Data analysis and visualization using R

using and writing functions in R

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Descriptive statistics

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Descriptive statistics

Descriptive stats functions

- R provides a wealth of descriptive statistics functions
- They are listed on the next two slides

Descriptive statistics functions (1)

function	purpose
mean( )	mean
median( )	median
var( )	variance s^2
sd( )	standard deviation s
min( )	minimum
max( )	maximum
range( )	min and max

Descriptive statistics functions (2)

function	purpose
quantile( )	quantiles
IQR( )	interquantile range
summary( )	6-number summary
hist( )	histogram
boxplot( )	boxplot

The quantile() function

- Gives the data alues corresponding to the specified quantiles
- Defaults to 0% 25% 50% 75% 100%

```
quantile(ChickWeight$weight)
```

```
##      0%     25%     50%     75%    100%
##   35.00   63.00 103.00 163.75 373.00
```

```
quantile(ChickWeight$weight, probs = seq(0, 1, 0.2))
```

```
##     0%    20%    40%    60%    80%   100%
##   35.0   57.0   85.0 126.0 181.6 373.0
```

Interquantile range IQR()

- Gives the range between 25% and 75% quantiles

```
IQR(ChickWeight$weight)
```

```
## [1] 100.75
```

```
## same as
quantile(ChickWeight$weight)[4] - quantile(ChickWeight$weig
```

```
##     75%
## 100.75
```

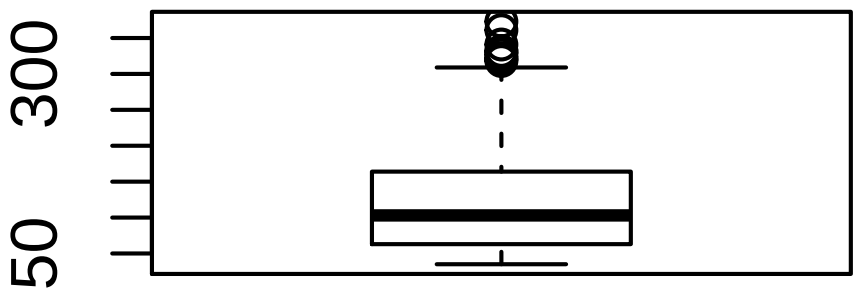
boxplot() is a picture of summary()

- Boxplot is a graph of the 5-number summary, but summary() also gives the mean

```
summary(ChickWeight$weight)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    35.0    63.0   103.0   121.8   163.8   373.0
```

```
boxplot(ChickWeight$weight)
```



Sorting and ordering

Sort and Order

- `sort()` sorts a vector
- `order()` returns a vector representing the ordered status of a vector

```
x <- c(2, 4, 6, 1, 3)
sort(x)
```

```
## [1] 1 2 3 4 6
```

```
ordr <- order(x); ordr
```

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

```
x[ordr]
```

```
## [1] 1 2 3 4 6
```

Use order when order matters

When you use `sort()`, a vector will be shuffled in-place. This is ususally *NOT* desirable when coupled vectors are being analysed (as in the most used data type Dataframes!)

Sorting dataframes

```
geneNames <- c("P53","BRCA1","VAMP1", "FHIT")
sig <- c(TRUE, TRUE, FALSE, FALSE)
meanExp <- c(4.5, 7.3, 5.4, 2.4)
genes <- data.frame(
    "name" = geneNames,
    "significant" = sig,
    "meanExp" = meanExp)
genes
```

```
##    name significant meanExp
## 1   P53        TRUE     4.5
## 2 BRCA1        TRUE     7.3
## 3 VAMP1       FALSE     5.4
## 4  FHIT       FALSE     2.4
```

```
## sort on gene name
genes[order(genes$name), ]
```

Multilevel sorting

You can also sort on multiple properties:

```
students <- data.frame(
    "st.names" = c("Henk", "Piet", "Sara", "Henk", "Henk"),
    "st.ages" = c(22, 23, 18, 19, 24))
students[order(students$st.names, students$st.ages), ]
```

```
##   st.names st.ages
## 4     Henk      19
## 1     Henk      22
## 5     Henk      24
## 2     Piet      23
## 3     Sara      18
```

Some general purpose functions (part 1)

Remove objects from memory

- When working with large datasets it may be usefull to free them from memory when no longer needed
- i.e. intermediate results
- use `rm()` to do this: `rm(genes)`, `rm(x, y, z)`

File system operations

- `getwd()` returns the current working directory
- `setwd()` sets the current working directory
- `dir()`, `dir(path)` lists the contents of the current directory or of *path*
- *path* can be defined as
  - Windows: `"E:\\emile\\datasets"`
  - Linux/Mac: `"~/datasets"` or `"/home/emile/datasets"`

