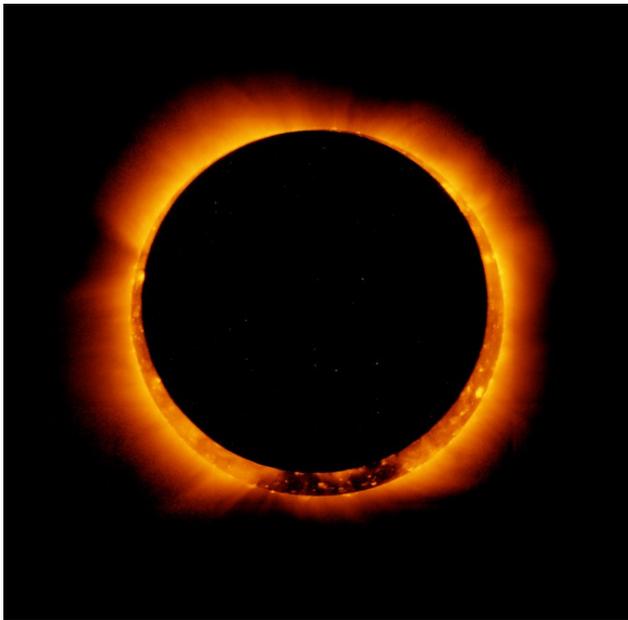


# Alignment and Atlases



## What does aligning mean and why do we want to do it?

- Alignment means to bring two objects into the same space so that each location within one object corresponds to the same location in the other
- Why?
  - ✧ motion correction across time
  - ✧ align EPI to anatomical data or vice versa – to assign a location with a functional result
  - ✧ compare data from longitudinal studies
  - ✧ compare data from different scanners, sites
  - ✧ compare results with a standard template or atlas for standardized locations and structures

## Alignment goals and tools in AFNI

- EPI data across time in a single run or across runs to a base image
  - ✧ **3dvolreg** – motion correction (rigid)
- Align data to template
  - ✧ **3dWarpDrive**, **@auto\_tlrc** – align similar volumes (affine) even across subjects
  - ✧ **3dQwarp**, **auto\_warp.py** – align similar volumes nonlinearly to template
- Align images across modalities – EPI to anat
  - ✧ **3dAllineate** – align different or similar volumes
  - ✧ **align\_epi\_anat.py** – general alignment script to align EPI with anatomical data
- Include motion correction, alignment of EPI to anatomical in fMRI processing pipeline script
  - ✧ **afni\_proc.py**
- Correct for motion between two volumes by aligning in two dimensions using corresponding slices
  - ✧ **@2dwarper.Allin** – non-linear alignment of slices
  - ✧ **@2dwarper**, **2dimreg** limit alignment to specific plane

## Alignment tools in AFNI (continued)

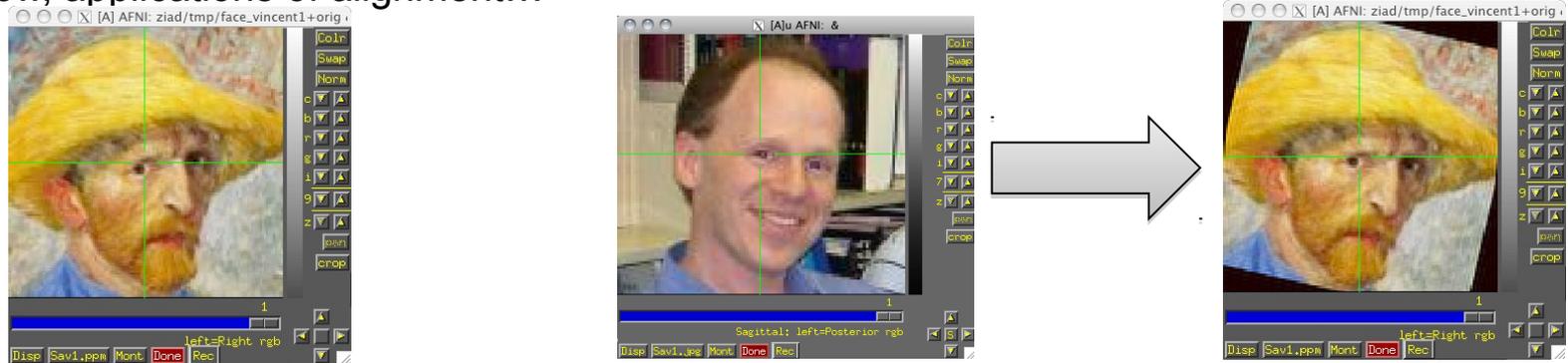
- Align partial data to roughly the right part of the brain
- **Nudge plug-in** - visually align two volumes
  - rotate by known amount between volumes
- ✧ **3drotate** – moves (shifts and rotates) volumes
- ✧ **3dWarp** – make oblique, deoblique to match another dataset
  - Put centers of data from outside sources in roughly the same space
- ✧ **@Align\_Centers, 3dCM** – put centers or centers of mass of dataset in same place
  - align specific regions across subjects
- ✧ **3dTagalign, tagset plugin** – place and align volumes using corresponding fiducial marker points
  - align one jpeg image to another
- ✧ **imreg** – align two 2D images

