HW2_jaeyounglee

Jaeyoung Lee

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Problem 3

First of all, it is to handle a mistake. Also, one can handle various versions of a code and see the history of a code. Furthermore, using version control, it is easy to collaborate with others. This is because one can share a code and work on the cloud such as GitHub.

Problem 4

a. Sensory data from five operators. http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/Sensory.dat

```
######## Sensory data ########
# Getting "https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/Sensory.dat"
url_sensory <- "https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/Sensory.dat"
sensory_rawdata <- fread(url_sensory, fill = TRUE, skip = 2, data.table = FALSE)
saveRDS(sensory_rawdata, 'sensory_rawdata.RDS')
sensory_rawdata <- readRDS('sensory_rawdata.RDS')
```

There are missing values in the raw data and the categories "Items" are in the data like oberservations. We need to remove missing values and extract the 'Item' numbers from the data.

```
# Using base R function only
# Convert data.frame to matrix and transpose the raw data
matrix_sensory <- t(as.matrix(sensory_rawdata))

# Find where the missing values are
na <- which(is.na(matrix_sensory==TRUE))

# The indexes where Item numbers are in the data
x <- 1
item <- x
for (i in 1:9){
  x <- x+18
  item <- c(item, x)
}

# Remove missing values and 'Item's from the data
Values <- matrix_sensory[-c(na,item)]

# Combine the values with 'Item' and 'Operator' columns
Item <- rep(paste('Item', 1:10), each = 15)   # Item names
Opr <- rep(paste('Opr', 1:5), 30)             # Operator names
sensory_data_base <- data.table(Item, Opr, Values)
```

```r
# Final tidy data with base R functions
head(sensory_data_base)
```

```
##      Item   Opr Values
## 1: Item 1 Opr 1    4.3
## 2: Item 1 Opr 2    4.9
## 3: Item 1 Opr 3    3.3
## 4: Item 1 Opr 4    5.3
## 5: Item 1 Opr 5    4.4
## 6: Item 1 Opr 1    4.3
```

Above is the converted tidy data frames using the base R functions only. A summary of the data is as follows:

Item	Opr	Values
Length:150	Length:150	Min. :0.700
Class :character	Class :character	1st Qu.:3.025
Mode :character	Mode :character	Median :4.700
NA	NA	Mean :4.657
NA	NA	3rd Qu.:6.000
NA	NA	Max. :9.400

Now, handle the same data with `tidyverse` package.

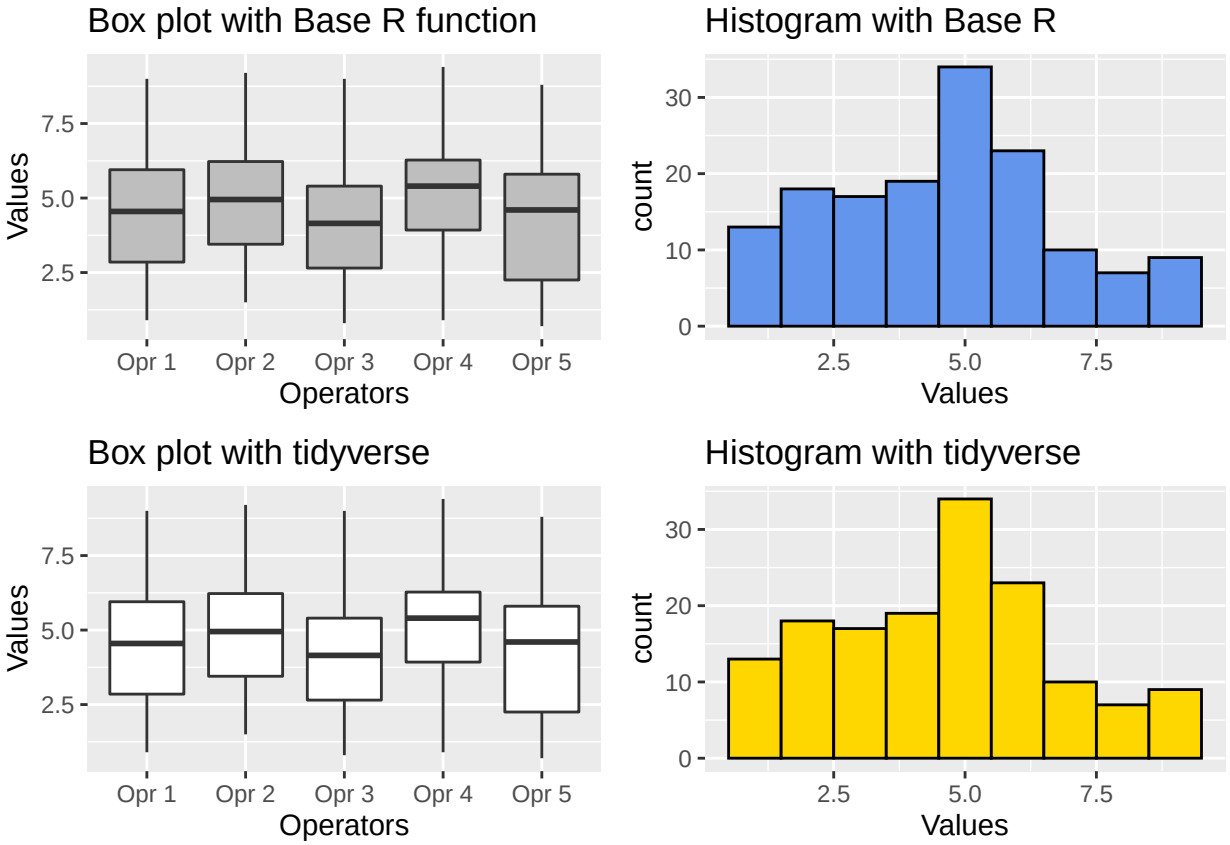
```
# Sensory data with tidyverse package
# Making matrix which is the same with base R function but using pipes.
matrix_sensory <- sensory_rawdata %>% as.matrix() %>% t()
na <- is.na(matrix_sensory==TRUE) %>% which()     # Find missing values

# The indexes where Item numbers are in the data
x <- 1
item <- x
for (i in 1:9){
  x <- x+18
  item <- c(item, x)
}

# Remove missing values and Item numbers from the data
Values <- matrix_sensory[-c(na,item)]

# Bind the values with 'Item' and 'Operator' columns
Item <- paste('Item', 1:10) %>% rep(each = 15)    # Item names
Opr <- paste('Opr', 1:5) %>% rep(30)              # Operator names
sensory_data_tidyverse <- data.table(Item, Opr, Values)

# Final tidy data with tidyverse
sensory_data_tidyverse %>% head()
```

```
##      Item   Opr Values
## 1: Item 1 Opr 1    4.3
## 2: Item 1 Opr 2    4.9
## 3: Item 1 Opr 3    3.3
## 4: Item 1 Opr 4    5.3
## 5: Item 1 Opr 5    4.4
## 6: Item 1 Opr 1    4.3
```

