Homework3

Hwasoo Shin

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Problem 3

For the analysis, we will be using tidyverse package. Within tidyverse package, we will especially use readr, dplyr, and ggplot package. In order to make better plots using ggplot, we will also import gridExtra package.

Sensory Data

```r
setwd('C:/Users/pc/Desktop/HWASOO/STUDY/StatPackage')
#Setting the path to read files.
library(tidyverse)
```

```
## Registered S3 method overwritten by 'rvest':
##   method            from
##   read_xml.response xml2

## -- Attaching packages ------------------------------------------------------------------------------

## v ggplot2 3.2.1     v purrr   0.3.2
## v tibble  2.1.1     v dplyr   0.8.3
## v tidyr   0.8.3     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.4.0

## -- Conflicts ---------------------------------------------------------------------------------------
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```r
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'

## The following object is masked from 'package:dplyr':
##
##     combine
```

```r
#We will use 'tidyverse' and 'gridExtra' package to do the analysis

Sensory<-read_table("Sensory.txt",skip=1)
```

```
## Parsed with column specification:
## cols(
##   `Item 1 2 3 4 5` = col_character()
## )
```

```
#read_table is in readr package, which is included in tidyverse package.
#Since the table we are reading has delimeters of white spaces and has one row to skip,
#we will use read_table with skip=1 option.
Sensory<-as.data.frame(Sensory)
#Change the data type into data.frame
class(Sensory)
```

```
## [1] "data.frame"
```

```
#Check the type of data. We can see it is changed to data frame.
dim(Sensory)
```

```
## [1] 30  1
```

```
#Check the dimension of data. Keep in mind that the data has only one column
SensoryName<-word(colnames(Sensory),sep=' ',1:6)
#We will fetch the names of data. We use word function to get the variables.
Sensory<-Sensory %>% separate(colnames(Sensory),SensoryName,sep=" ")
#Pipe operators (%>%). separate function will distribute the items in one column into
#multiple columns.
idx<-c(1:30)[-seq(1,30,by=3)]
#Since there are values where there isn't a item number, we will get rows without item numbers
Sensoryidx<-Sensory[idx,]
#Getting rows without item numbers
Sensory[,1]<-rep(1:10,each=3)
#Put item numbers on every row
Sensory[idx,2:6]<-Sensoryidx
#This is our modified data
#We can also make a data which columns are order of items.
Sensory2<-matrix(0,nrow=15,ncol=10)
for(i in 1:10){
Sensory2[,i]<-as.numeric(as.matrix(Sensory %>% filter(Item==i) %>% select(2:6)))
}
#We will arrange observations by item number
Sensory2Col<-paste('Item',1:10,sep='')
#Make column names for matrix Sensory2
Sensory2<-data.frame(Sensory2)
#Convert Sensory2 data type from matrix to data frame
colnames(Sensory2)<-Sensory2Col
#Give names of columns in Sensory2 data
Sensory3<-gather(Sensory,'Operator','value',-Item)
#Make it into a long data. 'gather' function helps convert wide data into long data.
head(Sensory3)
```

```
##   Item Operator value
## 1    1        1   4.3
## 2    1        1   4.3
## 3    1        1   4.1
## 4    2        1   6.0
## 5    2        1   4.9
## 6    2        1   6.0
```

```r
#We can see that the first variable indicates the number of item, and second
#indicates number of operation.
```

Through these steps we can successfully import and clean the data. We used pipe operations, dplyr, and readr package for effective data munging. Below is some syntax to help us glimpse the information implied in the data.

```r
summary(Sensory)
```

