

Open and Reprodubile Science in R

Technical Handbook

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Preface

The Open and Reproducible Science in R sub-module of the [MSc in International Health and Tropical Medicine](#) is designed to equip students with the knowledge and skills necessary to conduct both **academic research** and more importantly **real-world data analysis** that is transparent, reproducible, and in line with the principles of open science.

This technical handbook serves as the *go-to* guide for MSc IHTM students to the various tools, technologies, and processes that they will be learning and using within the module.

Organisation

This handbook is divided into three sections:

1. Tools

This section cover topics on the various tools and technologies that are to be used and/or introduced in the module. The [R language and environment for statistical computing and graphics](#) is primary of these as the module is specific to R. All other tools and technologies are either built specific for use with R (e.g. [RStudio](#) which is the IDE of choice for the module and for this handbook) or are general tools that enhance the *userR* experience and/or supports known and accepted best practices for open and reproducible science using R.

2. Practices

This section covers topics on recommended best practices for optimal usage and maintenance of R and RStudio.

3. Processes

This section covers topics on scientific/data analysis workflows with a focus on steps in initiating and setting up and participating and contributing to such projects within an open and reproducible framework.

How to use

Even though all efforts have been made to order the chapters in a way that is coherent and logical, this handbook is designed such that chapters are standalone topics in of themselves and uses cross-referencing between chapters to make links to the various learning topics/concepts. As such, the best use of this handbook is to use each chapter as a reference for more in-depth discussion of a topic discussed in class rather than a book to read from start to finish.

Introduction

All about R

R is a language and environment for statistical computing and graphics. It is a [GNU](#) project which is similar to the [S language and environment](#) which was developed at Bell Laboratories (formerly AT&T, now Lucent Technologies) by John Chambers and colleagues. R can be considered as a different implementation of S. There are some important differences, but much code written for S runs unaltered under R.

R provides a wide variety of statistical (linear and nonlinear modelling, classical statistical tests, time-series analysis, classification, clustering, etc.) and graphical techniques, and is highly extensible. The S language is often the vehicle of choice for research in statistical methodology, and R provides an open source route to participation in that activity.

One of R's strengths is the ease with which well-designed publication-quality plots can be produced, including mathematical symbols and formulae where needed. Great care has been taken over the defaults for the minor design choices in graphics, but the user retains full control.

R is available as free software under the terms of the Free Software Foundation's GNU General Public License in source code form. It compiles and runs on a wide variety of UNIX platforms and similar systems (including FreeBSD and Linux), Windows and MacOS.

R is unique in that it is not general-purpose. It does not compromise by trying to do a lot of things. It does a few things very well, mainly statistical analysis and data visualization. While you can find data analysis and machine learning libraries for languages like [Python](#), R has many statistical functionalities built into its core. No third-party libraries are needed for much of the core data analysis you can do with the language.

But even with this specific use case, it is used in every industry you can think of because a modern business runs on data. Using past data, data scientists and data analysts can determine the health of a business and give business leaders actionable insights into the future of their company.

Just because R is specifically used for statistical analysis and data visualization doesn't mean its use is limited. It's actually quite popular, ranking 19th in the [TIOBE index](#) of the most popular programming languages.

Academics, scientists, and researchers use R to analyze the results of experiments. In addition, businesses of all sizes and in every industry use it to extract insights from the increasing amount of daily data they generate.

Open and reproducible science

Open and reproducible science is the practice of science in such a way that others can collaborate and contribute and where research data, lab notes and other research processes are freely available, under terms that enable reuse, redistribution and reproduction of the research and its underlying data and methods. Reproducible research means that research data and code are made available so that others are able to reach the same results as are claimed in scientific outputs. Closely related is the concept of replicability, the act of repeating a scientific methodology to reach similar conclusions. These concepts are core elements of empirical research.

Open science is important because it enhances the **accessibility**, **transparency**, and **collaboration** of scientific research.

Open science makes research data, publications, and resources freely available to anyone, regardless of their location, institutional affiliation, or financial situation. This democratises knowledge and ensures that even those outside of well-funded research institutions can access the latest scientific findings.

By making data, methods, and results openly available, open science allows other researchers to verify, replicate, and build upon previous work. This transparency is essential for the self-correcting nature of science, helping to ensure the reliability and integrity of research findings.

When data and findings are openly shared, other researchers can more quickly build on existing work, leading to faster scientific progress. This is particularly important in fields like medicine or environmental science, where rapid advancements can have significant societal impacts.

Open science fosters collaboration across disciplines, institutions, and borders. Researchers can combine their expertise and resources to tackle complex problems, leading to more innovative solutions. Open data and resources also encourage citizen science, where the general public can contribute to scientific research.

By making research processes and findings open and accessible, science becomes more transparent to the public, which can increase trust in scientific research. Open science also allows the public to engage more directly with science, fostering a greater understanding and appreciation of scientific work.

Open science reduces duplication of effort by making data and methods available for reuse. Researchers can build on existing work rather than starting from scratch, which can save time

and resources. Additionally, open access to research outputs can reduce costs for institutions and researchers who would otherwise need to pay for access to publications.

Many of the world's most pressing challenges, such as climate change, pandemics, and poverty, require global collaboration and knowledge-sharing. Open science facilitates this by making research outputs accessible to scientists and policymakers worldwide, particularly in low- and middle-income countries that may lack access to expensive scientific resources.

In essence, open science enhances the efficiency, equity, and impact of scientific research, making it a critical approach for advancing knowledge and addressing global challenges.

The **Open and Reproducible Science in R** module is designed to give MSc IHTM students a foundational understanding and appreciation of the pillars of open science more broadly and within that the concepts, methods and tools for reproducible research more specifically. To further the students' learning, practical examples and exercises are walked through and discussed using the R language for statistical computing as a way to practically demonstrate these concepts.

Part I

Tools

1 Installing and setting up tools

Following are the steps to installing R, RStudio, and Git depending on your operating system.

1.1 Installing R, RStudio, and git

1.2 Windows

Step 1: Download and install R

Important that R is installed first. R is the main software and is needed for RStudio to work properly. R should always be installed first.

Go to <https://cran.r-project.org> and click on the link that says *Download R for Windows*. In the following page, click on the link that says *install R for the first time*.

Then click on *Download R-4.X.X for Windows* (latest release version). This will start the download process.

Once downloaded, go to the `.exe` file in your **Downloads** folder, double-click and follow all the install prompts, selecting recommended options all the time.

Step 2: Download and install RStudio

This step requires that **Step 1** has been done and was successful.

Go to <https://posit.co/download/rstudio-desktop/> and select the download specific for your Windows machine.

Once downloaded, double-click on `.exe` file downloaded to your **Downloads** folder and then follow all install prompts, always selecting recommended options.

Step 3: Download and install Rtools

For the things that you will be taught in the **Open and Reproducible Science** sub-module, you will need to expand the installation of R by installing the Rtools software.

Go to <https://cran.r-project.org/bin/windows/Rtools/> and choose to download the latest version of the installer (which is the Rtools version compatible with the R version you have installed in Step 1).

Once you have downloaded the .exe file, double-click on the .exe file and follow all install prompts. Choose all the recommended options.

Step 4: Download and install Git for Windows

For the things that you will be taught in the **Open and Reproducible Science** sub-module, you will need to install **Git for Windows**.

Go to this link - <https://github.com/git-for-windows/git/releases/latest> - to download the latest version of git. Make sure to select the version compatible with your Windows machine (64-bit or 32-bit).

Once you have downloaded the .exe file, double-click it and then follow all install prompts. Choose all recommended options.

1.3 macOS

Step 1: Download and install R

Important that R is installed first. R is the main software and is needed for RStudio to work properly. R should always be installed first.

Go to <https://cran.r-project.org> and click on the link that says **Download R for macOS**. In the following page, you will have two choices of R versions to install. Make sure to install the appropriate version for your macOS version (Apple Silicon vs Apple Intel version). Click on the download link for your macOS version. This will start the download process of the .pkg file specific for installing in macOS computers.

Once downloaded, go to the .pkg file in your **Downloads** folder, double-click and follow all the install prompts, selecting recommended options all the time.

1.3.1 Install RStudio

This step requires that **Step 1** has been done and was successful.

Go to <https://posit.co/download/rstudio-desktop/> and select the download specific for your macOS machine.

Once downloaded, double-click on `.dmg` file downloaded to your **Downloads** folder and then follow all install prompts, always selecting recommended options.

1.3.2 Install git for macOS

For the things that you will be taught in the **Open and Reproducible Science** sub-module, you will need to install **git for macOS**. Apple machines are already pre-installed with **git** but it is usually an Apple specific version of git and tends to be older and not configured in the way we need it. So we need to install another version of it that comes with Apple's **Xcode command line tools**.

To install, go to the macOS terminal and type the following command:

```
xcode-select --install
```

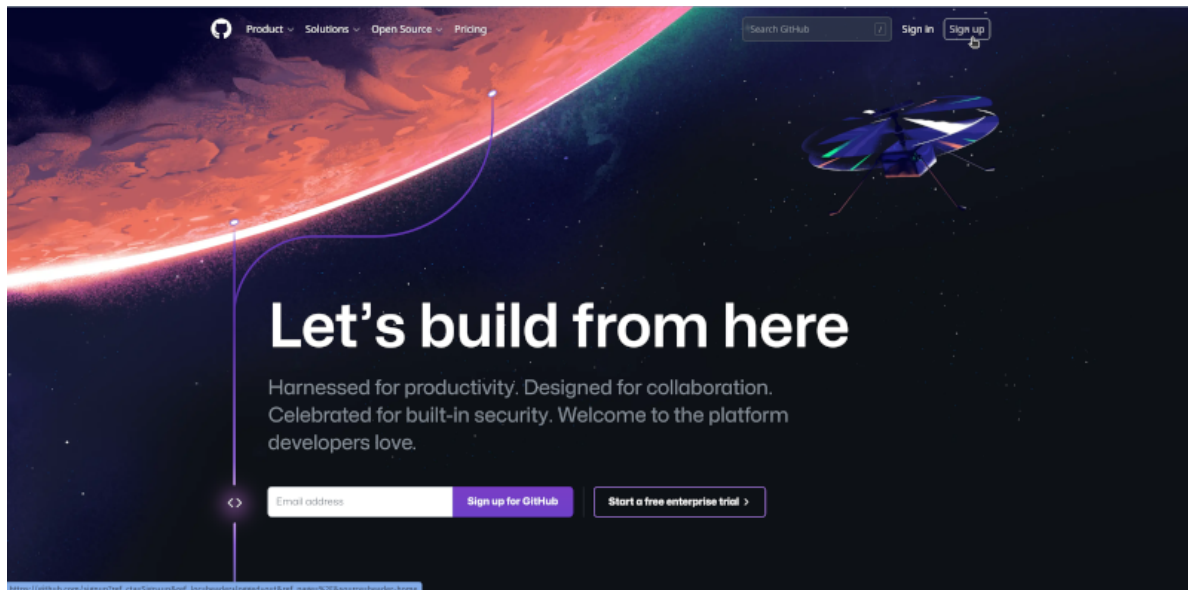
1.4 Register a GitHub account

For the **Open and Reproducible Science in R** sub-module, you will need a GitHub account to be able to receive the code materials and assignments that will be provided. This is the mechanism by which these materials will be distributed. Hence you will need to register an account with GitHub (if you don't already have one). It's free!

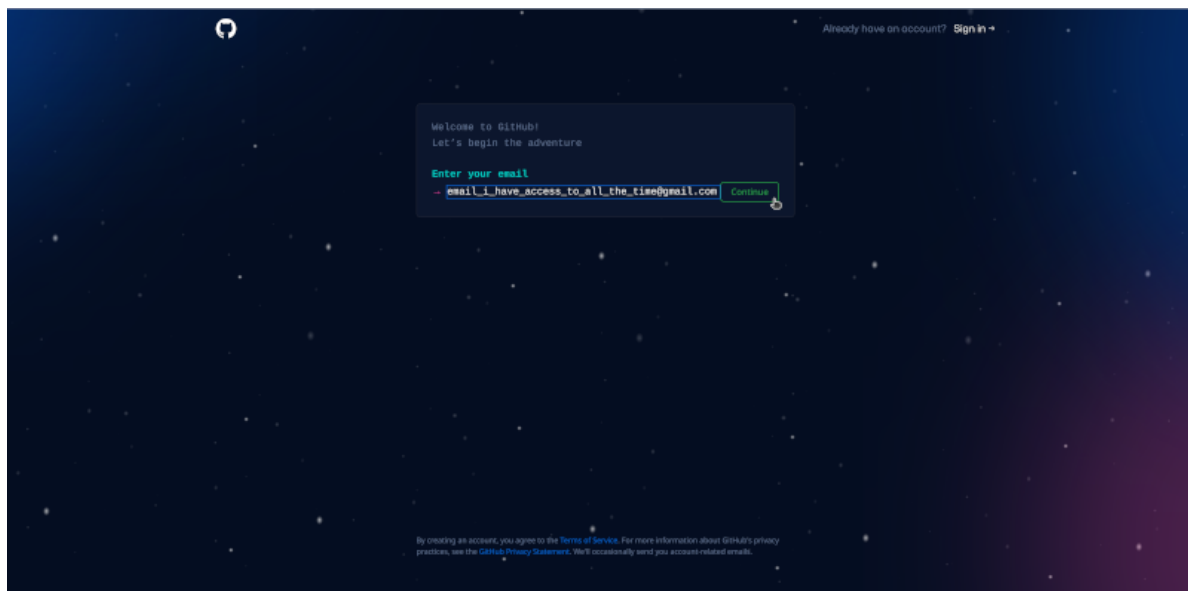
Step 1. Sign-up to GitHub

Go to <https://github.com>.

On the upper right hand corner of the page, click on ***Sign-up*** button



You will be then prompted to provide an email address to register your account with.

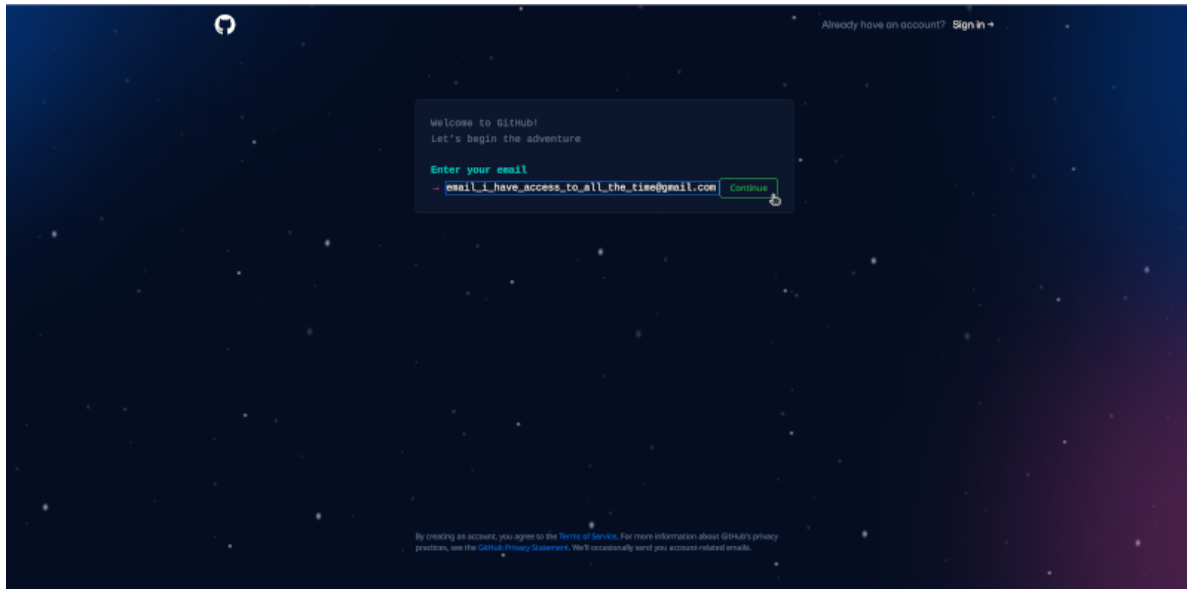


Note

With regard to the email address to use for creating a GitHub account, best practice is to use an email address that you will have access to all the time. Email addresses such as those for school (if you are a student) or for your current work may not always be the best email address to use as these email addresses tend to be time-limited (i.e., you lose

the email address once you graduate or once you leave your current work).

You will then be prompted for a password



Then follow all other prompts after this including confirmation of your email and creating a GitHub username (see next step).

Step 2. Set a GitHub username

With regard to creating/selecting a GitHub username, following are some best practice recommendations (Jenny Bryan and Jim Hester n.d.).

💡 Tips for selecting GitHub username

- Incorporate your actual name as this lets people know who they're dealing with and also makes your username easier for people to guess or remember.
- Reuse your username from other contexts, e.g., Twitter or Slack.
- Pick a username that will be appropriate revealing to a future boss.
- Shorter is better than longer.
- Be as unique as possible in as few characters as possible.
- Make it timeless and context-agnostic. Don't add a date or year or a reference to your current location, university, or employer.

- Avoid the use of upper vs. lower case to separate words. We highly recommend all lowercase. A better strategy for word separation is to use a hyphen (-).

Step 3. Setup two-factor authentication (2FA)

It is important to keep your GitHub account secure. Any breach in security of your online accounts, including GitHub, not only affects you but also those that you collaborate with. To increase the security of your GitHub account, please enable two-factor authentication (2FA) for your account. This can be done [here](#). There are 4 options for 2FA in GitHub. We recommended enabling at least 2 of these options. If you are familiar with use of passkeys, we recommend using this authentication approach in addition to 2FA.

Step 4. Get added to the Oxford IHTM CodeHub

The [Oxford iHealth CodeHub](#) is the organisational GitHub account for the MSc IHTM. To be included in the organisation, share your GitHub username to the sub-module lead who will then add you to the organisation. This is an important step as assignments and exercises for the sub-module are distributed through GitHub and GitHub Classroom via this organisational account.

! Important

The Oxford iHealth CodeHub organisational GitHub account requires members to have 2FA activated. It is therefore imperative that you enable 2FA on your account to be included in the organisation.

i Note

You will soon receive a message at the email address you registered to GitHub with inviting you to join the Oxford iHealth CodeHub organisation. Accept the invitation.

2 Introduction to R and RStudio

2.1 What is R?

R is a system for data manipulation, calculation, and graphics. It provides:

- Facilities for data handling and storage
- A large collection of tools for data analysis
- Graphical facilities for data analysis and display
- A simple but powerful programming language

R is often described as an environment for working with data. This is in contrast to a statistical *package* which is a collection of very specific tools. R is not strictly a statistics system but a system that provides many classical and modern statistical procedures as part of a broader data-analysis tool. This is an important difference between R and other statistical systems. In R a statistical analysis is usually performed as a series of steps with intermediate results being stored in objects. Systems such as SPSS and SAS provide copious output from (e.g.) a regression analysis whereas R will give minimal output and store the results of a fit for subsequent interrogation or use with other R functions. This means that R can be tailored to produce exactly the analysis and results that you want rather than produce an analysis designed to fit all situations.

R is a language based product. This means that you interact with R by typing commands such as:

```
table(SEX, LIFE)
```

rather than by using menus, dialog boxes, selection lists, and buttons. This may seem to be a drawback but it means that the system is considerably more flexible than one that relies on menus, buttons, and boxes. It also means that every stage of your data management and analysis can be recorded and edited and re-run at a later date. It also provides an audit trail for quality control purposes.

R is available under UNIX (including Linux), the Apple operating system macOS, and Microsoft Windows. The method used for starting R will vary from system to system. On UNIX systems you may need to issue the R command in a terminal session or click on an icon or menu option if your system has a windowing system. On Apple systems R will be available

as an application but can also be run in a terminal session. On Microsoft Windows systems there will usually be an icon on the Start menu or the desktop.