The result by tidyverse is the same with the base R function. The summary of the data converted by tidyverse is as follows.

Item	Opr	Values
Length:150	Length:150	Min. :0.700
Class :character	Class :character	1st Qu.:3.025
Mode :character	Mode :character	Median :4.700
NA	NA	Mean :4.657
NA	NA	3rd Qu.:6.000
NA	NA	Max. :9.400

Here are box plots and histograms of the sensory data using both base R functions and tidyverse.



b. Gold Medal performance for Olympic Men's Long Jump, year is coded as 1900=0. http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/LongJumpData.dat

```
######## Long Jump data ########
# Getting "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/LongJumpData.dat"
url_medal <- "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/LongJumpData.dat"
medal_rawdata <- fread(url_medal)
```

```
## Warning in fread(url_medal): Detected 12 column names but the data has 8
## columns. Filling rows automatically. Set fill=TRUE explicitly to avoid this
## warning.
```

```
saveRDS(medal_rawdata, 'medal_rawdata.RDS')
medal_rawdata <- readRDS('medal_rawdata.RDS')
```

The raw data has missing values and wide type data. It is better to reshape the data. Also, we need two vectors : 'Year' and 'Long Jump'.

```
# Using base R function only
# Year is coded as 1900 = 0
# Extract Year and Long Jump vectors
year <- c(medal_rawdata[[1]], medal_rawdata[[3]],
          medal_rawdata[[5]], medal_rawdata[[7]]) + 1900
longjump <- c(medal_rawdata[[2]], medal_rawdata[[4]],
              medal_rawdata[[6]], medal_rawdata[[8]])

# Bind the vectors as a data table and rename the categories
medal_data <- data.table(year[1:(length(year)-2)],
                         longjump[1:(length(longjump)-2)])
colnames(medal_data) <- c('Year', 'LongJump')
medal_data_base <- medal_data

# Final tidy data with base R functions
head(medal_data_base)
```

```
##    Year LongJump
## 1: 1896   249.75
## 2: 1900   282.88
## 3: 1904   289.00
## 4: 1908   294.50
## 5: 1912   299.25
## 6: 1920   281.50
```

Above is the converted tidy data frames using the base R functions. A summary of the data is as follows:

Year	LongJump
Min. :1896	Min. :249.8
1st Qu.:1921	1st Qu.:295.4
Median :1950	Median :308.1
Mean :1945	Mean :310.3
3rd Qu.:1971	3rd Qu.:327.5
Max. :1992	Max. :350.5

Now, handle the same data with `tidyverse` package.

```
# Using tidyverse package
# Year is coded as 1900 = 0
medal_data <- medal_rawdata[,1:8] # remove missing values only columns

# Extracting 'Year' columns and 'Long Jump' columns and remove missing values
colnames(medal_data) <- paste(rep(c('Year', 'Jump'),4), rep(1:4,each = 2))
year <- medal_data[,c(1,3,5,7)] %>%
  gather(key = 'name1', value = 'Year', 1,2,3,4) %>% filter(Year != na)
```

```
## Warning in Year != na: longer object length is not a multiple of shorter object
## length
```

```
year[,2] <- year[,2] + 1900
jump <- medal_data[,c(2,4,6,8)] %>%
  gather(key = 'name2', value = 'LongJump', 1,2,3,4) %>% filter(LongJump != na)
```

```
## Warning in LongJump != na: longer object length is not a multiple of shorter
## object length
```

```
# Bind the vectors as a data table and rename the categories
medal_data <- bind_cols(year[,2], jump[,2])
```

```
## New names:
## * NA -> ...1
## * NA -> ...2
```

