

4

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```

set.seed(501)
log_lik4= function (x,gam){ ##mu=3,gamma)
  n = length(x)
  if(!is.infinite((-sum(x)+ n*3)/gam - 2* sum(log(gam+exp(-x-3)))) &
    !is.nan((-sum(x)+ n*3)/gam - 2* sum(log(gam+exp(-x-3))))){
    ll=(-sum(x)+ n*3)/gam - 2* sum(log(gam+exp(-x-3)))} else{ll=0}
  return(-ll)
}
param = c(3, 1) # mu=3 , gamma = 1
n1=10
n2=500
gamma_1=rep(NA,100)
gamma_2=rep(NA,100)
gamma_3=rep(NA,100)
gamma_4=rep(NA,100)
for (i in 1:100){ # mle of gamma for n=10 and 500
  x1= rlogis(n1,3,1) #gamma=1
  x2=rlogis(n2,3,1)#gamma=1
  x3=rlogis(n1,3,10) #gamma=10
  x4=rlogis(n2,3,10)#gamma=10
  g1=optimize(log_lik4, interval = c(0.001,100), x=x1) # mle estimates
  g2=optimize(log_lik4, interval = c(0.001,100), x=x2)
  g3=optimize(log_lik4, interval = c(0.001,100), x=x3)
  g4=optimize(log_lik4, interval = c(0.001,100), x=x4)
  gamma_1[i]=g1$minimum
  gamma_2[i]=g2$minimum
  gamma_3[i]=g3$minimum
  gamma_4[i]=g4$minimum
}
mse1= 1/n1 *sum((gamma_1-mean(gamma_1))^2)
mse2= 1/n2 *sum((gamma_2-mean(gamma_2))^2)
mse3= 1/n1 *sum((gamma_3-mean(gamma_3))^2)
mse4= 1/n2 *sum((gamma_4-mean(gamma_4))^2)
mse1 # gamma =1 , n =10

## [1] 0.2485557
mse2 # gamma =1 , n =500

## [1] 0.0001154142
mse3 # gamma =10 , n =10

## [1] 35.17824
mse4 # gamma =10 , n =500

## [1] 0.02359754

```

Now we do the posterior mean by markov chain monte carlo:

```

# unnormalized pi will be :
pi_p = function(xvec , gam ){# assuming the same prior for gamma as in question 1
  -log_lik4(xvec, gam) * exp(-gam/10)
}

# full conditional : f(gamma| X,mu)
f_gamma_p = function(xvec , gam ){
  -log_lik4(xvec,gam) * exp(-gam/10)
}

x1= rlogis(n1,3,1) #gamma=1, n=10
x2=rlogis(n2,3,1)#gamma=1, n=500
x3=rlogis(n1,3,10) #gamma=10,n=10
x4=rlogis(n2,3,10)#gamma=10,n=500

chain_length= 10000
MH = matrix(NA, chain_length, 2,dimnames = list(NULL,c("index","gamma")))
MH[1,]= c(1, 2.6)
proposal = function(gam){
  rnorm(1,gam,1)
}
naccept = 1
i = 2
for (i in 2:chain_length){
  MH[i,1]=i
  propose = proposal(MH[i-1,2])
  alpha = min(f_gamma_p(x1,propose)*dnorm(MH[i-1,2],MH[i-1,2],1)/
             f_gamma_p(x1,MH[i-1,2])/dnorm(propose,MH[i-1,2],1) , 1)
  if (propose > 0 & is.finite(alpha)& !is.nan(alpha) & runif(1)< alpha){ MH[i,2]= propose }else{MH[i,2]=
}

