Interacting with R & RStudio

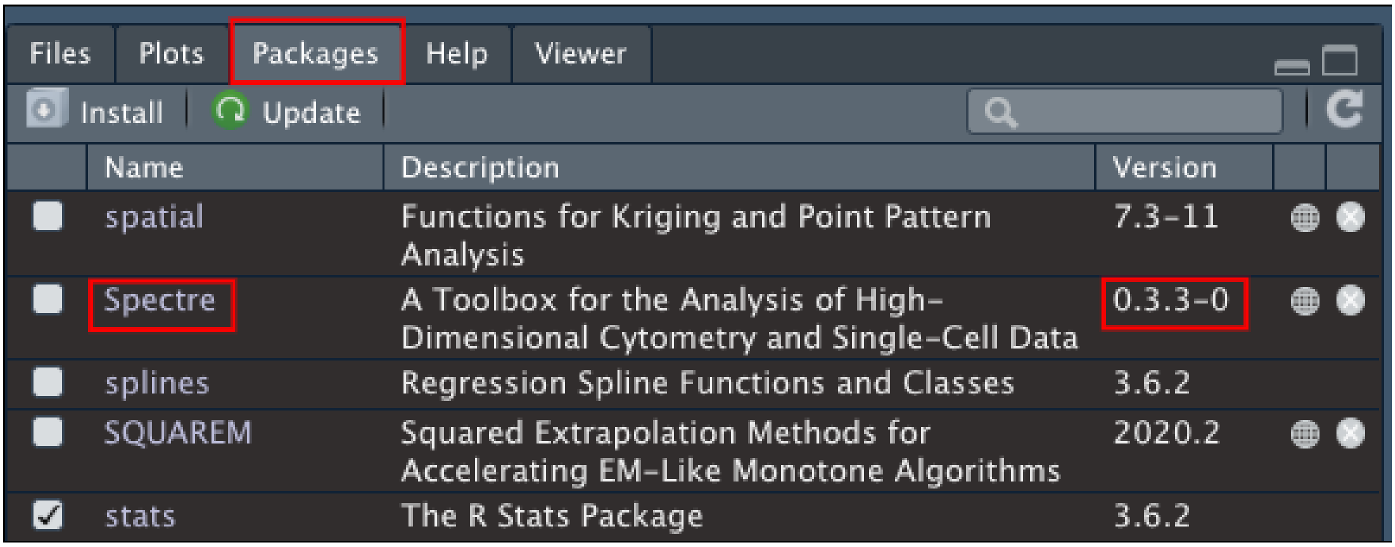
If you aren't familiar with using R and RStudio, check out our quick tutorial.

Install Spectre from Github

In v1.1 we have removed the package dependencies `rgeos` and `rgdal` as these are no longer available on CRAN. The package should install fine without these dependencies, but some spatial functions may not work properly. If required, one can download the archived packages, unzip them, and then placed them in the R library location.

Check Spectre version

To see if you have Spectre installed, you can open **RStudio** and look under the '**packages**' tab. The version will be listed in the right hand column. Hit the ⟳ button to refresh the package list if you need. If you have the latest version installed, R won't install it again. If you have an older version, the R will install the latest version. If you wish, you can check the Spectre Home Page for the latest version.



	Name	Description	Version
☐	spatial	Functions for Kriging and Point Pattern Analysis	7.3-11
☐	Spectre	A Toolbox for the Analysis of High-Dimensional Cytometry and Single-Cell Data	0.3.3-0
☐	splines	Regression Spline Functions and Classes	3.6.2
☐	SQUAREM	Squared Extrapolation Methods for Accelerating EM-Like Monotone Algorithms	2020.2
☑	stats	The R Stats Package	3.6.2

Tip

If you are updating Spectre, we advise deleting the previous installation to ensure a clean update.

```
remove.packages('Spectre')
```

Install Devtools

In R, install and load the 'devtools' package. The devtools package has a number of dependencies (packages that it needs to use) that it will automatically install when you install 'devtools' – this might take some time.

```
## Install (if not already installed)
if(!require('devtools')) {install.packages('devtools')}
```

Tip

After installing devtools, we recommend restarting RStudio, otherwise you may see an error like the following:

```
Downloading GitHub repo immunedynamics/spectre@HEAD
Error in utils::download.file(url, path, method = method, quiet = quiet,  :
```

```
download from 'https://api.github.com/repos/immunedynamics/spectre/tarball/HEAD' failed
```

