Code and Data Lab Management Guidelines

R and GitHub Starter Kit for New Team Members

Florencia D'Andrea

2024-11-29

Table of contents

Part I

Introduction

GitHub Organization: www.github.com/StringhiniLab

The use of programming languages has become an essential part of data analysis for most researchers today. In this context, a basic skill set in computer science knowledge is key to ensuring reliable and reproducible results (Wilson 2017). Although a variety of educational materials, tutorials, and recommended practices specifically designed to train researchers are available (Carpentry; Carpentries; Club; Community 2023), there is a trade-off: adopting and practicing these techniques often requires significant effort, which researchers must take from the time dedicated to studying their own disciplines.

In fact, one of the main barriers to sharing code at the time of publication is that scientists often do not know how to do it or have doubts about how to do it properly. Thus, the lack of training in computer science and best practices in data management impacts the reproducibility and transparency of scientific research (Ram 2013; Sharma et al. 2024). This issue is compounded by the lack of incentives from the scientific system, leading to a high number of publications in the not sharing their code despite the potential benefits of open science (Allen and Mehler 2019; Melvin et al. 2022; Tazare et al. 2024; Xu et al. 2025).

Where to Start?

We believe that the early adoption of basic tools and techniques to improve research data analysis by early-career researchers is fundamental. For this to happen, **training cannot be solely individual but should also be fostered within research groups**.

There are several advantages to this approach:

- **Establish minimum documentation practices**
  Defining a set of group-level criteria for code and data management helps standardize documentation and facilitate exchange among researchers in the group, saving time and avoiding confusion.
- **Teach where to learn more Data Science**
  Supporting new members of the research group in adopting basic computational techniques from the beginning sets the stage for researchers to explore additional tools early, based on the needs of their study topics.
- **Focus on domain-specific skills**
  Identifying and preselecting domain-specific computational skills can save time for new researchers.
  This knowledge is sometimes shared in publications tailored to each discipline but is too specific to be addressed by general training courses and tutorials for scientists, being the exception for some fields Carpentries. For example, it can be established that using a tool like GitHub is necessary for sharing code or collaborating, but learning to use a tool like Bash might not be essential.

- **Avoid messy projects from day one**
  Centralizing data analyses on a GitHub organization and creating standards for pushing code promotes improved repository structuring, version control, and better-documented code, ensuring a baseline quality of data analysis from the project's inception.
- **Early peer review**
  Sharing analyses from the beginning in private repositories shared only with team members enables peer review or feedback before publishing results. This should increase early-career researchers' confidence when sharing the code for publication and fuel open science practices.
- **Maintain the group's research history**
  This approach helps create and standardize a historical archive of the group's data analyses, ensuring continuity and avoiding dependence on researchers leaving behind their code and data when they move on.

Goal

The goal of this guide is not to be an exhaustive course in data analysis but to provide the **minimum necessary guidelines** for new members of Dr. Silvia Stringhini's lab to follow agreed-upon practices in data and code management.

References

What is the lab's policy for data and code usage?

Statement of Need

Dr. Silvia Stringhini is an epidemiologist with an extensive career. She has served as the Head of the Unit of Population Epidemiology at the Geneva University Hospitals and as an Assistant Professor at the University of Geneva, Switzerland. Her main research areas include social inequalities in chronic diseases and aging, the role of health behaviors in the genesis of social health inequalities, the biological consequences of social inequalities, and the role of environmental factors in social health disparities.

Recently, she moved her lab to the School of Population and Public Health at the University of British Columbia in Canada, where she is establishing a new team. Currently, she is in the process of welcoming new students and staff, making this an ideal time to outline how her new group will manage data and code in its publications.

We discussed with Dr. Stringhini the basic requirements that can be expected from a new student joining the group. A summary of the agreements reached and how they influenced the creation of this book can be found in Table 1.

Table 1: **Book content overview.** This table presents the benefits and selected topics included in the book to guide the team on each prioritized action.

Action	**Benefit**	**What does this book cover?**
Centralize the data analysis of the group in a GitHub organization	Preserve copies of the group's data analyses	- Steps to create a GitHub account and be added to the lab's organization - How to create a GitHub repository
Avoid sending confidential data to GitHub	Protection of sensitive data	- Use of `.gitignore` - Project structure recommendations including how to organize the data folder

Action	Benefit	What does this book cover?
Select R as the primary programming language and RStudio as the IDE	Standardize the software used in the lab	- Installation instructions - Recommendations on learning resources and good practices
Share a copy of each lab member's analyses in a private GitHub repository	- Create an initial version of the project that is organized and minimally documented so another lab member can understand it - Foster the habit of performing code backups - Receive feedback from colleagues early in the project development - Have access to analyses from other lab members that have not been published	- How to create a private GitHub repository and what information to include - Basic information to include in the README - Creating a GitHub team and defining procedures to manage access to private repositories - Develop a basic workflow for everyday use of Git and GitHub.
Store the code associated with scientific publications publicly in a GitHub repository	The benefits of conducting open science (citation)	This section will be developed at the time of the first paper's publication

Additionally, considering the lab's long-term evolution, onboarding and offboarding procedures were defined.

Why Use GitHub?

Git and GitHub were originally created for professional software development. However, their use has extended into the scientific field for various reasons:

- **Backup**
  Making it a habit to push to GitHub at least once a day allows you to keep an online copy of your data analysis.
- **Improved Documentation Practices**
  Having a complete README and knowing that your colleagues have access to your code encourages better organization of the project, making it clearer, more concise, and well-documented.

- **Version Control**
  It is easy to see how the project has evolved over time and recover changes from previous versions.
- **Reproducibility**
  When publishing scientific articles, maintaining reproducible results is considered a quality practice.

