Introduction to R

Summer Training for Research Scholar Program

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Installation

1. Install R using appropriate link from The Comprehensive R Archive Network.
2. Download and install RStudio for free. Just click the "Download RStudio" button and follow instructions.

Basics

When you type a command at the prompt of the *Console* window and hit Enter, your computer executes the command and shows you the results. Then RStudio displays a new prompt for your next command. For example, if you type 2 + 3 and hit Enter, RStudio will display:

```
2 + 3
```

```
[1] 5
```

or

```
21 / (4 + 3)
```

```
[1] 3
```

You can use common functions, like `log()`, `sin()`, `cos()` and many others:

```
log(2)
```

```
[1] 0.6931472
```

Objects (or variables)

You can assign values to `R` objects using `<-` symbol:

```
height <- 70
```

`R` is case sensitive, so variables `Height` and `height` are two distinct objects.

You can define an `R` object, that stores multiple values. For example, you can create a vector that contains a sequence of integer values (notice that both - start and end values are included):

```
id <- 1:10
id
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

Avoid using names c, t, cat, F, T, D as those are built-in functions/constants.

The variable name can contain letters, digits, underscores and dots and start with the letter or dot. The variable name cannot contain dollar sign or other special characters.

```
str.var  <- "oxygen"                # character variable
num.var  <- 15.99                   # numerical variable
bool.var <- TRUE                    # Boolean (or logical) variable
bool.var.1 <- F                     # logical values can be abbreviated
```

Vectors

Vector is an array of values of the same type: Vectors can be numeric, character or logical:

```
# Function c() is used to create a vector from a list of values
num.vector <- c( 5, 7, 9, 11, 4, -1, 0)

# Numeric vectors can be defined in a number of ways:
vals1 <- c (2, -7, 5, 3, -1 )              # concatenation
vals2 <- 25:75                             # range of values
vals3 <- seq(from=0, to=3, by=0.5)         # sequence definition
vals4 <- rep(1, times=7)                   # repeat value
vals5 <- rnorm(5, mean=2, sd=1.5 )         # normally distributed values
```

R Functions

There are many functions that come with R installation:

```
mean(1:99)
```

```
[1] 50
```

R Help

You can access the function's help topic in two ways:

```
?sd
help(sd)
```

If you do not know the function's name, you can search for a topic

```
??"standard deviation"
help.search("standard deviation")
```

Installing R packages

There are more than 20 thousand packages published officially on the CRAN's website. You can search them by name or by topic.

There are also many packages published on the Bioconductor site

To install an R package from the CRAN, use `install.packages("package_name")` command. For example, you may want to install a very popular `tidyverse` library of packages used by many data scientists:

```
install.packages("tidyverse")
```

Another very handy package is *table1*:

```
# To install package
install.packages("table1")
```

Once package is installed it can be loaded and used:

```
#Load R package
library(table1)
```

Vector operations in R

```
# Define a vector with values of body temperature in Fahrenheit
ftemp <- c(97.8, 99.5, 97.9, 102.1, 98.4, 97.7)

# Convert them to a vector with values in Celsius
ctemp <- (ftemp - 32) / 9 * 5
print(ctemp)
```

```
[1] 36.55556 37.50000 36.61111 38.94444 36.88889 36.50000
```

You can also perform operations on two or more vectors:

```
# Define values for body weight and height (in kg and meters)
weight <- c(65, 80, 73, 57, 84)
height <- c( 1.65, 1.80, 1.73, 1.68, 1.79)

# Calculate BMI
weight/height^2
```

```
[1] 23.87511 24.69136 24.39106 20.19558 26.21641
```

Vector Slicing (subsetting)

```
x <- c(36.6, 38.2, 36.4, 37.9, 41.0, 39.9, 36.8, 37.5)
x[2]         # returns second element
```

```
[1] 38.2
```

```
x[2:4]       # returns 2nd through 4th elements inclusive
```

```
[1] 38.2 36.4 37.9
```

```
x[c(1,3,5)]  # returns 1st, 3rd and 5th elements
```

```
[1] 36.6 36.4 41.0
```

```
# compare each element of the vector with a value
x < 37.0
```

```
[1]  TRUE FALSE  TRUE FALSE FALSE FALSE  TRUE FALSE
```

```
# return only those elements of the vector that satisfy a specific condition
x[ x < 37.0 ]
```

