Assignment2

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```r
rm(list = setdiff(ls(), lsf.str()))
```

Question 1

```r
q1mean <- 100
q1sd <- 15

meansamplex <- function(x) {
  mean(rnorm(x, mean=q1mean, sd=q1sd))
}

sdsamplex <- function(x) {
  sd(rnorm(x, mean=q1mean, sd=q1sd))
}

genMeanTrials <- function(trials, x) {
  df <- data.frame(matrix(ncol = 2, nrow = 0))
  colnames(df) <- c("Index", "Mean")

  for(i in 1:1000) {
    df <- rbind(df, c(i, mean(rnorm(x, mean=q1mean, sd=q1sd))))
  }
  df
}

genSDTrials <- function(trials, x) {
  df <- data.frame(matrix(ncol = 2, nrow = 0))
  colnames(df) <- c("Index", "Mean")

  for(i in 1:1000) {
    df <- rbind(df, c(i, sd(rnorm(x, mean=q1mean, sd=q1sd))))
  }
  df
}
```
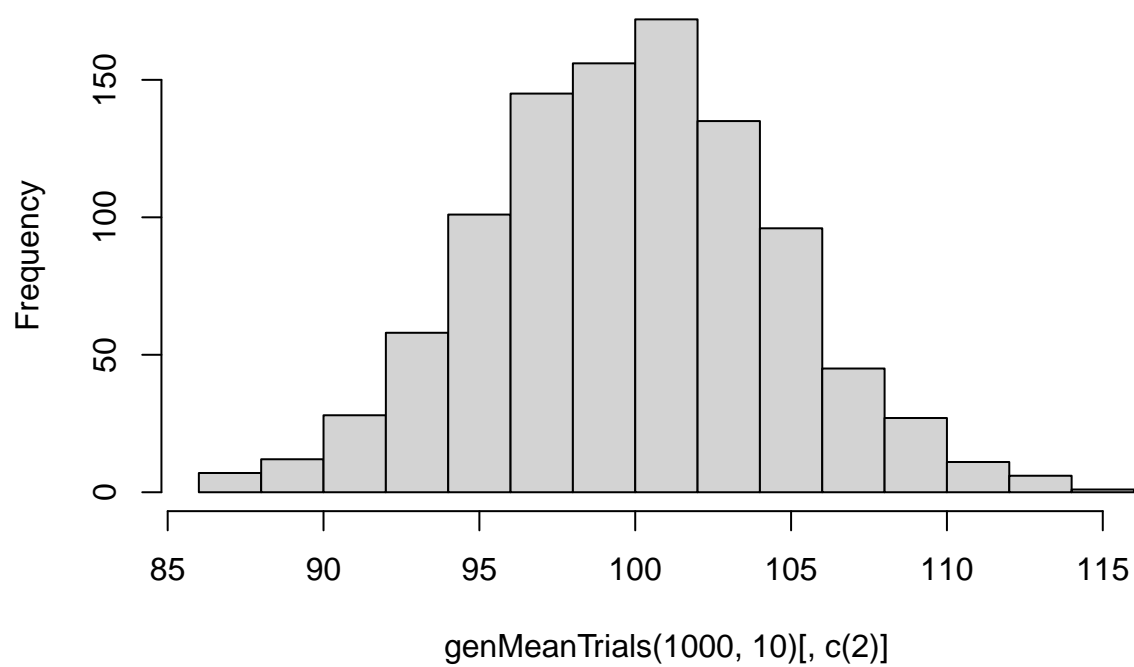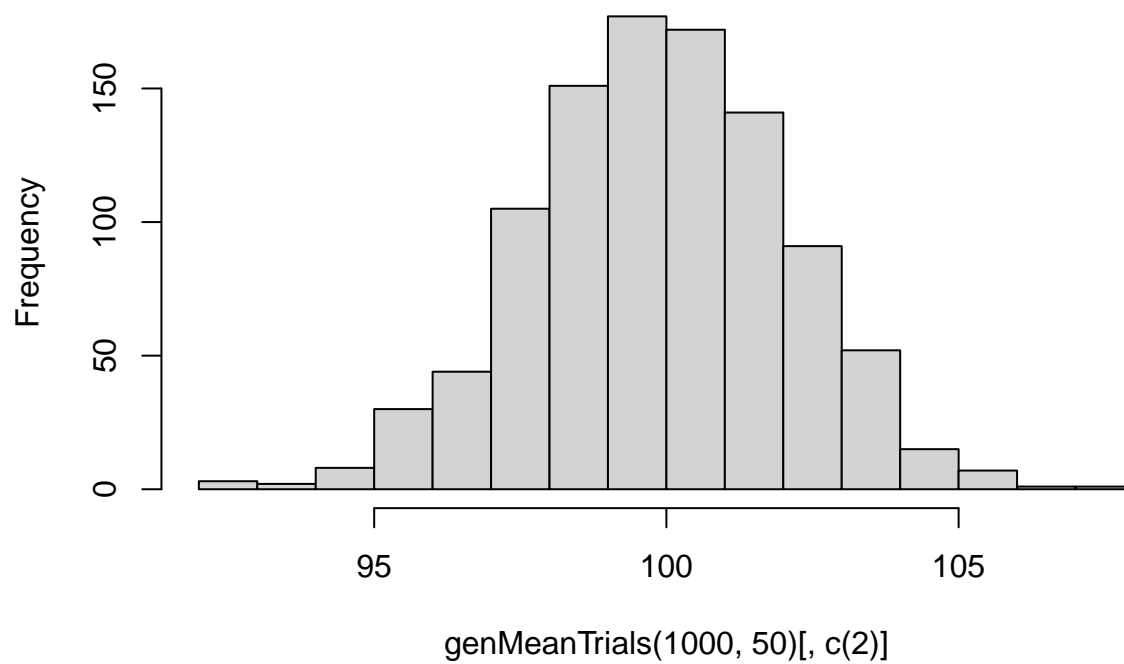
```r
hist(genMeanTrials(1000, 10)[, c(2)])
```

Histogram of genMeanTrials(1000, 10)[, c(2)]

