

# **NEUROIMAGING ANALYSIS IN R**

**ELIZABETH SWEENEY, SCM, PHD**

ASSISTANT PROFESSOR  
BIOSTATISTICS DIVISION  
HEALTHCARE POLICY AND RESEARCH  
WEILL CORNELL  
NEW YORK, NY

# Background:



Weill Cornell, Week 2!  
Assistant Professor  
Division of Biostatistics



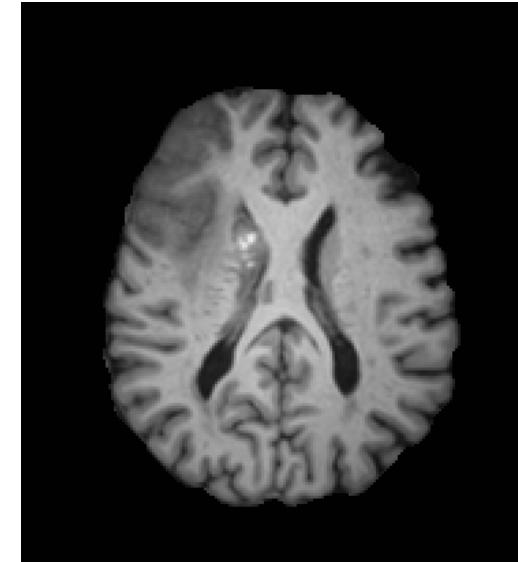
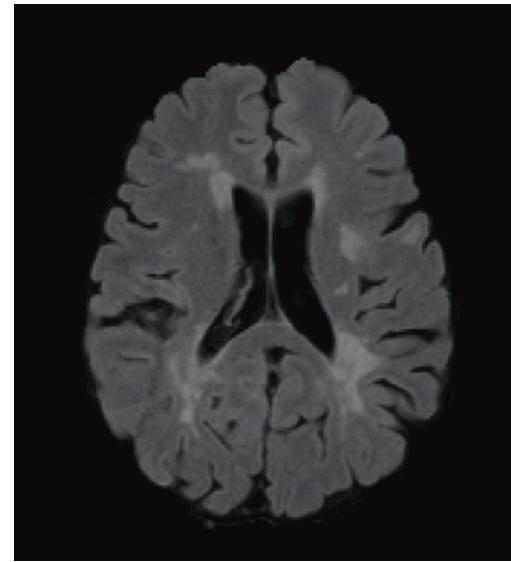
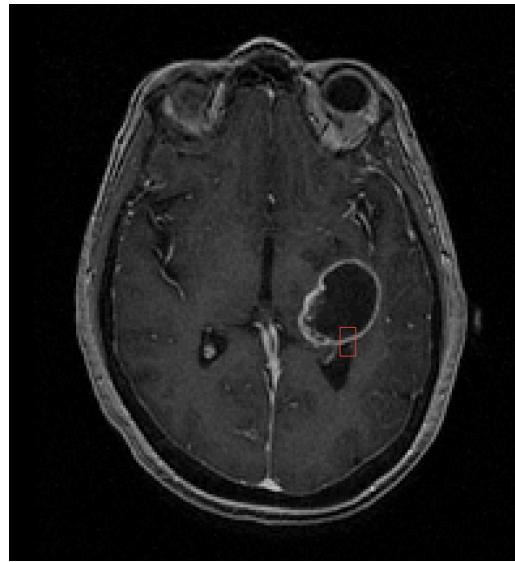
Covera Health, 2018 - 2019  
Senior Data Scientist

