

# RWorksheet\_6

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1. Create a data frame for the table below. Show your solution.

```
Student_score <- data.frame(  
  Student = c(1:10),  
  Pre_test = c(55,54,47,57,51,61,57,54,63,58),  
  Post_test = c(61,60,56,63,56,63,59,56,62,61)  
)  
Student_score
```

##	Student	Pre_test	Post_test
## 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

```
names(Student_score) <- c("Student", "Pre-test", "Post-test")
```

1a.

```
install.packages("Hmisc")
```

```
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.3'  
## (as 'lib' is unspecified)
```

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

```
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.3'  
## (as 'lib' is unspecified)
```

```
library(Hmisc)
```

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

```
library(pastecs)
```

```
#Hmisc
describe(Student_score)
```

```
## Student_score
##
## 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
##
## 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
##
## For the frequency table, variable is rounded to the nearest 0
## -----
## Pre-test
##      n missing distinct    Info    Mean      Gmd
##      10       0         8    0.988    55.7    5.444
##
## 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
##
## For the frequency table, variable is rounded to the nearest 0
## -----
## Post-test
##      n missing distinct    Info    Mean      Gmd
##      10       0         6    0.964    59.7    3.311
##
## 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
##
## For the frequency table, variable is rounded to the nearest 0
## -----
```

```
#pastecs
stat.desc(Student_score)
```

```
##      Student      Pre-test      Post-test
## 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.

The data were 10,10,10, 20,20,50,10,20,10,50,20,50,20,10.

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

ordered_lvl <- ordered(fertilizer_lvl, levels = c(10,20,50))

ordered_lvl
```

```
## [1] 10 10 10 20 20 50 10 20 10 50 20 50 20 10
## Levels: 10 < 20 < 50
```

*# The numbers inside the square brackets represent the observations or data points and below it are the levels.*

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

```
exercise_lvl <- c("l", "n", "n", "i", "l", "l", "n", "n", "i", "l")

factor_exercise <- factor(exercise_lvl, levels = c("n", "l", "i"))

factor_exercise
```

```
## [1] l n n i l l n n i l
## Levels: n l i
```

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")

factor_state <- factor(state, levels = c("act", "nsw", "nt", "qld", "sa", "tas", "vic", "wa"))

factor_state
```

```
## [1] tas sa qld nsw nsw nt wa wa qld vic nsw vic qld qld sa tas sa nt wa
## [20] vic qld nsw nsw wa sa act nsw vic vic act
## Levels: act nsw nt qld sa tas vic wa
```

*#the number inside the square brackets are the observations and below it are the levels. the levels rep*

5. From #4 - continuation:

```
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)

incmeans <- tapply(incomes, factor_state, mean)
```

```
incmeans
```

```
##      act      nsw      nt      qld      sa      tas      vic      wa
## 44.50000 57.33333 55.50000 53.60000 55.00000 60.50000 56.00000 52.25000
```

```
#b.
```

```
# we see that it calculates the means of every states.
```

6. Calculate the standard errors of the state income means (refer again to number 5)

```
stdError <- function(x) sqrt(var(x)/length(x))
incster <- tapply(incomes, factor_state, stdError)
incster
```

```
##      act      nsw      nt      qld      sa      tas      vic      wa
## 1.500000 4.310195 4.500000 4.106093 2.738613 0.500000 5.244044 2.657536
```

```
#b.
```

```
# in no.5 we see the means of every states while here, we calculate the standard error of each states.
```

```
# the standard errors provide a measure of the uncertainty associated with the sample mean incomes for
```

7.

