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

```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))
  # return(list(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
```

```r
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('/home/jane/Documents/SSME (Service Development Management)/Term2/
   MV013-Statistics for Computer Science/Assignment1')
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)

Peru <- data.frame(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’))

Australi <- 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),
                       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

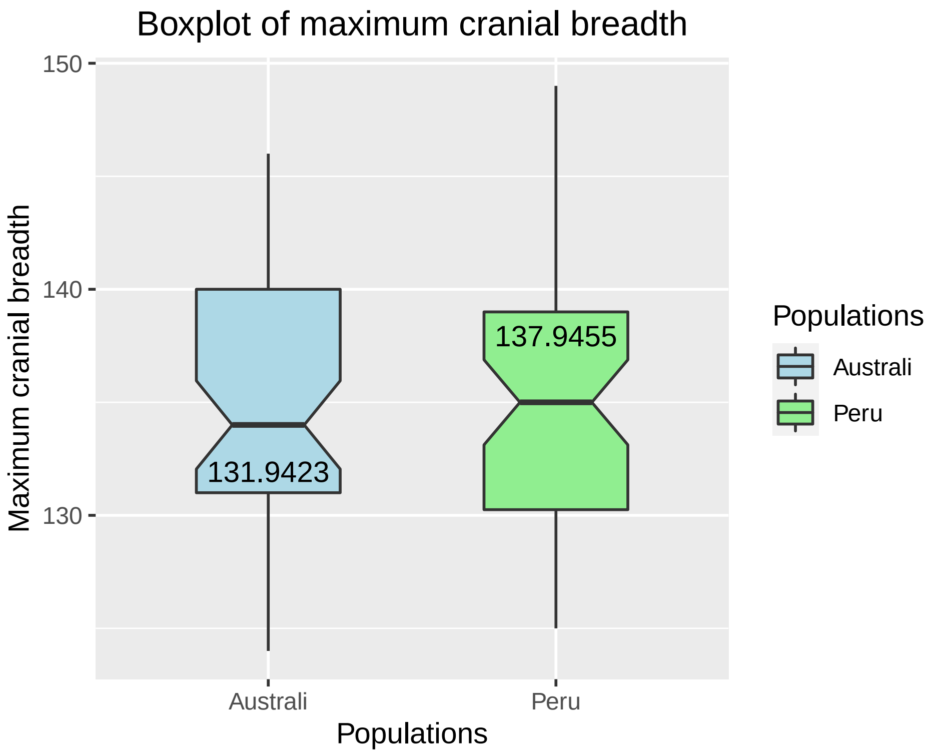
```
Australi.qq <- ggplot(data=data.frame(Australi=c(Howell.Male.Australi$XCB))) +
                aes(sample= Australi) +
                geom_qq(distribution = qnorm) +
                geom_qq_line(line.p = c(0.25, 0.75), col = "lightblue") +
                ylab('Maximum cranial breadth for Australi') +
                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. Interpret your results and graphics. Text. Results in table or graphic form. Commentaries and interpretation of the results.

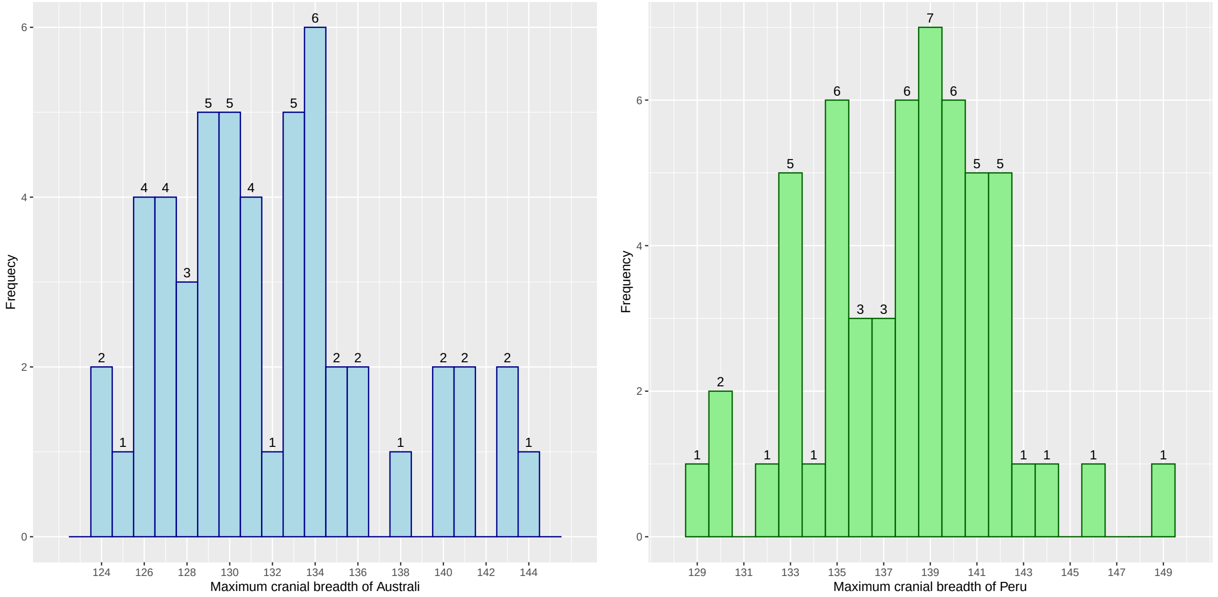
Characteristics of maximum cranial breadth

