Bios 6301: Assignment 9

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Due Tuesday, 29 November, 1:00 PM

$5^{n=day}$ points taken off for each day late.

40 points total.

Submit a single knitr file (named `homework9.rmd`), along with a valid PDF output file. Inside the file, clearly indicate which parts of your responses go with which problems (you may use the original homework document as a template). Add your name as `author` to the file's metadata section. Raw R code/output or word processor files are not acceptable.

Failure to name file `homework9.rmd` or include author name may result in 5 points taken off.

Question 1

15 points

Consider the following very simple genetic model (*very* simple – don't worry if you're not a geneticist!). A population consists of equal numbers of two sexes: male and female. At each generation men and women are paired at random, and each pair produces exactly two offspring, one male and one female. We are interested in the distribution of height from one generation to the next. Suppose that the height of both children is just the average of the height of their parents, how will the distribution of height change across generations?

Represent the heights of the current generation as a dataframe with two variables, m and f, for the two sexes. We can use `rnorm` to randomly generate the population at generation 1:

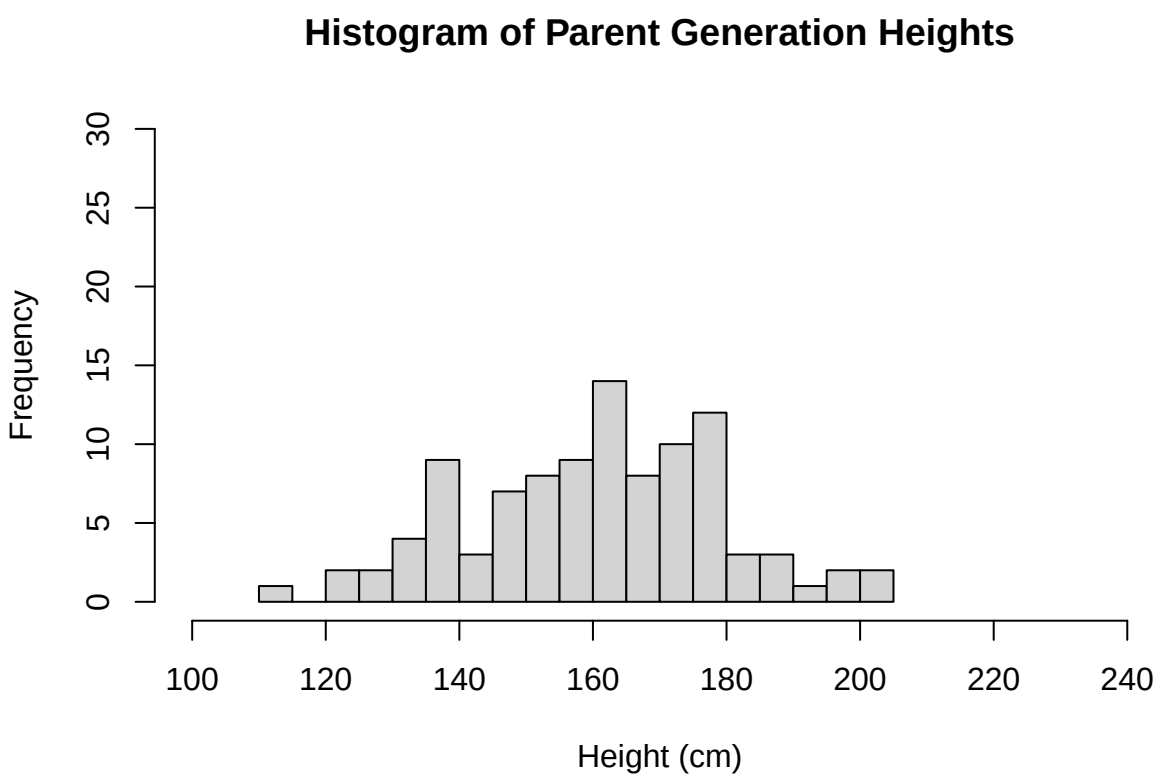
```
pop <- data.frame(m = rnorm(100, 160, 20), f = rnorm(100, 160, 20)) # rnorm(n, mean, sd)

# m and f are paired at random
# each pair makes 2 offspring (1 m and 1 f)
# height of offspring = avg of parents
```

The following function takes the data frame `pop` and randomly permutes the ordering of the men. Men and women are then paired according to rows, and heights for the next generation are calculated by taking the mean of each row. The function returns a data frame with the same structure, giving the heights of the next generation.