# Image and Volume Registration with AFNI

- Goal: bring images collected with different methods and at different times into spatial alignment
- Facilitates comparison of data on a voxel-by-voxel basis
  - ✧ Functional time series data will be less contaminated by artifacts due to subject movement
  - ✧ Can compare results across scanning sessions once images are properly registered
  - ✧ Can put volumes in standard space such as the stereotaxic Talairach-Tournoux coordinates
- Most (all?) image registration methods now in use do pair-wise alignment:
  - ✧ Given a base image  $\mathbf{J}(\mathbf{x})$  and target (or source) image  $\mathbf{I}(\mathbf{x})$ , find a geometrical transformation  $\mathbf{T}[\mathbf{x}]$  so that  $\mathbf{I}(\mathbf{T}[\mathbf{x}]) \approx \mathbf{J}(\mathbf{x})$
  - ✧  $\mathbf{T}[\mathbf{x}]$  will depend on some parameters
    - ☐ Goal is to find the parameters that make the transformed  $\mathbf{I}$  a 'best fit' to  $\mathbf{J}$
  - ✧ To register an entire time series, each volume  $\mathbf{I}_n(\mathbf{x})$  is aligned to  $\mathbf{J}(\mathbf{x})$  with its own transformation  $\mathbf{T}_n[\mathbf{x}]$ , for  $n=0, 1, \dots$ 
    - ☐ Result is time series  $\mathbf{I}_n(\mathbf{T}_n[\mathbf{x}])$  for  $n=0, 1, \dots$
    - ☐ User must choose base image  $\mathbf{J}(\mathbf{x})$

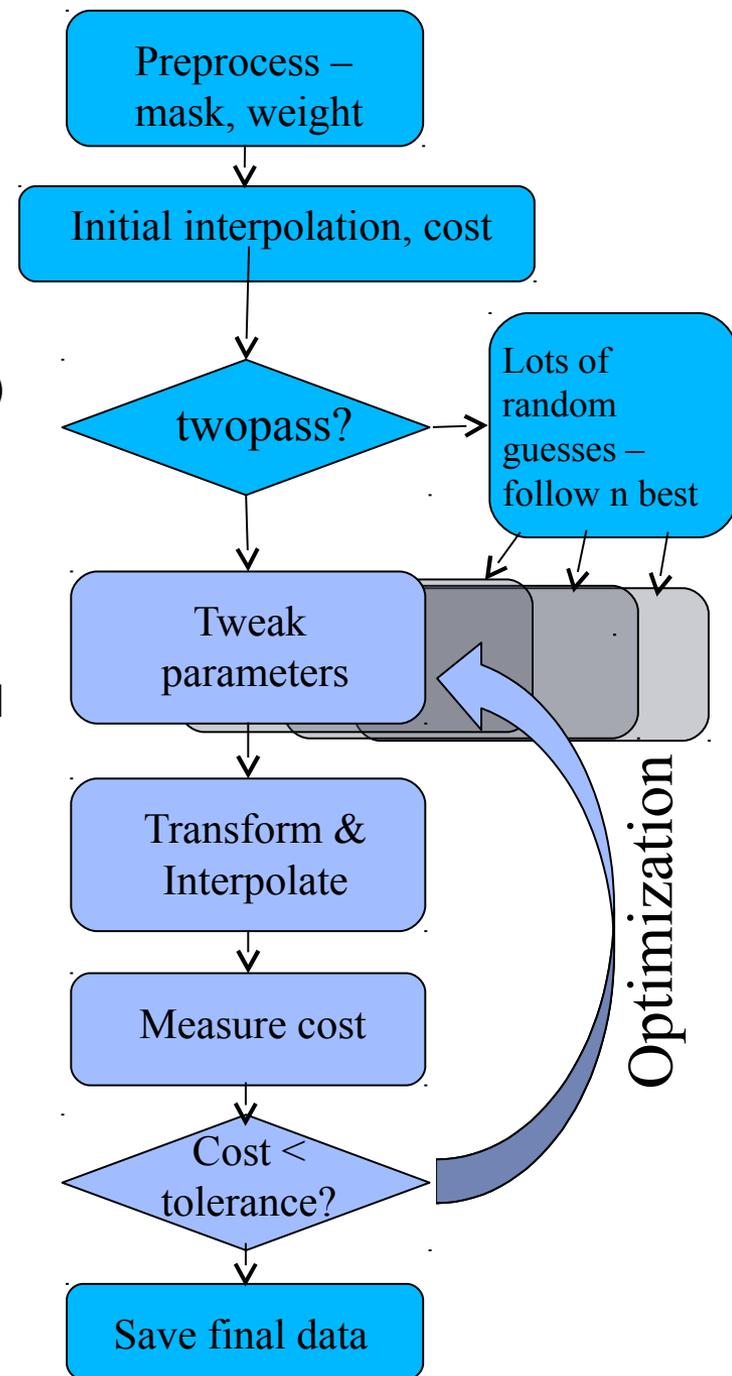
- Most image registration methods make 3 algorithmic choices:
  - ✧ How to measure mismatch **E** (for error) between  **$I(T[x])$**  and  **$J(x)$** ?
    - ❑ **Or ...** How to measure goodness of fit between  **$I(T[x])$**  and  **$J(x)$** ?
      - ❑  **$E(\text{parameters}) \equiv -\text{Goodness}(\text{parameters})$**
    - ✧ How to adjust parameters of  **$T[x]$**  to minimize **E**?
    - ✧ How to interpolate  **$I(T[x])$**  to the  **$J(x)$**  grid?
      - ❑ So we can compare voxel intensities directly
  - The input volume is transformed by the optimal  **$T[x]$**  and a record of the transform is kept in the header of the output.
  - Finding the transform to minimize **E** is the bulk of the registration work. Applying the transform is easy and is done on the fly in many cases.
  - If data starts off far from each other, may add a coarse pass (twopass) step
    - ✧ guess a lot among all the parameters (rotations, shifts, ...), measure cost
    - ✧ best guesses, tweak the parameters (optimize) and measure again

Now, applications of alignment...

