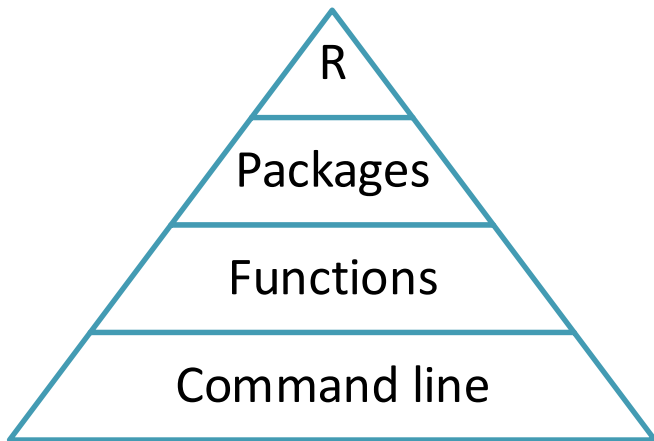


What is cran R?



What is cran R?

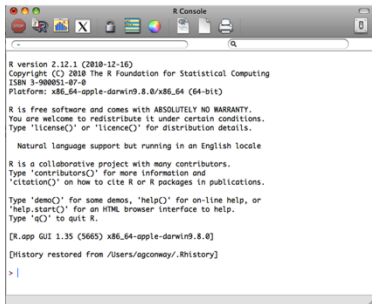


What is cran R?

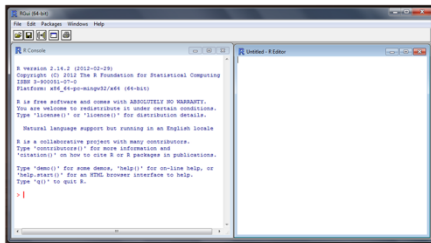
Here are some examples of the core packages that are commonly included with R:

1. **base** - This is the base R package that provides essential functions and data types.
2. **datasets** - This package contains various datasets that are frequently used for examples and testing.
3. **graphics** - Provides functions for creating graphical plots and charts.
4. **stats** - Includes statistical functions and models, such as linear regression and hypothesis testing.
5. ...

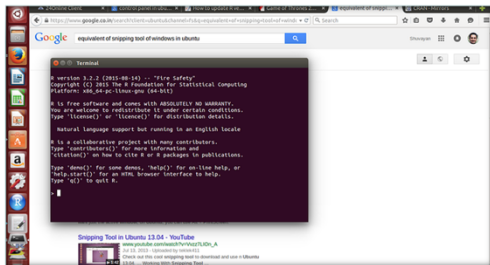
What is cran R?



```
R Console  
R version 2.12.1 (2010-12-16)  
Copyright (C) 2010 The R Foundation for Statistical Computing  
ISBN 3-900051-87-8  
Platform: x86_64-apple-darwin9.8.0/x86_64 (64-bit)  
  
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.  
  
Natural language support but running in an English locale  
  
R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.  
  
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.  
  
[R.app GUI 1.35 (5665) x86_64-apple-darwin9.8.0]  
[History restored from /Users/agconway/.Rhistory]  
> |
```



```
R R Console  
File Edit Packages Windows Help  
R Console  
R version 2.14.2 (2012-02-29)  
Copyright (C) 2012 The R Foundation for Statistical Computing  
ISBN 3-900051-07-0  
Platform: amd64-gnux86/x86_64 (64-bit)  
  
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.  
  
Natural language support but running in an English locale  
  
R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.  
  
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.  
  
> |
```



equivalent of snipping tool of windows in ubuntu

```
Terminal  
R version 3.2.2 (2013-09-14) -- "Fire Safety"  
Copyright (C) 2013 The R Foundation for Statistical Computing  
Platform: x86_64-pc-linux-gnu (64-bit)  
  
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.  
  
Natural language support but running in an English locale  
  
R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.  
  
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.  
  
- |
```

Snipping Tool in Ubuntu 12.04 - YouTube
www.youtube.com/watch?v=U3L0A
Jul 28, 2012 · Uploaded by mshelton11
Check out this cool snipping tool to download and use in Ubuntu
12.04... Ubuntu 12.04 Snipping Tool

