

RWorksheet_#7a

Jessa Mae Mirabuena

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```
library(Hmisc)

## Loading required package: lattice

## Loading required package: survival

## Loading required package: Formula

## Loading required package: ggplot2

##
## Attaching package: 'Hmisc'

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

library(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)

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

| | 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.

```
describe(a)
```

```
## a
##
## 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(a)

##      Student      PreTest      PostTest
## nbr.val 10.0000000 10.0000000 10.0000000
## nbr.null 0.0000000 0.0000000 0.0000000
## nbr.na   0.0000000 0.0000000 0.0000000
## min      1.0000000 47.0000000 56.0000000
## max      10.0000000 63.0000000 63.0000000
## range     9.0000000 16.0000000 7.0000000
```

```
## 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_Levels <- c(10,10,10,20,20,50,10,
                       20,10,50,20,50,20,10)
```

#a. Write the codes and describe the result.

```
order <- factor(Fertilizer_Levels, ordered = TRUE)
order

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

```
Df <- data.frame(Subjects)
Df

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

#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"

```

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

```

c <- factor(state)
c
## [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

levels(c)
## [1] "act" "nsw" "nt"  "qld" "sa"  "tas" "vic" "wa"

```

#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(): #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"

```

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

```

c <- factor(state)
c

```

```
## [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

levels(c)

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

#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()`:

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

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

meanincome <- tapply(incomes,state, mean )
meanincome

##      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. Copy the results and interpret. # act nsw nt #44.50000 57.33333 55.50000 # qld sa tas
#53.60000 55.00000 60.50000 # vic wa #56.00000 52.25000 #these are the mean of
income

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

```
stdError <- function(x) sqrt(var(x)/length(x))
```

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

```
incomestdr <- tapply(incomes, state, stdError)
incomestdr

##      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. Interpret the result. #It tells the sample mean of income #7. Use the titanic Data set

```
data("Titanic")
titanic<- data.frame(Titanic)
```

#a. subset the titatic dataset of those who survived and not survived. Show the #codes and its result.

```
#Survives <- subset(Titanic, Survived == "Yes") #Survives
```

```
#Died <- subset(Titanic, Survived == "No") #Died
```

#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.

```
getwd()
## [1] "/cloud/project"

breastcancer<- read.csv(file = "Breast_Cancer.csv", sep = "",stringsAsFactors
= F)
breastcancer
```

| | ID.CL. | thickness.Cell | size.Cell |
|-------|--|----------------|-----------|
| ## | Shape.Marg. | | |
| ## 1 | 1000025,5,1,1,1,2,1,3,1,1,benign | NA | NA |
| NA | | | |
| ## 2 | 1002945,5,4,4,5,7,10,3,2,1,benign | NA | NA |
| NA | | | |
| ## 3 | 1015425,3,1,1,1,2,2,3,1,1,benign | NA | NA |
| NA | | | |
| ## 4 | 1016277,6,8,8,1,3,4,3,7,1,benign | NA | NA |
| NA | | | |
| ## 5 | 1017023,4,1,1,3,2,1,3,1,1,benign | NA | NA |
| NA | | | |
| ## 6 | 1017122,8,10,10,8,7,10,9,7,1,malignant | NA | NA |
| NA | | | |
| ## 7 | 1018099,1,1,1,1,2,10,3,1,1,benign | NA | NA |
| NA | | | |
| ## 8 | 1018561,2,1,2,1,2,1,3,1,1,benign | NA | NA |
| NA | | | |
| ## 9 | 1033078,2,1,1,1,2,1,1,1,5,benign | NA | NA |
| NA | | | |
| ## 10 | 1033078,4,2,1,1,2,1,2,1,1,benign | NA | NA |
| NA | | | |
| ## 11 | 1035283,1,1,1,1,1,1,3,1,1,benign | NA | NA |
| NA | | | |
| ## 12 | 1036172,2,1,1,1,2,1,2,1,1,benign | NA | NA |
| NA | | | |
| ## 13 | 1041801,5,3,3,3,2,3,4,4,2,maligant | NA | NA |
| NA | | | |
| ## 14 | 1043999,1,1,1,1,2,3,3,1,1,benign | NA | NA |

