# Acosta-Worksheet7

ACOSTA, MELBOURNE BSIT2A

2022-12-22

```
#1. Create a data frame for the table below

Student <- seq(1:10)
PreTest <- c(55,54,47,57,51,61,57,54,63,58)
PostTest <- c(61,60,56,63,56,63,59,56,62,61)

DF <- data.frame(Student,PreTest,PostTest)
DF
```

```
##    Student PreTest PostTest
## 1        1      55       61
## 2        2      54       60
## 3        3      47       56
## 4        4      57       63
## 5        5      51       56
## 6        6      61       63
## 7        7      57       59
## 8        8      54       56
## 9        9      63       62
## 10      10      58       61
```

```
#a. Compute the descriptive statistics using different packages (Hmisc and pastecs).

#Write the codes and its result.

library(Hmisc)
```

```
## Warning: package 'Hmisc' was built under R version 4.2.2

## Loading required package: lattice

## Loading required package: survival

## Loading required package: Formula

## Loading required package: ggplot2

## Warning: package 'ggplot2' was built under R version 4.2.2
```

```
##
## Attaching package: 'Hmisc'

## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
library(pastecs)
```

```
## Warning: package 'pastecs' was built under R version 4.2.2
```

```
describe(DF)
```

```
## DF
##
##  3  Variables      10  Observations
## --------------------------------------------------------------------------------
## Student
##        n  missing distinct     Info     Mean      Gmd      .05      .10
##       10        0       10        1      5.5    3.667     1.45     1.90
##      .25      .50      .75      .90      .95
##     3.25     5.50     7.75     9.10     9.55
##
## lowest :  1  2  3  4  5, highest:  6  7  8  9 10
##
## Value        1   2   3   4   5   6   7   8   9  10
## Frequency    1   1   1   1   1   1   1   1   1   1
## Proportion 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
## --------------------------------------------------------------------------------
## PreTest
##        n  missing distinct     Info     Mean      Gmd
##       10        0        8    0.988     55.7    5.444
##
## lowest : 47 51 54 55 57, highest: 55 57 58 61 63
##
## Value       47  51  54  55  57  58  61  63
## Frequency    1   1   2   1   2   1   1   1
## Proportion 0.1 0.1 0.2 0.1 0.2 0.1 0.1 0.1
## --------------------------------------------------------------------------------
## PostTest
##        n  missing distinct     Info     Mean      Gmd
##       10        0        6    0.964     59.7    3.311
##
## lowest : 56 59 60 61 62, highest: 59 60 61 62 63
##
## Value       56  59  60  61  62  63
## Frequency    3   1   1   2   1   2
## Proportion 0.3 0.1 0.1 0.2 0.1 0.2
## --------------------------------------------------------------------------------
```

```
stat.desc(DF)
```

```
##                 Student      PreTest     PostTest
## nbr.val      10.0000000  10.00000000  10.00000000
## nbr.null      0.0000000   0.00000000   0.00000000
## nbr.na        0.0000000   0.00000000   0.00000000
## min           1.0000000  47.00000000  56.00000000
## max          10.0000000  63.00000000  63.00000000
## range         9.0000000  16.00000000   7.00000000
## sum          55.0000000 557.00000000 597.00000000
## median        5.5000000  56.00000000  60.50000000
## mean          5.5000000  55.70000000  59.70000000
## SE.mean       0.9574271   1.46855938   0.89504811
## CI.mean.0.95  2.1658506   3.32211213   2.02473948
## var           9.1666667  21.56666667   8.01111111
## std.dev       3.0276504   4.64399254   2.83039063
## coef.var      0.5504819   0.08337509   0.04741023
```

```
#2. The Department of Agriculture was studying the effects of several levels of a
#fertilizer on the growth of a plant. For some analyses, it might be useful to convert
#the fertilizer levels to an ordered factor.

DepartmentofAgriculture <- c(10,10,10,20,20,50,10,
                             20,10,50,20,50,20,10)
```

```
#a. Write the codes and describe the result.
In_Ord <- sort(DepartmentofAgriculture, decreasing = FALSE)
In_Ord
```

```
##  [1] 10 10 10 10 10 10 20 20 20 20 20 50 50 50
```

```
#3. Abdul Hassan, president of Floor Coverings Unlimited, has asked you to study
#the exercise levels undertaken by 10 subjects were "l", "n", "n", "i", "l" ,
#"l", "n", "n", "i", "l" ; n=none, l=light, i=intense
Subjects <- c("l","n","n","i","l","l","n","n","i","l")
```

```
#a. What is the best way to represent this in R?

