

Problem 6

```
set.seed(10)

MH <- function(n, init, h) {
  output <- matrix(0, nrow = n, ncol = 100)
  output[1,] = init
  accept_prob <- numeric(length = 100)
  for(i in 2:n) {

    for(j in 1:100) {
      proposed = rnorm(1, output[i-1, j], sd = sqrt(h))
      alpha = exp( log(dnorm(proposed)) - log(dnorm(output[i-1, j])) )

      if(runif(1) < alpha) {
        output[i, j] = proposed
        accept_prob[j] = accept_prob[j] + 1
      } else {
        output[i, j] = output[i-1, j]
      }
    }
  }
  accept_prob = accept_prob/n
  return(accept_prob)
}

init <- numeric(length = 100)
n <- 1e3
accept.vec <- MH(n, init, 1)
summary(accept.vec)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.6820  0.6960  0.7065  0.7052  0.7120  0.7410
```

Problem 7

```
set.seed(10)
library(mvtnorm)
```

```
Ftarget <- function(X, rho) {
  sigma <- rbind(c(1, rho), c(rho, 1))
  return(dmvnorm(X, mean = c(2, -2), sigma = sigma))
}

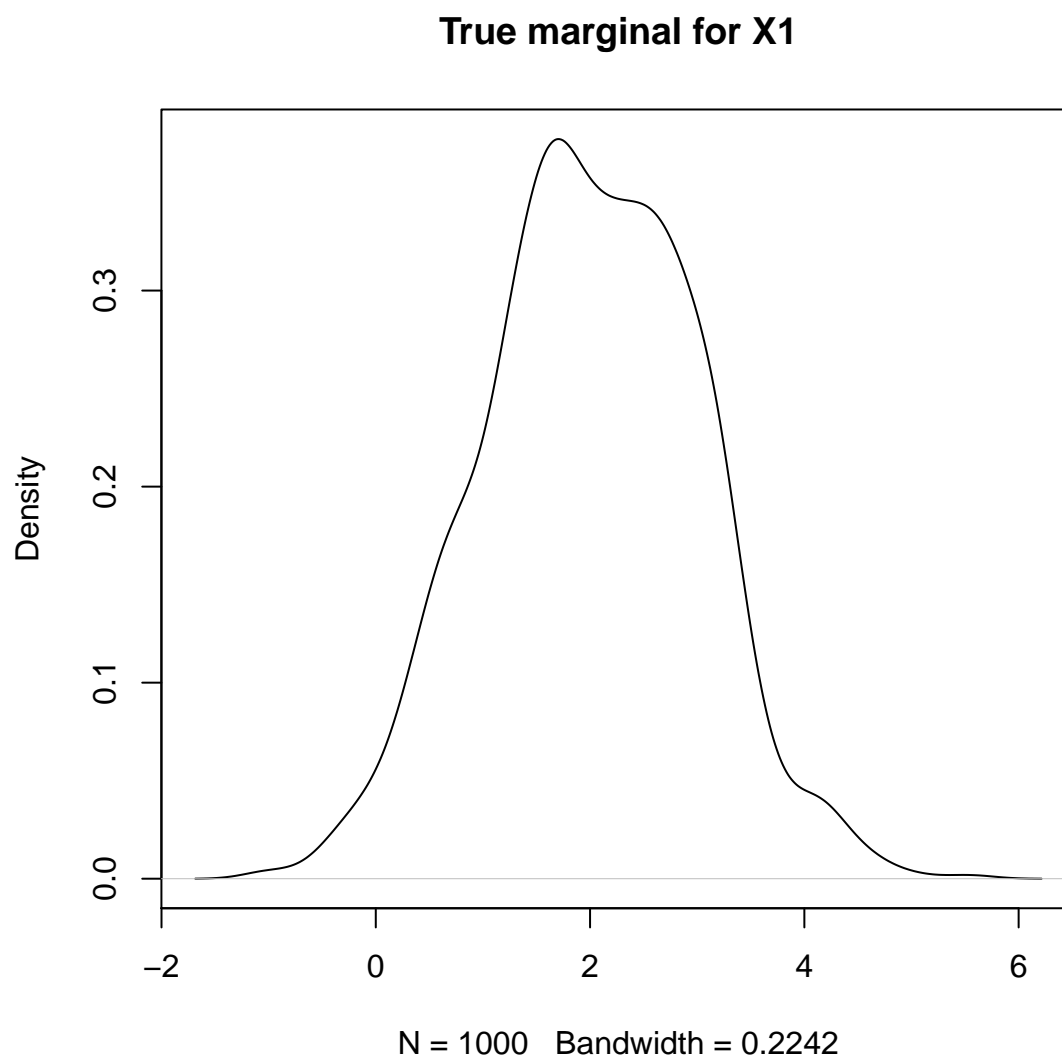
proposal <- function(x,h) {
  return(rmvnorm(1, mean = x, sigma = diag(h,2,2)))
}

MH <- function(n, init, h, rho) {
  output <- matrix(0, nrow = n, ncol = 2)
  output[1,] = init