Reading and writing textual data

Text data formats

Textual data comes in many forms. Here are a few examples:
`DesertBirdCensus.csv`

```
Species,"Count"
Black Vulture,64
Turkey Vulture,23
Harris's Hawk,3
Red-tailed Hawk,16
American Kestrel,7
```

BED_file.txt

```
browser position chr7:127471196-127495720
browser hide all
track name="ItemRGBDemo" description="Item RGB demonstratio
itemRgb="On"
chr7    127471196  127472363  Pos1  0  +  127471196  12747
chr7    127472363  127473530  Pos2  0  +  127472363  12747
chr7    127473530  127474697  Pos3  0  +  127473530  12747
chr7    127474697  127475864  Pos4  0  +  127474697  12747
chr7    127475864  127477031  Neg1  0  -  127475864  12747
chr7    127477031  127478198  Neg2  0  -  127477031  12747
```

mySNPdata.vcf

```
##fileformat=VCFv4.0
##fileDate=20100501
##reference=1000GenomesPilot-NCBI36
##assembly=ftp://ftp-trace.ncbi.nih.gov/1000genomes/ftp/rel
##INFO=<ID=BKPTID,Number=-1,Type=String,Description="ID of
##ALT=<ID=DEL,Description="Deletion">
##ALT=<ID=CNV,Description="Copy number variable region">
##FORMAT=<ID=GT,Number=1,Type=Integer,Description="Genotype
#CHROM  POS    ID  REF ALT    QUAL  FILTER  INFO  FORMAT  NAC
1 2827693    . CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGT
2 321682     . T <DEL>    6 PASS     IMPRECISE;SVTYPE=DEL;END=
2 14477084   . C <DEL:ME:ALU>  12  PASS  IMPRECISE;SVTYPE=DE
3 9425916    . C <INS:ME:L1> 23  PASS  IMPRECISE;SVTYPE=INS;
3 12665100   . A <DUP>    14  PASS  IMPRECISE;SVTYPE=DUP;END=
4 18665128   . T <DUP:TANDEM>  11  PASS  IMPRECISE;SVTYPE=DU
```

Data file structure

Whatever the contents of a file, you always need to address (some of) these questions:

- Are there comment lines at the top?
- Is there a header line with column names?
- What is the column separator? (fixed width?)
- Are there quotes around character data?
- How are missing values encoded?
- How are numeric values encoded?
- What is the type in each column?
  - character / numeric / factor / date/time

Some `read.table()` arguments

arg	specifies	example
sep	field separator	sep = ":"
header	is there a header	header = F
dec	decimal format	dec = ","
comment.char	comment line start	comment.char = ""
na.strings	NA value	na.strings = "-"
as.is	load as character	as.is = c(1,4)

Writing data to file

- writing a data frame / matrix / vector to file:
- `write.table(myData, file="file.csv")`
- Standard is a comma-separated file with both column- and row names, unless otherwise specified:
  - `col.names = F`
  - `row.names = F`
  - `sep = ";"`
  - `sep = "\t" # tab-separated`

Writing plot to file

- You can use a redirect to write a plot to file
- Usually this will be a png file
- Use `width` and `height` to specify size
- Default unit is pixels
- Use other unit: `units = "mm"`

```
png("/path/to/your/file.png",
    width = 700, height = 350, units = "mm")
plot(cars)
dev.off()
```

Some general purpose functions (part 2)

Glueing text pieces: paste()

- Use paste() to combine elements into a string

```
paste(1, 2, 3)
```

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

```
paste(1, 2, 3, sep="-")
```

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

```
paste(1:12, month.abb)
```

```
##  [1] "1 Jan"  "2 Feb"  "3 Mar"  "4 Apr"  "5 May"  "6 Jun"
##  [8] "8 Aug"  "9 Sep"  "10 Oct" "11 Nov" "12 Dec"
```

Investigate structure: `str()`

- Use `str()` to investigate the structure of a complex object

```
str(chickwts)
```

```
## 'data.frame':    71 obs. of  2 variables:
##  $ weight: num  179 160 136 227 217 168 108 124 143 140
##  $ feed  : Factor w/ 6 levels "casein","horsebean",..: 2
```

Convert numeric vector to factor: `cut()`

Sometimes, it is useful to work with a factor (ordinal) instead of a numeric vector (interval or ratio scale). For instance, when working with Body Mass Index (bmi) related variables, it may be noce to split this into a factor for further processing.
The function `cut()` can be used for this.