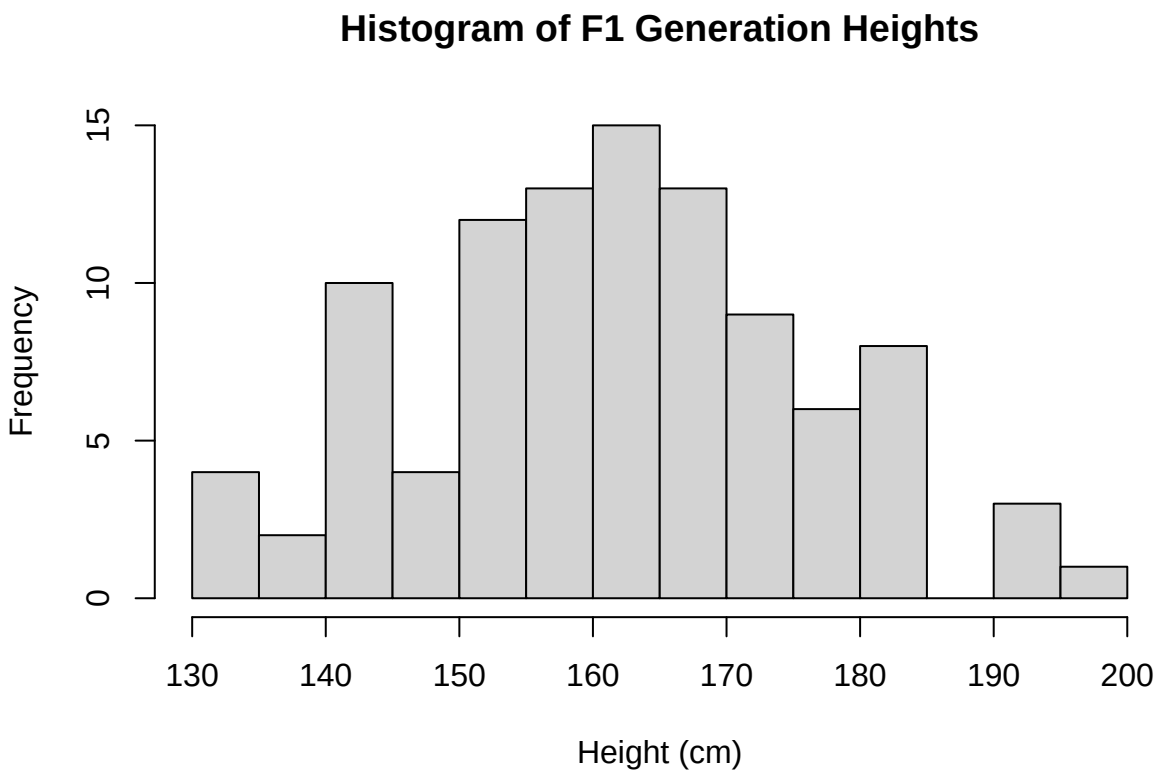
```
next_gen <- function(pop) {
    pop$m <- sample(pop$m) # randomly permutes order of the m
    pop$m <- rowMeans(pop) # finds mean of m & f (each row), defining it as the value for the next gene
    pop$f <- pop$m # both m & f offspring have avg height of parents
    pop # returns a data frame with the same structure
}
```

Use the function `next_gen` to generate nine generations (you already have the first), then use the function `hist` to plot the distribution of male heights in each generation (this will require multiple calls to `hist`). The phenomenon you see is called regression to the mean. Provide (at least) minimal decorations such as title and x-axis labels.

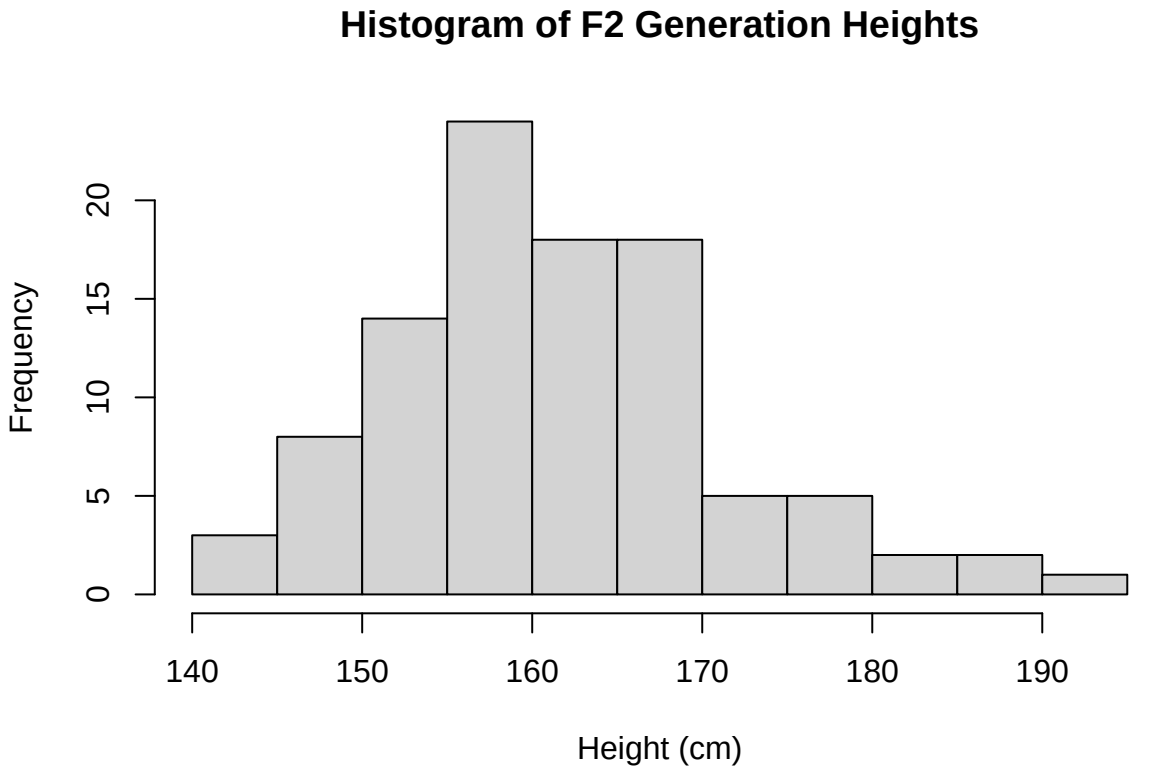
```r
# make it a loop with a counter
# 9 generations, 9 - 1 = 8
# 1:8 to 2:9 so I can include the parent generation in the same list

f_gens <- list(pop) # list of data frames

# generate another 8 generations
for (i in 2:9) {
  f_gens[[i]] <- next_gen(f_gens[[(i-1)]]) # be careful to reference the previous generation, not just
}

# histograms
hist(f_gens[[1]]$m, breaks=15, xlim=range(100,240), ylim=range(0,30), main='Histogram of Parent Generati
```