```
[1] 36.6 36.4 36.8
```

There are a number of functions that are useful to locate a value satisfying specific condition(s)

```
which.max(x)  # find the (first)maximum element and return its index
```

```
[1] 5
```

```
which.min(x)
```

```
[1] 3
```

```
which(x >= 37.0) # find the location of all the elements that satisfy a specific condition
```

```
[1] 2 4 5 6 8
```

Useful Functions:

Missing Values

Missing values in R are indicated with a symbol `NA`:

```
x <- c(734, 145, NA, 456, NA)

# check if there are any missing values:
anyNA(x)
```

```
[1] TRUE
```

To check which values are missing use `is.na()` function:

```
is.na(x)              # check if the element in the vector is missing
```

```
[1] FALSE FALSE  TRUE FALSE  TRUE
```

```
which(is.na(x))       # which elements are missing
```

```
[1] 3 5
```

By default statistical functions will not compute if the data contain missing values:

```
mean(x)
```

```
[1] NA
```

To view the arguments that need to be used to remove missing data, read help topic for the function:

```
?mean
```

```
#Perform computation removing missing data
mean(x, na.rm=TRUE)
```

```
[1] 445
```

Reading input files

There are many R functions to process files with various formats: Some come from base R:

- read.table()
- read.csv()
- read.delim()
- read.fwf()
- scan() and many others

```
# Read a regular csv file:
salt <- read.csv("http://rcs.bu.edu/classes/STaRS/intersalt.csv")
```

There are a few R packages which provide additional functionality to read files.

```
# Install package first
# You can install packages from the RStudio Menu (Tools -> Install packages)
#    or by executing the following R command:
#install.packages("foreign")

#Load R package "foreign"
```

```
library(foreign)

# Read data in Stata format
swissdata <- read.dta("http://rcs.bu.edu/classes/STaRS/swissfile.dta")

# Load R package haven to read SAS-formatted files (make sure it is installed! )
#install.packages("haven")
library(haven)

# Read data in SAS format
fhsdata <- read_sas("http://rcs.bu.edu/classes/STaRS/fhs.sas7bdat")
```

Exploring R dataframes

There are a few very useful commands to explore R's dataframes:

```
head(fhsdata)
```

```
# A tibble: 6 x 13
    SEX RANDID TOTCHOL   AGE SYSBP DIABP DIABETES BPMEDS PERIOD CIGPDAY HEARTRTE
  <dbl>  <dbl>   <dbl> <dbl> <dbl> <dbl>    <dbl>  <dbl>  <dbl>   <dbl>    <dbl>
1     1   2448     195    39  106   70           0      0      1       0       80
2     1   2448     209    52  121   66           0      0      3       0       69
3     2   6238     250    46  121   81           0      0      1       0       95
4     2   6238     260    52  105   69.5         0      0      2       0       80
5     2   6238     237    58  108   66           0      0      3       0       80
6     1   9428     245    48  128.  80           0      0      1      20       75
# i 2 more variables: HDLC <dbl>, LDLC <dbl>
```

```
tail(fhsdata)
```

```
# A tibble: 6 x 13
    SEX RANDID TOTCHOL   AGE SYSBP DIABP DIABETES BPMEDS PERIOD CIGPDAY HEARTRTE
  <dbl>  <dbl>   <dbl> <dbl> <dbl> <dbl>    <dbl>  <dbl>  <dbl>   <dbl>    <dbl>
1     1 1.00e7     185    40   141    98         0      0      1       0       67
2     1 1.00e7     173    46   126    82         0      0      2       0       70
3     1 1.00e7     153    52   143    89         0      0      3       0       65
4     2 1.00e7     196    39   133    86         0      0      1      30       85
5     2 1.00e7     240    46   138    79         0      0      2      20       90
```

```
6     2 1.00e7      NA    50   147    96         0      0      3      10       94
# i 2 more variables: HDLC <dbl>, LDLC <dbl>
```