Integrated development environment (IDE)

hello.qmd - _positron

```

python 3.12.1 (Python)
_positron

hello.qmd x
Preview Render on Save Source Visual Insert Code Cell Zoom 100%
SESSION HELP VIEWER CONNECTIONS
http://localhost:3750

python 3 hello.qmd 1 Meet the penguins
1
2 title: Hello, Quarto
3 format: html
4
5
6 # Run Cell (Run-Next Cell)
7 # (qysha)
8 # labels: load-packages
9 # include: false
10 from plotnine import *
11 from plotnine.data import penguins
12
13
14 ## Meet the penguins
15
16 The 'penguins' data from the 'plotnine' package contains size measurements for 344 penguins from three species observed on three islands in the Palmer Archipelago, Antarctica.
17
18 Figure 1 shows the relationship between flipper and bill lengths of these penguins.
19
20 # Run Cell (Run-Next Cell)
21 # (qysha)
22 # labels: fig-plot-penguins
23 # fig-caps: Flipper and bill length for penguins at Palmer Station LTER
24 # warnings: false
25 # echo: false
26
27 ggp<plot>(penguins, aes(x=flipper_length_mm, y=bill_length_mm)) +
  geom_point(aes(color=species), shape='diamond')
  
```

Meet the penguins

The `penguins` data from the `plotnine` package contains size measurements for 344 penguins from three species observed on three islands in the Palmer Archipelago, Antarctica.

Figure 1 shows the relationship between flipper and bill lengths of these penguins.

Bill length (mm)

Positron

<https://positron.posit.co/migrate-rstudio.html>

Rstudio

RStudio

```

File Edit Code View Project Workspace Plots Tools Help
diamonds.R plot.R diamonds
Source on Save Format Plot
library(ggplot2)
source("plot.R")
view(diamonds)
summary(diamonds)
summary(diamonds$price)
ave123 <- round(mean(diamonds$carat), 4)
clarity <- levels(diamonds$clarity)
p <- ggplot(carat, price,
  data=diamonds, color=clarity,
  xlab="Carat", ylab="Price",
  main="Diamond Pricing")
format(plot(p, size=24))
  
```

Workspace History

Data diamonds 53940 obs. of 10 variables

Values

ave123 0.7879

clarity character [8]

p ggplot [8]

Functions

format_plot(plot, size)

Files Plots Packages Help

Diamond Pricing

Price

Carat

Console

```

min. x: 0.000 min. y: 0.000 min. z: 0.000
1st Qu.: 4.710 1st Qu.: 4.720 1st Qu.: 2.910
median: 5.700 median: 5.710 median: 3.530
mean: 5.711 mean: 5.735 mean: 3.539
3rd Qu.: 6.540 3rd Qu.: 6.540 3rd Qu.: 4.040
Max.: 187.540 Max.: 18.900 Max.: 31.800
> summary(diamonds$price)
min. 1st Qu. median Mean 3rd Qu. Max.
326 950 2403 3933 5324 18620
> ave123 <- round(mean(diamonds$carat), 4)
> clarity <- levels(diamonds$clarity)
> p <- ggplot(carat, price,
+ data=diamonds, color=clarity,
+ xlab="Carat", ylab="Price",
+ main="Diamond Pricing")
> format(plot(p, size=24))
  
```

An editing window opens where you can write and save a series of instructions in a file: your **script**!

The screenshot displays the RStudio interface with three main panels:

- Source Editor (top left):** Contains an R script named 'diamondPricing.R'. The code is as follows:

```
1 library(ggplot2)
2 source("plots/formatPlot.R")
3
4 view(diamonds)
5 summary(diamonds)
6
7 summary(diamonds$price)
8 aveSize <- round(mean(diamonds$carat), 4)
9 clarity <- levels(diamonds$clarity)
10
11 p <- qplot(carat, price,
12           data=diamonds, color=clarity,
13           xlab="carat", ylab="price",
14           main="Diamond Pricing")
15
```
- Console (bottom left):** Shows the output of the script execution:

```
Min. : 0.000  Min. : 0.000  Min. : 0.000
1st Qu.: 4.710  1st Qu.: 4.720  1st Qu.: 2.910
Median : 5.700  Median : 5.710  Median : 3.530
Mean   : 5.731  Mean   : 5.735  Mean   : 3.539
3rd Qu.: 6.540  3rd Qu.: 6.540  3rd Qu.: 4.040
Max.   :10.740  Max.   :18.900  Max.   :31.800
> summary(diamonds$price)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  326   950   2401   3933   5324  18820
> aveSize <- round(mean(diamonds$carat), 4)
> clarity <- levels(diamonds$clarity)
> p <- qplot(carat, price,
+           data=diamonds, color=clarity,
+           xlab="carat", ylab="price",
+           main="Diamond Pricing")
> format.plot(p, size=24)
> |
```
- Plots Panel (bottom right):** Displays a scatter plot titled 'Diamond Pricing'. The x-axis is labeled 'Carat' (ranging from 0.0 to 3.5) and the y-axis is labeled 'Price' (ranging from 0 to 15000). The data points are colored by clarity, with a legend on the right showing categories: I1, SI2, SI1, VS2, VS1, VVS2, VVS1, and IF.

A terminal window giving all the output from the script

The screenshot displays the RStudio interface with three main panels:

- Source Editor:** Contains an R script with the following code:

```
1 library(ggplot2)
2 source("plots/formatPlot.R")
3
4 view(diamonds)
5 summary(diamonds)
6
7 summary(diamonds$price)
8 aveSize <- round(mean(diamonds$carat), 4)
9 clarity <- levels(diamonds$clarity)
10
11 p <- qplot(carat, price,
12           data=diamonds, color=clarity,
13           xlab="carat", ylab="price",
14           main="Diamond Pricing")
15
```
- Console:** Shows the output of the script, including summary statistics for the diamonds data and the execution of the plotting functions. The console output is highlighted with a red box:

```
Min. : 0.000 Min. : 0.000 Min. : 0.000
1st Qu.: 4.710 1st Qu.: 4.720 1st Qu.: 2.910
Median : 5.700 Median : 5.710 Median : 3.530
Mean : 5.731 Mean : 5.735 Mean : 3.539
3rd Qu.: 6.540 3rd Qu.: 6.540 3rd Qu.: 4.040
Max. :10.740 Max. :18.900 Max. :31.800
> summary(diamonds$price)
Min. 1st Qu. Median Mean 3rd Qu. Max.
326 950 2401 3933 5324 18820
> aveSize <- round(mean(diamonds$carat), 4)
> clarity <- levels(diamonds$clarity)
> p <- qplot(carat, price,
+           data=diamonds, color=clarity,
+           xlab="carat", ylab="price",
+           main="Diamond Pricing")
> format.plot(p, size=24)
> |
```
- Plots Panel:** Displays a scatter plot titled "Diamond Pricing". The x-axis is labeled "Carat" (ranging from 0.0 to 3.5) and the y-axis is labeled "Price" (ranging from 0 to 15000). The plot shows a positive correlation between carat weight and price, with points colored by clarity. A legend on the right lists clarity levels: I1, SI2, SI1, VS2, VS1, VVS2, VVS1, and IF.

A **Workspace** in which all the objects created/generated by the code are displayed (*i.e.* Matrices, Vectors, Functions, Constants...). It includes a **History** tab which returns all the executed instructions.

The screenshot displays the RStudio environment with the following components:

- Source Editor:** Contains R code for loading data, summarizing it, and creating a faceted plot.
- Workspace:** Shows the current environment with objects like 'diamonds', 'aveSize', 'clarity', 'p', and 'format.plot'.
- History:** Lists the executed R commands, such as 'library(ggplot2)', 'source()', 'view()', 'summary()', 'summary(diamonds\$price)', 'aveSize <- round(mean(diamonds\$carat), 4)', 'clarity <- levels(diamonds\$clarity)', 'p <- qplot(carat, price, data=diamonds, color=clarity, xlab="carat", ylab="price", main="Diamond Pricing")', and 'format.plot(p, size=24)'. This tab is highlighted with a red box.
- Console:** Shows the output of the executed code, including summary statistics for 'diamonds\$price' and 'diamonds\$carat', and the execution of the 'format.plot()' function.
- Plots:** A scatter plot titled 'Diamond Pricing' showing 'Price' on the y-axis (ranging from 0 to 10000) and 'Carat' on the x-axis (ranging from 0.0 to 3.0). The points are colored by 'Clarity', with a legend on the right showing categories: I1, SI2, SI1, VS2, VS1, VVS2, VVS1, and IF.