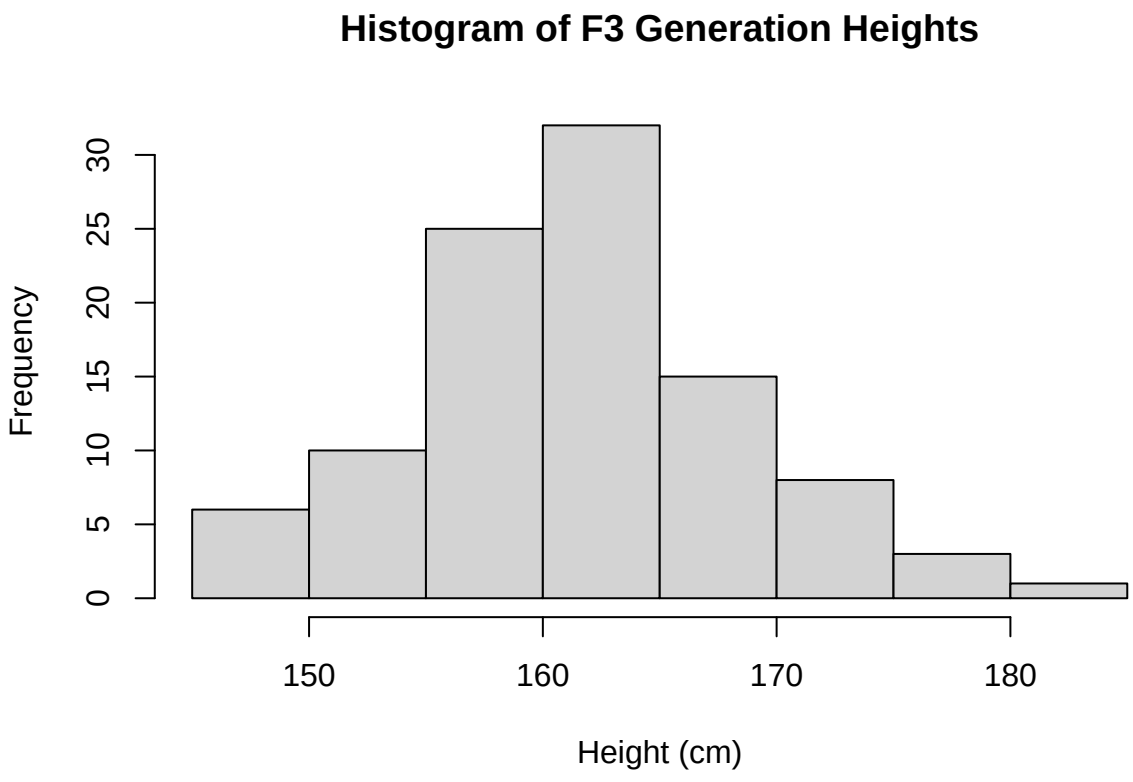

```r
hist(f_gens[[2]]$m, breaks=15, main='Histogram of F1 Generation Heights', xlab='Height (cm)')
```



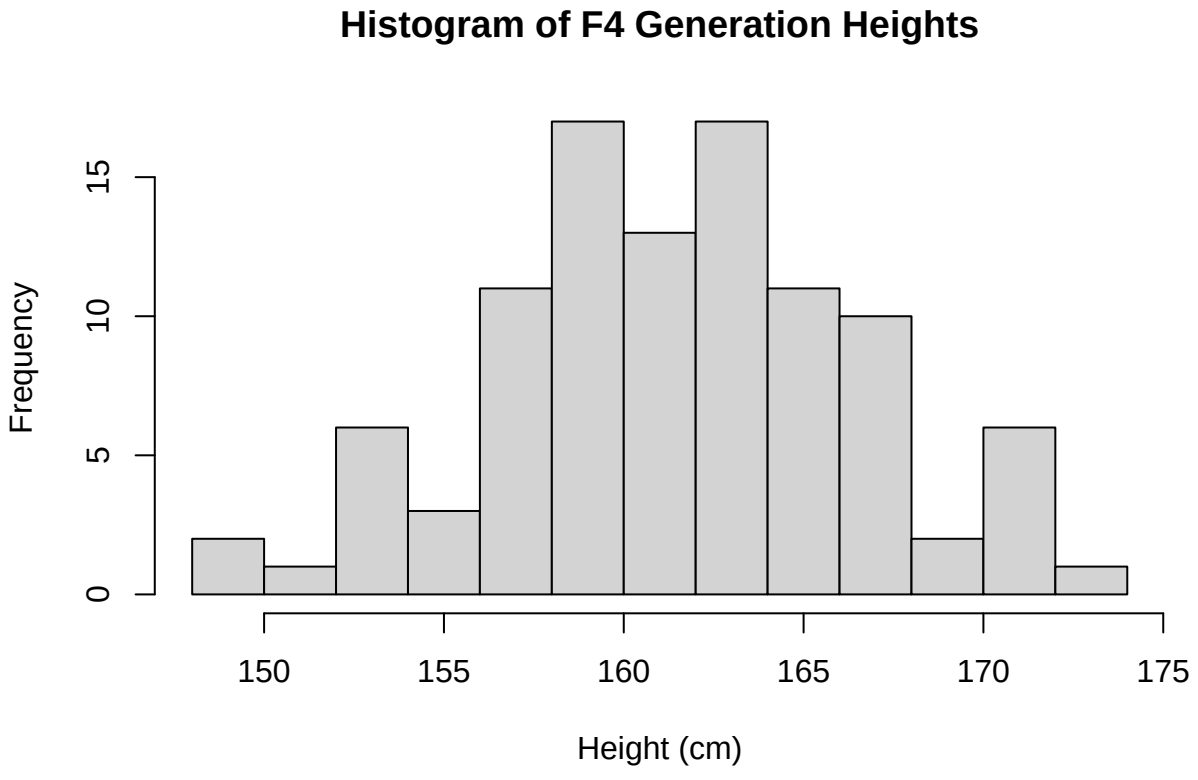

```
hist(f_gens[[3]]$m, breaks=15, main='Histogram of F2 Generation Heights', xlab='Height (cm)')
```



