#### R for Bioinformatics

Introduction, Programming, Data Analysis and Visualization
Introduction to Data Analysis and R

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## **Outline**

- Data Analysis
- Data Aanlysis and R
- Hello R!
- Development Environment
- S References

### Next

- Data Analysis
- Data Aanlysis and R
- Hello R!
- 4 Development Environment
- S References

# **Data Analysis**

#### Wikipedia

Analysis of data is a process of **inspecting**, **cleaning**, **transforming**, and **modeling** data with the goal of discovering useful information, suggesting conclusions, and supporting decision making.

#### **Data Analysis**

- Ollecting →
- ② Cleaning →
- $\odot$  Transforming  $\rightarrow$
- Modeling →
- **⑤** Visualizing →
- 6 Knowledge

#### **Biological Data Analysis**

- Sequencing →
- $QC \rightarrow$
- Alignment ...→
- **4** GWAS, EWAS ...→
- Manhattan Plot, Q-Q plot ...→
- Paper?

### Next

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## What is R?

#### R

R is a **free** software environment for statistical computing and graphics.

----R-project.org

#### **Data Analysis**

- Ollecting →
- $\bigcirc$  Cleaning  $\rightarrow$
- $\odot$  Transforming  $\rightarrow$
- Modeling →
- **⑤** Visualizing →
- 6 Knowledge

#### R

- Rcurl...
- gsub, unique...
- reshape...
- e1071...
- ggplot2...
- knitr...

# Biological Data Analysis and R

#### **Biological Data Analysis**

- $lue{1}$  Sequencing  $\rightarrow$
- $QC \rightarrow$
- Alignment ...→
- GWAS, EWAS ...
  →
- Manhattan Plot, Q-Q plot ...→
- Paper?

#### R

- Rsamtools, Affy...
- genomicRanges...
- reshape...
- e1071...
- ggbio...
- knitr, shiny...

# History

- Version 0.16, This is the last alpha version developed primarily by Ihaka and Gentleman. Much of the basic functionality from the "White Book" (see S history) was implemented. The mailing lists commenced on April 1, 1997.
- Version 0.49, April 23, 1997, This is the oldest available source release, and compiles on a limited number of Unix-like platforms. CRAN is started on this date, with 3 mirrors that initially hosted 12 packages. Alpha versions of R for Microsoft Windows and Mac OS are made available shortly after this version.
- Version 0.60, December 5, 1997, R becomes an official part of the GNU Project. The code is hosted and maintained on CVS.

# History

- Version 1.0.0, February 29, 2000, Considered by its developers stable enough for production use.[28]
- Version 1.4.0, S4 methods are introduced and the first version for Mac OS X is made available soon after.
- Version 2.0.0, October 4, 2004, Introduced lazy loading, which enables fast loading of data with minimal expense of system memory.
- Version 2.1.0, Support for UTF-8 encoding, and the beginnings of internationalization and localization for different languages.
- Version 2.11.0, April 22, 2010, Support for Windows 64 bit systems.
- Version 2.13.0, April 14, 2011, Adding a new compiler function that allows speeding up functions by converting them to byte-code.

# History

- Version 2.14.0, October 31, 2011, Added mandatory namespaces for packages. Added a new parallel package.
- Version 2.15.0, March 30, 2012, New load balancing functions. Improved serialization speed for long vectors.
- Version 3.0.0, April 3, 2013, Support for numeric index values 231 and larger on 64 bit systems.

### R in China

- 2004, official documents are translated into Chinese
- 2006, some books on R in Bioinformatics
- 2008, the first R conference was hold at Renming University, Beijing.
- 2009 to 2013, China R Conference is hold at Beijing and Shanghai each year.
- 2012, popular R books are translated into Chinese.
- 2013, R in Action ggplot2 R in a nutshell ...are published in China.
- 2013, CUHK-R course is launched.

# Applications of R

#### Applications '

- Statistical analysis
- Data Mining
- Life Science
- Business Intelligence
- Data Visualization
- Social Network

- eCommerce
- Integrated Circuit
- Financial
- Media
- Consoluting
- ...

