1.3.1: Introduction to R and R Studio

(Asynchronous-Online)

Session Objectives

1. Get acquainted with R and R Studio
2. Write simple R code in Console
3. Create your first R script
4. Install and load R packages (understanding your R session)
5. Create your first R Markdown report and produce output files in different formats (HTML, PDF, or DOCX)

---

0. Prework - Before You Begin

> ℹ R versus RStudio
>
> Note: **R** is the name of the programming language itself and **RStudio** is an integrated development environment (IDE) which is an enhanced interface for better organization, files management and analysis workflows.

Software and Applications to Download

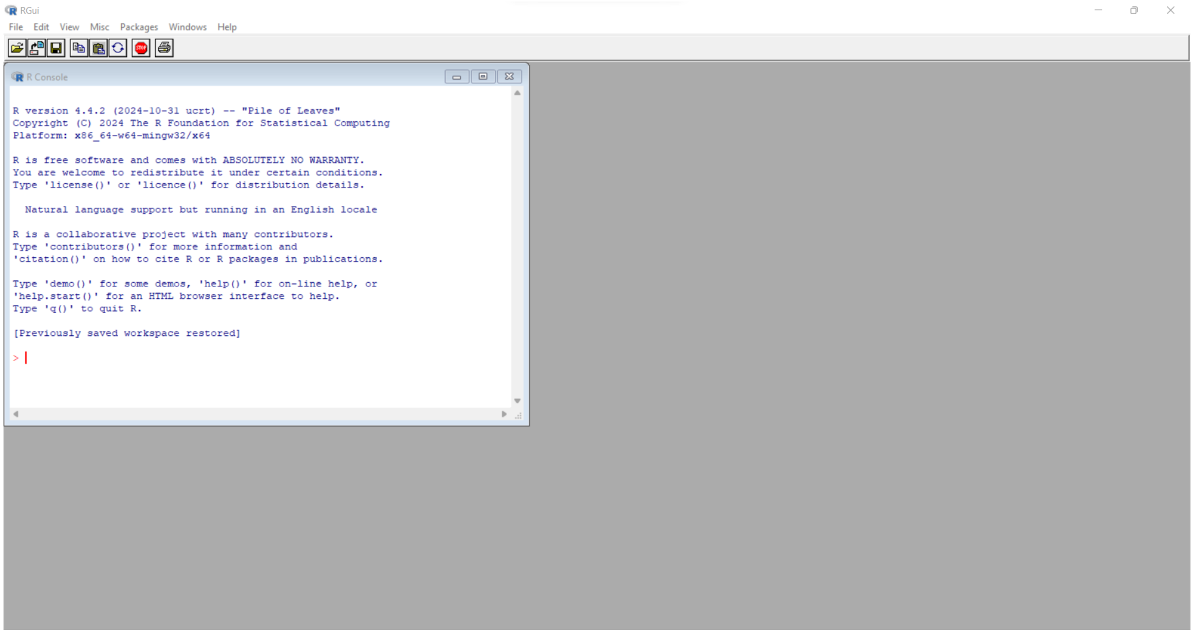
1. FIRST, Download and install R onto your computer from https://cran.r-project.org/.
2. NEXT, After installing R, download and install RStudio Desktop onto your computer from https://posit.co/download/rstudio-desktop/.

---

1. Get aquainted with R and R Studio

Basic R

When you download **R** from **CRAN** and install it on your computer, there is an R application that you can run. However, it is very bare bones. Here is a screenshot of what it looks like on my computer (Windows 11 operating system).



```
R version 4.4.2 (2024-10-31 ucrt) -- "Pile of Leaves"
Copyright (C) 2024 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64

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.
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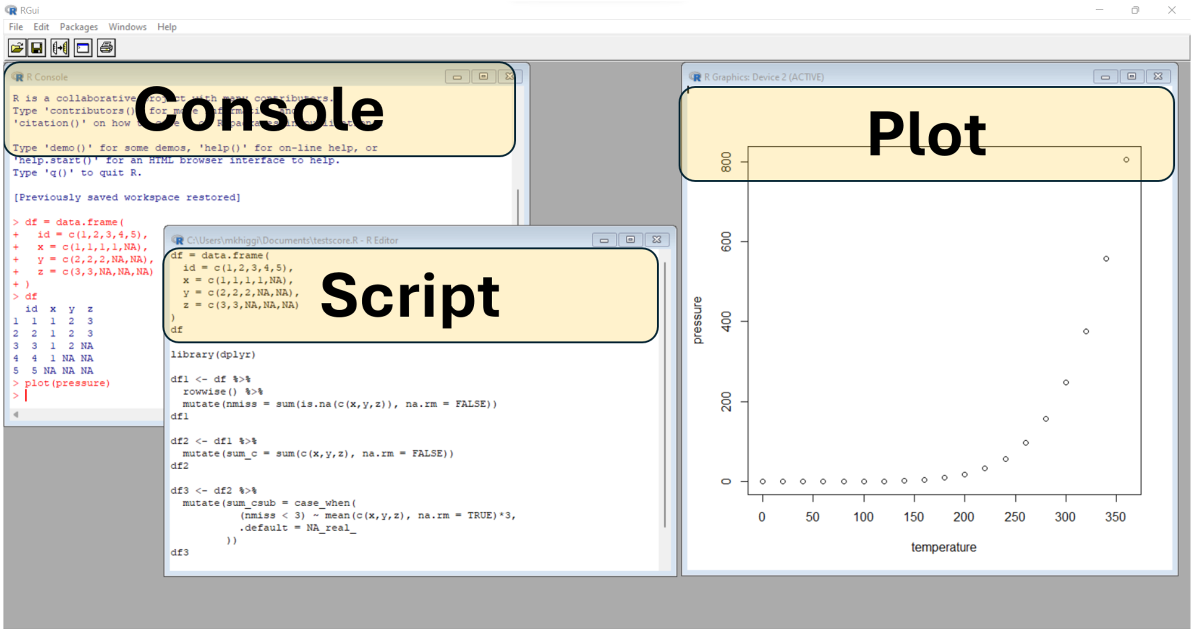
'citation()' on how to cite R or R packages in publications.

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.

[Previously saved workspace restored]

> 
```

You can type commands in the console window at the prompt ">" but this is slow and tedious. You can also write and execute scripts from inside this application and see the output back in the console window as well as creating plots. But managing large projects using this interface is not efficient.



```
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Type 'q()' to quit R.

[Previously saved workspace restored]

> df = data.frame(
+   id = c(1,2,3,4,5),
+   x = c(1,1,1,1,NA),
+   y = c(2,2,2,NA,NA),
+   z = c(3,3,NA,NA,NA)
+ )
> df
  id  x  y  z
1  1  1  2  3
2  2  1  2  3
3  3  1  2 NA
4  4  1 NA NA
5  5 NA NA NA
> plot(pressure)
> 
```

```
df = data.frame(
  id = c(1,2,3,4,5),
  x = c(1,1,1,1,NA),
  y = c(2,2,2,NA,NA),
  z = c(3,3,NA,NA,NA)
)
df

library(dplyr)

df1 <- df %>%
  rowwise() %>%
  mutate(nmiss = sum(is.na(c(x,y,z)), na.rm = FALSE))
df1

df2 <- df1 %>%
  mutate(sum_c = sum(c(x,y,z), na.rm = FALSE))
df2

df3 <- df2 %>%
  mutate(sum_csub = case_when(
            (nmiss < 3) ~ mean(c(x,y,z), na.rm = TRUE)*3,
            .default = NA_real_
          ))
df3
```

RStudio IDE

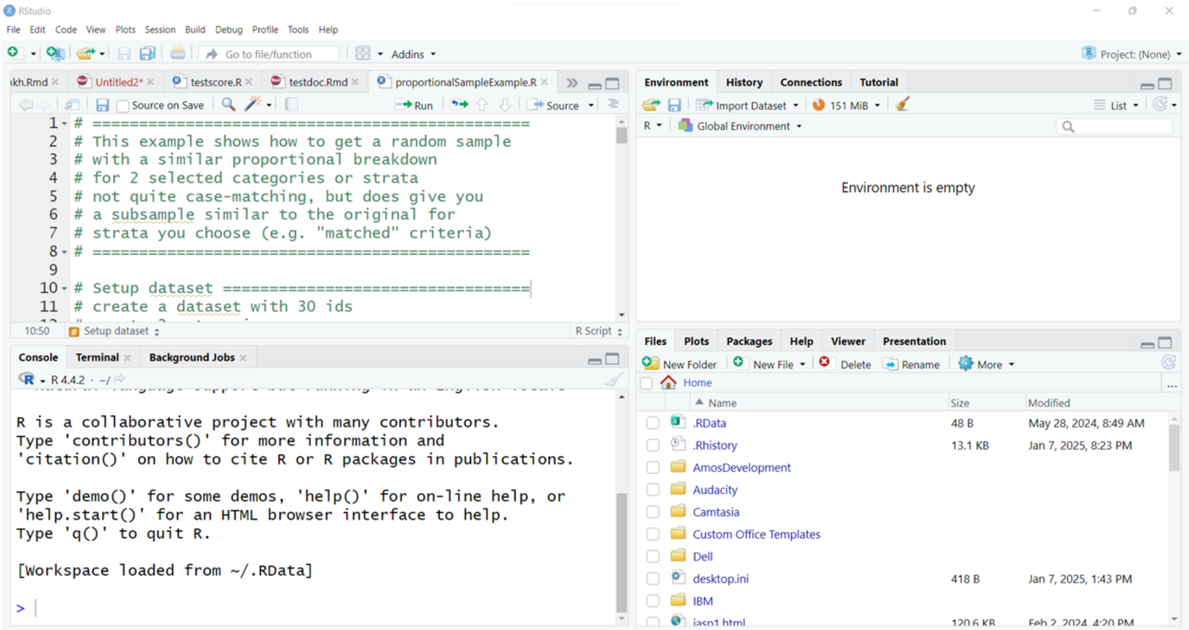
RStudio Desktop Software vs Posit the company

RStudio was founded in 2009 https://posit.co/about/ when it published the “free and open source” RStudio software. But over time, the RStudio application has expanded beyond just being used for the R programming language. You can now use RStudio for writing and managing projects with Python code, Markdown, LaTeX, Cascading Style Sheets and more.

So, in 2022, RStudio the company became Posit https://posit.co/blog/rstudio-is-becoming-posit/ to encompass the broader computing community.

The RStudio Integrated Development Environment (IDE) application provides much better tools for managing files within a given “project”. This biggest advantage of working in an IDE is everything is contained and managed within a given project, which is linked to a specific folder (container) on your computer (or cloud drive you may have access to).

However, you will still need to write and execute code using scripts and related files. An IDE is NOT a GUI (graphical user interface) which is the “point and click” workflow you may have experience with if you’ve used other analysis software applications such as SPSS, SAS Studio, Excel and similar.



```
# =============================================
# This example shows how to get a random sample
# with a similar proportional breakdown
# for 2 selected categories or strata
# not quite case-matching, but does give you
# a subsample similar to the original for
# strata you choose (e.g. "matched" criteria)
# =============================================

# Setup dataset ================================
# create a dataset with 30 ids
```

```
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'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Workspace loaded from ~/.RData]

>
```

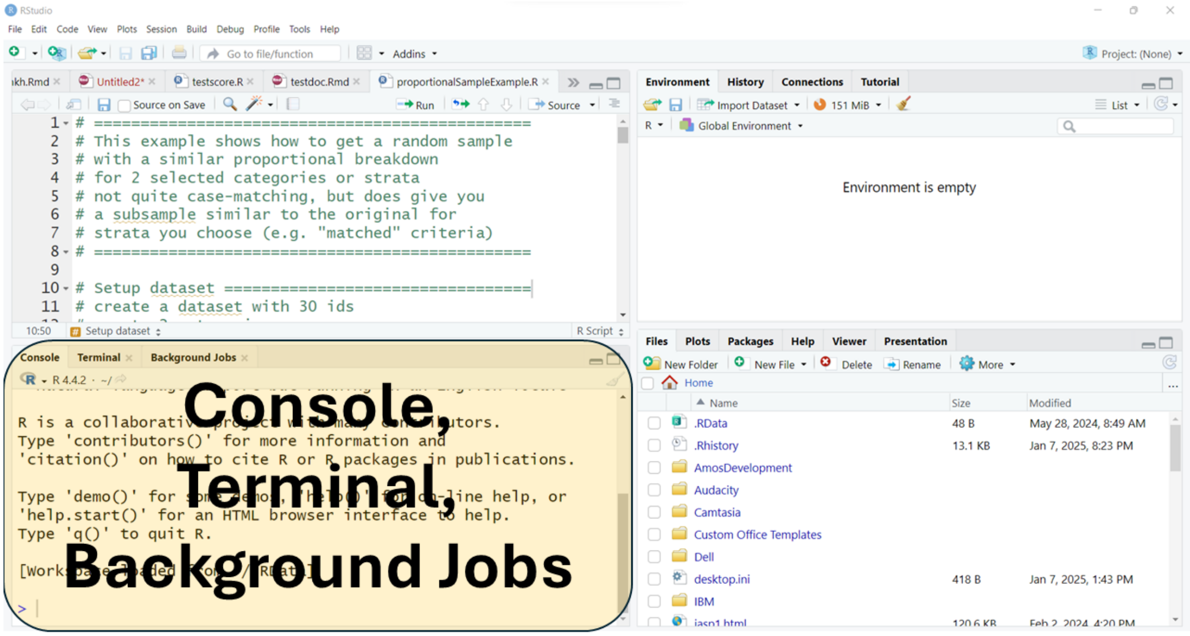
Environment is empty

Name	Size	Modified
.RData	48 B	May 28, 2024, 8:49 AM
.Rhistory	13.1 KB	Jan 7, 2025, 8:23 PM
AmosDevelopment		
Audacity		
Camtasia		
Custom Office Templates		
Dell		
desktop.ini	418 B	Jan 7, 2025, 1:43 PM
IBM		

The interface is usually arranged with the following 4 “window panes”:

- Console
- Source
- Environment
- Files

The typical arrangement, usually has the "Console" window pane at the bottom left. This window also usually has TABs for the "Terminal" and any "Background Jobs" that might be running.



```
# ================================================
# This example shows how to get a random sample
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>
```

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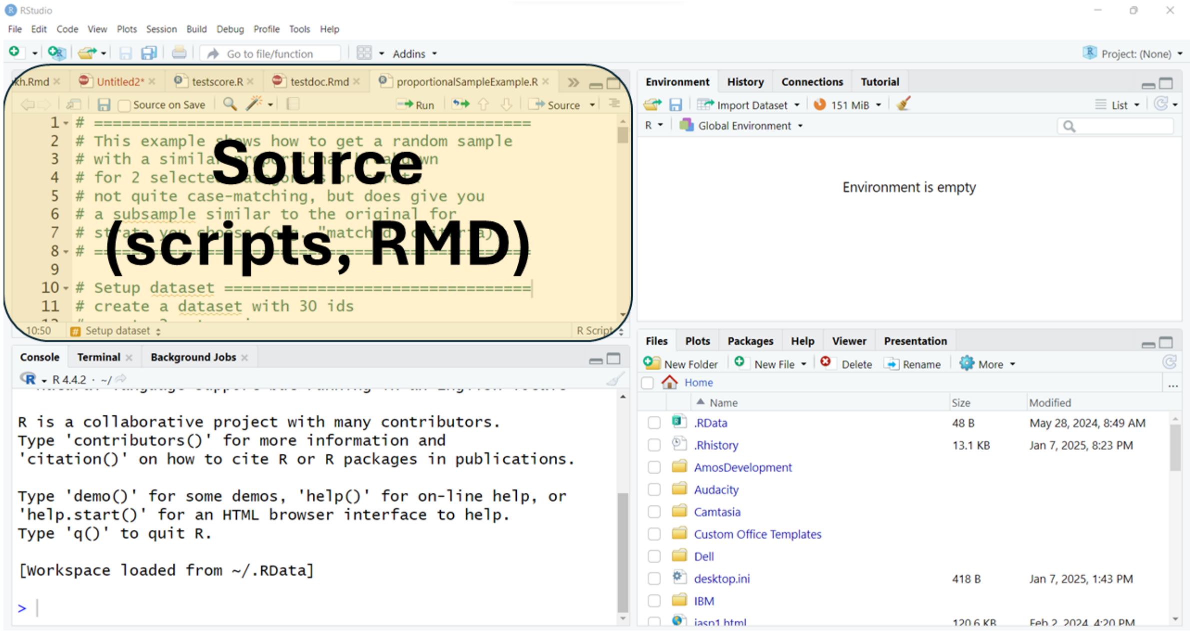
Custom Office Templates		
Dell		
desktop.ini	418 B	Jan 7, 2025, 1:43 PM
IBM		

The “Source” window pane is usually at the top left. This is where you will do most of your editing of your R program scripts (`*.R`) or Rmarkdown files (`*.Rmd`). This is also where the data viewer window will open. You can also open and edit other kinds of files here as well (`*.tex`, `*.css`, `*.txt`, and more).



```
# ==============================================
# This example [illegible] how to get a random sample
# with a simila[illegible]
# for 2 selecte[illegible]
# not quite case-matching, but does give you
# a subsample similar to the original for
# st[illegible]
# [illegible]

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[Workspace loaded from ~/.RData]

> 
```

Name	Size	Modified
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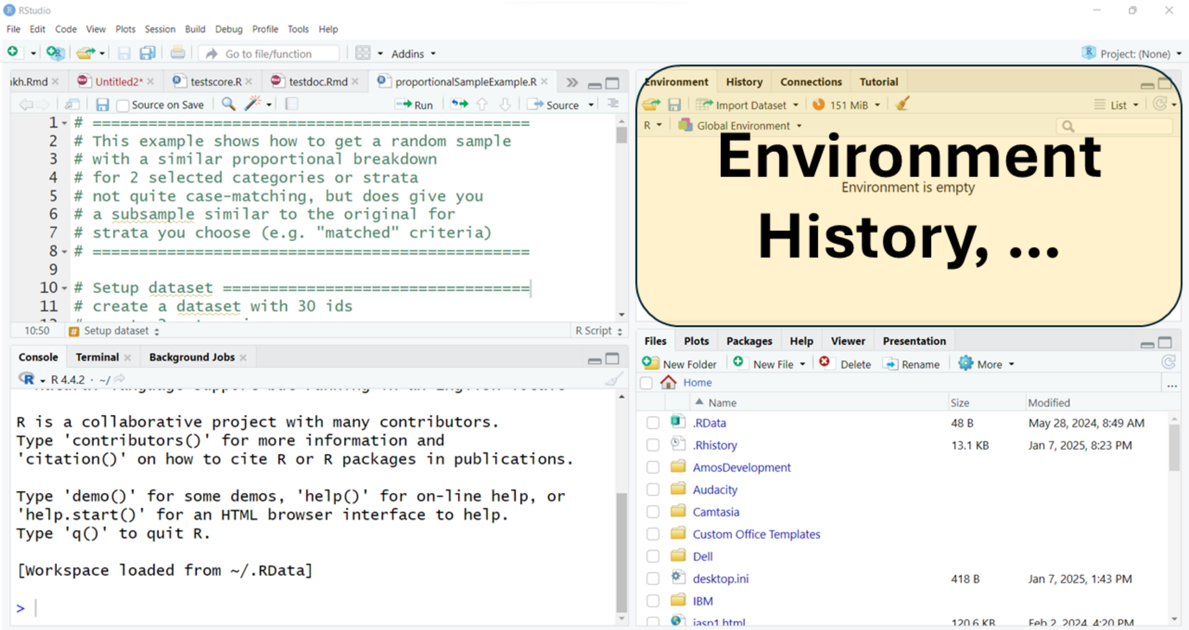
AmosDevelopment		
Audacity		
Camtasia		
Custom Office Templates		
Dell		
desktop.ini	418 B	Jan 7, 2025, 1:43 PM
IBM		

The top right window pane should always have your “Environment”, “History” and “Tutorial” TABs but may also have TABs for “Build” and “Git” and others depending on your project type and options selected.



```
# ===============================================
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# with a similar proportional breakdown
# for 2 selected categories or strata
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```

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[Workspace loaded from ~/.RData]

> 
```

Name	Size	Modified
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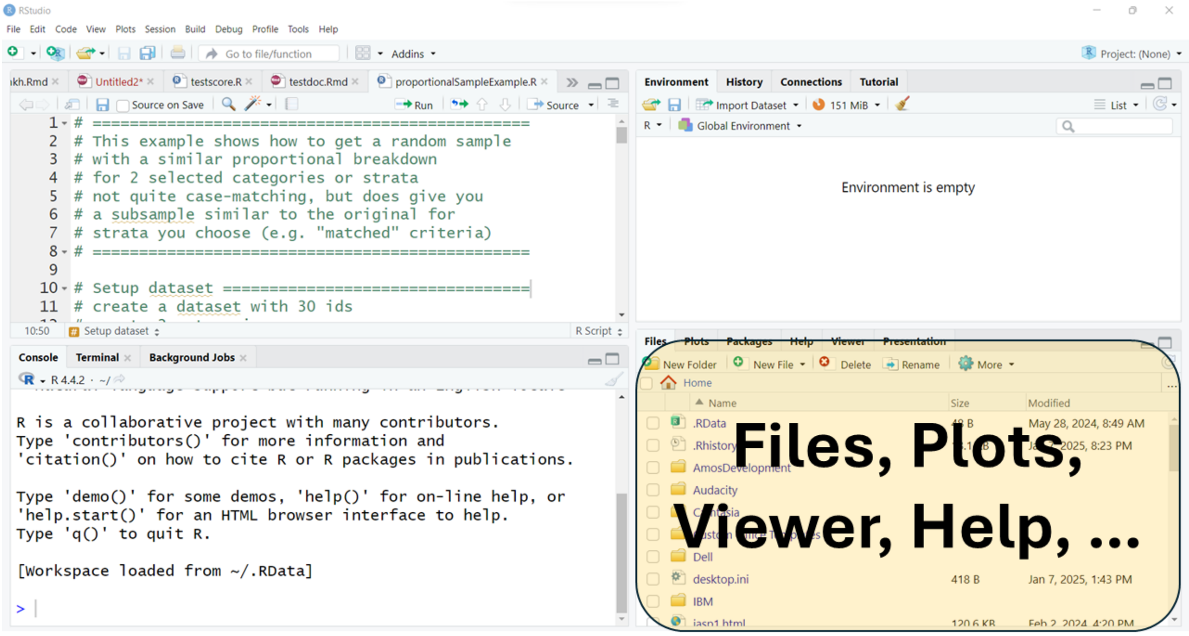
AmosDevelopment		
Audacity		
Camtasia		
Custom Office Templates		
Dell		
desktop.ini	418 B	Jan 7, 2025, 1:43 PM
IBM		
iasp1.html	120.6 KB	Feb 2, 2024, 4:20 PM

The bottom right window pane has TABs for your:

- "Files" directory
- "Plots" window for graphical output
- "Packages" - which lists all add-on R packages installed on your computer
- "Help" window
- as well as other TABs for "Viewer" and "Presentation" for viewing other kinds of output.



```r
# ==============================================
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Type 'q()' to quit R.

[Workspace loaded from ~/.RData]

> 
```
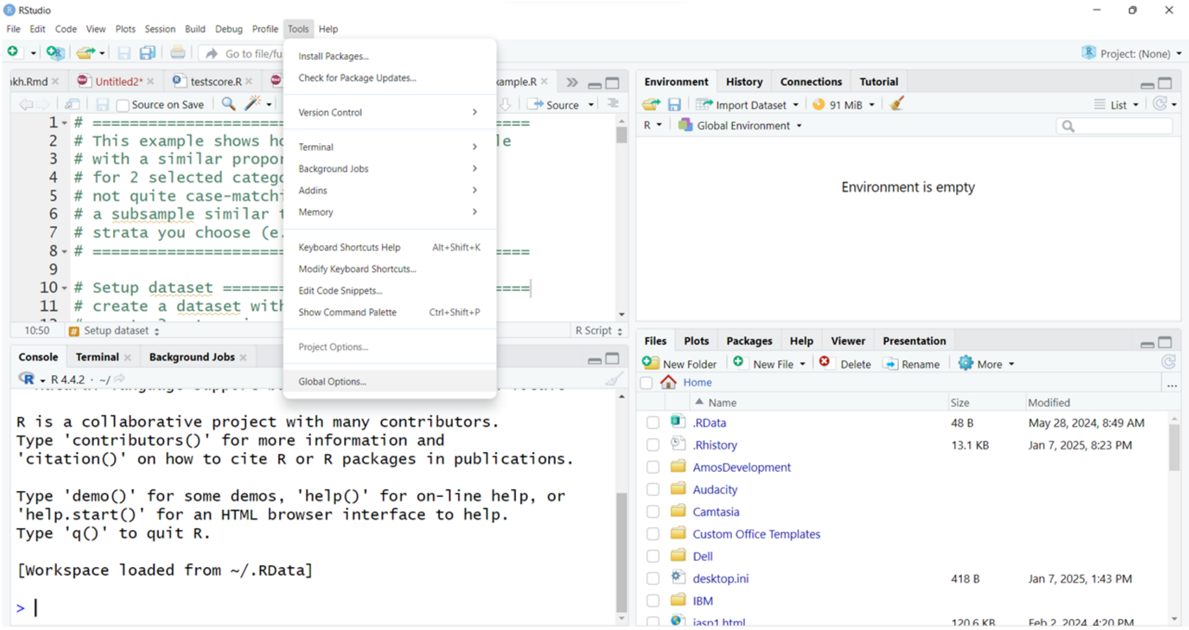

Customizing your RStudio interface

You also have the option to rearrange your window panes as well as change the look and feel of your programming interface and much more. To explore all of your options, click on the menu at the top for “Tools/Global Options”:



```
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'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Workspace loaded from ~/.RData]

> |
```
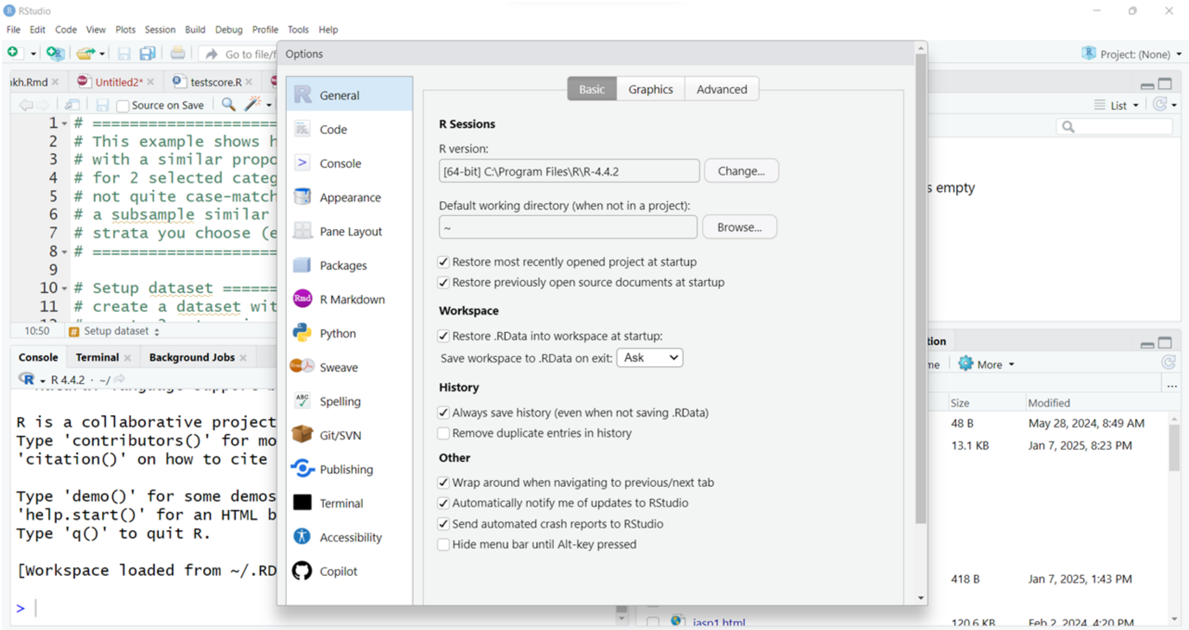

Take a look at the left side for the list of all of the options. Some of the most useful options to be aware of are:

- General
- Appearance, and
- Pane Layout

In the “General” TAB is where you can see and confirm that R is installed and where the R programming language executable is installed on your computer.



R Sessions

R version: [64-bit] C:\Program Files\R\R-4.4.2

Default working directory (when not in a project): ~

☑ Restore most recently opened project at startup
☑ Restore previously open source documents at startup

Workspace

☑ Restore .RData into workspace at startup:
Save workspace to .RData on exit: Ask

History

☑ Always save history (even when not saving .RData)
☐ Remove duplicate entries in history

Other

☑ Wrap around when navigating to previous/next tab
☑ Automatically notify me of updates to RStudio
☑ Send automated crash reports to RStudio
☐ Hide menu bar until Alt-key pressed

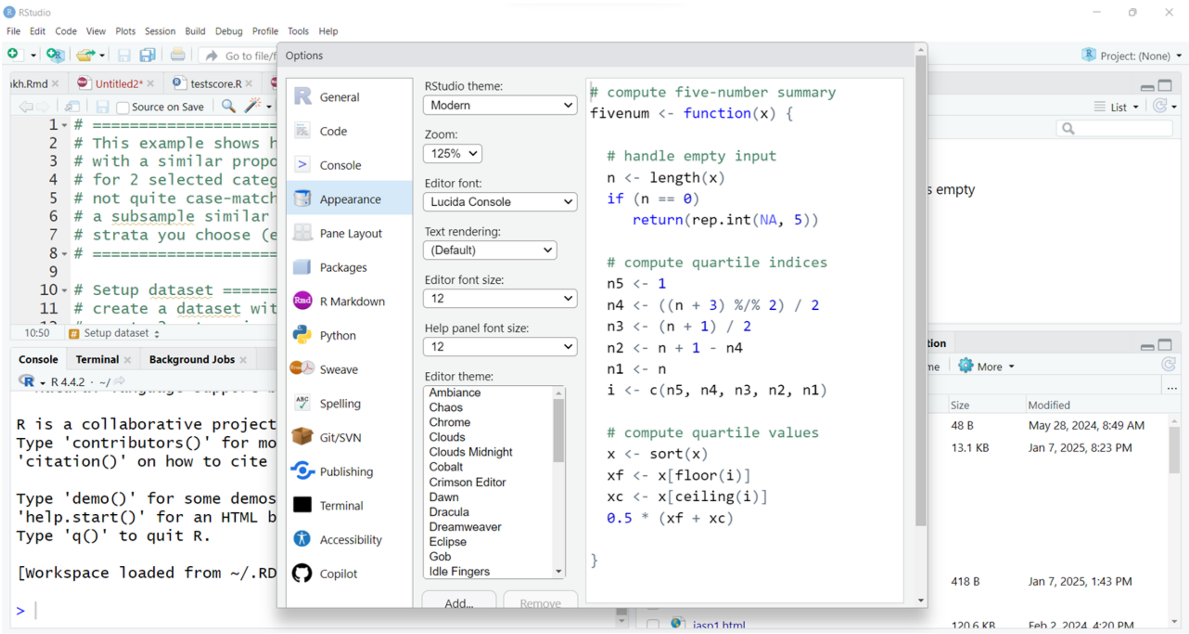
```
R is a collaborative project
Type 'contributors()' for mo
'citation()' on how to cite

Type 'demo()' for some demos
'help.start()' for an HTML b
Type 'q()' to quit R.

[Workspace loaded from ~/.RD

>
```

You will probably want to explore fine-tuning these parameters to customize the appearance of your RStudio preferences. For example, you can change the ZOOM level to improve readability. You may also want to change the FONT sizes for the Editor and Help windows as needed.

ZOOM + FONT

When making changes to your RStudio interface appearance, be aware that ZOOM and FONT size settings work together, so you may need to play around with the settings that work best for your monitor or device you are using.

I also encourage you to try out different "Editor Themes" which will change the colors of the R code as well as background colors (light or dark).



```
# ====================
# This example shows h
# with a similar propo
# for 2 selected categ
# not quite case-match
# a subsample similar
# strata you choose (e
# ====================

# Setup dataset ======
# create a dataset wit
```

```
R is a collaborative project
Type 'contributors()' for mo
'citation()' on how to cite

Type 'demo()' for some demos
'help.start()' for an HTML b
Type 'q()' to quit R.

[Workspace loaded from ~/.RD

>
```

RStudio theme: Modern

Zoom: 125%

Editor font: Lucida Console

Text rendering: (Default)

Editor font size: 12

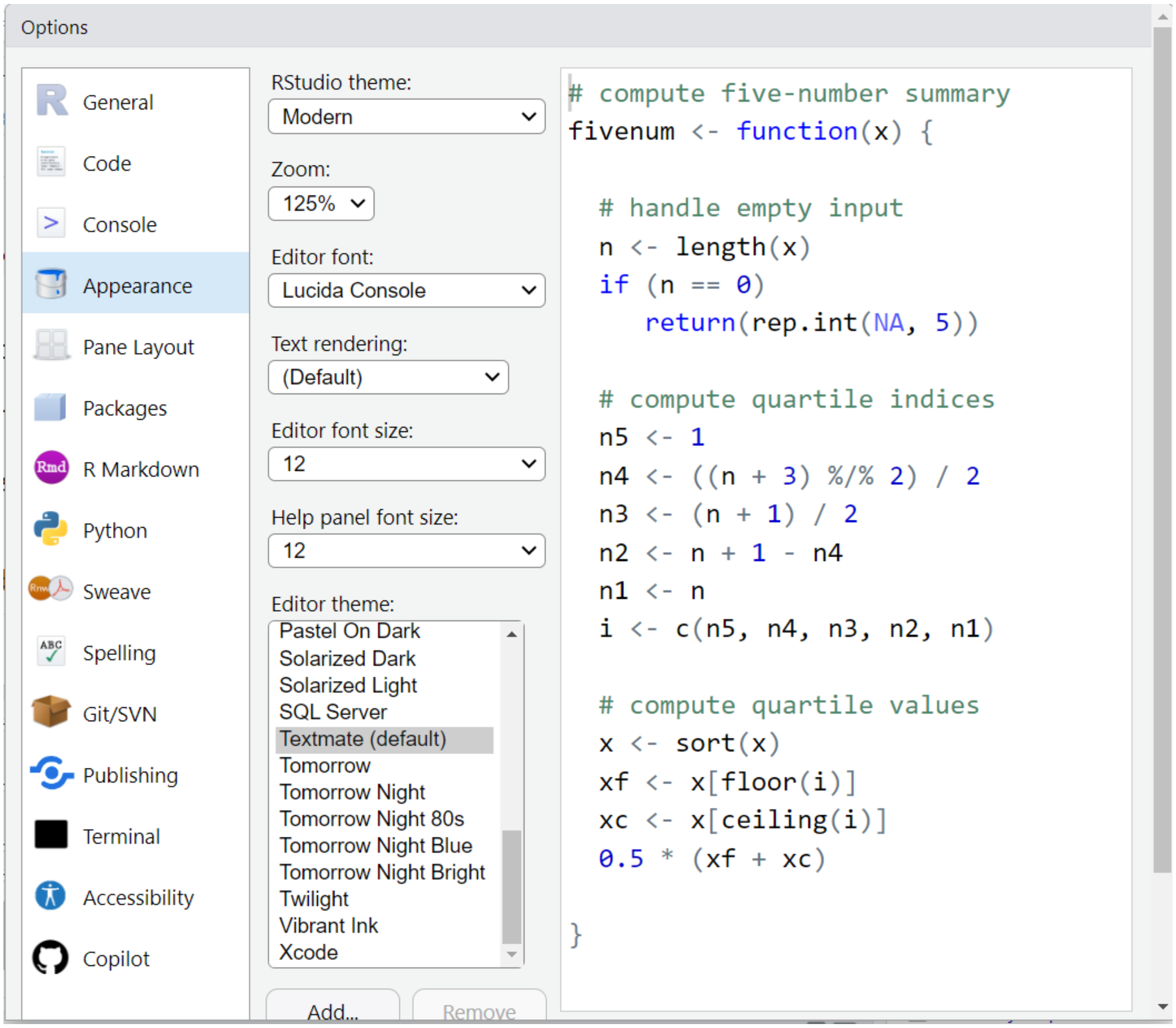
Help panel font size: 12

Editor theme:
- Ambiance
- Chaos
- Chrome
- Clouds
- Clouds Midnight
- Cobalt
- Crimson Editor
- Dawn
- Dracula
- Dreamweaver
- Eclipse
- Gob
- Idle Fingers

```
# compute five-number summary
fivenum <- function(x) {

  # handle empty input
  n <- length(x)
  if (n == 0)
     return(rep.int(NA, 5))

  # compute quartile indices
  n5 <- 1
  n4 <- ((n + 3) %/% 2) / 2
  n3 <- (n + 1) / 2
  n2 <- n + 1 - n4
  n1 <- n
  i <- c(n5, n4, n3, n2, n1)

  # compute quartile values
  x <- sort(x)
  xf <- x[floor(i)]
  xc <- x[ceiling(i)]
  0.5 * (xf + xc)

}
```

Size	Modified
48 B	May 28, 2024, 8:49 AM
13.1 KB	Jan 7, 2025, 8:23 PM
418 B	Jan 7, 2025, 1:43 PM

The default “Editor Theme” is textmate.



RStudio theme: Modern

Zoom: 125%

Editor font: Lucida Console

Text rendering: (Default)

Editor font size: 12

Help panel font size: 12

Editor theme: Textmate (default)

```
# compute five-number summary
fivenum <- function(x) {

  # handle empty input
  n <- length(x)
  if (n == 0)
     return(rep.int(NA, 5))

  # compute quartile indices
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  n3 <- (n + 1) / 2
  n2 <- n + 1 - n4
  n1 <- n
  i <- c(n5, n4, n3, n2, n1)

  # compute quartile values
  x <- sort(x)
  xf <- x[floor(i)]
  xc <- x[ceiling(i)]
  0.5 * (xf + xc)

}
```
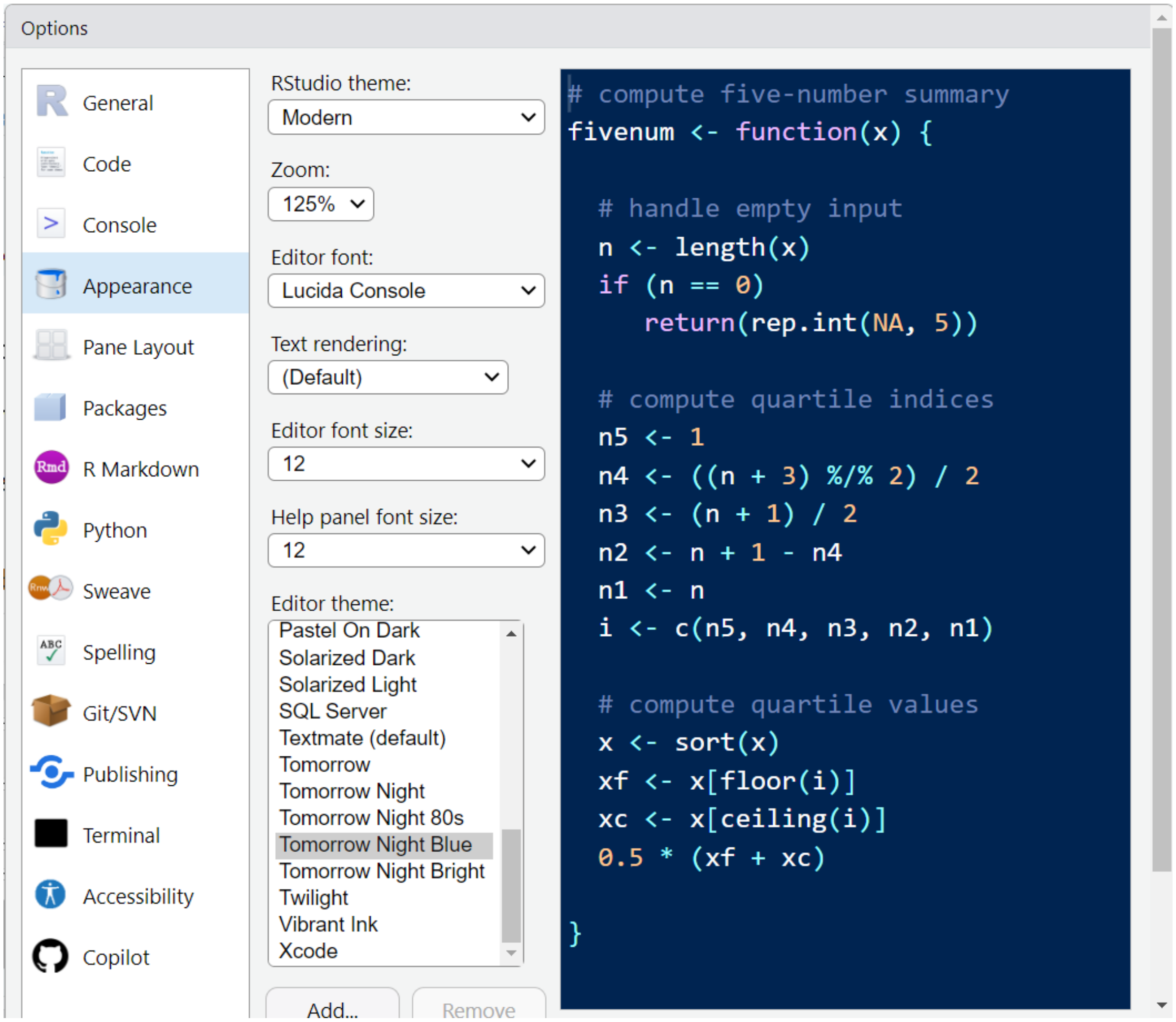

But here is an example of changing the theme to “Tomorrow Night Blue”.



RStudio theme: Modern

Zoom: 125%

Editor font: Lucida Console

Text rendering: (Default)

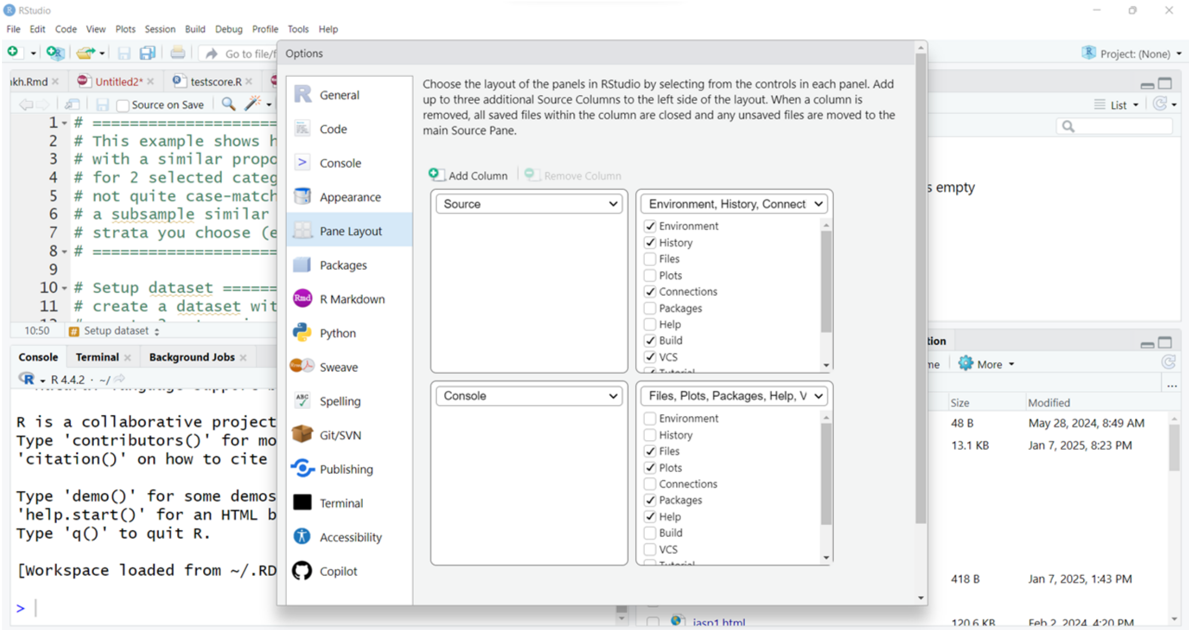
Editor font size: 12

Help panel font size: 12

Editor theme: Tomorrow Night Blue

```
# compute five-number summary
fivenum <- function(x) {

  # handle empty input
  n <- length(x)
  if (n == 0)
     return(rep.int(NA, 5))

  # compute quartile indices
  n5 <- 1
  n4 <- ((n + 3) %/% 2) / 2
  n3 <- (n + 1) / 2
  n2 <- n + 1 - n4
  n1 <- n
  i <- c(n5, n4, n3, n2, n1)

  # compute quartile values
  x <- sort(x)
  xf <- x[floor(i)]
  xc <- x[ceiling(i)]
  0.5 * (xf + xc)

}
```

I would also suggest NOT changing the layout of the window panes until you are very familiar with the default settings. But in “Pane Layout” is where you can see what the default layout settings are and what other options are available to you.



Choose the layout of the panels in RStudio by selecting from the controls in each panel. Add up to three additional Source Columns to the left side of the layout. When a column is removed, all saved files within the column are closed and any unsaved files are moved to the main Source Pane.

