Using MCMC to estimate unknown parameters of normal mixture

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Abstract

In this assignment, we will use the Gibbs sampling approach to design an MCMC to estimate all the unknown parameters.Use the **arms()** function in package HI.

1 Normal mixture revisited

Consider again the normal mixture example, except that the parameters of the normal distributions are considered unknown. Suppose that prior for μ_1 and μ_2 are $N(0, 10^2)$, that the prior for $1/\sigma_1^2$ and $1/\sigma_2^2$ are $\Gamma(a, b)$ with shape $a = .5$ and scale \$ b = 10\$. Further, all the priors are independent. Design an MCMC using the Gibbs sampling approach to estimate all 5 parameters. Use the **arms()** function in package **HI**. Run your chain for sufficiently long and drop the burn-in period. Plot the histogram of the results for all the parameters.

2 Likelihood function

First, let's consider the normal mixture example, the normal mixture distribution is a mixture of two normal distribution function:

$$N(\mu_1, \sigma_1^2); N(\mu_2, \sigma_2^2)$$

and the weight for each distribution is δ and $1 - \delta$.

```r
mixture_distribution <- function(delta, x, mu1, mu2, sigma1, sigma2) {
    delta * dnorm(x, mu1, sigma1) + (1 - delta) * dnorm(x, mu2, sigma2)
}
```

However, we don't know these 5 parameters of the mixture distribution function. Further, all the priors are independent. Now, we will generate some random sample:$\delta = 0.7, \mu_1 = 7, \sigma_1^2 = 0.5^2, \mu_2 = 10, \sigma_2^2 = 0.5^2$

```r
delta <- 0.7 # true value to be estimated based on the data
n <- 100
set.seed(123)
u <- rbinom(n, prob = delta, size = 1)
x0 <- rnorm(n, ifelse(u == 1, 7, 10), 0.5)
```

By sampling $n = 100$ data from the mixture distribution, we will get the likelihood function:

$$likelihood(x; \delta, \mu_1, \sigma_1^2, \mu_2, \sigma_2^2) = \prod_{i=1}^{n} \left[\delta N(\mu_1, \sigma_1^2) + (1 - \delta)N(\mu_2, \sigma_2^2)\right]$$

so does the loglikelihood function:

$$loglike(x; \delta, \mu_1, \sigma_1^2, \mu_2, \sigma_2^2) = \sum_{i=1}^{n} log(\delta N(\mu_1, \sigma_1^2) + (1 - \delta)N(\mu_2, \sigma_2^2))$$

```
loglike <- function(delta, x , mu1, mu2, sigma1, sigma2){
  sum(log(delta * dnorm(x, mu1, sigma1) + (1 - delta) * dnorm(x, mu2, sigma2)))
}
```

3 Posterior density

then, let's calculate posterior density, according to Bayes theory

$$p(\theta|x) = \frac{p(x|\theta)p(\theta)}{p(x)}$$

$p(\theta|x)$ is what we called posterior density, $p(x|\theta)$ is the likelihood function, $p(\theta)$ is prior probability, $p(x)$ is the normalization constant useful for Bayesian model selection. The prior for μ_1 and μ_2 are $N(0, 10^2)$, the prior for $\frac{1}{\sigma_1^2}$ and $\frac{1}{\sigma_2^2}$ are $\Gamma(0.5, 10)$, hence the prior for σ_1^2 and σ_2^2 are the inverse gamma distribution $IG(0.5, 10)$.

So we get the posterior density:

$$p(\delta, \mu_1, \sigma_1^2, \mu_2, \sigma_2^2|x) = \prod_{i=1}^{n} \left[\delta N(\mu_1, \sigma_1^2) + (1-\delta)N(\mu_2, \sigma_2^2)\right] N(\mu_1, 0, 10)N(\mu_2, 0, 10)IG(\sigma_1^2, 0.5, 10)IG(\sigma_2^2, 0.5, 10)$$

so does the log posterior function:

$$logposterior(\delta, \mu_1, \sigma_1^2, \mu_2, \sigma_2^2|x) = \sum_{i=1}^{n}(\delta N(\mu_1, \sigma_1^2)+(1-\delta)N(\mu_2, \sigma_2^2))+log(N(\mu_1, 0, 10))+log(N(\mu_2, 0, 10))+log(IG(\sigma_1^2, 0.5, 10)$$

```
library(invgamma)
logposterior <- function(delta, x, mu1, mu2, sigma1, sigma2){
  mu1.logprior <- dnorm(mu1, 0, 10, log = T)
  mu2.logprior <- dnorm(mu2, 0, 10, log = T)
  sigma1.logprior <- dinvgamma(sigma1^2, shape = 0.5, scale = 10, log = T)
  sigma2.logprior <- dinvgamma(sigma2^2, shape = 0.5, scale = 10, log = T)
  sum(mu1.logprior + mu2.logprior +sigma1.logprior + sigma2.logprior) + loglike(delta, x, mu1, mu2, sig
}
```