#DATAFRAME
out <- data.frame(Subjects)
out
```

```
##    Subjects
## 1         l
## 2         n
## 3         n
## 4         i
## 5         l
## 6         l
## 7         n
## 8         n
## 9         i
## 10        l
```

```r
#4.Sample of 30 tax accountants from all the states and territories of Australia and
#their individual state of origin is specified by a character vector of state mnemonics
#as:
state <- c("tas", "sa", "qld", "nsw", "nsw", "nt", "wa", "wa", "qld",
           "vic", "nsw", "vic", "qld", "qld", "sa", "tas", "sa", "nt",
           "wa", "vic", "qld", "nsw", "nsw", "wa", "sa", "act", "nsw",
           "vic", "vic", "act")
state
```

```
##  [1] "tas" "sa"  "qld" "nsw" "nsw" "nt"  "wa"  "wa"  "qld" "vic" "nsw" "vic"
## [13] "qld" "qld" "sa"  "tas" "sa"  "nt"  "wa"  "vic" "qld" "nsw" "nsw" "wa"
## [25] "sa"  "act" "nsw" "vic" "vic" "act"
```

```r
#a. Apply the factor function and factor level. Describe the results.
hello <- function(state)
  hello
```

```r
#5. From #4 - continuation:

#• Suppose we have the incomes of the same tax accountants in another vector (in
incomes <- c(60, 49, 40, 61, 64, 60, 59, 54,
             62, 69, 70, 42, 56, 61, 61, 61, 58, 51, 48,
             65, 49, 49, 41, 48, 52, 46, 59, 46, 58, 43)
```

```r
#a. Calculate the sample mean income for each state we can now use the special
#function tapply():
Calc <- tapply(state, incomes, mean)
```

```
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

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## returning NA

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## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA
```

```
Calc
```

```
## 40 41 42 43 46 48 49 51 52 54 56 58 59 60 61 62 64 65 69 70
## NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA
```

```
#b. Copy the results and interpret.
# 40 41 42 43 46 48 49 51 52 54 56 58 59 60 61 62 64 65 69 70
#NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA
```

```
#6.Calculate the standard errors of the state income means (refer again to number 3)

Calc_ST.n <- length(Calc)
Calc_1.sd <- sd(Calc)
Calc_Final.se <- Calc_1.sd/sqrt(Calc_ST.n)
Calc_Final.se
```

```
## [1] NA
```

```
#a. What is the standard error? Write the codes.
#NA
```

```
#b. Interpret the result.
#the result is not available because some variables are character type so it won't able to get the stan
```

```
#7. Use the titanic dataset.
data("Titanic")

head<- data.frame(Titanic)
```

```
#a. subset the titatic dataset of those who survived and not survived. Show the
#codes and its result.
head_subset <- subset(head, select = "Survived")
head_subset
```

```
##    Survived
## 1        No
## 2        No
## 3        No
## 4        No
## 5        No
## 6        No
## 7        No
## 8        No
## 9        No
## 10       No
## 11       No
## 12       No
## 13       No
## 14       No
## 15       No
## 16       No
## 17      Yes
## 18      Yes
## 19      Yes
## 20      Yes
## 21      Yes
## 22      Yes
## 23      Yes
## 24      Yes
## 25      Yes
## 26      Yes
## 27      Yes
## 28      Yes
## 29      Yes
## 30      Yes
## 31      Yes
## 32      Yes
```

```
#8. The data sets are about the breast cancer Wisconsin. The samples arrive periodically as Dr. Wolberg
#chronological grouping of the data. You can create this dataset in Microsoft Excel.
```

```
#a. describe what is the dataset all about.
#The dataset is all about Breast Cancer.
```

```
#b. Import the data from MS Excel. Copy the codes.

