

Setup instructions

Contents

R and RStudio	1
Packages	1
Testing testing	1
Further resources	4

You need to install R, RStudio, and several R packages before the workshop. The installation process is simple on all major platforms, and mostly consists of downloading and running the installers appropriate to your platform.

R and RStudio

- Install R, a free software environment for statistical computing and graphics. + It is *highly recommended* to install a precompiled binary distribution for your operating system – use the links up at the top of the page linked to above!
 - If you currently have R installed on your laptop, please make sure it is version 4.0.0 or later. *Please update if it is not!*
- Install RStudio, a powerful user interface for R.

Packages

Automatically install only new packages with the following.

```
#CRAN packages
pcks <- c("tidyverse", "msigdb", "fgsea", "BiocManager")

to.install <- pcks[!(pcks %in% installed.packages()[,"Package"])]

if(length(to.install)) install.packages(to.install)

#Bioconductor packages
pcks <- c("clusterProfiler")

to.install <- pcks[!(pcks %in% installed.packages()[,"Package"])]

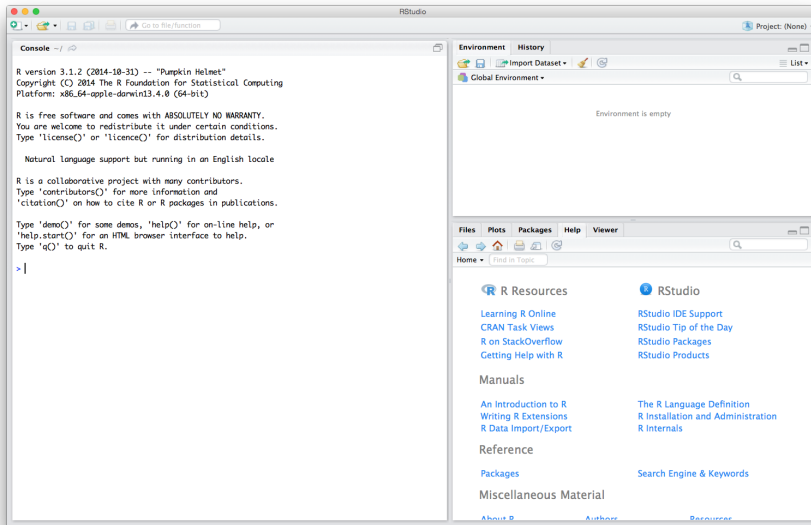
if(length(to.install)) BiocManager::install(to.install, ask = FALSE)
```

Testing testing

1. Do whatever is appropriate for your OS to launch RStudio. You should get a window similar to the screenshot below.
 - If you don't see a window that is divided into distinct areas labelled "Console", "Environment", etc., you are probably running the user interface that comes bundled with R. Check that RStudio



is present in your applications and start it instead.



2. Put your cursor in the left pane labelled “Console”, which is where you interact with the live R process. Create a simple object with code like `x <- 2 * 4` (followed by enter or return). In the “Environment” pane, to the right of the Console, you should see an entry for “x” with appropriate value (in this case, 8).
3. Then inspect the `x` object by typing `x` in the Console followed by enter or return. You should see the value 8 printed to the screen.
4. Test that the packages are installed by loading them.

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.1 --
## v ggplot2 3.3.5      v purrr   0.3.4
## v tibble  3.1.2      v dplyr  1.0.7
## v tidyr   1.1.3      v stringr 1.4.0
## v readr   1.4.0      v forcats 0.5.1

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
```

```
library(org.Hs.eg.db)
```

```
## Loading required package: AnnotationDbi
## Loading required package: stats4
## Loading required package: BiocGenerics
## Loading required package: parallel
##
## Attaching package: 'BiocGenerics'
##
## The following objects are masked from 'package:parallel':
##
##   clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##   clusterExport, clusterMap, parApply, parCapply, parLapply,
##   parLapplyLB, parRapply, parSapply, parSapplyLB
```

```

## The following objects are masked from 'package:dplyr':
##
##   combine, intersect, setdiff, union
## The following objects are masked from 'package:stats':
##
##   IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##   anyDuplicated, append, as.data.frame, basename, cbind, colnames,
##   dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##   grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
##   order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##   rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##   union, unique, unsplit, which, which.max, which.min
## Loading required package: Biobase
## Welcome to Bioconductor
##
##   Vignettes contain introductory material; view with
##   'browseVignettes()'. To cite Bioconductor, see
##   'citation("Biobase")', and for packages 'citation("pkgname)".
## Loading required package: IRanges
## Loading required package: S4Vectors
##
## Attaching package: 'S4Vectors'
## The following objects are masked from 'package:dplyr':
##
##   first, rename
## The following object is masked from 'package:tidyr':
##
##   expand
## The following object is masked from 'package:base':
##
##   expand.grid
##
## Attaching package: 'IRanges'
## The following objects are masked from 'package:dplyr':
##
##   collapse, desc, slice
## The following object is masked from 'package:purrr':
##
##   reduce
##
## Attaching package: 'AnnotationDbi'
## The following object is masked from 'package:dplyr':
##
##   select

```

##

```
library(msigdbr)
library(fgsea)
```

Further resources

The above is sufficient preparation for this workshop but here are some links if you are interested in reading a bit further.

- How to Use RStudio:
 - <https://support.rstudio.com/hc/en-us/sections/200107586-Using-RStudio>
- RStudio Public Discussion & Troubleshooting Guide:
 - <https://support.rstudio.com/hc/en-us/sections/203994097-RStudio-IDE>
- How to Install R:
 - <http://cran.r-project.org/doc/manuals/R-admin.html>
 - http://cran.stat.sfu.ca/doc/FAQ/R-FAQ.html#How-can-R-be-installed_003f
- R FAQ:
 - <http://cran.r-project.org/doc/FAQ/R-FAQ.html>
- More about add-on packages in the R Installation and Administration Manual
 - http://cran.r-project.org/doc/manuals/R-admin.html#Add_002don-packages