BST02: Using R for Statistics in Medical Research

Part B: Basic use of R

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Basic Use of R

In this Section

- Using R
- Examples with Data
- Getting Familiar with R
- Importing data and saving your work
- A lot of practice

Using R

- R is a command-based procedural language
  - write and execute commands
  - use and define functions
- You may write the commands in the R console (Windows) or in a shell (Linux)

You will become more familiar with the syntax as you use it

Using R

- Strongly advisable to use a suitable text editor - Some available options:
  - RWinEdt (for Windows; you also need WinEdt installed)
  - Tinn-R (for Windows; http://sciviews.org/Tinn-R/)
  - Rkward (for Linux)
  - Emacs (w. ESS, all platforms)
  - Visual Studio (for Windows)
  - Rstudio (all major platforms; http://www.rstudio.org/)
  - for more check https://r-dir.com/blog/2013/01/list-of-r-editors.html

Using R

- For this course: Rstudio (http://www.rstudio.org/)
  - free
  - works fine in Windows, MacOS and Linux
  - helpful with errors
  - alternative output options

Using R

- Can I use R without Rstudio?
- Can I use Rstudio without R?

Practical Examples

- **Package `survival` - pbc data set**

id	time	status	trt	age	sex	bili	chol
1	400	2	1	58.76523	f	14.5	261
2	4500	0	1	56.44627	f	1.1	302
3	1012	2	1	70.07255	m	1.4	176
4	1925	2	1	54.74059	f	1.8	244
5	1504	1	2	38.10541	f	3.4	279

Practical Examples

- **id**: case number
- **time**: number of days between registration and the earlier of death, transplantation, or study analysis in July, 1986
- **status**: status at endpoint, 0/1/2 for censored, transplant, dead
- **trt**: 1/2/NA for D-penicillamine, placebo, not randomised
- **age**: in years
- **sex**: m/f
- **bili**: serum bilirunbin (mg/dl)
- **chol**: serum cholesterol (mg/dl)

More details:
https://stat.ethz.ch/R-manual/R-devel/library/survival/html/pbc.html

Practical Examples

- What is a **scalar**/vector/matrix

id	time	status	trt	age	sex	bili	chol	dt
1	400	2	1	58.76523	f	14.5	261	1
2	4500	0	1	56.44627	f	1.1	302	2
3	1012	2	1	**70.07255**	m	1.4	176	3
4	1925	2	1	54.74059	f	1.8	244	4
5	1504	1	2	38.10541	f	3.4	279	5

Practical Examples

- What is a scalar/**vector**/matrix

id	time	status	trt	age	sex	bili	chol
1	400	**2**	1	58.76523	f	14.5	261
2	4500	**0**	1	56.44627	f	1.1	302
3	1012	**2**	1	70.07255	m	1.4	176
4	1925	**2**	1	54.74059	f	1.8	244
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Practical Examples

- What is a scalar/**vector**/matrix

id	time	status	trt	age	sex	bili	chol
1	**400**	2	1	58.76523	f	14.5	261
2	**4500**	0	1	56.44627	f	1.1	302
3	**1012**	2	1	70.07255	m	1.4	176
4	**1925**	2	1	54.74059	f	1.8	244
5	**1504**	1	2	38.10541	f	3.4	279

Practical Examples

- What is a scalar/vector/**matrix**

id	time	status	trt	age	sex	bili	chol
1	**400**	**2**	1	58.76523	f	14.5	261
2	**4500**	**0**	1	56.44627	f	1.1	302
3	**1012**	**2**	1	70.07255	m	1.4	176
4	**1925**	**2**	1	54.74059	f	1.8	244
5	**1504**	**1**	2	38.10541	f	3.4	279

Practical Examples

- What is a scalar/vector/**matrix**

id	time	status	trt	age	sex	bili	chol
1	400	2	1	58.76523	f	**14.5**	**261**
2	4500	0	1	56.44627	f	**1.1**	**302**
3	1012	2	1	70.07255	m	**1.4**	**176**
4	1925	2	1	54.74059	f	**1.8**	**244**
5	1504	1	2	38.10541	f	**3.4**	**279**

Practical Examples

- Common questions
  - What is the average age?
  - What is the average serum bilirubin?
  - What is the average serum cholesterol?
  - What is the percentage of females?
  - How many missing values do we have for serum cholesterol?

All these questions can be answered using R!

Getting Familiar with R

- Elementary commands: **expressions** and **assignments**
- An **expression** given as command is evaluated printed and discarded
- An **assignment** evaluates an expression and passes the value to a variable - the result is not automatically printed

Getting Familiar with R

Expression is given as a command,

```r
103473
```

```
[1] 103473
```

- However, it cannot be viewed again unless the command is rerun.

Getting Familiar with R

Expression is given as a command,

```r
103473
```

```
[1] 103473
```

- However, it cannot be viewed again unless the command is rerun.

In order to store information, the expression should assign the command

```r
x <- 103473
x
```

```
[1] 103473
```

Getting Familiar with R

You can use R as a calculator!

- Basic arithmetics

```
+, -, *, /, ^
```

```
y <- 103473 + 100000
y
```

```
[1] 203473
```

- Complicated arithmetics

Getting Familiar with R

Tips:

- R is case sensitive, e.g.,
  - **"sex"** is different than **"Sex"**
- Commands are separated by a semi-colon or by a newline
- Comments can be put anywhere, starting with a hashmark **#**: everything to the end of the line is a comment
- Assign a value to an object by **<-** or **=**
- Working directory: get with **getwd()** and set with **setwd()**

Getting Familiar with R

- Missing values
  - are coded as **NA** (i.e., not available) **is.na()**
- Infinity
  - is coded as **Inf** (plus infinity) or **-Inf** (minus infinity) **is.finite()**
- The Null objects
  - are coded as **NULL** (undefined) **is.null()**
- Not a number
  - is coded as **NaN** (Not a Number). Example:

```
0/0
```

```
[1] NaN
```

Importing Data

- function: **read.table()**, **read.csv()** and its variants
  - note: use forward slashes or double backward slashes in the file names, e.g.,
    "`C:/Documents and Settings/User/Data/file.txt`" or
    "`C:\\Documents and Settings\\User\\Data\\file.txt`"

- Specialized functions for importing data from other programs
  - package: **foreign**, function: **read.spss()**, **read.dta()**
  - package: **Hmisc**, function: **sas.get()**
  - package: **openxlsx**, function: **read.xlsx()**
  - package: **readxl**, function: **read_excel()**
  - package: **haven**, function: **read_spss()**
  - *etc*

Exporting Data

- Specialized functions for exporting data to other programs
  - function: **write.table()**, **write.csv()**
  - package: **foreign**, function: **write.spss()**, **write.dta()**
  - package: **openxlsx**, function: **write.xlsx()**
  - *etc*

Saving and Loading your Work

Multiple objects:

- You can save your R objects using **save()**
  - be careful about overwriting
- You can load your saved R objects using **load()**

Single object:

- Using **saveRDS()** you can save a single R object
- Using **readRDS()** you can load a single R object
  - we will need an assignment statement to store the results

Save your code by using the tab File in Rstudio!

