An introduction to R

Beginners session + Q&A

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What's R?

In origin was **S**, a programming language for statistical computing and interactive graphics. It was developed by John Chambers, Rick Becker and Allan Wilks of (NOKIA) Bell Laboratories in 1976.
S went through many version updates (1-4, 5 plus...) until in 1992 Ross Ihaka and Robert Gentleman (University of Auckland, New Zealand) worked on a further implementation and renamed it **R**.

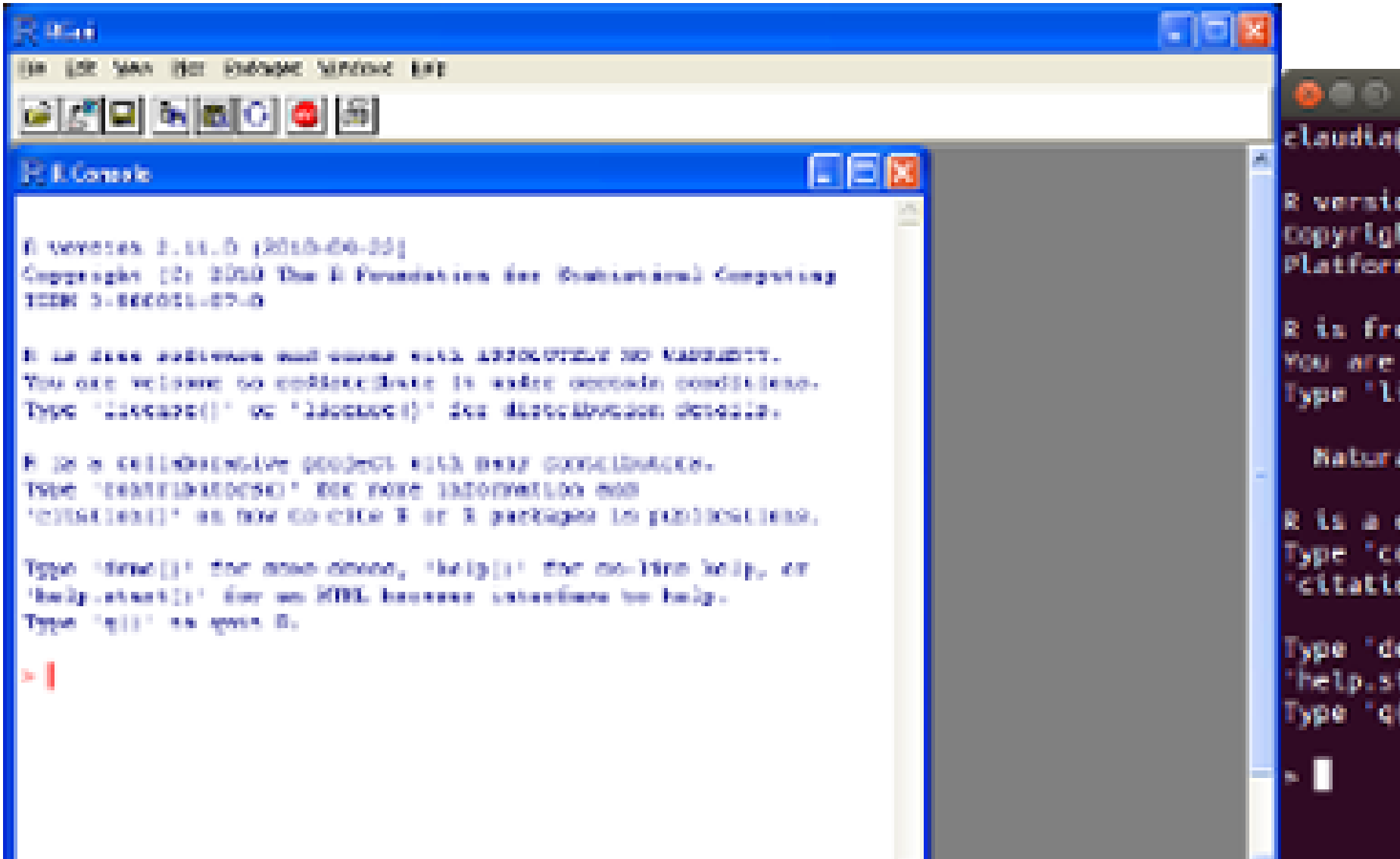
Let's install the software

Install R

Go to the R-project website, download and install R:

`https://www.r-project.org/`

The default Graphical User Interface (GUI) is basically a console!



