hw02

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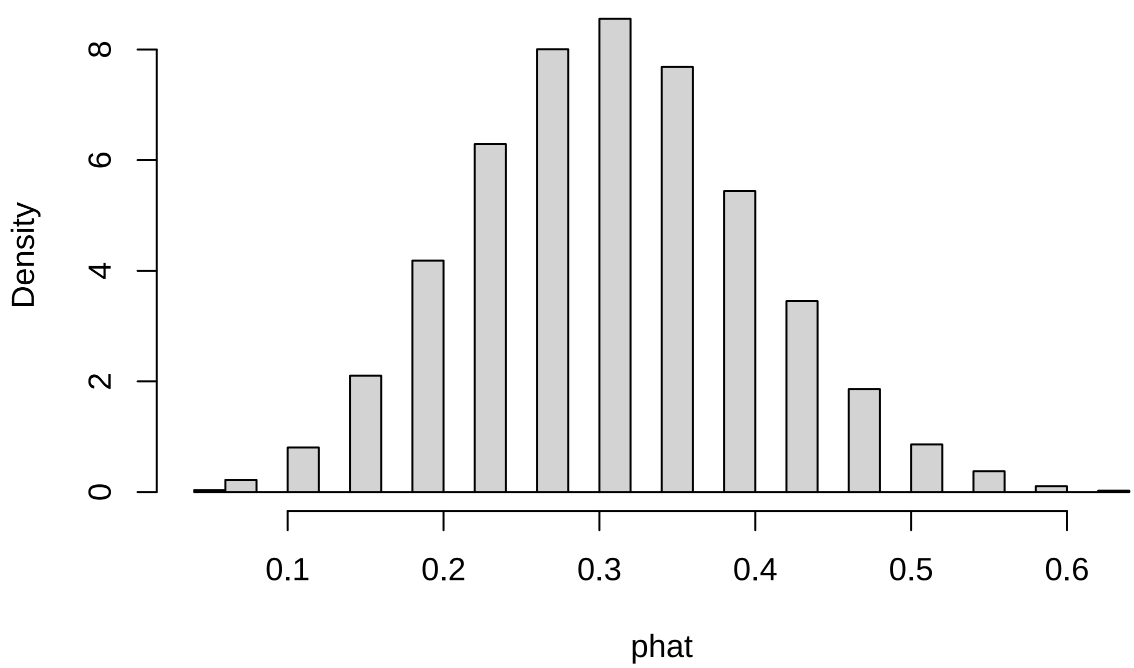
Q1. (Exercise 4.6)

a) We see that the sampling distribution is normally distributed, with the estimate mean at 0.315 with estimate standard error being 0.0922

b) Using the following equation $SE = \sqrt{\frac{\hat{p}(1-\hat{p})}{n}} = \sqrt{\frac{0.316(1-0.316)}{25}} = 0.09298258$ we get that theoretical standard error to be 0.09298258. This is relatively close to our initial 0.092 estimated standard error

```r
set.seed(69420)
Recidivism <- read.csv("https://sites.google.com/site/chiharahesterberg/data2/Recidivism.csv")
N <- 10^4
phat <- numeric(N)
for (i in 1:N)
{
  samp <- sample(Recidivism$Recid, 25)
  phat[i] <- mean(samp == "Yes")
}
hist(phat, freq = FALSE, main = NULL, breaks = 30)
```



```r
mean(phat) #0.315
```

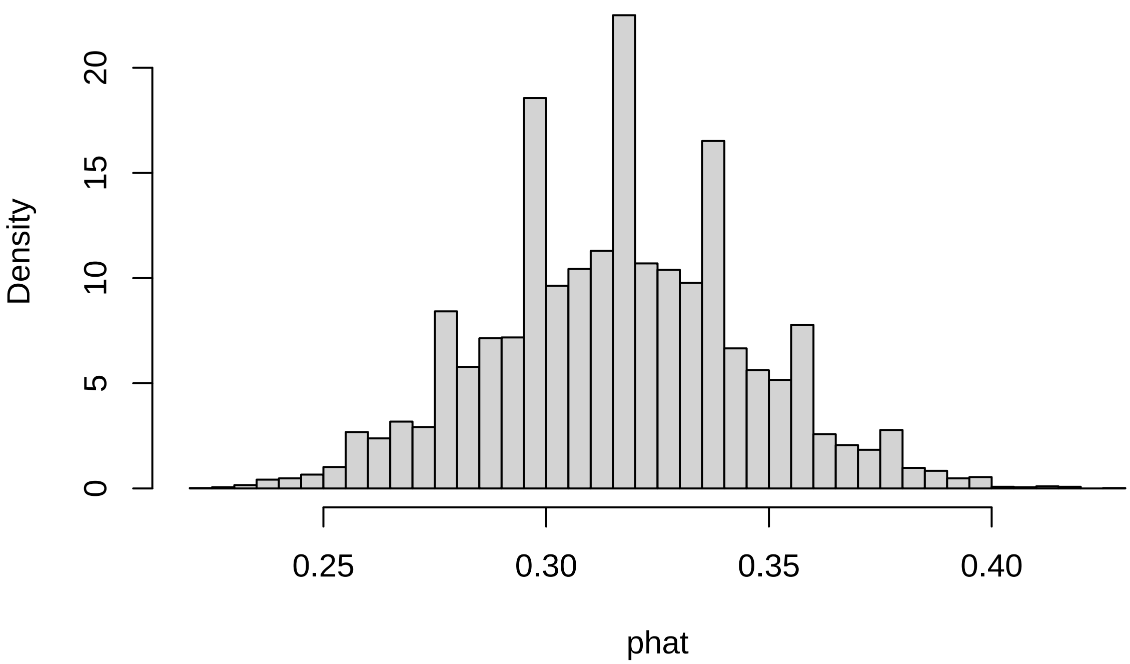
```
## [1] 0.317352
```

```r
sd(phat) #0.092
```

```
## [1] 0.09227394
```

c) Using the following equation $SE = \sqrt{\frac{\hat{p}(1-\hat{p})}{n}} = \sqrt{\frac{0.316(1-0.316)}{250}} = 0.02940367$ we get that theoretical standard error to be 0.02940367. This pair of theoretical standard error and estimated standard error is closer than the previous one with n = 25 cases.

```r
set.seed(69420)
Recidivism <- read.csv("https://sites.google.com/site/chiharahesterberg/data2/Recidivism.csv")
N <- 10^4
phat <- numeric(N)
for (i in 1:N)
{
  samp <- sample(Recidivism$Recid, 250)
  phat[i] <- mean(samp == "Yes")
}
hist(phat, freq = FALSE, main = NULL, breaks = 30)
```




```r
mean(phat)
```

```
## [1] 0.3169336
```

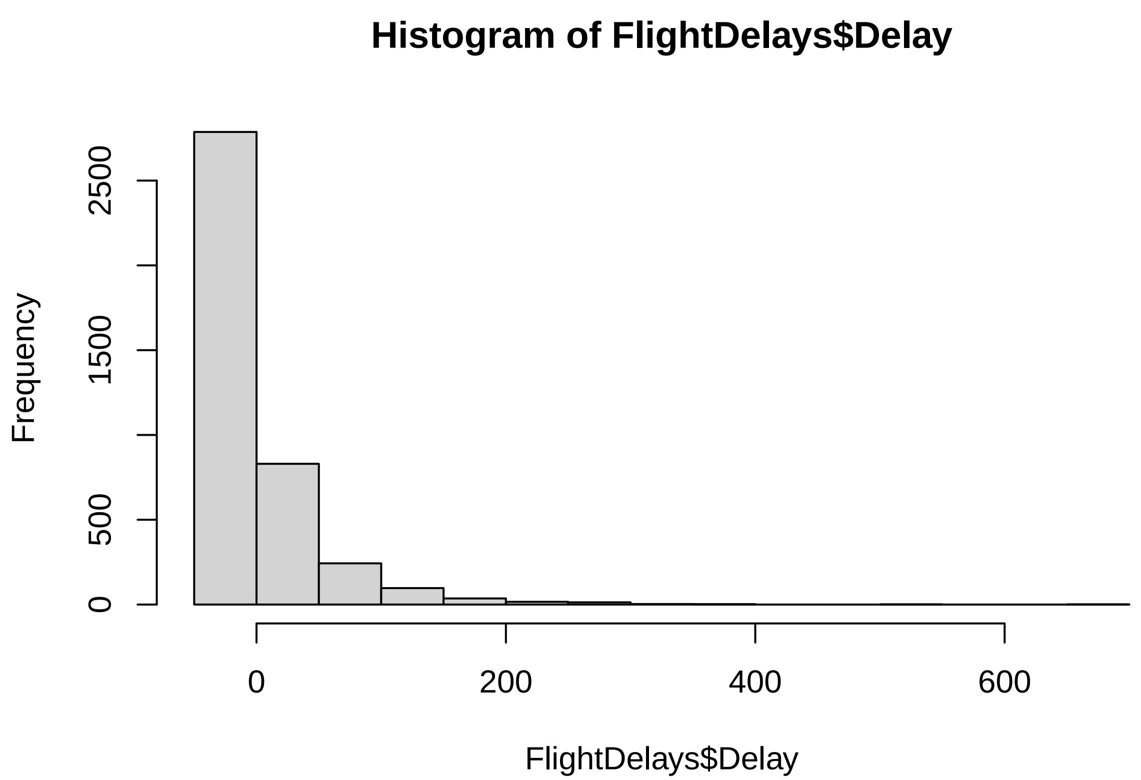
```r
sd(phat)
```

```
## [1] 0.02905113
```

