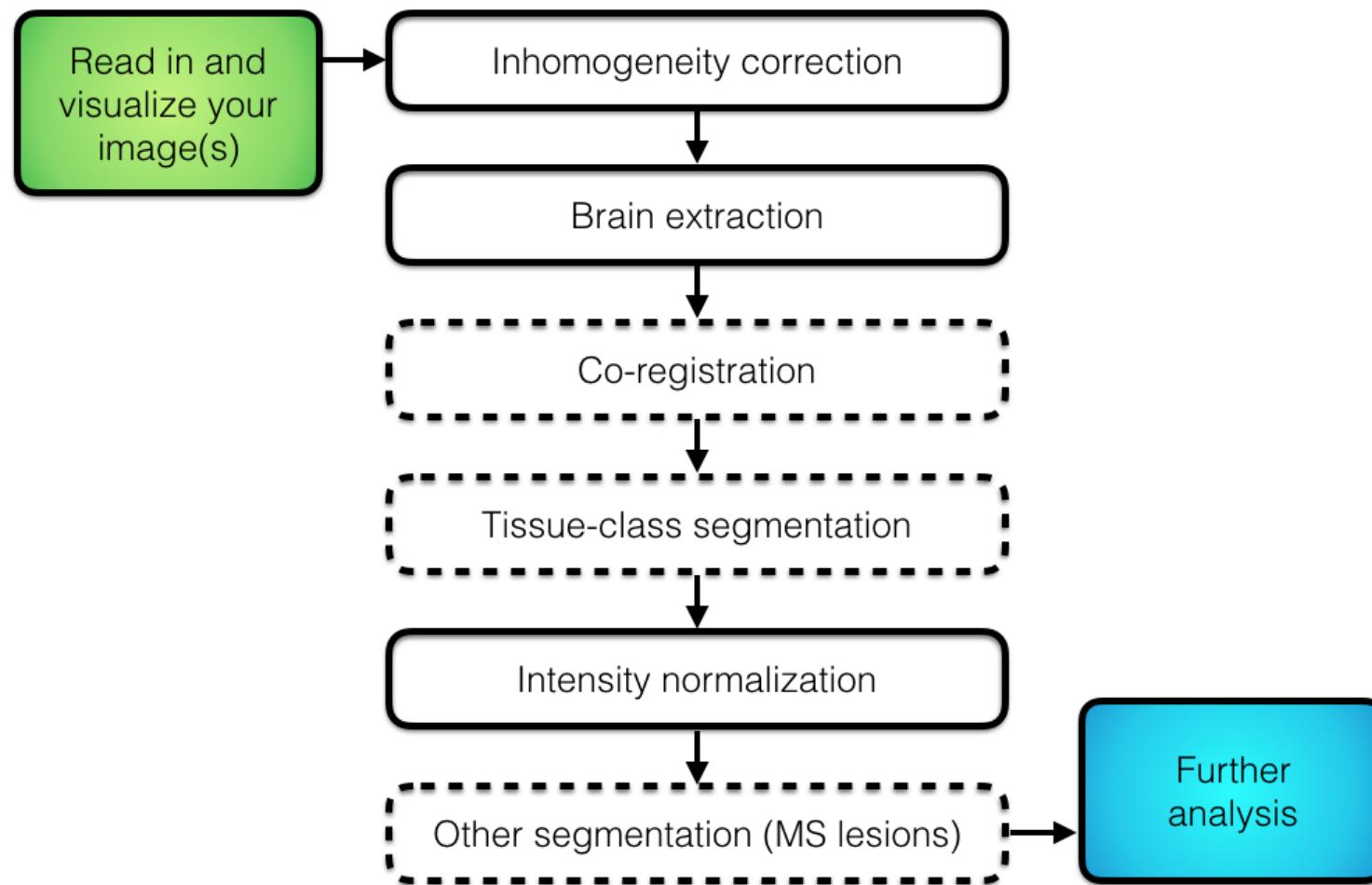


Image Registration

Overall Pipeline



Types of Registration

- Rigid-body registration (linear) - 6 degrees of freedom (dof)

