The >eR-Biostat initiative

Making R based education materials in statistics accessible for all

An introduction to R: Short Version (2017)

Developed by

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The course was developed as a part of the >eR-BioStat initiative.

Most of the datasets used in the course are available as R objects.

External datasets are available in the GitHub page of the course.

Overview

A (very) quick start: the cars data

Two sample t-test.

basic plots

1. Basic programming in R: objects in R
2. Reading external datasets
3. Basic plots functions
4. Programming in R: a for loop
5. Statistical modeling in R: simple linear regression
6. Statistical modeling in R: one-way ANOVA
7. Statistical modeling in R: logistic regression
8. Programming in R: user functions
9. Two-way ANOVA
10. More about two-way ANOVA,
11. More about linear regression
12. Application of a for loop: bootstrap.

A (very) quick Start

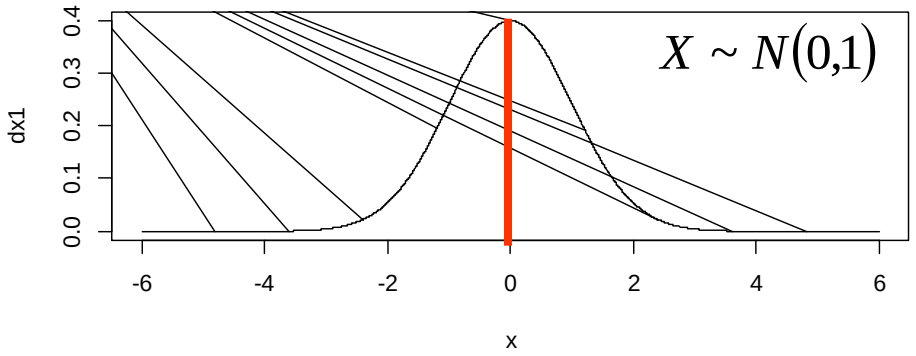
The R environment

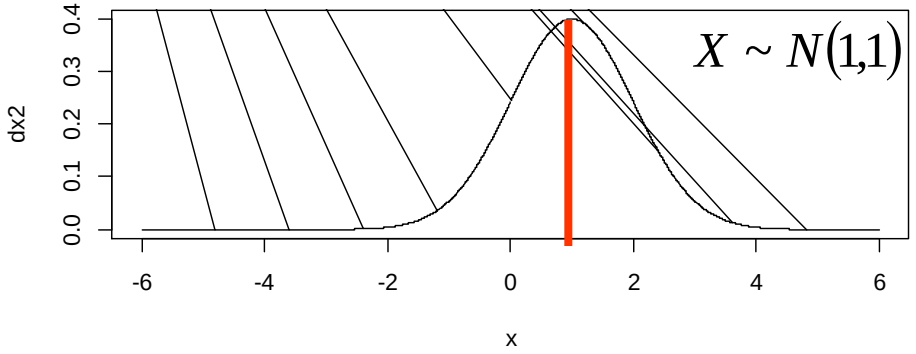
- Open R.
- Open a new script window.

The normal distribution: location

Density function of a normal distribution

$$X \sim N\left(\mu, \sigma^2\right)$$

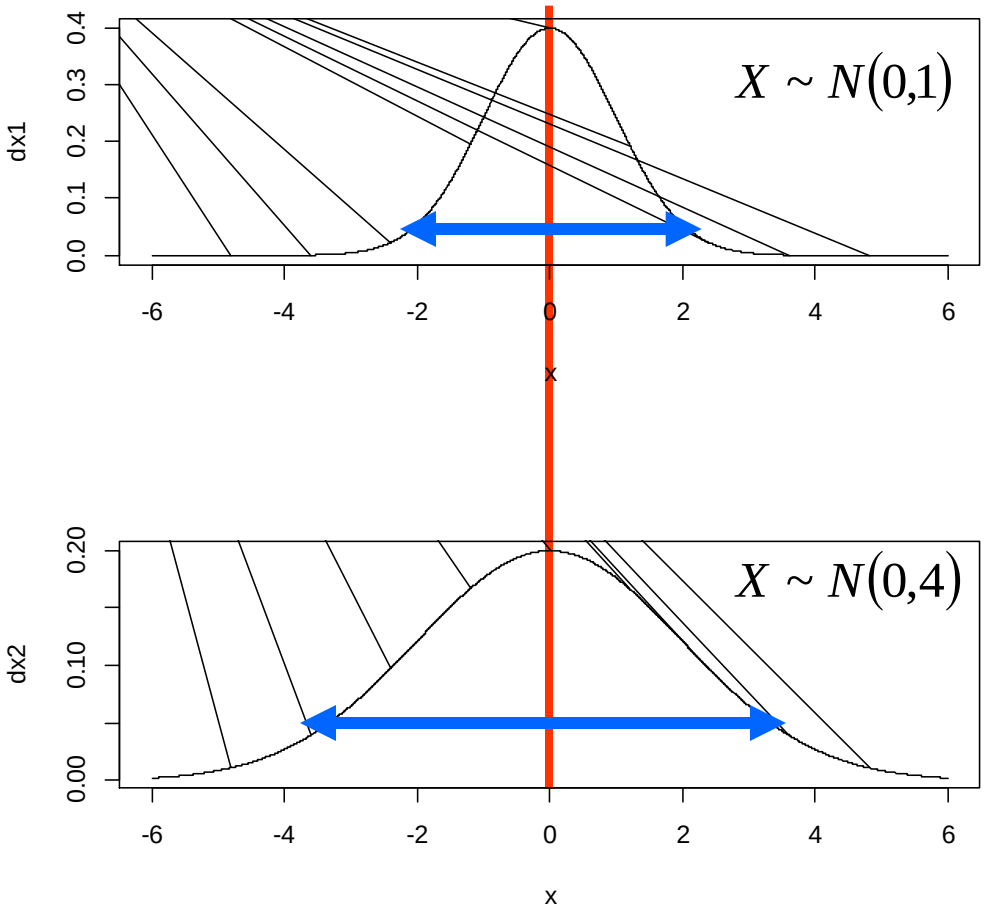




The normal distribution: variability

Density function of a normal distribution

$$X \sim N(\mu, \sigma^2)$$



Random sample from a normal distribution in R

Draw a random sample of size 100 from a normal distribution with mean – and variance 1

$$X \sim N(\mu, \sigma^2)$$

In R

```
rnorm(sample size, mean,standard deviation)
```

$$X \sim N(0,1)$$

```
rnorm(100,0,1)
```

Random sample from a normal distribution in R

Draw a random sample of size 100 from a normal distribution with mean – and variance 1

$$X \sim N\left(\mu, \sigma^2\right) \Rightarrow \; X \sim N(0,1)$$

```
> rnorm(100,0,1)
  [1] -0.173911348 -0.463196096 -1.084838332  2.373958677 -1.685884982
  [6] -1.952672126 -0.055601310 -0.241913096 -0.999586206  0.308335895
 [11]  0.556993818  2.337451275  0.778734465 -0.501354458  0.004525392
 [16] -1.468709822  0.109901143  0.109103689  0.662434110 -0.177097648
 [21] -1.442033566  0.615239368  0.254080126  1.152977602 -0.089559002
 [26]  0.065022482  0.300405204 -0.190196930 -0.244365328  0.886735849
 [31] -0.667671228 -1.009209277  0.388362272 -0.041883373  0.750480061
 [36] -2.103109677 -1.515839684 -0.477250540 -0.344581482  0.072570862
 [41] -0.364485234 -0.920898769  1.148778190  1.092225688 -0.832389361
 [46] -1.914844153 -0.384265110  0.528078353  1.319149374  0.226817654
 [51] -0.605867376 -0.658048328  0.086126314  0.711404951  1.190303122
 [56]  2.499314086  2.201924724  0.591527333 -0.733622099 -0.656031690
 [61] -0.194759316  0.864421699  0.813854743 -0.628803589  0.362077258
 [66]  0.312250497  1.451227963  1.107136623  0.680487861  1.585879056
 [71] -0.249983835 -1.436293634 -0.470710524 -2.330088808  0.265551343
 [76] -0.847238216 -1.199413581 -1.866542460  0.826973063 -0.592073631
 [81] -1.751735134  0.077115620 -0.306869702  0.120083596 -0.303521155
 [86] -0.644268518  0.295067198  2.004409939  0.310290927  0.221898330
 [91] -1.450606907 -1.264043444 -0.257282348  0.078120141 -0.902925645
 [96]  0.499980835 -0.596173525 -1.085097601 -0.773094391  0.693319162
```

Creating an R object

```
> x<-rnorm(100,0,1)
```

An R object contain the results

```
> x
 [1] -1.91083203  1.04955497 -2.40884482  0.33493954  1.45434660 -2.42198672
 [7]  0.44232862 -0.73804911 -0.36354587  0.39064194 -0.31993512 -1.30809569
[13]  0.11409195  0.43549125 -0.29501115  0.29197212  0.50983934 -0.80452037
[19] -0.61008244  1.80780477  1.31535974 -1.33155401  0.29044725 -0.63380504

[85]  1.03861350  0.89381884  0.86323215 -0.24199953  1.64380126  0.45445204
[91]  1.90708641  0.34088349 -0.25727644 -0.26498359  0.80095645  1.42711451
[97]  1.27998167 -0.54106317 -1.29443674  0.36046722
```

Print the R object

Summary statistics

```
 > mean(x)
[1] 0.02149641
```

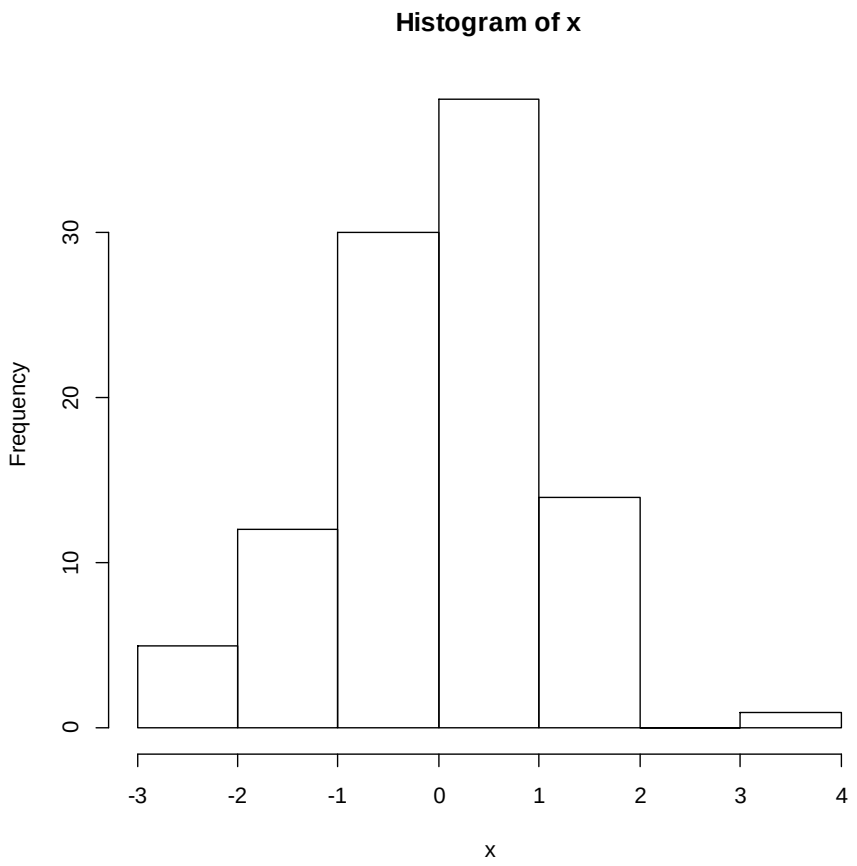
Sample mean

```
> var(x)
[1] 1.061159
```

Sample variance

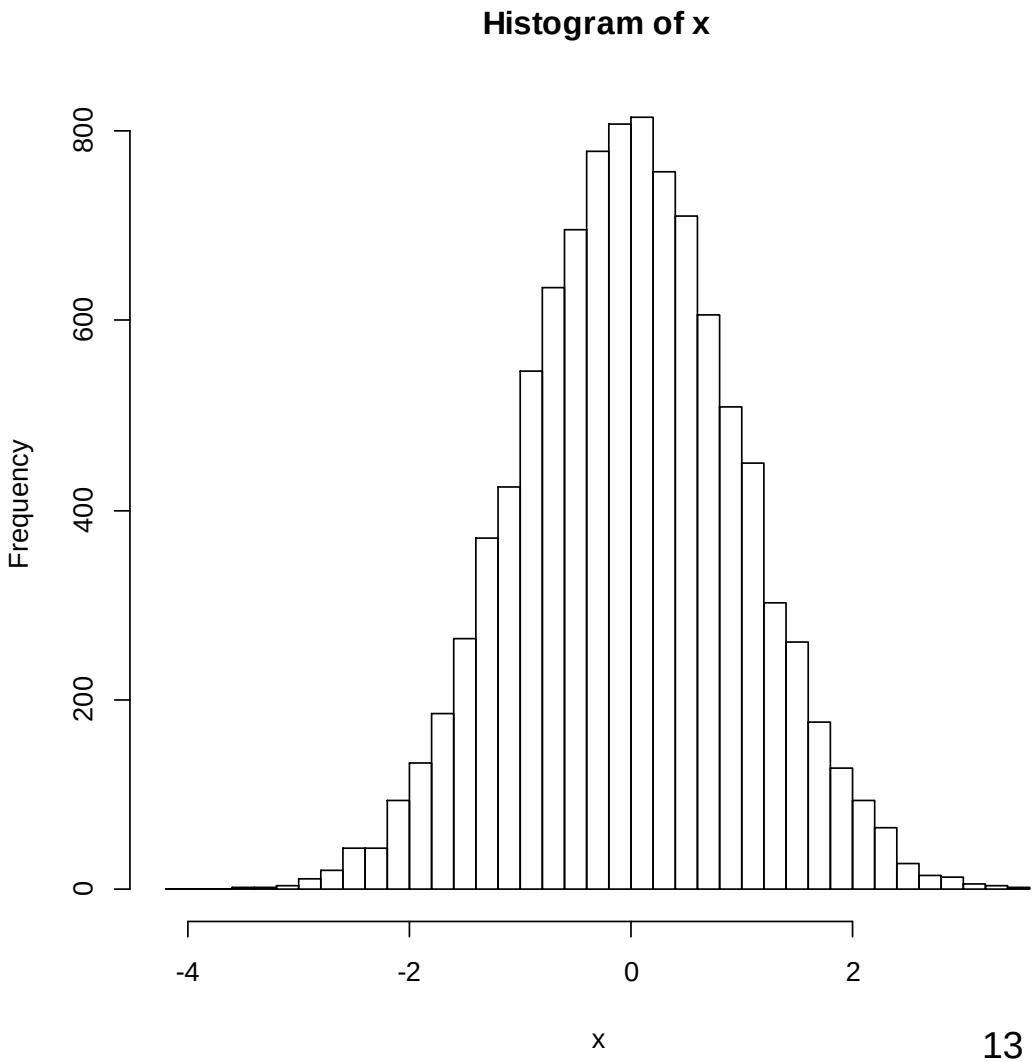
Histogram of the sample

```
> hist(x)
```



Histogram of the sample

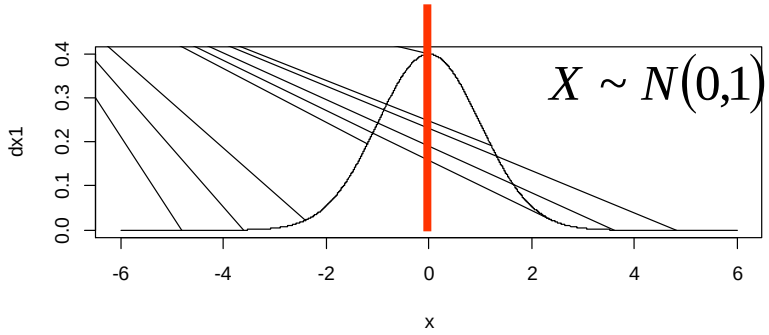
```
> x<-rnorm(10000,0,1)
> mean(x)
[1] -0.01259969
> var(x)
[1] 0.9871957
> hist(x,nclass=50)
```

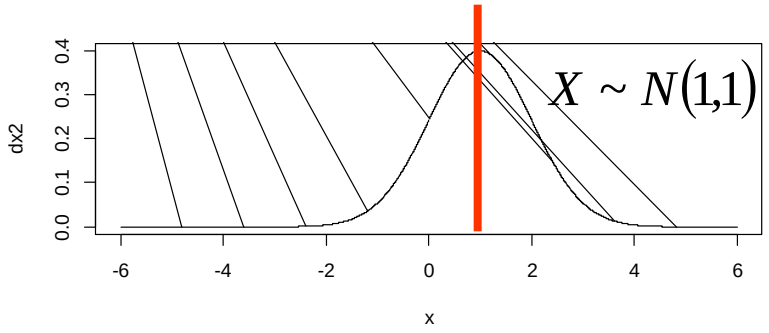


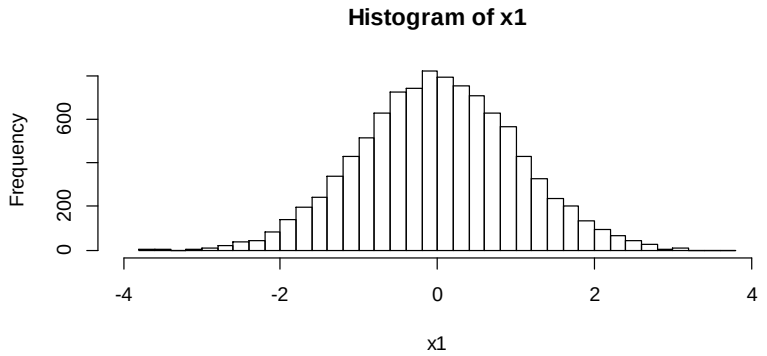
The normal distribution: location

$$X \sim N(\mu, \sigma^2)$$

```
> x1<-rnorm(10000,0,1)
> x2<-rnorm(10000,1,1)
> par(mfrow=c(2,1))
> hist(x1,nclass=50,xlim=c(-4,4))
> hist(x2,nclass=50,xlim=c(-4,4))
```



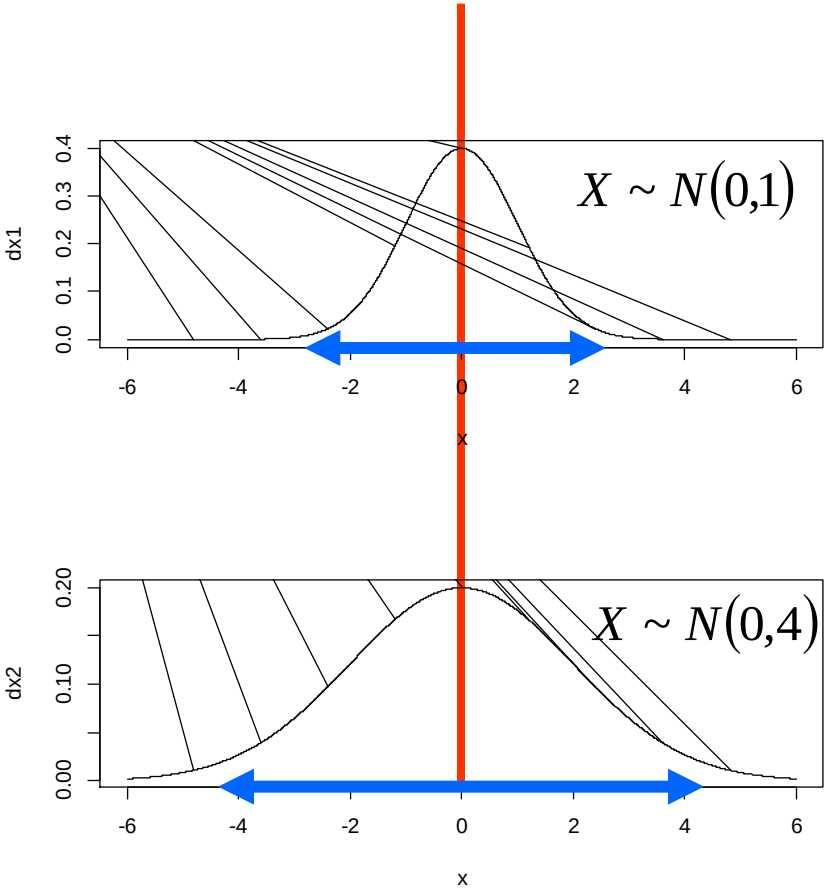


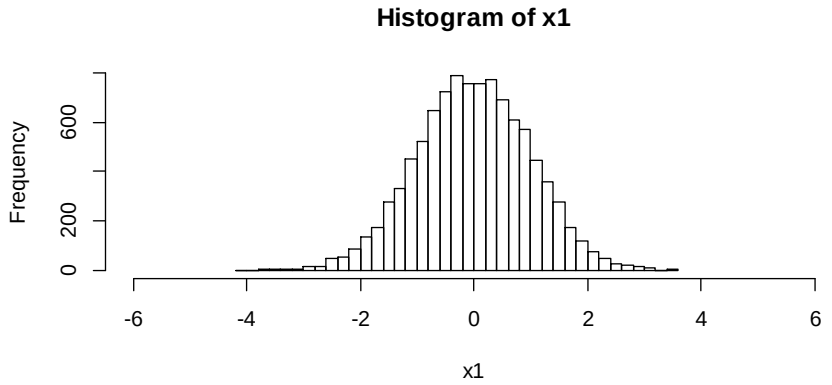


The normal distribution: variability

$$X \sim N(\mu, \sigma^2)$$

```
> x1<-rnorm(10000,0,1)
> x2<-rnorm(10000,0,2)
> par(mfrow=c(2,1))
> hist(x1,nclass=50,xlim=c(-6,6))
> hist(x2,nclass=100,xlim=c(-6,6))
```





The cars Data set in R

1. Write **cars** in the script window.
2. Submit

```
> cars
```

```
   speed dist
1      4    2
2      4   10
3      7    4
4      7   22
5      8   16
6      9   10
.      .    .
.      .    .
48    24   93
49    24  120
50    25   85
```

```
> help(cars)
>
```

Speed and Stopping Distances of Cars
Description

The data give the speed of cars and the distances taken to stop. Note that the data were recorded in the 1920s.