Using the prompt/console

To start R from command line, type **R** then hit enter (ONLY FOR LINUX/MAC USERS!).
When R is waiting for us to tell it what to do, it begins the line with the symbol:
>
If we give it an incomplete command and it can not finish the task requested it provides:
+
To get out of R we use the command
q()

Your turn!

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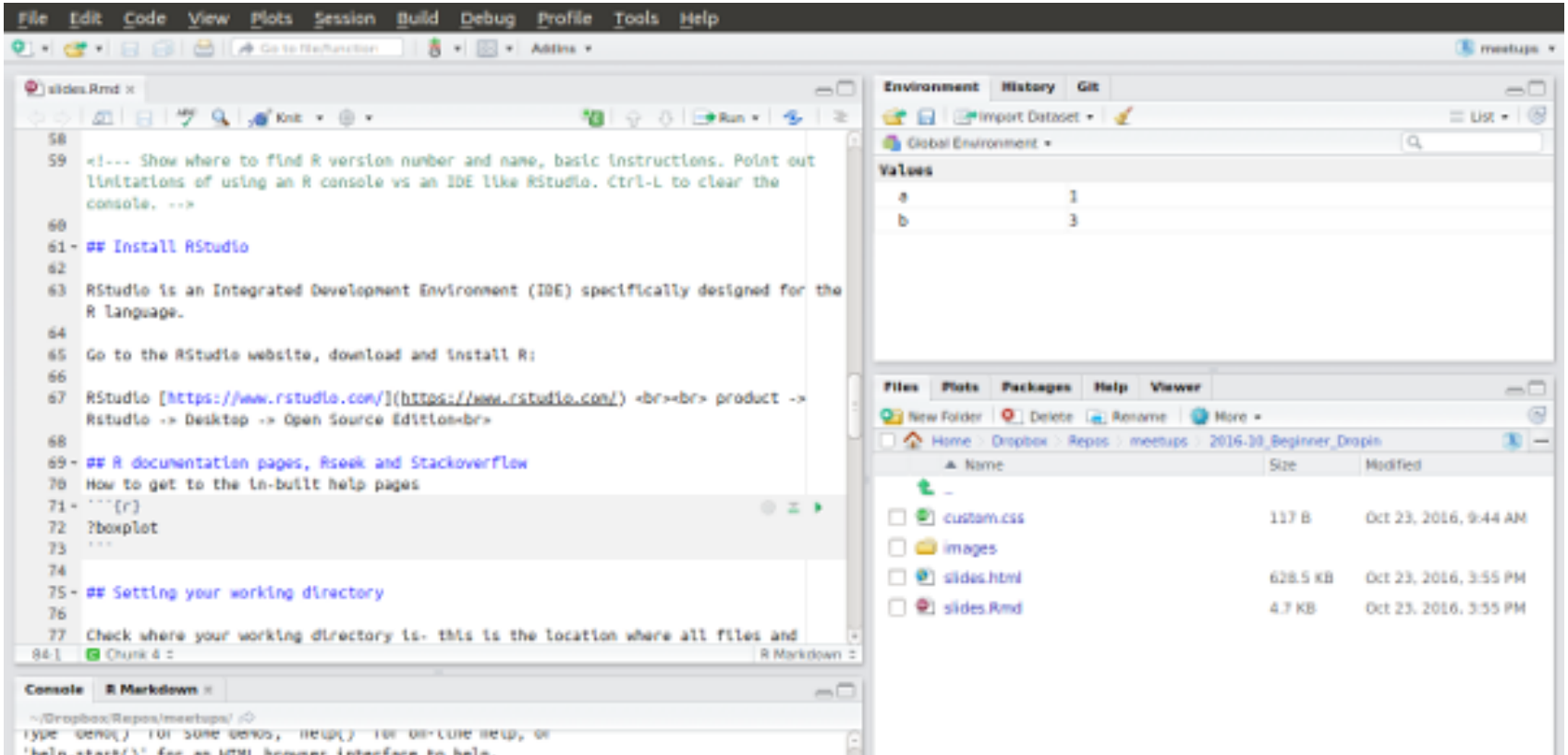
- Try the functions **license()**, **help()** and **q()**
- **For complex operations you might need to have an editor, check your environmental variables, visualise plots without switching window... that's why we recommend to use RStudio!**

