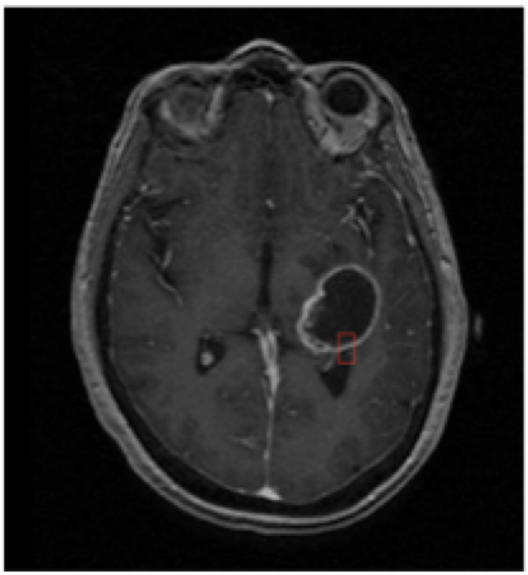
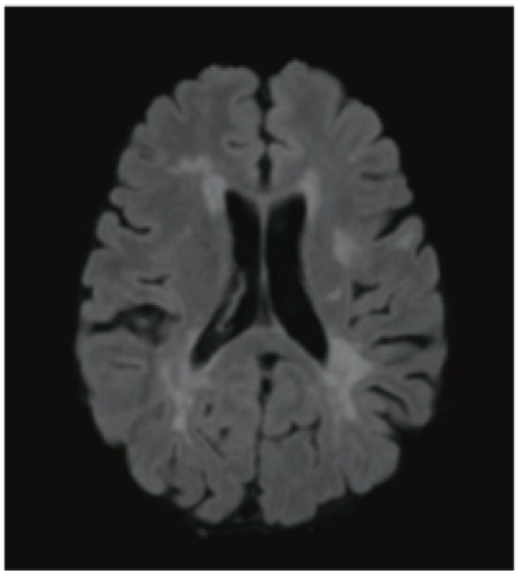
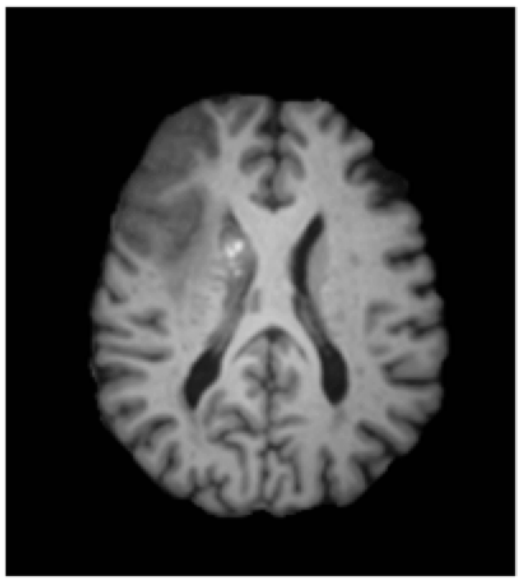
Neuroimaging Analysis in R: Image Preprocessing

Elizabeth M. Sweeney
Postdoctoral Fellow
Statistics Department, Rice University
Website: elizabethmargaretsweeney.wordpress.com
Twitter: @emsweene57
Github: emsweene