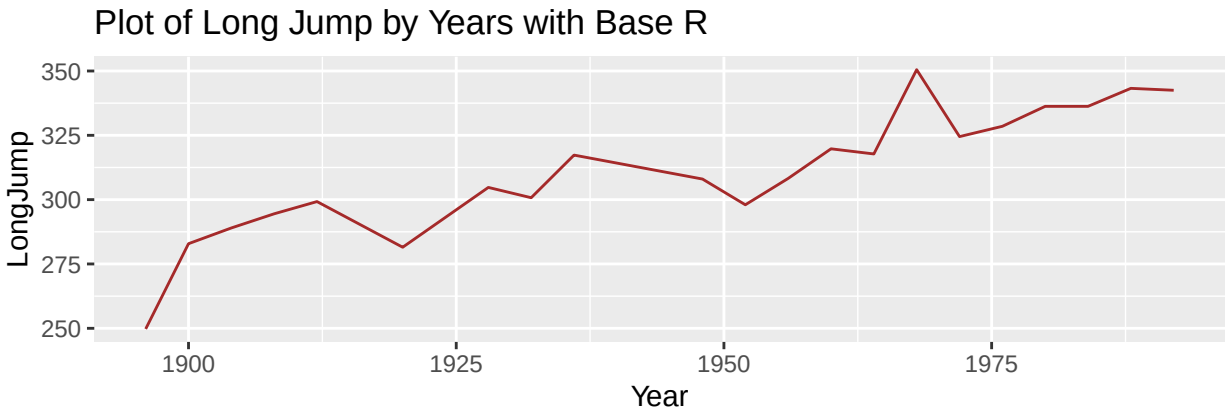
```
colnames(medal_data) <- c('Year', 'LongJump')
medal_data_tidyverse <- medal_data

# Final tidy data with tidyverse
medal_data_tidyverse %>% head()
```

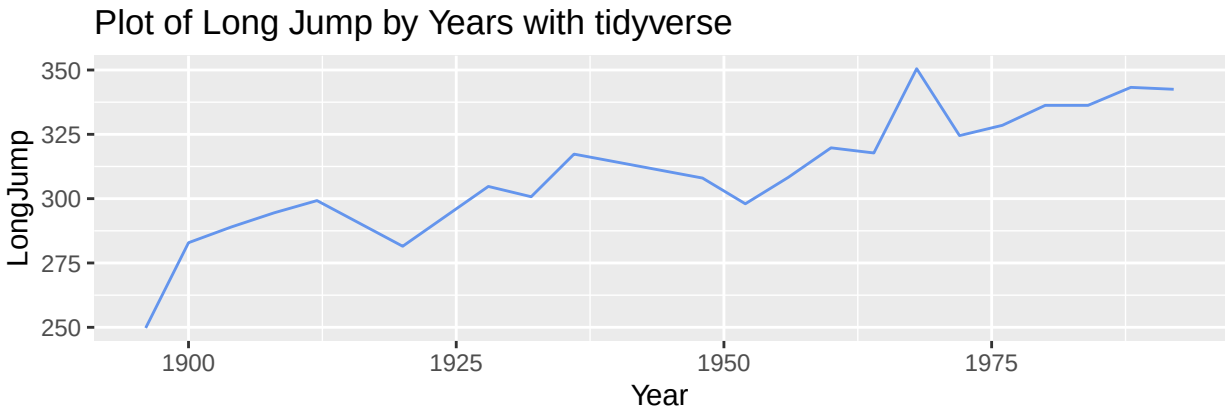
```
## # A tibble: 6 x 2
##    Year LongJump
##   <dbl>    <dbl>
## 1  1896     250.
## 2  1900     283.
## 3  1904     289
## 4  1908     294.
## 5  1912     299.
## 6  1920     282.
```

The result by tidyverse is the same with the base R function. The summary of the data converted by tidyverse is as follows.

Year	LongJump
Min. :1896	Min. :249.8
1st Qu.:1921	1st Qu.:295.4
Median :1950	Median :308.1
Mean :1945	Mean :310.3
3rd Qu.:1971	3rd Qu.:327.5
Max. :1992	Max. :350.5

As informative plots, line plots are used.





c. Brain weight (g) and body weight (kg) for 62 species.
http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/BrainandBodyWeight.dat

```
######## Brain weight data ########
# Getting "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/BrainandBodyWeight.dat"
url_brain <- "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/BrainandBodyWeight.dat"
brain_rawdata <- fread(url_brain)
```

```
## Warning in fread(url_brain): Detected 12 column names but the data has 6
## columns. Filling rows automatically. Set fill=TRUE explicitly to avoid this
## warning.
```

```
saveRDS(brain_rawdata, 'brain_rawdata.RDS')
brain_rawdata <- readRDS('brain_rawdata.RDS')
```

