

RWork- sheet_5

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```
#..
```

```
install.packages("htmltools")
```

```
## 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)
```

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

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

```
#1
```

```
library(Hmisc)
```

```
##
```

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

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      format.pval, units
```

```
library(pastecs)
```

```
student_score <- data.frame (
  Student = c(1,2,3,4,5,6,7,8,9,10),
  '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
```

```
summary(student_score)
```

```
##      Student      Pre.test      Post.test
## Min.   : 1.00   Min.   :47.00   Min.   :56.00
## 1st Qu.: 3.25   1st Qu.:54.00   1st Qu.:56.75
## Median : 5.50   Median :56.00   Median :60.50
## Mean   : 5.50   Mean   :55.70   Mean   :59.70
## 3rd Qu.: 7.75   3rd Qu.:57.75   3rd Qu.:61.75
## Max.   :10.00   Max.   :63.00   Max.   :63.00
```

```
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
```

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

```
fertilizer_levels <- factor(agri_data, levels = c(10, 20, 50), ordered = TRUE)
```

```
fertilizer_levels
```

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

```
#3
```

#The following represents the 10 exercise levels in which "n" stands for none, "l" stands for light, and "i" stands for intense.

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

```
## [1] "l" "n" "n" "i" "l" "l" "n" "n" "i" "l"
```

```
#4
```

```
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_factor <- factor(state, levels = unique (state))
state_factor
```

```
## [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: tas sa qld nsw nt wa vic act
```

```
#5
```

```
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, state_factor, mean)
incmeans
```

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

```
#5b
```

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

```
#The average income for tax accountants varies across different states in Australia. In Tasmania, tax a
```

```
#6a
```

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

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

```
#6b
```

```
#The accuracy of the average income estimate is very good for Tasmania, with a small standard error of
```

```
#7
```

```
data (Titanic)
Titanic
```

```
## , , Age = Child, Survived = No
```

```
##
```

```
##      Sex
```

```
## Class Male Female
```

```
## 1st      0      0
```

```
## 2nd      0      0
```

```
## 3rd     35     17
```

```
## Crew      0      0
```

```
##
```

```
## , , Age = Adult, Survived = No
```

```
##
```

```
##      Sex
```

```
## Class Male Female
```

```
## 1st    118      4
```

```
## 2nd    154     13
```

```
## 3rd    387     89
```

```
## Crew   670      3
```

```
##
```

```
## , , Age = Child, Survived = Yes
##
##      Sex
## Class  Male Female
## 1st      5      1
## 2nd     11     13
## 3rd     13     14
## Crew      0      0
##
## , , Age = Adult, Survived = Yes
##
##      Sex
## Class  Male Female
## 1st     57     140
## 2nd     14      80
## 3rd     75      76
## Crew   192      20
```

#7b

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   first, last

## The following objects are masked from 'package:Hmisc':
##
##   src, summarize

## The following objects are masked from 'package:base':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
```

```
Titanic_df <- as.data.frame(Titanic)
survivors <- Titanic_df %>%filter(Survived == "Yes")
head(survivors)
```

```
##   Class   Sex   Age Survived Freq
## 1  1st  Male Child    Yes     5
## 2  2nd  Male Child    Yes    11
## 3  3rd  Male Child    Yes    13
## 4  Crew  Male Child    Yes     0
## 5  1st Female Child    Yes     1
## 6  2nd Female Child    Yes    13
```

```
tail(survivors)
```

```
##   Class   Sex   Age Survived Freq
## 11  3rd  Male Adult    Yes    75
## 12  Crew  Male Adult    Yes   192
## 13  1st Female Adult    Yes   140
```

```
## 14 2nd Female Adult Yes 80
## 15 3rd Female Adult Yes 76
## 16 Crew Female Adult Yes 20
```

```
non_survivors <- Titanic_df %>%filter(Survived == "No")
head(non_survivors)
```

```
## Class Sex Age Survived Freq
## 1 1st Male Child No 0
## 2 2nd Male Child No 0
## 3 3rd Male Child No 35
## 4 Crew Male Child No 0
## 5 1st Female Child No 0
## 6 2nd Female Child No 0
```