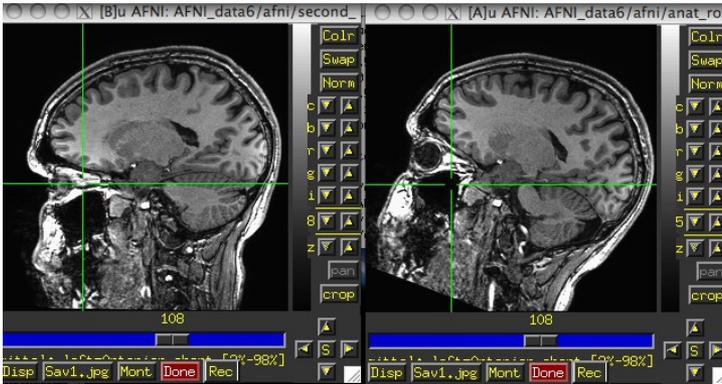


## Alignment process - overview

- Preprocess – mask data, weight data
- If far off, take some random guesses (-twopass)
- Optimize parameters on initial or best sets (6,12,39,1000's)
  - Use new parameters to transform input
    - Interpolate onto base data's grid
  - Measure alignment error with cost functional
    - Less than minimum error - finished
    - Better - keep adjusting with same direction
    - Worse – try other parameters
- Create final output by interpolating onto output grid
  - save datasets, transform parameters



# Within Modality Registration



- AFNI [3dvolreg](#) and [3dWarpDrive](#) programs match images by grayscale (intensity) values
  - ✧  $E =$  (weighted) sum of squares differences =  $\sum_x w(x) \cdot \{I(T[x]) - J(x)\}^2$ 
    - ☐ Only useful for registering ‘like images’:
      - ☐ Good for SPGR↔SPGR, EPI↔EPI, but **not** good for SPGR↔EPI
  - ✧ Several interpolation methods :
    - ☐ Fourier, linear, cubic, quintic, and heptic polynomials
  - ✧ [3dvolreg](#) is designed to run VERY fast for EPI↔EPI registration with small movements — good for fMRI purposes but restricted to 6-parameter rigid-body transformations.
  - ✧ [3dWarpDrive](#) is slower, but it allows for up to 12 parameters affine transformation. This corrects for scaling and shearing differences in addition to the rigid body transformations.

## Looking for Motion

afni GUI – graph-image  
video/ricochet, arrow keys.  
Graph spikes.

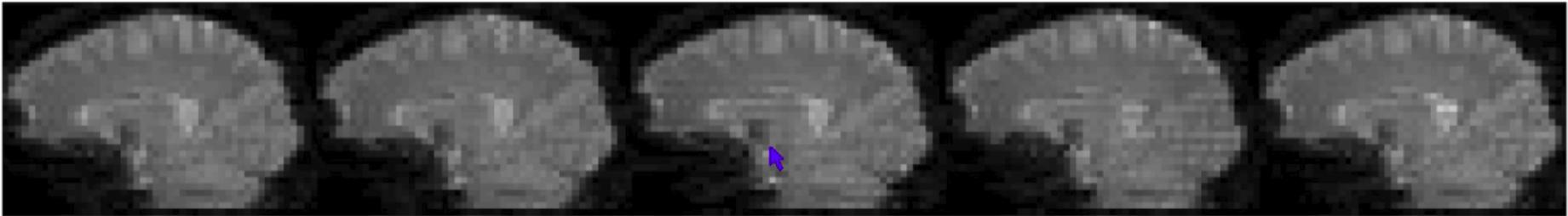


Image courtesy of Jonathan Power, NIMH

In statistical results, “activation” / “deactivation” occurs at high contrast boundaries like edge of brain or ventricles.

- AFNI program `3dvolreg` is for aligning 3D volumes by rigid movements
  - ✧ `T[x]` has 6 parameters:
    - ☐ Shifts along x-, y-, and z-axes; Rotations about x-, y-, and z-axes
  - ✧ Generically useful for intra- and inter-session alignment
  - ✧ Motions that occur within a single TR (2-3 s) cannot be corrected this way, since method assumes rigid movement of the entire volume
- AFNI program `3dWarpDrive` is for aligning 3D volumes by affine transformations
  - ✧ `T[x]` has up to 12 parameters:
    - ☐ Same as `3dvolreg` plus 3 Scales and 3 Shears along x-, y-, and z-axes
  - ✧ Generically useful for intra- and inter-session alignment
  - ✧ Generically useful for intra- and inter-subject alignment
- AFNI program `2dImReg` is for aligning 2D slices
  - ✧ `T[x]` has 3 parameters for each slice in volume:
    - ☐ Shift along x-, y-axes; Rotation about z-axis
    - ☐ No out of slice plane shifts or rotations!
  - ✧ Useful for **sagittal** EPI scans where dominant subject movement is ‘nodding’ motion that may be faster than TR
  - ✧ It is possible and sometimes even useful to run `2dImReg` to clean up sagittal nodding motion, followed by `3dvolreg` to deal with out-of-slice motion

- 11- • Intra-session registration example:

```
3dvolreg -base 4 -heptic -zpad 4 \
        -prefix fred1_epi_vr \
        -1Dfile fred1_vr_dfile.1D \
        fred1_epi+orig
```

Input dataset name

- ✧ **-base 4** ⇒ Selects sub-brick #4 of dataset **fred1\_epi+orig** as base image **J(x)**
- ✧ **-heptic** ⇒ Use 7<sup>th</sup> order polynomial interpolation
- ✧ **-zpad 4** ⇒ Pad each target image, **I(x)**, with layers of zero voxels 4 deep on each face prior to shift/rotation, then strip them off afterwards (before output)
  - ☐ Zero padding is particularly desirable for **-Fourier** interpolation
  - ☐ also good for large rotations, some data may get 'lost' if no zero padding
- ✧ **-prefix fred1\_epi\_vr** ⇒ Save output dataset into a new dataset with the given prefix name (e.g., **fred1\_epi\_vr+orig**)
- ✧ **-1Dfile fred1\_vr\_dfile.1D** ⇒ Save estimated movement parameters into a 1D (i.e., text) file with the given name
  - ☐ Movement parameters can be plotted with the **1dplot** command and used later....