Source

Environment, History, Connect
☑ Environment
☑ History
☐ Files
☐ Plots
☑ Connections
☐ Packages
☐ Help
☑ Build
☑ VCS

Console

Files, Plots, Packages, Help, V
☐ Environment
☐ History
☑ Files
☑ Plots
☐ Connections
☑ Packages
☑ Help
☐ Build
☐ VCS

2. Write simple R code in Console

Simple math

So, let's start with some simple R code using the Console window and typing commands at the `>` prompt (which is the greater than symbol).

You can write simple math expressions like `5 + 5`.

```r
5 + 5
```

```
[1] 10
```

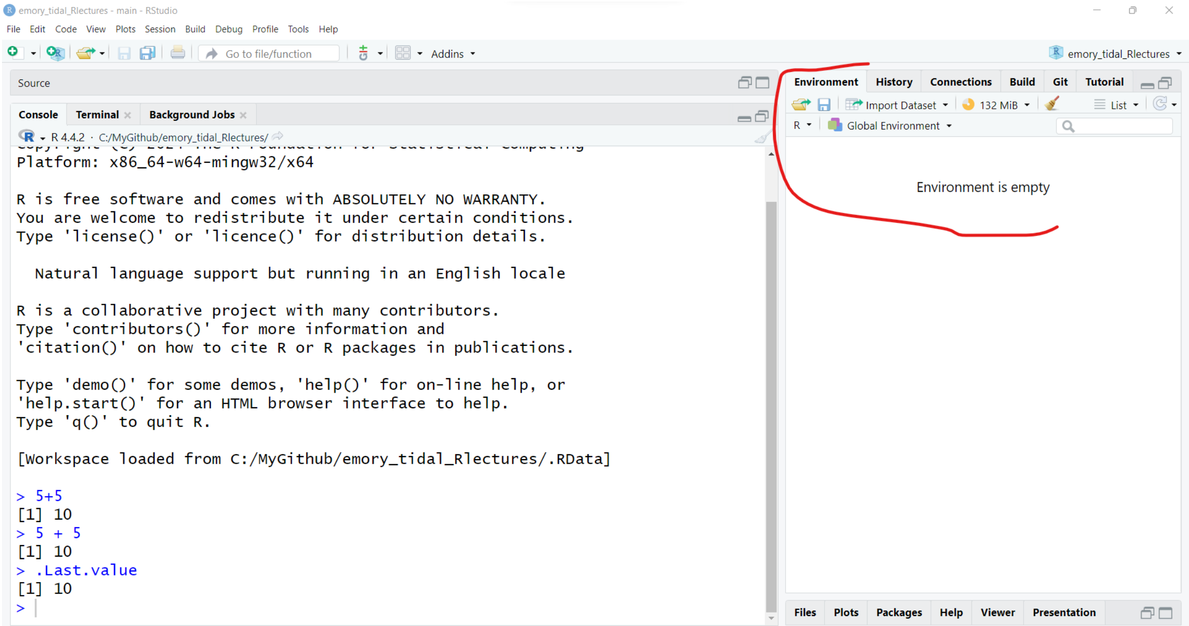
Notice that the output shows the number `1` enclosed in square brackets `[]` followed by the answer (or output) of `10`.

This is because R performed the addition operation using the `+` operator and then "saved" the output in temporary memory as a scalar object with 1 element, which is the number 10.

You can actually see this temporary object by typing `.Last.value` - which is only temporary and will be overwritten after the execution of the next R command.

```
.Last.value
[1] 10
```

However, if we look at our current computing environment (see “Global Environment” upper right window pane), it is still showing as empty.



```
Platform: x86_64-w64-mingw32/x64

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Type 'q()' to quit R.

[Workspace loaded from C:/MyGithub/emory_tidal_Rlectures/.RData]

> 5+5
[1] 10
> 5 + 5
[1] 10
> .Last.value
[1] 10
> 
```

This is because we have not yet “saved” the output into an object that we created. Let’s save the output from `5 + 5` into an object called `ten`.

To do this we need to do 2 things:

1. Create the object called `ten` by
2. Using the “assign” operator `<-` to take the result of `5 + 5` and move it (save it or pipe it) into the object `ten`.

```
ten <- 5 + 5
```

TL;DR What is the Assign Operator `<-`?

The "R" language is actually a derivative of the original "S" language which stood for the "language of statistics" - it was written by statisticians for statisticians (and now data scientists). *The original S language was written in the mid-1970's by programmers/statisticians at Bell Labs/AT&T.*

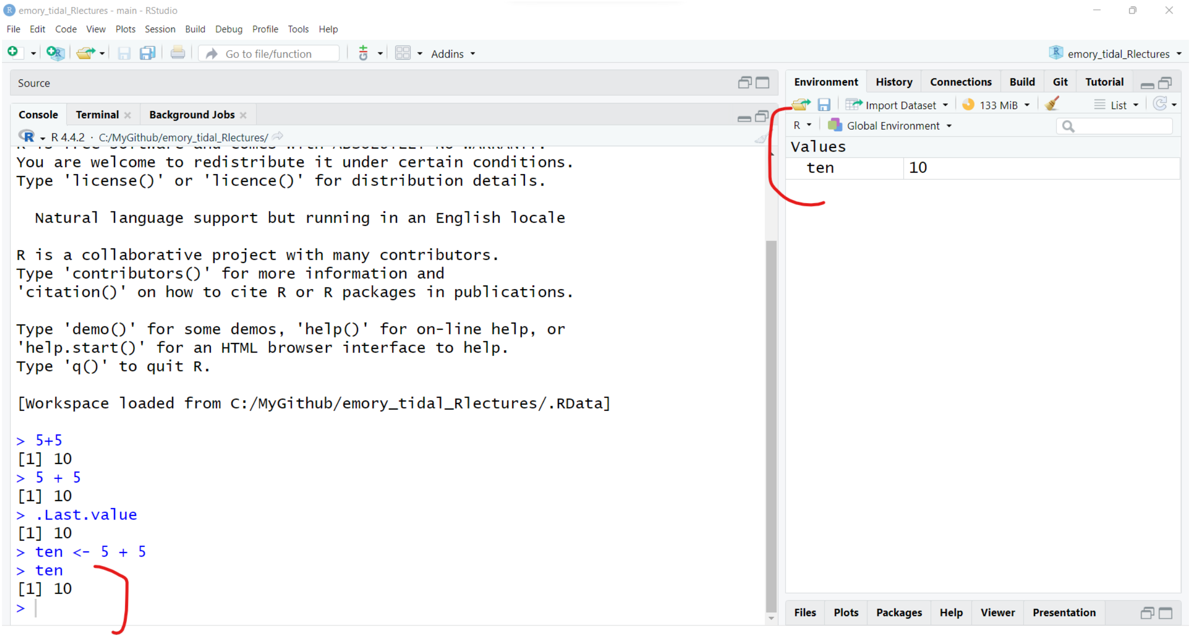
The `<-` actually comes from the physical key on their "APL" keyboards, for the APL programming language they were using at Bell Labs.

A Nice Blog Post on the History of `<-`

To "see" the output of this object called `ten` - you can either see it now in your Global Environment or type the object name in the Console to view it.

```
ten
```

```
[1] 10
```



```
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[Workspace loaded from C:/MyGithub/emory_tidal_Rlectures/.RData]

> 5+5
[1] 10
> 5 + 5
[1] 10
> .Last.value
[1] 10
> ten <- 5 + 5
> ten
[1] 10
>
```

```
Values
ten        10
```

It is important to remember that R is an "object-oriented" programming language - everything in R is an object.

Built in constants

There are several built in “constants” in R. Try typing these in at the Console to see the results.

```
pi
```

```
[1] 3.141593
```

```
letters
```

```
 [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q" "r"
 "s"
[20] "t" "u" "v" "w" "x" "y" "z"
```

```
LETTERS
```

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

```
month.name
```

```
 [1] "January"   "February"  "March"     "April"     "May"       "June"
 [7] "July"      "August"    "September" "October"   "November"  "December"
```

! R is Case Sensitive!

A pro and con of the R language is that it is case sensitive. Lower case `x` and uppercase `X` are different objects. As seen above, the lowercase `letters` object is a vector of the 26 lowercase letters, whereas `LETTERS` is a different object vector of the 26 uppercase letters. Be on the lookout for case sensitive spelling and formatting of object, package and function names in R.

For the constants like `letters` you get a list of the 26 lower case letters in the alphabet. Notice that the number in [square brackets] updates for each new line printed out. This allows you to keep track of the number of elements in the output object. `letters` is an “character” array (or vector) with 26 elements.

To confirm these details, we can use the `class()` function to determine that the `letters` object has all “character” elements. The `length()` function will let you know that there are 26 elements.

```r
class(letters)
```

```
[1] "character"
```

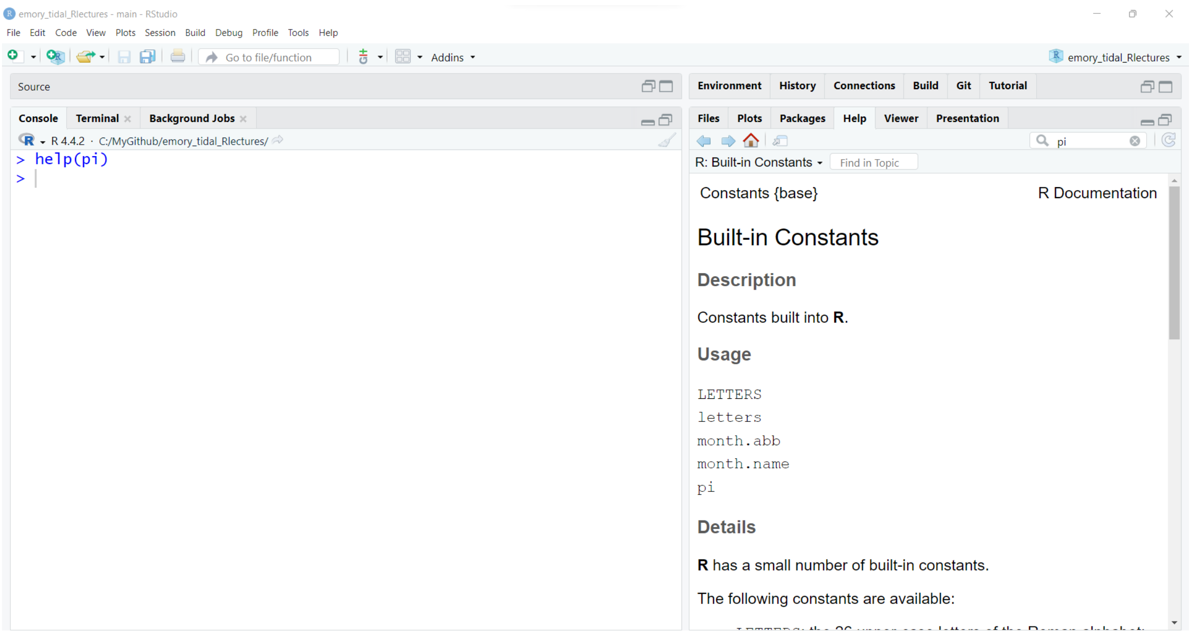
```r
length(letters)
```

```
[1] 26
```

Getting help

If you would like to learn more about these built-in "constants", you can get help in one of two ways. You can either type `help(pi)` in the "Console" (lower left) or type `pi` in the "Help" window (lower right).

```r
help(pi)
```



```
> help(pi)
> 
```

Constants {base} R Documentation

Built-in Constants

Description

Constants built into **R**.

Usage

```
LETTERS
letters
month.abb
month.name
pi
```

Details

R has a small number of built-in constants.

The following constants are available:

The `help()` function defaults to searching for a built-in object, function or dataset by default in the `base` R package. But some functions may exist in multiple packages, so it is always a good idea to add the package when running the `help()` function if possible.

Since `pi` is in the `base` R package, it would be better to run:

```r
help(pi, package = "base")
```

If you have no idea what package a function may be in, you can use the `??` search operator. For example, many packages include a plotting related function. If you want to see how many R packages currently installed on your computer have a `plot` related function, type the following:

```r
??plot
```

Try out a built-in R function

The majority of the R programming language is driven by functions. Technically the `+` operator is actually a function that performs a sum.

You can even get help on these operators, by typing `help("+")`. We have to add the quotes `""` so that R knows we are looking for this operator and not trying to perform an addition operation inside the function call.

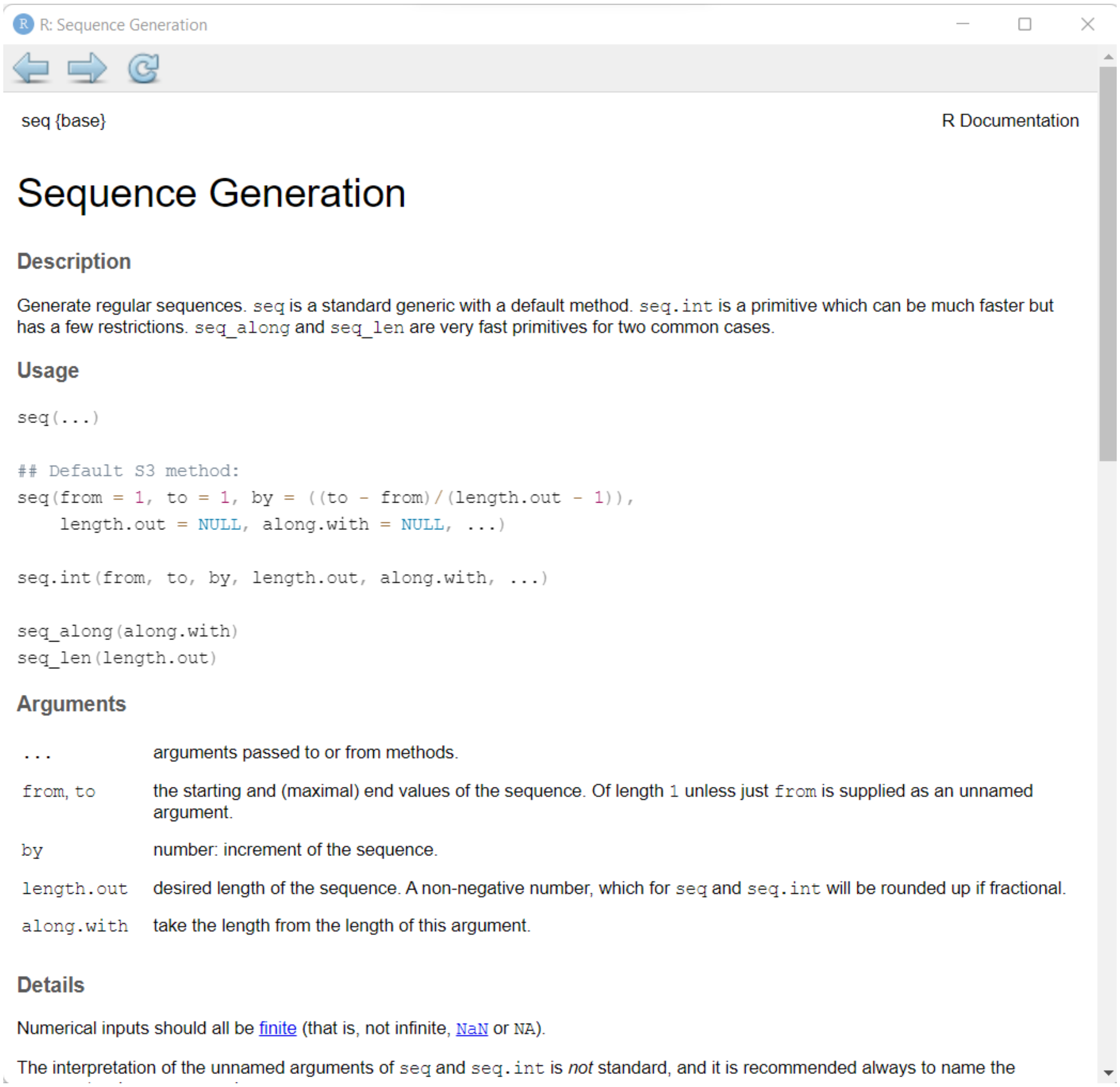
```
help("+")
```

But let's try a function to create a sequence of numbers - for example, let's use the `seq()` function to create a sequence of numbers from 1 to 10.

```
seq(10)
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

And let's look at the help page for the `seq()` function.



seq {base} R Documentation

Sequence Generation

Description

Generate regular sequences. `seq` is a standard generic with a default method. `seq.int` is a primitive which can be much faster but has a few restrictions. `seq_along` and `seq_len` are very fast primitives for two common cases.

Usage

```
seq(...)

## Default S3 method:
seq(from = 1, to = 1, by = ((to - from)/(length.out - 1)),
    length.out = NULL, along.with = NULL, ...)

seq.int(from, to, by, length.out, along.with, ...)

seq_along(along.with)
seq_len(length.out)
```

Arguments

`...`	arguments passed to or from methods.
`from, to`	the starting and (maximal) end values of the sequence. Of length `1` unless just `from` is supplied as an unnamed argument.
`by`	number: increment of the sequence.
`length.out`	desired length of the sequence. A non-negative number, which for `seq` and `seq.int` will be rounded up if fractional.
`along.with`	take the length from the length of this argument.

Details

Numerical inputs should all be finite (that is, not infinite, `NaN` or `NA`).

The interpretation of the unnamed arguments of `seq` and `seq.int` is *not* standard, and it is recommended always to name the

R allows for what is called "lazy" coding. This basically means you can provide very minimal input and R will try to figure out what you want using the default settings for a given function. In the case of `seq()` the function begins by default at 1 and creates the output in steps of 1 up to the value of 10.

While "lazy" coding practices are common with R, it would actually be better to explicitly define each **argument** to make sure you get the exact output you want. To do this, inside the parentheses `()` we should assign a value to each argument.

Notice in the "Help" page for `seq()` shown above that the first 3 arguments are: `from`, `to` and `by`. Each of these can be defined inside the `()` by using the syntax of the name of the argument, an equals sign `=`, and then the value (or object) you want to assign:

$$argument = value$$

For example, the explicit function call should be:

```r
seq(from = 1,
    to = 10,
    by = 1)
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

You could easily change these values to get a sequence from 0 to 5 in increments of 0.1 as follows:

```r
seq(from = 0,
    to = 5,
    by = 0.1)
```

```
 [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 1.1 1.2 1.3 1.4 1.5 1.6 1.7
 1.8
[20] 1.9 2.0 2.1 2.2 2.3 2.4 2.5 2.6 2.7 2.8 2.9 3.0 3.1 3.2 3.3 3.4 3.5 3.6
3.7
[39] 3.8 3.9 4.0 4.1 4.2 4.3 4.4 4.5 4.6 4.7 4.8 4.9 5.0
```

Notice the incremental counter `[#]` on the left to help you keep track of how many elements are in the resulting numeric vector that was the "result" or "output" from the `seq()` function.

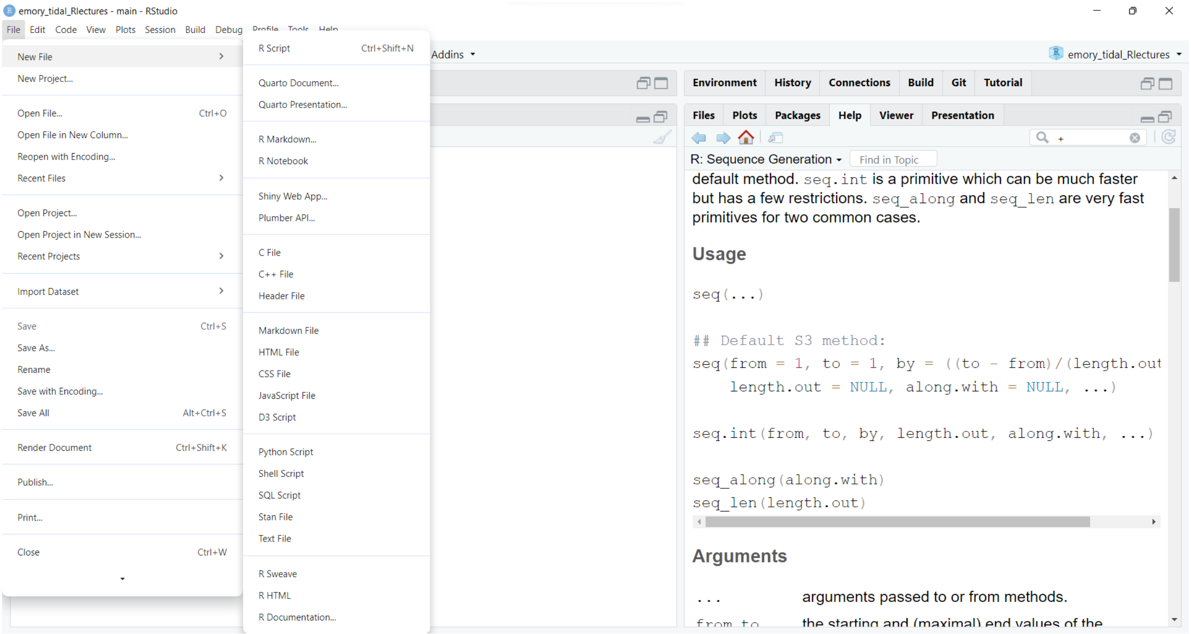
3. Create your first R script

Save your code in a new script

So, as you can tell, the R Console is useful but slow and tedious. Let's create an R script to save all of these commands in a file so that we can easily access everything we've done so far and re-run these commands as needed.

> **Good Reproducible Research Coding Practice**
>
> It is a good coding practice to create R code (saved in `*.R` script files or `*.Rmd` Rmarkdown files) for every step in your data preparation and analysis so that:
>
> - you have a record of everything you've done and why
> - other people on your team (including yourself in a few weeks) will know what you did and why
> - you can share your code with others so they will understand what you did and why *(and to publish your code and data with your research articles - YES you can get a DOI citation to add to your CV for data and code as well as for the article)*!

In RStudio go to the top menu "File/New File/R Script":



default method. `seq.int` is a primitive which can be much faster but has a few restrictions. `seq_along` and `seq_len` are very fast primitives for two common cases.