2.2 Why use R?

R is an open source system and is available under the *GNU general public license* (GPL) which means that it is available for free but that there are some restrictions on how you are allowed to distribute the system and how you may charge for bespoke data analysis solutions written using the R system. Details of the general public license are available from <http://www.gnu.org/copyleft/gpl.html>.

R is available for download from <http://www.r-project.org/>.

This is also the best place to get extension packages and documentation. You may also subscribe to the R mailing lists from this site. R is supported through mailing lists. The level of support is at least as good as for commercial packages. It is typical to have queries answered in a matter of a few hours.

Even though R is a free package it is more powerful than most commercial packages. Many of the modern procedures found in commercial packages were first developed and tested using R or S-Plus (the commercial equivalent of R).

2.3 What is RStudio

RStudio is an **integrated development environment (IDE)** for R. It includes a console, syntax-highlighting editor that supports direct code execution, as well as tools for plotting, history, debugging and workspace management.

RStudio is available in open source and commercial editions and runs on the desktop (Windows, macOS, and Linux) or in a browser connected to RStudio Server or RStudio Workbench (Debian/Ubuntu, Red Hat/CentOS, and SUSE Linux).

<https://youtu.be/n3uue28FD0w?si=DAMZrT6xhLS8ZMLH>

3 Introduction to git and GitHub

3.1 All about git

[git](#) is a version control system for software development. It allows developers to keep track of changes made to their code and collaborate with other developers on a project. [git](#) also allows for easy rollbacks and branch management. It is widely used in the software industry and is considered one of the best version control systems available.

[git](#) was developed by [Linus Torvalds](#) in 2005. He created [git](#) as a replacement for the proprietary version control system he was using at the time. The development of [git](#) was driven by the need for a distributed version control system, which allows multiple developers to work on a project simultaneously, without the need for a central server. [Linus Torvalds](#) is also known for creating the Linux operating system kernel.

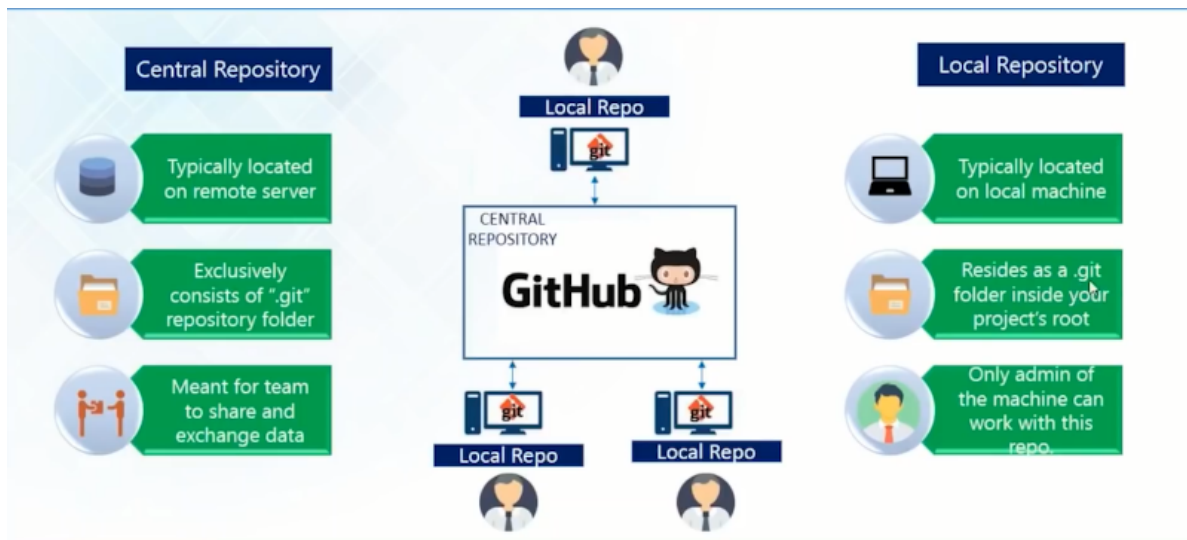
To use [git](#) in your machines, you will need to install it as described in [Section 1.1](#).

3.2 All about GitHub

[GitHub](#) is a web-based platform that provides hosting for software development and a community of developers to collaborate, share and learn from each other. It is built on top of [git](#), which is the version control system used for managing and tracking changes to the code. Developers can use [GitHub](#) to store and manage their code, collaborate with other developers, and track and manage issues and bugs. It also provides tools for code review, project management, and documentation. It is widely used by developers and organizations to host and share code, as well as to build and maintain open-source software.

[GitHub](#) is not a software you need to install. Rather it is a remote or cloud-based server that holds its users' code versioned using the [git](#) version control system and to which a user's local, [git](#)-versioned code syncs/communicates with.

A good illustration of the [git](#) and [GitHub](#) relationship can be viewed below:



4 Connecting RStudio with GitHub

Once RStudio is installed and a GitHub account has been created and registered, the final step in the R, RStudio, git, and GitHub dance is to create git-related settings on your machine that will identify you as a unique/specific git user and then creating a GitHub **personal access token (PAT)** which will serve as the key or proof that you will use to identify yourself as the git user you claim to be whenever you try to syn/connect to your GitHub account via RStudio or any other tool on your local computer.

Follow are the steps you will need to perform:

4.1 Introduce yourself to git

Open RStudio and then select the *Terminal* tab in the console pane.

The terminal is the tool used to interface with your computer through commands written in a programming language called **bash**. Most of you would have never used the terminal because we mostly use software built-in our computers that provide a *graphical user interface (GUI)* to perform operations and tasks.

RStudio comes with the terminal tool built in and usually is already available from the console pane as a separate table along side the R console (see below). By default, whenever you open RStudio, this tab for the terminal tool should already be available.

If it is not present, you can easily open a new terminal tab in the console pane by going to the RStudio menu ribbon and clicking on:

```
Tools --> Terminal --> New Terminal
```

or you can use the ALT + SHIFT + R keyboard shortcut.

In this step, you are basically going to issue a set of commands to your computer to save and store specific settings for the git software that you have installed.

Specifically, you are going to let git know who you are (your name) and what your email address (associated with your GitHub account) is.

The commands will be issued on the terminal. The commands are:

```
git config --global user.name 'YOUR FULL NAME'
git config --global user.email 'YOUR EMAIL ADDRESS'
```

Make sure to supply your full proper name (and not your username you created in GitHub).

Make sure that the email you provide is the email address you used to register and create an account with GitHub.

Unless there was an error in your syntax, you should not expect any output on the terminal after you issue the commands. To check that your name and email address have been recorded and/or that the name and email address recorded is correct, you can issue the following command:

```
git config --global --list
```

Here is an example of what you will see after issue this command:

```
user.name=YOUR FULL NAME
user.email=YOUR EMAIL ADDRESS
```

Check this output to what you expect it to be specified as. If the information is correct, then you've completed this step. If you need to correct any of this information, then repeat this step making sure that the name and email address you provide is correct.

4.2 Create a GitHub personal access token (PAT)

Now that you have introduced yourself to the git that is installed in your local machine/computer, you should now visit [GitHub](#) on a browser and create a *personal access token (PAT)*.

When you communicate/sync/interact with a remote git server, such as GitHub, you have to include credentials in the communication you are sending. These credentials prove that you are a specific GitHub user, who's allowed to do whatever you're asking to do.

git can communicate with a remote server using one of two protocols, HTTPS or SSH, and the different protocols use different credentials.

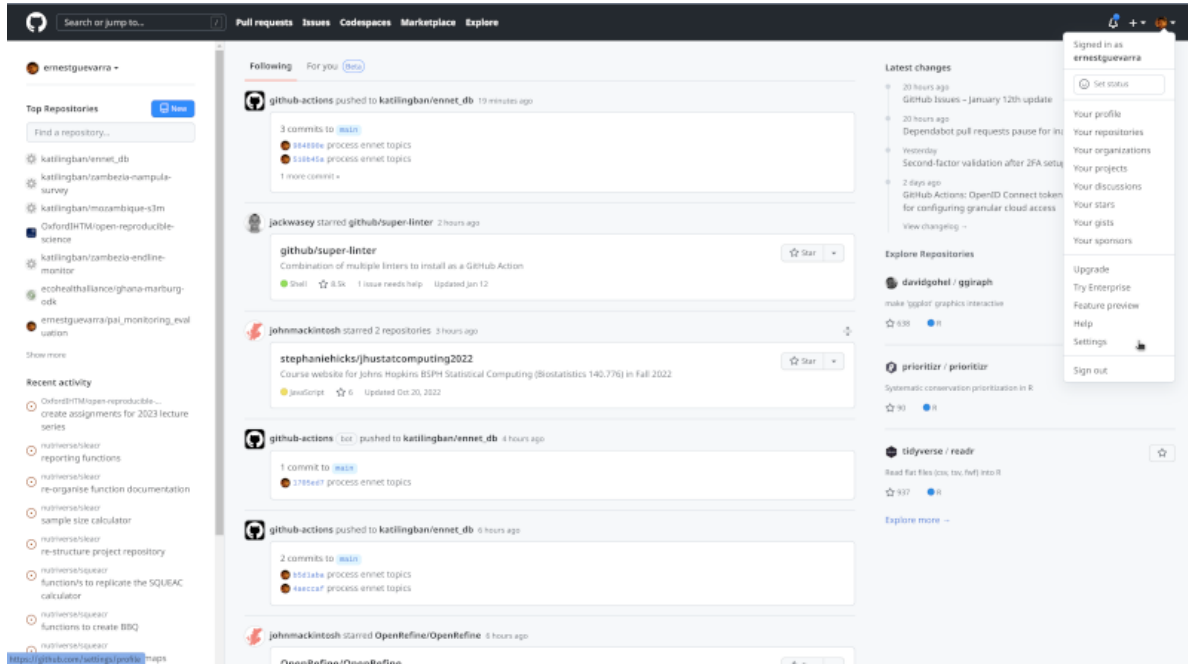
Here we describe the credential setup for the HTTPS protocol, which is what we recommend if you have no burning reason to pick SSH. With HTTPS, we will use a PAT to connect securely to GitHub from RStudio.

Please note that the PAT is not the same as the password you provided when registering for your GitHub account. Also, in performing a connection to GitHub via HTTPS protocol, your password is not an acceptable credential for communicating with GitHub.

To create a GitHub PAT, you need to:

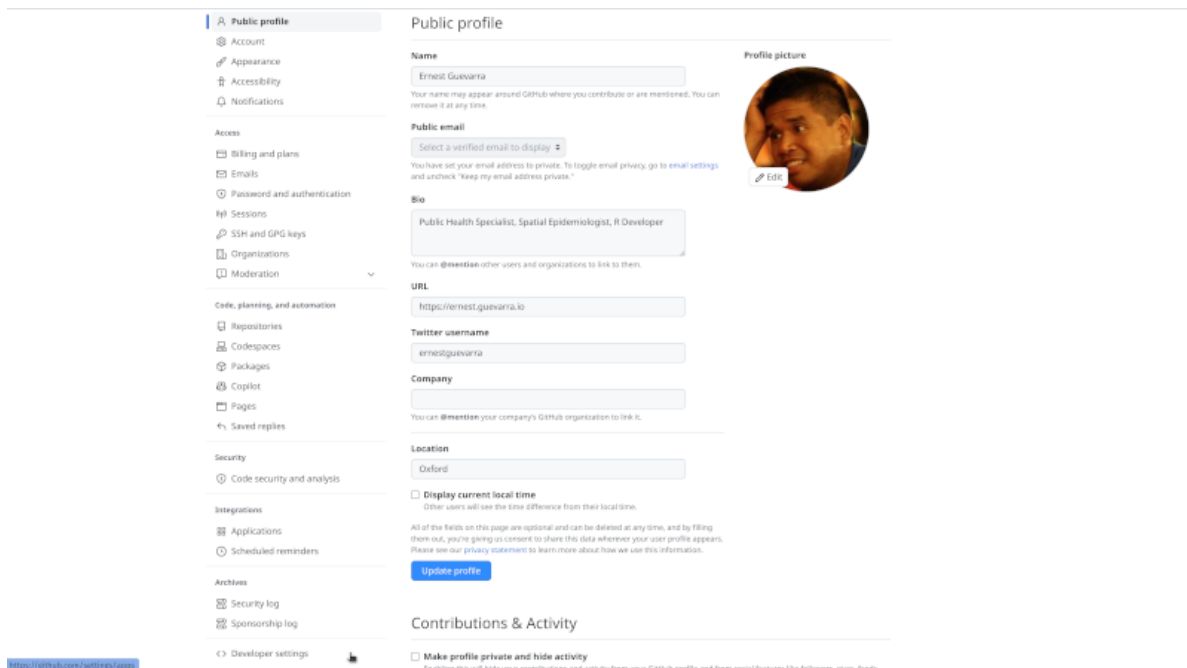
Step 1: Go to Settings from your GitHub account menu

Login to your GitHub account. On the upper right hand corner of the GitHub page you will see your account icon. Click on it to reveal a drop down menu as shown below. Select the *Settings* option.



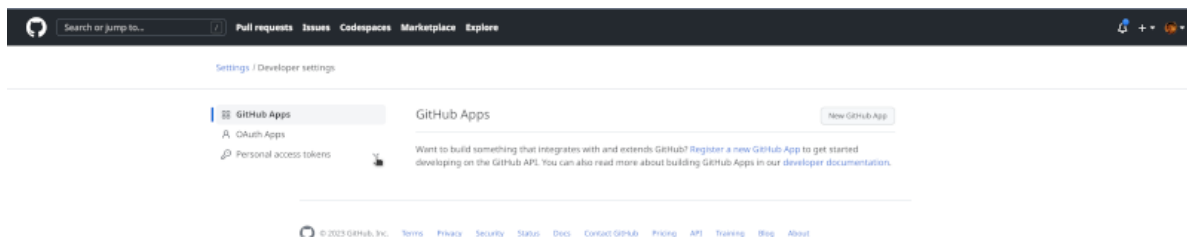
Step 2: From Settings navigate to Developer Settings

In the *Settings* page, find the *Developer Settings* option on the left hand sidebar as shown below:

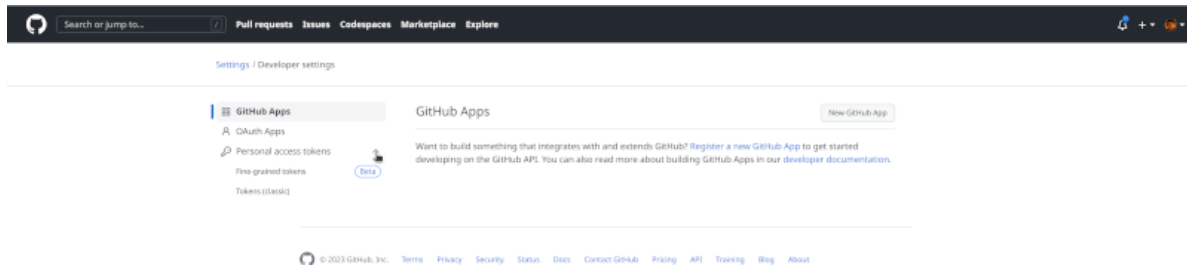


Step 3: From Developer Settings navigate to Personal Access Token

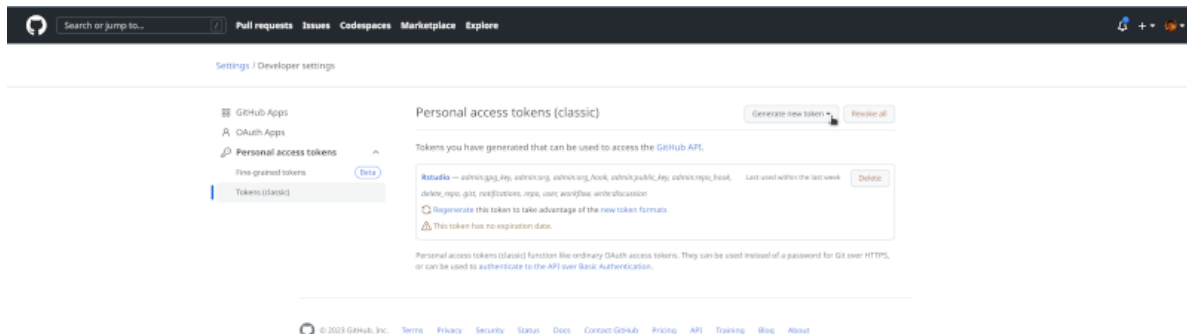
In the *Developer Settings* page, find the *Personal Access Token* option on the left hand sidebar as shown below:



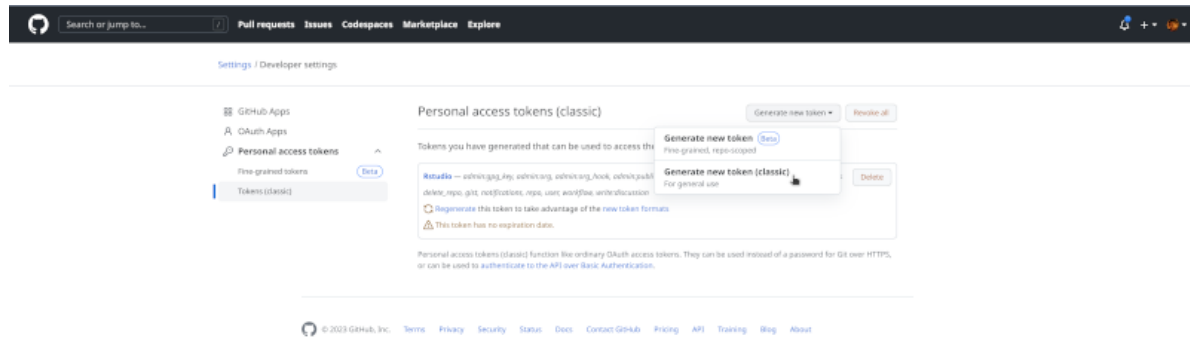
Step 4: Select Tokens (classic)



Step 5: Click on Generate new token

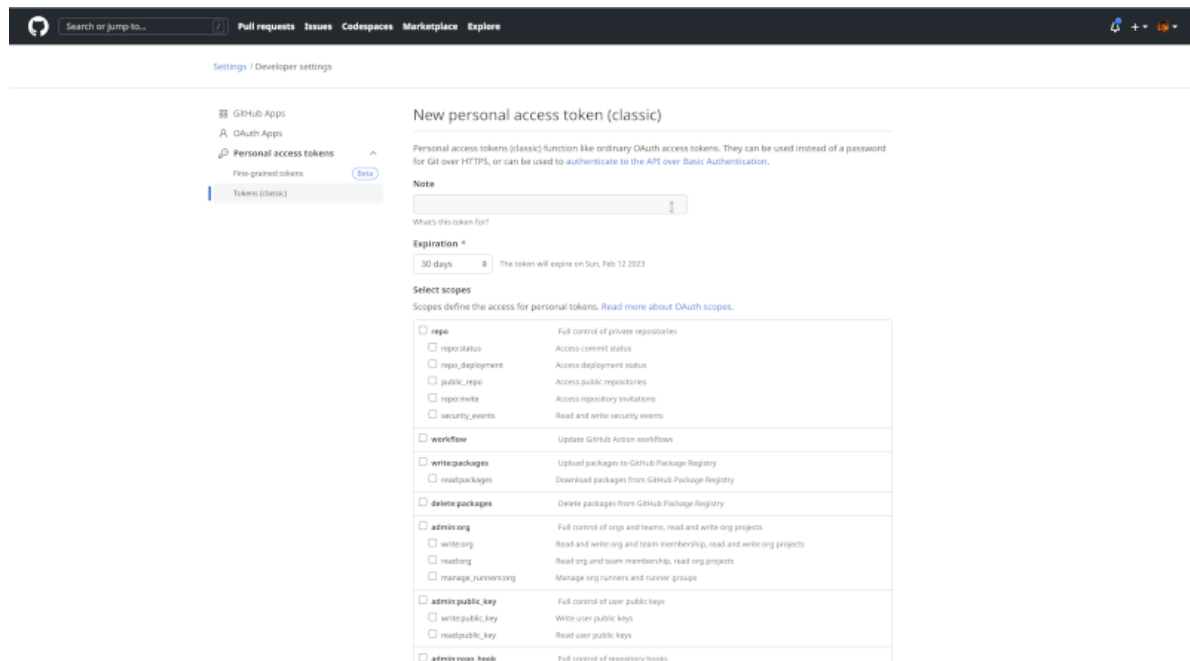


Step 6: Select Generate new token (classic)