```
hist(genMeanTrials(1000, 50)[, c(2)])
```
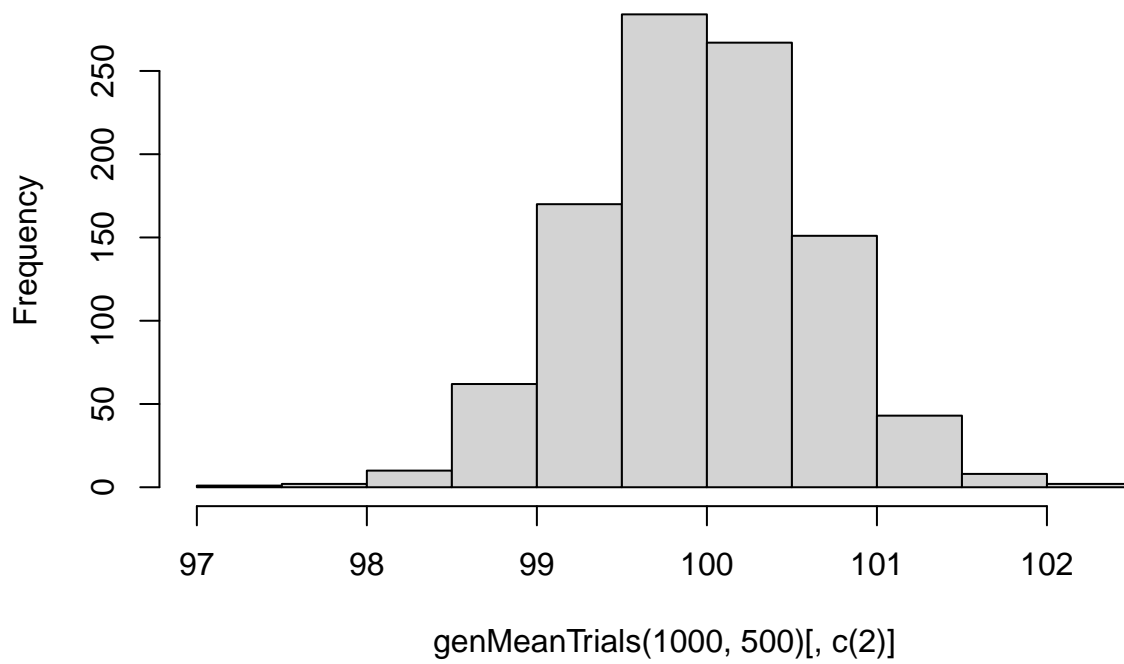
Histogram of genMeanTrials(1000, 50)[, c(2)]

genMeanTrials(1000, 50)[, c(2)]

```
hist(genMeanTrials(1000, 100)[, c(2)])
```

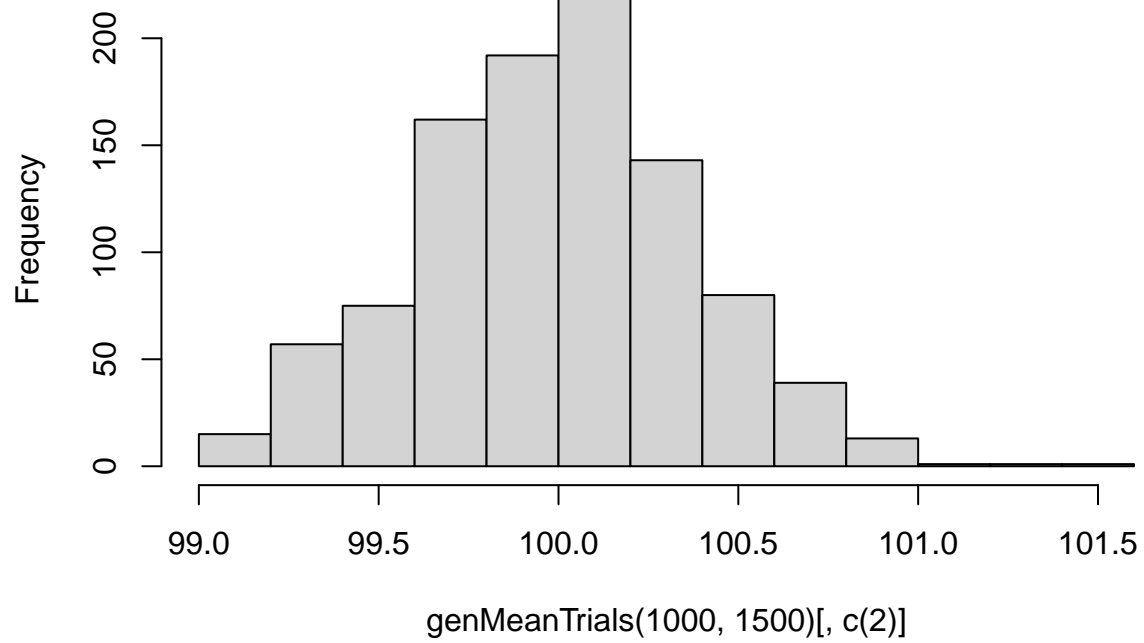## Histogram of genMeanTrials(1000, 100)[, c(2)]


```
hist(genMeanTrials(1000, 500)[, c(2)])
```

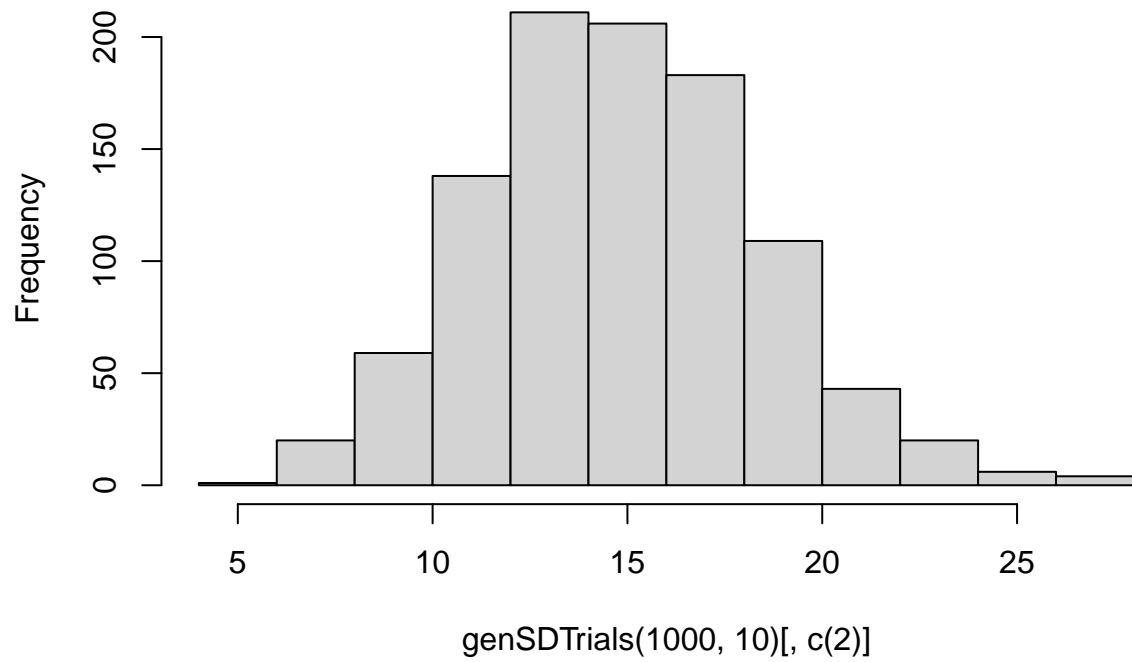## Histogram of genMeanTrials(1000, 500)[, c(2)]


