# Week 9: Reproducibility in RStudio

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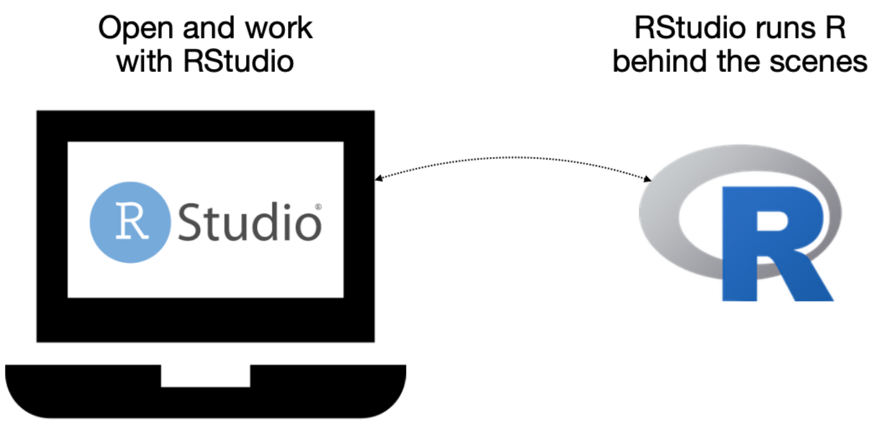
## Reproducibility in RStudio

In this week's lesson, we will be talking broadly about how to make our data analyses reproducible and how to start tackling larger projects.

For today's lesson, we will focus on how we can increase reproducibility within RStudio.

### R vs. RStudio

Before we begin, it is worth reminding ourselves of the difference between R and RStudio.




We are making the shift from working in Posit Cloud to using R and RStudio on your own device, meaning you should have both R and RStudio downloaded on your computer.

For most of us, even though we have downloaded the R software, we will likely never interact with the R program directly; I personally never open up R on my own computer.

Instead, in order to code in R and work with the R software, we will want to open up RStudio. Like it does in Posit Cloud, RStudio on our own computers connects to the R software that we have downloaded and let's us interact with R within the RStudio environment. So while I never personally open up R software directly, I frequently open up RStudio and work with R there!

### Introduction to Reproducibility

Throughout the course, we have talked about many of our topics in the context of "reproducibility," but what *exactly* does that mean?

When something is *reproducible*, it means we have the ability to recreate the same results (including cleaned data, tables, figures, and quantitative findings), using the same input data, computational methods, and conditions of analysis.

Our ultimate goal is to be able to rerun a fully analysis with a single click (or command).

Our first step is to make sure our code runs anytime and anywhere. That includes the next day or 5 years from now, on a desktop or a laptop, a Windows or a Mac, or on a collaborator or advisor's computer.

Below are some guidelines for making this happen:

### 1. Make sure things you did before don't matter (if they shouldn't)

Computers store the results of each command that we run in sequence. Occasionally, we will make a change to the code (perhaps we are testing a complicated piece of code) and the code will look like it still runs.

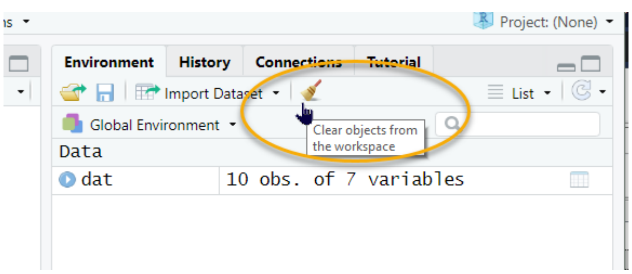
Sometimes, that line of code only works because of something we did earlier in the session, but if we restarted the session, it would get stuck because an object doesn't get created in the code or is created later on in the code.

We have actually been dealing with this scenario already. When we "knit" a .Rmd file–into a PDF, in our case–the document runs from scratch. If there is something in the code that is out of order or an object that isn't created in the code, the RMarkdown file won't create the PDF.

### 2. Clearing environments and restarting R

We can check that our code runs without having to knit, though. We have a few options.

- Clear R environment using the broom icon on the `Environment` tab.
  - Doesn't unload packages
  - Useful when developing code




- Restart R to get a clean environment
  - Does unload packages
  - Useful for making sure everything works
- Run entire file by selecting "Run All" in RMarkdown (`Ctrl + Alt + R` or `Cmd + Opt + R`)

For all of these options, we are trying to make sure that the code runs fully and produces the desired result without needed any tweaks.

