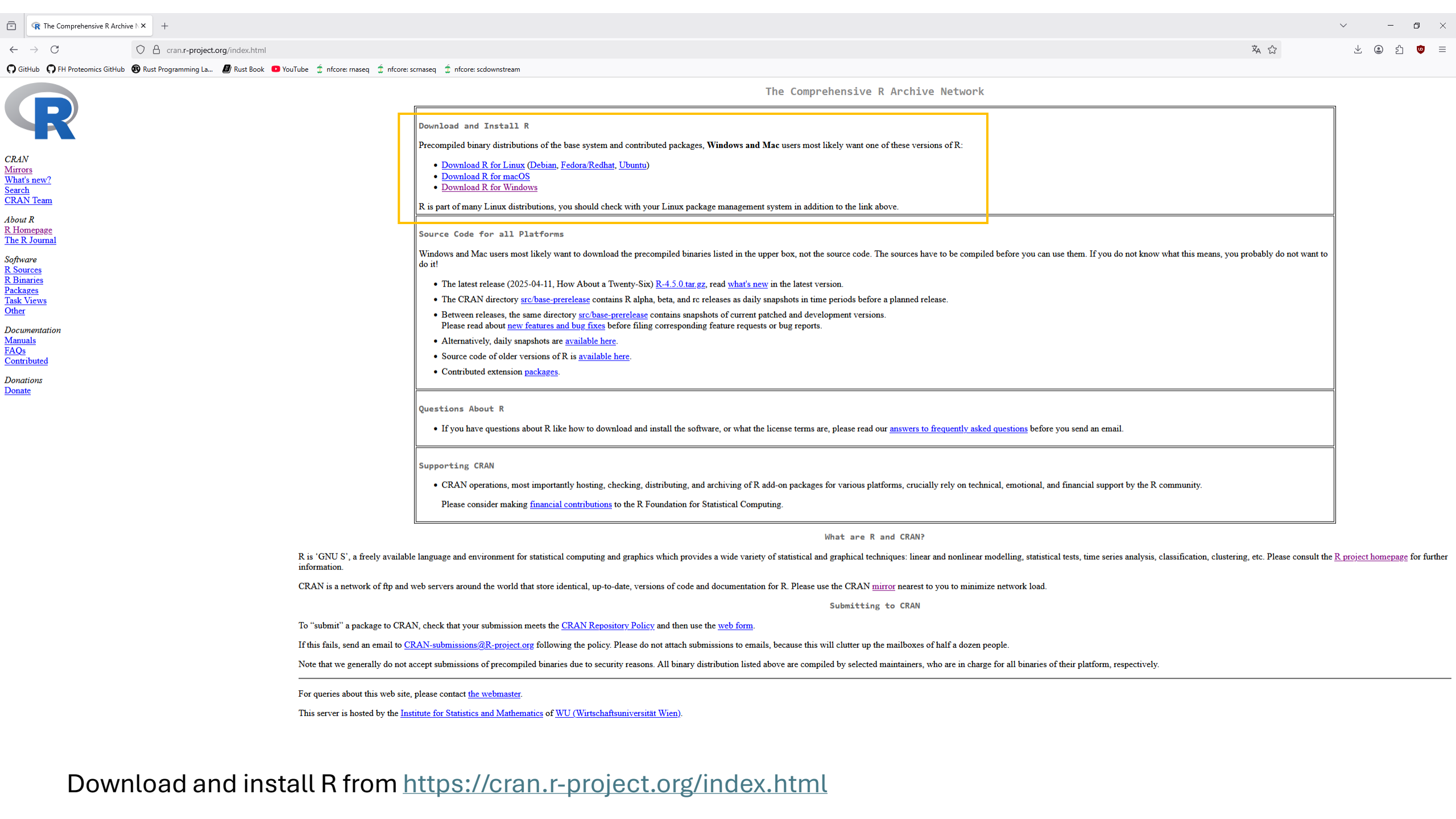
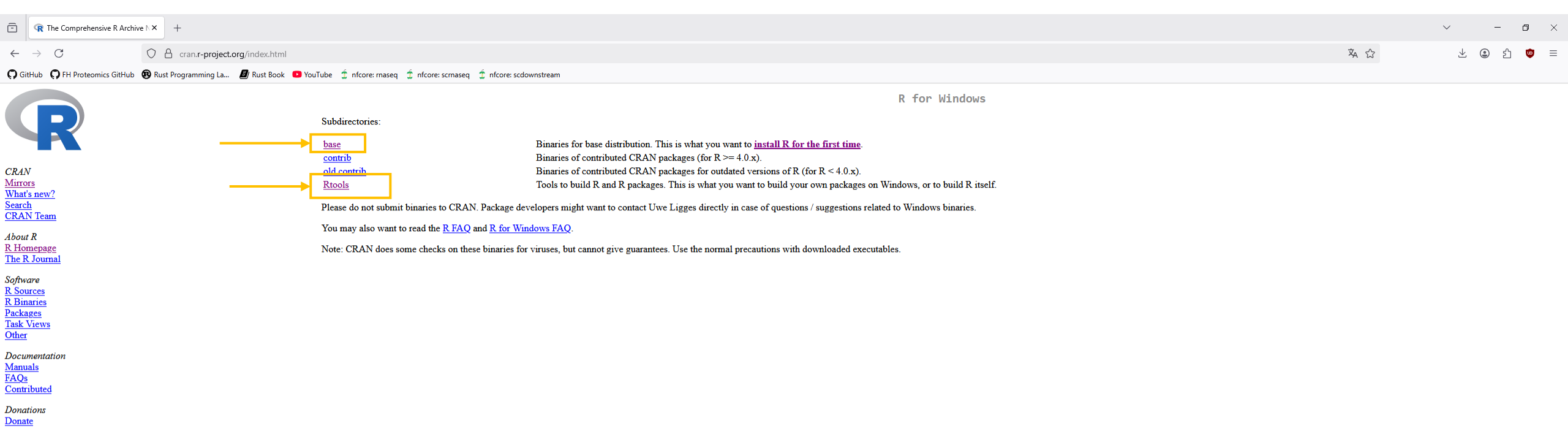