Install RStudio

RStudio is an Integrated Development Environment (IDE) specifically designed for the R language.
On the RStudio website (`https://www.rstudio.com/`) go to **product -> Rstudio -> Desktop -> Open Source Edition**
download and install RStudio Open Source Edition:



Basic operations, like a calculator

We have already R can be used as a calculator.
You can enter an expression to evaluated and hit enter (if you use the command line) or click the Run button (if you use Rstudio) to compute the result.

- Use * for multiply.
- Use ^ for raised to the power of.
- Use **parentheses** to ensure that it understands what you are trying to compute.
- The order of doing arithmetic operations is (left [done first] to right [done last]): ^ / * - +

Your turn!

Basic operations, like a calculator

```
1 + 2
```

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

```
5 * 6 + 9 * (10 ^ (-2) + 2 * 3)
```

```
## [1] 84.09
```

Literal operations

Like in algebra, we may want to store a computation under some variable name. The result is assigned to a variable with the <- ('less than' symbol followed by a hyphen):

```
a <- 1
```

- When you want to know what is in a variable simply ask by typing the variable name.

```
a
```

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

- We can store a computation under a new variable name or change the current value in an old variable.

```
b <- 2
b <- exp(b)
```

Something to remember

- Certain variable names are reserved for particular purposes (e.g. c q t C D F I T)
- Do not begin a variable name with a period or a number.
- Variable names are case (upper/lower) sensitive.

Data types and objects

R supports 5 basic data types:

- integer,
- numeric,
- character,
- logical and
- complex.

Missing values are labelled: **NA**.
Elements of basic type can be combined to form complex data objects such as:

- vectors,
- matrices,
- arrays,
- data frames and
- lists.

Objects

A **vector** is a sequence of data elements of the same basic type. To create a vector we can concatenate a list of numbers using the function **c()**.
A **matrix** is a 2 dimensional table in which every element is of the same type. To create a matrix we use the function **matrix()**.
An **array** is similar to a matrix but can have more than 2 dimensions. To create an array we use the function **array()**.
A matrix in which each column can be of a different type is called **data frame** and can be created using the function **data.frame()**.
A **list** is like a data frame but each column can be of different length or even a tree of data objects. A list is generated using the function **list()**.

Your turn!

Let's experiment with data objects

```r
a   <- 1

v1  <- c(1,2,3)
# Get the length of a vector
length(v1)
```

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

```r
m1  <- matrix(0, nrow = 3, ncol = 2)
# Count dimensions
dim(m1)
```

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

```r
df1 <- data.frame(v1, v1 * 10)

l1  <- list("a" = a, "v1" = v1, "m1" = m1, "df1" = df1)
# What would you use to count the elements of a list?
```

Explore data objects

```
typeof(l1)
```

```
## [1] "list"
```

```
str(l1)
```

```
## List of 4
##  $ a  : num 1
##  $ v1 : num [1:3] 1 2 3
##  $ m1 : num [1:3, 1:2] 0 0 0 0 0 0
##  $ df1:'data.frame': 3 obs. of  2 variables:
##   ..$ v1     : num [1:3] 1 2 3
##   ..$ v1...10: num [1:3] 10 20 30
```

Extract elements from data objects

Data objects in R are indexed. These indices can be used to extract/subset vectors, matrices, data frames and lists. Alternatively, named dimensions can be extracted using the operator **$**

```
v1[2]                # extract the second element of vector v
l1[2]                # extract the second element of list l1
m1[3,2]              # extract the element in the third row s
df1[3,2]             # extract the element in the third row s
```

```
l1$v1
```

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

R Base + core packages

All the basic R functions and operators seen so far are automatically loaded under the **R Base Package** (base).
There are additional built-in functions that are loaded grouped in separated packages. Each package is used for a specific purpose.
Some examples are: **base**, **stats**, **graphics**, **datasets**, etc.