**Try this** (in AFNI\_data6/afni) :

```
3dvolreg -base 3 -cubic -prefix epi_r1_vrt -1Dfile vr_dfile.1D epi_r1+orig
1dplot -volreg vr_dfile.1D &
```

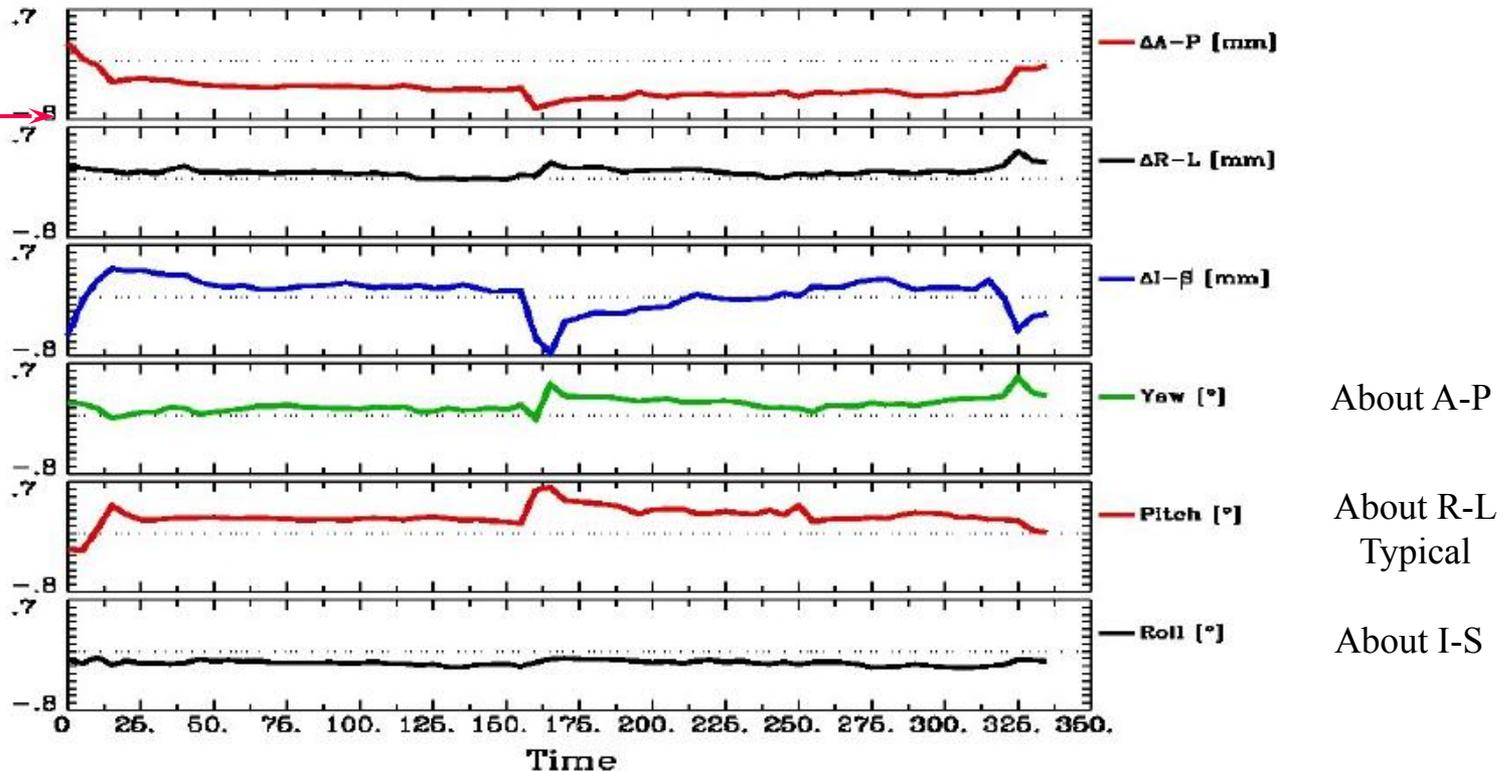
✧ Can now register second dataset from same session:

```
3dvolreg -base 'fred1_epi+orig[4]' -heptic -zpad 4 \
-prefix fred2_epi_vr -1Dfile fred2_vr_dfile.1D \
fred2_epi+orig
```

☐ Note base is from different dataset (`fred1_epi+orig`) than input (`fred2_epi+orig`)

☐ Aligning all EPI volumes from session to EPI closest in time to SPGR (if not aligning to anatomical)

```
1dplot -volreg -dx 5 -xlabel Time fred2_vr_dfile.1D
```



☐ Note motion peaks at time  $\approx 160$ s: subject jerked head up at that time

## "Fixing Motion"

- Motion occurs over slices and not volumes and moves data off original grid
- "Regressing out" – motion parameters, derivatives, displacement, euclidean norm of derivatives (summary parameters)
- Censoring ("scrubbing", "sweeping under the mat",...)
- Experimental design – kids, monkeys, juice, talking, waving hands wildly....
- Interpreting results – differences in motion between groups or something physiological
- Notice – activation following high contrast borders, "blinds" effects