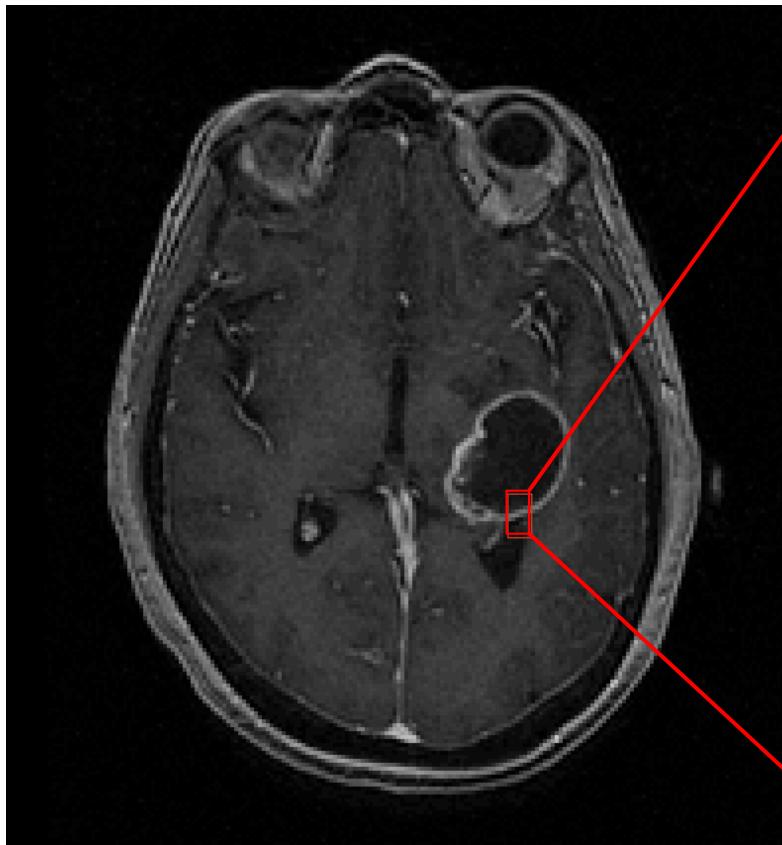


Flatiron Health, 2017 – 2018  
Senior Quantitative Scientist

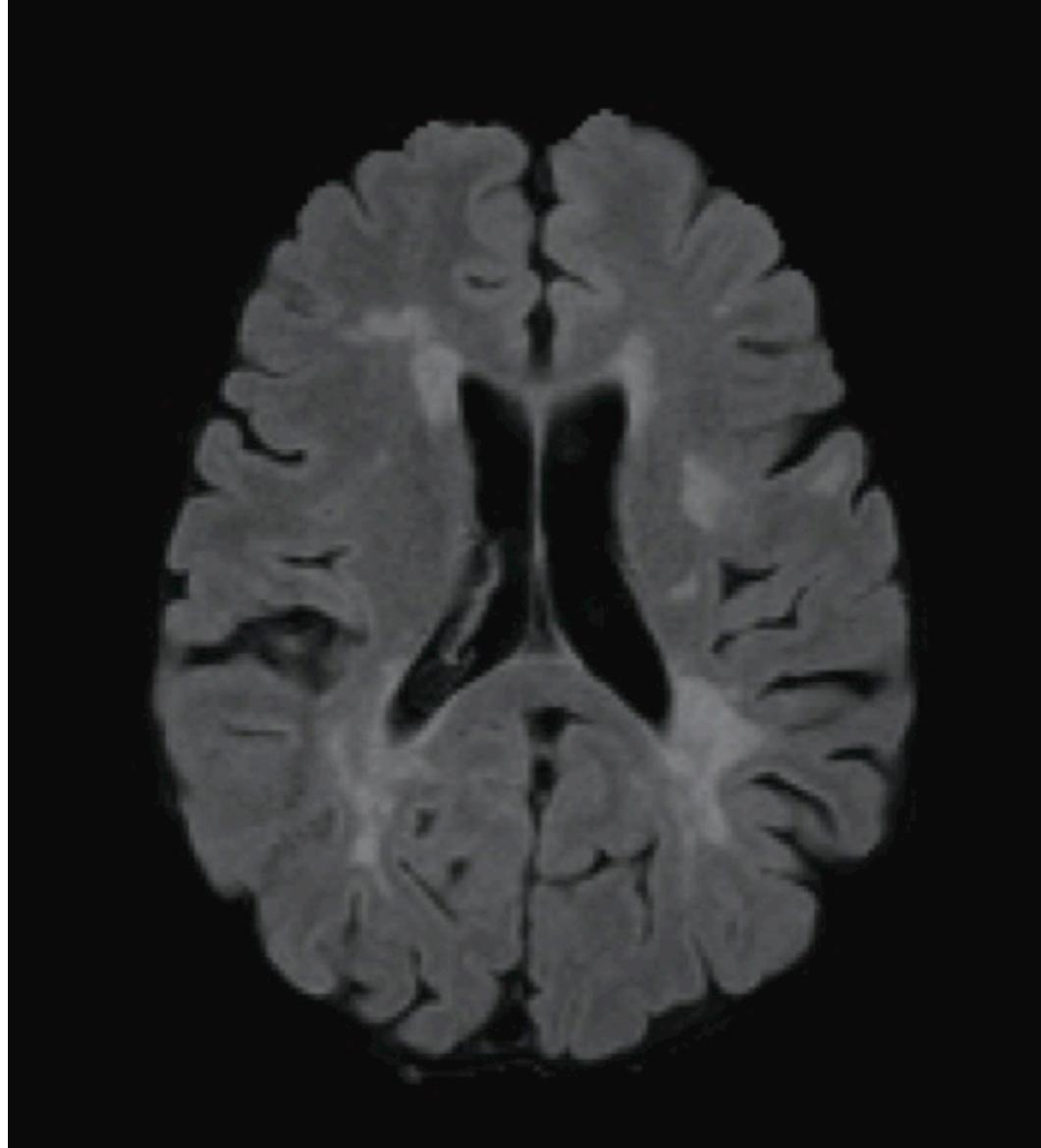
How to work with structural magnetic  
resonance imaging (sMRI) of the brain  
in R!

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

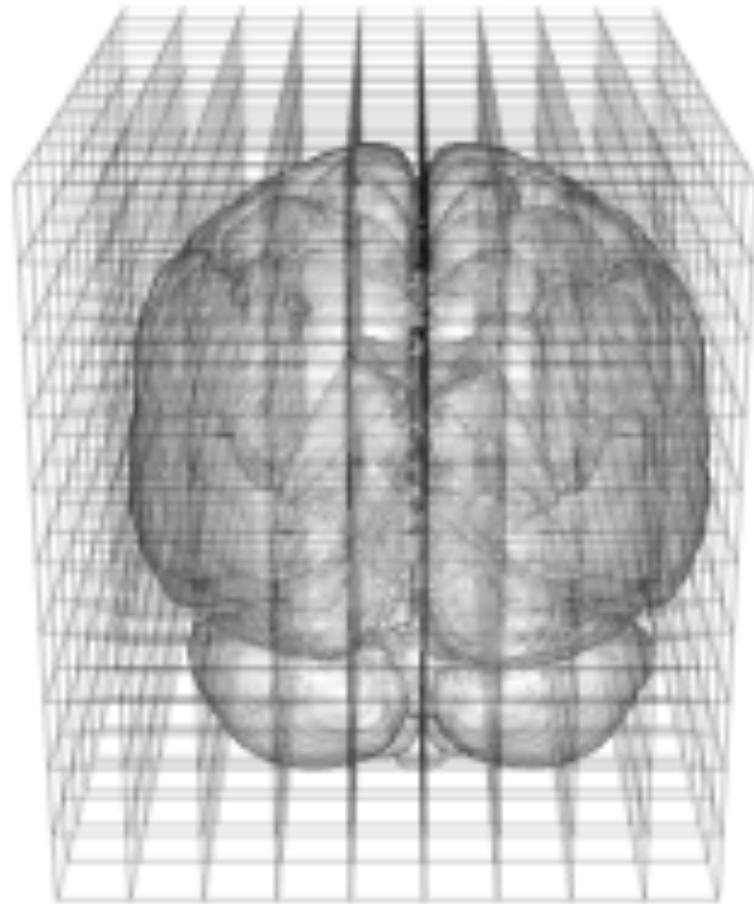




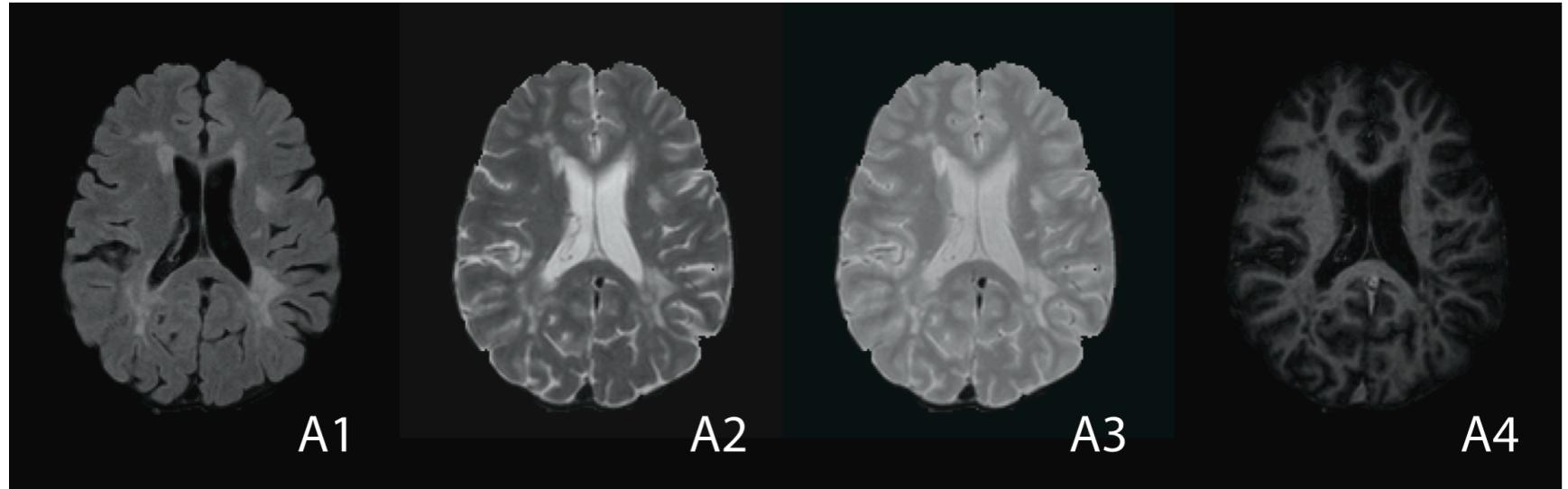
43	42	47	32	38	33
40	45	48	42	49	44
40	55	57	57	51	55
56	56	58	79	121	165
68	99	149	179	199	190
187	199	186	139	108	81
165	115	47	39	69	76
29	24	29	74	107	93
29	42	55	58	71	87
46	40	45	40	61	92
44	46	43	31	62	88