[,1]	speed	numeric	Speed (mph)
[,2]	dist	numeric	Stopping distance (ft)

The cars Data set in R: the $ sign

```
> speed
Error: object 'speed' not found
>
> cars$speed
 [1]  4  4  7  7  8  9 10 10 10 11 11 12 12 12 12 13 13 13 13 14 14 14 14 15 15
[26] 15 16 16 17 17 17 18 18 18 18 19 19 19 20 20 20 20 20 22 23 24 24 24 24
25
>
```

The cars Data set in R: creating a new object

```
> cars[,1]
 [1]  4  4  7  7  8  9 10 10 10 11 11 12 12 12 12 13 13 13 13 14 14 14 14 15 15
[26] 15 16 16 17 17 17 18 18 18 18 19 19 19 20 20 20 20 20 22 23 24 24 24 24
25

> x=cars[,1]

> print(x)
 [1]  4  4  7  7  8  9 10 10 10 11 11 12 12 12 12 13 13 13 13 14 14 14 14 15 15
[26] 15 16 16 17 17 17 18 18 18 18 19 19 19 20 20 20 20 20 22 23 24 24 24 24
25
>
```

Basic plot and descriptive statistics

- What is the average speed of the cars ?
- What is the variance of the cars' speed ?
- What is the min. (max.) speed ?

- What is the association between speed and stopping distance ?

Discussion

- R Objects: data frame.
- R functions.
- $.

Practical session 1

- The airquality is a dataset available in R.
- How many variables there are in the data ?
- Define an R object which contain the information about the wind speed.
- Calculate the mean, and variance for the wind speed.

Two-sample t-test

The sleep data in R

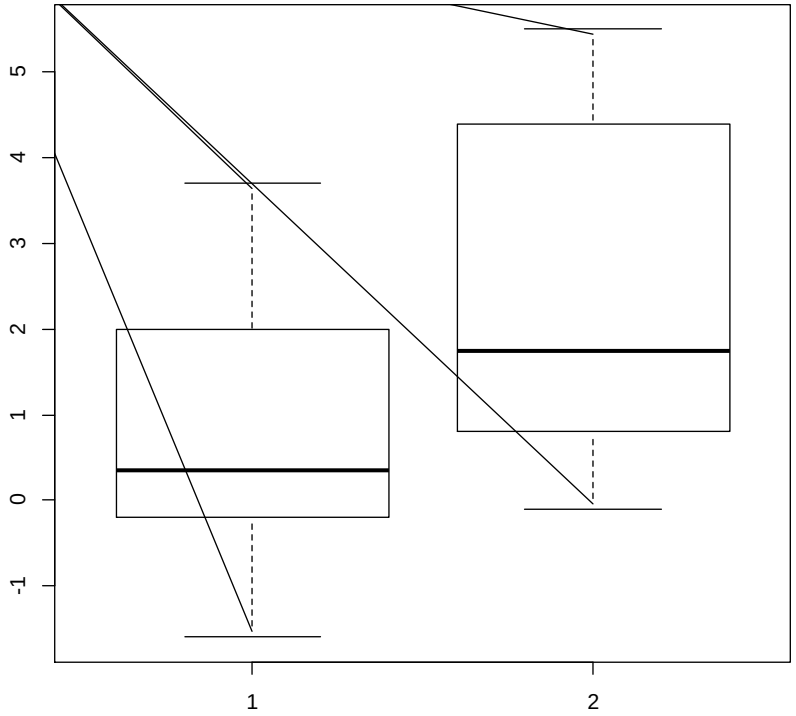
```
> help(sleep)
```

Data which show the effect of two soporific drugs (increase in hours of sleep compared to control) on 10 patients.

extra	numeric	increase in hours of sleep
group	factor	drug given
ID	factor	patient ID

```
> 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
.      .     .  .
14   0.1     2  4
15  -0.1     2  5
16   4.4     2  6
17   5.5     2  7
18   1.6     2  8
19   4.6     2  9
20   3.4     2 10
```

Two samples t-test




```
> extra=sleep$extra
> group=sleep$group
> boxplot(split(extra,group))
```

The aim of the analysis:

Test for a difference between the two soporific drugs

Two samples t-test

```
> t.test(extra~group,var.equal=TRUE)

        Two Sample t-test

data:  extra by group
t = -1.8608, df = 18, p-value = 0.07919
alternative hypothesis: true difference in means is not
equal to 0
95 percent confidence interval:
 -3.363874  0.203874
sample estimates:
mean in group 1 mean in group 2
           0.75            2.33
```

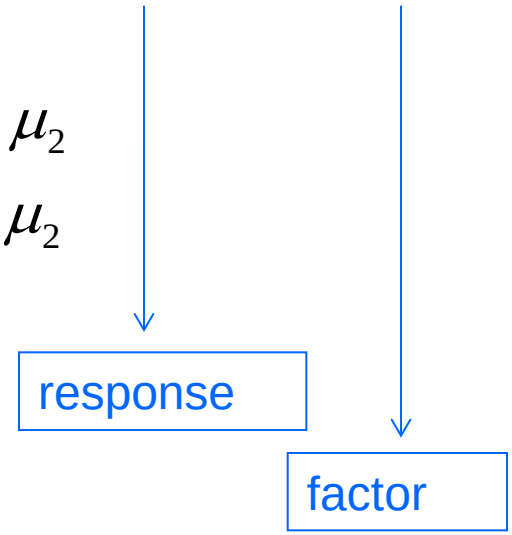
$$H_0 : \mu_1 = \mu_2$$
$$H_1 : \mu_1 \neq \mu_2$$

Two samples t-test

```
> t.test(extra~group,var.equal=TRUE)
```

$$H_0 : \mu_1 = \mu_2$$

$$H_1 : \mu_1 \neq \mu_2$$



R object for the output

```
> t.obj=t.test(extra~group,var.equal=TRUE)
> summary(t.obj)
```

```
             Length Class  Mode
statistic    1      -none- numeric
parameter    1      -none- numeric
p.value      1      -none- numeric
conf.int     2      -none- numeric
estimate     2      -none- numeric
null.value   1      -none- numeric
alternative  1      -none- character
method       1      -none- character
data.name    1      -none- character
```

R object for the output

```
> print(t.obj)

        Two Sample t-test

data:  extra by group
t = -1.8608, df = 18, p-value = 0.07919
alternative hypothesis: true difference in means is not
equal to 0
95 percent confidence interval:
 -3.363874  0.203874
sample estimates:
mean in group 1 mean in group 2
           0.75            2.33

> t.obj$p.value
[1] 0.07918671
> t.obj$statistic
        t
-1.860813
>
```

Discussion

- R Objects: output of the analysis.
- R functions: t.test
- $.

Practical session 2

- The ToothGrowth is a dataset available in R.
- Use `help(ToothGrowth)` for more details.
- The response variable is the Tooth length.
- Test if the Supplement type has an effect on the tooth length.

t.test(response ~ group, data = …)

Basic plots

The faithful data in R

```
> help(faithful)
```

Waiting time between eruptions and the duration of the eruption for the Old Faithful geyser in Yellowstone National Park, Wyoming, USA.

```
> Faithful
```

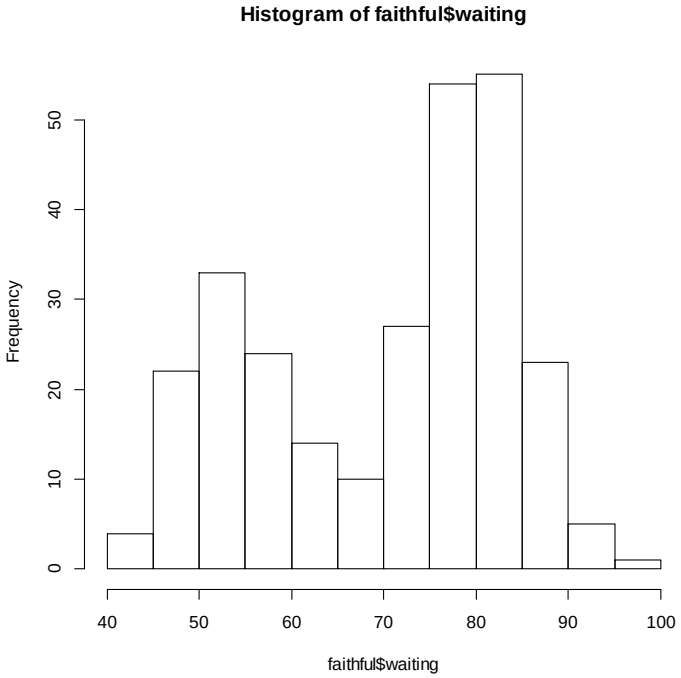
	eruptions	waiting
1	3.600	79
2	1.800	54
3	3.333	74
4	2.283	62
5	4.533	85
6	2.883	55
7	4.700	88
8	3.600	85
9	1.950	51

The faithful data in R

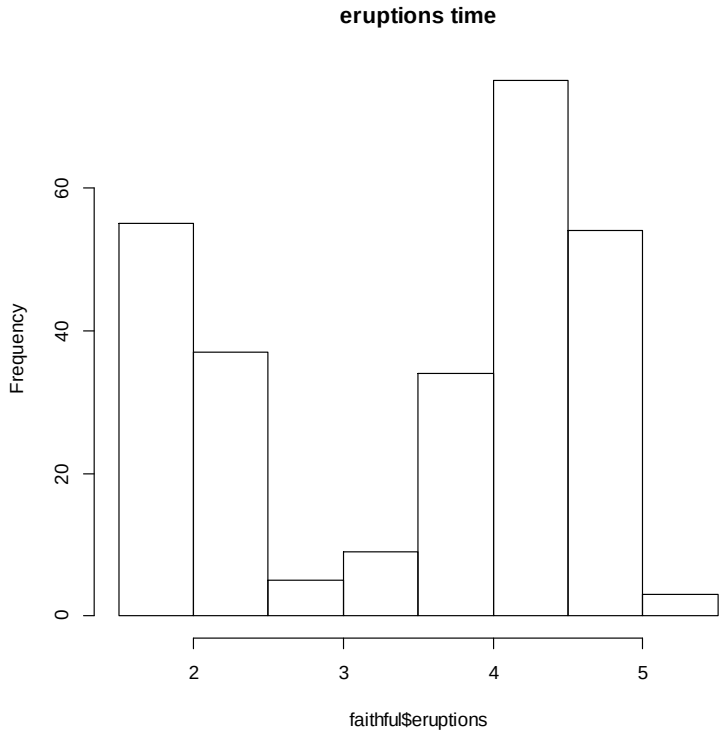
```
> faithful$eruption
  [1] 3.600 1.800 3.333 2.283 4.533 2.883 4.700 3.600 1.950
4.350 1.833 3.917 4.800 1.600 4.350 4.750 4.117 2.150 4.417 1.817 4.467

> mean(faithful$eruption)
[1] 3.487783

aithful$eruption
> mean(x)
[1] 3.487783
> median(x)
[1] 4
> range(x)
[1] 1.6 5.1
> min(x)
[1] 1.6
> max(x)
[1] 5.1
```

Basic plot

```
> hist(faithful$waiting)
```

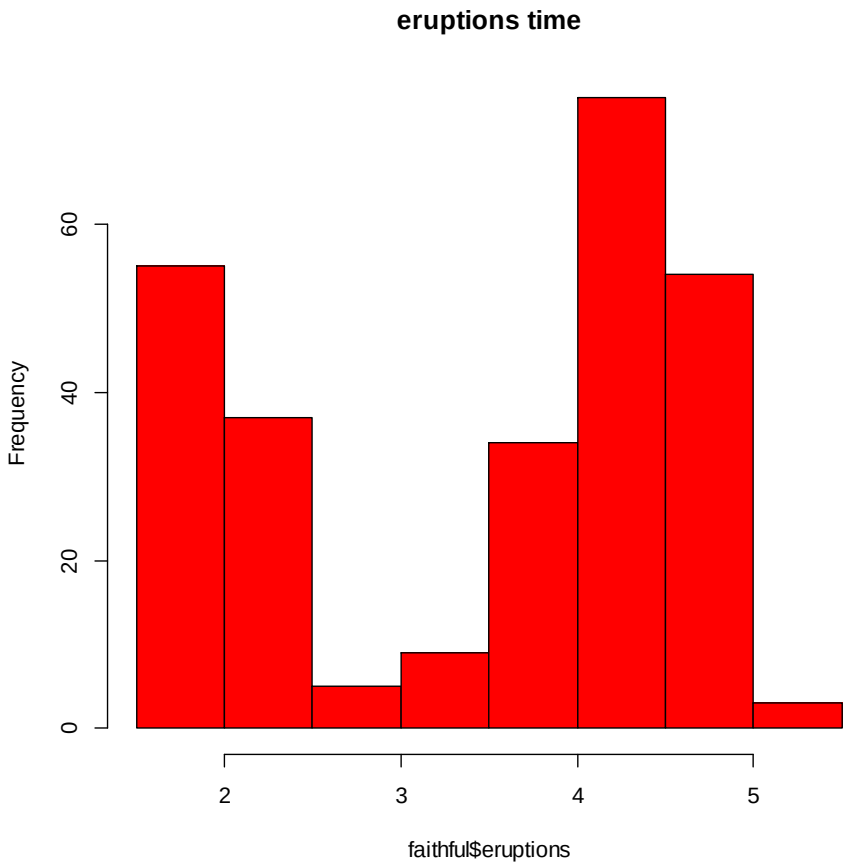



```
>hist(faithful$eruptions,
      main="eruptions time")
```

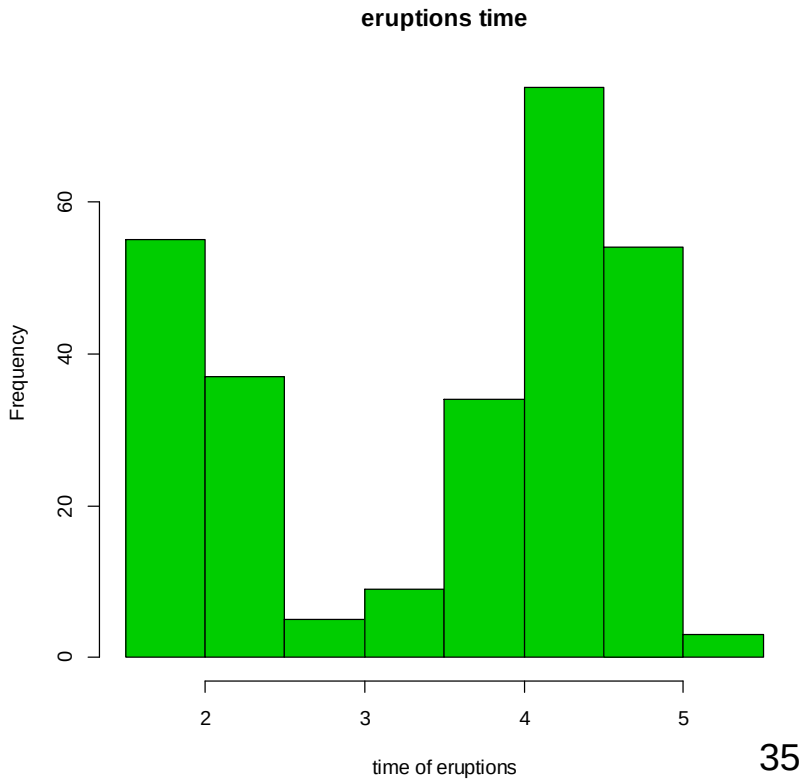


Basic plot

```
>hist(faithful$eruptions,
 main="eruptions time",
 col=2)
```

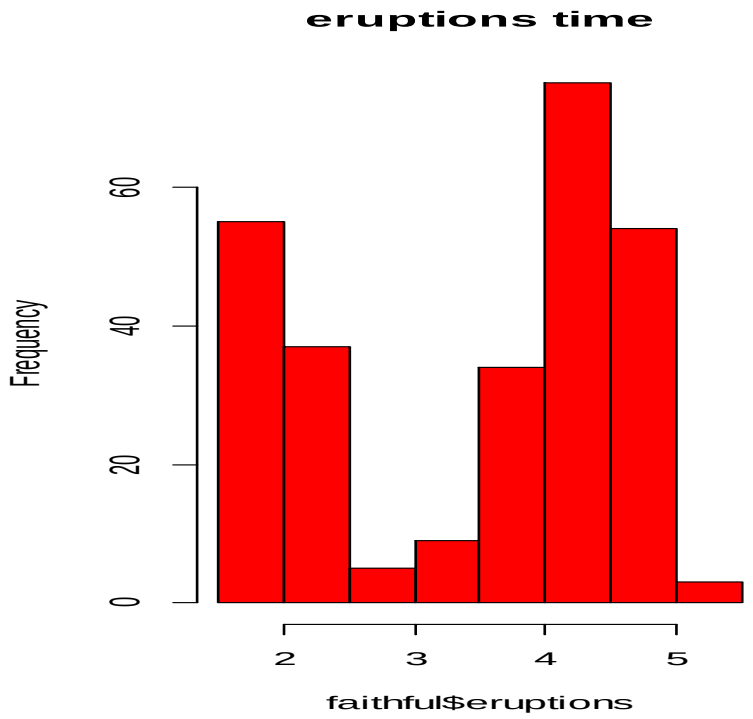


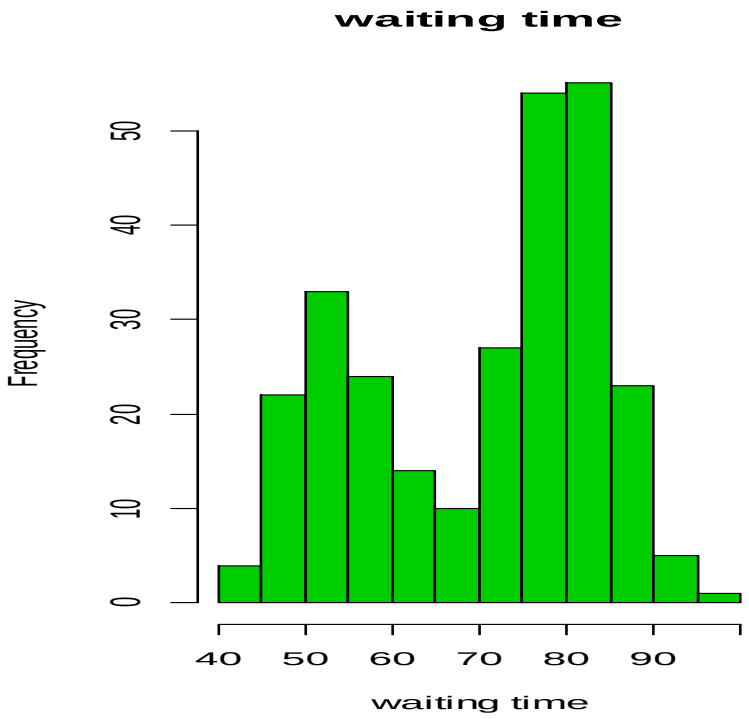

```
>hist(faithful$eruptions,
 main="eruptions time",
 col=3,
 xlab="time of eruptions")
```



Basic plot

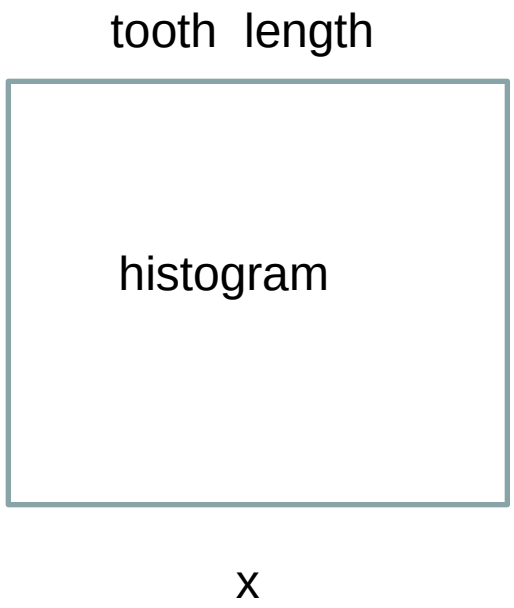
```
> mfrow=c(1,2))
> hist(faithful$eruptions,main="eruptions time",col=2)
> hist(faithful$waiting,main="waiting
  time",col=3,xlab="waiting time")
```





Practical session 3

- Use the ToothGrowth data.
- Produce an histogram for the tooth length with the following structure.