It's important to clarify that lab members are not expected to be expert users of Git and GitHub, but rather to handle basic commands necessary to achieve the use proposed.

Notes on Instructional Design

We recognize that creating the code for a scientific publication takes time and involves numerous attempts before deciding what figures and results effectively will be published. Keeping this in mind, it was decided that each student would generate a **private GitHub repository** by project to maintain a backup of daily data analyses conducted in the lab. This private repository could then serve as the foundation for a public version for the final GitHub repository with the scientific article's code. Also, publicly exposing the behind-the-scenes details of data management and analysis can be more challenging for early-career researchers, who can fear of public scrutiny of code (Gomes et al. (2022), Tazare et al. (2024)).

Maintaining this initial private repository has other benefits besides functioning as a backup: it allows sharing the code with other lab members (as part of a GitHub lab team), makes available analyses that may not be included in the final paper but could be relevant for another publication, helps keeping a clearer project structure from the beginning and **improves the overall documentation of the project**.

Specific characteristics of the research area were also discussed (Mathur and Fox (2023)), such as handling **sensitive data** (Community (2023)). As a result, practices like using `.gitignore` and setting up a structured data folder with `raw` and `processed` sub folders were suggested to prevent private data from being pushed to GitHub and to maintain an orderly system for storing such information within the project. Also, we created a friendly for non programmers README template, to be sure that the relevant information, as the database version in use and computational environment, is captured.

One of the more challenging aspects to adopt is using Git, as it has multiple utilities and a considerable learning curve. Considering this, it was decided that, in this initial stage, Git and GitHub's primary use would be to create an online and centralized backup of the projects, share repositories among team members, and manage version control instead of focusing in collaborative tools.

Since R is the most widely used programming language in the discipline, the team decided to leverage the Git integration provided by RStudio IDE's Git tab for committing changes and integrating students' local work into the GitHub repositories.

References

Roles

GitHub Organization Management

- **Adding new members**: Ensure that new lab members join the GitHub Organization once they have created their GitHub account.

GitHub Team Maintainer

At least one person in the lab will be assigned as the Team Maintainer of the GitHub organization. This role will allow them to add and remove members from the team, granting or revoking access to private repositories.

For this, it's important to assign the Lab Member in charge the **Team Maintainer** role for the Lab Team.
Follow the instructions in Assigning the team maintainer role to a team member

If properly assigned the label `mantainer` should appear next to they name in this repository: https://github.com/orgs/StringhiniLab/teams/lab-team.

Responsibilities of the Maintainer

- Add new lab members to the Lab Team.
- Remove team members who are no longer part of the lab.
- Assign other members as Team Maintainers if necessary.

References

Part II

Guidelines

1 Onboarding

Checklist

- □ Create your personal GitHub account.
- □ Request access to the GitHub Organization.
- □ Request access to the Lab Team.
- □ Install Git, R and RStudio.

1.1 Create Your Personal GitHub Account

First, you need to create an account on GitHub by following these steps: Creating an account on GitHub.

After creating your GitHub account, you'll notice that your profile is associated with a specific URL, structured as follows:

- `https://github.com/<username>`

This page allows you to access your account settings and all repositories you create.

1.2 Request Access to the GitHub Organization

Our lab has a GitHub organization that centralizes the repositories for everything produced in the lab.
Notice that the organization's URL is different from your profile's:

- https://github.com/StringhiniLab

To gain access, you need to provide your GitHub username to the person managing the organization. Having access to the organization will enable you to create repositories within it.

> ℹ Note that you have your personal GitHub url, and also there is the url of the GitHub organization.

1.3 Request Access to the Lab Team

Not all lab repositories are public. To access repositories owned by other lab members, you must also be added to the Lab Team.
Dr. Stringhini, as the owner of the organization, always has access to all repositories.

- Adding organization members to a team
- Managing team access to an organization repository

1.4 Installation Instructions

To work in the lab, you will need to have Git, R, and RStudio installed.
Please note that the installation process may vary depending on whether you have a computer with Windows, Linux, Mac (Intel), or Mac (Apple Silicon) operating systems.

- **Git**: Download Git

- **R**: Download R

- **RStudio**: Download RStudio

⚠ **Installation issues**

It could happen that you get into trouble during the installation process. Remember that we are a team and that you can use Slack to share your issues and look for support

Once you've completed these steps, you can move on to the next section.

1.5 References

- Best practices for organizations

2 Starting a New Project

These steps only need to be completed once, at the beginning of a project.