Q2. (Exercise 4.7)

a) Looking at the histogram below, we see that the data is skewed to the right, We get a mean of 11.7379 and a standard deviation 41.6305

```r
FlightDelays <- read.csv("https://sites.google.com/site/chiharahesterberg/data2/FlightDelays.csv")
hist(FlightDelays$Delay)
```




```r
mean(FlightDelays$Delay)
```

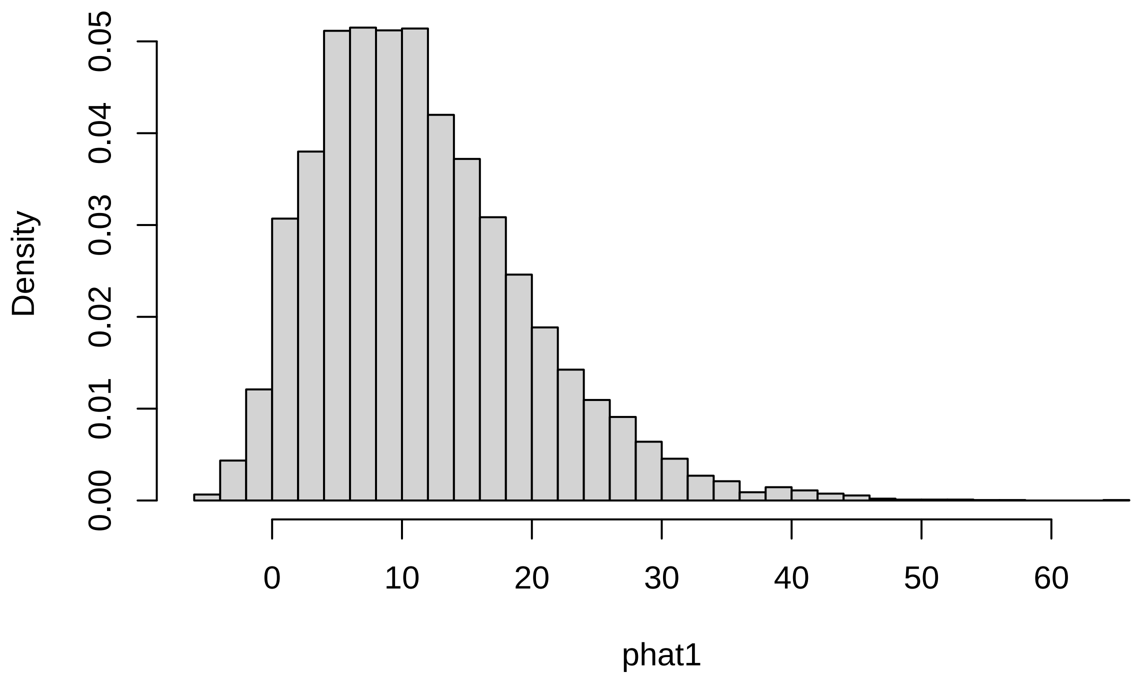
```
## [1] 11.7379
```

```r
sd(FlightDelays$Delay)
```

```
## [1] 41.6305
```

b) Looking at the histogram below, we see that the simulated sampling distribution is skewed to the right, We get an estimated mean of 11.64506 and a standard error 8.281396.

```r
set.seed(69420)
FlightDelays <- read.csv("https://sites.google.com/site/chiharahesterberg/data2/FlightDelays.csv")
N <- 10^4
phat1 <- numeric(N)
for (i in 1:N)
{
samp <- sample(FlightDelays$Delay, 25)
phat1[i] <- mean(samp)
}
hist(phat1, freq = FALSE, main = NULL, breaks = 30)
```




```r
mean(phat1)
```

```
## [1] 11.64506
```

```r
sd(phat1)
```

```
## [1] 8.281396
```

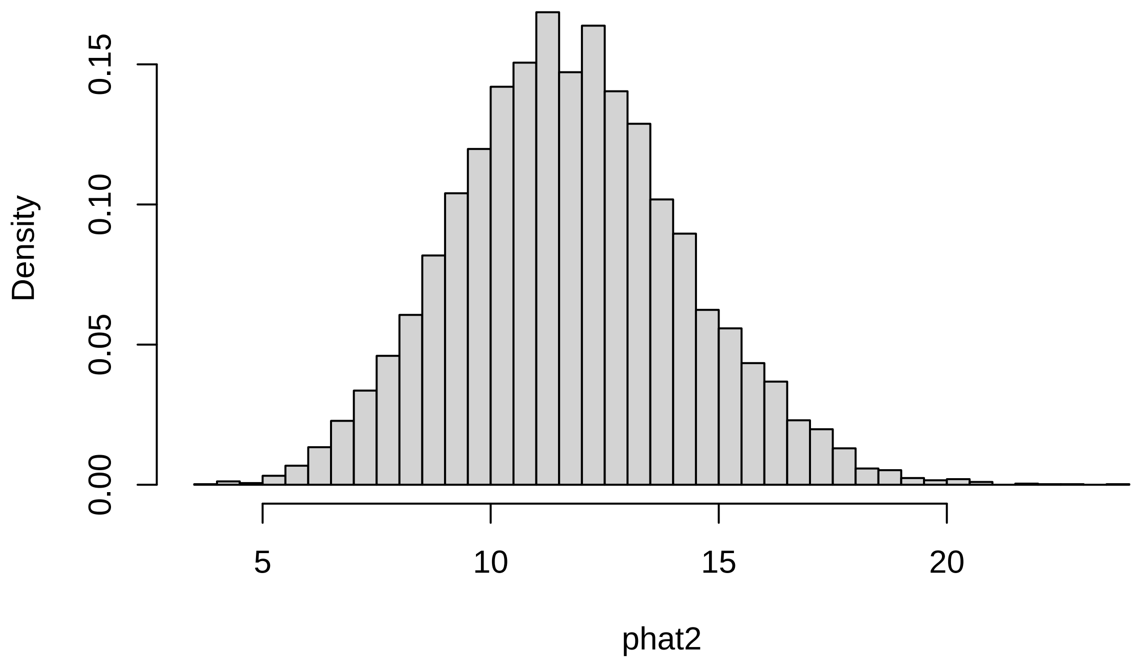
c) Our estimated standard error of 8.281396 is close to our theoretical standard error of 8.326099

```r
TSE <- sqrt(var(FlightDelays$Delay)/25)
TSE
```

```
## [1] 8.326099
```

d) Our estimated standard error is now 2.53198, which is slightly closer to the theoretical standard error of 2.632944 compared to when n = 25

```
set.seed(69420)
FlightDelays <- read.csv("https://sites.google.com/site/chiharahesterberg/data2/FlightDelays.csv")
N <- 10^4
phat2 <- numeric(N)
for (i in 1:N)
{
samp <- sample(FlightDelays$Delay, 250)
phat2[i] <- mean(samp)
}
hist(phat2, freq = FALSE, main = NULL, breaks = 30)
```




```
mean(phat2)
```

```
## [1] 11.75512
```

```
sd(phat2)
```

```
## [1] 2.53198
```

```
TSE1 <- sqrt(var(FlightDelays$Delay)/250)
TSE1
```

```
## [1] 2.632944
```

Q3. (Exercise 4.12)

Looking at the calculations below, we see that $P(\hat{X} \leq 4.6) = 0.02385744$

```r
n <- 20
mean <- 6
variance <- 10
val <- (4.6 - 6)/(sqrt(10)/sqrt(20))
pnorm(val)
```

```
## [1] 0.02385744
```

Q4. (Exercise 4.20)

a)

