
Local R Setup

1 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 (https://msdn.microsoft.com/en-us/commandline/wsl/install_guide), 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 (<http://www.nemotos.net/?p=1481>) as well as ANTsR on Windows ([https://github.com/stnava/ANTsR/wiki/Installing-ANTsR-in-Windows-10-\(along-with-FSL,-Rstudio,-Freesurfer,-etc\)\)](https://github.com/stnava/ANTsR/wiki/Installing-ANTsR-in-Windows-10-(along-with-FSL,-Rstudio,-Freesurfer,-etc)))).

1.1 Install R

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

We also recommend installing the RStudio IDE (<https://www.rstudio.com/products/rstudio/download/>)

1.2 CMake and Git

These are required by the `ANTsR` suite of tools. To install these, see the relevant sections in the Installing ANTsR tutorial (http://johnmuschelli.com/neuroc/installing_ANTsR/index.html)

1.3 FSL

See the installation instructions for FSL from <https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation> (<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation>).

1.3.1 Neurodebian

The following was done to make the Neurodebian installation look like that of Mac OSX:

```
#####  
# FSL  
#####  
sudo apt-get update \  
    && sudo apt-get install -y fsl-complete  
  
# Debian has a fixed FSLDIR  
export FSLDIR=/usr/local/fsl  
export FSLSHARE=/usr/share/data  
# add the fsl binary path to the search path  
export PATH=$PATH:${FSLDIR}/bin  
# export PATH=$PATH:/usr/lib/fsl/5.0  
# Possum is installed in the same directory  
export POSSUMDIR=$FSLDIR  
  
sudo mkdir -p ${FSLDIR}/bin  
sudo cp /usr/lib/fsl/5.0/* ${FSLDIR}/bin/  
sudo mkdir -p ${FSLDIR}/lib  
sudo mv ${FSLDIR}/bin/lib* ${FSLDIR}/lib/  
  
export FSLOUTPUTTYPE=NIFTI_GZ  
# export LD_LIBRARY_PATH=$LD_LIBRARY_PATH:/usr/lib/fsl/5.0  
export LD_LIBRARY_PATH=${FSLDIR}/lib:$LD_LIBRARY_PATH:  
  
# sudo cp /usr/share/fsl/5.0/etc/fslconf/fsl.sh $FSLDIR/etc/fslconf/fsl.sh  
export FSLOUTPUTTYPE=NIFTI_GZ  
# sudo rm $FSLDIR/etc/fslconf/fsl.sh  
sudo mkdir -p $FSLDIR/etc/fslconf/  
fname=${FSLDIR}/etc/fslconf/fsl.sh  
echo "FSLDIR=/usr/local/fsl" > ${fname}  
echo 'PATH=${PATH}:${FSLDIR}/bin' >> ${fname}  
echo 'LD_LIBRARY_PATH=${FSLDIR}/lib:$LD_LIBRARY_PATH' >> ${fname}  
echo "FSLOUTPUTTYPE=NIFTI_GZ" >> ${fname}  
  
#####  
# Setting global library  
#####  
sudo echo "${FSLDIR}/lib" > /etc/ld.so.conf.d/fsl.conf  
sudo ldconfig
```

```

sudo mkdir -p ${FSLDIR}/data/standard
sudo mkdir -p ${FSLDIR}/data/atlasses

#####
# Setting things up like other installers
#####
# setting up standard
sudo cp -R ${FSLSHARE}/fsl-mni152-templates/* ${FSLDIR}/data/standard/

# setting up atlases
sudo cp -R ${FSLSHARE}/harvard-oxford-atlasses/* ${FSLDIR}/data/atlasses/
sudo cp -R ${FSLSHARE}/juelich-histological-atlas/* ${FSLDIR}/data/atlasses/
sudo cp -R ${FSLSHARE}/bangor-cerebellar-atlas/* ${FSLDIR}/data/atlasses/
sudo cp -R ${FSLSHARE}/jhu-dti-whitematter-atlas/* ${FSLDIR}/data/atlasses/
sudo cp -R ${FSLSHARE}/forstmann-subthalamic-nucleus-atlas/* ${FSLDIR}/data/atlasses/
sudo cp -R ${FSLSHARE}/fsl-resting-connectivity-parcellation-atlasses/* ${FSLDIR}/data/atlasses/
sudo cp -R ${FSLSHARE}/mni-structural-atlas/* ${FSLDIR}/data/atlasses/
sudo cp -R ${FSLSHARE}/oxford-thalamic-connectivity-atlas/* ${FSLDIR}/data/atlasses/
sudo cp -R ${FSLSHARE}/talairach-daemon-atlas/* ${FSLDIR}/data/atlasses/

```

2 R Packages

2.1 Devtools Package

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

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

(<https://www.rstudio.com/products/rpackages/devtools/>). Please read through it as most of the code below requires `devtools`.

2.2 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, suppressAutoUpdate =
TRUE, ask = FALSE)
```

2.3 RGL

2.4 Mac and Linux

The `rgl` package can be installed using `install.packages` usually.

2.5 Linux

The `install.packages` command may have some problems on Linux machines. It can be installed in `bash` using:

```
sudo apt-get -y update && sudo apt-get build-dep -y r-cran-rgl
```

There may be an error that may be mitigated by the following command in `bash`:

```
sudo sed -i -- 's/#deb-src/deb-src/g' /etc/apt/sources.list && sudo sed -i
-- 's/# deb-src/deb-src/g' /etc/apt/sources.list
```

and re-running the code above.

2.6 Neuroimaging packages on Github

2.6.1 Standard Packages

```

source("https://neuroconductor.org/neurocLite.R")
# DICOM converter
neuro_install("dcm2niir")
library(dcm2niir); install_dcm2nii()
# HCP database connector
neuro_install("neurohcp")
# dcm2nii Rcpp implementation
neuro_install(c("RNifti", "divest", "oro.dicom", "oro.nifti",
"WhiteStripe"))
# data for whitestripe
library(WhiteStripe); download_img_data()

# neurobase package
neuro_install("neurobase")
neuro_install("fslr")

```

2.6.2 ANTsR

Please see the the Installing ANTsR tutorial

(http://johnmuschelli.com/neuroc/installing_ANTsR/index.html) if anything errors here:

```

#####
# ANTs
#####
neuro_install("ITKR")
neuro_install("ANTsRCore", upgrade_dependencies = FALSE)
neuro_install("ANTsR", upgrade_dependencies = FALSE)
neuro_install("extrantsr", upgrade_dependencies = FALSE)

```

2.6.3 Knitting using RStudio

```

install.packages(c("formatR", "caTools", "rprojroot", "rmarkdown"))

```

2.6.4 Imaging Packages and Data

The only package that isn't directly available is the `ms.lesion` package, which is due to restrictions on the data. This should be available from the tutorial

```
#####  
# Install MS LESION DATA!  
# INSTALL KIRBY21  
#####  
neuro_install("papayar")  
neuro_install("oasis")  
neuro_install("malf.templates")  
neuro_install("kirby21.t1")
```

3 Conclusion

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

3.1 Working installation of FSL and fslr test

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

3.2 Working installation of ANTsR and extrantsr

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