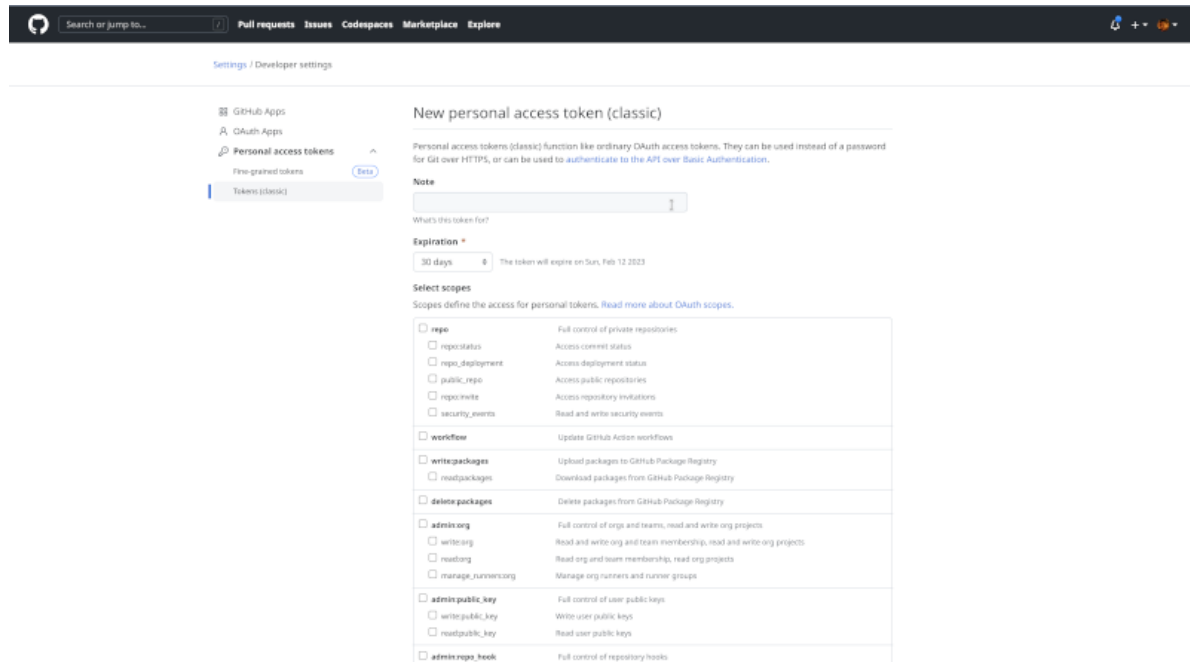
<https://github.com/settings/tokens/new>

Step 7: Give your token a name



The token name should be short but descriptive of the where or how you will use the token. Since we are using this to connect and allow communication between RStudio and GitHub, **rstudio** can be a good name that would remind you that this is what you are using to secure the connection/communication between your RStudio and your GitHub account.

Step 8: Set an expiry date for the token



The screenshot shows the GitHub interface for creating a new personal access token. The left sidebar has a search bar and navigation links for Pull requests, Issues, Codespaces, Marketplace, and Explore. Below these are links for Settings / Developer settings, GitHub Apps, OAuth Apps, Personal access tokens (selected), Fine-grained tokens, and Tokens (classic). The main content area is titled 'New personal access token (classic)' and includes a note about the token's function, an expiration dropdown set to '30 days', and a 'Select scopes' section with a table of permissions.

Select scopes	
Scopes define the access for personal tokens. Read more about OAuth scopes.	
<input type="checkbox"/> repo	Full control of private repositories
<input type="checkbox"/> repo:status	Access commit status
<input type="checkbox"/> repo:deployment	Access deployment status
<input type="checkbox"/> public_repo	Access public repositories
<input type="checkbox"/> repo:invite	Access repository invitations
<input type="checkbox"/> security_events	Read and write security events
<input type="checkbox"/> workflow	Update GitHub Action workflows
<input type="checkbox"/> write:packages	Upload packages to GitHub Package Registry
<input type="checkbox"/> read:packages	Download packages from GitHub Package Registry
<input type="checkbox"/> delete:packages	Delete packages from GitHub Package Registry
<input type="checkbox"/> admin:org	Full control of orgs and teams, read and write org projects
<input type="checkbox"/> write:org	Read and write org and team memberships, read and write org projects
<input type="checkbox"/> read:org	Read org and team memberships, read org projects
<input type="checkbox"/> manage:runnersorg	Manage org runners and runner groups
<input type="checkbox"/> admin:public_key	Full control of user public keys
<input type="checkbox"/> write:public_key	Write user public keys
<input type="checkbox"/> read:public_key	Read user public keys
<input type="checkbox"/> admin:repos_hooks	Full control of repository hooks

By default, GitHub will set a *30 day validity* for any new token created. Clicking on the option menu will show the other possible time periods to choose from including *No expiry date*.

It is best practice to assign an expiry date for security tokens such as the GitHub PAT. And a 30 day validity is standard practice. However, in reality, it is cumbersome to be creating new tokens frequently and for beginners, having to go through these steps again can be quite a chore. For the purposes of this lecture series, we would recommend setting the expiry for about 90 days to cover the whole period and then as a group, we'll have a *renew GitHub PAT party* on our last session.

Step 9: Set scopes

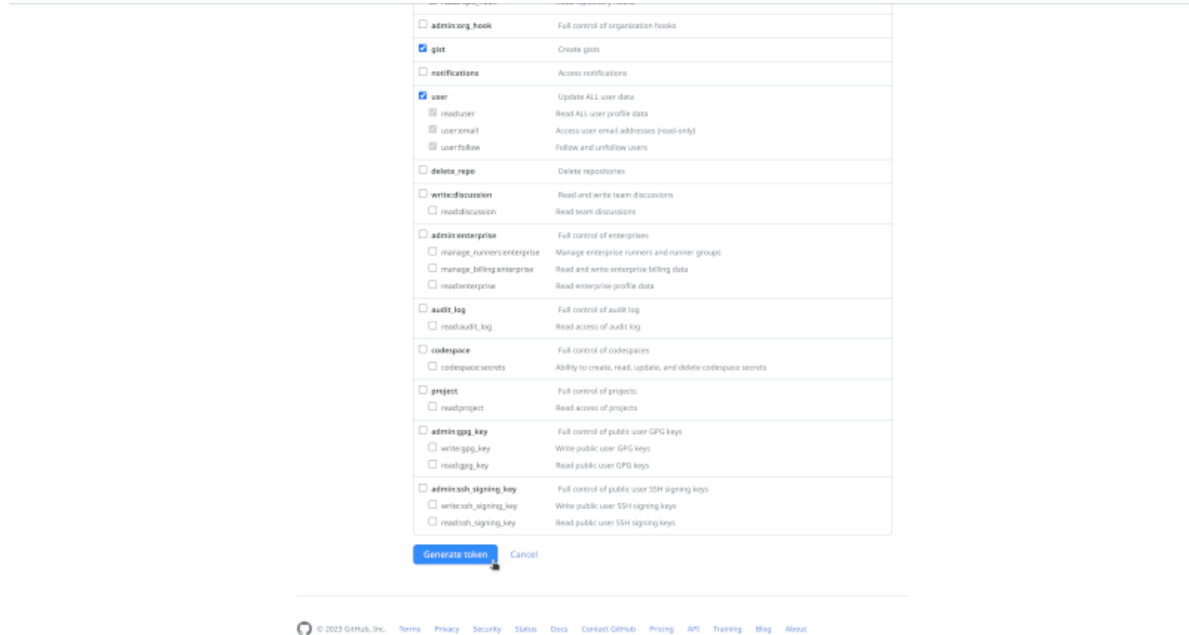
<input checked="" type="checkbox"/> repo	Full control of private repositories
<input type="checkbox"/> repo:status	Access commit status
<input type="checkbox"/> repo:deployment	Access deployment status
<input type="checkbox"/> public_repo	Access public repositories
<input type="checkbox"/> repo:invite	Access repository invitations
<input type="checkbox"/> security_events	Read and write security events
<input checked="" type="checkbox"/> workflow	Update GitHub Action workflows
<input type="checkbox"/> write:packages	Upload packages to GitHub Package Registry
<input type="checkbox"/> read:packages	Download packages from GitHub Package Registry
<input type="checkbox"/> delete:packages	Delete packages from GitHub Package Registry
<input type="checkbox"/> admin:org	Full control of orgs and teams, read and write org projects
<input type="checkbox"/> write:org	Read and write org and team membership, read and write org projects
<input type="checkbox"/> read:org	Read org and team membership, read org projects
<input type="checkbox"/> manage_runners:org	Manage org runners and runner groups
<input type="checkbox"/> admin:public_key	Full control of user public keys
<input type="checkbox"/> write:public_key	Write user public keys
<input type="checkbox"/> read:public_key	Read user public keys
<input type="checkbox"/> admin:repo_hook	Full control of repository hooks
<input type="checkbox"/> write:repo_hook	Write repository hooks
<input type="checkbox"/> read:repo_hook	Read repository hooks
<input type="checkbox"/> admin:org_hook	Full control of organization hooks
<input checked="" type="checkbox"/> gist	Create gists
<input type="checkbox"/> notifications	Access notifications
<input checked="" type="checkbox"/> user	Update ALL user data
<input type="checkbox"/> read:user	Read ALL user profile data
<input type="checkbox"/> user:email	Access user email addresses (read-only)
<input type="checkbox"/> user:follow	Follow and unfollow users
<input type="checkbox"/> delete:repo	Delete repositories
<input type="checkbox"/> write:discussion	Read and write team discussions
<input type="checkbox"/> read:discussion	Read team discussions
<input type="checkbox"/> admin:enterprise	Full control of enterprises
<input type="checkbox"/> manage_runners:enterprise	Manage enterprise runners and runner groups
<input type="checkbox"/> manage_billing:enterprise	Read and write enterprise billing data

Scopes are the types of permissions that you are attaching the token you are generating. This is again a security feature as tokens should only be given specific and limited permissions based on what you intend the token to be used for. It is not good practice to give a token complete or unlimited permissions as you are exposing your account to high risk if and when your token gets compromised.

For general R users, the following scopes are currently recommended:

- repo
- workflow
- gist
- user

Step 10: Click on Generate token



Permission	Description
<input type="checkbox"/> admin:org_hook	Full control of organization hooks
<input checked="" type="checkbox"/> gist	Create gists
<input type="checkbox"/> notifications	Access notifications
<input checked="" type="checkbox"/> user	Update ALL user data
<input type="checkbox"/> read:user	Read ALL user profile data
<input type="checkbox"/> user:email	Access user email addresses (read-only)
<input type="checkbox"/> user:follow	Follow and unfollow users
<input type="checkbox"/> delete_repo	Delete repositories
<input type="checkbox"/> write:discussion	Read and write team discussions
<input type="checkbox"/> read:discussion	Read team discussions
<input type="checkbox"/> admin:enterprise	Full control of enterprises
<input type="checkbox"/> manage_runners:enterprise	Manage enterprise runners and runner groups
<input type="checkbox"/> manage_billing:enterprise	Read and write enterprise billing data
<input type="checkbox"/> read:enterprise	Read enterprise profile data
<input type="checkbox"/> audit_log	Full control of audit log
<input type="checkbox"/> read:audit_log	Read access of audit log
<input type="checkbox"/> codespace	Full control of codespaces
<input type="checkbox"/> codespace:secrets	Ability to create, read, update, and delete codespace secrets
<input type="checkbox"/> project	Full control of projects
<input type="checkbox"/> read:project	Read access of projects
<input type="checkbox"/> admin:gpg_key	Full control of public user GPG keys
<input type="checkbox"/> write:gpg_key	Write public user GPG keys
<input type="checkbox"/> read:gpg_key	Read public user GPG keys
<input type="checkbox"/> admin:ssh_signing_key	Full control of public user SSH signing keys
<input type="checkbox"/> write:ssh_signing_key	Write public user SSH signing keys
<input type="checkbox"/> read:ssh_signing_key	Read public user SSH signing keys

[Generate token](#) [Cancel](#)

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After clicking you will now see a long string of characters and numbers which is your GitHub PAT. It is important to remember that once you see the generated GitHub PAT, you should copy this right away and store it securely.

Step 11: Store your PAT

Treat your GitHub PAT in the same way you would treat your password for online accounts. The best way to securely store the GitHub PAT is using a password manager ([1Password](#), [LastPass](#), [Bitwarden](#)). If you have a macOS computer, you can save your GitHub PAT into your computer's keychain.

⚠ Warning

Non-secure password/token storage practices that has been done by other students before are:

- Email their password/token to themselves

If you are using free email services such as Gmail, then this is a highly non-secure method. Others use their University of Oxford email address and argue that this is secure compared to using the free email services. Whilst it is true that a university email account is more

secure, email communications and email storage is still one of the most vulnerable places to keep something that is meant to be kept secret.

- Paste the token into a Word document and save in personal computer with the filename GITHUB_PAT.docx
- Paste the token into a Word document and save in Dropbox or in Google Drive

Please **AVOID** these methods.

Part II

Practices

5 Writing functions

For this topic, we will use data on weight and height to calculate body mass index. As a refresher, body mass index is calculated as follows:

$$\text{Body mass index} = \frac{\text{weight (kgs)}}{\text{height (m)}^2}$$

For this topic on writing functions in R, we will use BMI as an example to explore and demonstrate how we can create our own functions in R.

Let's say for example that you have been doing a research on children aged 11 years and older in 3 schools and you have collected the following data:

School 1516

school1516

	school	sex	ageMonths	weight	height
427	1516	1	138	24.5	126.0
428	1516	1	150	28.3	136.3
429	1516	1	162	32.2	143.5
430	1516	1	162	32.7	143.5
431	1516	1	150	28.6	137.0
432	1516	2	138	26.5	134.0
433	1516	1	150	29.9	139.2
434	1516	1	150	30.0	139.5
435	1516	1	162	34.0	148.0
436	1516	1	138	25.4	135.7
437	1516	1	150	32.3	143.0
438	1516	2	174	38.3	153.5
439	1516	2	162	41.6	151.0
440	1516	1	150	30.7	145.0
441	1516	2	186	46.8	155.2
442	1516	1	186	46.6	163.4
443	1516	1	150	33.5	145.5
444	1516	1	186	47.0	164.0
445	1516	1	174	41.1	159.5

446	1516	2	162	39.1	152.2
447	1516	2	174	40.9	155.5
448	1516	2	162	39.7	153.0
449	1516	2	162	40.9	153.2
450	1516	1	150	34.2	147.5
451	1516	2	150	41.8	149.4
452	1516	1	138	28.0	141.5
453	1516	1	138	30.0	142.0
454	1516	1	138	33.1	142.0
455	1516	1	186	46.1	167.5
456	1516	1	150	36.2	149.0
457	1516	2	162	47.4	156.0
458	1516	1	150	30.3	150.2
459	1516	2	150	36.4	152.1
460	1516	2	150	36.4	155.0
461	1516	2	150	44.1	155.0
462	1516	2	162	42.3	160.1
463	1516	2	179	50.4	163.5
464	1516	1	150	37.6	155.0
465	1516	2	138	36.0	154.5
466	1516	2	138	46.1	156.0

School 1522

school1522

	school	sex	ageMonths	weight	height
646	1522	1	203	30.6	140.5
647	1522	1	174	30.8	140.0
648	1522	1	162	29.3	136.3
649	1522	1	150	24.0	132.0
650	1522	1	150	28.1	132.1
651	1522	2	150	27.2	134.9
652	1522	1	162	34.2	139.2
653	1522	1	150	25.5	134.2
654	1522	1	138	24.6	129.0
655	1522	1	174	36.4	147.5
656	1522	1	150	28.7	137.5
657	1522	1	186	45.8	155.6
658	1522	1	174	36.3	151.6
659	1522	1	150	31.0	139.5
660	1522	1	138	29.0	134.3

661	1522	1	179	38.3	155.5
662	1522	2	138	31.3	138.4
663	1522	1	162	36.5	148.8
664	1522	1	155	36.8	145.2
665	1522	1	138	28.3	136.8
666	1522	1	138	26.8	137.3
667	1522	2	138	32.6	141.4
668	1522	2	138	31.9	143.0
669	1522	1	174	42.6	160.7
670	1522	2	198	57.8	158.0
671	1522	2	162	43.9	153.5
672	1522	2	150	35.1	150.6
673	1522	2	186	52.6	159.6
674	1522	2	150	45.1	152.8
675	1522	2	138	34.6	147.2
676	1522	2	150	45.3	153.1
677	1522	1	186	51.8	170.2
678	1522	2	150	57.1	154.2
679	1522	2	138	33.5	149.2
680	1522	1	150	36.3	154.1
681	1522	1	174	44.0	169.1
682	1522	2	150	44.5	158.3
683	1522	2	150	51.5	159.1
684	1522	2	138	47.4	157.8
685	1522	2	138	36.8	158.5
686	1522	2	138	52.0	161.0

School 1525

school1525

	school	sex	ageMonths	weight	height
752	1525	1	186	26.2	137
753	1525	1	186	32.7	138
754	1525	1	150	25.9	130
755	1525	1	162	30.4	137
756	1525	2	138	24.4	129
757	1525	2	138	23.8	130
758	1525	1	150	26.1	133
759	1525	1	150	26.4	135
760	1525	1	174	35.1	148
761	1525	1	162	28.7	142

762	1525	1	150	28.0	136
763	1525	1	174	34.0	149
764	1525	1	186	40.6	155
765	1525	2	150	35.8	142
766	1525	1	150	35.4	140
767	1525	2	138	27.8	137
768	1525	2	138	28.2	137
769	1525	2	138	29.7	139
770	1525	2	138	30.9	139
771	1525	1	138	28.2	137
772	1525	2	138	26.2	140
773	1525	2	138	26.6	140
774	1525	1	138	27.2	138
775	1525	2	138	27.0	141
776	1525	1	150	31.3	145
777	1525	2	162	33.9	152
778	1525	2	162	42.0	153
779	1525	2	185	38.3	157
780	1525	2	138	31.0	145
781	1525	2	138	32.3	145
782	1525	1	139	35.1	144
783	1525	2	150	36.4	152
784	1525	2	138	32.7	147
785	1525	1	174	44.9	166
786	1525	2	138	32.2	148
787	1525	2	138	36.4	148
788	1525	1	138	31.4	146
789	1525	2	138	45.0	149
790	1525	2	162	49.4	160
791	1525	2	138	34.3	150
792	1525	1	138	30.0	148
793	1525	2	150	37.0	156
794	1525	2	162	52.2	165
795	1525	2	138	42.9	158

In this dataset, the units of the height measurement is in centimetres.