4 Gibbs sampling

Next we will use an MCMC based the Gibbs sampler uses the ARMS algorithm from R package HI as recommended in the question:

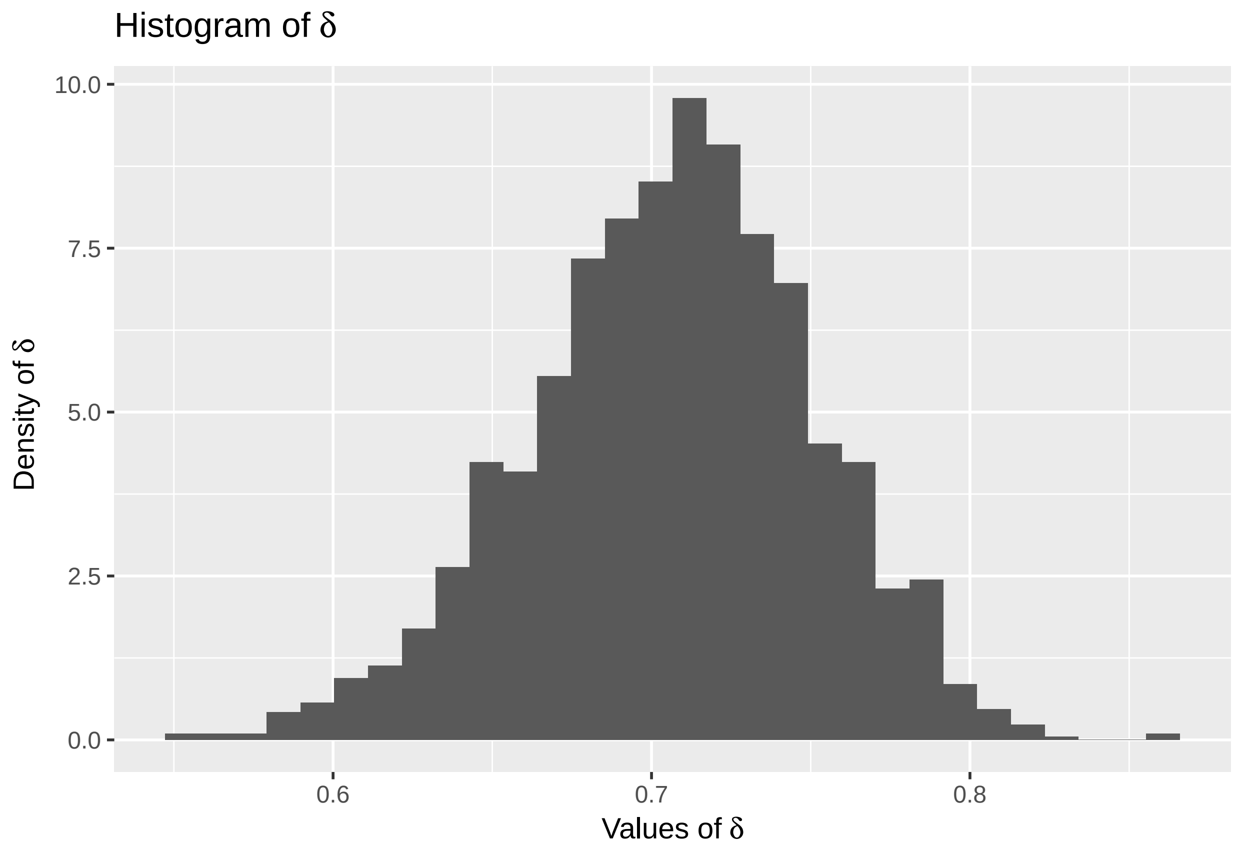
```
library(HI)
mymcmc <- function(niter, delta.init, mu1.init, mu2.init, sigma1.init, sigma2.init,x){
  data <- matrix(nrow = niter, ncol = 5)
  for(i in 1:niter){
    f1 <- function(x1)  logposterior(x1,x0,mu1.init,mu2.init,sigma1.init,sigma2.init)
    delta.init <- data[i,1] <- arms(delta.init, f1, function(x1) (x1 > 0) * (x1< 1), 1)

    f2 <- function(x2)  logposterior(delta.init,x0,x2,mu2.init,sigma1.init,sigma2.init)
    mu1.init <- data[i,2] <- arms(mu1.init, f2, function(x2) (x2 > -100) * (x2 < 100), 1)
    f3 <- function(x3)  logposterior(delta.init,x0,mu1.init,x3,sigma1.init,sigma2.init)
    mu2.init <- data[i,3] <- arms(mu2.init, f3, function(x3) (x3 > -100) * (x3 < 100), 1)

    f4 <- function(x4)  logposterior(delta.init,x0,mu1.init,mu2.init,x4,sigma2.init)
    sigma1.init <- data[i,4] <- arms(sigma1.init, f4, function(x4) (x4 > 0) * (x4 < 200), 1)

    f5 <- function(x5)  logposterior(delta.init,x0,mu1.init,mu2.init,sigma1.init,x5)
    sigma2.init <- data[i,5] <- arms(sigma2.init, f5, function(x5) (x5 > 0) * (x5 < 200), 1)
  }
  data
}
niter <- 3000
results <- mymcmc(niter, 0.5, 1,1,1,1,x0)
results <- results[-c(1:1000),]
options(warn=-1)
library(ggplot2)
plot1<- ggplot(data.frame(x = results[,1]), aes(x = x))+
  geom_histogram(aes(y=..density..))+labs(x = expression("Values of"~delta),
  y = expression(" Density of"~delta), title=expression("Histogram of"~delta))
plot1
```

