

Processing Neuroimaging Data in R: Capabilities

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What can we do in R?

1. Read/Write Images
2. Visualization of Images
3. Inhomogeneity/Bias Field Correction
4. Skull Stripping/Brain Extraction
5. Image Registration
6. Tissue-Class Segmentation
7. Image operations
8. Complex Modeling (yeah - it's R)

Starting from Raw Data

- `oro.dicom` - read/write DICOM data, the nifti object
 - Pure R implementation
- `dcm2niir` - uses `dcm2nii` from Chris Rorden
 - Can handle Par/Rec and many scanner types
- `matlabr` - could use `dicomread` matlab code and execute through R

Introduction: Packages

Medical Imaging Task View

- `oro.nifti`: read/write data, the nifti object
- `fslr`: process data (need FSL for most of the functionality)
- **ANTsR**: process data (full toolbox)
- **extrantsr**: makes ANTsR work with nifti objects
- `dti` - adaptive smoothing and diffusion tensor tools
- `fmri` - post-processing analysis: linear models and p-value smoothing
- `AnalyzeFMRI` - fMRI analysis (last updated in 2013)
- `spm12r` package calls out MATLAB using SPM

Data used from NITRC

Multi-modal dataset from HAMMER, (NIfTI conversion from ANALYZE).

- Data from https://www.nitrc.org/frs/?group_id=187 (testing folder in White_Matter_Lesion_Segmentation_Testdata.zip)
- 4 MRI sequences: **T1-weighted**, T2-weighted, PD, **FLAIR**

files

t1	t2	pd	flair
"T1.nii.gz"	"T2.nii.gz"	"PD.nii.gz"	"FLAIR.nii.gz"

Basics: Read in the Files!

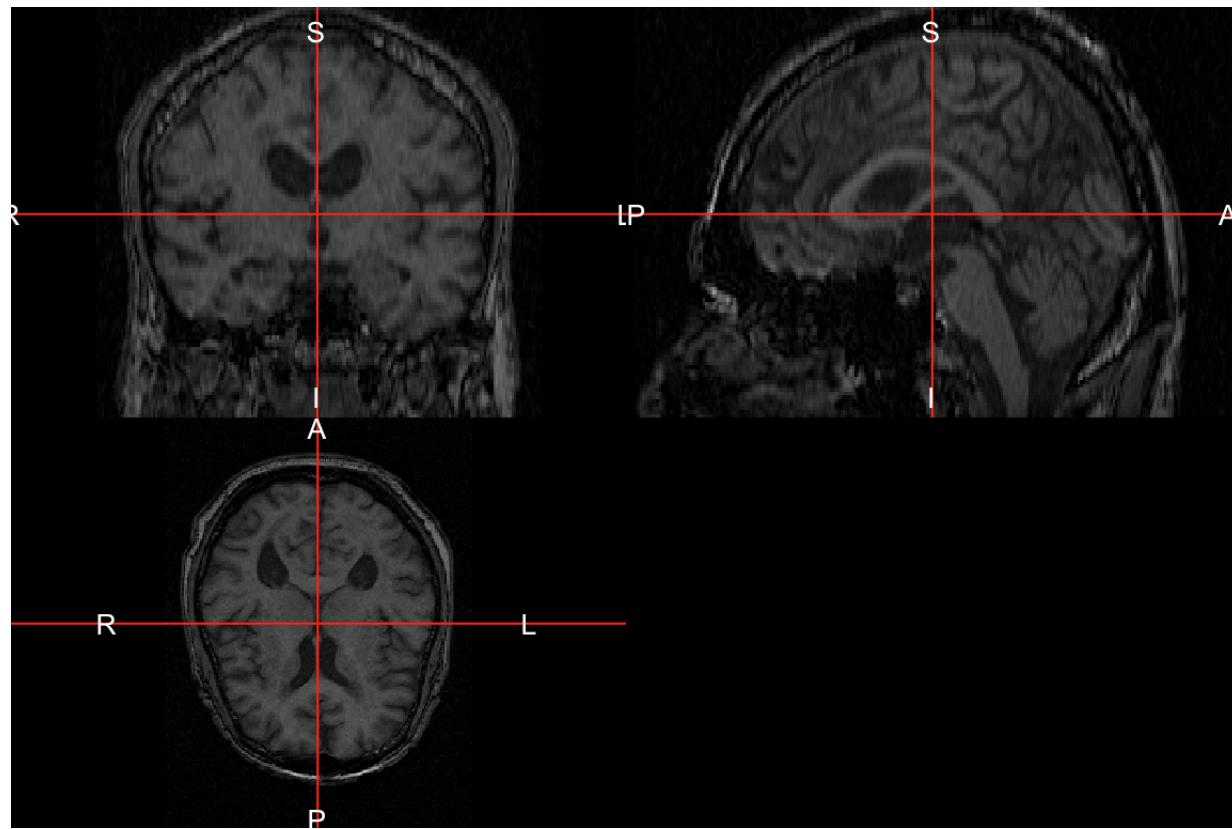
fslr: readnii uses `oro.nifti::readNIFTI`:

```
library(fslr)
base_t1 = readnii(files["t1"])
```

- like an array
- ANTsR uses pointers (faster), but not as intuitive

Orthographic View

```
library(fslr)  
fslr::ortho2(base_t1)
```



Orthographic Overlays

```
over_50 = mask_img(base_t1, base_t1 > 40); ortho2(base_t1, over_50)
```

