R tutorial

Updated by

Hilda Ibriga, Jincheng Bai and Qi Wang

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Originally created by

Hilda Ibriga, Linna Henry, Patricia Wahyu Haumahu, Qi Wang, Yixuan Qiu and Yuying Song

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Statistical Consulting Service

Purdue University

Getting and installing R

R is a free and open source statistical software. You can download R from the following website: https://cran.r-project.org/. R is available for Linux, OS X and Windows, just click download R according your operating system. For now we just need base distribution and you can choose base and click 'Download R x.x.x for ...' to get it.

Install packages

The R package comes with numerous basic functions, like `mean()` and `median()`, and procedures, such as lm for linear regression. More advanced functions and procedures will be in packages. In this example, we will be installing the ggplot2 package, which can be used to create advanced graphics.

The first step is to enter the following command in the R console window

```
install.packages("ggplot2")
```

You should see information appear in the R console window as it is installed. If there are no errors, the package is installed. To load the package for use, enter the following in the R console window

```
library(ggplot2)

## Warning: package 'ggplot2' was built under R version 3.1.3
```

You will often see these warning messages but there is rarely a compatibility issue. To use the functions and procedures in the package, you will need to load the package each time you open R, although you only need to install the package once. '##' is a prompt that indicates the message from the R console.

Basic data structure

Vector

A vector is a contiguous collection of objects of the same type. Common types of vectors include logical, integer, double, and character. Here are some examples of vectors

```
x <- c(3,2,5,6,55)
x

## [1]  3  2  5  6 55

y <- c("a", "d", "e", "hi")
y

## [1] "a"  "d"  "e"  "hi"
```

Here x is a vector of integers and y is a vector of characters. You can use the function `c()` to create a vector. The letter c stands for concatenate. You must separate the values using a comma. You can put as many items as you want inside a vector. Typing the name of a vector as a command prints the vector elements in order. To access one element of the vector, you can use the following code

```
x[3]

## [1] 5
```

This command asks for the third element of the vector x.

It is also possible to have a vector of length one (i.e., a named constant).

```
cool <- 4
cool

## [1] 4
```

Here cool is a vector with length one that contains the value 4.

List

A list is another data structure in R. It is similar to a vector, however it differs in that you can put objects of different types into a list. Here is an example:

```
person <- list("black hair", "brown eyes", 22, TRUE)
person

## [[1]]
## [1] "black hair"
##
## [[2]]
## [1] "brown eyes"
##
## [[3]]
## [1] 22
##
## [[4]]
## [1] TRUE
```

Here the person variable is a list with 4 objects. You can access elements in a list the same way you access elements in a vector. For example,

```
person[2]

## [[1]]
## [1] "brown eyes"
```

This will show us the second element in person.

Matrix

A matrix is a two dimensional data structure in R. Similar to a vector, matrices must contain objects of the same type.

```
mat <- matrix(NA, nrow = 4, ncol = 5)
mat

##      [,1] [,2] [,3] [,4] [,5]
## [1,]   NA   NA   NA   NA   NA
## [2,]   NA   NA   NA   NA   NA
## [3,]   NA   NA   NA   NA   NA
## [4,]   NA   NA   NA   NA   NA
```

In the preceding example, mat is a matrix with 4 rows and 5 columns. The values inside mat are all set to NA. This is essentially an empty (or missing) matrix.
You can access a row of a matrix by the following command.

```
mat[row.number,]
```

Where row.number is the row you want to look at. You must include a comma after the row number since the matrix is two dimensional. You can access a column of a matrix by having the comma first

```
mat[,col.number]
```

We can fill the matrix with whatever objects we like, provided all the objects are of the same type. In the following example, we fill in the rows of the matrix mat one at a time. Each row is basically a vector so we can use the same commands we can use to specify a vector.

```
mat[1,] <- c(2,3,7,5,8)
mat[2,] <- rep(4, 5)
mat[3,] <- 33:37
mat[4,] <- seq(23, 31, 2)
mat

##      [,1] [,2] [,3] [,4] [,5]
## [1,]    2    3    7    5    8
## [2,]    4    4    4    4    4
## [3,]   33   34   35   36   37
## [4,]   23   25   27   29   31
```

For the second row we used the `rep()` function, which stands for repeat. This function takes two numbers; the first number is the number you want to repeat and the second number is how many times you want this number to be repeated. For the third row, we used the : function. This function takes two numbers, the first number before the colon indicates the start and the second number after the colon indicates the end of a numeric sequence. The function, by default, will create a vector that increases by one from the start to the end. For the last row, we used the `seq()` function, which stands for sequence. This function takes 3 arguments. The first argument is the start value, the second argument is the ending value, and the last argument is how much you want to increment by. The seq()function will create a vector that starts at the start, ends at the end, and increases by the increment value. You will notice that all four rows are assigned vectors of length 5. This is because we have 5 columns.

You can set the column and row names of a matrix using the functions colnames() and rownames() respectively. Here is an example:

```
rownames(mat) <- c("r1", "r2", "r3", "r4")
rownames(mat)

## [1] "r1" "r2" "r3" "r4"
```

To look at the contents of one row of a matrix, we state the row number followed by a comma:

```
mat[2,]

## [1] 4 4 4 4 4
```

This shows us the second row. We can also look at a column putting the comma first

```
mat[,3]

## [1]  7  4 35 27
```

This shows us the third column. You can access one element of a matrix by specifying the element's row and column number

```
mat[4,5]

## [1] 31
```

This will show us the element in the fourth row and the fifth column.

Dataframe

A dataframe is another two-dimensional data structure in R. Much like a list, a dataframe can contain objects of different types. However objects within one column must be the same. Here is an example of a data frame

```
df <- data.frame(haircolor = c("red", "black", "blonde"), eyecolor = c(
"green", "brown", "blue"), age = c(22, 23, 25), phd = c(T, T, F))
df

##   haircolor eyecolor age   phd
## 1       red    green  22  TRUE
## 2     black    brown  23  TRUE
## 3    blonde     blue  25 FALSE
```

This dataframe has three rows and 4 columns. The 4 columns represent different variables. You can access one column of the dataframe by the following

```
df$age

## [1] 22 23 25
```

where df is the name of the dataframe and age is the column you want to look at. You can also use the matrix operators to access rows, columns, and elements of a data frame. Here is an example:

```
df[3,]

##   haircolor eyecolor age   phd
## 3    blonde     blue  25 FALSE

df[,2]

## [1] green brown blue
## Levels: blue brown green

df[3,3]

## [1] 25
```

Array

An array is a data structure in R that has 2 or more dimensions. Here is an example of an array

```
my_arr <- array(1:8, c(2,2,2))
my_arr

## , , 1
##
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
##
## , , 2
##
##      [,1] [,2]
## [1,]    5    7
## [2,]    6    8
```

Here we have created an array called my_arr using the function array(). The first argument in array() is a vector of the numeric values we want in the array. The second argument are the dimensions of my array presented as a vector. You can see in the output, the array is filled with the values 1 to 8, and there are two 2x2 matrices. The first 2 specifies the number of rows, the second 2 specifies the number of columns, and the third 2 specifies the number of matrices . You can access elements of the array with the following code:

```
my_arr[,,1]

##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
```

This returns the first 2x2 matrix.

```
my_arr[1,,1]

## [1] 1 3
```

This returns the first row in the first matrix.

```
my_arr[,1,1]

## [1] 1 2
```

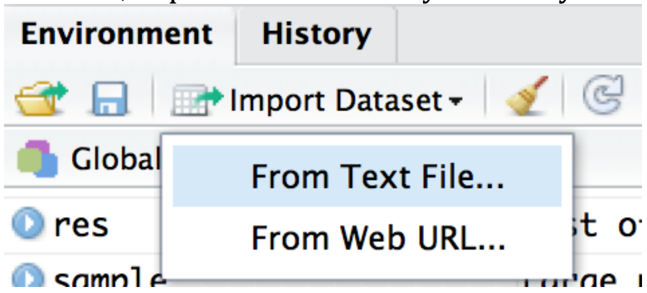
This returns the first column in the first matrix.