Download and install R from https://cran.r-project.org/index.html



We need both „base“ and „Rtools“

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.

Download and install Rstudio from https://posit.co/download/rstudio-desktop/

1: Install R

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

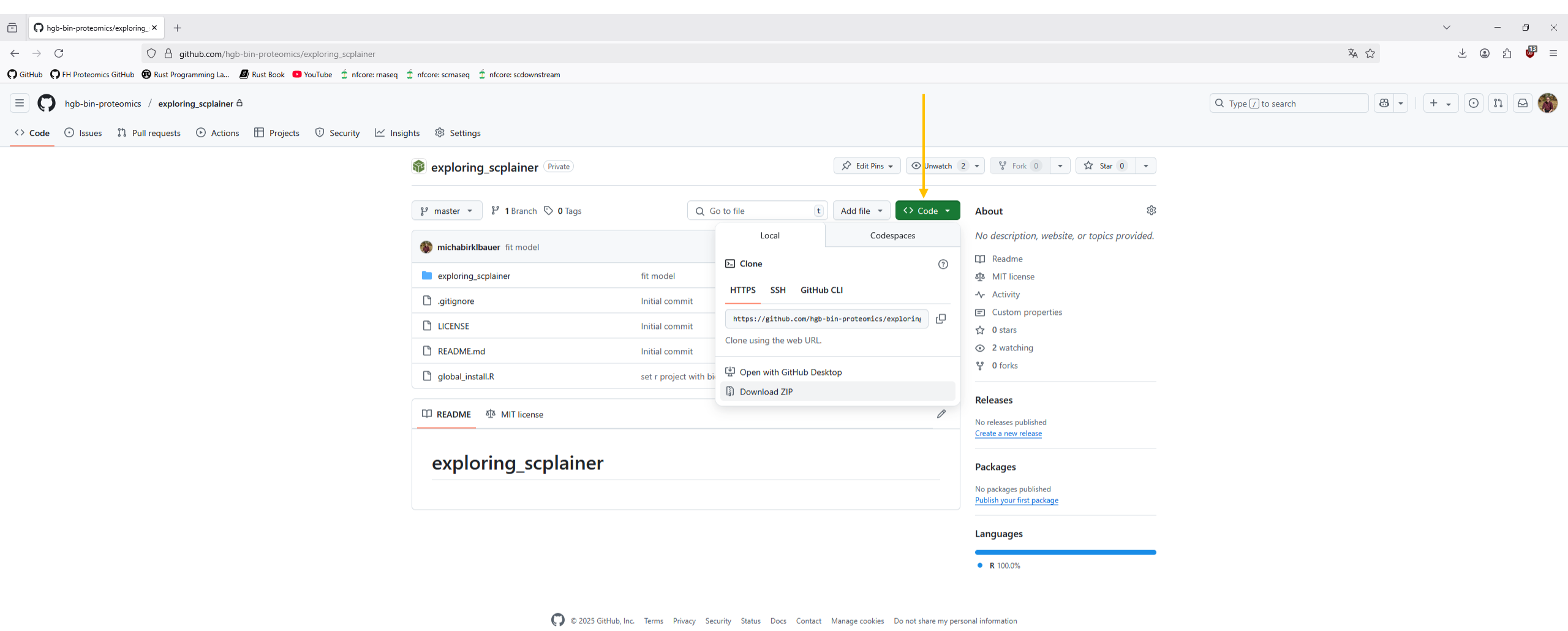
R is not a Posit product. By clicking on the link below to download and install R, you are leaving the Posit website. Posit disclaims any obligations and all liability with respect to R and the R website.