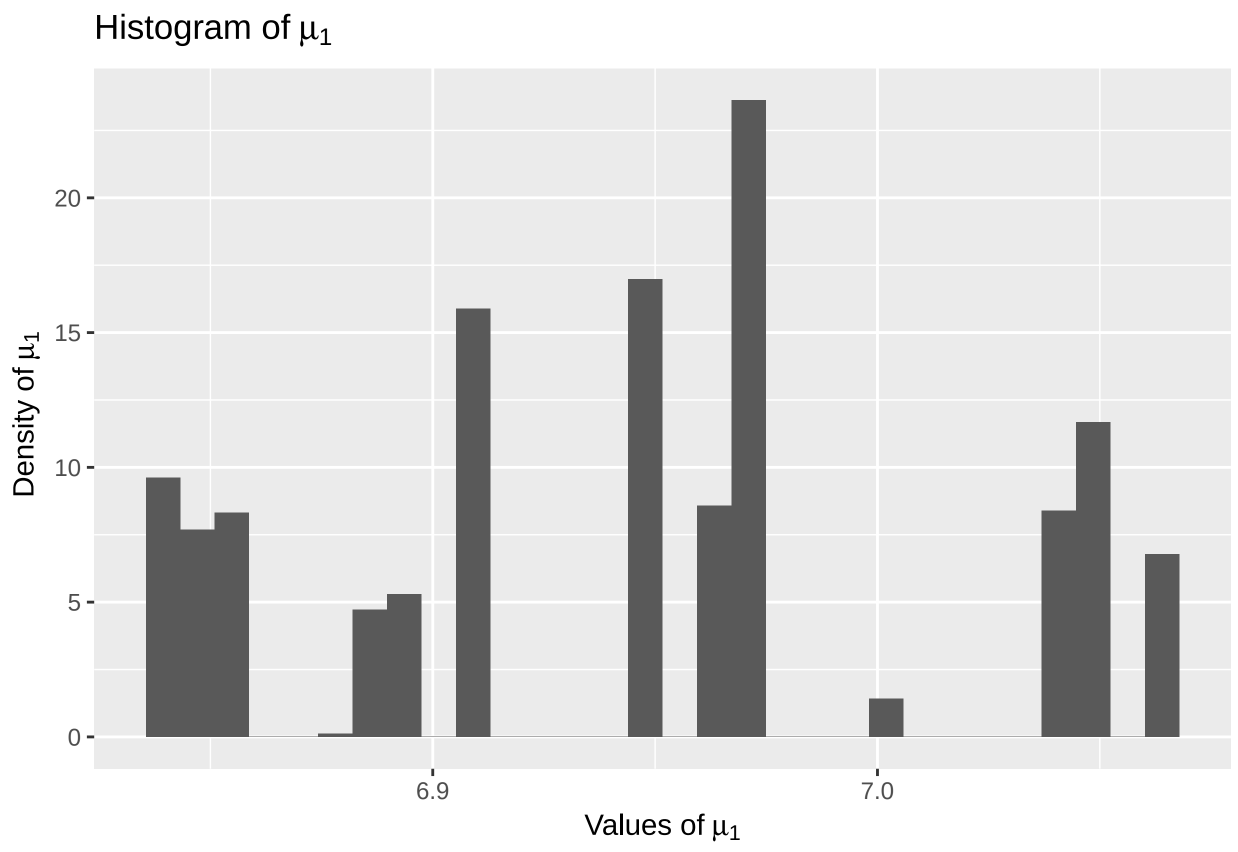
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



