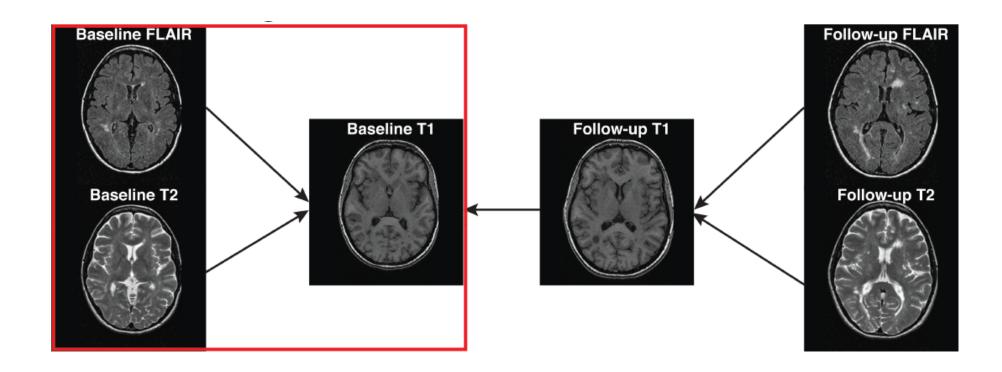
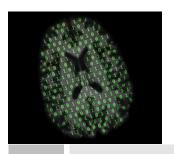


Wrapper Functions

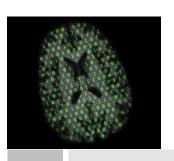




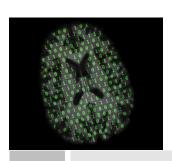
Wrapper Functions

The extrantsr function preprocess_mri_within will do the following steps:

- Inhomogeneity correction
- Registration of the files to the first filename

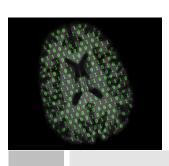


Within Visit 1 N4 Correction and Co-Registration

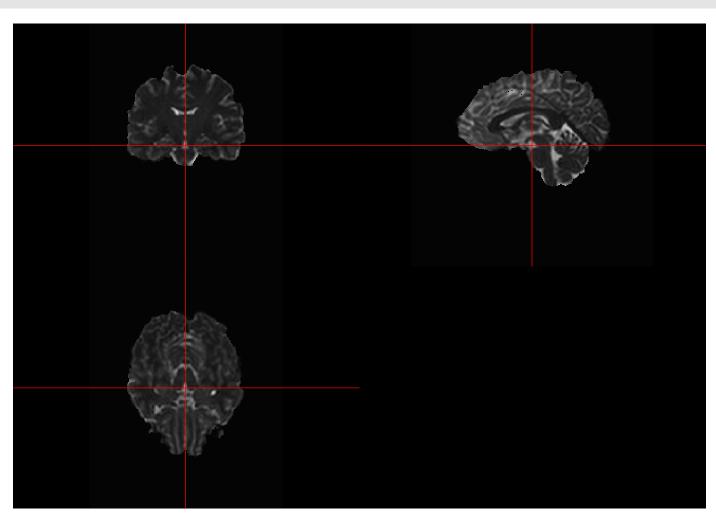


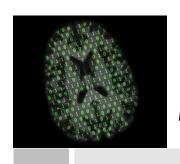
Applying a Brain Mask to All Registered Images

- Images from visit 1 are all in the same space as T1
- If we skull strip the T1 image then the mask can be applied to the other images to extract brain tissue

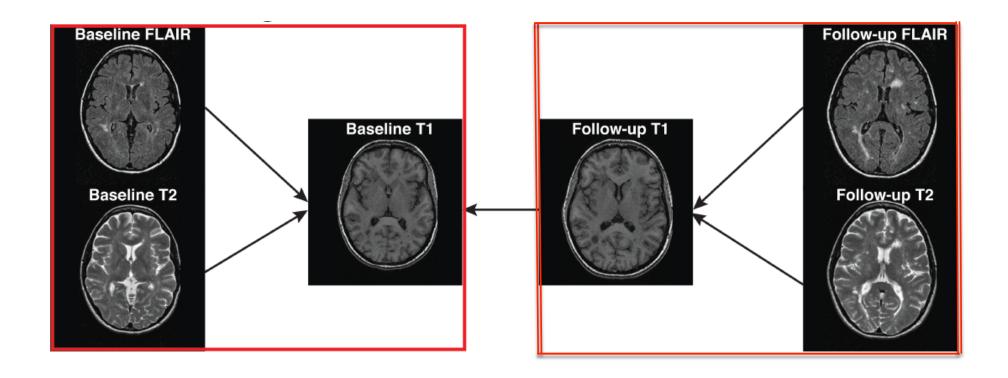


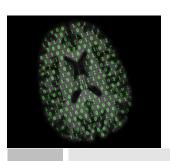
Results for Baseline Masking





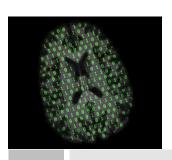
Multi-Sequence Within-visit Co-Registration





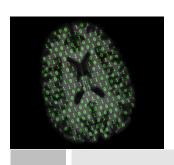
Within Visit 2 N4 Correction and Co-Registration

```
mridir2=file.path(kirbydir, "visit 2", "113")
files2 = c("113-02-MPRAGE.nii.qz",
          "113-02-T2w.nii.gz",
          "113-02-FLAIR.nii.gz")
files2 = file.path(mridir2, files2)
outfiles2 = c("113-02-MPRAGE processed.nii.gz",
             "113-02-T2w processed.nii.gz",
             "113-02-FLAIR processed.nii.gz")
outfiles2 = file.path(mridir2, outfiles2)
preprocess mri within (files = files2, retimg = FALSE,
outfiles = outfiles2, correction = "N4", skull strip = FALSE)
```



Applying a Brain Mask to All Registered Images

- Images from visit 1 are all in the same space as T1
- If we skull strip the T1 image then the mask can be applied to the other images to extract brain tissue



Results for Follow-up Masking