This last window contains 4 tabs :
Files (locates your working directory and allows you to navigate),
Plots (returns all graphic outputs),
Packages (package management)
Help (this is R's 112 or 911, contains all of R's help)

The screenshot displays the RStudio environment with the following components:

- Source Editor:** Contains R code for loading data, summarizing it, and creating a scatter plot. The code includes comments and function calls like `ggplot2`, `summary`, `round`, `levels`, `ggplot`, and `format.plot`.
- Console:** Shows the output of the code execution, including summary statistics for the `diamonds` dataset and the execution of the `format.plot` function.
- Environment/History:** Lists the loaded data (`diamonds` with 53940 observations) and the functions used (`format.plot`).
- Plots Panel:** Displays a scatter plot titled "Diamond Pricing" showing the relationship between Carat (x-axis) and Price (y-axis). The plot is color-coded by Clarity, with a legend on the right showing categories from I1 to IF.

The commandes on R:

An R command is either an expression or an assignment :

- ▶ Expression is directly evaluated, and the result is displayed on terminal

Exemple :

```
>2+3  
[1]5  
>sqrt(25)  
[1]5
```

Mathematical calcul

The commandes on R:

An R command is either an expression or an assignment :

- ▶ An assignement is an expression stored in object or variable

Exemple :

```
>a<-5  
>a  
[1]5
```



```
a <- 5
```

Object is named a

Value stored is 5

Sign used for d'affectation

<- ou =

Why store?

To manipulate later

The commandes on R:

An R command is either an expression or an assignment :

- ▶ An assignement is an expression stored in object or variable

Exemple :

```
>a<-5  
>a  
[1]5
```

```
a <- 5  
class(a)  
[1] Num
```

**It is very important to know
what type of object**

The commandes on R:

An R command is either an expression or an assignment :

▶ Object can be :

Character : ("A", "B", "C", ..)

Numeric : (1,2, 5.5, 6.7, ...)

Logic : (TRUE, FALSE)

▶ But also more complex:

Vector

Matrix

Data frame

List

The commandes on R:

Object Vector

- ▶ Vector contain only element with same mode (ex : numeric or character or logic ..)

```
Age = c(24, 26, 32, 54)
```

c() is the function to build a vector

Object type = Vector

There are the affected elements

The commandes on R:

What is the structure of my object ?

Function `class()` and `str()`

```
Age = c(24, 26, 32, 54)
```

```
str(Age)
```

```
Num[1:4]
```

```
class(Age)
```

```
Numeric
```

During the training we will see, how can we choose element inside a Vector or filter a vector

The commandes on R:

Object Matrix

- ▶ Matrix contains several vectors that build a table with columns and rows. The vectors belong to the same mode.

	[,1]	[,2]
[1,]	1	4
[2,]	2	5
[3,]	3	6

The commandes on R:

Object data frame

- ▶ Data frame contains several vectors that build a table with columns and rows. The vectors can belong to different modes

		colnames			
		Nom	Prenom	Age	Region_naissance
rownames	A	Keïta	Modibo	34	1
	B	Traoré	Moussa	23	2
	C	Konaré	Oumar	21	2
	D	Touré	Toumani	43	4
	E	Keïta	Boubacar	54	3

row.names() : row name (i.e. sample name)

colnames() : header(Nom, Prenom, etc)

The Workflow

Create Project

- Allow to save working environment automatically
- Keep the working environment open (scripts ...)