```
str(fhsdata)
```

```
tibble [11,627 x 13] (S3: tbl_df/tbl/data.frame)
 $ SEX     : num [1:11627] 1 1 2 2 2 1 1 2 2 2 ...
 $ RANDID  : num [1:11627] 2448 2448 6238 6238 6238 ...
  ..- attr(*, "label")= chr "Random ID"
 $ TOTCHOL : num [1:11627] 195 209 250 260 237 245 283 225 232 285 ...
 $ AGE     : num [1:11627] 39 52 46 52 58 48 54 61 67 46 ...
 $ SYSBP   : num [1:11627] 106 121 121 105 108 ...
 $ DIABP   : num [1:11627] 70 66 81 69.5 66 80 89 95 109 84 ...
 $ DIABETES: num [1:11627] 0 0 0 0 0 0 0 0 0 0 ...
 $ BPMEDS  : num [1:11627] 0 0 0 0 0 0 0 0 0 0 ...
 $ PERIOD  : num [1:11627] 1 3 1 2 3 1 2 1 2 1 ...
  ..- attr(*, "label")= chr "Examination cycle"
 $ CIGPDAY : num [1:11627] 0 0 0 0 0 20 30 30 20 23 ...
  ..- attr(*, "label")= chr "Cigarettes per day"
 $ HEARTRTE: num [1:11627] 80 69 95 80 80 75 75 65 60 85 ...
  ..- attr(*, "label")= chr "Ventricular Rate (beats/min)"
 $ HDLC    : num [1:11627] NA 31 NA NA 54 NA NA NA NA NA ...
  ..- attr(*, "label")= chr "HDL Cholesterol mg/dL"
 $ LDLC    : num [1:11627] NA 178 NA NA 141 NA NA NA NA NA ...
  ..- attr(*, "label")= chr "LDL Cholesterol mg/dL"
```

```
summary(fhsdata)
```

```
      SEX            RANDID           TOTCHOL            AGE
 Min.   :1.000   Min.   :   2448   Min.   :107.0   Min.   :32.00
 1st Qu.:1.000   1st Qu.:2474378   1st Qu.:210.0   1st Qu.:48.00
 Median :2.000   Median :5006008   Median :238.0   Median :54.00
 Mean   :1.568   Mean   :5004741   Mean   :241.2   Mean   :54.79
 3rd Qu.:2.000   3rd Qu.:7472730   3rd Qu.:268.0   3rd Qu.:62.00
 Max.   :2.000   Max.   :9999312   Max.   :696.0   Max.   :81.00
                                   NA's   :409
     SYSBP           DIABP           DIABETES           BPMEDS
 Min.   : 83.5   Min.   : 30.00   Min.   :0.00000   Min.   :0.0000
 1st Qu.:120.0   1st Qu.: 75.00   1st Qu.:0.00000   1st Qu.:0.0000
 Median :132.0   Median : 82.00   Median :0.00000   Median :0.0000
 Mean   :136.3   Mean   : 83.04   Mean   :0.04558   Mean   :0.5402
 3rd Qu.:149.0   3rd Qu.: 90.00   3rd Qu.:0.00000   3rd Qu.:0.0000
 Max.   :295.0   Max.   :150.00   Max.   :1.00000   Max.   :9.0000

     PERIOD          CIGPDAY          HEARTRTE           HDLC
 Min.   :1.000   Min.   :  0.00   Min.   : 37.00   Min.   : 10.00
 1st Qu.:1.000   1st Qu.:  0.00   1st Qu.: 69.00   1st Qu.: 39.00
 Median :2.000   Median :  0.00   Median : 75.00   Median : 48.00
 Mean   :1.899   Mean   : 14.98   Mean   : 77.26   Mean   : 49.37
 3rd Qu.:3.000   3rd Qu.: 20.00   3rd Qu.: 85.00   3rd Qu.: 58.00
 Max.   :3.000   Max.   :999.00   Max.   :999.00   Max.   :189.00
                                                   NA's   :8600
      LDLC
 Min.   : 20.0
 1st Qu.:145.0
 Median :173.0
 Mean   :176.5
 3rd Qu.:205.0
 Max.   :565.0
 NA's   :8601
```

```
# In this dataset, "999" is used to indicate missing values
fhsdata$HEARTRTE[fhsdata$HEARTRTE==999]<- NA
fhsdata$CIGPDAY[fhsdata$CIGPDAY==999]<- NA
summary(fhsdata)
```

