Worksheet-7a

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#Worksheet7a

install.packages("Hmisc")

install.packages("pastecs") #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
```

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

#Write the codes and its result.

library(Hmisc) library(pastecs)

describe(DF) stat.desc(DF)

#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
```

#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
```

#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
```

#a. Apply the factor function and factor level. Describe the results.

```
hello <- function(state) hello
```

#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) #a. Calculate the sample mean income for each state we can now use the special #function tapply():

```
Calc <- tapply(state, incomes, mean) Calc
```

#b. Copy the results and interpret.

4041424346484951525456585960616264656970

#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
```

#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 standard error. #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
```

#8. The data sets are about the breast cancer Wisconsin. The samples arrive periodically as Dr. Wolberg reports his clinical cases. The database therefore reflects this #chronological grouping of the data. You can create this dataset in Microsoft Excel.

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

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

```
library("readxl")

DATA <- read_excel("C:\\Users\\PC\\Desktop\\worksheets//Breast_Cancer.xlsx") DATA
```

#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
```

#c.2 Coefficient of variability for Marginal Adhesion.

```
COV <- sd(DATA$‘Marg. Adhesion‘) / mean(DATA$‘Marg. Adhesion‘)* 100 COV
```

#c.3 Number of null values of Bare Nuclei.

```
Null_Values <- subset(DATA,‘Bare. Nuclei‘ == "NA") #c.4 Mean and
```

standard deviation for Bland Chromatin

```
mean(DATA$‘Bl. Cromatin‘) sd(DATA$‘Bl.
Cromatin‘)
```

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

```
Calc_Mean <- mean(DATA$‘Cell Shape‘) Calc_Mean
```

#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
#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
```

#Constructing the confidence interval

```
numG <- numF * numC

#Lower numH <- Calc_Mean -

numG

#Upper

numI <- Calc_Mean + numG c(numH,numI)

#d. How many attributes? attributes(DATA)

#e. Find the percentage of respondents who are malignant. Interpret the results.

P_R <- subset(DATA, Class == "maligant")
P_R

#There 17 respondents who are malignant. #And there are total of 49 respondent. #Getting the
percentage

17 / 49 * 100

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

install.packages("AppliedPredictiveModeling")

library("AppliedPredictiveModeling")
data("abalone") View(abalone) head(abalone)
summary(abalone)

#Exporting the data abalone to the Microsoft excel file install.packages(“xlsxjars”)

library(xlsx) write.xlsx("abalone","C:\\Users\\PC\\Desktop\\worksheets\\abalone.xlsx")")
```