Usage

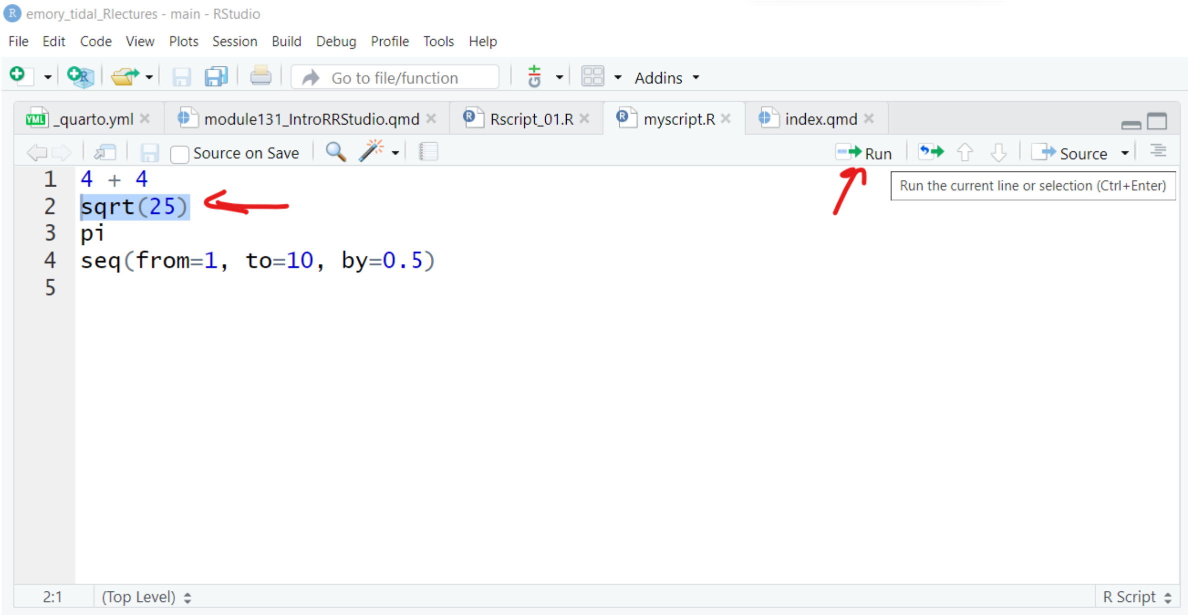
```
seq(...)

## Default S3 method:
seq(from = 1, to = 1, by = ((to - from)/(length.out
    length.out = NULL, along.with = NULL, ...)

seq.int(from, to, by, length.out, along.with, ...)

seq_along(along.with)
seq_len(length.out)
```

Arguments

`...`	arguments passed to or from methods.
`from, to`	the starting and (maximal) end values of the

Once the R Script file is created, type in some of the commands we did above in the Console and put one command on each line.

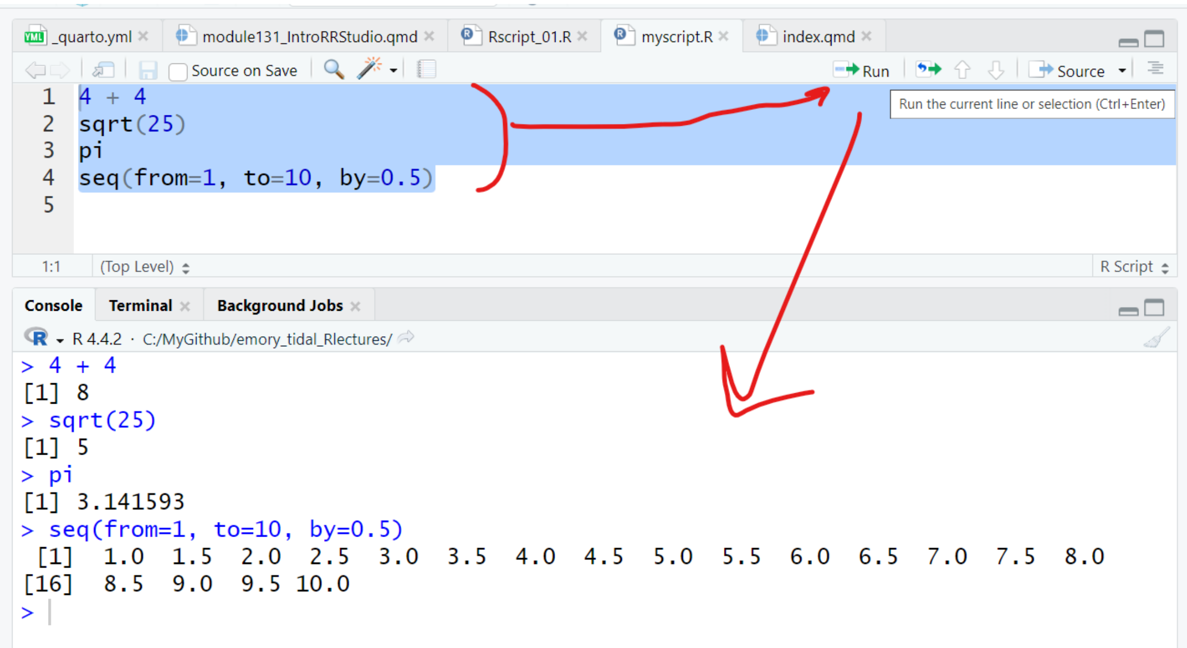
Just select each line and click "Run".



```r
4 + 4
sqrt(25)
pi
seq(from=1, to=10, by=0.5)
```

Then you can save the file on your computer as “myscript.R”, for example.

You can also select all of the rows and click run to execute all of the code in sequence and see the output in the “Console” Window.



```r
4 + 4
sqrt(25)
pi
seq(from=1, to=10, by=0.5)
```

```
> 4 + 4
[1] 8
> sqrt(25)
[1] 5
> pi
[1] 3.141593
> seq(from=1, to=10, by=0.5)
 [1]  1.0  1.5  2.0  2.5  3.0  3.5  4.0  4.5  5.0  5.5  6.0  6.5  7.0  7.5  8.0
[16]  8.5  9.0  9.5 10.0
> 
```

Here is the code and output:

```r
4 + 4
```

```
[1] 8
```

```r
sqrt(25)
```

```
[1] 5
```

```r
pi
```

```
[1] 3.141593
```

```r
seq(from=1, to=10, by=0.5)
```

```
 [1]  1.0  1.5  2.0  2.5  3.0  3.5  4.0  4.5  5.0  5.5  6.0  6.5  7.0  7.5
 8.0
[16]  8.5  9.0  9.5 10.0
```

Create R objects and Use Them

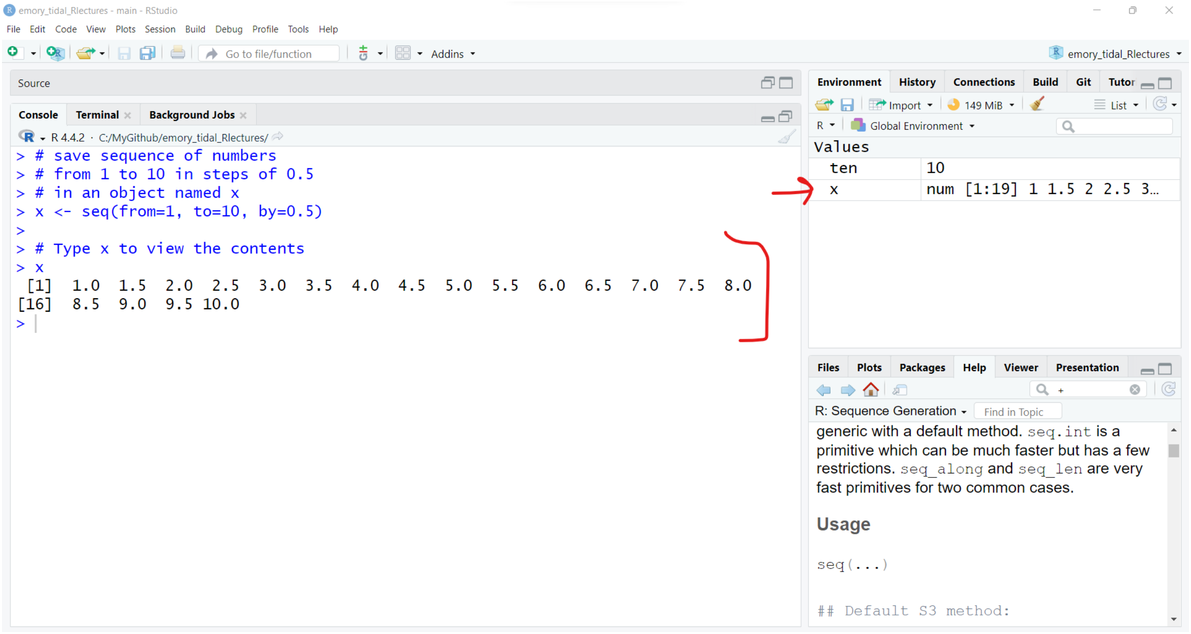
Let's try out some more built-in R functions, save the output in objects in your "Global Environment" and then use them in other functions and subsequent analysis steps.

Create a sequence of numbers and save them as an object called `x`. I also added a comment in the R code block below. Everything after the `#` hashtag is a comment which R will ignore. It is a good idea to add comments in your code to make sure that you and others understand what each part of your code does *(including yourself in a few weeks when you've forgotten why you wrote that code step)*.

```r
# save sequence of numbers
# from 1 to 10 in steps of 0.5
# in an object named x
x <- seq(from=1, to=10, by=0.5)

# Type x to view the contents
x
```

```
 [1]  1.0  1.5  2.0  2.5  3.0  3.5  4.0  4.5  5.0  5.5  6.0  6.5  7.0  7.5
 8.0
[16]  8.5  9.0  9.5 10.0
```

Also take a look at the "Global Environment" to see the new object `x`.



```
> # save sequence of numbers
> # from 1 to 10 in steps of 0.5
> # in an object named x
> x <- seq(from=1, to=10, by=0.5)
>
> # Type x to view the contents
> x
 [1]  1.0  1.5  2.0  2.5  3.0  3.5  4.0  4.5  5.0  5.5  6.0  6.5  7.0  7.5  8.0
[16]  8.5  9.0  9.5 10.0
> 
```

Values

ten	10
x	num [1:19] 1 1.5 2 2.5 3…

R: Sequence Generation

generic with a default method. `seq.int` is a primitive which can be much faster but has a few restrictions. `seq_along` and `seq_len` are very fast primitives for two common cases.

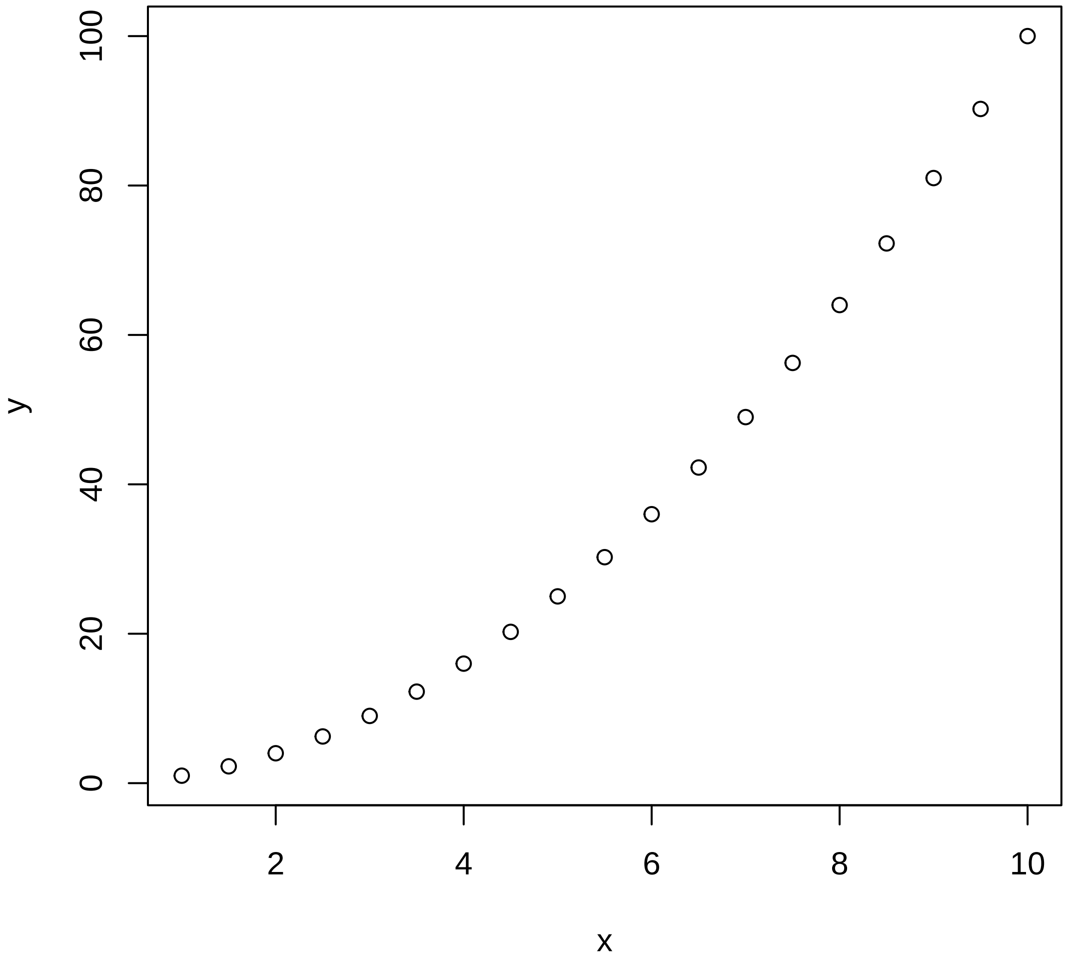
Usage

```
seq(...)

## Default S3 method:
```

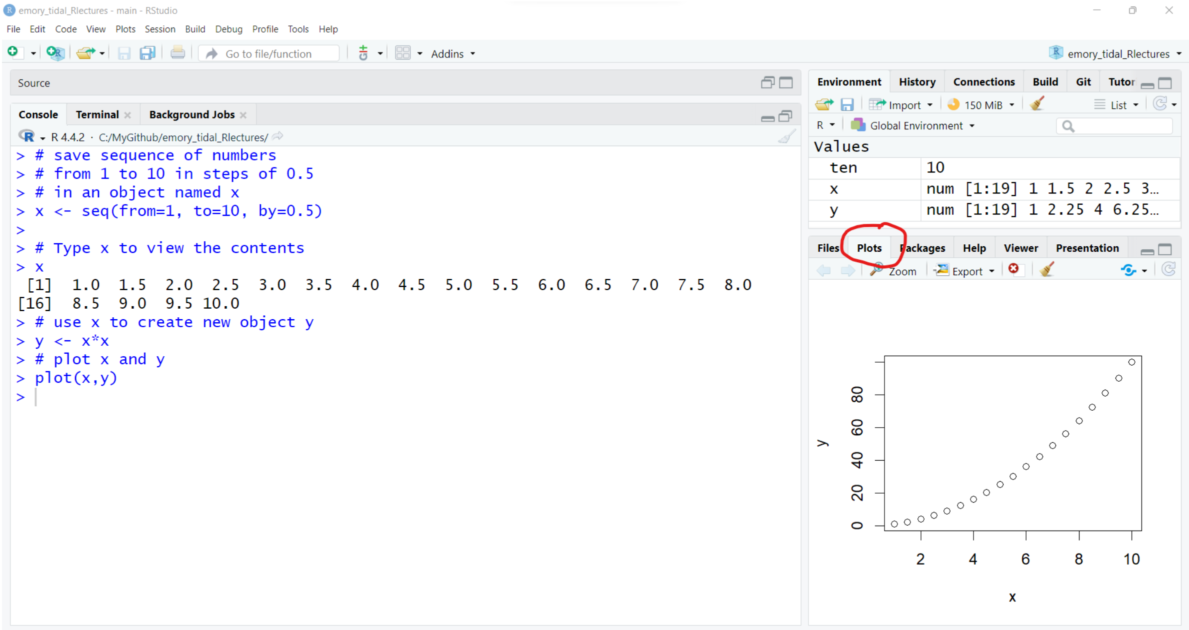
```
# use x to create new object y
y <- x*x
```

Once the object `y` is created, we can make a simple 2-dimensional scatterplot using the built-in `plot()` base R function.

```
# plot x and y
plot(x,y)
```



The plot is shown above, but if you are running this code interactively in the RStudio desktop, check the "Plots" window pane (lower right).



```
> # save sequence of numbers
> # from 1 to 10 in steps of 0.5
> # in an object named x
> x <- seq(from=1, to=10, by=0.5)
>
> # Type x to view the contents
> x
 [1]  1.0  1.5  2.0  2.5  3.0  3.5  4.0  4.5  5.0  5.5  6.0  6.5  7.0  7.5  8.0
[16]  8.5  9.0  9.5 10.0
> # use x to create new object y
> y <- x*x
> # plot x and y
> plot(x,y)
>
```

Values

ten	10
x	num [1:19] 1 1.5 2 2.5 3…
y	num [1:19] 1 2.25 4 6.25…

On your own

Download `Rscript_01.R` *(right click the linked file and "Save As" the file on your computer)*, then open it in your RStudio and run through the code. Try out new variations on your own.

4. Install and load R packages *(understanding your R session)*

Status of your current computing R session with `sessionInfo()`

While the base installation of R is pretty powerful on it's own, the beauty of R and the R programming community is that there are literally hundreds of thousands if not millions of people programming in R and creating new functions everyday.

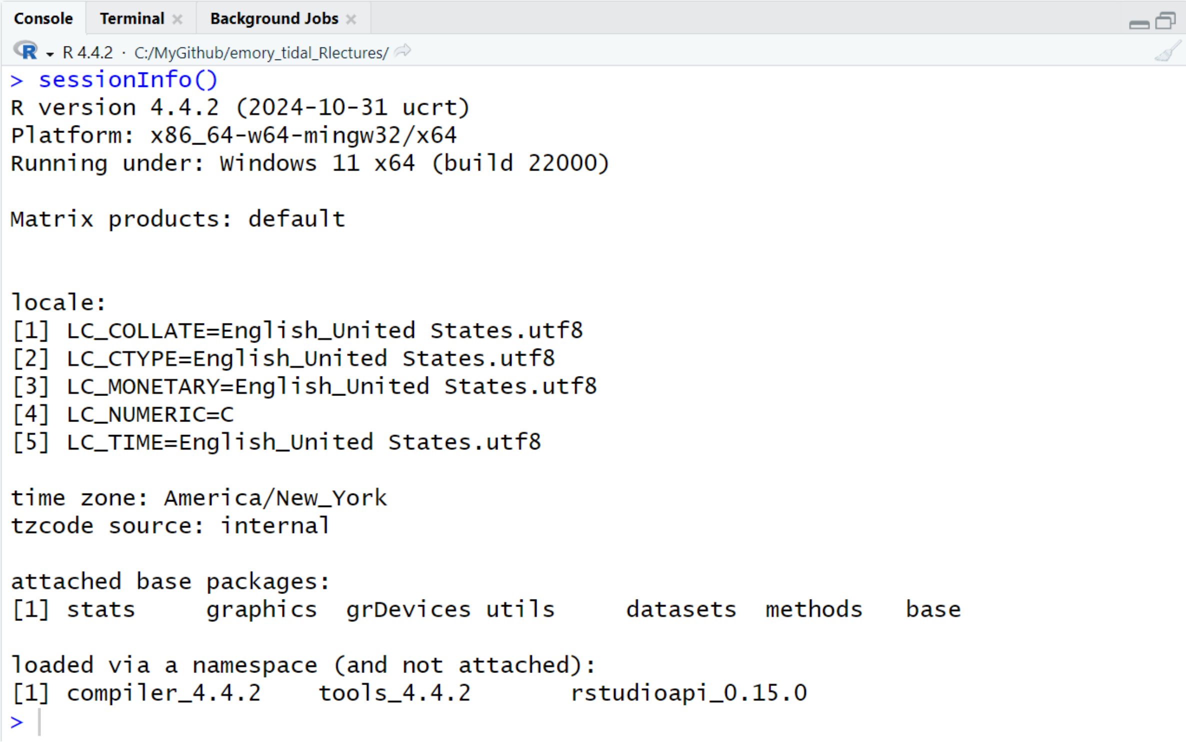
In order to use these new functions, the developers put them together in packages that we can install to extend the functionality of R.

But first, let's take a look at the packages that are part of the basic installation of R. One way to see which packages are currently installed and loaded into your current R computing session, is by running the command `sessionInfo()`.

> ⚠ Watch spelling - R is case sensitive!
>
> **Notice:** This function name is all lowercase except for the capital "I" in the middle. Be sure you are typing `sessionInfo()` and not `sessioninfo()`.

You will also notice that the `sessionInfo()` command also lists the version of R I'm currently running (4.4.2), my operating system (Windows 11) and and my locale (USA, East Coast). These details can sometimes be helpful for collaborating with others who may be working with different system settings and for debugging errors.

```
sessionInfo()
```



```
> sessionInfo()
R version 4.4.2 (2024-10-31 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 11 x64 (build 22000)

Matrix products: default


locale:
[1] LC_COLLATE=English_United States.utf8
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8

time zone: America/New_York
tzcode source: internal

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

loaded via a namespace (and not attached):
[1] compiler_4.4.2    tools_4.4.2       rstudioapi_0.15.0
>
```

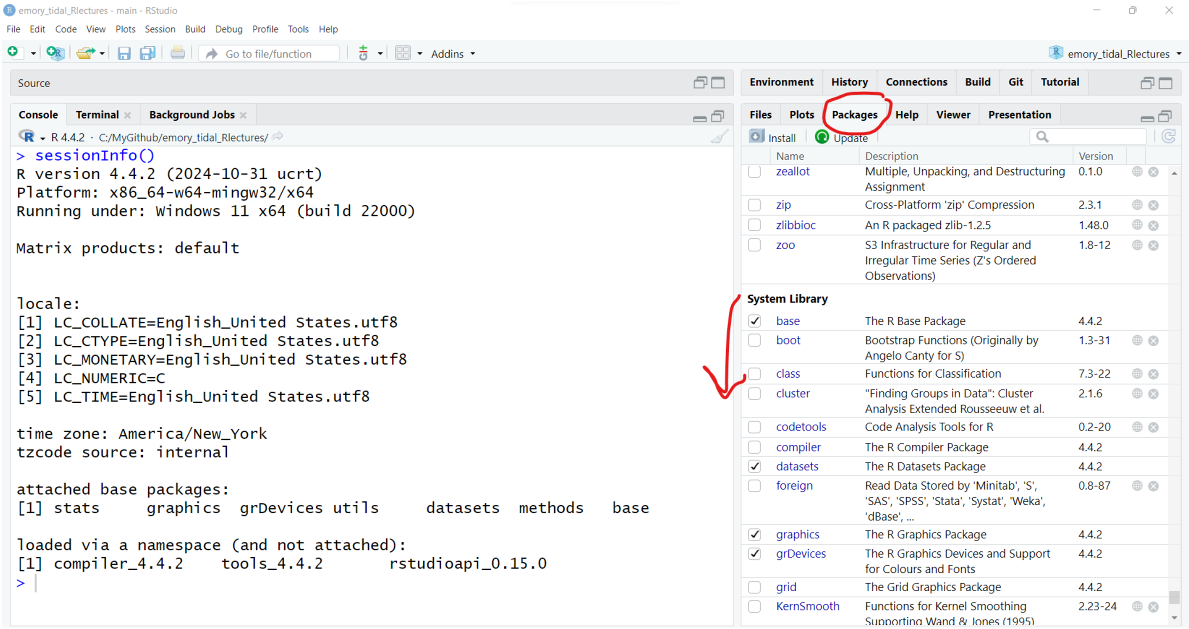
7 Base R Packages

The basic installation of R includes 7 packages:

- `stats`
- `graphics`
- `grDevices`
- `utils`
- `datasets`
- `methods`
- `base`

To learn more click on the "Packages" TAB in the lower right window pane to see the list of packages installed on your computer. I have a lot of packages on my computer, but here is a screenshot of the base R packages.