1/chain_length *sum((MH[,2]-mean(MH[,2]))^2) #mse posterior

## [1] 5725.959

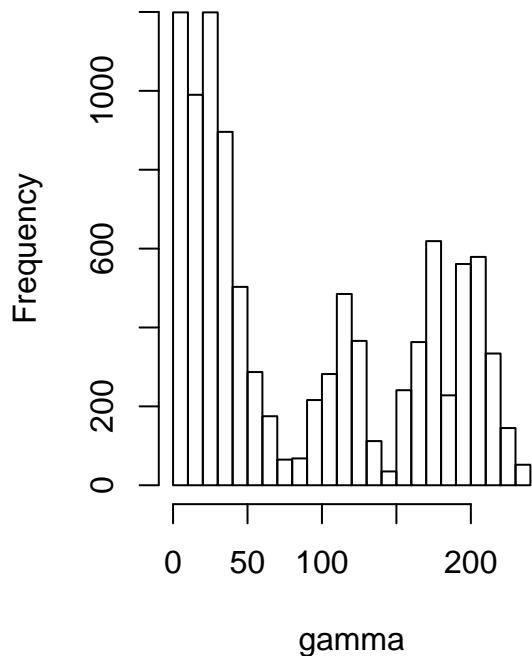
mean(MH[,2]) # posterior estimate

## [1] 90.60616

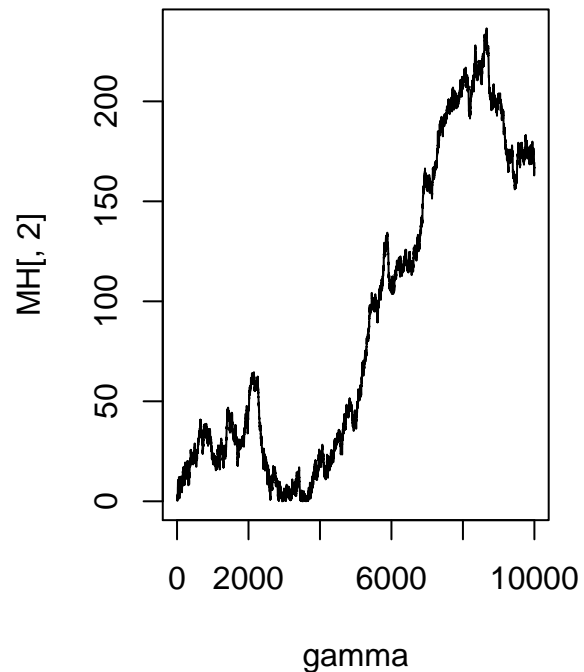
par(mfrow=c(1,2))
hist(MH[,2],breaks =30, main="Posterior of gamma" ,xlab="gamma")
plot(MH[,2], type = "l", xlab="gamma" , main = "Chain values of gamma")

```

Posterior of gamma



Chain values of gamma



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chain_length= 10000
MH = matrix(NA, chain_length, 2,dimnames = list(NULL,c("index","gamma")))
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  rnorm(1,gam,1)
}
naccept = 1
i = 2
for (i in 2:chain_length){
  MH[i,1]=i
  propose = proposal(MH[i-1,2])
  alpha = min(f_gamma_p(x2,propose)*dnorm(MH[i-1,2],MH[i-1,2],1)/
              f_gamma_p(x2,MH[i-1,2])/dnorm(propose,MH[i-1,2],1) , 1)
  if (propose > 0 & is.finite(alpha)& !is.nan(alpha) &runif(1)< alpha){ MH[i,2]= propose }else{MH[i,2]=
}
1/chain_length *sum((MH[,2]-mean(MH[,2]))^2) #mse posterior

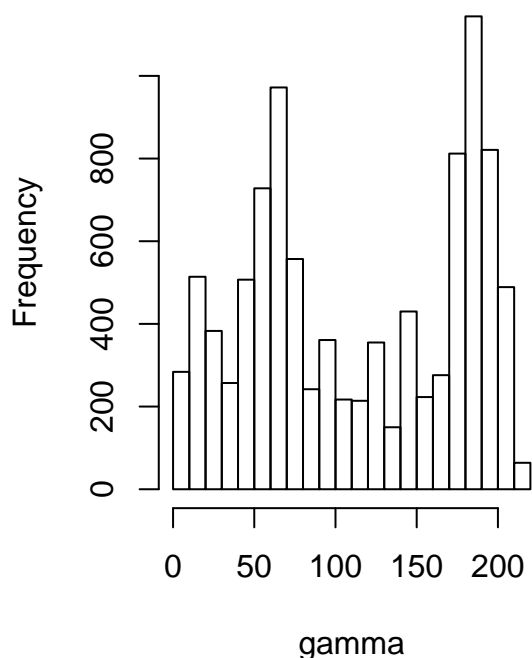