Chapter 1
Basic programming
Objects in R

Simple objects

Assign the value of 5 to the R object x


```
> x <- 5
> x
[1] 5
> x^2
[1] 25
> x + 6
[1] 11
```

Vectors

```
> x<-c("A","A","A","A","B","B","B","B")
> x
[1] "A" "A" "A" "A" "B" "B" "B" "B"
```

```
> y<-c(10,11,9,15,3,5,7,2)
> y
[1] 10 11  9 15  3  5  7  2
```

Index vectors

```
y[x=="A"]
```

All the elements in y for which x=A

```
> ya<-y[x=="A"]
> ya
[1] 10 11  9 15
```

```
> yb<-y[x=="B"]
> yb
[1] 3 5 7 2
```

```
> tapply(y,x,mean)
    A     B
11.25  4.25
```

Data frames

A data structure which contains more than 1 object.

Objects can be numeric objects and character objects

```
> z<-data.frame(x,y)
> z
   x  y
1  A 10
2  A 11
3  A  9
4  A 15
5  B  3
6  B  5
7  B  7
8  B  2
```

The $

The object x in z

```
> z$x
[1] A A A A B B B B
Levels: A B
> z$y
[1] 10 11  9 15  3  5  7  2
```

Matrix

```
> w<-c(1,2,40,2,3,9,200,4,6000)
> matw<-matrix(w,3,3)
> matw
     [,1] [,2] [,3]
[1,]    1    2  200
[2,]    2    3    4
[3,]   40    9 6000
```

Rows and columns

X_{ij}=x[i,j]

```
> w1<-matw[1,]
> w2<-matw[,2]
> w1
[1]   1   2 200
> w2
[1] 2 3 9
```

The matrix reloaded

```
> matw+10
     [,1] [,2] [,3]
[1,]   11   12  210
[2,]   12   13   14
[3,]   50   19 6010
```

```
>
[1]    1    3 6000
```

The inverse matrix

```
> solve(matw)
           [,1]       [,2]         [,3]
[1,] -0.687854189  0.39056517  0.0226680962
[2,]  0.453361924  0.07658141 -0.0151631184
[3,]  0.003905652 -0.00271864  0.0000382907
```

```
> solve(matw)%*%(matw)
                [,1]           [,2]          [,3]
[1,]  1.000000e+00  9.714451e-17  1.998401e-15
[2,]  5.551115e-17  1.000000e+00 -8.104628e-15
[3,]  4.336809e-19 -4.336809e-19  1.000000e+00
```

Example: data frame

```
> x<-c(25,36,21)
> gender<-c("M","M","F")
> data.frame(x,gender)
   x gender
1 25      M
2 36      M
3 21      F
```

Example: an R object of a data frame

```
> x<-c(25,36,21)
> gender<-c("M","M","F")
> xdat<-data.frame(x,gender)
> xdat
   x gender
1 25      M
2 36      M
3 21      F
> xdat$gender
[1] M M F
Levels: F M
```

Practical session 4

- Create the folowig data frame:

A	100
B	99
C	105
D	35
E	0
F	250

Chapter 2
Reading external datasets

Read an external file

```
> spwh3<-read.table('c:\\projects\\wseda\\spwh3.txt',
header=FALSE,na.strings="NA", dec=".")

> dim(spwh3)
[1] 60  4

> spwh3<-data.frame(spwh3)
> names(spwh3)<-c("id","y","x1","gender")
```

The data

```
> spwh3
   id          y x1 gender
1   1 10.111368  1      0
2   2  9.948930  1      0
3   3 10.322560  1      0
4   4 10.241052  1      0
5   5  9.911427  1      0
6   6  9.357969  1      0
7   7 10.649141  1      0
8   8 10.150197  1      0
9   9  9.403218  1      0
10 10  8.027072  1      0
11 11 20.020056  1      1
```

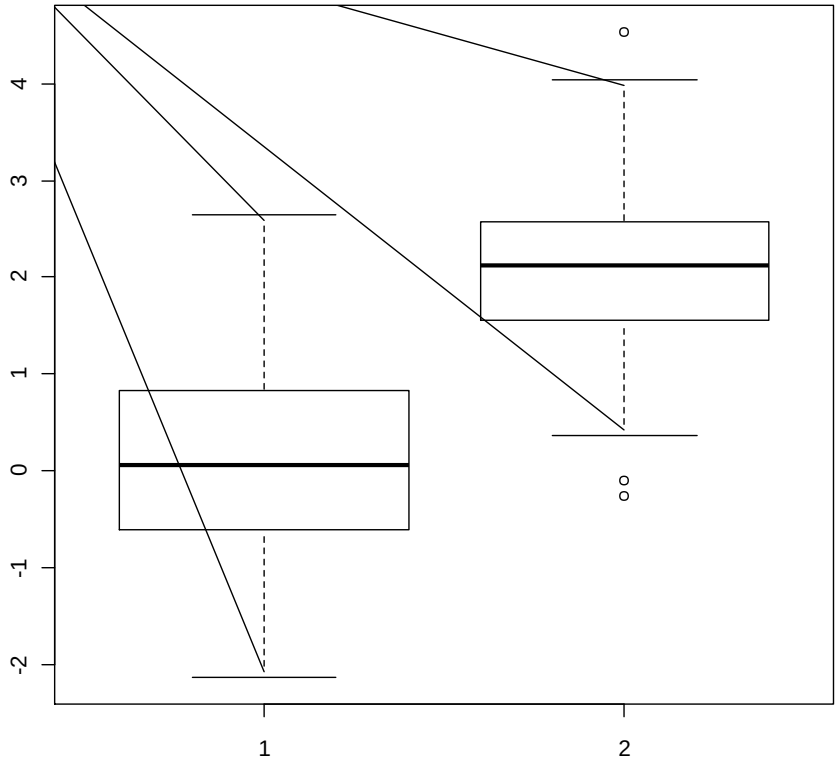
The sleep data in R

```
> 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
.      .     .  .
14   0.1     2  4
15  -0.1     2  5
16   4.4     2  6
17   5.5     2  7
18   1.6     2  8
19   4.6     2  9
20   3.4     2 10
```

Two samples t-test

```
> y1<-spwh3$y[spwh3$gender==0]
> y2<-spwh3$y[spwh3$gender==1]
> t.test(y1,y2)

        Welch Two Sample t-test

data:  y1 and y2
t = -9.1428, df = 58, p-value = 7.715e-13
alternative hypothesis: true difference in means is not
equal to 0
95 percent confidence interval:
 -12.229889  -7.836547
sample estimates:
mean of x mean of y
 14.99933  25.03254
```

Two samples t-test




```
> y1<-rnorm(100,0,1)
> y2<-rnorm(57,2,1)
> boxplot(y1,y2)
```

Two samples t-test

```
> t.test(y1,y2)

        Welch Two Sample t-test

data:  y1 and y2
t = -14.2203, df = 126.176, p-value < 2.2e-16
alternative hypothesis: true difference in means is not
equal to 0
95 percent confidence interval:
 -2.290641 -1.730980
sample estimates:
 mean of x  mean of y
-0.0063866  2.0044240
```

R object for the output

```
> t.t<-t.test(y1,y2)
```

```
> summary(t.t)
             Length Class  Mode
statistic    1      -none- numeric
parameter    1      -none- numeric
p.value      1      -none- numeric
conf.int     2      -none- numeric
estimate     2      -none- numeric
null.value   1      -none- numeric
alternative  1      -none- character
method       1      -none- character
data.name    1      -none- character
```

R object for the output

```
> t.t

        Welch Two Sample t-test

data:  y1 and y2
t = -14.2203, df = 126.176, p-value < 2.2e-16
alternative hypothesis: true difference in means is not
equal to 0
95 percent confidence interval:
 -2.290641 -1.730980
sample estimates:
 mean of x  mean of y
-0.0063866  2.0044240
> t.t$p.value
[1] 5.570543e-28
> t.t$statistic
        t
-14.22034
```

Practical session 5

- Create the following text file:

A	100
B	99
C	105
D	35
E	0
F	250

and read it to R as an external file

Chapter 3
Basic plots functions

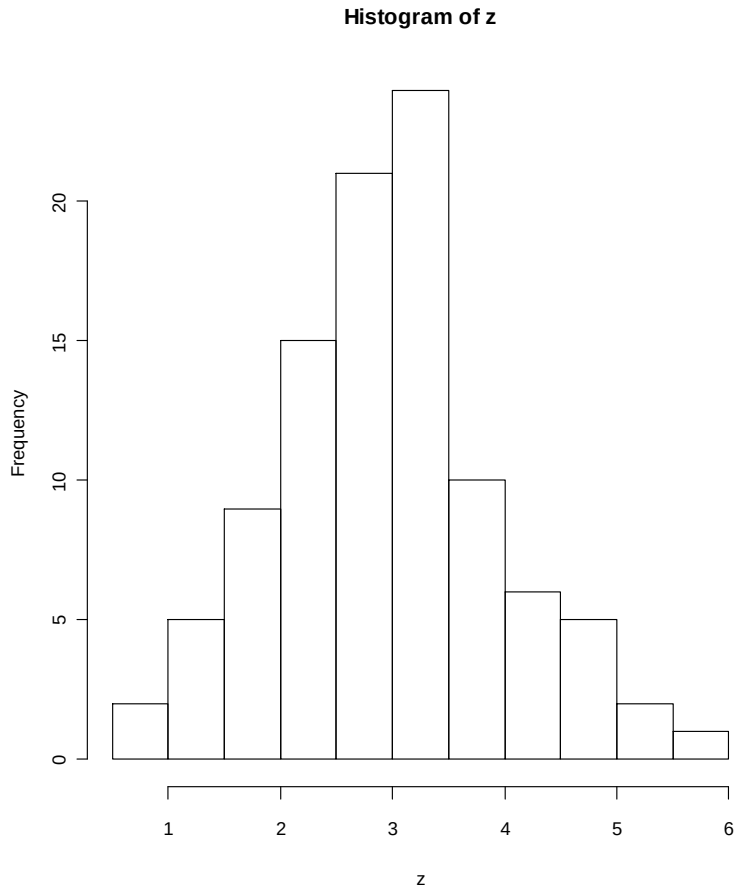
Descriptive statistics in R

```
> z<-rnorm(100,3,1)
> mean(z)
[1] 2.979706
> median(z)
[1] 2.958521
> max(z)
[1] 5.849559
> min(z)
[1] 0.877219
```

Generate random sample from N(3,1)

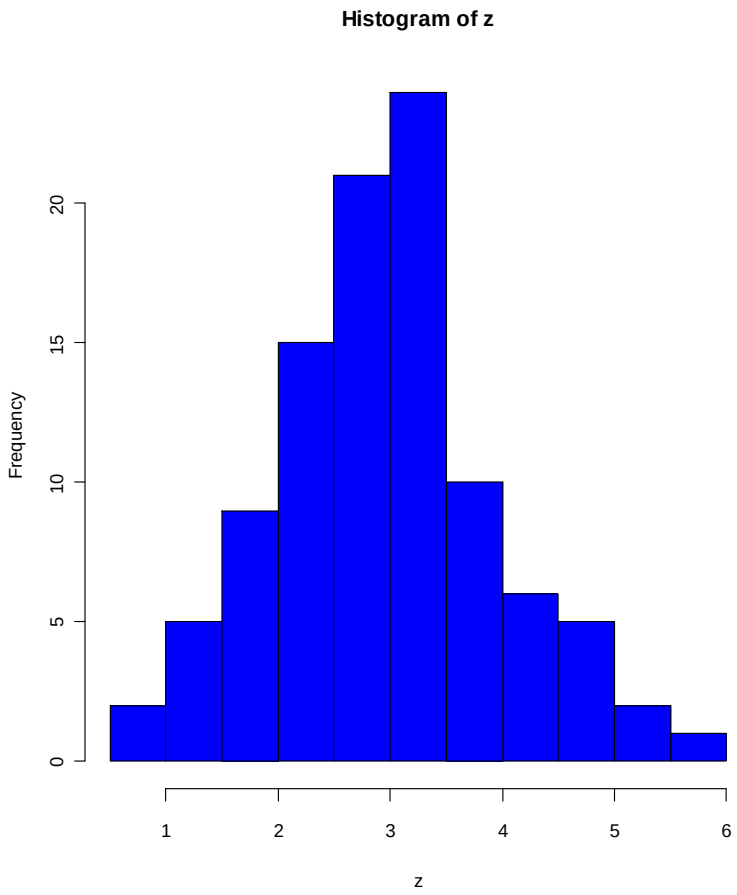
Histogram

```
> hist(z)
```

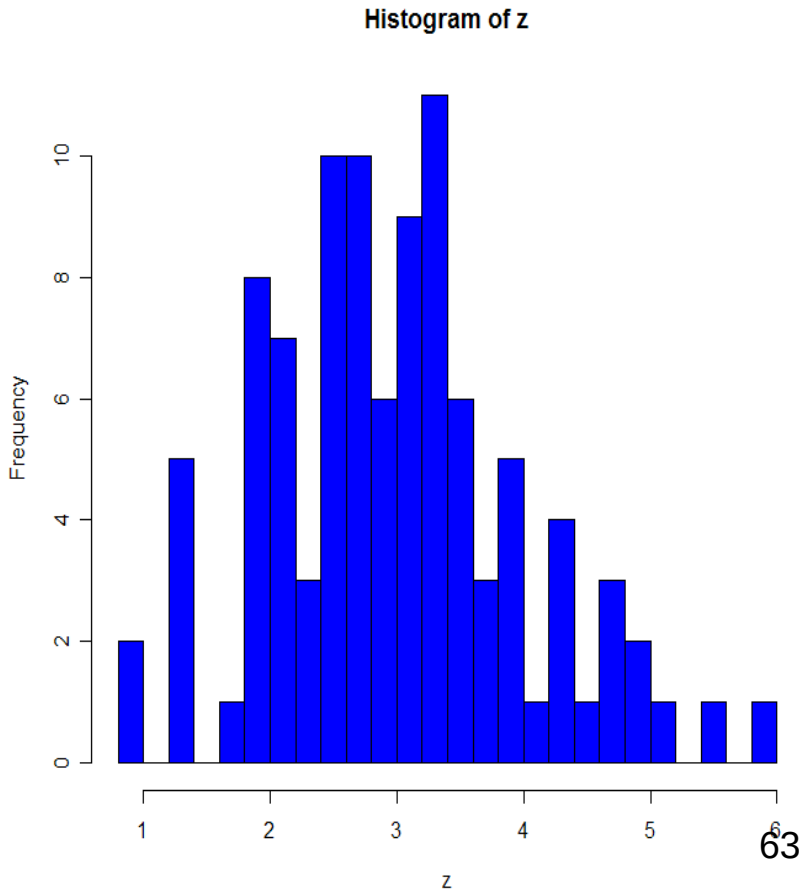


Plot options

```
> hist(z,col=4)
```

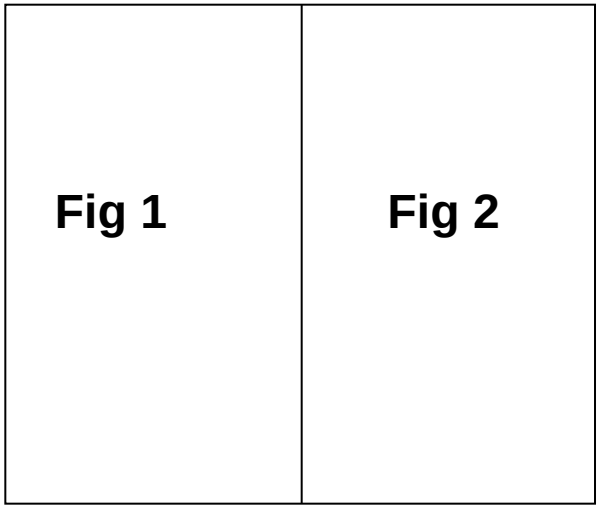


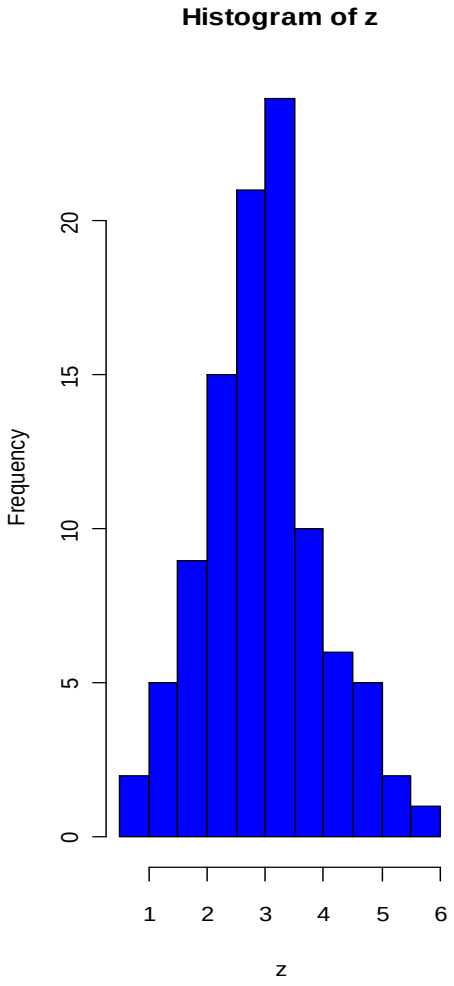

```
> hist(z,col=4,nclass=25)
```

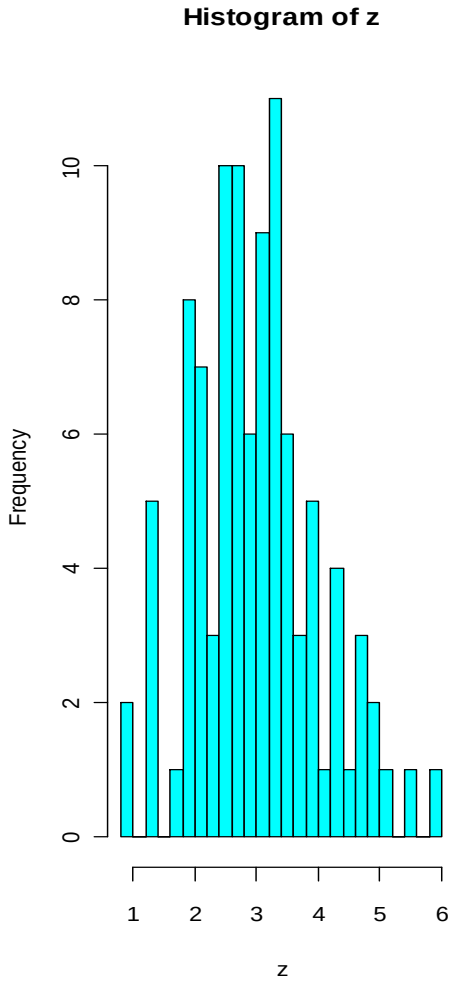


Controlling the graphical output: the par() function

```
> par(mfrow=c(1,2))
> hist(z,col=4)
> hist(z,col=5,nclass=25)
```