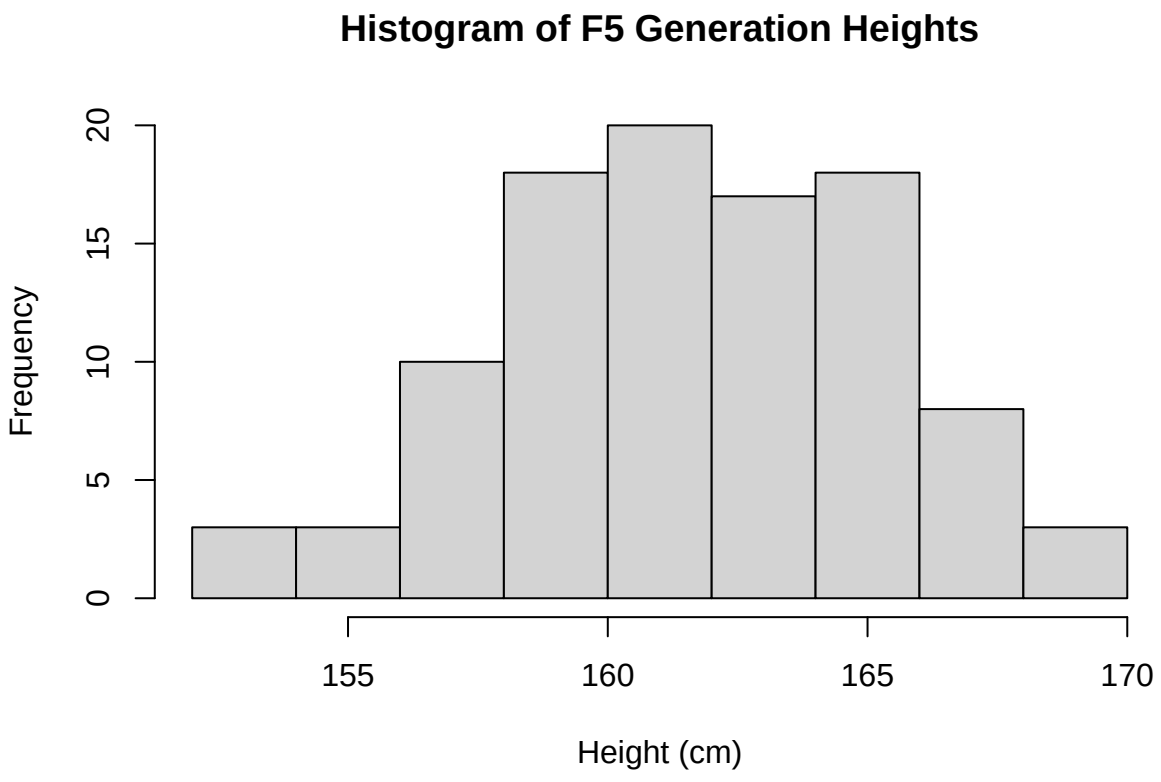

```
hist(f_gens[[4]]$m, breaks=13, main='Histogram of F3 Generation Heights', xlab='Height (cm)')
```



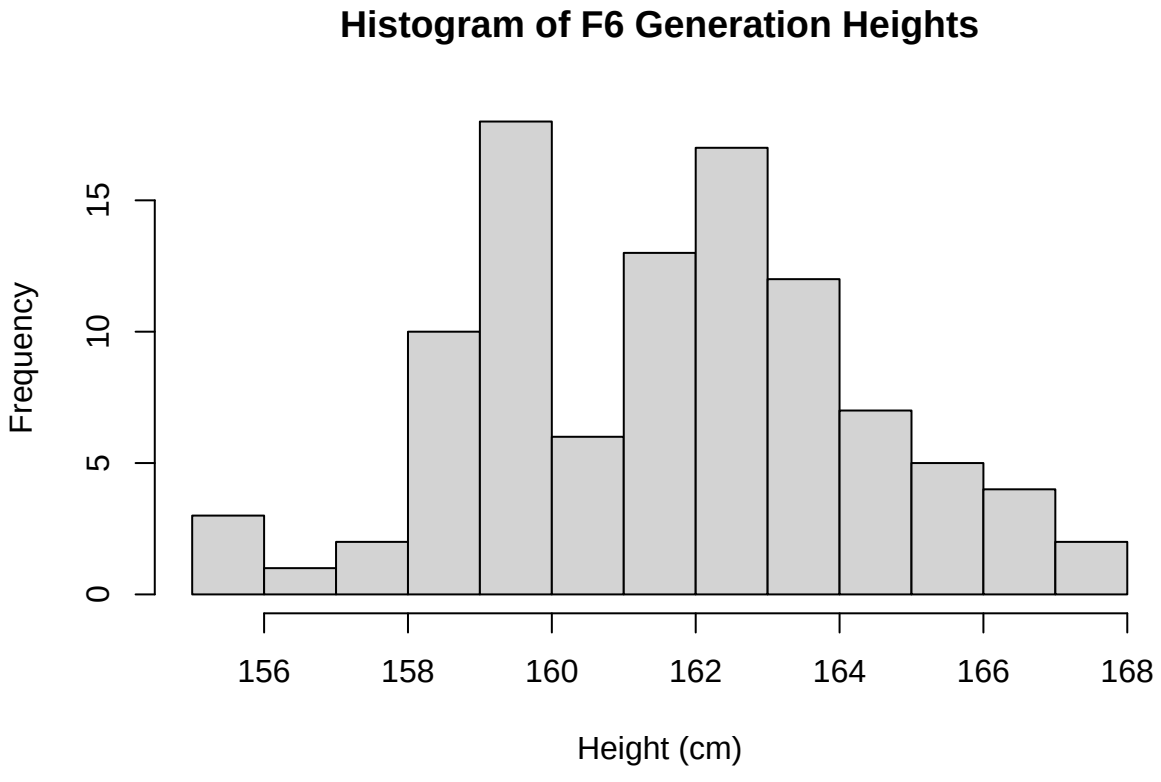

```
hist(f_gens[[5]]$m, breaks=10, main='Histogram of F4 Generation Heights', xlab='Height (cm)')
```