Reading and Exporting data

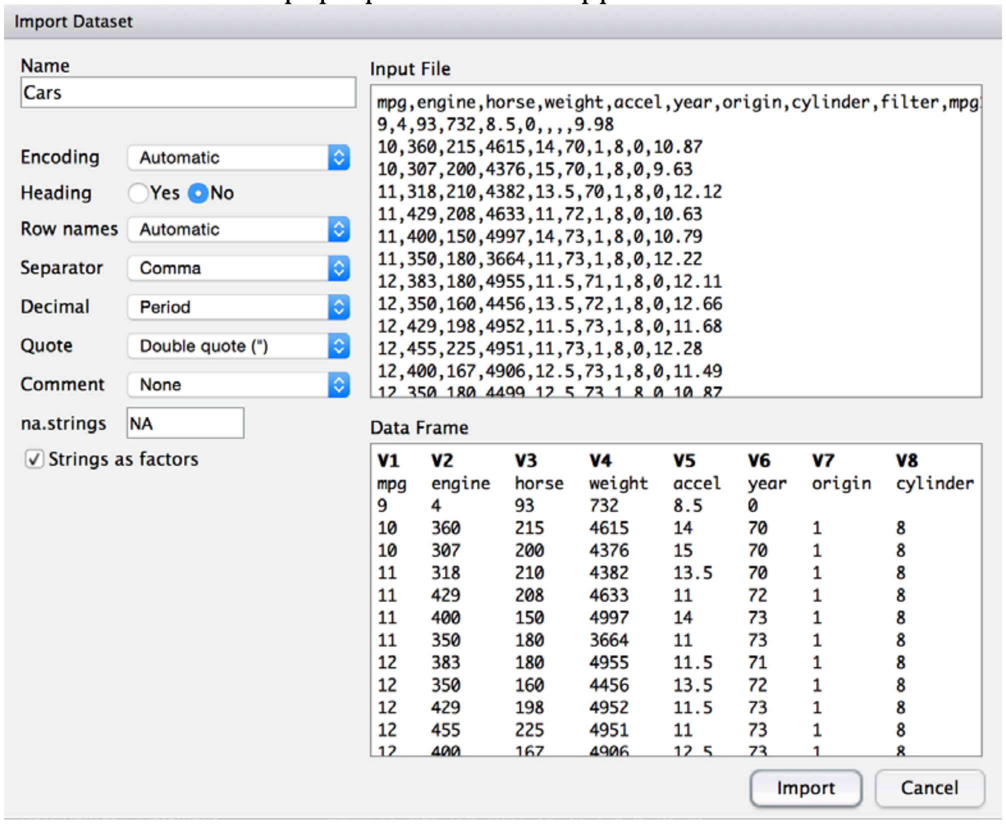
1. Reading in free formatted data using the built-in module in R Studio

R Studio is a popular IDE for R. It is free and available at https://www.rstudio.com/ for both Windows and OS X. Probably the easiest way to import data is using the built-in module in R Studio. It can take care of all the details for you. If you are new to R, it is highly recommended to do that. In this example, we will import a dataset with the name 'Cars.csv'. The dataset is available on our website (http://www.stat.purdue.edu/scs/help/Intro_stat_software.html) and you can download it and put it at your working directory.

1. Click *Import Dataset* in environment panel. It can either be *from text file* or *from web URL*, depends on whether you can try to import a local file.



2. Locate the file and a pop-up window will appear



Name: Cars

Encoding: Automatic

Heading: Yes [✓ No]

Row names: Automatic

Separator: Comma

Decimal: Period

Quote: Double quote (")

Comment: None

na.strings: NA

✓ Strings as factors

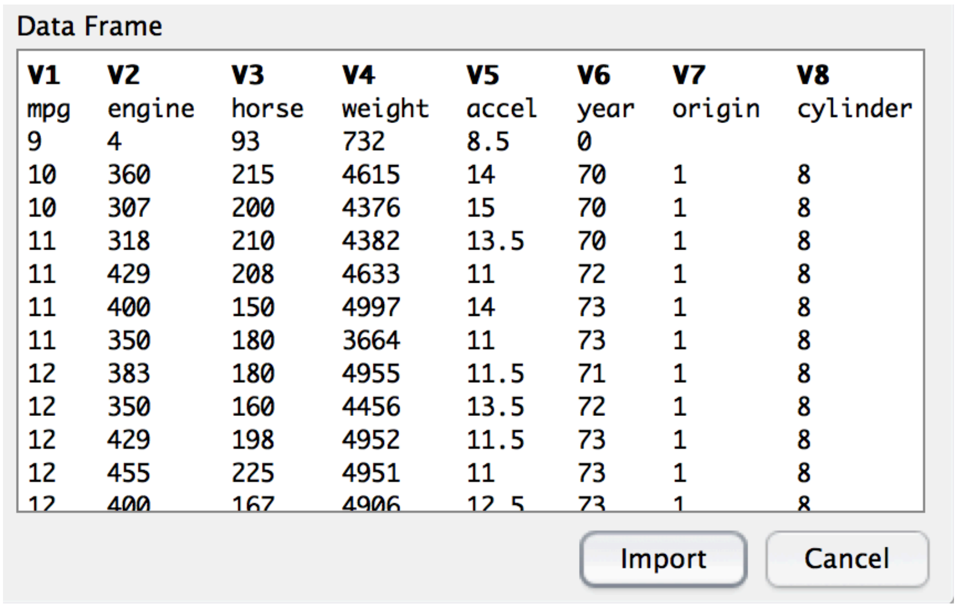
Input File

```
mpg,engine,horse,weight,accel,year,origin,cylinder,filter,mpg
9,4,93,732,8.5,0,,,,9.98
10,360,215,4615,14,70,1,8,0,10.87
10,307,200,4376,15,70,1,8,0,9.63
11,318,210,4382,13.5,70,1,8,0,12.12
11,429,208,4633,11,72,1,8,0,10.63
11,400,150,4997,14,73,1,8,0,10.79
11,350,180,3664,11,73,1,8,0,12.22
12,383,180,4955,11.5,71,1,8,0,12.11
12,350,160,4456,13.5,72,1,8,0,12.66
12,429,198,4952,11.5,73,1,8,0,11.68
12,455,225,4951,11,73,1,8,0,12.28
12,400,167,4906,12.5,73,1,8,0,11.49
12,350,180,4499,12.5,73,1,8,0,10.87
```

Data Frame

```
V1   V2      V3     V4      V5     V6    V7      V8
mpg  engine  horse  weight  accel  year  origin  cylinder
9    4       93     732     8.5    0
10   360     215    4615    14     70    1       8
10   307     200    4376    15     70    1       8
11   318     210    4382    13.5   70    1       8
11   429     208    4633    11     72    1       8
11   400     150    4997    14     73    1       8
11   350     180    3664    11     73    1       8
12   383     180    4955    11.5   71    1       8
12   350     160    4456    13.5   72    1       8
12   429     198    4952    11.5   73    1       8
12   455     225    4951    11     73    1       8
12   400     167    4906    12.5   73    1       8
```

3. Specify the name of the data frame of the file imported in the box under '*Name*', the default setting is the file name without its extended name. Click to choose whether there is a headings row in the data file or not. The content of the data frame will show up in the right lower part of the window. Be careful when it looks like this:

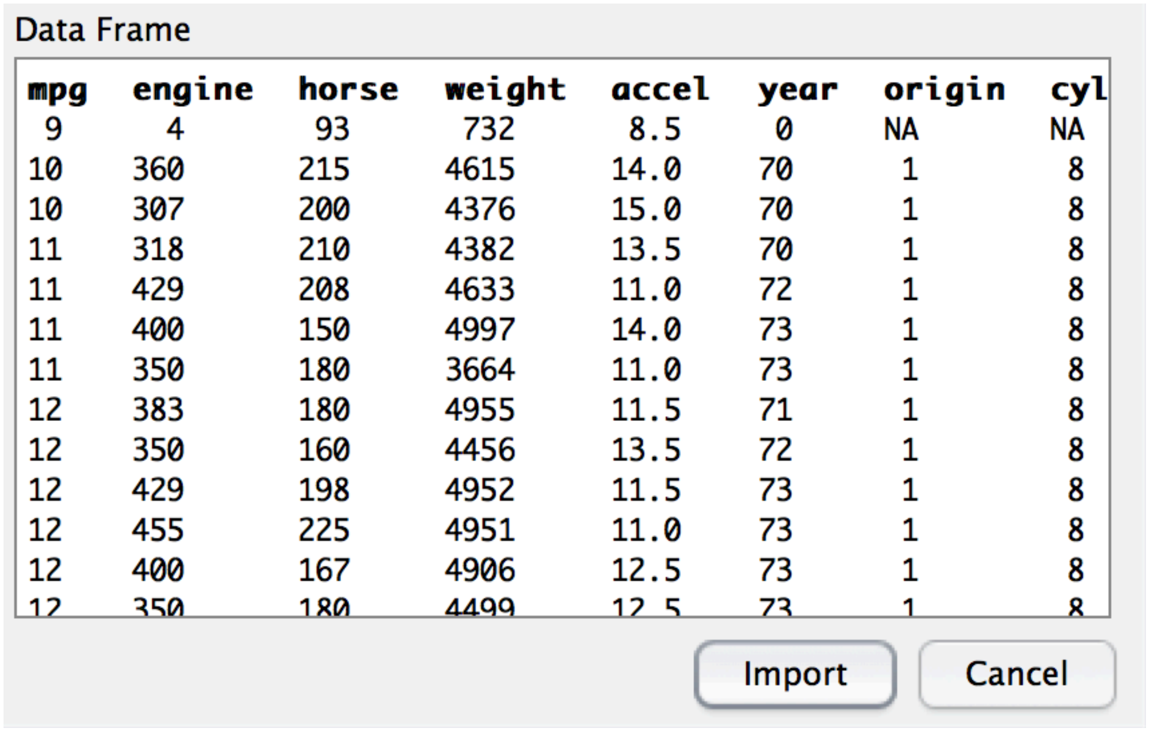


Data Frame

```
V1   V2      V3     V4      V5     V6    V7      V8
mpg  engine  horse  weight  accel  year  origin  cylinder
9    4       93     732     8.5    0
10   360     215    4615    14     70    1       8
10   307     200    4376    15     70    1       8
11   318     210    4382    13.5   70    1       8
11   429     208    4633    11     72    1       8
11   400     150    4997    14     73    1       8
11   350     180    3664    11     73    1       8
12   383     180    4955    11.5   71    1       8
12   350     160    4456    13.5   72    1       8
12   429     198    4952    11.5   73    1       8
12   455     225    4951    11     73    1       8
12   400     167    4906    12.5   73    1       8
```

This suggests there was a header row but the 'Yes' was not selected.