Checklist

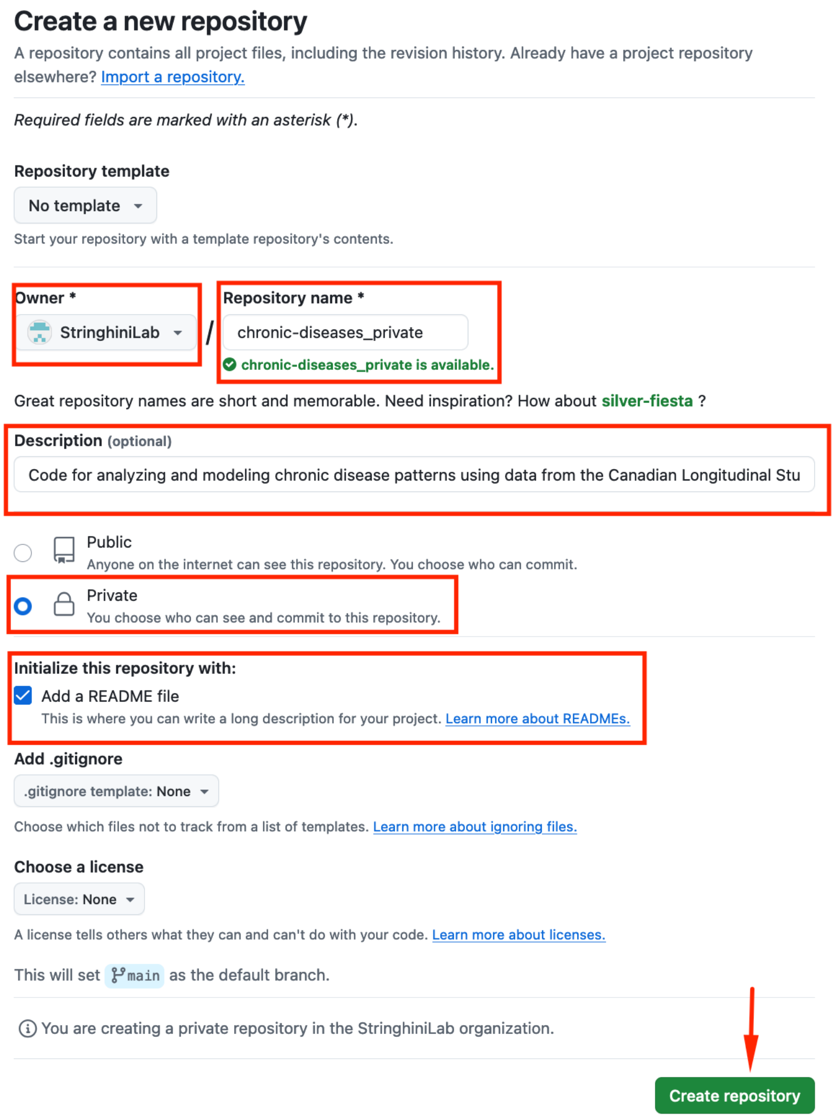
- □ Create a private repository by new project.

- □ Add the Lab Team to the repository.
- □ Clone the repository and associate it with an RStudio Project.
- □ Add your Data folder to `.gitignore`.
- □ Complete the `README` file using the template.

2.1 Create a private repository by new project

When starting to work on a new project, your first step is to create a **private** repository in the lab's GitHub organization: StringhiniLab GitHub.

1. Click the green **New** button to open a window like this:



Create a new repository

A repository contains all project files, including the revision history. Already have a project repository elsewhere? Import a repository.

Required fields are marked with an asterisk (*).

Repository template: No template

Start your repository with a template repository's contents.

Owner *: StringhiniLab / Repository name *: chronic-diseases_private

✓ chronic-diseases_private is available.

Great repository names are short and memorable. Need inspiration? How about **silver-fiesta** ?

Description (optional): Code for analyzing and modeling chronic disease patterns using data from the Canadian Longitudinal Stu

○ Public
Anyone on the internet can see this repository. You choose who can commit.

● Private
You choose who can see and commit to this repository.

Initialize this repository with:

☑ Add a README file
This is where you can write a long description for your project. Learn more about READMEs.

Add .gitignore: .gitignore template: None

Choose which files not to track from a list of templates. Learn more about ignoring files.

Choose a license: License: None

A license tells others what they can and can't do with your code. Learn more about licenses.

This will set main as the default branch.

ⓘ You are creating a private repository in the StringhiniLab organization.

2. Complete/select using the following criteria:

□ **Owner**
Select `StringhiniLab` as the owner, not your personal GitHub account.

□ **Repository Name**
Choose a name that represents your project. Since this repository will be private, append `_private` to the name.
For example, if the repository name is `chronic-diseases`, name it `chronic-diseases_private`.

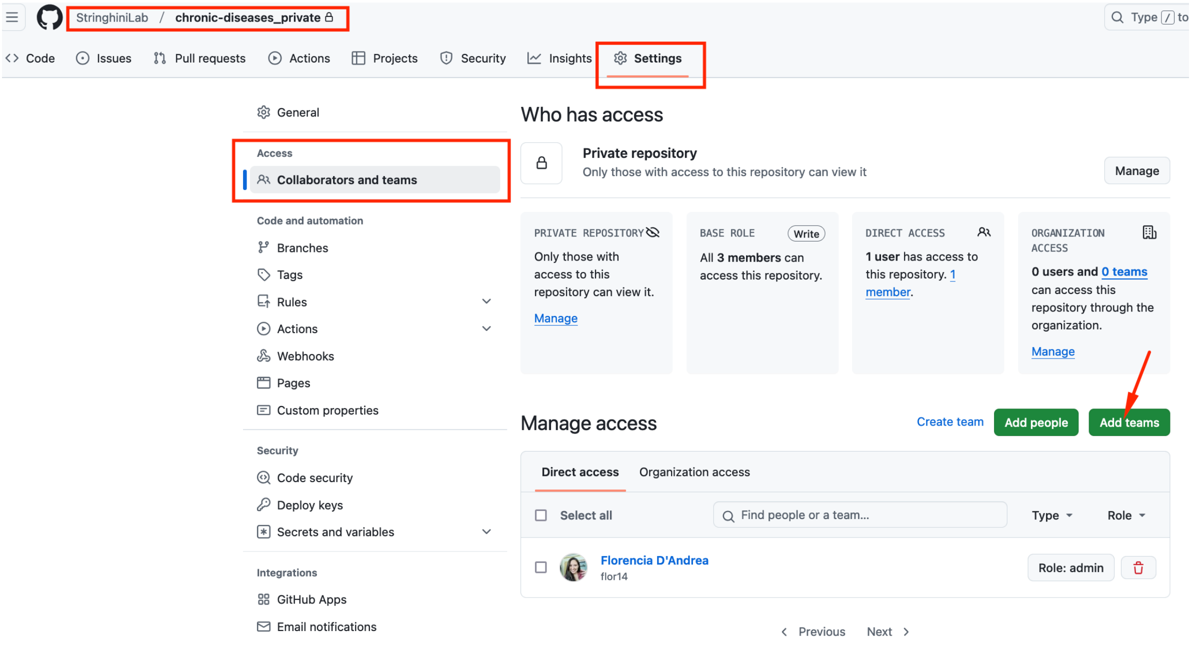
□ **Description**

Provide a more detailed description of the project here. This helps identify the repository's content in the organization.

