Statistics for Computer Science

Assignment 1

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Exercise 1

1. Create your own R-functions for calculating estimates of the following characteristics: sample mean, sample five number summary, sample skewness, sample kurtosis, sample variance, sample standard deviation, sample range, sample decile range, sample 0.1-trimmed average and sample 0.1-trimmed variance. Use Cramér's estimates for skewness and kurtosis. Do not use inbuilt functions min(), max(), mean(), quantile(), var(), sd(), range() or functions from external libraries.

Implementation in R

```
#function to calculate minimum
cal_minimum <- function(x){
  x <- sort(x)
  min_val <- x[1]
  return(min_val)
}

#function to calculate maximum
cal_maximum <- function(x){
  x <- sort(x)
  max_val <- tail(x,1)
  return(max_val)
}

#median, first quartile, thrid quartile, quartile_type should be, one,
   two(median), or three
cal_quartile <- function(x, quartile_type){
  x <- sort(x)
  result <- 0

  if(quartile_type == 'two'){
    if(length(x) %% 2 == 0){
      return((x[length(x)/2] + x[length(x+1)/2])/2)
    }else{
      return(x[length(x+1)/2])
    }
  }else if(quartile_type == 'one'){
    position <- (length(x) + 1)/4
    if (floor(position) == ceiling(position)){
      return(x[position])
    }else{
      return((x[floor(position)] + x[ceiling(position)])/2)
    }
  }else if(quartile_type == 'three'){
    position <- (3*(length(x) + 1))/4
    if (floor(position) == ceiling(position)){
      return(x[position])
```

```
    }else{
      return((x[floor(position)] + x[ceiling(position)])/2)
    }
  }
}

#Sample mean
cal_mean <- function(x){
  result <- sum(x) / length(x)
  return(result)
}

#Sample five number summary
cal_five_num_summary <- function(x){
  min <- cal_minimum(x)
  q1 <- cal_quartile(x, 'one')
  q2 <- cal_quartile(x, 'two')
  q3 <- cal_quartile(x, 'three')
  max <- cal_maximum(x)
  return(c(min, q1, q2, q3, max))
}

#Sample Skewness
cal_coef_skew <- function(x){
  s <- sqrt(cal_sample_variance(x))
  mean <- cal_mean(x)
  total <- 0
  for(i in x){
    total = total + (i - mean)^3
  }
  return(total/(s^3 * length(x)))
}

#Sample Kurtosis
cal_coef_kurt <- function(x){
  s <- sqrt(cal_sample_variance(x))
  mean <- cal_mean(x)
  total <- 0
  for(i in x){
    total = total + (i - mean)^4
  }
  total = total/(s^4 * length(x))
  return(total -3)
}

#Sample Variance
cal_sample_variance <- function(x){
  mean <- cal_mean(x)
  n_minus_one <- length(x) - 1
```

```
  total <- 0
  for(i in x){
    total = total + (i - mean)^2
  }
  return(total/n_minus_one)
}

#Sample Standard Deviation
cal_sd <- function(x){
  sample_variance <- cal_sample_variance(x)
  return(sqrt(sample_variance))
}

#Sample Range
cal_sample_range <- function(x){
  return(cal_maximum(x) - cal_minimum(x))
}

#Sample Decile Range
cal_sample_decile_range <- function(x){
  x_0.9 <- 90/100 * (length(x) +1)
  x_0.1 <- 10/100 * (length(x) +1)

  if (floor(x_0.9) == ceiling(x_0.9)){
    x_0.9 = x_0.9
  }else{
    x_0.9 = (x[floor(x_0.9)] + x[ceiling(x_0.9)])/2
  }

  if (floor(x_0.1) == ceiling(x_0.1)){
    x_0.1 = x_0.1
  }else{
    x_0.1 = (x[floor(x_0.1)] + x[ceiling(x_0.1)])/2
  }
  return(x_0.9 - x_0.1)
}

#Sample 0.1 trimmed average
cal_sample_0.1_trimmed_average <- function(x){
  g <- abs(0.1 * length(x))
  n <- length(x)
  total <- 0
  for(i in seq(g+1, n-g, 1)){
    total <- total + x[i]
  }
  return(total/(n - 2*g))
}

#Sample 0.1 trimmed variance
```

```
cal_sample_0.1_trimmed_variance <- function(x){
   g <- abs(0.1 * length(x))
   n <- length(x)
   x_gt <- cal_sample_0.1_trimmed_average(x)
   total <- 0
   for(i in seq(g+1, n-g, 1)){
     total <- total + (x[i] - x_gt)^2
   }
   return(total/(n - 2*g - 1))
}

library(xtable)
```

2. Separately for each population calculate sample size and these characteristics of maximum cranial breadth. Print them in a table with values rounded to 4 decimal places.