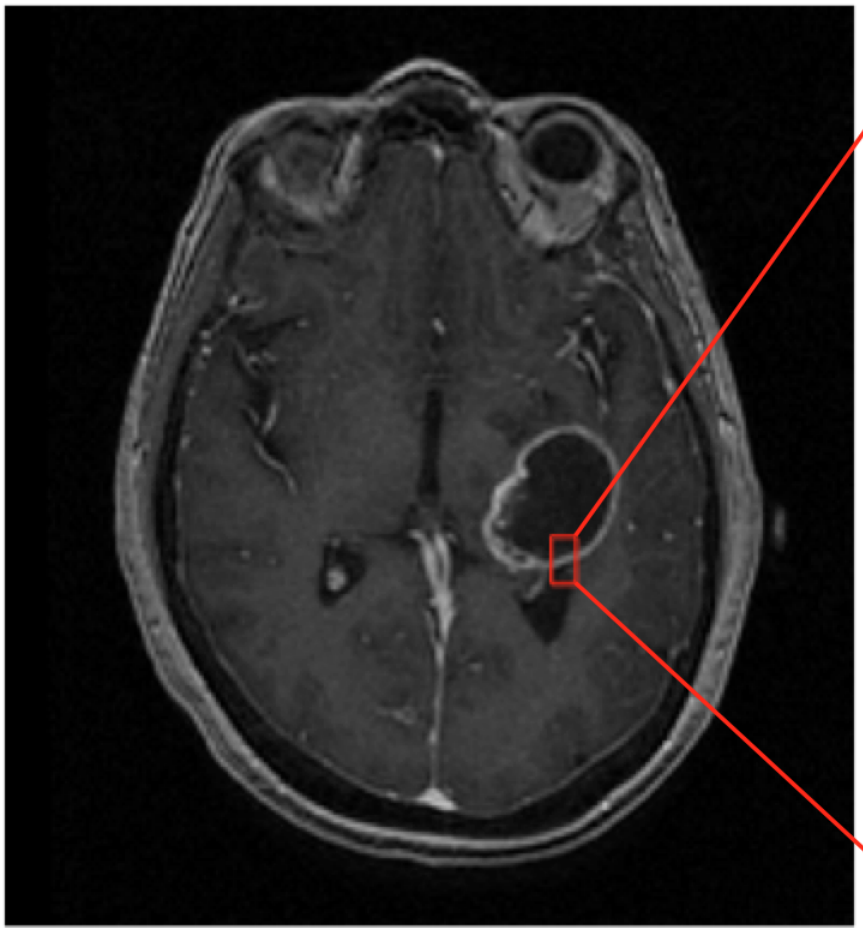
Houston R Users Group
September 5, 2016

Structural MRI

Structural MRI is used in clinical practice to diagnose disease and monitor disease progression.

