

# R and RStudio

## R Statistical Computing & Graphics

- Free open source software
- Available for Windows, Mac and Linux/Unix operating systems
- Large community of developers
- Many packages/libraries
  - CRAN repository
  - Bioconductor repository

## Download and Install

Download the latest stable release of R from <https://www.r-project.org>, latest version is 4.2.3

## RStudio

- Integrated development environment (IDE)
  - R
  - Python
- Console for running code
- Code editor with syntax colouring



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# The R Project for Statistical Computing

## Getting Started

R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS. To [download R](#), please choose your preferred [CRAN mirror](#).

If you have questions about R like how to download and install the software, or what the license terms are, please read our [answers to frequently asked questions](#) before you send an email.

## News

- **R version 4.3.0 (Already Tomorrow) prerelease versions** will appear starting Tuesday 2023-03-21. Final release is scheduled for Friday 2023-04-21.
- **R version 4.2.3 (Shortstop Beagle)** has been released on 2023-03-15.
- **R version 4.1.3 (One Push-Up)** was released on 2022-03-10.
- Thanks to the organisers of useR! 2020 for a successful online conference. Recorded tutorials and talks from the conference are available on the [R Consortium YouTube channel](#).

## Index of /src/base/R-4

<a href="#">Name</a>	<a href="#">Last modified</a>	<a href="#">Size</a>	<a href="#">Description</a>
<a href="#">Parent Directory</a>	-		
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<a href="#">R-4.0.1.tar.gz</a>	2020-06-06 09:05	32M	
<a href="#">R-4.0.2.tar.gz</a>	2020-06-22 09:05	32M	
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<a href="#">R-4.2.3.tar.gz</a>	2023-03-15 09:06	32M	

Apache Server at cran.r-project.org Port 443

- Workspace/file management
- Records history of commands

## RStudio

Download from <https://posit.co/download/rstudio-desktop/>

# RStudio Desktop

Used by millions of people weekly, the RStudio integrated development environment (IDE) is a set of tools built to help you be more productive with R and Python.

## 1: Install R

RStudio requires R 3.3.0+. Choose a version of R that matches your computer's operating system.

DOWNLOAD AND INSTALL R

- This page should detect your operating system
- Download RStudio
- Click on the install package
- Follow install instructions