```
hist(genMeanTrials(1000, 1500)[, c(2)])
```
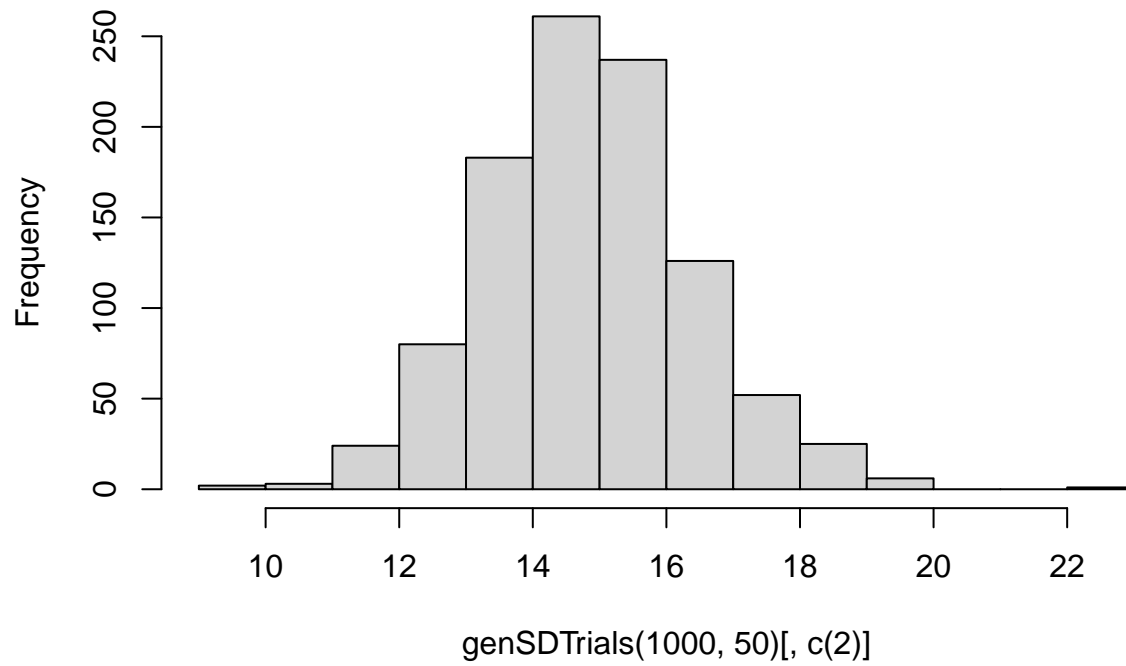
Histogram of genMeanTrials(1000, 1500)[, c(2)]


```
hist(genSDTrials(1000, 10)[, c(2)])
```
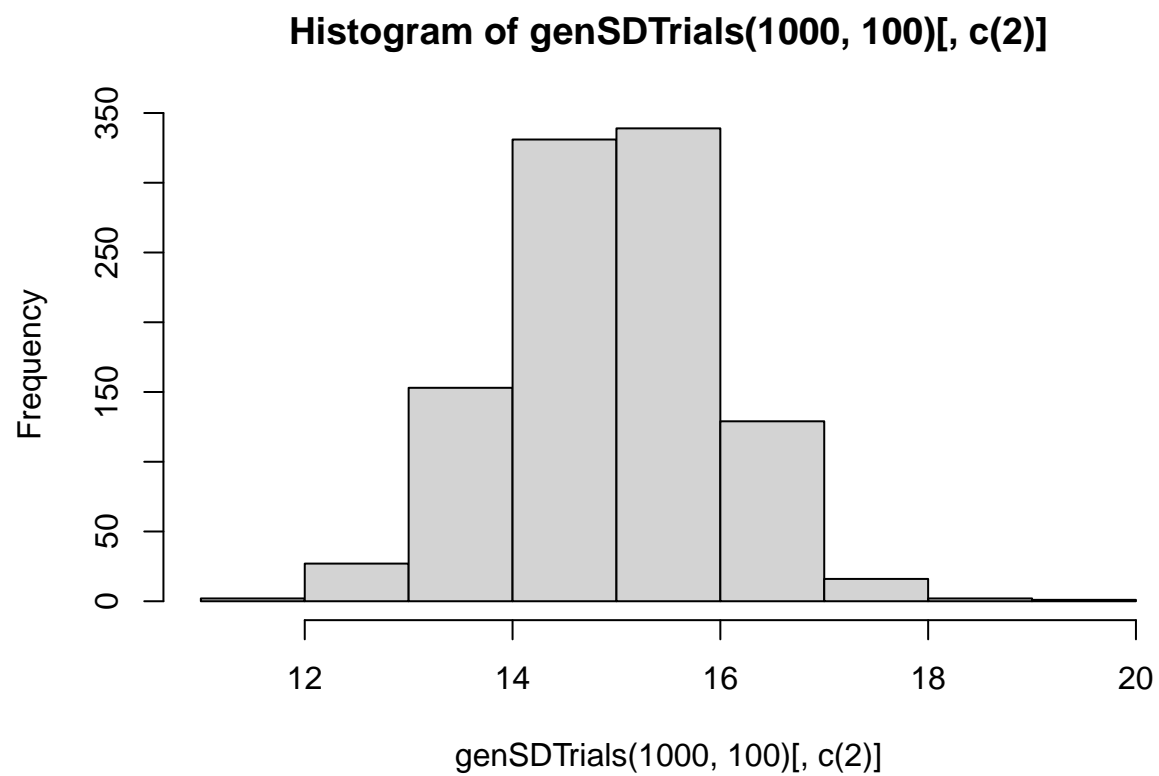
Histogram of genSDTrials(1000, 10)[, c(2)]

genSDTrials(1000, 10)[, c(2)]

```
hist(genSDTrials(1000, 50)[, c(2)])
```

Histogram of genSDTrials(1000, 50)[, c(2)]


