

Take-Home Test 1 R Work

Alex Burgos

```
1. homeruns <- read.csv("~/Downloads/hr.txt")
#a
aMean = tapply(homeruns$Distance, homeruns$Player, mean)
aMean
```

Judge	Ohtani	Ozuna	Santander	Soto
408.7500	414.2075	412.4615	395.4773	404.7500

```
aMedian = tapply(homeruns$Distance, homeruns$Player, median)
aMedian
```

Judge	Ohtani	Ozuna	Santander	Soto
407.0	415.0	413.0	400.5	409.5

```
myRange = function(homeruns){
  max(homeruns) - min(homeruns)
}
aRange = tapply(homeruns$Distance, homeruns$Player, myRange)
aRange
```

Judge	Ohtani	Ozuna	Santander	Soto
138	138	96	110	107

```
aVariance = tapply(homeruns$Distance, homeruns$Player, var)
aVariance
```

Judge	Ohtani	Ozuna	Santander	Soto
1099.7182	1022.3215	574.5182	724.3483	720.3462

```
aStdDev = tapply(homeruns$Distance, homeruns$Player, sd)
aStdDev
```

Judge	Ohtani	Ozuna	Santander	Soto
33.16200	31.97376	23.96911	26.91372	26.83927

```

cv = function(homeruns) {
  (sd(homeruns) / mean(homeruns)) * 100
}
aCV = tapply(homeruns$Distance, homeruns$Player, cv)
aCV

```

Judge	Ohtani	Ozuna	Santander	Soto
8.113027	7.719261	5.811235	6.805377	6.631072

```

aMin = tapply(homeruns$Distance, homeruns$Player, min)
aMin

```

Judge	Ohtani	Ozuna	Santander	Soto
339	338	352	332	340

```

aMax = tapply(homeruns$Distance, homeruns$Player, max)
aMax

```

Judge	Ohtani	Ozuna	Santander	Soto
477	476	448	442	447

```

# IQR
aiqr = summary(homeruns$Distance)
aQ1 = 384
aQ3 = 430
aQ3 - aQ1

```

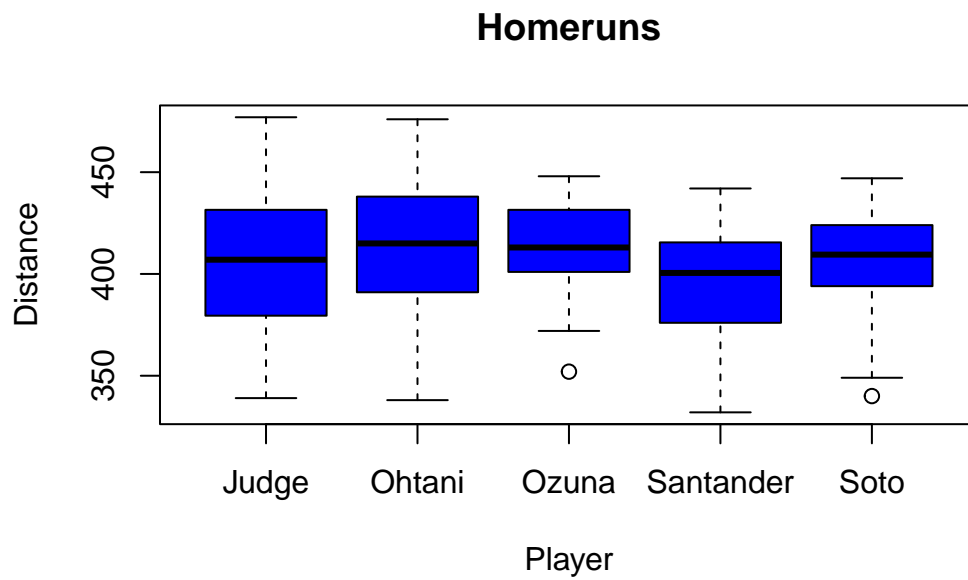
[1] 46

1b.

```

# Wrote in new lines to make it more legible in a code block.
boxplot(homeruns$Distance~homeruns$Player,
  main = "Homeruns",
  xlab = "Player",
  ylab = "Distance",
  col="blue")

```



2.

```
cholesterol <- read.csv("~/Downloads/cholesterol.txt")
```

```
# Males
```

```
mSummary = summary(cholesterol$M)
```

```
mSummary
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
73.0	173.0	200.0	201.2	227.0	373.0

```
# Females
```

```
fSummary = summary(cholesterol$F)
```

```
fSummary
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
78.0	178.0	208.0	210.7	239.0	452.0

```
mRange = max(cholesterol$M) - min(cholesterol$M)
mRange
```

```
[1] 300
```

```
fRange = max(cholesterol$F) - min(cholesterol$F)
fRange
```

```
[1] 374
```

```
mVar = var(cholesterol$M)
mVar
```

```
[1] 1620.777
```

```
fVar = var(cholesterol$F)
fVar
```

```
[1] 2156.532
```

```
mSD = sd(cholesterol$M)
mSD
```

```
[1] 40.25887
```

```
fSD = sd(cholesterol$F)
fSD
```

```
[1] 46.43847
```

```
mCV = mSD/mean(cholesterol$M) * 100
mCV
```

```
[1] 20.00532
```

```
fCV = fSD/mean(cholesterol$F) * 100  
fCV
```

```
[1] 22.0353
```

```
miqr = 227 - 173  
miqr
```