```
      SEX            RANDID            TOTCHOL           AGE
 Min.   :1.000   Min.   :   2448   Min.   :107.0   Min.   :32.00
 1st Qu.:1.000   1st Qu.:2474378   1st Qu.:210.0   1st Qu.:48.00
 Median :2.000   Median :5006008   Median :238.0   Median :54.00
 Mean   :1.568   Mean   :5004741   Mean   :241.2   Mean   :54.79
 3rd Qu.:2.000   3rd Qu.:7472730   3rd Qu.:268.0   3rd Qu.:62.00
 Max.   :2.000   Max.   :9999312   Max.   :696.0   Max.   :81.00
                                   NA's   :409
     SYSBP           DIABP           DIABETES            BPMEDS
 Min.   : 83.5   Min.   : 30.00   Min.   :0.00000   Min.   :0.0000
 1st Qu.:120.0   1st Qu.: 75.00   1st Qu.:0.00000   1st Qu.:0.0000
 Median :132.0   Median : 82.00   Median :0.00000   Median :0.0000
 Mean   :136.3   Mean   : 83.04   Mean   :0.04558   Mean   :0.5402
 3rd Qu.:149.0   3rd Qu.: 90.00   3rd Qu.:0.00000   3rd Qu.:0.0000
 Max.   :295.0   Max.   :150.00   Max.   :1.00000   Max.   :9.0000
```

```
     PERIOD         CIGPDAY         HEARTRTE           HDLC      
 Min.   :1.000   Min.   : 0.00   Min.   : 37.00   Min.   : 10.00  
 1st Qu.:1.000   1st Qu.: 0.00   1st Qu.: 69.00   1st Qu.: 39.00  
 Median :2.000   Median : 0.00   Median : 75.00   Median : 48.00  
 Mean   :1.899   Mean   : 8.25   Mean   : 76.78   Mean   : 49.37  
 3rd Qu.:3.000   3rd Qu.:20.00   3rd Qu.: 85.00   3rd Qu.: 58.00  
 Max.   :3.000   Max.   :90.00   Max.   :220.00   Max.   :189.00  
                 NA's   :79      NA's   :6        NA's   :8600    
      LDLC      
 Min.   : 20.0  
 1st Qu.:145.0  
 Median :173.0  
 Mean   :176.5  
 3rd Qu.:205.0  
 Max.   :565.0  
 NA's   :8601   
```

We can use *table1* package to get various summaries stratifying by one or more variable:

```r
# One level of stratification
table1(~ SEX + AGE + TOTCHOL | DIABETES, data=fhsdata)
```

	0	1	Overall
	(N=11097)	(N=530)	(N=11627)
SEX			
Mean (SD)	1.57 (0.495)	1.52 (0.500)	1.57 (0.495)
Median [Min, Max]	2.00 [1.00, 2.00]	2.00 [1.00, 2.00]	2.00 [1.00, 2.00]
AGE			
Mean (SD)	54.5 (9.52)	60.8 (8.54)	54.8 (9.56)
Median [Min, Max]	54.0 [32.0, 81.0]	61.0 [36.0, 80.0]	54.0 [32.0, 81.0]
TOTCHOL			
Mean (SD)	241 (44.9)	242 (53.6)	241 (45.4)
Median [Min, Max]	238 [107, 696]	236 [112, 638]	238 [107, 696]
Missing	381 (3.4%)	28 (5.3%)	409 (3.5%)