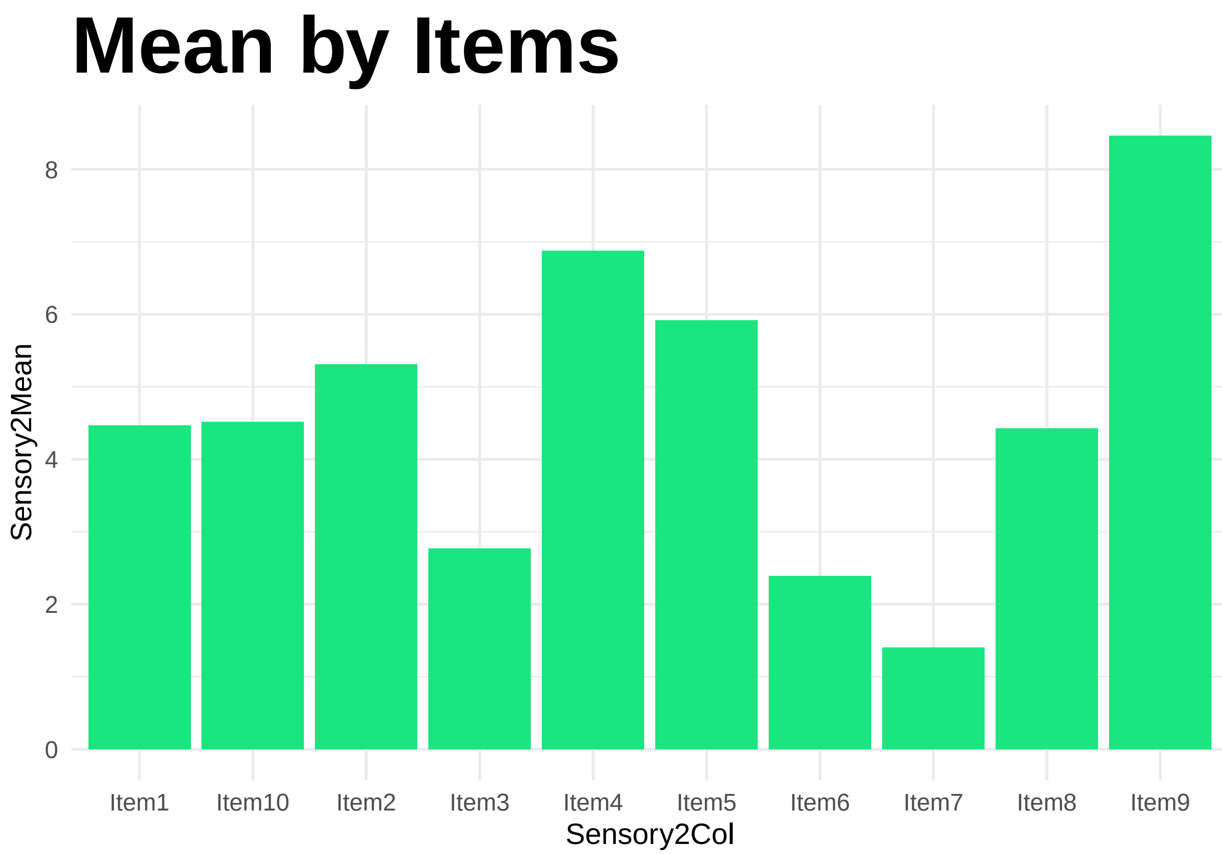
```
##       Item           1                  2                  3            
##  Min.   : 1.0   Length:30          Length:30          Length:30         
##  1st Qu.: 3.0   Class :character   Class :character   Class :character  
##  Median : 5.5   Mode  :character   Mode  :character   Mode  :character  
##  Mean   : 5.5                                                           
##  3rd Qu.: 8.0                                                           
##  Max.   :10.0                                                           
##       4                  5            
##  Length:30          Length:30         
##  Class :character   Class :character  
##  Mode  :character   Mode  :character  
##                                       
##                                       
## 
```

```r
#Summary of the first data file.
summary(Sensory2)
```

```
##      Item1           Item2           Item3           Item4     
##  Min.   :3.300   Min.   :4.200   Min.   :1.300   Min.   :5.90  
##  1st Qu.:4.050   1st Qu.:4.700   1st Qu.:2.350   1st Qu.:6.40  
##  Median :4.400   Median :5.300   Median :2.600   Median :6.90  
##  Mean   :4.467   Mean   :5.313   Mean   :2.773   Mean   :6.88  
##  3rd Qu.:5.100   3rd Qu.:5.950   3rd Qu.:3.050   3rd Qu.:7.20  
##  Max.   :5.700   Max.   :6.300   Max.   :4.600   Max.   :8.20  
##      Item5          Item6           Item7           Item8      
##  Min.   :4.90   Min.   :1.100   Min.   :0.700   Min.   :3.000  
##  1st Qu.:5.70   1st Qu.:1.750   1st Qu.:1.000   1st Qu.:4.400  
##  Median :5.90   Median :2.100   Median :1.200   Median :4.600  
##  Mean   :5.92   Mean   :2.393   Mean   :1.407   Mean   :4.427  
##  3rd Qu.:6.15   3rd Qu.:3.150   3rd Qu.:1.550   3rd Qu.:4.800  
##  Max.   :7.00   Max.   :4.000   Max.   :3.100   Max.   :4.900  
##      Item9           Item10     
##  Min.   :6.700   Min.   :2.80  
##  1st Qu.:7.950   1st Qu.:3.90  
##  Median :8.800   Median :4.80  
##  Mean   :8.467   Mean   :4.52  
##  3rd Qu.:9.000   3rd Qu.:5.10  
##  Max.   :9.400   Max.   :5.50
```

```r
#Summary of the second data file.
Sensory2Mean<-apply(Sensory2,2,mean)
#Mean by items.
```

```r
SensoryM<-data.frame(Sensory2Col,Sensory2Mean)
#Make two columns into variables into data frame
ggplot(SensoryM,aes(x=Sensory2Col,y=Sensory2Mean))+geom_bar(fill=rgb(0.1,0.9,0.5),
stat = "identity")+ ggtitle('Mean by Items')+
theme_minimal()+theme(plot.title = element_text(size=30,face="bold"))
```




```r
#Make a bar plot with the means by item. We can see that the Item9 has the biggest mean
#and Item7 has the smallet mean.
```

By modifiying the data we are able to see some information in each item. In this barplot, Item9 has the biggest mean and Item7 has the smallet mean.