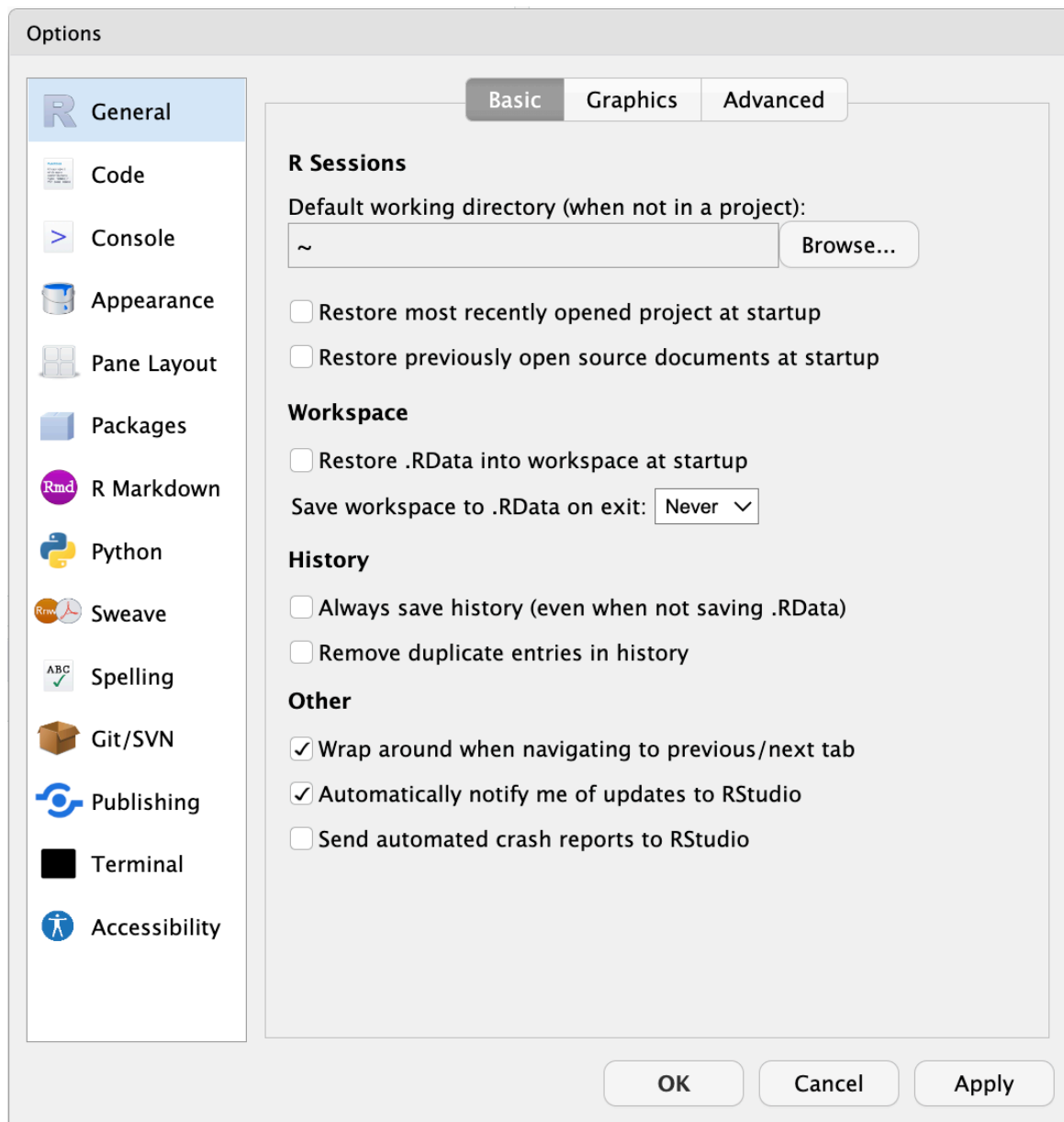
## 2: Install RStudio

DOWNLOAD RSTUDIO DESKTOP FOR MACOS 11+

This version of RStudio is only supported on macOS 11 and higher. For earlier