  accept_prob <- 0
  for(i in 2:n) {
    proposed = proposal(output[i-1,], h)
    alpha = exp( log(Ftarget(proposed, rho)) - log(Ftarget(output[i-1,], rho)) )
    if(runif(1) < alpha) {
      output[i,] = proposed
      accept_prob = accept_prob + 1
    } else {
      output[i,] = output[i-1,]
    }
  }
  accept_prob = accept_prob/n
  print(paste0("acceptance probaility is :", accept_prob))
  return(output)
}

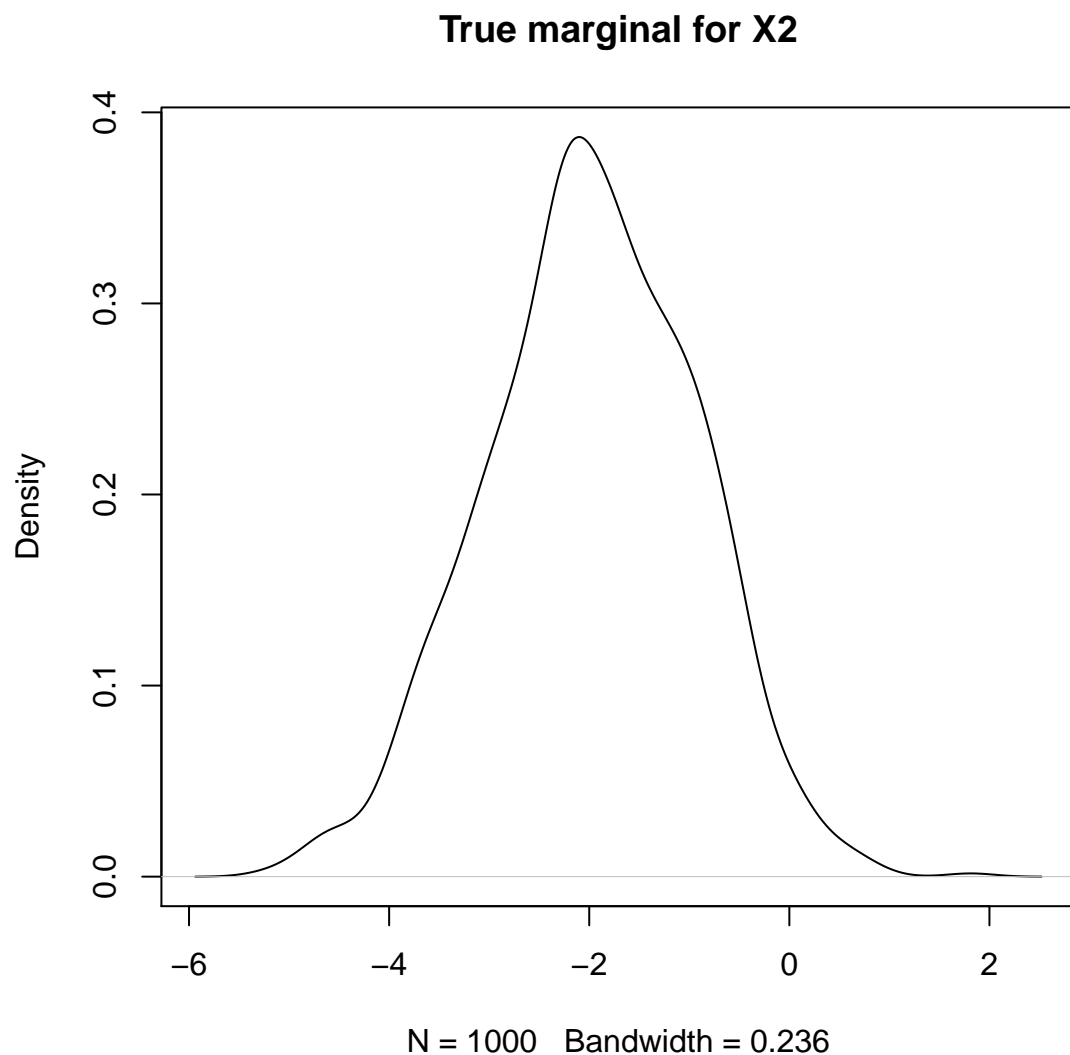
Gibbs <- function(n = 1e3, init = c(0,0), rho) {
  output <- matrix(0, nrow = n, ncol = 2)
  output[1,] = init
  output[1,2] = rnorm(1, mean = -2 + rho*(output[1,1] - 2), sd = sqrt(1 - rho^2))
  for(i in 2:n) {
    output[i,1] = rnorm(1, mean = 2 + rho*(output[i-1,2] + 2), sd = sqrt(1 - rho^2))
    output[i,2] = rnorm(1, mean = -2 + rho*(output[i,1] - 2), sd = sqrt(1 - rho^2))
  }
  return(output)
}

init <- numeric(length = 2)
rho_vec <- c(0, 0.5, 0.99)
```

```
h_vec <- c(3, 2.3, 0.1)
n <- 1e3
chain.mh <- matrix(nrow = n, ncol = 2)
chain.gibbs <- matrix(nrow = n, ncol = 2)
#par(mfrow=c(1,1,1,1))
t <- rnorm(n, mean = 2)
plot(density(t), main = "True marginal for X1")
```