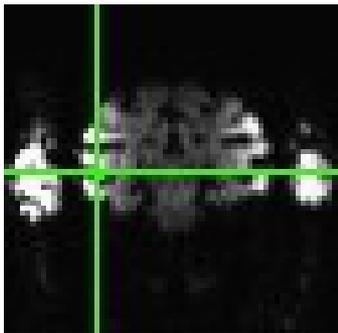
***Try this*** (in AFNI\_data6/afni) :

```
1d_tool.py -infile vr_dfile.1D -set_nruns 1 -censor_motion 1 ett  
1dplot ett_enorm.1D &  
cat ett_CENSORTR.txt
```

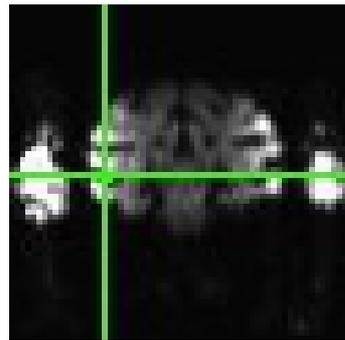
# Motion correction – caveats

- Motion is usually not completely correctable, so set motion parameters as regressors of no interest. Interpolation generally blurs data and depends on method and grid/resolution of EPI.
- Check in the AFNI GUI to be sure the data is not bouncing around after correction
- Example – Monkey sips juice at stimulus time, and large jaw muscles move. If the muscles are not masked, then motion correction may track muscles rather than brain.

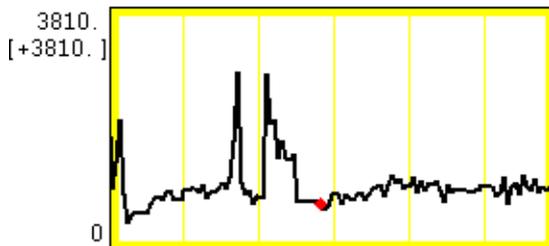
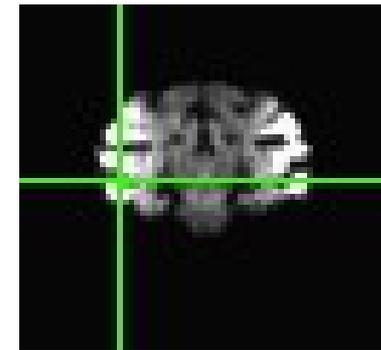
original



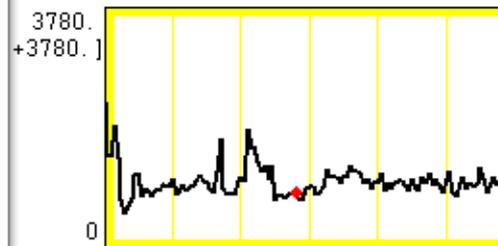
3dvolreg



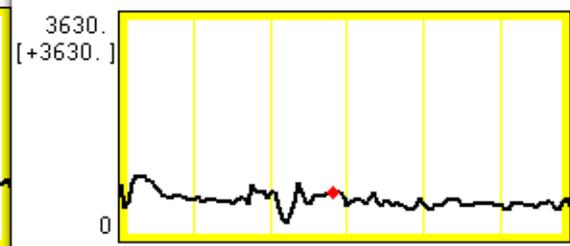
automask, 3dvolreg



CORONAL I: 46 #56=746@112.2222  
J: 32 Grid: 20 | Scale: 30 datum  
K: 6 # 0:118 | Base FIM Op



CORONAL I: 46 #56=889@112.2222  
J: 32 Grid: 20 | Scale: 30 da  
K: 6 # 0:118 | Base FIM Op



CORONAL I: 46 #56=801@112  
J: 32 Grid: 20 | Scale: 30 datum  
K: 6 # 0:118 | Base FIM Op

# Cross Modality Registration

- **3dAllineate** can be used to align images from different methods
  - ✧ For example, to align EPI data to SPGR / MPRAGE:
    - ❑ Run **3dSkullStrip** on the SPGR dataset so that it will be more like the EPI dataset (which will have the skull fat suppressed)
    - ❑ Use **3dAllineate** to align the EPI volume(s) to the skull-stripped SPGR volume
    - ❑ Program works well if the EPI volume covers most of the brain
  - ✧ Allows more general spatial transformations – affine, bilinear, non-linear (polynomial warping)
- **3dAllineate** has several different “cost” functions (**E**) available
  - ✧ **leastsq** = Least Squares (**3dvolreg**, **3dWarpDrive**)
  - ✧ **mutualinfo** = Mutual Information
  - ✧ **norm\_mutualinfo** = Normalized Mutual Information
  - ✧ **hellinger** = Hellinger Metric [the **default** cost function]
  - ✧ **corratio\_mul** = Correlation ratio (symmetrized by multiplication)
  - ✧ **corratio\_add** = Correlation ratio (symmetrized by addition)
  - ✧ **corratio\_uns** = Correlation ratio (unsymmetric)
    - **lpc** = Local Pearson Correlation (negative)
    - **lpa** = Local Pearson Correlation (absolute value)

## align\_epi\_anat.py

- Goal: Want to align anat and EPI (anat to EPI or EPI to anat or dset1to2 or dset2to1)

LPC method – Local Pearson Correlation to match dark CSF in anatomical data with bright CSF in EPI data.