DOWNLOAD AND INSTALL R

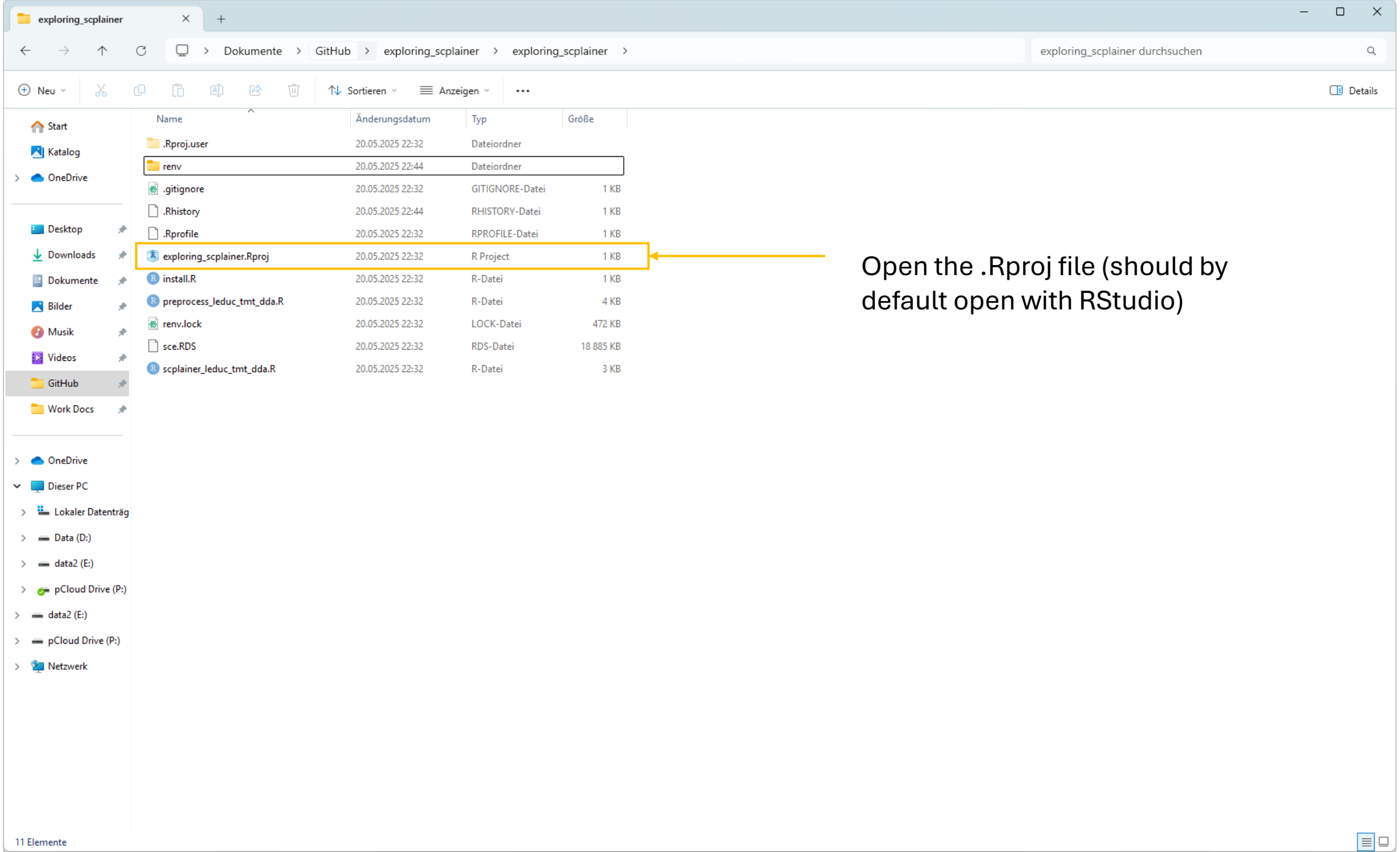
2: Install RStudio

DOWNLOAD RSTUDIO DESKTOP FOR WINDOWS

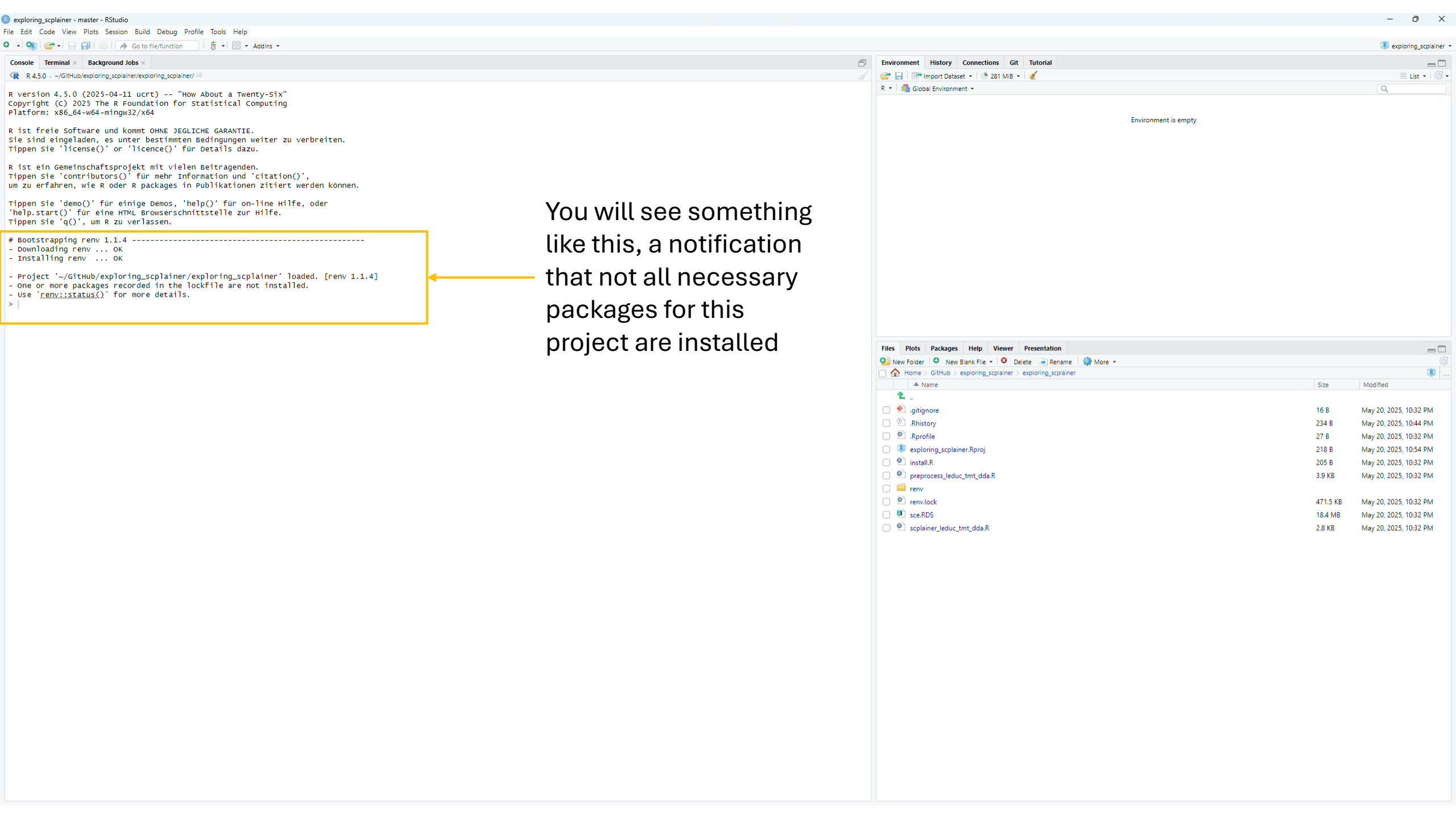
Size: 281.27 MB | SHA-256: 9E6F68CA | Version: 2025.05.0+496 | Released: 2025-05-05



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



Open the .Rproj file (should by default open with RStudio)


exploring_scplainer - master - RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function
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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
R ist freie Software und kommt OHNE JEGLICHE GARANTIE.
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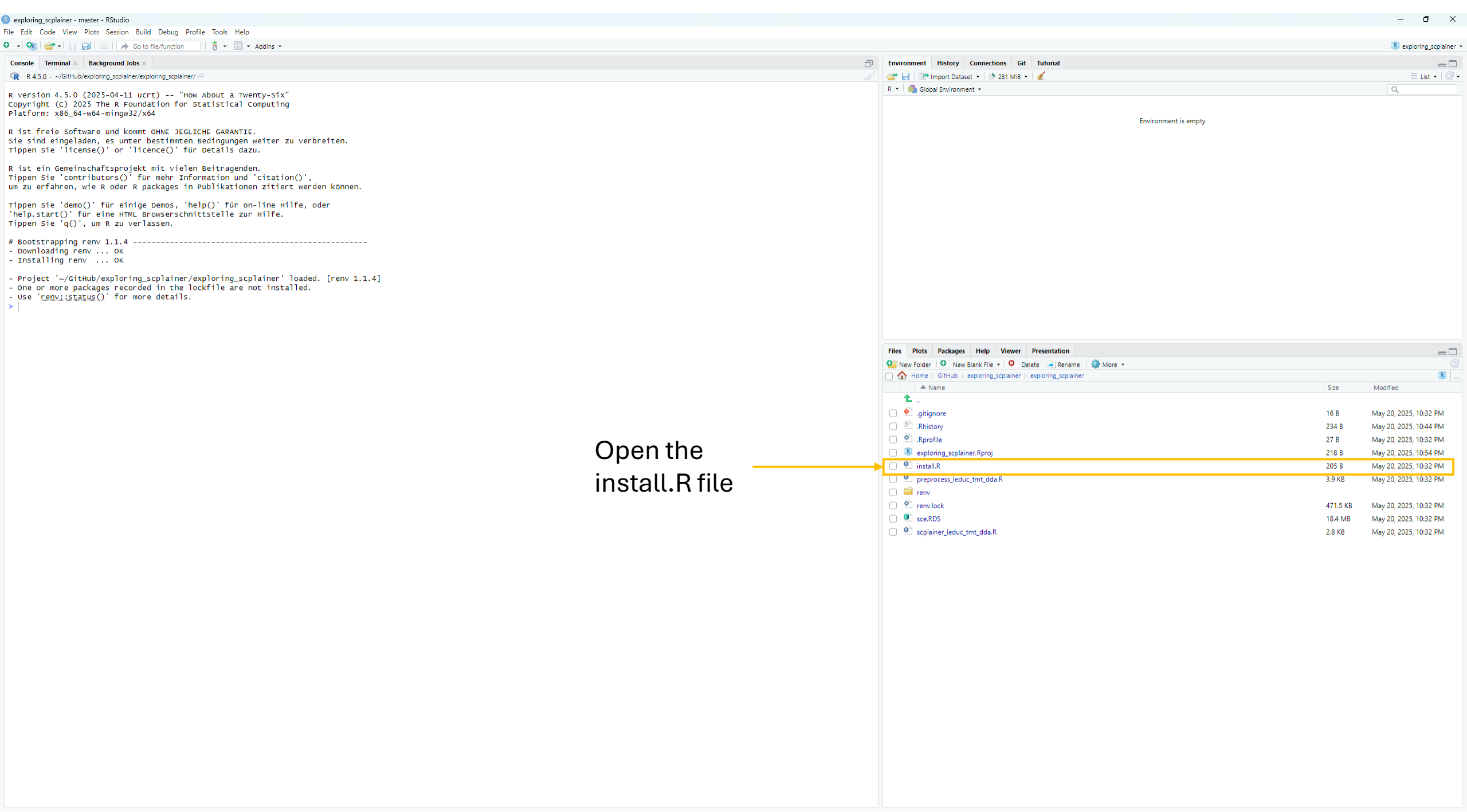
Tippen Sie 'demo()' für einige Demos, 'help()' für on-line Hilfe, oder
'help.start()' für eine HTML Browserschnittstelle zur Hilfe.
Tippen Sie 'q()', um R zu verlassen.
Bootstrapping renv 1.1.4 ----------
- Downloading renv ... OK
- Installing renv ... OK
- Project '~/GitHub/exploring_scplainer/exploring_scplainer' loaded. [renv 1.1.4]
- One or more packages recorded in the lockfile are not installed.
- Use `renv::status()` for more details.
>
You will see something like this, a notification that not all necessary packages for this project are installed
Environment
History
Connections
Git
Tutorial
Import Dataset
281 MiB
List
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
..
.gitignore 16 B May 20, 2025, 10:32 PM
.Rhistory 234 B May 20, 2025, 10:44 PM
.Rprofile 27 B May 20, 2025, 10:32 PM
exploring_scplainer.Rproj 218 B May 20, 2025, 10:54 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
renv.lock 471.5 KB May 20, 2025, 10:32 PM
sce.RDS 18.4 MB May 20, 2025, 10:32 PM
scplainer_leduc_tmt_dda.R 2.8 KB May 20, 2025, 10:32 PM


