4211 Homework 1

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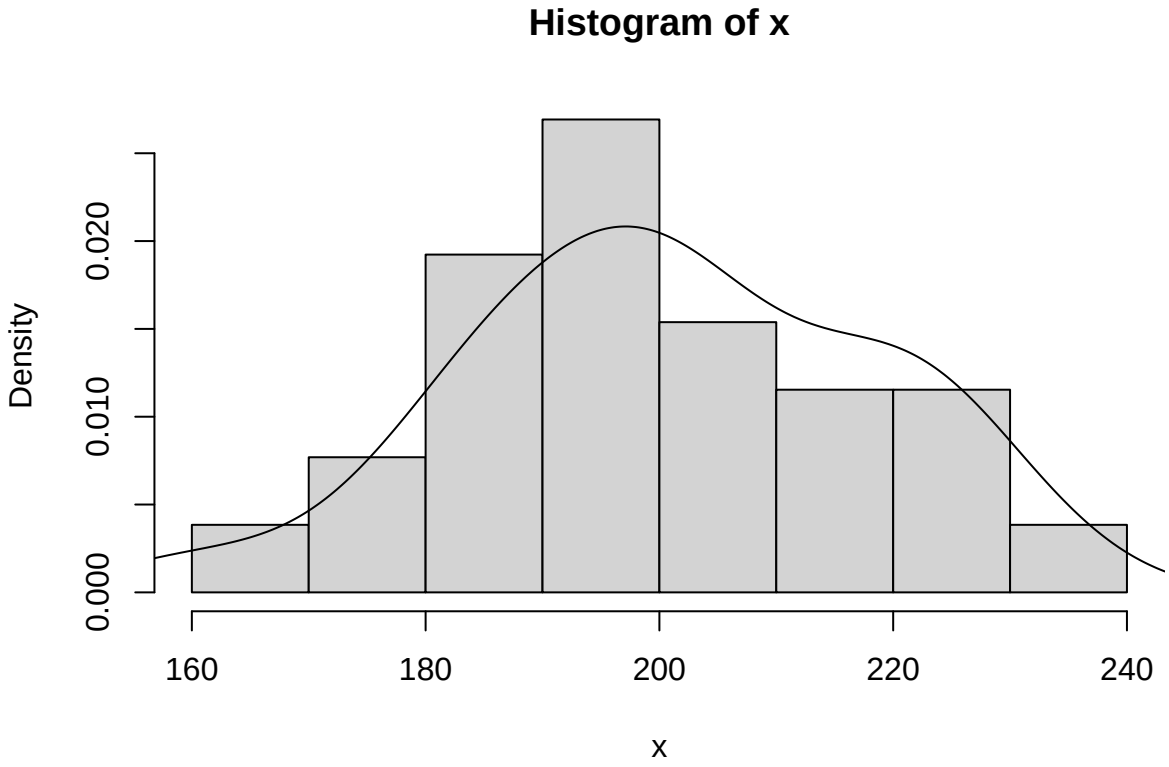
1

```
data(bb)
#x = bb$weight
x = c(160,175,180,185,185,185,190,190,195,195,195,200,200,200,200,205,205,210,210,218,219,220,222,225,2
```

(a)