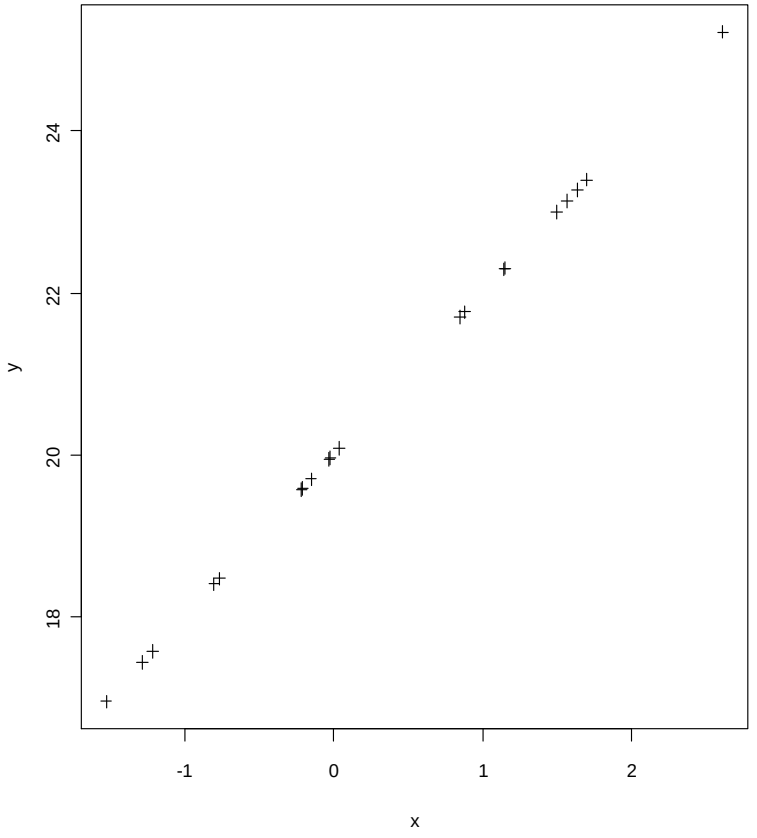






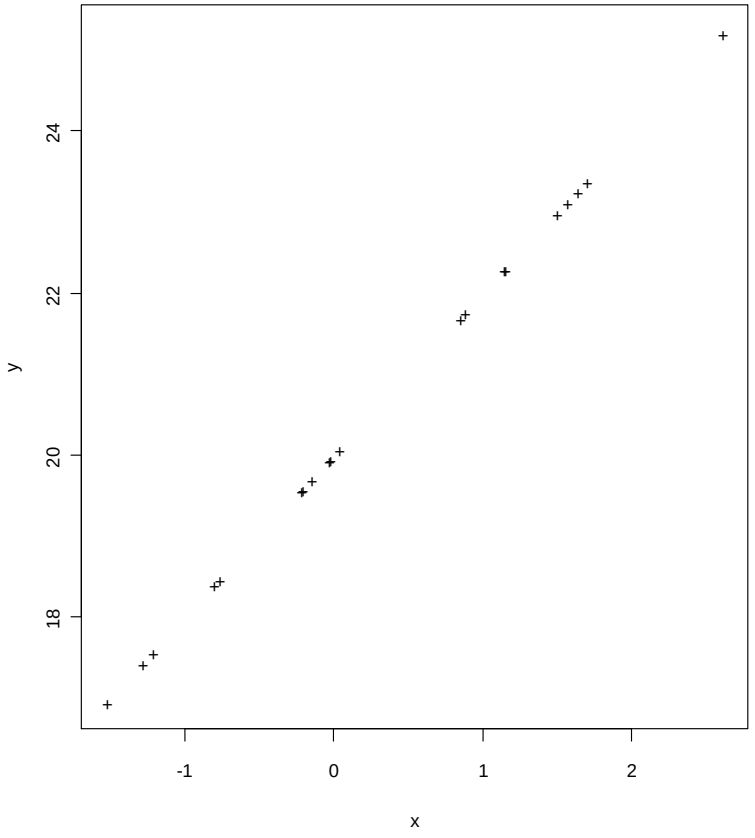
Type of points: the pch() function

```
> y<-2*x+20
> plot(x,y)
> plot(x,y,pch=3)
```



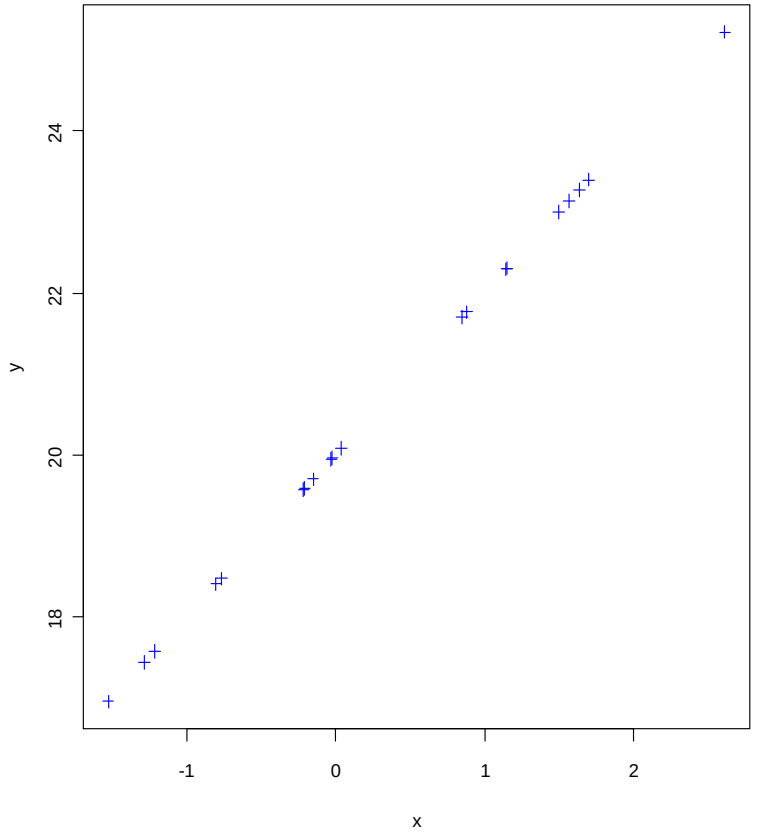
Type of points: the pch() function

```
>plot(x,y,pch="+")
```



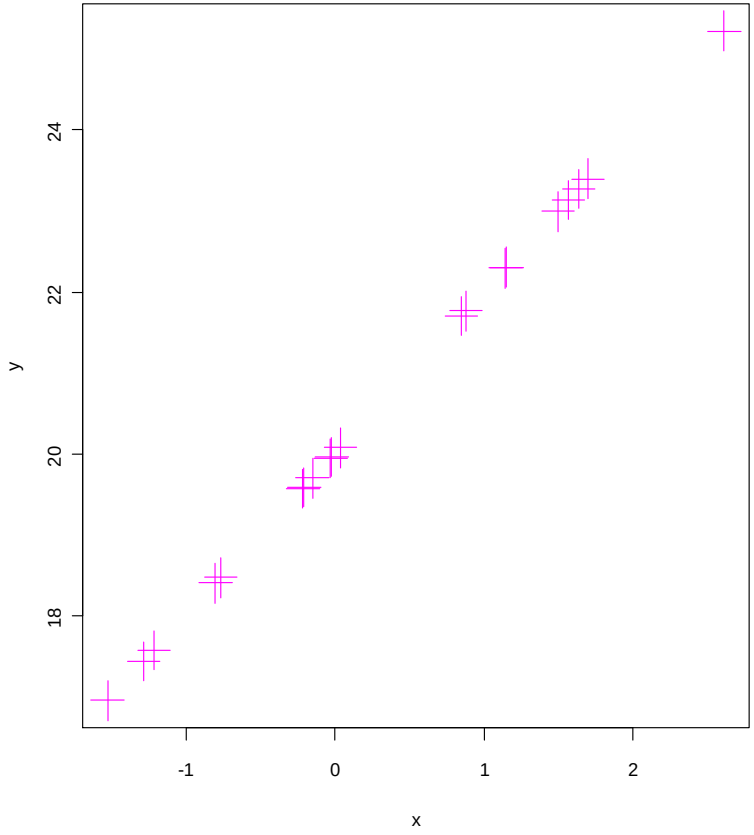
Colors: the option col

```
> plot(x,y,pch=" ")
> points(x,y,col=4,pch=3)
```



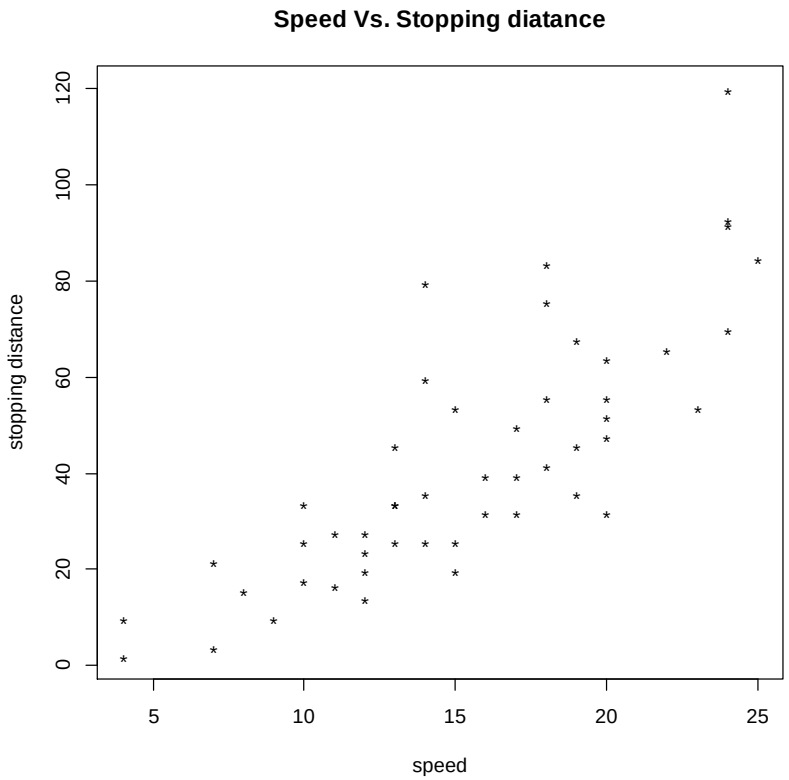
Size: the option cex

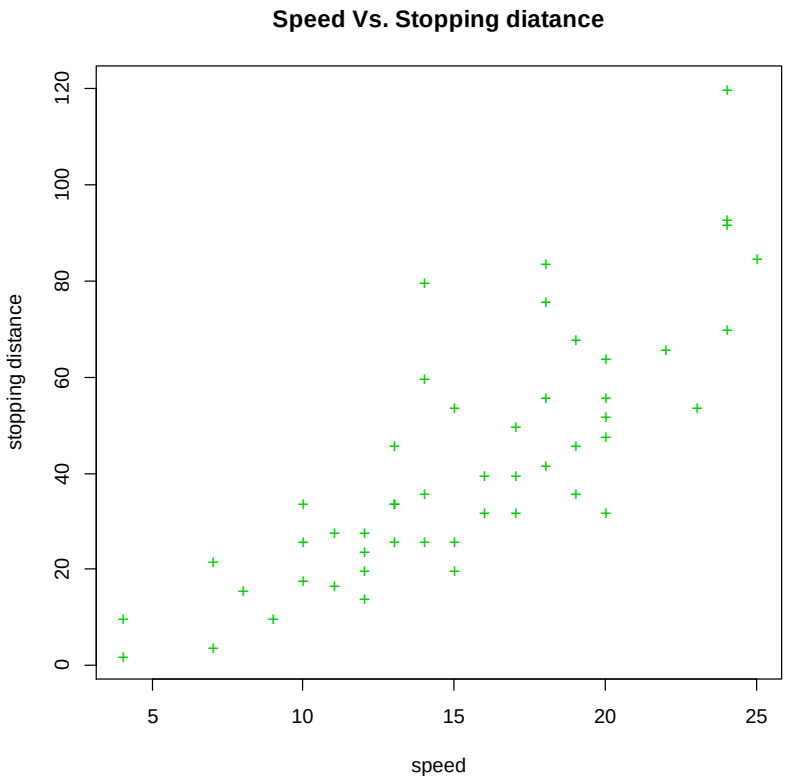
```
> plot(x,y,pch=" ")
> points(x,y,col=6,pch=3,cex=3)
```



Practical session 6

- Produce the following figures in R (use the cars data)





Practical session 7

- Use the airquality in R.

- Produce the following plots:
  - Histogram for the ozone level
  - Boxplot for the ozone level.

- What is the mean and the median of the ozone level.
- What is the minimum and maximum ozone levels.

Chapter 4
Programming I: A for loop

A for loop

```
for(i in 1:B)
{

}
```

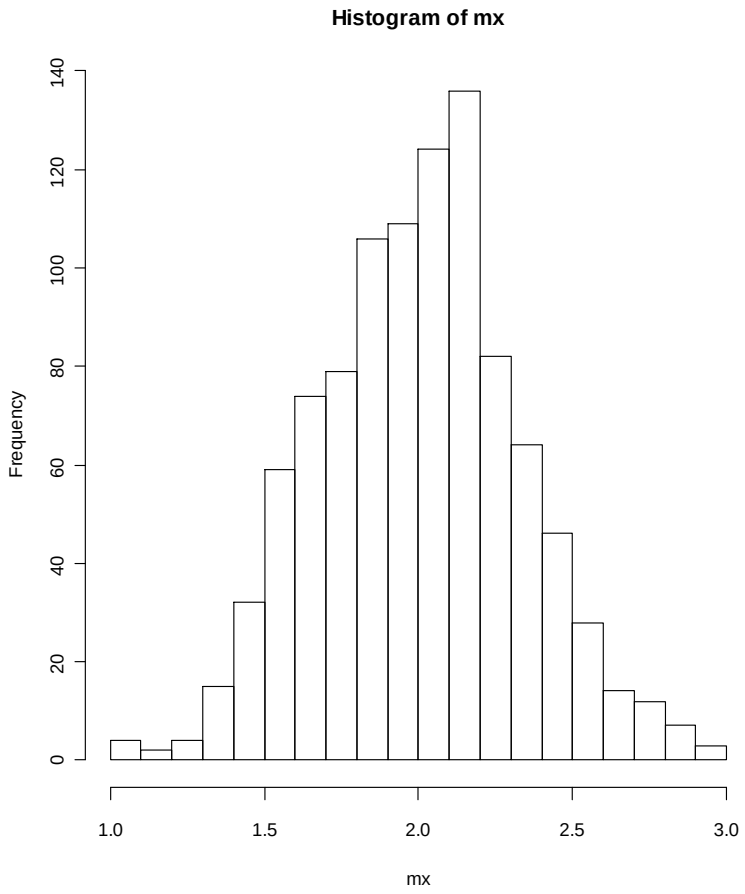
Here you ask from R to do the same thing B times…..

Generate 1000 samples from N(2,1)

```
> x<-rnorm(10,2,1)
> x
 [1]  2.1531462  2.4426189  0.8080064  1.4051178  1.9392356  0.6466574
 [7]  0.7519918 -0.1097367  2.3338487  3.7598694
> x<-rnorm(10,2,1)
> x
 [1] 2.9694328 1.1065506 1.5612572 0.3904008 1.6890423 3.7319756 0.9026146
 [8] 1.7763012 2.4356002 0.9643299
```

Generate 1000 samples from N(2,1)

```
> mx<-c(1:1000)
> for(i in 1:1000)
+ {
+ x<-rnorm(10,2,1)
+ mx[i]<-mean(x)
+ }
> hist(mx,nclass=25)
```



Example: distribution of the minimum in uniform distribution

- Generate 1000 samples (n=50) from U(0,1).
- Calculate the minimum of each sample.
- Estimate the density of the minimum.

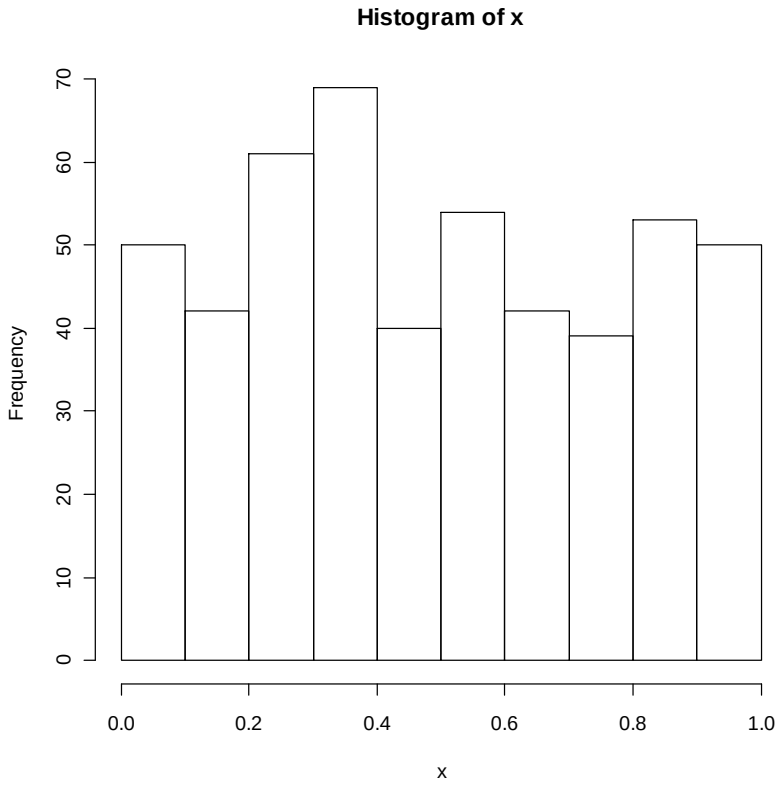
Example: distribution of the minimum in uniform distribution

- Generate 1000 samples (n=50) from U(0,1).
- Calculate the minimum of each sample.
- Estimate the density of the minimum.

Example: distribution of the minimum in uniform distribution

- Generate 1000 samples (n=50) from U(0,1).
- Calculate the minimum of each sample.

```
> x<-runif(500,0,1)
> hist(x)
> min(x)
[1] 0.004631357
```



Example: distribution of the minimum in uniform distribution

- Estimate the density of the minimum.

```
for(i in 1:B)
{

Generate 1000 samples (n=50) from U(0,1).
Calculate the minimum of each sample.

}
```

Example: distribution of the minimum in uniform distribution

- Estimate the density of the minimum.

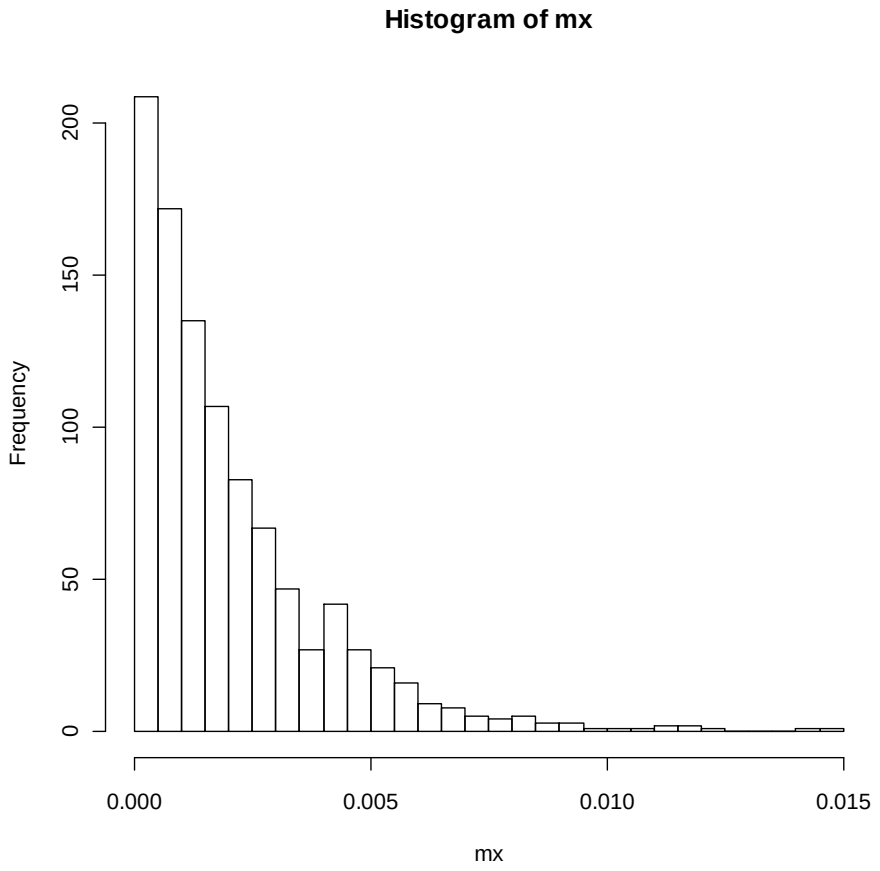
```
for(i in 1:B)
{
Generate 1000 samples (n=50) from U(0,1).
Calculate the minimum of each sample.
}
```

```
> mx<-c(1:1000)
> for(i in 1:1000)
+ {
+ x<-runif(500,0,1)
+ mx[i]<-min(x)
+ }
```

Example: distribution of the minimum in uniform distribution

- Estimate the density of the minimum.

```
> mx<-c(1:1000)
> for(i in 1:1000)
+ {
+ x<-runif(500,0,1)
+ mx[i]<-min(x)
+ }
>hist(mx)
```



Practical session 8

- Make a for loop that print your name 500 times.