Long Jump Data

We can similarly follow the steps as above;

```r
##### Long Jump Data #####

LongJump<-read_table('https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/LongJumpData.dat',skip=1)
```

```
## Parsed with column specification:
## cols(
##   `-4 249.75 24 293.13 56 308.25 80 336.25` = col_character()
## )
```

```r
#Read the file from url
LongJump<-as.data.frame(LongJump)
#Convert the type of data into data frame
dim(LongJump)
```

```
## [1] 5 1
```

```r
#We can see that the LongJump data only has 5 rows and one column. We will combine columns
#into Year and Long_Jump columns.
LongJump<-LongJump %>% separate(colnames(LongJump),LETTERS[1:8],sep=" ")
#Separate items into 8 arbitary columns
Year<-Long_Jump<-numeric()
#Make empty vectors of Year and Long_Jump
for(i in 1:4){
Year<-c(Year,LongJump[,2*i-1])
Long_Jump<-c(Long_Jump,LongJump[,2*i])
}
#Put multiple columns into each column
Year<-as.numeric(Year);Long_Jump<-as.numeric(Long_Jump)
#Convert each variable into numeric ones
Year<-Year+1900
#Since 0 means year 1900, we will add 1900 for each value
LongJump<-data.frame(Year,Long_Jump)
#Make it into a data frame
tail(LongJump)
```

```
##    Year Long_Jump
## 15 1976    328.50
## 16 1984    336.25
## 17 1988    343.25
## 18 1992    342.50
## 19   NA        NA
## 20   NA        NA
```

```r
#We can see that there are NAs in last two rows.
LongJump<-LongJump[-c(19,20),]
#Remove last two rows
```

Through these steps we can import and clean the data. Unlike the first data, this data had repeated columns. So we can first assign these repeating columns as independent columns at first, and then merge the columns that should belong the same variable.

Following is some syntax to finish our analysis.

```r
summary(lm(data=LongJump,Long_Jump~Year))
```

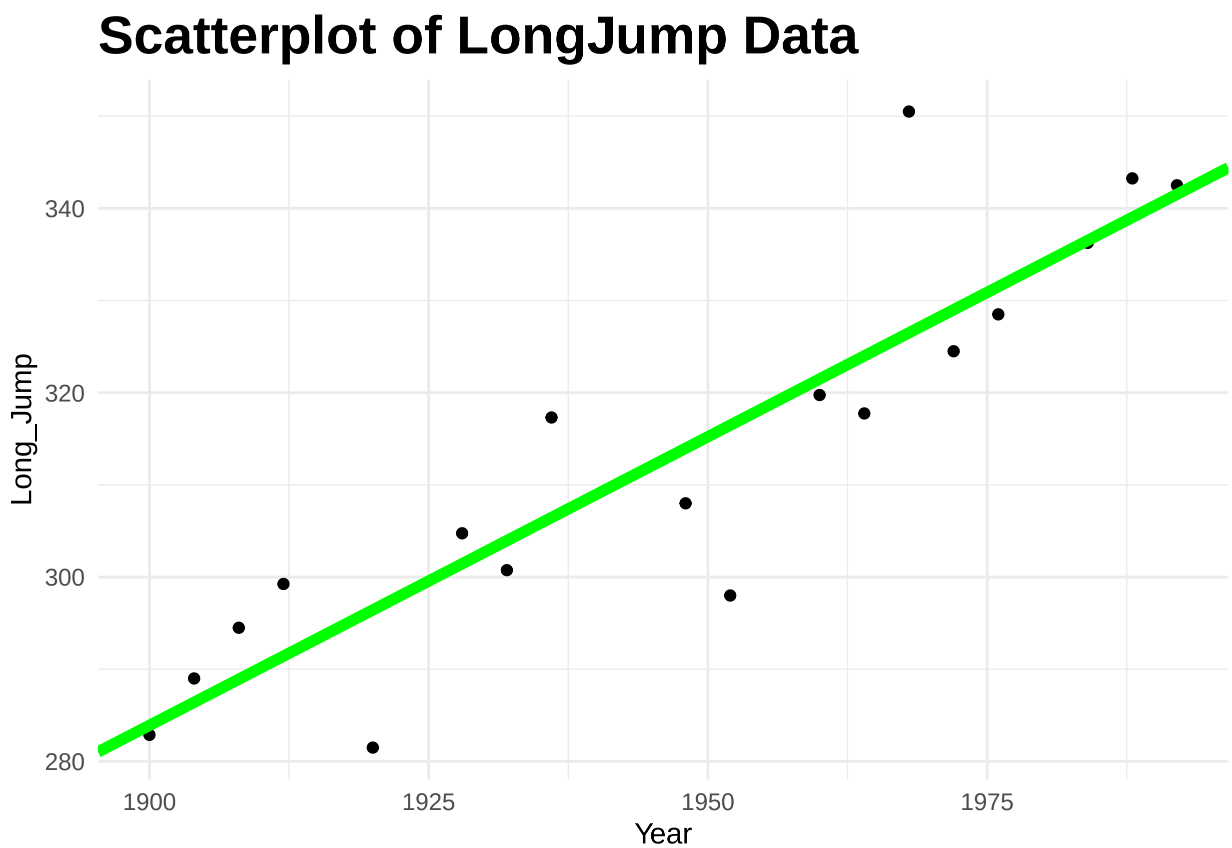
```
##
## Call:
## lm(formula = Long_Jump ~ Year, data = LongJump)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -18.4752  -4.1751  -0.6478   3.9988  24.0050
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -905.9381   150.7102  -6.011 1.81e-05 ***
## Year           0.6262     0.0774   8.091 4.79e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.7 on 16 degrees of freedom
## Multiple R-squared:  0.8036, Adjusted R-squared:  0.7913
## F-statistic: 65.46 on 1 and 16 DF,  p-value: 4.789e-07
```

```
#Summary of linear model in LongJump data. The independent variable will be Year and the
#target variable will be Long_Jump.We can see that the slope will be 0.6262. Since the
#p-value is both smaller than 0.05, we can say that the coefficients are significant under
#significane level 0.05.
cor(LongJump$Long_Jump,LongJump$Year)
```

```
## [1] 0.8964282
```

```
#Correlation between Long_Jump and Year variable. It is highly correlated, which is, it is
#likely the data are algined in a line.
LMLongJump<-lm(data=LongJump,Long_Jump~Year)
#Assign the information about linear model of LongJump
ggplot(LongJump,aes(x=Year,y=Long_Jump))+geom_point()+ggtitle('Scatterplot of LongJump Data')+
geom_abline(slope=LMLongJump$coefficients[2],intercept=LMLongJump$coefficients[1],color='green',size=2)+
theme_minimal()+theme(plot.title = element_text(size=20,face="bold"))
```




```
#We can see that the points are on ascending order, which is, those two variables are in a
#positive relationship.
```