Change the Heading to be 'Yes', the file will load properly. Also it will take care of the missing values which are coded as 'NA' in this document.



```
mpg  engine  horse  weight  accel  year  origin  cyl
 9     4      93     732     8.5    0     NA      NA
10   360     215    4615    14.0   70      1       8
10   307     200    4376    15.0   70      1       8
11   318     210    4382    13.5   70      1       8
11   429     208    4633    11.0   72      1       8
11   400     150    4997    14.0   73      1       8
11   350     180    3664    11.0   73      1       8
12   383     180    4955    11.5   71      1       8
12   350     160    4456    13.5   72      1       8
12   429     198    4952    11.5   73      1       8
12   455     225    4951    11.0   73      1       8
12   400     167    4906    12.5   73      1       8
12   350     180    4499    12.5   73      1       8
```

2. Reading in free formatted data from an ASCII file using the read.table function

The read.table() function can read in any type of delimited ASCII file. It works pretty much the same as import dataset procedures in R studio. Actually, what this R module does is translate your specifications into function calls. So, read.table is doing that directly.

Here is an example for reading in the Car.csv file we just loaded by using '*Import Dataset*' module.

```
cars <- read.table(file = "Cars.csv", header = TRUE, sep = ",")
```

The data will be stored as a data frame and be assigned to the variable 'cars' on the left hand side of '<-". Three most important argument of read.table are:

- file: Specify the file location, if no specific path is specified, it will look for files in current working directory. So we can either specify the full path or just the file name if it is in the working directory.

- header: Whether the file's first row is a header row or not, default value is FALSE
- sep: Specifies the separator, default value is ' '.

For more detail, read the help document by using the 'help()' function. You can also learn similar functions which are developed for a certain type of files there. For example, the following command will give you the help document for read.table function.

```
help("read.table")
```

3.Exporting files using write.table function

The write.table function outputs data frame. Suppose we made some changes on 'cars' that we just read in and would like to save somewhere then write.table function can be used . The arguments it takes are similar to read.table. Here is an example:

```
write.table(cars, file = "Cars2.csv", sep = "\t", row.names = FALSE,
            col.names = TRUE)
```

- The first argument is to specify which data frame to be exported.
- file: the path of file to be created.
- sep: separator, the default separator is a blank space but any separator can be specified in the sep option. In the example we used a *Tab* separator.
- row.names and col.names: whether those names will appear in the output file. The default values are both TRUE.

Basic Statistics

The following commands are commonly used to explore and describe a data set.

Here is a print out the data set for reference:

```
Cars
## 	mpg engine horse weight accel year origin cylinder filter_.  mpg1
## 1   9.0    4.0    93    732   8.5    0     NA       NA       NA  9.98
## 2  10.0  360.0   215   4615  14.0   70      1        8        0 10.87
## 3  10.0  307.0   200   4376  15.0   70      1        8        0  9.63
## 4  11.0  318.0   210   4382  13.5   70      1        8        0 12.12
## 5  11.0  429.0   208   4633  11.0   72      1        8        0 10.63
## .
## .
## .
## 398 46.6   86.0    65   2110  17.9   80       3         4         1 47.93
## 399   NA  133.0   115   3090  17.5   70       2         4         1    NA
## 400   NA  350.0   165   4142  11.5   70       1         8         0    NA
## 401   NA  351.0   153   4034  11.0   70       1         8         0    NA
## 402   NA  383.0   175   4166  10.5   70       1         8         0    NA
## 403   NA  360.0   175   3850  11.0   70       1         8         0    NA
## 404   NA  302.0   140   3353   8.0   70       1         8         0    NA
## 405   NA   97.0    48   1978  20.0   71       2         4         1    NA
## 406   NA  121.0   110   2800  15.4   81       2         4         1    NA
```

There are some missing values, so we need to remove these missing values first.

Removing missing values:

```
cars=cars[-which(is.na(cars),arr.ind=T),]
```

Summary of Statistics

```
#summary(dataset/variable)
summary(cars)

##       mpg            engine          horse           weight
##  Min.   :10.00   Min.   : 68.0   Min.   : 46.0   Min.   :1613
##  1st Qu.:17.50   1st Qu.:105.0   1st Qu.: 75.0   1st Qu.:2220
##  Median :23.00   Median :151.0   Median : 92.0   Median :2790
##  Mean   :23.64   Mean   :193.6   Mean   :103.4   Mean   :2958
##  3rd Qu.:29.00   3rd Qu.:261.0   3rd Qu.:123.5   3rd Qu.:3590
##  Max.   :46.60   Max.   :455.0   Max.   :230.0   Max.   :5140
##      accel            year           origin         cylinder
##  Min.   : 8.00   Min.   :70.00   Min.   :1.000   Min.   :4.000
##  1st Qu.:14.00   1st Qu.:73.00   1st Qu.:1.000   1st Qu.:4.000
##  Median :15.50   Median :76.00   Median :1.000   Median :4.000
##  Mean   :15.57   Mean   :76.03   Mean   :1.567   Mean   :5.462
##  3rd Qu.:17.05   3rd Qu.:79.00   3rd Qu.:2.000   3rd Qu.:8.000
##  Max.   :24.80   Max.   :82.00   Max.   :3.000   Max.   :8.000
##     filter_.           mpg1
##  Min.   :0.0000   Min.   :10.63
##  1st Qu.:0.0000   1st Qu.:17.16
##  Median :1.0000   Median :22.71
##  Mean   :0.7441   Mean   :23.58
##  3rd Qu.:1.0000   3rd Qu.:29.34
##  Max.   :1.0000   Max.   :47.93
```

Data Structure

```
#str(dataset/variable)
str(cars)

## 'data.frame':    379 obs. of  10 variables:
##  $ mpg     : num  10 11 11 11 12 12 12 13 13 13 ...
##  $ engine  : num  360 318 429 400 455 400 350 400 400 350 ...
##  $ horse   : int  215 210 208 150 225 167 180 170 175 165 ...
##  $ weight  : int  4615 4382 4633 4997 4951 4906 4499 4746 5140 ...
##  $ accel   : num  14 13.5 11 14 11 12.5 12.5 12 12 12 ...
##  $ year    : int  70 70 72 73 73 73 73 71 71 72 ...
##  $ origin  : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ cylinder: int  8 8 8 8 8 8 8 8 8 8 ...
##  $ filter_.: int  0 0 0 0 0 0 0 0 0 0 ...
##  $ mpg1    : num  10.9 12.1 10.6 10.8 12.3 ...
```

Mean and Variance

```
#mean(variable,na.rm(removing NA)=True)
mean(cars$mpg)

## [1] 23.64248

#var(variable)
var(cars$mpg)

## [1] 59.8734
```

Number of Observation in the Variable

```
#length(variable)
length(cars$mpg)

## [1] 379
```

Median

```
#median(variable,na.rm=T)
median(cars$mpg)

## [1] 23
```

Quantile

```
#quantile(variable,level,na.rm=T), the argument na.rm==T means any NA a
nd NaN's are removed from x before the quantiles are computed.
quantile(cars$mpg,0.25)

##  25%
## 17.5
```

These commands are used for basic statistical inference

T-test

The default options of t-test in R are “x”, ”y”, “alternative”, “mu”, “paired”, “var.equal” and “conf.level”, and their default values are as follows:

```
t.test(x, y = NULL,
       alternative = c("two.sided", "less", "greater"),
       mu = 0, paired = FALSE, var.equal = FALSE,
       conf.level = 0.95, ...)
```

One Sample t-test

```
#t.test(variable, mean under null hypothesis)
t.test(cars$mpg,mu=25)

##
##  One Sample t-test
##
## data:  cars$mpg
## t = -3.4155, df = 378, p-value = 0.0007058
## alternative hypothesis: true mean is not equal to 25
## 95 percent confidence interval:
##  22.86096 24.42400
## sample estimates:
## mean of x
##  23.64248
```