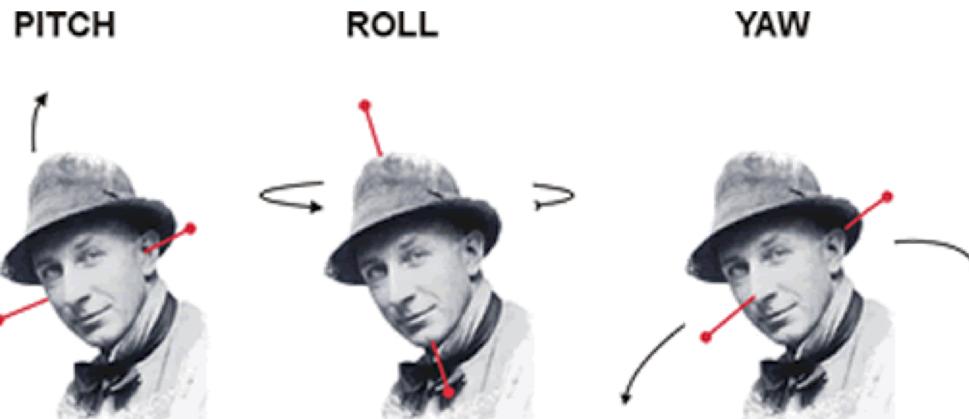
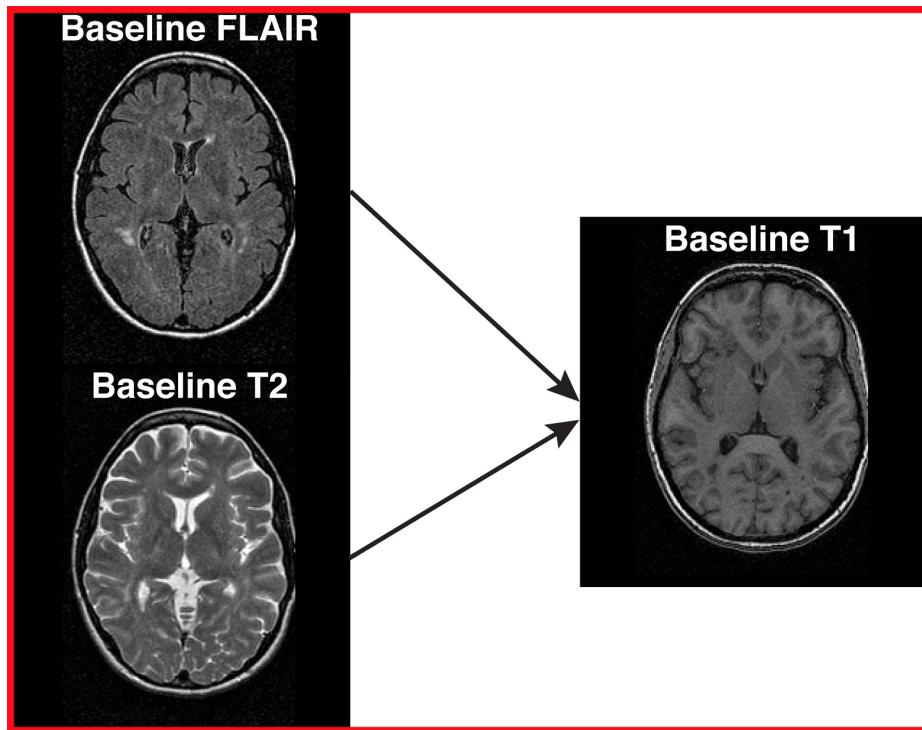


Image taken from <http://cnl.web.arizona.edu/imageprops.htm>

- Pitch - Think of nodding ("yes")
- Yaw - Think of shaking head ("no")
- Roll - Think of shoulder shrugging ("I don't know")
- x – left/right
- y – forward/backward
- z – jump up/down

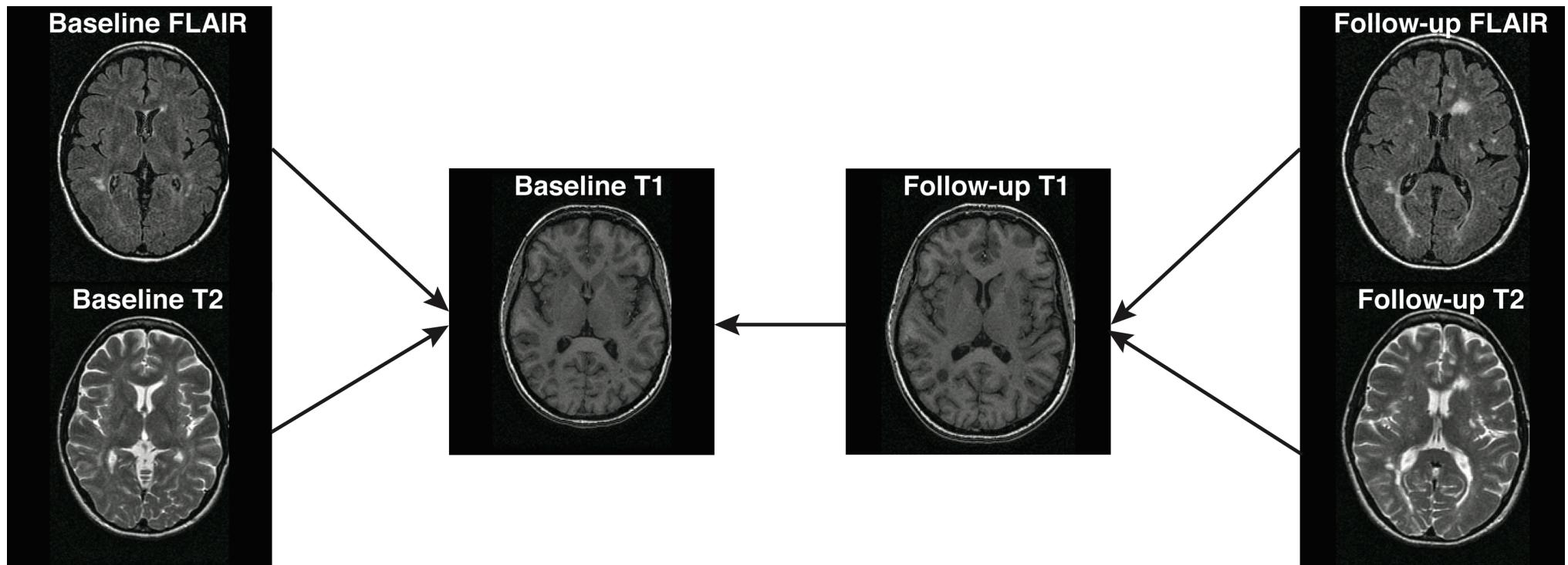
Types of Registration

- Rigid-body registration (linear) - 6 degrees of freedom (dof)
 - Co-registration (within the same person)
 - **Cross-sectional between-sequences**
 - Longitudinal between-sequences
 - Longitudinal within-sequence