See the packages listed under "System Library" which are the ones that were installed with base R. You'll notice that only some of these have checkmarks next to them. The checkmark means those are also loaded into your R session. Only some of them are loaded into memory by default to minimize the use of your computer's memory.



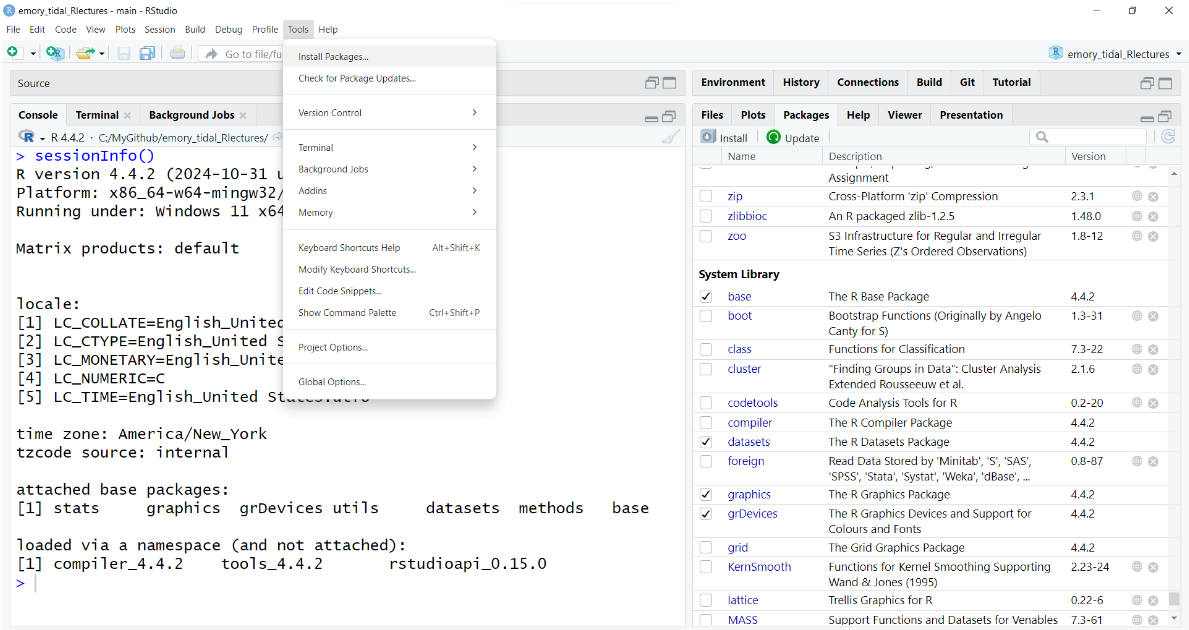
```
> sessionInfo()
R version 4.4.2 (2024-10-31 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 11 x64 (build 22000)

Matrix products: default


locale:
[1] LC_COLLATE=English_United States.utf8
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8

time zone: America/New_York
tzcode source: internal

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

loaded via a namespace (and not attached):
[1] compiler_4.4.2    tools_4.4.2       rstudioapi_0.15.0
> 
```

	Name	Description	Version
☐	zeallot	Multiple, Unpacking, and Destructuring Assignment	0.1.0
☐	zip	Cross-Platform 'zip' Compression	2.3.1
☐	zlibbioc	An R packaged zlib-1.2.5	1.48.0
☐	zoo	S3 Infrastructure for Regular and Irregular Time Series (Z's Ordered Observations)	1.8-12
System Library			
☑	base	The R Base Package	4.4.2
☐	boot	Bootstrap Functions (Originally by Angelo Canty for S)	1.3-31
☐	class	Functions for Classification	7.3-22
☐	cluster	"Finding Groups in Data": Cluster Analysis Extended Rousseeuw et al.	2.1.6
☐	codetools	Code Analysis Tools for R	0.2-20
☐	compiler	The R Compiler Package	4.4.2
☑	datasets	The R Datasets Package	4.4.2
☐	foreign	Read Data Stored by 'Minitab', 'S', 'SAS', 'SPSS', 'Stata', 'Systat', 'Weka', 'dBase', ...	0.8-87
☑	graphics	The R Graphics Package	4.4.2
☑	grDevices	The R Graphics Devices and Support for Colours and Fonts	4.4.2
☐	grid	The Grid Graphics Package	4.4.2
☐	KernSmooth	Functions for Kernel Smoothing Supporting Wand & Jones (1995)	2.23-24

Install a Package and Load it into R session memory

Let’s install a “new” R package, like `ggplot2`.

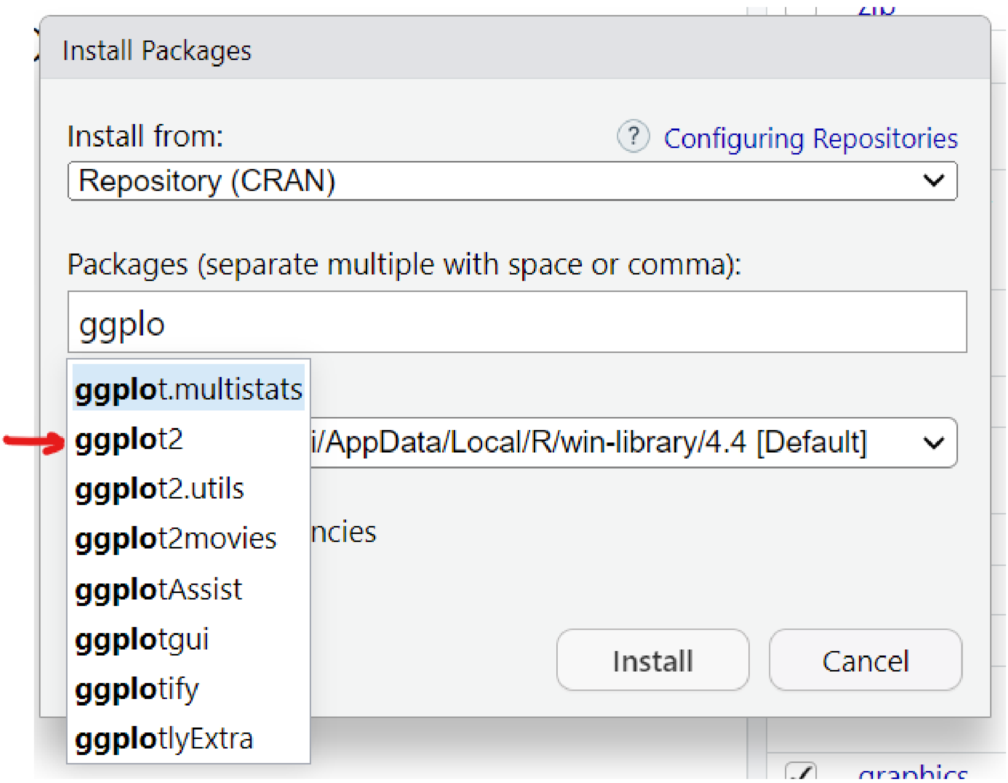
Go to the RStudio menu “Tools/Install” Packages



```
> sessionInfo()
R version 4.4.2 (2024-10-31 u
Platform: x86_64-w64-mingw32/
Running under: Windows 11 x64

Matrix products: default


locale:
[1] LC_COLLATE=English_Unitec
[2] LC_CTYPE=English_United S
[3] LC_MONETARY=English_Unite
[4] LC_NUMERIC=C
[5] LC_TIME=English_United St

time zone: America/New_York
tzcode source: internal

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

loaded via a namespace (and not attached):
[1] compiler_4.4.2    tools_4.4.2       rstudioapi_0.15.0
> 
```

	Name	Description	Version
		Assignment	
☐	zip	Cross-Platform 'zip' Compression	2.3.1
☐	zlibbioc	An R packaged zlib-1.2.5	1.48.0
☐	zoo	S3 Infrastructure for Regular and Irregular Time Series (Z's Ordered Observations)	1.8-12
System Library			
☑	base	The R Base Package	4.4.2
☐	boot	Bootstrap Functions (Originally by Angelo Canty for S)	1.3-31
☐	class	Functions for Classification	7.3-22
☐	cluster	"Finding Groups in Data": Cluster Analysis Extended Rousseeuw et al.	2.1.6
☐	codetools	Code Analysis Tools for R	0.2-20
☐	compiler	The R Compiler Package	4.4.2
☑	datasets	The R Datasets Package	4.4.2
☐	foreign	Read Data Stored by 'Minitab', 'S', 'SAS', 'SPSS', 'Stata', 'Systat', 'Weka', 'dBase', ...	0.8-87
☑	graphics	The R Graphics Package	4.4.2
☑	grDevices	The R Graphics Devices and Support for Colours and Fonts	4.4.2
☐	grid	The Grid Graphics Package	4.4.2
☐	KernSmooth	Functions for Kernel Smoothing Supporting Wand & Jones (1995)	2.23-24
☐	lattice	Trellis Graphics for R	0.22-6
☐	MASS	Support Functions and Datasets for Venables	7.3-61

This will then open up a window where you can type in the name of the package you want. As soon as we start typing `ggplot2` the menu begins listing all packages with that partial spelling...

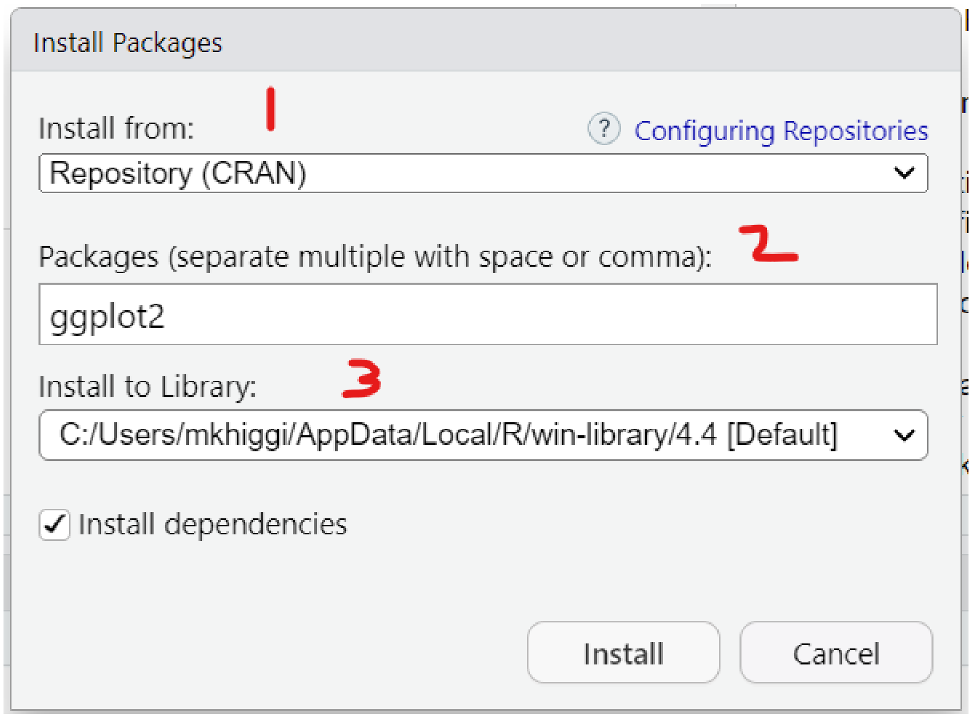


Install from: Repository (CRAN)

Packages (separate multiple with space or comma): ggplo

You'll notice that there are 3 parts to the installation:

1. Where you want to get the package from *(i.e., which repository - more on repositories below)*.
2. The name of the package. You can actually type more than one package name at a time separated by commas if you want to install several packages at once.
3. The file location on your computer where the new package is installed - your file location may be different than mine. But this is useful to know in case something goes wrong. **I would suggest keeping the default settings.**



Install from: Repository (CRAN)

Packages (separate multiple with space or comma): ggplot2

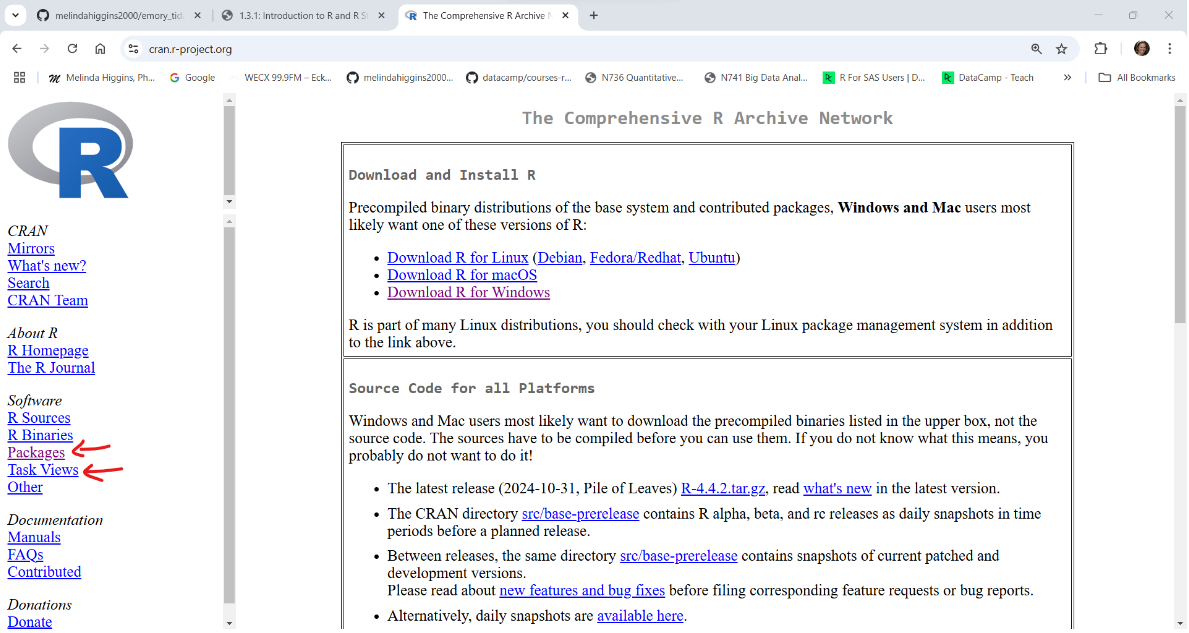
Install to Library: C:/Users/mkhiggi/AppData/Local/R/win-library/4.4 [Default]

☑ Install dependencies

Where to get packages - CRAN Repository

Using the "Tools/Install" Packages menu from within RStudio automatically links to CRAN, which is the "The Comprehensive R Archive Network". You've already been here once to download and install the R programming language application.

Here is a screenshot of the CRAN homepage.



The Comprehensive R Archive Network

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- Download R for Linux (Debian, Fedora/Redhat, Ubuntu)
- Download R for macOS
- Download R for Windows

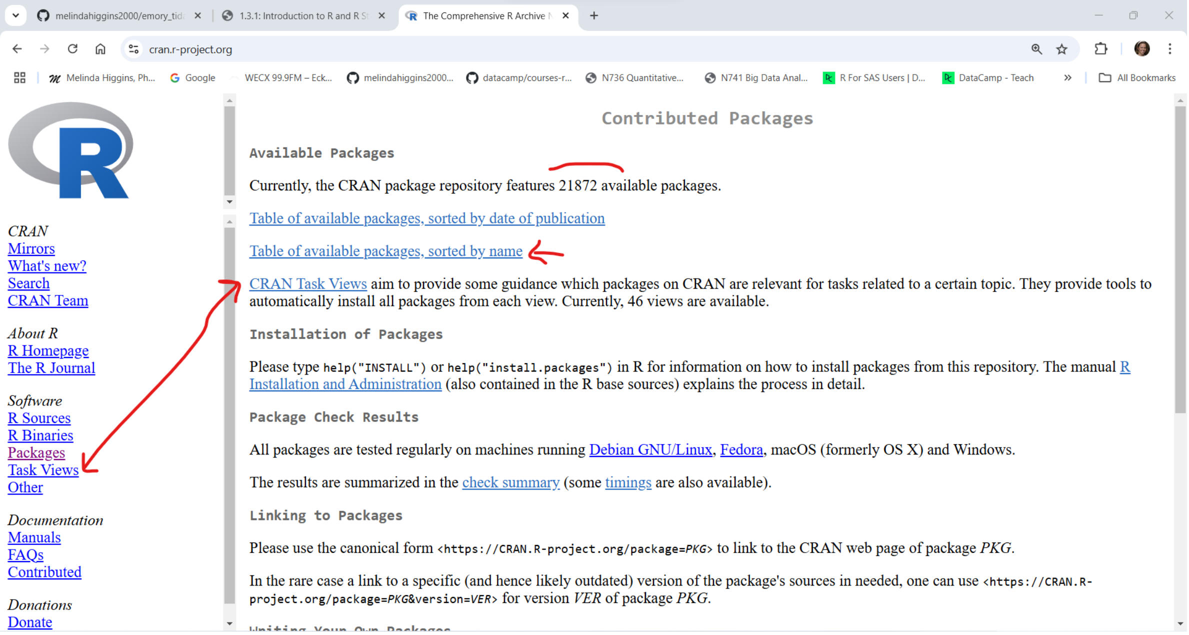
R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

Source Code for all Platforms

Windows and Mac users most likely want to download the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- The latest release (2024-10-31, Pile of Leaves) R-4.4.2.tar.gz, read what's new in the latest version.
- The CRAN directory src/base-prerelease contains R alpha, beta, and rc releases as daily snapshots in time periods before a planned release.
- Between releases, the same directory src/base-prerelease contains snapshots of current patched and development versions.
  Please read about new features and bug fixes before filing corresponding feature requests or bug reports.
- Alternatively, daily snapshots are available here.

Next click on “Packages” at the left to see the full list of packages currently available. As of right now (01/10/2025 at 5:12pm EST) there are 21,872 packages. This number increases every day as people create, validate and publish their packages on CRAN. You can get a list of all of the packages or if you have no idea what package you need, you can also look at the “Task Views” to see groupings of packages.



Contributed Packages

Available Packages

Currently, the CRAN package repository features 21872 available packages.

Table of available packages, sorted by date of publication

Table of available packages, sorted by name

CRAN Task Views aim to provide some guidance which packages on CRAN are relevant for tasks related to a certain topic. They provide tools to automatically install all packages from each view. Currently, 46 views are available.

Installation of Packages

Please type `help("INSTALL")` or `help("install.packages")` in R for information on how to install packages from this repository. The manual R Installation and Administration (also contained in the R base sources) explains the process in detail.

Package Check Results

All packages are tested regularly on machines running Debian GNU/Linux, Fedora, macOS (formerly OS X) and Windows.

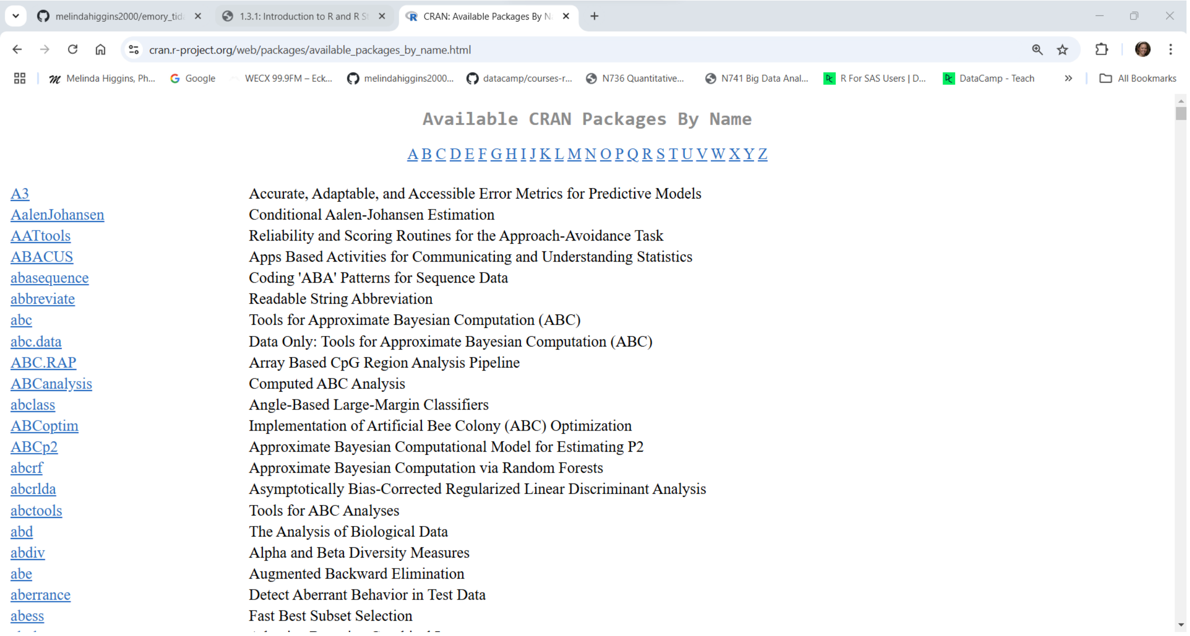
The results are summarized in the check summary (some timings are also available).

Linking to Packages

Please use the canonical form `<https://CRAN.R-project.org/package=PKG>` to link to the CRAN web page of package *PKG*.

In the rare case a link to a specific (and hence likely outdated) version of the package's sources in needed, one can use `<https://CRAN.R-project.org/package=PKG&version=VER>` for version *VER* of package *PKG*.