Independent Sample t-test (Unequal Variance)

```
#t.test(variable1,variable2)
t.test(cars$mpg,cars$mpg1)

##
##  Welch Two Sample t-test
##
## data:  cars$mpg and cars$mpg1
## t = 0.10196, df = 755.88, p-value = 0.9188
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -1.052830  1.168186
## sample estimates:
## mean of x mean of y
##  23.64248  23.58480
```

Independent Sample t-test (Equal Variance)

```
#t.test(variable1,variable2,var.equal=True)
t.test(cars$mpg,cars$mpg1,var.equal=T)

##
##  Two Sample t-test
##
## data:  cars$mpg and cars$mpg1
## t = 0.10196, df = 756, p-value = 0.9188
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -1.052830  1.168186
## sample estimates:
## mean of x mean of y
##  23.64248  23.58480
```

Paired t-test

```
#t.test(variable1,variable2,paired=T)
t.test(cars$mpg,cars$mpg1,paired=T)

##
##  Paired t-test
##
## data:  cars$mpg and cars$mpg1
## t = 1.0662, df = 378, p-value = 0.287
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.0486872  0.1640434
## sample estimates:
## mean of the differences
##               0.0576781
```

Chi-Squared Tests

We are going to use a made-up a data set in the following example as Cars.csv does not lend itself to a Chi-Squared test. The data set will be a two-way contingency table, where the two factors are Degree (levels are High and Low) and clinic (5 levels from Worse to Marked Improvement), and the response variable is y.

Data input:

```
y1<-c(1,13,16,15,7)
y2<-c(11,53,42,27,11)

y<-cbind(y1,y2)
dimnames(y)<-list(clinic=c("Worse","Stationary","Slight Improvement",
                          "Moderate Improvement","Marked Improvement"),
                  Degree=(c("High","Low")))
```

```
y
```

```
##                          Degree
## clinic                    High Low
##   Worse                      1  11
##   Stationary                13  53
##   Slight Improvement        16  42
##   Moderate Improvement      15  27
##   Marked Improvement         7  11
```

Performing the Chi-squared test:

```
chi.test<-chisq.test(y)
```

```
## Warning in chisq.test(y): Chi-squared approximation may be incorrect
```

```
chi.test
```

```
## 
##  Pearson's Chi-squared test
## 
## data:  y
## X-squared = 6.8807, df = 4, p-value = 0.1423
```

To see the other data produced by chisq.test:

```
names(chi.test)
```

```
## [1] "statistic" "parameter" "p.value"   "method"    "data.name" "obs
erved"
## [7] "expected"  "residuals" "stdres"
```

To get the expected values, for example:

```
chi.test$expected
```

```
##                          Degree
## clinic                         High       Low
##   Worse                    3.183673  8.816327
##   Stationary              17.510204 48.489796
##   Slight Improvement      15.387755 42.612245
##   Moderate Improvement 11.142857 30.857143
##   Marked Improvement       4.775510 13.224490
```

Correlation

By default, the correlation function in R is as follows:

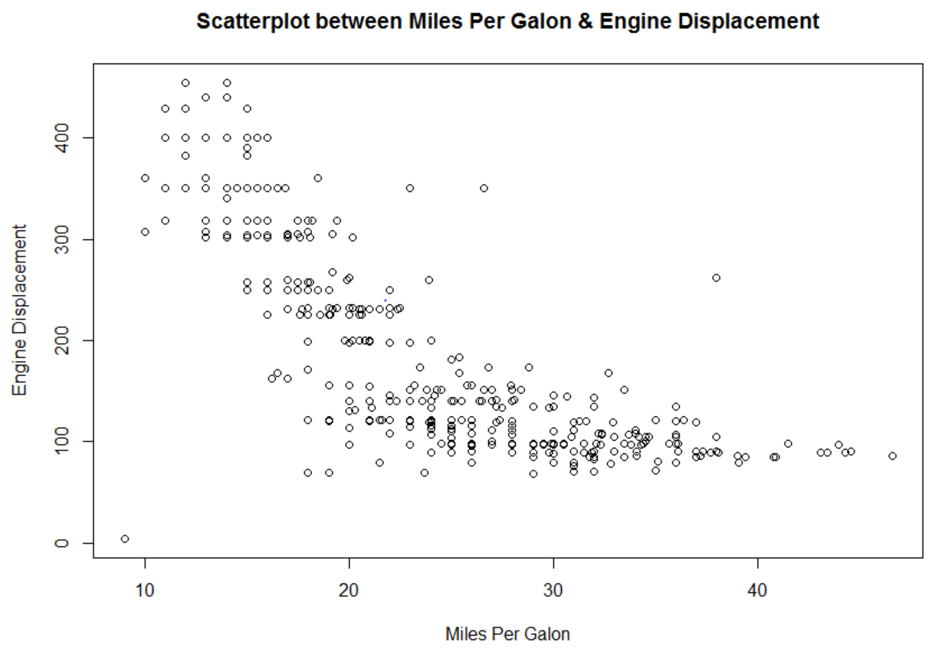
```
cor(x, y = NULL, use = "everything",
    method = c("pearson", "kendall", "spearman"))
#by default it uses Pearson method

#cor(variable1,variable2)
cor(cars$mpg,cars$engine)

## [1] -0.812826

cor(cars$mpg,cars$engine,method="spearman")

## [1] -0.8729739
```

Correlation Significance Test

```
#cor.test(variable1,variable2)
cor.test(cars$mpg,cars$engine)

##
##  Pearson's product-moment correlation
##
## data:  cars$mpg and cars$engine
## t = -27.094, df = 377, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.8444198 -0.7755971
## sample estimates:
##       cor
## -0.812826

cor.test(cars$mpg,cars$engine,method="spearman")

## Warning in cor.test.default(cars$mpg, cars$engine, method = "spearma
n"):
## Cannot compute exact p-value with ties

##
##  Spearman's rank correlation rho
##
## data:  cars$mpg and cars$engine
## S = 16994000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##        rho
## -0.8729739
```

Plotting a Scatterplot

```
plot(cars$mpg,cars$engine,xlab="Miles Per Gallon", ylab="Engine Displac
ement",
     main="Scatterplot between Miles Per Gallon & Engine Displacement")
```



Hypothesis testing (t-tests done previously)

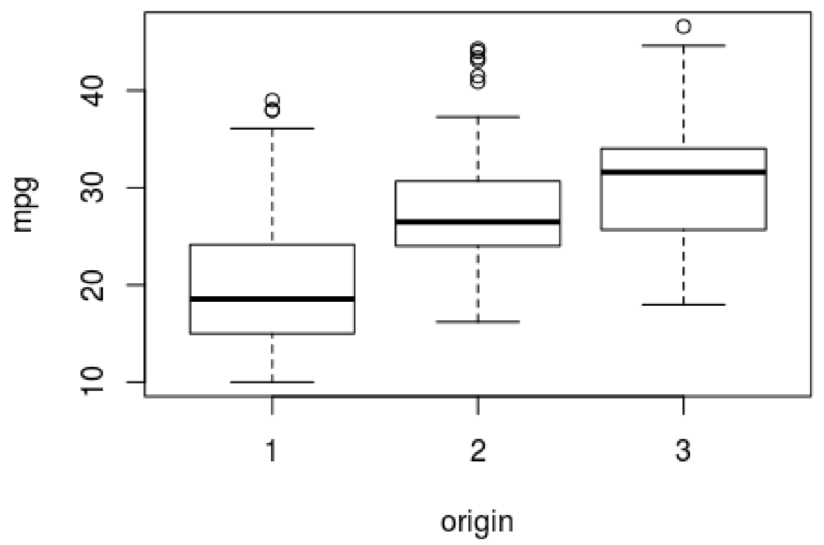
One-Way ANOVA

We will introduce how to do One-Way ANOVA (analysis of variance) in R based on the dataset **Cars.csv**. The response variable is *mpg*. The factor is *origin*. The One-Way ANOVA can be carried out by using the R function *aov()*
We read in the dataset and name it as *cars* and change the class of the variable *origin* to be a factor. There are three levels of *origin* as 1, 2 and 3.

```
cars <- read.csv("Cars.csv")

#Use read.csv to import a csv file

cars$origin <- as.factor(cars$origin)
levels(cars$origin)

## [1] "1" "2" "3"
```

The first step in our analysis is to graphically compare mpgs among three distributions with different origins.

```
plot(mpg ~ origin, data=cars)
```



From the boxplot it appears that the median of *mpg* for origin 1 is lower than for origin 2 and 3.

Next, the R function *aov()* can be used for fitting ANOVA models.

```
results = aov(mpg ~ origin, data=cars)
summary(results)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)    
## origin        2   7985    3992   97.97 <2e-16 ***
## Residuals   394  16056      41                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 9 observations deleted due to missingness
```

From the output of *summary()*, The F value is 97.97 with a p-value smaller than 0.05. We clearly reject the null hypothesis of equal means of *mpg* for all three origin.