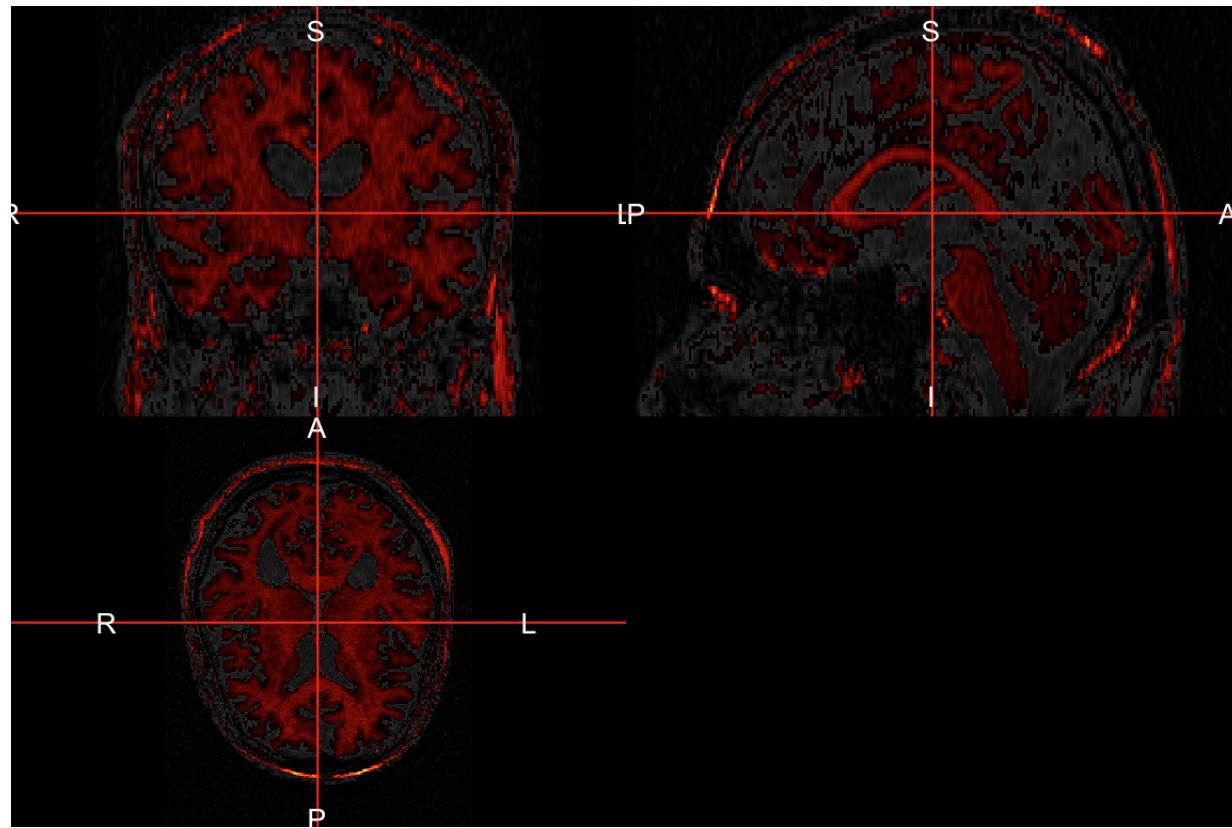


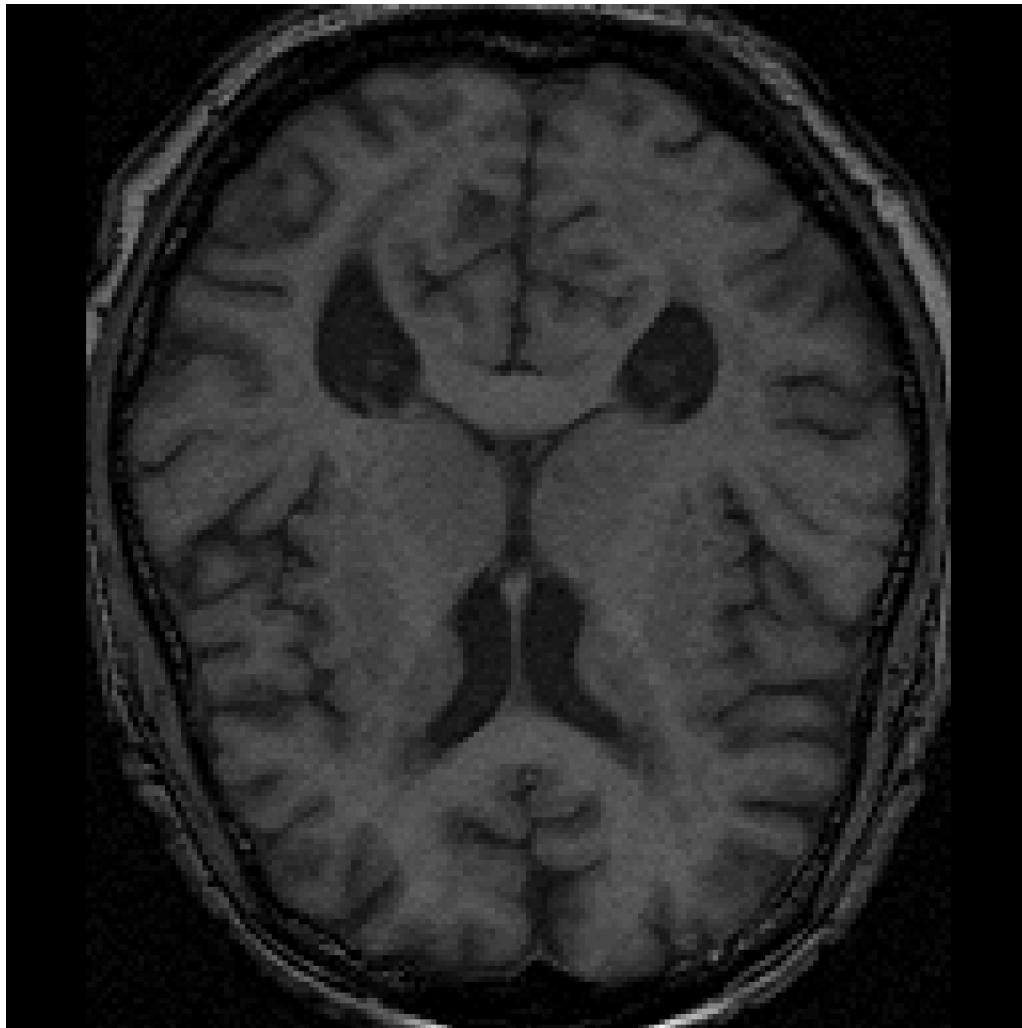
Image Slices

```
image(base_t1, z = 55, plot.type = "single")
```

Slice Overlays

```
over_50[over_50 <= 0] = NA; over_50 = cal_img(over_50)
overlay(base_t1, over_50, z = 55, plot.type = "single")
```

Cropped Image Slices



Bias Field Correction

ANTsR/extrantsr

- `bias_correct` from `extrantsr` package calls
`ANTsR::n4BiasFieldCorrection` (N. J. Tustison et al. 2010)
- EM-like, assumes bias is smooth over space, logs the data

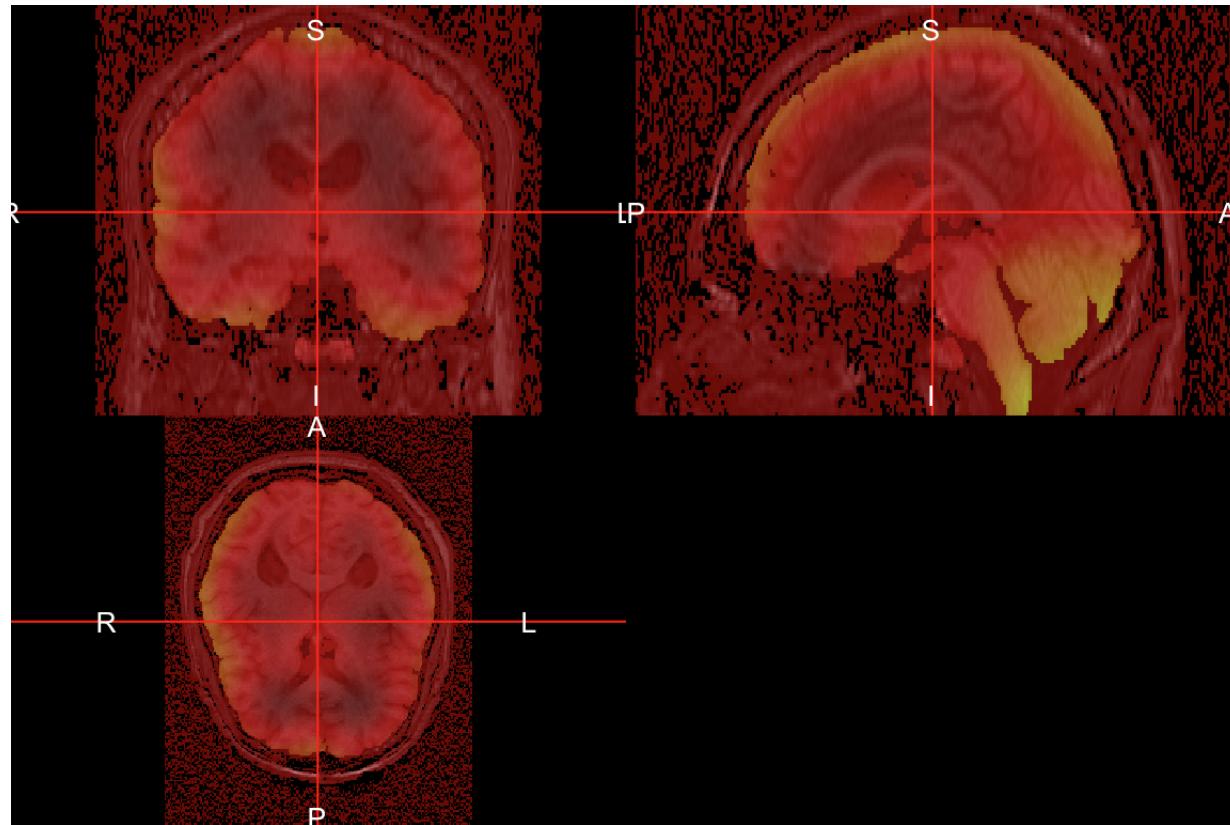
```
library(extrantsr)
n4_t1 = bias_correct(file = base_t1, correction = "N4", retimg = TRUE)
```

