



IAVS-LAC

The Workshop

This Session

R

RMarkdown

Reconciliation

From the field to the desk

[Session 1]

Miguel Alvarez

21st April 2023



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Welcome!

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- ▶ 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**
 - ▶ *20:00 to 21:00 Coaching by João*
- ▶ Style
 - ▶ Slides for Introductions
 - ▶ Life Code
 - ▶ Exercises / Homeworks

Time Conversions

- ▶ 11:00 to 14:00 in **Colombia** (COT)
- ▶ 18:00 to 21:00 in **Germany** (CEST)



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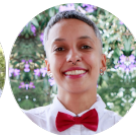
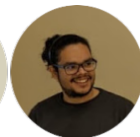
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Trainers

- ▶ Miguel: Main Trainer
- ▶ João: Coaching
- ▶ Marius: Technical support on R
- ▶ Coordination and Assistance:
 - ▶ Glenda
 - ▶ Gabriella



See [biosketches](#)



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Motivation

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

To describe a numerical variable, you can use the function `summary()`, for instance:

```
options(width = 40)
summary(iris$Petal.Length)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.
##   1.000   1.600   4.350   3.758   5.100
##      Max.
##   6.900
```



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Installing Instructions

Required Software

R Script

Data Sets

Download Data

Downloads Sessions Exercises

Downloads

Installing Software and Packages

A list of links to the required software is [here](#).

Once you mastered to get your system running, you will need to install some packages in **R**. For it, run [following skript](#) in your R session.

Download Data

A zip file with the data sets required for the R sessions can be downloaded [here](#).

Alternatively, you load the data in your working directory by running following code in your R session:

```
download.file(  
  url = "https://kamapu.github.io/r-vegetation/documents/course-data  
  destfile = "course-data.zip", method = "curl")  
unlink("course-data.zip", overwrite = TRUE)  
unlink("course-data.zip")
```



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- ▶ Refreshing R
- ▶ Introduction to RMarkdown
- ▶ Taxonomic Names 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] "8" "9" "10"
is.numeric(B)
## [1] FALSE
```



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integer

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logical (condition)

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character (names)

```
# index as integer
```

```
letters[15]
```

```
##      o
```

```
## "o"
```

```
# index as logical
```

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

```
##      d      e      f      g      h      i      j      k      l      m
```

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

```
##      n      o      p      q      r      s      t      u      v      w
```

```
## "n" "o" "p" "q" "r" "s" "t" "u" "v" "w"
```

```
##      x      y      z
```

```
## "x" "y" "z"
```

```
# index as character
```

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

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

```
##      m
```

```
## "m"
```



Special Values

- ▶ 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.

- ▶ 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"
```



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Data Frame

Column-oriented Table

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

A special case of list!

```
head(iris)
```

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

```
##   Petal.Width Species
## 1           0.2  setosa
## 2           0.2  setosa
## 3           0.2  setosa
## 4           0.2  setosa
## 5           0.2  setosa
## 6           0.4  setosa
```

```
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 ...
```




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S4 Objects

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► Structured in slots

► slotNames()

► @

► Validation

► validObject()

► Prototype

► new()

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

```
library(taxlist)
str(Easplst)
```

```
## 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':  311 ob
```



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.
```

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

```
##      Max.
```

```
##      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
abcrlda
abctools
abd
abdiv
abe
abess
abjlasso
ABHgenotypeR
abind
abjData
abjutils
abmR
abn
abnormality
abodOutlier
ABPS
abstr
abstractr
abtest
abundant
Ac3net
ACA
academictwitter

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 Jurimetrics 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/vegtable")
```

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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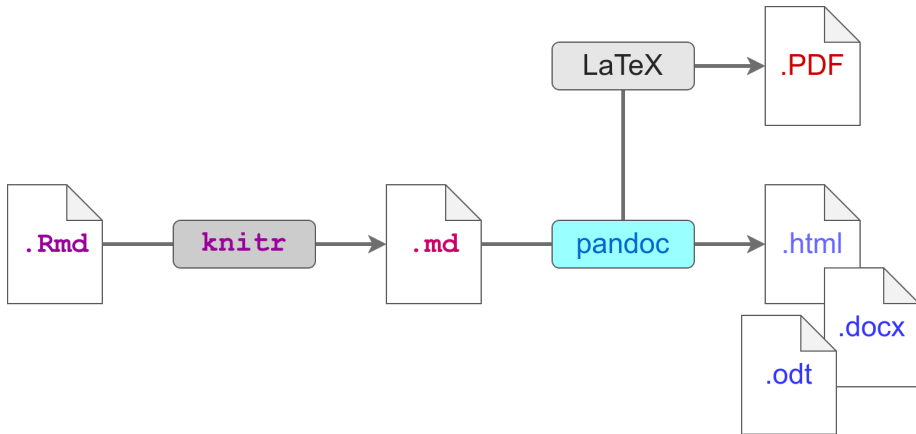
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r-vegetation - RStudio

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     serf_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

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

01-rmarkdown.html

Open in Browser

Find

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

- ▶ Taxonomy Equalization
- ▶ Taxonomic Standardization
- ▶ Taxonomic Harmonization
- ▶ Taxonomic Normalization
- ▶ Taxonomic Reconciliation

```
library(taxlist)
summary(Easplist, "Cyclosorus interruptus")

## -----
## concept ID: 50074
## view ID: 1
## level: species
## parent: 55055 Cyclosorus Link
##
## # accepted name:
## 50074 Cyclosorus interruptus (Willd.) H. Itô
##
## # synonyms (13):
## 52002 Dryopteris gongylodes (Schkuhr) Kuntze
## 52008 Thelypteris interrupta (Willd.) K. Iwa
## 52009 Cyclosorus striatus Ching
## 53097 Pteris interrupta Willd.
## 53098 Aspidium continuum Desv.
## 53099 Aspidium ecklonii Kunze
## 53100 Aspidium gongylodes Schkuhr
## 53101 Aspidium obtusatum Sw
```



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Online Databases

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[IPNI](#)

[Tropicos](#)

[TNRS](#)

[WFO](#)

[GBIF](#)

[Flora del Conosur](#)

[African Plant Database](#)



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Several R Packages

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[taxize](#)

[Taxonstand](#)

For a review, see [Grenié et al. \(2022\)](#)



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Thank You!

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