Shi.Chunlin.Hw7code

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Question 5

We first set up the parameters

```
n_1 = 20
n_2 = 50
lambda = 5
N = 10^5
```

We now create a vector to store the proportion of value between 0.19 and 0.21

```
proportions_1 = numeric(N)
proportions_2 = numeric(N)
```

Now, we generate the distribution

```
for (i in 1:N) {
  X_1 = rexp(n_1, rate = lambda)
  Mean_1 = mean(X_1)
  X_2 = rexp(n_2, rate = lambda)
  Mean_2 = mean(X_2)

  proportions_1[i] <- as.numeric(Mean_1 >= 0.19 & Mean_1 <= 0.21)
  proportions_2[i] <- as.numeric(Mean_2 >= 0.19 & Mean_2 <= 0.21)
}
```

Now we calculate the results:

```
res_n1 = sum(proportions_1) / N
res_n2 = sum(proportions_2) / N

res_n1
```

```
## [1] 0.17587
```

```
res_n2
```

```
## [1] 0.27492
```

From above, we can see that there are about 18% of the M_20 and 28% of M_50 values are between the limits, which reflects increasing concentration of M_n as n increases.

Question 6

(d)

For the exact distribution

```
# (a) n = 16
p_exact_a = pgamma(2.5, shape = 16, rate = 16*0.5)
p_exact_a
```

```
## [1] 0.8434869
```

```
# (b) n = 36
p_exact_b = pgamma(2.5, shape = 36, rate = 36*0.5)
p_exact_b
```

```
## [1] 0.9257825
```

```
# (c) n = 100
p_exact_c = pgamma(2.5, shape = 100, rate = 100*0.5)
p_exact_c
```

```
## [1] 0.9906209
```

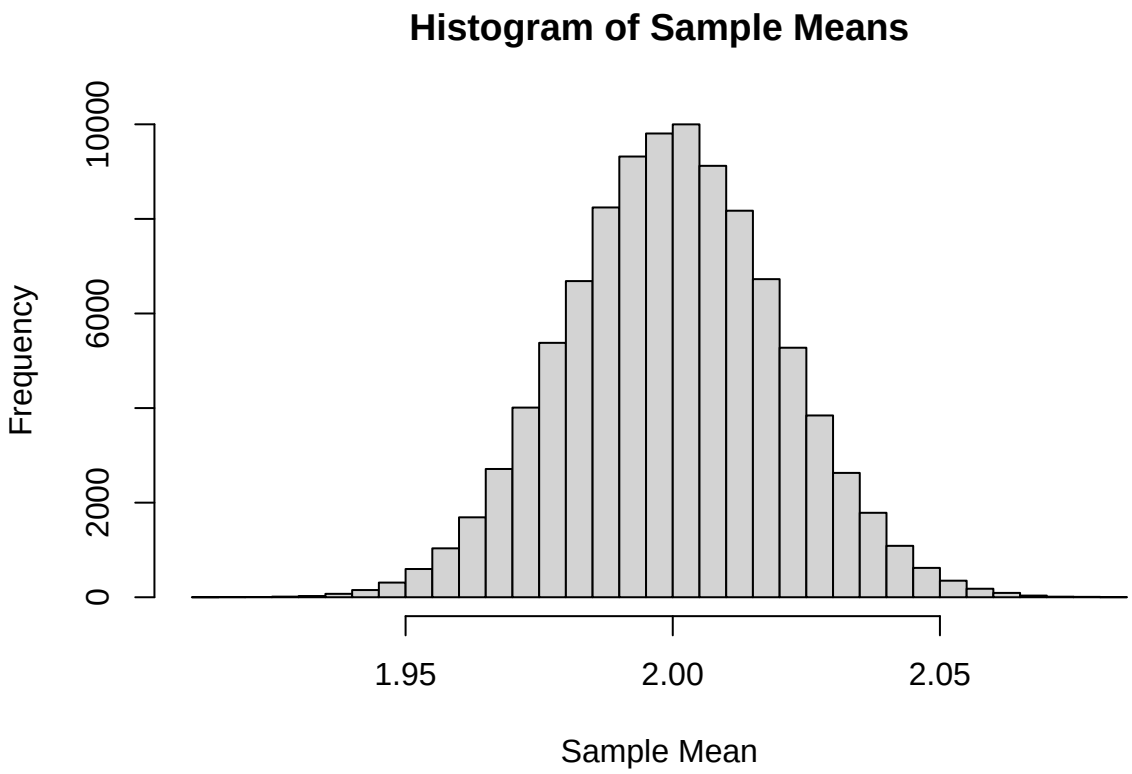
(e)

In this case

```
N = 10^5
n = 100

samples = matrix(rgamma(N*n, shape =n, rate = n*0.5), ncol = n)
sample_means <- rowMeans(samples)

# Plot a histogram
hist(sample_means, breaks = 30, main = "Histogram of Sample Means", xlab = "Sample Mean")
```



From the graph above, it looks normal.