### 3. Stop saving the current state of the environment

The typical default in RStudio is to automatically save the state of the environment when you close out of RStudio. Alternatively, it might ask if you want to save or not.

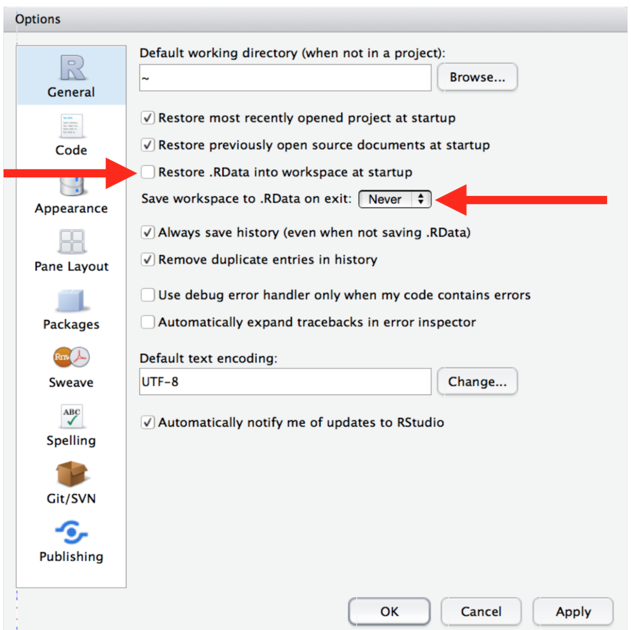
If you choose to save the workspace, everything in the environment will get reloaded when you start R, even when you restart it as described above.

While that might sound convenient, it can actually cause a lot of problems (see #1 above). To reduce the risk of having code that doesn't fully run on one click, we want to stop R from storing the state of the environment when we close RStudio.

To set the default in RStudio to not save the workspace, we want to do the following:

`Tools` -> `Global Options` -> `General` -> `Save workspace to ~/.RData on exit` -> `Never`

Uncheck `Restore .RData into workspace at startup`




### 4. Make sure code works on other computers

We will talk a lot more in-depth about this in a few minutes, but generally speaking, we want to do the following things to increase the likelihood that our code will run on another computer:

- Avoid using `setwd()` and absolute file paths (e.g., `C:\Users\Batman\DataCarp\data\mydata.csv`)
- Instead, use RStudio Projects and relative paths (e.g, `data/mydata.csv`)
- Write code that will work on all operating systems
  - Filenames in code should match actual names exactly, including capitalization
  - Use `/` instead of `\` or `\\` in paths

### 5. Clean up extra code

- Remove `install.packages()` lines from your code to avoid reinstalling packages repeatedly
- Remove experiments from your code
- If you don't want to remove them, comment them out by putting a `#` in front of the line of code.
  - A shortcut for this is `Ctrl + Shift + C` or `Cmd + Shift + C`

For example, now that we are using our own computers, we need to ensure that we have the correct packages *installed* on our local computers before we will be able to load them.

```
# download the package to your computer
# only needs to be done once
# install.packages("tidyverse")

# load the package for use
# needs to be done every time you open RStudio
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.4     v tidyr     1.3.1
## v purrr     1.0.4
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

## File Paths

In the course so far, we've been using Posit Cloud and placing data files where R knows to find them for you without any fuss.

Working with data files on your own computer is a little more complicated, but in this lesson we'll learn how to do this effectively.

In order to use data (or other files) stored on a computer, we need to be able to tell R where to find the data.

This is done using file paths. They are a description of the directories where our files are stored.

If you click here, this should download the Shrub Dimensions dataset that we have used before. But where does it get downloaded?

The details will look a bit different depending on the operating system but, generally, across the top or bottom of your file finder, you'll see the folder that things are stored in.

If we try to load this dataset just using its filename, as we have been doing in Posit Cloud, it probably won't work.

