

## Local R Setup

## 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")
```