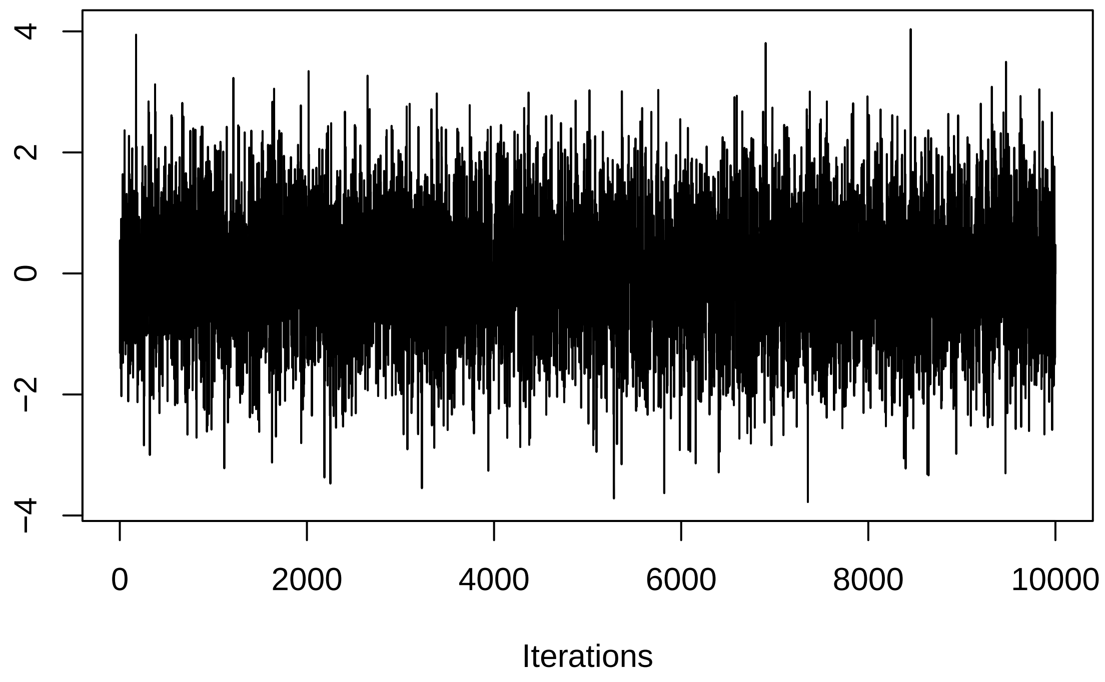
Looking at the histogram, we can see that our S1 histogram looks very similar to our Cauchy Distribution since they are both bimodal which makes sense since we're generating samples for it, while our S2 does not. Hence, we can say that S1 or C=3 better approximates our distribution.

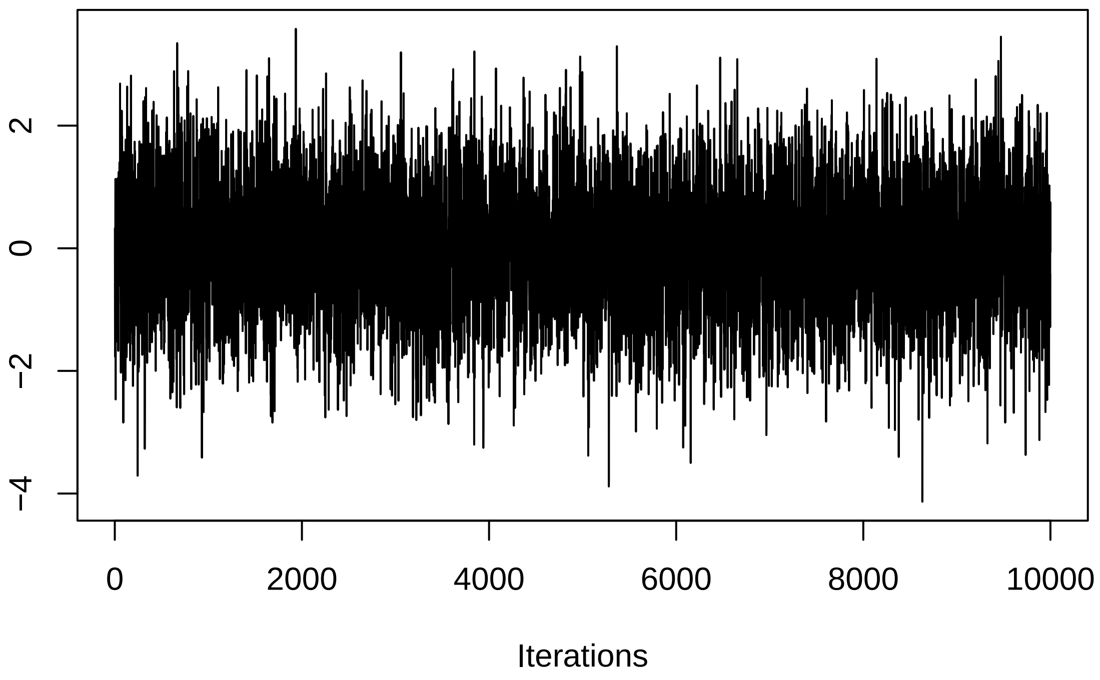
We will now implement the Gibbs sampling MCMC method

```
gaussian_gibbs = function(burn_in, keep_draws, theta0, rho){
theta_sample = matrix(0, nrow = 1+ burn_in + keep_draws, ncol = 2)
theta_sample[1,1] = theta0[1]
theta_sample[1,2] = theta0[2]
for(i in 2:(burn_in + keep_draws)){
  theta_sample[i,1] = rnorm(1, rho * theta_sample[i-1,2], sqrt(1-rho^2))
  theta_sample[i,2] = rnorm(1, rho * theta_sample[i,1], sqrt(1-rho^2))
}
theta_sample_out = theta_sample[(2+burn_in):(1+ burn_in + keep_draws), ]
return(theta_sample_out)
}
```