Since we had only two continuous variables for this data, we can use scatterplot to see the general relationship of the data. The points are aligned in a line, which we can assume that those two variables will have high correlation.

Brain Body Data

As previous data, the columns are repeated. We can go similar steps as we have just before done on the data.

```
BrainBody<-read_table('https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/BrainandBodyWeight.dat',
                      skip=1,col_names=F)
```

```
## Parsed with column specification:
## cols(
##   X1 = col_character()
## )
```

```
#Read data from Internet. For convenience, we will remove the first row and don't get the
#column names.
BrainBody<-as.data.frame(BrainBody)
#Convert format of the read data into data.frame
```

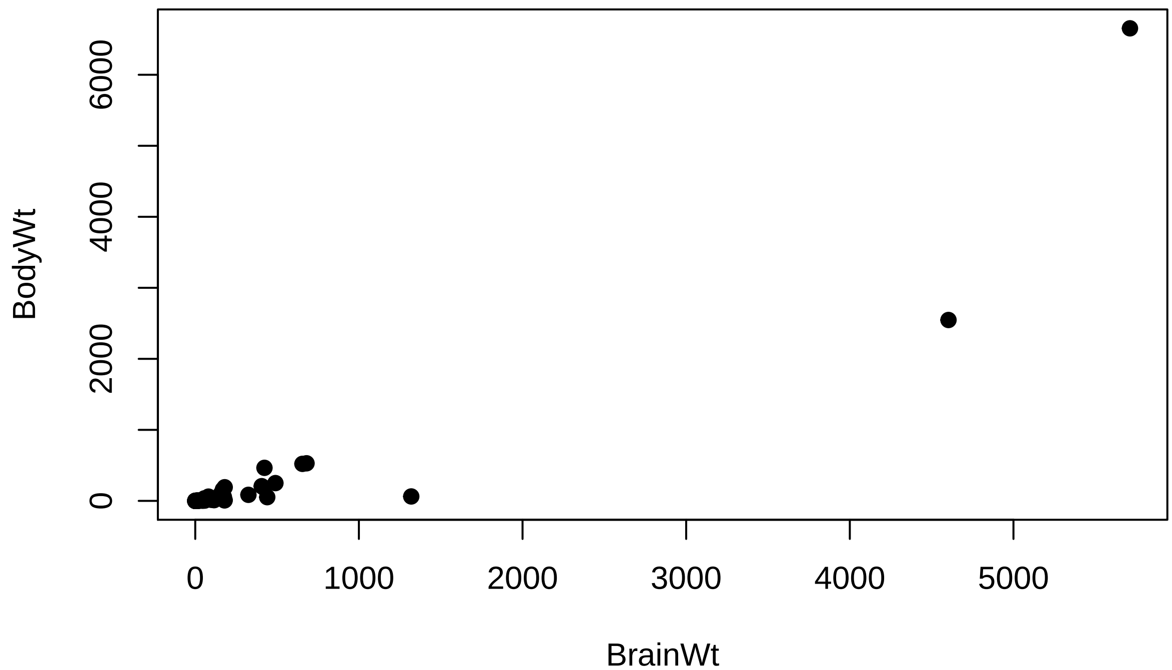
```r
BrainBody<-BrainBody %>% separate(colnames(BrainBody),LETTERS[1:6],sep=' ')
#Separate items into individual row. We will combine the variables into BrainWt and BodyWt
#variables.
BrainWt<-BodyWt<-numeric()
for(i in 1:3){
BodyWt<-c(BodyWt,BrainBody[,2*i-1])
BrainWt<-c(BrainWt,BrainBody[,2*i])