Using what we have learned earlier on calculating BMI using R, I can perform the following R commands to get the BMI for each child in each of the schools:

```
## Calculate BMI for children in school 1516
school1516$weight / (school1516$height / 100) ^ 2
```

```
## Calculate BMI for children in school 1516
school1522$weight / (school1516$height / 100) ^ 2
```

```
## Calculate BMI for children in school 1516
school1525$weight / (school1516$height / 100) ^ 2
```

Because the commands are repetitive, I can easily copy and paste my initial line of code to calculate BMI for children in school 1516 and then just change the object names accordingly to calculate the BMI for children in the two other schools.

When I run these lines of code, I get the following results:

```
[1] 15.43210 15.23333 15.63695 15.87976 15.23789 14.75830 15.43095 15.41604
[9] 15.52228 13.79349 15.79539 16.25481 18.24481 14.60166 19.42954 17.45347
[17] 15.82409 17.47472 16.15550 16.87903 16.91463 16.95929 17.42632 15.71962
[25] 18.72730 13.98444 14.87800 16.41539 16.43128 16.30557 19.47732 13.43083
[33] 15.73414 15.15088 18.35588 16.50280 18.85363 15.65036 15.08153 18.94313
```

Warning in school1522\$weight/(school1516\$height/100)^2: longer object length is not a multiple of shorter object length

```
[1] 19.27438 16.57903 14.22865 11.65487 14.97150 15.14814 17.65012 13.10363
[9] 11.23083 19.76704 14.03492 19.43787 15.92035 14.74435 12.03967 14.34481
[17] 14.78490 13.57079 14.46527 12.21679 11.08343 13.92627 13.59168 19.58058
[25] 25.89564 21.92561 17.40726 26.08609 16.07485 15.58488 18.61440 22.96095
[33] 24.68185 13.94381 15.10926 17.16604 16.64656 21.43600 19.85735 15.12163
[41] 32.75384
```

Warning in school1525\$weight/(school1516\$height/100)^2: longer object length is not a multiple of shorter object length

```
[1] 16.50290 17.60176 12.57755 14.76284 13.00016 13.25462 13.46983 13.56612
[9] 16.02447 15.58555 13.69260 14.42986 17.80624 17.02735 14.69670 10.41216
[17] 13.32058 11.04253 12.14611 12.17362 10.83529 11.36315 11.58914 12.41023
[25] 14.02307 16.93116 20.82920 18.99425 11.04923 14.54889 14.42308 16.13472
[33] 14.13479 18.68887 13.40271 14.20099 11.74611 18.73049 20.69522 14.09435
[41] 18.89645 19.91636 25.34934 20.83308
```

The calculation for the BMI of children in school 1516 seems to have completed without issues and a vector of BMI results have been produced. However, for school 1522 and school 1525, there is a warning saying:

```
## Warning in school1522$weight/(school1516$height)^2: longer object length is not a multiple
## of shorter object length
```

Although a result has been provided, the warning gives me an indication that something is not quite right with my calculation and when I inspect further, I notice that in my formula for school 1522 and for school 1525, my denominator is still using data for school 1516 and this is most likely what is causing the warning message.

So, to correct this I go back to my lines of code and edit the denominators for school 1522 and school 1525 as follows:

```
## Calculate BMI for children in school 1516
school1516$weight / (school1516$height / 100) ^ 2
```

```
## Calculate BMI for children in school 1516
school1522$weight / (school1522$height / 100) ^ 2
```

```
## Calculate BMI for children in school 1516
school1525$weight / (school1525$height / 100) ^ 2
```

which gives me:

```
[1] 15.43210 15.23333 15.63695 15.87976 15.23789 14.75830 15.43095 15.41604
[9] 15.52228 13.79349 15.79539 16.25481 18.24481 14.60166 19.42954 17.45347
[17] 15.82409 17.47472 16.15550 16.87903 16.91463 16.95929 17.42632 15.71962
[25] 18.72730 13.98444 14.87800 16.41539 16.43128 16.30557 19.47732 13.43083
[33] 15.73414 15.15088 18.35588 16.50280 18.85363 15.65036 15.08153 18.94313
```

```
[1] 15.50132 15.71429 15.77161 13.77410 16.10277 14.94669 17.65012 14.15908
[9] 14.78277 16.73082 15.18017 18.91674 15.79459 15.92991 16.07852 15.83937
[17] 16.34076 16.48493 17.45479 15.12217 14.21653 16.30492 15.59978 16.49597
[25] 23.15334 18.63150 15.47594 20.65000 19.31656 15.96837 19.32626 17.88178
[33] 24.01416 15.04898 15.28626 15.38741 17.75817 20.34543 19.03550 14.64837
[41] 20.06095
```

```
[1] 13.95919 17.17076 15.32544 16.19692 14.66258 14.08284 14.75493 14.48560
[9] 16.02447 14.23329 15.13841 15.31463 16.89906 17.75441 18.06122 14.81166
[17] 15.02477 15.37188 15.99296 15.02477 13.36735 13.57143 14.28271 13.58081
[25] 14.88704 14.67278 17.94182 15.53816 14.74435 15.36266 16.92708 15.75485
[33] 15.13258 16.29409 14.70051 16.61797 14.73072 20.26936 19.29687 15.24444
[41] 13.69613 15.20381 19.17355 17.18475
```

I now do not get the warning message and the expected length of BMI values for each school has now been produced.

From this short example above, we realise how tedious a task it is to type in the code above every time we need to calculate BMI. Also, it becomes even challenging to debug issues with the code because we have to review and edit (as needed) each iteration of the calculation to see where it may have gone wrong (especially when doing a cut and paste approach).

It would be better (and easier) to have a function that calculates and displays the BMI values automatically. Fortunately, R allows us to do just that.

The `function()` function allows us to create new functions in R with the following generic syntax:

```
function_name <- function(argument1, argument2, ...) {  
  ## Your code here  
}
```

Using this template/generic syntax, we apply it to create a function called `calculate_bmi` as follows:

```
calculate_bmi <- function(weight, height) {  
  weight / height ^ 2  
}
```

We now have a function for calculating and outputting BMI values.

Let us now test it with our 3 sets of data:

School 1516

```
calculate_bmi(  
  weight = school1516$weight,  
  height = school1516$height / 100  
)
```

```
[1] 15.43210 15.23333 15.63695 15.87976 15.23789 14.75830 15.43095 15.41604  
[9] 15.52228 13.79349 15.79539 16.25481 18.24481 14.60166 19.42954 17.45347  
[17] 15.82409 17.47472 16.15550 16.87903 16.91463 16.95929 17.42632 15.71962  
[25] 18.72730 13.98444 14.87800 16.41539 16.43128 16.30557 19.47732 13.43083  
[33] 15.73414 15.15088 18.35588 16.50280 18.85363 15.65036 15.08153 18.94313
```

School 1522

```
calculate_bmi(
  weight = school1522$weight,
  height = school1522$height / 100
)
```

```
[1] 15.50132 15.71429 15.77161 13.77410 16.10277 14.94669 17.65012 14.15908
[9] 14.78277 16.73082 15.18017 18.91674 15.79459 15.92991 16.07852 15.83937
[17] 16.34076 16.48493 17.45479 15.12217 14.21653 16.30492 15.59978 16.49597
[25] 23.15334 18.63150 15.47594 20.65000 19.31656 15.96837 19.32626 17.88178
[33] 24.01416 15.04898 15.28626 15.38741 17.75817 20.34543 19.03550 14.64837
[41] 20.06095
```

School 1525

```
calculate_bmi(
  weight = school1525$weight,
  height = school1525$height / 100
)
```

```
[1] 13.95919 17.17076 15.32544 16.19692 14.66258 14.08284 14.75493 14.48560
[9] 16.02447 14.23329 15.13841 15.31463 16.89906 17.75441 18.06122 14.81166
[17] 15.02477 15.37188 15.99296 15.02477 13.36735 13.57143 14.28271 13.58081
[25] 14.88704 14.67278 17.94182 15.53816 14.74435 15.36266 16.92708 15.75485
[33] 15.13258 16.29409 14.70051 16.61797 14.73072 20.26936 19.29687 15.24444
[41] 13.69613 15.20381 19.17355 17.18475
```

In our example here, the `calculate_bmi()` function helped a little bit in making the code to calculate BMI for each student in each school more efficient. But the efficiency that functions provide become more evident when you need to make more complex operations. For example, what if you need to get the mean BMI for students in each school? Without a function, we will have to do the following script for each school:

School 1516

```
## Calculate BMI for children in school 1516
bmi_school1516 <- school1516$weight / (school1516$height / 100) ^ 2

## Get the mean BMI for children in school 1516
mean_bmi_school1516 <- mean(bmi_school1516)

mean_bmi_school1516
```



```
[1] 16.28491
```

School 1522

```
## Calculate BMI for children in school 1522
bmi_school1522 <- school1522$weight / (school1522$height / 100) ^ 2

## Get the mean BMI for children in school 1522
mean_bmi_school1522 <- mean(bmi_school1522)

mean_bmi_school1522
```

```
[1] 16.89955
```

School 1525

```
## Calculate BMI for children in school 1525
bmi_school1525 <- school1525$weight / (school1525$height) ^ 2

## Get the mean BMI for children in school 1525
mean_bmi_school1525 <- mean(bmi_school1525)

mean_bmi_school1525
```

```
[1] 0.001564695
```

As the operations/calculations we want to perform become more complex, the copy and paste method becomes more and more tedious. With the function approach, we can use the following:

```
calculate_mean_bmi <- function(weight, height) {
  bmi <- weight / height ^ 2

  mean_bmi <- mean(bmi)

  return(mean_bmi)
}
```

Applying the function to the datasets, we get:

School 1516

```
calculate_mean_bmi(  
  weight = school1516$weight,  
  height = school1516$height / 100  
)
```

```
[1] 16.28491
```

School 1522

```
calculate_mean_bmi(  
  weight = school1522$weight,  
  height = school1522$height / 100  
)
```

```
[1] 16.89955
```

School 1525

```
calculate_mean_bmi(  
  weight = school1525$weight,  
  height = school1525$height / 100  
)
```

```
[1] 15.64695
```

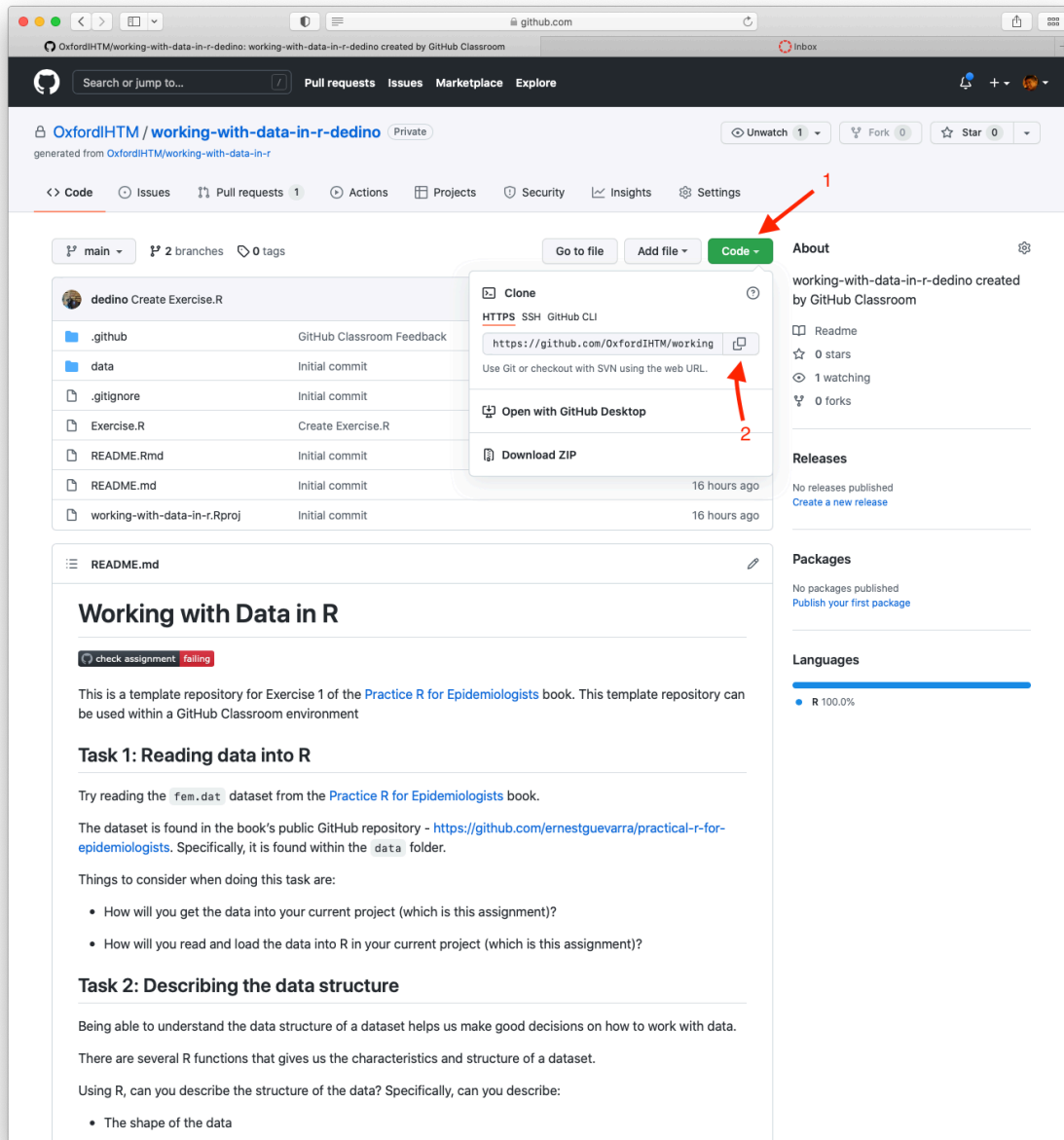
Part III

Processes

6 Cloning a GitHub repository into your local computer using RStudio

This tutorial is a summary of the the instructions described [here](#).

6.1 Get the GitHub repository URL



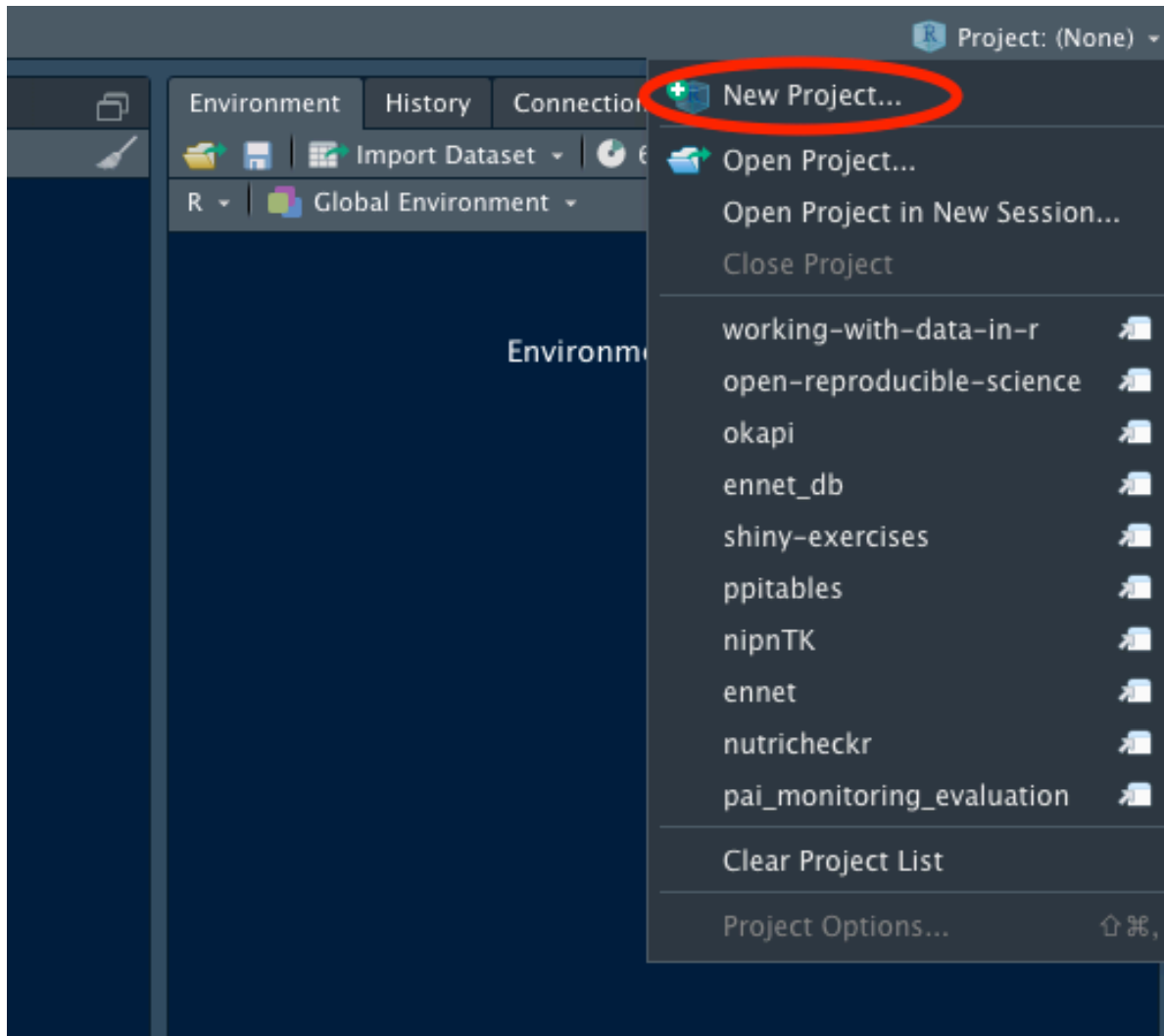
1. Go to the repository's GitHub page

Click on the green button that is labeled code.

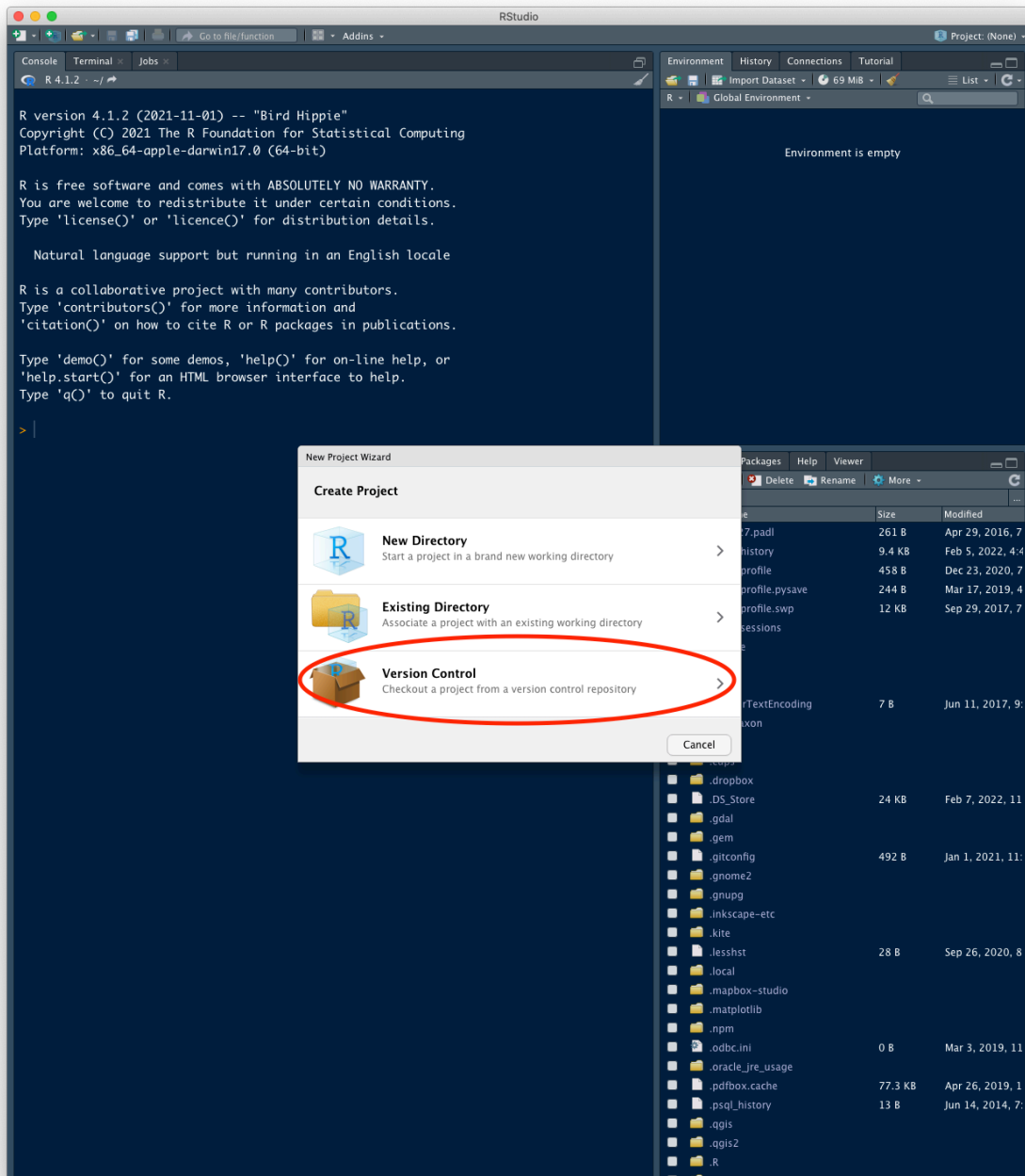
2. Copy the repository URL

Click on the copy to clipboard icon to copy the repository URL.