**180 x 216 = 38,800 voxels**



**180 x 180 x 216 ≈ 7 million voxels**



A1) Fluid Attenuated Inversion Recovery (FLAIR)

A2) T2-weighted (T2)

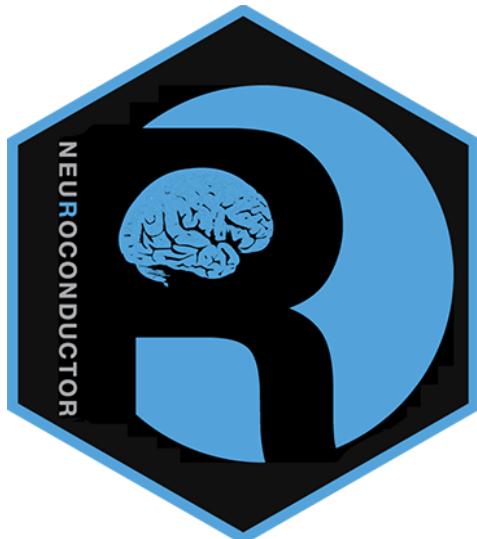
A3) Proton Density (PD)

A4) T1-weighted (T1)

**4 x 7million = 28 million voxels**

**Back in the day...**

# Neuroconductor: [neuroconductor.org](https://neuroconductor.org)



Neuroconductor<sup>1</sup> is an open-source platform for rapid testing and dissemination of reproducible computational imaging software. The goals of the project are to:

- provide a centralized repository of R software dedicated to image analysis;
- disseminate quickly software updates;
- educate a large, diverse community of scientists using detailed tutorials and short courses;
- ensure quality via automatic and manual quality controls; and
- promote reproducibility of image data analysis.

<sup>1</sup>Muschelli, John, et al. "Neuroconductor: an R platform for medical imaging analysis." *Biostatistics* 20.2 (2018): 218-239.

# Neuroconductor: neuroconductor.org

The screenshot shows the Neuroconductor website's package list page. At the top, there is a dark blue header bar with the Neuroconductor logo, navigation links (Install, Submit Package, List Packages, Developers, Help, About, Log in), a search input field, and a blue 'Search' button. Below the header, a breadcrumb navigation shows 'Home / All Neuroconductor Packages'. The main title 'All Neuroconductor Packages' is displayed prominently. Below the title are three buttons: 'View Dependency Graph', 'Browse releases', and 'View Pending Packages'. To the left, there is a 'Show' dropdown set to '100' entries and a 'Search:' input field. The main content area is a table listing four packages:

Package	Version	Title	Maintainer	GitHub	Last Updated
aal	0.1.1	Automated Anatomical Labeling ('AAL') Atlas	John Muschelli	<a href="#">muschellij2/aal</a>	2019-04-29
afnir	0.4.6	Wrapper Functions for 'AFNI' (Analysis of Functional 'NeuroImages')	John Muschelli	<a href="#">muschellij2/afnir</a>	2019-04-29
ANTsR	0.4.9	ANTs in R: Quantification Tools for Biomedical Images	Brian B. Avants	<a href="#">stnava/ANTsR</a>	2019-05-02
ANTsRCore	0.6.3.9	Core Software Infrastructure for 'ANTsR'	Brian B. Avants	<a href="#">ANTsX/ANTsRCore</a>	2019-05-06

# Neuroconductor: [neuroconductor.org](http://neuroconductor.org)



**Adi Gherman, MSE**

Lead developer



**John Muschelli, PhD**

R package guru



**Brian Caffo, PhD**

Professor



**Ciprian Crainiceanu, PhD**

Professor

# Neuroconductor: [neuroconductor.org](https://neuroconductor.org)

```
> source("https://neuroconductor.org/neurocLite.R")
```

# NIfTI File Format

Much of neuroimaging data is stored in a NIfTI file format.  
These files have 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

# oro.nifti Package

```
> neuro_install('oro.nifti')
> library(oro.nifti)
```

# oro.nifti Package

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

# Kirby 21: [www.nitrc.org/projects/multimodal](http://www.nitrc.org/projects/multimodal)

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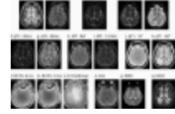
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**MRI SIMULATOR™** SIMULATE THE MRI ENVIRONMENT  
INCREASE DATA QUALITY   REDUCE PARTICIPANT ANXIETY   REDUCE PARTICIPANT DROPOUT RATE  
PSYCHOLOGY SOFTWARE TOOLS

**Multi-Modal MRI Reproducibility Resource** Visit Website

We have acquired scan-rescan imaging sessions on 21 healthy volunteers (no history of neurological disease). Imaging modalities include MPRAGE, FLAIR, DTI, resting state fMRI, B0 and B1 field maps, ASL, VASO, quantitative T1 mapping, quantitative T2 mapping, and magnetization transfer imaging. All data have been converted to NIFTI format.

  
Image 1 of 2  
Click for more.

**Statistics** i

Home Page  
NeuroLex ID: nlx\_1...  
RRID: SCR\_002442  
Funding: NIH/NCRR...  
Forums: 6 message...  
News Items: 3  
Total Downloads: ...  
Registered: Dec 16,...