The model is significant, then we would like to carry out the multiple comparisons to get information how *mpg* differs in three different origin by using R function *pairwise.t.test()*. This function *pairwise.t.test* computes the pair-wise comparisons between group means with corrections for multiple testing.

```
pairwise.t.test(cars$mpg, cars$origin, p.adjust="bonferroni")
```

```
## 
##  Pairwise comparisons using t tests with pooled SD 
## 
## data:  cars$mpg and cars$origin 
## 
```

```
##   1      2
## 2 <2e-16 -
## 3 <2e-16 0.045
##
## P value adjustment method: bonferroni
```

This result states that the means of these three origins are all significantly different.

Another multiple comparisons procedure is Tukey's method by using R function *TukeyHSD()*. This function creates a set of confidence intervals on the differences between means.

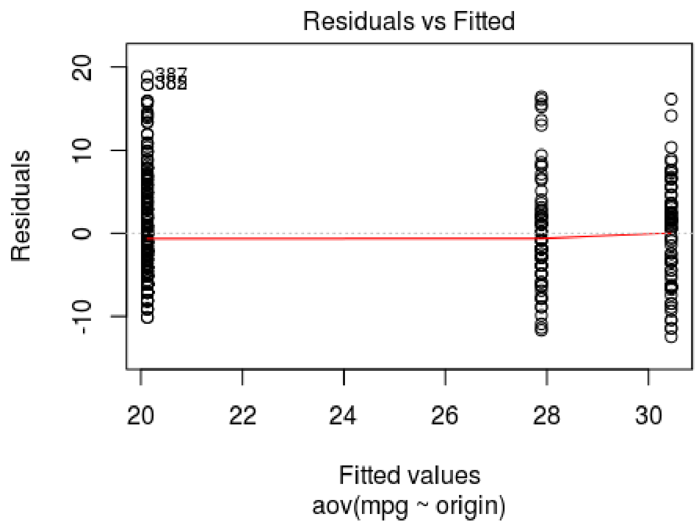
```
results = aov(mpg ~ origin, data=cars)
TukeyHSD(results,conf.level=0.95)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = mpg ~ origin, data = cars)
##
## $origin
##          diff        lwr       upr     p adj
## 2-1  7.763203 5.73054715  9.795858 0.0000000
## 3-1 10.322407 8.38214860 12.262666 0.0000000
## 3-2  2.559204 0.09398439  5.024424 0.0397888
```

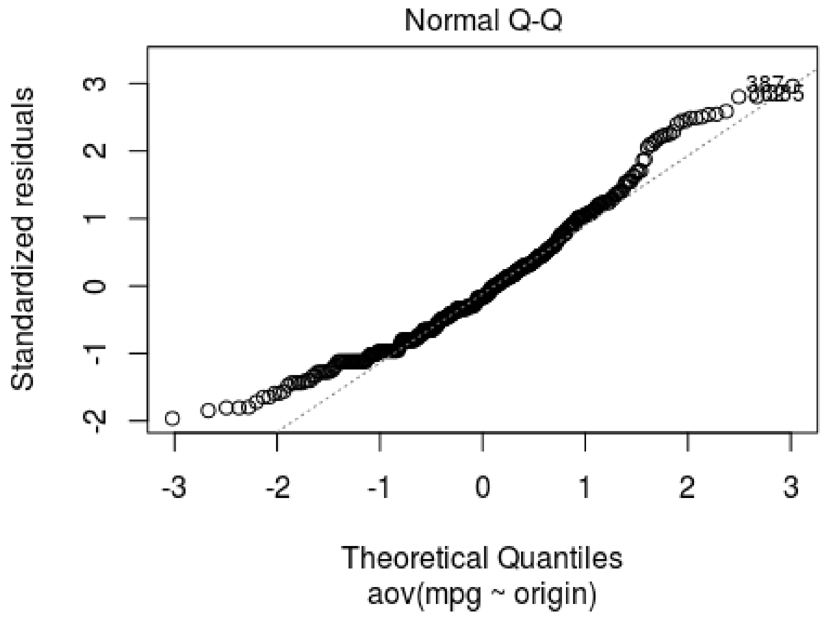
The results show that all the three differences are significant.

Then we want to carry out the diagnostic of the model assumption, and we can use the plot function to plot the model:

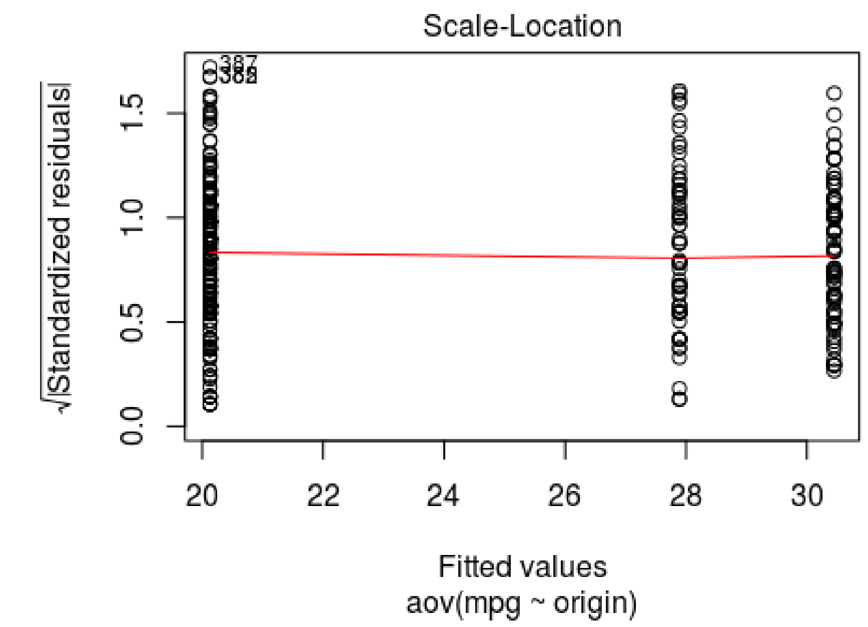
```
plot(results)
```

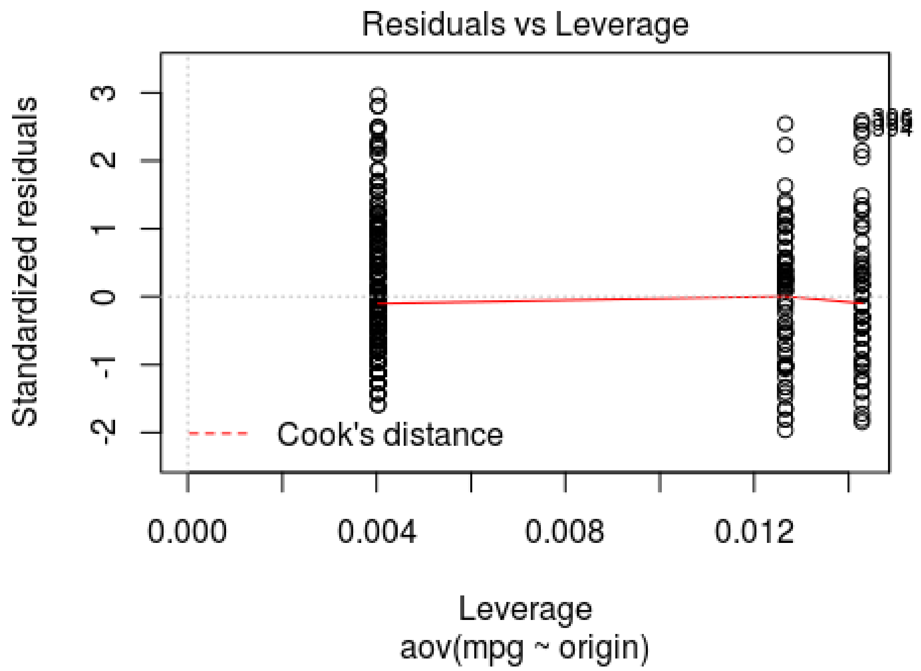


The redline connects the medians across different groups.



The points are mostly close to the straight line, however, we can observe a small pattern in the beginning and in the end, which suggests the distribution of residuals is a little skewed.