- □ **Public or Private?**
  Ensure the repository is set to `Private`.
- □ **Initialize Repository With**
  Add a `README.md`.

Ignore the other options for now.
If everything works, you'll see your repository within the GitHub organization labeled as `Private`.

2.2 Add the Lab Team to the repository



Only those with access to this repository can view it

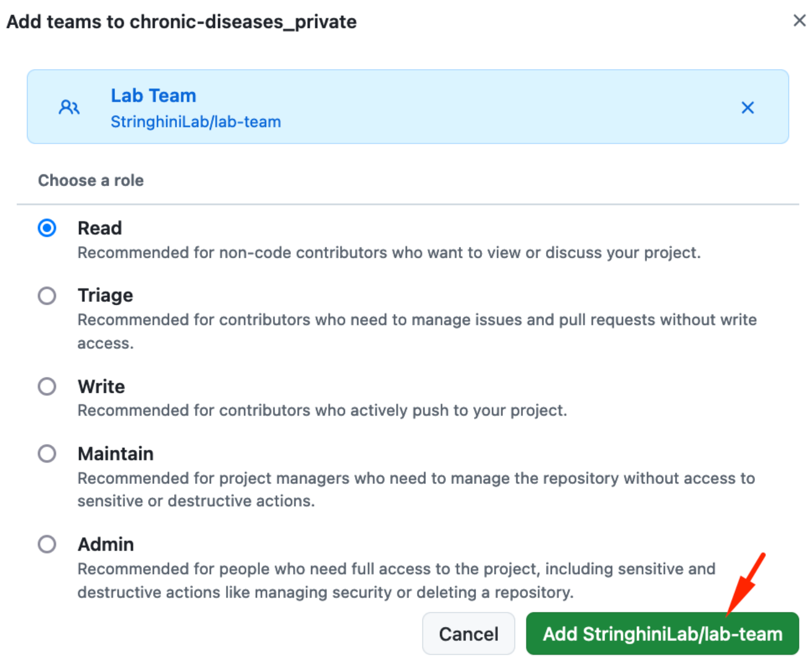
Only those with access to this repository can view it.

All 3 members can access this repository.

1 user has access to this repository. 1 member.

0 users and 0 teams can access this repository through the organization.

1. **Navigate to the repository's `Settings` tab.**
   In the left-hand sidebar, find and click on `Collaborators and teams`.
2. Click **Add teams** and add `Lab Team`.
   By default, you will select the Read role for the team. The idea is that other Lab Members can view the repository but will not be able to edit it by mistake.



Add teams to chronic-diseases_private

Lab Team
StringhiniLab/lab-team

Choose a role

● **Read**
Recommended for non-code contributors who want to view or discuss your project.

○ **Triage**
Recommended for contributors who need to manage issues and pull requests without write access.

○ **Write**
Recommended for contributors who actively push to your project.

○ **Maintain**
Recommended for project managers who need to manage the repository without access to sensitive or destructive actions.

○ **Admin**
Recommended for people who need full access to the project, including sensitive and destructive actions like managing security or deleting a repository.

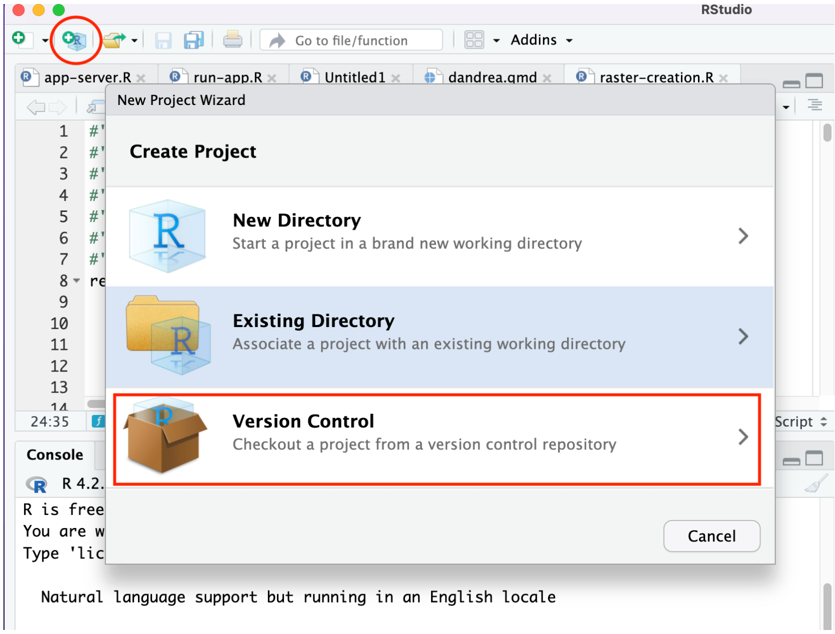
This allows all current Lab Members to view (but not modify) your project.
If you don't want to share an analysis with other Lab Members, you can create a repository in your personal GitHub account instead. However, **always ensure sensitive data is not pushed to GitHub** for confidentiality reasons.

All repositories in `StringhiniLab` should be accessible to the Lab Team, which is why these repositories are hosted in the organization instead of personal accounts. Remember that individuals who are Owners of the organization can view all repositories even if there are not part of the Team.