exploring_scplainer - master - RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function
Addins
exploring_scplainer
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"
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Platform: x86_64-w64-mingw32/x64
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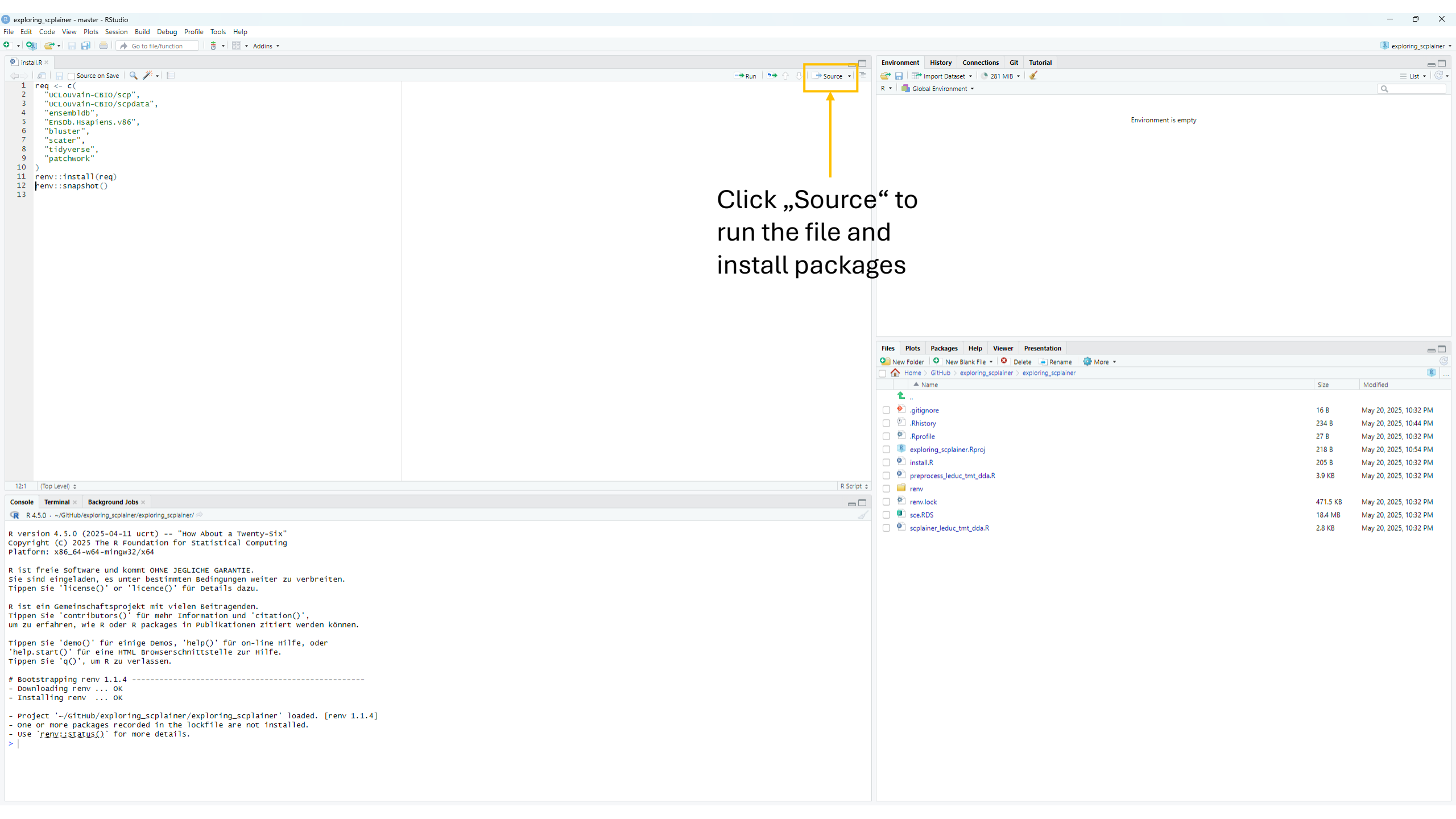
Tippen Sie 'demo()' für einige Demos, 'help()' für on-line Hilfe, oder
'help.start()' für eine HTML Browserschnittstelle zur Hilfe.
Tippen Sie 'q()', um R zu verlassen.
Bootstrapping renv 1.1.4 ----------
- Downloading renv ... OK
- Installing renv ... OK
- Project '~/GitHub/exploring_scplainer/exploring_scplainer' loaded. [renv 1.1.4]
- One or more packages recorded in the lockfile are not installed.
- Use `renv::status()` for more details.
>
Environment
History
Connections
Git
Tutorial
Import Dataset
281 MiB
List
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
..
.gitignore 16 B May 20, 2025, 10:32 PM
.Rhistory 234 B May 20, 2025, 10:44 PM
.Rprofile 27 B May 20, 2025, 10:32 PM
exploring_scplainer.Rproj 218 B May 20, 2025, 10:54 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
renv.lock 471.5 KB May 20, 2025, 10:32 PM
sce.RDS 18.4 MB May 20, 2025, 10:32 PM
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
exploring_scplainer
install.R
Source on Save
Run
Source
req <- c(
"UCLouvain-CBIO/scp",
"UCLouvain-CBIO/scpdata",
"ensembldb",
"EnsDb.Hsapiens.v86",
"bluster",