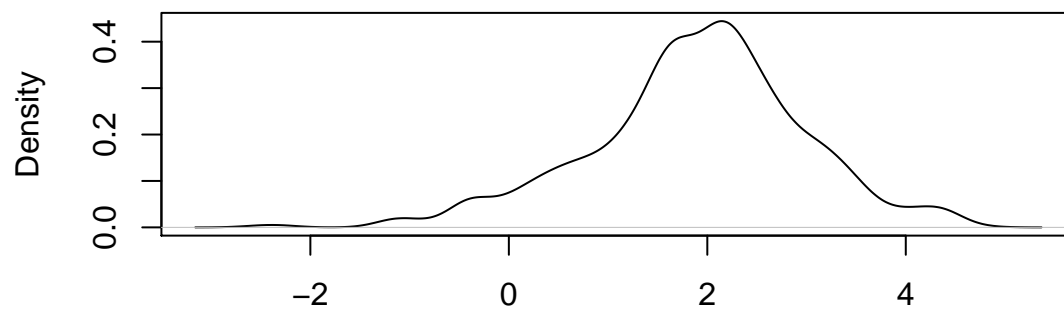
```
plot(density(rnorm(n, mean = -2)), main = "True marginal for X2")
```



```
for(i in 1:3) {  
  par(mfrow=c(2,1))  
  chain.mh = MH(n, init, h_vec[i], rho_vec[i])  
  chain.gibbs = Gibbs(n,init, rho_vec[i])  
  print(paste0("rho is :", rho_vec[i]))  
  plot(density(chain.mh[,1]), main = "marginal for X1 in chain.mh")  
  plot(density(chain.mh[,2]), main = "marginal for X2 in chain.mh")  
  plot.ts(chain.mh)  
  plot(density(chain.gibbs[,1]), main = "marginal for X1 in chain.gibbs")  
  plot(density(chain.gibbs[,2]), main = "marginal for X2 in chain.gibbs")  
  plot.ts(chain.gibbs)
```

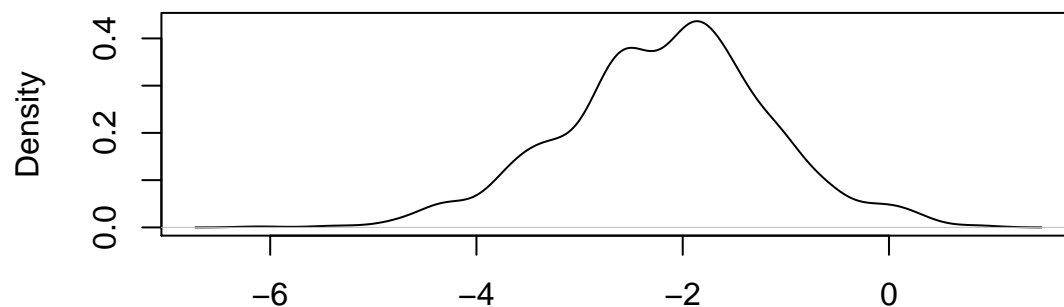
```
}  
  
## [1] "acceptance probaility is :0.35"  
## [1] "rho is :0"
```