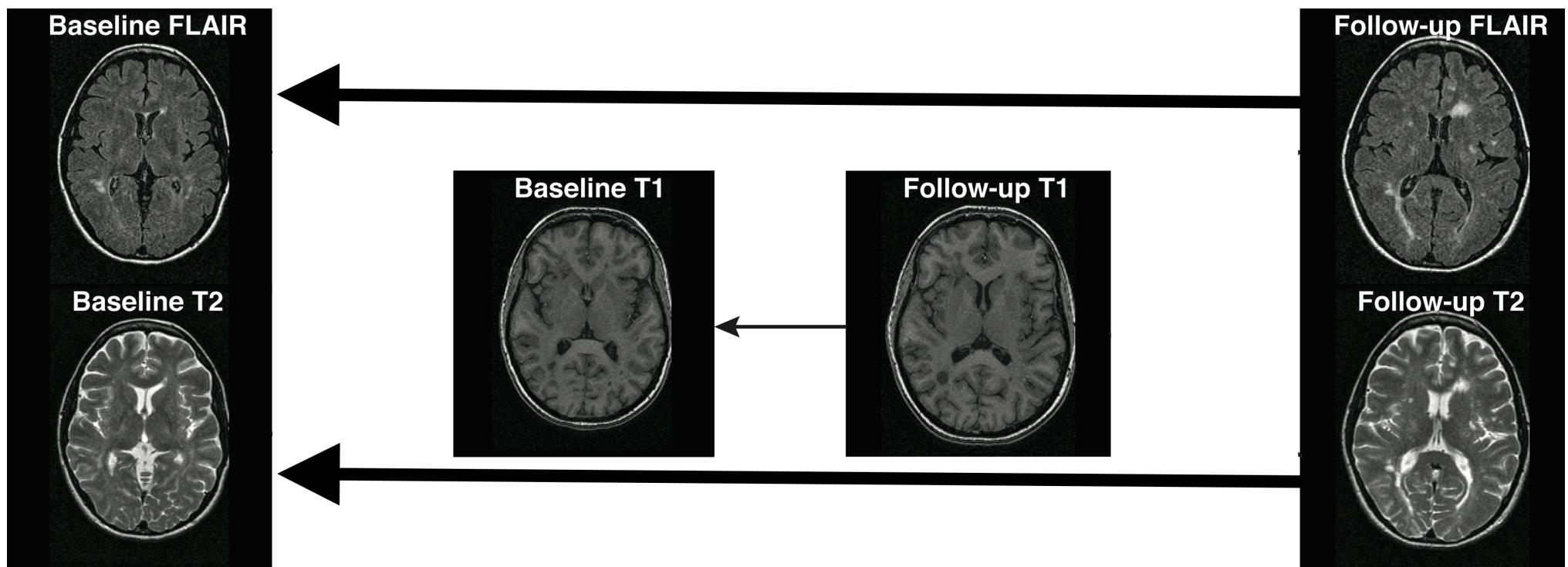
Types of Registration

- Rigid-body registration (linear) - 6 degrees of freedom (dof)
 - Co-registration (within the same person)
 - **Cross-sectional between-sequences**
 - **Longitudinal between-sequences**
 - Longitudinal within-sequence