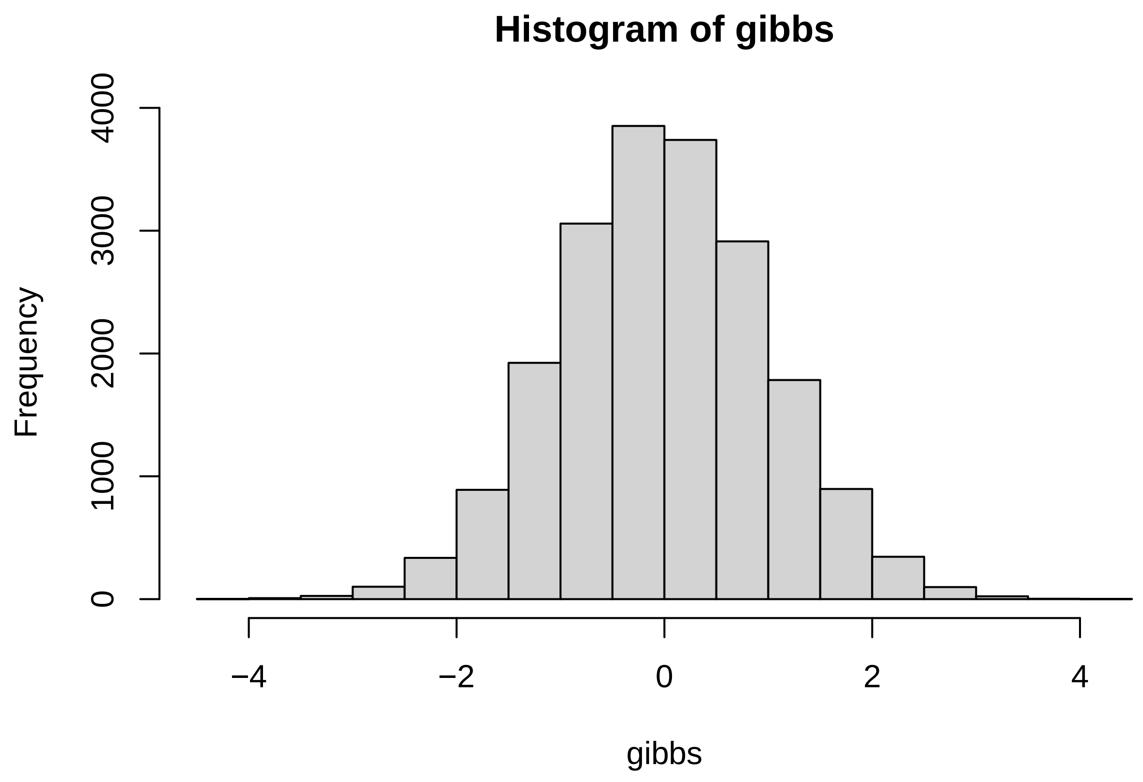
Making traceplots to deterine how our Gibbs MCMC samples look:

```r
# traceplot from our gibbs sampling
gibbs <- gaussian_gibbs(1000, 10000, c(0,0), 0.6)
coda::traceplot(as.mcmc(gibbs))
```



