

Homework 7

Xiaokang Liu

26 October 2018

Contents

1 The likelihood function

1

1 The likelihood function

From the normal mixture example, we know that the likelihood function for the data is

$$f(x|\theta) = \prod_{i=1}^n [\delta \phi(x_i, \mu_1, \sigma_1^2) + (1 - \delta) \phi(x_i, \mu_2, \sigma_2^2)]$$

where $\phi()$ is the density function of a normal variable. Suppose that prior for μ_1 and μ_2 are $N(0, 100)$, that the prior for $1/\sigma_1^2$ and $1/\sigma_2^2$ are $\Gamma(a, b)$ with shape $a = 0.5$ and scale $b = 10$, and for δ we use noninformative prior, the uniform distribution. Further, all the priors are independent. For simplicity, let's write the prior densities for $\mu_1, \mu_2, \sigma_1^2, \sigma_2^2$ are f_1, f_2, f_3 and f_4 , respectively. Thus, the joint posterior distribution for those five parameters is

$$p(\theta|x) \propto f(x|\theta) f_1(\mu_1) f_2(\mu_2) f_3(\sigma_1^2) f_4(\sigma_2^2)$$

where $\theta = (\mu_1, \mu_2, \sigma_1^2, \sigma_2^2)$. For applying Gibbs sampling, we have to get the full conditional distribution for each parameter, they are:

$$\begin{aligned} p(\delta|x, \mu_1, \mu_2, \sigma_1^2, \sigma_2^2) &\propto f(x|\theta) \\ p(\mu_1|x, \delta, \mu_2, \sigma_1^2, \sigma_2^2) &\propto f(x|\theta) f_1(\mu_1) \\ p(\mu_2|x, \delta, \mu_1, \sigma_1^2, \sigma_2^2) &\propto f(x|\theta) f_2(\mu_2) \\ p(\sigma_1^2|x, \delta, \mu_2, \mu_1, \sigma_2^2) &\propto f(x|\theta) f_3(\sigma_1^2) \\ p(\sigma_2^2|x, \delta, \mu_2, \mu_1, \sigma_1^2) &\propto f(x|\theta) f_4(\sigma_2^2). \end{aligned}$$

Or we can directly use the relationship:

$$\begin{aligned} p(\delta|x, \mu_1, \mu_2, \sigma_1^2, \sigma_2^2) &\propto f(x|\theta) \\ p(\mu_1|x, \delta, \mu_2, \sigma_1^2, \sigma_2^2) &\propto f(x|\theta) \\ p(\mu_2|x, \delta, \mu_1, \sigma_1^2, \sigma_2^2) &\propto f(x|\theta) \\ p(\sigma_1^2|x, \delta, \mu_2, \mu_1, \sigma_2^2) &\propto f(x|\theta) \\ p(\sigma_2^2|x, \delta, \mu_2, \mu_1, \sigma_1^2) &\propto f(x|\theta). \end{aligned}$$