}
#We will put the geneated variables into two variables
BodyWt<-as.numeric(BodyWt);BrainWt<-as.numeric(BrainWt)
#Make the two variable types to numeric vectors
BrainBody<-data.frame(BodyWt,BrainWt)
#Put the variables into data frame
tail(BrainBody)
```

```
##     BodyWt BrainWt
## 58 160.000   169.0
## 59   0.900     2.6
## 60   1.620    11.4
## 61   0.104     2.5
## 62   4.235    50.4
## 63      NA      NA
```

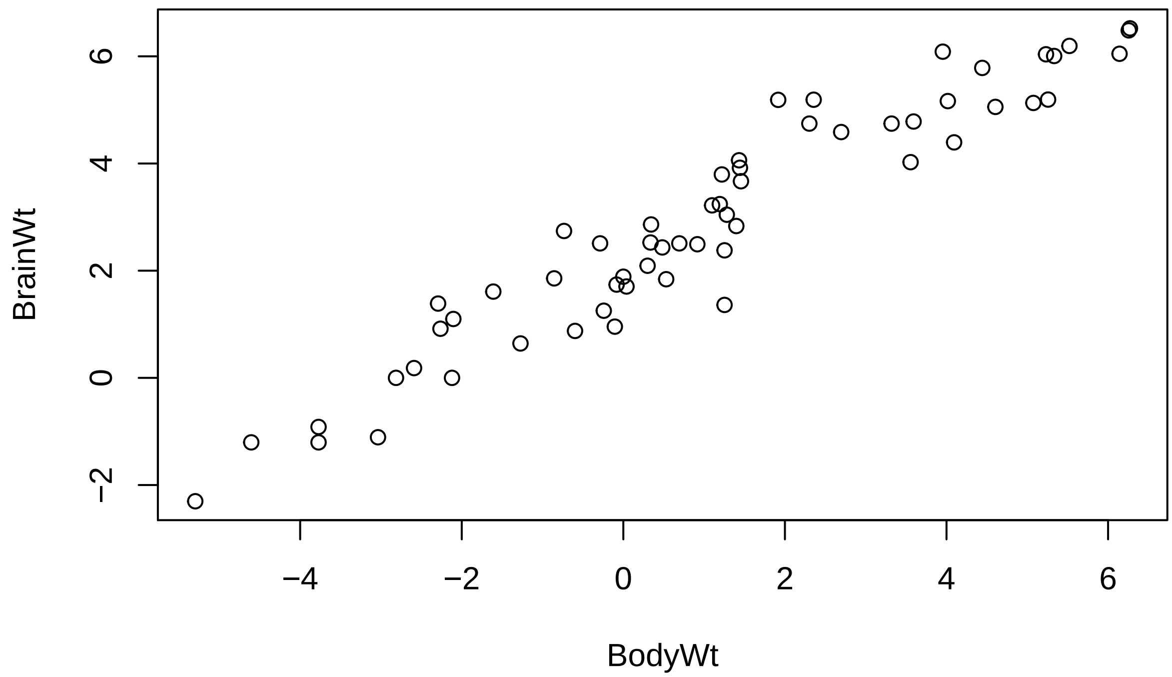
```r
#We can check that there are NA values on the last row.
BrainBody<-BrainBody[-63,]
#Remove the last row of the data frame
```

Through these steps we are able to import the data.

```r
plot(data=BrainBody,BodyWt~BrainWt,pch=19)
```




```r
#The scatter plot of Brain Weight and Body Weight. It is hard to see how the variables are related
#because of some extreme values. For analysis, we will only select values that are smaller than 1000
#for each variable.
BrainBody2<-BrainBody %>% filter(BrainWt<1000&BodyWt<1000)
BrainBody2<-log(BrainBody2)
#Since the data has large numbers with very small numbers, we will put log on our data
plot(BrainBody2)
```