Implementation in R

```
setwd(getwd())
Howell <- read.csv('Howell.csv')
Howell.Male <- Howell[Howell$Sex == 'M', ]
Howell.Male.Australi <- Howell.Male[(Howell.Male$Population == 'AUSTRALI'), ]
Howell.Male.Peru <- Howell.Male[(Howell.Male$Population == 'PERU'), ]

#Working on population of 'AUSTRALI'
Australi.sample_size <- length(Howell.Male.Australi$XCB)
Australi.sample_mean <- cal_mean(Howell.Male.Australi$XCB)
Australi.sample_five_num_summary <- cal_five_num_summary(Howell.Male.Australi$XCB)
Australi.sample_skewness <- cal_coef_skew(Howell.Male.Australi$XCB)
Australi.sample_kurtosis <- cal_coef_kurt(Howell.Male.Australi$XCB)
Australi.sample_variance <- cal_sample_variance(Howell.Male.Australi$XCB)
Australi.sample_sd <- cal_sd(Howell.Male.Australi$XCB)
Australi.sample_range <- cal_sample_range(Howell.Male.Australi$XCB)
Australi.sample_decile_range <- cal_sample_decile_range(Howell.Male.Australi$XCB)
Australi.sample_0.1_trimmed_average <- cal_sample_0.1_trimmed_average(Howell.Male.Australi$XCB)
Australi.sample_0.1_trimmed_variance <- cal_sample_0.1_trimmed_variance(Howell.Male.Australi$XCB)

#Working on population of 'PERU'
Peru.sample_size <- length(Howell.Male.Peru$XCB)
Peru.sample_mean <- cal_mean(Howell.Male.Peru$XCB)
Peru.sample_five_num_summary <- cal_five_num_summary(Howell.Male.Peru$XCB)
Peru.sample_skewness <- cal_coef_skew(Howell.Male.Peru$XCB)
Peru.sample_kurtosis <- cal_coef_kurt(Howell.Male.Peru$XCB)
```

```
Peru.sample_variance <- cal_sample_variance(Howell.Male.Peru$XCB)
Peru.sample_sd <- cal_sd(Howell.Male.Peru$XCB)
Peru.sample_range <- cal_sample_range(Howell.Male.Peru$XCB)
Peru.sample_decile_range <- cal_sample_decile_range(Howell.Male.Peru$XCB
   )
Peru.sample_0.1_trimmed_average <- cal_sample_0.1_trimmed_average(Howell
   .Male.Peru$XCB)
Peru.sample_0.1_trimmed_variance <- cal_sample_0.1_trimmed_variance(
   Howell.Male.Peru$XCB)

Howell.characteristics <- data.frame(Australi=c(Australi.sample_size,
                        Australi.sample_mean,
                        Australi.sample_five_num_summary,
                        Australi.sample_skewness,
                        Australi.sample_kurtosis,
                        Australi.sample_variance,
                        Australi.sample_sd,
                        Australi.sample_range,
                        Australi.sample_decile_range,
                        Australi.sample_0.1_trimmed_average,
                        Australi.sample_0.1_trimmed_variance),
                  Peru=c(Peru.sample_size, Peru.sample_mean,
                         Peru.sample_five_num_summary,
                         Peru.sample_skewness,
                         Peru.sample_kurtosis,
                         Peru.sample_variance,
                         Peru.sample_sd,
                         Peru.sample_range,
                         Peru.sample_decile_range,
                         Peru.sample_0.1_trimmed_average,
                         Peru.sample_0.1_trimmed_variance),
                  row.names = c('Size', 'Mean', 'Minimum',
                                'Q1', 'Q2', 'Q3', 'Maximum',
                                'Skewness', 'Kurtosis',
                                'Variance', 'Standard Deviation',
                                'Range', 'Decile Range',
                                'Sampe 0.1 trimmed average',
                                'Sample 0.1 trimmed variance'))

library(xtable)
```

3. Create boxplots of maximum cranial breadth of each population side by side in one figure. Set the width of boxes to be proportional to sample sizes, add notches and arithmetic averages for both groups.

Implementation in R

```
max.len = max(length(Howell.Male.Australi$XCB), length(Howell.Male.Peru$
   XCB))
x=c(Howell.Male.Australi$XCB, rep(NA, max.len - length(Howell.Male.
```

```
   Australi$XCB)))
y=c(Howell.Male.Peru$XCB, rep(NA, max.len - length(Howell.Male.Peru$XCB)))

Populations <- c('Australi', 'Peru')
values <- c(x, y)
df <- data.frame(Populations, values)

library(ggplot2)
boxplot <- ggplot(df, aes(x=Populations, y=values, fill=Populations)) +
          geom_boxplot(notch = TRUE, width=(55/110)) +
          scale_fill_manual(values=c("lightblue", "lightgreen")) +
          ylab('Maximum cranial breadth') +
          xlab('Populations') +
          annotate("text", x=1, y=Australi.sample_mean,
                   label= round(Australi.sample_mean, 4)) +
          annotate("text", x=2, y=Peru.sample_mean,
                   label= round(Peru.sample_mean, 4)) +
          ggtitle('Boxplot of maximum cranial breadth') +
          theme(plot.title = element_text(hjust = 0.5))
```

4. Separately for each population create histogram of maximum cranial breadth. Make sure that the histograms can be easily compared (without using back-to-back histogram).