```
hist(genSDTrials(1000, 100)[, c(2)])
```
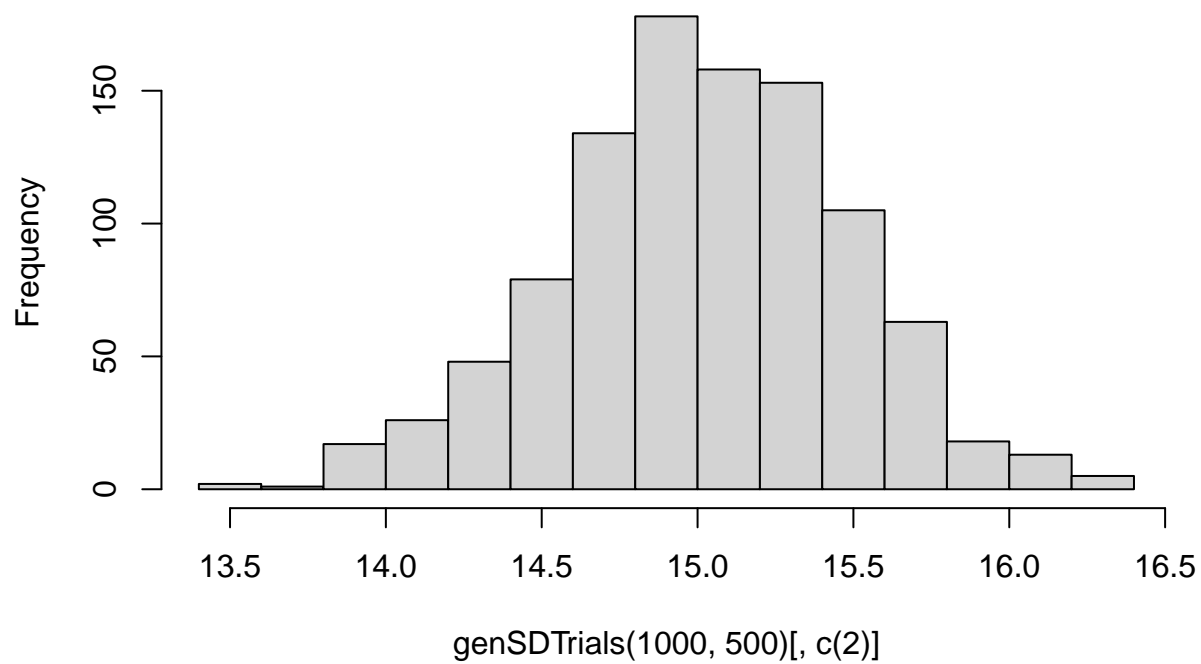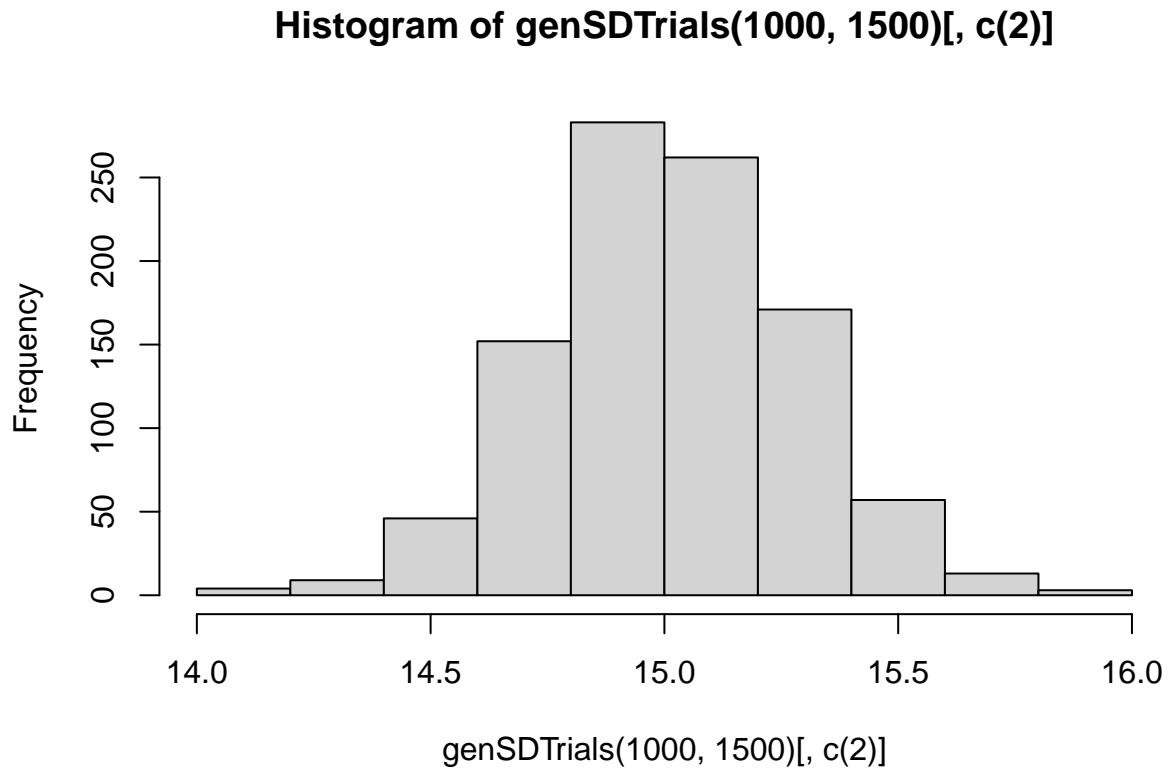
Histogram of genSDTrials(1000, 100)[, c(2)]

genSDTrials(1000, 100)[, c(2)]

```r
hist(genSDTrials(1000, 500)[, c(2)])
```

Histogram of genSDTrials(1000, 500)[, c(2)]

genSDTrials(1000, 500)[, c(2)]

```r
hist(genSDTrials(1000, 1500)[, c(2)])
```

Histogram of genSDTrials(1000, 1500)[, c(2)]

As the number of sampled number increases, the means of the histograms approach the actual mean and standard deviations supplied to the sampling functions.

Question 2

```
q2a <- 2
q2b<- 5

genMeanTrials <- function(trials, x) {
  df <- data.frame(matrix(ncol = 2, nrow = 0))
  colnames(df) <- c("Index", "Mean")

  for(i in 1:1000) {
    df <- rbind(df, c(i, mean(rbeta(x, shape1=q2a, shape2=q2b))))
  }
  df
}

genSDTrials <- function(trials, x) {
  df <- data.frame(matrix(ncol = 2, nrow = 0))
  colnames(df) <- c("Index", "Mean")

  for(i in 1:1000) {
    df <- rbind(df, c(i, sd(rbeta(x, shape1=q2a, shape2=q2b))))
```