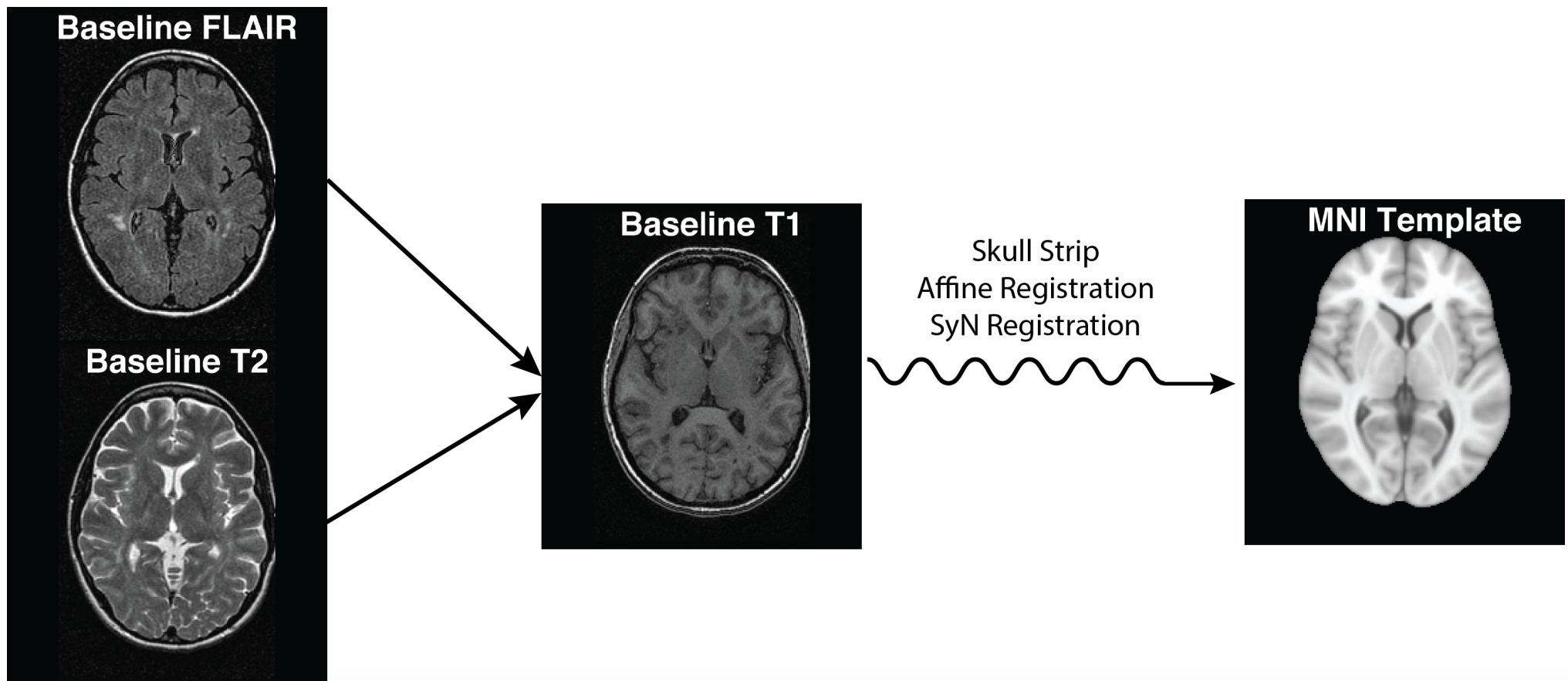
Types of Registration

- Rigid-body registration (linear) - 6 degrees of freedom (dof)
 - Co-registration (within the same person)
 - Cross-sectional between-sequences**
 - Longitudinal between-sequences
 - **Longitudinal within-sequence**



Types of Registration

- Affine registration – 12 dof (scaling)
- Non-linear (> 12 dof): usually requires a prior affine registration
 - Across-subject registration
 - Registration to a template: There are many different templates



Rigid Registration: The Math

For a voxel v , the rigid transformation can be written as:

$$T_{\text{rigid}}(v) = Rv + t \text{ where } R =$$

$$\begin{bmatrix} \cos\beta\cos\gamma & \cos\alpha\sin\gamma + \sin\alpha\sin\beta\cos\gamma & \sin\alpha\sin\gamma - \cos\alpha\sin\beta\cos\gamma & -\cos\beta\sin\gamma & \cos\alpha\cos\gamma - \sin\alpha\sin\beta\cos\gamma \\ \sin\beta\cos\gamma & \sin\alpha\cos\gamma + \cos\alpha\sin\beta\sin\gamma & -\sin\alpha\sin\gamma & \sin\beta\sin\gamma & \sin\alpha\cos\beta\cos\gamma \\ \sin\beta\sin\gamma & -\sin\alpha\cos\gamma + \cos\alpha\sin\beta\sin\gamma & \cos\alpha\cos\gamma & \sin\beta\cos\gamma & -\sin\alpha\sin\beta\cos\gamma \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

- 6 degrees of freedom
- 3 associated with the translation vector: $t = (t_x, t_y, t_z)$
- 3 associated with the rotation parameters: $\theta = (\alpha, \beta, \gamma)$.

Aside into Lists

- Initialize an empty list and add two elements to it

```
l = list()  
l[[1]] = c(1, 2, 4, 5)  
l[[2]] = matrix(1:10, nrow = 2)  
print(l)
```

```
[[1]]  
[1] 1 2 4 5  
  
[[2]]  
[,1] [,2] [,3] [,4] [,5]  
[1,]    1    3    5    7    9  
[2,]    2    4    6    8   10
```

- Subsetting uses double brackets:

```
print(l[[1]])
```

```
[1] 1 2 4 5
```

Subsetting by name

If a `vector` has names, you can also put the - Initialize an empty list and add two elements to it

```
x = c(one = 1, three = 14, two = 5)  
print(x)
```

```
one three two  
1     14    5
```

```
x[c("three")]
```

```
three  
14
```

If a `list` has names, you can subset with the `$`

- Subsetting with double brackets:

```
names(l) = c("V", "m"); l[["V"]]
```

```
[1] 1 2 4 5
```

Subsetting by name

If a list has names, you can also subset with the \$

```
l$v
```

```
[1] 1 2 4 5
```

Reading in more than the T1: `ms.lesion` package

- `get_image_filenames_list_by_subject` - returns a list, each element is a subject, and each subject has a vector of filenames, named for each modality

```
library(ms.lesion)
all_files = get_image_filenames_list_by_subject()
class(all_files); names(all_files)

[1] "list"

[1] "test01"      "test02"      "test03"      "training01"   "training02"
[6] "training03"  "training04"  "training05"

files = all_files$training01; class(files); names(files)

[1] "character"

[1] "T1"        "T2"        "FLAIR"

t1_fname = files["T1"]
t1 = readnii(t1_fname)
rt1 = robust_window(t1, probs = c(0, 0.975))
```

Image Registration

The `registration` function from `extrantsr` can register 2 images. The main arguments are:

- `filename` - either `nifti` object or filename of image to be registered (moving)
- `template.file` - either `nifti` object or filename of target image (fixed)
- `typeofTransform` - transformation of moving to fixed image (Rigid/Affine/SyN)
- `interpolator` - how are voxels averaged in fixed space
(Linear/NearestNeighbor/LanczosWindowedSinc)

It can also perform bias correction if `correct = TRUE`.