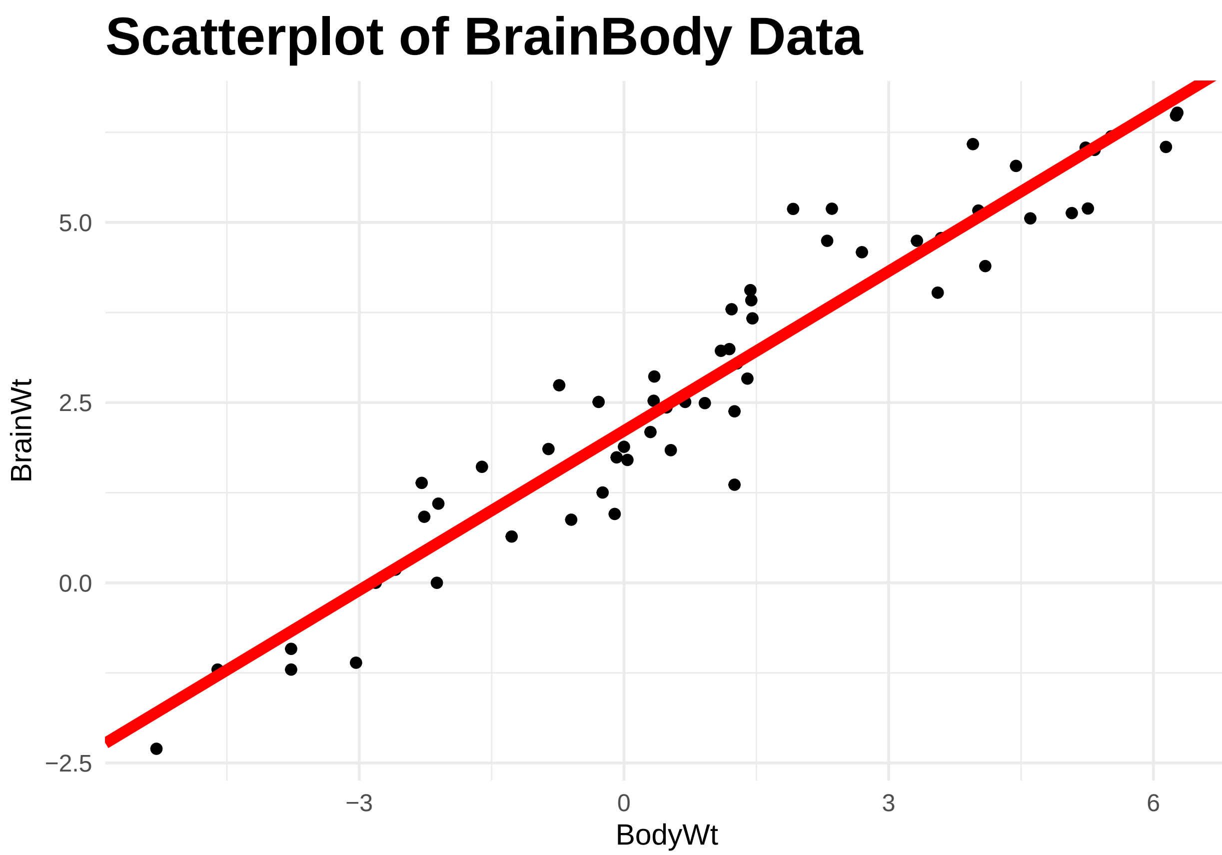



```r
#Since the extreme data are now modified, we can see the relationship between variables more clearly
summary(lm(data=BrainBody2,BrainWt~BodyWt))
```

```
##
## Call:
## lm(formula = BrainWt ~ BodyWt, data = BrainBody2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.67191 -0.51590 -0.03111  0.48139  1.66464
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.10890    0.09179   22.97   <2e-16 ***
## BodyWt       0.73756    0.03007   24.53   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6618 on 57 degrees of freedom
## Multiple R-squared:  0.9135, Adjusted R-squared:  0.9119
## F-statistic: 601.7 on 1 and 57 DF,  p-value: < 2.2e-16
```

```r
#This is the summary of simple linear model of the modified data.
#We can see that the p-value for both coefficients are all smaller than 0.05. Therefore, we can conclud
#that the both coefficients are significant under significance level 0.05.
```

```
LMBrainBody2<-lm(data=BrainBody2,BrainWt~BodyWt)
#Assign the information about linear model of BrainBody2
ggplot(BrainBody2,aes(x=BodyWt,y=BrainWt))+geom_point()+ggtitle('Scatterplot of BrainBody Data')+
geom_abline(slope=LMBrainBody2$coefficients[2],intercept=LMBrainBody2$coefficients[1],
            color='red',size=2)+
  theme_minimal()+theme(plot.title = element_text(size=20,face="bold"))
```




```
#We can see that the points are on ascending order, which is, those two variables are in a
#positive relationship.
```

We can see that the data is positively related as the previous data. But we have to keep in mind that there are some extreme values, which are too small or large compared to some other values. To successfully do the analysis we had to remove some data points and use logarithms to deal with some rest of the extreme values. We can see the variables with logarithms are usually distributed in a line. Therefore, we can conclude that log(Long_Jump) and log(Year) are highly correlated.