```
  }
  df
}
```

```
print("Expected mean:")
```

```
## [1] "Expected mean:"
```

```
(q2a)/(q2a+q2b) # 0.2857143
```

```
## [1] 0.2857143
```

```
print("Expected SD:")
```
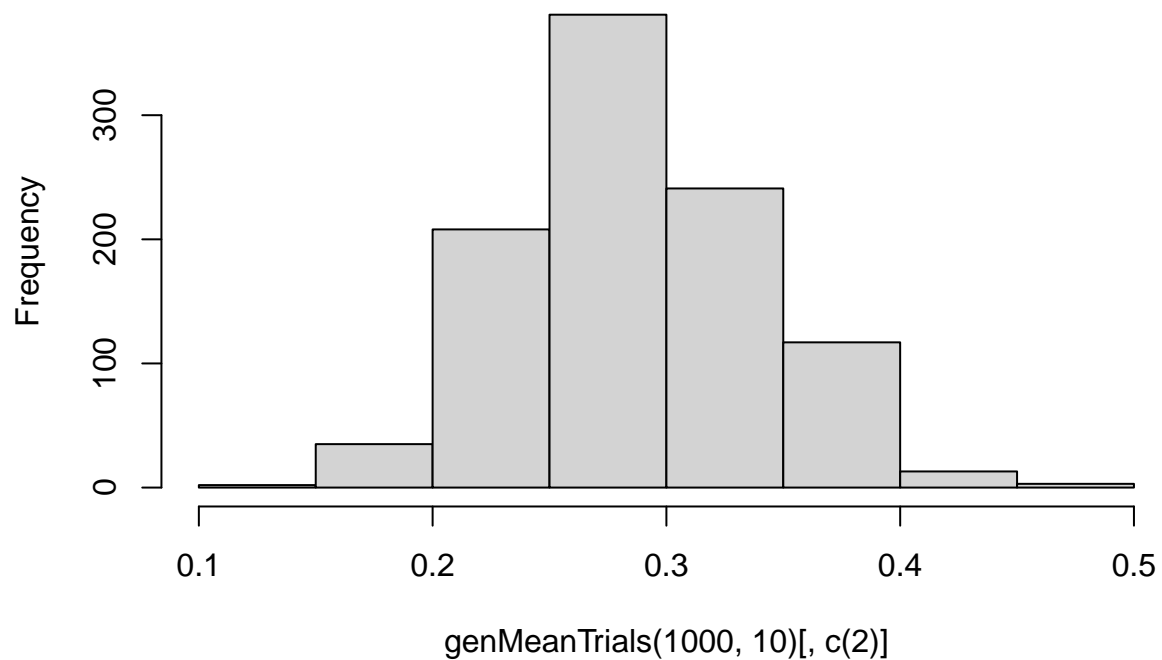
```
## [1] "Expected SD:"
```

```
((q2a * q2b) / (((q2a + q2b)^2) * (q2a + q2b + 1)))^(1/2) # 0.1597191
```
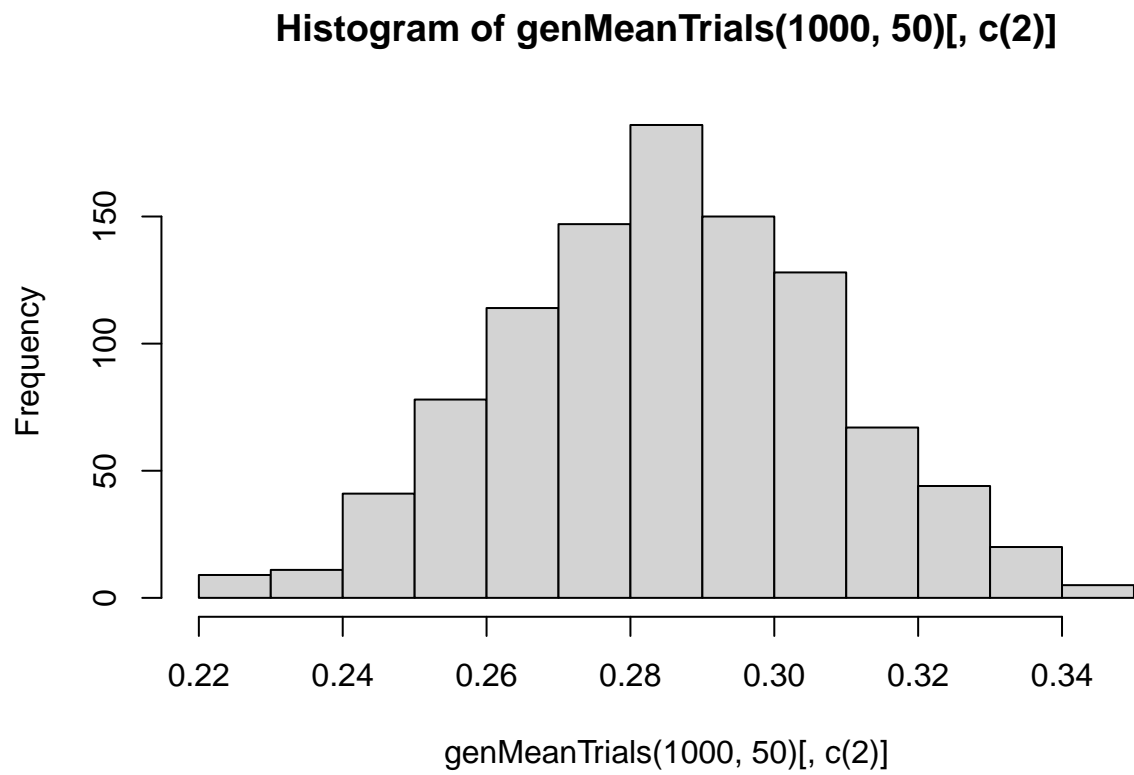
```
## [1] 0.1597191
```