Saving and Loading your Work

Tips:

- Short names are preferred over longer names
- Try to avoid using names that contain symbols
- Avoid spaces in names
- Remove any comments in your data set
- Make sure that any missing values in your data set are indicated with the same value (or no value)

Summary

Basic functions

- `getwd()`, `setwd()`,
- `is.na()`, `is.finite()`, `is.null()`

Import/Export

- `read.csv()`, `write.csv()`
- `read.xlsx()`, `write.xlsx()`
- `read.table()`, `write.table()`

Save/Load

- `save()`, `saveRDS()`
- `load()`, `readRDS()`

Practice

Demos

- Basic R R html
- Importing and Saving R html

Practicals

- Importing and Saving html

Common Objects in R

In this Section

- Objects in R
- Data types
- Data structures
- A lot of practice

Objects in R

- In R Everything (data, results, ...) is an object
- In order to list the created objects use the following functions

```r
objects()
ls()
```

Objects in R

- In R Everything (data, results, ...) is an object
- In order to list the created objects use the following functions

```r
objects()
ls()
```

- In order to remove objects

```r
rm()
rm(list=ls(all=TRUE))
```

Objects in R

- To investigate a specific object (e.g. pbc)

```r
str(pbc[,c("id", "time", "status", "trt", "age", "sex", "bili", "chol")])
```

```
'data.frame':   418 obs. of  8 variables:
 $ id    : int  1 2 3 4 5 6 7 8 9 10 ...
 $ time  : int  400 4500 1012 1925 1504 2503 1832 2466 2400 51 ...
 $ status: int  2 0 2 2 1 2 0 2 2 2 ...
 $ trt   : int  1 1 1 1 2 2 2 2 1 2 ...
 $ age   : num  58.8 56.4 70.1 54.7 38.1 ...
 $ sex   : Factor w/ 2 levels "m","f": 2 2 1 2 2 2 2 2 2 2 ...
 $ bili  : num  14.5 1.1 1.4 1.8 3.4 0.8 1 0.3 3.2 12.6 ...
 $ chol  : int  261 302 176 244 279 248 322 280 562 200 ...
```

Data Types

The simplest data types are:

- **numeric** : quantitative data
- **character** : qualitative data
- **integer** : whole numbers
- **logical** : TRUE or FALSE
- **factors** : qualitative data (levels)

Data Types in R

To find out what type of object you have, you can use the following function

```r
mode(pbc$age)
```

```
[1] "numeric"
```

```r
str(pbc$age)
```

```
 num [1:418] 58.8 56.4 70.1 54.7 38.1 ...
```

Data Structures

The most important data structures are:

- **Scalar** a single element
- **Vectors** have the same type of elements
- **Matrices** have the same type of elements with the same length
- **Arrays** have the same type of elements with the same length but can store the data in more than two dimensions
- **Data frames** have elements of different type with the same length
- **Lists** have elements of different type and length

Data Structures

How do these data structures look like?

Data Structures

- Differences between **vector**, matrix, array, data.frame and list

```
pbc[1:6, c("age")]
```

```
[1] 58.76523 56.44627 70.07255 54.74059 38.10541 66.25873
```

Data Structures

- Differences between vector, **matrix**, array, data.frame and list

```
pbc[1:6, c("age", "bili", "chol")]
```

```
       age bili chol
1 58.76523 14.5  261
2 56.44627  1.1  302
3 70.07255  1.4  176
4 54.74059  1.8  244
5 38.10541  3.4  279
6 66.25873  0.8  248
```

Data Structures

- Differences between vector, matrix, **array**, data.frame and list

```
pbc[1:3, c("age", "bili", "chol")]
```

```
       age bili chol
1 58.76523 14.5  261
2 56.44627  1.1  302
3 70.07255  1.4  176
```

```
pbc[4:6, c("age", "bili", "chol")]
```

```
       age bili chol
4 54.74059  1.8  244
5 38.10541  3.4  279
6 66.25873  0.8  248
```

Data Structures

- Differences between vector, matrix, **array**, data.frame and list

```
pbc[1:2, c("protime", "time")]
```

```
  protime time
1    12.2  400
2    10.6 4500
```

```
pbc[3:4, c("protime", "time")]
```

```
  protime time
3    12.0 1012
4    10.3 1925
```

Data Structures

- Differences between vector, matrix, array, **data.frame** and list

```
pbc[1:6, c("id", "sex", "bili", "chol")]
```

```
  id sex bili chol
1  1   f 14.5  261
2  2   f  1.1  302
3  3   m  1.4  176
4  4   f  1.8  244
5  5   f  3.4  279
6  6   f  0.8  248
```

Data Structures

- Differences between vector, matrix, array, data.frame and **list**

```r
pbc[1:6, c("sex")]
```

```
[1] f f m f f f
Levels: m f
```

```r
pbc[1:2, c("sex", "bili")]
```

```
  sex bili
1   f 14.5
2   f  1.1
```

```r
pbc[1:4, c("age")]
```

```
[1] 58.76523 56.44627 70.07255 54.74059
```

Data Structures in R

Let’s now create different data structure in R!

