From the field to the desk

[Session 1]

Miguel Alvarez

21st April 2023

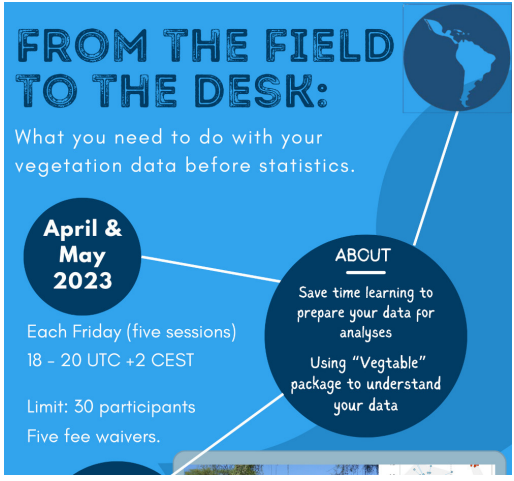
The Workshop

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



The Workshop

- 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)

The Workshop

Trainers

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

See biosketches

The Workshop

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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The Workshop

This Session

R

RMarkdown

Reconciliation

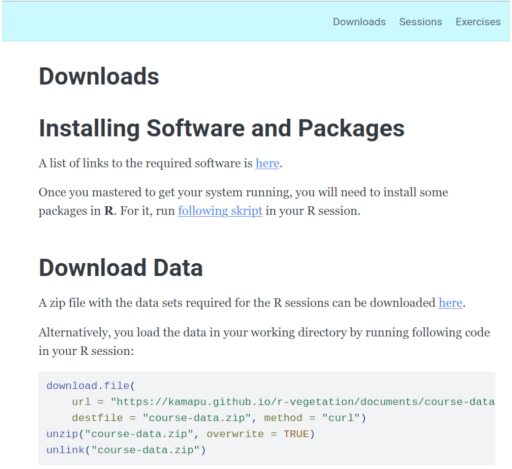
Installing Instructions

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")
unzip("course-data.zip", overwrite = TRUE)
unlink("course-data.zip")
```

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- Refreshing R
- Introduction to RMarkdown
- Taxonomic Names Resolution

R

- 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

- 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

- []
- Index
  - integer
  - logical (condition)
  - 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
```

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"
```

R

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 4
##  $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3
```

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':   311 obs
```

R

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
```

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

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

A3	Accurate, Adaptable, and Accessible Error Metrics for Predictive Models
AATtools	Reliability and Scoring Routines for the Approach-Avoidance Task
ABACUS	Apps Based Activities for Communicating and Understanding Statistics
abbreviate	Readable String Abbreviation
abbyyR	Access to Abbyy Optical Character Recognition (OCR) API
abc	Tools for Approximate Bayesian Computation (ABC)
abc.data	Data Only: Tools for Approximate Bayesian Computation (ABC)
ABC.RAP	Array Based CpG Region Analysis Pipeline
abcADM	Fit Accumulated Damage Models and Estimate Reliability using ABC
ABCanalysis	Computed ABC Analysis
abclass	Angle-Based Large-Margin Classifiers
ABCoptim	Implementation of Artificial Bee Colony (ABC) Optimization
ABCp2	Approximate Bayesian Computational Model for Estimating P2
abcrf	Approximate Bayesian Computation via Random Forests
abcrlda	Asymptotically Bias-Corrected Regularized Linear Discriminant Analysis
abctools	Tools for ABC Analyses
abd	The Analysis of Biological Data
abdiv	Alpha and Beta Diversity Measures
abe	Augmented Backward Elimination
abess	Fast Best Subset Selection
abglasso	Adaptive Bayesian Graphical Lasso
ABHgenotypeR	Easy Visualization of ABH Genotypes
abind	Combine Multidimensional Arrays
abjData	Databases Used Routinely by the Brazilian Jurimetrics Association
abjutils	Useful Tools for Jurimetrical Analysis Used by the Brazilian Jurimetrics Association
abmR	Agent-Based Models in R
abn	Modelling Multivariate Data with Additive Bayesian Networks
abnormality	Measure a Subject's Abnormality with Respect to a Reference Population
abodOutlier	Angle-Based Outlier Detection
ABPS	The Abnormal Blood Profile Score to Detect Blood Doping
abstr	R Interface to the A/B Street Transport System Simulation Software
abstractr	An R-Shiny Application for Creating Visual Abstracts
abtest	Bayesian A/B Testing
abundant	High-Dimensional Principal Fitted Components and Abundant Regression
Ac3net	Inferring Directional Conservative Causal Core Gene Networks
ACA	Abrupt Change-Point or Aberration Detection in Point Series
academictwitteR	Access the Twitter Academic Research Product Track V2 API Endpoint