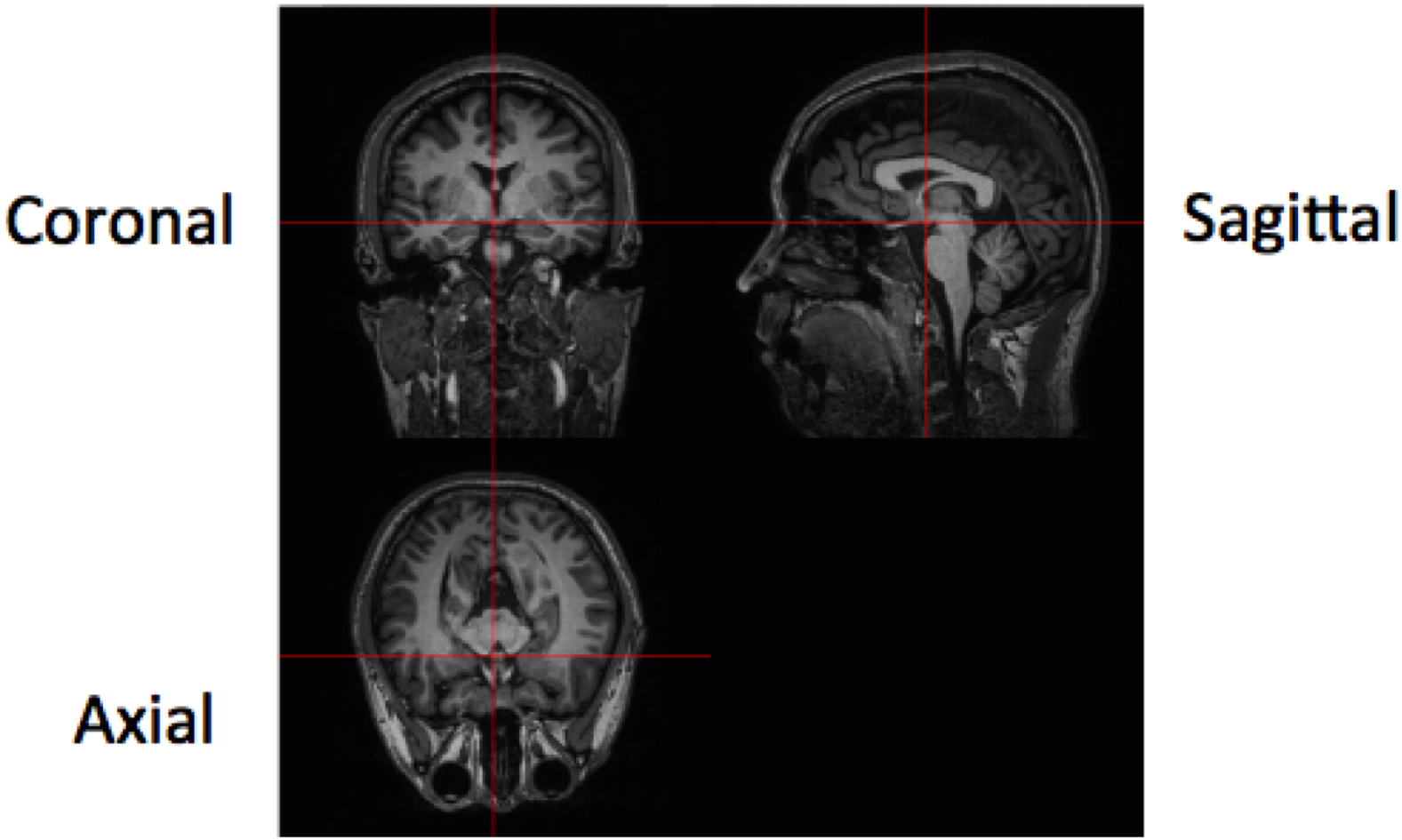




Structural MRI

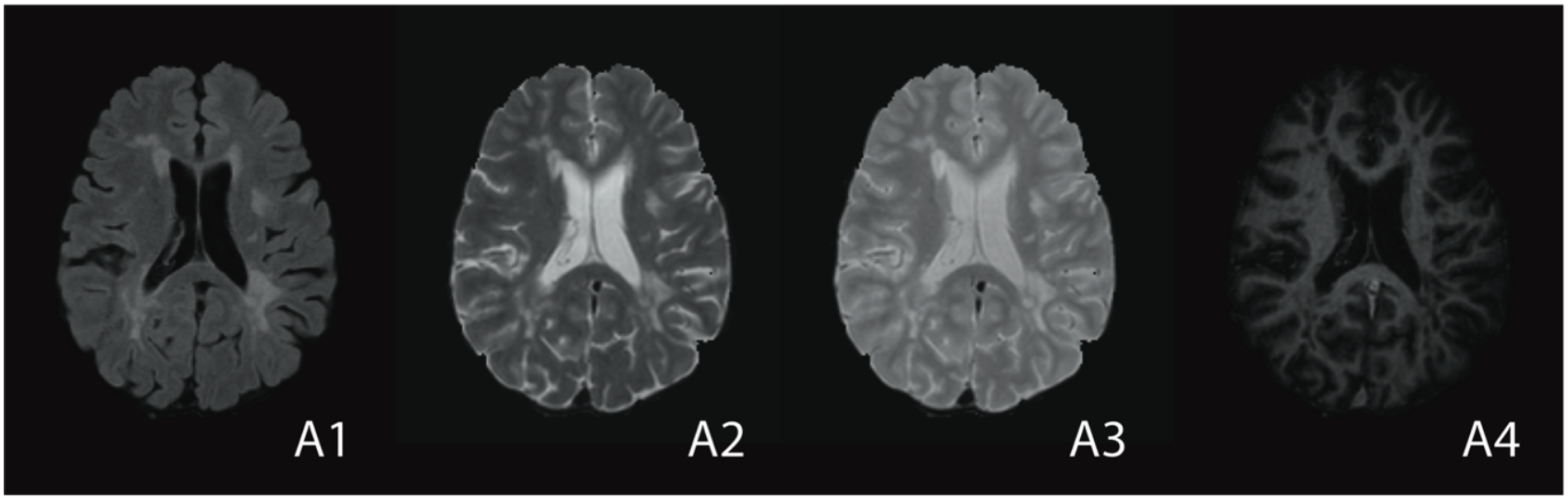


43	42	47	32	38	33
40	45	48	42	49	44
40	55	57	57	51	55
56	56	58	79	121	165
68	99	149	179	199	190
187	199	186	139	108	81
165	115	47	39	69	76
29	24	29	74	107	93