Data Structures in R

Create a vector

```r
vec <- c(1, 2, 3, 4, 5)
vec
```

```
[1] 1 2 3 4 5
```

```r
vec <- c(1:5)
vec
```

```
[1] 1 2 3 4 5
```

Data Structures in R

Create a matrix

```r
vec <- c(1, 2, 3, 4, 5, 6, 7, 8, 9)
mat <- matrix(data = vec,
              nrow = 3, ncol = 3)
mat
```

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

Data Structures in R

Create a matrix

```
vec <- c(1, 2, 3, 4, 5, 6, 7, 8, 9)
mat <- matrix(data = vec,
              nrow = 3, ncol = 3)
mat
```

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

```
vec <- c(1, 2, 3, 4, 5, 6, 7, 8, 9)
mat <- matrix(data = vec,
              nrow = 3, ncol = 3,
              byrow = TRUE)
mat
```

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

Data Structures in R

Create an array

```r
ar <- array(data = c(1, 2, 3, 4, 5, 6, 7, 8), dim = c(2, 2, 2))
ar
```

```
, , 1

     [,1] [,2]
[1,]    1    3
[2,]    2    4

, , 2

     [,1] [,2]
[1,]    5    7
[2,]    6    8
```

Data Structures in R

Create an array

```r
ar <- array(data = c(1, 2, 3, 4), dim = c(2, 2, 1))
ar
```

```
, , 1

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

Data Structures in R

Create a data frame

```
dtf <- data.frame(pbc[, "sex"],
                  pbc[, "age"])
dtf[1:3,]
```

```
  pbc....sex.. pbc....age..
1            f     58.76523
2            f     56.44627
3            m     70.07255
```

Data Structures in R

Create a data frame

```
dtf <- data.frame(pbc[, "sex"],
                  pbc[, "age"])
dtf[1:3,]
```

```
  pbc....sex.. pbc....age..
1            f     58.76523
2            f     56.44627
3            m     70.07255
```

```
dtf <- data.frame(Gender = pbc[, "sex"],
                  Age = pbc[, "age"])
dtf[1:3,]
```

```
  Gender      Age
1      f 58.76523
2      f 56.44627
3      m 70.07255
```

Data Structures in R

Create a list

```
list1 <- list(vec = c(1:5), mat = pbc[1:2, c("age", "sex")])
list1
```

```
$vec
[1] 1 2 3 4 5

$mat
       age sex
1 58.76523   f
2 56.44627   f
```

Summary

Data types

- `numeric`
- `character`
- `integer`
- `logical`
- `factors`
- `str()`, `mode()`

Data structures

- `c()`
- `matrix()`
- `array()`
- `data.frame()`
- `list()`

Other

- `ls()`, `objects()`

Practice

Demos

- Common R Objects R html

Practicals

- Common R Objects html

Indexing and Subsetting

In this Section

- Indexing
- Subsetting
- A lot of practice

Indexing/Subsetting

- When transforming and analyzing data we often need to select specific observations or variables
  - Examples: Select …
    - the 3rd element of vector age
    - the 3rd column of the pbc data set
    - the sex of the 10th patient
    - all information of the 5th patient
    - the serum cholesterol for all males
    - the age for male patients or patients that have serum bilirubin > 3
    - the first measurement per patient

Indexing/Subsetting

- This can be done using square bracket (**[ ]**) notation and indices.
- Three basic types
    - position indexing
    - logical indexing
    - name indexing

Vectors

Indexing with `vector`

- For position indexing, use a **positive** value to select an element

```
x <- c(6:17)
x
```

```
 [1]  6  7  8  9 10 11 12 13 14 15 16 17
```

```
x[2]
```

```
[1] 7
```

- Use multiple positive values to select multiple elements

```
x[c(2,3,4)]
```

```
[1] 7 8 9
```

Vectors

Indexing with `vector`

- For position indexing, use duplicated **positive** values to select the same elements

```r
x <- c(6:17)
x
```

```
 [1]  6  7  8  9 10 11 12 13 14 15 16 17
```

```r
x[c(2,2,2)]
```

```
[1] 7 7 7
```

Vectors

Indexing with `vector`

- For position indexing, use a **negative** value to remove an element

```r
x <- c(6:17)
x
```

```
 [1]  6  7  8  9 10 11 12 13 14 15 16 17
```

```r
x[-5]
```

```
 [1]  6  7  8  9 11 12 13 14 15 16 17
```

- **Positive and negative indices cannot be combined**

Vectors

Indexing with `vector`

- Use logical index of the same length to select elements where the value is **TRUE**

```
x <- c(6:10)
y <- c(TRUE, FALSE, FALSE, FALSE, FALSE)
x[y]
```

```
[1] 6
```

Vectors

Indexing with `vector`

- Use logical indexing in combination with conditions

```
x <- c(6:10)
x[x > 7]
```

```
[1]  8  9 10
```

```
x[x > 7 & x > 9]
```

```
[1] 10
```

```
x[x > 7 | x > 9]
```

```
[1]  8  9 10
```

Vectors

Indexing with `vector`

- For name/character indexing, use the name of the element

```
x <- c(foo=5, bar=4, one=7, two=12, three=2)
x[c('foo', 'one')]
```

```
foo one
  5   7
```

- Use the function `names` to obtain the names

Matrices

Indexing with `matrix`

- Indexing matrices is similar to indexing vectors but with double index
  - The first position denotes the rows **["index",]**
  - The first position denotes the columns **[, "index"]**

Matrices

Indexing with `matrix`

- Indexing matrices is similar to indexing vectors but with double index
  - The first position denotes the rows **["index",]**
  - The first position denotes the columns **[, "index"]**

```
mat <- matrix(data = 1:4,
              nrow = 2, ncol = 2)
mat
```

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

- Use position indexing as:

```
mat <- matrix(data = 1:4,
              nrow = 2, ncol = 2)
mat[2, 2]
```

```
[1] 4
```

Matrices

Indexing with `matrix`

- Be cautious, it also works with a single index. In this case, it selects the particular element of the vector that will be included in the matrix

```
mat <- matrix(data = 1:4,
              nrow = 2, ncol = 2)
mat[2]
```

```
[1] 2
```

```
mat[[2]]
```

```
[1] 2
```

Matrices

Indexing with `matrix`

- When we leave a position blank all elements are selected

```r
mat <- matrix(data = 1:4,
              nrow = 2, ncol = 2)
mat
```

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

```r
mat[2, ]
```

```
[1] 2 4
```

Arrays

Indexing with `array`

```r
ar <- array(data = 1:4,
            dim = c(1,2,2))
ar
```

```
, , 1

     [,1] [,2]
[1,]    1    2

, , 2

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

```r
ar[1, 1, ]
```

```
[1] 1 3
```