Implementation in R

```
Australi.hist <- ggplot(data=data.frame(Australi=c(Howell.Male.Australi$XCB)),
                        aes(x=Howell.Male.Australi$XCB)) +
                geom_histogram(color="darkblue", fill="lightblue", binwidth = 1) +
                xlab('Maximum cranial breadth of Australi') +
                ylab('Frequecy') +
                scale_x_continuous(breaks = seq(124, 144, 2), lim = c(122, 146)) +
                geom_text(stat = 'count', aes(label =..count.., vjust = -0.5))

Peru.hist <- ggplot(data=data.frame(Peru=c(Howell.Male.Peru$XCB)),
                    aes(x=Howell.Male.Peru$XCB)) +
            geom_histogram(color="darkgreen", fill="lightgreen", binwidth = 1) +
            xlab('Maximum cranial breadth of Peru') +
            ylab('Frequency') +
            scale_x_continuous(breaks = seq(129, 149, 2), lim = c(128, 150)) +
            geom_text(stat = 'count', aes(label =..count.., vjust = -0.5))
```

5. Create normal qq-plot of maximum cranial breadth for each population.

Implementation in R

```
Australi.qq <- ggplot(data=data.frame(Australi=c(Howell.Male.Australi$XCB))) +
                  aes(sample= Australi) +
                  geom_qq(distribution = qnorm) +
                  geom_qq_line(line.p = c(0.25, 0.75), col = "lightblue") +
                  ylab('Maximum cranial breadth for Australi') +
                  ggtitle('QQ-Plot of maximum cranial breadth of Australi') +
                  theme(plot.title = element_text(hjust = 0.5))

Peru.qq <- ggplot(data=data.frame(Peru=c(Howell.Male.Peru$XCB))) +
              aes(sample= Peru) +
              geom_qq(distribution = qnorm) +
              geom_qq_line(line.p = c(0.25, 0.75), col = "lightgreen") +
              ylab('Maximum cranial breadth for Peru') +
              ggtitle('QQ-Plot of maximum cranial breadth of Peru') +
              theme(plot.title = element_text(hjust = 0.5))
```

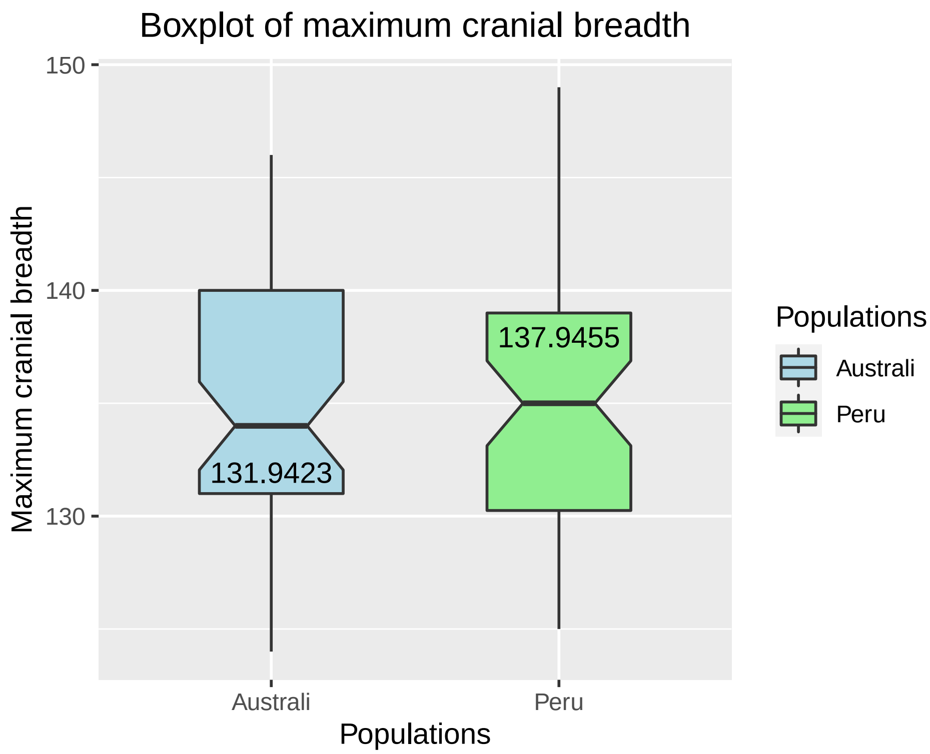
6. Interpretion of results and graphics.

Characteristics of maximum cranial breadth

Table represents the characteristics of maximum cranial breadth. The selected populations are male people from Austali and Peru.

	Australi	Peru
Size	52.0000	55.0000
Mean	131.9423	137.9455
Minimum	124.0000	129.0000
Q1	128.0000	135.0000
Q2	131.0000	138.0000
Q3	134.0000	141.0000
Maximum	144.0000	149.0000
Skewness	0.6436	-0.0037
Kurtosis	-0.3390	0.0616
Variance	26.0554	15.8673
Standard Deviation	5.1045	3.9834
Range	20.0000	20.0000
Decile Range	15.0000	-4.0000
Sampe 0.1 trimmed average	129.4712	138.1364
Sample 0.1 trimmed variance	26.3226	15.1438

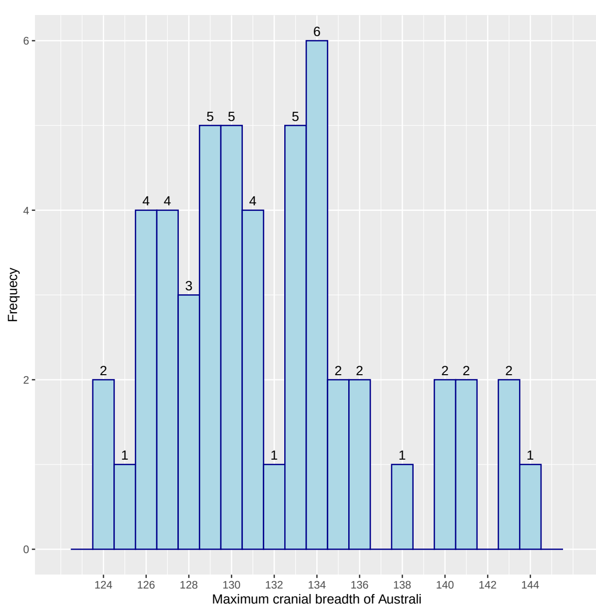
Table 1: Characteristics of maximum cranial breadth