```
data <- read_csv("shrub-dimensions-labeled.csv")
```

This doesn't work because R cannot find the file where we've tried to load it from.

### Absolute vs. Relative Paths

File paths can be either *absolute* or *relative*. Spoiler alert: we prefer relative paths!

**Absolute Paths** Absolute file paths describe exactly where something is on the computer.

The data file that we downloaded is now being stored in the `Downloads` sub-directory of our `Home` directory on our computer. The `Home` directory will vary a little bit by operating system.

For example, on a Mac or Linux computer, the `Home` directory is `/home/username`. Within the `username` directory is the `Downloads` directory (or folder).

```
# OSX/Linux
data <- read_csv('/home/ellenbledsoe/Downloads/shrub-dimensions-labeled.csv')
```

On a Windows machine, change `home` to `Users`.

```
# Windows
data <- read_csv('/Users/ebledsoe/Downloads/shrub-dimensions-labeled.csv')
```

Folders (another name for directories) are separated by `/`, a forward slash. We then have the file name at the end.

As an important note, Windows shows `\` or `\\` (backslashes) as the separator between folders. However, this does not work universally. Because `/` works on all operating systems, we want to use it to promote reproducibility across operating systems.

As we've done in the past, we always need to include the file extension (the part after the `.`) when reading in a file.

**Relative Paths** Relative paths don't specify exactly where on a computer the file is located. Instead, they point to the location of the file of interest in *relation* to what we call the "current working directory", meaning the directory that we are currently in.

```
'Downloads/shrub-dimensions-labeled.csv'
```

The relative file path above is saying "From where I am currently, the shrub-dimensions file is in the `Downloads` sub-directory."

### Find Out Where You Are

So how do we find out which directory R thinks that we are in? We can use a function called `getwd()`

```
getwd()
```

This function stands for "get working directory". The "working directory" is where the program starts from; any relative paths will need to start from this directory.

### Loading Data

If we have data that is in our current working directly, we can use the file name alone to read in the data.