fslr: Uses method by Sled, Zijdenbos, and Evans (1998) (slow)

```
bc_t1 = fsl_biascorrect(file = base_t1)
FSLDIR='/usr/local/fsl/'; export FSLDIR; sh "${FSLDIR}/etc/fslconf/fsl.sh"; FS:
```

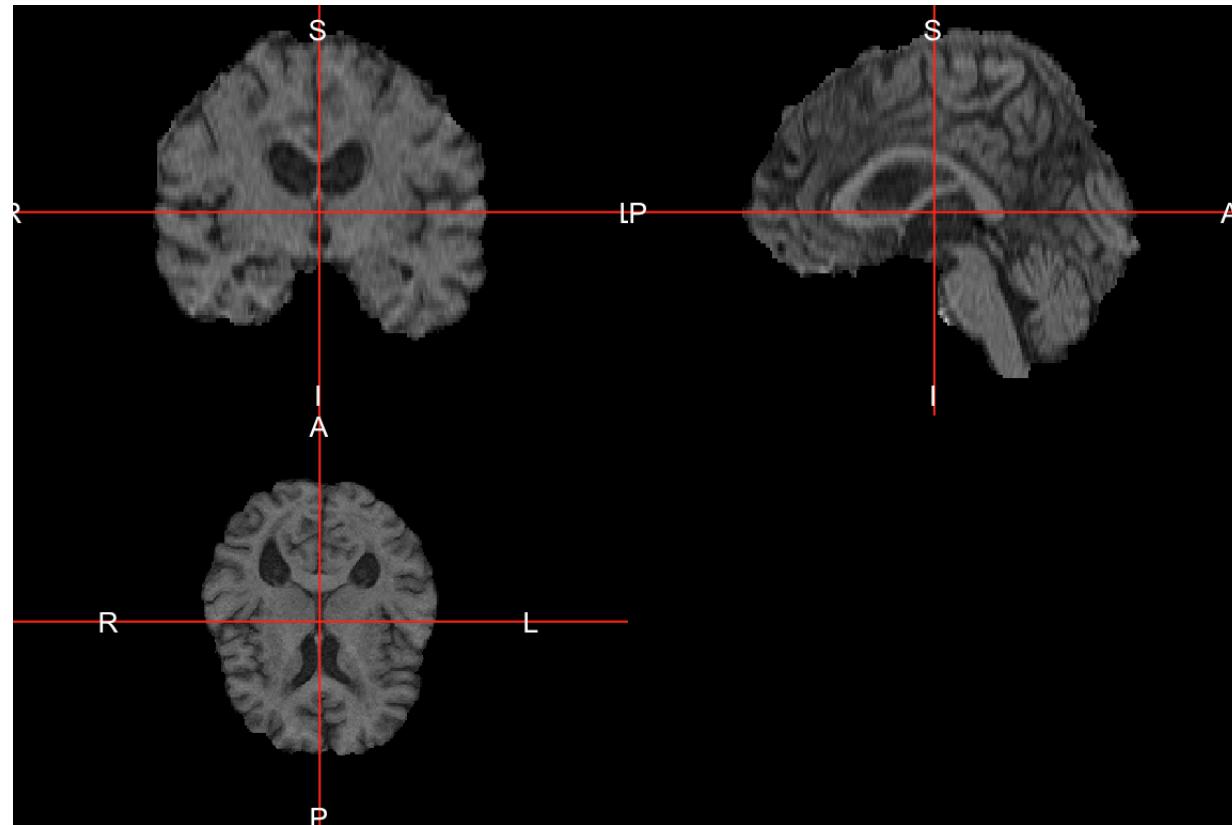
Bias Field Correction: Results

```
ratio = finite_img(n4_t1 / base_t1)
ortho2(n4_t1, ratio, col.y = alpha(hotmetal(), 0.5))
```



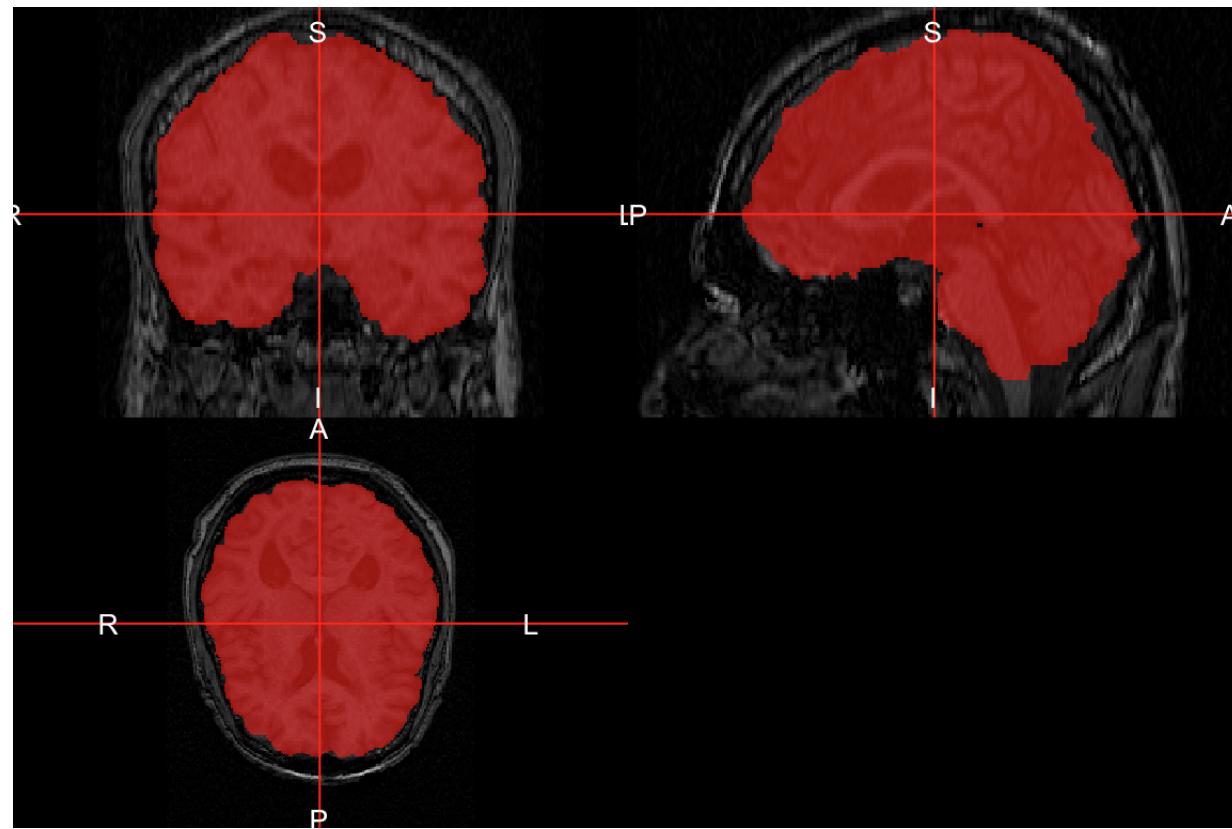
Skull Stripping: FSL BET

```
ss_t1 = fslbet(n4_t1, outfile = "SS_Image")  
FSLDIR='/usr/local/fsl/'; export FSLDIR; sh "${FSLDIR}/etc/fslconf/fsl.sh"; FS:
```