δ is about 0.7

```r
plot2<- ggplot(data.frame(x = results[,2]), aes(x = x))+
  geom_histogram(aes(y=..density..))+labs(x = expression("Values of"~mu[1]),
  y = expression(" Density of"~mu[1]), title=expression("Histogram of"~mu[1]))
plot2
```

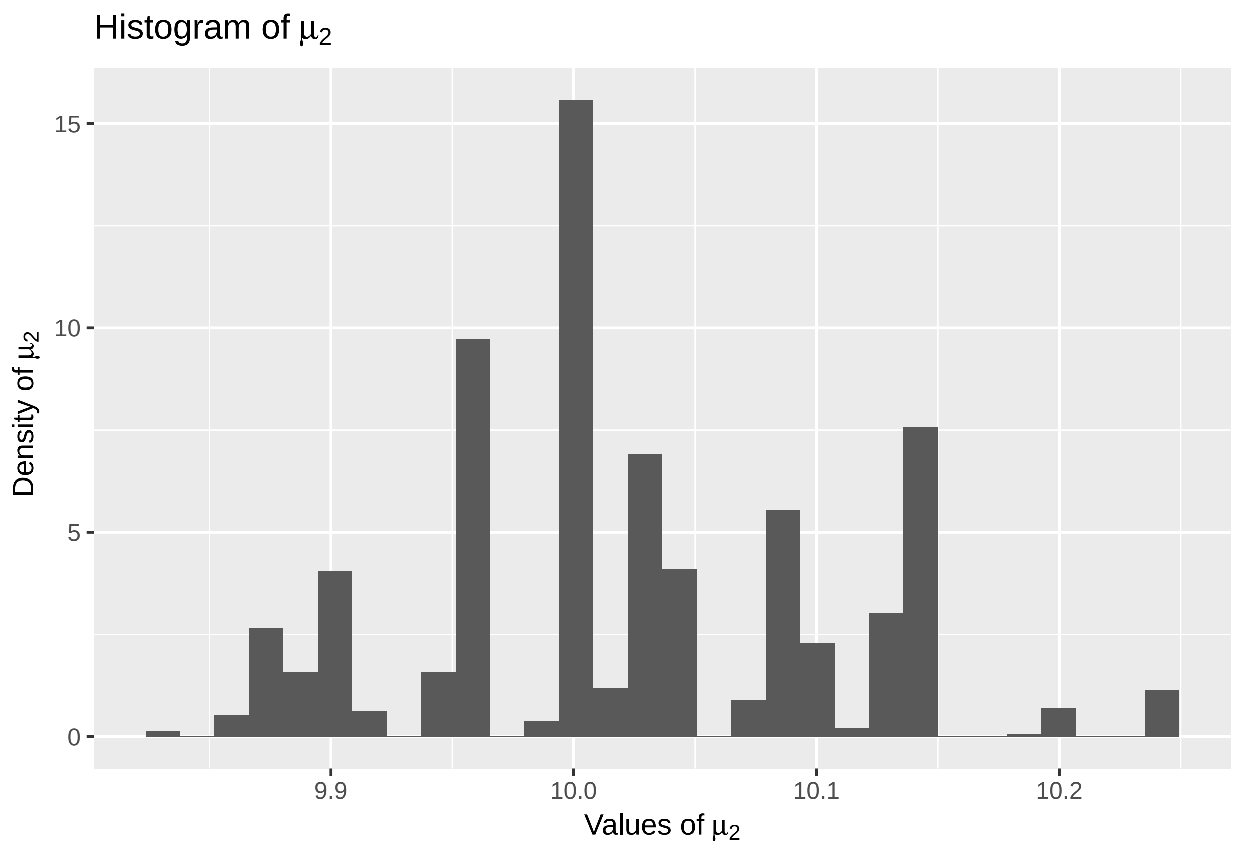
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