## [1] 4194.211

mean(MH[,2]) # posterior estimate

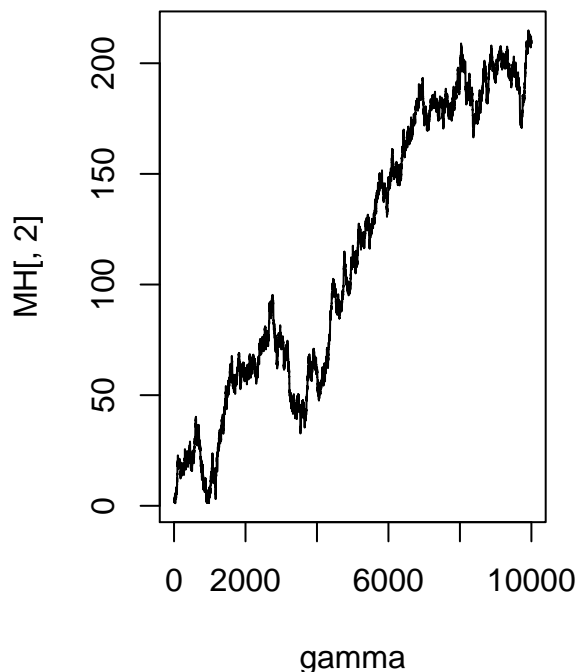
## [1] 113.3182

par(mfrow=c(1,2))
hist(MH[,2],breaks =30, main="Posterior of gamma",xlab="gamma")
plot(MH[,2], type = "l", xlab="gamma", main = "Chain values of gamma")
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Posterior of gamma



Chain values of gamma



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}
naccept = 1
i = 2
for (i in 2:chain_length){
  MH[i,1]=i
  propose = proposal(MH[i-1,2])
  alpha = min(f_gamma_p(x3,propose)*dnorm(MH[i-1,2],MH[i-1,2],1)/
              f_gamma_p(x3,MH[i-1,2])/dnorm(propose,MH[i-1,2],1) , 1)
  if (propose > 0 & is.finite(alpha)& !is.nan(alpha) &runif(1)< alpha){ MH[i,2]= propose }else{MH[i,2]=
}

1/chain_length *sum((MH[,2]-mean(MH[,2]))^2) #mse posterior

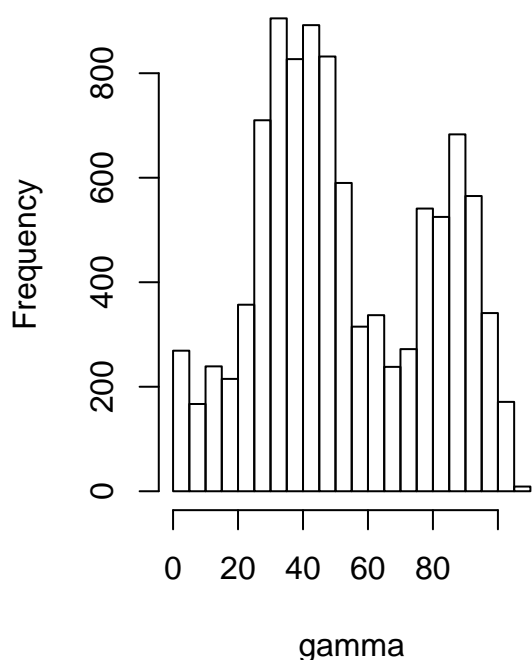
## [1] 700.8453

mean(MH[,2]) # posterior estimate

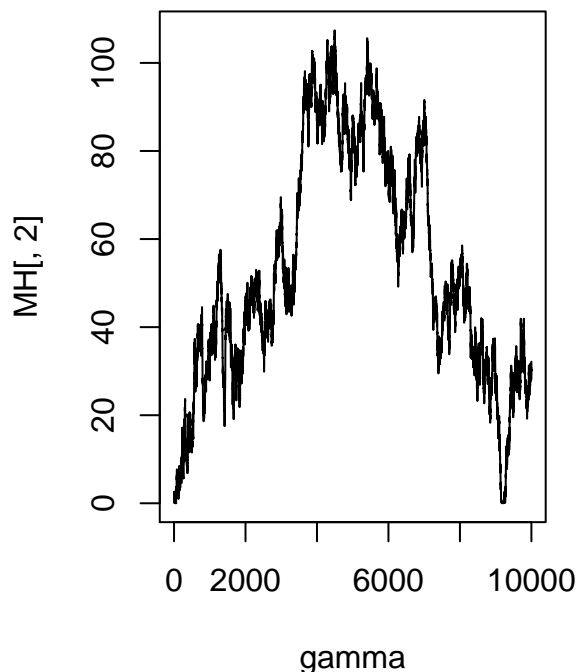
## [1] 52.86894

par(mfrow=c(1,2))
hist(MH[,2],breaks =30, main="Posterior of gamma" ,xlab="gamma")
plot(MH[,2], type = "l", xlab="gamma" , main = "Chain values of gamma")
```