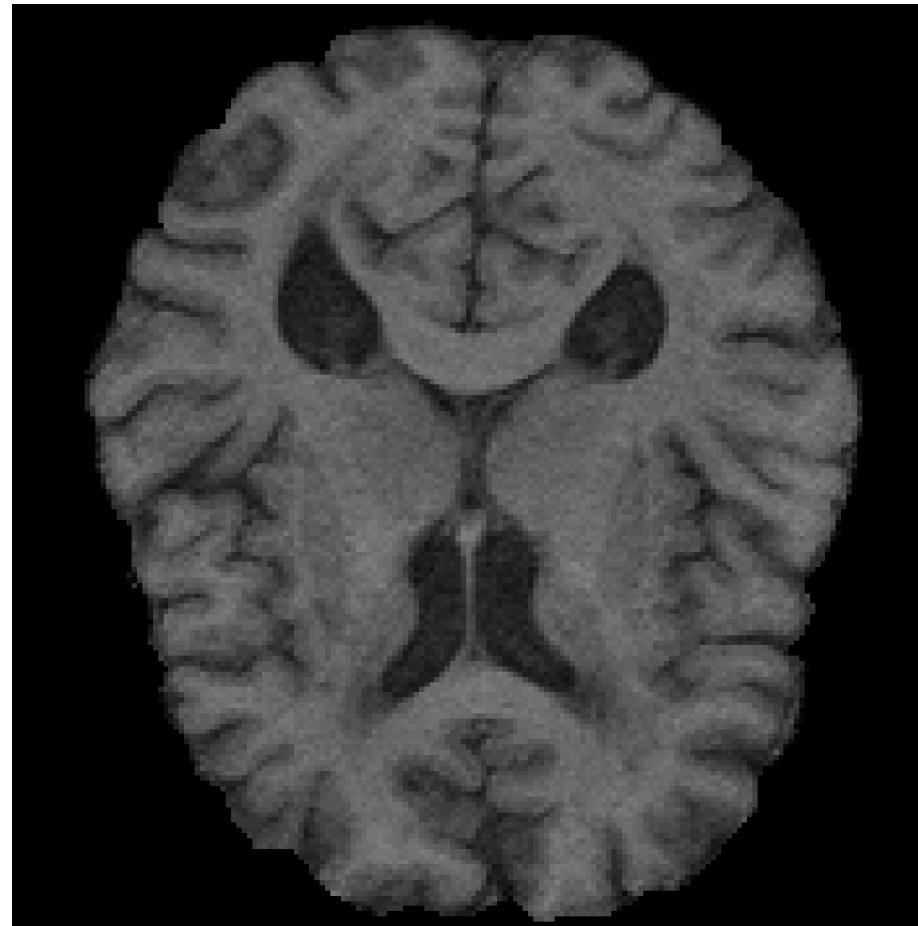
Overlaying Skull Stripped mask

```
mask = ss_t1 > 0  
ortho2(base_t1, y = mask, col.y = alpha("red", 0.5))
```



Visualization: Cropped Image Slices

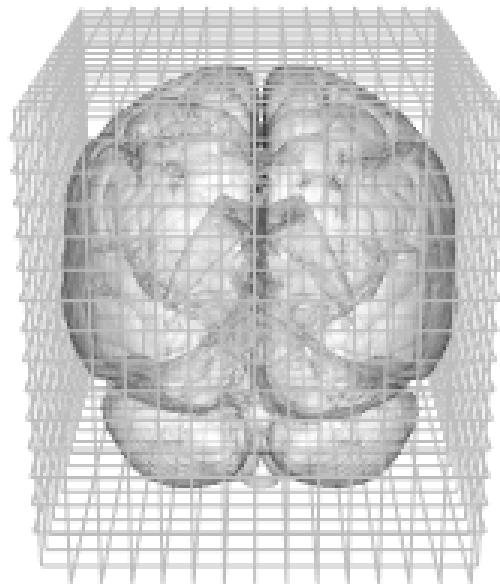
```
cropped = dropEmptyImageDimensions(ss_t1)
image(cropped, z = floor(dim(cropped)[3]/2), plot.type = "single")
```



Visualization: 3-dimensions

- `rgl, misc3d` (`contour3d` function)
- `brainR` - put on a webpage with some controls

```
devtools:::source_gist("bd40d10afabc503d71e8")
```



Rigid-Body Registration

ANTsR/extrantsr

- `antsRegistration` - rigid/affine/non-linear diffeomorphic
- `extrantsr::registration` - wraps `antsRegistration` to use `nifti` objects

fslr

- `flirt` - linear/affine registration
- `fnirt` - non-linear registration (need affine first)
- `fnirt_with_affine` - wraps above 2