```
hist(genMeanTrials(1000, 10)[, c(2)])
```
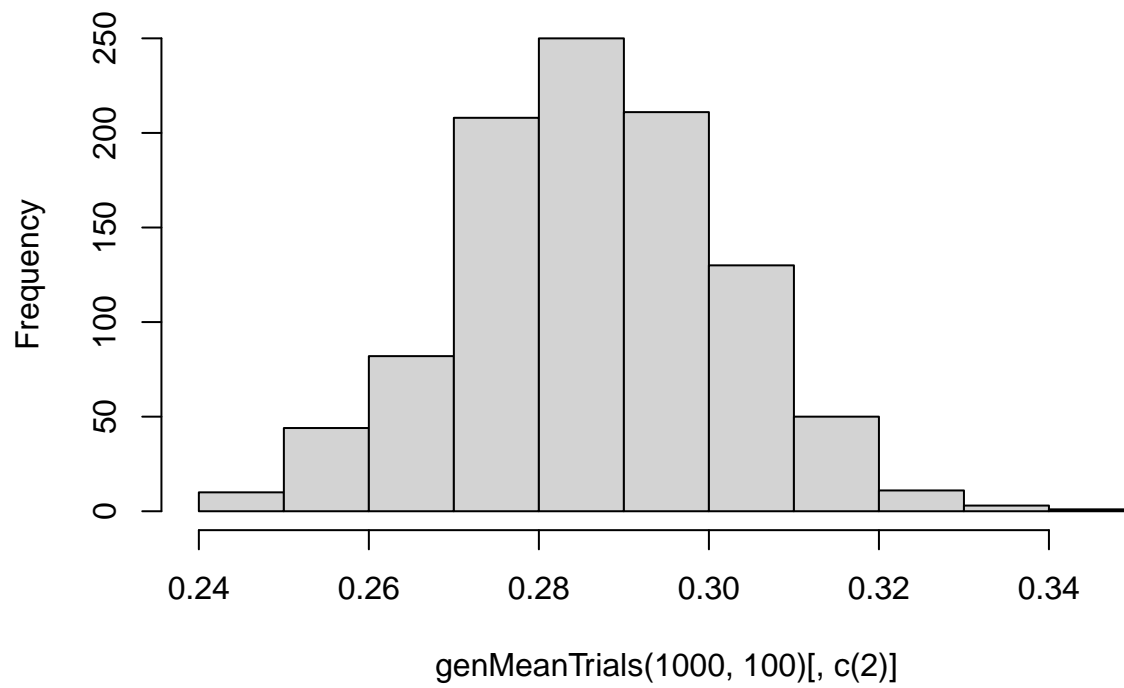

Histogram of genMeanTrials(1000, 10)[, c(2)]
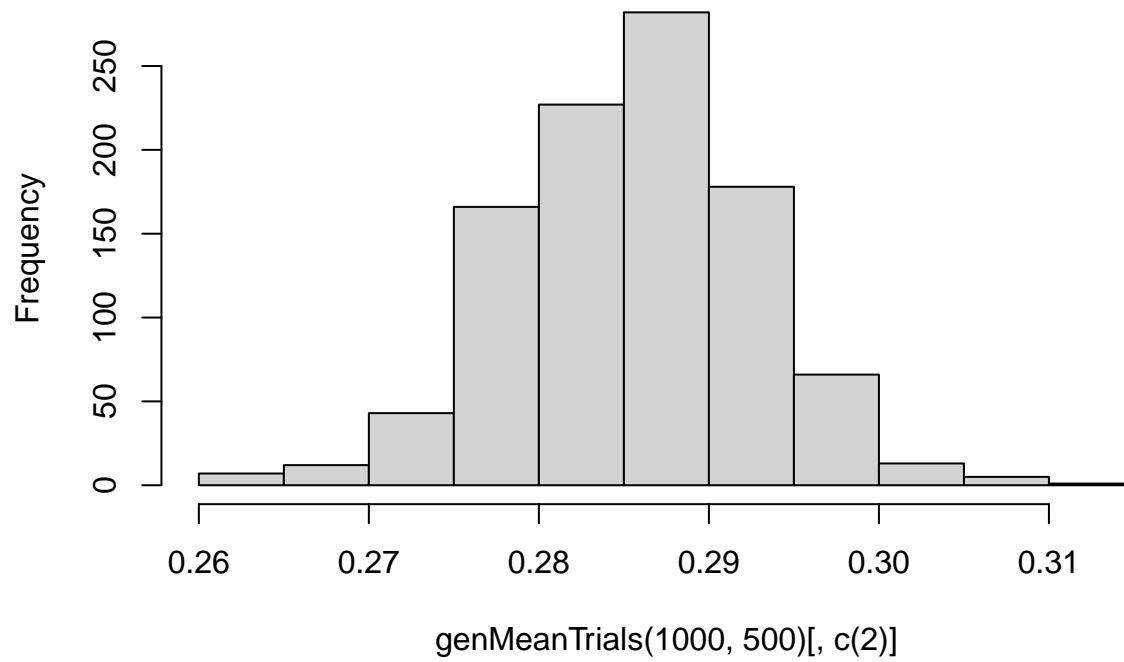
```r
hist(genMeanTrials(1000, 50)[, c(2)])
```

Histogram of genMeanTrials(1000, 50)[, c(2)]

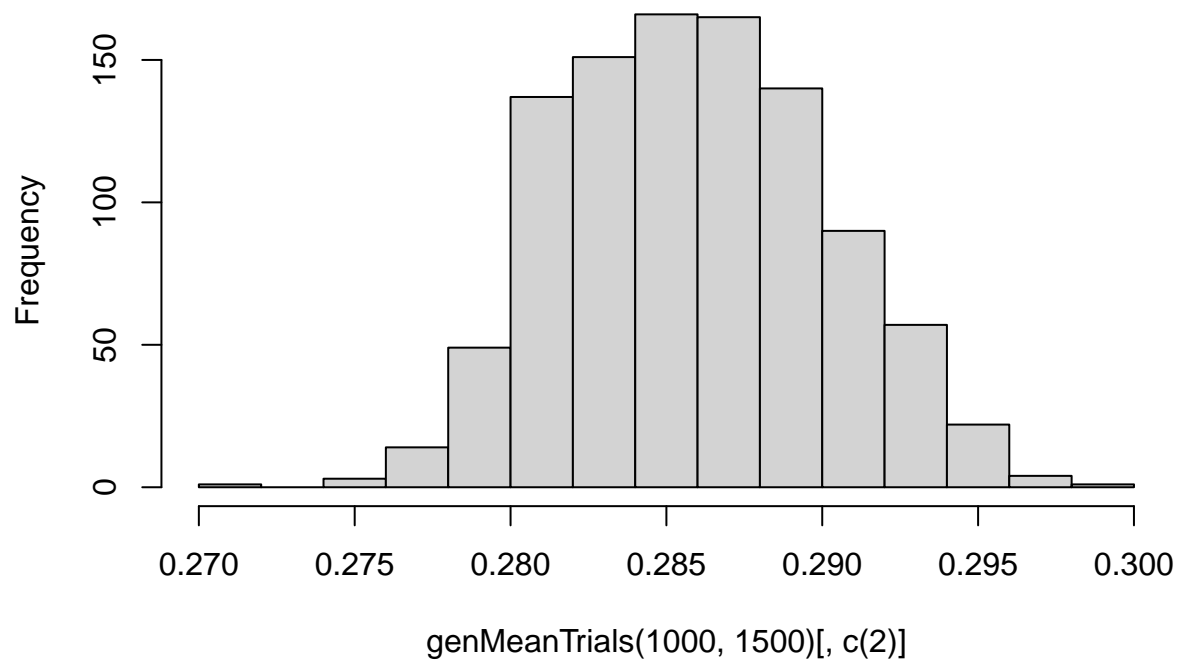genMeanTrials(1000, 50)[, c(2)]

```r
hist(genMeanTrials(1000, 100)[, c(2)])
```

Histogram of genMeanTrials(1000, 100)[, c(2)]