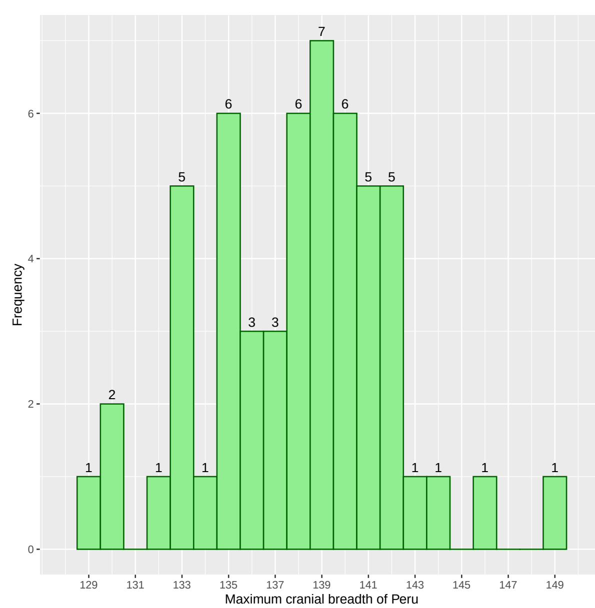


Boxplot represent maximum cranial breadth of Austali and Peru with the arithmetic average of each population placed on each box. X-axis shows the population and y-axis show the number of maximum cranial breadth.

Histograms represent maximum cranial breadth of each population

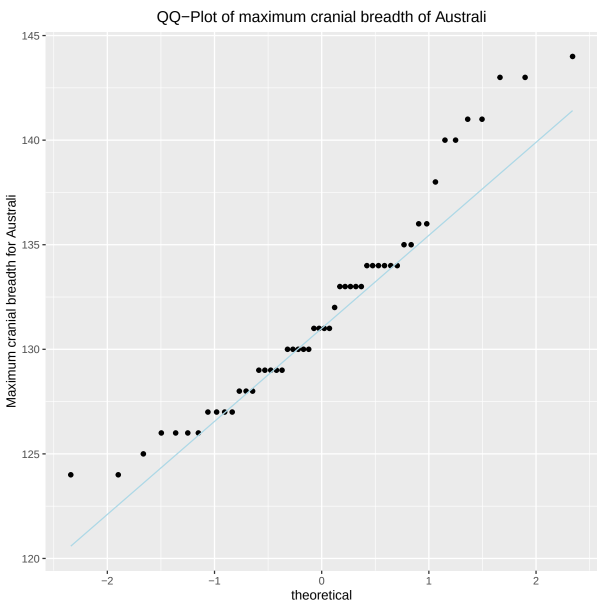
Histograms show frequency of maximum cranial breadth of Australi(on the left) and Peru(on the right) with the number of frequency on top of each bar. X-axis shows the number of maximum cranial breadth and y-axis shows the frequency.

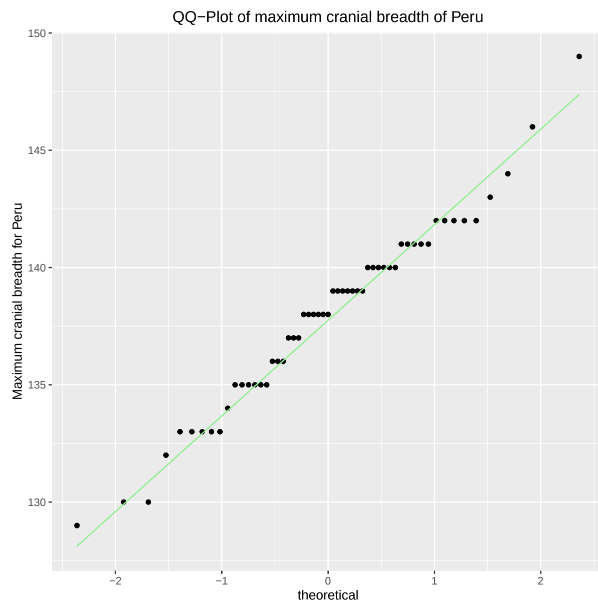




QQ-plot represent maximum cranial breadth of each population

The left figure shows qq-plot represent maximum cranial breadth of Australi while the right one is for Peru.





Exercise 2

1. Calculate the number of men and women in Spain for each year and print them in a table together with the total population.