marginal for X1 in chain.mh



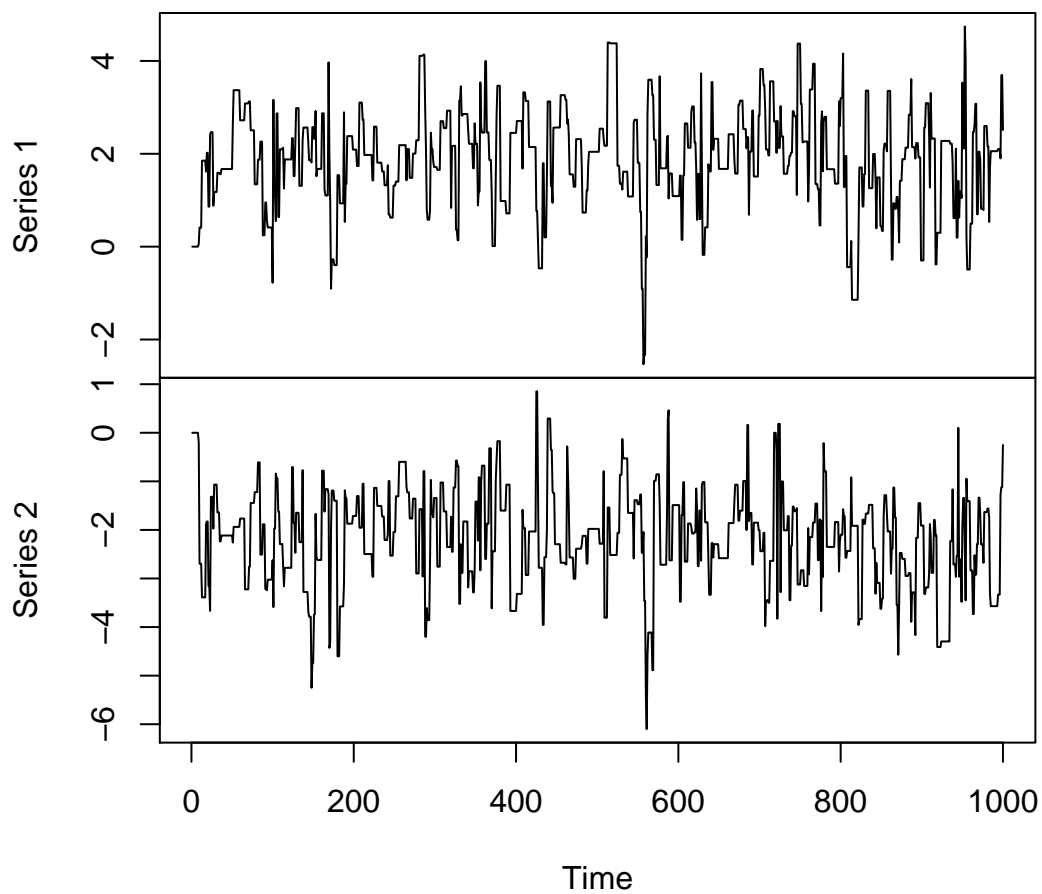
N = 1000 Bandwidth = 0.2087

marginal for X2 in chain.mh

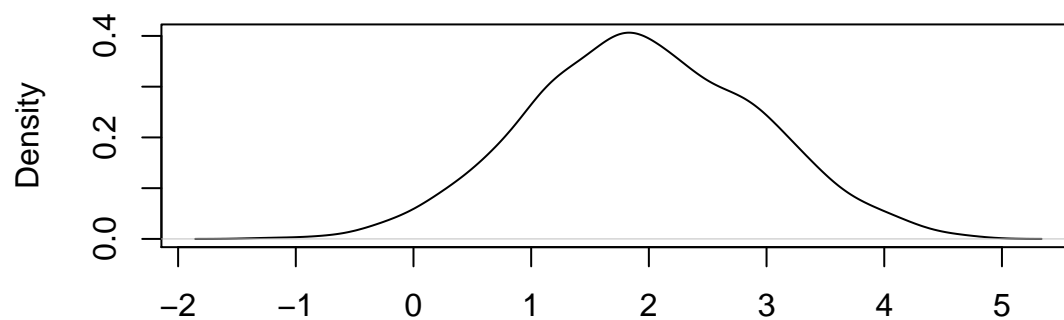


N = 1000 Bandwidth = 0.2085

chain.mh

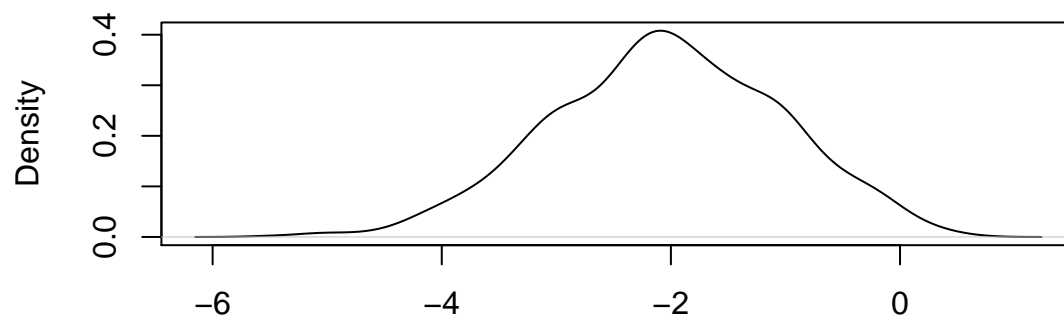


marginal for X1 in chain.gibbs