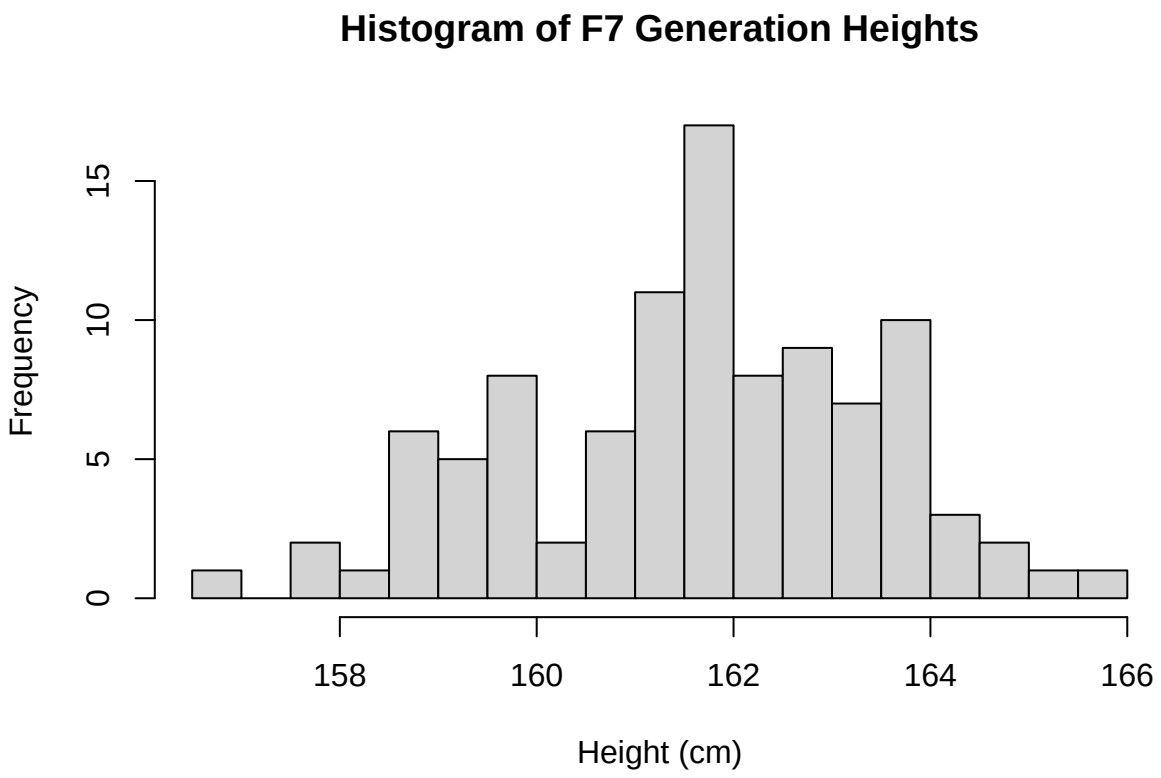

```
hist(f_gens[[6]]$m, breaks=10, main='Histogram of F5 Generation Heights', xlab='Height (cm)')
```



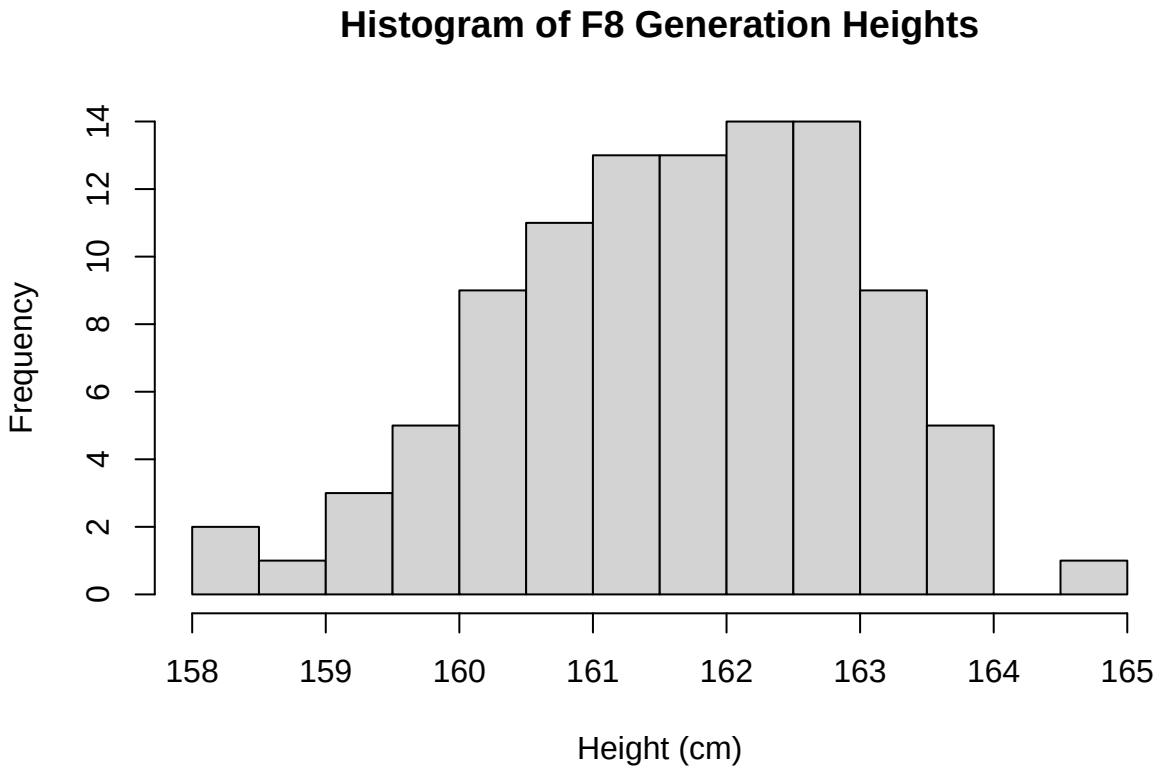

```
hist(f_gens[[7]]$m, breaks=15, main='Histogram of F6 Generation Heights', xlab='Height (cm)')
```




```
hist(f_gens[[8]]$m, breaks=13, main='Histogram of F7 Generation Heights', xlab='Height (cm)')
```




```
hist(f_gens[[9]]$m, breaks=10, main='Histogram of F8 Generation Heights', xlab='Height (cm)')
```