Chapter 5

Statistical modeling 1: Simple linear regression

Reading the cars data

```
> carsdat<-read.table('c:\\projects\\wseda\\Rintro\\cars.txt',
   header=FALSE,na.strings="NA", dec=".")
> dim(carsdat)
[1] 50  3
```

The data is available in R, use, help(cars)

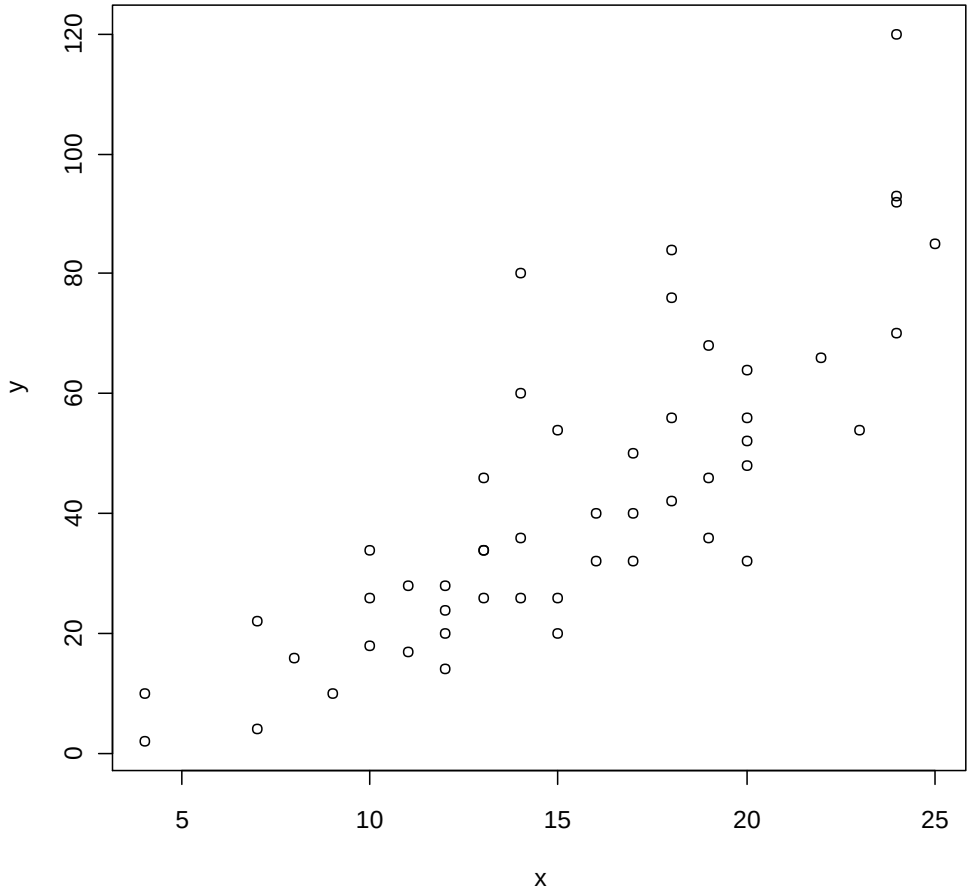
The cars data

```
> help(cars)
```

```
cars                  package:datasets                  R Documentation

Speed and Stopping Distances of Cars

Description:

     The data give the speed of cars and the distances taken to stop.
     Note that the data were recorded in the 1920s.

Usage:

     cars

Format:

     A data frame with 50 observations on 2 variables.

       [,1]  speed  numeric  Speed (mph)
       [,2]  dist   numeric  Stopping distance (ft)

Source:

     Ezekiel, M. (1930) _Methods of Correlation Analysis_.  Wiley.
```

The cars data

```
> x<-carsdat[,2]
> y<-carsdat[,3]
> plot(x,y)
```



The lm() function

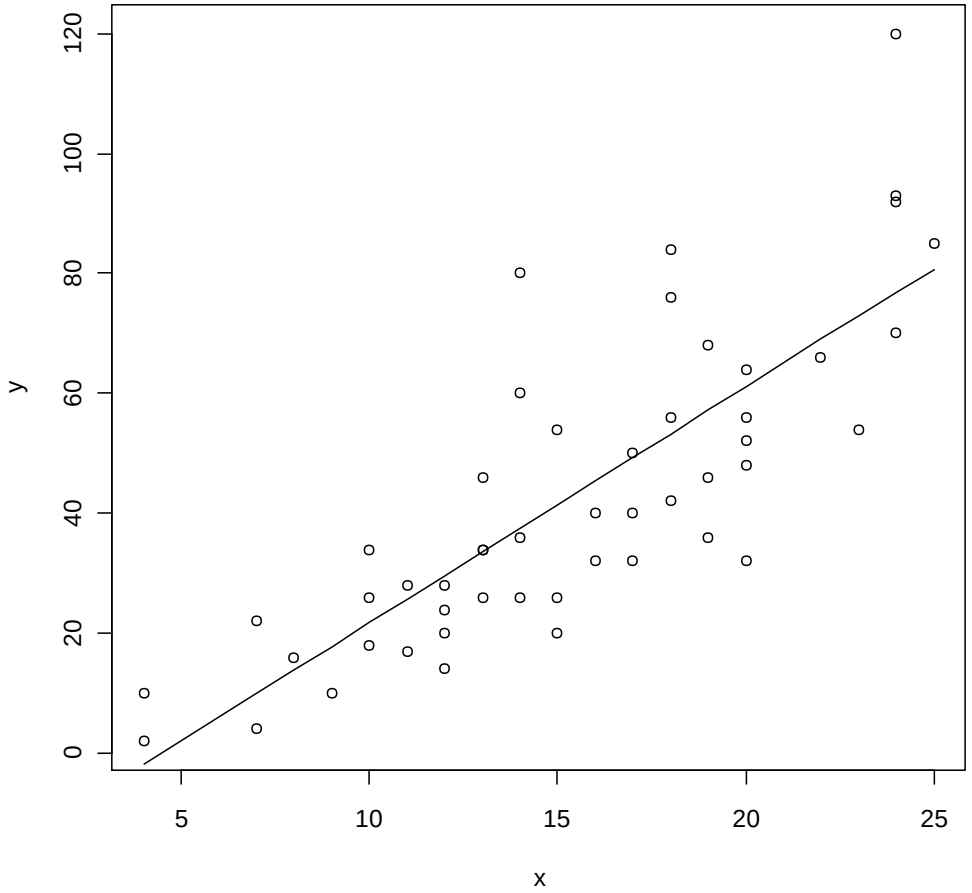
$$y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$$

General call of the `lm()` function

```
lm(response~predictor)
```

Data and predicted model

```
> fit.1<-lm(y~x)
> plot(x,y)
> lines(x,fit.1$fit)
```



The “output”

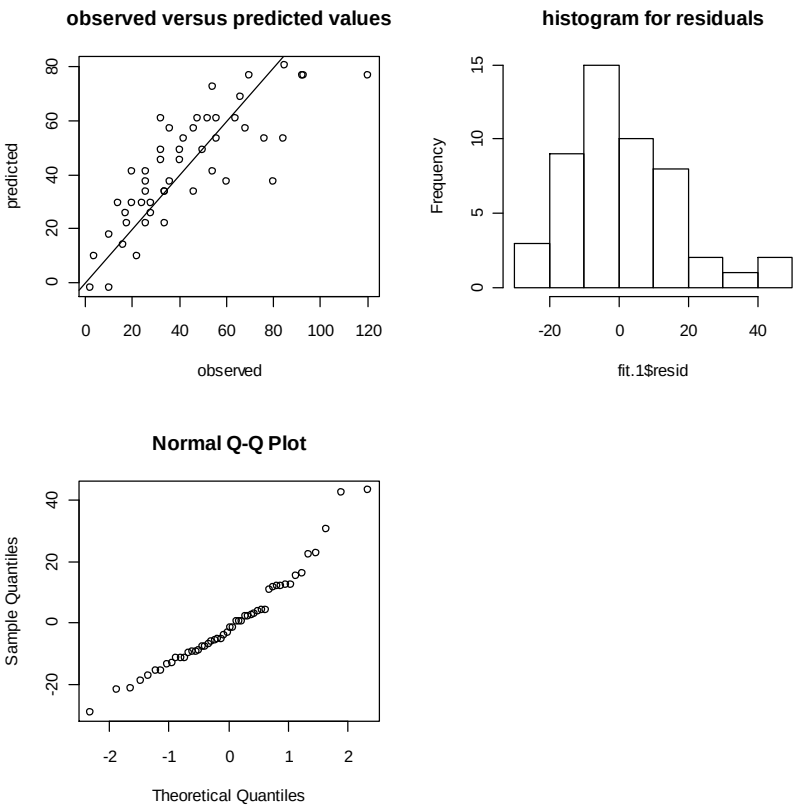
ANOVA table for the model

```
Analysis of Variance Table

Response: y
          Df Sum Sq Mean Sq F value    Pr(>F)
x          1  21186 21185.5  89.567 1.490e-12
    ***
Residuals 48  11354   236.5
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’
    0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> summary(fit.1)

Call:
lm(formula = y ~ x)

Residuals:
    Min      1Q  Median      3Q     Max
-29.069  -9.525  -2.272   9.215  43.201

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -17.5791     6.7584  -2.601   0.0123 *
x             3.9324     0.4155   9.464 1.49e-12 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
    0.1 ‘ ’ 1

Residual standard error: 15.38 on 48 degrees of
    freedom
Multiple R-squared: 0.6511,     Adjusted R-squared:
    0.6438
F-statistic: 89.57 on 1 and 48 DF,  p-value: 1.490e-12
```

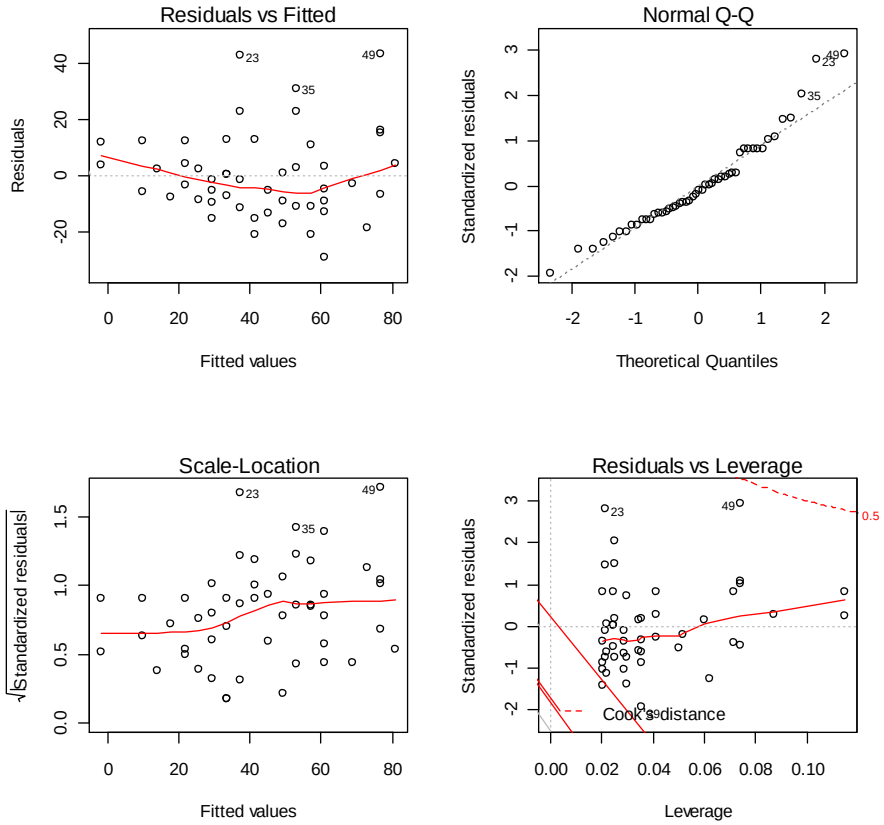
Graphical output

```
> par(mfrow=c(2,2))
> plot(y,fit.1$fit,xlab="observed",
  ylab="predicted")
> abline(0,1)
> title("observed versus predicted
   values")
> hist(fit.1$resid,col=0,main=" ")
> title("histogram for residuals")
> qqnorm(fit.1$resid)
```



Default plots

```
> plot(fit.1)
```



Practical session 9

- The airquality is a dataset available in R.
- Fit a simple linear regression model in which the ozone level is the response and the wind speed is the predictor.
- Test the hypothesis that the slope is zero.
- Use the default plots of an lm() object to produce the diagnostic plot.

Chapter 6

Statistical modeling 2: One way ANOVA

Examples:

The chick data

The cash data

Example 1: The chick dataset in R

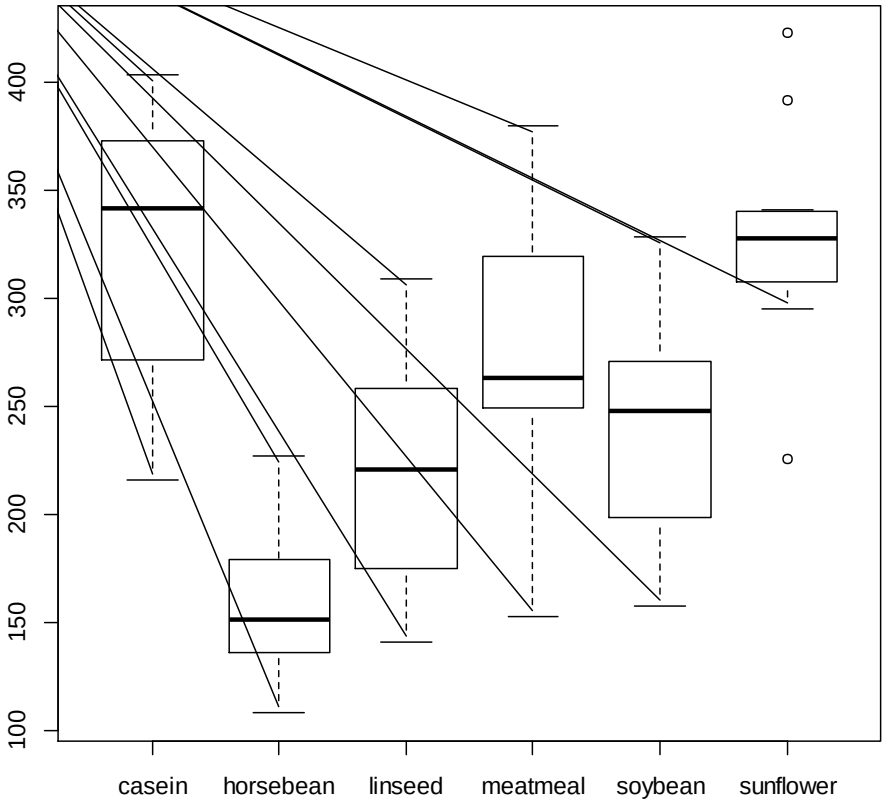
```
>  chickwts
   weight      feed
1     179 horsebean
2     160 horsebean
3     136 horsebean
4     227 horsebean

16    203   linseed
17    148   linseed
18    169   linseed

23    243   soybean
24    230   soybean
25    248   soybean
```

> help(chickwts)

An experiment was conducted to measure the effectiveness of various feed supplements on the growth rate of chickens.

Boxplot by group

```
> w<-chickwts[,1]
> feed<-chickwts[,2]
> boxplot(split(w,feed))
```



Mean by group

```
> tapply(w,feed,mean)
   casein horsebean   linseed  meatmeal   soybean sunflower
 323.5833  160.2000  218.7500  276.9091  246.4286  328.9167
```

One-Way ANOVA model: model formulation

$$Y_{ij} = \mu_i + \varepsilon_{ij}$$

Parameters: fixed but unknown and needed to be estimated

Random error, assumed to follow normal distribution with constant varaince.

$$\varepsilon_{ij} \sim N\left(0, \sigma^2\right)$$

Model assumptions are:

1. The random error is nornal distributed.
2. The varaince is constant across the factor levels.

The Null Hypothesis: No diet effect

- For a model in which the factor has 5 (the diet group) levels we wish to test the null hypothesis:

$$H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5 = \mu_6$$

- This means that we want to test if the means across all factor levels are equal.

- Mind that: we test if the parameters (μ_j) are equal, not is the sample means ($\bar{Y}_j$).

Test Statistic

Within group sum of squares

$$SSW = \sum_{i=1}^{I} \sum_{j=1}^{n_i} \left(Y_{ij} - \bar{Y}_{i.} \right)^2$$

Between group sum of squares

$$SSB = \sum_{i=1}^{I} n_i \left(\bar{Y}_{i.} - \bar{Y}.. \right)^2$$

$$F = \frac{SSB/(I-1)}{SSW/(N-I)} = \frac{MSB}{MSW}$$

The test statistic, F, is the ratio between the mean of the between sum of squares (SSB) and the mean of the within sum of squares.