```
tail(survivors)
```

```
## Class Sex Age Survived Freq
## 11 3rd Male Adult Yes 75
## 12 Crew Male Adult Yes 192
## 13 1st Female Adult Yes 140
## 14 2nd Female Adult Yes 80
## 15 3rd Female Adult Yes 76
## 16 Crew Female Adult Yes 20
```

```
#8
```

```
library(readr)
```

```
breastcancer_wisconsin <- read_csv("/cloud/project/Rworksheet6/breastcancer_wisconsin.csv", show_col_types = FALSE)
breastcancer_wisconsin
```

```
## # A tibble: 699 x 11
```

```
##      id clump_thickness size_uniformity shape_uniformity marginal_adhesion
##      <dbl>          <dbl>          <dbl>          <dbl>          <dbl>
## 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
## 7 1018099           1             1             1             1
## 8 1018561           2             1             2             1
## 9 1033078           2             1             1             1
## 10 1033078          4             2             1             1
```

```
## # i 689 more rows
```

```
## # i 6 more variables: epithelial_size <dbl>, bare_nucleoli <chr>,
```

```
## # bland_chromatin <dbl>, normal_nucleoli <dbl>, mitoses <dbl>, class <dbl>
```

```
#id: A unique identifier for each biopsy. clump_thickness: Describes the thickness of the clumps in the
```

```
#8d.1
```

```
sd_clump_thickness <- sd(breastcancer_wisconsin$clump_thickness)
```

```
sample_size <- length(breastcancer_wisconsin$clump_thickness)
```

```
sem_clump_thickness <- sd_clump_thickness / sqrt(sample_size)
```

```
cat("Standard Error of the Mean for Clump Thickness:", sem_clump_thickness, "\n")
```

```
## Standard Error of the Mean for Clump Thickness: 0.1065011
```

```
#8d.2
```

```
mean_marginal_adhesion <- mean(breastcancer_wisconsin$marginal_adhesion)
```

```
sd_marginal_adhesion <- sd(breastcancer_wisconsin$marginal_adhesion)
```

```
cv_marginal_adhesion <- (sd_marginal_adhesion / mean_marginal_adhesion) * 100
```

```
cat("Coefficient of Variation for Marginal Adhesion:", cv_marginal_adhesion, "%\n")
```

```
## Coefficient of Variation for Marginal Adhesion: 101.7283 %
```

```
#8d.3
```

```
num_null_bare_nuclei <- sum(is.na(breastcancer_wisconsin$bare_nucleoli))
```

```
cat("Number of null values for Bare Nuclei:", num_null_bare_nuclei, "\n")
```

```
## Number of null values for Bare Nuclei: 15
```

```
#8d.4
```

```
mean_bland_chromatin <- mean(breastcancer_wisconsin$bland_chromatin, na.rm = TRUE)
```

```
sd_bland_chromatin <- sd(breastcancer_wisconsin$bland_chromatin, na.rm = TRUE)
```

```
cat("Mean for Bland Chromatin:", mean_bland_chromatin, "\n")
```

```
## Mean for Bland Chromatin: 3.437768
```

```
cat("Standard Deviation for Bland Chromatin:", sd_bland_chromatin, "\n")
```

```
## Standard Deviation for Bland Chromatin: 2.438364
```

```
#8d.5
```

```
mean_value <- mean(breastcancer_wisconsin$shape_uniformity, na.rm = TRUE)
```

```
se <- sd(breastcancer_wisconsin$shape_uniformity, na.rm = TRUE) / sqrt(length(breastcancer_wisconsin$shape_uniformity))
```

```
confidence_level <- 0.95
```

```
margin_of_error <- qt((1 + confidence_level) / 2, df = length(breastcancer_wisconsin$shape_uniformity))
```

```
confidence_interval <- c(mean_value - margin_of_error, mean_value + margin_of_error)
```

```
cat("Confidence Interval (", confidence_level * 100, "%) :", confidence_interval, "\n")
```