The data needs two columns which are 'Body Wt' and 'Brain Wt'.

```
# Using base R function only
# The method is the same with the data from part (b)
# Extract Body Wt and Brain Wt vectors
bodywt <- c(brain_rawdata[[1]], brain_rawdata[[3]], brain_rawdata[[5]])
brainwt <- c(brain_rawdata[[2]], brain_rawdata[[4]], brain_rawdata[[6]])

# Remove missing values
brain_data <- data.table(bodywt[-length(bodywt)], brainwt[-length(brainwt)])
colnames(brain_data) <- c('Body_Wt', 'Brain_Wt')
brain_data_base <- brain_data

# Final tidy data with base R functions
head(brain_data_base)
```

```
##    Body_Wt Brain_Wt
## 1:   3.385     44.5
## 2:   0.480     15.5
## 3:   1.350      8.1
## 4: 465.000    423.0
## 5:  36.330    119.5
## 6:  27.660    115.0
```

Above is the converted tidy data frames using the base R functions. A summary of the data is as follows:

Body_Wt	Brain_Wt
Min. : 0.005	Min. : 0.10
1st Qu.: 0.600	1st Qu.: 4.25
Median : 3.342	Median : 17.25
Mean : 198.790	Mean : 283.13
3rd Qu.: 48.202	3rd Qu.: 166.00
Max. :6654.000	Max. :5712.00

Now, handle the same data with `tidyverse` package.

```
# Tidy data with tidyverse
# Remove vectors which have only missing values
brain_data <- brain_rawdata[,1:6]

# Extracting 'Year' columns and 'Long Jump' columns and remove missing values
colnames(brain_data) <- paste(rep(c('bw', 'brw'),3), rep(1:3,each = 2))
bw <- brain_data[,c(1,3,5)] %>% gather(key = 'name1', value = 'BW', 1,2,3) %>%
  filter(BW != na)
```

```
## Warning in BW != na: longer object length is not a multiple of shorter object
## length
```

```
brw <- brain_data[,c(2,4,6)] %>% gather(key = 'name2', value = 'BRW', 1,2,3) %>%
  filter(BRW != na)
```

```
## Warning in BRW != na: longer object length is not a multiple of shorter object
## length
```

```
# Bind the vectors as a data table and rename the categories
brain_data <- bind_cols(bw[,2], brw[,2])
```

```
## New names:
## * NA -> ...1
## * NA -> ...2
```

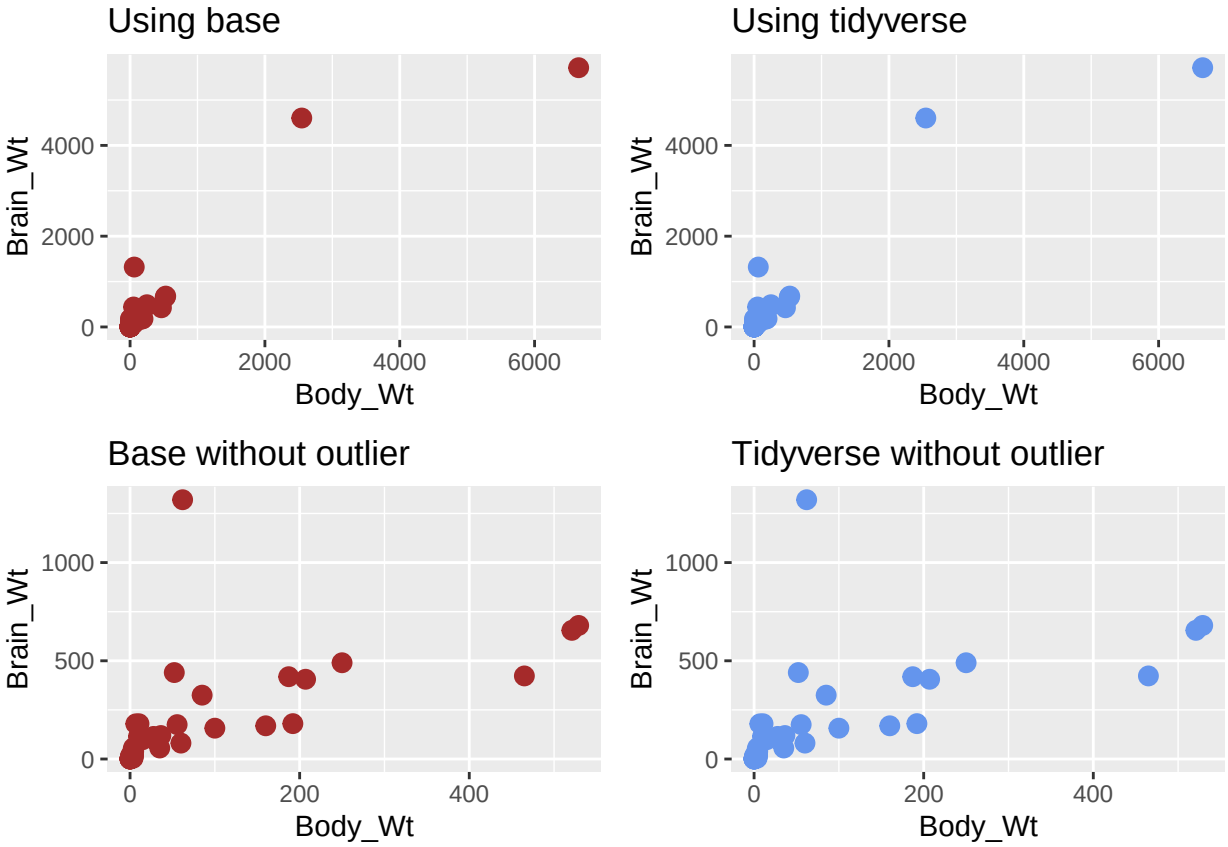
```
colnames(brain_data) <- c('Body_Wt', 'Brain_Wt')
brain_data_tidyverse <- brain_data

# Final tidy data with tidyverse
brain_data_tidyverse %>% head()
```

```
## # A tibble: 6 x 2
##   Body_Wt Brain_Wt
##     <dbl>    <dbl>
## 1    3.38     44.5
## 2    0.48     15.5
## 3    1.35      8.1
## 4  465       423
## 5   36.3     120.
## 6   27.7     115
```

The result by tidyverse is the same with the base R function. The summary of the data converted by tidyverse is as follows.

