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The Comprehensive R Archive Network

Download and Install R

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

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

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

Source Code for all Platforms

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

- The latest release (2025-04-11, How About a Twenty-Six) [R-4.5.0 tar.gz](#), read [what's new](#) in the latest version.
- The CRAN directory [src/base-prerelease](#) contains R alpha, beta, and rc releases as daily snapshots in time periods before a planned release.
- Between releases, the same directory [src/base-prerelease](#) contains snapshots of current patched and development versions. Please read about [new features and bug fixes](#) before filing corresponding feature requests or bug reports.
- Alternatively, daily snapshots are [available here](#).
- Source code of older versions of R is [available here](#).
- Contributed extension [packages](#).

Questions About R

- 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.

Supporting CRAN

- CRAN operations, most importantly hosting, checking, distributing, and archiving of R add-on packages for various platforms, crucially rely on technical, emotional, and financial support by the R community.

Please consider making [financial contributions](#) to the R Foundation for Statistical Computing.

What are R and CRAN?

R is 'GNU S', a freely available language and environment for statistical computing and graphics which provides a wide variety of statistical and graphical techniques: linear and nonlinear modelling, statistical tests, time series analysis, classification, clustering, etc. Please consult the [R project homepage](#) for further information.

CRAN is a network of ftp and web servers around the world that store identical, up-to-date, versions of code and documentation for R. Please use the CRAN [mirror](#) nearest to you to minimize network load.

Submitting to CRAN

To "submit" a package to CRAN, check that your submission meets the [CRAN Repository Policy](#) and then use the [web form](#).


If this fails, send an email to CRAN-submissions@R-project.org following the policy. Please do not attach submissions to emails, because this will clutter up the mailboxes of half a dozen people.

Note that we generally do not accept submissions of precompiled binaries due to security reasons. All binary distribution listed above are compiled by selected maintainers, who are in charge for all binaries of their platform, respectively.

For queries about this web site, please contact [the webmaster](#).

This server is hosted by the [Institute for Statistics and Mathematics](#) of [WU \(Wirtschaftsuniversität Wien\)](#).

Download and install R from <https://cran.r-project.org/index.html>



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R for Windows

Subdirectories:

base	Binaries for base distribution. This is what you want to install R for the first time .
contrib	Binaries of contributed CRAN packages (for R \geq 4.0.x).
old-contrib	Binaries of contributed CRAN packages for outdated versions of R (for R $<$ 4.0.x).
Rtools	Tools to build R and R packages. This is what you want to build your own packages on Windows, or to build R itself.

Please do not submit binaries to CRAN. Package developers might want to contact Uwe Ligges directly in case of questions / suggestions related to Windows binaries.

You may also want to read the [R FAQ](#) and [R for Windows FAQ](#).

Note: CRAN does some checks on these binaries for viruses, but cannot give guarantees. Use the normal precautions with downloaded executables.

We need both „base“ and „Rtools“

RStudio Desktop - Posit

posit.co/download/rstudio-desktop/

GitHubFH Proteomics GitHubRust Programming La...Rust BookYouTubenfcorn: maseqnfcorn: scrnaseqnfcorn: scdownstream

POSIT

PRODUCTSOPEN SOURCEUSE CASESPARTNERSLEARN & SUPPORTABOUT

DOWNLOAD

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.

Don't want to download or install anything? Get started with RStudio on [Posit Cloud for free](#). If you're a professional data scientist looking to download RStudio and also need common enterprise features, don't hesitate to [book a call with us](#).

Want to learn about core or advanced workflows in RStudio? Explore the [RStudio User Guide](#) or the [Getting Started](#) section.

1: Install R

RStudio requires R 3.6.0+. Choose a version of R that matches your computer's operating system.