```
install.packages("titanic")
```

```
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.3'
```

```
## (as 'lib' is unspecified)
```

```
library(titanic)
```

```
data("titanic_train")
```

```
survived <- subset(titanic_train, Survived == 1)
```

```
not_survived <- subset(titanic_train, Survived == 0)
```

```
head(survived)
```

```
##      PassengerId Survived Pclass
## 2             2         1       1
## 3             3         1       3
## 4             4         1       1
## 9             9         1       3
## 10            10         1       2
## 11            11         1       3
##
##                                Name      Sex Age SibSp Parch
## 2  Cumings, Mrs. John Bradley (Florence Briggs Thayer) female  38     1     0
## 3                                Heikkinen, Miss. Laina female  26     0     0
## 4      Futrelle, Mrs. Jacques Heath (Lily May Peel) female  35     1     0
## 9    Johnson, Mrs. Oscar W (Elisabeth Vilhelmina Berg) female  27     0     2
## 10                               Nasser, Mrs. Nicholas (Adele Achem) female  14     1     0
## 11                               Sandstrom, Miss. Marguerite Rut female   4     1     1
##
##      Ticket      Fare Cabin Embarked
## 2      PC 17599 71.2833   C85         C
## 3  STON/O2. 3101282  7.9250         S
## 4      113803 53.1000  C123         S
```

```
## 9          347742 11.1333          S
## 10         237736 30.0708          C
## 11         PP 9549 16.7000      G6      S
```

```
head(not_survived)
```

```
##      PassengerId Survived Pclass                Name Sex Age SibSp
## 1             1         0       3      Braund, Mr. Owen Harris male  22     1
## 5             5         0       3      Allen, Mr. William Henry male  35     0
## 6             6         0       3            Moran, Mr. James male  NA     0
## 7             7         0       1      McCarthy, Mr. Timothy J male  54     0
## 8             8         0       3      Palsson, Master. Gosta Leonard male   2     3
## 13           13         0       3      Saunderson, Mr. William Henry male  20     0
##      Parch      Ticket    Fare Cabin Embarked
## 1         0 A/5 21171   7.2500          S
## 5         0  373450   8.0500          S
## 6         0  330877   8.4583          Q
## 7         0   17463  51.8625     E46     S
## 8         1  349909  21.0750          S
## 13        0 A/5. 2151   8.0500          S
```

8.

```
breastcancer_data <- read.csv("breastcancer_wisconsin.csv")
```

```
str(breastcancer_data)
```

```
## 'data.frame':    699 obs. of  11 variables:
## $ id          : int  1000025 1002945 1015425 1016277 1017023 1017122 1018099 1018561 1033078 1033078 1033078
## $ clump_thickness : int  5 5 3 6 4 8 1 2 2 4 ...
## $ size_uniformity : int  1 4 1 8 1 10 1 1 1 2 ...
## $ shape_uniformity : int  1 4 1 8 1 10 1 2 1 1 ...
## $ marginal_adhesion: int  1 5 1 1 3 8 1 1 1 1 ...
## $ epithelial_size : int  2 7 2 3 2 7 2 2 2 2 ...
## $ bare_nucleoli    : chr  "1" "10" "2" "4" ...
## $ bland_chromatin   : int  3 3 3 3 3 9 3 3 1 2 ...
## $ normal_nucleoli   : int  1 2 1 7 1 7 1 1 1 1 ...
## $ mitoses          : int  1 1 1 1 1 1 1 1 5 1 ...
## $ class            : int  2 2 2 2 2 4 2 2 2 2 ...
```

```
head(breastcancer_data)
```

```
##      id clump_thickness size_uniformity shape_uniformity marginal_adhesion
## 1 1000025             5             1             1             1
## 2 1002945             5             4             4             5
## 3 1015425             3             1             1             1
## 4 1016277             6             8             8             1
## 5 1017023             4             1             1             3
## 6 1017122             8            10            10             8
##      epithelial_size bare_nucleoli bland_chromatin normal_nucleoli mitoses class
## 1             2             1             3             1             1     2
## 2             7            10             3             2             1     2
## 3             2             2             3             1             1     2
## 4             3             4             3             7             1     2
## 5             2             1             3             1             1     2
## 6             7            10             9             7             1     4
```