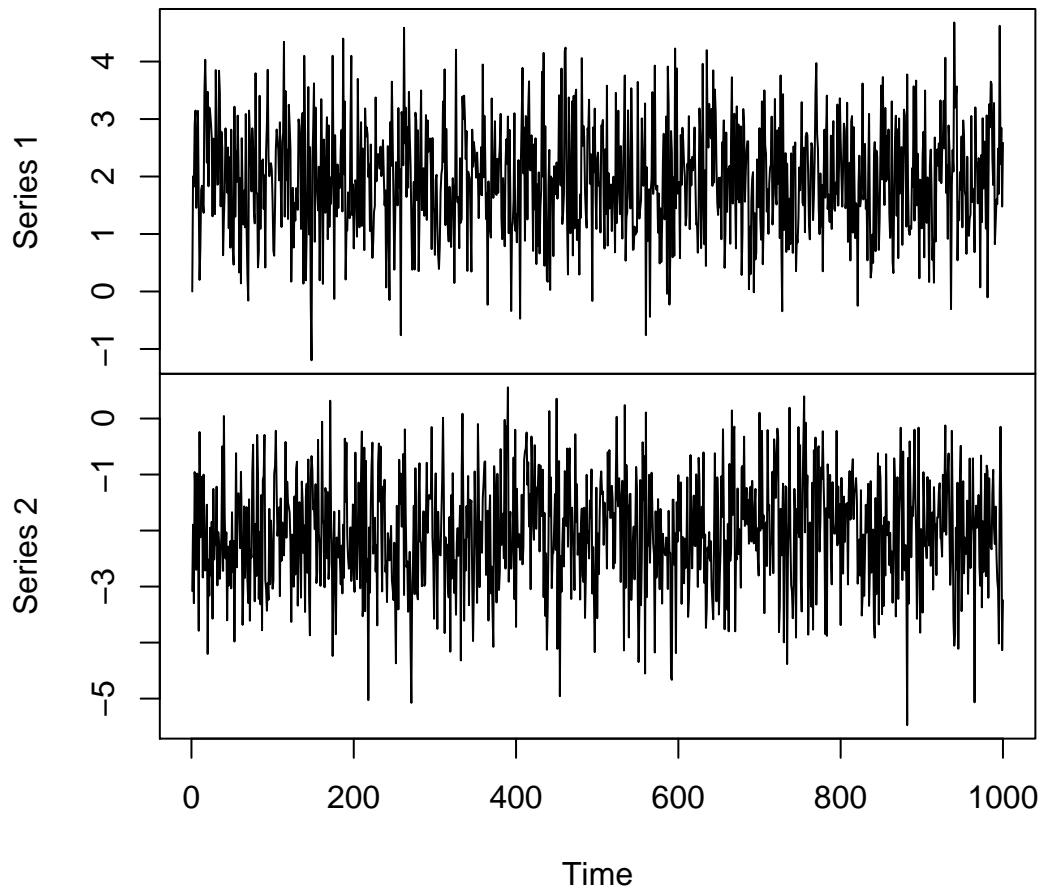
N = 1000 Bandwidth = 0.219

marginal for X2 in chain.gibbs



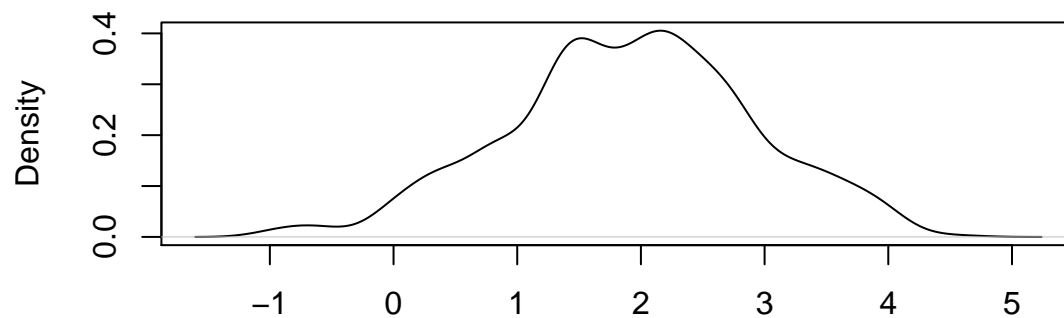
N = 1000 Bandwidth = 0.226

chain.gibbs



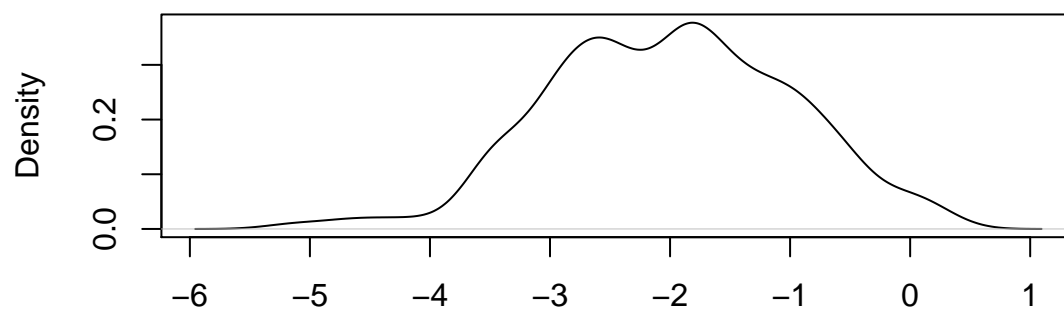
```
## [1] "acceptance probaility is :0.364"  
## [1] "rho is :0.5"
```