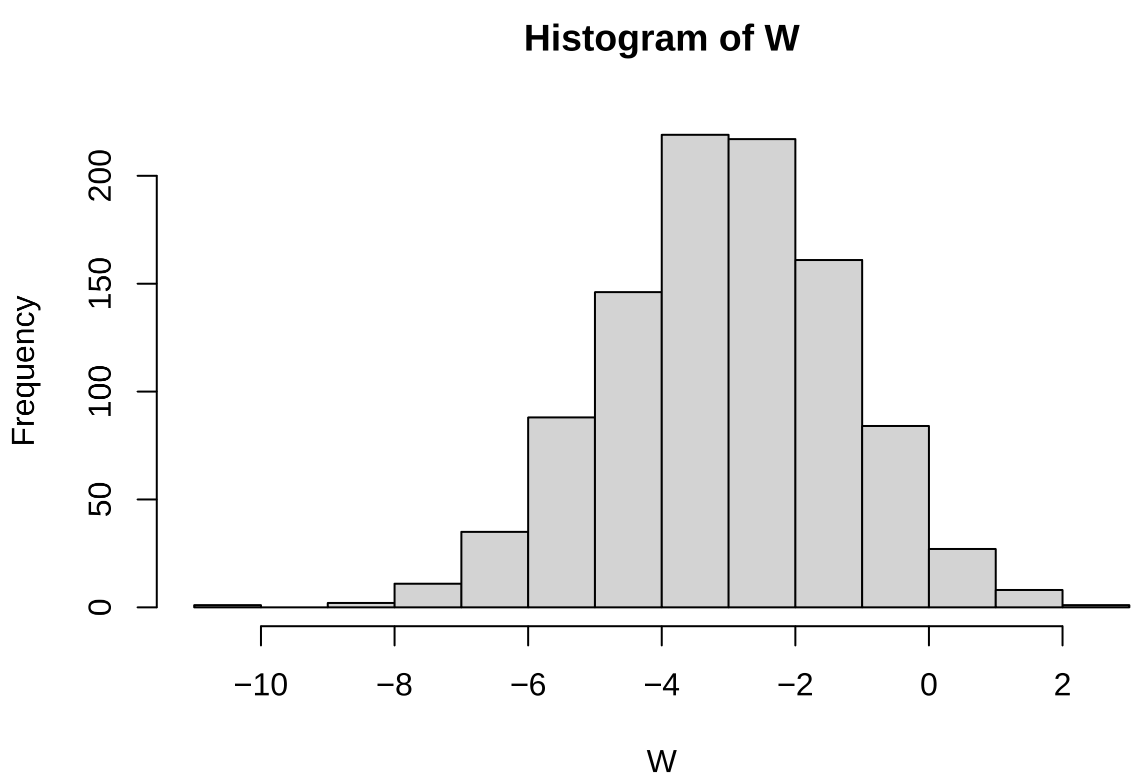
$$E(\bar{Z}) = E(\bar{X}) - E(\bar{Y}) = 7 - 10 = -3$$

$$Var(\bar{Z}) = Var(\bar{X}) + Var(\bar{Y}) = \frac{3^2}{9} + \frac{5^2}{12} = 1 + \frac{25}{12} = \frac{37}{12} \approx 3.083$$

Because of the Central Limit Theorem, we can get that $W \sim N(-3, 3.083)$

b) We get simulated mean and standard error as -3.046 and 3.051, these are close to the theoretical mean and stdard error of -3 and 3.083

```r
set.seed(69420)
W <- numeric(1000)
for (i in 1:1000)
{
x <- rnorm(9,7,3)
y <- rnorm(12,10,5)
W[i] <- mean(x) - mean(y)
}
hist(W)
```



```r
mean(W)
```

```
## [1] -3.046227
```

```r
sum((W - mean(W))^2/ length(W))
```

```
## [1] 3.050577
```

c) We get that $P(W < -1.5) = 0.82$, our exact answer is 0.804, which is pretty close to our estimated answer

```r
prob<- (-1.5 + 3)/(sqrt(3.083))
bleh <- pnorm(prob)
bleh
```

```
## [1] 0.8035274
```

```r
mean(W < -1.5)
```

```
## [1] 0.82
```

Q5. (Exercise 4.14)

We get the probability that between 220 and 230 people, 29.6% of people will have a high school diploma

```r
n <- 800
p <- 0.286
pbinom(220, 800, 0.286)
```

```
## [1] 0.259103
```

```r
pbinom(230, 800, 0.286)
```

```
## [1] 0.5550674
```

```r
pbinom(230, 800, 0.286) - pbinom(220, 800, 0.286)
```

```
## [1] 0.2959644
```

Q6. (Exercise 4.28)

$$f(x) = 3x^2$$

$$P(X \leq x) = \int_0^x 3x^2 dx$$

$$P(X \leq x) = x^3$$

a)

$$f(x_{min}) = n[1 - x_1^n]^{n-1} f(x_n)$$
$$f(x_{min}) = n[1 - x_1^3]^{n-1} 3x_n^2$$
$$f(x_{min}) = 3n[1 - x_1^3]^{n-1} x_n^2 (0 \leq x \leq 1)$$

b)

$$f(x_{max}) = n[f(x_n)]^{n-1} f(x_n)$$
$$f(x_{max}) = 3n \cdot x_n^{n-1} x_n^2$$
$$f(x_{max}) = 3n \cdot x_n^{3n-1} (0 \leq x_n \leq 1)$$

c)

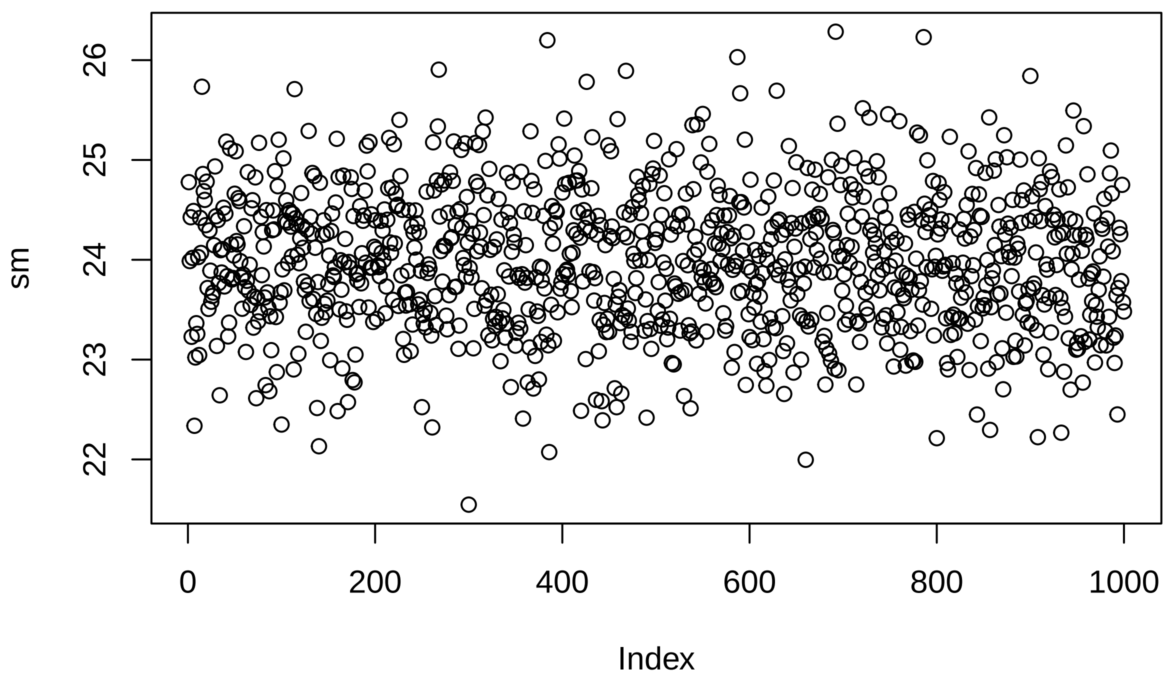
$$P[x_{max} > 0.92] = \int_{0.92}^{1} 3 \cdot 10 x_n^{3 \cdot 10 - 1} dx_n$$
$$\ldots$$

$$P[x_{max} > 0.92] = 1 - (0.92)^{30}$$

Q7. (Exercise 5.9)

a) The plot seems normally distributed.

```
set.seed(69420)
sm <- numeric(1000)
for (i in 1:1000)
{
sm[i] = mean(rgamma(200,6,0.25))
}
plot(sm)
```



```r
mean(sm)
```