# Attendee of R community































#### **Pros and Cons**

#### Bo Cowgill, Google

"The best thing about R is that it was developed by statisticians. The worst thing about R is that ... it was developed by statisticians."

### Next

- Data Analysis
- Data Aanlysis and R
- Hello R!
  - Hello R!
  - Hello Statistical Analysis!
  - Hello Plot!
- Development Environment
- References

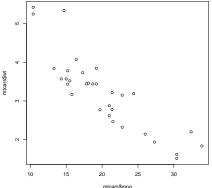
## Hello R!

```
print("Hello R!")
## [1] "Hello R!"
```

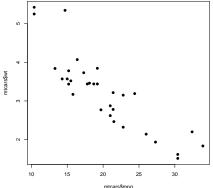
# **Hello Statistical Analysis**

```
data(mtcars)
cor(mtcars$mpg, mtcars$wt)
## [1] -0.8677
```

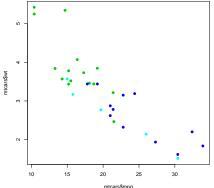
```
data(mtcars)
plot(mtcars$mpg, mtcars$wt)
```



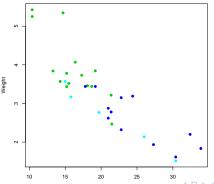
```
data(mtcars)
plot(mtcars$mpg, mtcars$wt, pch = 19)
```



```
data(mtcars)
plot(mtcars$mpg, mtcars$wt, pch = 19, col = mtcars$gear)
```

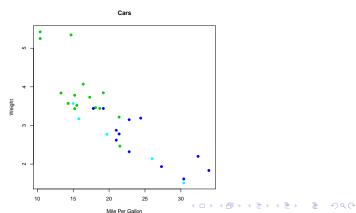


```
data(mtcars)
plot(mtcars$mpg, mtcars$wt, pch = 19, col = mtcars$gear, xlab = "Mi
    ylab = "Weight")
```

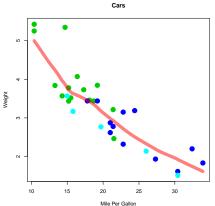


Mile Per Gallon

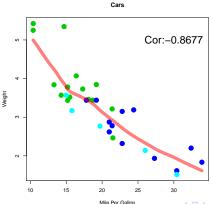
```
data(mtcars)
plot(mtcars$mpg, mtcars$wt, pch = 19, col = mtcars$gear, xlab = "Mi
    ylab = "Weight", main = "Cars")
```



```
data(mtcars)
plot(mtcars$mpg, mtcars$wt, pch = 19, col = mtcars$gear, xlab = "Mile Per Gallon",
    ylab = "Weight", main = "Cars", cex = 2)
lines(loess.smooth(mtcars$mpg, mtcars$wt), col = rgb(1, 0, 0, 0.5), lwd = 10)
```



```
data(mtcars)
plot(mtcars$mpg, mtcars$wt, pch = 19, col = mtcars$gear, xlab = "Mile Per Gallon",
    ylab = "Weight", main = "Cars", cex = 2)
lines(loess.smooth(mtcars$mpg, mtcars$wt), col = rgb(1, 0, 0, 0.5), lwd = 10)
text(30, 5, paste("Cor", round(cor(mtcars$mpg, mtcars$wt), 4), sep = ":"), cex = 2)
```



### Next

- Data Analysis
- Data Aanlysis and R
- 3 Hello R!
- Development Environment
  - Obtaining and installing R
  - R in Command Line
  - Editors and IDEs
- References

## Download and Installation

#### Download

# CRAN

#### Installation

- R: Linux(apt, yum), Mac OS, Windows
- Rtools: Windows
- packages: CRAN, devtools, github, local file

## **R** Commands

#### **R** Commands

R CMD command args

"command":