Scale-Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
387
382
20
22
24
26
28
30
Fitted values
aov(mpg ~ origin)


Residuals vs Leverage
Standardized residuals
-2
-1
0
1
2
3
Cook's distance
0.000
0.004
0.008
0.012
Leverage
aov(mpg ~ origin)

Regression

As before, we remove the missing values first:

```
cars<-cars[-which(is.na(cars),arr.ind=T),]
```

To get the names of variables in the dataset, we can use the basic function "names":

```
names(cars)

##  [1] "mpg"      "engine"   "horse"    "weight"   "accel"    "year"
##  [7] "origin"   "cylinder" "filter_." "mpg1"
```

Linear Regression Models

To fit a linear regression model with all variables in the dataset without interaction:

```
mod.reg<-lm(mpg~.,data=cars)
summary(mod.reg)

##
## Call:
## lm(formula = mpg ~ ., data = cars)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.3196 -0.6958  0.0189  0.6254  3.0243
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.5673545  1.5809687  -0.359  0.71990
## engine       0.0025929  0.0024279   1.068  0.28622
## horse        0.0004493  0.0046635   0.096  0.92330
## weight      -0.0006067  0.0002320  -2.615  0.00930 **
## accel        0.0159285  0.0316724   0.503  0.61533
## year         0.0662729  0.0200110   3.312  0.00102 **
## origin       0.0964715  0.0902488   1.069  0.28579
## cylinder    -0.2033509  0.1193718  -1.704  0.08931 .
## filter_.    -0.4577229  0.2929970  -1.562  0.11910
## mpg1         0.9102985  0.0167311  54.407  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.023 on 369 degrees of freedom
## Multiple R-squared:  0.9829, Adjusted R-squared:  0.9825
## F-statistic:  2362 on 9 and 369 DF,  p-value: < 2.2e-16
```

To fit a linear regression model with several variables in the dataset:

```
mod1<-lm(mpg~engine+horse+weight,data=cars)
summary(mod1)
##
## Call:
```

```
## lm(formula = mpg ~ engine + horse + weight, data = cars)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.4431 -2.7307 -0.3825  2.2516 16.1406
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 44.7774973  1.2369586  36.200  < 2e-16 ***
## engine      -0.0098511  0.0069098  -1.426   0.1548
## horse       -0.0278049  0.0133328  -2.085   0.0377 *
## weight      -0.0055278  0.0007289  -7.584 2.67e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.169 on 375 degrees of freedom
## Multiple R-squared:  0.7121, Adjusted R-squared:  0.7098
## F-statistic: 309.1 on 3 and 375 DF,  p-value: < 2.2e-16
```

To fit a linear regression model with interaction:

```
mod2<-lm(mpg~engine*horse+weight,data=cars)

#engine*horse means the main effects of engine and horse as well as the
ir interaction effect.


summary(mod2)

##
## Call:
## lm(formula = mpg ~ engine * horse + weight, data = cars)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -9.936 -2.216 -0.238  1.871 16.781
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.373e+01  1.568e+00  34.278  < 2e-16 ***
## engine       -7.268e-02  9.879e-03  -7.357 1.20e-12 ***
## horse        -1.796e-01  2.201e-02  -8.161 5.11e-15 ***
## weight       -2.895e-03  7.417e-04  -3.903 0.000113 ***
## engine:horse  4.724e-04  5.686e-05   8.308 1.81e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.835 on 374 degrees of freedom
## Multiple R-squared:  0.7569, Adjusted R-squared:  0.7543
## F-statistic: 291.2 on 4 and 374 DF,  p-value: < 2.2e-16
```

To fit a linear regression model with higher order interaction:

```
mod3<-lm(mpg~(engine+horse+weight)^3,data=cars)
summary(mod3)

##
## Call:
## lm(formula = mpg ~ (engine + horse + weight)^3, data = cars)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.5411 -2.2346 -0.4175  1.7745 17.3233
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)          6.163e+01  5.560e+00  11.085  < 2e-16 ***
## engine              -1.208e-01  3.819e-02  -3.163  0.00169 **
## horse               -1.871e-01  7.713e-02  -2.426  0.01573 *
## weight              -6.913e-03  2.398e-03  -2.883  0.00417 **
## engine:horse         5.980e-04  2.627e-04   2.277  0.02338 *
## engine:weight        1.982e-05  9.870e-06   2.008  0.04541 *
## horse:weight         1.461e-05  2.680e-05   0.545  0.58582
## engine:horse:weight -7.848e-08  6.647e-08  -1.181  0.23848
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.817 on 371 degrees of freedom
## Multiple R-squared:  0.7612, Adjusted R-squared:  0.7567
## F-statistic:   169 on 7 and 371 DF,  p-value: < 2.2e-16
```

To view the contents of model summary:

```
sum=summary(mod.reg)
names(sum)

##  [1] "call"          "terms"         "residuals"     "coefficients"
##  [5] "aliased"       "sigma"         "df"            "r.squared"
##  [9] "adj.r.squared" "fstatistic"    "cov.unscaled"
```

To get model coefficients:

```
sum$coefficients

##                  Estimate  Std. Error     t value     Pr(>|t|)
## (Intercept) -0.5673545304 1.580968723 -0.35886512 7.199012e-01
## engine       0.0025929429 0.002427858  1.06799595 2.862205e-01
## horse        0.0004492931 0.004663497  0.09634253 9.233008e-01
## weight      -0.0006066500 0.000232019 -2.61465725 9.297769e-03
## accel        0.0159284879 0.031672447  0.50291308 6.153254e-01
## year         0.0662728753 0.020011017  3.31181941 1.018461e-03
## origin       0.0964715379 0.090248782  1.06895114 2.857905e-01
## cylinder    -0.2033509048 0.119371772 -1.70350915 8.931478e-02
## filter_.    -0.4577229299 0.292996952 -1.56221055  1.190956e-01
## mpg1          0.9102985190 0.016731122 54.40749836 2.447556e-178
```

To get specific values in the model coefficients, for example p-values:

```
sum$coefficients[,4]
```

```
##   (Intercept)        engine         horse        weight          acce
l
##  7.199012e-01  2.862205e-01  9.233008e-01  9.297769e-03  6.153254e-0
1
##          year        origin      cylinder      filter_.           mpg
1
##  1.018461e-03  2.857905e-01  8.931478e-02  1.190956e-01 2.447556e-17
8
```

Logistic regression

For the logistic regression case, suppose we are interested in how variables, such as GRE (Graduate Record Exam scores), GPA (grade point average) and prestige of the undergraduate institution, effect admission into graduate school. The response variable, admit/don't admit, is a binary variable.

Let's first read in the dataset online.

```
admission <- read.csv("http://www.ats.ucla.edu/stat/data/binary.csv")
head(admission)
```

```
##   admit gre  gpa rank
## 1     0 380 3.61    3
## 2     1 660 3.67    3
## 3     1 800 4.00    1
## 4     1 640 3.19    4
## 5     0 520 2.93    4
## 6     1 760 3.00    2
```

This dataset has a binary response (outcome, dependent) variable called *admit*. There are three predictor variables: *gre, gpa* and *rank*. We will treat the variables *gre* and *gpa* as continuous. The variable *rank* takes on the values 1 through 4. Institutions with a rank of 1 have the highest prestige, while those with a rank of 4 have the lowest. We can get basic descriptives for the entire data set by using *summary* function.

```
summary(admission)
```

```
##      admit             gre             gpa             rank      
##  Min.   :0.0000   Min.   :220.0   Min.   :2.260   Min.   :1.000  
##  1st Qu.:0.0000   1st Qu.:520.0   1st Qu.:3.130   1st Qu.:2.000  
##  Median :0.0000   Median :580.0   Median :3.395   Median :2.000  
##  Mean   :0.3175   Mean   :587.7   Mean   :3.390   Mean   :2.485  
##  3rd Qu.:1.0000   3rd Qu.:660.0   3rd Qu.:3.670   3rd Qu.:3.000  
##  Max.   :1.0000   Max.   :800.0   Max.   :4.000   Max.   :4.000
```

First, we convert *rank* to a factor to indicate that *rank* should be treated as a categorical variable.

```
admission$rank <- factor(admission$rank)
levels(admission$rank)

## [1] "1" "2" "3" "4"
```

Then we fit a logistic regression model using the *glm* function and use *summary* function to get the estimate of the model.

```
results <- glm(admit ~ gre + gpa + rank, data = admission, family = "bi
nomial")
summary(results)

##
## Call:
## glm(formula = admit ~ gre + gpa + rank, family = "binomial",
##     data = admission)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6268  -0.8662  -0.6388   1.1490   2.0790
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.989979   1.139951  -3.500 0.000465 ***
## gre          0.002264   0.001094   2.070 0.038465 *
## gpa          0.804038   0.331819   2.423 0.015388 *
## rank2       -0.675443   0.316490  -2.134 0.032829 *
## rank3       -1.340204   0.345306  -3.881 0.000104 ***
## rank4       -1.551464   0.417832  -3.713 0.000205 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 499.98  on 399  degrees of freedom
## Residual deviance: 458.52  on 394  degrees of freedom
## AIC: 470.52
##
## Number of Fisher Scoring iterations: 4
```

The outputs from *summary* can show us a lot of useful information. In the 'Coefficients' section of the output, we can check whether the predictor variables are significant or not by checking the p-value. As we can see from the output, both *gre* and *gpa* are statistically significant, as are the three terms for *rank*. The logistic regression coefficients give the change in the log odds of the outcome for a one unit increase in the predictor variable.