"scater",
"tidyverse",
"patchwork"
)
renv::install(req)
renv::snapshot()
12:1
(Top Level)
R Script
Click „Source“ to run the file and install packages
Environment
History
Connections
Git
Tutorial
Import Dataset
281 MiB
List
R
Global Environment
Environment is empty
Files
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New Folder
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exploring_scplainer
Name
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.gitignore 16 B May 20, 2025, 10:32 PM
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.Rprofile 27 B May 20, 2025, 10:32 PM
exploring_scplainer.Rproj 218 B May 20, 2025, 10:54 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
renv.lock 471.5 KB May 20, 2025, 10:32 PM
sce.RDS 18.4 MB May 20, 2025, 10:32 PM
scplainer_leduc_tmt_dda.R 2.8 KB May 20, 2025, 10:32 PM
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"
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Platform: x86_64-w64-mingw32/x64
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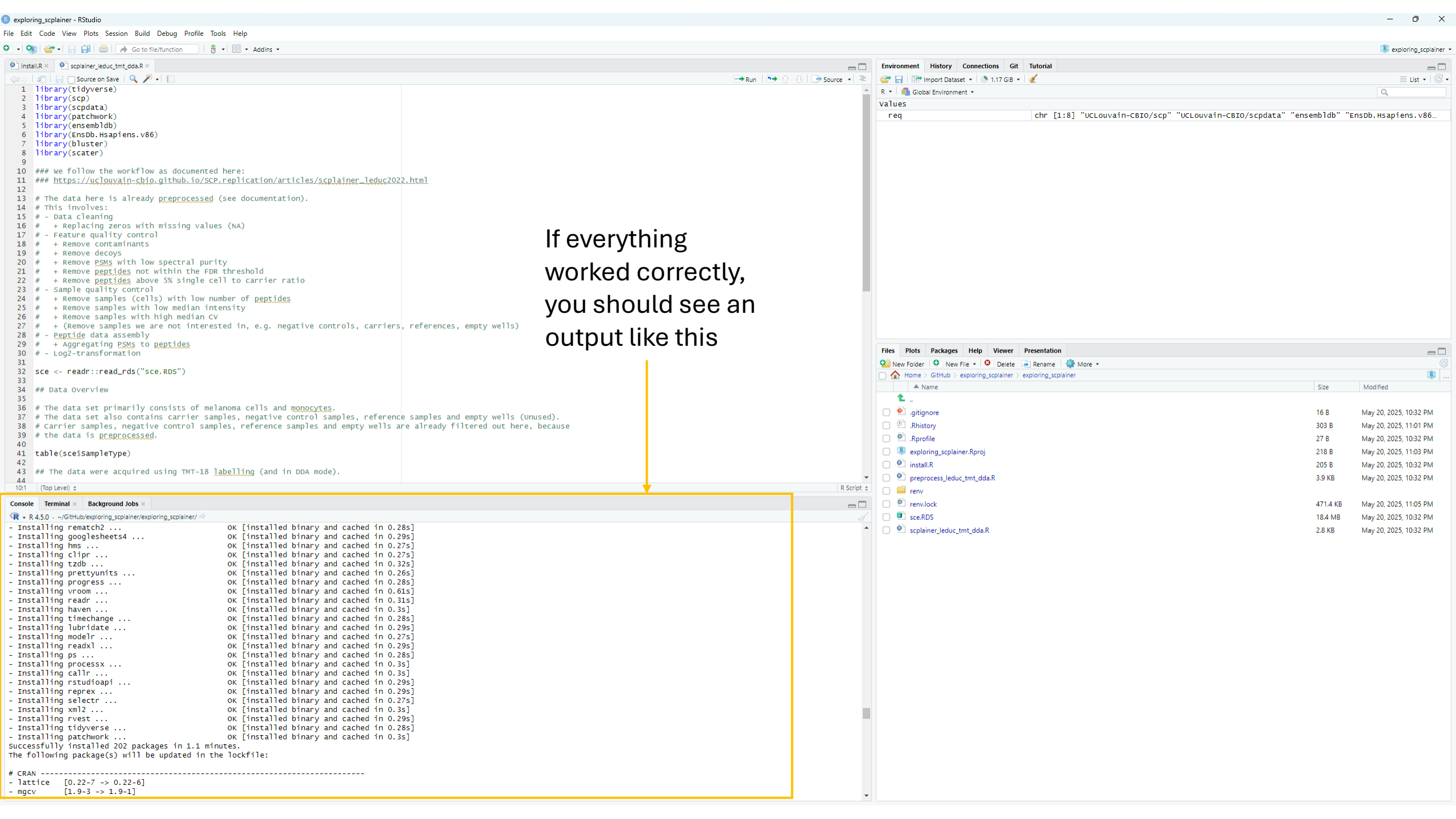
'help.start()' für eine HTML Browserschnittstelle zur Hilfe.
Tippen Sie 'q()', um R zu verlassen.
Bootstrapping renv 1.1.4 ----------
- Downloading renv ... OK
- Installing renv ... OK
- Project '~/GitHub/exploring_scplainer/exploring_scplainer' loaded. [renv 1.1.4]
- One or more packages recorded in the lockfile are not installed.
- Use `renv::status()` for more details.
>