INSTALL Install add-on packages

**REMOVE** Remove add-on packages

**BATCH** Run R in batch mode

# **R Command Options**

#### **R Command Options**

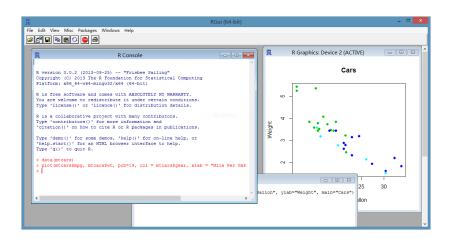
- -h, --help Print usage message and exit
- --version Print version information and exit
  - --save Do save workspace at the end of the session
- --no-save Don't save it
- --restore Do restore previously saved objects
- --no-restore Don't restore anything
  - --vanilla Combine --no-save, --no-restore,
    - --no-site-file, --no-init-file and --no-environ
- -f file, --file=file Take input from "file"
- -e expression Use 'exression' as input

## **Editors and IDEs**

#### **Editors**

- R terminal
- Rgui
- VIM + Vim-R-plugin
- Emacs + ESS
- Notepad++ + NppToR
- ..

# R Terminal and Rqui



# R Terminal and Rgui

#### R

- Ctrl + R: run
- Tab: auto complete
- arrow up and down: history

#### R and Texteditor

- copy and paste
- source("source.R")

#### source

```
sourceDir <- function(path, trace = TRUE, ...) {
  for (nm in list.files(path, pattern = "[.][RrSsQq]$")) {
    if (trace)
        cat(nm, ":")
    source(file.path(path, nm), ...)
    if (trace)
        cat("\n")
  }
}</pre>
```

```
R for Bioinformatics
```

Development Environment

Editors and IDEs

st.svg

7.R

ps\_and\_trick

as.matrix(d)[1:4,1:4]

## VIM + Vim-R-plugin

```
t2.R ZZZ.R RNA-Seq.R
                                                                           X q9 0.1416941
            x, Rowy = NULL, Colv = if (symm) "Rowy" else NULL, distfun, hclust g10 0.5772262 0.3061073
fmcsR-manual
fmcsR-manual
                                                                            > as.matrix(c)[1:4,1:4]
fmcsR-manual
Rdlatex.loa
                                                                                1,0000000 -0,7240061 0,8050921 0,2327069
            y <- matrix(rnorm(50), 10, 5, dimnames=list(paste("a", 1:10, sep="|q2 -0.7240061 1.0000000 -0.5586679 -0.7823333
package.Rche
00 pkg src/
             # Row clustering
                                                                               0.8050921 -0.5586679 1.0000000 0.2567203
            hr <- hclust(as.dist(1-cor(t(v), method="pearson")), method="compl a4
mypackage/
                                                                               0.2327069 -0.7823333 0.2567203 1.0000000
             # Column clustering
eecheck.log
eeinstall.ou
             nc <- hclust(as.dist(1-cor(v, method="spearman")), method="complet
                                                                                        til
                                                                                                   t2
mypackage-Ex
             ## Plot heatmap
                                                                                -0.2608109 -2.1287458 0.5436205 -0.1962956 0.5136432
mypackage-Ex
            heatmap.2(y, Rowy-as,dendrogram(hr), Coly-as,dendrogram(hc), scale a2
                                                                                -2.0478162 -0.2318061 -2.1907113 -0.9185012 -1.1459074
mypackage-Ex
            ## Return matrix with row/column sorting as in heatmap
                                                                                -0.1814785 -0.5137189 1.2004188 -0.2185163
/package/
            y[rev(hr$labels[hr$order]), hc$labels[hc$order]]
                                                                                 0.2493454 -0.5782053
                                                                                                      0.7562372 -0.6441311 -1.0792957
            heat.colors
mon/
                                                                                 0.1082261 -1.8310231 -0.3319702 0.5535095
I-colAg.Rd
            heat.colors function arDevices
                                                                                 0.2596634 -0.8048402 -0.3751721 -0.6061271 -1.4533725
-mypackage-
                        function stats
                                           ample
                                                                                 0.4497986 -0.6475571
             fmcs(sdfset[[1]], sdfset[[2]], fast=T)
                                                                                 -1.0501454 -0.3717143 0.2831488 -1.6238084
             result <- fmcs(sdfset[[1]], sdfset[[2]])
-myfct.R
                                                                                -0.7831244 0.8490208 1.1253892 -0.4341535 0.691246S
            mcs <- fmcs(sdfset[[1]], sdfset[[2]], au=2, bu=1, matching.mode="a| q10 -1.7273262 0.3621398 2.2920425 -0.9175735 -1.6735589
DESCRIPTION
NAMESPACE
            script2.R F+1
Read-and-del
                                                                         339/5
icsR 1.0.tar
                                                                                                    package:aplots
tter.pnq
                                                                            heatmap.2
                                                                                                                                  R Documente
             ______
trix.xls
fct.R
             ## code chunk number 3: dist2
             ................
package_1.0
                                                                            Enhanced Heat Map
tes.R
              <- cor(t(v), method="pearson")
verLapper.R
            as.matrix(c)[1:4,1:4]
                                                                            Description:
angeoverlappe
                                                                                 A heat map is a false color image (basically 'image(t(x))')
M-Seq.R
ript1.R
                                                                             a
ript2.R
             ## code chunk number 4: dist2
                                                                                 dendrogram added to the left side and/or to the top. Typica
Fstreamer.R
             .................
                                                                                 reordering of the rows and columns according to some set of
st.sdf
            d <- as.dist(1-c)
                                                                            es
```