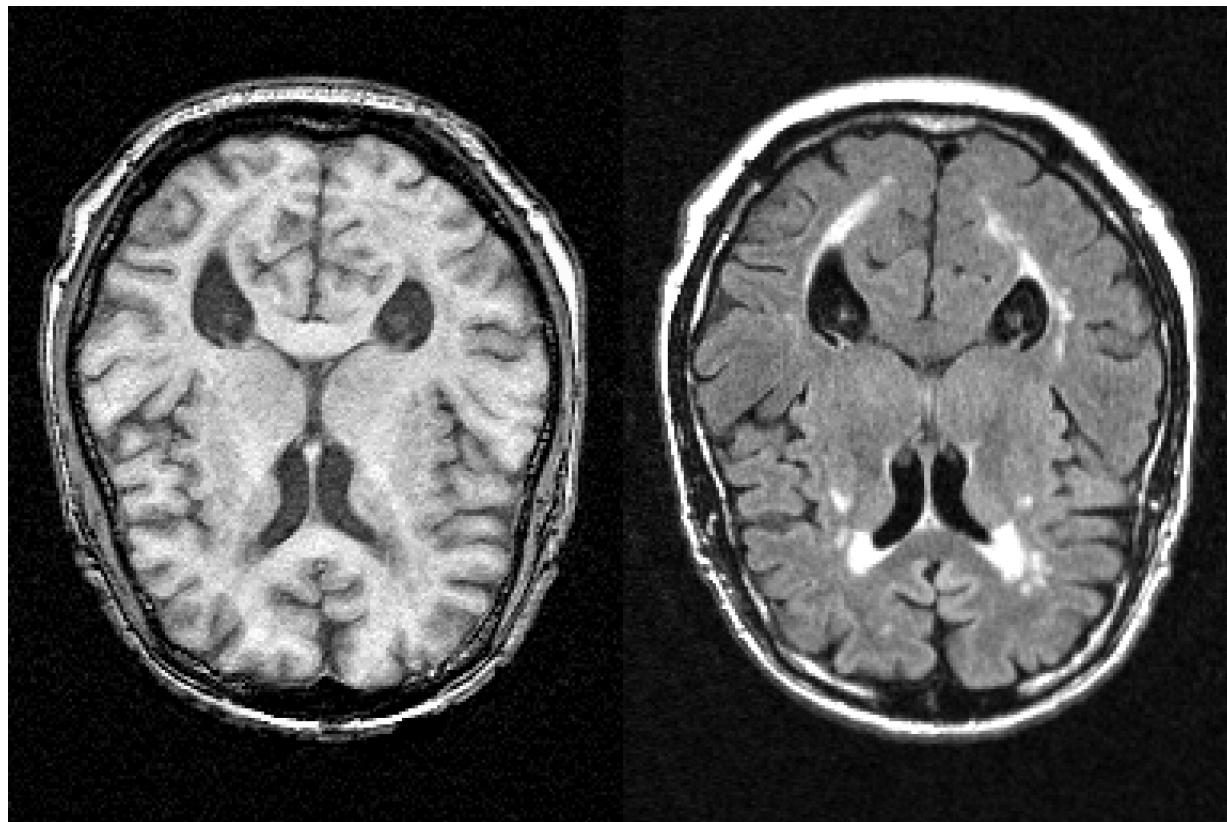
Rigid-Body Registration

- `registration` from `extrantsr` is a general function to do linear/non-linear registration, using `antsRegistration`

```
ants_reg_flair = registration(  
    filename = files["flair"],  
    template.file = n4_t1,  
    typeofTransform = "Rigid")
```

Rigid-Body Registration Results

Rigid-Body Registration Slice



Non-linear Registration

- Registering the skull-stripped T1-weighted image to the MNI 152 brain image
- Uses Symmetric Normalization (SyN) (B. B. Avants et al. 2008)

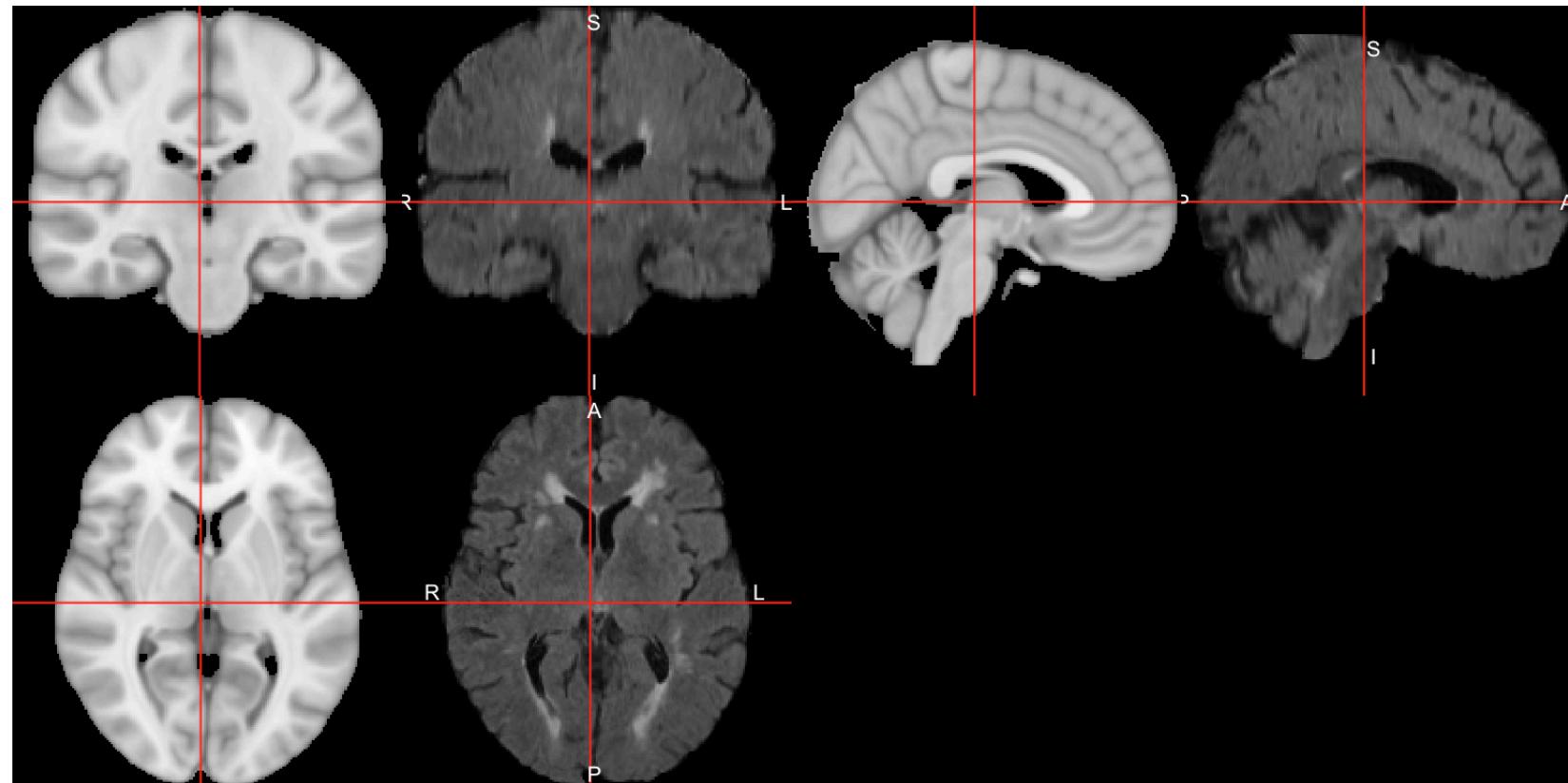
```
template.file = mni_fname(mm = "1", brain = TRUE)
ss_t1_to_mni = registration(
  filename = ss_t1,
  template.file = template.file,
  typeofTransform = "SyN", remove.warp = FALSE,
  outprefix = "temp")
```

Non-linear Registration Results

Applying Registration Transformations

```
reg_flair_to_mni = ants_apply_transforms(  
    fixed = template.file,  
    moving = ants_reg_flair$outfile, # registered FLAIR  
    interpolator = "Linear",  
    transformlist = ss_t1_to_mni$fwdtransforms )
```

Non-linear Transformation of FLAIR



Preprocess MRI: within a visit

We can develop pipelines/full analyses!