- align\_epi\_anat.py script – preprocessing and calls 3dAllineate for alignment
- @AddEdge – for visualization

- Simple Example:

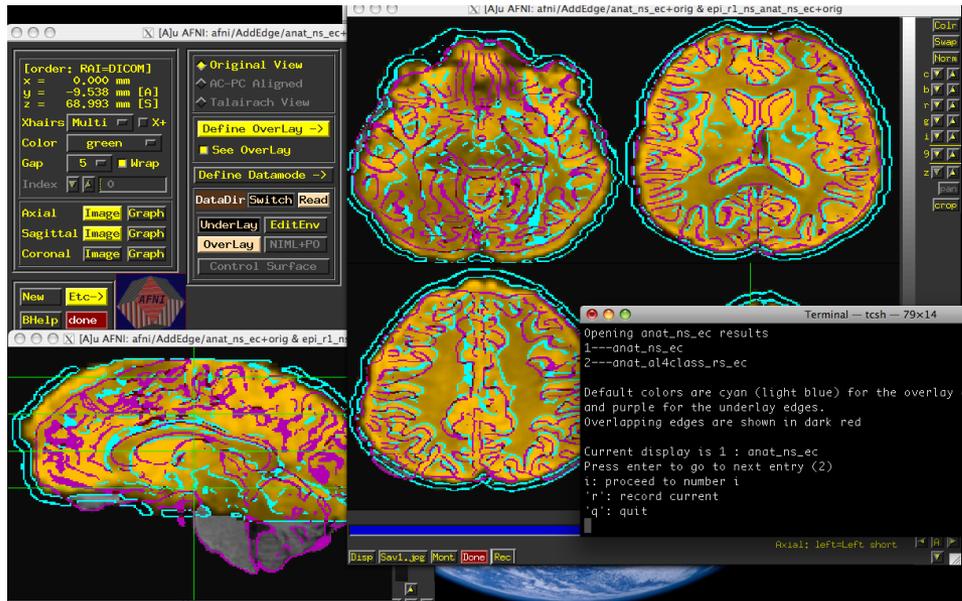
```
align_epi_anat.py -anat anat+orig \  
                -epi epi_r1+orig \  
                -AddEdge -epi_base 0 -suffix _al4class
```

```
cd AddEdge
```

```
afni -niml -yesplugouts &
```

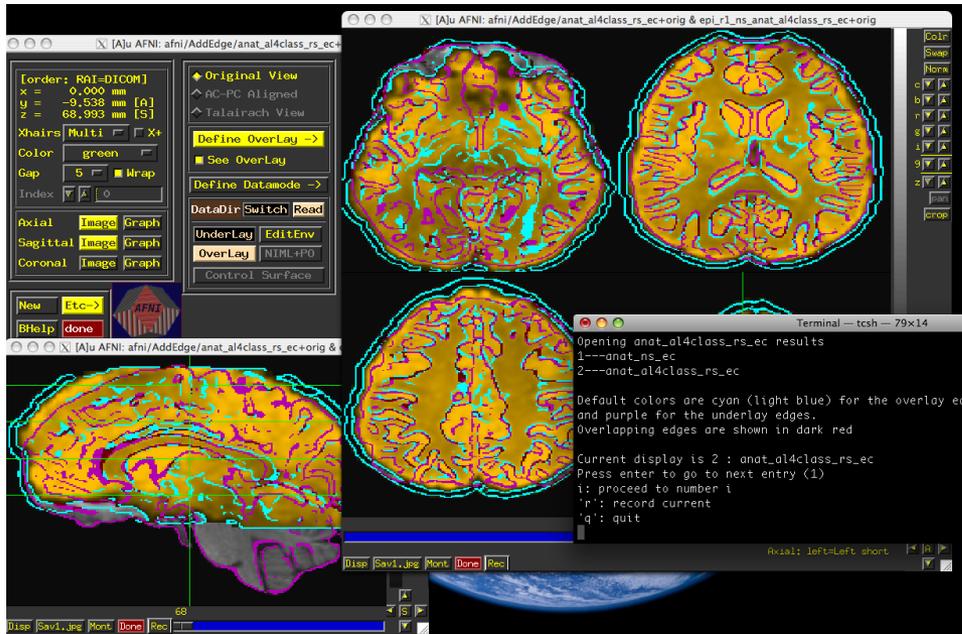
```
@AddEdge
```

Combines deoblique, motion correction, alignment and talairach transformations into a single transformation. Also performs slice timing correction and applies transformations to “child” datasets.