Here is what the list of Packages looks like sorted by name:

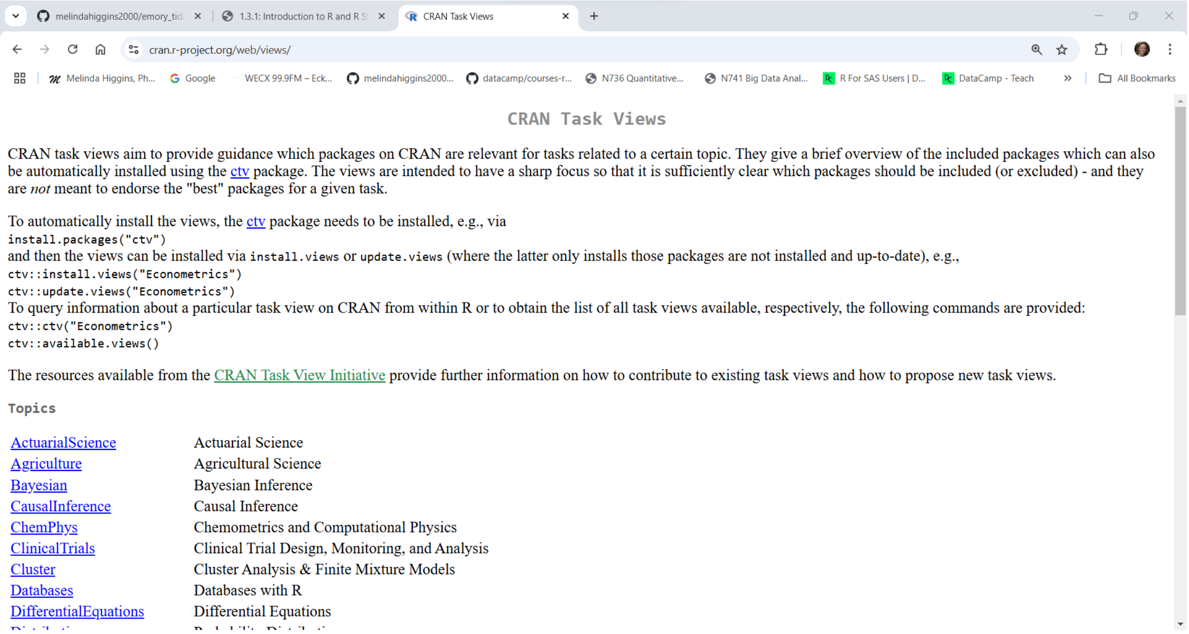


Available CRAN Packages By Name

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
AalenJohansen	Conditional Aalen-Johansen Estimation
AATtools	Reliability and Scoring Routines for the Approach-Avoidance Task
ABACUS	Apps Based Activities for Communicating and Understanding Statistics
abasequence	Coding 'ABA' Patterns for Sequence Data
abbreviate	Readable String Abbreviation
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
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
aberrance	Detect Aberrant Behavior in Test Data
abess	Fast Best Subset Selection

However, you can also browse Packages by “Task View”:



CRAN Task Views

CRAN task views aim to provide guidance which packages on CRAN are relevant for tasks related to a certain topic. They give a brief overview of the included packages which can also be automatically installed using the ctv package. The views are intended to have a sharp focus so that it is sufficiently clear which packages should be included (or excluded) - and they are *not* meant to endorse the "best" packages for a given task.

To automatically install the views, the ctv package needs to be installed, e.g., via

```
install.packages("ctv")
```

and then the views can be installed via `install.views` or `update.views` (where the latter only installs those packages are not installed and up-to-date), e.g.,

```
ctv::install.views("Econometrics")
ctv::update.views("Econometrics")
```

To query information about a particular task view on CRAN from within R or to obtain the list of all task views available, respectively, the following commands are provided:

```
ctv::ctv("Econometrics")
ctv::available.views()
```

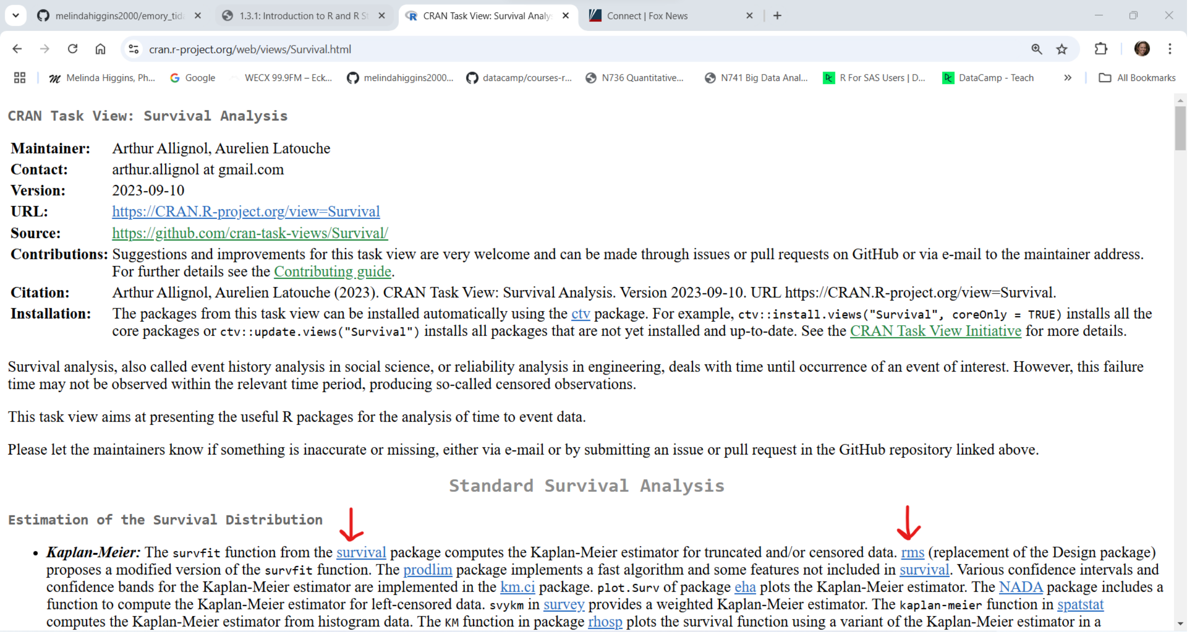
The resources available from the CRAN Task View Initiative provide further information on how to contribute to existing task views and how to propose new task views.

Topics

ActuarialScience	Actuarial Science
Agriculture	Agricultural Science
Bayesian	Bayesian Inference
CausalInference	Causal Inference
ChemPhys	Chemometrics and Computational Physics
ClinicalTrials	Clinical Trial Design, Monitoring, and Analysis
Cluster	Cluster Analysis & Finite Mixture Models
Databases	Databases with R
DifferentialEquations	Differential Equations

For example, suppose you are interested in survival analysis, here is a screenshot of the Survival Task View.

As you can see each Task View has a person(s) listed who help to maintain these collections. As you scroll through the webpage, you'll see links to packages they recommend along with a description of what the packages do. For example, see the links below to the `survival` and `rms` packages.



CRAN Task View: Survival Analysis

Maintainer:	Arthur Allignol, Aurelien Latouche
Contact:	arthur.allignol at gmail.com
Version:	2023-09-10
URL:	https://CRAN.R-project.org/view=Survival
Source:	https://github.com/cran-task-views/Survival/
Contributions:	Suggestions and improvements for this task view are very welcome and can be made through issues or pull requests on GitHub or via e-mail to the maintainer address. For further details see the Contributing guide.
Citation:	Arthur Allignol, Aurelien Latouche (2023). CRAN Task View: Survival Analysis. Version 2023-09-10. URL https://CRAN.R-project.org/view=Survival.
Installation:	The packages from this task view can be installed automatically using the ctv package. For example, `ctv::install.views("Survival", coreOnly = TRUE)` installs all the core packages or `ctv::update.views("Survival")` installs all packages that are not yet installed and up-to-date. See the CRAN Task View Initiative for more details.

Survival analysis, also called event history analysis in social science, or reliability analysis in engineering, deals with time until occurrence of an event of interest. However, this failure time may not be observed within the relevant time period, producing so-called censored observations.

This task view aims at presenting the useful R packages for the analysis of time to event data.

Please let the maintainers know if something is inaccurate or missing, either via e-mail or by submitting an issue or pull request in the GitHub repository linked above.

Standard Survival Analysis

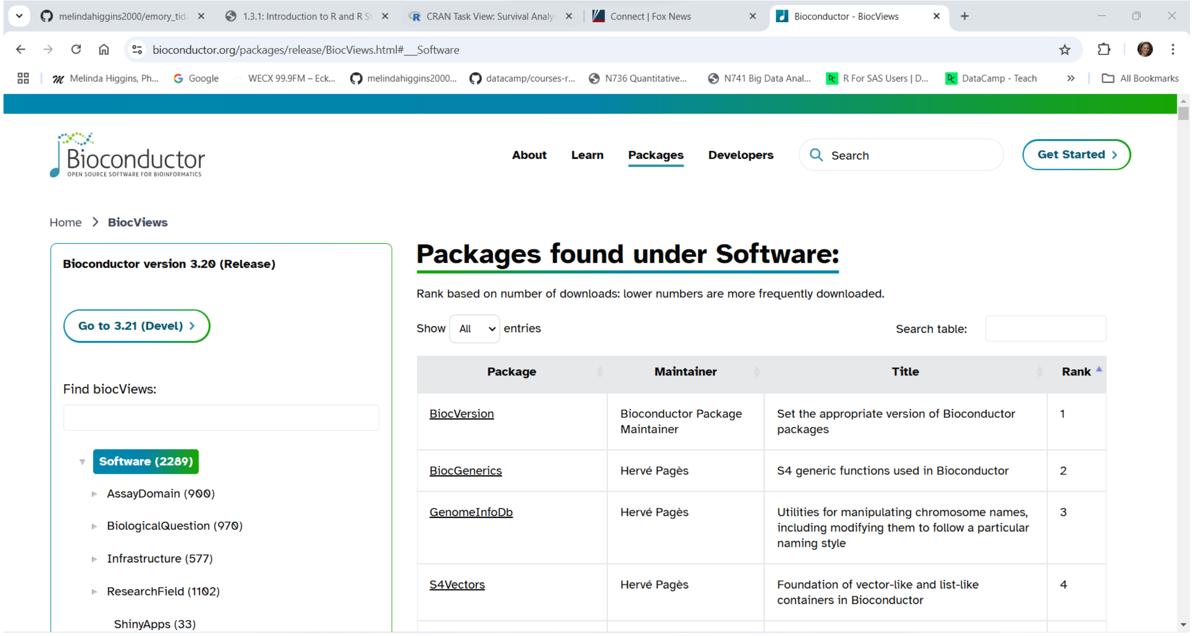
Estimation of the Survival Distribution

- ***Kaplan-Meier:*** The `survfit` function from the survival package computes the Kaplan-Meier estimator for truncated and/or censored data. rms (replacement of the Design package) proposes a modified version of the `survfit` function. The prodlim package implements a fast algorithm and some features not included in survival. Various confidence intervals and confidence bands for the Kaplan-Meier estimator are implemented in the km.ci package. `plot.Surv` of package eha plots the Kaplan-Meier estimator. The NADA package includes a function to compute the Kaplan-Meier estimator for left-censored data. `svykm` in survey provides a weighted Kaplan-Meier estimator. The `kaplan-meier` function in spatstat computes the Kaplan-Meier estimator from histogram data. The `KM` function in package rhosp plots the survival function using a variant of the Kaplan-Meier estimator in a

Where to get packages - Bioconductor Repository

While the list of R packages on CRAN is impressive, if you plan to do analyses of biological data, there is a good chance you will need a package from Bioconductor.org.

As of right now (01/10/2025 at 6:45pm EST) there are 2289 packages on Bioconductor. Similar to CRAN, Bioconductor requires each package to meet certain validation criteria and code testing requirements but these criteria are even more stringent on Bioconductor than on CRAN. You'll notice that you can search for packages under the `biocViews` (left side column) or you can sort them alphabetically or search for individual packages in the section on the right side.



Packages found under Software:

Rank based on number of downloads: lower numbers are more frequently downloaded.

Package	Maintainer	Title	Rank
BiocVersion	Bioconductor Package Maintainer	Set the appropriate version of Bioconductor packages	1
BiocGenerics	Hervé Pagès	S4 generic functions used in Bioconductor	2
GenomeInfoDb	Hervé Pagès	Utilities for manipulating chromosome names, including modifying them to follow a particular naming style	3
S4Vectors	Hervé Pagès	Foundation of vector-like and list-like containers in Bioconductor	4

The one disadvantage of R packages from Bioconductor is that you cannot install them directly using the RStudio menu for "Tools/Install" Packages because you cannot "see" the Bioconductor repository from inside RStudio. Instead you have to install Bioconductor packages using R code.

For example, here is what you need to do to install the `phyloseq` package which "… provides a set of classes and tools to facilitate the import, storage, analysis, and graphical display of microbiome census data".

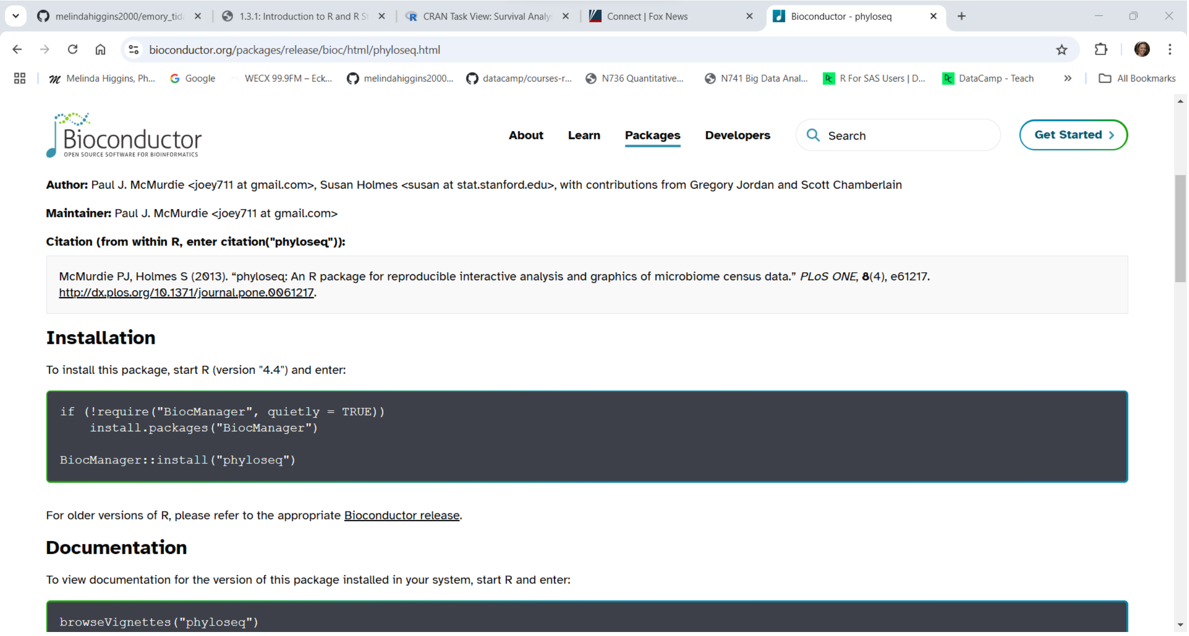
To install `phyloseq` you need to *(see the black box of code in the screenshot shown below)*:

1. Install `BiocManager` from CRAN - this package you can install from the RStudio menu for "Tools/Install Packages" - or you can run the code shown below for `install.packages()`.

```r
install.packages("BiocManager")
```

2. Then go to the Console or open an R script and run:

```r
BiocManager::install("phyloseq")
```



Author: Paul J. McMurdie <joey711 at gmail.com>, Susan Holmes <susan at stat.stanford.edu>, with contributions from Gregory Jordan and Scott Chamberlain

Maintainer: Paul J. McMurdie <joey711 at gmail.com>

Citation (from within R, enter citation("phyloseq")):

McMurdie PJ, Holmes S (2013). "phyloseq: An R package for reproducible interactive analysis and graphics of microbiome census data." *PLoS ONE*, **8**(4), e61217. http://dx.plos.org/10.1371/journal.pone.0061217.

Installation

To install this package, start R (version "4.4") and enter:

```
if (!require("BiocManager", quietly = TRUE))
    install.packages("BiocManager")

BiocManager::install("phyloseq")
```

For older versions of R, please refer to the appropriate Bioconductor release.

Documentation

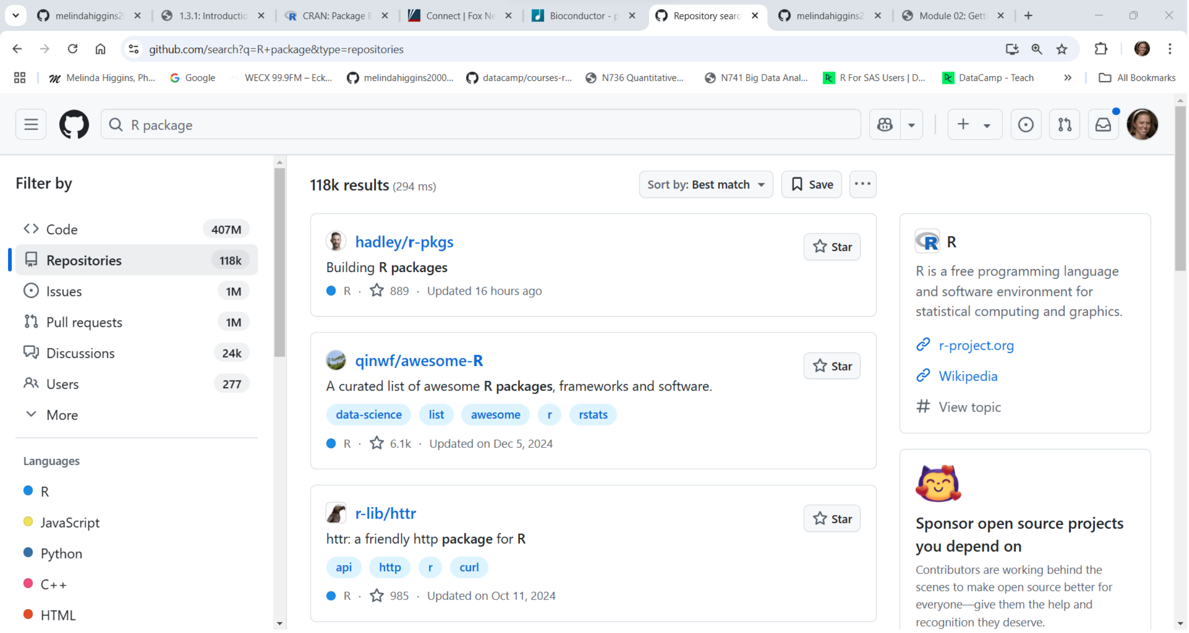
To view documentation for the version of this package installed in your system, start R and enter:

```
browseVignettes("phyloseq")
```

Where to get packages - Github, friends, teammates, ...

In addition to the CRAN and Bioconductor repositories, you can also get packages from Github (and other cloud-based repositories), friends, teammates or write your own.

To get an idea of how many packages may be currently on Github, we can "search" for "R package" at https://github.com/search?q=R+package&type=repositories and as you can see this is well over 118,000+ packages.



118k results (294 ms)

hadley/r-pkgs
Building R packages
R · 889 · Updated 16 hours ago

qinwf/awesome-R
A curated list of awesome R packages, frameworks and software.
data-science list awesome r rstats
R · 6.1k · Updated on Dec 5, 2024

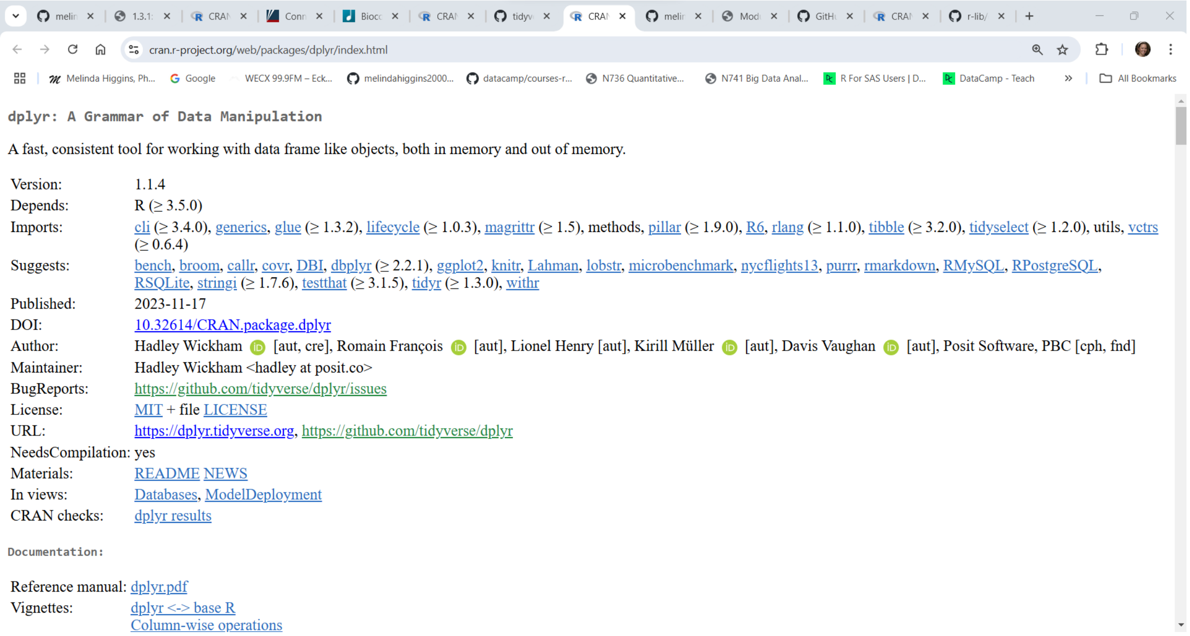
r-lib/httr
httr: a friendly http package for R
api http r curl
R · 985 · Updated on Oct 11, 2024

R
R is a free programming language and software environment for statistical computing and graphics.
r-project.org
Wikipedia
View topic

Sponsor open source projects you depend on
Contributors are working behind the scenes to make open source better for everyone—give them the help and recognition they deserve.

While you can find packages on Github that have not (yet) been published on CRAN or Bioconductor, the developers of packages currently on CRAN and Bioconductor also often publish their development version *(think of these as in "beta" and still undergoing testing)* on Github.

For example, the current published version of the data wrangling R package `dplyr` on CRAN was last updated on 11/17/2023 *(over a year ago)*.



dplyr: A Grammar of Data Manipulation

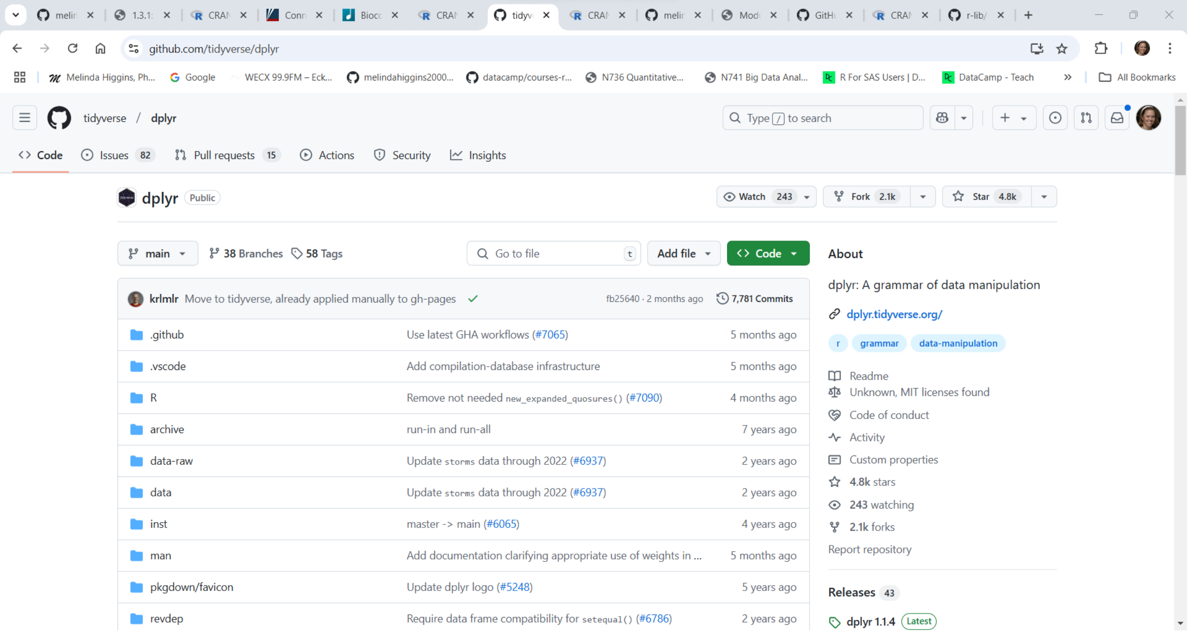
A fast, consistent tool for working with data frame like objects, both in memory and out of memory.