You can also calculate odds ratio.

```
exp(coef(results))

## (Intercept)         gre       gpa       rank2       rank3       rank4

##   0.0185001   1.0022670   2.2345448  0.5089310  0.2617923  0.2119375
```

Power calculation

We now take a look at how to conduct power analysis for a simple t test, a paired t test and a One-way ANOVA.

The power of a test is the probability of detecting an effect given that the effect exists. In statistical jargon, it is the probability of rejecting the null hypothesis when the alternative hypothesis of interest is true.

Conducting a power analysis is generally done for two of the following reasons:

1) To determine the number of subjects (sample size) needed in order to detect a given effect size at a specified power.
2) To determine the power of the test given an effect size and the sample size available for the study.

In the first case, the power analysis is done before the data collection stage. In the second case, the power analysis is often used when there is a limit to the number of subjects the researcher can use in the study. The power analysis is therefore run in this case in order to determine how likely the study conducted using the limited sample size at hand is to detect an effect. A low power, would be a good reason to rethink whether to proceed with the study.

In order to conduct a power analysis, three out of four of the following values need to be specified: (i.e. given three of the quantities below the fourth one can be computed using the power analysis)

- Sample size
- Effect size
- Significance level (Type I error: the probability of finding an effect when the effect is present)
- Power (1- Type II error: The probability of failing to detect an effect when the effect is present)

Important: There is no golden rule for the minimum power required for a study. However, it is important to remember that a larger power is more desirable as it reduces the risk of a Type II error. Scientists often follow the rule proposed by Cohen (1988) in his book "Statistical Power Analysis for the Behavioral Sciences " which states that studies should be designed to allow for a power of at least 0.8. For more information on power and how to determine the minimum effect size of a test please refer to Cohen's book mentioned above.

The R package "**pwr**" allows us to run power analysis for a wide variety of models. The R code below makes the "pwr" package available in the R library.

```
library(pwr)
```

Power analysis: One sample t-test.

In the case of the one sample t-test, the null hypothesis is that the mean of the data of interest is equal to a constant and the alternative could be one of the three options:

1. The mean is greater than the constant (right-tailed hypothesis),
2. The mean is less than the constant (left-tailed hypothesis)
3. The mean is not equal to the constant (two-tailed hypothesis).

The R function for carrying the one sample t-test is provided below where "n" is the total sample size, "d" is the effect size, "sig.level" is the significance level, "power" is the power of the test and "type" is set to be "one.sample".

Specifying any three of the four values will generate the value of the non-specified parameter.

```
#pwr.t.test(n = , d = , sig.level = , power = , type = "one.sample")
```

In the example below, we compute the sample size required for a two-tailed One Sample t-test at a 0.05 significance level and a power of 80%. We make an educated guess based on previous studies that the minimum effect size we would like to detect is 0.40.

```
pwr.t.test(n = , d =0.40 , sig.level =0.05 , power = 0.8, type =  "one.
sample",  alternative = "two.sided")

## 
##      One-sample t test power calculation 
## 
##               n = 51.00945
##               d = 0.4
##       sig.level = 0.05
##           power = 0.8
##     alternative = two.sided
```

The results show that a total sample size of 51 subjects is required to achieve 80% power at the specified significance level.

In the second example below, we compute the power of a One-sample t-test with a two-tailed alternative hypothesis at a 0.05 significance level, with a sample size of 30 and a minimum effect size of 0.40.

```
pwr.t.test(n = 30 , d =0.40 , sig.level =0.05 , power = , type =  "one.
sample", alternative = "two.sided")

##
##      One-sample t test power calculation
##
##               n = 30
##               d = 0.4
##       sig.level = 0.05
##           power = 0.5628136
##     alternative = two.sided
```

The results show that with a sample size of 30 the power of the test will approximately 56%.

Power Analysis: Two sample t-test.

A two sample t-test tests whether the means of two different groups are equal or not. A two sample t-test is only valid if the data between the two groups are not correlated. In the example below, we determine the total sample size required for detecting an effect size of 0.6 given that we want to achieve a 90% power with a 0.05 significance level.

```
pwr.t.test(n = , d =0.6 , sig.level =0.05 , power = 0.9 , type =  "two.
sample",alternative = "two.sided")

##
##      Two-sample t test power calculation
##
##               n = 59.35155
##               d = 0.6
##       sig.level = 0.05
##           power = 0.9
##     alternative = two.sided
##
## NOTE: n is number in *each* group
```

The results show that we need a total sample size of about 60. Which means that the two groups will have a sample size of 30 each. We can use the same function in order to find the power of a two sample t-test with balanced samples given the total sample size by leaving the "power" option empty.

If the samples are unbalanced, that is if the data is such that one of the groups has more samples than the other group then we can use the R function'pwr.t2n.test' in order to find the power of the two sample t-test as illustrated below.

```
pwr.t2n.test(n1 = 40 , n2=57 , d =0.6 , sig.level = 0.05, power = ,alte
rnative = "two.sided")

##
##      t test power calculation
##
##               n1 = 40
##               n2 = 57
##                d = 0.6
##        sig.level = 0.05
##            power = 0.821067
##      alternative = two.sided
```

The power in this case is about 82%.

Power analysis: Paired t-test.

A paired t-test is used to compare the means of two groups when we believe the data between the groups are correlated. For example, the paired t-test can be used to compare the mean responses of an outcome of interest before and after an intervention is operated on the subjects. The following R code shows how to get the sample size for a paired t-test in order to achieve a power of 0.9 at a significance level of 0.05 with an estimated minimum effect size of 0.8.

```
pwr.t.test(n = , d =0.8 , sig.level =0.05 , power = 0.9 , type =  "pair
ed",alternative= "two.sided")

##
##      Paired t test power calculation
##
##                n = 18.44623
##                d = 0.8
##        sig.level = 0.05
##            power = 0.9
##      alternative = two.sided
##
## NOTE: n is the number of *pairs*.
```

The results show that we need a sample size of about 18 pairs for the paired t-test with a 90% power.

Power analysis: One-way ANOVA

Power analysis for a one-way ANOVA model with “k” number of levels can be carried using the "pwr.anova.test" function in R. In the example below we determine the sample size for carrying a one-way ANOVA with 4 levels, an 80% power and an effect size of 0.4 at a 0.05 significance level. Here "n" represents the number of sample per level and "f" is the effect size.

```
pwr.anova.test(k = 4 , n = , f = 0.4 , sig.level = 0.05 , power = 0.8)

##
##      Balanced one-way analysis of variance power calculation
##
##               k = 4
##               n = 18.04262
##               f = 0.4
##       sig.level = 0.05
##           power = 0.8
##
## NOTE: n is the number of samples in each group.
```

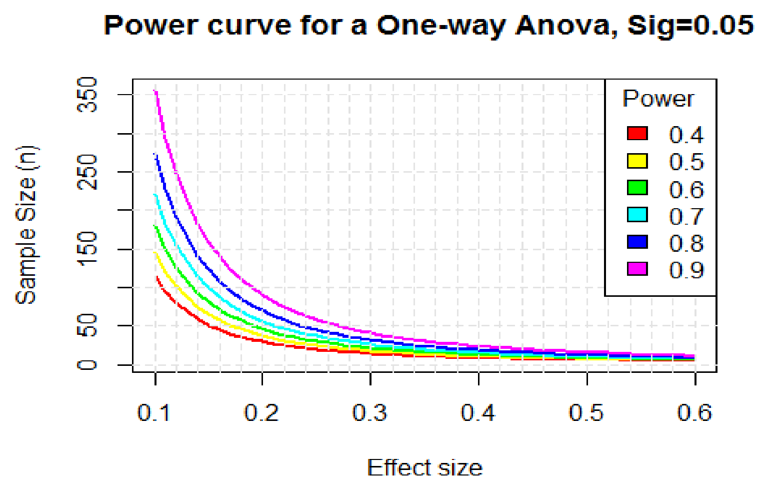
The results show that in order to detect a treatment effect size of 0.4 or greater if one exists with an 80% power each of the four treatments groups should have a sample size of 18. Hence the total sample size for the study would be 18*4= 72. The power for the ANOVA can be computed if the sample size for each level is known, by leaving the power option in the function call empty. Note that in such a case the group sample size should be equal.

Power curves

A power curve is often a better option for representing how the power of the test varies with different values of the sample size and effect size. Below is a code that the user can change in order to generate a power curve for any type of test. In the specific example below, the power curve for a one-way ANOVA is generated using different effect sizes and sample size at a 0.05 significance level.