```
shrub_data <- read_csv('shrub-dimensions-labeled.csv')
```

This is considered a relative path, because the file is in the working directory. The only remaining piece of the path that we need to specify is the name of the file itself.

One way to ensure that a file is in the working directory is to download it using the `download.file()` function, which we have done a number of times while in Posit Cloud.

When we have data that is not in the working directory, we have two options:

- tell R where it is
- change the working directory to where it is

Changing the working directory is a common approach. To do so, people use the `setwd()` function, which sets the working directory to a specific location.

This, however, can cause a number of issues. If you are working with someone else's files or on another computer, the directory that you want to be working from is likely different from the file path that has been put in the `setwd()` function.

In general, using `setwd()` means that your code will only work on a single computer. This breaks a core tenet of reproducibility, so we want to avoid doing this.

Ideally, we want to have the working directory set automatically, regardless of what computer we are using, and we use relative paths.

## RStudio Projects

The simplest way to ensure that we are always using relative paths is to use RStudio Projects (or R Projects, same thing).

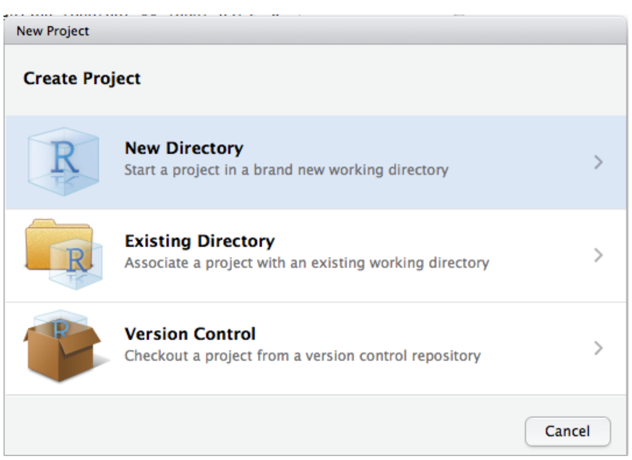
In fact we've already been using them! Every time you click on an assignment or click `New Project` in Posit Cloud, this was actually creating a new R Project. Now we need to learn how to do this on our own computers.

Each project is a self-contained unit of work in a specific folder/directory. It treats all locations as relative to that specific directory.

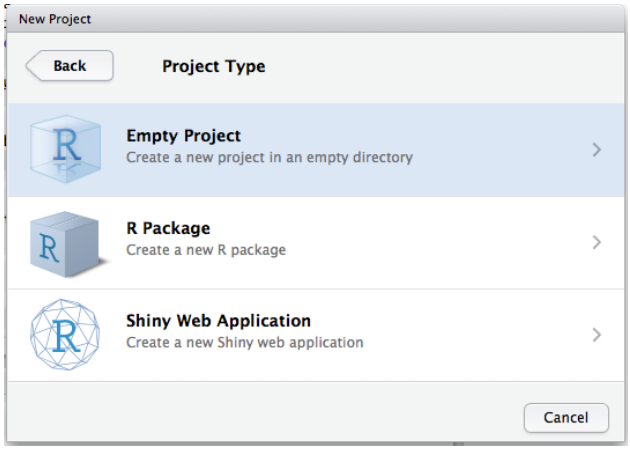
Let's set up an R Project on our own computers.

> `File` -> `New Project` -> `New Directory` -> `New Project` -> [insert_name_here]

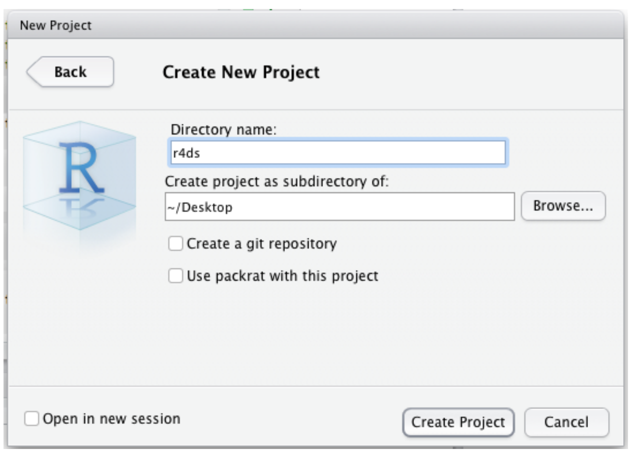
1. Select "New Directory"



2. Select “Empty Project”



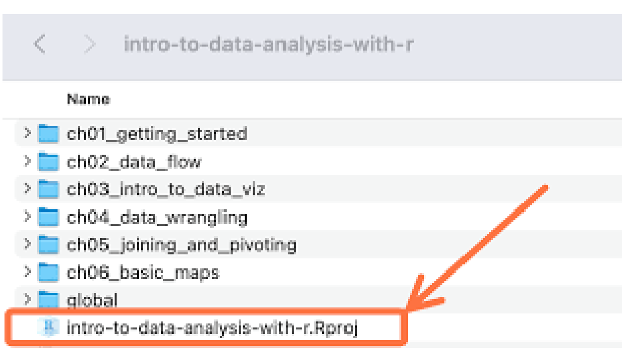

3. Use the “Browse” button to find a location for your project folder and name it appropriately.




If you prefer, you can use the `Existing Directory` option to choose a folder that already exists that you want to turn into an R Project.

Once we create our new project, RStudio will create a `.Rproj` file in that directory. This file is not the project itself, but it does contain information about the project. We do not manually change this file.

To open an RStudio Project, you will want to open the `.Rproj` file.




We probably want to move this file into our project directory! We can also add our Shrub Dimensions data into the project directory as well. I will demonstrate how to do this manually.

Now when we try to run the line of code that we are familiar with when reading in datasets, we should have success!

```
data <- read_csv('shrub-dimensions-labeled.csv')
```

**Sub-directories** As we will discuss shortly, it is common to store data in a sub-directory, such as a `data` folder. Let's create a new folder in our project.

Create the new folder: > `New Folder` -> `data_raw` -> `OK`

Move the data file into the new folder: > `File checkbox` -> `More` -> `Move` -> `data_raw`

Now, in order to successfully read in the shrub data file, we need to point R into the `data_raw` directory first before we specify the file name.

```
data <- read_csv('data_raw/shrub-dimensions-labeled.csv')
```

### Writing Data

We we have made some kind of change to our dataset and want to save that resulting dataset, we can use a function called `write_csv()` to do so.

Let's pretend we've made some type of change to our shrub dataset and want to save it.

The arguments for `write_csv()` are:

- the name of the object with the data you want to save
- the file path for where you want the new file to end up. This should include the name of the file you want to create, also with the file extension (.csv, in this case)