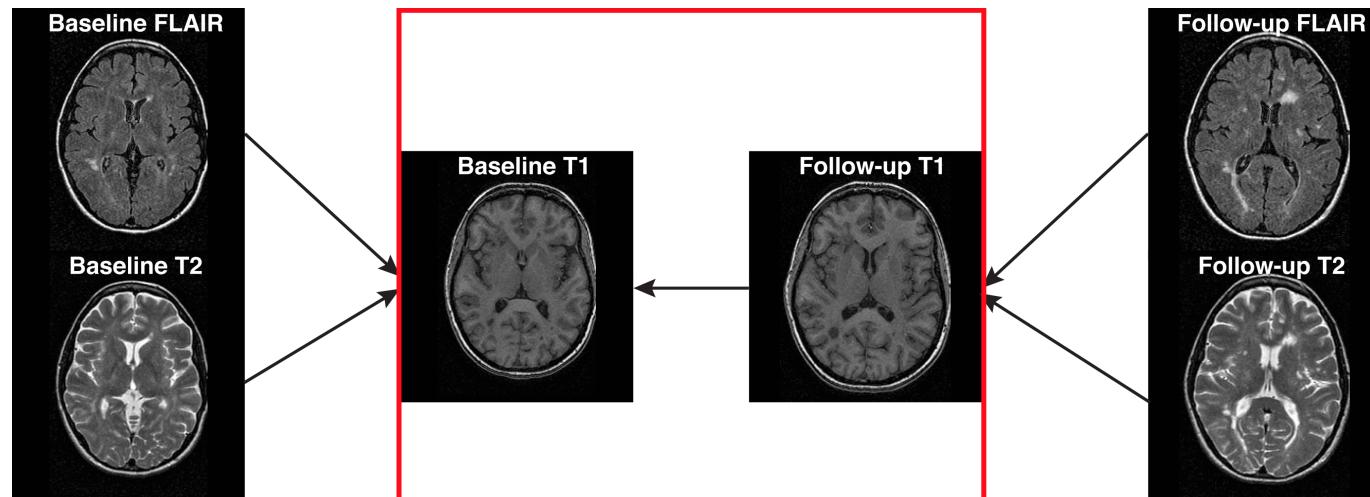
`extrantsr::preprocess_mri_within` will do inhomogeneity correction, skull strip (or mask), and register to the first scan.

```
proc_images = preprocess_mri_within(  
  files = files[c("t1", "t2", "pd", "flair")],  
  maskfile = ss_t1 > 0)
```

Preprocess MRI: across visits

`preprocess_mri_across` combines `preprocess_mri_within` and `registration`. If you had baseline/follow-up data:

```
outfiles = gsub("[.]nii", '_process.nii', files)
preprocess_mri_across(
  baseline_files, followup_files,
  baseline_outfiles, followup_outfiles,
  maskfile)
```



Tissue-Class Segmentation

ANTsR/extrantsr: uses Atropos (Brian B Avants et al. 2011)

- ANTsR - `atropos`, extrantsr - `otropos`

```
tissue_seg = otropos(  
    a = ss_t1,  
    x = mask)
```

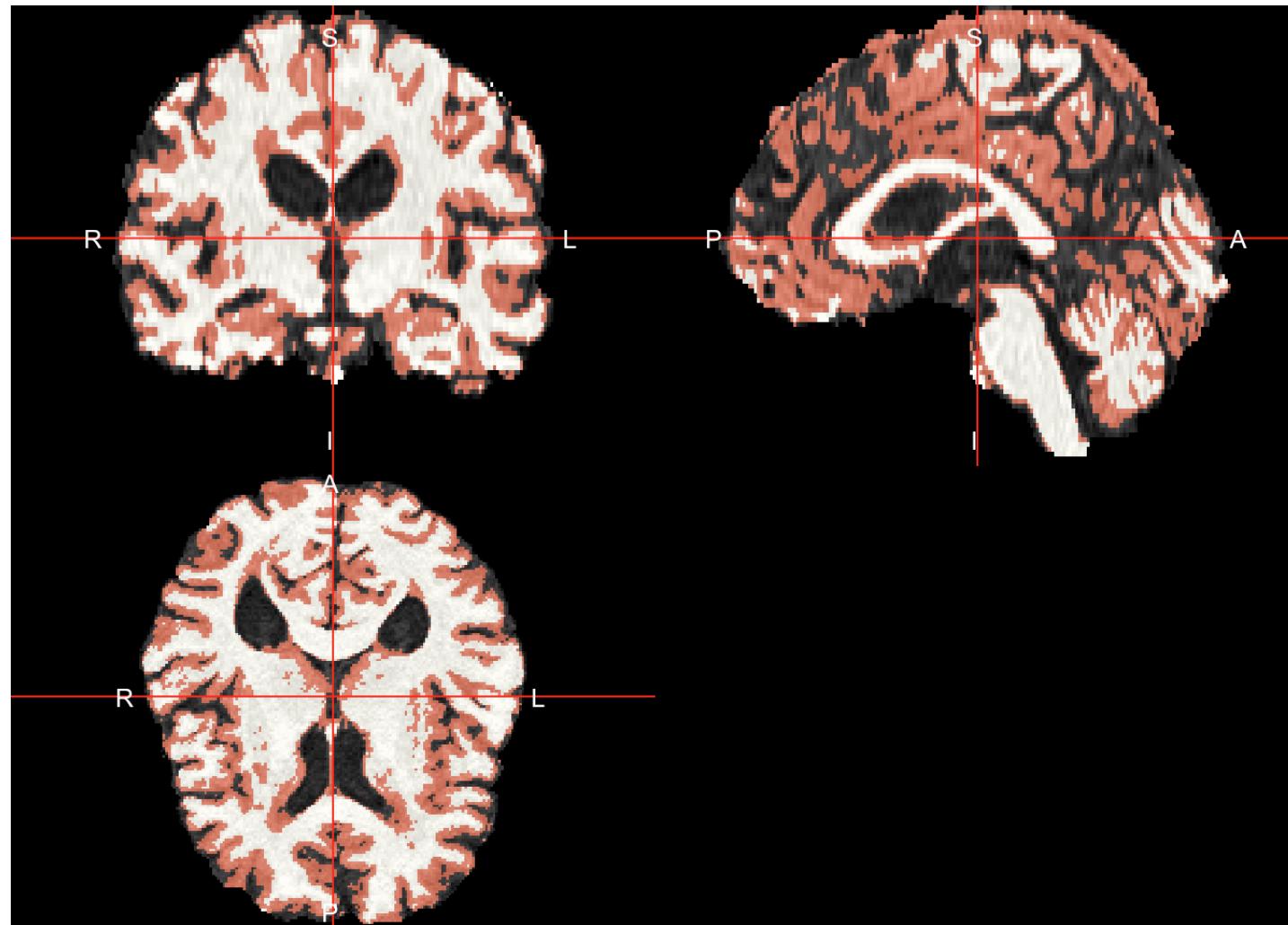
fslr: uses FAST (Zhang, Brady, and Smith 2001)