(row or column means) within the restrictions imposed by the

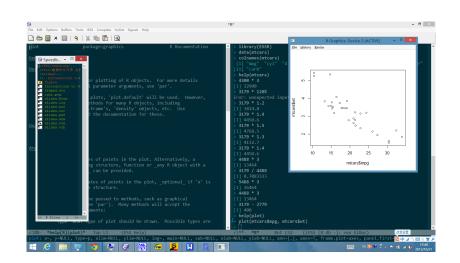
dendrogram is carried out.

# Notepad++ + NppToR

```
*C:\Program Files\Notepad++\test.r - Notepad++
                                                                                File Edit Search View Encoding Language Settings Macro Run TextFX Plugins Window ?
  test.r
      A=matrix(c(1,2,3,3,4,3,2,1,1),3,3)
      b=c(3,2,1)
     x=solve(A,b)
User Define 57 chars 65 bytes 5 lines
                                Ln:1 Col:1 Sel:0(0 bytes) in 0 ranges
                                                                Dos\Windows
                                                                        ANSI
                                                                                   INS
```

**Editors and IDEs** 

### Emacs + ESS



### Emacs + ESS

#### What is ESS?

Emacs Speaks Statistics (ESS) is an add-on package for emacs text editors such as **GNU Emacs** and XEmacs. It is designed to support editing of scripts and interaction with various statistical analysis programs such as **R**, S-Plus, SAS, Stata and JAGS.

#### **ESS** Website

http://ess.r-project.org/

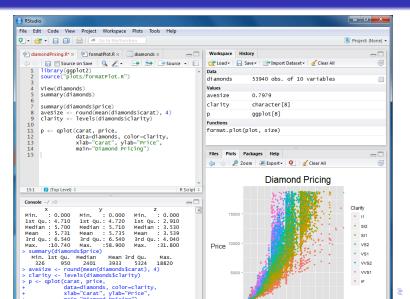
## **IDEs**

#### **IDEs**

- RStudio: local and cloud-based
- TinnR
- StatET: eclipse for R
- ..

Editors and IDEs

## **RStudio**



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#### **Books**

- R in action (also in Chinese)
- Introduction to R (also in Chinese)
- R for beginner (also in Chinese)
- R in a Nutshell (Chinese version is in press)
- The art of R programming (also in Chinese)
- ggplot2. Elegant Graphics for Data Analysis (also in Chinese)

## Websites

- R-project and CRAN
- COS.name (Chinese)
- Quick-R
- http://had.co.nz/, Hadley Wickham
- Twitter, github, RForge
- Google

## Websites

- R-project and CRAN
- COS.name (Chinese)
- Quick-R
- http://had.co.nz/, Hadley Wickham
- Twitter, github, RForge
- Google Baidu?

#### **Journals**

- The R Journal
- Journal of Statistical Software
- BMC Bioinformatics: Software
- Bioinformatics: Application Note