Body_Wt	Brain_Wt
Min. : 0.005	Min. : 0.10
1st Qu.: 0.600	1st Qu.: 4.25
Median : 3.342	Median : 17.25
Mean : 198.790	Mean : 283.13
3rd Qu.: 48.202	3rd Qu.: 166.00
Max. :6654.000	Max. :5712.00

As informative plots, scatter plots are used.



d. Triplicate measurements of tomato yield for two varieties of tomatos at three planting densities. http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/tomato.dat

```
######## Tomato data ########
# Getting "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/tomato.dat"
url_tomato <- "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/tomato.dat"
tomato_rawdata <- fread(url_tomato, skip = 1)
```

```
## Warning in fread(url_tomato, skip = 1): Detected 3 column names but the data has
## 4 columns (i.e. invalid file). Added 1 extra default column name for the first
## column which is guessed to be row names or an index. Use setnames() afterwards
## if this guess is not correct, or fix the file write command that created the
## file to create a valid file.
```

```
saveRDS(tomato_rawdata, 'tomato_rawdata.RDS')
tomato_rawdata <- readRDS('tomato_rawdata.RDS')
```

The values are grouped in the cells of the data above. Therefore, we should split the cells into single values.

```
# Using base R function only
# Need to split the values
cells <- strsplit(unlist(tomato_rawdata), split = ',', fixed = T) # split the data
values <- as.numeric(unlist(c(cells[3:8]))) # numerical data

# Combine the split values into data frame
tomato_matrix <- matrix(values, byrow = T, ncol = 3)
tomato_matrix <- t(cbind(tomato_matrix[1:2,], tomato_matrix[3:4,], tomato_matrix[5:6,]))

# Bind the data with the densities (categories)
tomato_data <- data.frame(tomato_matrix, as.character(rep(c(10000,20000,30000), each=3)))
colnames(tomato_data) <- c('IFE1', 'PusaEarlyDwarf','Density')
tomato_data_base <- tomato_data

# Final tidy data with base R functions
tomato_data_base
```

```
##   IFE1 PusaEarlyDwarf Density
## 1 16.1            8.1   10000
## 2 15.3            8.6   10000
## 3 17.5           10.1   10000
## 4 16.6           12.7   20000
## 5 19.2           13.7   20000
## 6 18.5           11.5   20000
## 7 20.8           14.4   30000
## 8 18.0           15.4   30000
## 9 21.0           13.7   30000
```

Above is the converted tidy data frames using the base R functions. A summary of the data is as follows:

IFE1	PusaEarlyDwarf	Density
Min. :15.30	Min. : 8.10	Length:9
1st Qu.:16.60	1st Qu.:10.10	Class :character
Median :18.00	Median :12.70	Mode :character
Mean :18.11	Mean :12.02	NA
3rd Qu.:19.20	3rd Qu.:13.70	NA
Max. :21.00	Max. :15.40	NA

Now, handle the same data with `tidyverse` package.

```
# Using tidyverse package
# Need to split the values
tomato_data <- tomato_rawdata[,-1] %>%
  separate(col = '10000', into = c("1","2","3"), sep = ",", convert = T) %>%
  separate(col = '20000', into = c("4","5","6"), sep = ",", convert = T) %>%
  separate(col = '30000', into = c("7","8","9"), sep = ",", convert = T) %>%
  as.matrix() %>% t()
```

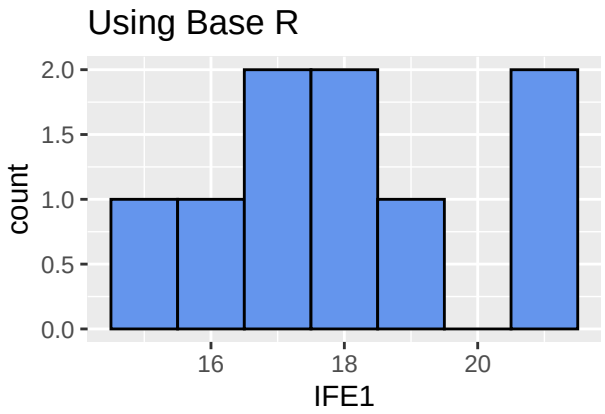
```
## Warning: Expected 3 pieces. Additional pieces discarded in 1 rows [2].
```