μ_1 is about 7

```
plot3<- ggplot(data.frame(x = results[,3]), aes(x = x))+
  geom_histogram(aes(y=..density..))+labs(x = expression("Values of"~mu[2]),
  y = expression(" Density of"~mu[2]), title=expression("Histogram of"~mu[2]))
plot3
```

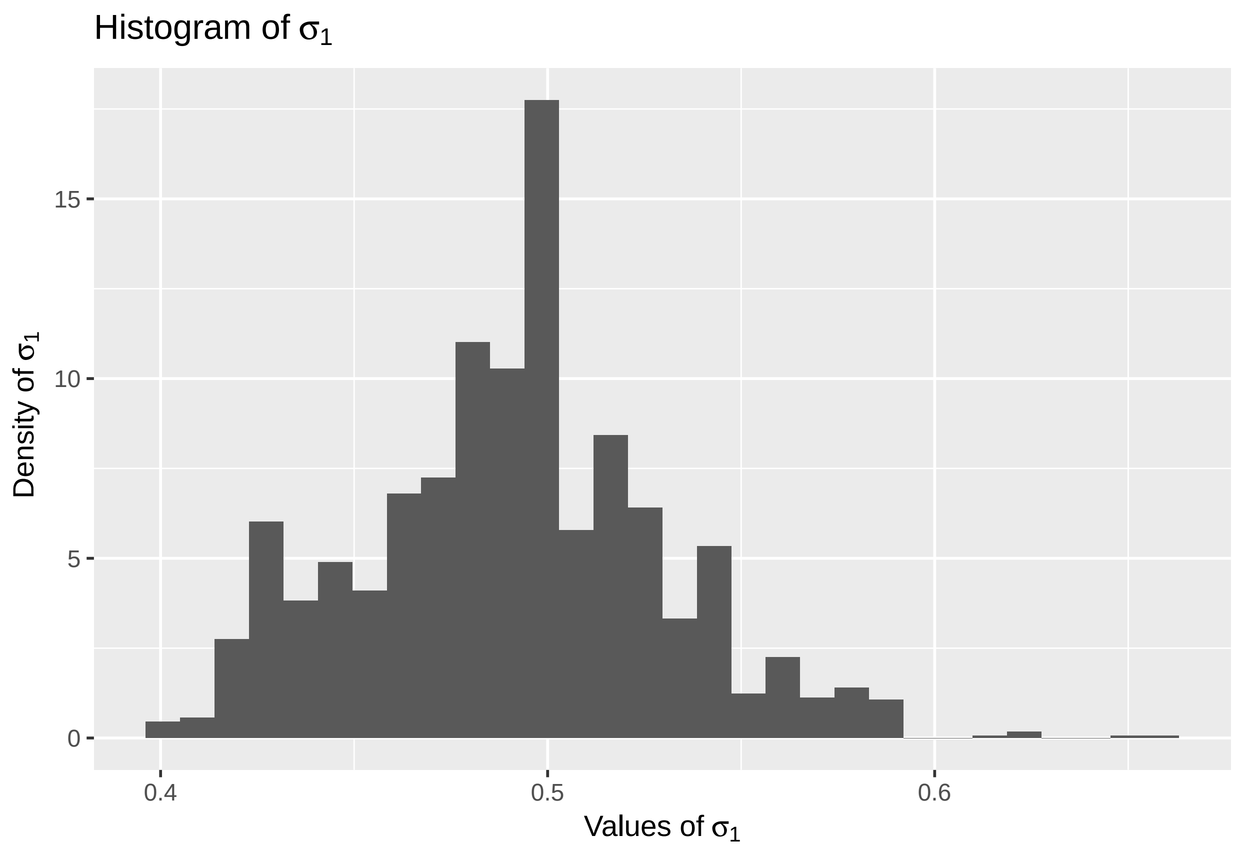
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