	Australi
Size	52.0000
Mean	131.9423
Minimum	124.0000
Q1	128.0000
Q2	131.0000
Q3	134.0000
Maximum	144.0000
Skewness	0.6436
Kurtosis	-0.3390
Variance	26.0554
Standard Deviation	5.1045
Range	20.0000
Decile Range	15.0000
Sampe 0.1 trimmed average	129.4712
Sample 0.1 trimmed variance	26.3226

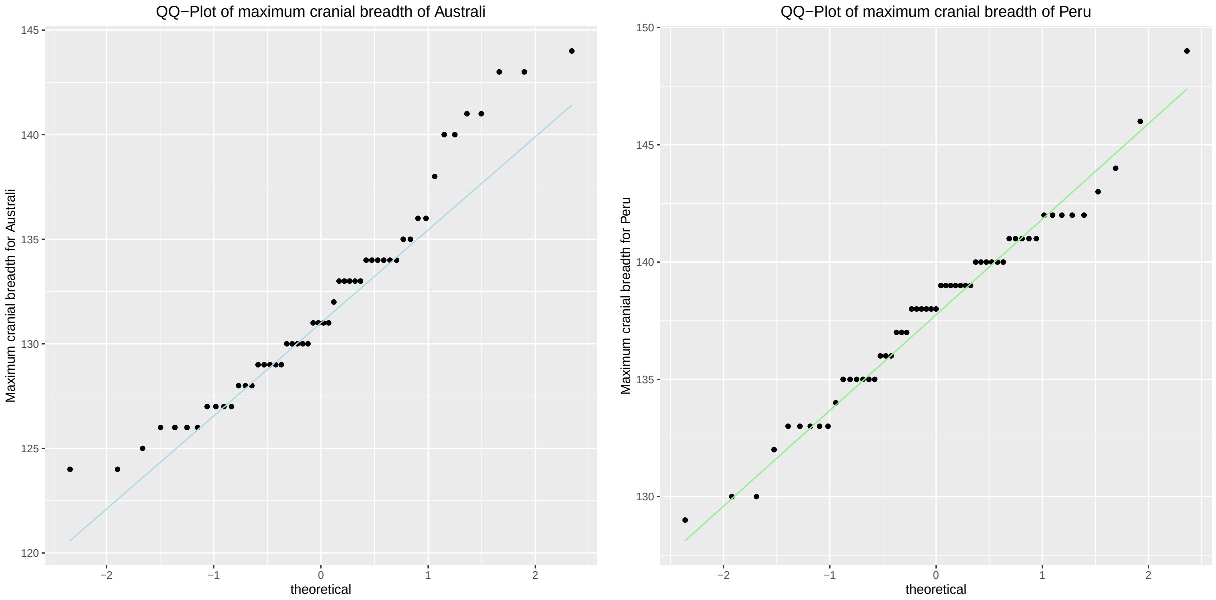
	Peru
Size	55.0000
Mean	137.9455
Minimum	129.0000
Q1	135.0000
Q2	138.0000
Q3	141.0000
Maximum	149.0000
Skewness	-0.0037
Kurtosis	0.0616
Variance	15.8673
Standard Deviation	3.9834
Range	20.0000
Decile Range	-4.0000
Sampe 0.1 trimmed average	138.1364
Sample 0.1 trimmed variance	15.1438



Histograms represent maximum cranial breadth of each population



QQ-plot represent maximum cranial breadth of each population



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('/home/jane/Documents/SSME (Service Development Management)/Term2/MV013-Statistics for Computer Science/Assignment1')
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]))

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(df) <- c('1998', '2003', '2008', '2013', '2018', 'Total')
df[6,1] <- sum(df$Male)
df[6,2] <- sum(df$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))
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 = sprintf("%.0fk", population/1000)) +
  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.province.gender <- c(proportion.male, proportion.female)
```

```
Error in eval(expr, envir, enclos): object ’proportion.male’ not found
```

```
df.proportion <- data.frame(proportion.province, proportion.province.
   gender, proportion.gender)
```