The aov() function

$$Y_{ij} = \mu_i + \varepsilon_{ij}$$

```
aov(response ~ factor)
```

```
> a.model=aov(w~feed)
> summary(a.model)
```

Test Statistic

Between group sum of squares/dgree of fredom

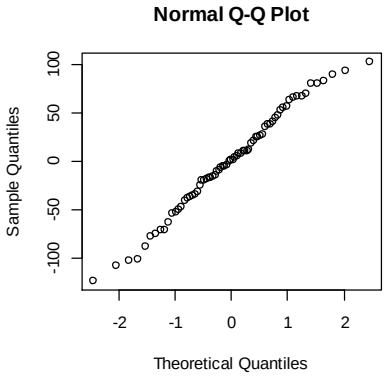
Within group sum of squares/dgree of fredom

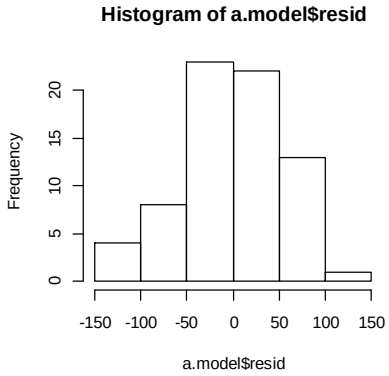
$$= \frac{SSB/(I-1)}{SSW/(N-I)} = \frac{MSB}{MSW} = F$$

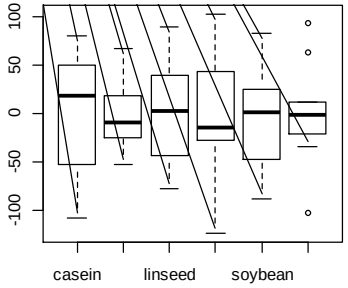
```
> a.model=aov(w~feed)
> summary(a.model)
            Df Sum Sq Mean Sq F value   Pr(>F)
feed         5 231129   46226   15.37 5.94e-10 ***
Residuals   65 195556    3009
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Diagnostic plot

```
> par(mfrow=c(2,2))
> qqnorm(a.model$resid)
> hist(a.model$resid,col=0)
> boxplot(split(a.model$resid,feed))
```







One-Way ANOVA model: alternative model formulation

$$Y_{ij} = \mu_0 + \alpha_i + \varepsilon_{ij}$$

Mean of the reference group

Diet effect

$$\sum_{i=1}^{I} \alpha_i = 0$$

Random error, assumed to follow normal distribution with constant varaince.

$$\varepsilon_{ij} \sim N\left(0, \sigma^2\right)$$

Model assumptions are:

1. The random error is nornal distributed.
2. The varaince is constant across the factor levels.

Estimation of the model in R

$$Y_{ij} = \mu_0 + \alpha_i + \varepsilon_{ij}$$

```
lm(response~predictor)
```

```
> lm.fit<-lm(w~feed)
```

Estimation of the model in R

```
> summary(lm.fit)

Call:
lm(formula = w ~ feed)

Residuals:
     Min       1Q   Median       3Q      Max
-123.909  -34.413    1.571   38.170  103.091

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   323.583     15.834  20.436  < 2e-16 ***
feedhorsebean -163.383     23.485  -6.957 2.07e-09 ***
feedlinseed   -104.833     22.393  -4.682 1.49e-05 ***
feedmeatmeal   -46.674     22.896  -2.039 0.045567 *
feedsoybean    -77.155     21.578  -3.576 0.000665 ***
feedsunflower    5.333     22.393   0.238 0.812495
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 54.85 on 65 degrees of freedom
Multiple R-squared:  0.5417,    Adjusted R-squared:  0.5064
F-statistic: 15.36 on 5 and 65 DF,  p-value: 5.936e-10
```

323.583: the mean of the casein

323.583-163.383= 160.2000, the mean of the horsebeen group

The AVOVA table

```
Residual standard error: 54.85 on 65 degrees of freedom
Multiple R-squared:  0.5417,    Adjusted R-squared:  0.5064
F-statistic: 15.36 on 5 and 65 DF,  p-value: 5.936e-10
```

$$54.85 = \sqrt{3009}$$

```
> anova(lm.fit)
Analysis of Variance Table

Response: w
          Df Sum Sq Mean Sq F value    Pr(>F)
feed       5 231129   46226  15.365 5.936e-10 ***
Residuals 65 195556    3009
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Example 2: Reading the cash data

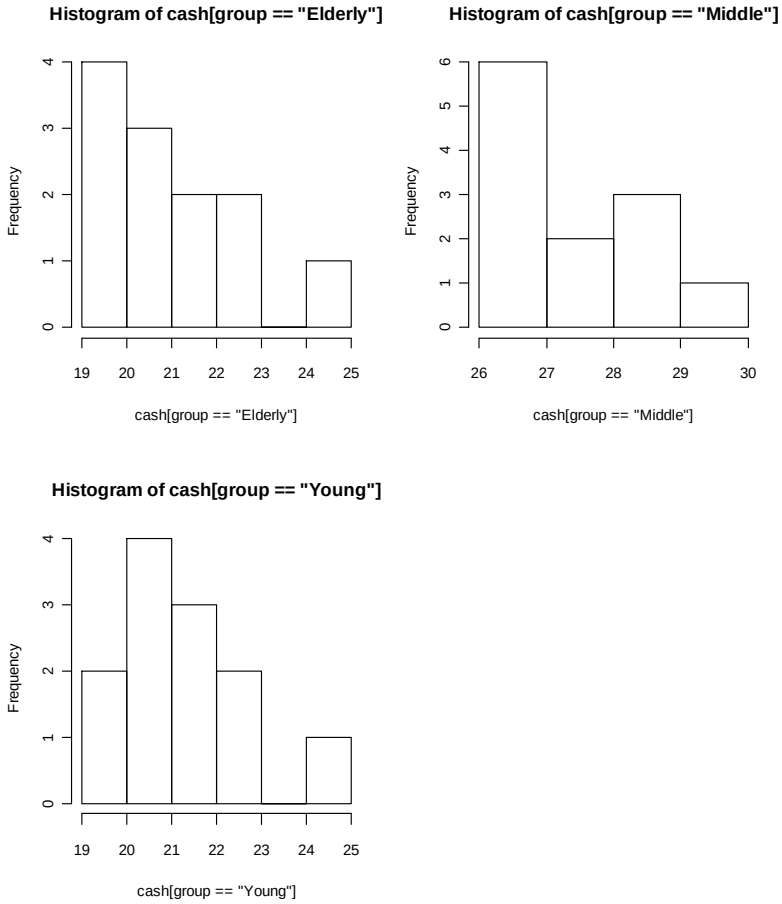
```
> cashdat<-
  read.table('c:\\projects\\wseda\\Rintro\\cashdat.txt',
  header=FALSE,na.strings="NA", dec=".")
> dim(cashdat)
[1] 36  2
> names(cashdat)<-c("cash","group")
> attach(cashdat)
```

The data

```
> print(cashdat)
   cash   group
1    23   Young
2    25   Young
.     .      .
.     .      .
11   21   Young
12   21   Young
13   28  Middle
.     .      .
.     .      .
24   29  Middle
25   23 Elderly
26   20 Elderly
35   22 Elderly
36   21 Elderly
```

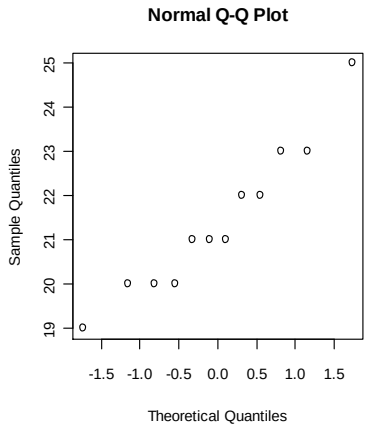
Histograms by group

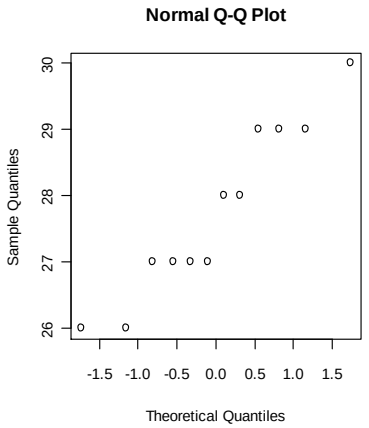
```
> par(mfrow=c(2,2))
> hist(cash[group=="Elderly"],col=0)
> hist(cash[group=="Middle"],col=0)
> hist(cash[group=="Young"],col=0)
```

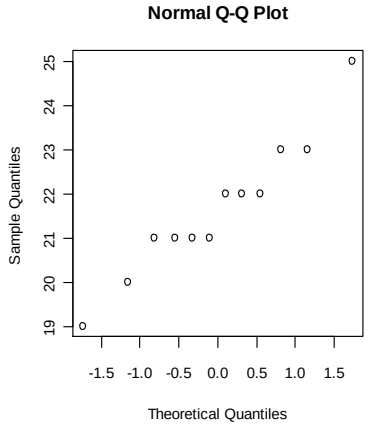


qq normal plots by group

```
> par(mfrow=c(2,2))
> qqnorm(cash[group=="Elderly"])
> qqnorm(cash[group=="Middle"])
> qqnorm(cash[group=="Young"])
```





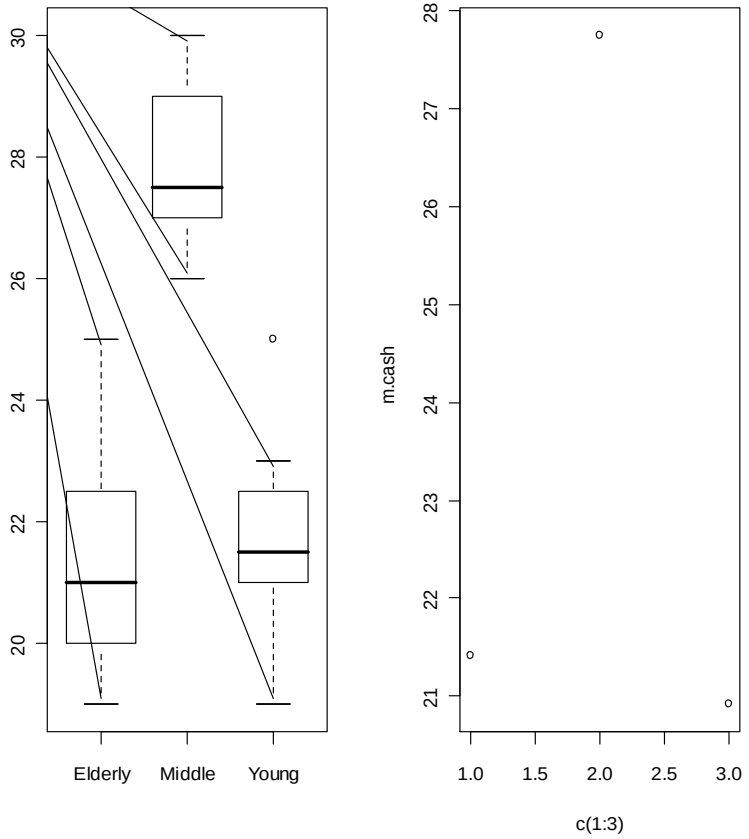


Boxplot and dotplot

```
> par(mfrow=c(1,2))
> boxplot(split(cash,group))
```

```
> tapply(cash,group,mean)
 Elderly   Middle    Young
21.41667 27.75000 21.66667
```

```
> m.cash<-c(21.41667,27.75,20.91667)
> names1<-c("Elderly","Middle","Young")
> plot(c(1:3),m.cash)
```



One-Way ANOVA model: model formulation

$$Y_{ij} = \mu_i + \varepsilon_{ij}$$

Parameters: fixed but unknown and needed to be estimated

Random error, assumed to follow normal distribution with constant varaince.

$$\varepsilon_{ij} \sim N\left(0, \sigma^2\right)$$

Model assumptions are:

1. The random error is nornal distributed.
2. The varaince is constant across the factor levels.

The Null Hypothesis: No treatment effect

- For a model in which the factor has three levels we wish to test the null hypothesis:

$$H_0 : \mu_1 = \mu_2 = \mu_3$$

- This means that we want to test if the means across all factor levels are equal.

- Mind that: we test if the parameters (μ_j) are equal, not is the sample means ($\bar{Y}_j$).

Test Statistic

Within group sum of squares

$$SSW = \sum_{i=1}^{I} \sum_{j=1}^{n_i} \left(Y_{ij} - \bar{Y}_{i.} \right)^2$$

Between group sum of squares

$$SSB = \sum_{i=1}^{I} n_i \left(\bar{Y}_{i.} - \bar{Y}.. \right)^2$$

$$F = \frac{SSB/(I-1)}{SSW/(N-I)} = \frac{MSB}{MSW}$$

The test statistic, F, is the ratio between the mean of the between sum of squares (SSB) and the mean of the within sum of squares.

The aov() function

$$Y_{ij} = \mu_i + \varepsilon_{ij}$$

```
aov(response ~ factor)
```

```
>Fit.aov<-aov(cash~group)
>summary(Fit.aov)
```

Test Statistic

Between group sum of squares/dgree of fredom

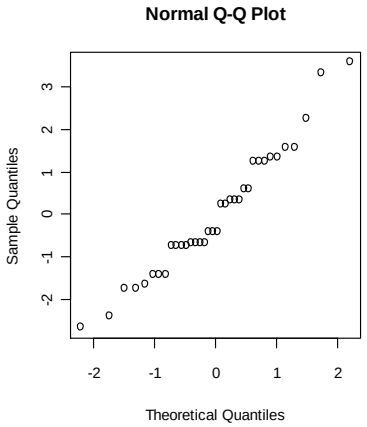
Within group sum of squares/dgree of fredom

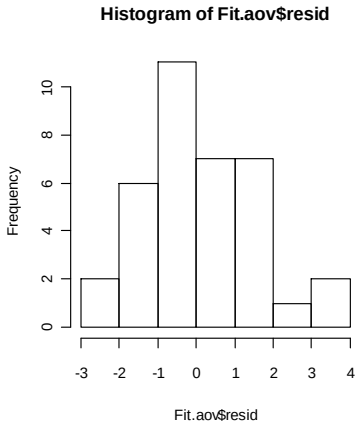
$$= \frac{SSB/(I-1)}{SSW/(N-I)} = \frac{MSB}{MSW} = F$$

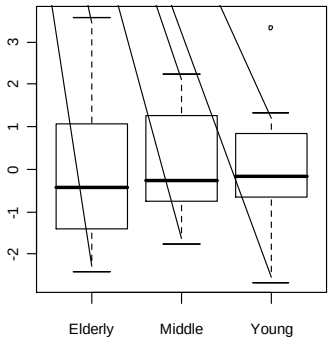
```
> summary(Fit.aov)
             Df  Sum Sq Mean Sq F value    Pr(>F)
group         2 308.722 154.361  67.172 2.322e-12 ***
Residuals    33  75.833   2.298
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Diagnostic plot

```
> par(mfrow=c(2,2))
> qqnorm(Fit.aov$resid)
> hist(Fit.aov$resid,col=0)
> boxplot(split(Fit.aov$resid,group))
```







Practical session 10 (a)

- Create the following data frame in R

	y	treatment
1	10	A
2	12	A
3	13	A
4	15	A
5	10	B
6	9	B
7	9	B
8	11	B
9	10	C
10	15	C
11	13	C
12	8	C

- Use one-way ANOVA model to test the null hypothesis of no treatment effect

Practical session 10 (b)

- Create the following data frame in R

	y	treatment
1	10	A
2	12	A
3	13	A
4	15	A
5	10	B
6	9	B
7	9	B
8	11	B
9	10	C
10	15	C
11	13	C
12	8	C

- Use one-way ANOVA model to test the null hypothesis of no treatment effect

Chapter 7

Statistical modeling 3: Logistic regression

Examples:

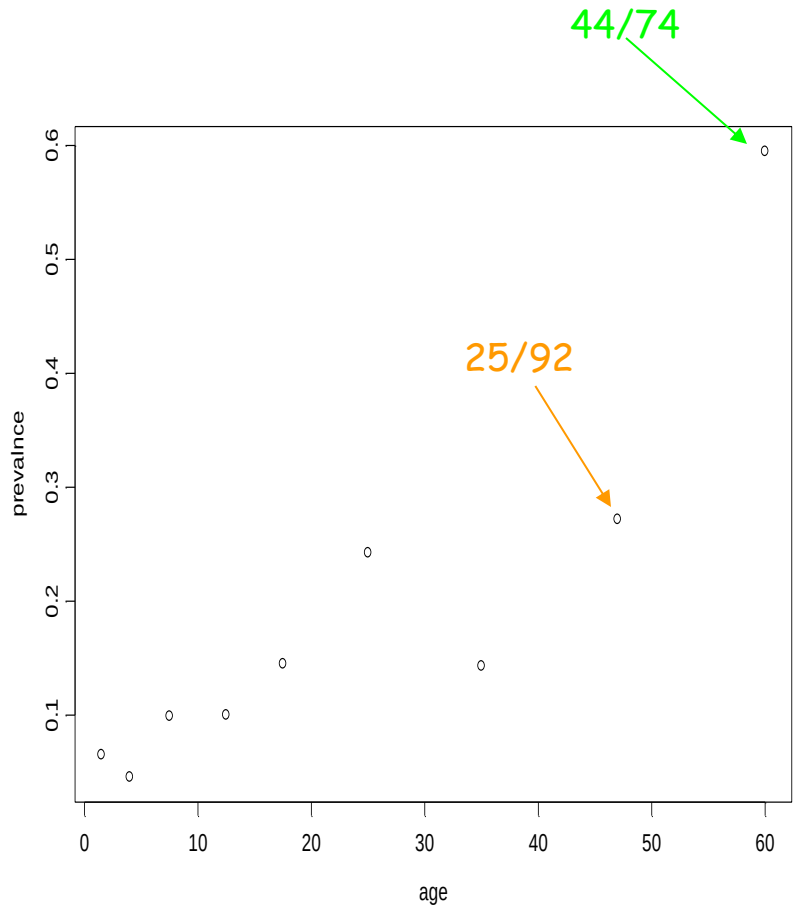
Serological data

Example : Serological data of malaria

- In this example the information about each subject in the experiment is the disease status (infected or not by malaria) and the age group of the subject.
- The variables are: the sample size, the number of sero-positive at each sample size (=the number of infected subjects) and the age.

Example : serological data

Age group	Mid age	Sero positive	Sample size
	1.5	8	123
	4.0	6	132
	7.5	18	182
	12.5	14	140
	17.5	20	138
	25.0	39	161
	35.0	19	133
	47.0	25	92
	60.0	44	74



Reading the data

```
> sero<-read.table('c:\\projects\\wseda\\Rintro\\sero1.txt',
header=FALSE,na.strings="NA", dec=".")

> print(sero)
  V1   V2  V3 V4
1  1  1.5 123  8
2  2  4.0 132  6
3  3  7.5 182 18
4  4 12.5 140 14
5  5 17.5 138 20
6  6 25.0 161 39
7  7 35.0 133 19
8  8 47.0  92 25
9  9 60.0  74 44
```

Example : serological data

Mid age	Sero positive	Sample size
1.5	8	123
4.0	6	132
7.5	18	182
12.5	14	140
17.5	20	138
25.0	39	161
35.0	19	133
47.0	25	92
60.0	44	74

$$Z_i = \begin{cases} 1 & sero \quad pos. \\ 0 & sero \quad neg. \end{cases}$$

$$Y_i = \sum Z_i$$

Number of sero-positive at each age group

$$Y_i \sim B(n_i, \quad P_i)$$

n_i: sample size at each age group

P_i is the probability to be infected (the prevalence). We use logistic regression in order to model the prevalence as a function of age

$$\log it(P_i) = \alpha + \beta \times age$$

The probability of infection

$$P = \frac{e^{\alpha+\beta\ age}}{1+e^{\alpha+\beta\ age}}$$

If β>0 then there is a positive association between the probability and age. This means that the probability of infection increase with age.

If β<0 then there is a negative association between the probability and age. This means that the probability of infection decrease with age.

The glm() function

$$Y_i \sim B(n_i, \quad P_i) \qquad \log it(P_i) = \alpha + \beta \times age$$

glm(pos/ntot ~ age, family=binomial(link = "logit"))

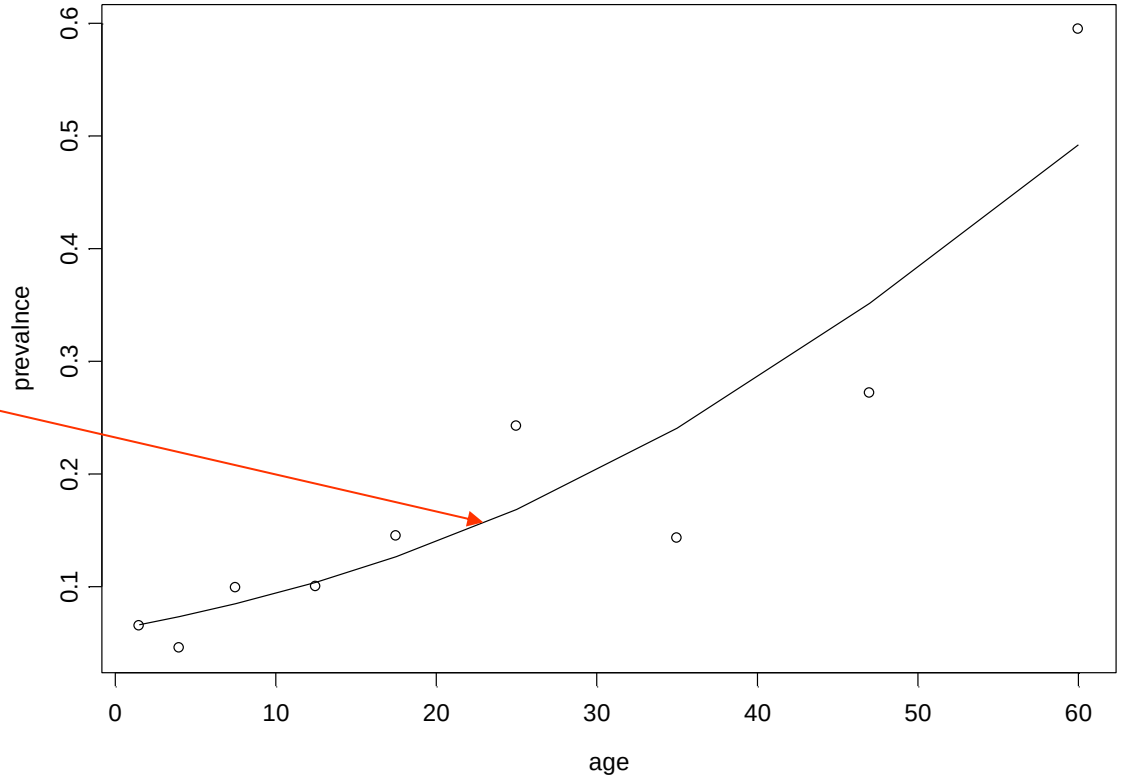
The glm() function

```
> fit.glm<- glm(pos/ntot ~ age, family=binomial(link = "logit"))
> summary(fit.glm)

Call:
glm(formula = pos/ntot ~ age, family = binomial(link = "logit"))