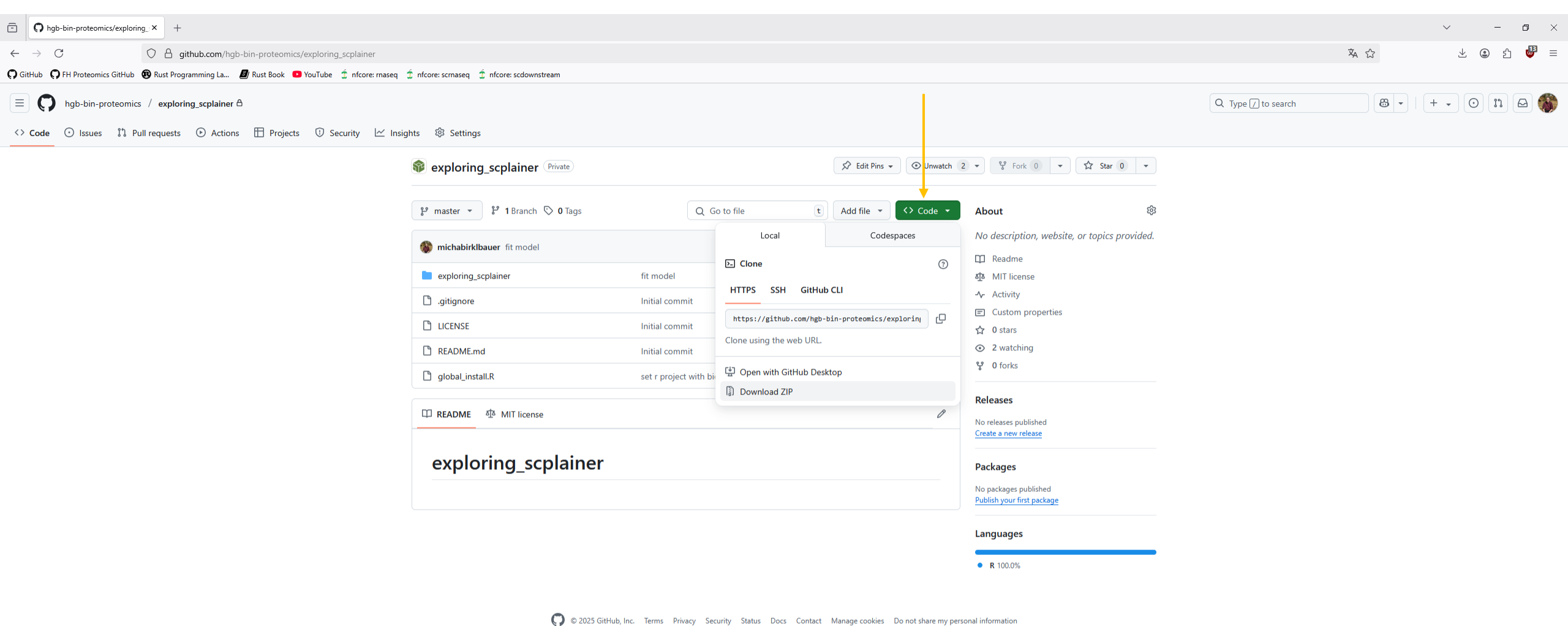
R is not a Posit product. By clicking on the link below to download and install R, you are leaving the Posit website. Posit disclaims any obligations and all liability with respect to R and the R website.