Built-in functions

```r
x <- c(1,2,3,4,5,6,7,8,9)

# Core functions from the "base" package
print("Hello world!")   # Print messages
sum(x)          # calculates the sum of the elements in the ve
mean(v1)        # average
max(x)          # the largest value
min(x)          # the smallest value
log(b)          # natural logarithm (log10 computes logarith w
sort(x)         # re-arrange elements of x in ascending order
summary(v1)     # summary statistics

# Core functions from the "stats" package
median(x)       # the sample median
var(x)          # the sample variance (has n-1 in denominator)
sd(x)           # the standard deviation
```

NAMESPACE

```
stats::cov
cov
```

But... be careful!

```
cov <- function(x){x+1}
cov
stats::cov                  # the original cov function is not
rm(cov)                     # remove the last definition
```

Setting your working directory

Check where your working directory is- this is the location where all files and functions will be read and written to

```
getwd()
```

```
## [1] "/home/claudia/Dropbox/Repos/meetups/2016-10_Beginne
```

If this isn't where your files are then you can set it through (put your own path in the quotes!)

```
setwd("C:\Documents\mypath")
```

Or in Rstudio you can go: Session>Set Working Directory>Choose Directory and navigate to your folder

Example data

R comes with a number of example datasets. To browse the complete list use the function **data()**, with no inputs.
For example, the **iris** dataset consists of 50 samples from three species of Iris (Iris setosa, Iris virginica and Iris versicolor). Four features were measured from each sample: the length and the width of the sepals and petals, in centimetres.

```
head(iris)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Spec
## 1          5.1         3.5          1.4         0.2  set
## 2          4.9         3.0          1.4         0.2  set
## 3          4.7         3.2          1.3         0.2  set
## 4          4.6         3.1          1.5         0.2  set
## 5          5.0         3.6          1.4         0.2  set
## 6          5.4         3.9          1.7         0.4  set
```

Look at the in-built data set on trees

```
trees
```

```
##    Girth Height Volume
## 1    8.3     70   10.3
## 2    8.6     65   10.3
## 3    8.8     63   10.2
## 4   10.5     72   16.4
## 5   10.7     81   18.8
## 6   10.8     83   19.7
## 7   11.0     66   15.6
## 8   11.0     75   18.2
## 9   11.1     80   22.6
## 10  11.2     75   19.9
## 11  11.3     79   24.2
## 12  11.4     76   21.0
## 13  11.4     76   21.4
## 14  11.7     69   21.3
## 15  12.0     75   19.1
```