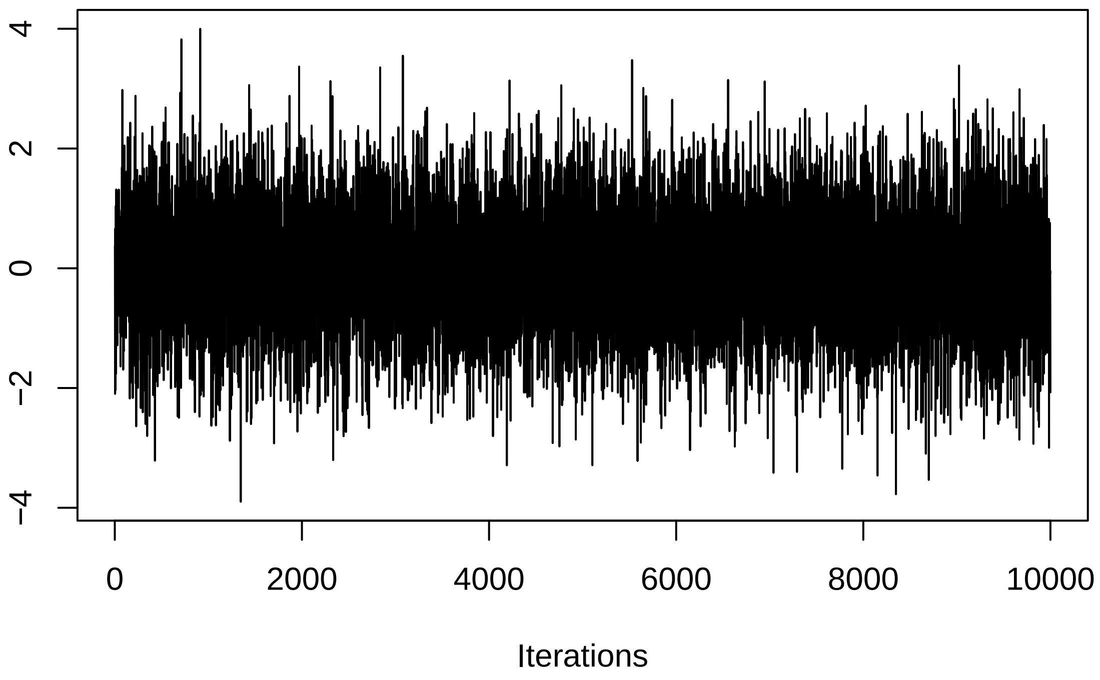


```r
hist(gibbs)
```

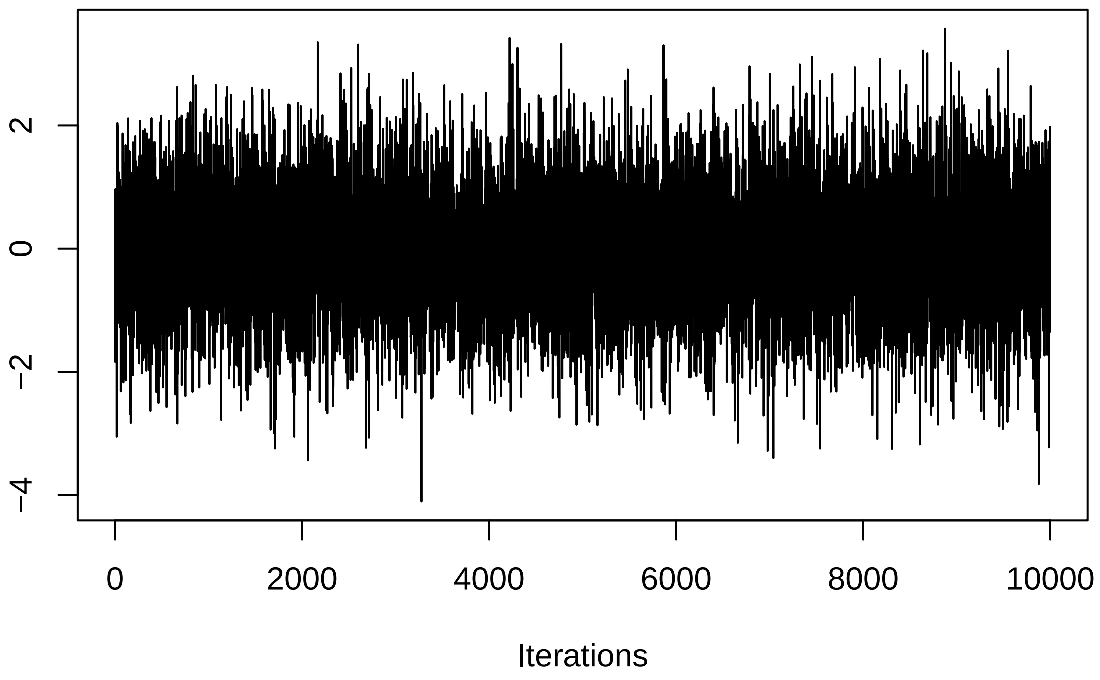


We can see that the traceplots for both theta 1 and theta 2 converges since stays in the general vicinity of 0 and looks horizontal for both traceplots after the burn-in period. Our histogram shows that we follow a normal distribution, which is true of the joint posterior since a normal-normal gives us a normal posterior, so the graph makes sense.