DOWNLOAD AND INSTALL R

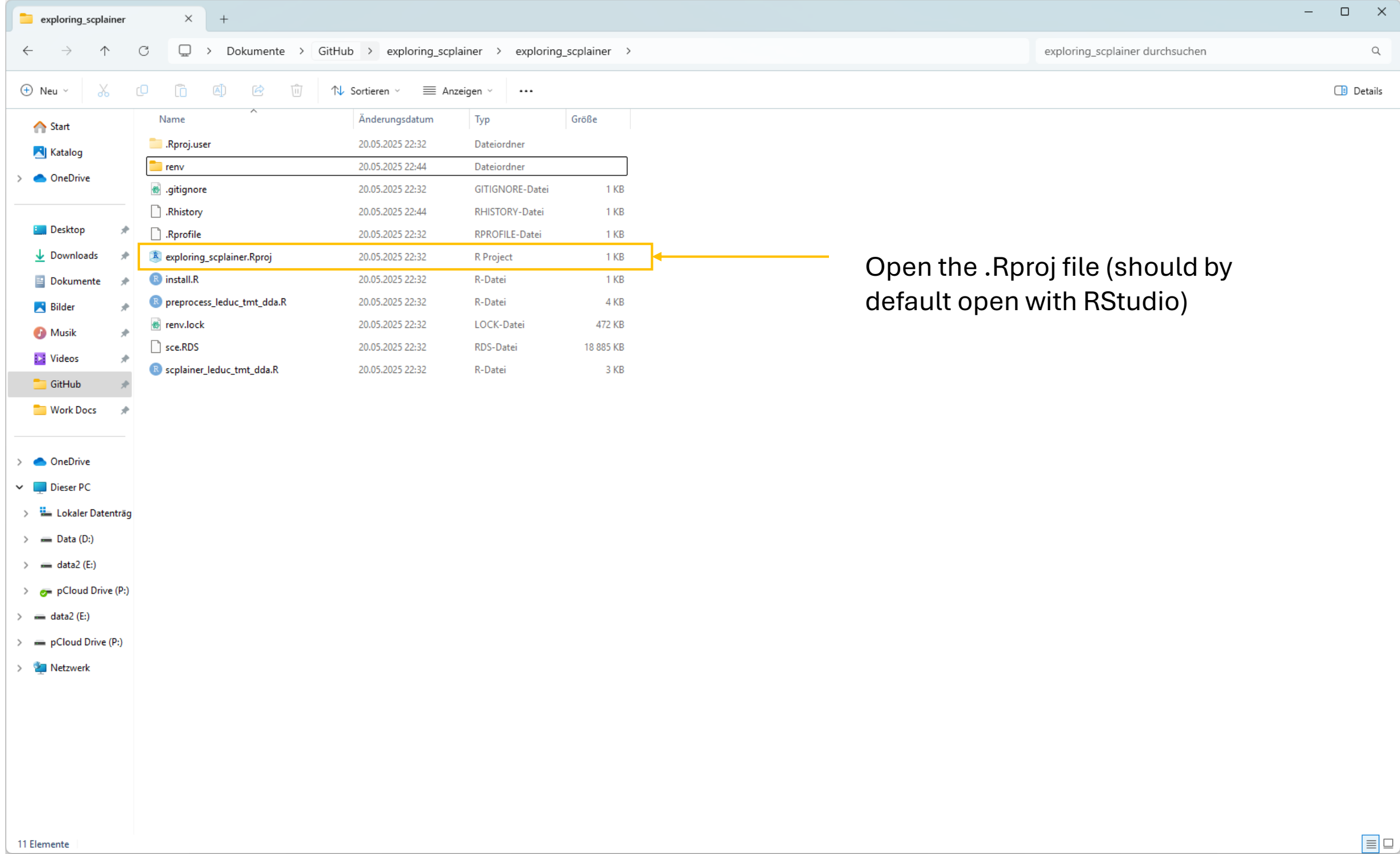
2: Install RStudio

DOWNLOAD RSTUDIO DESKTOP FOR WINDOWS

Size: 281.27 MB | [SHA-256: 9E6F68CA](#) | Version: 2025.05.0+496 | Released: 2025-05-05



Download the project from https://github.com/hgb-bin-proteomics/exploring_scplainer



exploring_scplainer - master - RStudio

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Go to file/function

Addins

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R 4.5.0 · ~/GitHub/exploring_scplainer/exploring_scplainer/

R version 4.5.0 (2025-04-11 ucrt) -- "How About a Twenty-six"
Copyright (C) 2025 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64

R ist freie Software und kommt OHNE JEGLICHE GARANTIE.
Sie sind eingeladen, es unter bestimmten Bedingungen weiter zu verbreiten.
Tippen Sie 'license()' or 'licence()' für Details dazu.

R ist ein Gemeinschaftsprojekt mit vielen Beitragenden.
Tippen Sie 'contributors()' für mehr Information und 'citation()',
um zu erfahren, wie R oder R packages in Publikationen zitiert werden können.

Tippen Sie 'demo()' für einige Demos, 'help()' für on-line Hilfe, oder
'help.start()' für eine HTML Browserschnittstelle zur Hilfe.
Tippen Sie 'q()', um R zu verlassen.

Bootstrapping renv 1.1.4 -----
- Downloading renv ... OK
- Installing renv ... OK

- Project '~/GitHub/exploring_scplainer/exploring_scplainer' loaded. [renv 1.1.4]
- One or more packages recorded in the lockfile are not installed.
- Use 'renv::status()' for more details.
> |

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R · Global Environment ·

Environment is empty

Files Plots Packages Help Viewer Presentation

New Folder New Blank File Delete Rename More

Home > GitHub > exploring_scplainer > exploring_scplainer

	Name	Size	Modified
	..		
<input type="checkbox"/>	.gitignore	16 B	May 20, 2025, 10:32 PM
<input type="checkbox"/>	.Rhistory	234 B	May 20, 2025, 10:44 PM
<input type="checkbox"/>	.Rprofile	27 B	May 20, 2025, 10:32 PM
<input type="checkbox"/>	exploring_scplainer.Rproj	218 B	May 20, 2025, 10:54 PM
<input type="checkbox"/>	install.R	205 B	May 20, 2025, 10:32 PM
<input type="checkbox"/>	preprocess_leduc_tmt_dda.R	3.9 KB	May 20, 2025, 10:32 PM
<input type="checkbox"/>	renv		
<input type="checkbox"/>	renv.lock	471.5 KB	May 20, 2025, 10:32 PM
<input type="checkbox"/>	sce.RDS	18.4 MB	May 20, 2025, 10:32 PM
<input type="checkbox"/>	scplainer_leduc_tmt_dda.R	2.8 KB	May 20, 2025, 10:32 PM