29	42	55	58	71	87
46	40	45	40	61	92
44	46	43	31	62	88

Structural MRI



Structural MRI



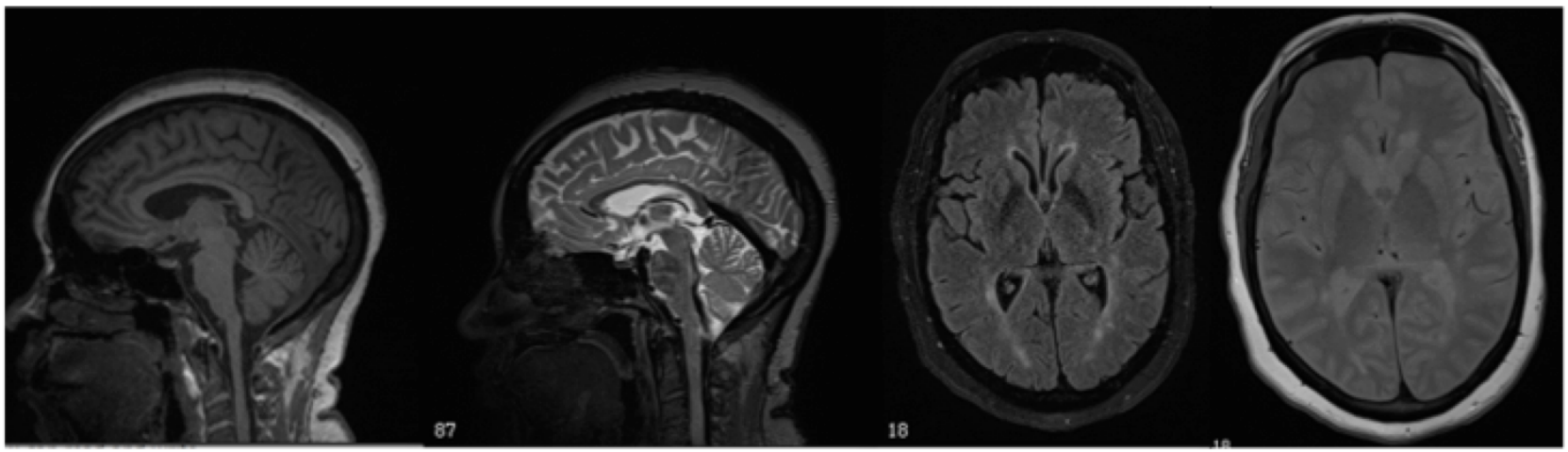
A1. Fluid-attenuated inversion recovery (FLAIR)
A2. T2-weighted (T2-w)
A3. Proton density (PD)
A4. T1-weighted (T1-w)