| | | | |
|-------|---------------------------------------|----|----|
| NA | | | |
| ## 15 | 1044572,8,7,5,10,7,9,5,5,4,maligant | NA | NA |
| NA | | | |
| ## 16 | 1047630,7,4,6,4,6,1,4,3,1,maligant | NA | NA |
| NA | | | |
| ## 17 | 1048672,4,1,1,1,2,1,2,1,1,benign | NA | NA |
| NA | | | |
| ## 18 | 1049815,4,1,1,1,2,1,3,1,1,benign | NA | NA |
| NA | | | |
| ## 19 | 1050670,10,7,7,6,4,10,4,1,2,maligant | NA | NA |
| NA | | | |
| ## 20 | 1050718,6,1,1,1,2,1,3,1,1,benign | NA | NA |
| NA | | | |
| ## 21 | 1054590,7,3,2,10,5,10,5,4,4,maligant | NA | NA |
| NA | | | |
| ## 22 | 1054593,10,5,5,3,6,7,7,10,1,maligant | NA | NA |
| NA | | | |
| ## 23 | 1056784,3,1,1,1,2,1,2,1,1,benign | NA | NA |
| NA | | | |
| ## 24 | 1057013,8,4,5,1,2,NA,7,3,1,maligant | NA | NA |
| NA | | | |
| ## 25 | 1059552,1,1,1,1,2,1,3,1,1,benign | NA | NA |
| NA | | | |
| ## 26 | 1065726,5,2,3,4,2,7,3,6,1,maligant | NA | NA |
| NA | | | |
| ## 27 | 1066373,3,2,1,1,1,1,2,1,1,benign | NA | NA |
| NA | | | |
| ## 28 | 1066979,5,1,1,1,2,1,2,1,1,benign | NA | NA |
| NA | | | |
| ## 29 | 1067444,2,1,1,1,2,1,2,1,1,benign | NA | NA |
| NA | | | |
| ## 30 | 1070935,1,1,3,1,2,1,1,1,1,benign | NA | NA |
| NA | | | |
| ## 31 | 1070935,3,1,1,1,1,1,2,1,1,benign | NA | NA |
| NA | | | |
| ## 32 | 1071760,2,1,1,1,2,1,3,1,1,benign | NA | NA |
| NA | | | |
| ## 33 | 1072179,10,7,7,3,8,5,7,4,3,maligant | NA | NA |
| NA | | | |
| ## 34 | 1074610,2,1,1,2,2,1,3,1,1,benign | NA | NA |
| NA | | | |
| ## 35 | 1075123,3,1,2,1,2,1,2,1,1,benign | NA | NA |
| NA | | | |
| ## 36 | 1079304,2,1,1,1,2,1,2,1,1,benign | NA | NA |
| NA | | | |
| ## 37 | 1080185,10,10,10,8,6,1,8,9,1,maligant | NA | NA |
| NA | | | |
| ## 38 | 1081791,6,2,1,1,1,1,7,1,1,benign | NA | NA |
| NA | | | |
| ## 39 | 1084584,5,4,4,9,2,10,5,6,1,maligant | NA | NA |

| | | | | | |
|-------|--|--------------|------------|-----------------|----|
| NA | | | | | |
| ## 40 | 1091262,2,5,3,3,6,7,7,5,1,maligant | | NA | | NA |
| NA | | | | | |
| ## 41 | 1096800,6,6,6,9,6,NA,7,8,1,benign | | NA | | NA |
| NA | | | | | |
| ## 42 | 1099510,10,4,3,1,3,3,6,5,2,maligant | | NA | | NA |
| NA | | | | | |
| ## 43 | 1100524,6,10,10,2,8,10,7,3,3,maligant | | NA | | NA |
| NA | | | | | |
| ## 44 | 1102573,5,6,5,6,10,1,3,1,1,maligant | | NA | | NA |
| NA | | | | | |
| ## 45 | 1103608,10,10,10,4,8,1,8,10,1,maligant | | NA | | NA |
| NA | | | | | |
| ## 46 | 1103722,1,1,1,1,2,1,2,1,2,benign | | NA | | NA |
| NA | | | | | |
| ## 47 | 1105257,3,7,7,4,4,9,4,8,1,maligant | | NA | | NA |
| NA | | | | | |
| ## 48 | 1105524,1,1,1,1,2,1,2,1,1,benign | | NA | | NA |
| NA | | | | | |
| ## 49 | 1106095,4,1,1,3,2,1,3,1,2,benign | | NA | | NA |
| NA | | | | | |
| ## | Adhesion.Epith. | C.size.Bare. | Nuclei.Bl. | Cromatin.Normal | |
| ## 1 | NA | NA | NA | NA | |
| ## 2 | NA | NA | NA | NA | |
| ## 3 | NA | NA | NA | NA | |
| ## 4 | NA | NA | NA | NA | |
| ## 5 | NA | NA | NA | NA | |
| ## 6 | NA | NA | NA | NA | |
| ## 7 | NA | NA | NA | NA | |
| ## 8 | NA | NA | NA | NA | |
| ## 9 | NA | NA | NA | NA | |
| ## 10 | NA | NA | NA | NA | |
| ## 11 | NA | NA | NA | NA | |
| ## 12 | NA | NA | NA | NA | |
| ## 13 | NA | NA | NA | NA | |
| ## 14 | NA | NA | NA | NA | |
| ## 15 | NA | NA | NA | NA | |
| ## 16 | NA | NA | NA | NA | |
| ## 17 | NA | NA | NA | NA | |
| ## 18 | NA | NA | NA | NA | |
| ## 19 | NA | NA | NA | NA | |
| ## 20 | NA | NA | NA | NA | |
| ## 21 | NA | NA | NA | NA | |
| ## 22 | NA | NA | NA | NA | |
| ## 23 | NA | NA | NA | NA | |
| ## 24 | NA | NA | NA | NA | |
| ## 25 | NA | NA | NA | NA | |
| ## 26 | NA | NA | NA | NA | |
| ## 27 | NA | NA | NA | NA | |
| ## 28 | NA | NA | NA | NA | |