Data Frames

Indexing with `data.frame`

- Works with single and double index

```r
DF <- data.frame(x = 1:3,
          y = c("male", "male", "female"))
DF
```

```
  x      y
1 1   male
2 2   male
3 3 female
```

Data Frames

Indexing with `data.frame`

- Works with single and double index

```
DF <- data.frame(x = 1:3,
                 y = c("male", "male", "female"))
DF
```

```
  x      y
1 1   male
2 2   male
3 3 female
```

- Use position single indexing

```
DF[2]
```

```
       y
1   male
2   male
3 female
```

```
DF[[2]]
```

```
[1] "male"   "male"   "female"
```

Data Frames

Indexing with `data.frame`

- When using double index, indexing works like a matrix

```
DF <- data.frame(x = 1:3,
         y = c("male", "male", "female"))
DF
```

```
  x      y
1 1   male
2 2   male
3 3 female
```

- Use position indexing

```
DF[2, ]
```

```
  x    y
2 2 male
```

- Use logical indexing

```
DF[DF$x < 2, ]
```

```
  x    y
1 1 male
```

Data Frames

Indexing with `data.frame`

- **$** provides a convenient notation to extract an element by name

```
head(pbc$time)
```

```
[1]  400 4500 1012 1925 1504 2503
```

```
head(pbc[ ,"time"])
```

```
[1]  400 4500 1012 1925 1504 2503
```

Data Frames

Indexing with `data.frame`

- Combine logical and position indexing in data frame

```r
head(pbc[pbc$sex == "m", 1:7])
```

```
   id time status trt      age sex ascites
3   3 1012      2   1 70.07255   m       0
14 14 1217      2   2 56.22177   m       1
21 21 3445      0   2 64.18891   m       0
24 24 4079      2   1 44.52019   m       0
48 48 4427      0   2 49.13621   m       0
52 52 2386      2   1 50.54073   m       0
```

Data Frames

Indexing with `data.frame`

- Combine logical and position indexing in data frame

```r
head(pbc[pbc$age > 30 | pbc$sex == "f", 1:7])
```

```
  id time status trt      age sex ascites
1  1  400      2   1 58.76523   f       1
2  2 4500      0   1 56.44627   f       0
3  3 1012      2   1 70.07255   m       0
4  4 1925      2   1 54.74059   f       0
5  5 1504      1   2 38.10541   f       0
6  6 2503      2   2 66.25873   f       0
```

Data Frames

Indexing with `data.frame`

- Combine logical and position indexing in data frame

```r
head(pbc[pbc$age > 30 & pbc$sex == "f", 1:7])
```

```
  id time status trt      age sex ascites
1  1  400      2   1 58.76523   f       1
2  2 4500      0   1 56.44627   f       0
4  4 1925      2   1 54.74059   f       0
5  5 1504      1   2 38.10541   f       0
6  6 2503      2   2 66.25873   f       0
7  7 1832      0   2 55.53457   f       0
```

Lists

Indexing with `list`

- Lists can be subsetted in the same way as vectors using single brackets - Note that the output is a list

- Use position indexing

```r
mylist <- list(y = c(14, 45), z = c("m", "f", "f"))
mylist[2]
```

```
$z
[1] "m" "f" "f"
```

Lists

Indexing with `list`

- Double square brackets can be also used - Note that the output is a vector

- Use position indexing

```
mylist <- list(y = c(14, 45), z = c("m", "f", "f"))
mylist[[2]]
```

```
[1] "m" "f" "f"
```

Lists

Indexing with `list`

- **$** provides a convenient notation to extract an element by name - Note that the output is a vector

```r
mylist <- list(y = c(14, 45), z = c("m", "f", "f"))
mylist
```

```
$y
[1] 14 45

$z
[1] "m" "f" "f"
```

```r
mylist$y
```

```
[1] 14 45
```

Summary

Vectors

- `[]`
- `[""]` - for categorical variables

Matrices

- `[,]`
- `[[]], []`

Arrays

- `[ , , ]`

Data frames

- `[,]`
- `[[]], []`
- `$`

Lists

- `[]`
- `[[]]`
- `$`

Practice

- Use the following webpage to further investigate indexing and subsetting
  https://emcbiostatistics.shinyapps.io/indexing/

Demos

- Shiny app indexing subsetting R

In order to run the app you will need to install the packages:

- `survival`
- `shiny`

Practice

Demos

- Indexing/Subsetting R html

Practicals

- Indexing/Subsetting html

Data Transformation Exploration Visualization

In this Section

- Data transformation
- Data exploration
- Data visualization
- A lot of practice

Data Transformation

You will never receive the perfect data set!

- **Round** continuous variables
- Convert **numeric** variables to **factors**
- Compute **new variables**
  - transform variables
- **Sort** the data set
- Data sets of **wide** $\Longleftrightarrow$ **long** format

Data Transformation

- **Round** continuous variables

```
pbc[1:3, c("time", "age", "bili", "chol")]
```

```
  time      age bili chol
1  400 58.76523 14.5  261
2 4500 56.44627  1.1  302
3 1012 70.07255  1.4  176
```

```
round(pbc[1:3, c("time", "age", "bili", "chol")], digits = 2)
```

```
  time   age bili chol
1  400 58.77 14.5  261
2 4500 56.45  1.1  302
3 1012 70.07  1.4  176
```

Data Transformation

- Convert **numeric** variables to **factors**

```r
DF <- pbc[,c("id", "time", "status", "trt", "age",
                    "sex", "bili", "chol")]
head(DF)
```

```
  id time status trt      age sex bili chol
1  1  400      2   1 58.76523   f 14.5  261
2  2 4500      0   1 56.44627   f  1.1  302
3  3 1012      2   1 70.07255   m  1.4  176
4  4 1925      2   1 54.74059   f  1.8  244
5  5 1504      1   2 38.10541   f  3.4  279
6  6 2503      2   2 66.25873   f  0.8  248
```