- `--nobias` as an option does not do bias field correction

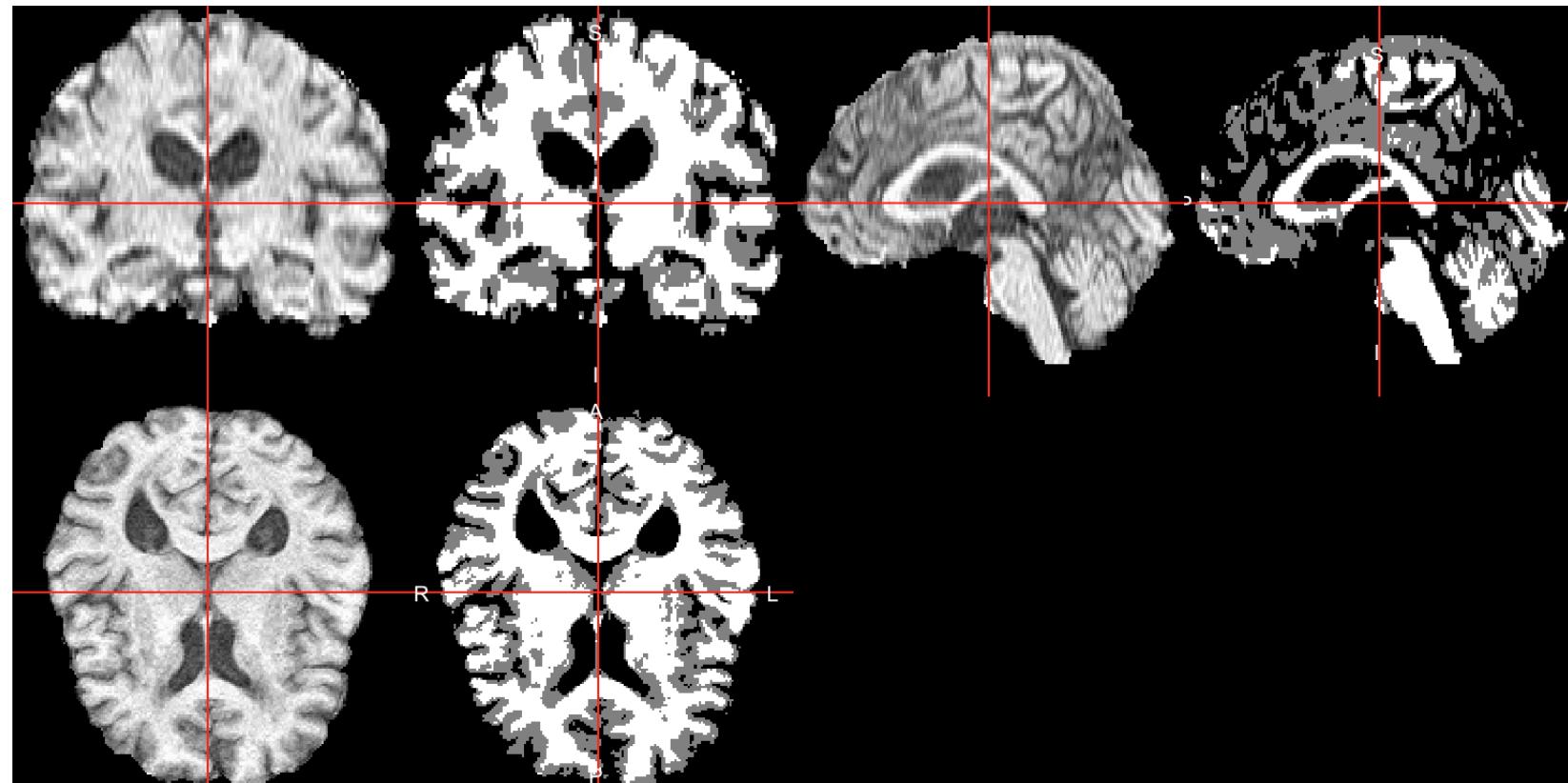
```
fast_t1 = fast(ss_t1, opts = "--nobias")  
FSLDIR='/usr/local/fsl/'; export FSLDIR; sh "${FSLDIR}/etc/fslconf/fsl.sh"; FS
```

