



Introduction to R



Computational Genomics

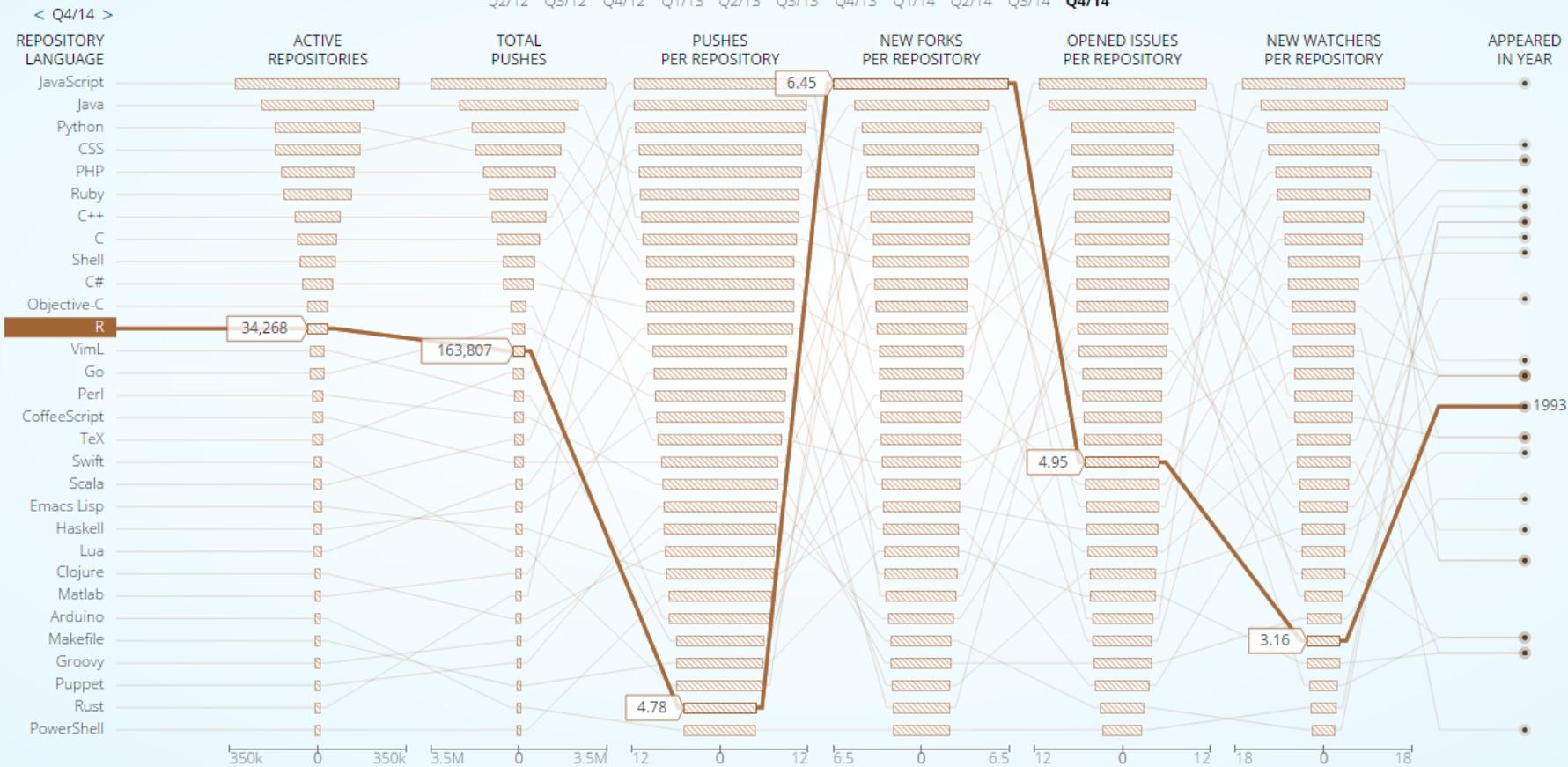
Weiguang (Wayne) Mao

Significant content courtesy by Silvia Liu

2M ACTIVE REPOSITORIES

1M

Q2/12 Q3/12 Q4/12 Q1/13 Q2/13 Q3/13 Q4/13 Q1/14 Q2/14 Q3/14 Q4/14



Why or Why not

Statistical models can be written with only a few lines.