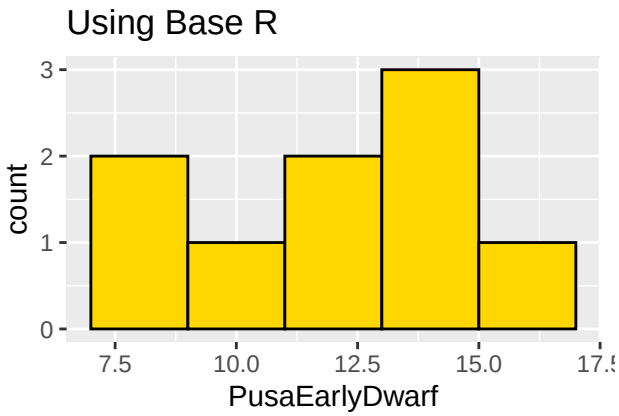
```
dens <- rep(c(10000,20000,30000), each = 3) %>% as.character() # Densities

# Bind the data with the densities vector
tomato_data <- tomato_data %>% data.frame(dens)
colnames(tomato_data) <- c('IFE1', 'PusaEarlyDwarf','Density')
tomato_data_tidyverse <- tomato_data

# Final tidy data with tidyverse
tomato_data_tidyverse
```

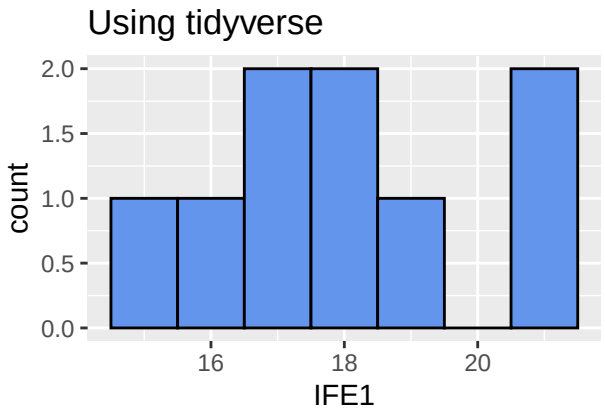
```
##   IFE1 PusaEarlyDwarf Density
## 1 16.1            8.1   10000
## 2 15.3            8.6   10000
## 3 17.5           10.1   10000
## 4 16.6           12.7   20000
## 5 19.2           13.7   20000
## 6 18.5           11.5   20000
## 7 20.8           14.4   30000
## 8 18.0           15.4   30000
## 9 21.0           13.7   30000
```

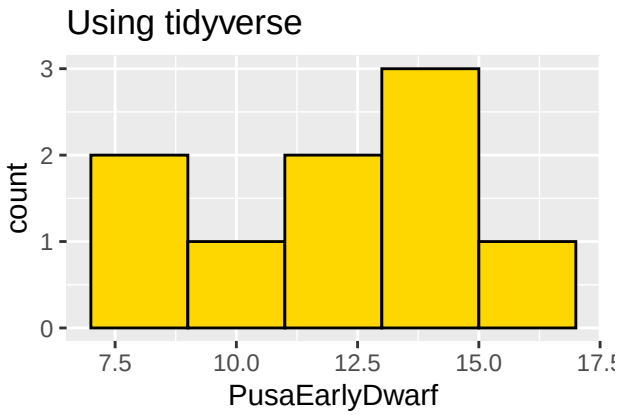
IFE1	PusaEarlyDwarf	Density
Min. :15.30	Min. : 8.10	Length:9
1st Qu.:16.60	1st Qu.:10.10	Class :character
Median :18.00	Median :12.70	Mode :character
Mean :18.11	Mean :12.02	NA
3rd Qu.:19.20	3rd Qu.:13.70	NA
Max. :21.00	Max. :15.40	NA

Here are the histograms of above data based on both base R and tidyverse.