```r
# Two levels of stratification (nesting)
table1(~ AGE + TOTCHOL + HDLC | DIABETES*SEX, data=fhsdata)
```

	1	2	1	2	1	2
	(N=4769)	(N=6328)	(N=253)	(N=277)	(N=5022)	(N=6605)
AGE						
Mean (SD)	54.2 (9.49)	54.7 (9.53)	59.8 (8.39)	61.7 (8.59)	54.5 (9.51)	55.0 (9.60)
Median [Min, Max]	54.0 [33.0, 80.0]	54.0 [32.0, 81.0]	60.0 [39.0, 79.0]	62.0 [36.0, 80.0]	54.0 [33.0, 80.0]	55.0 [32.0, 81.0]
TOTCHOL						
Mean (SD)	235 (42.4)	246 (46.2)	228 (42.8)	255 (59.4)	234 (42.4)	247 (46.9)
Median [Min, Max]	232 [113, 696]	243 [107, 625]	230 [115, 366]	248 [112, 638]	232 [113, 696]	243 [107, 638]
Missing	100 (2.1%)	281 (4.4%)	7 (2.8%)	21 (7.6%)	107 (2.1%)	302 (4.6%)
HDL Cholesterol mg/dL						
Mean (SD)	43.7 (13.1)	54.0 (15.8)	43.8 (15.2)	49.3 (17.1)	43.7 (13.3)	53.6 (15.9)
Median [Min, Max]	42.0 [10.0, 138]	52.0 [11.0, 189]	41.0 [17.0, 118]	48.0 [15.0, 93.0]	42.0 [10.0, 138]	52.0 [11.0, 189]
Missing	3578 (75.0%)	4724 (74.7%)	140 (55.3%)	158 (57.0%)	3718 (74.0%)	4882 (73.9%)

To see more examples of *table1* package usage, see. https://cran.r-project.org/web/packages/table1/vignettes/table1-examples.html

Correlation

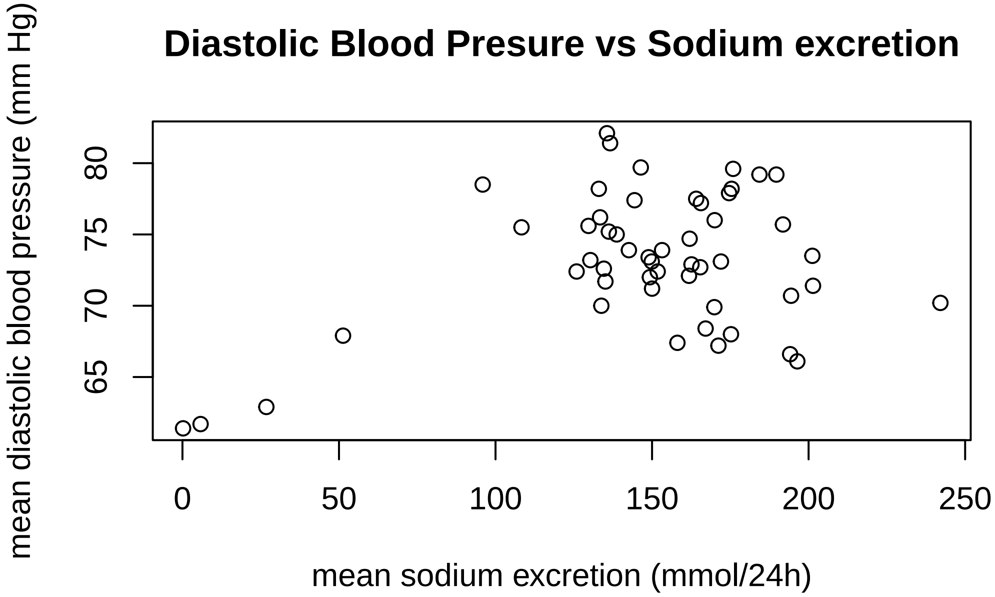
To explain this test, we will use the *salt* dataset we imported earlier:

```
str(salt)
```

```
'data.frame':   52 obs. of  4 variables:
 $ b      : num  0.512 0.226 0.316 0.042 0.086 0.265 0.384 0.501 0.352 0.443 ...
 $ bp     : num  72 78.2 73.9 61.7 61.4 73.4 79.2 66.6 82.1 75 ...
 $ sodium : num  149.3 133 142.6 5.8 0.2 ...
 $ country: chr  "Argentina" "Belgium" "Belgium" "Brazil" ...
```

The correlation test is used to test the linear relationship of 2 continuous variables. We can first display two variables using scatter plot:

```r
plot(x = salt$sodium,
     y = salt$bp,
     xlab = "mean sodium excretion (mmol/24h)",
     ylab = "mean diastolic blood pressure (mm Hg)",
     main = "Diastolic Blood Presure vs Sodium excretion")
```



As we can see in this plot, there is little correlation between these 2 variables and there are a few "outlier" points that will affect the correlation calculation!!!

Let's perform the test:

```r
cor.test(salt$bp, salt$sodium)
```

```

    Pearson's product-moment correlation

data:  salt$bp and salt$sodium
t = 2.7223, df = 50, p-value = 0.008901
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.09577287 0.57573339
sample estimates:
      cor
0.3592828
```

The **Null Hypothesis** : the true correlation between bp and sodium (blood pressure and salt intake) is 0 (they are independent);
The **Alternative hypothesis**: true correlation between bp and sodium is not equal to 0.

The *p-value* is less that 0.05 and the 95% CI does not contain 0, so at the significance level of 0.05 we reject null hypothesis and state that there is some (positive) correlation (0.359) between these 2 variables.

Important:

- The order of the variables in the test is not important
- Correlation provide evidence of association, not causation!
- Correlation values is always between -1 and 1 and does not change if the units of either or both variables change
- Correlation describes linear relationship
- Correlation is strongly affected by outliers (extreme observations)

In this case the correlation is weak and there are a few points that significantly affect the result.

Linear Model