```
hist(genMeanTrials(1000, 500)[, c(2)])
```
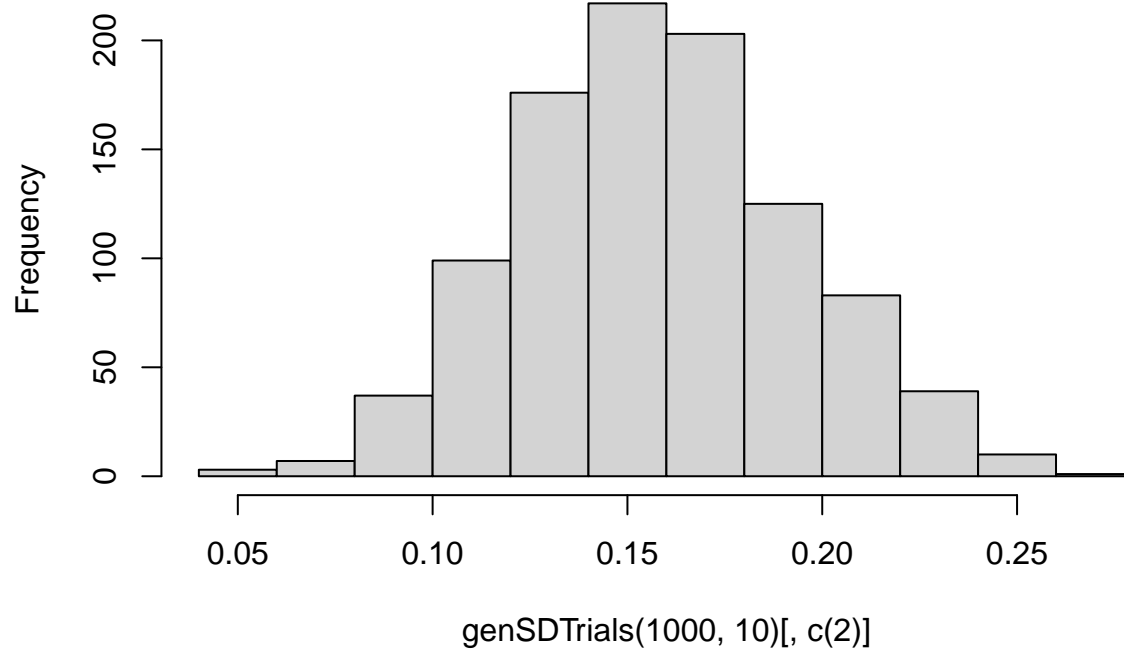
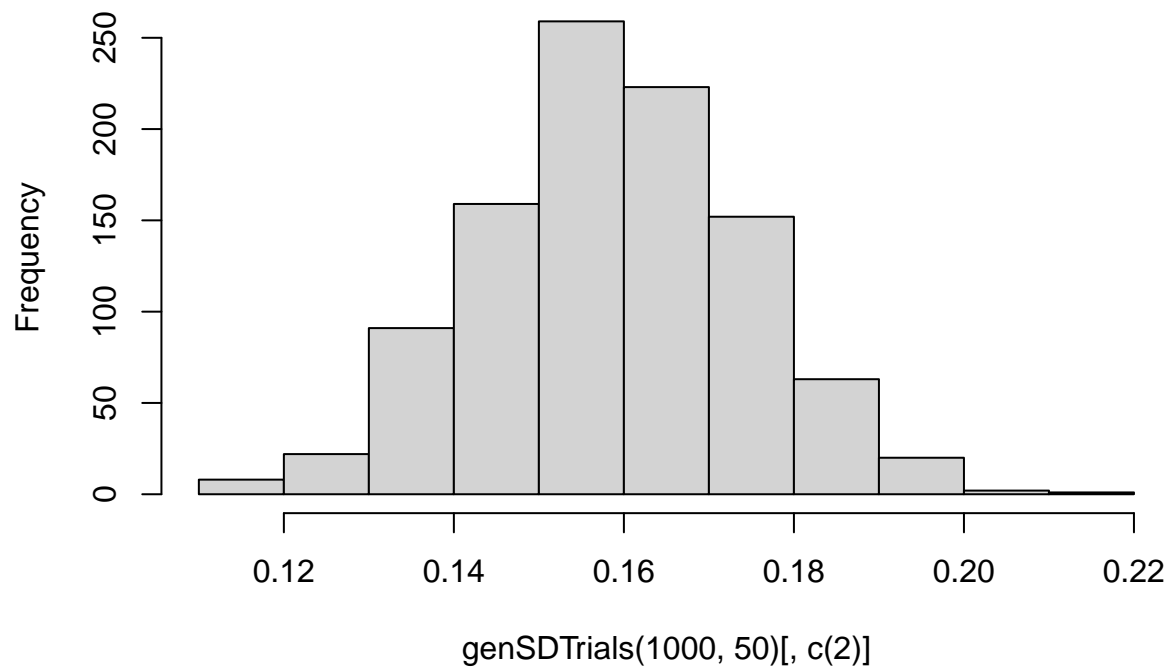**Histogram of genMeanTrials(1000, 500)[, c(2)]**


```r
hist(genMeanTrials(1000, 1500)[, c(2)])
```

Histogram of genMeanTrials(1000, 1500)[, c(2)]

genMeanTrials(1000, 1500)[, c(2)]

```
hist(genSDTrials(1000, 10)[, c(2)])
```

Histogram of genSDTrials(1000, 10)[, c(2)]

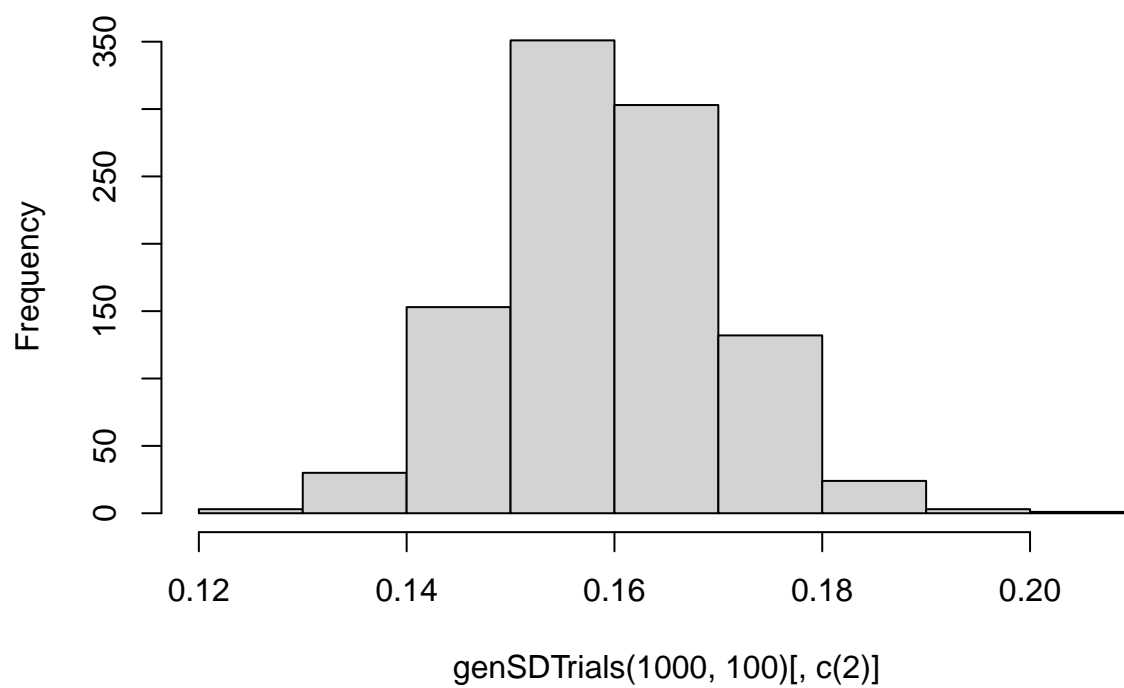genSDTrials(1000, 10)[, c(2)]