R + visualization
= perfect match 

Cran "Task Views" page lists a wide range of tasks for which R packages are available

6789 packages, 6/18/2015

Bioconductor Open source software for bioinformatics

1104 packages

Statisticians, engineers and scientists without computer programming skills find it easy to use.

- Your mission
- Free, open source



REVOLUTION
ANALYTICS

<http://dataconomy.com/r-vs-python-the-data-science-wars/>

<http://blog.revolutionanalytics.com/2015/06/how-many-packages-are-there-really-on-cran.html>



VS.



As a full-fledged programming language, Python is a good tool to implement algorithms for production use.



Statisticians, engineers and scientists without computer programming skills find it easy to use.

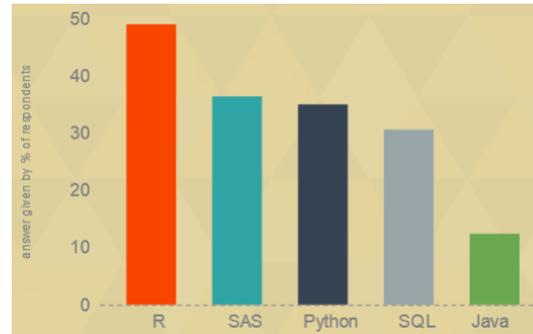
R is slow, on purpose



Developed by statisticians, for statisticians

R has been used primarily in academics and research. However, R is rapidly expanding into the enterprise market.

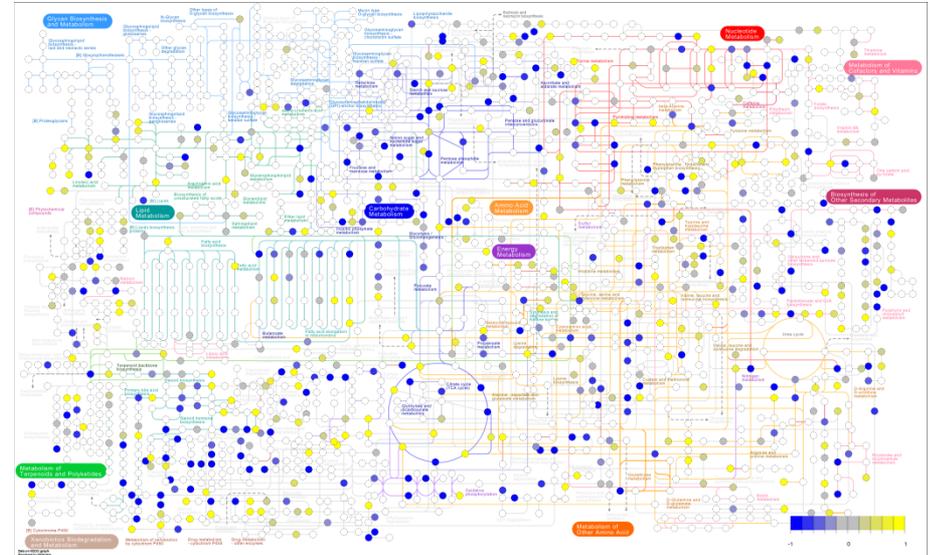
Python is used by programmers that want to delve into data analysis or apply statistical techniques, and by developers that turn to data science.