```
Error in data.frame(proportion.province, proportion.province.gender,
   proportion.gender): object ’proportion.province.gender’ not found
```

```
proportion.barplot <- ggplot(data=dffff, aes(x=proportion.province, y=
   proportion.province.gender, fill=proportion.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") +
          ggtitle(’Barplot of population proportion’)
```

```
Error in ggplot(data = dffff, aes(x = proportion.province, y =
   proportion.province.gender, : object ’dffff’ not found
```

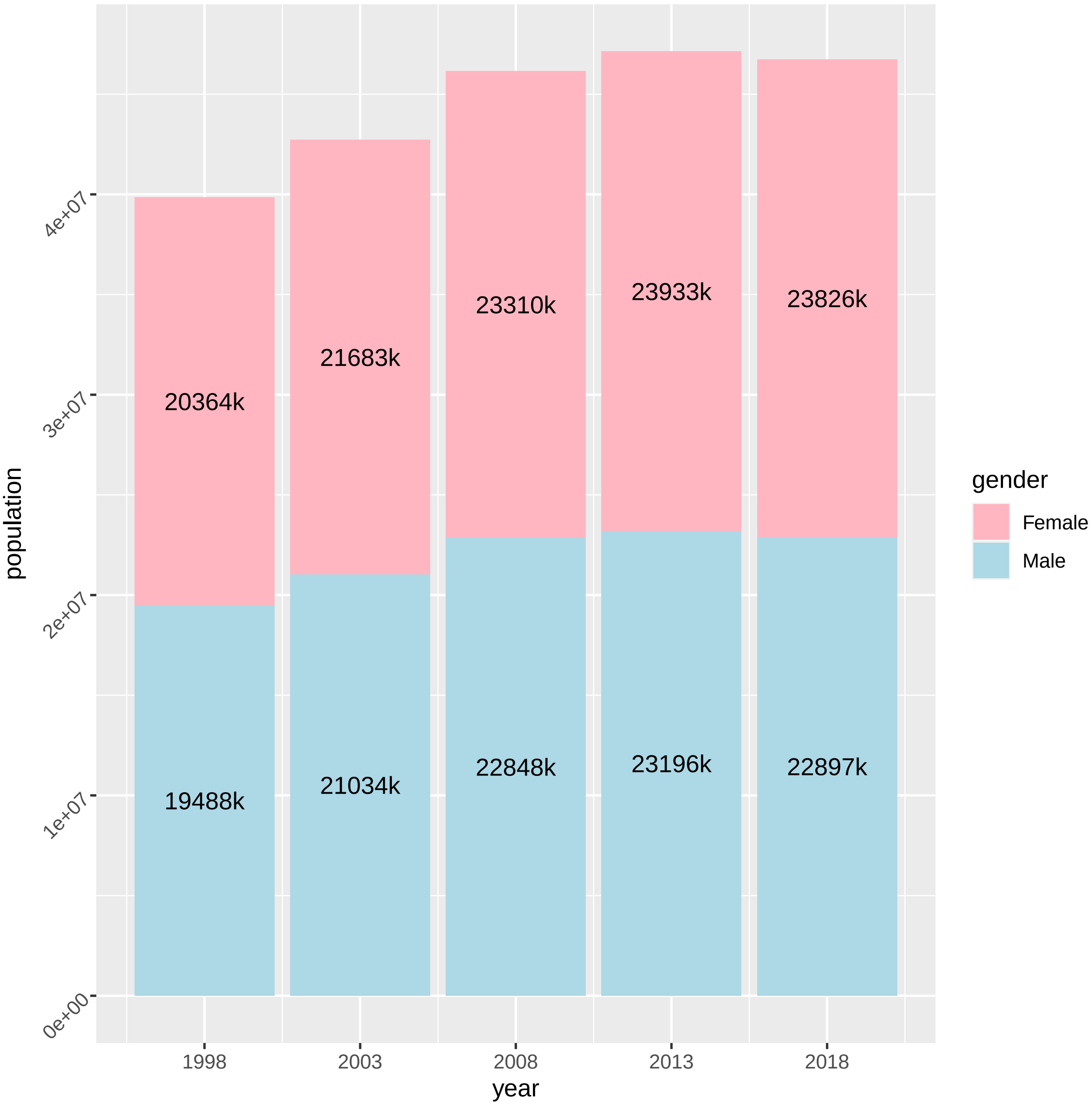
```
proportion.barplot
```

```
Error in eval(expr, envir, enclos): object ’proportion.barplot’ not
   found
```

5. Interpret your results and graphics.

	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 1: Population of Spanish


population
4e+07
3e+07
2e+07
1e+07
0e+00
20364k
21683k
23310k
23933k
23826k
19488k
21034k
22848k
23196k
22897k
1998
2003
2008
2013
2018
year
gender
Female
Male