Version:	1.1.4
Depends:	R (≥ 3.5.0)
Imports:	cli (≥ 3.4.0), generics, glue (≥ 1.3.2), lifecycle (≥ 1.0.3), magrittr (≥ 1.5), methods, pillar (≥ 1.9.0), R6, rlang (≥ 1.1.0), tibble (≥ 3.2.0), tidyselect (≥ 1.2.0), utils, vctrs (≥ 0.6.4)
Suggests:	bench, broom, callr, covr, DBI, dbplyr (≥ 2.2.1), ggplot2, knitr, Lahman, lobstr, microbenchmark, nycflights13, purrr, rmarkdown, RMySQL, RPostgreSQL, RSQLite, stringi (≥ 1.7.6), testthat (≥ 3.1.5), tidyr (≥ 1.3.0), withr
Published:	2023-11-17
DOI:	10.32614/CRAN.package.dplyr
Author:	Hadley Wickham [aut, cre], Romain François [aut], Lionel Henry [aut], Kirill Müller [aut], Davis Vaughan [aut], Posit Software, PBC [cph, fnd]
Maintainer:	Hadley Wickham <hadley at posit.co>
BugReports:	https://github.com/tidyverse/dplyr/issues
License:	MIT + file LICENSE
URL:	https://dplyr.tidyverse.org, https://github.com/tidyverse/dplyr
NeedsCompilation:	yes
Materials:	README NEWS
In views:	Databases, ModelDeployment
CRAN checks:	dplyr results

Documentation:

Reference manual:	dplyr.pdf
Vignettes:	dplyr <-> base R Column-wise operations

However, the development version of `dplyr` on Github was last updated 5 months ago in August 2024. *So, there is probably a new version of* ***`dplyr`*** *coming soon for CRAN.*



krlmlr Move to tidyverse, already applied manually to gh-pages ✓ fb25640 · 2 months ago 7,781 Commits

.github	Use latest GHA workflows (#7065)	5 months ago
.vscode	Add compilation-database infrastructure	5 months ago
R	Remove not needed `new_expanded_quosures()` (#7090)	4 months ago
archive	run-in and run-all	7 years ago
data-raw	Update `storms` data through 2022 (#6937)	2 years ago
data	Update `storms` data through 2022 (#6937)	2 years ago
inst	master -> main (#6065)	4 years ago
man	Add documentation clarifying appropriate use of weights in ...	5 months ago
pkgdown/favicon	Update dplyr logo (#5248)	5 years ago
revdep	Require data frame compatibility for `setequal()` (#6786)	2 years ago

About

dplyr: A grammar of data manipulation

dplyr.tidyverse.org/

r grammar data-manipulation

Readme
Unknown, MIT licenses found
Code of conduct
Activity
Custom properties
4.8k stars
243 watching
2.1k forks
Report repository

Releases 43

dplyr 1.1.4 Latest

While the developers haven't published this "Github" version of **`dplyr`** yet on CRAN, if you want to test out new **`dplyr`** functions and updates under development, you can go to the R Console or write an R script to install the development version using these commands (see below) which is explained on the `dplyr` on Github website.

```r
# install.packages("pak")
pak::pak("tidyverse/dplyr")
```

Finding and vetting R packages

So, as you have seen there are numerous ways to find R packages and there are hundreds of thousands of them out there. Your company or team may also have their own custom R package tailored for your specific research areas and data analysis workflows.

Finding R packages is similar to finding new questionnaires, surveys or instruments for your research. For example, if you want to measure someone's depression levels, you should use a validated instrument like the Center for Epidemiological Studies-Depression (CESD) or the Beck Depression Index (BDI). These measurement instruments have both been well published and are well established for depression research.

Finding R packages is similar - do your research! Make sure that the R package has been published and is well established to do the analysis you want. In terms of reliability, getting packages from CRAN or Bioconductor are the best followed by Github or other individuals. The best suggestion is look to see which R packages are being used by other people in your field.

⚠ No oversight company or agency

While it may seem worrisome that there is no governing company or organization that verifies and validates and certifies all R packages, the good news is that the R community is a vast Global community. The development of R is not controlled by a limited number of people hired within a single company - instead there are literally millions of R programmers across the Globe testing and providing feedback on a 24/7 basis. If there is a problem with a package or function, there will be people posting about these issues - see Additional Resources.

This is the power of Open Source computing!!

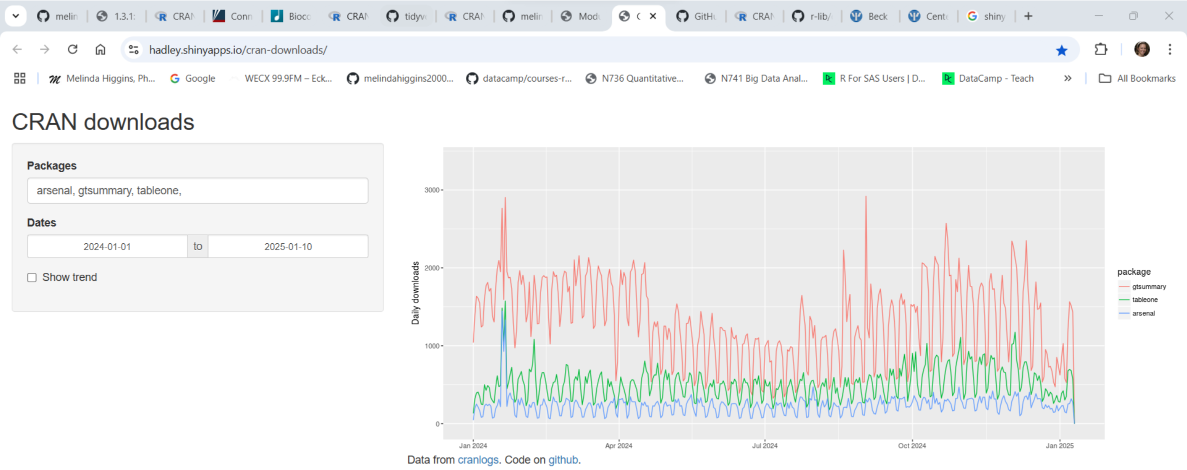
Popularity of R Packages

To get an idea of how long a package has been in use and if it is still being actively supported and how it relates to other similar packages, check out this interactive Shiny app website for package downloads from CRAN https://hadley.shinyapps.io/cran-downloads/. Type in the packages you want (separated by commas) to compare and put in the date range of interest.

Here is an example comparing the `arsenal`, `gtsummary`, and `tableone` packages all of which are useful for making tables of summary statistics (aka, "Table 1") - showing the number of downloads since the beginning of Jan 1, 2024.

As you can see the most downloaded of these 3 packages is `gtsummary` followed by `tableone` and then `arsenal` having the fewest downloads. This does NOT necessarily imply quality, but it does give you some insight into the popularity of these packages. I actually prefer the `arsenal` table package but `tableone` has been around longer and `gtsummary` is written by members of the RStudio/Posit development community and is more well known and popular. All 3 of these packages can be found in use in current research literature.

You will see examples of all 3 of these table-making packages in Module lesson 1.3.2



CRAN downloads

Packages

arsenal, gtsummary, tableone,

Dates

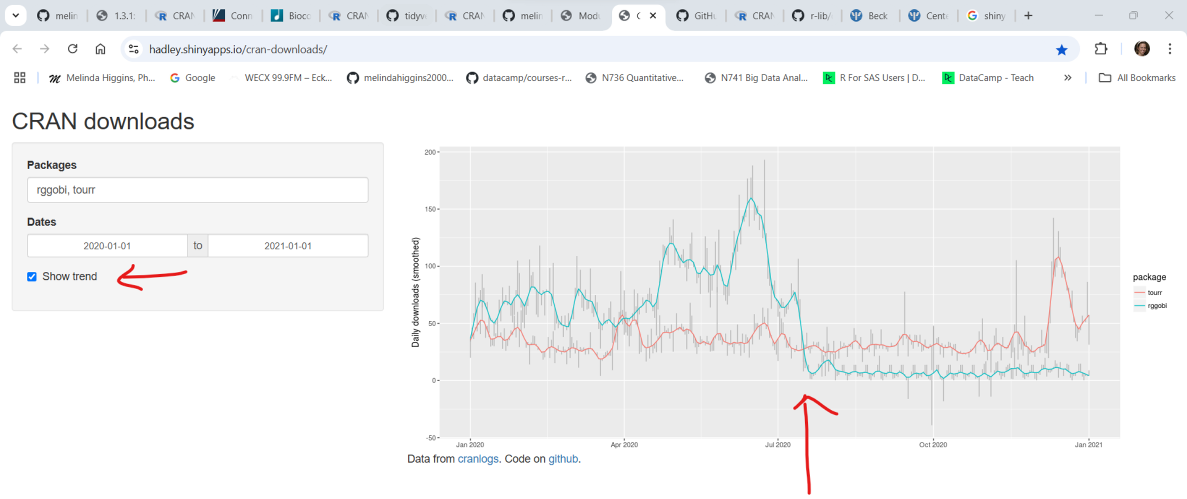
2024-01-01 to 2025-01-10

☐ Show trend

Data from cranlogs. Code on github.

Here is an example of two specific packages I like. The `rggobi` package which was great for visualizing multiple dimensions of data simultaneously but which is no longer supported. But there is now a newer `tourr` package which was written by the same developers to replace the `rggobi` package. You can see that in the middle of 2020, the number of downloads for `rggobi` dropped almost to 0 and the `tourr` package downloads started to rise - this is about when `rggobi` was archived on CRAN and they switched over to maintaining the newer `tourr` package.

- `rggobi` on CRAN moved to archived status in July 2020, but
- `tourr` on CRAN was last updated in April 2024.



CRAN downloads

Packages
rggobi, tourr

Dates
2020-01-01 to 2021-01-01

☑ Show trend

Data from cranlogs. Code on github.

In summary:

- do your homework,
- check to see when the package was last updated,
- research who maintains it and
- review how good their documentation is for the package and what it does, and
- see if the package has been used by others in your research area.

Load the new R package into your R session

After you've decided what package you want and have installed it onto your computer, you **must load it into memory for EVERY new R session** for which you want those functions available.

> Packages - install once, (re)-load every R session
>
> Unless you upgrade R or change computers, you only need to install a given R package once. But you do need to (re)-load the package into your current R session every time you (re)-start R (or RStudio).

For example, suppose I want to make a plot using the `ggplot2` package. Before I can use the `ggplot()` function, I have to load that package into my computing session.

Here is my current R session status **BEFORE** I load the `ggplot2` package.

```r
# show current sessionInfo
sessionInfo()
```

```
R version 4.5.1 (2025-06-13 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 11 x64 (build 22000)

Matrix products: default
  LAPACK version 3.12.1

locale:
[1] LC_COLLATE=English_United States.utf8
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8

time zone: America/New_York
tzcode source: internal

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

loaded via a namespace (and not attached):
 [1] compiler_4.5.1    fastmap_1.1.1     cli_3.6.3         tools_4.5.1
 [5] htmltools_0.5.8.1 rstudioapi_0.15.0 yaml_2.3.8        rmarkdown_2.26
```

```
 [9] knitr_1.50       jsonlite_1.8.8    xfun_0.52         digest_0.6.35
[13] rlang_1.1.4      evaluate_0.23
```

Since I have not yet loaded the `ggplot2` package into the session, I will get an error.

```
# I have not yet loaded ggplot2 into the session
# try the ggplot() function with the
# built-in pressure dataset to see error
ggplot(pressure, aes(temperature, pressure)) +
  geom_point()
```

```
Error in ggplot(pressure, aes(temperature, pressure)): could not find
function "ggplot"
```

The code above generates an error since these functions are not yet available in our session.

To fix this error, we need to use the `library()` function to load the `ggplot2` functions into current working memory.

```
# load ggplot2 package
library(ggplot2)

# look at sessionInfo again
sessionInfo()
```

```
R version 4.5.1 (2025-06-13 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 11 x64 (build 22000)

Matrix products: default
  LAPACK version 3.12.1

locale:
[1] LC_COLLATE=English_United States.utf8
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8

time zone: America/New_York
tzcode source: internal

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

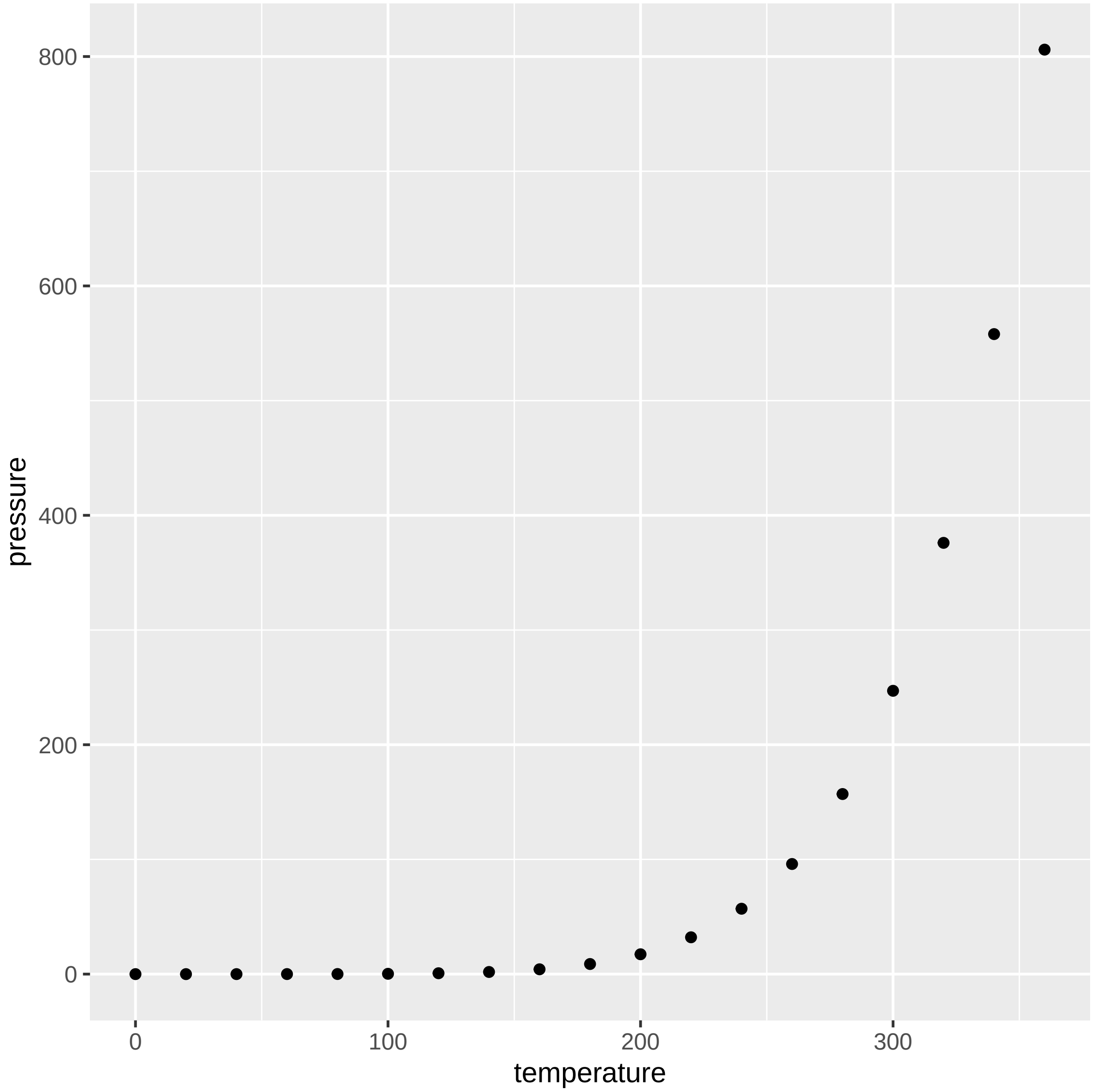
other attached packages:
[1] ggplot2_3.5.1

loaded via a namespace (and not attached):
 [1] vctrs_0.6.5       cli_3.6.3         knitr_1.50        rlang_1.1.4
 [5] xfun_0.52         generics_0.1.3    jsonlite_1.8.8    glue_1.8.0
 [9] colorspace_2.1-0  htmltools_0.5.8.1 scales_1.3.0      fansi_1.0.6
[13] rmarkdown_2.26    grid_4.5.1        evaluate_0.23     munsell_0.5.0
[17] tibble_3.2.1      fastmap_1.1.1     yaml_2.3.8        lifecycle_1.0.4
[21] compiler_4.5.1    dplyr_1.1.4       pkgconfig_2.0.3   rstudioapi_0.15.0
[25] digest_0.6.35     R6_2.5.1          tidyselect_1.2.1  utf8_1.2.4
[29] pillar_1.9.0      magrittr_2.0.3    withr_3.0.2       tools_4.5.1
[33] gtable_0.3.6
```

Notice that under `other attached packages` we can now see `ggplot2_3.5.1` indicating that yes `ggplot2` is installed and in memory and that version 3.5.1 is the version I am currently using.

Let's try the plot again with the `ggplot()` function from the `ggplot2` package.

```
# try the plot again
ggplot(pressure, aes(temperature, pressure)) +
  geom_point()
```



⚠ Reload packages for every new R session

Everything you close out your R/RStudio computing session (or restart your R session) you will need to load all of your package again. I know this seems like a HUGE pain, but there is a rationale for this.

1. You may not need the same packages for every new computing session - so R begins with the minimum loaded to save computing memory.
2. The GOOD NEWS is you do not have to re-install the packages - these are already saved on your computer. You only have to re-load them into memory using the `library()` function.
3. This workflow forces you to document (in your code) which packages you need for your computing sessions and why you are using them.

BUT … If you do have a core set of packages that you would like to make sure get loaded into memory every time you start R/RStudio, see these helpful posts on customizing your startup:

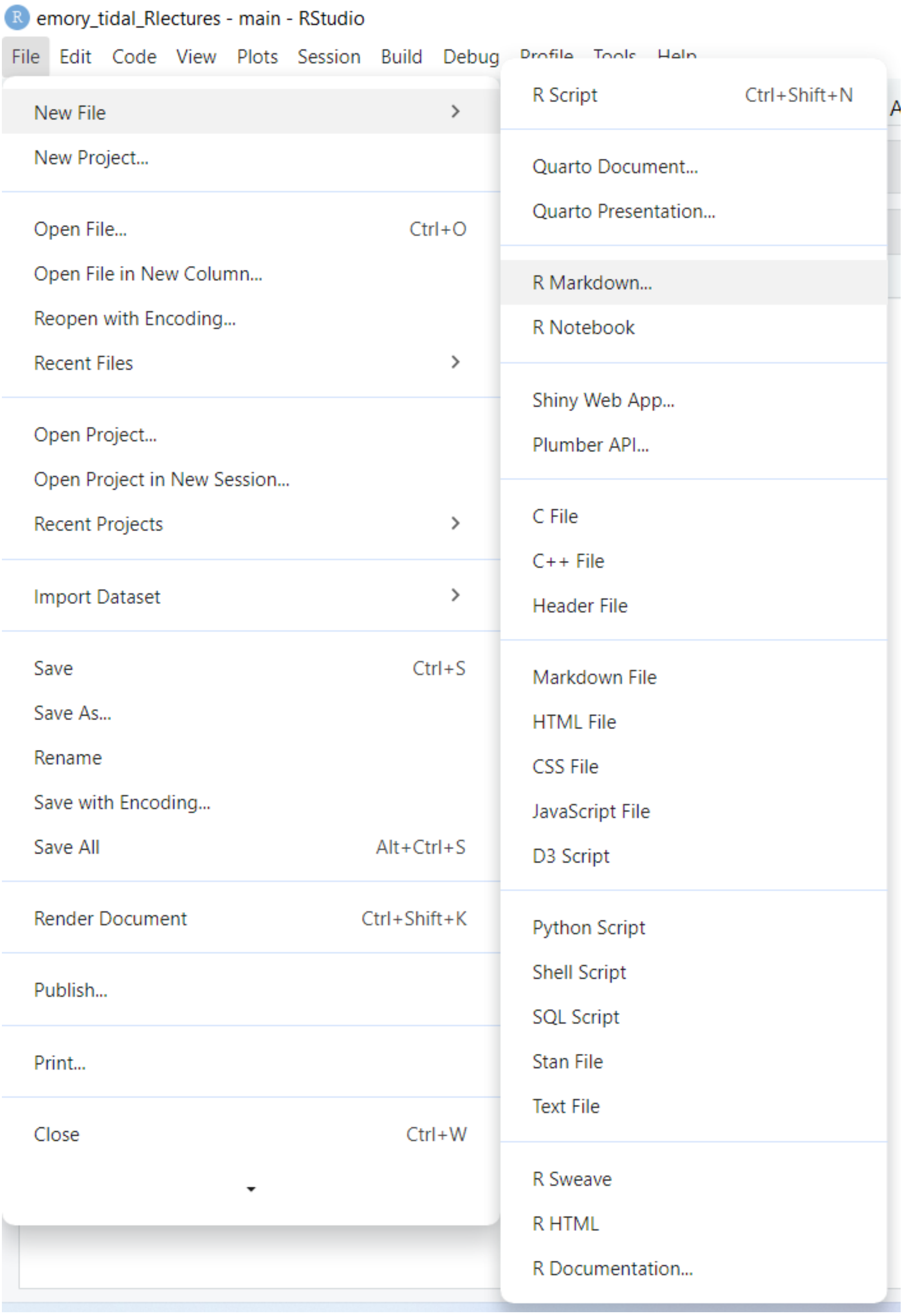
- https://www.datacamp.com/doc/r/customizing
- https://www.r-bloggers.com/2014/09/fun-with-rprofile-and-customizing-r-startup/

5. Create your first R Markdown report and produce output files in different formats (HTML, PDF, or DOCX)

Create a new Rmarkdown File

We will do more in the later lesson 1.3.6: Putting reproducible research principles into practice, but let's take a look at an Rmarkdown file and how we can use it to create a report that combines together `data + code + documentation` to produce a seamless report.