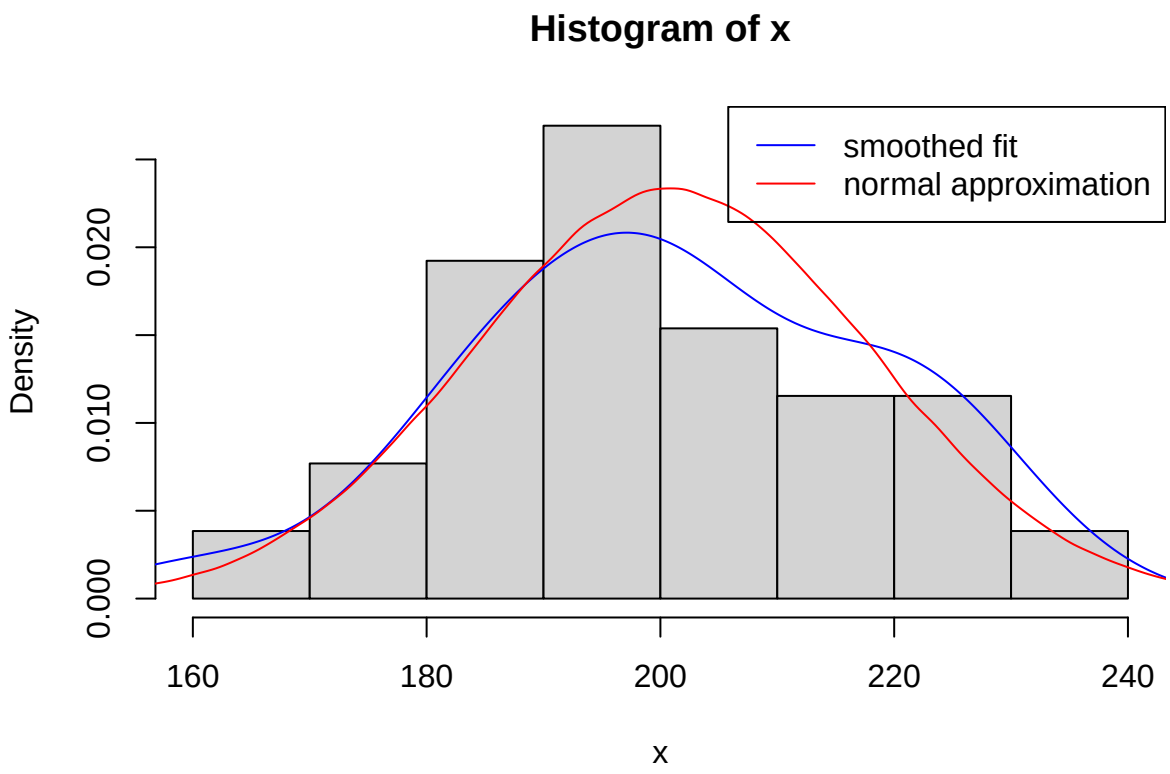
```
hist(x,pr=T)
lines(density(x))
```



The normal distribution looks like it may be fairly accurate in this case.

(b)

```
muhat = mean(x)
varhat = mean((x-muhat)**2)
sdhat = sqrt(varhat)
variationhat = muhat/sdhat
hist(x,pr=T)
lines(density(x), col = "blue")
lines(density(rnorm(1000000, mean = muhat, sd = sdhat)), col = "red")
legend('topright', lty = 1, col=c("blue", "red"), legend = c("smoothed fit", "normal approximation"))
```




```
muhat
```

```
## [1] 201
```

```
varhat
```

```
## [1] 293.9231
```

```
sdhat
```

```
## [1] 17.14418
```

```
variationhat
```

```
## [1] 11.72409
```

(c)

```
phat = sum(as.integer(x>215))/length(x)
phat
```

```
## [1] 0.2692308
```

(d)

```
1 - pnorm(215, mean = muhat, sd = sdhat)
```

```
## [1] 0.2070776
```

2

```
getcis <- function(mat,cc=.90){
numb <- length(mat[,1]); ci <- c()
for(j in 1:numb)
{ci<-rbind(ci,t.test(mat[j,],conf.level=cc)$conf.int)}
return(as.data.frame(ci))}

getcisz = function(mat, cc=.90, sd = TRUE){
  numb = length(mat[,1])
  ci = c()

  if(sd){
    for (j in 1:numb){
    alpha = 1-cc
    xbar = mean(mat[j,])
    upper = xbar + sd*qnorm(alpha/2)/sqrt(length(mat[j,]))
    lower = xbar - sd*qnorm(alpha/2)/sqrt(length(mat[j,]))
    ci = rbind(ci, c(upper, lower))
  }
  return(as.data.frame(ci))
  }

   for (j in 1:numb){
    alpha = 1-cc
    xbar = mean(mat[j,])
    sd = sd(mat[j,])
    upper = xbar + sd*qnorm(alpha/2)/sqrt(length(mat[j,]))
    lower = xbar - sd*qnorm(alpha/2)/sqrt(length(mat[j,]))
    ci = rbind(ci, c(upper, lower))
  }
  return(as.data.frame(ci))

}
```