Data Transformation

- Convert **numeric** variables to **factors**

```
DF <- pbc[,c("id", "time", "status", "trt", "age",
                    "sex", "bili", "chol")]
DF$trt <- factor(x = DF$trt, levels = c(1, 2),
                 labels = c("D-penicillmain", "placebo"))
head(DF)
```

```
  id time status            trt      age sex bili chol
1  1  400      2 D-penicillmain 58.76523   f 14.5  261
2  2 4500      0 D-penicillmain 56.44627   f  1.1  302
3  3 1012      2 D-penicillmain 70.07255   m  1.4  176
4  4 1925      2 D-penicillmain 54.74059   f  1.8  244
5  5 1504      1        placebo 38.10541   f  3.4  279
6  6 2503      2        placebo 66.25873   f  0.8  248
```

Data Transformation

- Compute **new variables**
  - transform variables

```
DF <- pbc[,c("id", "time", "status", "trt", "age",
                    "sex", "bili", "chol")]
head(DF)
```

```
  id time status trt      age sex bili chol
1  1  400      2   1 58.76523   f 14.5  261
2  2 4500      0   1 56.44627   f  1.1  302
3  3 1012      2   1 70.07255   m  1.4  176
4  4 1925      2   1 54.74059   f  1.8  244
5  5 1504      1   2 38.10541   f  3.4  279
6  6 2503      2   2 66.25873   f  0.8  248
```

Data Transformation

- Compute **new variables**
  - transform variables

```
DF <- pbc[,c("id", "time", "status", "trt", "age",
                    "sex", "bili", "chol")]
DF$time <- DF$time/30
DF$time_years <- DF$time/12
head(DF)
```

```
  id      time status trt      age sex bili chol time_years
1  1  13.33333      2   1 58.76523   f 14.5  261   1.111111
2  2 150.00000      0   1 56.44627   f  1.1  302  12.500000
3  3  33.73333      2   1 70.07255   m  1.4  176   2.811111
4  4  64.16667      2   1 54.74059   f  1.8  244   5.347222
5  5  50.13333      1   2 38.10541   f  3.4  279   4.177778
6  6  83.43333      2   2 66.25873   f  0.8  248   6.952778
```

Data Transformation

- **Sort** the data set in either ascending or descending order
    - The variable by which we sort can be a numeric, string or factor

```r
head(sort(pbc$bili))
```

```
[1] 0.3 0.3 0.3 0.4 0.4 0.4
```

Data Transformation

- **Sort** the data set in either ascending or descending order
  - The variable by which we sort can be a numeric, string or factor

```r
head(pbc[order(pbc$bili), ])
```

```
     id time status trt      age sex ascites hepato spiders edema bili chol albumin copper
8     8 2466      2   2 53.05681   f       0      0       0     0  0.3  280    4.00     52
36   36 3611      0   2 56.41068   f       0      0       0     0  0.3  172    3.39     18
163 163 2055      2   1 53.49760   f       0      0       0     0  0.3  233    4.08     20
84   84 4032      0   2 55.83025   f       0      0       0     0  0.4  263    3.76     29
108 108 2583      2   1 50.35729   f       0      0       0     0  0.4  127    3.50     14
135 135 3150      0   1 42.96783   f       0      0       0     0  0.4  263    3.57    123
```

Data Transformation

- **Sort** the data set in either ascending or descending order
  - The variable by which we sort can be a numeric, string or factor

```r
head(pbc[order(pbc$bili, pbc$age), ])
```

```
     id time status trt      age sex ascites hepato spiders edema bili chol albumin copper
8     8 2466      2   2 53.05681   f       0      0       0   0.0  0.3  280    4.00     52
163 163 2055      2   1 53.49760   f       0      0       0   0.0  0.3  233    4.08     20
36   36 3611      0   2 56.41068   f       0      0       0   0.0  0.3  172    3.39     18
135 135 3150      0   1 42.96783   f       0      0       0   0.0  0.4  263    3.57    123
320 320 2403      0  NA 44.00000   f      NA     NA      NA   0.5  0.4   NA    3.81     NA
168 168 2713      0   2 47.75359   f       0      1       0   0.0  0.4  257    3.80     44
```

Data Transformation

- Data sets of **wide** $\Longleftrightarrow$ long format

```
head(pbc[,c("id", "time", "status", "trt", "age",
                         "sex", "bili", "chol")])
```

```
  id time status trt      age sex bili chol
1  1  400      2   1 58.76523   f 14.5  261
2  2 4500      0   1 56.44627   f  1.1  302
3  3 1012      2   1 70.07255   m  1.4  176
4  4 1925      2   1 54.74059   f  1.8  244
5  5 1504      1   2 38.10541   f  3.4  279
6  6 2503      2   2 66.25873   f  0.8  248
```

Data Transformation

- Data sets of wide $\Longleftrightarrow$ **long** format

```r
head(pbcseq[, c("id", "futime", "status", "trt", "age", "day",
                      "sex", "bili", "chol")])
```

```
  id futime status trt      age day sex bili chol
1  1    400      2   1 58.76523   0   f 14.5  261
2  1    400      2   1 58.76523 192   f 21.3   NA
3  2   5169      0   1 56.44627   0   f  1.1  302
4  2   5169      0   1 56.44627 182   f  0.8   NA
5  2   5169      0   1 56.44627 365   f  1.0   NA
6  2   5169      0   1 56.44627 768   f  1.9   NA
```

Data Transformation

- Data sets of **wide** $\Longleftrightarrow$ **long** format

```
?reshape
```

Data Exploration

- Common questions for the pbc data set
  - What is the mean and standard deviation for age?
  - What is the mean and standard deviation for time?
  - What is the median and interquartile range for age?
  - What is the percentage of placebo patients?
  - What is the percentage of females?
  - What is the mean and standard deviation for age in males?
  - What is the mean and standard deviation for baseline serum bilirubin?
  - What is the percentage of missings in serum bilirubin?

All these questions can be answered using R!