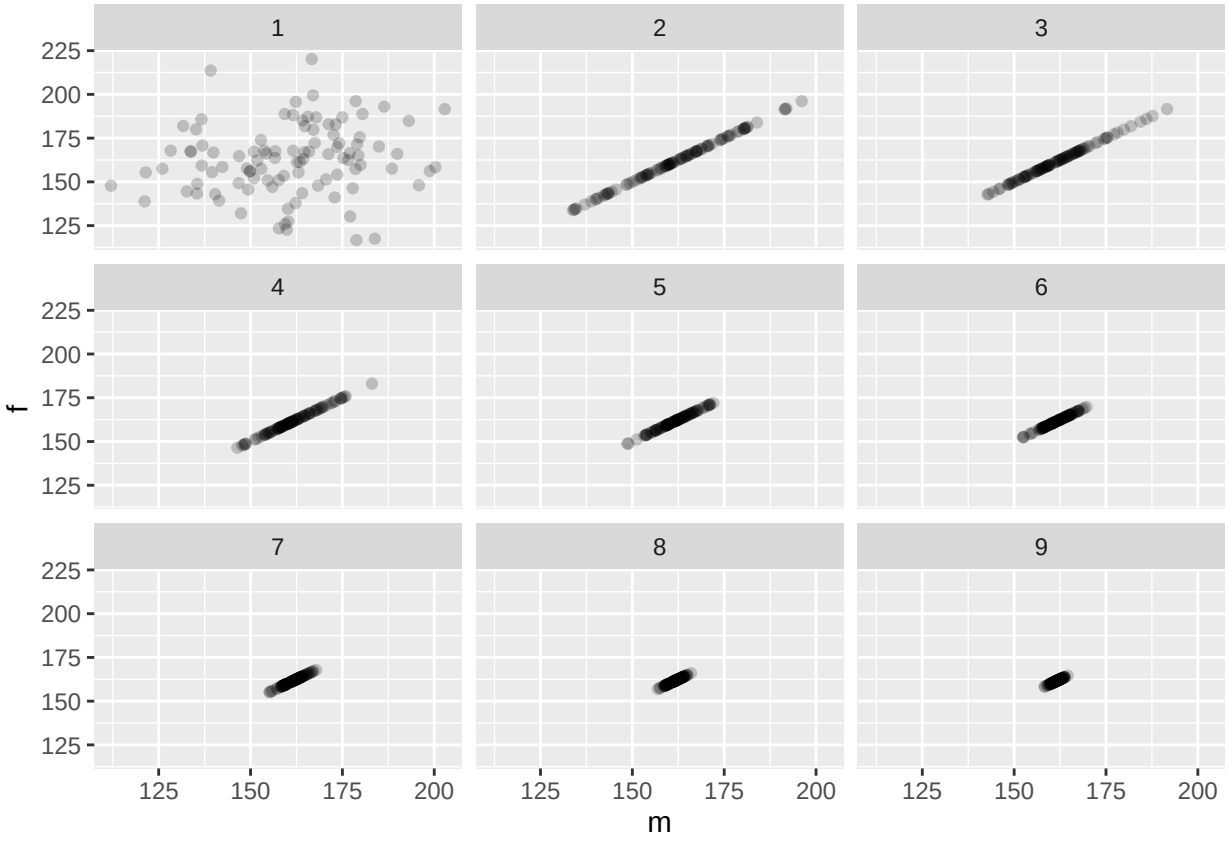


Question 2

10 points

Use the simulated results from question 1 to reproduce (as closely as possible) the following plot in ggplot2.

```
library(ggplot2)
# make a generation variable, I need everything in one dataframe
gen_count <- rep(c(seq(1, 9)), each=100)

multi_gen <- rbind(f_gens[[1]], f_gens[[2]], f_gens[[3]], f_gens[[4]], f_gens[[5]], f_gens[[6]], f_gens

total <- cbind(multi_gen, gen_count)

# scatter plot
# all 9 are displayed on 1 device, 3x3
# m along x axis, f along y axis

p = ggplot(data=total) + geom_point(mapping = aes(x=m, y=f), alpha = 0.2)
p + facet_wrap(~ gen_count)
```



Question 3

15 points

You calculated the power of a study design in question #1 of assignment 3. The study has two variables, treatment group and outcome. There are two treatment groups (0, 1) and they should be assigned randomly with equal probability. The outcome should be a random normal variable with a mean of 60 and standard deviation of 20. If a patient is in the treatment group, add 5 to the outcome.