μ_2 is about 10

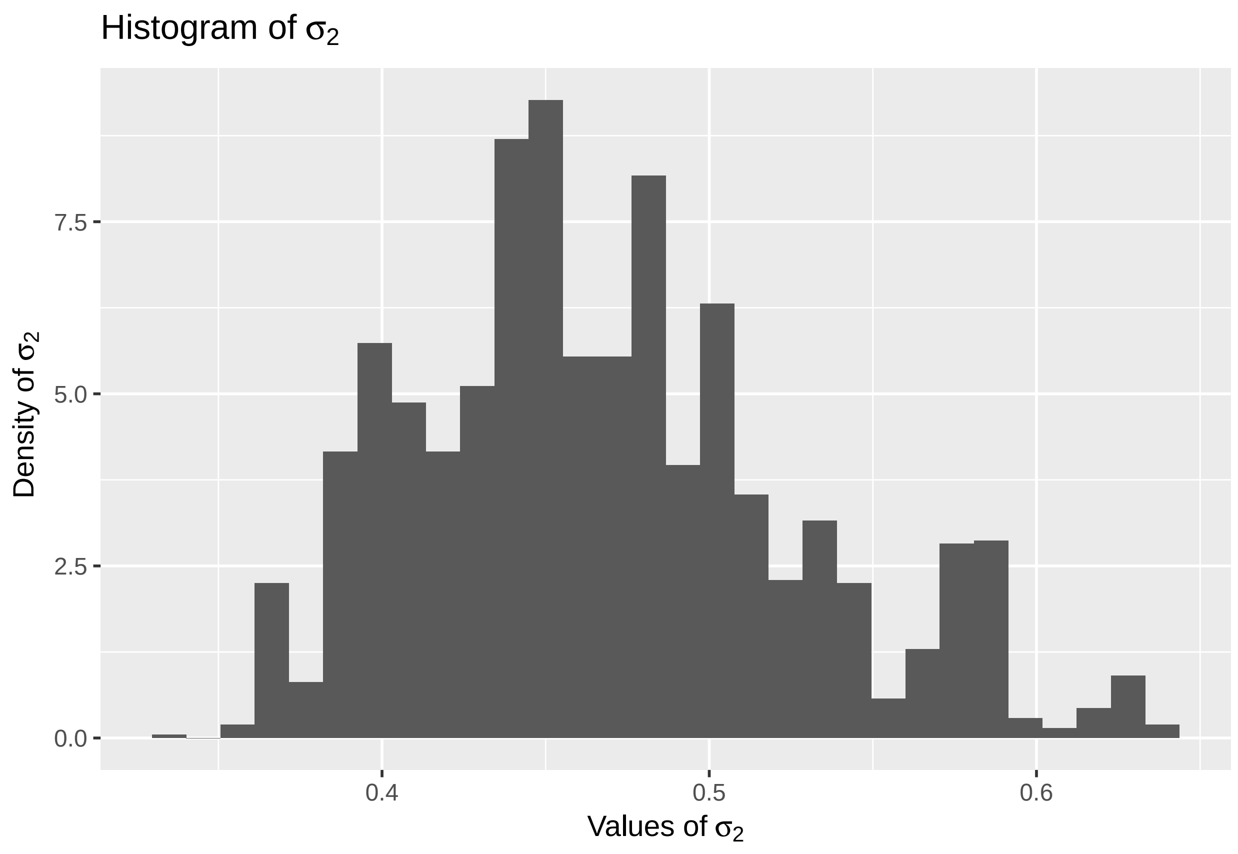
```r
plot4<- ggplot(data.frame(x = results[,4]), aes(x = x))+
  geom_histogram(aes(y=..density..))+labs(x = expression("Values of"~sigma[1]),
  y = expression(" Density of"~sigma[1]), title=expression("Histogram of"~sigma[1]))
plot4
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
plot5<- ggplot(data.frame(x = results[,5]), aes(x = x))+
  geom_histogram(aes(y=..density..))+labs(x = expression("Values of"~sigma[2]),
  y = expression(" Density of"~sigma[2]), title=expression("Histogram of"~sigma[2]))
plot5
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```


Histogram of σ_2
Density of σ_2
Values of σ_2