

The Workshop
This Session
R
RMarkdown

TNRS

From the field to the desk [Session 1]

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This Session

R

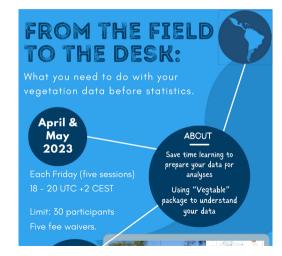
RMarkdown

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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





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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)



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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
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
```

```
## [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" "v" "z"
# index as character
names(letters) <- letters
letters["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(</pre>
   A = 1:10,
    B = matrix(1:10, nrow = 2),
    C = "This is a list")
my_list
## $A
## [1] 1 2 3 4 5 6
##
## $B
##
        [,1] [,2] [,3] [,4] [,5]
## [1,]
## [2,]
           2 4
                              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 Peta ## 1 5.1 3.5 1.4 ## 2 4.9 3.0 1.4

3 4.7 3.2 1.3 1.5 ## 4 4.6 3.1

5 5.0 3.6 1.4 ## 6 5.4 3.9 1.7

str(iris)

##

'data.frame':

\$ 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"

150 obs. of 5 variables:



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S4 Objects

Structured in slots

slotNames() **o**

Validation

validObject()

Prototype

library(taxlist) str(Easplist)

Formal class 'taxlist' [package "taxlist"] w ## ... 0 taxonNames

##

##

##

##

##

##

##

##

##

##

##

##

##

....\$ TaxonUsageID : int [1:5393] 1 5231\$ TaxonConceptID: int [1:5393] 1 1 2\$ TaxonName

.. ..\$ AuthorName .. @ taxonRelations: 'data.frame':

.. ..\$ TaxonConceptID: int [1:3887] 1 2 3\$ AcceptedName : int [1:3887] 1 2 3

.. ..\$ ViewID

.. ..\$ secundum

.. ..\$ Basionym\$ Parent

: int [1:3887] 54753\$ Level : Factor w/ 7 levels\$ ViewID

: int [1:3887] 1 1 1 ..@ taxonViews

0 towarTraita .ldata framal.

:'data.frame':

:'data.frame':

5393 ob

3887 ob

3 obs.

: int [1:3] 1 2 3 : chr [1:3] "African \$\sie view bibtexkey: chr [1:3] "CJBGSANB

: chr [1:5393] "Abelm

: chr [1:5393] "(L.)

: logi [1:3887] NA NA

new()

There is also S3 and R6



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Functions and Methods

 $foo(par_1 = arg_1, ..., par_n = arg_n)$

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

Methods are defined for an specific object class.

```
A \leftarrow 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



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Packages

R

- 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

ABCDEFGHIIKLMNOPORSTUVWXYZ

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 abbreviate Readable String Abbreviation Access to Abbyy Optical Character Recognition (OCR) API

abbyyR 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

A3

AATtools

ABACUS

abctools abd

abdiv

abess

abind

abiData

abjutils

abmR

abnormality

abodOutlier

abn

ABPS

abstr

abtest abundant

Ac3net

academictwitteR

ACA

abstractr

abglasso

ABHgenotypeR

abe

abcADM Fit Accumulated Damage Models and Estimate Reliability using ABC ARCanalysis Computed ABC Analysis Angle-Based Large-Margin Classifiers abelass

ABCoptim Implementation of Artificial Ree Colony (ARC) Optimization ABCp2 Approximate Bayesian Computational Model for Estimating P2

aberf Approximate Bayesian Computation via Random Forests abcrida 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 Broduct Track V2 ADI Endpoint



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- ▶ 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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Example of self-contained HTML as notebook.

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Taxonomic Names Resolution.

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