```
lm.res <- lm( bp ~ sodium, data = salt)
summary(lm.res)
```

```

Call:
lm(formula = bp ~ sodium, data = salt)

Residuals:
    Min      1Q  Median      3Q     Max 
-8.8625 -2.8906  0.0299  3.6470  9.4283 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 67.56245    2.14643  31.477   <2e-16 ***
sodium       0.03768    0.01384   2.722   0.0089 ** 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.511 on 50 degrees of freedom
Multiple R-squared:  0.1291,    Adjusted R-squared:  0.1117 
```

```
F-statistic: 7.411 on 1 and 50 DF,  p-value: 0.008901
```

Here we estimated that relationship between the predictor (*sodium*) and response (*bp*) variables.
The summary statistics here reports a number of things. *p-value* tells us if the model is statistically significant.
In Linear Regression, the *Null Hypothesis* is that the coefficient associated with the variables are equal to zero.
Multiple R-squared value is equal to the square of the correlation value we calculated in the previous test.

When the model fits the data;

- R-squared - The higher - the better
- F-statistics - The higher the better
- Std. Error - The closer to 0 - the better

One Sample t-Test

This test is used to test the mean of a sample from a normal distribution

```
t.test(salt$bp, mu=70)
```

```

    One Sample t-test

data:  salt$bp
t = 4.7485, df = 51, p-value = 1.703e-05
alternative hypothesis: true mean is not equal to 70
95 percent confidence interval:
 71.81934 74.48451
sample estimates:
mean of x
 73.15192
```

The *null hypothesis*: The true mean is equal to 70. The *alternative hypothesis*: true mean is not equal to 70. Since *p-value* is small (1.703e-05) - less than 0.05, 95% percent CI does not contain the value 70, we can reject the *null hypothesis*.

Two Sample t-TEST

Let’s load some other dataset. It comes with R. This dataset shows the effect of two soporific drugs (increase in hours of sleep compared to control) on 10 patients. There are 3 variables:

- extra: (numeric) increase in hours of sleep.
- group: (factor) categorical variable indicating which drug is given
- ID: (factor) patient ID

```r
data(sleep)
head(sleep)
```

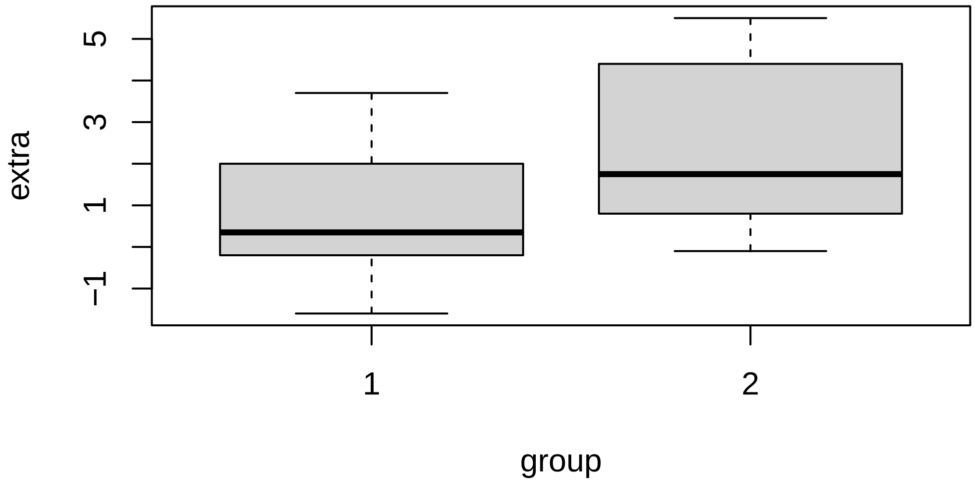
```
  extra group ID
1   0.7     1  1
2  -1.6     1  2
3  -0.2     1  3
4  -1.2     1  4
5  -0.1     1  5
6   3.4     1  6
```