library("readxl")
```

```
## Warning: package ’readxl’ was built under R version 4.2.2
```

```
DATA <- read_excel("B:\\Git\\Worksheets\\Acsota_Workesheet7\\Breast_Cancer.xlsx")
DATA
```

```
## # A tibble: 49 x 11
##         ID CL. thickne~1 Cell ~2 Cell ~3 Marg.~4 Epith~5 Bare.~6 Bl. C~7 Norma~8
##      <dbl>         <dbl>   <dbl>   <dbl>   <dbl>   <dbl> <chr>     <dbl>   <dbl>
##  1 1000025             5       1       1       1       2 1             3       1
##  2 1002945             5       4       4       5       7 10            3       2
##  3 1015425             3       1       1       1       2 2             3       1
##  4 1016277             6       8       8       1       3 4             3       7
##  5 1017023             4       1       1       3       2 1             3       1
##  6 1017122             8      10      10       8       7 10            9       7
##  7 1018099             1       1       1       1       2 10            3       1
##  8 1018561             2       1       2       1       2 1             3       1
##  9 1033078             2       1       1       1       2 1             1       1
## 10 1033078             4       2       1       1       2 1             2       1
## # ... with 39 more rows, 2 more variables: Mitoses <dbl>, Class <chr>, and
## #   abbreviated variable names 1: ‘CL. thickness‘, 2: ‘Cell size‘,
## #   3: ‘Cell Shape‘, 4: ‘Marg. Adhesion‘, 5: ‘Epith. C.size‘,
## #   6: ‘Bare. Nuclei‘, 7: ‘Bl. Cromatin‘, 8: ‘Normal nucleoli‘
```

```
#c. Compute the descriptive statistics using different packages. Find the values of:

#c.1 Standard error of the mean for clump thickness.
Clump <- length(DATA$`CL. thickness`)
Clump_A <- sd(DATA$`CL. thickness`)
Clump_B <- Clump_A/sqrt(DATA$`CL. thickness`)
Clump_B
```

```
##  [1] 1.2812754 1.2812754 1.6541194 1.1696391 1.4325095 1.0129371 2.8650189
##  [8] 2.0258743 2.0258743 1.4325095 2.8650189 2.0258743 1.2812754 2.8650189
## [15] 1.0129371 1.0828754 1.4325095 1.4325095 0.9059985 1.1696391 1.0828754
## [22] 0.9059985 1.6541194 1.0129371 2.8650189 1.2812754 1.6541194 1.2812754
## [29] 2.0258743 2.8650189 1.6541194 2.0258743 0.9059985 2.0258743 1.6541194
## [36] 2.0258743 0.9059985 1.1696391 1.2812754 2.0258743 1.1696391 0.9059985
## [43] 1.1696391 1.2812754 0.9059985 2.8650189 1.6541194 2.8650189 1.4325095
```

```
#c.2 Coefficient of variability for Marginal Adhesion.
COV <- sd(DATA$`Marg. Adhesion`) / mean(DATA$`Marg. Adhesion`)* 100
COV
```

```
## [1] 97.67235
```

```r
#c.3 Number of null values of Bare Nuclei.
Null_Values <- subset(DATA,`Bare. Nuclei` == "NA")
```

```r
#c.4 Mean and standard deviation for Bland Chromatin
mean(DATA$`Bl. Cromatin`)
```

```
## [1] 3.836735
```

```r
sd(DATA$`Bl. Cromatin`)
```

```
## [1] 2.085135
```

```r
#c.5 Confidence interval of the mean for Uniformity of Cell Shape

#Calculate the mean
Calc_Mean <- mean(DATA$`Cell Shape`)
Calc_Mean
```

```
## [1] 3.163265
```

```r
#Calculate the standard error of the mean
SE_M <- length(DATA$`Cell Shape`)
SD_B <- sd(DATA$`Cell Shape`)
Ans_1 <- SD_B/sqrt(SE_M)
Ans_1
```

```
## [1] 0.4158294
```

```r
#Find the t-score that corresponds to the confidence level
D = 0.05
numE = SE_M - 1
numF = qt(p = D/ 2, df = numE,lower.tail = F)
numF
```

```
## [1] 2.010635
```

```r
#Constructing the confidence interval
numG <- numF * numE
```

```r
#Lower
numH <- Calc_Mean - numG
```

```r
#Upper
numI <- Calc_Mean + numG

c(numH,numI)
```

```
## [1] -93.34720  99.67373
```

```
#d. How many attributes?
attributes(DATA)
```

```
## $class
## [1] "tbl_df"     "tbl"        "data.frame"
##
## $row.names
##  [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
## [26] 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49
##
## $names
##  [1] "ID"              "CL. thickness"   "Cell size"       "Cell Shape"
##  [5] "Marg. Adhesion"  "Epith. C.size"   "Bare. Nuclei"    "Bl. Cromatin"
##  [9] "Normal nucleoli" "Mitoses"         "Class"
```

```
#e. Find the percentage of respondents who are malignant. Interpret the results.