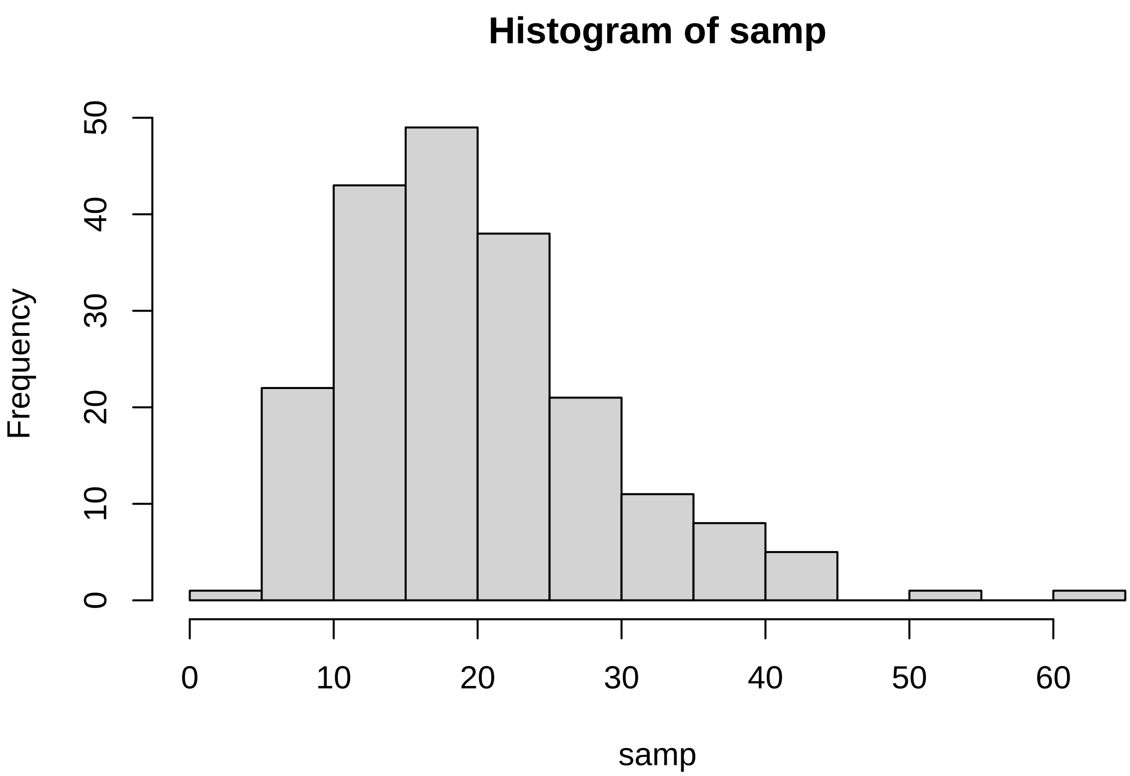
```
## [1] 23.98305
```

```r
sd(sm)
```

```
## [1] 0.698026
```

b) We get a slightly right skewed histogram with estimated mean at 20 and estimated standard error at 9.36

```r
set.seed(69420)
samp <- rgamma(200,5,0.25)
hist(samp)
```




```r
mean(samp)
```

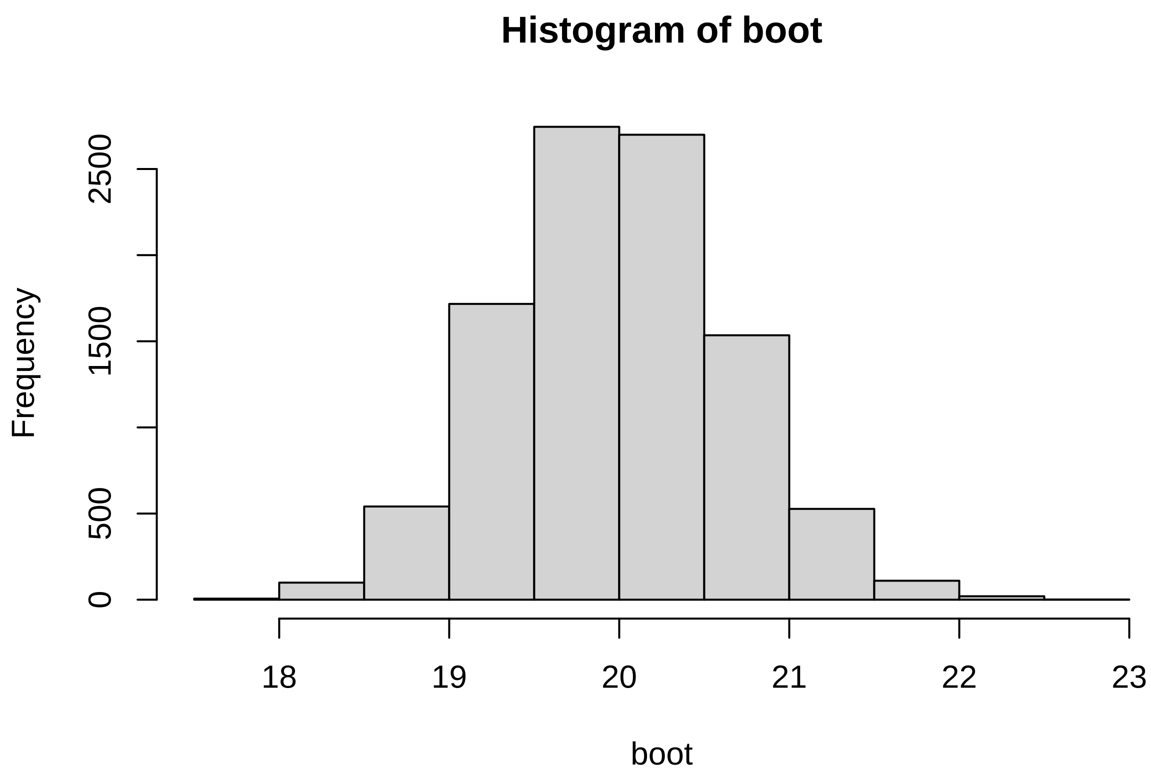
```
## [1] 20.00015
```

```r
sd(samp)
```

```
## [1] 9.359762
```

c) Bootstrap mean is 19.98796 and standard error is 0.665884

```
N <- 10^4
boot<- numeric(N)
for(i in 1:N){
  boot[i] <- mean(sample(samp, 200, replace = TRUE))
}
hist(boot)
```



d) The mean for sampling distribution and bootstrap distribution are very close (approximately 24 for both). The standard error is a bit different with smapling distribution having a 0.6881 SE and bootstrap distribution having an 0.221 SE.

```
data.frame(
    Distribution = c("Population", "Sampling distribution", "Sample",
                     "Bootstrap distribution"),
    Mean = c(20, 20,mean(sm), mean(boot)),
    SE = c(9, 0.6,sd(sm), sd(boot))
)
```

```
##             Distribution     Mean        SE
## 1             Population 20.00000 9.0000000
## 2  Sampling distribution 20.00000 0.6000000
## 3                 Sample 23.98305 0.6980260
## 4 Bootstrap distribution 19.98770 0.6649944
```

e) As the sample size gets smaller, shilw the means stay about the same, the SE gets significantly worse and more different as sample size decreases

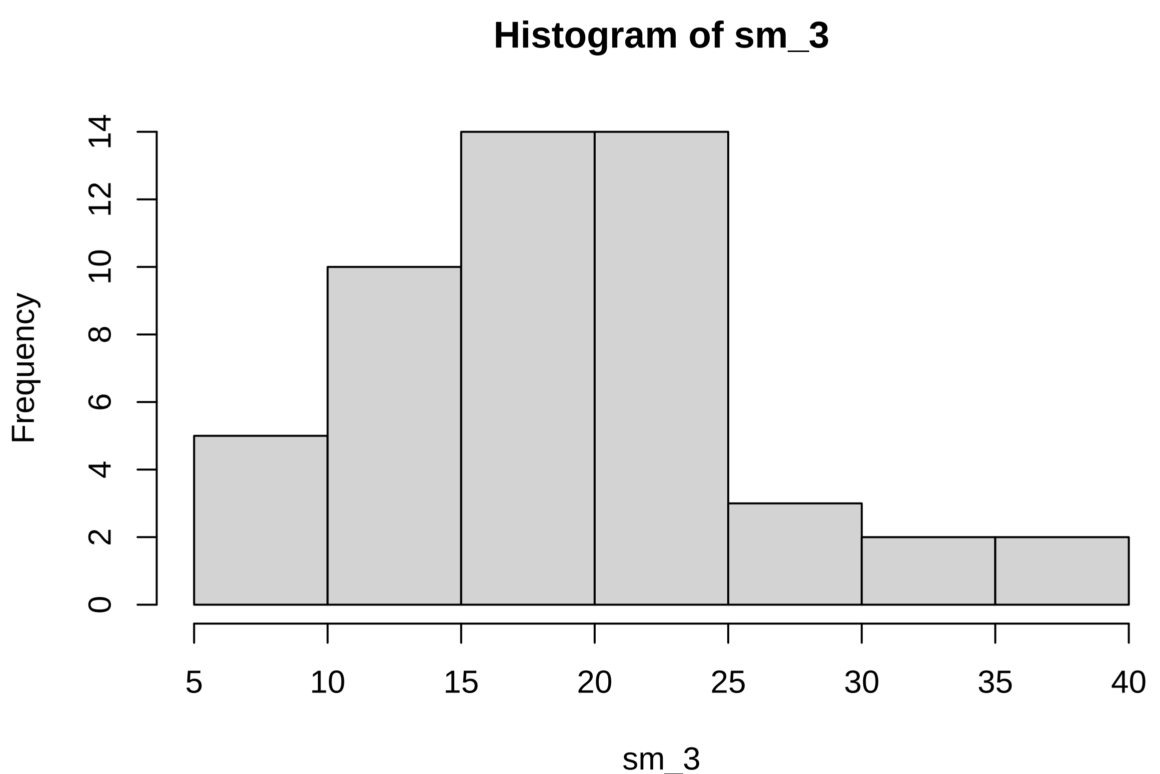
```r
set.seed(69420)
sm_1 <- numeric(1000)
for (i in 1:1000)
{
sm_1[i] = mean(rgamma(50,5,0.25))
}
mean(sm_1)
```

```
## [1] 20.03551
```

```r
sd(sm_1)
```

```
## [1] 1.245621
```

```r
sm_3 <- rgamma(50,5,0.25)
hist(sm_3)
```