```r
summary(sleep)
```

```
     extra         group        ID
 Min.   :-1.600   1:10    1      :2
 1st Qu.:-0.025   2:10    2      :2
 Median : 0.950           3      :2
 Mean   : 1.540           4      :2
 3rd Qu.: 3.400           5      :2
 Max.   : 5.500           6      :2
                          (Other):8
```

To compare the means of 2 samples:

```r
boxplot(extra ~ group, data = sleep)
```



```
t.test(extra ~ group, data = sleep)
```

```

	Welch Two Sample t-test

data:  extra by group
t = -1.8608, df = 17.776, p-value = 0.07939
alternative hypothesis: true difference in means between group 1 and group 2 is not equal
95 percent confidence interval:
 -3.3654832  0.2054832
sample estimates:
mean in group 1 mean in group 2 
           0.75            2.33 
```

Here the *Null Hypothesis* is that the true difference between 2 groups is equal to 0 And the *Alternative Hypothesis* is that it does not equal to 0 In this test the p-value is above significance level of 0.05 and 95% CI contains 0, so we cannot reject the NULL hypothesis.

Note, that t.test has a number of options, including *alternative* which can be set to "two.sided", "less", "greater", depending which test you would like to perform. Using option *var.equal* you can also specify if the variances of the values in each group are equal or not.

One-way ANOVA test

The one-way analysis of variance ($ANOVA$) test is an extension of two-samples t.test for comparing means for datasets with more than 2 groups.

Assumptions:

- The observations are obtained independently and randomly from the population defined by the categorical variable
- The data of each category is normally distributed
- The populations have a common variance.

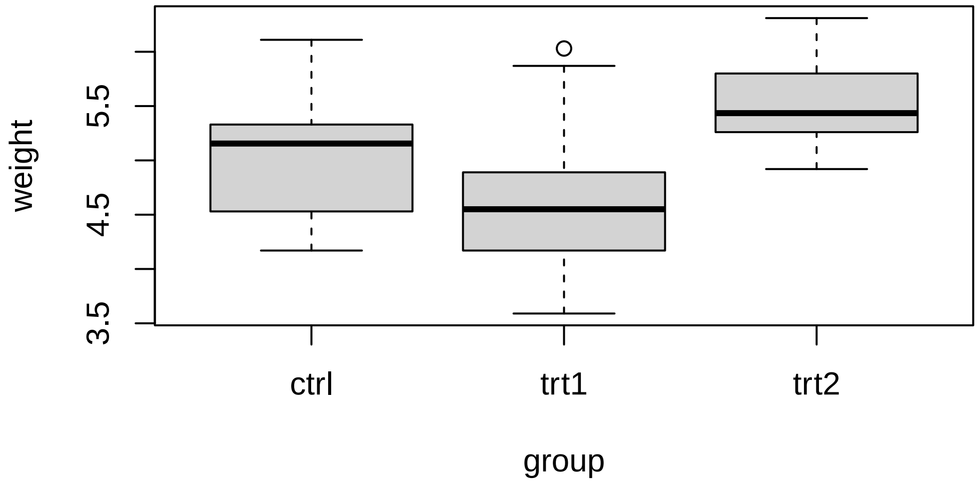
```
data("PlantGrowth")
head(PlantGrowth)
```

```
  weight group
1   4.17  ctrl
2   5.58  ctrl
3   5.18  ctrl
4   6.11  ctrl
5   4.50  ctrl
6   4.61  ctrl
```

```
summary(PlantGrowth)
```

```
     weight       group   
 Min.   :3.590   ctrl:10  
 1st Qu.:4.550   trt1:10  
 Median :5.155   trt2:10  
 Mean   :5.073            
 3rd Qu.:5.530            
 Max.   :6.310            
```

```
boxplot(weight~group, data=PlantGrowth)
```



As visible from the side-by-side boxplots, there is some difference in the weights of 3 groups, but we cannot determine from the plot if this difference is significant.

```
aov.res <- aov(weight~group, data=PlantGrowth)
summary( aov.res )
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
group        2  3.766  1.8832   4.846 0.0159 *
Residuals   27 10.492  0.3886
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

As we can see from the summary output the *p-value* is 0.0159 < 0.05 which indicates that there is a statistically significant difference in weignt between these groups. We can check the confidence intervals for the treatment parameters:

```
confint(aov.res)
```

```
                  2.5 %    97.5 %
(Intercept)  4.62752600 5.4364740
grouptrt1   -0.94301261 0.2010126
grouptrt2   -0.07801261 1.0660126
```

Important: In one-way ANOVA test a small p-value indicates that some of the group means are different, but it does not say which ones!