Install Spectre

Subsequently, use the 'install_github' function to install and load the Spectre package. By default this will load the 'master' branch, which is the same as the latest stable release version (listed at https://github.com/ImmuneDynamics/Spectre/releases). To install a specific release version, see https://cran.r-project.org/web/packages/githubinstall/vignettes/githubinstall.html.

```
## Install Spectre
library('devtools')

options(timeout=6000) # this changes the 'timeout' limit for downloading the package
devtools::install_github("immunedynamics/spectre") # this will download and install Spectre
```

ⓘ If you are trying to install the 'development' version of Spectre, use:
options(timeout=6000)
devtools::install_github("immunedynamics/spectre", ref = 'development')

Confirm or decline updates

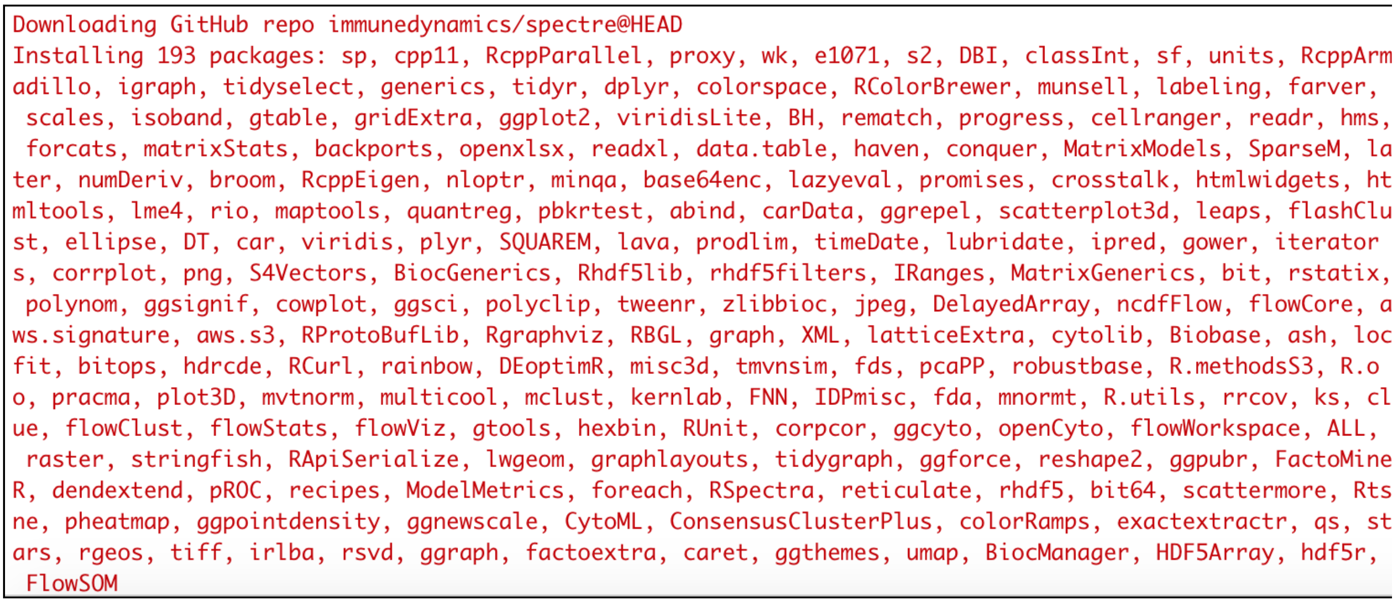
During installation, you may see a message like the following. You can update all the packages if you wish, but if you are unsure, or using multiple packages in other contexts, it might be wise to wait until you have time to update everything and test your scripts afterwards.

```
These packages have more recent versions available.
Which would you like to update?

1: All
2: CRAN packages only
3: None
4: rlang    (0.4.1  -> 0.4.2 ) [CRAN]
5: digest   (0.6.22 -> 0.6.23) [CRAN]
6: roxygen2 (7.0.0  -> 7.0.1 ) [CRAN]

Enter one or more numbers, or an empty line to skip updates:
```

```
# Type '1' and press enter to update all packages, or '3' and press enter for no updates
3
```