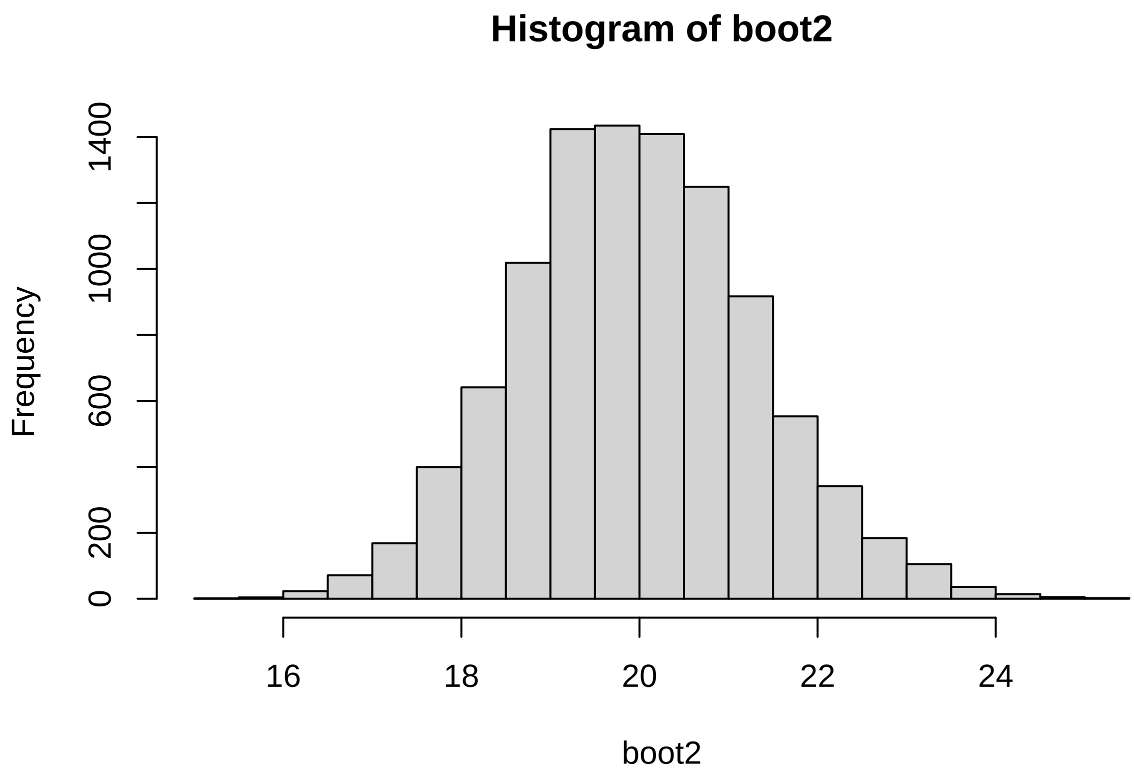

```r
mean(sm_3)
```

```
## [1] 18.77944
```

```r
sd(sm_3)
```

```
## [1] 7.337662
```

```r
N <- 10^4
boot2<- numeric(N)
for(i in 1:N){
  boot2[i] <- mean(sample(samp, 50, replace = TRUE))
}
hist(boot2)
```




```r
mean(boot2)
```

```
## [1] 19.97334
```

```r
sd(boot2)
```

```
## [1] 1.331857
```

```r
data.frame(
    Distribution = c("Population", "Sampling distribution", "Sample",
                     "Bootstrap distribution"),
    Mean = c(20, 20,mean(sm_3), mean(boot2)),
    SE = c(9, 1.262298,sd(sm_3), sd(boot2))
)
```

```
##             Distribution     Mean       SE
## 1             Population 20.00000 9.000000
## 2  Sampling distribution 20.00000 1.262298
## 3                 Sample 18.77944 7.337662
## 4 Bootstrap distribution 19.97334 1.331857
```

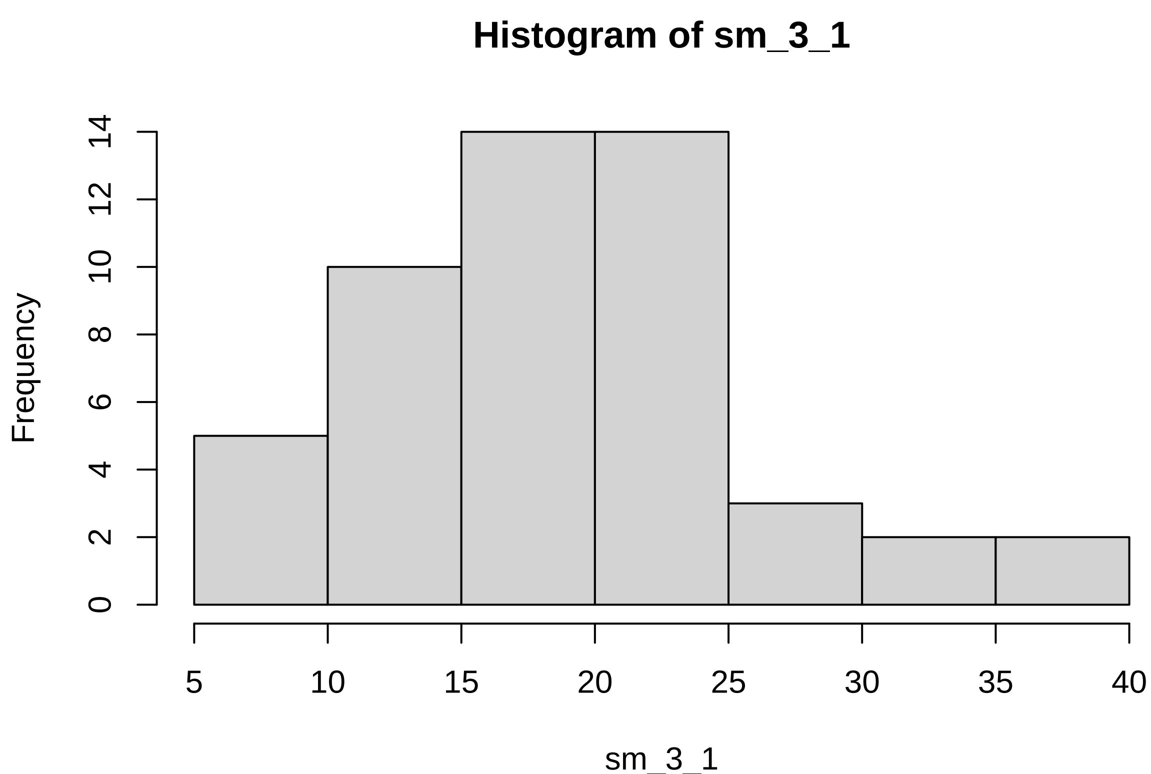
```r
set.seed(69420)
sm_1_1 <- numeric(1000)
for (i in 1:1000)
{
sm_1_1[i] = mean(rgamma(50,5,0.25))
}
mean(sm_1_1)
```

```
## [1] 20.03551
```

```r
sd(sm_1_1)
```

```
## [1] 1.245621
```

```r
sm_3_1 <- rgamma(50,5,0.25)
hist(sm_3_1)
```