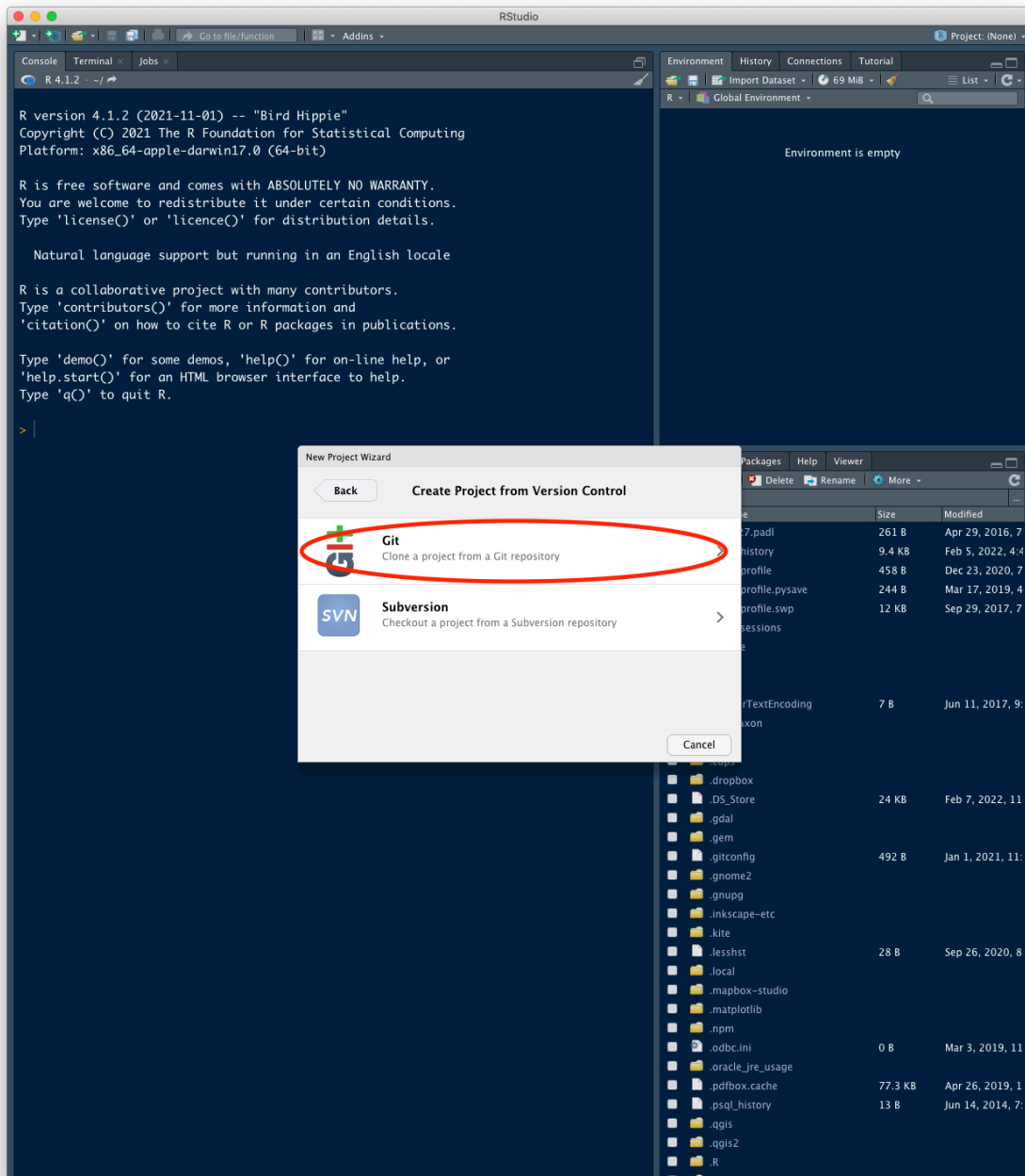
6.2 Go to RStudio and create new project



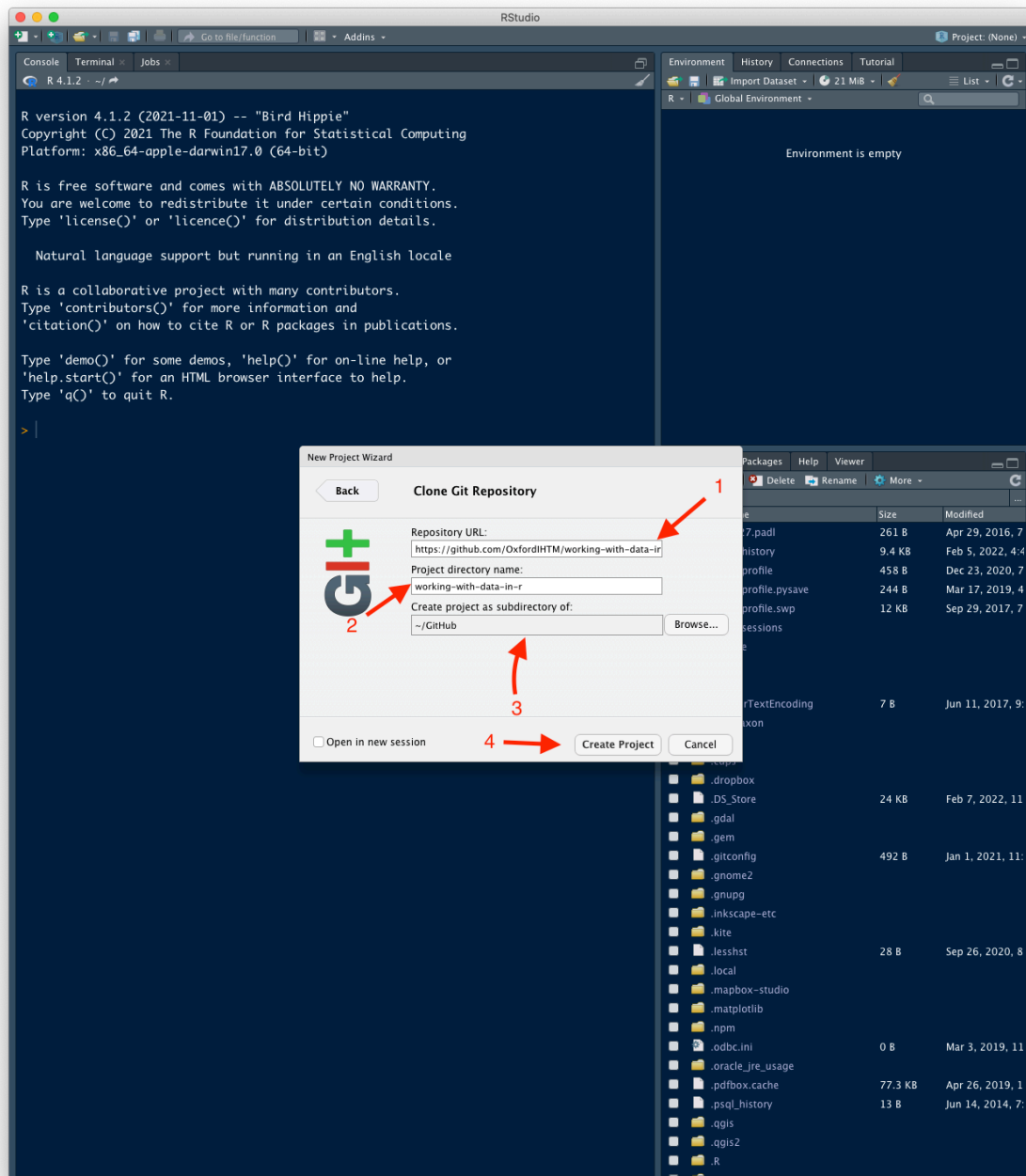
6.3 Choose Version Control



6.4 Select Git



6.5 Setup repository settings



1. Paste the repository URL you copied earlier

2. Set the project directory name

The project directory name should be specified already after you paste the repository URL. Use the suggested directory name.

3. Set local directory

Browse for the directory on your local computer where you want to save the files for the specified project.

4. Create project

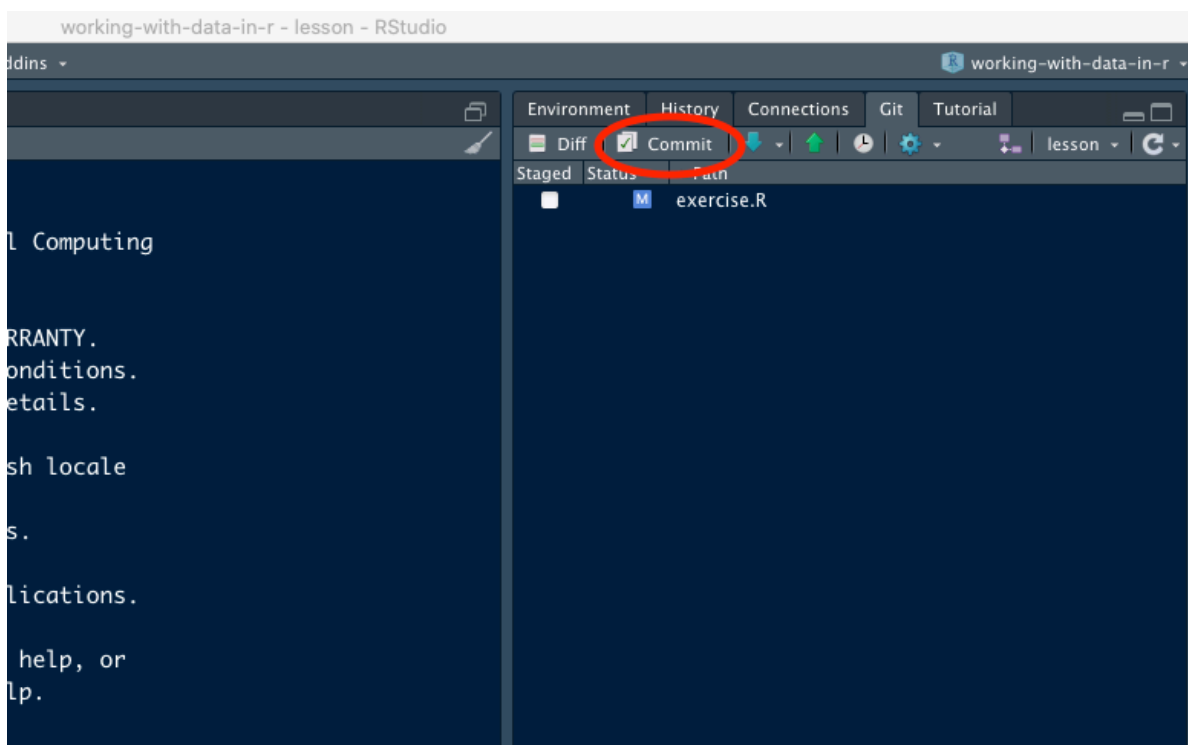
Click on the **Create Project** button/icon.

You will now have the GitHub repository in your local computer.

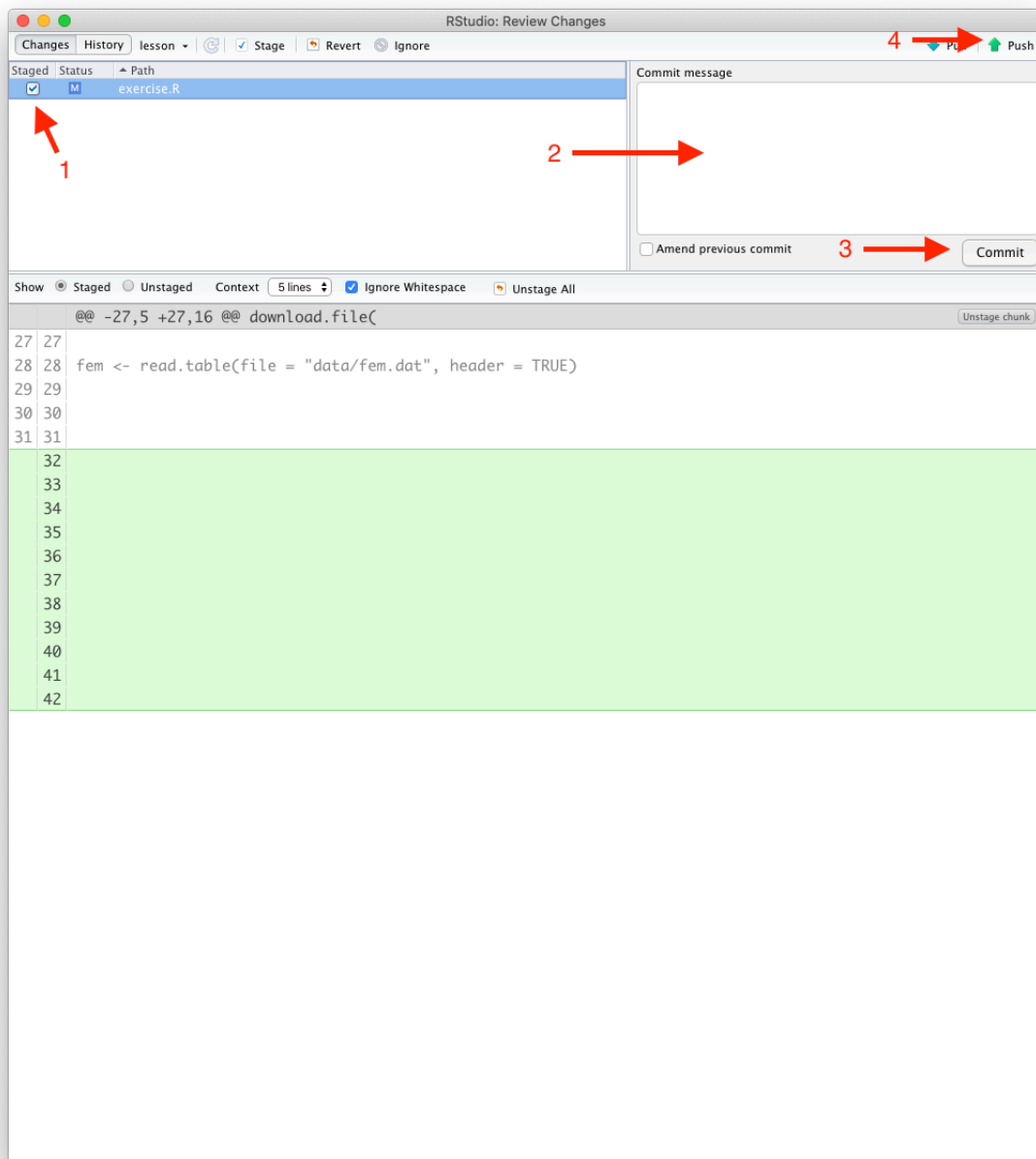
7 Committing your changes and pushing them to GitHub

Following are the steps to take in committing your changes in RStudio and pushing them to GitHub.

7.1 Click on Commit in the Git tab on RStudio



7.2 Getting changes saved and push to GitHub



1. Stage changes

Tick the box beside the file that has changed to stage the changes.

2. Add a commit message

Every time you make a commit you must also write a short commit message.

Write a commit message in the **Commit message** dialog box. In the commit message, describe the changes that you made.

3. Click on the Commit button

4. Click on the Push button

7.3 Initiate a pull request

1. Click on the branches link from your repository

The screenshot shows the GitHub interface for the repository `OxfordIHTM/working-with-data-in-r`. The repository is a private template. The navigation bar includes links for Code, Issues, Pull requests, Actions, Projects, Wiki, Security, Insights, and Settings. The repository name is `main` with `2 branches` and `0 tags`. The `2 branches` link is circled in red. Below the navigation bar, there is a table of commits and a list of files. The commit history table shows the following commits:

Commit	Author	Message	Time
5111243	ernestguevarra	update R version in container	2 weeks ago
		update assignment	2 weeks ago
		initial commit	last year
		update assignment	2 weeks ago
		update assignment	2 weeks ago
		initial commit	last year

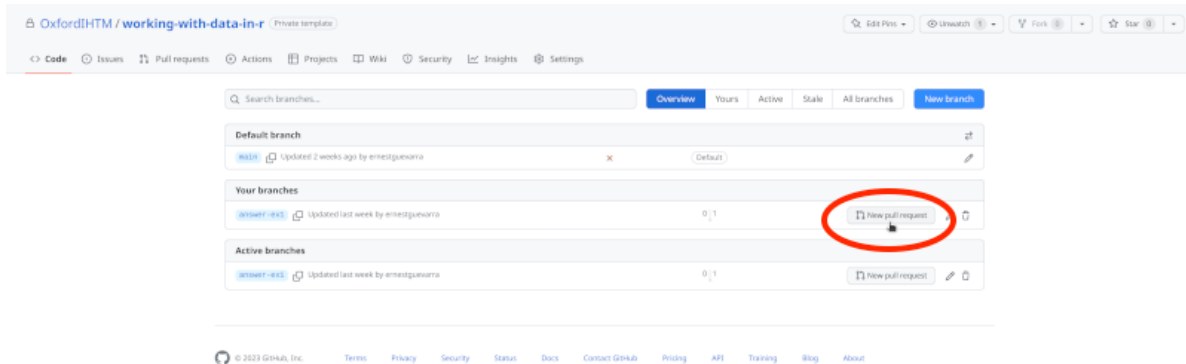
The files list includes:

- `.github/workflows`
- `data`
- `.gitignore`
- `README.Rmd`
- `README.md`
- `working-with-data-in-r.Rproj`

The `README.md` file is selected, showing the title **Working with Data in R**. The README content includes a section titled **Retrieving the assignment locally to your computer via RStudio** and a link to a tutorial: <https://oxford-ihtm.io/ihtm-handbook/clone-repository.html>.