Explore the trees data set

The top of the data

```
head(trees)
```

The end of the data set

```
tail(trees)
```

The size and type of the data

```
str(trees)
```

Summary statistics on each of the fields

```
summary(trees)
```

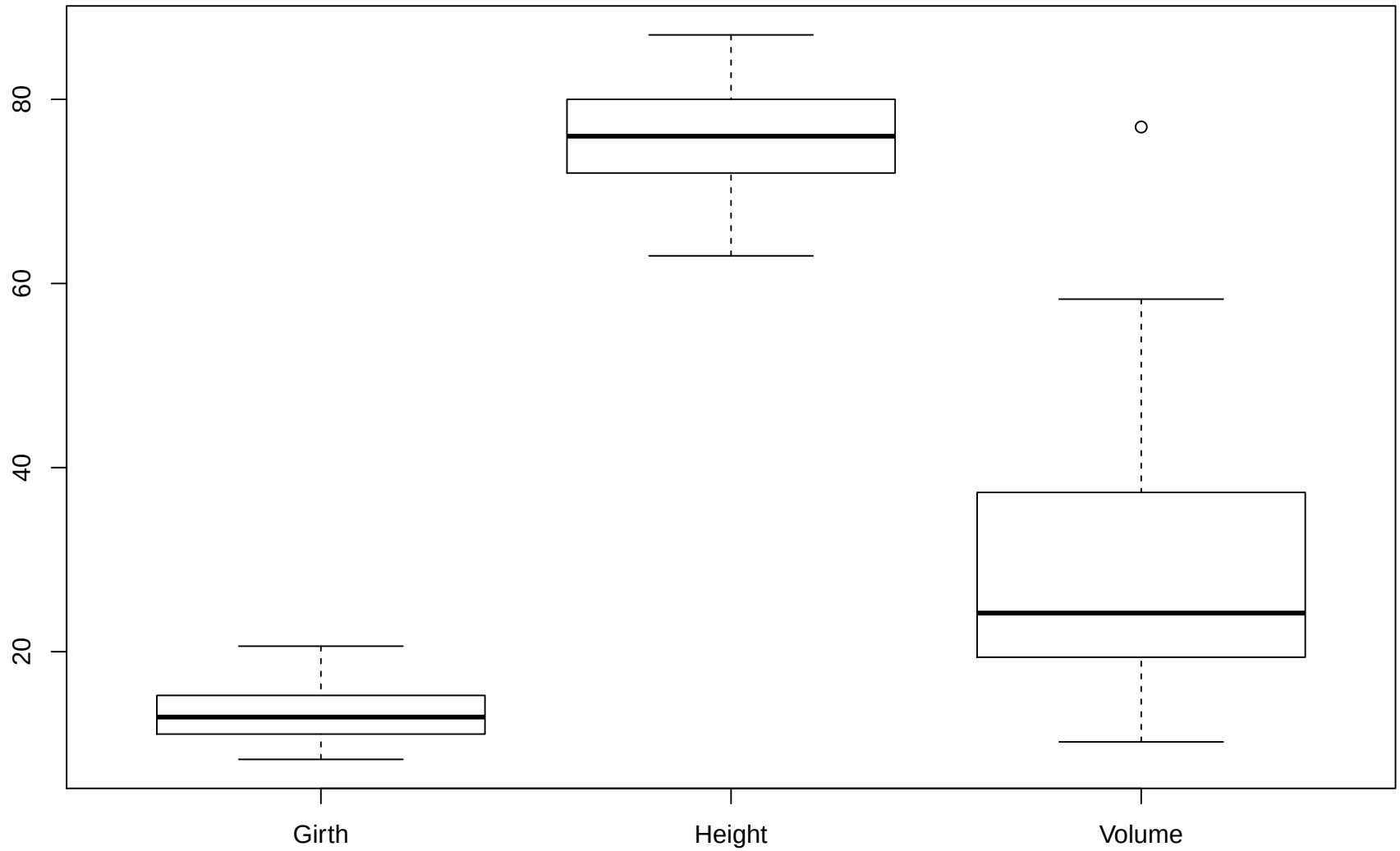
Pull out only one of the fields

```
summary(trees$Girth)
```