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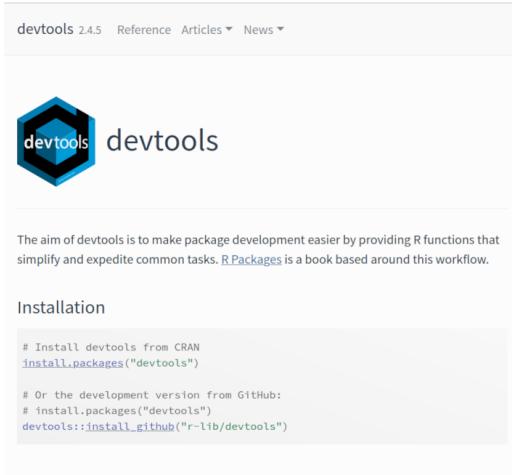
devtools

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

For instance...

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



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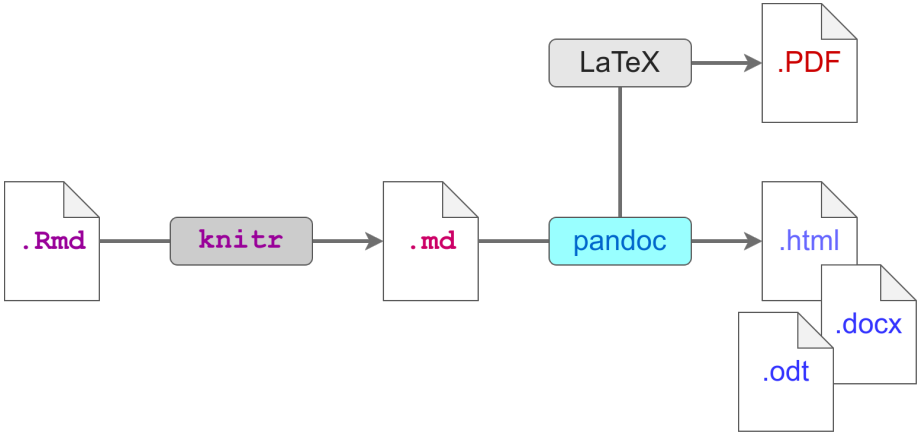
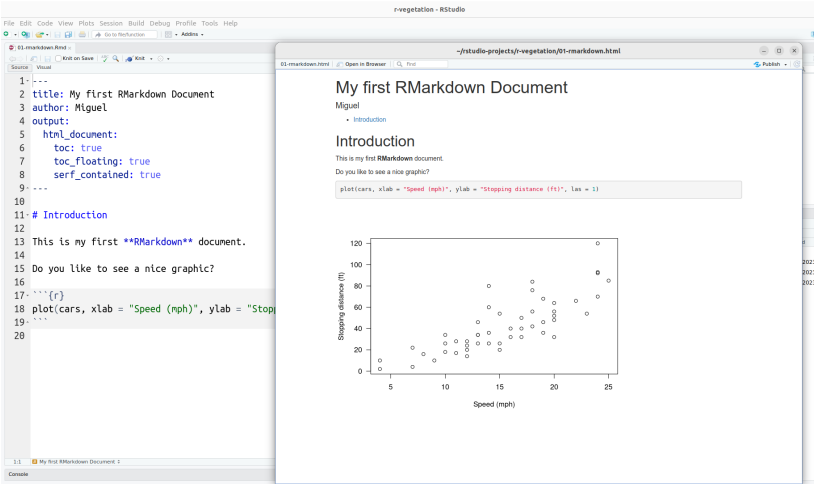


RMarkdown


r-vegetation - RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
01-rmarkdown.Rmd
Knit on Save
Knit
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 = "Stop
19 ```
20
1:1 My first RMarkdown Document 1
Console
~/rstudio-projects/r-vegetation/01-rmarkdown.html
01-rmarkdown.html
Open in Browser
Find
Publish
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)
0
0
20
40
60
80
100
120
5
10
15
20
25

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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.
```

Reconciliation

Online Databases

IPNI
Tropicos
TNRS
WFO
GBIF
Flora del Conosur
African Plant Database

Reconciliation

Several R Packages

taxize
Taxonstand

For a review, see Grenié et al. (2022)

Thank You!