You will see something like this, a notification that not all necessary packages for this project are installed

exploring_scplainer - master - RStudio

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Go to file/function

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R 4.5.0 · ~/GitHub/exploring_scplainer/exploring_scplainer/

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- Use 'renv::status()' for more details.
> |

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Import Dataset 281 MiB

R Global Environment

Environment is empty

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New Folder New Blank File Delete Rename More

Home > GitHub > exploring_scplainer > exploring_scplainer

	Name	Size	Modified
	..		
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<input type="checkbox"/>	.Rhistory	234 B	May 20, 2025, 10:44 PM
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<input type="checkbox"/>	sce.RDS	18.4 MB	May 20, 2025, 10:32 PM
<input type="checkbox"/>	scplainer_leduc_tmt_dda.R	2.8 KB	May 20, 2025, 10:32 PM

Open the
install.R file

exploring_scplainer - master - RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

Go to file/function Addins

install.R

```
1 req <- c(
2   "UCLouvain-CBIO/scp",
3   "UCLouvain-CBIO/scpdata",
4   "ensemldb",
5   "Ensembl.Hsapiens.v86",
6   "bluster",
7   "scater",
8   "tidyverse",
9   "patchwork"
10 )
11 renv::install(req)
12 renv::snapshot()
13
```

Run Source

Click „Source“ to run the file and install packages

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Environment is empty

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New Folder New Blank File Delete Rename More

Home > GitHub > exploring_scplainer > exploring_scplainer

	Name	Size	Modified
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Console Terminal Background Jobs

R 4.5.0 ~/GitHub/exploring_scplainer/exploring_scplainer/

```
R version 4.5.0 (2025-04-11 ucrt) -- "How About a Twenty-six"
Copyright (C) 2025 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64

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Tippen Sie 'q()', um R zu verlassen.

# Bootstrapping renv 1.1.4 -----
- Downloading renv ... OK
- Installing renv ... OK

- Project '~/GitHub/exploring_scplainer/exploring_scplainer' loaded. [renv 1.1.4]
- One or more packages recorded in the lockfile are not installed.
- Use 'renv::status()' for more details.
> |
```


install.R

scplainer_leduc_tmt_dda.R

Run

Source

```
1 library(tidyverse)
2 library(scp)
3 library(scpdata)
4 library(patchwork)
5 library(ensemblDb)
6 library(EnsDb.Hsapiens.v86)
7 library(bluster)
8 library(scater)
9
10 ## we follow the workflow as documented here:
11 ## https://uclouvain-cbio.github.io/SCP.replication/articles/scplainer_leduc2022.html
12
13 # The data here is already preprocessed (see documentation).
14 # This involves:
15 # - Data cleaning
16 #   + Replacing zeros with missing values (NA)
17 # - Feature quality control
18 #   + Remove contaminants
19 #   + Remove decoys
20 #   + Remove psm's with low spectral purity
21 #   + Remove peptides not within the FDR threshold
22 #   + Remove peptides above 5% single cell to carrier ratio
23 # - Sample quality control
24 #   + Remove samples (cells) with low number of peptides
25 #   + Remove samples with low median intensity
26 #   + Remove samples with high median cv
27 #   + (Remove samples we are not interested in, e.g. negative controls, carriers, references, empty wells)
28 # - Peptide data assembly
29 #   + Aggregating psm's to peptides
30 # - Log2-transformation
31
32 sce <- readr::read_rds("sce.RDS")
33
34 ## Data Overview
35
36 # The data set primarily consists of melanoma cells and monocytes.
37 # The data set also contains carrier samples, reference samples and empty wells (Unused).
38 # carrier samples, negative control samples, reference samples and empty wells are already filtered out here, because
39 # the data is preprocessed.
40
41 table(sce$SampleType)
42
43 ## The data were acquired using TMT-18 labelling (and in DDA mode).
```

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req chr [1:8] "UCLouvain-CBio/scp" "UCLouvain-CBio/scpdata" "ensemldb" "EnsDb.Hsapiens.v86..."

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exploring_scplainer

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..