Basic plots

Create your first plot

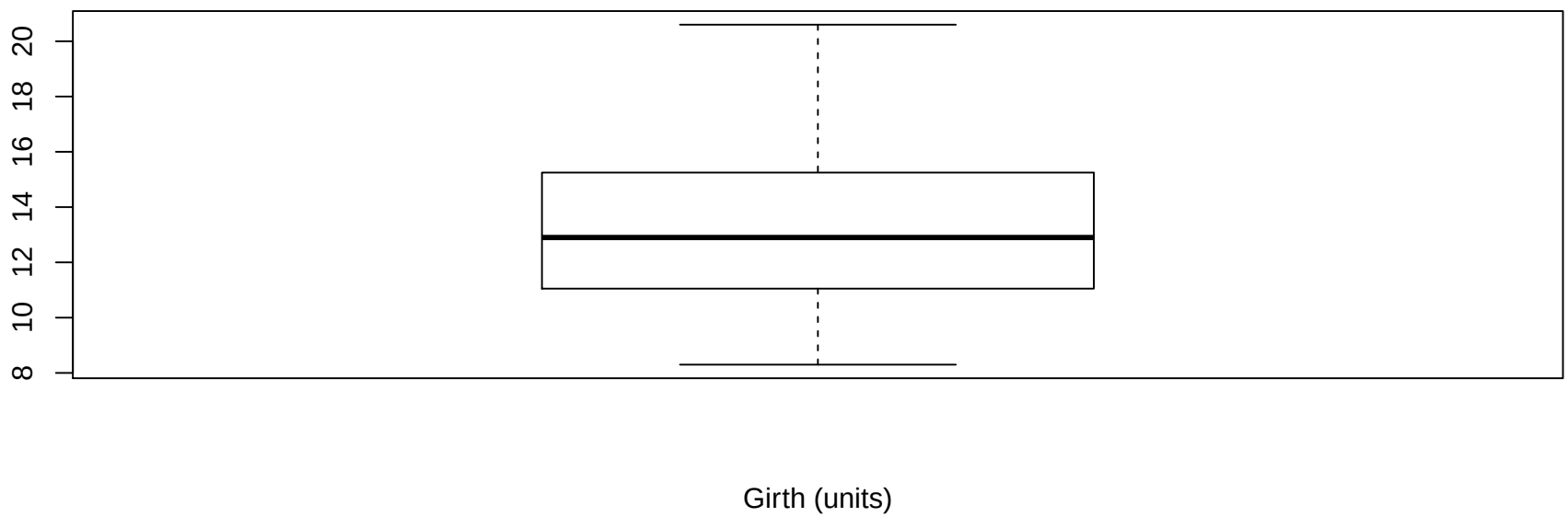
```
boxplot(trees)
```



Basic plots

Create another variable with only one of the fields and plot that

```
treeGirth <- trees$Girth
boxplot(treeGirth, xlab="Girth (units)", title="Tree Girths
```



Export/Import a table (data.frame) to/from text file

```
write.csv(iris,"~/iris.csv")

myTable <- read.csv("~/iris.csv")

head(myTable)
```

```
##   X Sepal.Length Sepal.Width Petal.Length Petal.Width Sp
## 1 1          5.1         3.5          1.4         0.2  s
## 2 2          4.9         3.0          1.4         0.2  s
## 3 3          4.7         3.2          1.3         0.2  s
## 4 4          4.6         3.1          1.5         0.2  s
## 5 5          5.0         3.6          1.4         0.2  s
## 6 6          5.4         3.9          1.7         0.4  s
```

Work with remote files

```
myTable2 <- read.csv("http://www.ats.ucla.edu/stat/data/hsb

head(myTable2)
```

```
##    id female race ses schtyp prog read write math scienc
## 1  70      0    4   1      1    1   57    52   41       4
## 2 121      1    4   2      1    3   68    59   53       6
## 3  86      0    4   3      1    1   44    33   54       5
## 4 141      0    4   3      1    3   63    44   47       5
## 5 172      0    4   2      1    2   47    52   57       5
## 6 113      0    4   2      1    2   44    52   51       6
```

R data formats

Rds stores a single R object, use readRDS() and saveRDS() to read in and save respectively.

```
## save a single object to file
pippo <- c(1,2,4)
saveRDS(pippo, "pippo.rds")

## restore it under a different name
pippo2 <- readRDS("pippo.rds")
```

RData (or rda) allows to save(), load(), attach() multiple data objects in one file.

```
## save two objects to one file
pippo <- c(1,2,4)
pluto <- c(3,5,4)
save(pippo, pluto, file= "x.rda")

## restore the objects
```

Other data formats

There are dedicated R packages to handle the most commonly used data formats.
Some examples are:

- Text files (e.g. csv)
- Spreadsheets (e.g. .xls)
- GIS files (e.g. .shp, ascii, .tif)
- Binaries (e.g. .nc)
- Markups (e.g. xml, gml)

R can also connect to databases (e.g. postgresql)

Install additional packages

There are ~8000 R packages available on the Comprehensive R Archive Network (CRAN).

```r
# Install a new package for advanced graphics
install.packages("ggplot2")

# Load the package
library("ggplot2")
```

Custom functions

You can create a custom function as in the example below:

```
myFunction <- function(x){

   y <- x + 1

   return(y)
}

myFunction( x = 32 )
```

```
## [1] 33
```

Help

Each function comes with a documentation page that can be visualised typing **help(*name of the function*)** in the console. Alternatively, you can type **?** (question mark) before the name of the function.

```
help(print)
?print
```

You can also:

- Browse Rseek to find out what packages are available for a given topic (e.g. cluster analysis)
- Join the R users forum
- Google your problem
- Post a question on Stackoverflow

Cheat Sheets & Reference Guides

- R Reference Card
- Writing R extensions
- Google's R Style Guide
- RStudio website
  - Data Visualization
  - Package Development
  - Data Wrangling
  - R Markdown
  - R Markdown Reference Guide
  - Shiny

Where to go next

Great tutorials:

- edx MiT course: `https://www.edx.org/course/analytics-edge-mitx-15-071x-2`
- DataCamp: `https://www.datacamp.com/`
- Coursera: `https://www.coursera.org/learn/r-programming`
- Great Kaggle Tutorials: `https://www.kaggle.com/mrisdal/titanic/exploring-survival-on-the-titanic`