R + visualization
= perfect match

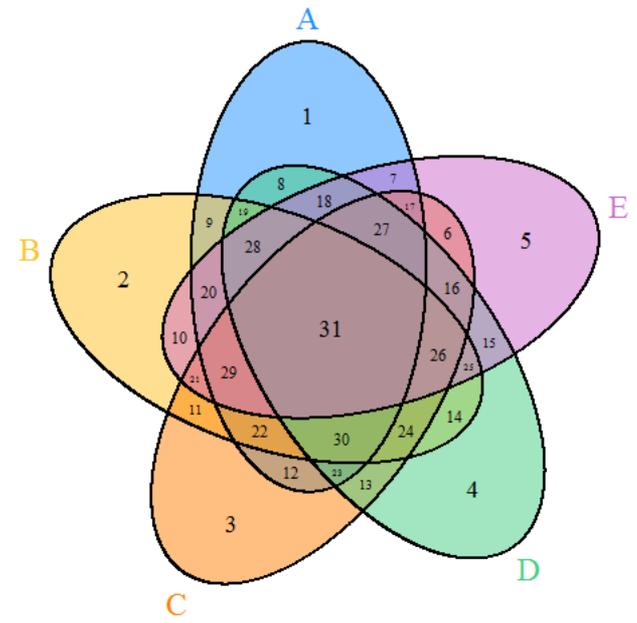
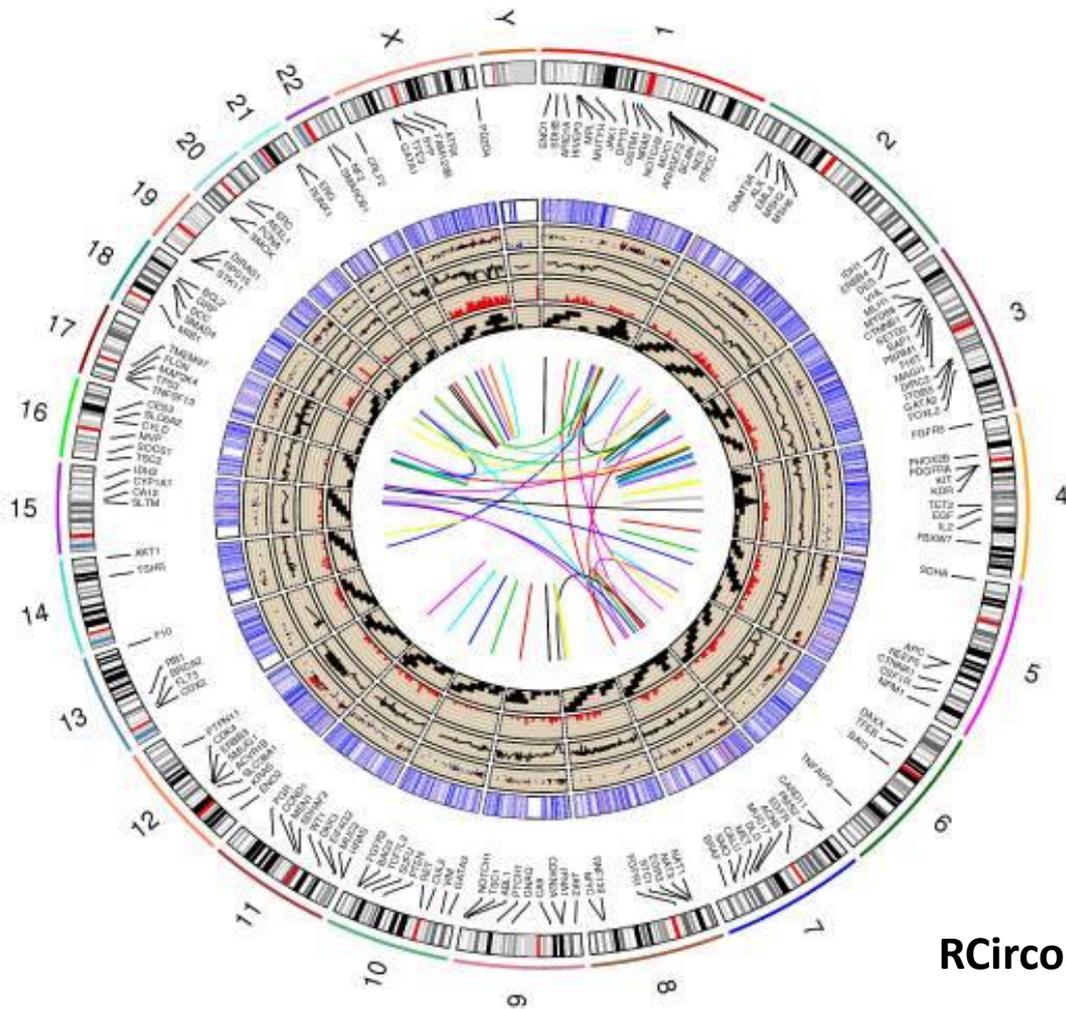


- ggplot2
- API (cytoscape)



Pathview: An R package for pathway based data integration and visualization

RCircos 2D Track Plot with Human Genome



VennDiagram: Generate High-Resolution Venn and Euler Plots

RCircos: an R package for Circos 2D track plots.