marginal for X1 in chain.mh



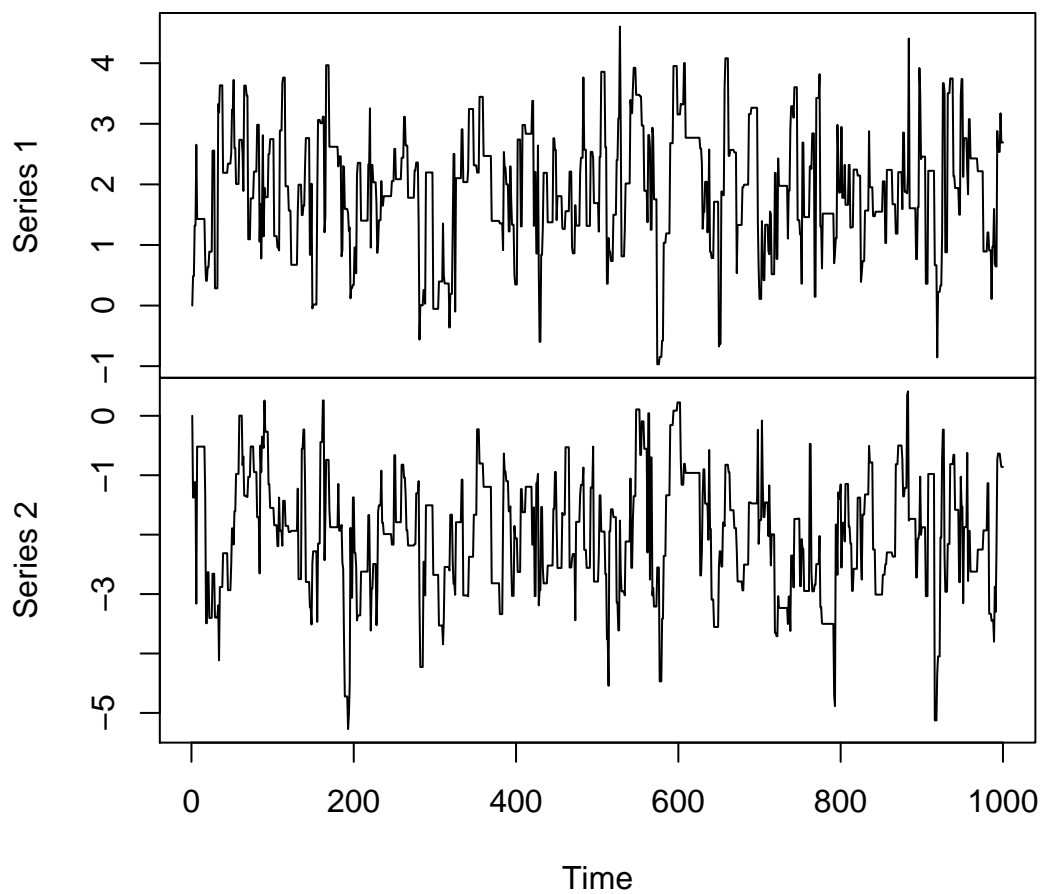
N = 1000 Bandwidth = 0.2111

marginal for X2 in chain.mh

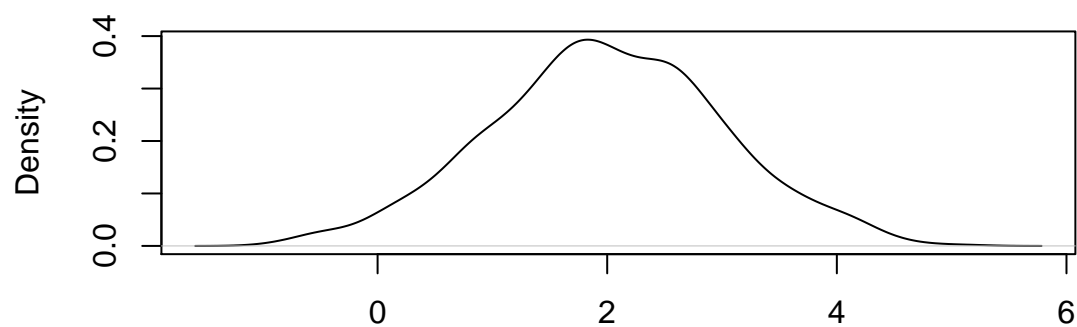


N = 1000 Bandwidth = 0.2275

chain.mh

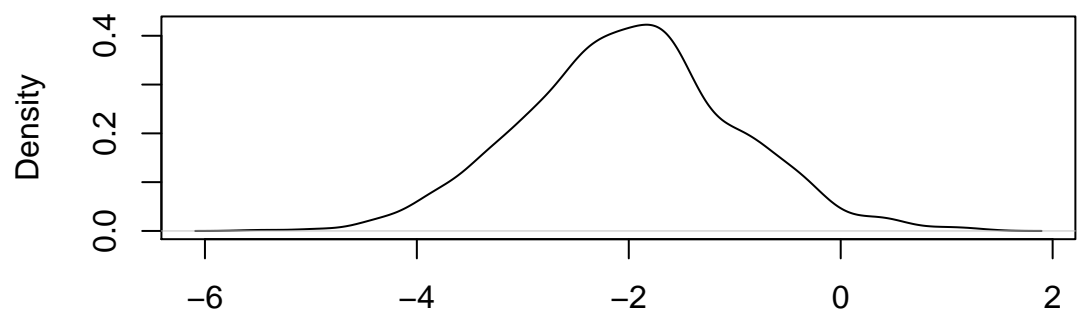


marginal for X1 in chain.gibbs



