

Local R Setup

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System Requirements

The functionality of some of these packages requires Linux, Mac OSX, or a Unix-type system. This excludes Windows in some cases. The code was run on Linux and Mac OSX. Although we do not currently support it, Windows 10 has a Linux subsystem, which may allow for a working installation of all the dependencies of Neuroconductor.

Although still untested there is a good tutorial on running FSL on Windows as well as ANTsR on Windows.

Install R

You can install the latest R from <http://cran.r-project.org/>.

We also recommend installing the RStudio IDE

CMake and Git

These are required by the ANTsR suite of tools. To install these, see the relevant sections in the Installing ANTsR tutorial

FSL

R Packages

Devtools Package

The tutorial and breakdown for installing the devtools package is located at:

<https://www.rstudio.com/products/rpackages/devtools/>.

Please read through it as most of the code below requires devtools.

Bioconductor

We need Bioconductor packages in some cases and we can install it with the code below:

```
# Installing Bioconductor  
library(utils);  
source("http://bioconductor.org/biocLite.R");  
biocLite(pkgs = c("Biobase"), suppressUpdates = TRUE, suppress
```

RGL

Conclusion

If all of these install correctly, restart R and test:

Working installation of FSL and fsLR test

```
library(fsLR)
have_fsl()
example("fsl_smooth")
```

Working installation of ANTsR and extrantsr

```
library(extrantsr)
example("smooth_image")
```