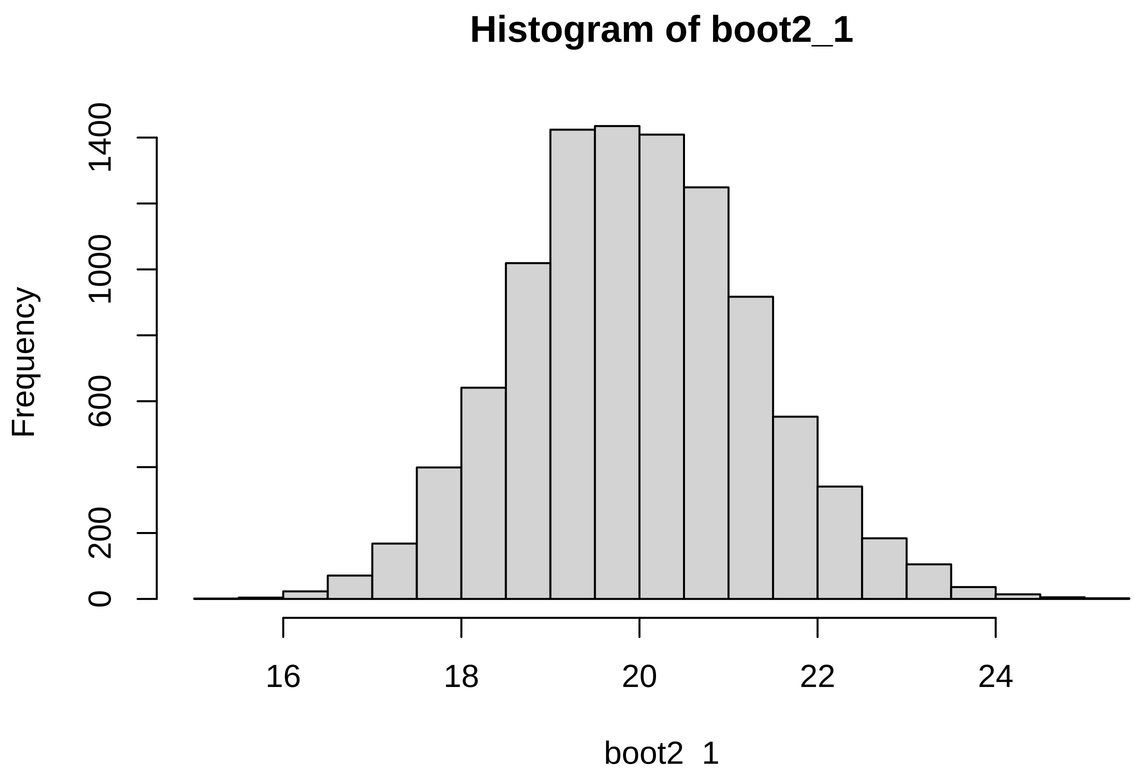

```r
mean(sm_3_1)
```

```
## [1] 18.77944
```

```r
sd(sm_3_1)
```

```
## [1] 7.337662
```

```r
N <- 10^4
boot2_1<- numeric(N)
for(i in 1:N){
  boot2_1[i] <- mean(sample(samp, 50, replace = TRUE))
}
hist(boot2_1)
```




```r
mean(boot2_1)
```

```
## [1] 19.97334
```

```r
sd(boot2_1)
```

```
## [1] 1.331857
```

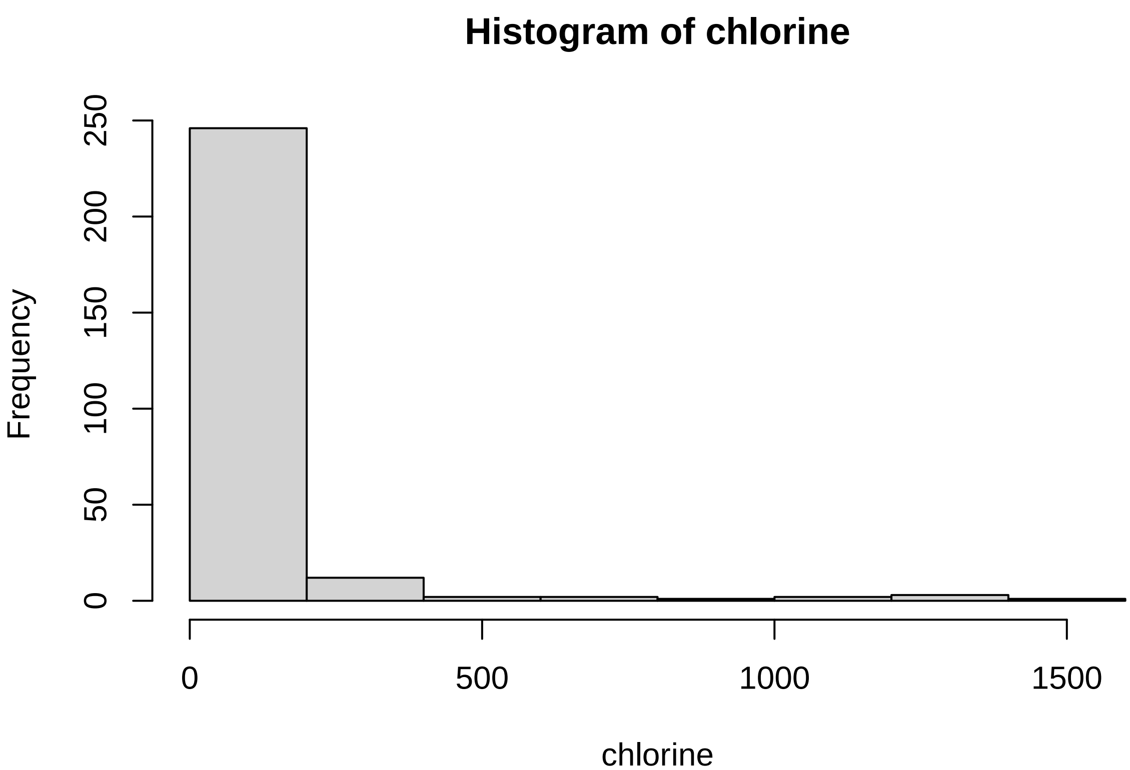
```r
data.frame(
    Distribution = c("Population", "Sampling distribution", "Sample",
                     "Bootstrap distribution"),
    Mean = c(20, 20,mean(sm_3_1), mean(boot2_1)),
    SE = c(9, 1.262298,sd(sm_3_1), sd(boot2_1))
)
```

```
##             Distribution     Mean       SE
## 1             Population 20.00000 9.000000
## 2  Sampling distribution 20.00000 1.262298
## 3                 Sample 18.77944 7.337662
## 4 Bootstrap distribution 19.97334 1.331857
```

Q8. (Exercise 5.11)

a) The histogram is extremely right skewed with a boxplot that fits that as well. The summary for the chlorine consist of min = 1.00, 1st quantile = 5.00, median = 14.05, Mean = 78.31, 3rd quantile = 55.70, and max = 1550.00

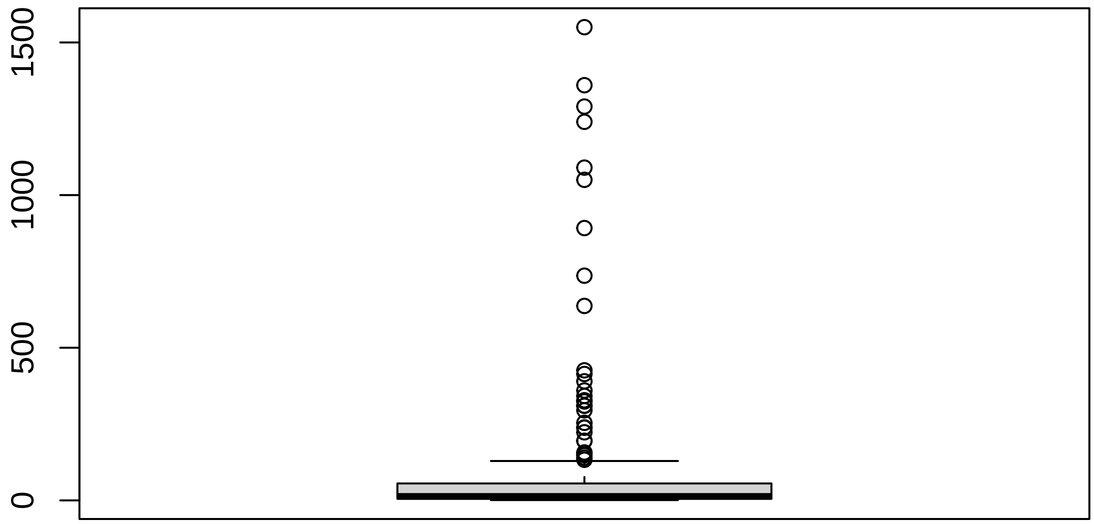
```
set.seed(69420)
Bangladesh <- read.csv("https://sites.google.com/site/chiharahesterberg/data2/Bangladesh.csv")
chlorine <-subset(Bangladesh, select = Chlorine, subset = !is.na(Chlorine), drop = T)
hist(chlorine)
```