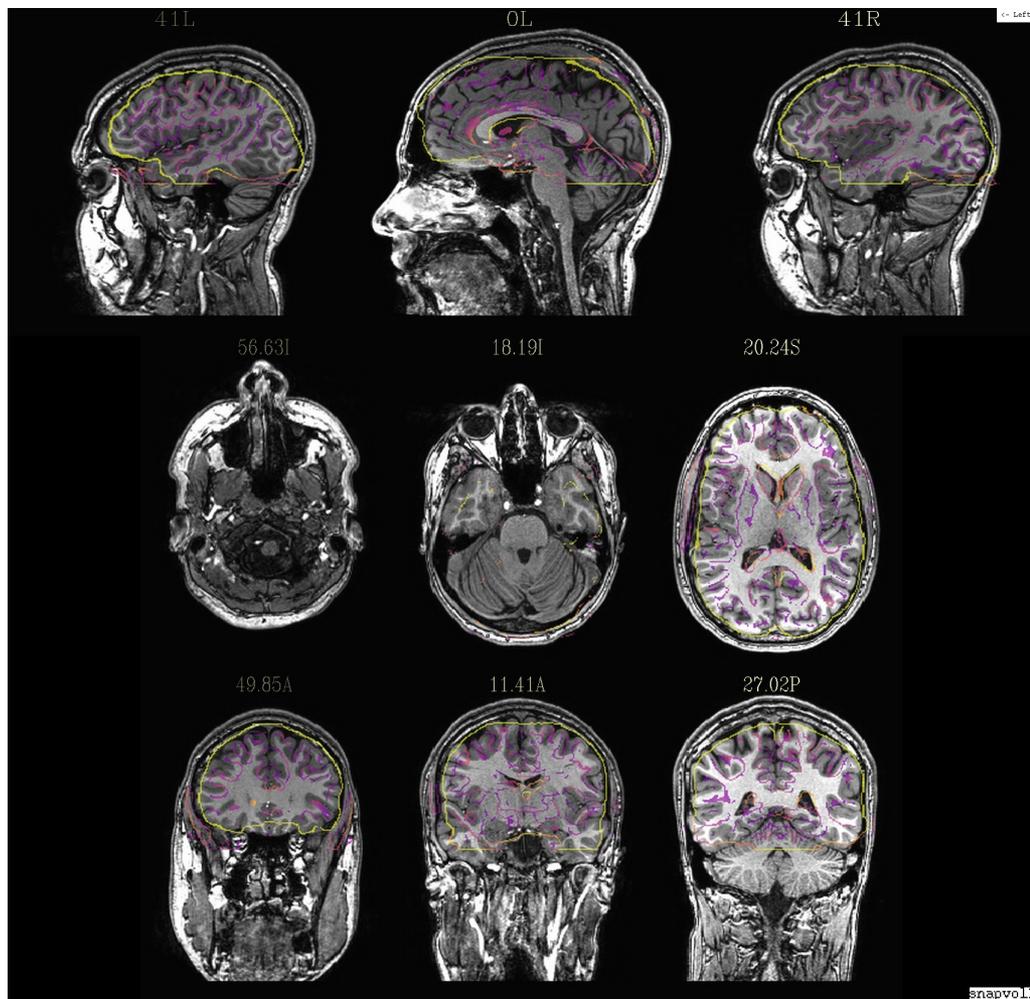


@AddEdge  
display

Before



After



@snapshot\_volreg anat+orig. epi\_r1+orig edges.jpg  
aiv edges.jpg

## Alignment Visualization in AFNI

- Graph and image – travel through time for motion correction or for a thousand datasets in a row.
- Multiple controllers and crosshairs – up to ten datasets at a time, quick and rough.
- Overlay display – opacity control, thresholding. A single pair – good for different or similar datasets.
- Overlay toggle, Underlay toggle – wiggle, good but a little tricky ('o' and 'u' keys in image viewer)
- Sliding Overlay ('4'/'5' keys), Fade-in overlay ('6' key), Checkerboard Underlay – ('#' key) two similar datasets in underlay but must be virtually identical. Good for comparing two processing methods
- Edge display for underlay – effective pairwise comparison for quick fine structure display and comparison with overlay dataset with opacity. One dataset should have reliable structure and contrast. Now with 'e' toggle.
- @AddEdge – single or dual edges with good contrast for pairwise comparison.

## Alignment strategies with align\_epi\_anat.py

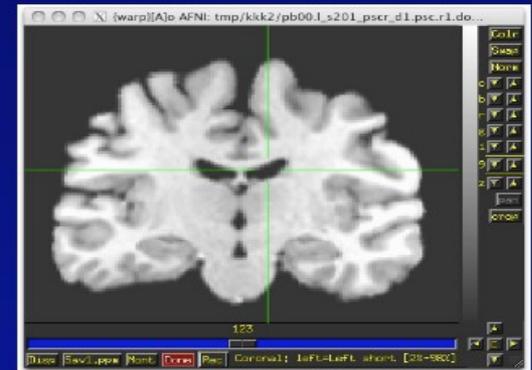
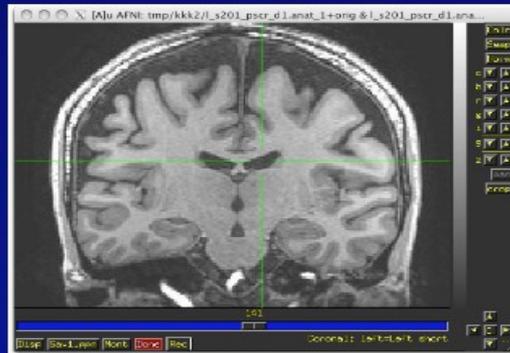
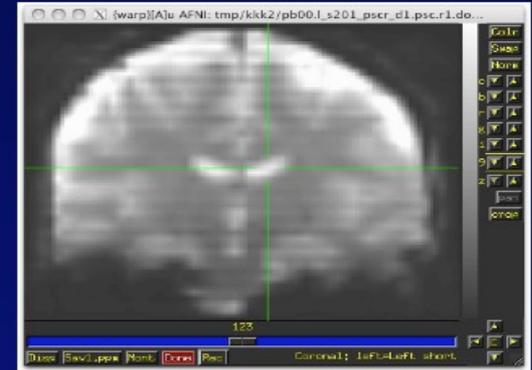
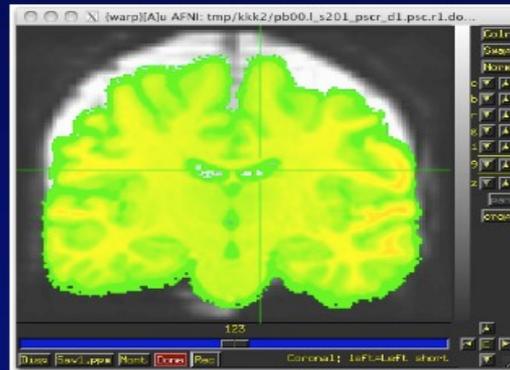
- Defaults work usually (>90% - FCON1000)
  - Problems:
    - ◆ Far off start – “-big\_move”, “-giant\_move”, “-ginormous\_move”
    - ◆ Poor contrast – “-cost lpa”, “-cost nmi”, “-cost lpc+ZZ”
    - ◆ Poor non-uniformity – “-edge”, “-cost lpa”
    - ◆ stroke/MS lesions, tumors, monkeys, rats, multi-modality (CT/PET/DTI/...), something else? – see us, post message