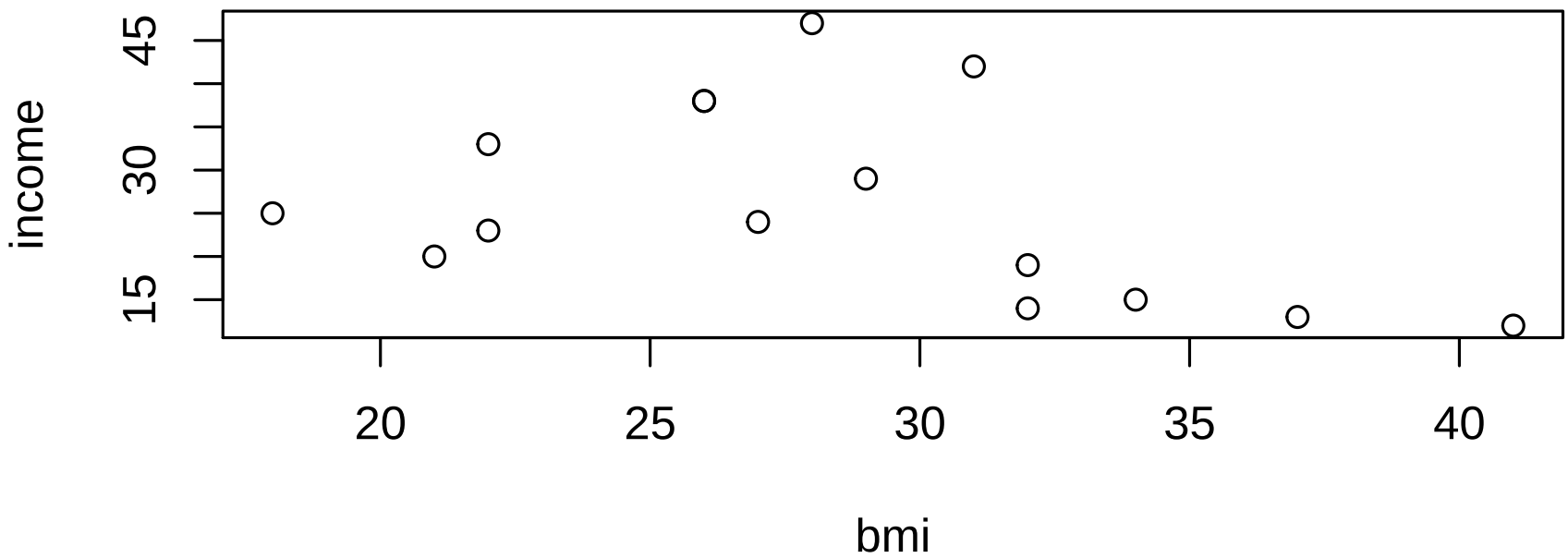
cut() demo

- suppose you have the following dataset

```
## body mass index
bmi <- c(22, 32, 21, 37, 28,   34, 26, 29, 41, 18,   22, 27
## year income * 1000 euros
income <- c(23, 14, 20, 13, 47,   15, 38, 29, 12, 25,   33,
my.data <- data.frame(bmi = bmi, income = income)
```

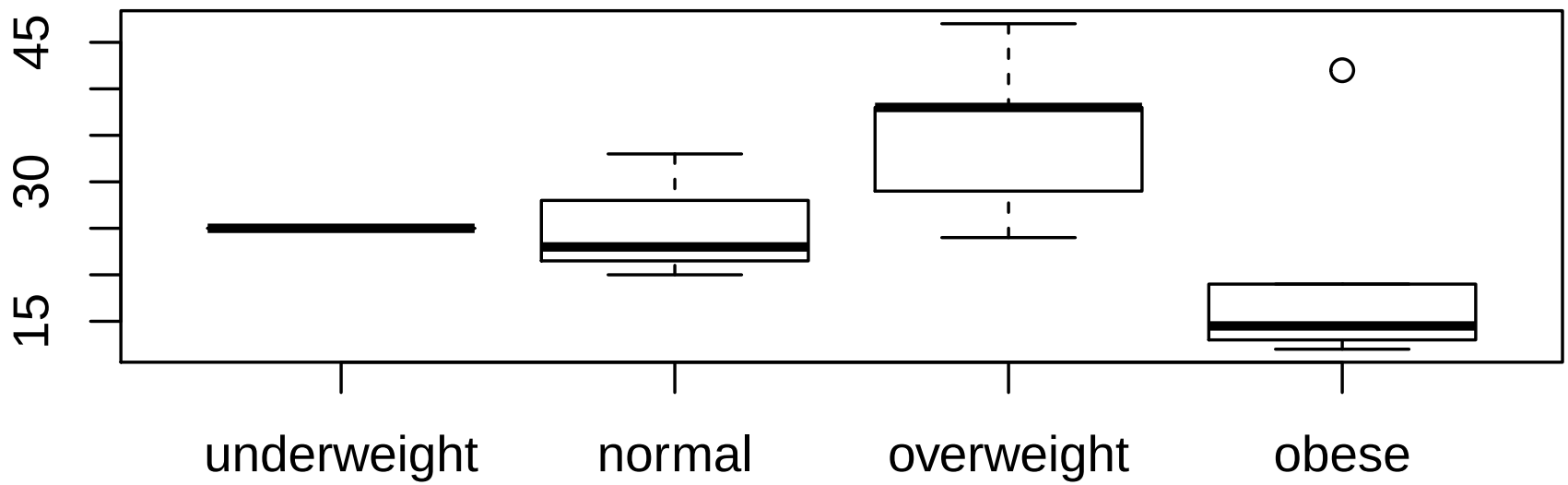
- You can of course look at income as a function of bmi using a plot:

```
with(my.data, plot(income ~ bmi))
```