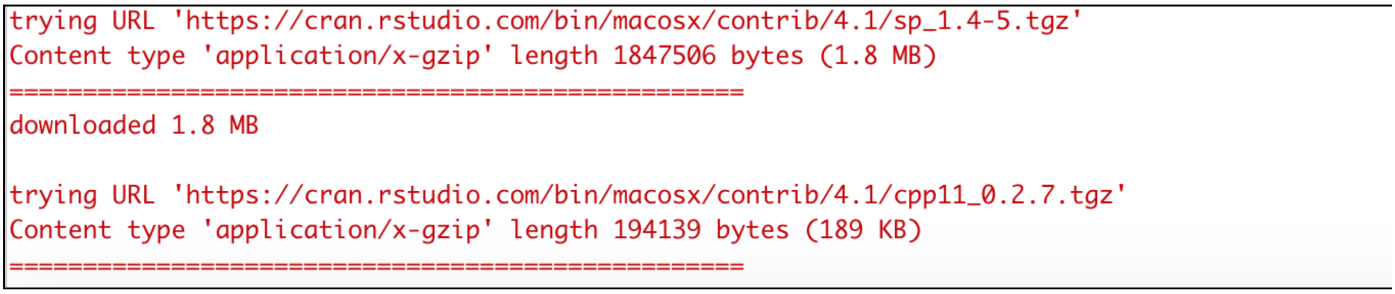
Possible queries during installation

R will inform you of which additional package are being installed.



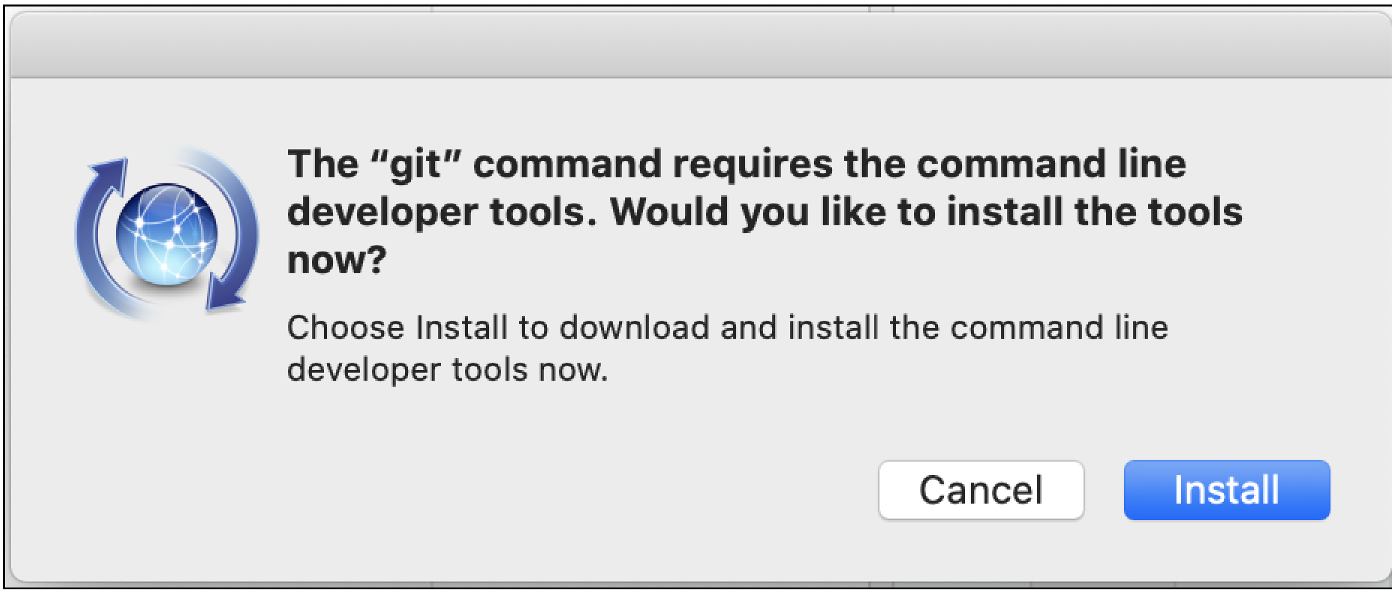
```
Downloading GitHub repo immunedynamics/spectre@HEAD
Installing 193 packages: sp, cpp11, RcppParallel, proxy, wk, e1071, s2, DBI, classInt, sf, units, RcppArm
adillo, igraph, tidyselect, generics, tidyr, dplyr, colorspace, RColorBrewer, munsell, labeling, farver,
 scales, isoband, gtable, gridExtra, ggplot2, viridisLite, BH, rematch, progress, cellranger, readr, hms,
 forcats, matrixStats, backports, openxlsx, readxl, data.table, haven, conquer, MatrixModels, SparseM, la
ter, numDeriv, broom, RcppEigen, nloptr, minqa, base64enc, lazyeval, promises, crosstalk, htmlwidgets, ht
mltools, lme4, rio, maptools, quantreg, pbkrtest, abind, carData, ggrepel, scatterplot3d, leaps, flashClu
st, ellipse, DT, car, viridis, plyr, SQUAREM, lava, prodlim, timeDate, lubridate, ipred, gower, iterator
s, corrplot, png, S4Vectors, BiocGenerics, Rhdf5lib, rhdf5filters, IRanges, MatrixGenerics, bit, rstatix,
 polynom, ggsignif, cowplot, ggsci, polyclip, tweenr, zlibbioc, jpeg, DelayedArray, ncdfFlow, flowCore, a
ws.signature, aws.s3, RProtoBufLib, Rgraphviz, RBGL, graph, XML, latticeExtra, cytolib, Biobase, ash, loc
fit, bitops, hdrcde, RCurl, rainbow, DEoptimR, misc3d, tmvnsim, fds, pcaPP, robustbase, R.methodsS3, R.o
o, pracma, plot3D, mvtnorm, multicool, mclust, kernlab, FNN, IDPmisc, fda, mnormt, R.utils, rrcov, ks, cl
ue, flowClust, flowStats, flowViz, gtools, hexbin, RUnit, corpcor, ggcyto, openCyto, flowWorkspace, ALL,
 raster, stringfish, RApiSerialize, lwgeom, graphlayouts, tidygraph, ggforce, reshape2, ggpubr, FactoMine
R, dendextend, pROC, recipes, ModelMetrics, foreach, RSpectra, reticulate, rhdf5, bit64, scattermore, Rts
ne, pheatmap, ggpointdensity, ggnewscale, CytoML, ConsensusClusterPlus, colorRamps, exactextractr, qs, st
ars, rgeos, tiff, irlba, rsvd, ggraph, factoextra, caret, ggthemes, umap, BiocManager, HDF5Array, hdf5r,
 FlowSOM
```