Tomato data

Unlike the data we have seen on the other steps, there are multiple observations in one cell in tomato data. We first have to separate these repeated measurements into respective entries in matrix. Then, we will use each tomato brand as our variables.

```r
Tomato<-read_table('https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/tomato.dat',
                   skip=1,col_names=F)
```

```
## Parsed with column specification:
## cols(
##   X1 = col_character(),
##   X2 = col_character(),
##   X3 = col_character(),
##   X4 = col_character()
## )
```

```r
#Since the first row will be the message we will read the data from the second line.
#Also, to assign variables on our own we will not put column names at first.
Tomato<-data.frame(Tomato)
#Convert the data type into data.frame
Tomato2<-Tomato[2:3,2:4]
#Tomato2 is a data frame with observations only.
Tomato3<-matrix(0,nrow=2,ncol=9)
#Make an empty matrix to put values in Tomato2
for(j in 1:2){
for(i in 1:3){
Tomato3[j,c(3*i-2,3*i-1,3*i)]<-word(Tomato2[j,i],1:3,sep=',')
#Extract each observations into a matrix
}
}
Ife<-Tomato3[1,];PursaEarlyDwarf<-Tomato3[2,]
#Extract the rows to make columns, which will be the name of brand
Ife<-as.numeric(Ife);PursaEarlyDwarf<-as.numeric(PursaEarlyDwarf)
#Change the variable types to numeric variables
Tomato<-data.frame(Ife,PursaEarlyDwarf)
#Put two variables together to make a data.frame
TomatoRow<-paste(rep(c('10k','20k','30k'),each=3),'_',rep(1:3,3),sep='')
#Making row names for data frame 'Tomato'
rownames(Tomato)<-TomatoRow
#Put row names to the data
Operator<-rep(c('10k','20k','30k'),each=3)
Tomato<-data.frame(Tomato,Operator)
#Put the Operator value into the data frame
TomatoL<-gather(Tomato,'Brand','Value',-Operator)
#Make a narrow data
head(TomatoL)
```

```
##   Operator Brand Value
## 1      10k   Ife  16.1
## 2      10k   Ife  15.3
## 3      10k   Ife  17.5
## 4      20k   Ife  16.6
## 5      20k   Ife  19.2
## 6      20k   Ife  18.5
```

```r
#We can see that the data is transformed into a 'narrow' data
```

We can consider rows as columns in our raw data with each 3 trial. The names of rows will be '(Raw data column)_(trial number)', and columns will be each tomato brand.