```r
hist(genSDTrials(1000, 50)[, c(2)])
```
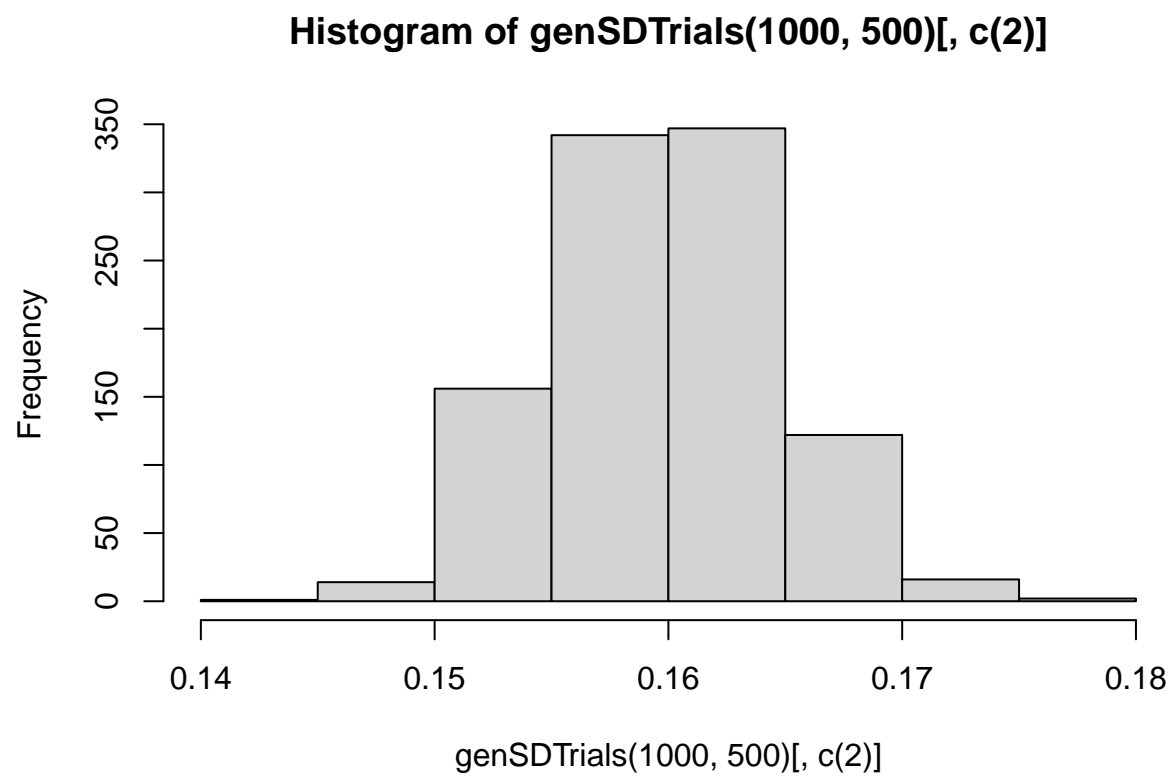
Histogram of genSDTrials(1000, 50)[, c(2)]


```
hist(genSDTrials(1000, 100)[, c(2)])
```
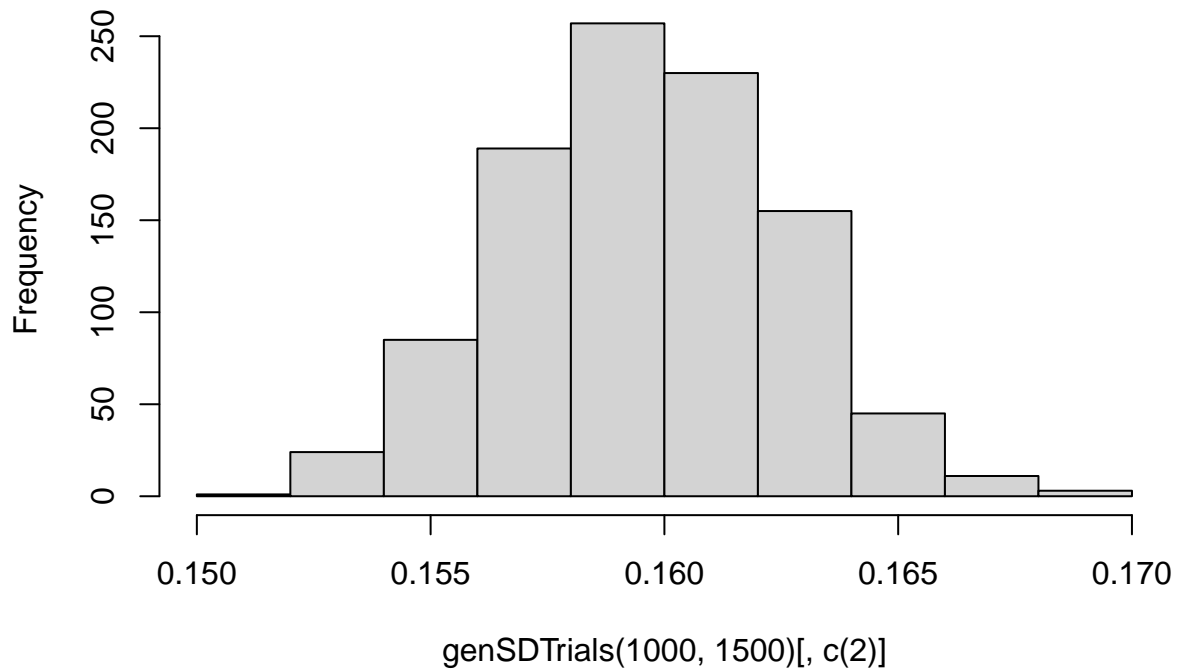
Histogram of genSDTrials(1000, 100)[, c(2)]


```
hist(genSDTrials(1000, 500)[, c(2)])
```

Histogram of genSDTrials(1000, 500)[, c(2)]

genSDTrials(1000, 500)[, c(2)]

```
hist(genSDTrials(1000, 1500)[, c(2)])
```

Histogram of genSDTrials(1000, 1500)[, c(2)]

Expected mean: 0.1597191

Expected SD: 0.2857143

Similar to the normal distribution, the more sample numbers are considered, the closer the means of the trials come to the expected mean and SD of the Beta distribution. Although, more trials are required to bring about the same degree of convergence.