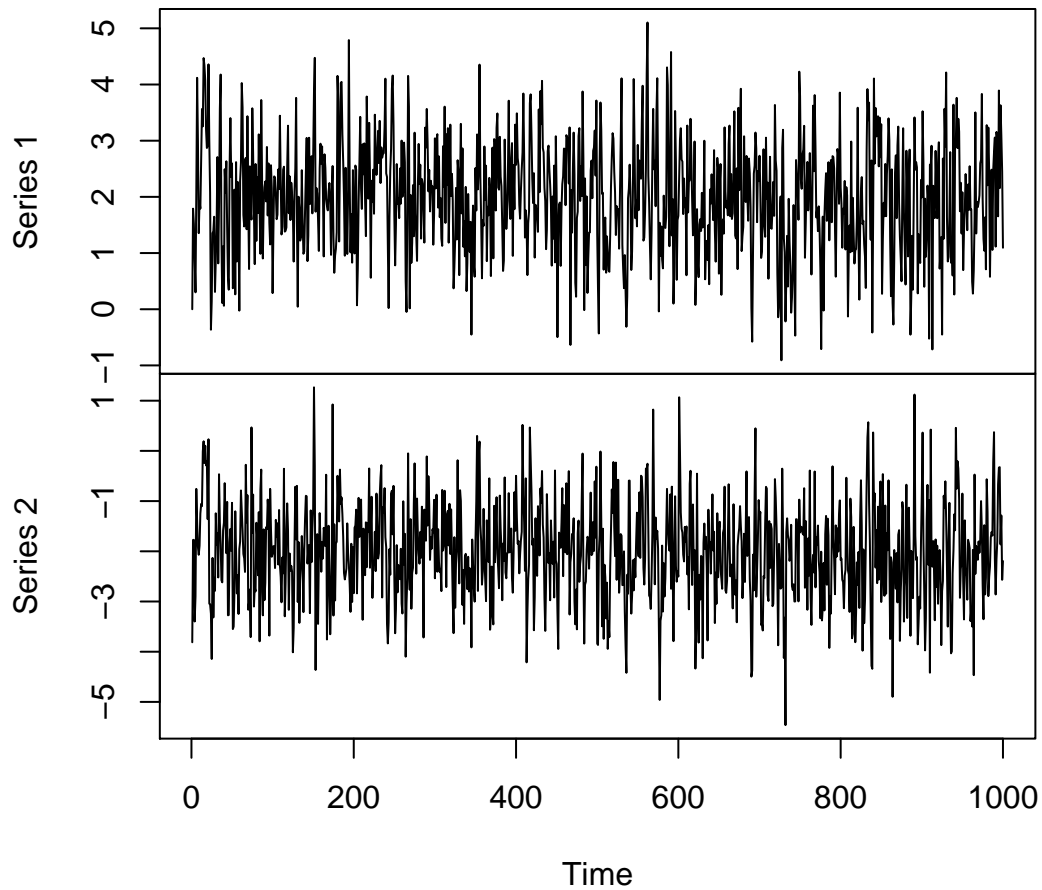
N = 1000 Bandwidth = 0.2263

marginal for X2 in chain.gibbs



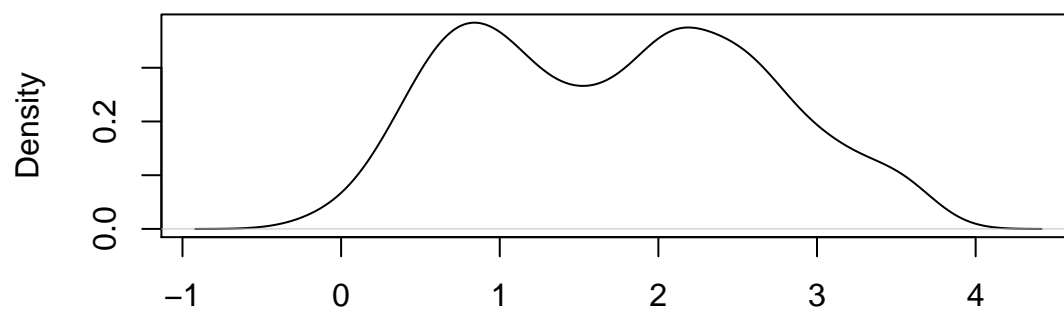
N = 1000 Bandwidth = 0.2097

chain.gibbs



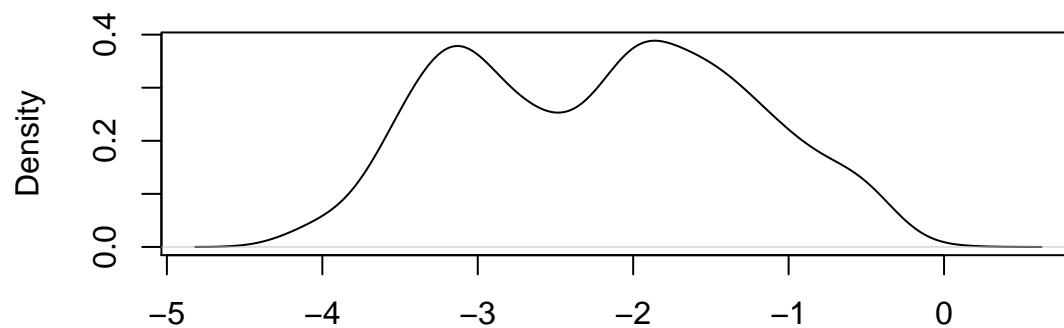
```
## [1] "acceptance probaility is :0.353"  
## [1] "rho is :0.99"
```