Posterior of gamma



Chain values of gamma



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MH[1,]= c(1, 2.6)
proposal = function(gam){
  rnorm(1,gam,1)
}
naccept = 1
i = 2
for (i in 2:chain_length){
  MH[i,1]=i
  propose = proposal(MH[i-1,2])
  alpha = min(f_gamma_p(x4,propose)*dnorm(MH[i-1,2],MH[i-1,2],1)/
              f_gamma_p(x4,MH[i-1,2])/dnorm(propose,MH[i-1,2],1) , 1)
  if (propose > 0 & is.finite(alpha)& !is.nan(alpha) &runif(1)< alpha){ MH[i,2]= propose }else{MH[i,2]=
}

1/chain_length*sum((MH[,2]-mean(MH[,2]))^2) #mse posterior

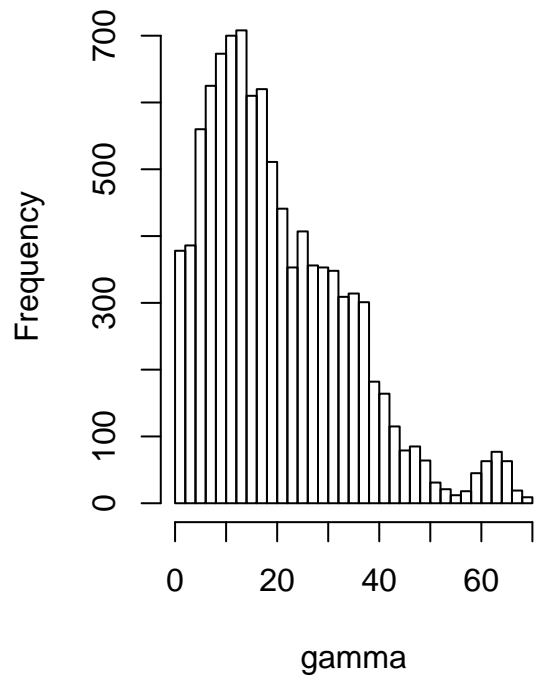
## [1] 194.8782

mean(MH[,2]) # posterior estimate

## [1] 20.27006

par(mfrow=c(1,2))
hist(MH[,2],breaks =30, main="Posterior of gamma",xlab="gamma")
plot(MH[,2], type = "l", xlab="gamma" , main = "Chain values of gamma")
```

Posterior of gamma



Chain values of gamma