```
summary(breastcancer_data)
```

```
##           id           clump_thickness size_uniformity shape_uniformity
## Min.      : 61634    Min.      : 1.000    Min.      : 1.000    Min.      : 1.000
## 1st Qu.: 870688    1st Qu.: 2.000    1st Qu.: 1.000    1st Qu.: 1.000
## Median : 1171710    Median : 4.000    Median : 1.000    Median : 1.000
## Mean     : 1071704    Mean     : 4.418    Mean     : 3.134    Mean     : 3.207
## 3rd Qu.: 1238298    3rd Qu.: 6.000    3rd Qu.: 5.000    3rd Qu.: 5.000
## Max.     :13454352    Max.     :10.000    Max.     :10.000    Max.     :10.000
## marginal_adhesion epithelial_size bare_nucleoli      bland_chromatin
## Min.      : 1.000    Min.      : 1.000    Length:699      Min.      : 1.000
## 1st Qu.: 1.000    1st Qu.: 2.000    Class :character 1st Qu.: 2.000
## Median : 1.000    Median : 2.000    Mode  :character Median : 3.000
## Mean     : 2.807    Mean     : 3.216                      Mean     : 3.438
## 3rd Qu.: 4.000    3rd Qu.: 4.000                      3rd Qu.: 5.000
## Max.     :10.000    Max.     :10.000                      Max.     :10.000
## normal_nucleoli      mitoses           class
## Min.      : 1.000    Min.      : 1.000    Min.      :2.00
## 1st Qu.: 1.000    1st Qu.: 1.000    1st Qu.:2.00
## Median : 1.000    Median : 1.000    Median :2.00
## Mean     : 2.867    Mean     : 1.589    Mean     :2.69
## 3rd Qu.: 4.000    3rd Qu.: 1.000    3rd Qu.:4.00
## Max.     :10.000    Max.     :10.000    Max.     :4.00
```

```
#the dataset is about the data of the breast cancer.
```

8d.

```
install.packages("psych")
```

```
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.3'
## (as 'lib' is unspecified)
```

```
library(psych)
```

```
##
## Attaching package: 'psych'
## The following object is masked from 'package:Hmisc':
##
##      describe
```

```
clump_thickness <- breastcancer_data$ClumpThickness
marginal_adhesion <- breastcancer_data$MarginalAdhesion
bare_nuclei <- breastcancer_data$BareNuclei
bland_chromatin <- breastcancer_data$BlandChromatin
uniformity_cell_shape <- breastcancer_data$UniformityCellShape
```

```
#d.1 Standard error of the mean for clump thickness.
```

```
SE_clumpthickness <- sd(clump_thickness) / sqrt(length(clump_thickness))
SE_clumpthickness
```

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

```
#d.2 Coefficient of variability for Marginal Adhesion.
```

```
CV_marginaladhesion <- sd(marginal_adhesion) / mean(marginal_adhesion)
```

```
## Warning in mean.default(marginal_adhesion): argument is not numeric or logical:
## returning NA
```

```
CV_marginaladhesion
```

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

```
#d.3 Number of null values of Bare Nuclei.
```

```
nullval_barenuclei <- sum(is.na(bare_nuclei))
```

```
nullval_barenuclei
```

```
## [1] 0
```

```
#d.4 Mean and standard deviation for Bland Chromatin
```

```
mean_blandchromatin <- mean(breastcancer_data$bland_chromatin)
```

```
sd_blandchromatin <- sd(breastcancer_data$bland_chromatin)
```

```
mean_blandchromatin
```

```
## [1] 3.437768
```

```
sd_blandchromatin
```

```
## [1] 2.438364
```

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

```
ci_uniformitycellshape <- tryCatch(  
  t.test(breastcancer_data$`uniformity_cell_shape`)$conf.int,  
  error = function(e) NULL  
)
```

```
## Warning in mean.default(x): argument is not numeric or logical: returning NA
```

```
ci_uniformitycellshape
```

```
## NULL
```

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

```
install.packages("AppliedPredictiveModeling")
```

```
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.3'
```

```
## (as 'lib' is unspecified)
```

```
library(AppliedPredictiveModeling)
```

```
data("abalone")
```

```
install.packages("openxlsx")
```

```
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.3'
```

```
## (as 'lib' is unspecified)
```

```
library(openxlsx)
```

```
write.xlsx(abalone, file = "abalone.xlsx")
```

```
View(abalone)
```

```
## Warning in View(abalone): unable to open display
```

```
## Error in .External2(C_dataviewer, x, title): unable to start data viewer
```

```
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
```