IDE & Versions



3.2.3 (12/10/2015) Wooden Christmas-Tree



0.99.491 (desktop version/cluster version)



Workspace: fileName.rdata = fileName.mat

Installation

- R & Rstudio

<http://lib.stat.cmu.edu/R/CRAN/>

<https://www.rstudio.com/products/rstudio/download/>

- R package

- CRAN

```
install.package("packageName")
```

- Bioconductor

```
source("http://bioconductor.org/biocLite.R")
```

```
biocLite("packageName")
```

Importing

- `library(packageName)`

How to run R scripts

- Command line

Rscript myscript.R

```
print("Hello world")
```

```
D:\Software\R Language\bin>Rscript Recitation.R  
[1] "Hello World"
```

- ✓ • Within R/Rstudio

Select the code blocks you want to run and press Ctrl+R/Enter

```
> print("Hello world")  
[1] "Hello world"
```

-2. = and <-

- Long time ago
= (equal) <- (assignment)
== (equal)



```
> print(x=3)
[1] 3
> print(y<-3)
[1] 3
```

```
f <- function(x){
  print(x)
}
```

```
> f(a<-3)
[1] 3
> f(a=3)
Error in f(a = 3) : unused argument (a = 3)
> f(x=3)
[1] 3
```

-1. data.frame

```
> x <- data.frame("SN"=1:2,"Age"=c(21,15),"Name"=c("John","Dora"),stringsAsFactors=FALSE)
```

```
> x
  SN Age Name
1  1  21 John
2  2  15 Dora
```

```
> str(x)
'data.frame':  2 obs. of  3 variables:
 $ SN  : int  1 2
 $ Age : num  21 15
 $ Name: chr  "John" "Dora"
```

```
> x[x$Name=="John",]
  SN Age Name
1  1  21 John
```

- Treat it as matrices
- Take care of strings/texts (factor or character)

0. Start from 1

```
> m0
      [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6
> apply(m0,1,sum)
[1]  9 12
```

```
SumOfRow = [0,0]
for i in range(2):
    for j in range(3):
        SumOfRow[i] = SumOfRow[i]+m0[i][j]
print SumOfRow
```

```
[[1, 3, 5], [2, 4, 6]]
[9, 12]
```

R, like S, is designed **around a true** computer language, and it allows users to add additional functionality by defining new functions.

1. Types and Variables

- Use `class(x)` to check what type the variable is
- Basic types
 - Numeric
 - Integer
 - Logical: True(T)/ False (F)
 - ~~String~~ Character

```
> as.numeric()  
numeric(0)  
> as.integer()  
integer(0)  
> as.character()  
character(0)
```

2. ~~String~~ Character

- `nchar()`

```
> str <- "HelloWorld"
> nchar(str)
[1] 10
```
- `paste()`

```
> paste("Hello", "world", sep="-")
[1] "Hello-world"
```
- `grep()`, `regexpr()`, `gregexpr()`

```
> grep("a", c("a", "b", "c"))
[1] 1

> regexpr("o", "HelloWorld")
[1] 5
attr(,"match.length")
[1] 1
attr(,"useBytes")
[1] TRUE

> gregexpr("o", "HelloWorld")
[[1]]
[1] 5 7
attr(,"match.length")
[1] 1 1
attr(,"useBytes")
[1] TRUE
```
- `strsplit()`

```
> strsplit("Hello,world", ",")
[[1]]
[1] "Hello" "world"
```
- `substring()`

```
> substring("HelloWorld", 1, 5)
[1] "Hello"
```
- `sub()`, `gsub()`

```
> sub("o", "*", "HelloWorld")
[1] "Hell*world"

> gsub("o", "*", "HelloWorld")
[1] "Hell*w*rld"
```

3. Data Structures

- Vector

```
> v1 <- 2:5
> v1
[1] 2 3 4 5

> v3 <- c(3, 2, 7.2, 0.9, 100)
> v3
[1] 3.0 2.0 7.2 0.9 100.0

> v4 <- seq(4, 7, 0.5)
> v4
[1] 4.0 4.5 5.0 5.5 6.0 6.5 7.0
```

```
> v2 <- c(2, "Hello")
> v2
[1] "2" "Hello"
```

