



IAVS-LAC

The
Workshop

This Session

R

RMarkdown

Name
Resolution

From the field to the desk

[Session 1]

Miguel Alvarez

21st April 2023



The Workshop

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Welcome!

- ▶ 21-04-2023 **Session 1**
- ▶ 28-04-2023 **Session 2**
- ▶ 05-05-2023 **Session 3**
- ▶ 12-05-2023 **Session 4**
- ▶ 19-05-2023 **Session 5**

<https://kamapu.github.io/r-vegetation/>
detailed program

FROM THE FIELD TO THE DESK:

What you need to do with your vegetation data before statistics.

April & May 2023

Each Friday (five sessions)
18 - 20 UTC +2 CEST

Limit: 30 participants
Five fee waivers.

ABOUT

Save time learning to prepare your data for analyses

Using "Vegetable" package to understand your data



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- ▶ Time Slots
 - ▶ 18:00 to 19:00 Course
 - ▶ 19:00 to 19:10 Break
 - ▶ 19:10 to 20:00 Course
- ▶ Style
 - ▶ Slides for Introductions
 - ▶ Life Code
 - ▶ Exercises / Homeworks

Time Conversions

- ▶ 18:00 to 20:30 in **UTC**
- ▶ 13:00 to 15:30 in **COT**
- ▶ 20:00 to 22:30 in **CEST**



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Intro to the trainers

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Motivation

- ▶ Collaborative work
- ▶ Reproducible data assessment
- ▶ Literate Programming



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- ▶ Installing instructions
- ▶ Data sets



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Thanks!

A collage with avatars and logos.

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- ▶ Refreshing R
- ▶ Introduction to RMarkdown
- ▶ Taxonomic Resolution



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- ▶ Console
- ▶ Workspace (Global environment)
- ▶ History
- ▶ Script
- ▶ Working directory

- ▶ Graphic devices
- ▶ Packages (extensions)



Vector

The fundamental data structure in **R**

- ▶ `length()`
- ▶ `class()`
- ▶ `names()` (optional)

```
c(1:10)
```

```
## [1] 1 2 3 4 5 6 7 8 9 10
```

```
rep(5, times = 10)
```

```
## [1] 5 5 5 5 5 5 5 5 5 5
```

```
LETTERS[1:5]
```

```
## [1] "A" "B" "C" "D" "E"
```



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Type of data

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- ▶ integer
- ▶ numeric
- ▶ logical
- ▶ factor
- ▶ character

```
A <- c(1:10)
is.numeric(A)
## [1] TRUE
```

```
B <- as.character(A)
B
## [1] "1" "2" "3" "4" "5" "6" "7" "8"
is.numeric(B)
## [1] FALSE
```



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Index



[]



Index



integer



logical (condition)



character (names)

```
# index as integer
```

```
letters[15]
```

```
## [1] "o"
```

```
# index as logical
```

```
letters[!letters %in% c("a", "b", "c")]
```

```
## [1] "d" "e" "f" "g" "h" "i" "j" "k" "l" "m"
```

```
## [20] "w" "x" "y" "z"
```

```
# index as character
```

```
names(letters) <- letters
```

```
letters["m"]
```

```
## m
```

```
## "m"
```



Special Values

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- ▶ NA
- ▶ NaN
- ▶ NULL
- ▶ Inf
- ▶ -Inf

5/0

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

```
log(0)
```

```
## [1] -Inf
```

```
sqrt(-1)
```

```
## Warning in sqrt(-1): NaNs produced
```

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



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Lists

A listing of objects.