Then we can conduct Gibbs sampling step by step. For δ , we can just use the rejection sampling method from the example to sample from the conditional density. For all other methods, we can use rejection sampling function *arms* in R-package *HI*. The codes for applying the algorithm is like follows:

```

### Generate data: delta=0.7, mu_1=7, mu_2=10, sigma_1=sigma_2=0.5
delta <- 0.7
n <- 100
set.seed(254)
u <- rbinom(n, prob = delta, size = 1)
x <- rnorm(n, ifelse(u == 1, 7, 10), 0.5)

mylike <- function(delta,mu1,mu2,sigma1,sigma2,x) {
  # prod(delta * dnorm(x, mu1, sqrt(sigma1)) + (1 - delta) * dnorm(x, mu2, #sqrt(sigma2))) * dnorm(x, mu1, sqrt(sigma1))
  prod(delta * dnorm(x, mu1, sqrt(sigma1)) + (1 - delta) * dnorm(x, mu2, sqrt(sigma2))) * dnorm(x, mu1, sqrt(sigma1))
}

mymcmc5 <- function(niter, init, x){
  res <- matrix(nrow = niter, ncol = 5)
  for (i in 1:niter){
    init.delta <- init[1]
    init.mu1 <- init[2]
    init.mu2 <- init[3]
    init.sigma1 <- init[4]
    init.sigma2 <- init[5]

    f0 <- function(x0) log(mylike(x0,init.mu1,init.mu2,init.sigma1,init.sigma2,x))
    new.delta <- res[i,1] <- arms(init.delta, f0, function(x0) (x0>0)*(x0<1), 1)

    f1 <- function(x1) log(mylike(new.delta,x1,init.mu2,init.sigma1,init.sigma2,x))
    new.mu1 <- res[i,2] <- arms(init.mu1, f1, function(x1) (x1>-50)*(x1<100), 1)
    #new.mu1 <- res[i,2] <- arms(rnorm(1,6,1), f1, function(x1) (x1>-50)*(x1<100), 1)

    f2 <- function(x2) log(mylike(new.delta,new.mu1,x2,init.sigma1,init.sigma2,x))
    new.mu2 <- res[i,3] <- arms(init.mu2, f2, function(x2) (x2>-50)*(x2<100), 1)

    f3 <- function(x3) log(mylike(new.delta,new.mu1,new.mu2,x3,init.sigma2,x))
    new.sigma1 <- res[i,4] <- arms(init.sigma1, f3, function(x3) (x3>0)*(x3<5), 1)

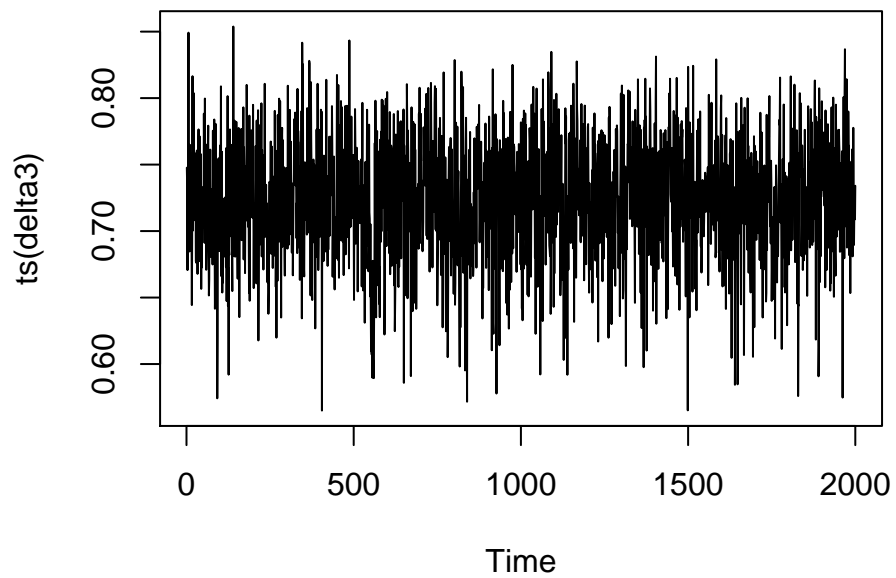
    f4 <- function(x4) log(mylike(new.delta,new.mu1,new.mu2,new.sigma1,x4,x))
    new.sigma2 <- res[i,5] <- arms(init.sigma2, f4, function(x4) (x4>0)*(x4<5), 1)

    new.par <- c(new.delta,new.mu1,new.mu2,new.sigma1,new.sigma2)
    init <- new.par
  }
  res
}

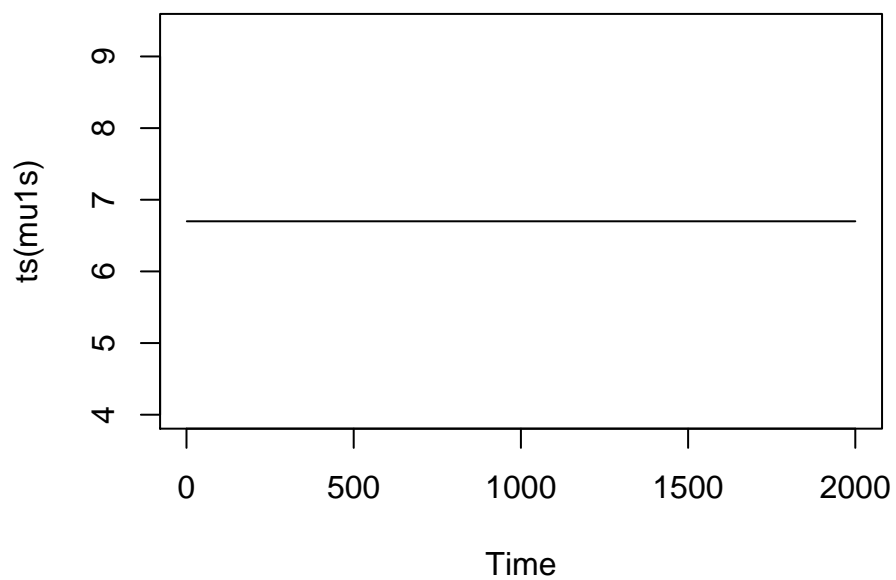
niter <- 3000
init <- c(0.5,5.7,9,0.2,0.2)
res <- mymcmc5(niter, init, x)