Image registration

For example, if we wanted to register the FLAIR to the T1 image, we would run:

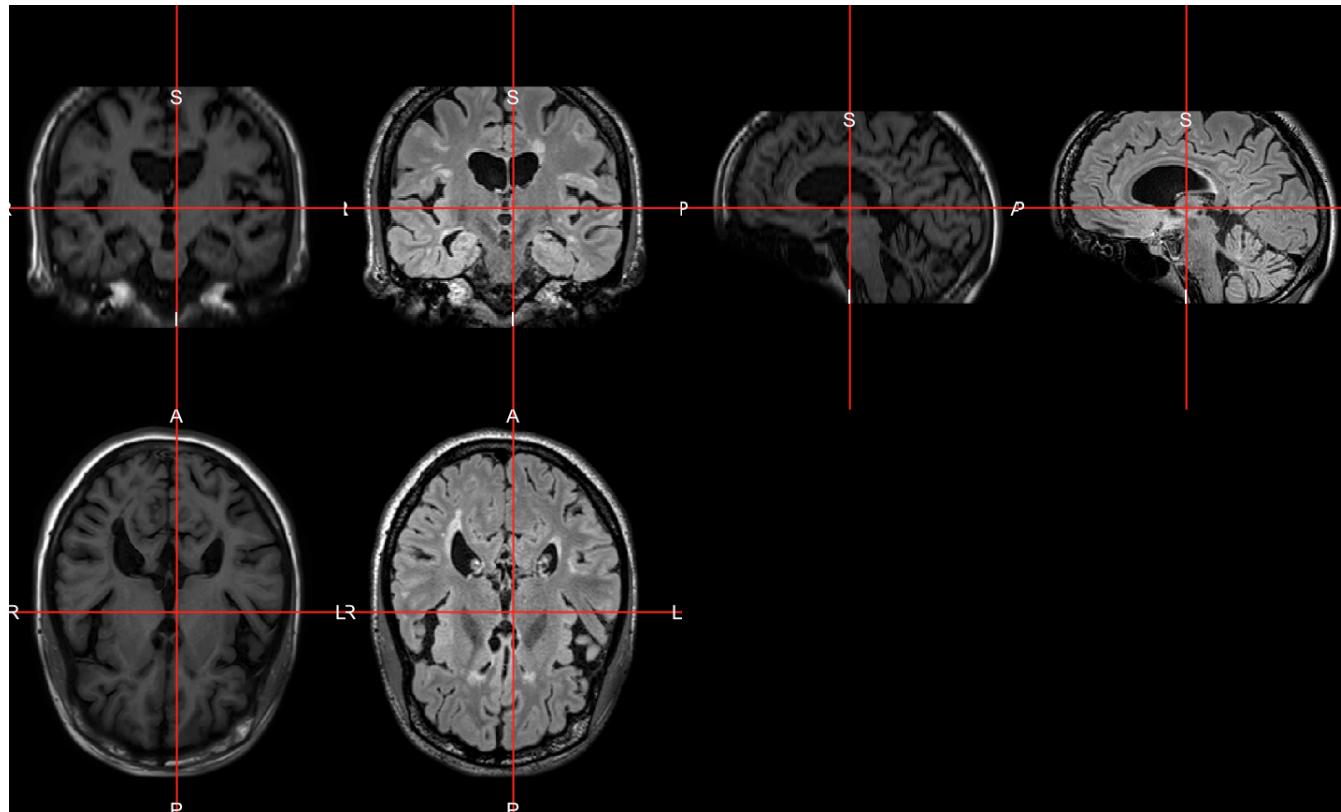
```
library(extrantsr)
reg = registration(
  filename = files["FLAIR"], template.file = files["T1"],
  typeOfTransform = "Rigid", interpolator = "Linear", verbose = FALSE)
names(reg)

[1] "outfile"           "fwdtransforms"      "invtransforms"
[4] "interpolator"      "other_interpolator" "invert_interpolator"
[7] "typeOfTransform"    "retimg"
```

The output in `reg` would contain the transformed image and paths to the estimated transformations.