- which(), sort(), length(), rev()

```
> v0 <- 5:2
> v0
[1] 5 4 3 2
> which(v0>2)
[1] 1 2 3

> sort(v0)
[1] 2 3 4 5

> length(v0)
[1] 4

> rev(v0)
[1] 2 3 4 5
```

3. Data Structures

- Lists

```
> l1 <- list(name=c("Peter","Lily","Emma"),c("yes","no"),
+ age=c(20,40,33,rep(18,times=3)),
+ value=matrix(1:6,2,3))
> l1
$name
[1] "Peter" "Lily"  "Emma"

[[2]]
[1] "yes" "no"

$age
[1] 20 40 33 18 18 18

$value
      [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6

> l1$name
[1] "Peter" "Lily"  "Emma"
> l1[[1]]
[1] "Peter" "Lily"  "Emma"
```

3. Data Structures

- Linked lists

```
> tree <- list(list(1, 2), list(3, list(4, 5)))
> # left child: list(1, 2)
> tree[[1]]
[[1]]
[1] 1

[[2]]
[1] 2

> # right child
> tree[[2]]
[[1]]
[1] 3

[[2]]
[[2]][[1]]
[1] 4

[[2]][[2]]
[1] 5

> # right child of right child: list(4, 5)
> tree[[2]][[2]]
[[1]]
[1] 4

[[2]]
[1] 5
```



4. Matrices

- 2-dimension

```
> d <- sample(1:20)
> d
[1] 14 20  4  3 17 10 18 19  1  9 12  2 16 13 15  7  6  8 11  5
```

```
> m1 <- matrix(data=d,nrow=4,ncol=5,byrow=TRUE,
+ dimnames=list(rows=c("cat","dog","rat","fish"),
+ cols=c("a","b","c","d","e")))
> m1
```

| | cols | | | | |
|------|------|----|----|----|----|
| rows | a | b | c | d | e |
| cat | 14 | 20 | 4 | 3 | 17 |
| dog | 10 | 18 | 19 | 1 | 9 |
| rat | 12 | 2 | 16 | 13 | 15 |
| fish | 7 | 6 | 8 | 11 | 5 |

```
> m1["cat",]
a b c d e
14 20 4 3 17
> m1[,1]
cat dog rat fish
14 10 12 7
```

```
> dim(m1)
[1] 4 5
> nrow(m1)
[1] 4
> ncol(m1)
[1] 5
> rownames(m1)
[1] "cat" "dog" "rat" "fish"
> colnames(m1)
[1] "a" "b" "c" "d" "e"
```

4. Matrices

- 2-dimension

 `> m3 <- matrix(1:6,2,3)`
`> m3`

| | [,1] | [,2] | [,3] |
|------|------|------|------|
| [1,] | 1 | 3 | 5 |
| [2,] | 2 | 4 | 6 |

 `> m4 <- matrix(11:16,2,3,byrow=TRUE)`
`> m4`

| | [,1] | [,2] | [,3] |
|------|------|------|------|
| [1,] | 11 | 12 | 13 |
| [2,] | 14 | 15 | 16 |

`> m5 <- matrix(21:26,3,2)`
`> m5`

| | [,1] | [,2] |
|------|------|------|
| [1,] | 21 | 24 |
| [2,] | 22 | 25 |
| [3,] | 23 | 26 |

`> m3*m4`

| | [,1] | [,2] | [,3] |
|------|------|------|------|
| [1,] | 11 | 36 | 65 |
| [2,] | 28 | 60 | 96 |

`> m3%%m5`

| | [,1] | [,2] |
|------|------|------|
| [1,] | 202 | 229 |
| [2,] | 268 | 304 |

`> rbind(m3,m4)`

| | [,1] | [,2] | [,3] |
|------|------|------|------|
| [1,] | 1 | 3 | 5 |
| [2,] | 2 | 4 | 6 |
| [3,] | 11 | 12 | 13 |
| [4,] | 14 | 15 | 16 |

`> t(m3)`

| | [,1] | [,2] |
|------|------|------|
| [1,] | 1 | 2 |
| [2,] | 3 | 4 |
| [3,] | 5 | 6 |