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▶ class list

▶ length()

▶ index

▶ []

▶ [[]]

▶ \$

```
my_list <- list(  
  A = 1:10,  
  B = matrix(1:10, nrow = 2),  
  C = "This is a list")  
my_list  
  
## $A  
## [1] 1 2 3 4 5 6 7 8 9 10  
##  
## $B  
##      [,1] [,2] [,3] [,4] [,5]  
## [1,] 1    3    5    7    9  
## [2,] 2    4    6    8   10  
##  
## $C  
## [1] "This is a list"
```




Data Frame

Column-oriented Table

- ▶ `class` list
- ▶ `length()`
- ▶ `index`
 - ▶ `[]`
 - ▶ `[[]]`
 - ▶ `$`

A special case of list!

```
head(iris)
```

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

```
str(iris)
```

```
## 'data.frame':   150 obs. of  5 variables:
##  $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4
##  $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9
##  $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7
##  $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.2
##  $ Species     : Factor w/ 3 levels "setosa"
```



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S4 Objects

► Structured in slots

► slotNames()

► @

► Validation

► validObject()

► Prototype

► new()

There is also **S3** and **R6**

```
library(taxlist)
```

```
str(Easplist)
```

```
## Formal class 'taxlist' [package "taxlist"] w
## ..@ taxonNames      : 'data.frame':  5393 ob
## .. ..$ TaxonUsageID  : int [1:5393] 1 5231
## .. ..$ TaxonConceptID: int [1:5393] 1 1 2
## .. ..$ TaxonName     : chr [1:5393] "Abelm
## .. ..$ AuthorName    : chr [1:5393] "(L.)
## ..@ taxonRelations: 'data.frame':  3887 ob
## .. ..$ TaxonConceptID: int [1:3887] 1 2 3
## .. ..$ AcceptedName  : int [1:3887] 1 2 3
## .. ..$ Basionym      : logi [1:3887] NA NA
## .. ..$ Parent        : int [1:3887] 54753
## .. ..$ Level         : Factor w/ 7 levels
## .. ..$ ViewID        : int [1:3887] 1 1 1
## ..@ taxonViews      : 'data.frame':  3 obs.
## .. ..$ ViewID       : int [1:3] 1 2 3
## .. ..$ secundum     : chr [1:3] "African
## .. ..$ view_bibtexkey: chr [1:3] "CJBGSANB
## ..@ taxonTraits     : 'data.frame':  314/27bs
```



Functions and Methods

`foo(par1 = arg1, ..., parn = argn)`

- Parameters (par)
- Arguments (arg)
- Output or Action

Methods are defined for an specific object class.

```
A <- c(1, NA, 3, 5)
```

```
mean(A)
```

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

```
mean(A, na.rm = TRUE)
```

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

```
summary(iris$Species)
```

```
##      setosa versicolor  virginica
```

```
##           50           50           50
```

```
summary(iris$Petal.Length)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
```

```
##      1.000   1.600   4.350   3.758   5.100   6.900
```



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Packages

- ▶ `install.packages()`
- ▶ Load Package to session
 - ▶ `library()`
 - ▶ `require()`
- ▶ `update.packages()`

```
install.packages("ade4")  
update.packages(ask = FALSE)
```

<https://cran.r-project.org/>

Available CRAN Packages By Name

ABCDEFGHIJKLMNOPQRSTUVWXYZ

A3
AATools
ABACUS
abbreviate
abbyyR
abc
abc.data
ABC.RAP
abcADM
ABCanalysis
abclass
ABCOptim
ABCp2
abcrf
abcrda
abctools
abd
abdiv
abe
abess
abglasso
ABHgenotypeR
abind
abjData
abjutils
abmR
abn
abnormality
abodOutlier
ABPS
abstr
abstractr
abtest
abundant
Ac3net
ACA
academictwitterR