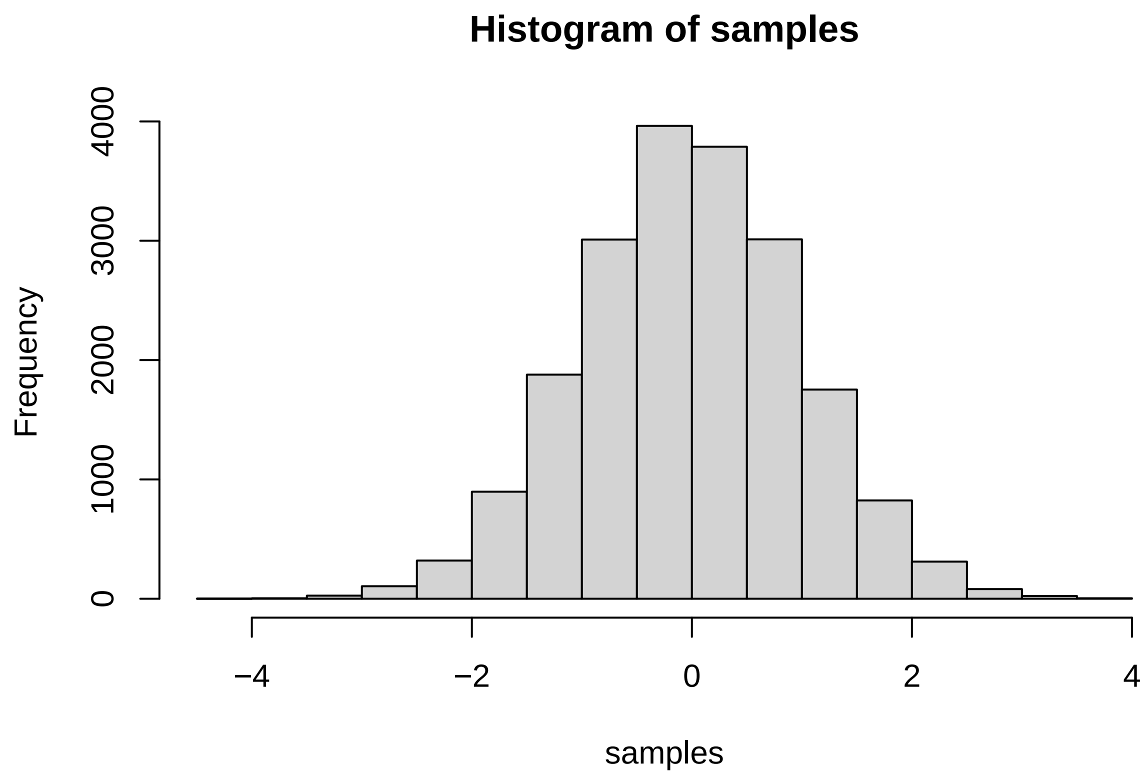
```r
# traceplot from our rmvnorm samples
cov <- matrix(c(1,0.6,0.6,1), nrow=2, ncol=2, byrow = T)

samples <- mvtnorm::rmvnorm(n=10000, mean=c(0,0), sigma=cov)
coda::traceplot(as.mcmc(samples))
```



4
2
0
−2
−4
0
2000
4000
6000
8000
10000
Iterations



```r
hist(samples)
```



The samples from our rmvnorm look very similar with our gibbs sampling traceplots. The histogram of our samples resembles a normal distribution and our gibbs sampling.