Check/Install packages

- `install.packages("your packages")`
- `BiocManager::install("dada2")`

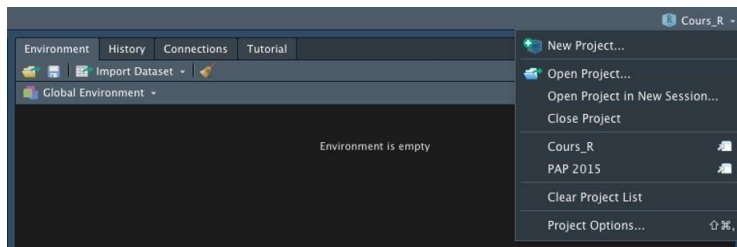
Load library

- `library("dada2")`
- `dada2::function`

Execute function

- `merge.Pairs(dadaFs, derepFS, verbose = TRUE)`




Work with projects with RStudio



Work with projects with RStudio

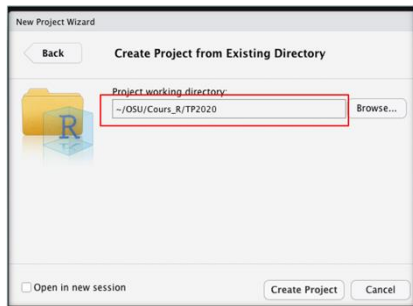
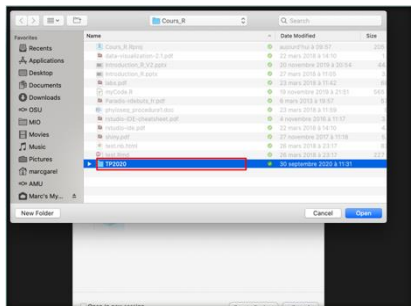
New Project

Create Project

-  **New Directory**
Start a project in a brand new working directory >
-  **Existing Directory**
Associate a project with an existing working directory >
-  **Version Control**
Checkout a project from a version control repository >

Cancel

Work with projects with RStudio



Check install packages

The screenshot shows the RStudio interface with the following components:

- Source Editor:** Contains R code for installing and loading packages. The code includes `install.packages()` for 'gridExtra' and 'vegan', `library()` for 'dada2', 'phyloseq', 'ggplot2', 'gridExtra', 'DECIPHER', and 'phangorn', and `setwd()` to set the working directory. A path is also defined for 'DATA_GAB'.
- Console:** Shows the execution of `install.packages()` for 'gridExtra' and 'vegan', followed by `library(phyloseq)`. The output indicates that 'phyloseq' is attached to the search path.
- Environment Pane:** Shows the 'Global Environment' with a variable 'a' having a value of 5.
- Packages Pane:** Lists installed and available packages. The 'crayon' package is highlighted with a red oval. The list includes packages like 'codetools', 'colorspace', 'compiler', 'crayon', 'curl', 'dada2', 'data.table', 'datasets', 'DBI', 'DECIPHER', and 'DelayedArray'.

```
13 install.packages("gridExtra")
14 install.packages("vegan")
15
16
17 library("dada2"); packageVersion("dada2")
18 library("phyloseq")
19 library("ggplot2")
20 library("gridExtra")
21 library("DECIPHER")
22 library("phangorn")
23 library("vegan")
24 setwd("~/Formation2019TUN/")
25
26 path=~/"Formation2019TUN/DATA_GAB"
27
28 (Untitled) R Script
```

~/Desktop/...
m3G/downloaded_packages
Update old packages: 'cluster', 'formatR', 'GenomicAlignments',
'GenomicFeatures',
'ggplot2', 'markdown', 'mime', 'phangorn', 'rlang', 'rtracklaye
r', 'tibble', 'xfun',
'XML'
Update all/some/none? [a/s/n]:
n
> library("phyloseq")
Attachment du package : 'phyloseq'

Name	Description	Version
<input type="checkbox"/> codetools	Code Analysis Tools for R et al.	0.2-16
<input type="checkbox"/> colorspace	A Toolbox for Manipulating and Assessing Colors and Palettes	1.4-1
<input type="checkbox"/> compiler	The R Compiler Package	3.6.0
<input checked="" type="checkbox"/> crayon	Colored Terminal Output	1.3.4
<input type="checkbox"/> curl	A Modern and Flexible Web Client for R	3.3
<input type="checkbox"/> dada2	Accurate, high-resolution sample inference from amplicon sequencing data	1.12.1
<input type="checkbox"/> data.table	Extension of 'data.frame'	1.12.2
<input checked="" type="checkbox"/> datasets	The R Datasets Package	3.6.0
<input type="checkbox"/> DBI	R Database Interface	1.0.0
<input checked="" type="checkbox"/> DECIPHER	Tools for curating, analyzing, and manipulating biological sequences	2.12.0
<input type="checkbox"/> DelayedArray	A unified framework for working transparently with on-disk and	0.10.0