Accurate, Adaptable, and Accessible Error Metrics for Predictive Models
Reliability and Scoring Routines for the Approach-Avoidance Task
Apps Based Activities for Communicating and Understanding Statistics
Readable String Abbreviation
Access to Abbyy Optical Character Recognition (OCR) API
Tools for Approximate Bayesian Computation (ABC)
Data Only: Tools for Approximate Bayesian Computation (ABC)
Array Based CpG Region Analysis Pipeline
Fit Accumulated Damage Models and Estimate Reliability using ABC
Computed ABC Analysis
Angle-Based Large-Margin Classifiers
Implementation of Artificial Bee Colony (ABC) Optimization
Approximate Bayesian Computational Model for Estimating P2
Approximate Bayesian Computation via Random Forests
Asymptotically Bias-Corrected Regularized Linear Discriminant Analysis
Tools for ABC Analyses
The Analysis of Biological Data
Alpha and Beta Diversity Measures
Augmented Backward Elimination
Fast Best Subset Selection
Adaptive Bayesian Graphical Lasso
Easy Visualization of ABH Genotypes
Combine Multidimensional Arrays
Databases Used Routinely by the Brazilian Jurimetrics Association
Useful Tools for Jurimetrical Analysis Used by the Brazilian Jurimetrics Association
Agent-Based Models in R
Modelling Multivariate Data with Additive Bayesian Networks
Measure a Subject's Abnormality with Respect to a Reference Population
Angle-Based Outlier Detection
The Abnormal Blood Profile Score to Detect Blood Doping
R Interface to the A/B Street Transport System Simulation Software
An R-Shiny Application for Creating Visual Abstracts
Bayesian A/B Testing
High-Dimensional Principal Fitted Components and Abundant Regression
Inferring Directional Conservative Causal Core Gene Networks
Abrupt Change-Point or Aberration Detection in Point Series
Access the Twitter Academic Research Product Track V2 API Endpoint



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devtools

- ▶ `install()`
- ▶ `install_github()`

For instance...

```
library(devtools)
install_github("ropensci/taxlist")
install_github("kamapu/vegetable")
```

devtools 2.4.5 Reference Articles ▼ News ▼



devtools

The aim of devtools is to make package development easier by providing R functions that simplify and expedite common tasks. [R Packages](#) is a book based around this workflow.

Installation

```
# Install devtools from CRAN
install.packages("devtools")

# Or the development version from GitHub:
install.packages("devtools")
devtools::install_github("r-lib/devtools")
```



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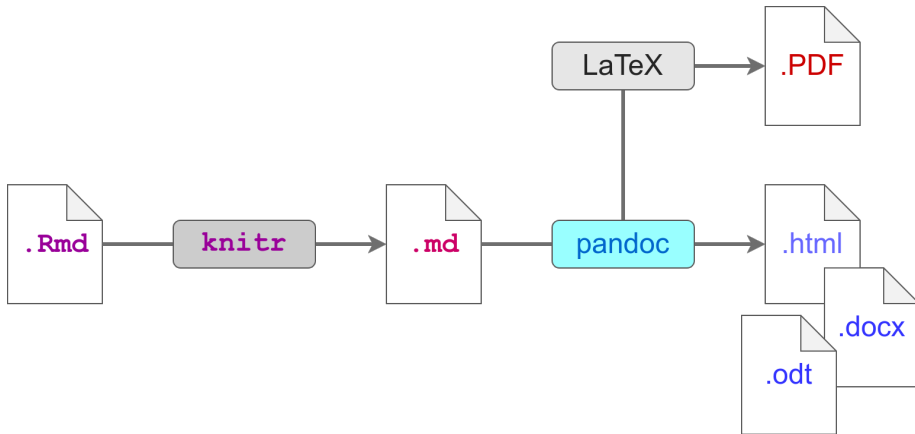
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r-vegetation - RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

61-rmarkdown.Rmd

```
1 ---
2 title: My first RMarkdown Document
3 author: Miguel
4 output:
5   html_document:
6     toc: true
7     toc_floating: true
8     serif_contained: true
9 ---
10
11 # Introduction
12
13 This is my first RMarkdown document.
14
15 Do you like to see a nice graphic?
16
17 ```{r}
18 plot(cars, xlab = "Speed (mph)", ylab = "Stopping distance (ft)", las = 1)
19 ```
20
```

1:1 My first RMarkdown Document

Console

~/.rstudio-projects/r-vegetation/01-rmarkdown.html

01-rmarkdown.html

My first RMarkdown Document

Miguel

- Introduction

Introduction

This is my first RMarkdown document.

Do you like to see a nice graphic?

```
plot(cars, xlab = "Speed (mph)", ylab = "Stopping distance (ft)", las = 1)
```

Stopping distance (ft)

Speed (mph)



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Taxonomic Names Resolution

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Thank You!

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