```

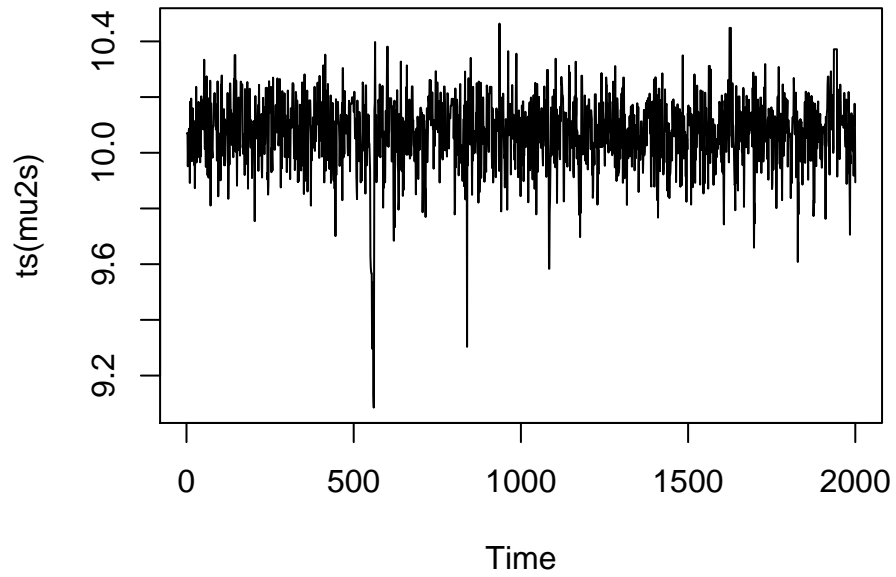
```
res <- res[-c(1:1000),]  
delta3 <- res[,1]  
mu1s <- res[,2]  
mu2s <- res[,3]  
sigma1s <- res[,4]  
sigma2s <- res[,5]  
  
plot(ts(delta3))
```