FLAIR comparison

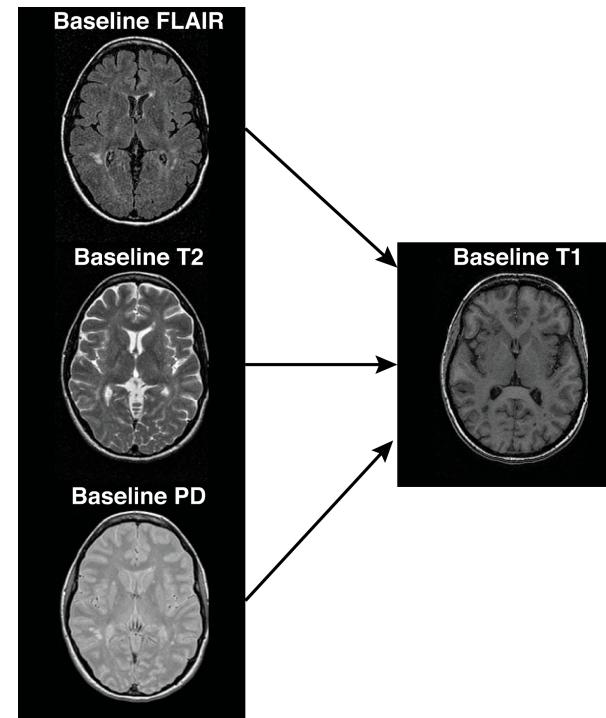
```
double_ortho(rt1, reg$outfile)
```



Wrapper function to perform preprocessing

We would like to perform registration within a visit for all modalities. The `extrantsr` function `within_visit_registration` will do the following steps:

1. Inhomogeneity correction (N3 or N4): could also use images from previous lecture
2. Registration to a fixed image (T1)



Registration within a visit

The function `within_visit_registration` arguments take in:

- `fixedImage` - the image to be registered to
- `movingImages` - images to register to the `fixed`
- `typeofTransform` - transformation of moving to fixed image (Rigid/Affine)
- `interpolator` - how are voxels averaged in `fixed` space
- `correct` - should correction be done, if so, specify `correction = "N4"`

and outputs a list of transformations (`fwdtransforms`) and output filenames (`outfile`)

Lists: lapply

With lists and vectors, there are apply functions. These apply a function to every element of the list. In this course, we will use:

- lapply - apply function and return the elements as a list
 - `lapply(LIST, FUNCTION, OTHER_ARGUMENTS_TO_FUNCTION)`
- sapply - apply function and return a “simplified” version
 - if all elements returned are a one-element vector, return a vector
 - if element 1 is a vector of length 3 and element 2 is a vector of length 1, return a list

Register to the T1 image

```
res = within_visit_registration(
  fixed = files["T1"], moving = files[c("T2", "FLAIR")],
  correct = TRUE, correction = "N4",
  typeofTransform = "Rigid", interpolator = "Linear")
output_imgs = lapply(res, function(x) x$outfile)
out = c(T1 = list(t1), output_imgs)

# Running Bias-Field Correction on file

# Running Registration of file to template

# Applying Registration output is

$fwdtransforms
[1] "/var/folders/1s/wrtqcpxn685_zk570bnx9_rr0000gr/T//RtmpN4MXsP/file12bc91f0b4b400G

$invtransforms
[1] "/var/folders/1s/wrtqcpxn685_zk570bnx9_rr0000gr/T//RtmpN4MXsP/file12bc91f0b4b400G

$prev_transforms
character(0)

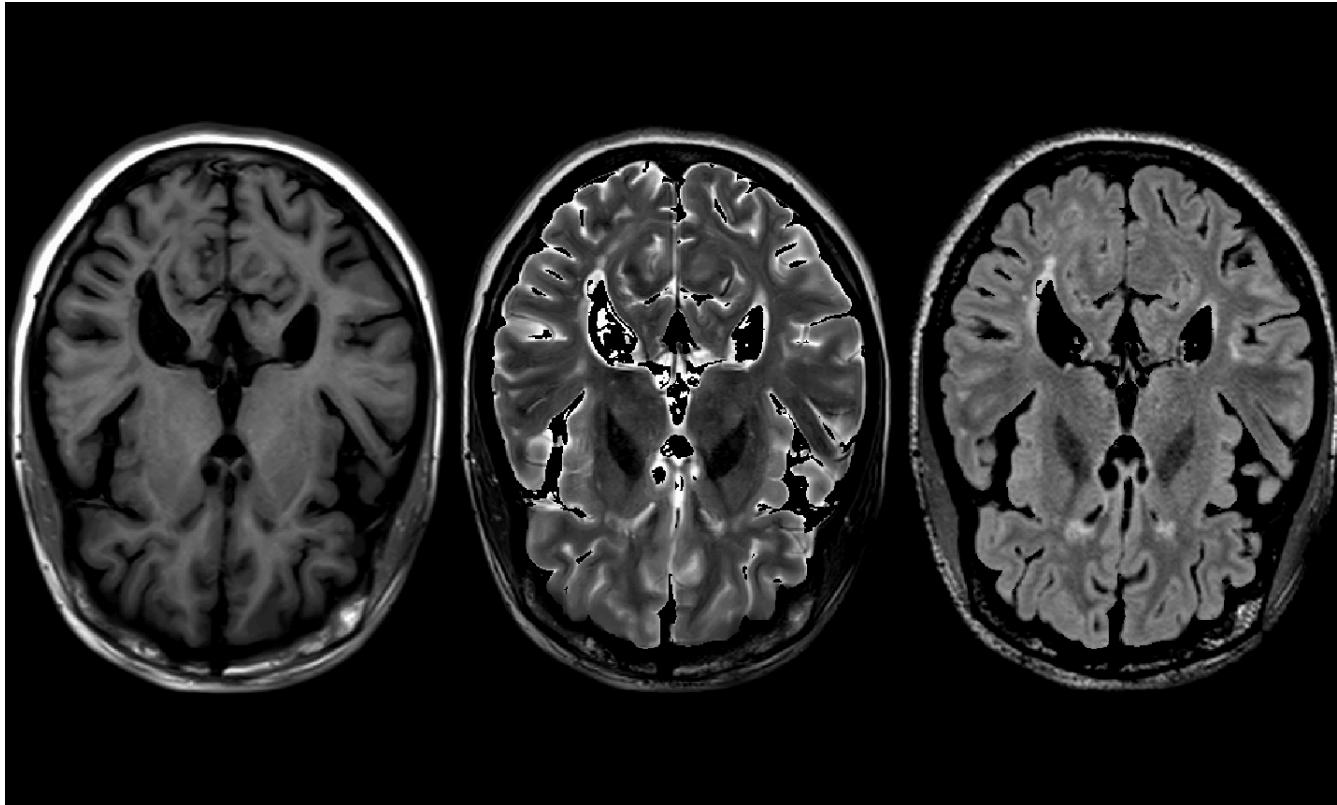
# Applying Transformations to file

[1] "-d"
[2] "3"
[3] "-i"
[4] "<pointer: 0x7fdb04b572c0>"
[5] "-o"
[6] "<pointer: 0x7fdb04a70fa0>"
```