`> apply(m3,1,sum)`

| [1] | 9 12 |
|-----|------|
|-----|------|

`> as.vector(m3)`

| [1] | 1 2 3 4 5 6 |
|-----|-------------|
|-----|-------------|

4. Matrices

- Multi-dimension (array)

```
> a <- array(1:24,dim=c(4,3,2),
+ dimnames=list(c("a","b","c","d"),c("x","y","z"),c("old","new") ))
> a
, , old
  x y z
a 1 5 9
b 2 6 10
c 3 7 11
d 4 8 12

, , new
  x y z
a 13 17 21
b 14 18 22
c 15 19 23
d 16 20 24
```

5. Dictionaries

- names(), rownames(), colnames()

```
> v1
[1] 2 3 4 5
> names(v1) <- c("a","b","c","d")
> v1[1]
a
2
> v1["a"]
a
2
```

```
> m1 <- matrix(data=d,nrow=4,ncol=5,byrow=TRUE,
+ dimnames=list(rows=c("cat","dog","rat","fish"),
+ cols=c("a","b","c","d","e")))
> m1
      cols
rows  a  b  c  d  e
cat  14 20  4  3 17
dog  10 18 19  1  9
rat  12  2 16 13 15
fish  7  6  8 11  5
```

```
> m1["cat",]
 a  b  c  d  e
14 20  4  3 17
> m1[,1]
cat dog rat fish
 14  10  12  7
```

6. Conditionals

- If, else if, else

```
> x<-3
> if (x < 0){
+   print("Negative")
+ }else if (x == 0){
+   print("Zero")
+ }else{
+   print("Positive")
+ }
[1] "Positive"
```

```
> x <- 1
> if (x < 0){
+   print("Negative")
+ }
> else if (x == 0){
Error: unexpected 'else' in "else"
>   print("Zero")
[1] "Zero"
> }else{
Error: unexpected '}' in "}"
>   print("Positive")
[1] "Positive"
> }
Error: unexpected '}' in "}"
```

7. Iteration

- for

```
> sum <- 0
> for (i in 1:10){
+   sum <- sum+i
+ }
> sum
[1] 55
```

- while

```
> sum <- 0
> i <- 1
> while (i <= 10){
+   sum <- sum+i
+   i <- i+1
+ }
> sum
[1] 55
```

- repeat

```
> sum <- 0
> i <- 0
> repeat{
+   i <- i+1
+   sum <- sum+i
+   if (i > 9) break
+ }
> sum
[1] 55
```


9. Writing Files

#write data to a file

```
write(x, file = "data", ncolumns = if(is.character(x)) 1 else 5, append = FALSE, sep = " ")
```

#write data to a file in a table format

```
write.table(x, file = "", append = FALSE, quote = TRUE, sep = " ", eol = "\n", na = "NA",  
            dec = ".", row.names = TRUE, col.names = TRUE, qmethod = c("escape",  
            "double"), fileEncoding = "")
```

#save R objects into a file

```
save(..., file="")
```

#save the current workspace

```
save.image(file = ".RData", version = NULL, ascii = FALSE, compress = !ascii, safe =  
TRUE)
```

10. Reading Files

#Reads a file in table format and creates a data frame from it

```
read.table(file, header = FALSE, sep = "", quote = "\"\"", dec = ".", numerals =  
  c("allow.loss", "warn.loss", "no.loss"), row.names, col.names, as.is  
  = !stringsAsFactors, na.strings = "NA", colClasses = NA, nrow = -1, skip = 0,  
  check.names = TRUE, fill = !blank.lines.skip, strip.white = FALSE,  
  blank.lines.skip = TRUE, comment.char = "#", allowEscapes = FALSE, flush =  
  FALSE, stringsAsFactors = default.stringsAsFactors(), fileEncoding = "",  
  encoding = "unknown", text, skipNul = FALSE)
```

#read a csv file

```
read.csv(file, header = TRUE, sep = ",", quote = "\"\"", dec = ".", fill = TRUE,  
comment.char = "", ...) #load the
```

#load datasets written with function *save*

```
load(file, envir = parent.frame(), verbose = FALSE)
```