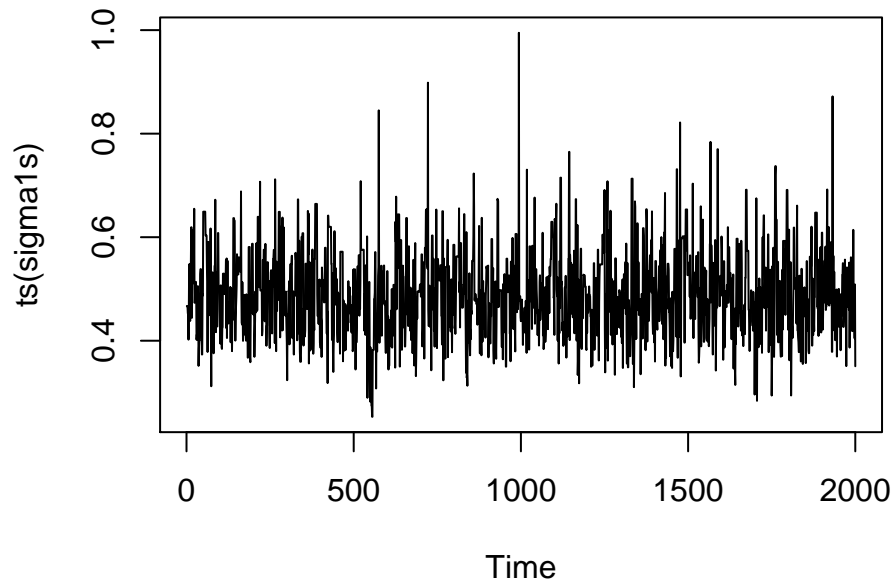
```
plot(ts(mu1s))
```



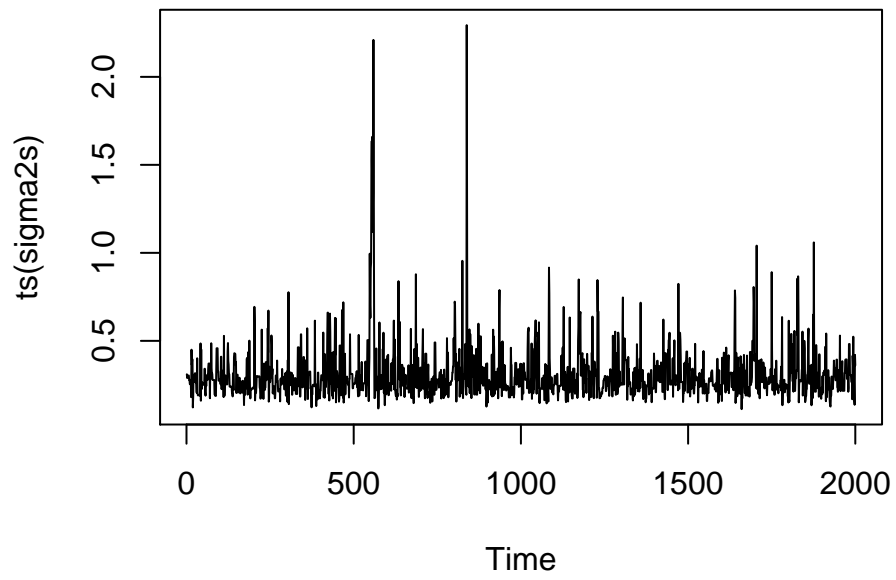
```
plot(ts(mu2s))
```



```
plot(ts(sigma1s))
```