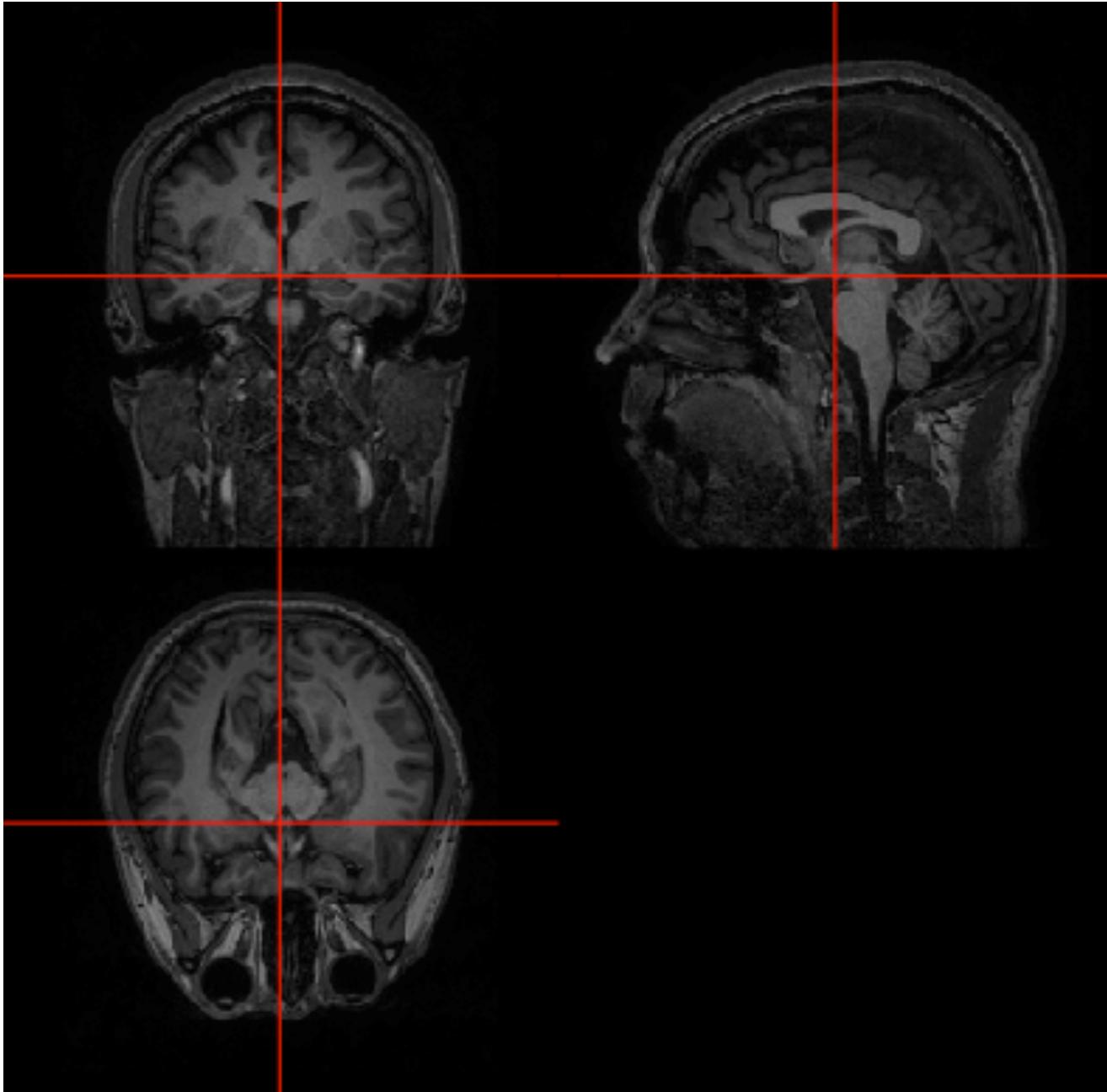
# oro.nifti Package

We will use a subject from the Kirby 21, an open source multi-modal MRI reproducibility study with 21 healthy subjects ([www.nitrc.org/projects/multimodal](http://www.nitrc.org/projects/multimodal)) to show what we can do with the oro.nifti package:

```
> Image <- readNIFTI('SUBJ0001-01-MPRAGE.nii.gz',  
+ reorient=FALSE)  
> dim(Image)  
[1] 170 256 256
```

# oro.nifti Package

> orthographic(Image)