(a)

```
n = 9
m = 1000
mat = matrix(rnorm(m*n, mean = 1, sd = 1), ncol=n)
CIn = getcisz(mat, cc = 0.95)
mean(CIn$V2-CIn$V1)
```

```
## [1] 1.306643
```

(b)

```
CIt = getcis(mat, cc = 0.95)
mean(CIt$V2-CIt$V1)
```

```
## [1] 1.481781
```

(c)

As expected, when we use the t confidence interval rather than the z one, our confidence intervals are longer.

3

(a)

```
CIn$Successful = CIn$V1 < 1 & CIn$V2 > 1
mean(CIn$Successful)
```

```
## [1] 0.96
```

```
CIt$Successful = CIt$V1 < 1 & CIt$V2 > 1
mean(CIt$Successful)
```

```
## [1] 0.958
```

Both values are very close to the nominal coverage probability.

(b)

```
CIn2 = getcisz(mat, cc = 0.95, sd = FALSE)
CIn2$Successful = CIn2$V1 < 1 & CIn2$V2 > 1
mean(CIn2$Successful)
```

```
## [1] 0.929
```

The coverage probability no longer conforms to the nominal coverage probability. It performed worse than both of the other test types.

4

```
getcib = function(x, cc=0.95, type = "z", n = 30){
  ci = c()
  alpha = 1-cc

  if(type == "z"){
    for (j in 1:length(x)){
      phat = x[j]/n
      sd = sqrt(phat*(1-phat))
      upper = phat + sd*qnorm(alpha/2)/sqrt(n)
      lower = phat - sd*qnorm(alpha/2)/sqrt(n)
      ci = rbind(ci, c(upper, lower))
    }
    return(as.data.frame(ci))
  }

  if(type == "t"){
    df = n-1
    for (j in 1:length(x)){
      phat = x[j]/n
      sd = sqrt(phat*(1-phat))
      upper = phat + sd*qt(alpha/2, df = df)/sqrt(n)
      lower = phat - sd*qt(alpha/2, df = df)/sqrt(n)
      ci = rbind(ci, c(upper, lower))
    }
    return(as.data.frame(ci))
  }

}
```

(a)

```
data = rbinom(1000, size=30, p=0.5)
CIbn = getcib(data)
```

(b)

```
CIbt = getcib(data, type = "t")
```

(c)

```
CIbn.length = mean(CIbn$V2-CIbn$V1)
CIbt.length = mean(CIbt$V2-CIbt$V1)

CIbn$Successful = CIbn$V1 < 0.5 & CIbn$V2 > 0.5
```

```r
CIbn.coveragep = mean(CIbn$Successful)

CIbt$Successful = CIbt$V1 < 0.5 & CIbt$V2 > 0.5
CIbt.coveragep = mean(CIbt$Successful)

CIbn.length
```

```
## [1] 0.3520576
```

```r
CIbn.coveragep
```

```
## [1] 0.964
```

```r
CIbt.length
```

```
## [1] 0.3673735
```

```r
CIbt.coveragep
```

```
## [1] 0.964
```

They have the same coverage probability (0.95), but the t interval has a slightly larger length.

5

n = 1/sqrt(1+1/n)

```
k = qt(0.9, df=7)*sqrt(1+1/8)
k
```

```
## [1] 1.500753
```