Implementation in R

```
setwd(getwd())
Spanish.province <- read.csv('area_spanish_provinces.csv')
Spanish.population <- read.csv('population-spain-1998-2018.csv', sep=";"
   )

population.2018 <- sum(Spanish.population$males.2018, Spanish.population
   $females.2018)
population.2013 <- sum(Spanish.population$males.2013, Spanish.population
   $females.2013)
population.2008 <- sum(Spanish.population$males.2008, Spanish.population
   $females.2008)
population.2003 <- sum(Spanish.population$males.2003, Spanish.population
   $females.2003)
population.1998 <- sum(Spanish.population$males.1998, Spanish.population
   $females.1998)

total.population <- sum(colSums(Spanish.population[ ,-1]))

```

```
population.df <- data.frame(Male=c(sum(Spanish.population$males.1998),
                                   sum(Spanish.population$males.2003),
                                   sum(Spanish.population$males.2008),
                                   sum(Spanish.population$males.2013),
                                   sum(Spanish.population$males.2018),
                                      0),
                            Female=c(sum(Spanish.population$females.1998),
                                     sum(Spanish.population$females.2003),
                                     sum(Spanish.population$females.2008),
                                     sum(Spanish.population$females.2013),
                                     sum(Spanish.population$females.2018), 0),
                            Total=c(population.1998, population.2003,
                                    population.2008, population.2013,
                                    population.2018, total.population))

row.names(population.df) <- c(’1998’, ’2003’, ’2008’, ’2013’, ’2018’, ’
   Total’)
population.df[6,1] <- sum(population.df$Male)
population.df[6,2] <- sum(population.df$Female)
```

2. Display barplot plot of total population of Spain in each of the years, with each bar divided between men and women.

Implementation in R

```
library(ggplot2)
year <- c(1998, 1998, 2003, 2003, 2008, 2008, 2013, 2013, 2018, 2018)
population <- c(sum(Spanish.population$males.1998),
                sum(Spanish.population$females.1998),
                sum(Spanish.population$males.2003),
                sum(Spanish.population$females.2003),
                sum(Spanish.population$males.2008),
                sum(Spanish.population$females.2008),
                sum(Spanish.population$males.2013),
                sum(Spanish.population$females.2013),
                sum(Spanish.population$males.2018),
                sum(Spanish.population$females.2018))
options(scipen = 999)
gender <- c(’Male’, ’Female’, ’Male’, ’Female’, ’Male’,
            ’Female’, ’Male’, ’Female’, ’Male’, ’Female’ )

df.population <- data.frame(year, population, gender)
population.barplot<-ggplot(data=df.population,
                           aes(x=year, y=population, fill=gender )) +
                    geom_col() +
                    scale_fill_manual(values=c("lightpink", "lightblue")
                       ) +
                    scale_x_continuous(breaks = seq(1998, 2018, 5)) +
                    scale_y_continuous(breaks = seq(0, 50000000,
                       5000000)) +
```

```
                    geom_text(aes(label = sprintf("%.0fk", population/1000)),
                              position = position_stack(0.5)) +
                    theme(axis.text.y=element_text(angle = 45))
```

3. Display barplot of relative proportions of men and women within each province in 2018

Implementation in R

```
proportion.province <-c(as.vector(Spanish.population$province), as.vector(Spanish.population$province))
proportion.gender <- c(rep('Male', 52), rep('Female', 52))
proportion.male <- round(Spanish.population$males.2018 / (Spanish.population$males.2018 + Spanish.population$females.2018), 4)
proportion.female <- round(Spanish.population$females.2018 / (Spanish.population$males.2018 + Spanish.population$females.2018), 4)

proportion.province.gender <- c(proportion.male, proportion.female)

df.proportion <- data.frame(Provinces=proportion.province,
                            Proportion=proportion.province.gender,
                            Gender=proportion.gender)

proportion.barplot <- ggplot(data=df.proportion,
                             aes(x=Provinces, y=Proportion, fill=Gender)) +
                      geom_col() +
                      theme(axis.text.x=element_text(angle = 90, size=6),
                            plot.title = element_text(vjust=0.5, hjust=1)) +
                      scale_fill_manual(values=c("lightpink", "lightblue")) +
                      scale_x_discrete(name= "Provinces") +
                      scale_y_continuous(name= "Population proportion")
```

4. Calculate population density in each province in 1998 and in 2018.

Implementation in R

```
province.population.2018 <- Spanish.population$males.2018 + Spanish.population$females.2018
province.population.1998 <- Spanish.population$males.1998 + Spanish.population$females.1998
provinces <- sapply(strsplit(as.vector(Spanish.population$province), ", "), '[', 1)

df <- data.frame(province = provinces,
                 population.1998 = province.population.1998,
                 population.2018 =province.population.2018)