P_R <- subset(DATA, Class == "maligant")
P_R
```

```
## # A tibble: 17 x 11
##          ID CL. thickne~1 Cell ~2 Cell ~3 Marg.~4 Epith~5 Bare.~6 Bl. C~7 Norma~8
##       <dbl>         <dbl>   <dbl>   <dbl>   <dbl>   <dbl> <chr>     <dbl>   <dbl>
##   1 1041801             5       3       3       3       2 3             4       4
##   2 1044572             8       7       5      10       7 9             5       5
##   3 1047630             7       4       6       4       6 1             4       3
##   4 1050670            10       7       7       6       4 10            4       1
##   5 1054590             7       3       2      10       5 10            5       4
##   6 1054593            10       5       5       3       6 7             7      10
##   7 1057013             8       4       5       1       2 NA            7       3
##   8 1065726             5       2       3       4       2 7             3       6
##   9 1072179            10       7       7       3       8 5             7       4
##  10 1080185            10      10      10       8       6 1             8       9
##  11 1084584             5       4       4       9       2 10            5       6
##  12 1091262             2       5       3       3       6 7             7       5
##  13 1099510            10       4       3       1       3 3             6       5
##  14 1100524             6      10      10       2       8 10            7       3
##  15 1102573             5       6       5       6      10 1             3       1
##  16 1103608            10      10      10       4       8 1             8      10
##  17 1105257             3       7       7       4       4 9             4       8
## # ... with 2 more variables: Mitoses <dbl>, Class <chr>, and abbreviated
## #   variable names 1: ‘CL. thickness‘, 2: ‘Cell size‘, 3: ‘Cell Shape‘,
## #   4: ‘Marg. Adhesion‘, 5: ‘Epith. C.size‘, 6: ‘Bare. Nuclei‘,
## #   7: ‘Bl. Cromatin‘, 8: ‘Normal nucleoli‘
```

```
#There 17 respondents who are malignant.
#And there are total of 49 respondent.
```

```
#Getting the percentage
17  / 49 * 100
```

```
## [1] 34.69388
```

```
#9. Export the data abalone to the Microsoft excel file. Copy the codes.

library("AppliedPredictiveModeling")
```

```
## Warning: package 'AppliedPredictiveModeling' was built under R version 4.2.2
```

```
data("abalone")
View(abalone)
head(abalone)
```

```
##   Type LongestShell Diameter Height WholeWeight ShuckedWeight VisceraWeight
## 1    M        0.455    0.365  0.095      0.5140        0.2245        0.1010
## 2    M        0.350    0.265  0.090      0.2255        0.0995        0.0485
## 3    F        0.530    0.420  0.135      0.6770        0.2565        0.1415
## 4    M        0.440    0.365  0.125      0.5160        0.2155        0.1140
## 5    I        0.330    0.255  0.080      0.2050        0.0895        0.0395
## 6    I        0.425    0.300  0.095      0.3515        0.1410        0.0775
##   ShellWeight Rings
## 1       0.150    15
## 2       0.070     7
## 3       0.210     9
## 4       0.155    10
## 5       0.055     7
## 6       0.120     8
```

```
summary(abalone)
```

```
##  Type      LongestShell      Diameter          Height        WholeWeight
##  F:1307   Min.   :0.075   Min.   :0.0550   Min.   :0.0000   Min.   :0.0020
##  I:1342   1st Qu.:0.450   1st Qu.:0.3500   1st Qu.:0.1150   1st Qu.:0.4415
##  M:1528   Median :0.545   Median :0.4250   Median :0.1400   Median :0.7995
##           Mean   :0.524   Mean   :0.4079   Mean   :0.1395   Mean   :0.8287
##           3rd Qu.:0.615   3rd Qu.:0.4800   3rd Qu.:0.1650   3rd Qu.:1.1530
##           Max.   :0.815   Max.   :0.6500   Max.   :1.1300   Max.   :2.8255
##  ShuckedWeight    VisceraWeight     ShellWeight         Rings
##  Min.   :0.0010   Min.   :0.0005   Min.   :0.0015   Min.   : 1.000
##  1st Qu.:0.1860   1st Qu.:0.0935   1st Qu.:0.1300   1st Qu.: 8.000
##  Median :0.3360   Median :0.1710   Median :0.2340   Median : 9.000
##  Mean   :0.3594   Mean   :0.1806   Mean   :0.2388   Mean   : 9.934
##  3rd Qu.:0.5020   3rd Qu.:0.2530   3rd Qu.:0.3290   3rd Qu.:11.000
##  Max.   :1.4880   Max.   :0.7600   Max.   :1.0050   Max.   :29.000
```

```
#Exporting the data abalone to the Microsoft excel file

library(xlsx)
```

```
## Warning: package 'xlsx' was built under R version 4.2.2
```

```
write.xlsx("abalone","B:\\Git\\Worksheets\\Acsota_Workesheet7\\abalone.xlsx")
```