16 B

May 20, 2025, 10:32 PM

.gitignore

303 B

May 20, 2025, 11:01 PM

.Rhistory

27 B

May 20, 2025, 10:32 PM

.Rprofile

218 B

May 20, 2025, 11:03 PM

exploring_scplainer.Rproj

205 B

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preprocess_leduc_tmt_dda.R

471.4 KB

May 20, 2025, 11:05 PM

renv

18.4 MB

May 20, 2025, 10:32 PM

renv.lock

2.8 KB

May 20, 2025, 10:32 PM

sce.RDS

scplainer_leduc_tmt_dda.R

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R 4.5.0

~/GitHub/exploring_scplainer/exploring_scplainer/

- Installing rematch2 ...

OK [installed binary and cached in 0.28s]

- Installing googlesheets4 ...

OK [installed binary and cached in 0.29s]

- Installing hms ...

OK [installed binary and cached in 0.27s]

- Installing clipr ...

OK [installed binary and cached in 0.27s]

- Installing tzdb ...

OK [installed binary and cached in 0.32s]

- Installing prettyunits ...

OK [installed binary and cached in 0.26s]

- Installing progress ...

OK [installed binary and cached in 0.28s]

- Installing vroom ...

OK [installed binary and cached in 0.61s]

- Installing readr ...

OK [installed binary and cached in 0.31s]

- Installing haven ...

OK [installed binary and cached in 0.3s]

- Installing timechange ...

OK [installed binary and cached in 0.28s]

- Installing lubridate ...

OK [installed binary and cached in 0.29s]

- Installing modelr ...

OK [installed binary and cached in 0.27s]

- Installing readxl ...

OK [installed binary and cached in 0.29s]

- Installing ps ...

OK [installed binary and cached in 0.28s]

- Installing processx ...

OK [installed binary and cached in 0.3s]

- Installing callr ...

OK [installed binary and cached in 0.3s]

- Installing rstudioapi ...

OK [installed binary and cached in 0.29s]

- Installing reprex ...

OK [installed binary and cached in 0.29s]

- Installing selectr ...

OK [installed binary and cached in 0.27s]

- Installing xml2 ...

OK [installed binary and cached in 0.3s]

- Installing rvest ...

OK [installed binary and cached in 0.29s]

- Installing tidyverse ...

OK [installed binary and cached in 0.28s]

- Installing patchwork ...

OK [installed binary and cached in 0.3s]

Successfully installed 202 packages in 1.1 minutes.

The following package(s) will be updated in the lockfile:

CRAN

- lattice [0.22-7 -> 0.22-6]

- mgcv [1.9-3 -> 1.9-1]

If everything worked correctly, you should see an output like this

exploring_scplainer - RStudio

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Go to file/function

Addins

install.R x scplainer_leduc_tmt_dda.R x

Source on Save

Run

Source

```
1 library(tidyverse)
2 library(scp)
3 library(scpdata)
4 library(patchwork)
5 library(ensemldb)
6 library(EnsDb.Hsapiens.v86)
7 library(bluster)
8 library(scater)
9
10 ## we follow the workflow as documented here:
11 ## https://uclouvain-cbio.github.io/SCP.replication/articles/scplainer_leduc2022.html
12
13 # The data here is already preprocessed (see documentation).
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44
```

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Name

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Modified

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.gitignore 16 B May 20, 2025, 10:32 PM

.Rhistory 303 B May 20, 2025, 11:01 PM

.Rprofile 27 B May 20, 2025, 10:32 PM

exploring_scplainer.Rproj 218 B May 20, 2025, 11:03 PM

install.R 205 B May 20, 2025, 10:32 PM

preprocess_leduc_tmt_dda.R 3.9 KB May 20, 2025, 10:32 PM

renv 471.4 KB May 20, 2025, 11:05 PM

renv.lock 18.4 MB May 20, 2025, 10:32 PM

sce.RDS 2.8 KB May 20, 2025, 10:32 PM

scplainer_leduc_tmt_dda.R

Console

Terminal

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R 4.5.0 - ~/GitHub/exploring_scplainer/exploring_scplainer/

> library(ensemldb)

Lade nötiges Paket: GenomicFeatures

Lade nötiges Paket: AnnotationDbi

Attache Paket: 'AnnotationDbi'

Das folgende Objekt ist maskiert 'package:dplyr':

select

Lade nötiges Paket: AnnotationFilter

Attache Paket: 'ensemldb'

Das folgende Objekt ist maskiert 'package:dplyr':

filter

Das folgende Objekt ist maskiert 'package:stats':

filter

> library(EnsDb.Hsapiens.v86)

> library(bluster)

> library(scater)

Lade nötiges Paket: SingleCellExperiment

Lade nötiges Paket: scuttle

> |

You should also be able to load all the packages in the „scplainer_leduc_tmt_dda.R“ file