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.24364  -0.09726   0.01479   0.06756   0.19568

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.79677    1.79832  -1.555    0.120
age          0.04718    0.04668   1.011    0.312

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1.31775  on 8  degrees of freedom
Residual deviance: 0.18094  on 7  degrees of freedom
AIC: 8.062

Number of Fisher Scoring iterations: 5
```

Data and predicted values

$$\log it\left(\hat{P}_i\right) = -2.71 + 0.044 \times age$$

$$\hat{P}_i = \frac{e^{-2.71+0.044\times age}}{1+e^{-2.71+0.044\times age}}$$



Chapter 8

Programming in R II: User functions

Generate s random sample pf size 1000 from N(0,3)

```
> x<-rnorm(100,0,3)
> mean(x)
[1] 0.3080260
> median(x)
[1] 0.4176008
> quantile(x)
        0%         25%         50%         75%        100%
-5.9877043 -1.7844439  0.4176008  1.5712923  8.5930491
```

A user function: general form

```
function name<-function(x)
{
```

R commands (what do you what that the function will do for you……)

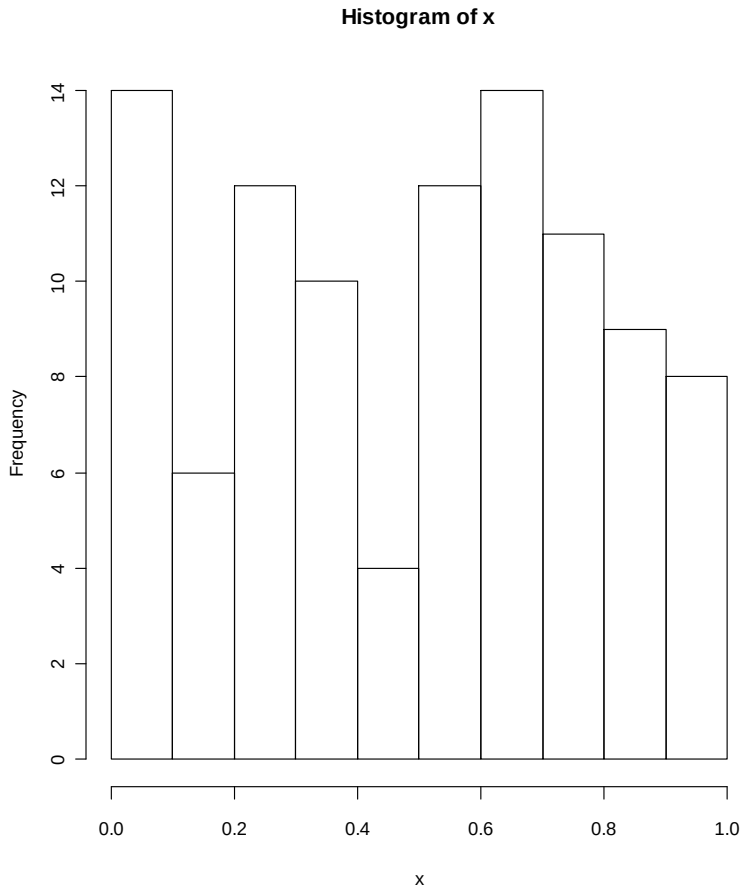
```
}
```

A user function: example

```
fch20<-function(x)
{
mean.x<-mean(x)
med.x<-median(x)
q.x<-quantile(x)
hist(x)
return(mean.x,med.x,q.x)
}
```

A user function: output

```
> z<-runif(100,0,1)
> fch20(z)
$mean.x
[1] 0.4947539

$med.x
[1] 0.5291341

$q.x
         0%         25%
   50%         75%        100%
0.01240262 0.24212404
   0.52913405 0.72482479
   0.98413912

Warning message:
In return(mean.x, med.x, q.x) :
   multi-argument returns are
   deprecated
>
```



Practical session 11

- Write a function which receive a numerical vector as an input and calculate the mean of the vector.

Chapter 9:

Statistical modeling : Two-way ANOVA

Model formulation

$$Y_{ijk} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \varepsilon_{ijk}$$

μ	Overall mean
α_i	Main effect of factor A
β_j	Main effect of factor B
$\alpha\beta_{ij}$	Interaction effect
ε_{ijk}	Random error

Example 1: Reading the data

```
> spwh3<-read.table('c:\\projects\\wseda\\spwh3.txt',
   header=FALSE,na.strings="NA", dec=".")
> names(spwh3)<-c("id","y","x1","gender")
```

Example 1: The data

```
> print(spwh3)
   id          y x1 gender
1   1 10.111368  1      0
2   2  9.948930  1      0
3   3 10.322560  1      0
.   .    .       .      .
.   .    .       .      .
59 59 30.030490  3      1
60 60 29.541542  3      1
>
```

Both x1 and gender are numerical objects !!!!

For an ANOVA model the independent variables are suppose to be factors.

Example 2: The data

	y	f1	f2
1	10	A1	B1
2	11	A1	B1
3	12	A1	B1
4	9	A2	B1
5	7	A2	B1
6	6	A2	B1
7	11	A1	B2
8	13	A1	B2
9	14	A1	B2
10	7	A2	B2
11	5	A2	B2
12	8	A2	B2

Two factors: f1 and f2

Three observations per combination.

```
> f1<-c("A1","A1","A1","A2","A2","A2","A1","A1","A1","A2","A2","A2")
> f2<-c("B1","B1","B1","B1","B1","B1","B2","B2","B2","B2","B2","B2")
> y<-c(10,11,12,9,7,6,11,13,14,7,5,8)
> data.frame(y,f1,f2)
```

Which null hypotheses we test ?

$$H_0: \quad \alpha_1 = \alpha_2$$

No treatment effect of factor A

$$H_0: \quad \beta_1 = \beta_2$$

No treatment effect of factor B

No interaction effects

$$H_0: \quad \alpha\beta_{11} = \alpha\beta_{12} = \alpha\beta_{21} = \alpha\beta_{22}$$

Example 1: A model without interaction

```
> fit.1<-aov(y~as.factor(x1)+as.factor(gender))
> anova(fit.1)
Analysis of Variance Table

Response: y
                   Df  Sum Sq Mean Sq F value    Pr(>F)
as.factor(x1)       2 1034.81  517.40  2244.8 < 2.2e-16 ***
as.factor(gender)   1 1509.98 1509.98  6551.3 < 2.2e-16 ***
Residuals          56   12.91    0.23
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘
   ’ 1
```

Example 1: A model with interaction

```
fit.2<-aov(y~as.factor(x1)+as.factor(gender)
           +as.factor(x1)*as.factor(gender))
```

```
> anova(fit.2)
Analysis of Variance Table

Response: y
                               Df  Sum Sq Mean Sq  F value Pr(>F)
as.factor(x1)                   2 1034.81  517.40 2171.959 <2e-16 ***
as.factor(gender)               1 1509.98 1509.98 6338.599 <2e-16 ***
as.factor(x1):as.factor(gender)  2    0.04    0.02    0.091 0.9131
Residuals                      54   12.86    0.24
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
>
```

Example 1: Testing model 1 versus model 2

```
> anova(fit.1,fit.2)
```

```
Analysis of Variance Table
Model 1: y ~ as.factor(x1) + as.factor(gender)
Model 2: y ~ as.factor(x1) + as.factor(gender) + as.factor(x1) * as.factor(gender)
```

```
  Res.Df   RSS    Df  Sum of Sq      F    Pr(>F)
1     56 12.9073
2     54 12.8639  2    0.0434     0.091  0.9131
```


F-test for the interaction

Example 2: A model without interaction

```
> fit.1<-aov(y~f1+f2)
> anova(fit.1)

Analysis of Variance Table

Response: y
          Df Sum Sq Mean Sq F value    Pr(>F)
f1         1 70.083  70.083 31.4066 0.0003325 ***
f2         1  0.750   0.750  0.3361 0.5763122
Residuals  9 20.083   2.231
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘
   ’ 1
```

Example 2: A model with interaction

```
> fit.2<-aov(y~f1+f2+f1*f2)
> anova(fit.2)
```

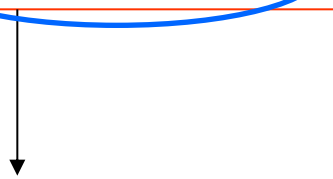
```
Analysis of Variance Table

Response: y
          Df Sum Sq Mean Sq F value    Pr(>F)
f1         1 70.083  70.083 35.0417 0.0003539 ***
f2         1  0.750   0.750  0.3750 0.5572922
f1:f2      1  4.083   4.083  2.0417 0.1909016
Residuals  8 16.000   2.000
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Example 2: Testing model 1 versus model 2

```
> anova(fit.1,fit.2)
```

```
Analysis of Variance Table

Model 1: y ~ f1 + f2
Model 2: y ~ f1 + f2 + f1 * f2
```

```
  Res.Df    RSS Df Sum of Sq      F Pr(>F)
1      9 20.083
2      8 16.000  1    4.0833 2.0417 0.1909
```



F-test for the interaction

Example 2: means by factor level

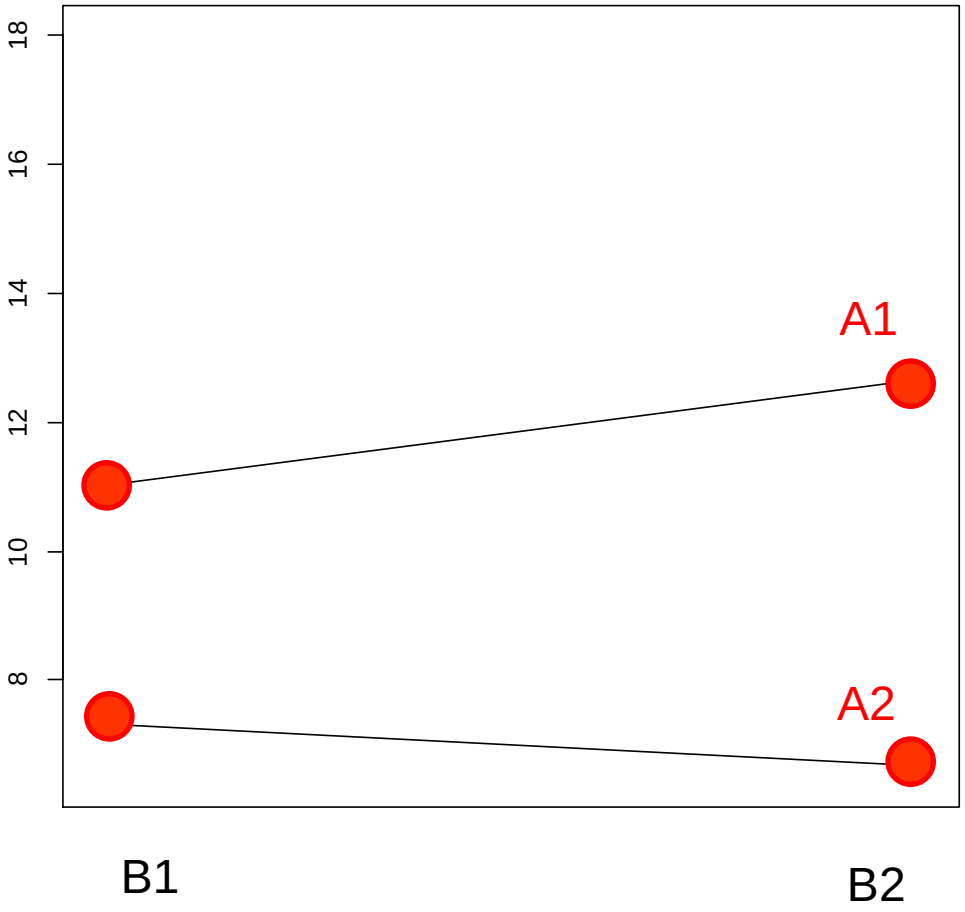
```
> tapply(y,f1,mean)
      A1       A2
11.83333 12.00000
> tapply(y,f2,mean)
       B1        B2
 9.166667 14.666667
> ind<-list(f1,f2)
> ind
[[1]]
 [1] "A1" "A1" "A1" "A2" "A2" "A2" "A1" "A1" "A1" "A2" "A2" "A2"

[[2]]
 [1] "B1" "B1" "B1" "B1" "B1" "B1" "B2" "B2" "B2" "B2" "B2" "B2"

> m<-tapply(y,ind,mean)
> m
          B1       B2
A1 11.000000 12.66667
A2  7.333333 16.66667
```

Factor 1

Factor 2

Cell means

Interaction plot: Example 2



Cell means

	B1	B2
A1	11.000000	12.666667
A2	7.333333	6.666667

Example 3: The data

	y	f1	f2
1	10	A1	B1
2	11	A1	B1
3	12	A1	B1
4	9	A2	B1
5	7	A2	B1
6	6	A2	B1
7	11	A1	B2
8	13	A1	B2
9	14	A1	B2
10	17	A2	B2
11	15	A2	B2
12	18	A2	B2

Two factors: f1 and f2

Three observations per combination.

```
> f1<-c("A1","A1","A1","A2","A2","A2","A1","A1","A1","A2","A2","A2")
> f2<-c("B1","B1","B1","B1","B1","B1","B2","B2","B2","B2","B2","B2")
> y<-c(10,11,12,9,7,6,11,13,14,17,15,18)
> data.frame(y,f1,f2)
```

Example 3: A model with interaction

```
> fit.2<-aov(y~f1+f2+f1*f2)
> anova(fit.2)
```

```
Analysis of Variance Table

Response: y
          Df Sum Sq Mean Sq F value    Pr(>F)
f1         1  0.083   0.083  0.0417 0.8433536
f2         1 90.750  90.750 45.3750 0.0001471 ***
f1:f2      1 44.083  44.083 22.0417 0.0015517 **
Residuals  8 16.000   2.000
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Example 3: means by factor level

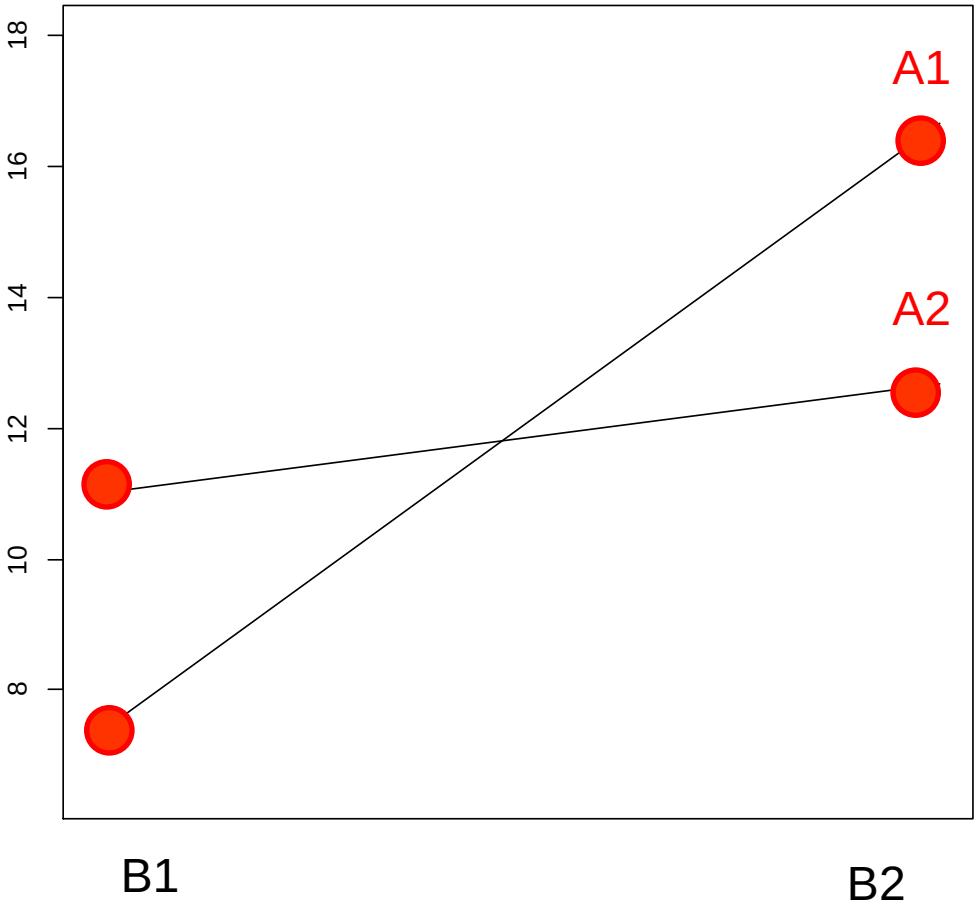
```
> tapply(y,f1,mean)
      A1       A2
11.83333 12.00000
> tapply(y,f2,mean)
       B1        B2
 9.166667 14.666667
> ind<-list(f1,f2)
> ind
[[1]]
 [1] "A1" "A1" "A1" "A2" "A2" "A2" "A1" "A1" "A1" "A2" "A2" "A2"

[[2]]
 [1] "B1" "B1" "B1" "B1" "B1" "B1" "B2" "B2" "B2" "B2" "B2" "B2"

> m<-tapply(y,ind,mean)
> m
          B1       B2
A1 11.000000 12.66667
A2  7.333333 16.66667
```

Factor 1

Factor 2

Cell means

Interaction plot: Example 3



Cell means

	B1	B2
A1	11.000000	12.66667
A2	7.333333	16.66667

Chapter 10
Statistical modeling :
More about two-way ANOVA

Reading the data

```
> spwh3<-read.table('c:\\projects\\wseda\\spwh3.txt',
header=FALSE,na.strings="NA", dec=".")
> names(spwh3)<-c("id","y","x1","gender")
> attach(spwh3)
```

Two-way ANOVA model

```
> fit.2<-aov(y~as.factor(x1)+as.factor(gender)+as.factor(x1)*as.factor(gender))

> anova(fit.2)

Analysis of Variance Table

Response: y
                               Df  Sum Sq Mean Sq  F value Pr(>F)
as.factor(x1)                   2 1034.81  517.40 2171.959 <2e-16 ***
as.factor(gender)               1 1509.98 1509.98 6338.599 <2e-16 ***
as.factor(x1):as.factor(gender)  2    0.04    0.02    0.091 0.9131
Residuals                      54   12.86    0.24
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Stepwise procedure

```
> slm1 <- step(fit.2)
Start:  AIC=-80.4
y ~ as.factor(x1) + as.factor(gender) + as.factor(x1) * as.factor(gender)

                                    Df Sum of Sq     RSS     AIC
- as.factor(x1):as.factor(gender)  2     0.043  12.907 -84.193
<none>                                         12.864 -80.395

Step:  AIC=-84.19
y ~ as.factor(x1) + as.factor(gender)

                    Df Sum of Sq     RSS     AIC
<none>                           12.91  -84.19
- as.factor(x1)      2   1034.81 1047.72  175.60
- as.factor(gender)  1   1509.98 1522.89  200.04
```

Stepwise procedure

```
> summary(slm1)
                  Df  Sum Sq Mean Sq F value    Pr(>F)
as.factor(x1)      2 1034.81  517.40  2244.8 < 2.2e-16 ***
as.factor(gender)  1 1509.98 1509.98  6551.3 < 2.2e-16 ***
Residuals         56   12.91    0.23
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘
’ 1
```

Chapter 11
Statistical modeling :
More about Linear regression

Reading the data

```
> spwh2<-read.table('c:\\projects\\wseda\\spwh2.txt',
header=FALSE,
+                              ,na.strings="NA", dec=".")
> dim(spwh2)
[1] 100   5
>
> names(spwh2)<-c("id","y","x1","x2","x3")
> attach(spwh2)

        The following object(s) are masked from spwh2 (
position 3 ) :

         id x1 x2 x3 y
```

Fitting two models

```
> fit.1<-lm(y~x1+x2)
> anova(fit.1)
```

```
Analysis of Variance Table

Response: y
          Df Sum Sq Mean Sq  F value    Pr(>F)
x1         1  164.2   164.2   27.152 1.059e-06 ***
x2         1 7409.7  7409.7 1224.980 < 2.2e-16 ***
Residuals 97  586.7     6.0
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05
     ‘.’ 0.1 ‘ ’ 1
```