11. Plot

```
#2-by-2 sub graph  
par(mfrow=c(2,2))
```

```
#graph 1: plot
```

```
x <- 1:10
```

```
y <- seq(0.1, 1, by=0.1)
```

```
z <- y+rnorm(10, mean=0, sd=0.1)
```

```
plot(x, z, type="p", col="red", main="Plot", xlab="x label", ylab="value")
```

```
lines(x,y)
```

```
#graph 2: histogram
```

```
age <- rnorm(1000, mean=20, sd=3)
```

```
hist(age, main="Histogram", xlab="age", ylab="counts")
```

```
#graph 3: boxplot
```

```
boxplot(age, main="boxplot", ylab="age")
```

```
#graph 4: qq plot
```

```
qqnorm(age, main="qq plot")
```

11. Plot

```
#2-by-2 sub graph  
par(mfrow=c(2,2))
```

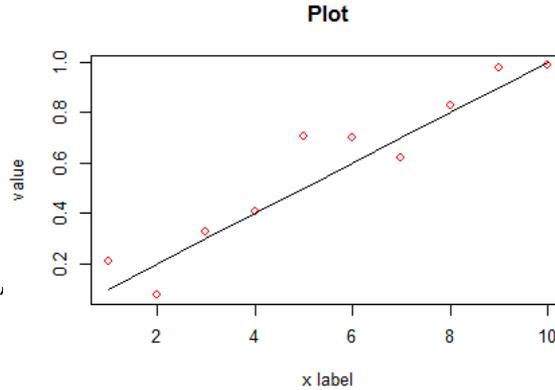
```
#graph 1: plot
```

```
x <- 1:10
```

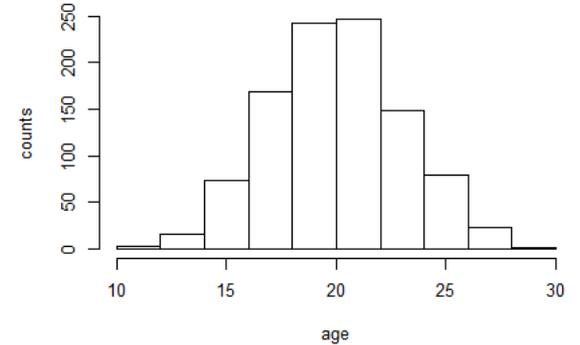
```
y <- seq(0.1, 1, by=0.1)
```

```
z <- y+rnorm(10, mean=0, sd=0.1)
```

```
plot(x, z, type="p", col="red", main="Plot")  
lines(x,y)
```



Histogram



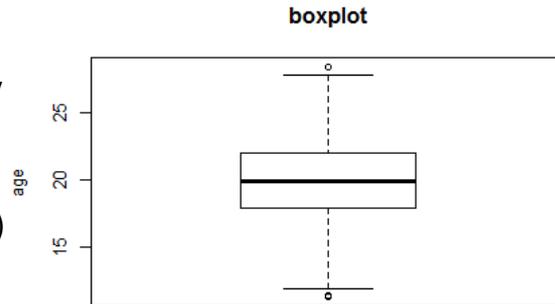
```
#graph 2: histogram
```

```
age <- rnorm(1000, mean=20, sd=3)
```

```
hist(age, main="Histogram", xlab="age", y
```

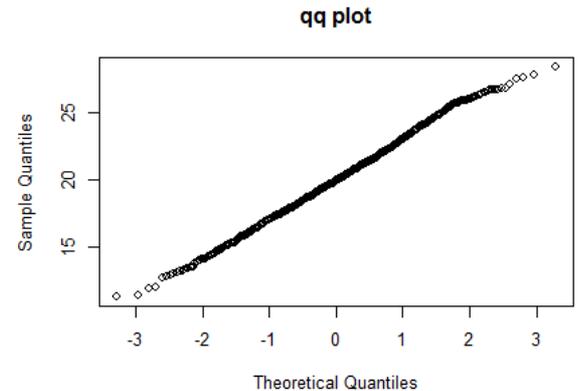
```
#graph 3: boxplot
```

```
boxplot(age, main="boxplot", ylab="age")
```



```
#graph 4: qq plot
```

```
qqnorm(age, main="qq plot")
```



Look it up!

Google