Checking registration: new visualization!

The `multi_overlay` function takes in a list of images and then plots one slice across modalities (assumes center slice):

```
multi_overlay(out)
```



Coregistration within a visit results

- Overall, there seems to be good overlap after registration
- It is usually beneficial to do inhomogeneity correction before registration.
 - just set `correct = TRUE` or pass in the bias-corrected images

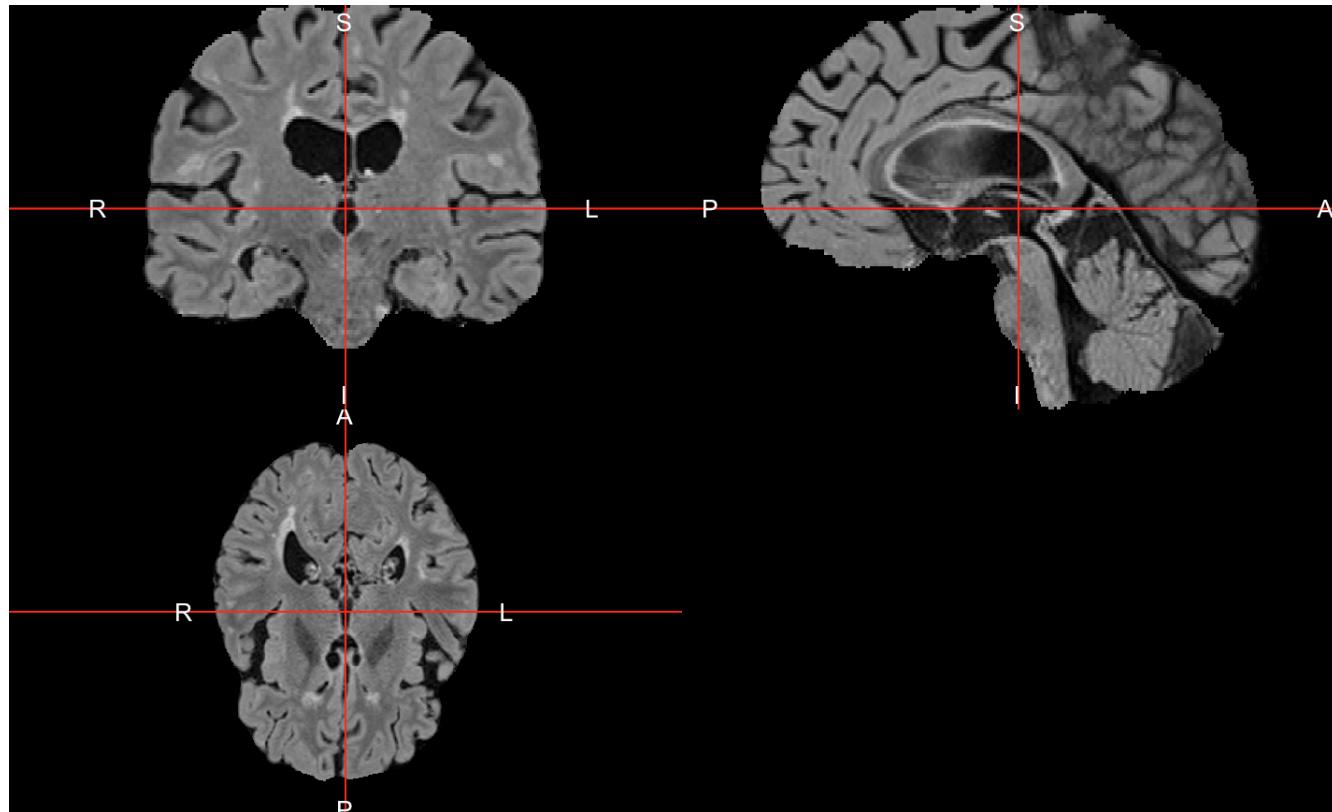
Applying a Brain mask to all registered images