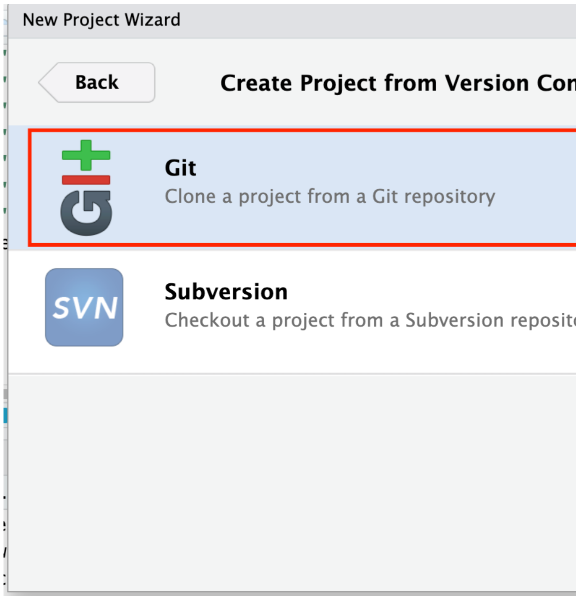
2.3 Clone the repository and associate it with an RStudio Project

1. **Open RStudio**
   If RStudio is not installed, complete first the installation instructions in the Onboarding section.

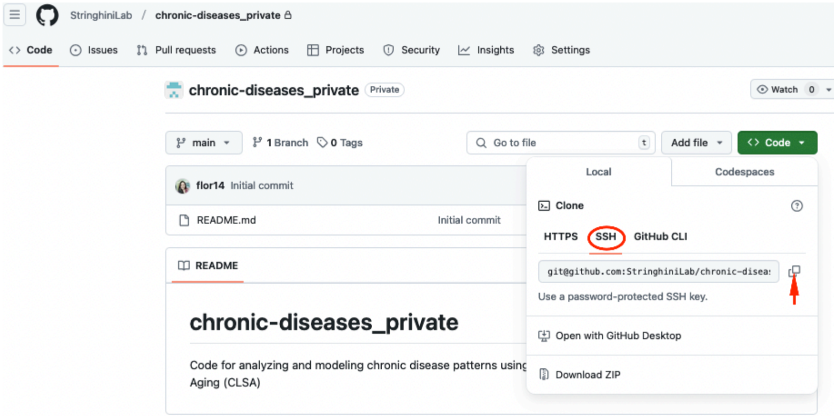
2. **Clone the Repository**
   In RStudio:
   `File > New Project > Version Control > Clone a Project from a Git Repository`.



```
R is free
You are w
Type 'lic

 Natural language support but running in an English locale
```


New Project Wizard
Back
Create Project from Version Con
Git
Clone a project from a Git repository
SVN
Subversion
Checkout a project from a Subversion reposit

Go back to the repository and copy the repository's URL.



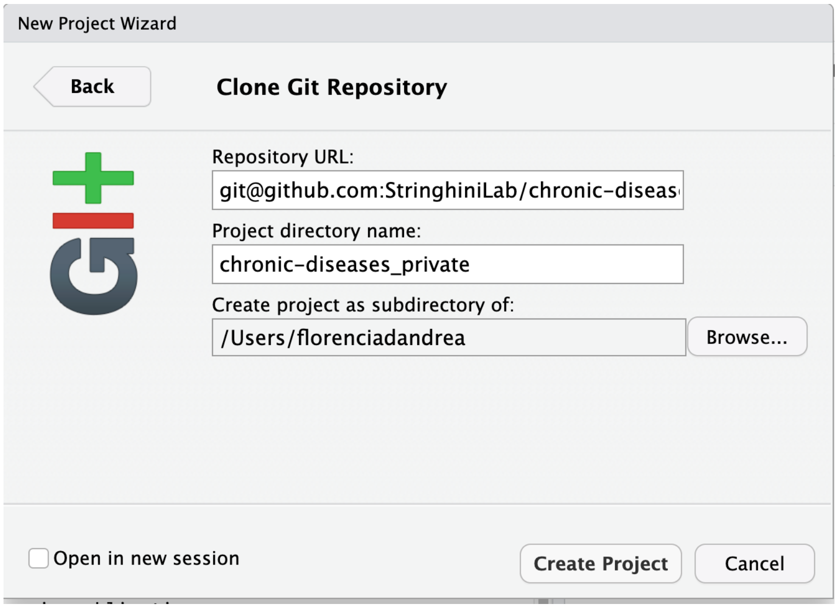
```
git@github.com:StringhiniLab/chronic-diseas
```

Use a password-protected SSH key.

chronic-diseases_private

Code for analyzing and modeling chronic disease patterns using
Aging (CLSA)

And paste it in the correct field:



New Project Wizard

Clone Git Repository

Repository URL: git@github.com:StringhiniLab/chronic-diseas

Project directory name: chronic-diseases_private

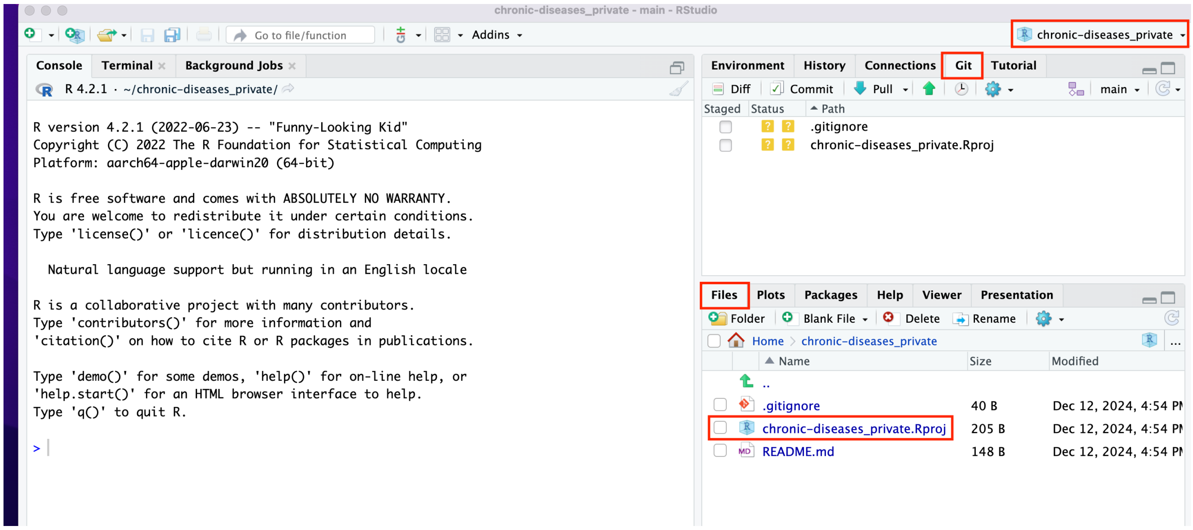
Create project as subdirectory of: /Users/florenciadandrea

If successful, you'll see a folder containing your project, including the README file that we created on GitHub, in the Files tab at the bottom-right of RStudio.

Note that an .Rproj icon has appeared. Clicking on this icon outside of RStudio will open RStudio directly within the project.

Additionally, the project name now appears in the top-right corner. By opening that menu, you can easily switch between projects without leaving the RStudio IDE.

You'll also notice a tab named Git in the top-right panel.



chronic-diseases_private - main - RStudio

R 4.2.1 · ~/chronic-diseases_private/

```
R version 4.2.1 (2022-06-23) -- "Funny-Looking Kid"
Copyright (C) 2022 The R Foundation for Statistical Computing
Platform: aarch64-apple-darwin20 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

Staged	Status	Path
□	? ?	.gitignore
□	? ?	chronic-diseases_private.Rproj

Home › chronic-diseases_private

Name	Size	Modified
..		
.gitignore	40 B	Dec 12, 2024, 4:54 PM
chronic-diseases_private.Rproj	205 B	Dec 12, 2024, 4:54 PM
README.md	148 B	Dec 12, 2024, 4:54 PM

2.3.1 Add your Data folder to `.gitignore`

We work with sensitive data. If working locally, create a `data` folder (e.g., click the `+ Folder` icon in the `Files` tab). Move your data files into this folder.

Open the `.gitignore` file and add the line `data/`. This tells Git to ignore the contents of the `data` folder, preventing accidental data pushes.

We recommend creating at least two sub-folders within `data/`:

- `raw/`: Use this folder to store the original datasets.
- `processed/`: Use this folder to save any datasets generated as preliminary or final results from your analyses.

If `data/` is listed in your `.gitignore` file, both subfolders will automatically be ignored by Git since they are located within the `data/` folder.

If the folder is not in the project root or has a different name, adjust the `.gitignore` settings accordingly.

Your project structure should look like this:

```
project-folder/
  .gitignore # Specifies files and folders to ignore in version control
  README.md # Documentation about the project
  data/ # Folder to store datasets
      raw/ # Original datasets (never modified directly)
      processed/ # Cleaned and processed datasets
```

> **What file to use for your analysis?**
>
> There are many files you can use for analyzing the data. You can use a basic R script, or files as RMarkdown and its more current version Quarto, that allow you to merge the code with blocks of text.

and you `.gitignore` file should look like this:

```
.Rproj.user
.Rhistory
.RData
.Ruserdata
/.quarto/
data/
```

2.4 Complete the README using the template

Before starting work, fill out the `README.md` file with the following information:

```
# Title

## Author
**Name:** [Your Name]
**Email:** [Your Name]

## Start Date
[YYYY-MM-DD]

## Objective
The objective of this project is to ...

## Database Used and Version
**Database Name:** [Name]
**Data Version:** [Specify version or date accessed]

-[] Sensitive data is stored locally and excluded from version control using `.gitignore.`
-[] All analyses comply with the data use agreements.

## Project Structure

chronic-diseases/
  data/ # Folder for datasets
    raw/ # Original datasets (never modified directly)
    processed/ # Cleaned and processed datasets
  scripts/ # R scripts for analysis
  outputs/ # Figures, tables, and other results
  README.md # Project overview and documentation
  .Rproj # RStudio project file