Data Exploration

- **Hints**
- Check functions: **mean(...)**, **sd(...)**, **percent(...)**, **median(...)**, **IQR(...)**, **table(...)**

Data Exploration

- **Hints**

- Check functions: **mean(...)**, **sd(...)**, **percent(...)**, **median(...)**, **IQR(...)**, **table(...)**

What is the mean value for age?

```r
mean(pbc$age)
```

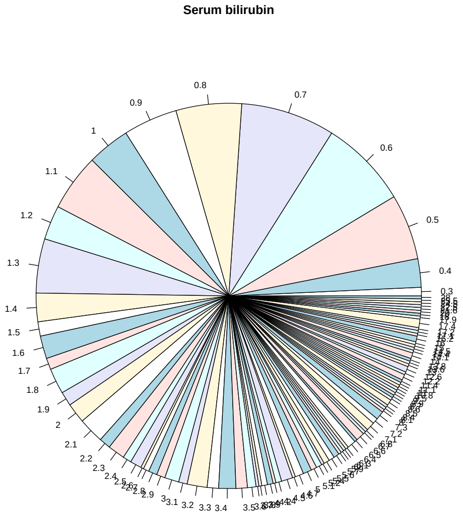
```
[1] 50.74155
```

Data Visualization

- It is important to investigate each variable in our data set using plots
  - Descriptive statistics for continuous and categorical variables
  - Distributions of variables
  - Distributions of variables per group
  - Extreme values
  - Linear/nonlinear evolutions

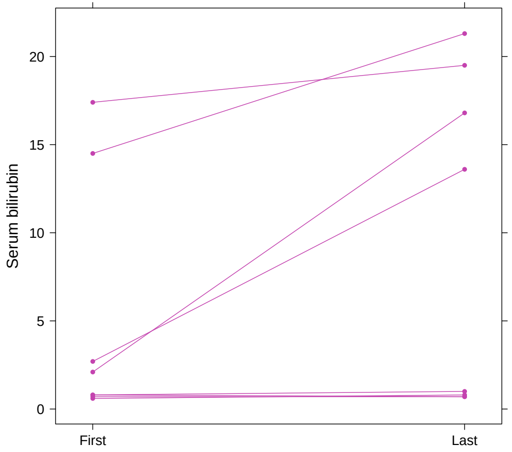
Data Visualization

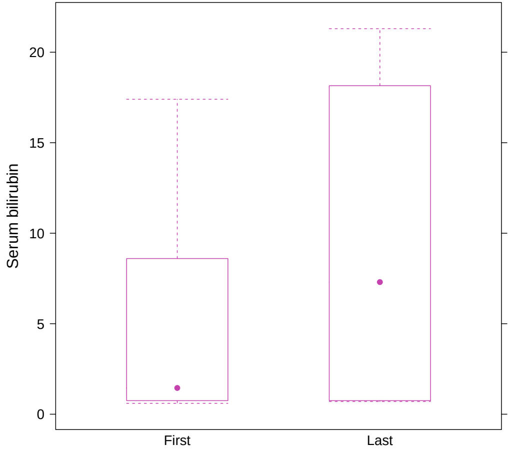
Take care!



Data Visualization

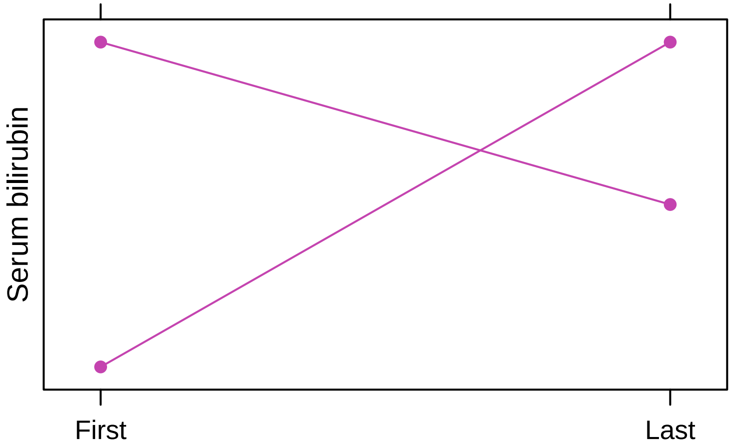
Take care!





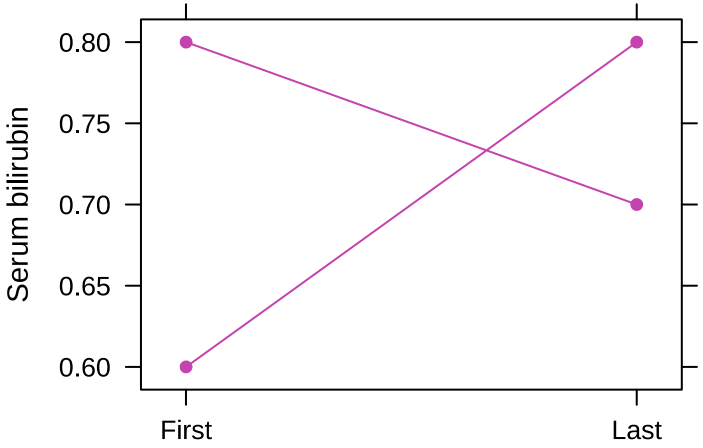
Data Visualization

Take care!



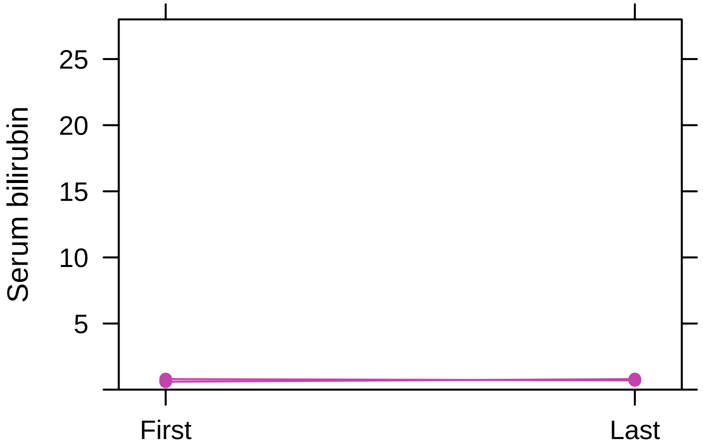
Data Visualization

Take care!



Data Visualization

Take care!



Data Visualization

- R has very powerful graphics capabilities
- Some good references are
  - Murrel, P. (2005) R Graphics. Boca Raton: Chapman & Hall/CRC.
  - Sarkar, D. (2008) Lattice Multivariate Data Visualization with R. New York: Springer-Verlag.