For multiple pairwise-comparisions we use **Tukey** test:

```
TukeyHSD(aov.res)
```

```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = weight ~ group, data = PlantGrowth)

$group
            diff        lwr       upr     p adj
trt1-ctrl -0.371 -1.0622161 0.3202161 0.3908711
trt2-ctrl  0.494 -0.1972161 1.1852161 0.1979960
trt2-trt1  0.865  0.1737839 1.5562161 0.0120064
```

This result indicates that the significant difference in between treatment 1 and treatment 2 with the adjusted *p-value* of 0.012.

Chi-Squred test of independence in R

The chi-square test is used to analyze the frequency table (or contengency table) formed by two categorical variables. It evaluates whether there is a significant association between the categories of the two variables.

```
treat <- read.csv("http://rcs.bu.edu/classes/STaRS/treatment.csv")
head(treat)
```

```
  id treated improved
1  1       1        1
2  2       1        1
3  3       0        1
4  4       1        1
5  5       1        0
6  6       1        0
```

```
summary(treat)
```

```
       id          treated          improved
 Min.   :  1   Min.   :0.0000   Min.   :0.000
 1st Qu.: 27   1st Qu.:0.0000   1st Qu.:0.000
 Median : 53   Median :0.0000   Median :1.000
 Mean   : 53   Mean   :0.4762   Mean   :0.581  
 3rd Qu.: 79   3rd Qu.:1.0000   3rd Qu.:1.000  
 Max.   :105   Max.   :1.0000   Max.   :1.000  
```

In the above dataset there are 2 categorical variables:

- treated - 0 or 1
- improved - 0 or 1

We would like to test if there is an improvement after the treatment. In other words if these 2 categorical variables are dependent.

First let's take a look at the tables:

```
# Frequency table: "treated will be rows, "improved" - columns"
table(treat$treated, treat$improved)
```

```

     0  1
  0 29 26
  1 15 35
```

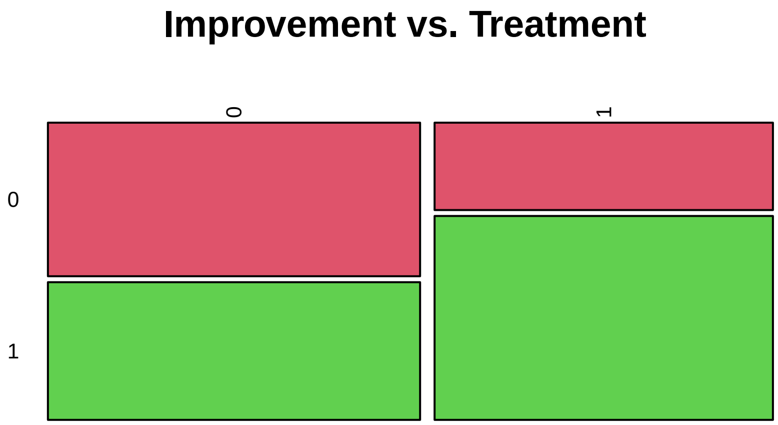
```
# Proportion table
prop.table(table(treat$treated, treat$improved))
```

```

            0         1
  0 0.2761905 0.2476190
  1 0.1428571 0.3333333
```

We can visualize this contingency table with a mosaic plot:

```
tbl <- table(treat$treated, treat$improved)
mosaicplot( tbl, color = 2:3, las = 2, main = "Improvement vs. Treatment" )
```



Compute chi-squred test

```
chisq.test (tbl)
```

```

    Pearson's Chi-squared test with Yates' continuity correction

data:  tbl
X-squared = 4.6626, df = 1, p-value = 0.03083
```

The *Null Hypothesis* is that *treated* and *improved* variables are independent.
In the above test the *p-value* is 0.03083, so at the significance level of 0.05 we can reject the null hypothesis

Additional resources

1. R for applied epidemiology and public health
2. R for data science
3. The R Graph Gallery
4. FAQ in R and other R topics by UCLA
5. Which Statistical Test to use