## Reproducibility

sessionInfo()
```

There is more material available on organizing project structures Eugene Barsky, using `.gitignore` (**theturingwayKeepingSensitive?**) or other resources listed here, or creating good README files (The Turing Way - Readme File) and name conventions Eugene Barsky if you want to explore further.

Now you're ready to start writing code!

2.5 References

3 Regular Project Workflow

These steps should be completed every day you work on the project. Although they may seem complex at first, once you get accustomed to them, you won't need to think about it anymore.

Checklist

□ Add all the files you want to commit to the staging area.

□ Create a commit message.

□ Push the changes to the GitHub repository.

3.1 How to use the Git tab in RStudio

Pay attention to the Git tab located in the top-right corner. Git will only display files that have been added, modified, or deleted since the project was initialized or since the last commit (we'll cover what that means shortly).

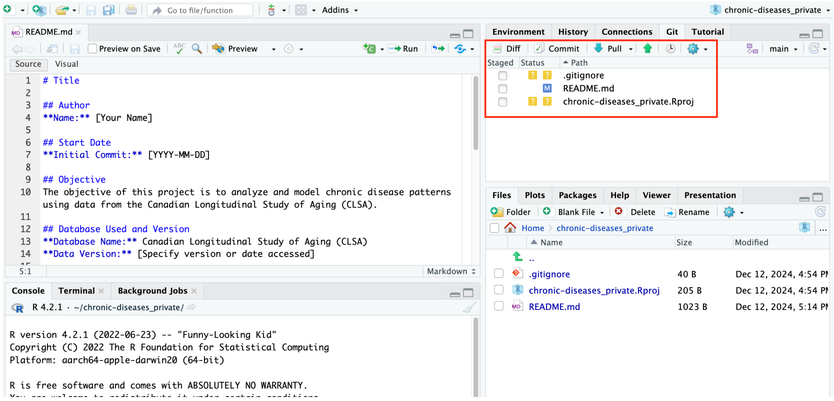
Keep in mind that when we cloned the project from GitHub, two new files were added:

- The `.Rproj` file, created because we based our RStudio project on the repository.
- The `.gitignore` file, automatically generated as part of the project setup in RStudio.

These files will appear with a yellow question mark, indicating they are *untracked*—in other words, Git is aware of them but has not yet saved them under version control.

The `README.md` file initially did not appear in the Git tab. However, after adding the template and saving the changes, it now shows a blue "M," which indicates that the file has been *modified*.

If you were to remove a file, you would see it next to a red 'D', indicating that it has been *deleted* from the project.



```
# Title

## Author
**Name:** [Your Name]

## Start Date
**Initial Commit:** [YYYY-MM-DD]

## Objective
The objective of this project is to analyze and model chronic disease patterns
using data from the Canadian Longitudinal Study of Aging (CLSA).

## Database Used and Version
**Database Name:** Canadian Longitudinal Study of Aging (CLSA)
**Data Version:** [Specify version or date accessed]
```

Staged	Status	Path
□	? ?	.gitignore
□	M	README.md
□	? ?	chronic-diseases_private.Rproj

Name	Size	Modified
..		
.gitignore	40 B	Dec 12, 2024, 4:54 PM
chronic-diseases_private.Rproj	205 B	Dec 12, 2024, 4:54 PM
README.md	1023 B	Dec 12, 2024, 5:14 PM

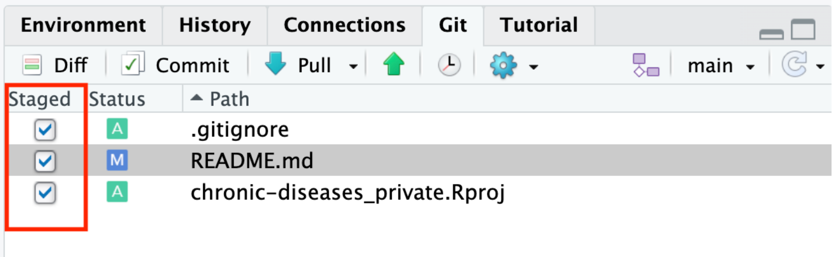
```
R version 4.2.1 (2022-06-23) -- "Funny-Looking Kid"
Copyright (C) 2022 The R Foundation for Statistical Computing
Platform: aarch64-apple-darwin20 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
```

The next step is to save these changes in the project and add a descriptive title. Each time you save a new version of the project, we say you are making a commit, which you label with a title.

3.1.1 Add all the files you want to commit to the staging area.

The first thing you need to do is check in the Staged section of the Git tab all the changes you want to save under the same title. You will notice that sometimes a green 'A' appears. You can ignore this. The important part is that you check all the changes you want to save.

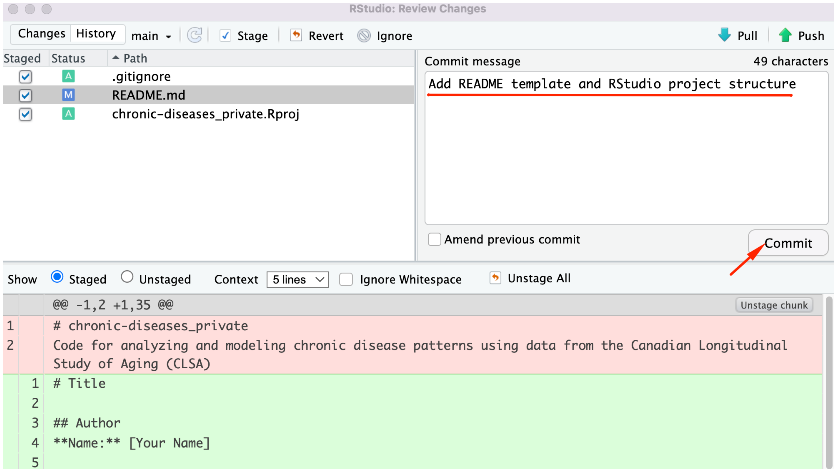
In our case, since we are working with non-collaborative repositories and the main purpose of using GitHub is to share data with other coworkers and maintain a backup, there's no need to focus too much on the details in this section.



Staged	Status	Path
☑	A	.gitignore
☑	M	README.md
☑	A	chronic-diseases_private.Rproj

3.1.2 Create a commit message.

After doing this, you need to click the commit button to make these changes permanent in the project. You will then choose a message for the commit and click the `Commit` button.



Staged	Status	Path
☑	A	.gitignore
☑	M	README.md
☑	A	chronic-diseases_private.Rproj

Commit message — 49 characters

Add README template and RStudio project structure

□ Amend previous commit

Show ● Staged ○ Unstaged Context 5 lines □ Ignore Whitespace

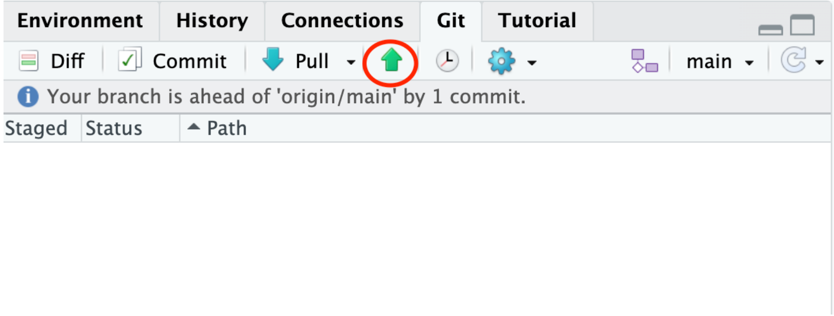
```
@@ -1,2 +1,35 @@
# chronic-diseases_private
Code for analyzing and modeling chronic disease patterns using data from the Canadian Longitudinal
Study of Aging (CLSA)
# Title