Data Visualization

- Traditional graphics system
  - package **graphics**
- Trellis graphics system
  - package **lattice** (which is based on package grid)
- Grammar of Graphics implementation (i.e., Wilkinson, L. (1999) The Grammar of Graphics. New York: Springer-Verlag)
  - packages **ggplot** & **ggplot2**

Data Visualization

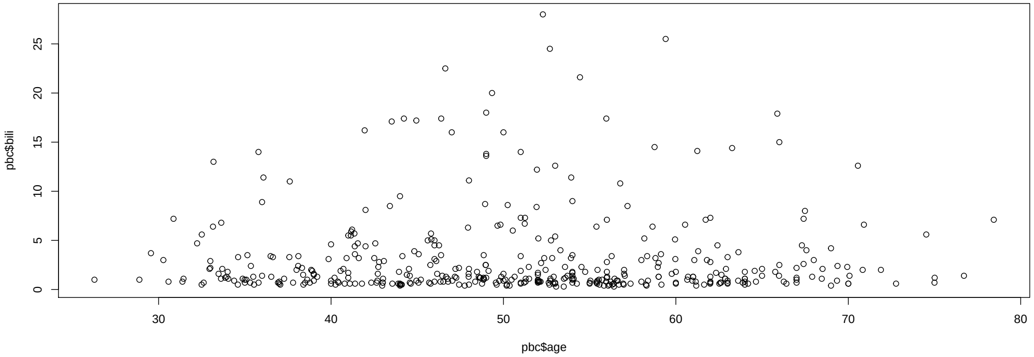
Important plotting basic functions

- **plot()**: scatter plot (and others)
- **barplot()**: bar plots
- **boxplot()**: box-and-whisker plots
- **hist()**: histograms
- **dotchart()**: dot plots
- **pie()**: pie charts
- **qqnorm()**, **qqline()**, **qqplot()**: distribution plots
- **pairs()**: for multivariate data

Data Visualization

Continuous variables

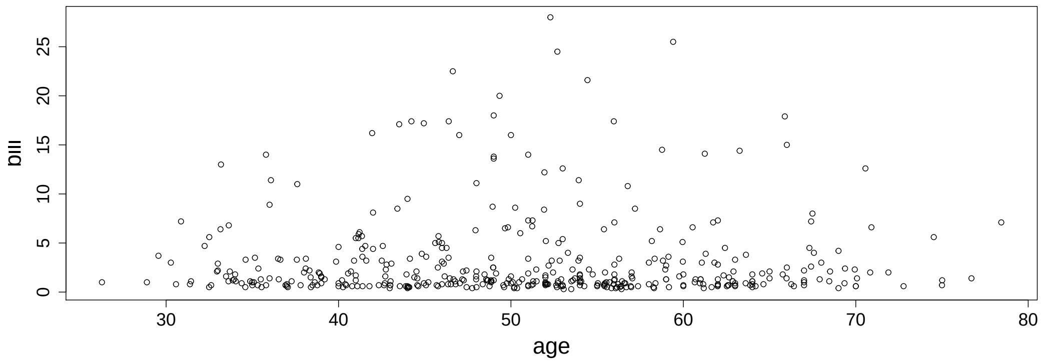
```r
plot(x = pbc$age, y = pbc$bili)
```



Data Visualization

Continuous variables

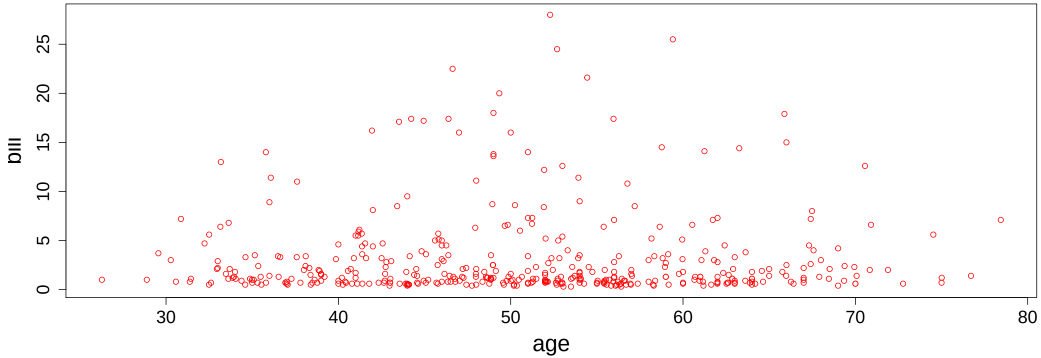
```
plot(x = pbc$age, y = pbc$bili, xlab = "age", ylab = "bili",
     cex.lab = 1.9, cex.axis = 1.5)
```



Data Visualization

Continuous variables

```
plot(x = pbc$age, y = pbc$bili, xlab = "age", ylab = "bili",
     cex.lab = 1.9, cex.axis = 1.5, col = "red")
```