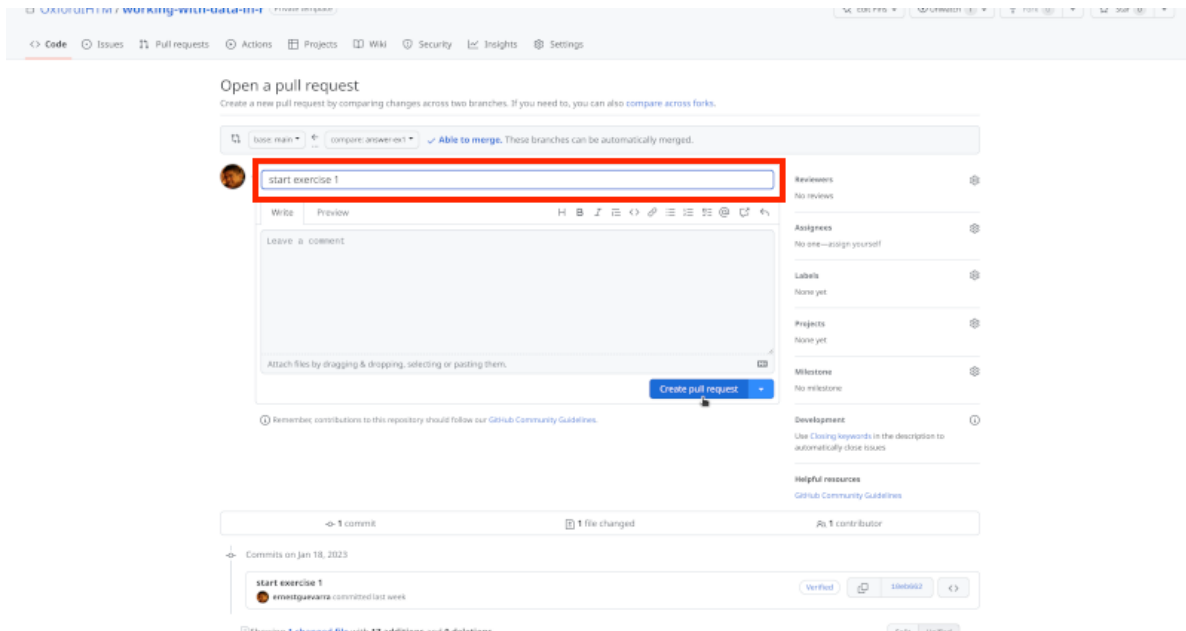
2. Make a pull request

Click on the **Make pull request** link on the appropriate branch.



<https://github.com/OxfordH1M/working-with-data-in-r/compare/answer-ext:spadoc>

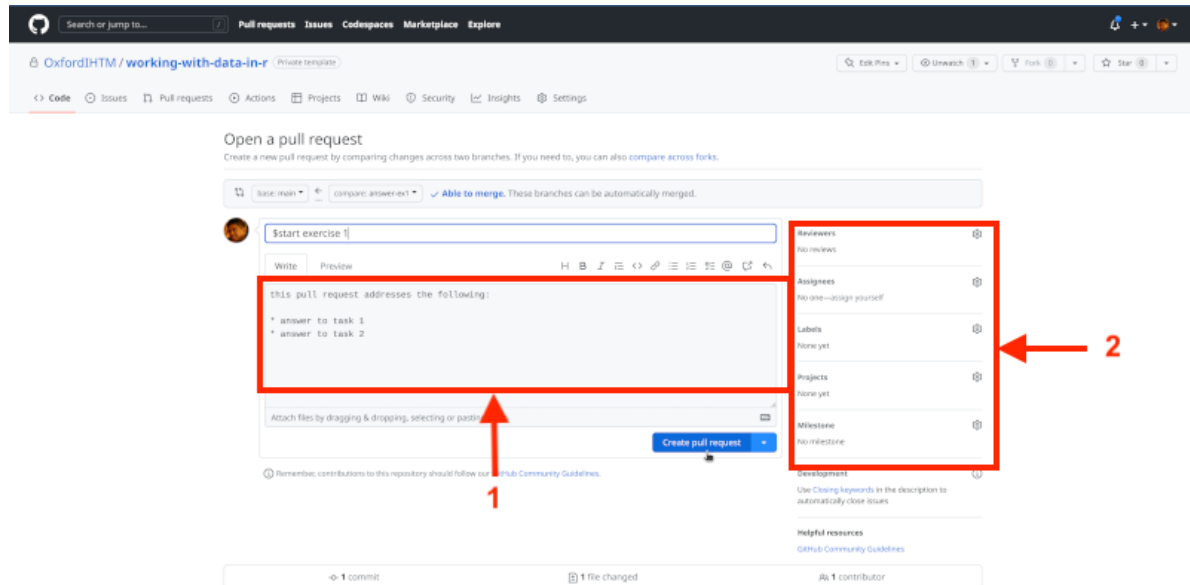
3. Enter a title for your pull request



Make the title as short but as informative as possible.

4. Create a pull request

Add further description about the pull request (optional) and then click on **Create pull request** button



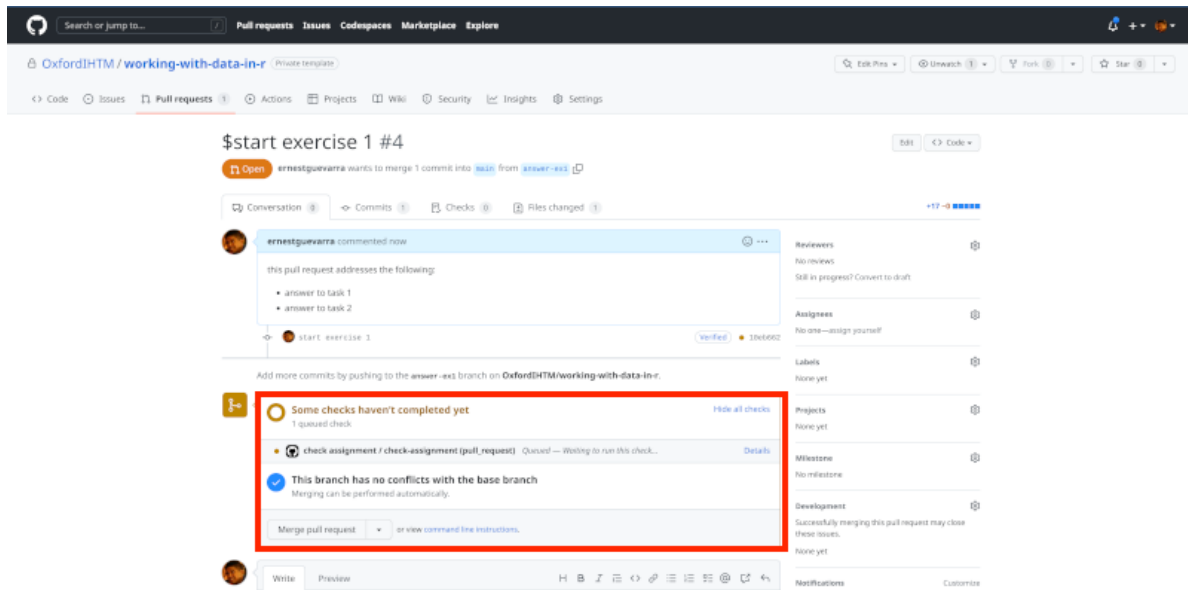
i Note

If you think more information will help the reviewer navigate through the changes you have made, use the comment box to add more details. This comments box can interpret Markdown syntax so you can format your text accordingly.

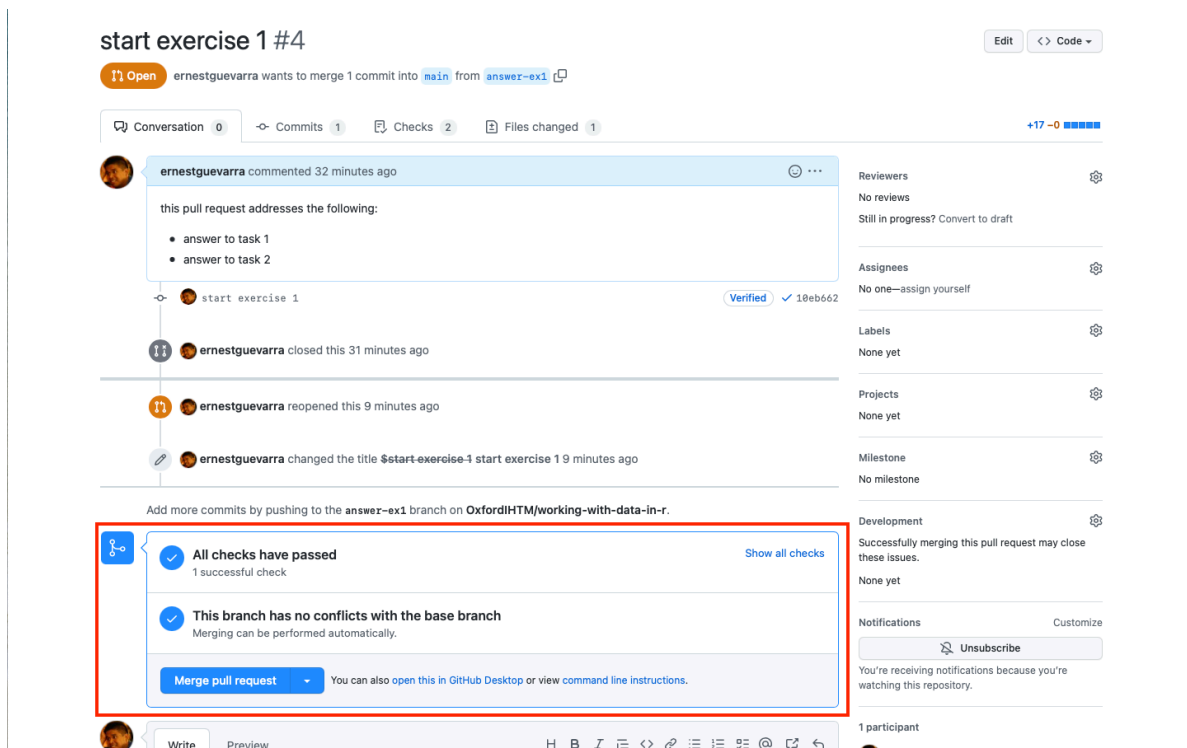
On the right hand side of the pull request page, you can set a specific reviewer for your pull request (recommended). Also, given that you are making this pull request, assign this pull request to you so you are notified of the progress of this pull request.

5. Wait for review

If the project has automated checks included, you will see that these checks will get initiated.



If there are no issues with the code, the automated checks should show that all checks have passed.



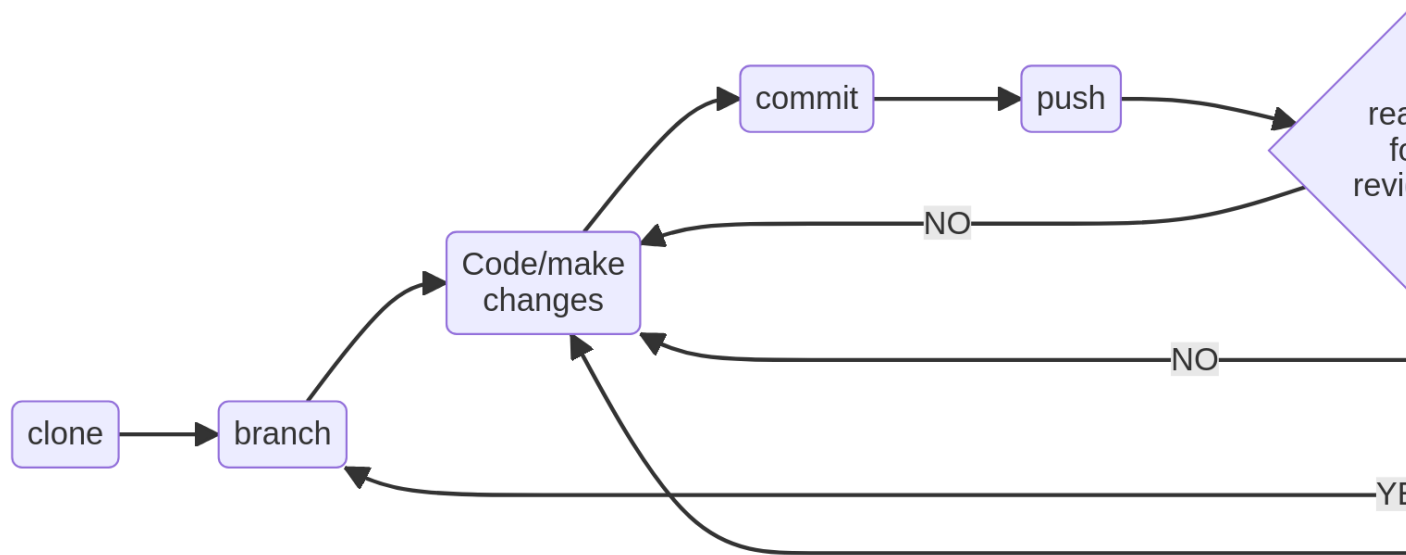
i Note

Wait for reviewer's feedback/comments. If reviewer request's changes, make changes to your code and then commit and push again (as above). If your project has automated checks, this will get triggered again within the same pull request. Your reviewer will be notified of the changes you have made and should review your work again. Once reviewer approves changes, you can then merge your work to the main branch.

8 Participating in an existing R/RStudio project

Following are the general steps to take when participating in an existing R/RStudio project that has been initiated and led by someone else.

The following diagram illustrates the steps in this process:



A flowchart of a git-based development workflow

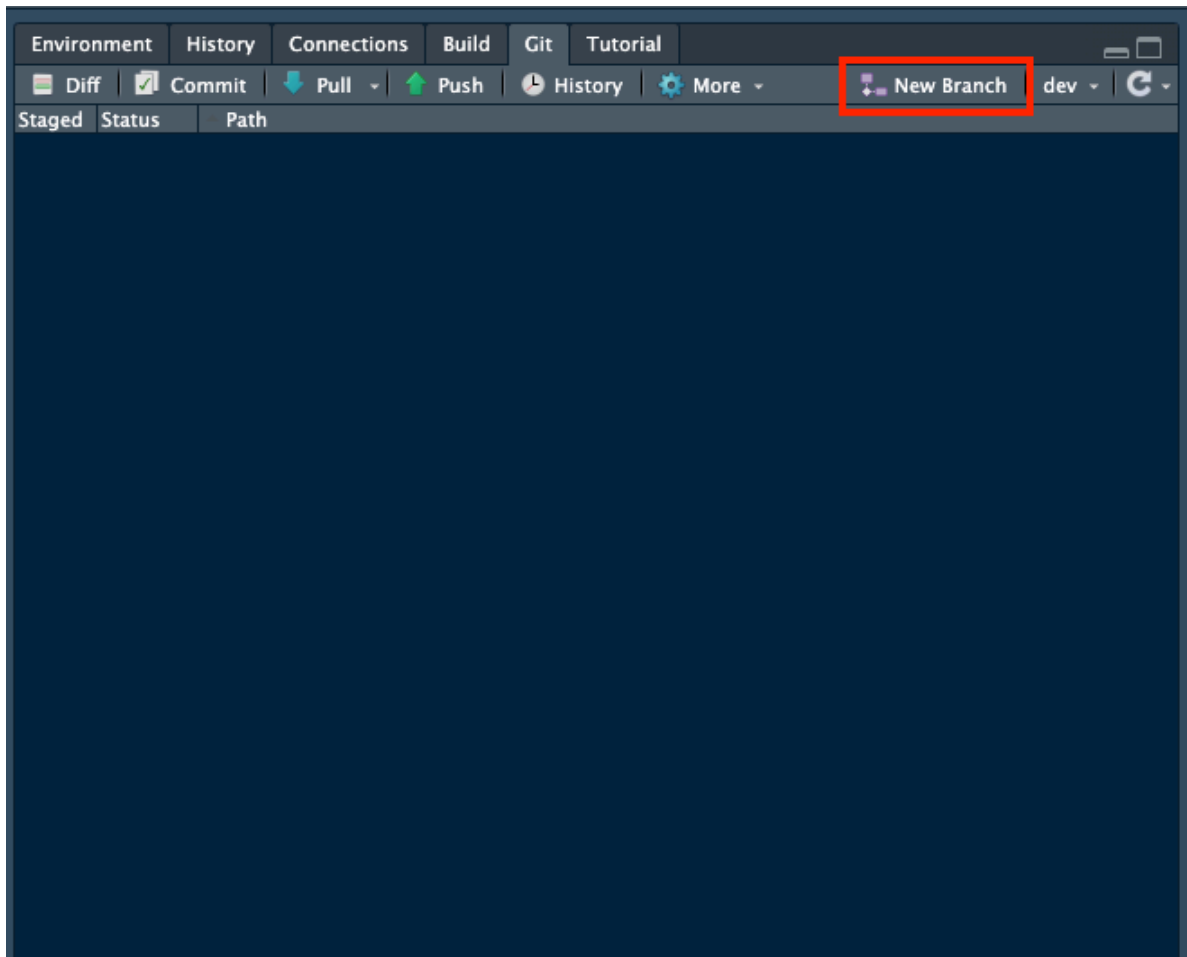
8.1 Clone the project to your local machine

Steps in cloning a project to your local machine is described in [Chapter 6](#).