Check install packages :CRAN package

```
ECIPHER")  
hangorn")  
egan")  
ormation2019TUN/")
```

```
rmation2019TUN/DATA_GAB"
```

```
Jobs
```

```
ackages  
s: 'cluster', 'formatR', 'GenomicAlignments',  
'arrow', 'rmarkdown', 'phangorn', 'rlang', 'r  
'
```

```
one? [a/s/n]:
```

```
sq")
```

```
ackage : 'phyloseq'
```

```
act is masked from 'package:IRanges':
```

The screenshot shows the RStudio interface with the 'Install Packages' dialog box open. The background is a terminal window with R code. The dialog box has the following fields and options:

- Install from:** Repository (CRAN) (with a link to 'Configuring Repositories')
- Packages (separate multiple with space or comma):** (empty text box)
- Install to Library:** /Library/Frameworks/R.framework/Versions/3.6/Resources/libra (dropdown menu)
- Install dependencies
- Buttons: Install, Cancel

Below the dialog box, a list of installed or available packages is visible:

- dichromat Color Schemes for Dichromats
- digest Create Compact Hash Digests of R Objects
- ensembledb Utilities to create and use Ensembl-based annotat

Check install packages :Bioconductor package

Command line is mandatory

```
19 library("ggplot2")
20 library("gridExtra")
21 library("DECIPHER")
22 library("phangorn")
23 library("vegan")
24 setwd("~/Formation2019TUN/")
25
26 path "~/Formation2019TUN/DATA_GAB"
20:21 (Untitled) R Script
```

Console Terminal x Jobs x

```
~/Desktop/
>
>
> BiocManager::install("dada2", version = "3.9")
Bioconductor version 3.9 (BiocManager 1.30.4), R 3.6.0 (2019-04-26)
Installing package(s) 'dada2'
essai de l'URL 'https://bioconductor.org/packages/3.9/bioc/bin/macosx/el-capitan/contrib/3.6/dada2_1.12.1.tgz'
Content type 'application/x-gzip' length 2576762 bytes (2.5 MB)
=====
downloaded 2.5 MB
```

Files	Plots	Packages	Help
Name	Description		
<input type="checkbox"/> fastmatch	Fast match() fun		
<input type="checkbox"/> foreach	Provides Foreac		
<input type="checkbox"/> foreign	Read Data Store		
<input type="checkbox"/> formatR	Format R Code		
<input type="checkbox"/> Formula	Extended Mode		
<input type="checkbox"/> futile.logger	A Logging Utilit		
<input type="checkbox"/> futile.options	Futile Options M		
<input type="checkbox"/> gdata	Various R Progr		
<input type="checkbox"/> GenomeInf...	Utilities for mar		

Load library to execute function

```
8 ~/Desktop/
9 installing package(s)
essai de l'URL 'https://bioconductor.org/packages/3.9/bioc/bin/macosx/el-capitan/contrib/3.6/dada2_1.12.1.tgz'
10 Content type 'application/x-gzip' length 2576762 bytes (2.5 MB)
=====
11 downloaded 2.5 MB

12 The downloaded binary packages are in
   /var/folders/j0/8vvynk7d3ws46jrp4z4d005r0000gn/T//Rtmp7mum3G/downloaded_packages
13 >
14 >
15 > library("dada2")
16 Le chargement a nécessité le package : Rcpp
> |
```

Diapositive 11 sur 16 Français (France) Notes

Or use command as : `package::function()`

```
---  
title: "ggplot2 demo"  
author: "Norah Jones"  
date: "5/22/2021"  
format:  
  html:  
    code-fold: true  
---  
  
## Air Quality  
  
@fig-airquality further explores the impact of temperature on ozone level.  
```${r}``  
#| label: fig-airquality
#| fig-cap: "Temperature and ozone level."
#| warning: false

library(ggplot2)