exploring_scplainer - RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
install.R
scplainer_leduc_tmt_dda.R
Source on Save
Run
Source
library(tidyverse)
library(scp)
library(scpdata)
library(patchwork)
library(ensembldb)
library(EnsDb.Hsapiens.v86)
library(bluster)
library(scater)
We follow the workflow as documented here:
https://uclouvain-cbio.github.io/SCP.replication/articles/scplainer_leduc2022.html
# The data here is already preprocessed (see documentation).
# This involves:
# - Data cleaning
#   + Replacing zeros with missing values (NA)
# - Feature quality control
#   + Remove contaminants
#   + Remove decoys
#   + Remove PSMs with low spectral purity
#   + Remove peptides not within the FDR threshold
#   + Remove peptides above 5% single cell to carrier ratio
# - Sample quality control
#   + Remove samples (cells) with low number of peptides
#   + Remove samples with low median intensity
#   + Remove samples with high median CV
#   + (Remove samples we are not interested in, e.g. negative controls, carriers, references, empty wells)
# - Peptide data assembly
#   + Aggregating PSMs to peptides
# - Log2-transformation
sce <- readr::read_rds("sce.RDS")
Data Overview
# The data set primarily consists of melanoma cells and monocytes.
# The data set also contains carrier samples, negative control samples, reference samples and empty wells (Unused).
# Carrier samples, negative control samples, reference samples and empty wells are already filtered out here, because
# the data is preprocessed.
table(sce$SampleType)
The data were acquired using TMT-18 labelling (and in DDA mode).
10:1
(Top Level)
R Script
If everything worked correctly, you should see an output like this
Console
Terminal
Background Jobs
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]
Environment
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1.17 GiB
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req
chr [1:8] "UCLouvain-CBIO/scp" "UCLouvain-CBIO/scpdata" "ensembldb" "EnsDb.Hsapiens.v86…
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New Folder
New File
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Rename
More
Home › GitHub › exploring_scplainer › exploring_scplainer
Name
Size
Modified
.gitignore 16 B May 20, 2025, 10:32 PM
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.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
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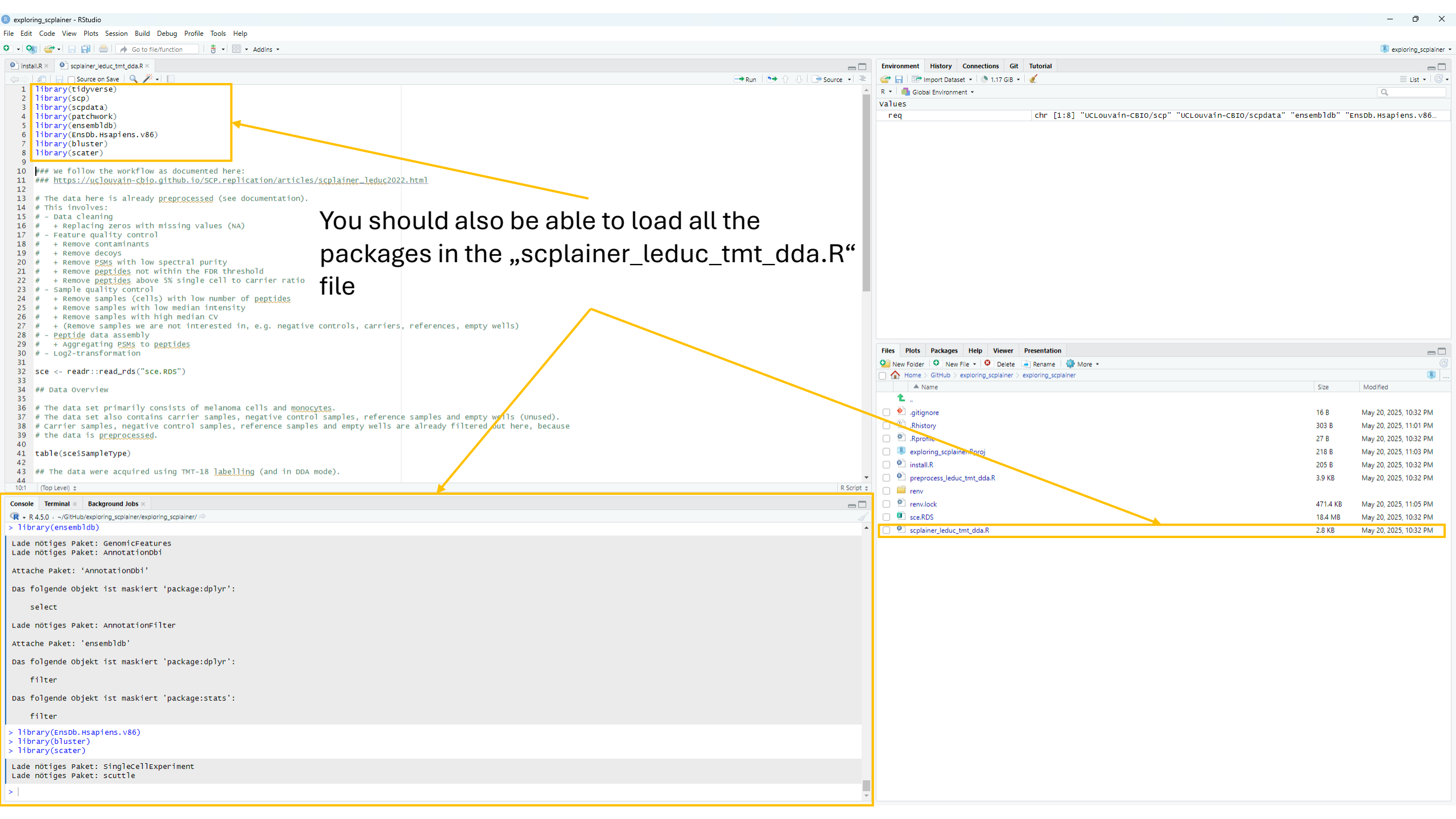
renv.lock 471.4 KB May 20, 2025, 11:05 PM
sce.RDS 18.4 MB May 20, 2025, 10:32 PM
scplainer_leduc_tmt_dda.R 2.8 KB May 20, 2025, 10:32 PM