Now that the images are in the same space as the T1, if we skull-strip the T1 image (we did with MALF), we can apply this mask to those images to extract brain tissues using the `neurobase::mask_img` command:

```
mask = readnii("../output/training01_01_t1_mask.nii.gz") # MALF mask
masked_imgs = lapply(out, mask_img, mask)
```

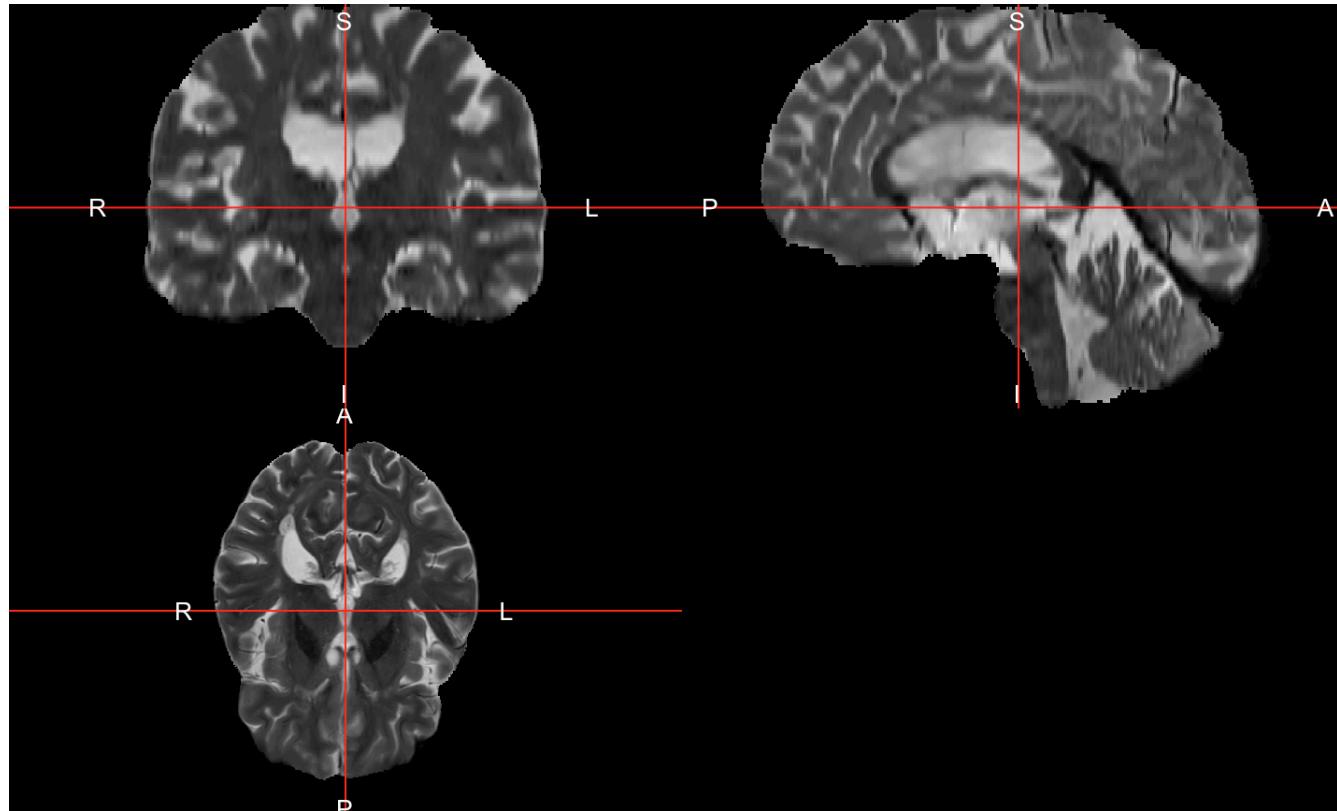
Masked FLAIR Result

ortho2 (masked_imgs\$FLAIR)



Masked T2 Result

ortho2 (masked_imgs\$T2)



Overview of functions

- Registration within a subject can be done in R
 - `registration` wraps around the reading/writing of images and applying transformations (uses ANTsR functions)
 - `double_ortho`, `ortho2`, and `multi_overlay` can provide some basic visual checks to assess registration quality
 - `within_visit_registration` is a registration wrapper function
 - `preprocess_mri_within` - wraps multiple steps above (`inhomo`, `reg`, `extract`)
- Once images are registered in the same space, operations can be applied to all the images, such as:
 - Masking with a brain mask
 - Transforming images to new spaces with one modality

Co-registration overview

- Co-registration requires a few degrees of freedom (usually 6)
 - sequences from the same individual/brain are more alike than images from different subjects
- Example analyses that do not require a reference template
 - Identify location-specific longitudinal changes within an individual
 - Tissue class or structural segmentation
 - Analysis of individual-subject change in intensities

Population template registration

We have only done registration within a subject, but many times you want to perform a population-level analysis. This requires registration to a **template**:

- The registration can be done for this as well, just the `template`.`file` is now the template image and `filename` is the subject image.
 - other files (in the same space) can be transformed using the `other.files` and `other.outfiles` arguments. Or:
 - `ants_apply_transforms` can be used to apply this transformations to the other files

Website

http://johnmuschelli.com/imaging_in_r