



IAVS-LAC

The Workshop

This Session

R

RMarkdown

Reconciliation

# From the field to the desk

## [Session 1]

Miguel Alvarez

21<sup>st</sup> April 2023



# The Workshop

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## Welcome!

### The Workshop

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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





# The Workshop

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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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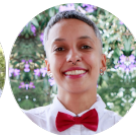
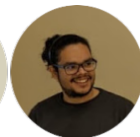
R

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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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# This Session

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





# R

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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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## Index

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Index

R



integer

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logical (condition)

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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"
```

```
## [10] "m" "n" "o" "p" "q" "r" "s" "t" "u"
```

```
## [19] "v" "w" "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

### ► 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] "Abelma
## .. ..$ 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")
```



## IAVS-LAC

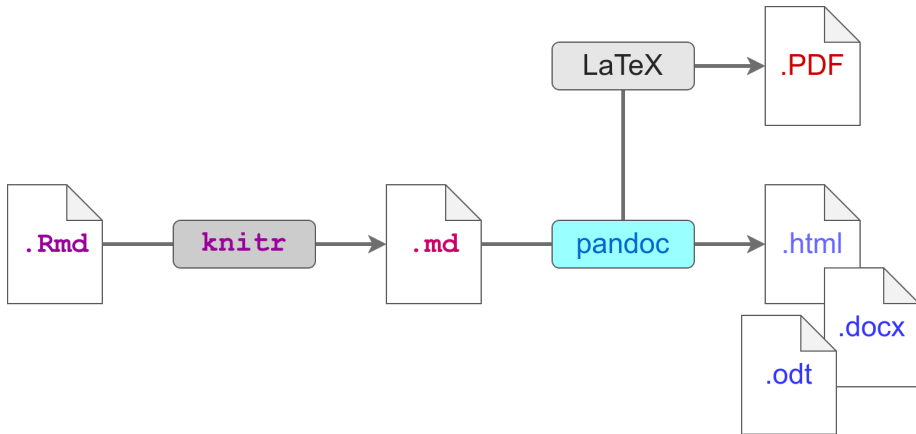
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# RMarkdown

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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](#)



# Reconciliation

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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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