exploring_scplainer - RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
install.R
scplainer_leduc_tmt_dda.R
Source on Save
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)
10 ### We follow the workflow as documented here:
11 ### https://uclouvain-cbio.github.io/SCP.replication/articles/scplainer_leduc2022.html
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 PSMs 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 PSMs to peptides
30 # - Log2-transformation
32 sce <- readr::read_rds("sce.RDS")
34 ## Data Overview
36 # The data set primarily consists of melanoma cells and monocytes.
37 # The data set also contains carrier samples, negative control 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.
41 table(sce$SampleType)
43 ## The data were acquired using TMT-18 labelling (and in DDA mode).
10:1 (Top Level)
R Script
You should also be able to load all the packages in the „scplainer_leduc_tmt_dda.R“ file
Console
Terminal
Background Jobs
R 4.5.0 · ~/GitHub/exploring_scplainer/exploring_scplainer/
> library(ensembldb)
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: 'ensembldb'
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
>
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Tutorial
Import Dataset
1.17 GiB
List
Global Environment
Values
req
chr [1:8] "UCLouvain-CBIO/scp" "UCLouvain-CBIO/scpdata" "ensembldb" "EnsDb.Hsapiens.v86...
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New File
Delete
Rename
More
Home > GitHub > exploring_scplainer > exploring_scplainer
Name
Size
Modified
.gitignore 16 B May 20, 2025, 10:32 PM
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