```
write_csv(data, "data_clean/shrubs_modified.csv")
```

### Changing Projects

If you want to switch between projects, you can do so: > `File` -> `Recent Projects` or `Open Project`

Alternatively, you can click on the arrow next to the name of the project in the upper right-hand corner, which will provide the same options.

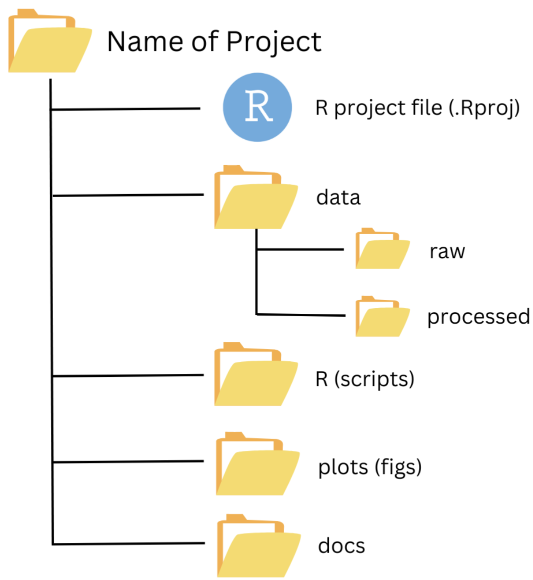
## Project Structure

Next in our journey of reproducibility is project structure.

There are a lot of potential benefits to creating a good organizational structure from the beginning, including helpful documentation. This can help us understand all of the project components, work more efficiently, and make collaboration easier (including with our future selves!).

Setting up a good structure will save you a lot of frustration in long run, even if it might be a bit time-consuming and frustrating to do it right initially.

### File Structure




If possible, we want to have all files associated with the project in one main folder. This main folder should be the RStudio Project folder.

From there, we can (and should…) have sub-folders. What exactly those sub-folders are is up to you. A good starting place is to have something like this (or like the image above):

- `data_raw`
  - keeping the raw data in a separate folder helps ensure that the original copy always exists
  - metadata about the included files can go in this folder as well
- `data_clean`
- `docs`
- `outputs`
  - big analysis files, data visualizations, etc.
- `scripts`
  - any files in the scripts folder (.R or .Rmd) should have relative file paths to read in and create files
  - lots of descriptive text and/or comments
  - good object names (and column names)
  - general order is packages, data, any functions we have created, everything else

Both folder and file names should follow good naming conventions. They should be descriptive but not too long, have a consistent formatting, and include no spaces or special characters.

The R Project folder should also contain a README file with descriptions of the file structure, the files in the project, and any other relevant information for how to reproduce analyses or outputs.

### File Paths in RMarkdown Files vs. Scripts

Using documents that combine code output and text in single document, such as with RMarkdown files (which we are already doing!), is another great way to promote reproducibility.

There is an odd quirk that comes with using file paths in .Rmd files, however.

For reasons I haven't quite been able to nail down, file paths work a little bit different in R scripts (.R file that only understand the R language) and RMarkdown files (.Rmd files, like we use) in RProjects.

- For R scripts, the R Project folder is the working directory, which is standard.
- For RMarkdown files, the folder that contains the file is the home folder.

What this means is that if your .Rmd file is in a sub-directory, that sub-directory is that file's reference point. To read in data from another sub-directory, we have to tell R that we want to go up one level in directory structure (to the project folder) and then into the other sub-directory.

To move "up" in your folder structure (or back to the larger folder), we use `...`

```
data <- read_csv("../data_raw/shrub-dimensions-labeled.csv")
```

#### Goal of Good Project Structure

Ultimately, the goal of setting up a good project structure is reproducibility. We are aiming to get the same results from a set of data and code without having to make any adjustments, regardless of who is running the code or what computer it is on.

It also has important implications for how we share code with others.

For example, we can zip/compress the project folder and send it to someone else. When they work with the files in the project folder, as long as all of the paths are relative instead of absolute, they will work seemlessly.

When we start talking about version control using git and GitHub, they are nicely integrated into the RStudio Project structure.

Ultimately, reproducibility is meant to make our lives easier, for ourselves and our collaborators.

## Helpful Resources

Below I'm including some resources that you might find helpful while you're starting out understanding file paths and R Projects.

- R for Epidemiologists: File Paths (and R Projects)
- Reproducible Data Science for Ecologists: Project Organization
- RStudio Projects and Working Directories: A Beginner's Guide
- Posit: RStudio Projects
- R 4 Data Science: Workflow: Projects