As each dependency (package) is being installed, you will see updates.



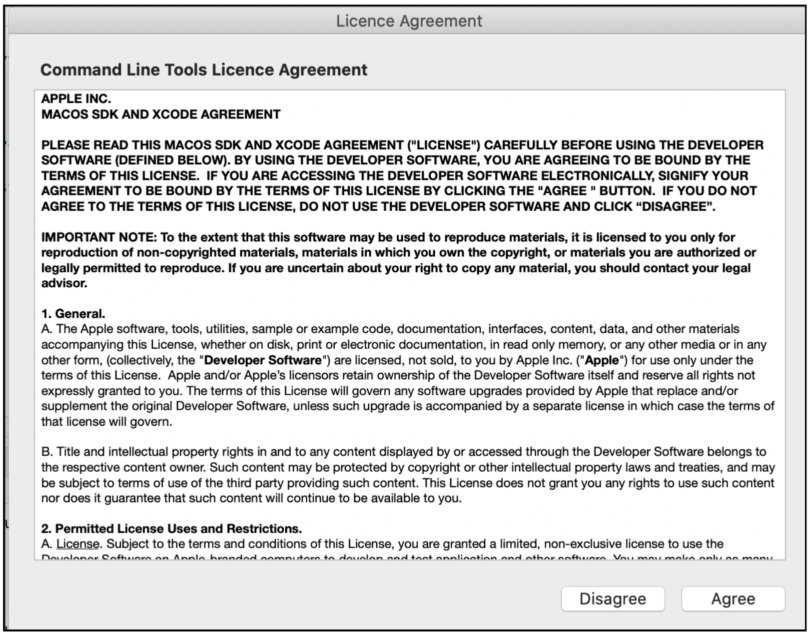
```
trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.1/sp_1.4-5.tgz'
Content type 'application/x-gzip' length 1847506 bytes (1.8 MB)
==================================================
downloaded 1.8 MB

trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.1/cpp11_0.2.7.tgz'
Content type 'application/x-gzip' length 194139 bytes (189 KB)
==================================================
```

If you see the following prompt, click '**Install**'.