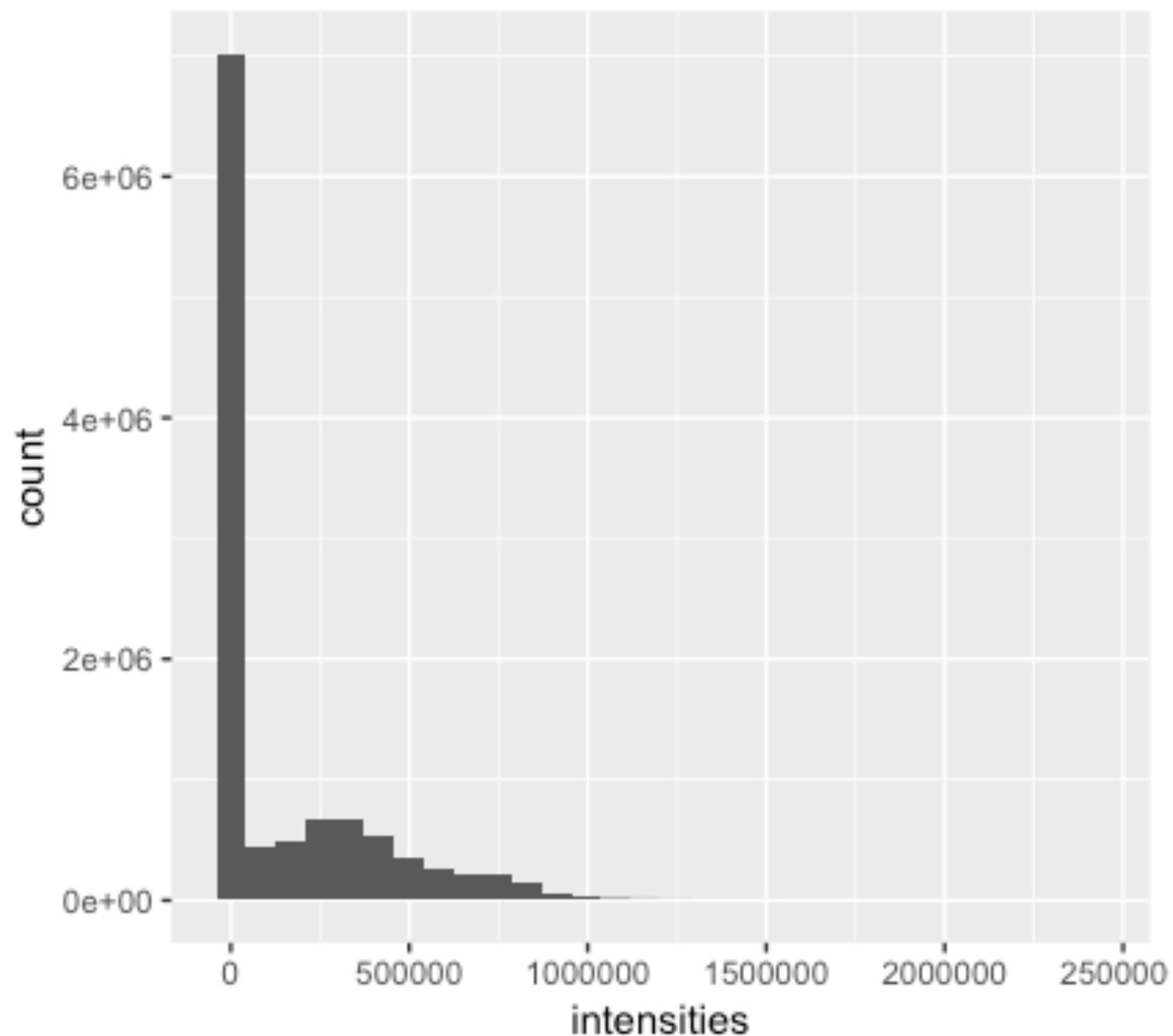
# oro.nifti Package

```
> summary(Image)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0	0	3416	143789	256204	2408322

# oro.nifti Package

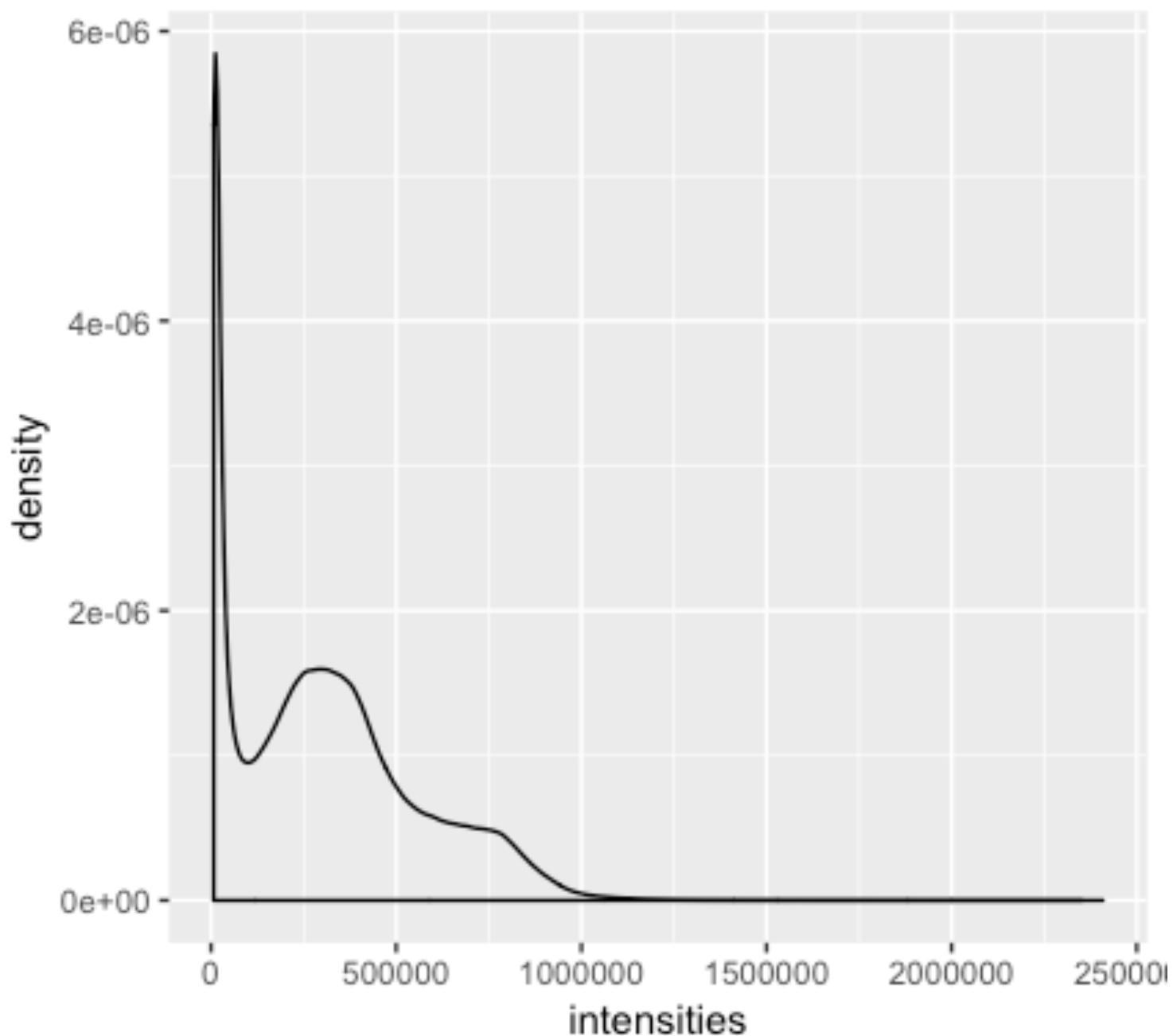
```
> Image.frame <- data.frame(intensities = c(Image))  
  
> ggplot(Image.frame , aes(x = intensities))  
+ geom_histogram()
```



# oro.nifti Package

```
> Image.frame.5000 <- Image.frame %>%
  filter(intensities >= 5000)