Data Visualization

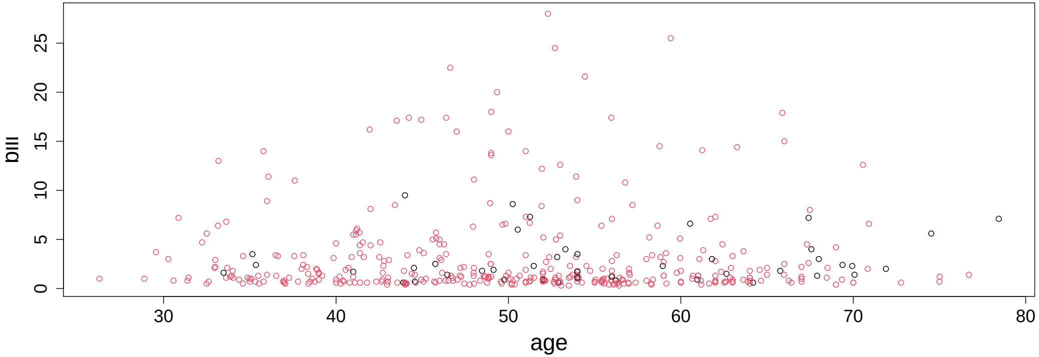
- For more options check

```
?plot
```

Data Visualization

Continuous variables per group

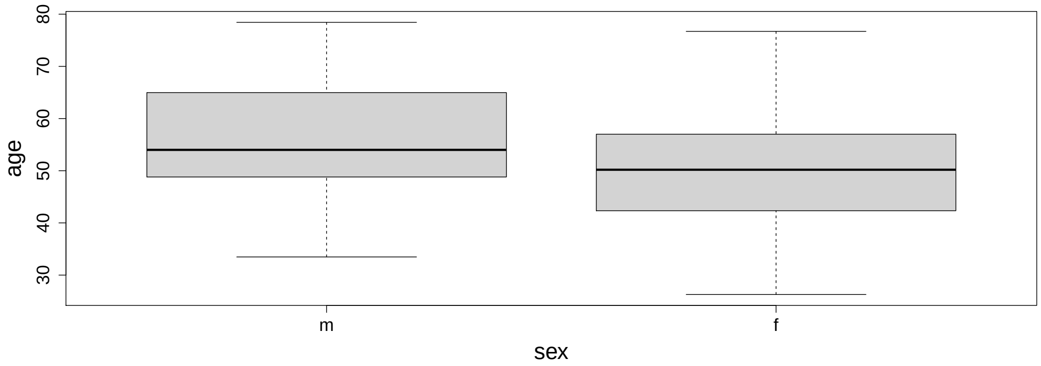
```r
plot(x = pbc$age, y = pbc$bili, xlab = "age", ylab = "bili",
     cex.lab = 1.9, cex.axis = 1.5, col = pbc$sex)
```



Data Visualization

Continuous variables per group

```
boxplot(formula = pbc$age ~ pbc$sex, xlab = "sex", ylab = "age",
     cex.lab = 1.9, cex.axis = 1.5)
```



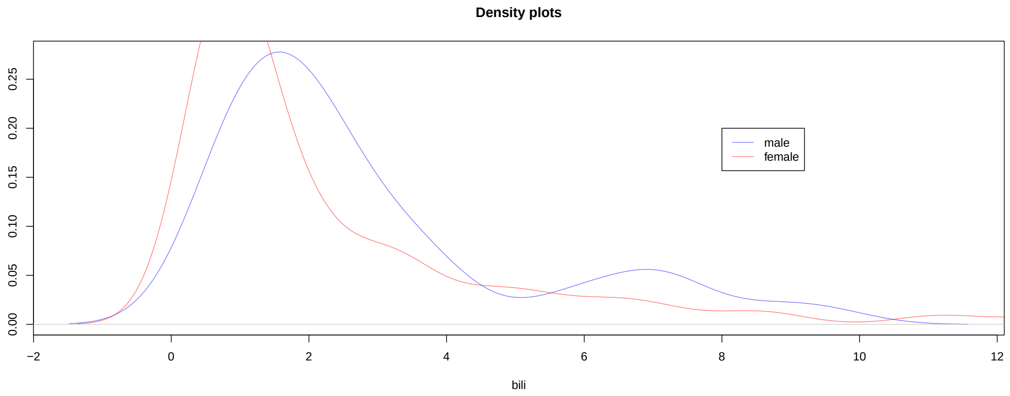
Data Visualization

Continuous variables per group

```r
pbc_male_bili <- pbc$bili[pbc$sex == "m"]
pbc_female_bili <- pbc$bili[pbc$sex == "f"]
plot(density(x = pbc_male_bili), col = rgb(0,0,1,0.5),
     main = "Density plots", xlab = "bili", ylab = "")
lines(density(x = pbc_female_bili), col = rgb(1,0,0,0.5))
legend(x = 8, y = 0.2, legend = c("male", "female"),
       col = c(rgb(0,0,1,0.5), rgb(1,0,0,0.5)), lty = 1)
```

Data Visualization

Continuous variables per group



Data Visualization

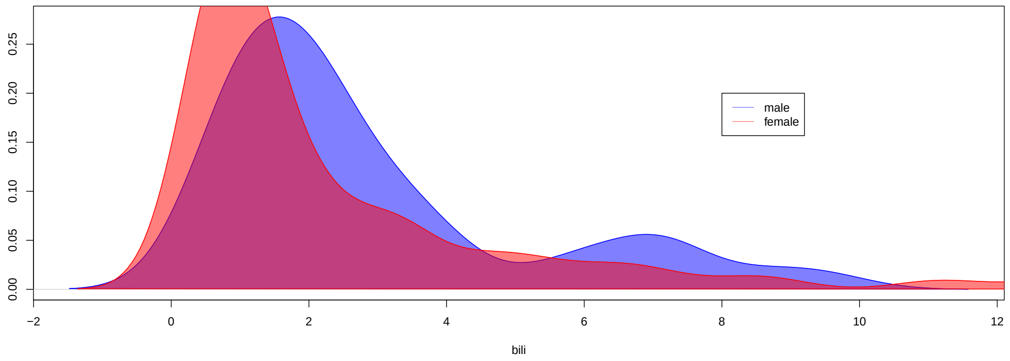
Continuous variables per group

```r
pbc_male_bili <- pbc$bili[pbc$sex == "m"]
pbc_female_bili <- pbc$bili[pbc$sex == "f"]
plot(density(x = pbc_male_bili), col = rgb(0,0,1,0.5),
     main = "Density plots", xlab = "bili", ylab = "")
polygon(density(x = pbc_male_bili), col = rgb(0,0,1,0.5),
        border = "blue")
lines(density(x = pbc_female_bili), col = rgb(1,0,0,0.5))
polygon(density(x = pbc_female_bili), col = rgb(1,0,0,0.5),
        border = "red")
legend(x = 8, y = 0.2, legend = c("male", "female"),
       col = c(rgb(0,0,1,0.5), rgb(1,0,0,0.5)), lty = 1)
```

Data Visualization

Continuous variables per group

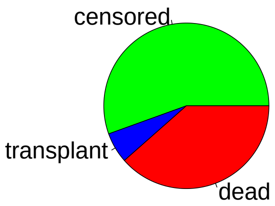
Density plots



Data Visualization

Categorical variables

```r
pbc$status <- factor(x = pbc$status, levels = c(0, 1, 2),
                     labels = c("censored", "transplant", "dead"))
pie(table(pbc$status), col = c("green", "blue", "red"), cex = 2)
```



Summary

Transformation

- `round()`
- `factor()`
- `order()`
- `reshape()`

Exploration

- `mean()`, `sd()`
- `median()`, `IQR()`
- `table()`

Visualization

- `plot()`, `legend()`
- `hist()`
- `barchart()`
- `boxplot()`
- `xyplot()`, `ggplot()`
- `par()`

Practice

Demos

- Data Transformation R html
- Data Exploration R html
- Data Visualization R html

Practicals

- Data Manipulation html