```

```
area.provinces <- sapply(strsplit(as.vector(Spanish.province$Province)," "), tail, 1)
df1 <- data.frame(province = area.provinces, area = Spanish.province$Area)

for(i in 1:52){
  for(j in 1:52){
    if(grepl(df1$province[j], df$province[i])){
      df$area[i] <- df1$area[j]
    }
  }
}

df$province <- Spanish.population$province
df$density.1998 <- round(df$population.1998 / df$area, 4)
df$density.2018 <- round(df$population.2018 / df$area, 4)

density.2018.sample_size <- length(df$density.2018)
density.2018.sample_mean <- cal_mean(df$density.2018)
density.2018.sample_five_num_summary <- cal_five_num_summary(df$density.2018)
density.2018.sample_skewness <- cal_coef_skew(df$density.2018)
density.2018.kurtosis <- cal_coef_kurt(df$density.2018)
density.2018.sample_sd <- cal_sd(df$density.2018)

density.1998.sample_size <- length(df$density.1998)
density.1998.sample_mean <- cal_mean(df$density.1998)
density.1998.sample_five_num_summary <- cal_five_num_summary(df$density.1998)
density.1998.sample_skewness <- cal_coef_skew(df$density.1998)
density.1998.kurtosis <- cal_coef_kurt(df$density.1998)
density.1998.sample_sd <- cal_sd(df$density.1998)

density.characteristics <- data.frame("1998"=c(density.1998.sample_size,
                                               density.1998.sample_mean,
                                               density.1998.sample_five_num_summary,
                                               density.1998.sample_skewness,
                                               density.1998.kurtosis,
                                               density.1998.sample_sd),
                                      "2018"=c(density.2018.sample_size,
                                               density.2018.sample_mean,
                                               density.2018.sample_five_num_summary,
                                               density.2018.sample_skewness,
                                               density.2018.kurtosis,
                                               density.2018.sample_sd),
```

```
                                     row.names = c('Size', 'Mean', 'Minimum',
                                                   'Q1', 'Q2', 'Q3', 'Maximum',
                                                   'Skewness', 'Kurtosis', 'Standard Deviation'))

colnames(density.characteristics) <- c("Year 1998", "Year 2018")

year.1998 <- rep('1998', 52)
year.2018 <- rep('2018', 52)
year <- c(year.1998, year.2018)
values <- c(df$density.1998, df$density.2018)
density.df <- data.frame(year, values)

density.boxplot <- ggplot(density.df, aes(x=year, y=values, fill=year)) +
                  geom_boxplot(notch = TRUE) +
                  scale_fill_manual(values=c("lightblue", "lightgreen")) +
                  ylab('Population density') +
                  xlab('Year') +
                  ggtitle('Boxplot of population density in Spain') +
                  theme(plot.title = element_text(hjust = 0.5))

hist.1998 <- ggplot(data=df, aes(x=density.1998)) +
                geom_histogram(color="darkblue", fill="lightblue", binwidth = 50) +
                xlab('Population density in 1998') +
                ylab('Frequecy') +
                scale_x_continuous(breaks = seq(0, 5000, 500))

hist.2018 <- ggplot(data=df, aes(x=density.2018)) +
                geom_histogram(color="darkgreen", fill="lightgreen", binwidth = 50) +
                xlab('Population density in 2018') +
                ylab('Frequecy') +
                scale_x_continuous(breaks = seq(0, 7000, 500))

histogram.group <- ggplot(density.df, aes(x = values)) +
              geom_histogram(aes(color = year, fill = year),
                             position = "identity", bins = 30, alpha = 0.4, binwidth = 50) +
              scale_color_manual(values = c("#00AFBB", "#E7B800")) +
              scale_fill_manual(values = c("#00AFBB", "#ffffff00")) +
              scale_x_continuous(breaks = seq(0, 7000, 500)) +
              xlab('Population density') +
```

```
                ylab('Frequecy')
```

5. Interpretion of results and graphics.

Table of population in Spain

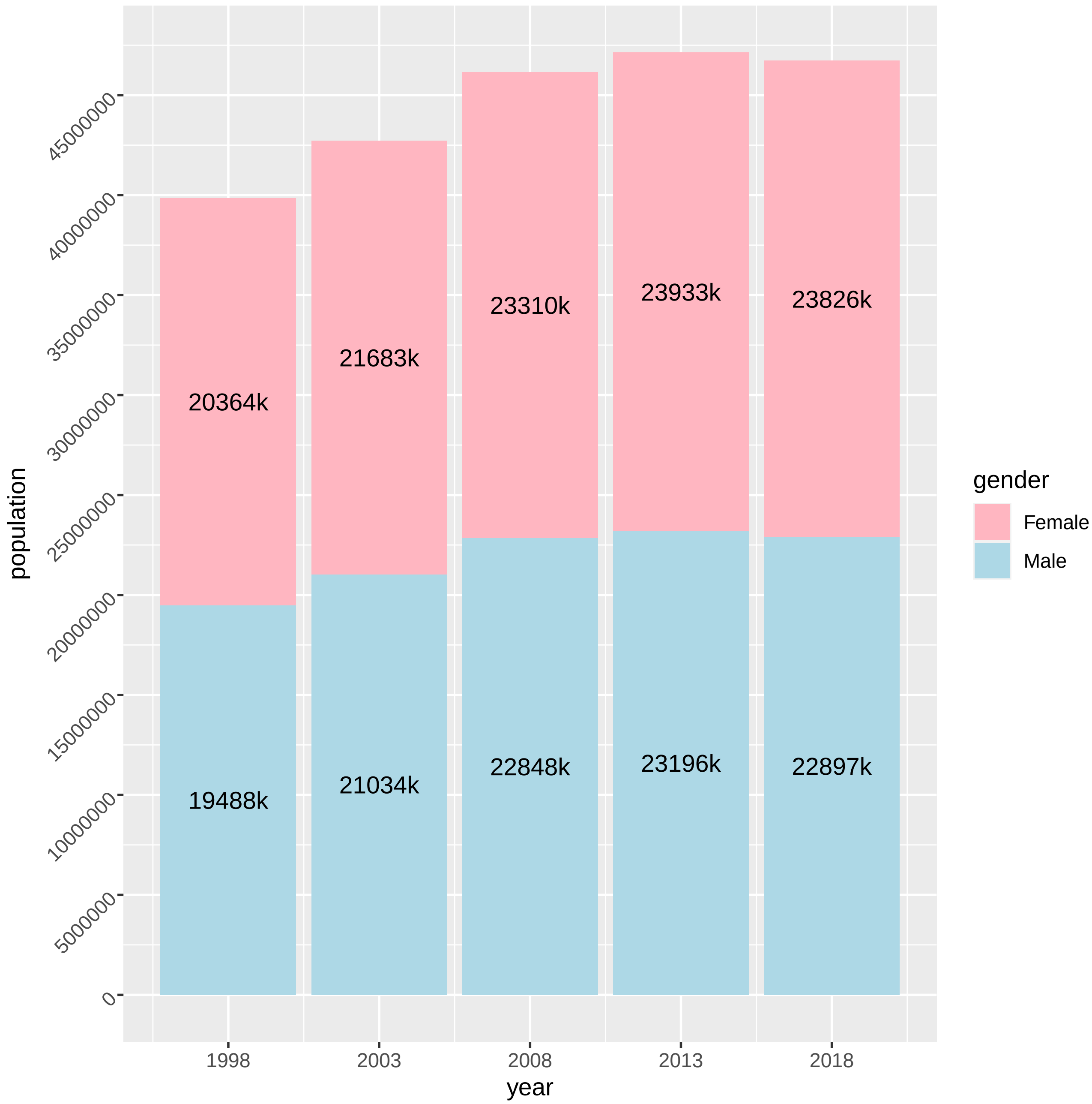
Table represents the population of Spain in 1998, 2003, 2008, 2013 and 2018. It shows the total population based on gender between each year, the total population between each year, and the total population of the 5 selected year.