Go to the RStudio menu and click "File/New File/R Markdown":


emory_tidal_Rlectures - main - RStudio
File
Edit
Code
View
Plots
Session
Build
Debug
Profile
Tools
Help
New File
New Project...
Open File... Ctrl+O
Open File in New Column...
Reopen with Encoding...
Recent Files
Open Project...
Open Project in New Session...
Recent Projects
Import Dataset
Save Ctrl+S
Save As...
Rename
Save with Encoding...
Save All Alt+Ctrl+S
Render Document Ctrl+Shift+K
Publish...
Print...
Close Ctrl+W
R Script Ctrl+Shift+N
Quarto Document...
Quarto Presentation...
R Markdown...
R Notebook
Shiny Web App...
Plumber API...
C File
C++ File
Header File
Markdown File
HTML File
CSS File
JavaScript File
D3 Script
Python Script
Shell Script
SQL Script
Stan File
Text File
R Sweave
R HTML
R Documentation...

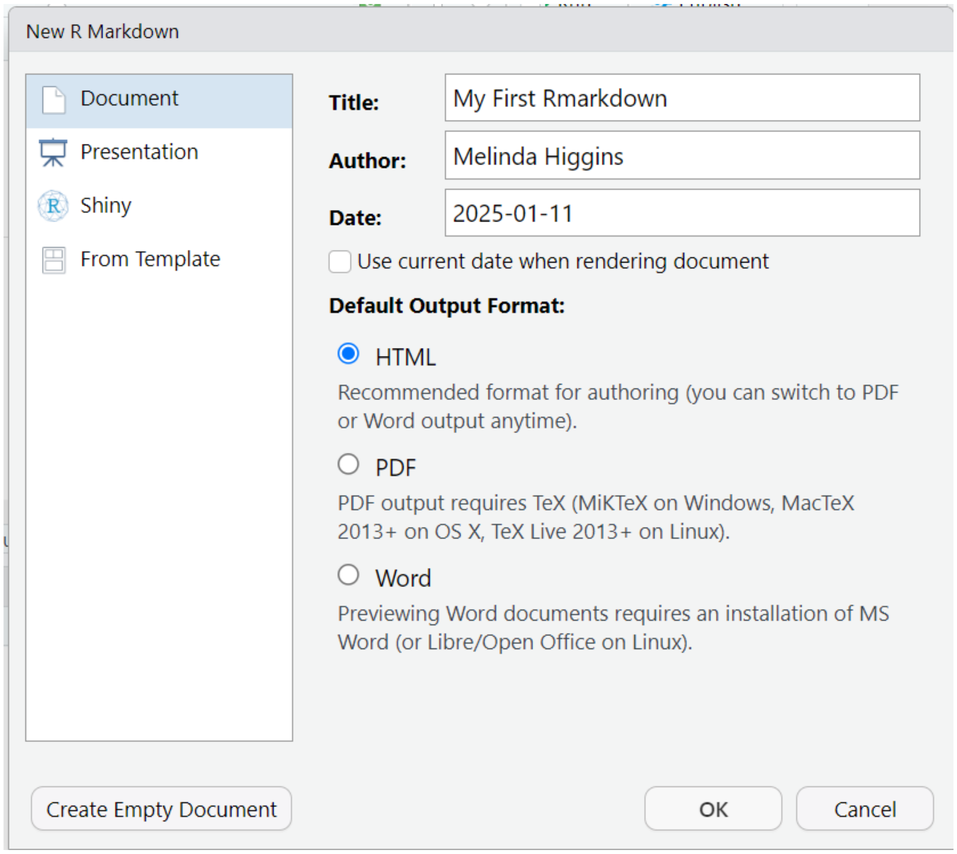
Type in a title, your name, the date and choose the format you'd like to create. For your first document I encourage you to try HTML. But you can create WORD (DOC) documents and even PDFs. In addition to documents, you can also create slide deck presentations, Shiny apps and other custom products like R packages, websites, books, dashboards and many more.

Rmarkdown ideas and inspiration

- Rmarkdown Gallery
- Rmarkdown Formats
- Rmarkdown Cookbook

To get started, use the built-in template:

- Type in a title
- Type in your name as author
- Choose and output document format
    - HTML is always a good place to start - **only need a browser to read the output `*.html` file.**
    - DOC usually works OK - **but you need MS Word or Open Office installed on your computer.**
    - PDF **NOTE: You need a TEX compiler on your computer** - Learn about installing the `tinytex` https://yihui.org/tinytex/ R package to create PDFs.



Title: My First Rmarkdown

Author: Melinda Higgins

Date: 2025-01-11

☐ Use current date when rendering document

Default Output Format:

● HTML

Recommended format for authoring (you can switch to PDF or Word output anytime).

○ PDF

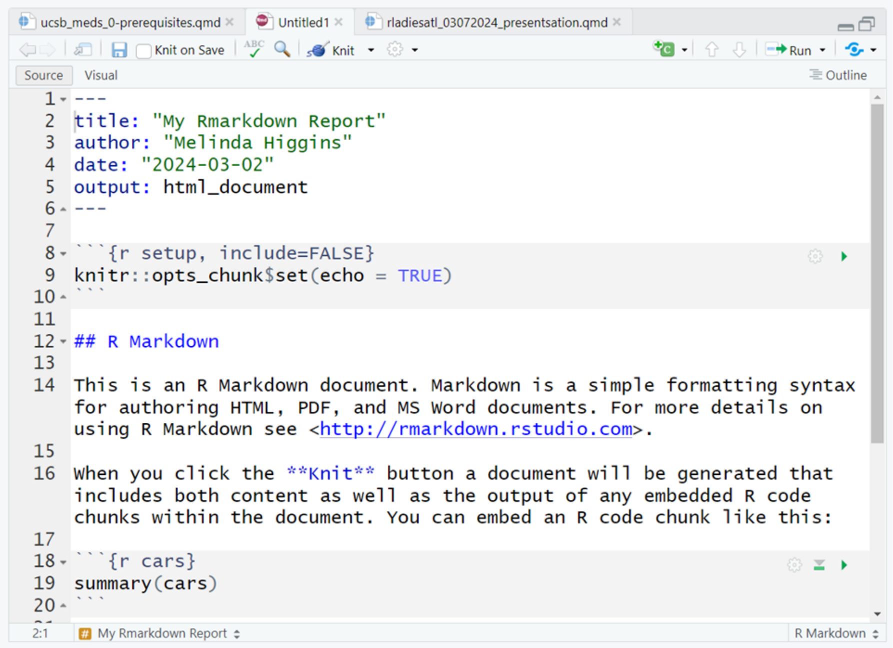
PDF output requires TeX (MiKTeX on Windows, MacTeX 2013+ on OS X, TeX Live 2013+ on Linux).

○ Word

Previewing Word documents requires an installation of MS Word (or Libre/Open Office on Linux).

Rmarkdown sections

Here is the **Example RMarkdown Template** provided by RStudio to help you get started with your first Rmarkdown document.



~~~
---
title: "My Rmarkdown Report"
author: "Melinda Higgins"
date: "2024-03-02"
output: html_document
---

```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
```

## R Markdown

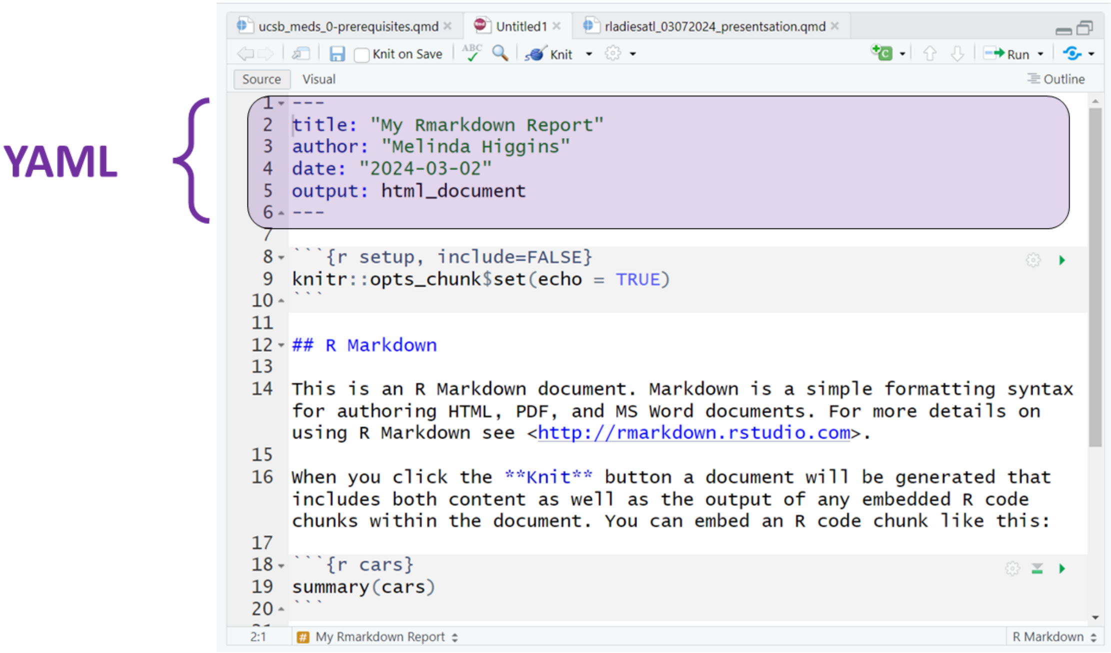
This is an R Markdown document. Markdown is a simple formatting syntax
for authoring HTML, PDF, and MS Word documents. For more details on
using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that
includes both content as well as the output of any embedded R code
chunks within the document. You can embed an R code chunk like this:

```{r cars}
summary(cars)
```
~~~

This document consists of the following 3 key sections:

1. YAML (yet another markup language) - this is essentially the metadata for your document and defines elements like the title, author, date and type of output document to be created (HTML in this example).



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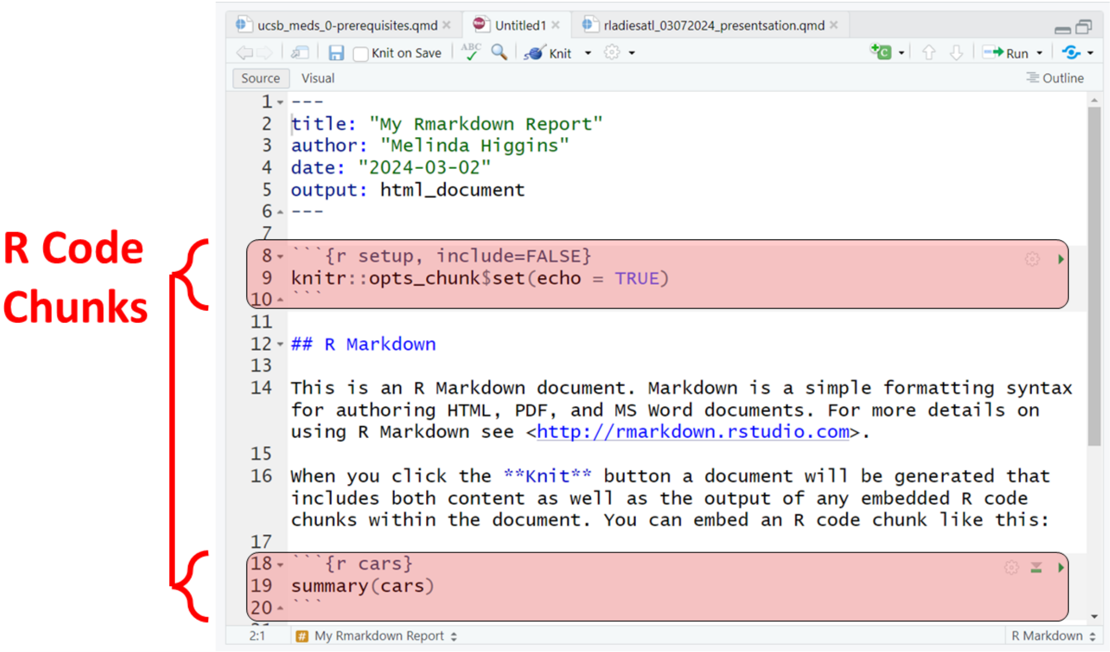
```
```
```

2. R code blocks - the goal is to "interweave" code and documentation so these 2 elements live together. That way the analysis output and any associated tables or figures are updated automatically without having to cut-and-paste from other applications into your document - which is time consuming and prone to human errors.

Notice that the code block starts and ends with 3 backticks ` ``` ` and includes the `{r}` Rlanguage designation inside the curly braces.

> **ℹ Rmarkdown**
>
> Rmarkdown can be used for many different programming languages including `python`, `sas`, and more, see rmarkdown - language-engines.



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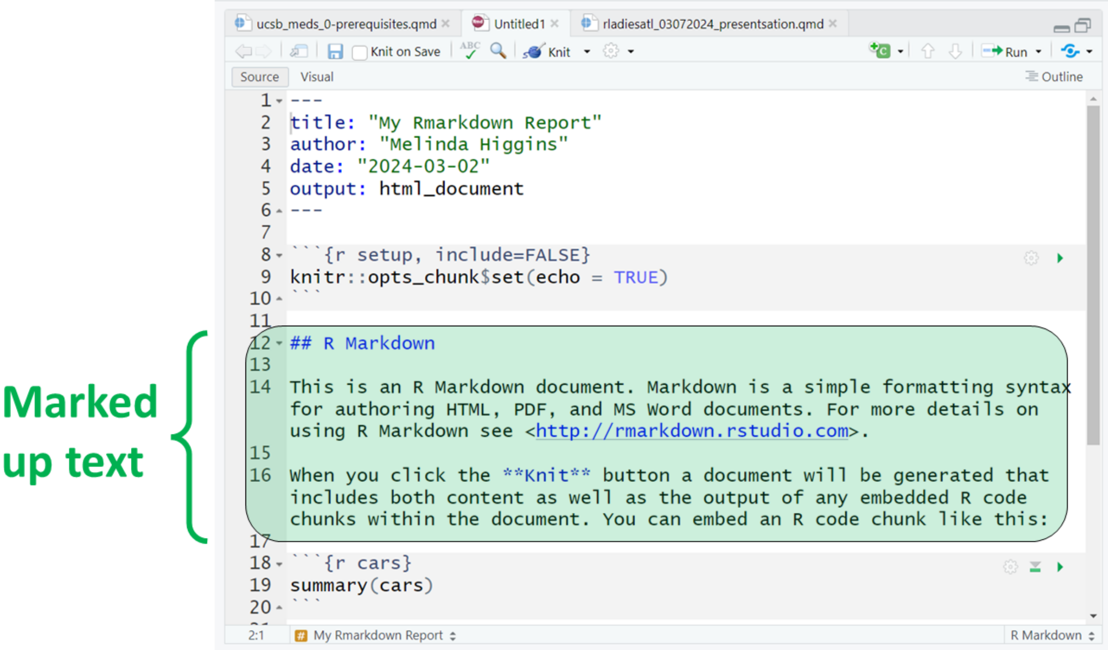
3. Along with the R code blocks, we can also create our document with "marked up (or marked down)" text. Rmarkdown is a version of "markdown" which is a simplified set of tags that tell the computer how you want a piece of text formatted.

For example putting 2 asterisks `**` before and after a word will make it **bold**, putting one `_` underscore before and after a word will make the word *italics*; one or more hashtags `#` indicate a header at certain levels, e.g. 2 hashtags `##` indicate a header level 2.

> **Rmarkdown Tutorial**
>
> I encourage you to go through the step by step tutorial at https://rmarkdown.rstudio.com/lesson-1.html.



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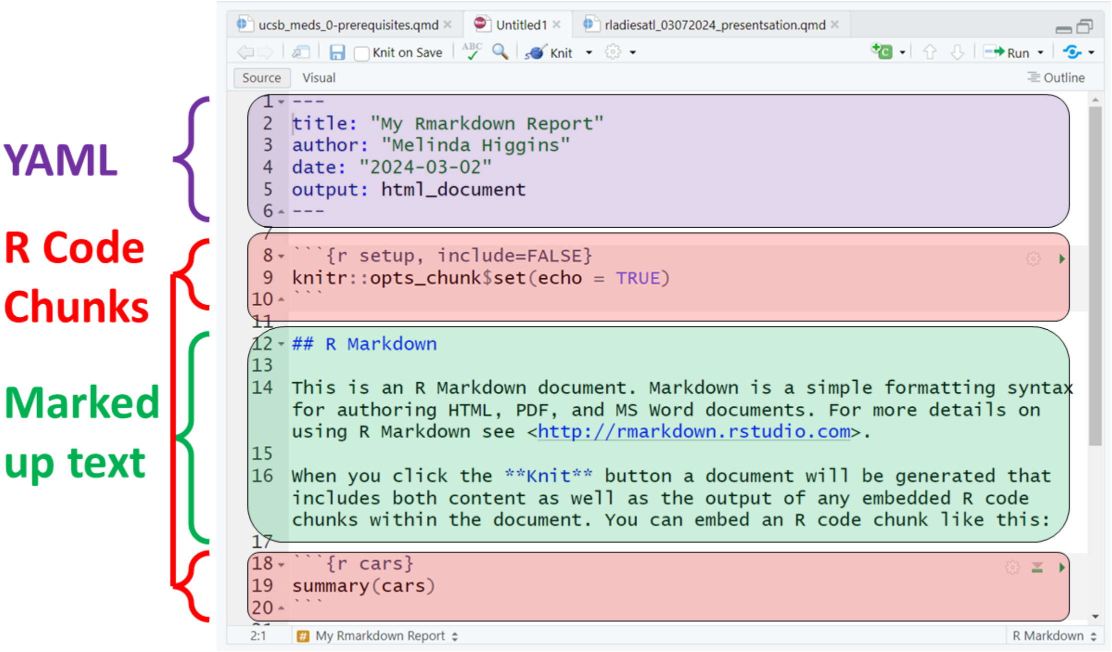
```{r cars}
summary(cars)
```
```
```

Here are all 3 sections outlined.



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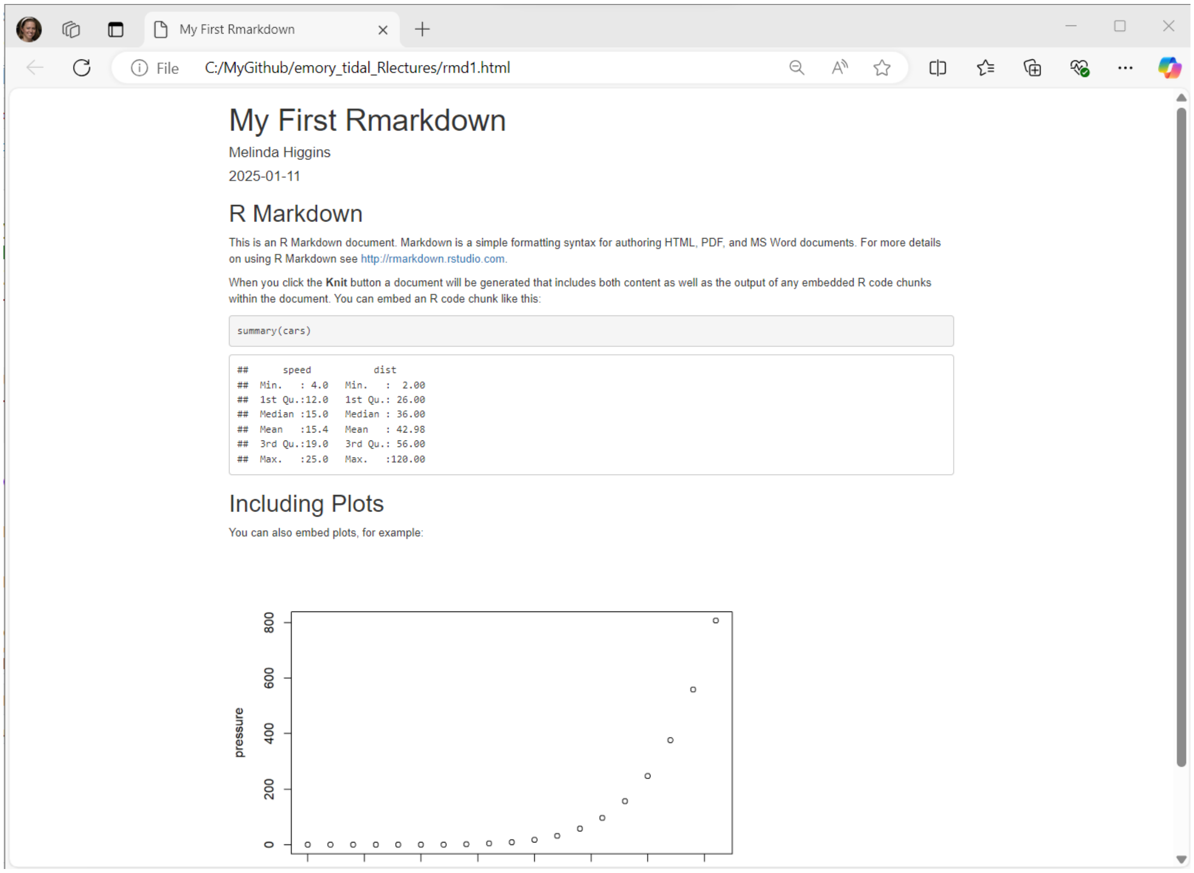
```
~~~

At the top of the page you'll notice a little blue button that says "knit" - this will "knit" (or combine) the output from the R code chunks and format the text as "marked up" and produce this HTML file *(which will open in a browser window)*:



My First Rmarkdown

Melinda Higgins

2025-01-11

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```
summary(cars)
```

```
##      speed           dist       
##  Min.   : 4.0   Min.   :  2.00  
##  1st Qu.:12.0   1st Qu.: 26.00  
##  Median :15.0   Median : 36.00  
##  Mean   :15.4   Mean   : 42.98  
##  3rd Qu.:19.0   3rd Qu.: 56.00  
##  Max.   :25.0   Max.   :120.00  
```

Including Plots

You can also embed plots, for example:

R Code For This Module

- `module_131.R`
- `Rscript_01.R`

References

R Core Team. 2025. *R: A Language and Environment for Statistical Computing.* Vienna, Austria: R Foundation for Statistical Computing. https://www.R-project.org/.

Wickham, Hadley. 2016. *Ggplot2: Elegant Graphics for Data Analysis.* Springer-Verlag New York. https://ggplot2.tidyverse.org.

Wickham, Hadley, Winston Chang, Lionel Henry, Thomas Lin Pedersen, Kohske Takahashi, Claus Wilke, Kara Woo, Hiroaki Yutani, Dewey Dunnington, and Teun van den Brand. 2024. *Ggplot2: Create Elegant Data Visualisations Using the Grammar of Graphics.* https://ggplot2.tidyverse.org.

Other Helpful Resources

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