Image Preprocessing

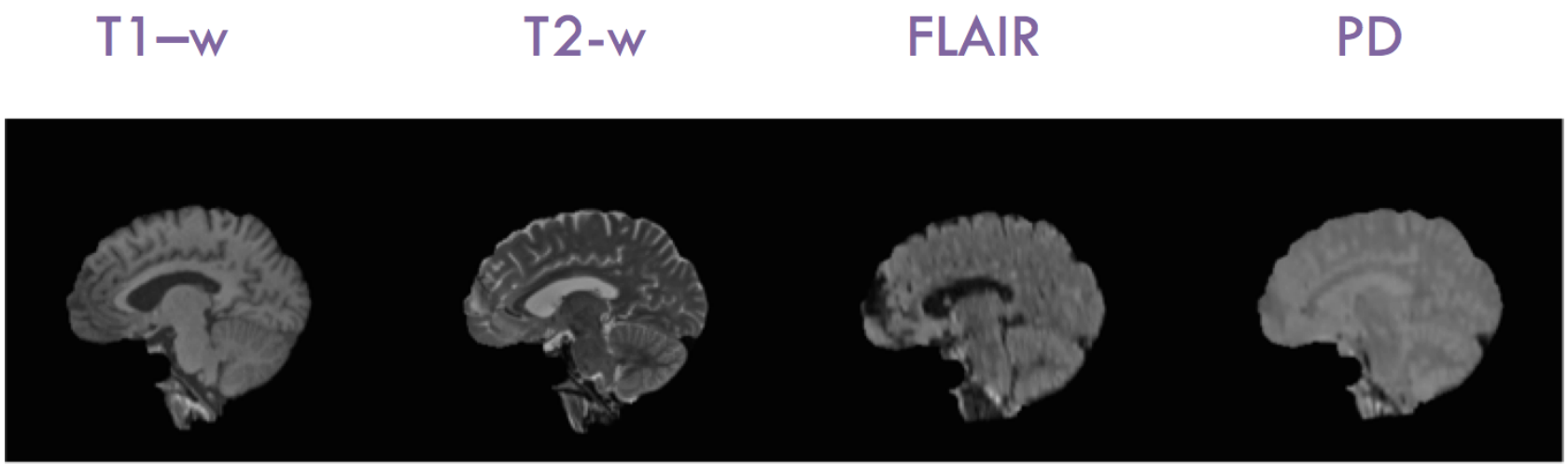
The stuff you have to do before you perform statistical analysis.

Before

T1–w T2-w FLAIR PD



After



Outline

- NIfTI file format (oro.nifti)
- Image preprocessing (fslr)
- Other R packages (ANTsR , oro.dicom, extrantsr)
- Multiple sclerosis lesion segmentation (oasisr, SuBLIME)

NIfTI file format

Neuroimaging Informatics Technology Initiative (NIfTI) file format:

- Files with a .nii or .nii.gz extension
- Standardized representation of images
- Most commonly used type of analytic file
- Developed to facilitate cross-platform, cross-software interpretability
- 3-dimensional (3D) array: stacking individual slices on top of each other

NIfTI file format

The R package oro.nifti:

- Use the writeNIfTI, readNIfTI functions in the oro.nifti package
- Reads and writes NIfTI files
- Works with nifti R objects (S4 objects)
- Default for writeNIfTI is to save compressed NIfTI files

NIfTI file format

Let's switch to R and explore the NIfTI file format with oro.nifti.

Using data from Kirby 21, an open source multi-modal MRI reproducibility study with 21 healthy subjects (www.nitrc.org/projects/multimodal)

fslr: an FSL port to R

1. FSL is useful, open-source, scriptable software for neuroimaging analysis
2. Problem: Requires coding in bash
3. Solution: fslr Ports many of the main functions of FSL into R
4. Disclaimer: May not work on Windows operating systems

Package: fslr

Setting up fslr:

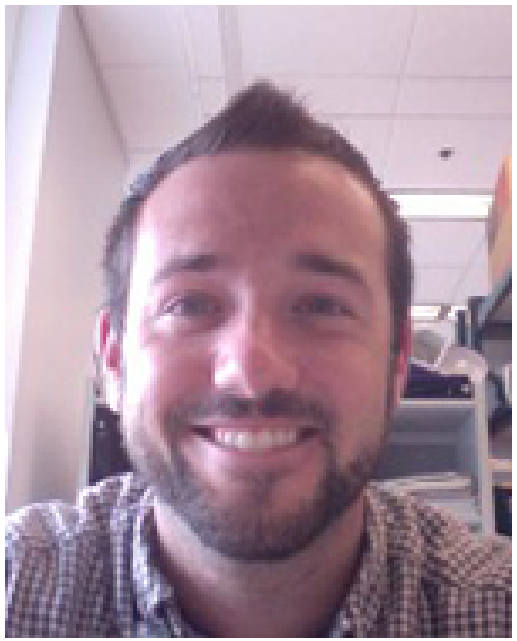
1. Install FSL
   http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation#Installing_FSL
2. Install the R packages fslr and oro.nifti

   ```
   install.packages("fslr")
   ```

3. In R, set your part to fsl with

   ```
   options(fsl.path= "/path/to/fsl/")
   ```

The creator of fslR: John Muschelli



Blog: hopstat.wordpress.com
Twitter: @StrictlyStat

Under the Hood

```
fsl_bet : function (infile, outfile = NULL, retimg = TRUE,
reorient = FALSE, intern = FALSE, opts = "",
betcmd = c("bet2", "bet"), ...)

{betcmd = match.arg(betcmd)
cmd <- get.fsl()
cmd <- paste0(cmd, sprintf("%s \"%s\" \"%s\" %s", betcmd,
infile, outfile, opts))
res = system(cmd, intern = intern)
ext = get.imgext()
outfile = paste0(outfile, ext)
if (retimg) {
img = readnii(outfile, reorient = reorient, ...)
return(img)
}
return(res) }
```

ANTsR

ANTsR (http://stnava.github.io/ANTsR/) is apackage providing ANTs features in R as well as imaging-specific data representations, spatially regularized dimensionality reduction and segmentation tools

```
install.packages("devtools")
```

```
library(devtools)
install_github("stnava/cmaker")
install_github("stnava/ITKR")
install_github("stnava/ANTsR")
```

More R packages

More R packages for structural MRI analysis:

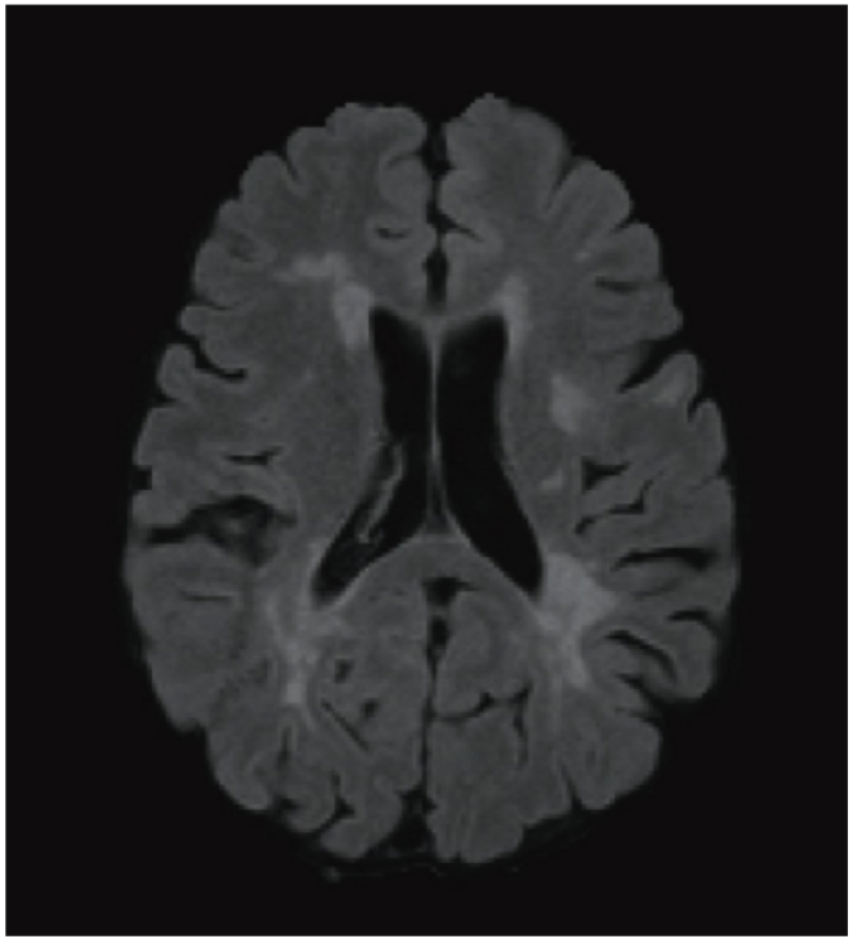
```
install.packages("oro.dicom") # working with DICOM images
install_github("muschellij2/extrantsr") # EXTRA ANTsR functions
```