```
## Confidence Interval ( 95 %) : 2.986741 3.428138
```

```
#8d
```

```
column_names <- names(breastcancer_wisconsin)
```

```
column_names
```

```
## [1] "id" "clump_thickness" "size_uniformity"
```

```
## [4] "shape_uniformity" "marginal_adhesion" "epithelial_size"
```

```
## [7] "bare_nucleoli" "bland_chromatin" "normal_nucleoli"
```

```
## [10] "mitoses" "class"
```

```

#8e
malignant_count <- sum(breastcancer_wisconsin$class == 4)

malignant_percentage <- (malignant_count / nrow(breastcancer_wisconsin)) * 100

cat("Percentage of respondents who are malignant:", malignant_percentage, "%\n")

## Percentage of respondents who are malignant: 34.47783 %

#9
library("AppliedPredictiveModeling")
library(readr)
abalone <- read_csv("/cloud/project/Rworksheet6/abalone.csv")

## Rows: 4177 Columns: 9
## -- Column specification -----
## Delimiter: ","
## chr (1): Sex
## dbl (8): Length, Diameter, Height, Whole weight, Shucked weight, Viscera wei...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
abalone

## # A tibble: 4,177 x 9
##   Sex    Length Diameter Height `Whole weight` `Shucked weight` `Viscera weight`
##   <chr>   <dbl>   <dbl>  <dbl>         <dbl>         <dbl>         <dbl>
## 1 M      0.455    0.365  0.095         0.514         0.224         0.101
## 2 M      0.35     0.265  0.09         0.226         0.0995        0.0485
## 3 F      0.53     0.42   0.135        0.677         0.256         0.142
## 4 M      0.44     0.365  0.125        0.516         0.216         0.114
## 5 I      0.33     0.255  0.08         0.205         0.0895        0.0395
## 6 I      0.425    0.3     0.095        0.352         0.141         0.0775
## 7 F      0.53     0.415  0.15         0.778         0.237         0.142
## 8 F      0.545    0.425  0.125        0.768         0.294         0.150
## 9 M      0.475    0.37   0.125        0.509         0.216         0.112
## 10 F     0.55     0.44   0.15         0.894         0.314         0.151
## # i 4,167 more rows
## # i 2 more variables: `Shell weight` <dbl>, Rings <dbl>
head(abalone)

## # A tibble: 6 x 9
##   Sex    Length Diameter Height `Whole weight` `Shucked weight` `Viscera weight`
##   <chr>   <dbl>   <dbl>  <dbl>         <dbl>         <dbl>         <dbl>
## 1 M      0.455    0.365  0.095         0.514         0.224         0.101
## 2 M      0.35     0.265  0.09         0.226         0.0995        0.0485
## 3 F      0.53     0.42   0.135        0.677         0.256         0.142
## 4 M      0.44     0.365  0.125        0.516         0.216         0.114
## 5 I      0.33     0.255  0.08         0.205         0.0895        0.0395
## 6 I      0.425    0.3     0.095        0.352         0.141         0.0775
## # i 2 more variables: `Shell weight` <dbl>, Rings <dbl>
summary(abalone)

```

##	Sex	Length	Diameter	Height
##	Length:4177	Min. :0.075	Min. :0.0550	Min. :0.0000
##	Class :character	1st Qu.:0.450	1st Qu.:0.3500	1st Qu.:0.1150
##	Mode :character	Median :0.545	Median :0.4250	Median :0.1400
##		Mean :0.524	Mean :0.4079	Mean :0.1395
##		3rd Qu.:0.615	3rd Qu.:0.4800	3rd Qu.:0.1650
##		Max. :0.815	Max. :0.6500	Max. :1.1300
##	Whole weight	Shucked weight	Viscera weight	Shell weight
##	Min. :0.0020	Min. :0.0010	Min. :0.0005	Min. :0.0015
##	1st Qu.:0.4415	1st Qu.:0.1860	1st Qu.:0.0935	1st Qu.:0.1300
##	Median :0.7995	Median :0.3360	Median :0.1710	Median :0.2340
##	Mean :0.8287	Mean :0.3594	Mean :0.1806	Mean :0.2388
##	3rd Qu.:1.1530	3rd Qu.:0.5020	3rd Qu.:0.2530	3rd Qu.:0.3290
##	Max. :2.8255	Max. :1.4880	Max. :0.7600	Max. :1.0050
##	Rings			
##	Min. : 1.000			
##	1st Qu.: 8.000			
##	Median : 9.000			
##	Mean : 9.934			
##	3rd Qu.:11.000			
##	Max. :29.000			