The “git” command requires the command line developer tools. Would you like to install the tools now?

Choose Install to download and install the command line developer tools now.



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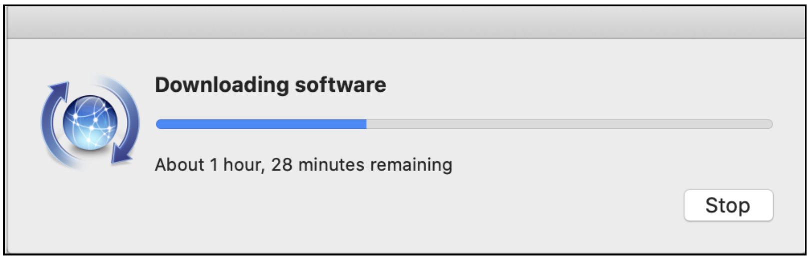
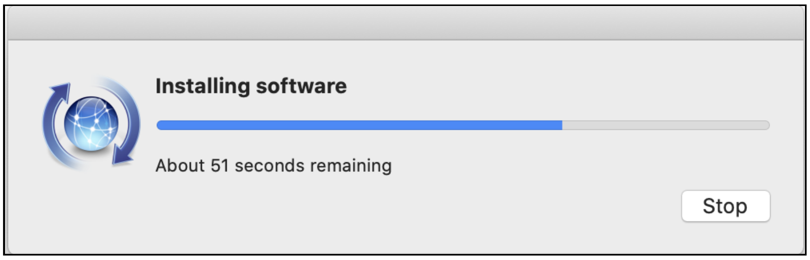
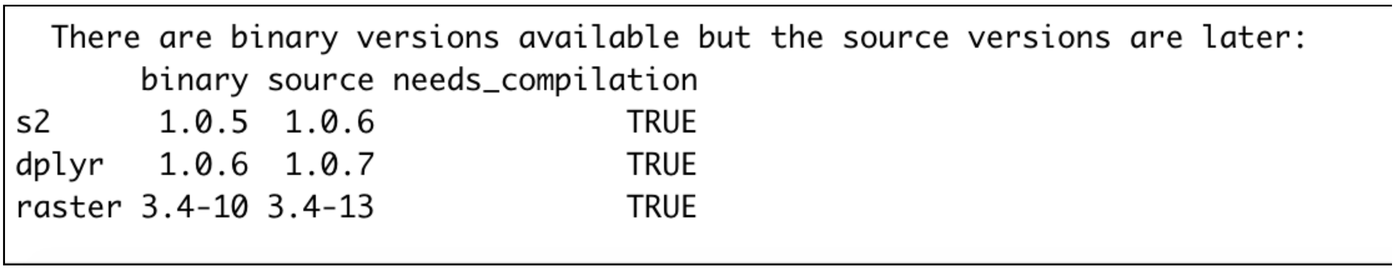




You may be asked for permission to compile the code for certain pages, type '**Yes**' and run the code.



```
  There are binary versions available but the source versions are later:
       binary source needs_compilation
s2      1.0.5  1.0.6              TRUE
dplyr   1.0.6  1.0.7              TRUE
raster 3.4-10 3.4-13              TRUE
```

```
Do you want to attempt to install these from sources? (Yes/no/cancel)
```

```
Yes
```

Successful installation

If the installation was successful, you should see something similar to the following:

```
✓  checking for file ‘/private/var/folders/zf/7wygqzns5vx7ycttdgcc4byc0000gp/T/RtmpDchxP7/
remotes9a66a1a4064/ImmuneDynamics-Spectre-c1401e6/DESCRIPTION’ ...
─  preparing ‘Spectre’: (879ms)
✓  checking DESCRIPTION meta-information ...
─  checking for LF line-endings in source and make files and shell scripts
─  checking for empty or unneeded directories
─  building ‘Spectre_0.5.4.tar.gz’

* installing *source* package ‘Spectre’ ...
** using staged installation
** R
** data
*** moving datasets to lazyload DB
** inst
** byte-compile and prepare package for lazy loading
** help
Warning: /private/var/folders/zf/7wygqzns5vx7ycttdgcc4byc0000gp/T/RtmpQekn8e/R.INSTALL231e7ae0ba82/
Spectre/man/demo.exp.Rd: docType ‘demo.exp’ is unrecognized
*** installing help indices
** building package indices
** testing if installed package can be loaded from temporary location
** testing if installed package can be loaded from final location
** testing if installed package keeps a record of temporary installation path
* DONE (Spectre)
```