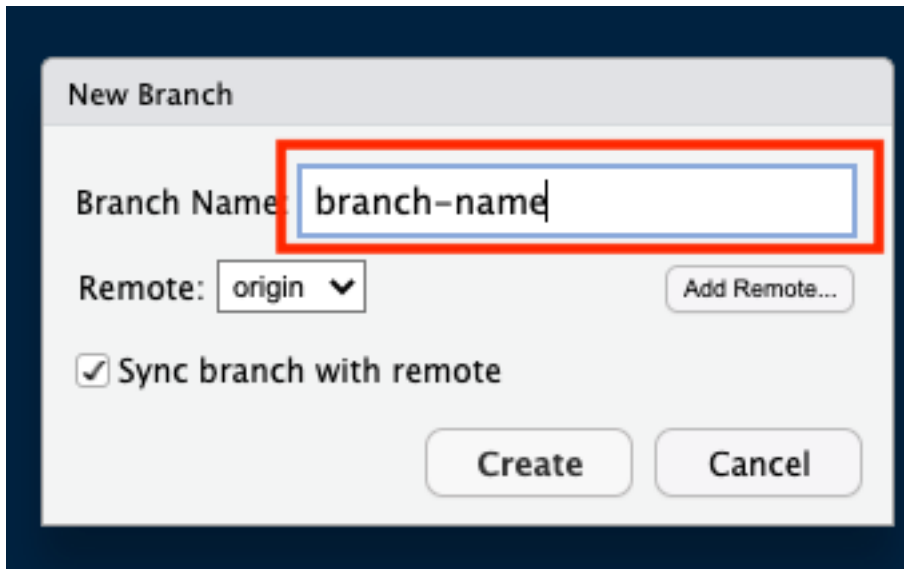
8.2 Create a new branch from the main branch

Before making any changes to the project, create a new branch as follows:

8.2.1 Click on New Branch



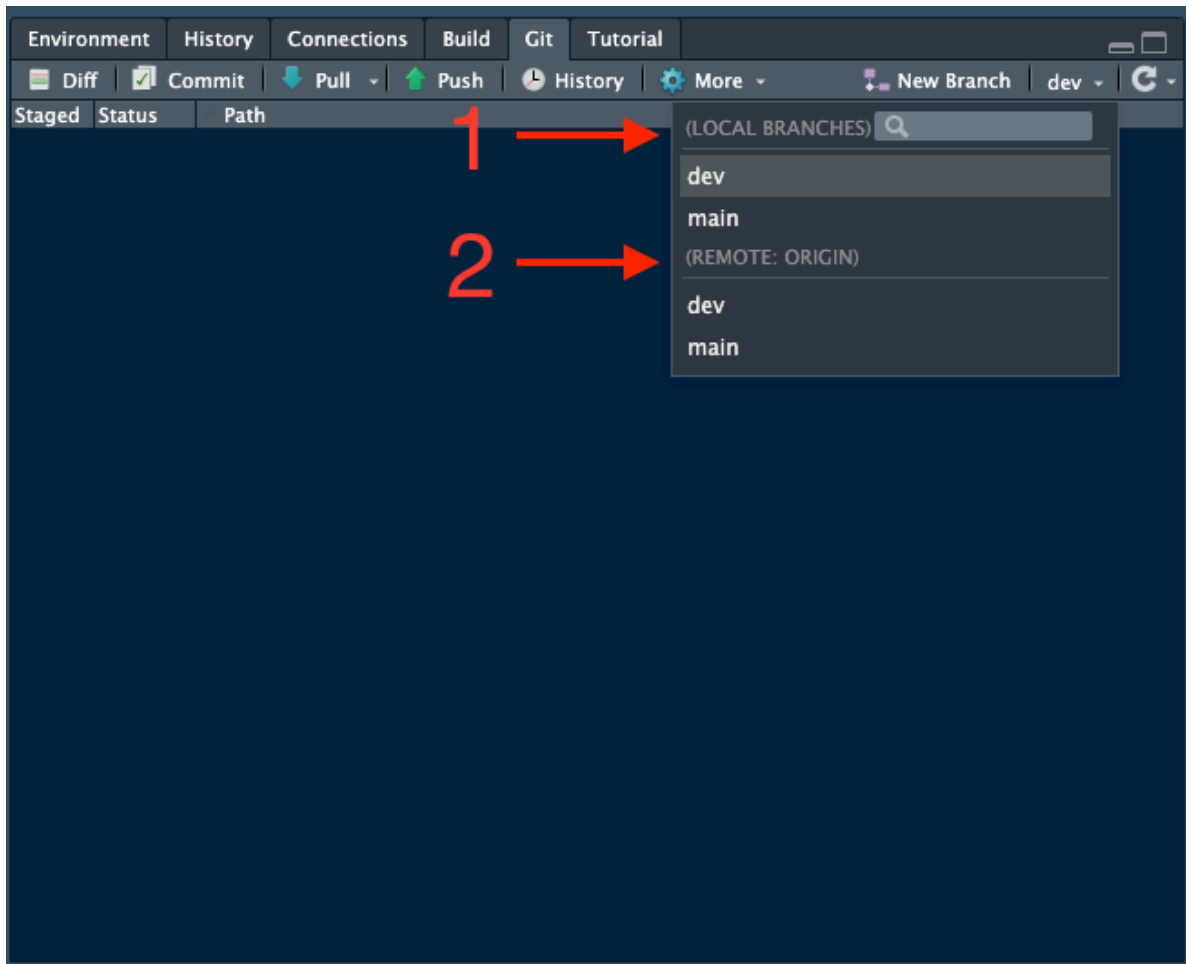
8.2.2 Name the new branch



Name the branch uniquely. The best way to name a branch will be based on how the team/person you are working with prefers to name branches. Some would like the branch name to succinctly describe the type of change that is being made. Some may ask you to name your branch with your username. Some may ask you to name your branch using coded values.

Once named, click on **Create**

You will now see the new branch in the list of branches



8.3 Code and make changes to your branch

Start coding and implement the changes you want to make or the changes that your collaborator/s asked you to make.

8.4 Commit and push your changes and initiate a pull request

After making changes, you should **commit** and **push** your changes. This process is described in Chapter 7. Your code and your changes do not have to be complete already for you to commit and push changes. It is good practice to commit and push frequently (at least once a day usually at the end of your coding session). See this as similar to saving your work at multiple stages.

Once your code and the changes you want to make are complete (and ideally that they are working correctly on your local machine), and that you are ready to have your work reviewed, you can now make a **pull request**. This process is also described in [Chapter 7](#).

8.5 Merge pull request

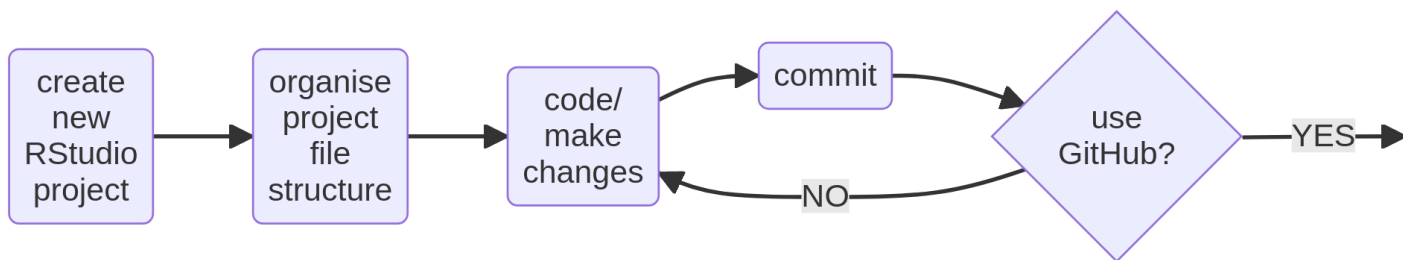
Once your chosen reviewer has seen your work, they may ask you to make changes based on what they see with your code. If so, then start coding again on the same branch and address the reviewers comments, commit those changes and push the changes to your remote repository. Your changes will push into the same existing open pull request that is waiting approval. The reviewer can then view your changes and make the necessary feedback.

Once reviewer approves your changes, they may either merge your pull request themselves or they may let you know in their feedback that they are happy with your changes and that you can now merge your pull request. If so, then click on the **Merge pull request** button.

Your changes have now been integrated into the main branch of the project.

9 Initiating an R/RStudio project

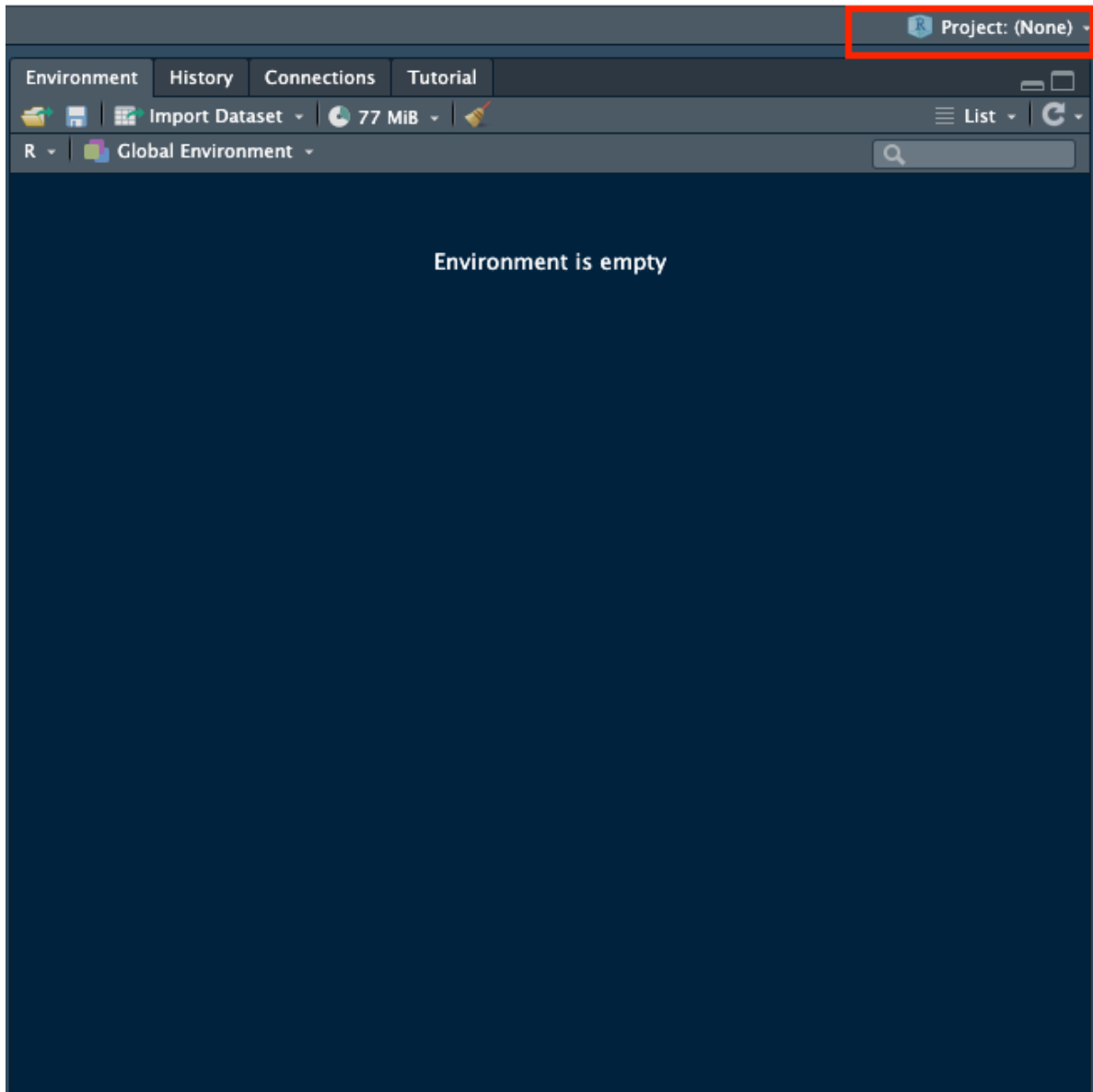
Following is a diagram of the steps in initiating your own R/RStudio project.

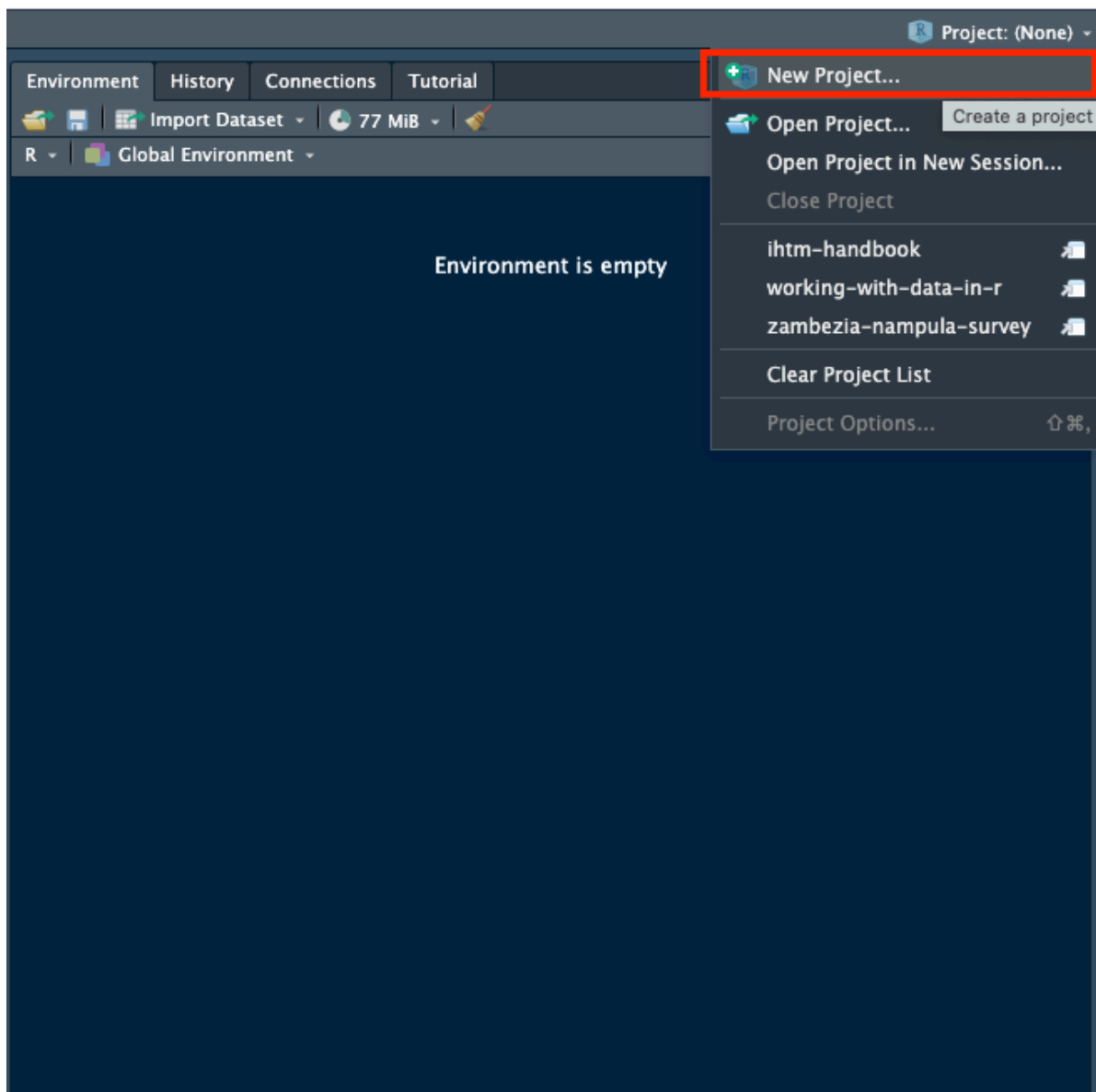


A flowchart for initiating an R project

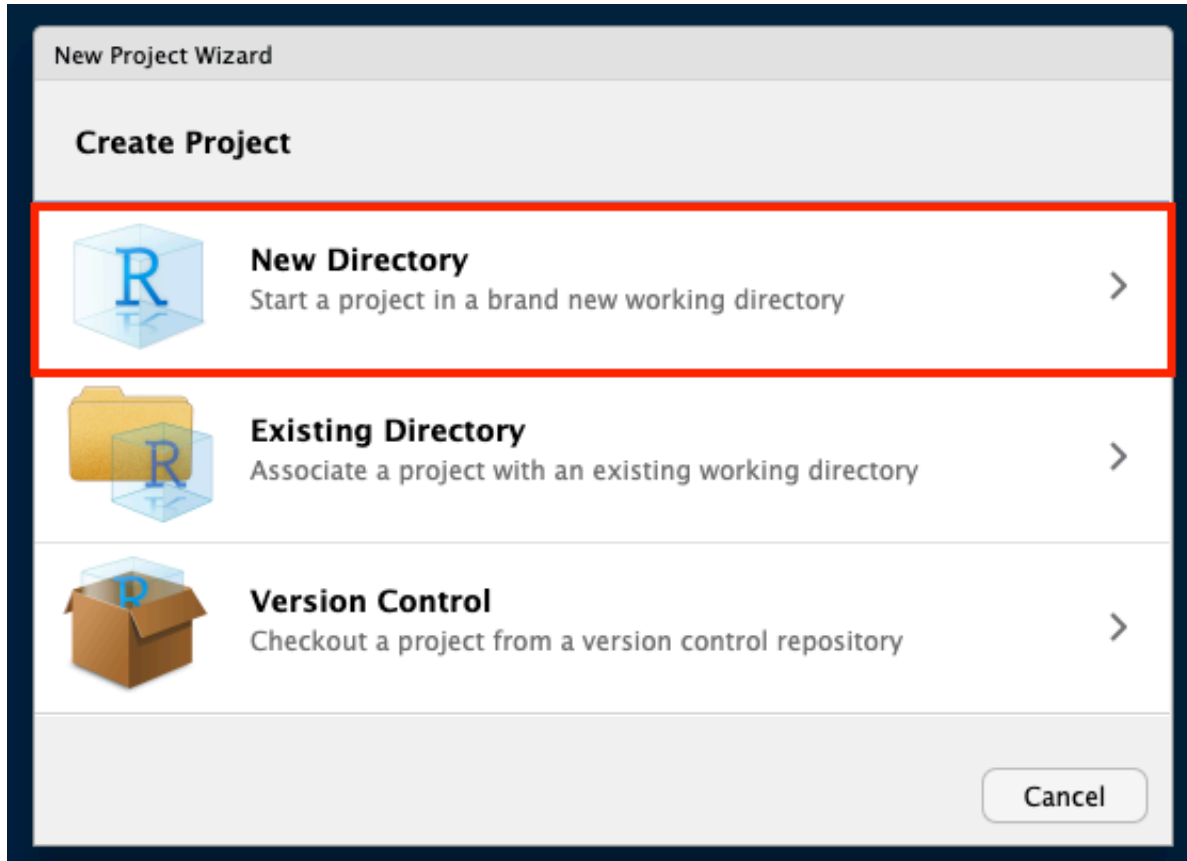
9.1 Create a new project in RStudio

9.1.1 Click on New Project button on RStudio

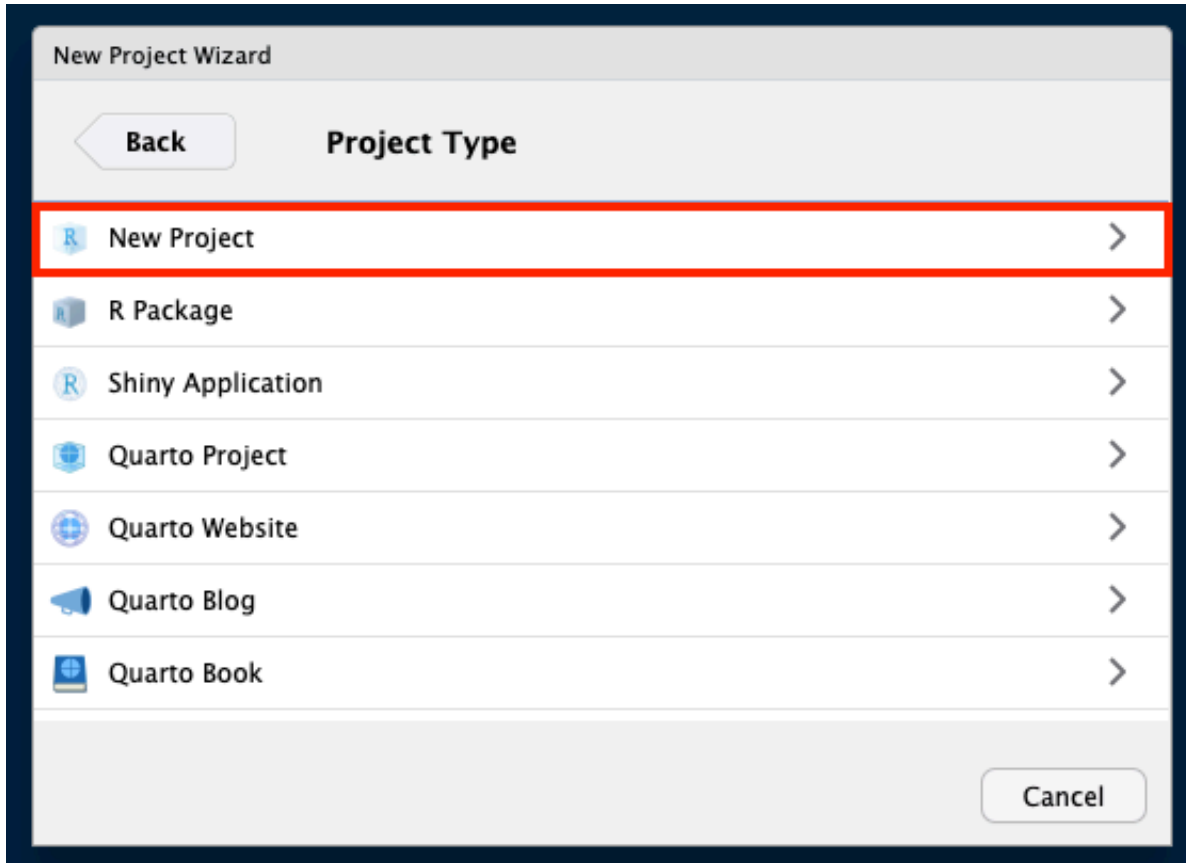




9.1.2 Create a New Directory



9.1.3 Select New Project as project type



9.1.4 Specify details for new project

New Project Wizard

Back Create New Project

Directory name: project-name

Create project as subdirectory of: ~/GitHub Browse...