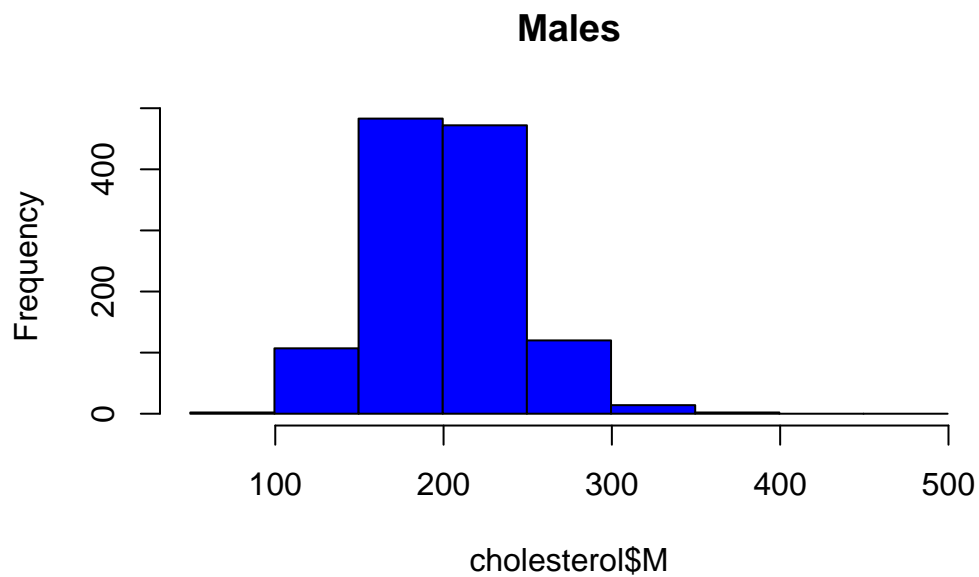
```
[1] 54
```

```
fiqr = 239 - 178  
fiqr
```

```
[1] 61
```

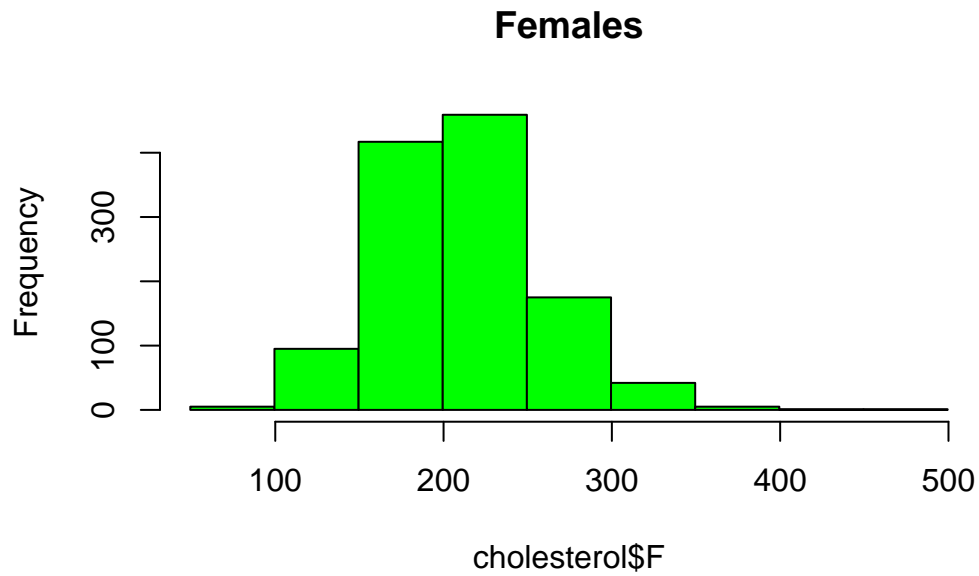
2b.

```
# Males  
hist(cholesterol$M, breaks=seq(49.5, 500, by=50), col = "blue", main = "Males", )
```



```
# Females
```

```
hist(cholesterol$F, breaks=seq(49.5, 500, 50), col = "green", main = "Females")
```



5.

```
a = dbinom(6, 10, 0.65) * 100  
a
```

```
[1] 23.76685
```

```
b = sum(dbinom(4:8, 10, 0.65)) * 100  
b
```

```
[1] 88.80213
```

6.

```
a = pnorm(11, 14, 1)
a
```

```
[1] 0.001349898
```

```
b = 1 - pnorm(18, 14, 1)
b
```

```
[1] 3.167124e-05
```

```
c = qnorm(0.05, 0, 1)
c
```

```
[1] -1.644854
```

```
d = pnorm(20, 14, 1) - pnorm(15, 14, 1)
d
```

```
[1] 0.1586553
```