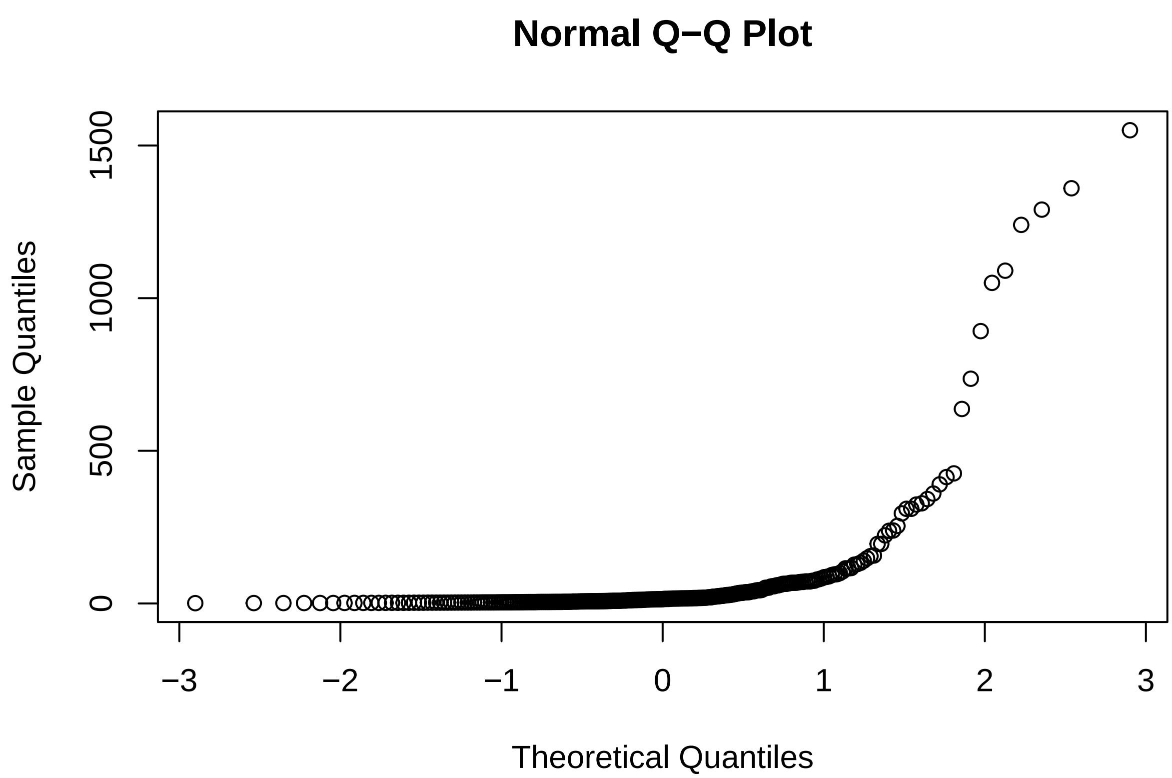

```
summary(chlorine)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##    1.00    5.00   14.20   78.08   55.50 1550.00
```

```
boxplot(chlorine)
```



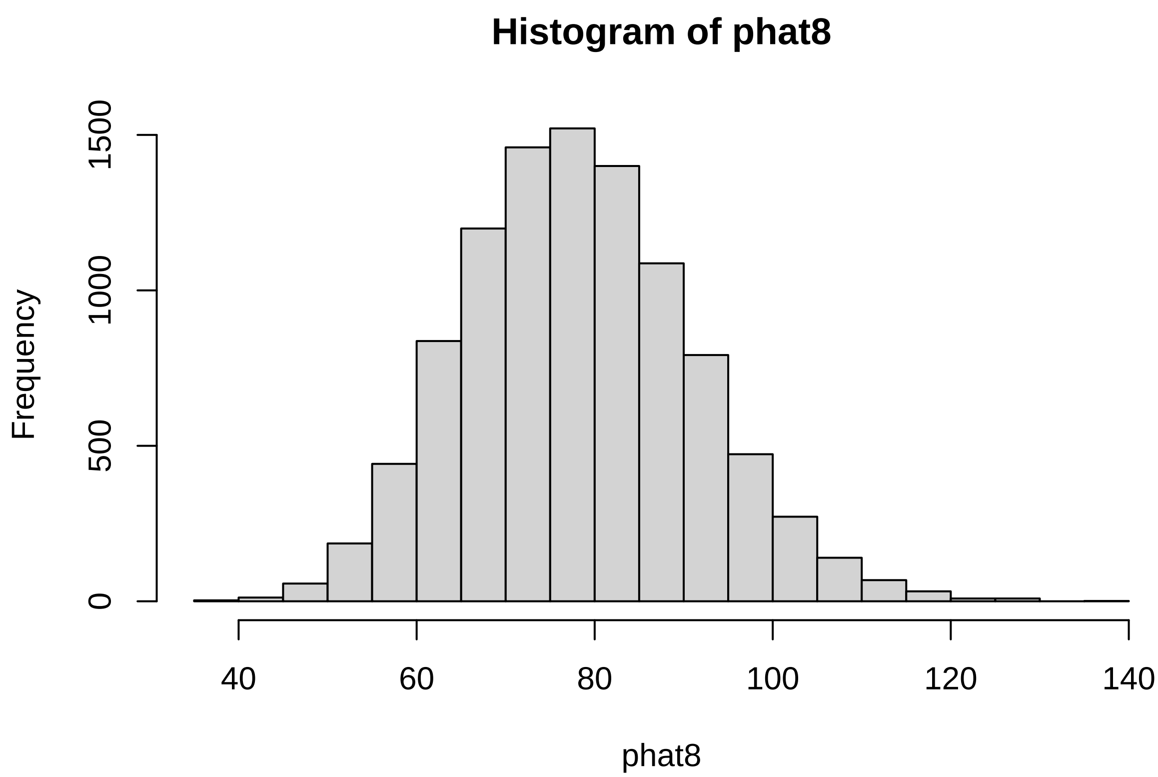

```
qqnorm(chlorine)
```



b) Bootstrap is shown below

```
set.seed(69420)
N <- 10^4
phat8 <- numeric(N)
n <- nrow(Bangladesh)
for (i in 1:N)
{
  samp8 <- sample(Bangladesh$Chlorine, size = n, replace = TRUE)
```

```r
  phat8[i] <- mean(samp8, na.rm = TRUE)
}
hist(phat8)
```




```r
mean(phat8)
```

```
## [1] 78.22395
```

```r
sd(phat8)
```

```
## [1] 12.9174
```

c) We get a 95% confidence interval from 54.92034 to 105.20690 What this means is that we are 95% confident that the mean chlorine concentration from the 271 wells in the data set will fall between those two values inclusive.

```r
quantile(phat8, probs = c(0.025,0.975))
```

```
##       2.5%     97.5%
##   54.92034 105.20690
```

d) The bootstrap estimated of the bias is -0.1399, this represents -0.010 of the standard error

```r
chlorine <- subset(Bangladesh, select = Chlorine, subset = !is.na(Chlorine), drop = T)
bias <- mean(chlorine) - mean(phat8)
bias / sd(phat8)
```

```
## [1] -0.01083329
```

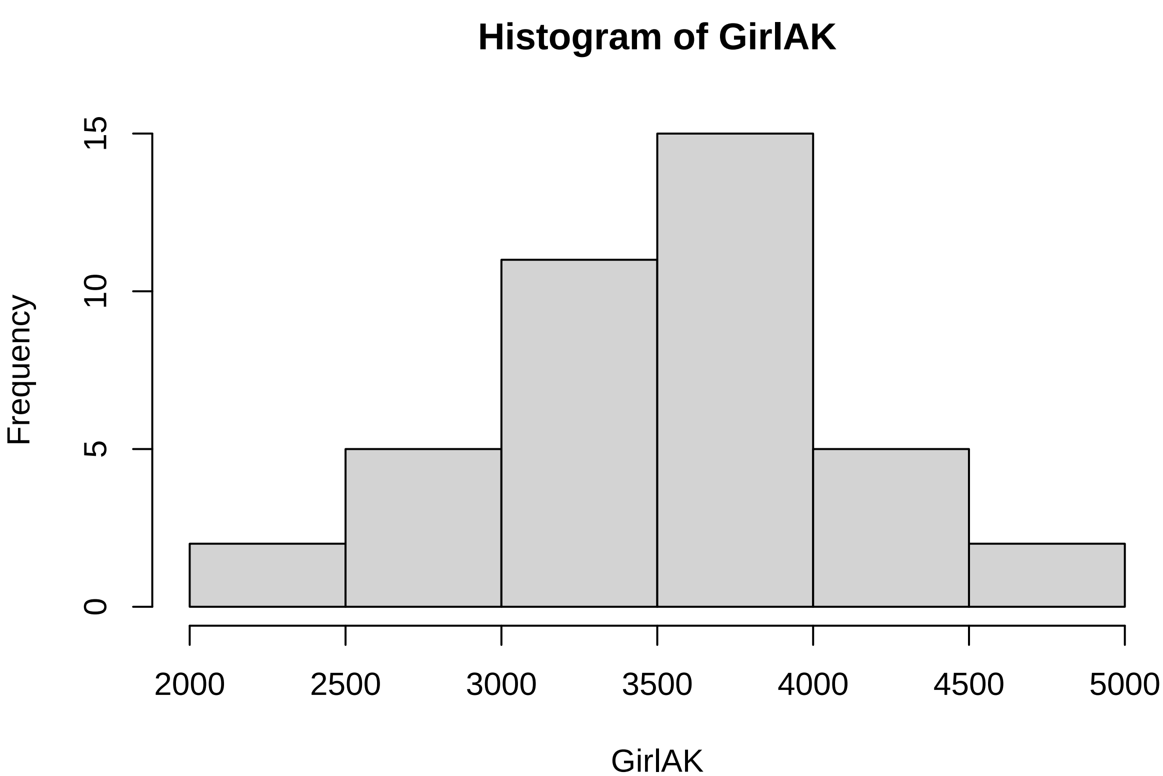
Q9. (Exercise 5.17)

a) Both look normally distributed, GirlAK has a min of 2182, 1st Q of 3558, Median of 3516, Mean of 3516, 3rd Q of 3926, and Max of 4592. GirlWY has a min of 2212, 1st Q of 2934, Median of 3278, Mean of 3208, 3rd Q of 3515, and Max of 3995

```r
Girls2004 <- read.csv("https://sites.google.com/site/chiharahesterberg/data2/Girls2004.csv")
GirlWY <- Girls2004 %>% filter (State == "WY") %>% pull(Weight) %>% na.omit()
GirlAK <- Girls2004 %>% filter (State == "AK") %>% pull(Weight) %>% na.omit()
summary(GirlAK)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    2182    3170    3558    3516    3926    4592
```