	Male	Female	Total
1998	19488465	20364186	39852651
2003	21034326	21682738	42717064
2008	22847737	23310085	46157822
2013	23196386	23933397	47129783
2018	22896602	23826378	46722980
Total	109463516	113116784	222580300

Table 2: Population of Spain

Barplot of population in Spain

Barplot of total popuation in Spain in 1998, 2003, 2008, 2013 and 2018 with bar separated by gender. Male in blue and Female in pink. Each bar has two numbers represents total population based on gender in each year. X-axis shows the years and y-axis shows population. The number of population in Spain slightly increased till 2013 and slightly dropped in 2018.



Barplot of proportions of men and women in Spain (2018)

Barplot represents population proportion of each province in Spain in 2018. X-axis shows provinces in Spain while y-axis show the relative proportion. Each bar is divided between men and women of each province. The blue part is for men and the pink part is for women. The proportion of men and women in each province is almost equal with men are slightly less than women.

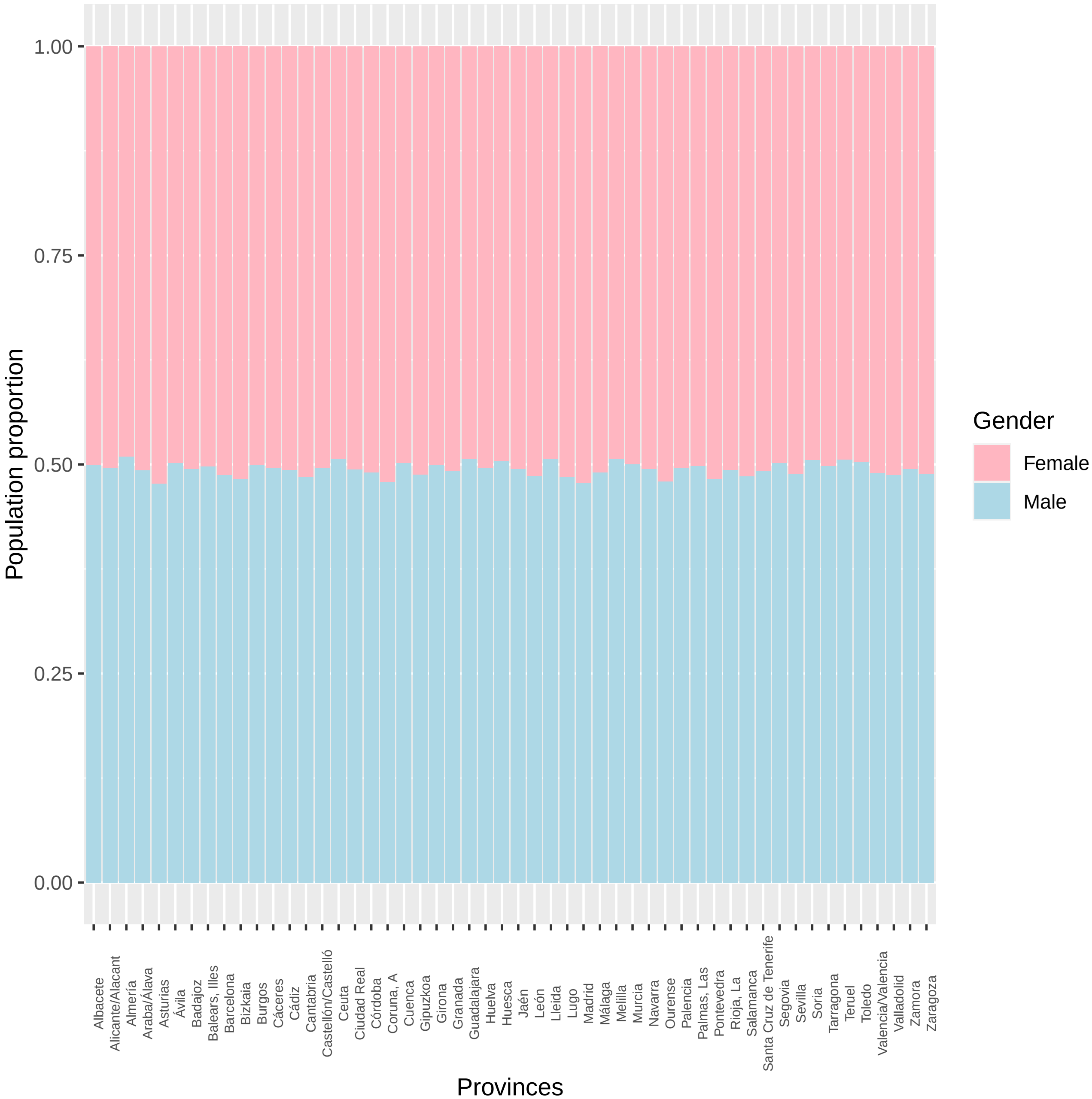
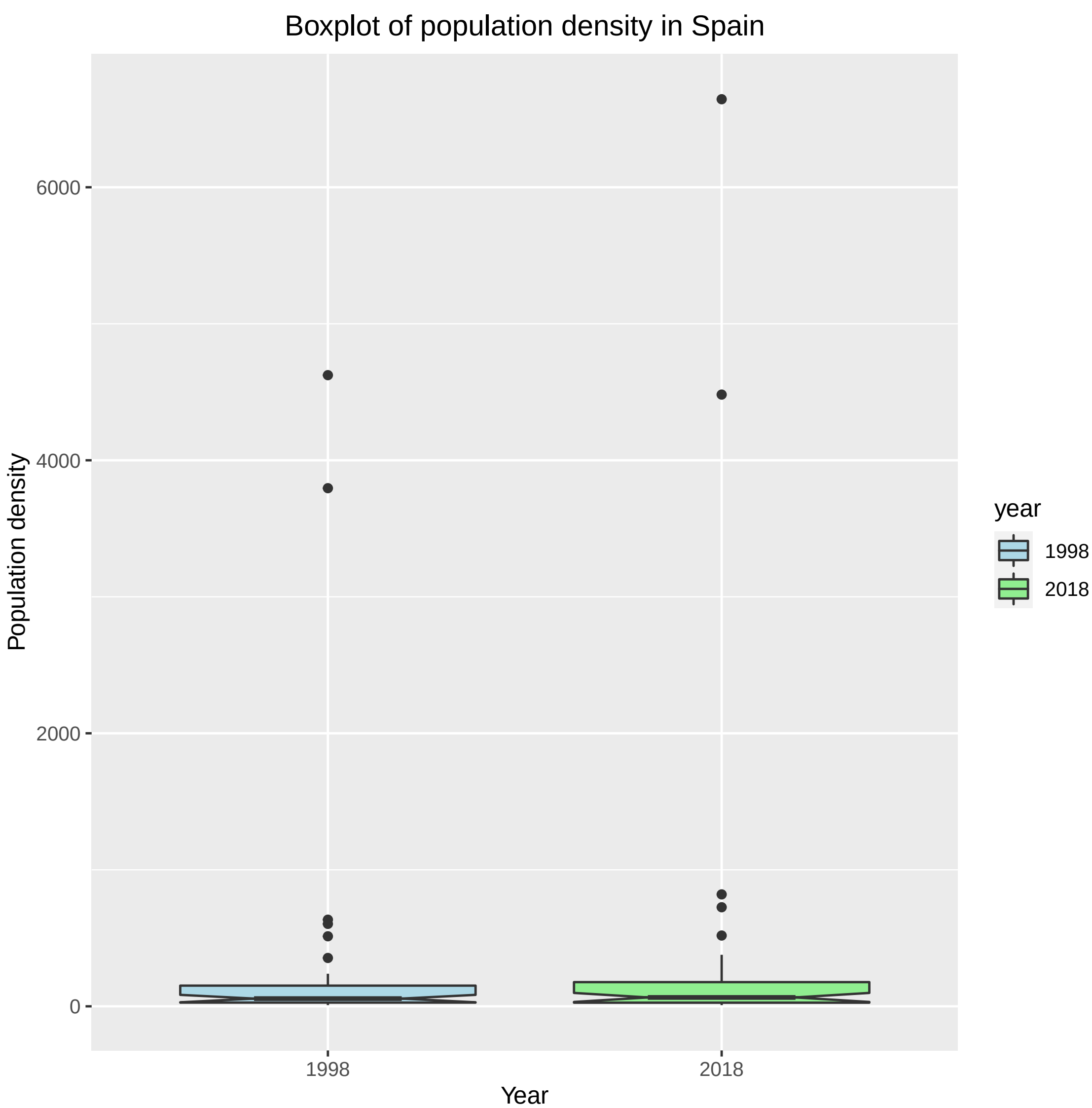


Table of characteristics of population density in Spain (1998 and 2018)

	Year 1998	Year 2018
Size	52.0000	52.0000
Mean	268.3568	339.0729
Minimum	8.8899	8.5994
Q1	26.5034	26.4518
Q2	55.7095	64.1000
Q3	154.2437	188.0495
Maximum	4623.6923	6644.9231
Skewness	4.5286	4.7737
Kurtosis	19.7477	22.5997
Standard Deviation	812.2020	1089.5388

Table 3: Characteristics of Population density of Spain



Histograms represent population density in Spain

First two histograms show population density in Spain in 1998 and 2018. The x-axis shows population density while the y-axis shows frequency. The last histogram shows the joining of population density in Spain in 1998 and 2018.