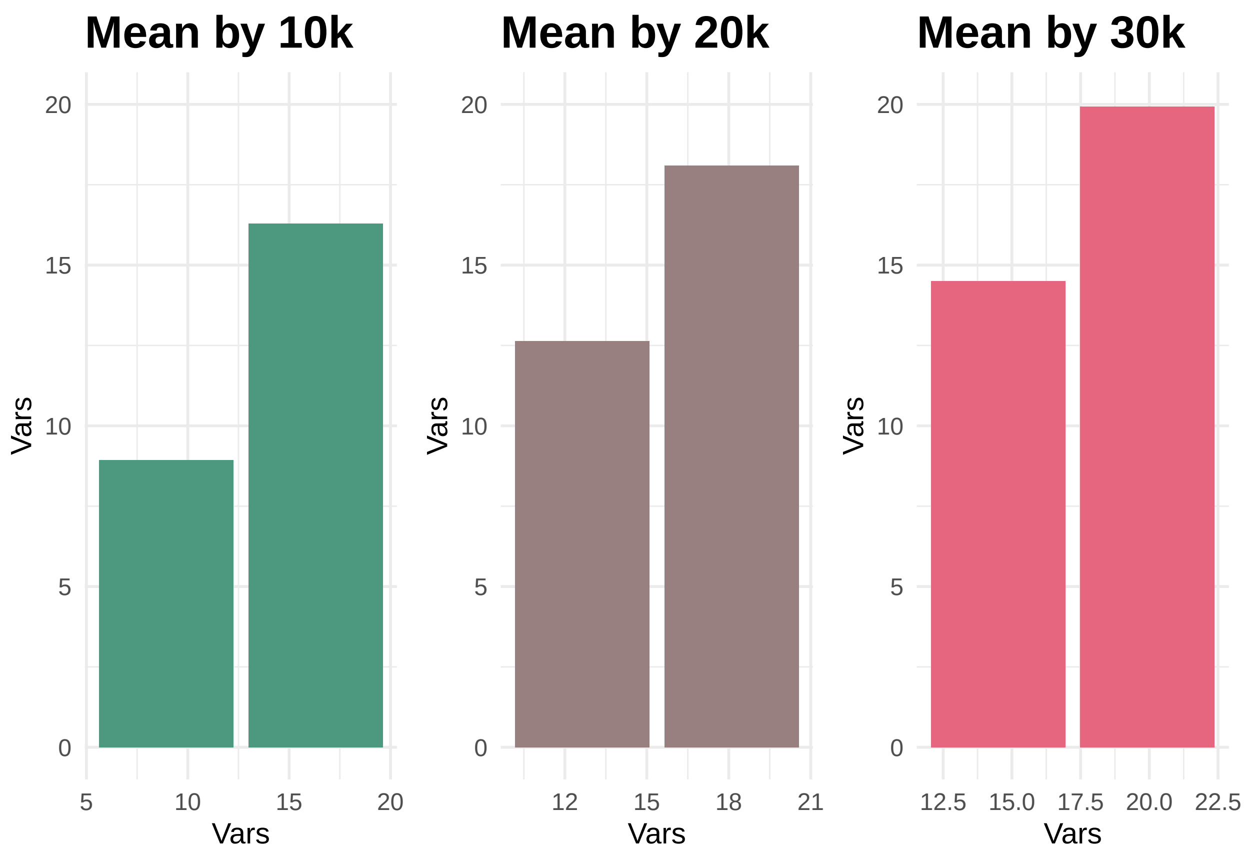
```
summary(Tomato)
```

```
##       Ife        PursaEarlyDwarf Operator
##  Min.   :15.30   Min.   : 8.10   10k:3
##  1st Qu.:16.60   1st Qu.:10.10   20k:3
##  Median :18.00   Median :12.70   30k:3
##  Mean   :18.11   Mean   :12.02
##  3rd Qu.:19.20   3rd Qu.:13.70
##  Max.   :21.00   Max.   :15.40
```

```
#Basic summary of variables in Tomato
t1<-Tomato[1:3,] %>% summarise(Ife_Mean=mean(Ife),Pursa_Mean=mean(PursaEarlyDwarf))
#Getting the mean of each brand from the first variable in our raw data.
t1<-data.frame(TName=c('Ife','Tomato'),Vars=as.numeric(as.matrix(t1)))
#Making into a 'ggplot's barplot-firendly' data frame. The first column will be the names of
#brand and second column will be the mean of each variable.
#We will keep making these kinds of data frames on following process.
t2<-Tomato[4:6,] %>% summarise(Ife_Mean=mean(Ife),Pursa_Mean=mean(PursaEarlyDwarf))
t2<-data.frame(TName=c('Ife','Tomato'),Vars=as.numeric(as.matrix(t2)))
t3<-Tomato[7:9,] %>% summarise(Ife_Mean=mean(Ife),Pursa_Mean=mean(PursaEarlyDwarf))
t3<-data.frame(TName=c('Ife','Tomato'),Vars=as.numeric(as.matrix(t3)))

p1<-ggplot(t1,aes(x=Vars,y=Vars))+geom_bar(fill=rgb(0.3,0.6,0.5), stat = "identity")+
  ggtitle('Mean by 10k')+
theme_minimal()+theme(plot.title = element_text(size=17,face="bold"))+ylim(0,20)
#Make the data frame we made above into a ggplot barplot. This one will show the means
#in 10k variable.
#We will take the same process on other data frames as well.
p2<-ggplot(t2,aes(x=Vars,y=Vars))+geom_bar(fill=rgb(0.6,0.5,0.5), stat = "identity")+
  ggtitle('Mean by 20k')+
theme_minimal()+theme(plot.title = element_text(size=17,face="bold"))+ylim(0,20)
p3<-ggplot(t3,aes(x=Vars,y=Vars))+geom_bar(fill=rgb(0.9,0.4,0.5), stat = "identity")+
  ggtitle('Mean by 30k')+
theme_minimal()+theme(plot.title = element_text(size=17,face="bold"))+ylim(0,20)

grid.arrange(p1,p2,p3,layout_matrix=rbind(c(1,2,3))) #Put the bar plots in one window.
```




```
#From the graph, we can learn that the bars get slightly higher for each trial groups. Also,
#PursaEarlyDwarf brand has higher observation values than Ife brand.
```

Considering the variables in the raw data and each trials, we used the means by trials as the y-value for the barplot. From '10000', '20000', and '30000' variables in the raw data the values became larger. Also, Pursa Early Dwarf brand had larger values on observations than the ones form Ife brand.