Note: The user is advised to read the comments (sentences that come after the "#" symbols, in order to determine how to modify the code for the type of power curve they want to generate.)

```
# This code generates a power curve for a One-Way ANOVA model with 4 le
vels of equal sample size.


#Step1: Load pwr package in R working library.
 library(pwr)

#Step2: Define the range of effect size for building the power curve us
ing the R function "seq". In this case we generate an effect size which
 ranges from 0.1 to 0.6 with intervals of 0.01.

f <- seq(.1,.6,.01)
 nf <- length(f)
 #Step 3: Define the range of power acceptable for the study. The code
below generated power which ranges from 0.4 to 0.95 with intervals of 0
.1.
 p <- seq(.4,.95,.1)
 np <- length(p)

 # obtain sample sizes.
 samsize <- array(numeric(nf*np), dim=c(nf,np))
 for (i in 1:np){
   for (j in 1:nf){

     # you can specify the specific type of power analysis to run here
by replacing the pwr.anova.test() function with the power function suit
ed for your analysis Example: pwr.t.test() for one-sample t-test for or
 pwr.t2n.test() for a two-sample t-test.
     result <- pwr.anova.test(k= 4, n = , f =  f[j], sig.level = .05, p
ower = p[i])


     samsize[j,i] <- ceiling(result$n)
   }
 }

 # set up graph
 xrange <- range(f)
 yrange <- round(range(samsize))
 colors <- rainbow(length(p))
 plot(xrange, yrange, type="n",
   xlab="Effect size",
   ylab="Sample Size (n)" )

 # add power curves
 for (i in 1:np){
   lines(f, samsize[,i], type="l", lwd=2, col=colors[i])
 }

 # add annotation (grid lines, title, legend)
 abline(v=0, h=seq(0,yrange[2],50), lty=2, col="grey89")
 abline(h=0, v=seq(xrange[1],xrange[2],.02), lty=2,
    col="grey89")

# Add title for the curve
 title(" Power curve for a One-way Anova, Sig=0.05")  legend("topright"
, title="Power", as.character(p),
    fill=colors)
```



Linear Mixed Models

When analyzing some experimental data, one or more of the factors in the study may be treated as **random factors**. That is, their levels can be thought of as being **randomly sampled** from a larger population of levels. When one or more random factors exist in a linear model, we call it a **Linear Mixed Model** (LMM) to highlight the fact that independent variables are a mixture of fixed factors and random factors.

LMM in R

In R we use the **lme4** package to build and fit LMM, and use the **car** package to do significance test.

Building LMM in R is very similar to building a linear regression via `lm()`, except that we need to declare which variables are random.

We use the car data set to illustrate how to fit LMM in R. First we read in the data:

```
dat = read.csv("Cars.csv")
head(dat, 10)
```

```
##    mpg engine horse weight accel year origin cylinder filter  mpg1
## 1    9      4    93    732   8.5    0     NA       NA     NA  9.98
## 2   10    360   215   4615  14.0   70      1        8      0 10.87
## 3   10    307   200   4376  15.0   70      1        8      0  9.63
## 4   11    318   210   4382  13.5   70      1        8      0 12.12
## 5   11    429   208   4633  11.0   72      1        8      0 10.63
## 6   11    400   150   4997  14.0   73      1        8      0 10.79
## 7   11    350   180   3664  11.0   73      1        8      0 12.22
## 8   12    383   180   4955  11.5   71      1        8      0 12.11
## 9   12    350   160   4456  13.5   72      1        8      0 12.66
## 10  12    429   198   4952  11.5   73      1        8      0 11.68
```

We will treat origin, cylinder and filter as categorical variables, so we convert them to factors:

```
dat$origin = as.factor(dat$origin)
dat$cylinder = as.factor(dat$cylinder)
dat$filter = as.factor(dat$filter)
```

Assume that we want to build a model taking mpg1 as response, origin as fixed factor, and cylinder as random factor, then we can build the model as follows:

```
library(lme4)

## Loading required package: Matrix
model = lmer(mpg1 ~ origin + (1 | cylinder), data = dat, REML = FALSE)
```

The REML parameter controls whether to use the maximum likelihood (ML) or the restricted maximum likelihood (REML) to fit the model. In this example, we choose REML = FALSE to use the ML approach.

After building the model we can use the summary() method to print the estimates of model parameters.

```
summary(model)

## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: mpg1 ~ origin + (1 | cylinder)
##    Data: dat
##
##      AIC      BIC   logLik deviance df.resid
##   2373.4   2393.3  -1181.7   2363.4      392
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4654 -0.6018 -0.1019  0.4598  3.9633
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  cylinder (Intercept) 24.22    4.921
##  Residual             21.54    4.642
## Number of obs: 397, groups:  cylinder, 5
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  20.8890     2.3251   8.984
## origin2       0.7503     0.7459   1.006
## origin3       3.9086     0.7173   5.449
##
## Correlation of Fixed Effects:
##         (Intr) orign2
## origin2 -0.115
## origin3 -0.117  0.437
```

In the "Random effects" section, we can see that the estimated standard deviation of the random factor `cylinder` is 4.921, and the estimated standard deviation of residual is 4.642.

In the "Fixed effects" section, the table gives the estimated fixed effects of different levels of `origin`, where `origin = 1` is taken to be the reference level.

Significance Test

The **lme4** package itself does not provide functions to calculate p-values of fixed effects. Instead, the **car** package has a function called `Anova()` to do the work.

```
library(car)
Anova(model)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: mpg1
##         Chisq Df Pr(>Chisq)
## origin 32.038  2  1.104e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The Wald test result shows that `origin` has a significant effect on `mpg1`.

Nested Factors

If we wish to specify a random factor `g2` nested in a fixed factor `g1`, the formula can be written as `g1 + (1 | g1:g2)`. Similarly, if `g1` is also random, the formula is `(1 | g1) + (1 | g1:g2)`, which can be simplified to be `(1 | g1/g2)`.

For example, if we treat `filter` as a fixed factor, and `cylinder` is nested in `filter`, the model can be coded as

```
model2 = lmer(mpg1 ~ origin + filter + (1 | filter:cylinder),
              data = dat, REML = FALSE)
summary(model2)

## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: mpg1 ~ origin + filter + (1 | filter:cylinder)
##    Data: dat
##
##      AIC      BIC   logLik deviance df.resid
##   2326.5   2350.3  -1157.3   2314.5      384
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4593 -0.5981 -0.1003  0.4635  3.9561
##
```

```
## Random effects:
##  Groups          Name        Variance Std.Dev.
##  filter:cylinder (Intercept) 10.80    3.287
##  Residual                    21.44    4.630
## Number of obs: 390, groups:  filter:cylinder, 3
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  14.8941     3.3184   4.488
## origin2       0.7022     0.7473   0.940
## origin3       3.9518     0.7184   5.501
## filter1       8.7999     4.0693   2.163
##
## Correlation of Fixed Effects:
##         (Intr) orign2 orign3
## origin2  0.000
## origin3  0.000  0.436
## filter1 -0.815 -0.049 -0.051
```

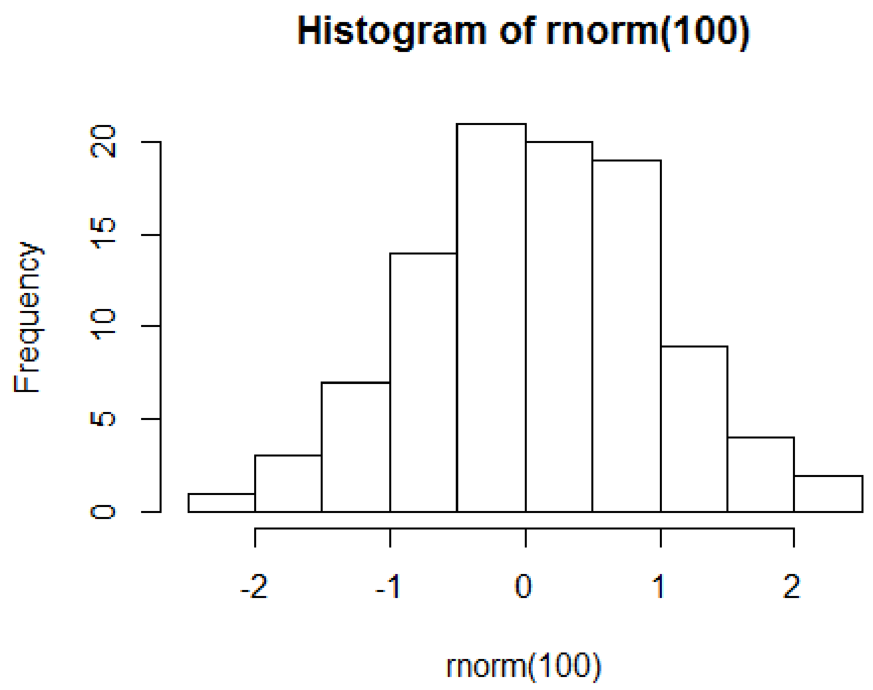
```
Anova(model2)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: mpg1
##          Chisq Df Pr(>Chisq)
## origin 32.8924  2  7.203e-08 ***
## filter  4.6764  1    0.03058 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Graphics

Create a plot.

```
set.seed(1)
 hist(rnorm(100))
```


Histogram of rnorm(100)
Frequency
0
5
10
15
20
-2
-1
0
1
2
rnorm(100)