> ggplot(Image.frame.5000 , aes(x = intensities))
  + geom_density()
```



# fslr Package

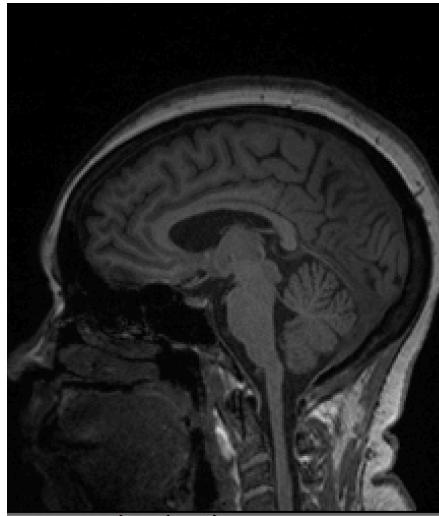
```
> neuro_install('fslr')
> library(fslr)
```

# fslr Package

- FSL is useful, open-source, scriptable software for neuroimaging analysis.
- One of the main problems with using FSL is that it requires coding in bash!
- The solution is to use the `fslr` package.
- The `fslr` package ports many of the main functions of FSL into R.

# fsdr Package

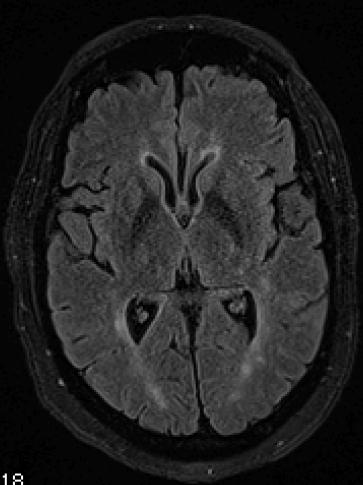
T1-w



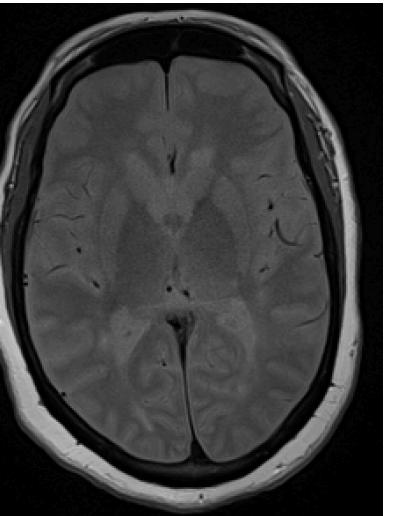
T2-w



FLAIR



PD



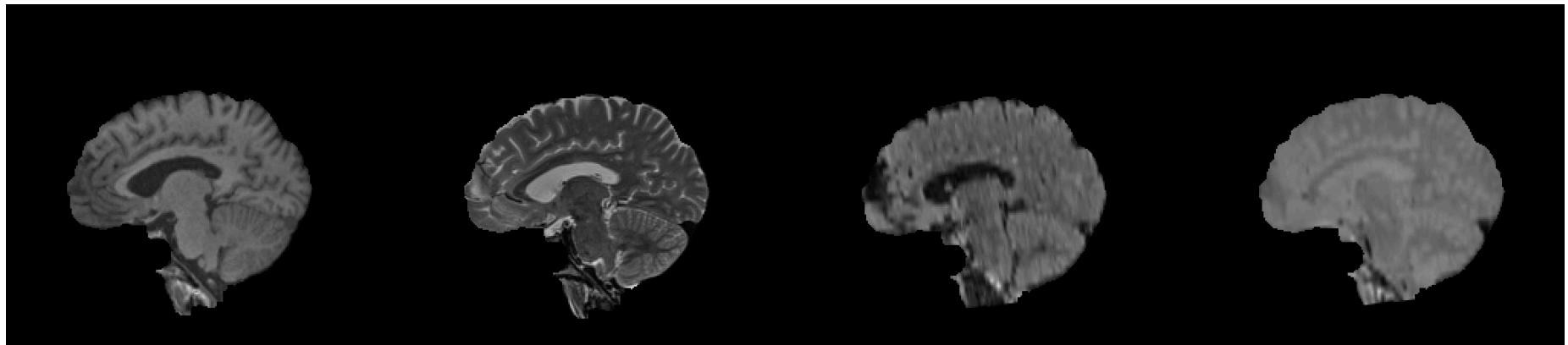
# fsdr Package

T1-w

T2-w

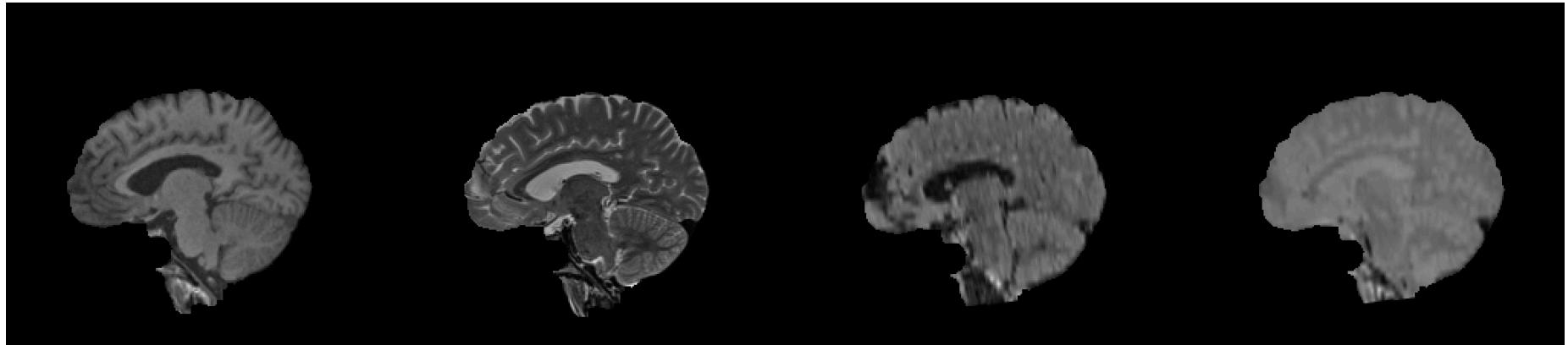
FLAIR

PD



# fslr Package

Entirely in R!<sup>1</sup>



<sup>1</sup> Muschelli, J., Sweeney, E. M., Lindquist, M. A., and Crainiceanu, C. M. (2015). fslr: Connecting the FSL Software with R. *The R Journal*.

# fslr Package

- `fsl_biascorrect` – image inhomogeneity correction
- `fslbet` – skull stripping
- `flirt` – image coregistration

# fslr Package