macOS environments, please [download a previous version](#).

## RStudio

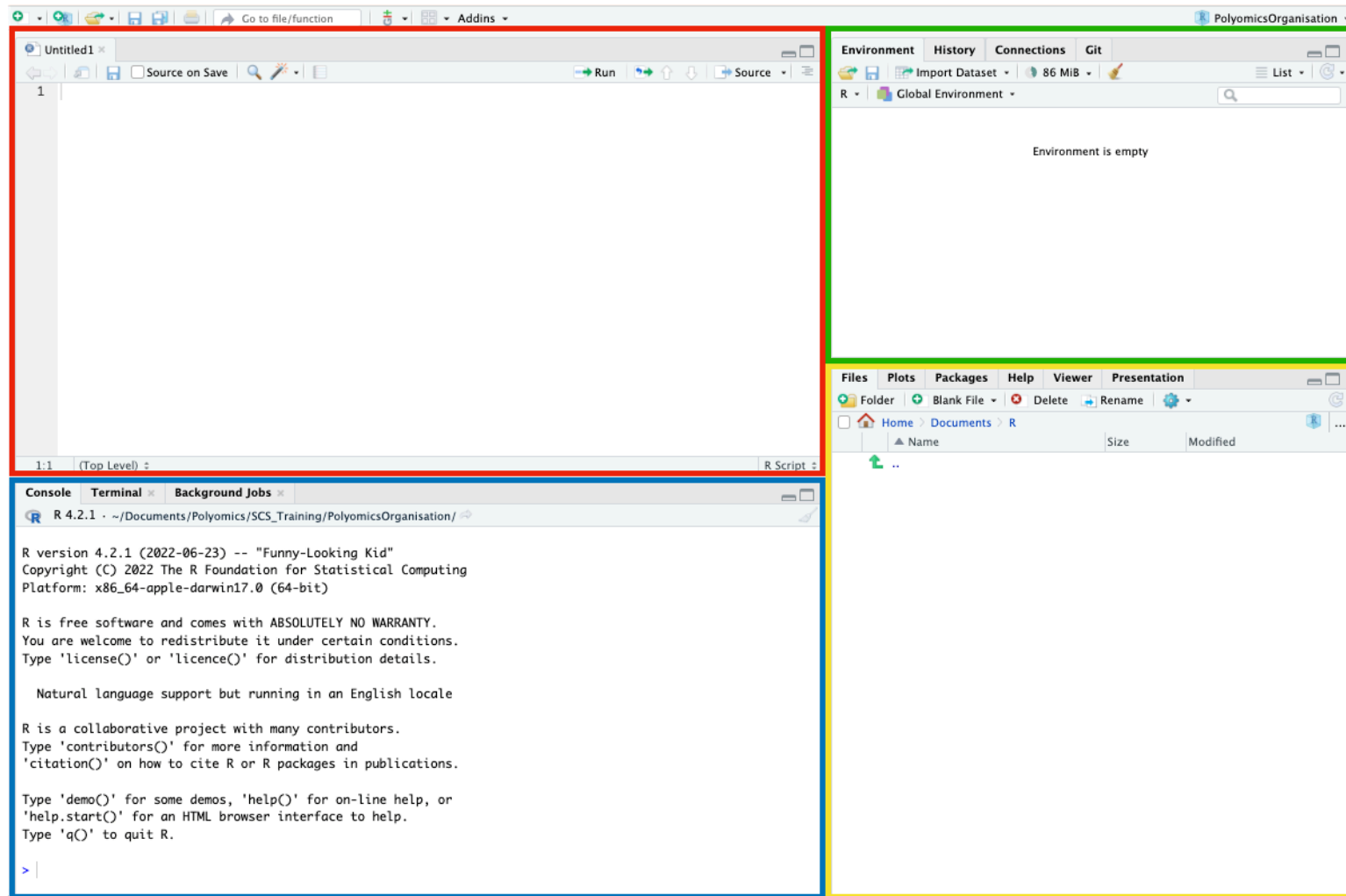
Set up Rstudio - Set options in **Tools** and **Global Options...**