| | | | | |
|-------|------------------------|----|----|----|
| ## 29 | NA | NA | NA | NA |
| ## 30 | NA | NA | NA | NA |
| ## 31 | NA | NA | NA | NA |
| ## 32 | NA | NA | NA | NA |
| ## 33 | NA | NA | NA | NA |
| ## 34 | NA | NA | NA | NA |
| ## 35 | NA | NA | NA | NA |
| ## 36 | NA | NA | NA | NA |
| ## 37 | NA | NA | NA | NA |
| ## 38 | NA | NA | NA | NA |
| ## 39 | NA | NA | NA | NA |
| ## 40 | NA | NA | NA | NA |
| ## 41 | NA | NA | NA | NA |
| ## 42 | NA | NA | NA | NA |
| ## 43 | NA | NA | NA | NA |
| ## 44 | NA | NA | NA | NA |
| ## 45 | NA | NA | NA | NA |
| ## 46 | NA | NA | NA | NA |
| ## 47 | NA | NA | NA | NA |
| ## 48 | NA | NA | NA | NA |
| ## 49 | NA | NA | NA | NA |
| ## | nucleoli.Mitoses.Class | | | |
| ## 1 | NA | | | |
| ## 2 | NA | | | |
| ## 3 | NA | | | |
| ## 4 | NA | | | |
| ## 5 | NA | | | |
| ## 6 | NA | | | |
| ## 7 | NA | | | |
| ## 8 | NA | | | |
| ## 9 | NA | | | |
| ## 10 | NA | | | |
| ## 11 | NA | | | |
| ## 12 | NA | | | |
| ## 13 | NA | | | |
| ## 14 | NA | | | |
| ## 15 | NA | | | |
| ## 16 | NA | | | |
| ## 17 | NA | | | |
| ## 18 | NA | | | |
| ## 19 | NA | | | |
| ## 20 | NA | | | |
| ## 21 | NA | | | |
| ## 22 | NA | | | |
| ## 23 | NA | | | |
| ## 24 | NA | | | |
| ## 25 | NA | | | |
| ## 26 | NA | | | |
| ## 27 | NA | | | |
| ## 28 | NA | | | |

```
## 29          NA
## 30          NA
## 31          NA
## 32          NA
## 33          NA
## 34          NA
## 35          NA
## 36          NA
## 37          NA
## 38          NA
## 39          NA
## 40          NA
## 41          NA
## 42          NA
## 43          NA
## 44          NA
## 45          NA
## 46          NA
## 47          NA
## 48          NA
## 49          NA
```

#c. Compute the descriptive statistics using different packages. Find the values of: #c.1 Standard error of the mean for clump thickness.

```
num8c1.n <- length(breastcancer$`CL. thickness`)
```

```
num8c1.sd <- sd(breastcancer$`CL. thickness`)
```

```
#num8c1.se <- num8c1.sd/sqrt (breastcancer$CL. thickness) #num8c1.se
```

#c.2 Coefficient of variability for Marginal Adhesion. Marginal_Adhesion <- as.numeric(breastcancer\$V5) stat.desc(Marginal_Adhesion)

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

```
Bare_Nuclei <- as.numeric(breastcancer$V7)
stat.desc( Bare_Nuclei)
```

```
## Warning in min(x): no non-missing arguments to min; returning Inf
```

```
## Warning in max(x): no non-missing arguments to max; returning -Inf
```

```
## Warning in qt((0.5 + p/2), (Nbrval - 1)): NaNs produced
```

| ## | nbr.val | nbr.null | nbr.na | min | max | |
|-------|---------|----------|--------|---------|--------------|---|
| range | | | | | | |
| ## | 0 | 0 | 0 | Inf | -Inf | - |
| Inf | | | | | | |
| ## | sum | median | mean | SE.mean | CI.mean.0.95 | |
| var | | | | | | |
| ## | 0 | NA | NaN | NA | NaN | |

```
NA
##      std.dev      coef.var
##      NA          NA
```

```
#c.4 Mean and standard deviation for Bland Chromatin ``{r, include = TRUE}
Bland_Chromatin <- as.numeric(breastcancer$V8)

mean(Bland_Chromatin , na.rm = TRUE) sd(Bland_Chromatin , na.rm = TRUE)

stat.desc( Bland_Chromatin)
```

```
#c.5 Confidence interval of the mean for Uniformity of Cell Shape
``{r, include = TRUE}
cell_shape <- as.numeric(breastcancer$V4)
stat.desc(cell_shape )
```

#d. How many attributes? #e. Find the percentage of respondents who are malignant. Interpret the results.

```
describe(breastcancer$V11, na.rm =TRUE)

##
## NULL
```

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

```
library("AppliedPredictiveModeling")
data("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
```

```
library(xlsx)
```

```
write.xlsx("abalone", "/cloud/project/Worksheet7a/abalone.xlsx")
```