Starting with a sample size of 250, create a 95% bootstrap percentile interval for the mean of each group. Then create a new bootstrap interval by increasing the sample size by 250 until the sample is 2500. Thus you will create a total of 10 bootstrap intervals. Each bootstrap should create 1000 bootstrap samples. (9 points)

```r
# power function from assignment 3
power <- function(sample_size) {
  mean(replicate(1000, {
  treatment <- rbinom(sample_size, 1, 0.5)
  outcome <- rnorm(sample_size, mean=60, sd=20)
  for (i in 1:sample_size) {
    if (treatment[i]==1){
      outcome[i] <- outcome[i] + 5}
    }
  t.test(outcome ~ treatment, alternative='two.sided', mu=0)$p.value
  }) < 0.05)
}

# now working on the homework problem

# another attempt at bootstrapping
sim_sample <- function (sample_size) {
  treatment <- rbinom(sample_size, 1, 0.5)
  outcome <- rnorm(sample_size, mean=60, sd=20)
      for (i in 1:sample_size) {
        if (treatment[i]==1){
          outcome[i] <- outcome[i] + 5
        }
      }
  df <- data.frame(treatment, outcome)
  df
}

boot_interval <- function(sample_size) {
  x <- sim_sample(sample_size)
  # set up the empty matrix
  bootmean <- matrix(nrow=1000, ncol=2)

  # bootstrapping
  for(i in 1:nrow(bootmean)) {
    boot.x <- x[sample(nrow(x), nrow(x), replace=TRUE),] # bootstrap sample
    controls <- boot.x[which(boot.x[,1]==as.integer(0)),][,2]
    exp <- boot.x[which(boot.x[,1]==as.integer(1)),][,2]
    bootmean[i,] <- c(mean(controls), mean(exp))
  }

  # separate the control and treatment groups, and find the mean of each
  controls <- bootmean[,1]
  exp <- bootmean[,2]
  means <- c(mean(controls), mean(exp))
  # find the 5% and 95% bootstrap intervals for the mean of each group
  control_interval <- means[1] + qnorm(c(0.05, 0.95)) * sd(controls) #/ sqrt(length(controls))
  exp_interval <- means[2] + qnorm(c(0.05, 0.95)) * sd(exp) #/ sqrt(length(exp))

  # get set up for the data frame - these will both be columns
  low_ci <- c(control_interval[1], exp_interval[1])
  high_ci <- c(control_interval[2], exp_interval[2])
  # data frame
```

```
  boot_data <- data.frame(
    means,
    low_ci, # low, rows still match up
    high_ci, # high
    rep(sample_size, 2),
    as.factor(c(0,1)) # controls first, then treatment group
  )
  names(boot_data) <- c('means', 'low_ci', 'high_ci', 'sample_size', 'treatment') # I want the names of
  boot_data
}

boot_interval(250) # yay! It works
```

```
##      means   low_ci  high_ci sample_size treatment
## 1 60.61821 58.16414 63.07228         250         0
## 2 63.55807 60.59618 66.51997         250         1
```

```
# on to running with different sample sizes!
boot_list <- seq(from=250, to=2500, by=250) # now to increase the sample size

# I originally wanted to combine these into one dataframe using a loop, but I was having trouble gettin
final <- rbind(boot_interval(250), boot_interval(500), boot_interval(750), boot_interval(1000), boot_in

final # all info in one dataframe, with a column clarifying treatment vs control
```

```
##       means   low_ci  high_ci sample_size treatment
## 1  60.79092 57.99886 63.58298         250         0
## 2  65.35693 62.34823 68.36564         250         1
## 3  58.86207 56.81408 60.91006         500         0
## 4  65.25631 63.19170 67.32091         500         1
## 5  60.41323 58.71466 62.11179         750         0
## 6  65.57532 63.97300 67.17763         750         1
## 7  61.15414 59.62587 62.68242        1000         0
## 8  65.73127 64.35333 67.10920        1000         1
## 9  61.72783 60.47388 62.98178        1250         0
## 10 65.25564 63.91463 66.59664        1250         1
## 11 59.64445 58.39162 60.89729        1500         0
## 12 63.81874 62.60547 65.03201        1500         1
## 13 60.29592 59.16402 61.42782        1750         0
## 14 64.49748 63.39462 65.60034        1750         1
## 15 60.51955 59.53366 61.50543        2000         0
## 16 64.79029 63.67525 65.90534        2000         1
## 17 60.41594 59.49348 61.33839        2250         0
## 18 65.14273 64.15801 66.12746        2250         1
## 19 60.03375 59.10943 60.95807        2500         0
## 20 64.89775 64.00796 65.78754        2500         1
```

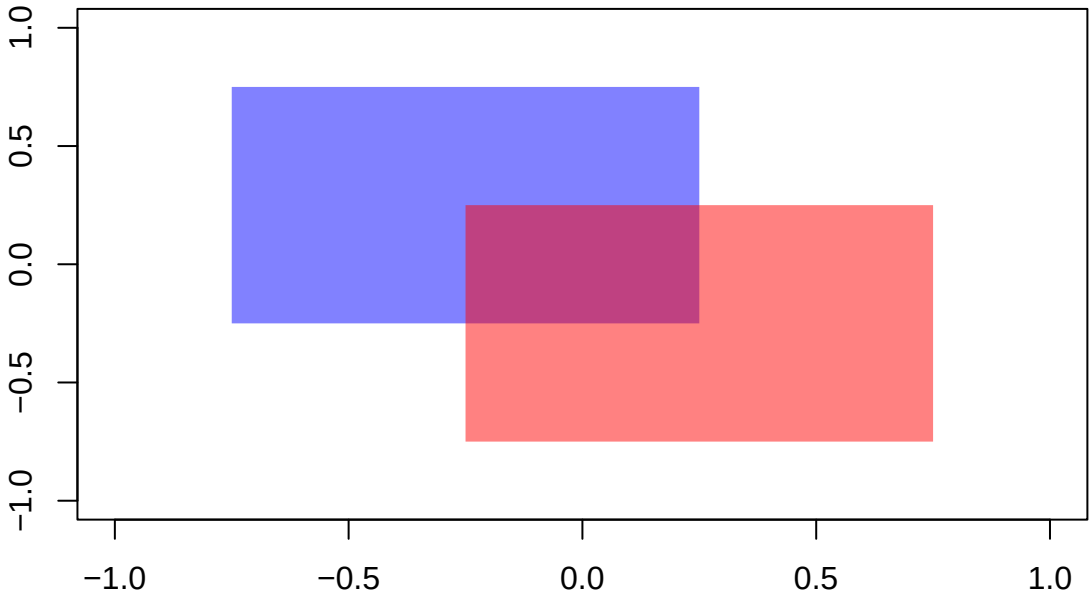
Produce a line chart that includes the bootstrapped mean and lower and upper percentile intervals for each group. Add appropriate labels and a legend. (6 points)

You may use base graphics or ggplot2. It should look similar to this (in base).