- Uncheck the boxes as shown in the example
- Ensure that *Save workspace to .RData on exit* is set to **Never**

YouTube video on installing and setting up RStudio <https://www.youtube.com/watch?v=D6CunpqF04E>

# RStudio



- Source pane
  - Write R commands as R scripts or Notebooks

- Console Pane
  - Where the R commands are executed
- Environment pane
  - Details of the R variables
- Files pane
  - View the directory and file structure

## **RStudio Libraries**

R packages or libraries are extensions to the R language.

R packages contain:

- Code
- Data
- Documentation

The packages are in a standardised format and can be installed from repositories

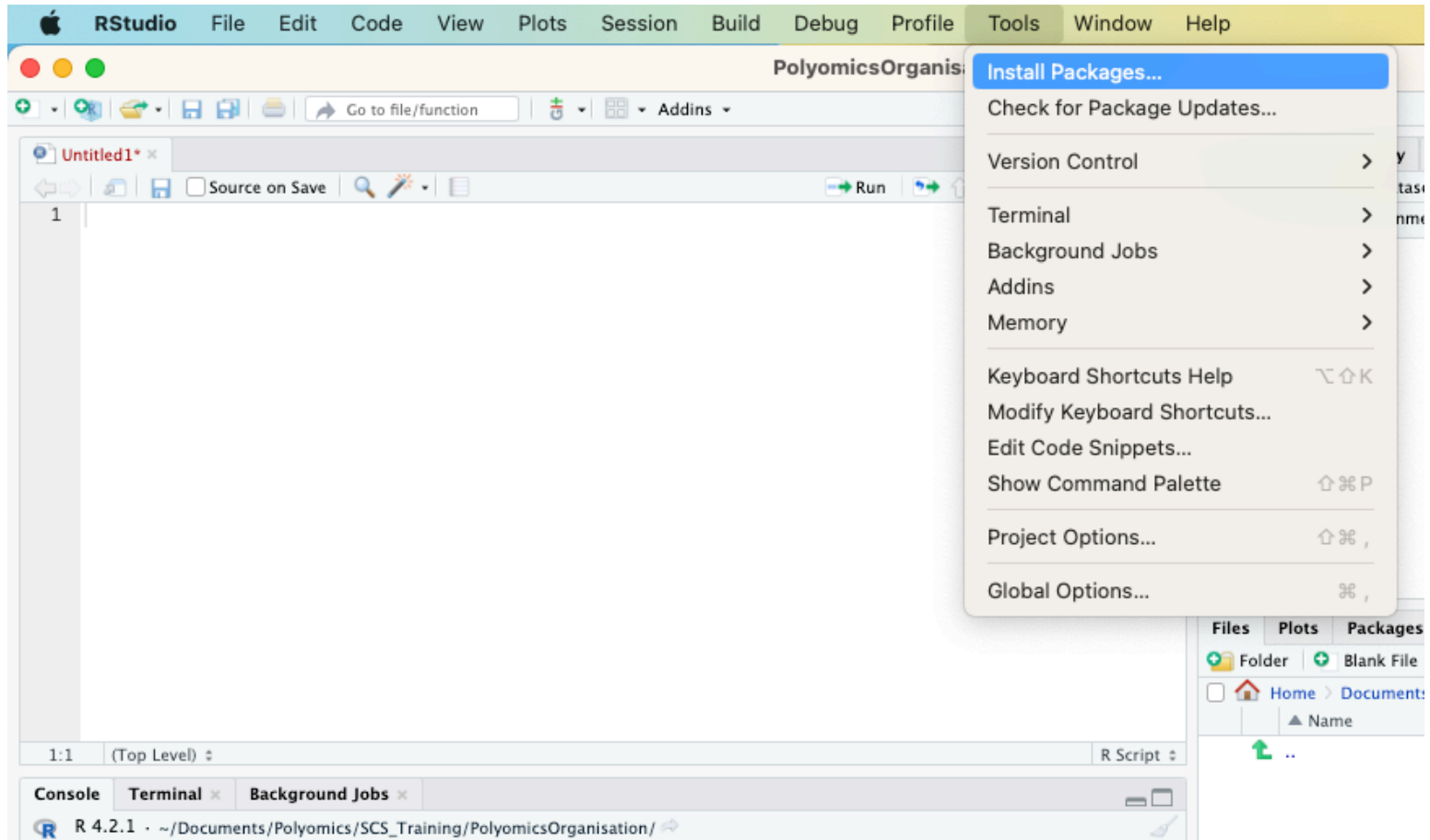
## **R Repositories**

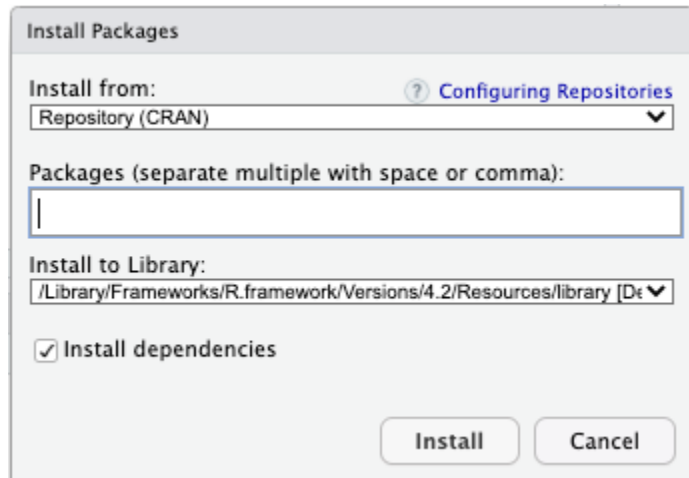
- Comprehensive R Archive Network (CRAN)
  - Main software repository, supported by the R Foundation
- Bioconductor
  - R packages for the analysis of biological data
- GitHub
  - Alternative repository for R packages, often in active development



## Installing Libraries

### RStudio





## Installing Packages

### Terminal

From CRAN using the R command `install.packages`

```
install.packages("tidyverse")
```

From Bioconductor First need to install a package manager program

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

Then can install specific packages

```
BiocManager::install(c("GenomicFeatures", "AnnotationDbi"))
```

## Installing Packages

### Terminal

From GitHub First need to install devtools from CRAN

```
install.packages("devtools")  
require("devtools")
```

Then can install GitHub packages. Github packages are usually named after the repository name then the package name  
e.g. grahamhamilton/Rpackage

```
install_github("GitHubPackage")
```

## Installing Packages

Now install these packages

- CRAN
  - tidyverse
  - devtools

## Loading Packages

Packages have to be loaded prior to use. There are two ways to load packages in R.

- `library()`
  - `library()` will output an error and stop the execution of the code