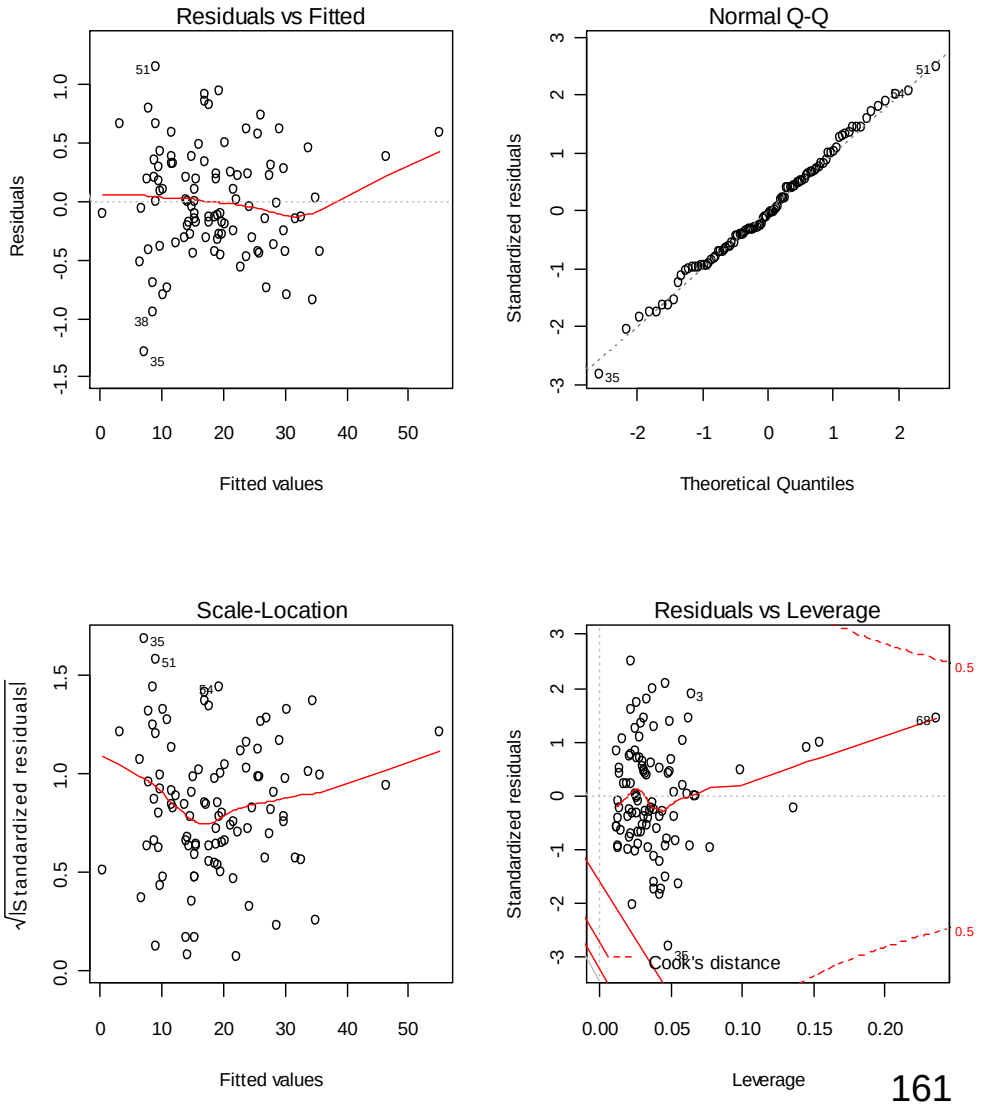
```
> fit.2<-lm(y~x1+x2+x3)
> anova(fit.2)
```

```
Analysis of Variance Table

Response: y
          Df Sum Sq Mean Sq  F value    Pr(>F)
x1         1  164.2   164.2   758.98 < 2.2e-16 ***
x2         1 7409.7  7409.7 34241.81 < 2.2e-16 ***
x3         1  566.0   566.0  2615.44 < 2.2e-16 ***
Residuals 96   20.8     0.2
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
    0.1 ‘ ’ 1
```

Testing model 1 versus model 2

```
> anova(fit.1,fit.2)
Analysis of Variance Table

Model 1: y ~ x1 + x2
Model 2: y ~ x1 + x2 + x3
  Res.Df    RSS Df Sum of Sq      F    Pr(>F)
1     97 586.74
2     96  20.77  1    565.97 2615.4 < 2.2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1
```

```
> par(mfrow=c(2,2))
> plot(fit.2)
```



Single terms deletions

```
> drop1(fit.2, test="F")
Single term deletions

Model:
y ~ x1 + x2 + x3
       Df Sum of Sq    RSS    AIC  F value     Pr(F)
<none>                20.8 -149.1
x1      1      76.6   97.4    3.4   354.21 < 2.2e-16 ***
x2      1    7865.3 7886.1  442.8 36347.01 < 2.2e-16 ***
x3      1     566.0  586.7  182.9  2615.44 < 2.2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘
’ 1
```

AIC and likelihood

```
> AIC(fit.2)
[1] 136.6403
> logLik(fit.2)
'log Lik.' -63.32017 (df=5)
```

Chapter 12

Application : the for loop

The bootstrap estimate of the standard error for the mean

The observed data

A sample of 10 observations:

```
> x <- c(11.201, 10.035, 11.118, 9.055, 9.434, 9.663, 10.403, 11.662, 9.285,8.84)
> mean(x)
[1] 10.0696
```

We wish to estimate the standard error of the sample mean

$$S.E(\bar{x}) = \frac{\sigma_F}{\sqrt{n}}$$

Parametric and nonparametric bootstrap

nonparametric bootstrap

$$F \rightarrow (x_1, x_2, ..., x_n)$$

We resample from the empirical distribution

parametric bootstrap

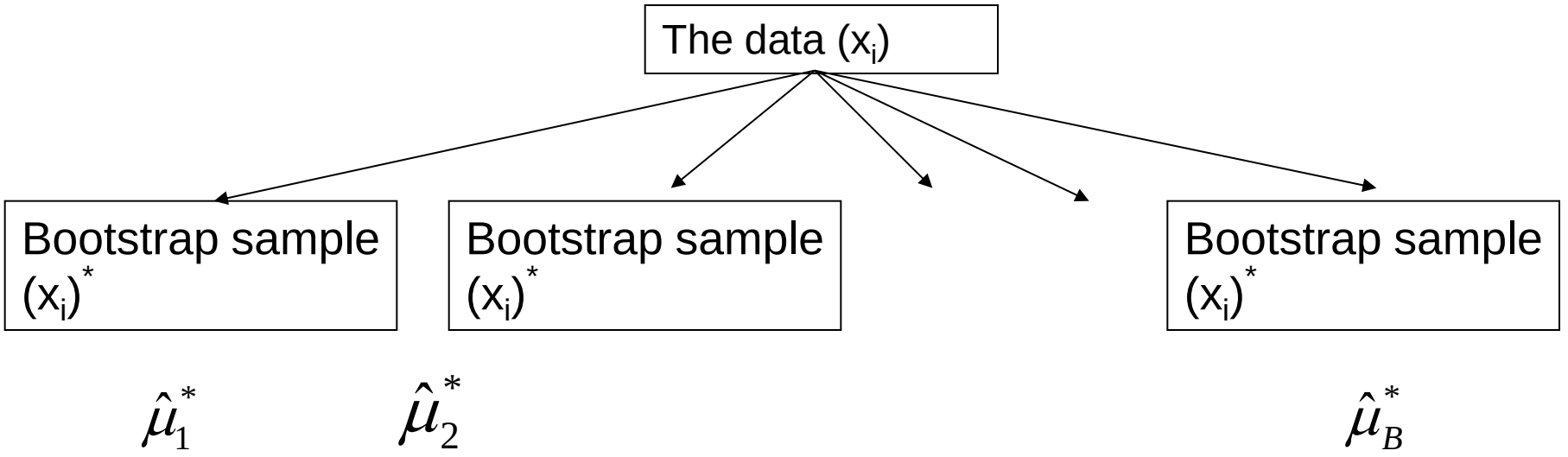
We assume a parametric model for F

$$F(\theta)$$

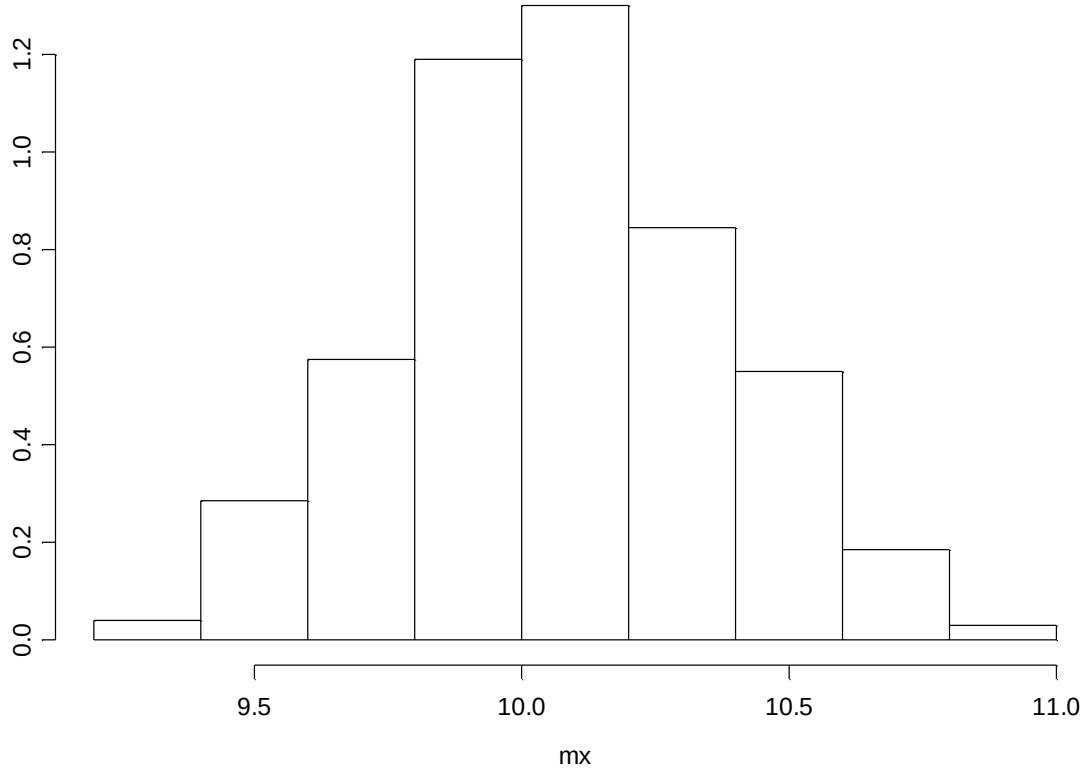
We resample from

$$F(\hat{\theta})$$

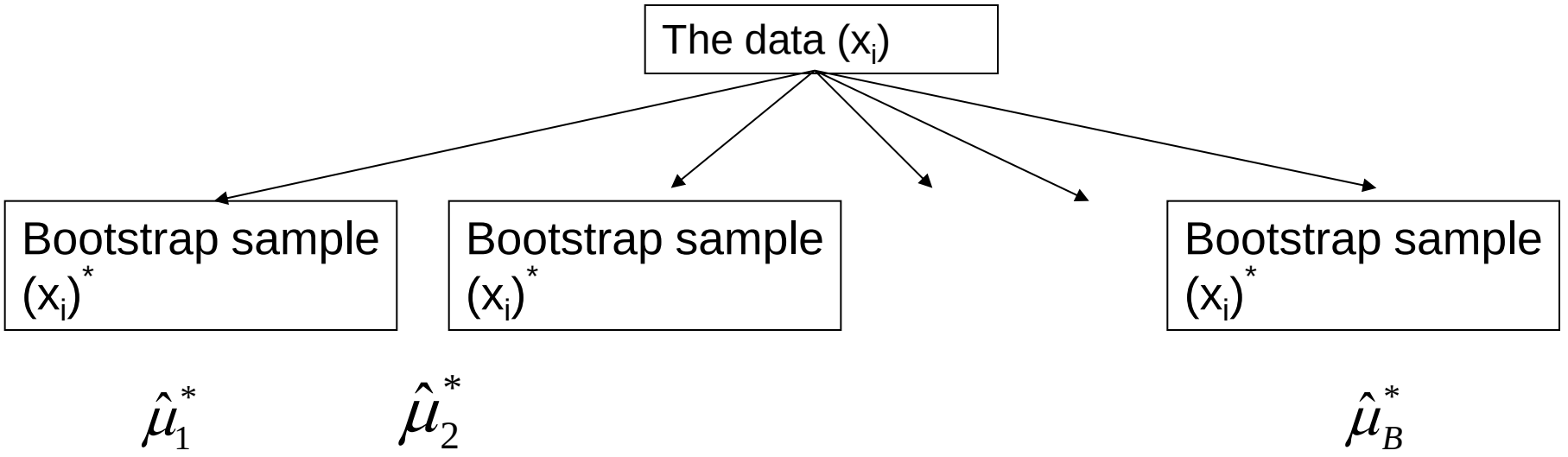
Nonparametric bootstrap



Nonparametric bootstrap



Nonparametric bootstrap



$$S.E.(\hat{\mu}) = \left\{ \frac{1}{B-1} \sum_{b=1}^{B} \left(\hat{\mu}_b^* - \hat{\mu}^* \right)^2 \right\}^{0.5}$$

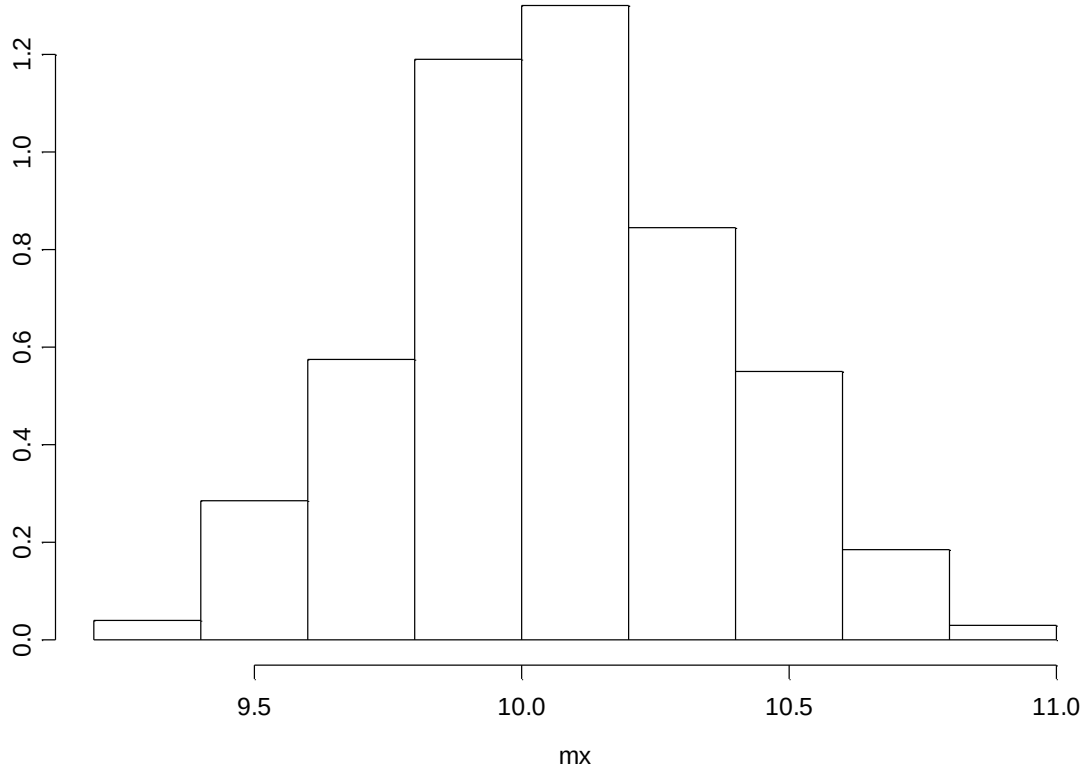
R code

```
> var(mx)
[1] 0.09357364
```

The estimated standard error 0.093

```
n<-length(x)
B<-1000
mx<-c(1:B)
for(i in 1:B){
cat(i)
boot.i<-sample(x,n,replace=T)
mx[i]<-mean(boot.i)
}
```

Nonparametric bootstrap



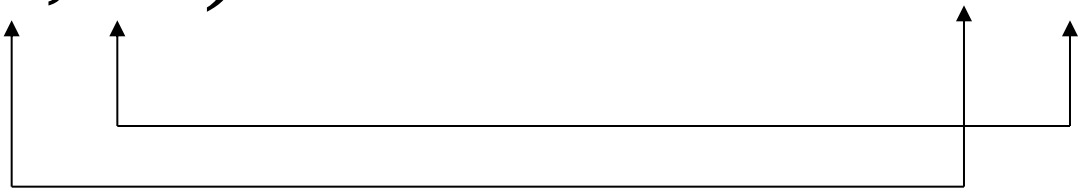
Parametric bootstrap

We assume a parametric model for F

$$F = N(\mu, \sigma^2)$$

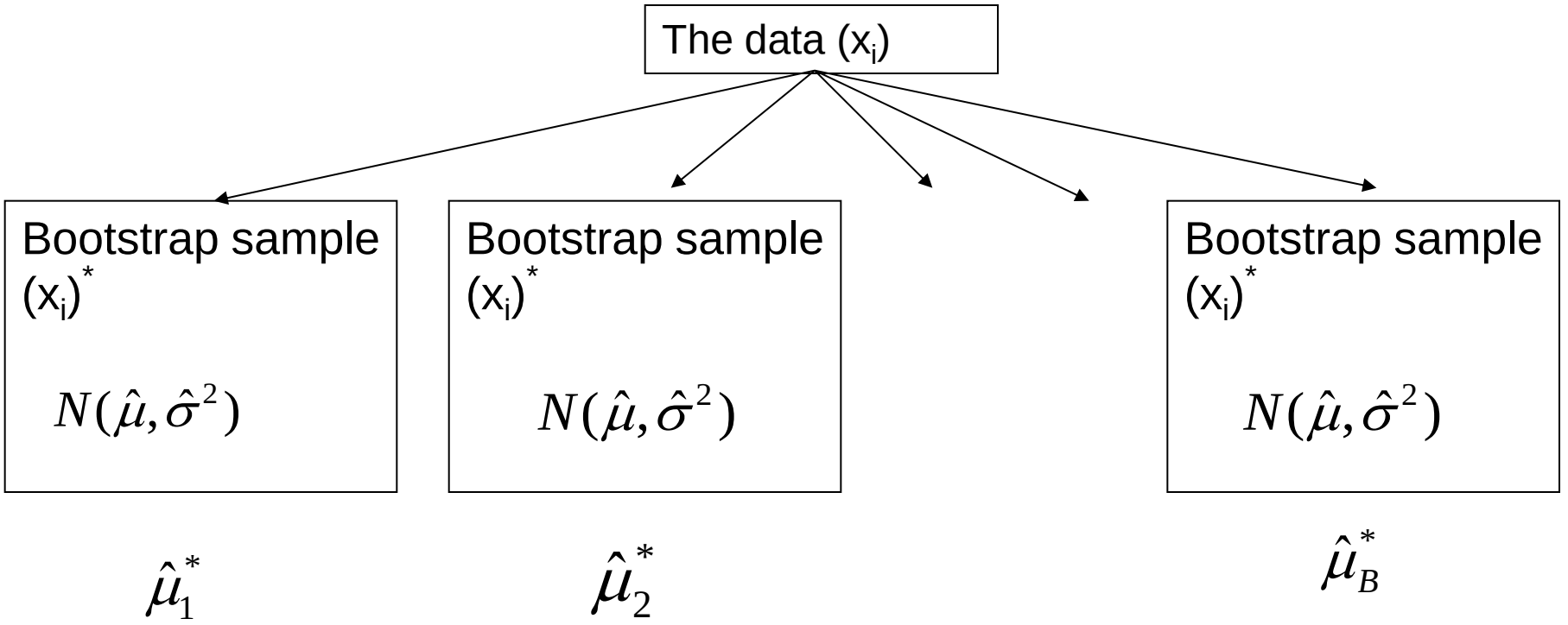
We estimate F by

$$\hat{F} = N(\hat{\mu}, \hat{\sigma}^2)$$



We replace the unknown parameters in F with their plug-in estimates

Parametric bootstrap



$$S.E.(\hat{\mu}) = \left\{ \frac{1}{B+1} \sum_{b=1}^{B} \left(\hat{\mu}_b^* - \hat{\mu}^* \right)^2 \right\}^{0.5}$$

R code

> var(mx)
[1] 0.1007613

Bootstrap estimate for the standard error for the mean

```
B<-1000
MLx<-mean(x)
Varx<-var(x)
mx<-c(1:B)
for(i in 1:B){
cat(i)
boot.i<-rnorm(n,MLx,sqrt(Varx))
mx[i]<-mean(boot.i)
}
```

Parametric bootstrap