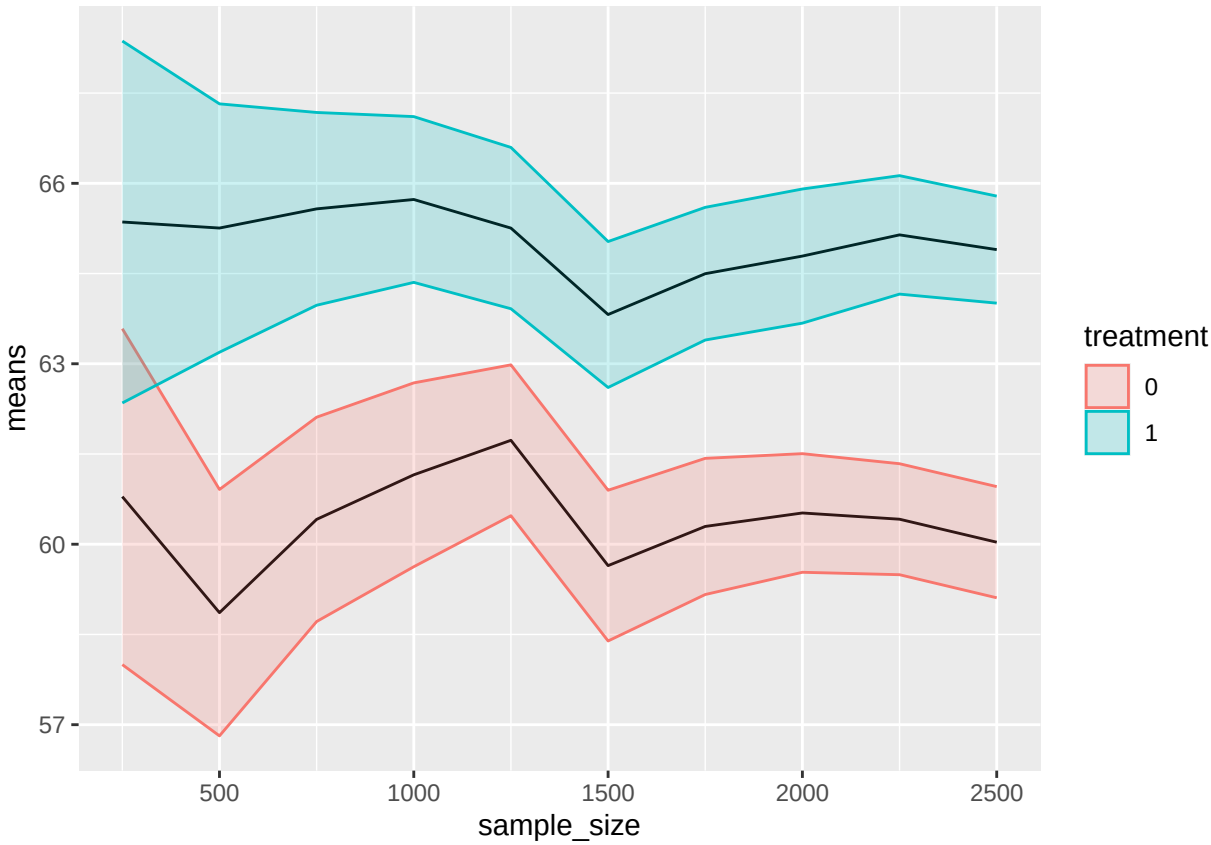
Here's an example of how you could create transparent shaded areas.

```
makeTransparent = function(..., alpha=0.5) {
  if(alpha<0 | alpha>1) stop("alpha must be between 0 and 1")
```

```
  alpha = floor(255*alpha)
  newColor = col2rgb(col=unlist(list(...)), alpha=FALSE)
  .makeTransparent = function(col, alpha) {
    rgb(red=col[1], green=col[2], blue=col[3], alpha=alpha, maxColorValue=255)
  }
  newColor = apply(newColor, 2, .makeTransparent, alpha=alpha)
  return(newColor)
}

par(new=FALSE)
plot(NULL,
  xlim=c(-1, 1),
  ylim=c(-1, 1),
  xlab="",
  ylab=""
)

polygon(x=c(seq(-0.75, 0.25, length.out=100), seq(0.25, -0.75, length.out=100)),
        y=c(rep(-0.25, 100), rep(0.75, 100)), border=NA, col=makeTransparent('blue',alpha=0.5))
polygon(x=c(seq(-0.25, 0.75, length.out=100), seq(0.75, -0.25, length.out=100)),
        y=c(rep(-0.75, 100), rep(0.25, 100)), border=NA, col=makeTransparent('red',alpha=0.5))
```




```
library(ggplot2)

ggplot(data=final, aes(x=sample_size, y=means, group=treatment, color=treatment, fill=treatment)) +
  geom_line(col="black") +
  geom_ribbon(aes(ymin=low_ci, ymax=high_ci), alpha=0.2)
```


means
66
63
60
57
500
1000
1500
2000
2500
sample_size
treatment
0
1