See also `spm12r_segment`

ANTsR Tissue-Class Segmentation



ANTsR Tissue-Class Segmentation



fslr Tissue-Class Segmentation

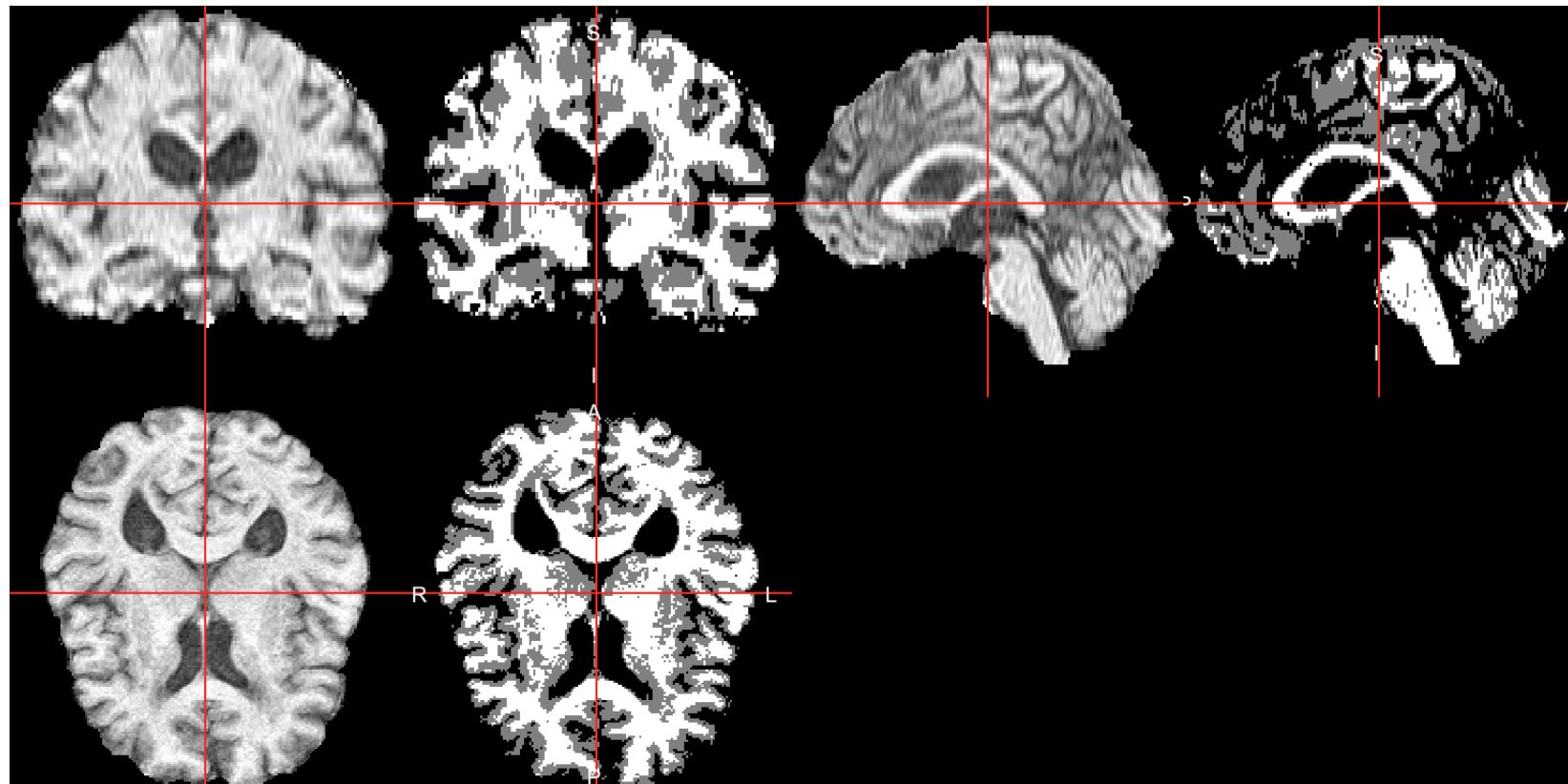


Image operations

fslr

- `fslsmooth` - Gaussian/box smoothing
- `fslerode/fsldilate` - erosion/dilation
- `fslfill/fslfill2` - fill holes

spm12r

- `spm_bwlabel` - label connected components

ANTsR

- `smooth_image` - Gaussian smoothing
- `oMath("ME")/oMath("MD")` - erosion/dilation
- `oMath("FillHoles")` - fill holes
- `oMath("GetLargestComponent")` - find largest components

fMRI

- `fsl_slicetimer` - slice timing correction
- `ANTsR::preprocessfMRI`
- `spm12r`
 - slice timing correction
 - realignment - get motion correction parameters
 - co-registration
 - segmentation/normalization to a template

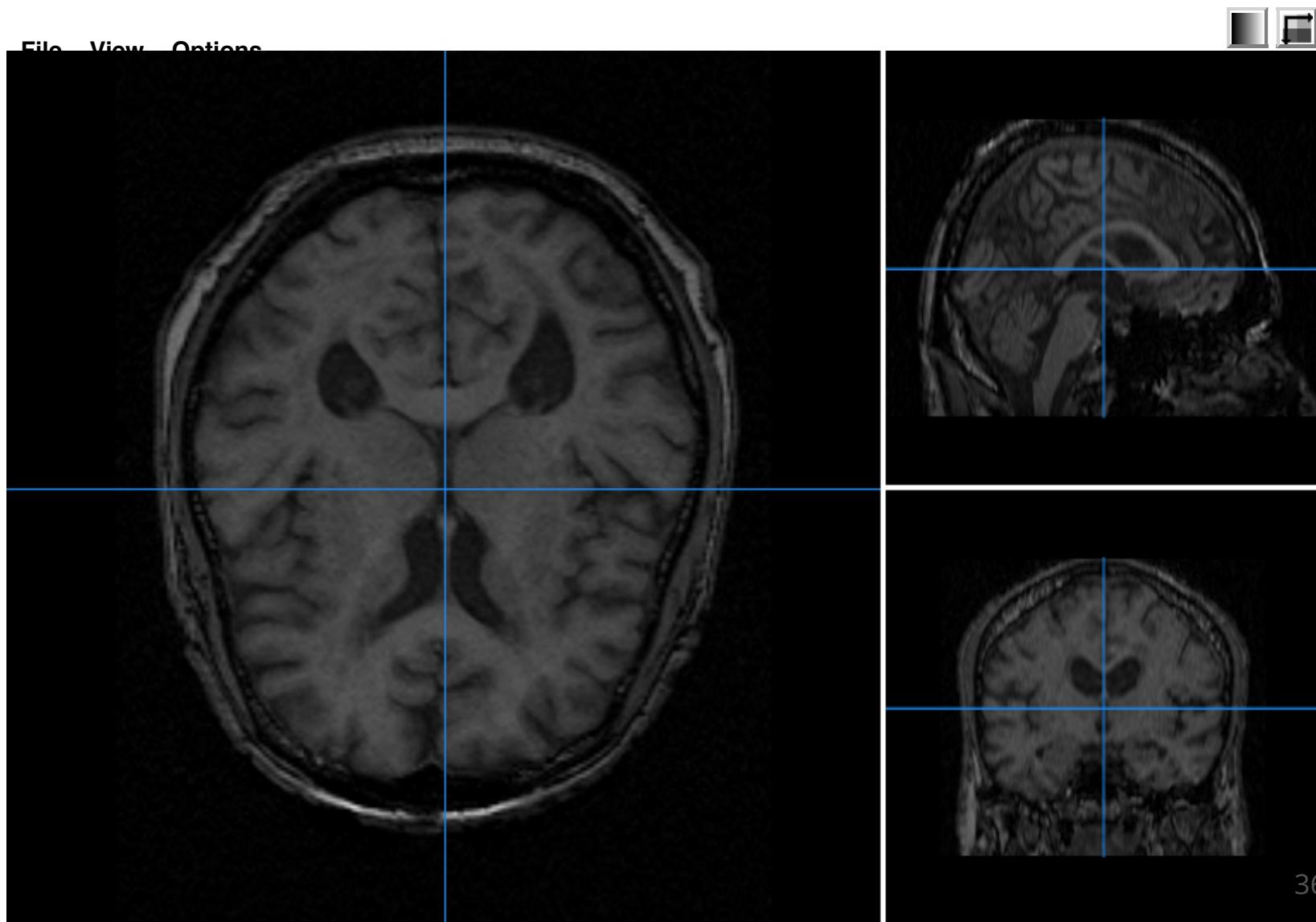
Intensity Normalization

- WhiteStripe (Shinohara et al. 2014)
- Whole brain z-scoring
- Histogram matching
- General standardization methods
- RAVEL (talk to Taki)

Overview

- Many methods are being developed for processing neuroimaging in R
- Analysis tools are largely already in R
- These are not standardized nor centralized
- Develop something like BioConductor
 - standard data structures
 - standard data sets
 - NITRC isn't exactly what we want
- GitHub and Neuroconductor

Interactive Visualization using papayar



Bibliography

- Avants, B. B., C. L. Epstein, M. Grossman, and J. C. Gee. 2008. "Symmetric Diffeomorphic Image Registration with Cross-Correlation: Evaluating Automated Labeling of Elderly and Neurodegenerative Brain." *Medical Image Analysis*, Special issue on the third international workshop on biomedical image registration - WBIR 2006, 12 (1): 26–41. doi:[10.1016/j.media.2007.06.004](https://doi.org/10.1016/j.media.2007.06.004).
- Avants, Brian B, Nicholas J Tustison, Jue Wu, Philip A Cook, and James C Gee. 2011. "An Open Source Multivariate Framework for N-Tissue Segmentation with Evaluation on Public Data." *Neuroinformatics* 9 (4). Springer: 381–400.
- Shinohara, Russell T., Elizabeth M. Sweeney, Jeff Goldsmith, Navid Shiee, Farrah J. Mateen, Peter A. Calabresi, Samson Jarso, Dzung L. Pham, Daniel S. Reich, and Ciprian M. Crainiceanu. 2014. "Statistical Normalization Techniques for Magnetic Resonance Imaging." *NeuroImage: Clinical* 6: 9–19.