marginal for X1 in chain.mh



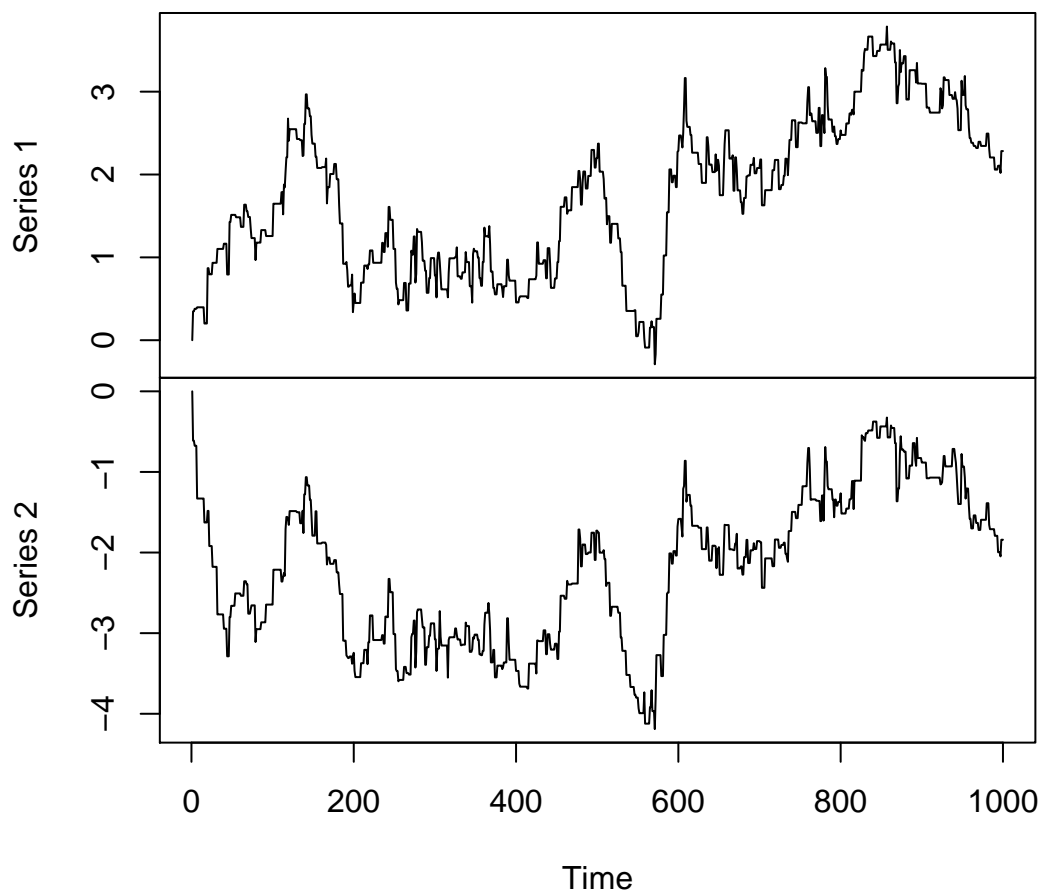
N = 1000 Bandwidth = 0.2096

marginal for X2 in chain.mh

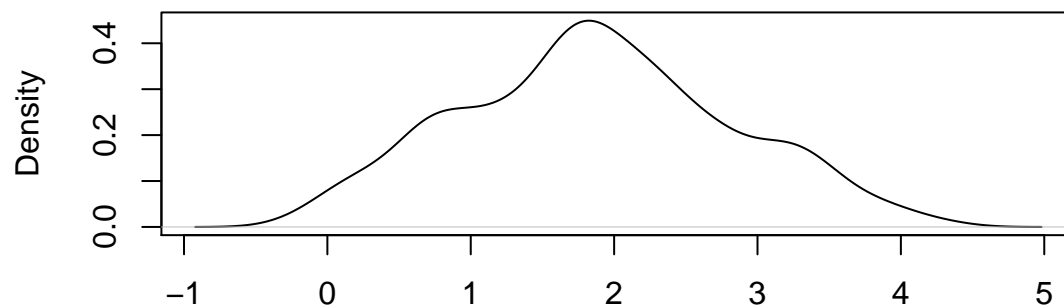


N = 1000 Bandwidth = 0.2091

chain.mh

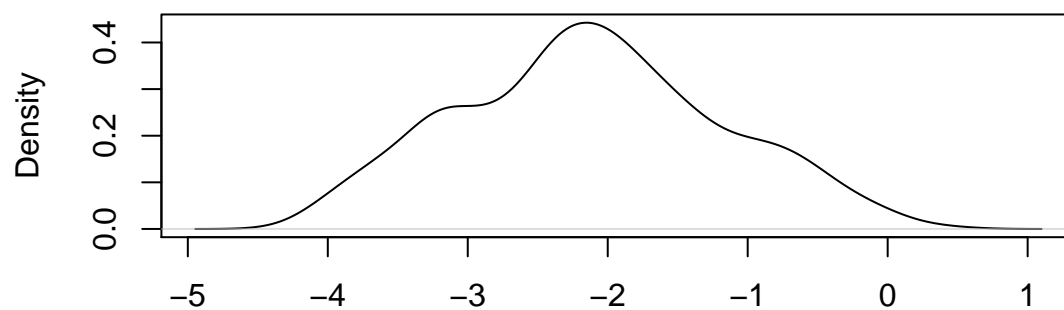


marginal for X1 in chain.gibbs



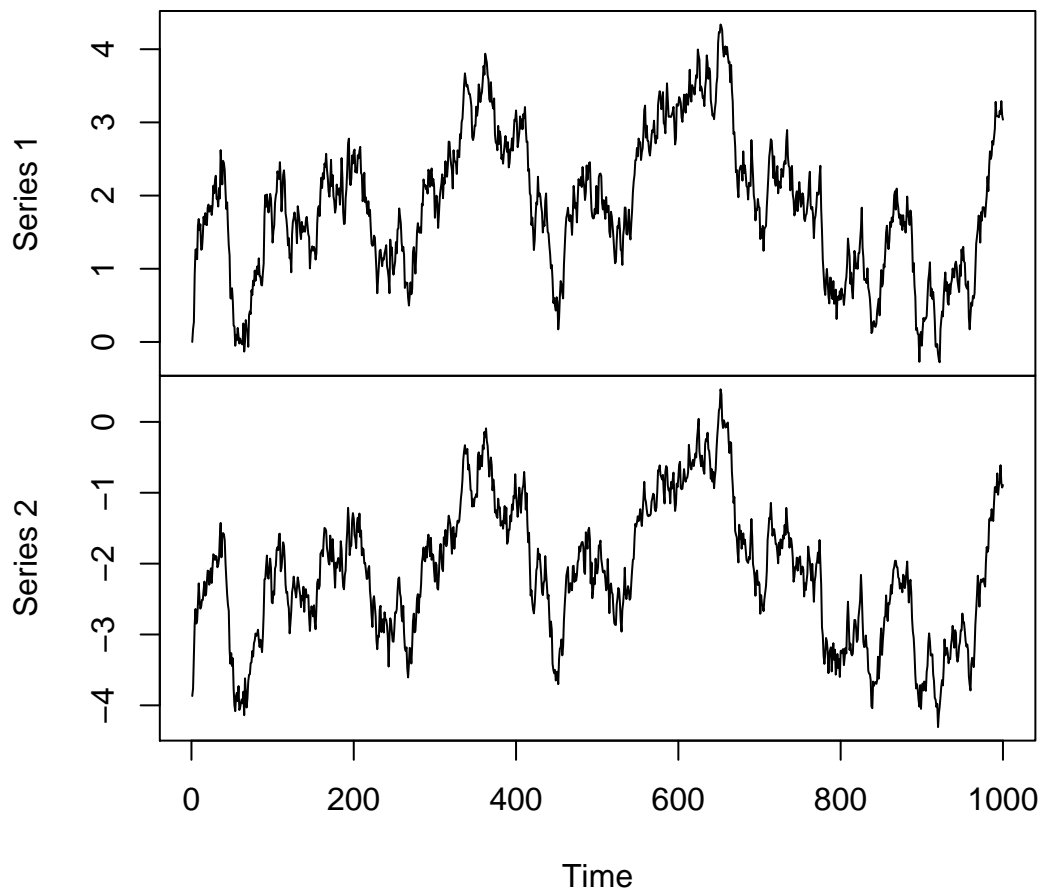
N = 1000 Bandwidth = 0.2146

marginal for X2 in chain.gibbs



N = 1000 Bandwidth = 0.2132

chain.gibbs



MH is better for $\rho = 0$ Gibbs is better for $\rho = 0$ because these values of ρ induce 0 correlation between the components, keeping the auto-correlation between the components to a minimum and thus improving the quality of samples of the Markov chain.