From the field to the desk

[Session 1]

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21st April 2023

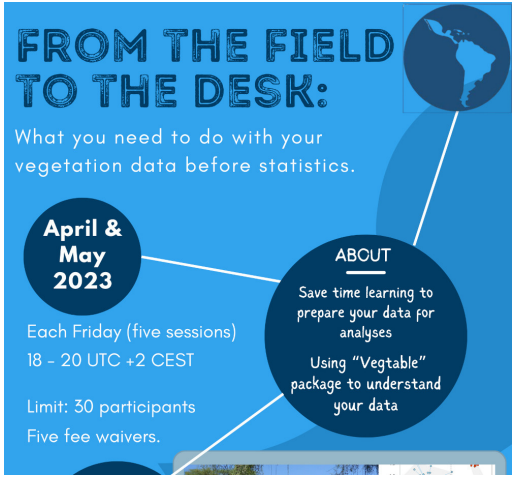
The Workshop

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

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The Workshop
This Session
R
RMarkdown
Name Resolution

- 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

- 11:00 to 13:00 in **Colombia** (COT)
- 18:00 to 22:00 in **Germany** (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

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"
```

```
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   n
## "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n"
##   x   y   z
## "x" "y" "z"
```

```
# index as character
names(letters) <- letters
letters["m"]
```

```
##   m
## "m"
```

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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"
```

Data Frame

Column-oriented Table

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

A special case of list!

```
head(iris)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal
## 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
```

```
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.
##  $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.
##  $ Species     : Factor w/ 3 levels "setosa"
```

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
```

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.    M
##   1.000   1.600   4.350   3.758   5.100   6.
```

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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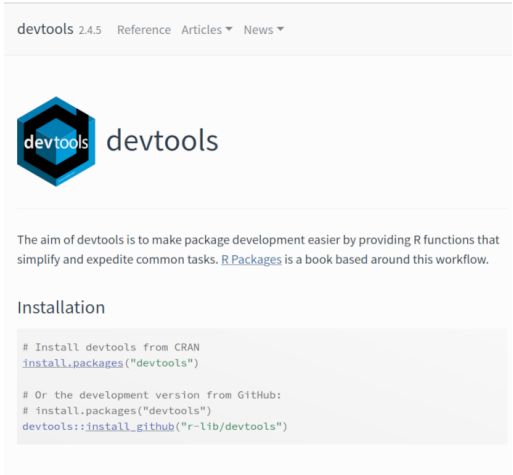
devtools

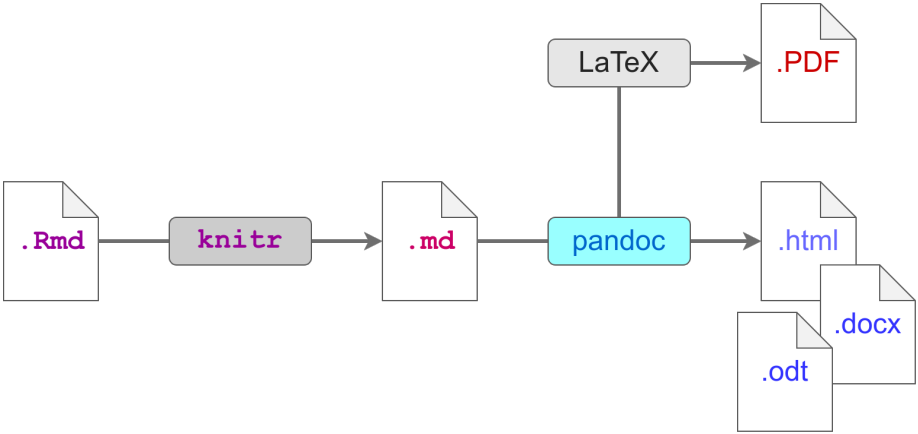
- `install()`
- `install_github()`

For instance...

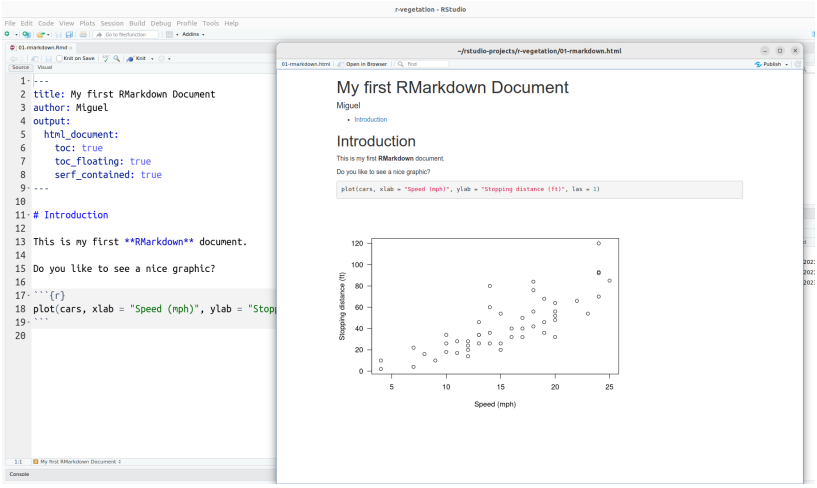
```
library(devtools)
install_github("ropensci/taxlist")
install_github("kamapu/vegtable")
```



RMarkdown



RMarkdown


r-vegetation - RStudio
01-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 = "Stop
19 ```
20
~/studio-projects/r-vegetation/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

Thank You!