You can check on the status of Spectre and the other package dependencies by running '**package.check()**'.

```
## Check if all required packages have been installed
Spectre::package.check()
```

You should see something like the following returned, but with the most recent version of Spectre.

```
Package: Spectre
 -- Version (on disk): 0.5.3
 -- Version (loaded):  0.5.3
 -- Install date:      2021-06-19
 -- Install source:    Github (immunedynamics/spectre@c1401e6)
 -- Install path:      /Library/Frameworks/R.framework/Versions/4.1/Resources/library/Spectre
 -- R version:         R version 4.1.0 (2021-05-18)
 -- OS:                macOS Catalina 10.15.7

Checking dependency packages...
 -- All packages successfully installed.

Check out 'https://immunedynamics.github.io/spectre/' for protocols
```

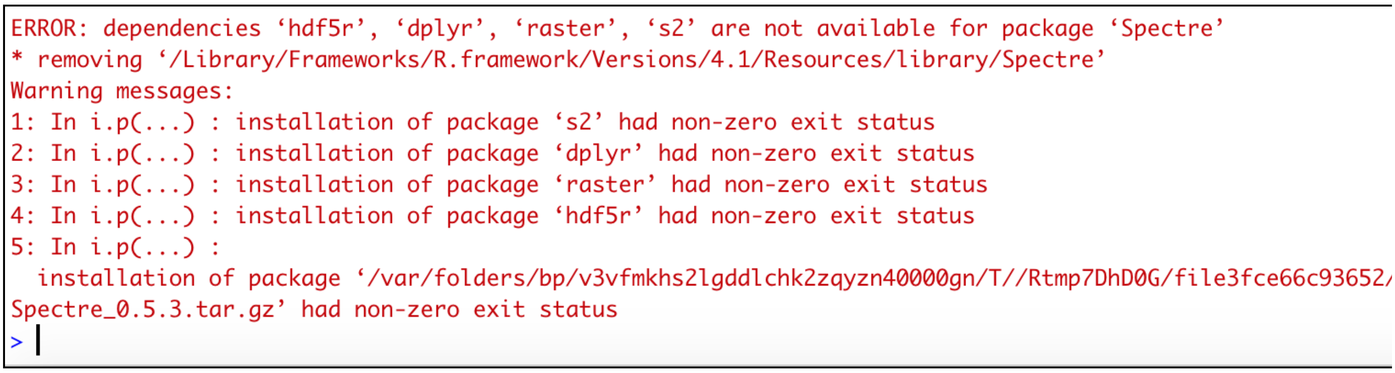
Load libraries (packages)

You can then load the required packages using the '*package.load()*' function.

```
## Load all required packages
Spectre::package.load()
```

Unsuccessful installation

If Spectre or any of the dependencies was not installed successfully, you may see some error messages like the following.



```
ERROR: dependencies ‘hdf5r’, ‘dplyr’, ‘raster’, ‘s2’ are not available for package ‘Spectre’
* removing ‘/Library/Frameworks/R.framework/Versions/4.1/Resources/library/Spectre’
Warning messages:
1: In i.p(...) : installation of package ‘s2’ had non-zero exit status
2: In i.p(...) : installation of package ‘dplyr’ had non-zero exit status
3: In i.p(...) : installation of package ‘raster’ had non-zero exit status
4: In i.p(...) : installation of package ‘hdf5r’ had non-zero exit status
5: In i.p(...) :
  installation of package ‘/var/folders/bp/v3vfmkhs2lgddlchk2zqyzn40000gn/T//Rtmp7DhD0G/file3fce66c93652/
Spectre_0.5.3.tar.gz’ had non-zero exit status
> 
```

Alternatively, if Spectre was successfully installed, but when running '**package.check()**' some of the dependencies were not been installed correctly, you will see something like the following:

```
Checking dependency packages...
 -- Biobase is required but not installed. Please install from BioConductor.

Check out 'https://immunedynamics.github.io/spectre/getting-started/' for help with installation
```

Installation troubleshooting

If you run into problems during installation, check out our installation troubleshooting page. Alternatively, you can report an issue on Github, ask for help on our discussion board, or email us.