Appendix

```
knitr::opts_chunk$set(echo = TRUE)
library(data.table)
library(tidyverse)
library(ggplot2)
library(ggpubr)
######## Sensory data ########
# Getting "https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/Sensory.dat"
url_sensory <- "https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/Sensory.dat"
sensory_rawdata <- fread(url_sensory, fill = TRUE, skip = 2, data.table = FALSE)
saveRDS(sensory_rawdata, 'sensory_rawdata.RDS')
sensory_rawdata <- readRDS('sensory_rawdata.RDS')

# Using base R function only
# Convert data.frame to matrix and transpose the raw data
matrix_sensory <- t(as.matrix(sensory_rawdata))

# Find where the missing values are
na <- which(is.na(matrix_sensory==TRUE))

# The indexes where Item numbers are in the data
x <- 1
item <- x
for (i in 1:9){
  x <- x+18
  item <- c(item, x)
}

# Remove missing values and 'Item's from the data
Values <- matrix_sensory[-c(na,item)]

# Combine the values with 'Item' and 'Operator' columns
Item <- rep(paste('Item', 1:10), each = 15)   # Item names
Opr <- rep(paste('Opr', 1:5), 30)             # Operator names
sensory_data_base <- data.table(Item, Opr, Values)

# Final tidy data with base R functions
head(sensory_data_base)

knitr::kable(summary(sensory_data_base))
# Sensory data with tidyverse package
# Making matrix which is the same with base R function but using pipes.
matrix_sensory <- sensory_rawdata %>% as.matrix() %>% t()
na <- is.na(matrix_sensory==TRUE) %>% which()     # Find missing values

# The indexes where Item numbers are in the data
x <- 1
item <- x
for (i in 1:9){
  x <- x+18
  item <- c(item, x)
}
```

```r
# Remove missing values and Item numbers from the data
Values <- matrix_sensory[-c(na,item)]

# Bind the values with 'Item' and 'Operator' columns
Item <- paste('Item', 1:10) %>% rep(each = 15)   # Item names
Opr <- paste('Opr', 1:5) %>% rep(30)             # Operator names
sensory_data_tidyverse <- data.table(Item, Opr, Values)

# Final tidy data with tidyverse
sensory_data_tidyverse %>% head()

knitr::kable(summary(sensory_data_tidyverse))
# box plots for item 1 to 4
base_boxplot <- ggplot(sensory_data_base, aes(x=Opr, y= sensory_data_base$Values)) +
  geom_boxplot(fill = 'gray') +
  labs(title="Box plot with Base R function",x="Operators", y = "Values")

base_hist = ggplot(sensory_data_base, aes(x=Values)) +
  geom_histogram(binwidth = 1, fill=I("cornflowerblue"), col = I("black")) +
  labs(title = 'Histogram with Base R')

tidy_boxplot <- ggplot(sensory_data_tidyverse,
                       aes(x=Opr, y= sensory_data_base$Values)) +
  geom_boxplot(fill = 'white') +
  labs(title="Box plot with tidyverse",x="Operators", y = "Values")

tidy_hist = ggplot(sensory_data_tidyverse, aes(x=Values)) +
  geom_histogram(binwidth = 1, fill=I("gold"), col = I("black")) +
  labs(title = 'Histogram with tidyverse')


ggarrange(base_boxplot, base_hist, tidy_boxplot, tidy_hist, ncol = 2, nrow = 2)

######## Long Jump data ########
# Getting "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/LongJumpData.dat"
url_medal <- "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/LongJumpData.dat"
medal_rawdata <- fread(url_medal)
saveRDS(medal_rawdata, 'medal_rawdata.RDS')
medal_rawdata <- readRDS('medal_rawdata.RDS')

# Using base R function only
# Year is coded as 1900 = 0
# Extract Year and Long Jump vectors
year <- c(medal_rawdata[[1]], medal_rawdata[[3]],
          medal_rawdata[[5]], medal_rawdata[[7]]) + 1900
longjump <- c(medal_rawdata[[2]], medal_rawdata[[4]],
              medal_rawdata[[6]], medal_rawdata[[8]])

# Bind the vectors as a data table and rename the categories
medal_data <- data.table(year[1:(length(year)-2)],
                         longjump[1:(length(longjump)-2)])
colnames(medal_data) <- c('Year', 'LongJump')
medal_data_base <- medal_data
```

```r
# Final tidy data with base R functions
head(medal_data_base)

knitr::kable(summary(medal_data_base))
# Using tidyverse package
# Year is coded as 1900 = 0
medal_data <- medal_rawdata[,1:8] # remove missing values only columns

# Extracting 'Year' columns and 'Long Jump' columns and remove missing values
colnames(medal_data) <- paste(rep(c('Year', 'Jump'),4), rep(1:4,each = 2))
year <- medal_data[,c(1,3,5,7)] %>%
  gather(key = 'name1', value = 'Year', 1,2,3,4) %>% filter(Year != na)
year[,2] <- year[,2] + 1900
jump <- medal_data[,c(2,4,6,8)] %>%
  gather(key = 'name2', value = 'LongJump', 1,2,3,4) %>% filter(LongJump != na)

# Bind the vectors as a data table and rename the categories
medal_data <- bind_cols(year[,2], jump[,2])
colnames(medal_data) <- c('Year', 'LongJump')
medal_data_tidyverse <- medal_data

# Final tidy data with tidyverse
medal_data_tidyverse %>% head()


# Plot of Long Jump by Years
medal_base_plot <- ggplot(data = medal_data_base, aes(x = Year, y= LongJump)) +
  geom_line(col = 'brown') +
  labs(title = 'Plot of Long Jump by Years with Base R')

medal_tidyverse_plot <- ggplot(data = medal_data_tidyverse, aes(x = Year, y= LongJump)) +
  geom_line(col = 'cornflowerblue') +
  labs(title = 'Plot of Long Jump by Years with tidyverse')

ggarrange(medal_base_plot, medal_tidyverse_plot, ncol = 1, nrow = 2)