## Author
**Name:** [Your Name]

```

How Often Should You Commit?

Think of commits as checkpoints for related changes. If you might want to revert a set of changes later, commit them together.

3.2 Push the changes to the GitHub repository.

Finally, to push the changes to GitHub, click the `Push` button.



Your branch is ahead of 'origin/main' by 1 commit.

You'll notice that the files in the Git tab disappear after you commit. This is expected, as Git only tracks changes between commits. Remember, if you don't click the green arrow representing push, the changes will not take effect on GitHub.

If everything went smoothly, you should navigate to the repository URL and see the changes you made.

How Often Should You Push?

Push your changes **at least once a day** after completing your work.

Moving foward with Git and GitHUb

If you want to learn more about Git and GitHub, we recommend the following books and tutorials Carpentry, Bryan (2018), Club, Tiffany Timbers and Lee, (**theturingwayGettingStarted?**)
Additionally, UBC Library offers some basic data management courses that might be helpful to you: Short courses

---

3.3 References

- Article: Research Data Management

4 Offboarding

- The Lab Member must be removed from the GitHub Lab Team.

When leaving the organization, you will lose access to private repositories created by other team members but will retain access to those you created yourself.

Allen, Christopher, and David MA Mehler. 2019. "Open Science Challenges, Benefits and Tips in Early Career and Beyond." *PLoS Biology* 17 (5): e3000246.

Bryan, Jennifer. 2018. *Happy Git and GitHub for the useR*. GitHub.

Carpentries, The. "Data Carpentry." https://datacarpentry.org/.

Carpentry, Software. "Version Control with Git: Summary and Setup - Version Control with Git." https://swcarpentry.github.io/git-novice/.

Club, Our Coding. "Setting up a GitHub Repository for Your Lab - Version Control and Code Management with GitHub." https://ourcodingclub.github.io/tutorials/git-for-labs/.

Community, The Turing Way. 2023. "The Turing Way: A Handbook for Reproducible, Ethical and Collaborative Research." Zenodo. https://doi.org/10.5281/zenodo.7625728.

Eugene Barsky, Paul Lesack, Billie Hu. "Introduction to Research Data Management." https://ubc-library-rc.github.io/rdm/.

Gomes, Dylan GE, Patrice Pottier, Robert Crystal-Ornelas, Emma J Hudgins, Vivienne Foroughirad, Luna L Sánchez-Reyes, Rachel Turba, et al. 2022. "Why Don't We Share Data and Code? Perceived Barriers and Benefits to Public Archiving Practices." *Proceedings of the Royal Society B* 289 (1987): 20221113.

Mathur, Maya B, and Matthew P Fox. 2023. "Toward Open and Reproducible Epidemiology." *American Journal of Epidemiology* 192 (4): 658–64. https://doi.org/10.1093/aje/kwad007.

Melvin, Ryan L, Steven J Barker, Joe Kiani, and Dan E Berkowitz. 2022. "Pro-Con Debate: Should Code Sharing Be Mandatory for Publication?" *Anesthesia & Analgesia* 135 (2): 241–45.

Ram, Karthik. 2013. "Git Can Facilitate Greater Reproducibility and Increased Transparency in Science." *Source Code for Biology and Medicine* 8: 1–8.

Sharma, Nitesh Kumar, Ram Ayyala, Dhrithi Deshpande, Yesha Patel, Viorel Munteanu, Dumitru Ciorba, Viorel Bostan, et al. 2024. "Analytical Code Sharing Practices in Biomedical Research." *PeerJ Computer Science* 10: e2066.

Tazare, John, Shirley V Wang, Rosa Gini, Daniel Prieto-Alhambra, Peter Arlett, Daniel R Morales Leaver, Caroline Morton, et al. 2024. "Sharing Is Caring? International Society for Pharmacoepidemiology Review and Recommendations for Sharing Programming Code." *Pharmacoepidemiology and Drug Safety* 33 (9): e5856.

Tiffany Timbers, Trevor Campbell, and Melissa Lee. "Chapter 12 Collaboration with Version Control | Data Science — Datasciencebook.ca." https://datasciencebook.ca/version-control.html.

Wilson, Jennifer AND Cranston, Greg AND Bryan. 2017. "Good Enough Practices in Scientific Computing." *PLOS Computational Biology* 13 (6): 1–20. https://doi.org/10.1371/journal.pcbi.1005510.

Xu, Edward, Anna Catharina V. Armond, David Moher, and Kelly Cobey. 2025. "Key Challenges in Epidemiology: Embracing Open Science." *Journal of Clinical Epidemiology* 178: 111618. https://doi.org/https://doi.org/10.1016/j.jclinepi.2024.111618.