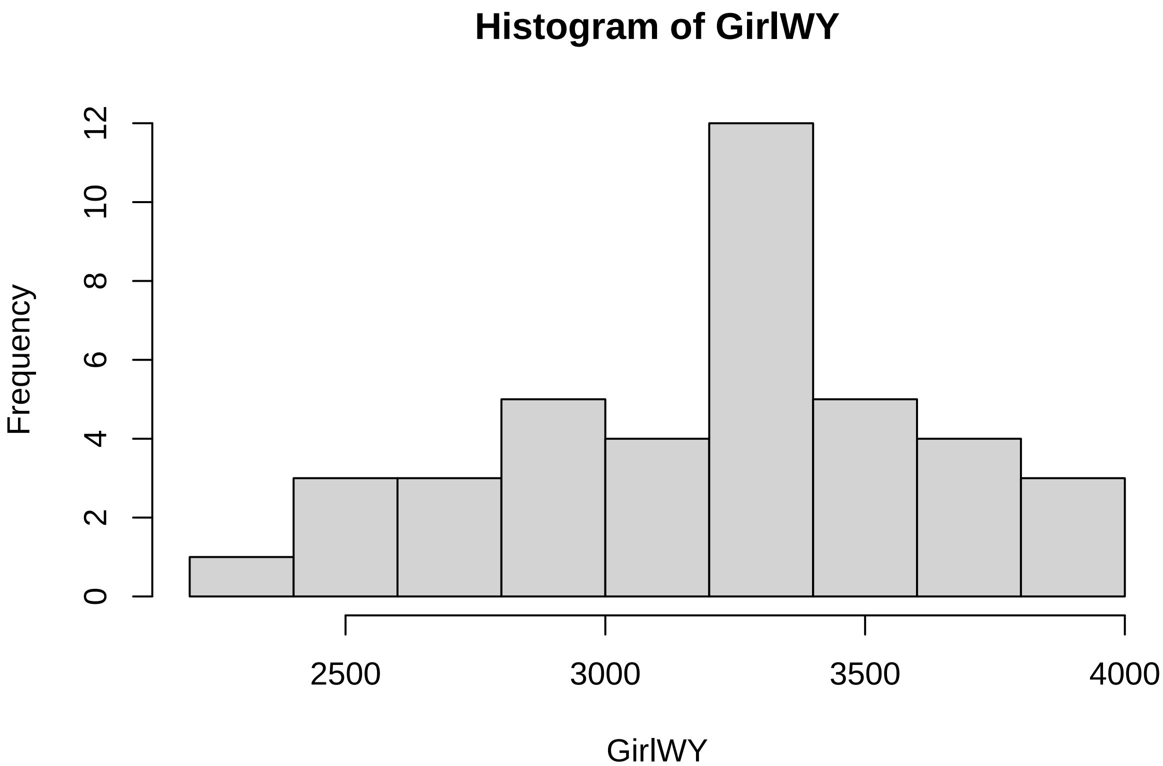
```r
hist(GirlAK)
```




```r
summary(GirlWY)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    2212    2934    3278    3208    3515    3995
```

```r
hist(GirlWY)
```



b) We get a 95% confidence interval between -529.65313 and -85.54687. What this means is that we are 95% confident that the average weight of a baby girl born in WY is 529.65313 to 85.54687 less than the average weight of a baby girl born in Arkansas.

```r
set.seed(69420)
N <- 10^4
phat9 <- numeric(N)
n <- nrow(Bangladesh)
for (i in 1:N)
{
  WYboot <- sample (GirlWY, replace = TRUE)
  AKboot <- sample (GirlAK, replace = TRUE)
  phat9[i] <- mean(WYboot) - mean(AKboot)
}
quantile(phat9, probs = c(0.025, 0.975))
```

```
##       2.5%      97.5%
## -529.65313  -85.54687
```

c) We get an estimate bias of 0.5158875, which represents a 0.004596454 fraction of the bootstrap standard error

```r
true9 <- mean(GirlWY) - mean(GirlAK)
bias9 <- mean(phat9) - true9
bias9
```

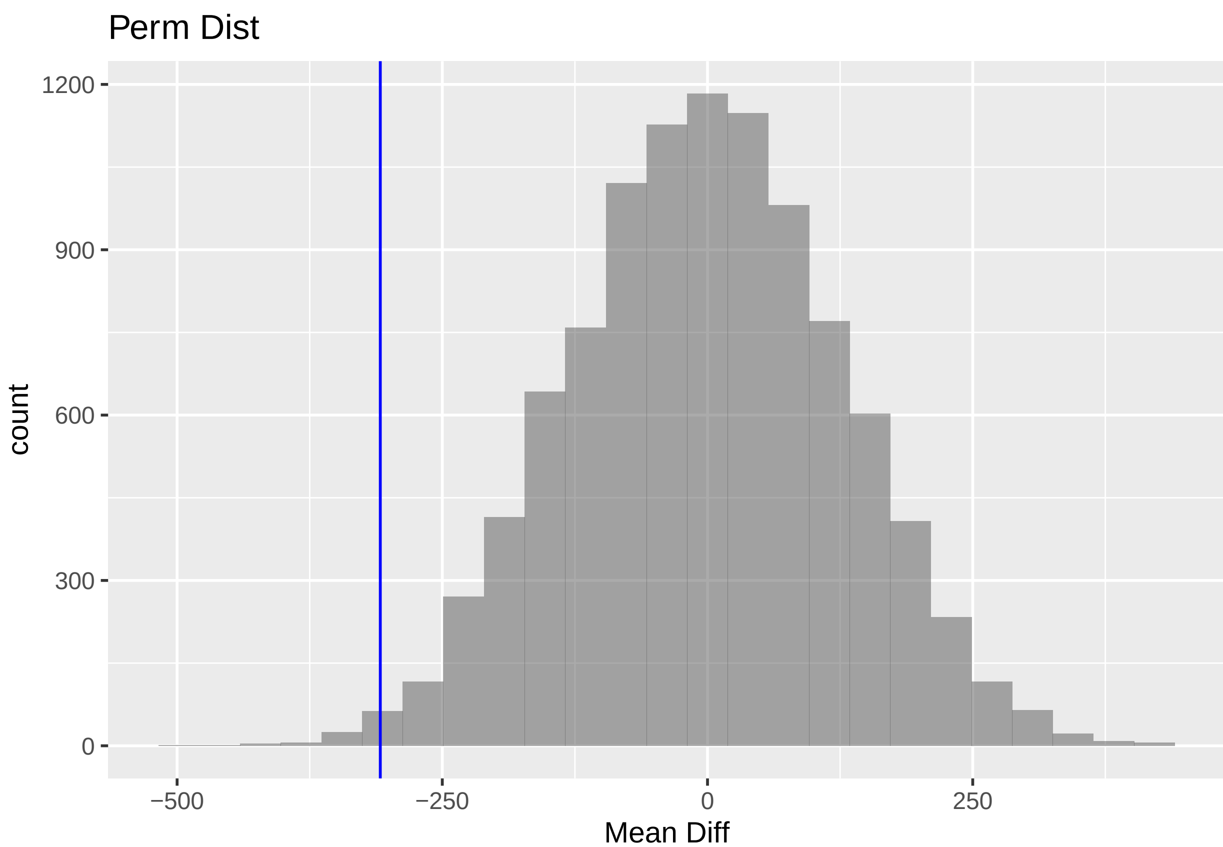
```
## [1] 0.5158875
```

```
bias9 / sd(phat9)
```

```
## [1] 0.004596454
```

d) Our null hypothesis is that there is no weight difference between baby girls born in Arkansas and Wyoming. Our alternative hypothesis is that there is a difference. We get a p-value of 0.01239876 which is small enough to indicate a statisticaly discernible difference between the mean baby girl weight in Wypming and in Arkansas.

```
set.seed(69420)
N <- 10^4
result9 <- numeric(N)
n <- nrow(Bangladesh)
for (i in 1:N)
{
  index <- sample(nrow(Girls2004), size = 40, replace = TRUE)
  result9[i] <- mean(Girls2004$Weight[index], trim = 0.25) - mean(Girls2004$Weight[-index], trim = 0.25
}
gf_histogram(~result9, title = "Perm Dist", xlab = "Mean Diff") %>% gf_vline(xintercept = ~true9, color
```




```
2*(sum(result9 <= true9) + 1)/(N+1)
```

```
## [1] 0.01239876
```

e) Our conclusion holds for the baby girls born in Syoming and Arkansas in 2004 where the gestation period is at least 37 weeks and where there are no twins.