- but wouldn't it be nice to look at the bmi categories as defined by the WHO? - use `cut()`

```
my.data$bmi.class <- cut(bmi,
    breaks = c(0, 18.5, 25.0, 30.0, Inf), right = F,
    labels = c("underweight", "normal", "overweight", "obes
    ordered_result = T)
with(my.data, boxplot(income ~ bmi.class))
```



Flow control

what is flow control

- used to control the execution of different commands
- these structures are used for flow control
  - if(){} else if(){} else{}
  - for(){}
  - while(){}

if and else

- Since flow control is used primarily within functions it is dealt with here
- The first is `if & else` for conditional code

```
x <- 43
if (x > 40) {
    print("TRUE")
} else {
    print("FALSE")
}
```

```
## [1] "TRUE"
```

if/else real life example

- this code chunk checks if a file exists and only downloads it if it is not present

```
my_data_file <- "/some/file/on/disk"
## fetch file
if (!file.exists(my_data_file)) {
    print(paste("downloading", my_data_file))
    download.file(url = remote_url, destfile = my_data_file
} else {
    print(paste("reading cached copy of", my_data_file))
}
```

ifelse ternary

There is also a shorthand for `if(){}else{}`

```
a <- 3
x <- if (a == 1) 1 else 2
x
```

```
## [1] 2
```

for

- `for` is used for looping vectors
- However, the prefered way to do this is by `apply()` and its relatives (see above)

```
for (i in 1:3) {
    print(i)
}
```

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

for

- Sometimes, a `for` loop is handy with index

```
x <- c("foo", "bar", "baz")
for (i in 1 : length(x)) {
    print(x[i])
}
```

```
## [1] "foo"
## [1] "bar"
## [1] "baz"
```

Creating functions

Functions are reusable code

- Functions are named pieces of code with a single well-defined purpose
- They ususally have some data as input: **arguments**
- They usually have some **return** value

A first function

- Here is a simple function determining whether some number is even

```
IsEven <- function(x) {
    y <- x %% 2 == 0
    return(y) ##explicit return not required
}
IsEven(1:5)
```

```
## [1] FALSE  TRUE FALSE  TRUE FALSE
```

Function basics

- The result of the last statement within a function is the return value of that function
- Use `return()` for forcing return values at other points:

```
MyMessage <- function(age) {
    if (age < 18) return("have a lemonade!")
    else return("have a beer!")
}
MyMessage(20)
```

```
## [1] "have a beer!"
```

Default argument values

- Use default values for function arguments whenever possible
- Almost all functions in R packages have many arguments with default values

```
MyPower <- function(x, power = 2) {
    x ^ power
}
MyPower(10, 3) ## custom power
```

```
## [1] 1000
```

```
MyPower(10) ## defaults to 2
```

```
## [1] 100
```

Errors and warnings

- When someting is not right, but not enought to quit execution, use a warning to let the user (or yourself) know
- `warning("I am not happy")`
- When something is terribly wrong, stop execution with an error message
- `stop("I can't go on")`

Errors and warnings demo

```
DemoInv <- function(x) {
    if (!is.numeric(x)) {
        stop("non-numeric vector")
    }
    return(x/3)
}
b <- DemoInv(c("a", "b")) # b not created!
b <- DemoInv(1:4)
```

```
> b <- DemoInv(c("a", "b")) # b not created!
Error in DemoInv(c("a", "b")) : non-numeric vector
> b <- DemoInv(1:4)
```