

RWorksheet_Sadural#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
```