ggplot(airquality, aes(Temp, Ozone)) +
 geom_point() +
 geom_smooth(method = "loess")
...
```

## ggplot2 demo

Norah Jones  
May 22nd, 2021

### Air Quality

[Figure 1](#) further explores the impact of temperature on ozone level.

► Code

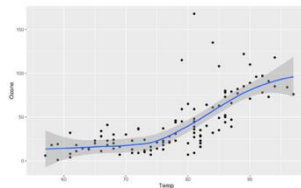
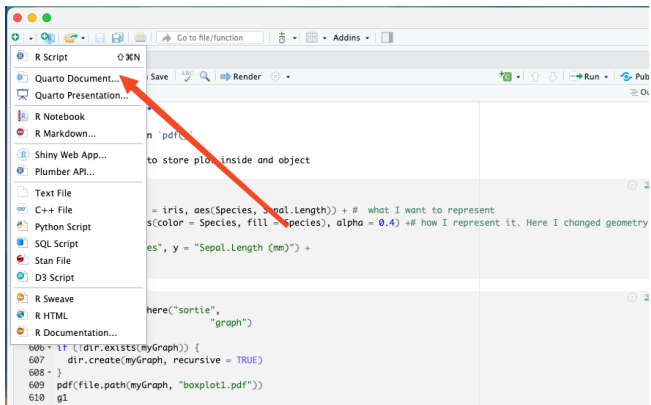


Figure 1: Temperature and ozone level.

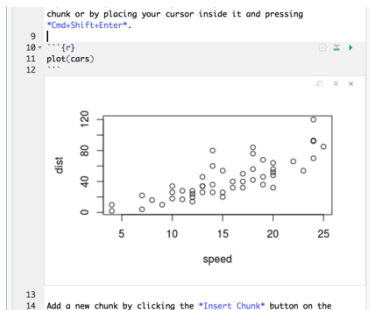
An R Quarto, is a document with chunks that can be executed independently and interactively, with output visible immediately beneath the input. It is more flexible than Markdown

# R Quarto



# Creating a Quarto instead of the classical script

- ▶ You can create a new notebook in RStudio with the menu command `File` → `New File` → `Quarto document`.
- ▶ Notebook chunks can be inserted quickly using the keyboard shortcut `Ctrl + Alt + I` (macOS: `Cmd + Option + I`), or via the `Insert` menu in the editor toolbar.
- ▶ Between chunks, you can comment all your results.



```

title: "ggplot2 demo"
author: "Norah Jones"
date: "5/22/2021"
format:
 html:
 fig-width: 8
 fig-height: 4
 code-fold: true

Air Quality

@fig-airquality further explores the impact of
temperature on ozone level.

``{r}
#| label: fig-airquality
#| fig-cap: "Temperature and ozone level."
#| warning: false

library(ggplot2)
ggplot(airquality, aes(Temp, Ozone)) +
 geom_point() +
 geom_smooth(method = "loess")
...
```

## ggplot2 demo

Norah Jones

May 22nd, 2021

### Air Quality

[Figure 1](#) further explores the impact of temperature on ozone level.

► Code

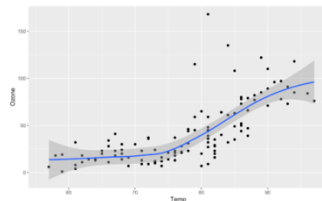


Figure 1: Temperature and ozone level.

manuscript-template-rstudio-test - main - RStudio

manuscript-template-rstudio-test

index.qmd

```

1 ---
2 title: La Palma Earthquakes
3 author:
4 - name: Steve Purves
5 orcid: 0000-0002-0760-5497
6 corresponding: true
7 email: steve@curvenote.com
8 roles:
9 - Investigation
10 - Project administration
11 - Software
12 - Visualization
13 affiliations:
14 - Curvenote
15 - name: Rowan Cockett
16 orcid: 0000-0002-7859-8394
17 corresponding: false
18 roles: []
19 affiliations:
20 - Curvenote
21 keywords:
22 - La Palma
23 - Earthquakes
24 abstract: |
25 In September 2021, a significant jump in seismic activity on

```

6:22 La Palma Earthquakes

Preview: index.qmd Running 42:28

Output created: index.html

Watching files for changes  
GET: /index.html

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La Palma Earthquakes

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ABSTRACT  
In September 2021, a significant jump in seismic activity on the island of La Palma (Canary Islands, Spain) signaled the start of a volcanic crisis that still continues at the time of writing. Earthquake data is continually collected and published by the Instituto Geográfico Nacional (IGN). ...

## 1 Introduction

Figure 1: Timeline of recent earthquakes on La Palma

<https://quarto.org/docs/manuscripts/authoring/rstudio.html>

A demo before practice...