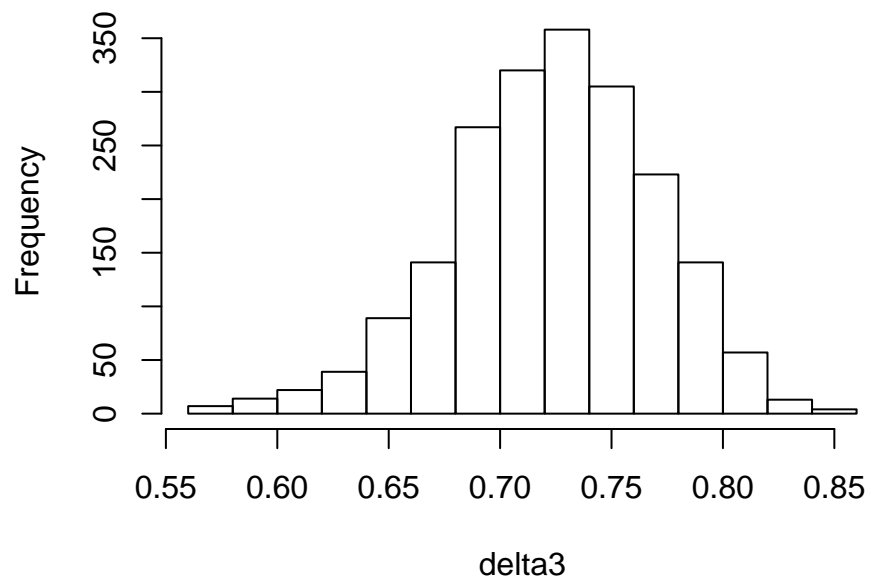


```
plot(ts(sigma2s))
```



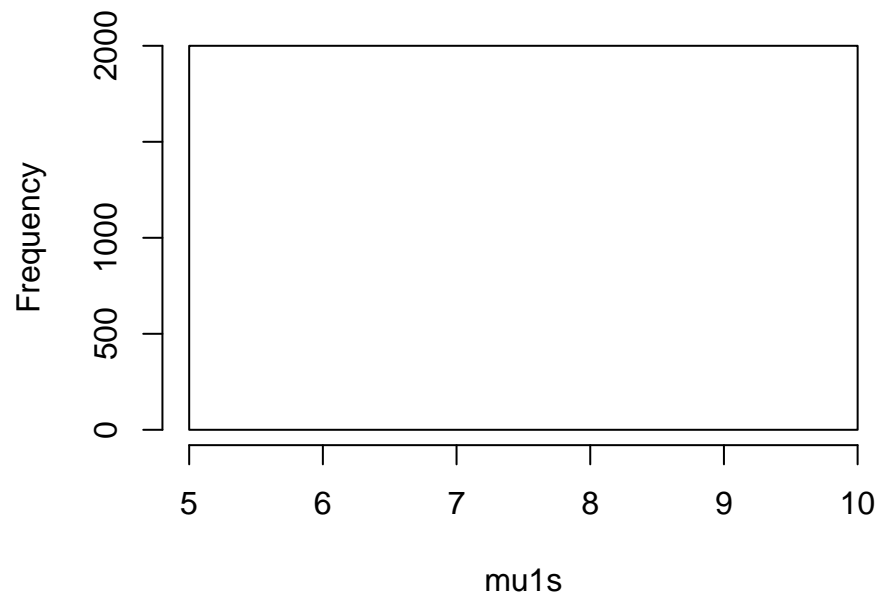
```
hist(delta3)
```

Histogram of delta3



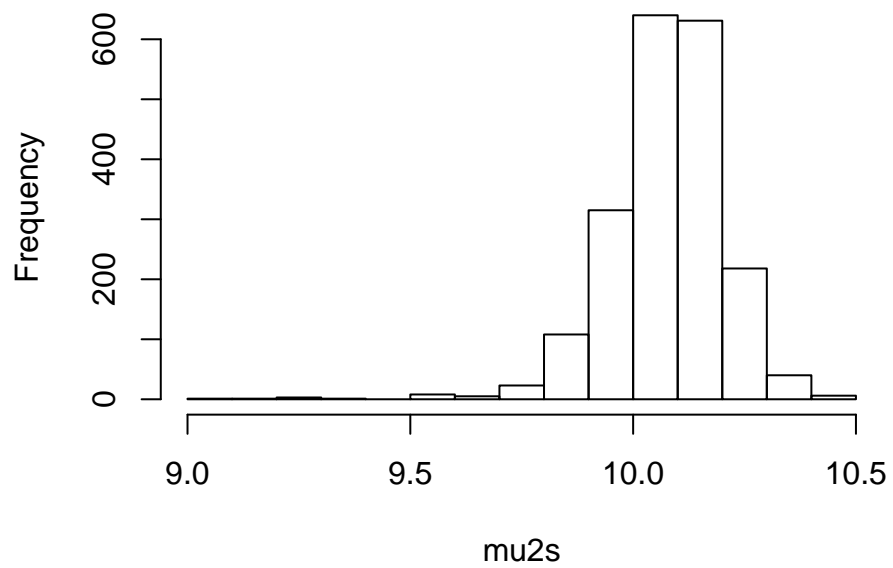
```
hist(mu1s)
```

Histogram of mu1s



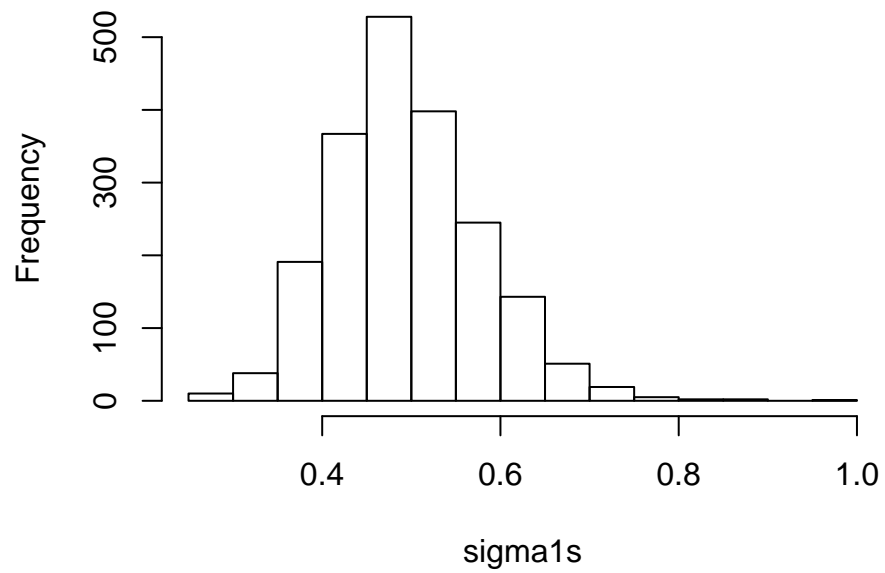
```
hist(mu2s)
```

Histogram of mu2s



```
hist(sigma1s)
```

Histogram of sigma1s



```
hist(sigma2s)
```

Histogram of sigma2s