######## Brain weight data ########
# Getting "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/BrainandBodyWeight.dat"
url_brain <- "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/BrainandBodyWeight.dat"
brain_rawdata <- fread(url_brain)
saveRDS(brain_rawdata, 'brain_rawdata.RDS')
brain_rawdata <- readRDS('brain_rawdata.RDS')
# Using base R function only
# The method is the same with the data from part (b)
# Extract Body Wt and Brain Wt vectors
bodywt <- c(brain_rawdata[[1]], brain_rawdata[[3]], brain_rawdata[[5]])
brainwt <- c(brain_rawdata[[2]], brain_rawdata[[4]], brain_rawdata[[6]])

# Remove missing values
brain_data <- data.table(bodywt[-length(bodywt)], brainwt[-length(brainwt)])
colnames(brain_data) <- c('Body_Wt', 'Brain_Wt')
brain_data_base <- brain_data
```

```r
# Final tidy data with base R functions
head(brain_data_base)

knitr::kable(summary(brain_data_base))
# Tidy data with tidyverse
# Remove vectors which have only missing values
brain_data <- brain_rawdata[,1:6]

# Extracting 'Year' columns and 'Long Jump' columns and remove missing values
colnames(brain_data) <- paste(rep(c('bw', 'brw'),3), rep(1:3,each = 2))
bw <- brain_data[,c(1,3,5)] %>% gather(key = 'name1', value = 'BW', 1,2,3) %>%
  filter(BW != na)
brw <- brain_data[,c(2,4,6)] %>% gather(key = 'name2', value = 'BRW', 1,2,3) %>%
  filter(BRW != na)

# Bind the vectors as a data table and rename the categories
brain_data <- bind_cols(bw[,2], brw[,2])
colnames(brain_data) <- c('Body_Wt', 'Brain_Wt')
brain_data_tidyverse <- brain_data

# Final tidy data with tidyverse
brain_data_tidyverse %>% head()

# Scatter plots of "Body Wt" and "Brain Wt"
brain_base_plot <-
  ggplot(data = brain_data_base, aes(x = Body_Wt, y= Brain_Wt)) +
  geom_point(col = 'brown', size = 3, shape = 19) +
  labs(title = 'Using base')

brain_tidyverse_plot <-
  ggplot(data = brain_data_tidyverse, aes(x = Body_Wt, y= Brain_Wt)) +
  geom_point(col = 'cornflowerblue', size = 3, shape = 19) +
  labs(title = 'Using tidyverse')

# Scatter plots without outliers
brain_base_plot_wo_outlier <-
  ggplot(data = brain_data_base[-c(19,33),], aes(x = Body_Wt, y= Brain_Wt)) +
  geom_point(col = 'brown', size = 3, shape = 19) +
  labs(title = 'Base without outlier')

brain_tidyverse_plot_wo_outlier <-
  ggplot(data = brain_data_tidyverse[-c(19,33),], aes(x = Body_Wt, y= Brain_Wt)) +
  geom_point(col = 'cornflowerblue', size = 3, shape = 19) +
  labs(title = 'Tidyverse without outlier')



ggarrange(brain_base_plot, brain_tidyverse_plot,
          brain_base_plot_wo_outlier,
          brain_tidyverse_plot_wo_outlier,
          ncol = 2, nrow = 2)

######## Tomato data ########
```

```r
# Getting "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/tomato.dat"
url_tomato <- "http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/tomato.dat"
tomato_rawdata <- fread(url_tomato, skip = 1)
saveRDS(tomato_rawdata, 'tomato_rawdata.RDS')
tomato_rawdata <- readRDS('tomato_rawdata.RDS')

# Using base R function only
# Need to split the values
cells <- strsplit(unlist(tomato_rawdata), split = ',', fixed = T) # split the data
values <- as.numeric(unlist(c(cells[3:8]))) # numerical data

# Combine the split values into data frame
tomato_matrix <- matrix(values, byrow = T, ncol = 3)
tomato_matrix <- t(cbind(tomato_matrix[1:2,], tomato_matrix[3:4,], tomato_matrix[5:6,]))

# Bind the data with the densities (categories)
tomato_data <- data.frame(tomato_matrix, as.character(rep(c(10000,20000,30000), each=3)))
colnames(tomato_data) <- c('IFE1', 'PusaEarlyDwarf','Density')
tomato_data_base <- tomato_data

# Final tidy data with base R functions
tomato_data_base

knitr::kable(summary(tomato_data_base))
# Using tidyverse package
# Need to split the values
tomato_data <- tomato_rawdata[,-1] %>%
  separate(col = '10000', into = c("1","2","3"), sep = ",", convert = T) %>%
  separate(col = '20000', into = c("4","5","6"), sep = ",", convert = T) %>%
  separate(col = '30000', into = c("7","8","9"), sep = ",", convert = T) %>%
  as.matrix() %>% t()
dens <- rep(c(10000,20000,30000), each = 3) %>% as.character() # Densities

# Bind the data with the densities vector
tomato_data <- tomato_data %>% data.frame(dens)
colnames(tomato_data) <- c('IFE1', 'PusaEarlyDwarf','Density')
tomato_data_tidyverse <- tomato_data

# Final tidy data with tidyverse
tomato_data_tidyverse

# Histograms of tomato data

hist_ife_base = ggplot(tomato_data_base, aes(x=IFE1)) +
  geom_histogram(binwidth = 1, fill=I("cornflowerblue"), col = I("black")) +
  labs(title = 'Using Base R')

hist_pusa_base = ggplot(tomato_data_base, aes(x=PusaEarlyDwarf)) +
  geom_histogram(binwidth = 2, fill=I("gold"), col = I("black")) +
  labs(title = 'Using Base R')

hist_ife_tidyverse = ggplot(tomato_data_tidyverse, aes(x=IFE1)) +
  geom_histogram(binwidth = 1, fill=I("cornflowerblue"), col = I("black")) +
```

```
  labs(title = 'Using tidyverse')

hist_pusa_tidyverse = ggplot(tomato_data_tidyverse, aes(x=PusaEarlyDwarf)) +
  geom_histogram(binwidth = 2, fill=I("gold"), col = I("black")) +
  labs(title = 'Using tidyverse')


ggarrange(hist_ife_base, hist_pusa_base,
          hist_ife_tidyverse, hist_pusa_tidyverse, ncol = 2, nrow = 2)
```