☐ Create a git repository

☐ Use renv with this project

☐ Open in new session

Create Project Cancel

Specify a project name

Note

Best practices for naming a project are:

- Make sure that name is succinct (as short as possible while at the same time descriptive of the project);
- Don't use spaces for your project name. If you need to separate words, use a *hyphen* or an *underscore*;
- Avoid using capital letters.

Specify a directory/location

Select a directory in your local machine where to place the directory of your new project

Decide whether to use git to version this project

Here you can decide whether you want to use git to version your project. Remember that using git doesn't mean you have to use GitHub. git is software installed in your local machine and it versions what you have on your local machine. You don't need GitHub or any other similar service to version your code with git in your local machine.

I would recommend that you tick this option for any new project you create so that you can version your work in your local machine even if you don't want or decide not to use GitHub or any other remote git service.

Do you want to open a new session

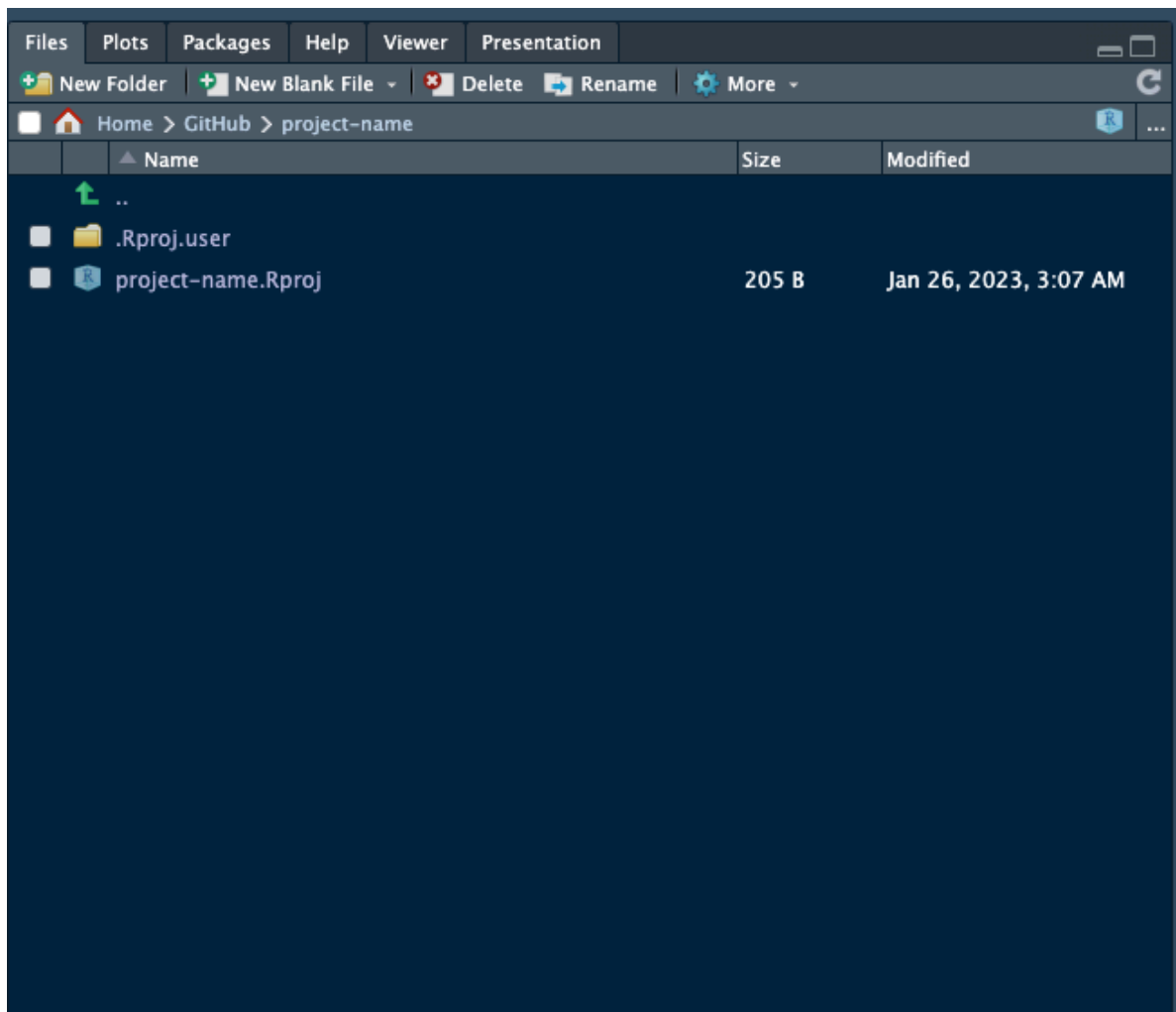
This is by default unticked and will open the new project within the existing RStudio session (if any). This means that if you have an existing RStudio session with another project that you are working on, that project will be closed and the new project you are creating will open in the existing RStudio session.

If you need your existing RStudio session and the project within it to remain open alongside the new project you are creating, tick this box/option.

Click on Create New Project

Once you click on *Create New Project*, you will now see the new project open in RStudio.

You will also see something like below within the file explorer pane of RStudio.



9.2 2. Structure/organise your new project appropriately

Note

Project organisation is vital because:

- supports productivity because the different components of the project are placed in directories where they should be;
- enables clarity in communicating project structure;
- facilitates collaboration.

Organising an R project can be user- and project-dependent but there are generally accepted project organising structure that is common to most well-organised projects. Below is an example:

```
|-- my-project
  |-- data
  |-- output
    |-- figures
  |-- R
  |-- my-project.Rproj
  |-- analysis_workflow.R
  |-- README.md
```

9.3 3. Start coding

This will include creating bespoke R functions (as required) and creating an Rscript for the step-by-step processes in your scientific workflow.

9.4 Next steps

The next steps will depend on whether you will use git and GitHub for versioning your project and whether or not you will work on your project as a solo scientist or work and collaborate with other scientists.

10 Creating portable and reproducible scientific workflows

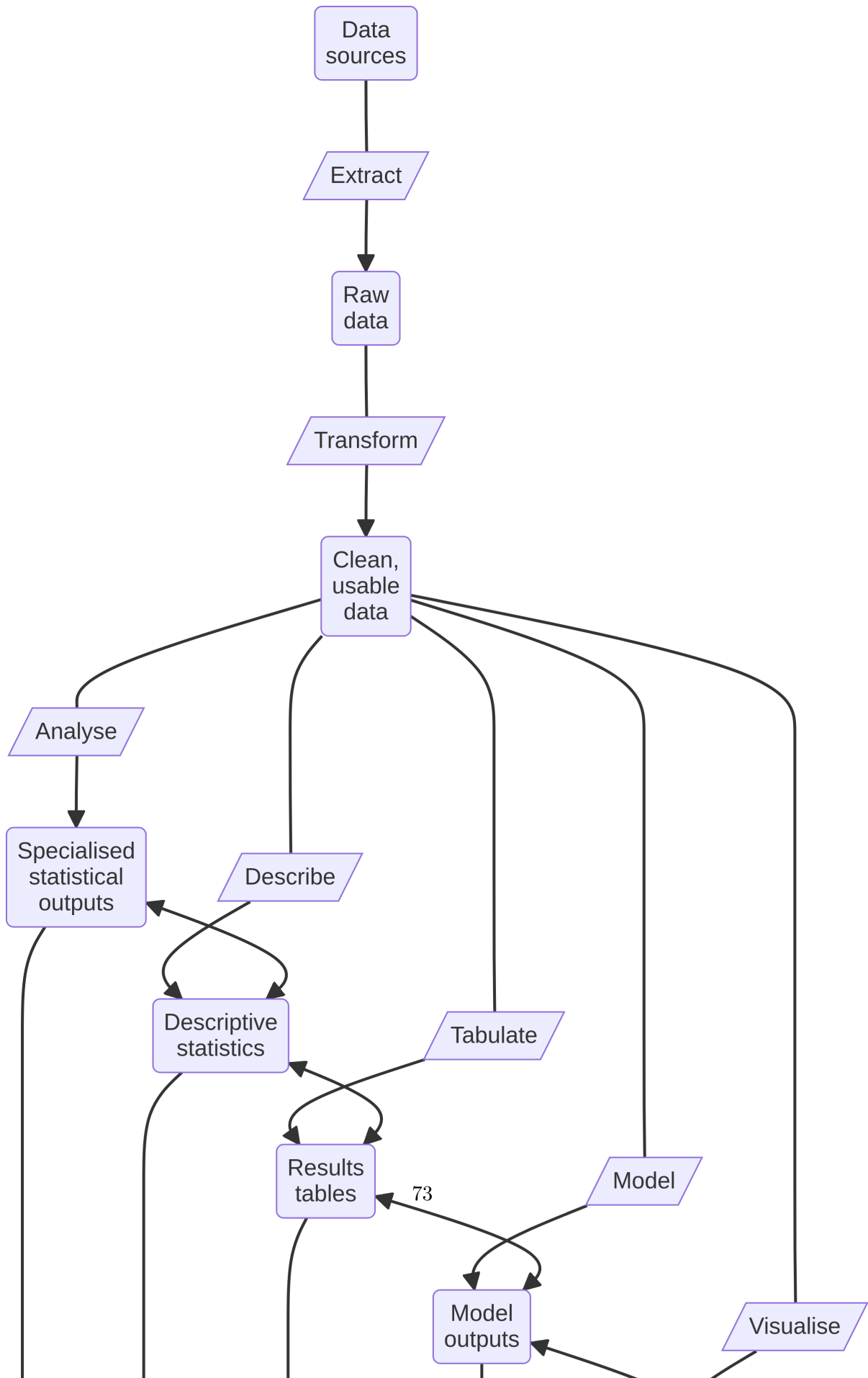
At this point, you would have written your own R code and R scripts and saved these within an R file (.R file extension).

By now, you would have also appreciated how extensible R is through built-in packages and/or through functions that you have created yourself.

So far, in the examples that we have worked on, the operations and the problems have been quite straightforward. But from your own experience dealing with your own data, real world data is far from straightforward and far from simple. Complexity is almost always a given.

R's scripting capability and R's extensibility are its main characteristics that make R a good tool for creating robust scientific workflows particularly for complex data and research projects.

A typical scientific workflow would have the following steps:



A flowchart for an example scientific workflow

In general, an R script should reflect the different steps outlined above. Hence, an R script of a scientific workflow would tend to look like this:

```
## Load libraries

## Retrieve and read data

## Process data

## Analyse data

### Descriptive analysis

### Statistical tests

### Model specifications

## Outputs

### Tabulation of results

### Model outputs

### Plots

## Report
```

In this chapter, we will go through a step-by-step walkthrough of how to build a robust scientific workflow in R. A robust workflow is one that is *portable* i.e., not dependent on hardware and software and instead can be run on almost any machine with very minimal, if any, additional setup or configuration required, and one that is *reproducible* i.e., can be run over and over again without issues, providing the expected results with the same data or providing updated results with new and/or updated data.

10.1 Create a new RStudio project

The steps here are a summary of what is found in [Section 9.1](#).

Tip

- Open RStudio
- Click on the **File** option in the RStudio menu. In the dropdown menu, select **New Project**
- In the menu window, select **New directory** option.
- In the next menu window, select **New project** option.
- In the next menu window, enter the following details:
 - Name of the project - important to make the project name as short as possible but descriptive of the project you are creating; don't use spaces, instead use dash (or underscore) and avoid using capital letters;
 - Select the directory in your computer in which you want to save the project in. Click on **Browse** to open your computers file manager and navigate to the directory you want to save your project in;
 - Tick the selection box to make this project a git repository (whilst this is not necessary, this is highly recommended especially if you are collaborating with others);
 - Tick the selection box to enable **renv** in this project (this is what mainly contribute to the portability of your project); and,
 - Click on **Create project**

10.2 Create an R file for package dependencies

It is best practice to create a standalone R file specific for invoking/calling on R package dependencies. I recommend calling this file `packages.R` and this file should be saved in the root directory of the project you just created.

These are steps on how you can create this file.

💡 Tip

Steps for creating an R package dependencies file:

- Click on the **File** option in the RStudio menu. In the dropdown menu, select **New File** and then in the next dropdown menu, select **R script**.
- A new tab will open in your text editor pane of RStudio (upper left pane) with the name *Untitled1*. Save this file by clicking on the disk icon on the text editor menu or do a keyboard shortcut with **CTRL + s**. Give this empty R script the filename `packages.R`.
- You should now see a file in the main directory/root directory of your project named `packages.R`
- Add code in the `packages.R` file specifying the packages you will be using in this project. There will be standard packages that we will always use with this type of workflow. So a template/generic `packages.R` file will contain the following:

```
#####  
#  
#'  
# ' General packages needed for a targets workflow  
#'  
#  
#####  
  
library(targets)  
library(tarchetypes)  
library(here)  
library(rmarkdown)  
library(knitr)  
library(kableExtra)  
library(dplyr)  
library(openxlsx)  
library(ggplot2)  
  
#####  
#  
#'  
# ' Add other packages that will be used in the project below  
#'
```

```
#  
#####
```

10.3 Create placeholder directories

Create placeholder directories for different components of the workflow. These placeholder directories will provide an organising structure to the project and remind you of where to save/store specific files and outputs.

Tip

Following are steps on how to create placeholder directories:

- In the lower right pane of RStudio (the file manager pane), find the menu button labelled ***Folder***.
- Give this new folder the label of ***R***. This folder will hold all bespoke functions that we will create to use for this project workflow;
- Repeat these steps to create new folders with the following labels:
 - ***data*** - This folder will hold any data that we retrieve as part of this workflow.
 - ***outputs*** - This folder will hold all our workflow outputs such as plots/figures, tables (in Excel or CSV files), HTML and/or Word and/or PDF outputs
 - ***reports*** - This folder will hold all our RMarkdown report (***.Rmd***) files
 - ***docs*** - This folder will hold any of our deployed outputs such as HTML report, dashboard, etc.

These are placeholder directories which we will populate as we work through the workflow for this project.

10.4 Create the target script file

The next task is to create a `{targets}` script file (`_targets.R`) which is the file that will define the workflow that we will be creating.

Tip

The `_targets.R` script file can be created through these steps:

- Clicking on **File** → **New File** → **R Script** in RStudio.
- A new tab will show in your Source window on the top left quadrant of your RStudio screen. This tab will usually be called `Untitled1`.
- Save this file first and change its name to `_targets.R`. Make sure to save it in the current project directory.
- You know that you were successful in doing this once you see a file called `_targets.R` in the file system window in the lower right quadrant of your RStudio screen.

10.5 Edit the targets script file

Now, the next step is to edit your script file by adding sets of R code that does the following:

- Loads the packages required
- Loads custom functions (if any)
- Defines individual targets using `tar_targets` function
- Ends with a list of targets objects

A basic `{targets}` workflow will look like this:

```
## Load libraries -----  
library(targets)  
  
  
## Load custom functions -----  
for (f in list.files("R", full.names = TRUE)) source (f)  
for (f in list.files(here::here("R"), full.names = TRUE)) source (f)  
  
  
## Create targets and list targets objects -----
```

11 Contributing to Oxford IHTM CodeHub projects

This section would be relevant to you if:

1. You have completed the **Open and Reproducible Science in R** sub-module of the MSc for International Health and Tropical Medicine; or,
2. If you are an MSc for International Health and Tropical Medicine alumni and have experience and knowledge using R.

The Oxford IHTM CodeHub actively runs projects focused on either research software development (based in R) or R-based scientific research workflows. Our list of previous and current projects can be found [here](#).

11.1 Research software development

Oxford IHTM CodeHub develops research software using the R package system. Our collection of research software tools are found [here](#) and the underlying code is available from our [organisational GitHub](#).

If you would like to contribute to Oxford IHTM CodeHub's software development, following is a list of steps on how to.

11.1.1 Get familiar with R's package writing process

We build our research software tools using R. Hence, we use the R package writing process. This is described in the official [R manual for writing extensions](#). This manual is the official reference for what is considered acceptable R software development by the R Core Team and are the guides that will ensure that your R package can pass submission and entry into the Comprehensive R Archive Network (CRAN). So, from an academic perspective, you can see this as the official guide of a publisher/publication on what your manuscript should look like so you can submit to their journal for publication. It is not a guarantee of publication, but that you are meeting their publication standards.

However, the R manual for writing extensions is not as easy to navigate and not as easy to read. For beginners, we would recommend starting off with Hadley Wickham's online book called [R Packages](#). The book is free to use online and has clearly delineated chapters and sections for specific R package writing tasks required. We would expect anyone wanting to contribute to the CodeHub's software development projects to have been able to go through this book.

11.1.2 Get familiar and reach intermediate level git and GitHub skills

Our software development process uses git and GitHub to facilitate code sharing and versioning. It is paramount that anyone wanting to contribute to any software project should have at least intermediate level git and GitHub skills. These include:

- Competent in cloning and/or forking software project repositories;
- Competent in the branching process of git and GitHub;
- Competent in the pull request process of GitHub;
- Competent in GitHub's issues tracker and project tracker system;
- Competent in code review process of GitHub.

If you want to brush up on your git and GitHub, please go through Jenny Bryan's [Happy Git and GitHub for the useR](#).

11.1.3 Review our portfolio of research software

Visit the project page of the Oxford IHTM CodeHub website - <https://oxford-ihtm.io/projects/> to see our current line-up of CodeHub software projects.

Have a look at our R Universe of research software - <https://oxfordihtm.r-universe.dev> - for the build status of each project.

Have a look at our GitHub organisation - <https://github.com/OxfordIHM> - to see the code for each of these projects.

Each project is in continuous development. We recommend looking at the repository for each of the projects, understand via the README what the project is trying to achieve and then review each projects issues page to see what the current line up of tasks or issues that the development requires. If for some reason there is no issues listed in a project, this is most likely that current developers have not gotten around to documenting their tasks/issues at hand. If so, you can make an issue to ask developers what the best task is to do for a beginner to contribute to.

11.1.4 Communicate with developers

Once you have found a project and an issue that you want to work on, make a comment on that issue making sure to tag the developer/maintainer stating that you are going to have a go at this issue and then will make a pull request of your contribution.

This communication is important as this will trigger the developer/maintainer to confirm that you are an eligible member of the CodeHub (the pre-requisites above) and then will add you as a collaborator on the project. This step is important because your status in the project as a collaborator will determine your next step on contributing. We prefer that CodeHub members are internal collaborators as this simplifies their participation (see next section).

11.1.5 Clone or fork the project repository

Once you have been added to the project repository as a collaborator, you can now `clone` the repository to your local machine and then start making your contribution.

If for some reason you haven't been added to the project repository as a collaborator yet but you are itching to contribute, you can still start contributing but instead of cloning, you will need to `fork` the repository. This is similar to cloning but your `fork` is identified as being from someone outside the organisation. This means you will need to make your own GitHub repository under your own username of the project as a fork of the original, write your code contribution and commit to your repository and then make a pull request to the original repository.

These forking steps are described in all the CONTRIBUTING notes/guidance in each project as we open contributions from anyone (not just CodeHub members) but not all are eligible to be internal collaborators.

We would like to avoid this for eligible members of CodeHub so will endeavour to keep up with collaborator requests. So, if you are impatient and would really like to contribute already, consider forking but be warned that this has a lot more complicated steps than simple cloning. Either follow-up your request to be made a collaborator.

References

Jenny Bryan, and Jim Hester. n.d. *Happy Git and GitHub for the useR*. Accessed September 3, 2024. <https://happygitwithr.com/>.