Biostatistics: Theory and Applications in R (Virtual)

Week2_Session2_R_training2

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#Logical operators

```
4 == 4  #"==" equal to....

4!=4    # "!=" not equal to...

7>6     # TRUE

7<6     # FALSE

"hello" == "bye bye"    #FALSE

"hello" == "hello"      #TRUE

"hello" > "good afternnon"   #Alphabetical Order!

TRUE < FALSE       #TRUE = 1, FALSE = 0

TRUE==1   # binary number of TRUE is 1
FALSE==1

FALSE==0  # binary number of FALSE is 0
TRUE==0
```

#Create your first R-Objects!

```
n <- 5    # "<-" is used to assign a name for a R-Object
n
#  <-       # click Alt -

n = 6     # "=" you can also use it,
         #but "=" is also used for mathematical function, so better use "<-"
n

s <- 10
S          #R is case sensitive so capital "S" not found
s          # working, so do not try to mix capital and small letters
           # specially for "C" "O" "S" "V" "X"

my_basket <- 5
my_basket
```

#Special values

```
# R can also deal with infinity values

5/0  # Inf = infinity
-5/0 # -Inf = negative infinity
0/0  # NaN = not a number
# "NA" = "not available", "no data"
```

#Basic data types in R

```
my_numeric <- 4
my_character <- "universe"
my_logical <- FALSE

#Check class or mode and typeof of my_numeric, my_character and my_logical
class(my_numeric)
class(my_character)
class(my_logical)

mode(my_numeric)
mode(my_character)
mode(my_logical)

typeof(my_numeric)  #"double" is identical to "numeric".
typeof(my_character)
typeof(my_logical)

?typeof()
```

#Create a vector

```
my.vector <- c(1,2,3,4,5)
my.vector

is.vector(my.vector)  # TRUE
as.vector(my.vector)

my.new.vector <- 1:100
my.new.vector

seq(from=10, to=20)
seq(from=10, to=20, by=2)  #even numbers
seq(from=11, to=20, by=2)  #odd numbers


x <- c(a = 1, b = 2)
is.vector(x)
as.vector(x)
```

#Some simple functions that are useful for vector math

```
min  #minimum value of a set of numbers
max  #maximum of a set of numbers
sum #sum of all elements
mean #arithmetic mean
sd #standard deviationlength #length of a vector (or the number of columns in a data frame)
NROW #number of rows in a vector or data frame

my.vector <- c(1,2,3,4,5)

min(my.vector)
max(my.vector)
sum(my.vector)
mean(my.vector)
sd(my.vector)
NROW(my.vector)
```

#Assign name to a vector

```
#sum(my.new.vector) to the name ‚w2'
w1 <- sum(my.vector)

w2 <- sum(my.new.vector)

w1
w2
```

#Useful Functions for data transformation

```
x<- c(10, 100, 1000, 10000)

#natural log of x
log(x)
```

```
#base 10 log of x
log10(x)

#ex
exp(x)

#sine of x
sin(x)

#cosine of x
cos(x)

#tangent of x
tan(x)

#square root of x
sqrt(x)
sqrt((x[1]))
#absolute value of x
abs(x)
```

#Import data set from xlsx file

```
setwd("C:/Users/Fahmida Sultana/Desktop/R training/R_training_Class_02")
getwd()
setwd("C:/Users/Fahmida Sultana/Desktop/R training/R_training_Class_02")

#install openxlsx package or xlsx package
library(openxlsx)
library(readxl)

study_1 <- read.xlsx("Tree_height.xlsx")
str(study_1)


study_2 <- read_excel("Tree_height.xlsx", sheet = "study_2")
str(study_2)
```

#import CSV and text file

```
# directly via import Dataset
study_3 <- read.csv("C:/Users/Fahmida Sultana/Desktop/R
training/R_training_Class_02/Tree_height1.csv")
str(study_3)

Tree_height1 <- read.csv("C:/Users/Fahmida Sultana/Desktop/R
training/R_training_Class_02/Tree_height1.csv")
str(Tree_height1)

# By setting working directory

setwd("C:/Users/Fahmida Sultana/Desktop/R training/R_training_Class_02")
getwd()

study_4 <- read.csv("Tree_height1.csv")
str(study_4)

#OR
#dir.create("C:/Users/Fahmida Sultana/Desktop/R training/R_training_Class_02/R2")

# import tab delimited file
# directly via import Dataset
study_5 <- read.delim("C:/Users/Fahmida Sultana/Desktop/R
training/R_training_Class_02/Tree_height2.txt")
str(study_5)


# By setting working directory

study_6 <- read.delim("Tree_height2.txt")
str(study_6)
```

#How to check data structure

```
#The functions unique(), sort(), and range() can also be useful for checking data.
#x <- read.csv("C:/Users/Fahmida Sultana/Desktop/R training/R_training_Class_02/Tree_height1.csv")

x <- read.xlsx("Tree_height.xlsx")

#to see the whole file
```

```
str(x)
summary(x)
head(x)

# to see into the file, rows, columns, data levels
unique(x$treatment)  # to the the all treatment name
sort(x$year)         # to see the all input in year column
range(x$year)        # to see the range of the year column
x[3,]    # see the 3rd row
x[,2]    # see the 6th column
```