More R packages

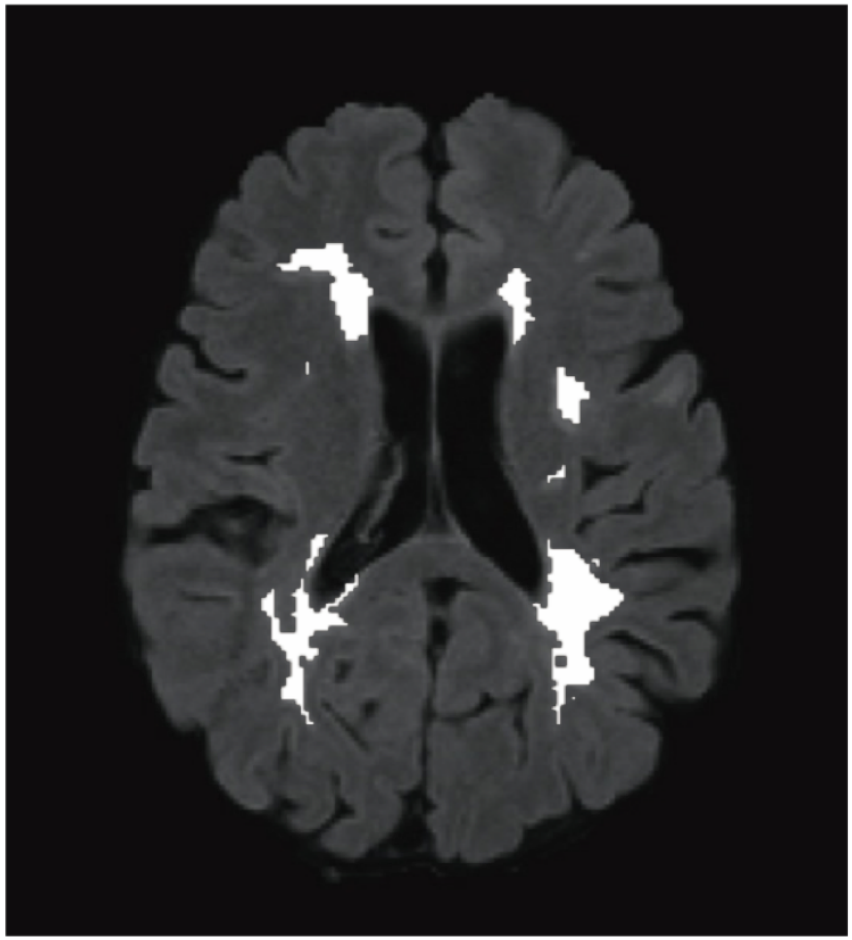
More R packages for structural MRI analysis:

```
install.packages("oro.dicom") # working with DICOM images
install_github("muschellij2/extrantsr") # EXTRA ANTsR functions
```

MS Lesion Segmentation



MS Lesion Segmentation



MS Lesion Segmentation

- R package: oasis

  `install.packages(oasis)`

- R package: SuBLIME

  `library(devtools) install_github("emsweene/SuBLIME_package")`

Want to learn more?

Introduction to Neurohacking in R (Coursera)
(www.coursera.org/learn/neurohacking/)