```
> fslbet
function (infile, outfile = NULL, retimg = TRUE, reorient = FALSE,
    intern = FALSE, opts = "", betcmd = c("bet2", "bet"), verbose = TRUE,
    ...)
{
  betcmd = match.arg(betcmd)
  cmd <- get.fsl()
  outfile = check_outfile(outfile = outfile, retimg = retimg,
    fileext = "")
  infile = checkimg(infile, ...)
  outfile = checkimg(outfile, ...)
  outfile = nii.stub(outfile, ...)
  cmd <- paste0(cmd, sprintf("%s \"%s\" \"%s\" %s", betcmd,
    infile, outfile, opts))
  if (verbose) {
    message(cmd, "\n")
  }
  res = system(cmd, intern = intern)
  ext = get.imgext()
  outfile = paste0(outfile, ext)
  if (retimg) {
    img = readnii(outfile, reorient = reorient, ...)
    return(img)
  }
  return(res)
}
```

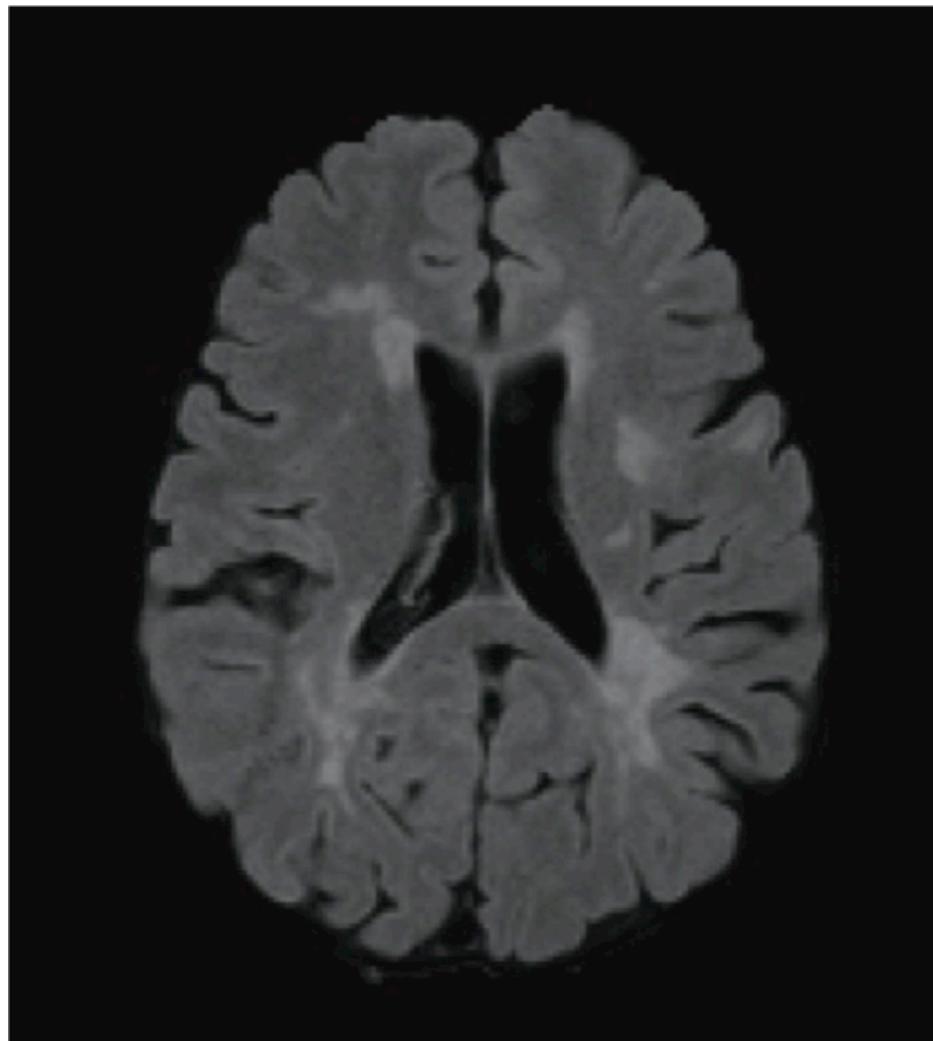
# Resources

“The Statistical Analysis of Structural MRI Neuroimaging Data”<sup>1</sup>

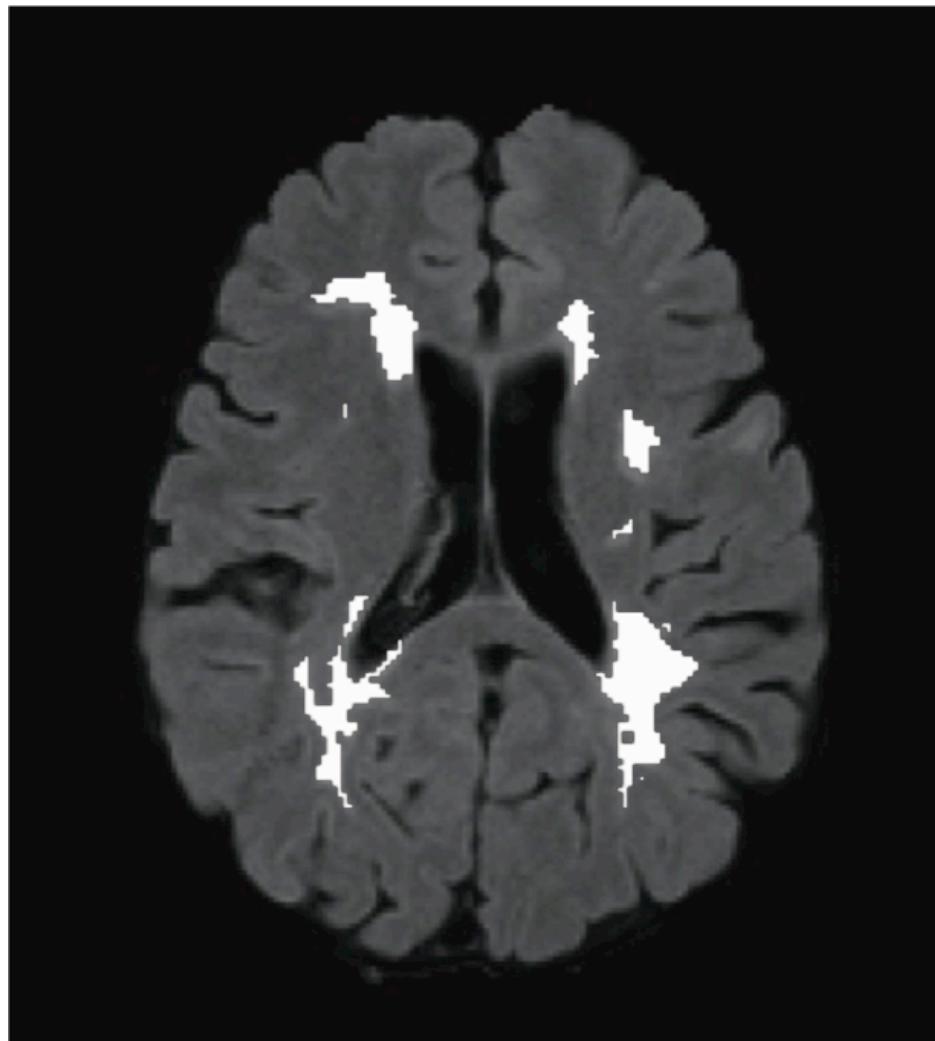
“Neurohacking in R” on 

<sup>1</sup> Sweeney, E. M., Eloyan, A., Shinohara, R. T., and Crainiceanu, C. M. (In Press). The Statistical Analysis of Structural MRI Neuroimaging Data. *Handbook of Modern Statistical Methods: Neuroimaging Data Analysis*. CRC Press.

# Structural MRI in Multiple Sclerosis

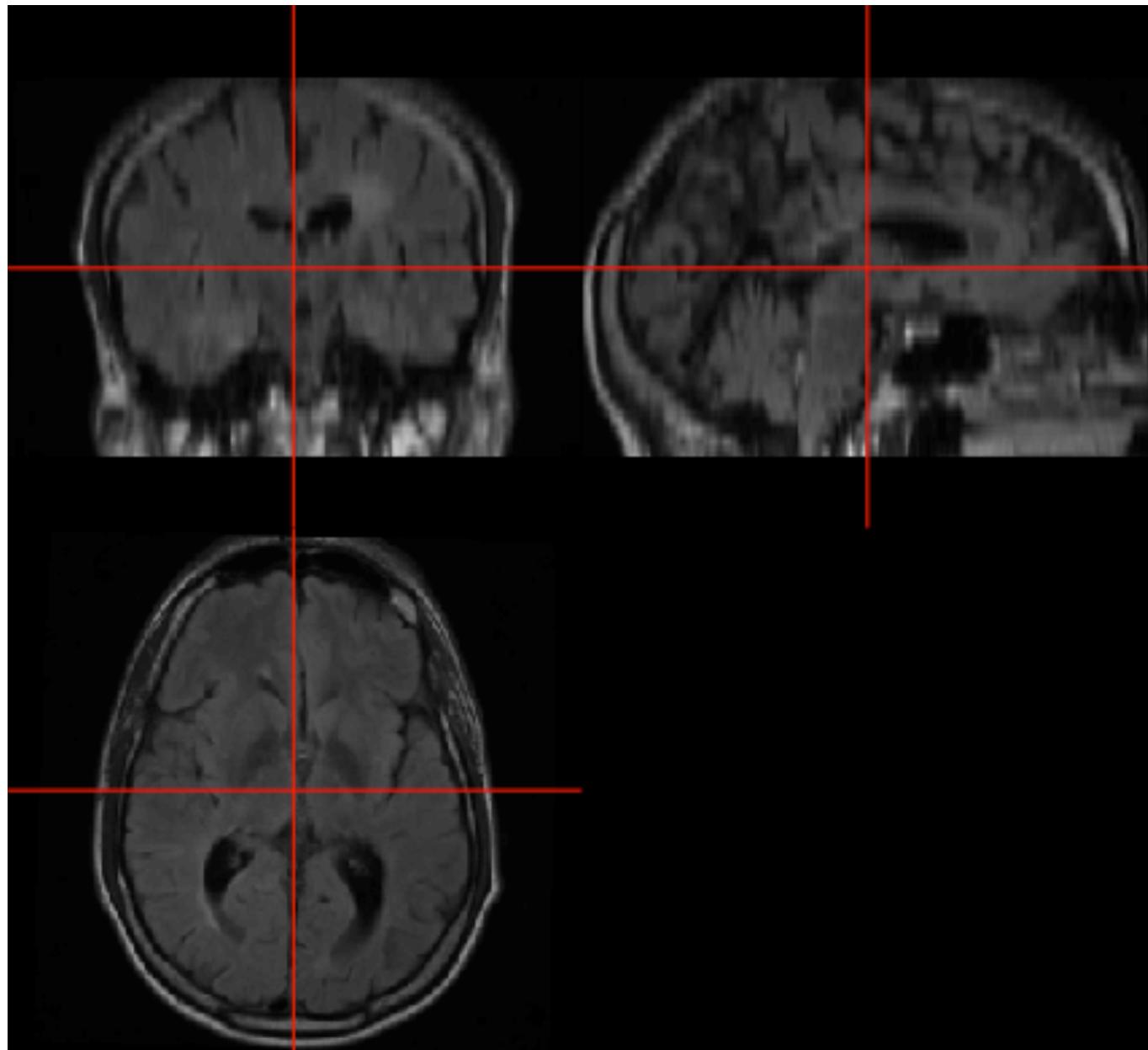


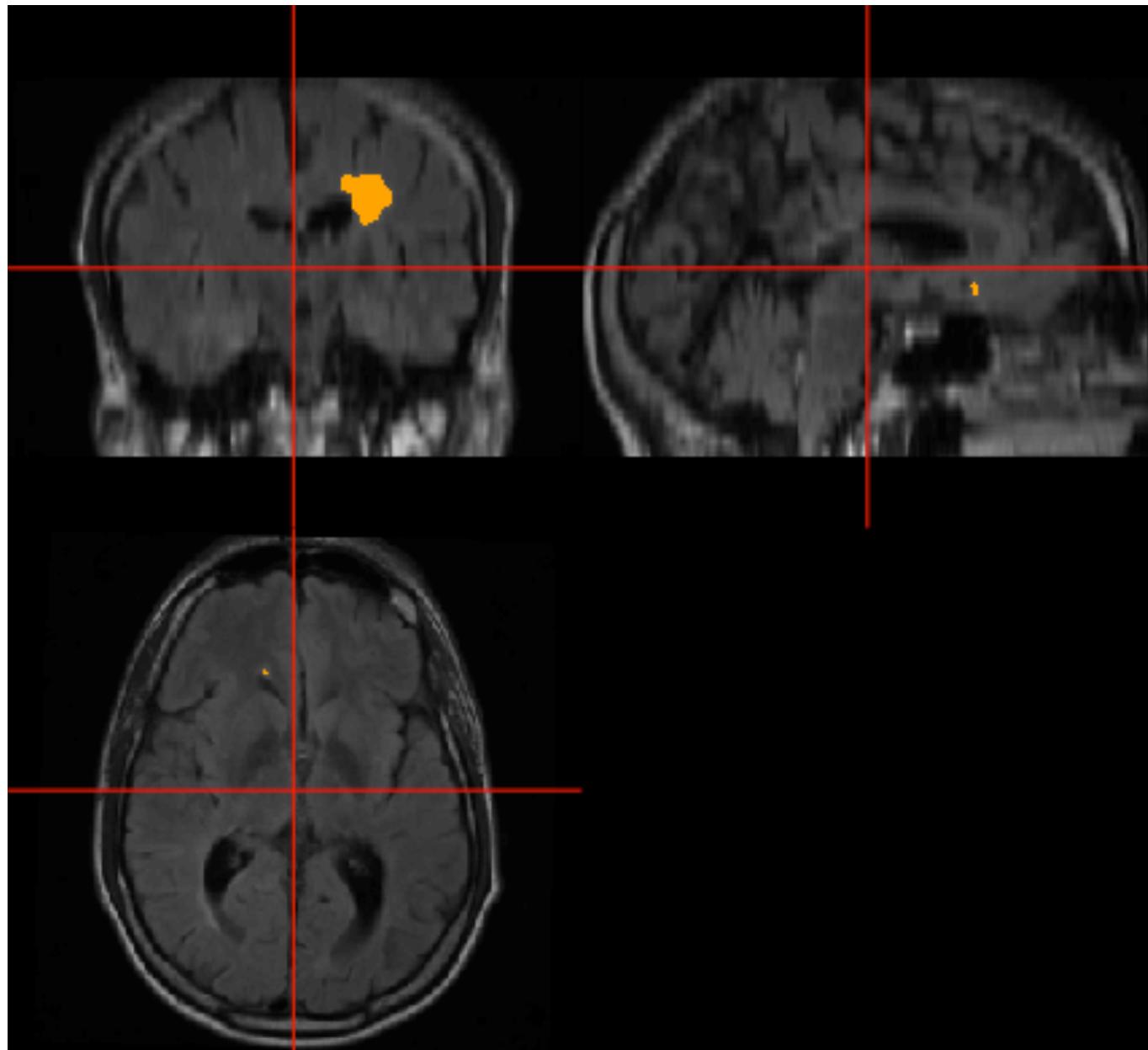
# Structural MRI in Multiple Sclerosis



# **oasis Package**

```
> neuro_install('oasis')
> library(oasis)
```





Thank you!