## Real and Imaginary Problems

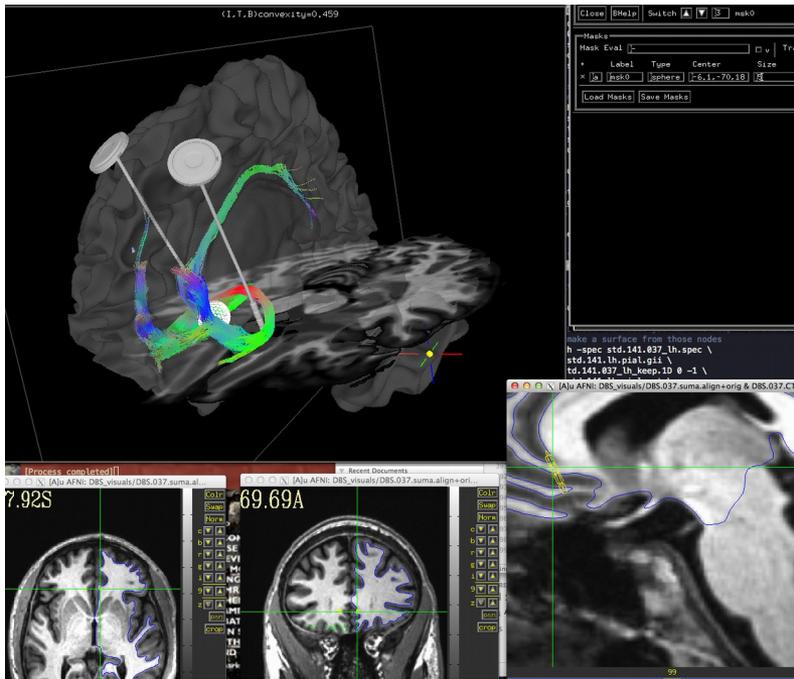
# Saved by the contrast

- However, bias may result in erroneous group differences



## Alignment –special cases

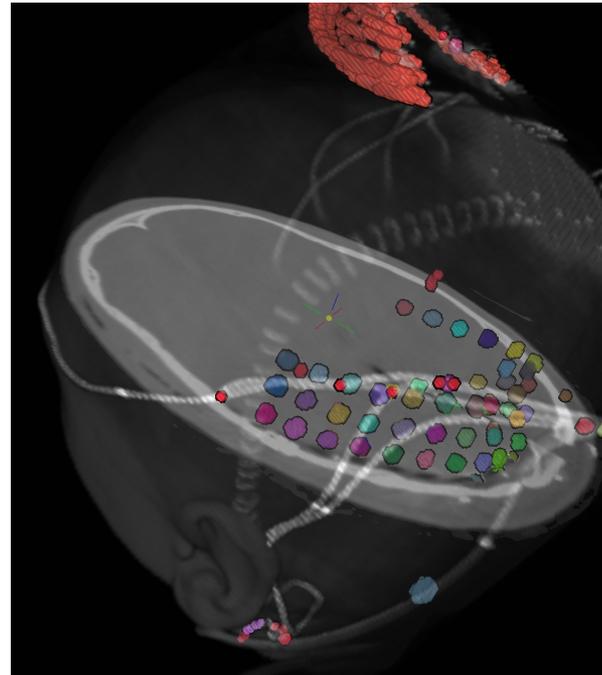
DBS – align CT with electrodes to pre-surgical MRI, PET



Dataset courtesy of Justin Rajendra,  
(Formerly at Emory, Now in our group.  
Woohoo!)

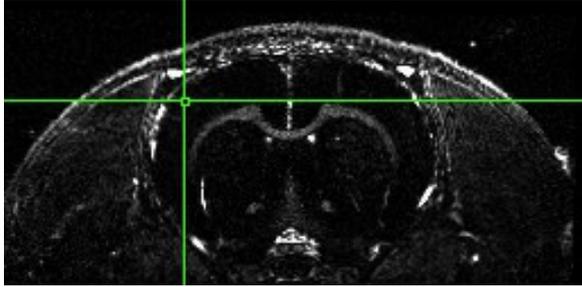
Also see @Install\_DBSPROC for DBS with  
CT and DTI processing (S. Horovitz)

ECOG – align CT with electrodes to pre-surgical MRI

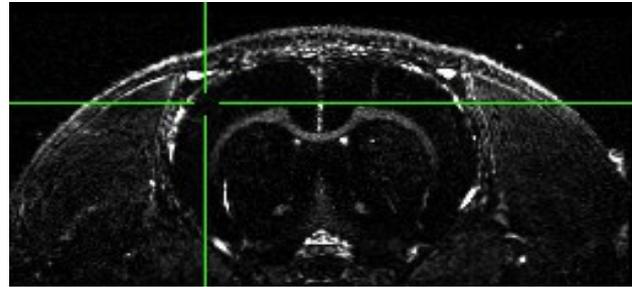


Dataset courtesy of Anna Gaglianese  
(University of Utrecht, Netherlands)

## Rat Brains



Alignment of 12 hour  
Manganese enhanced MRI scan  
(MEMRI) to start

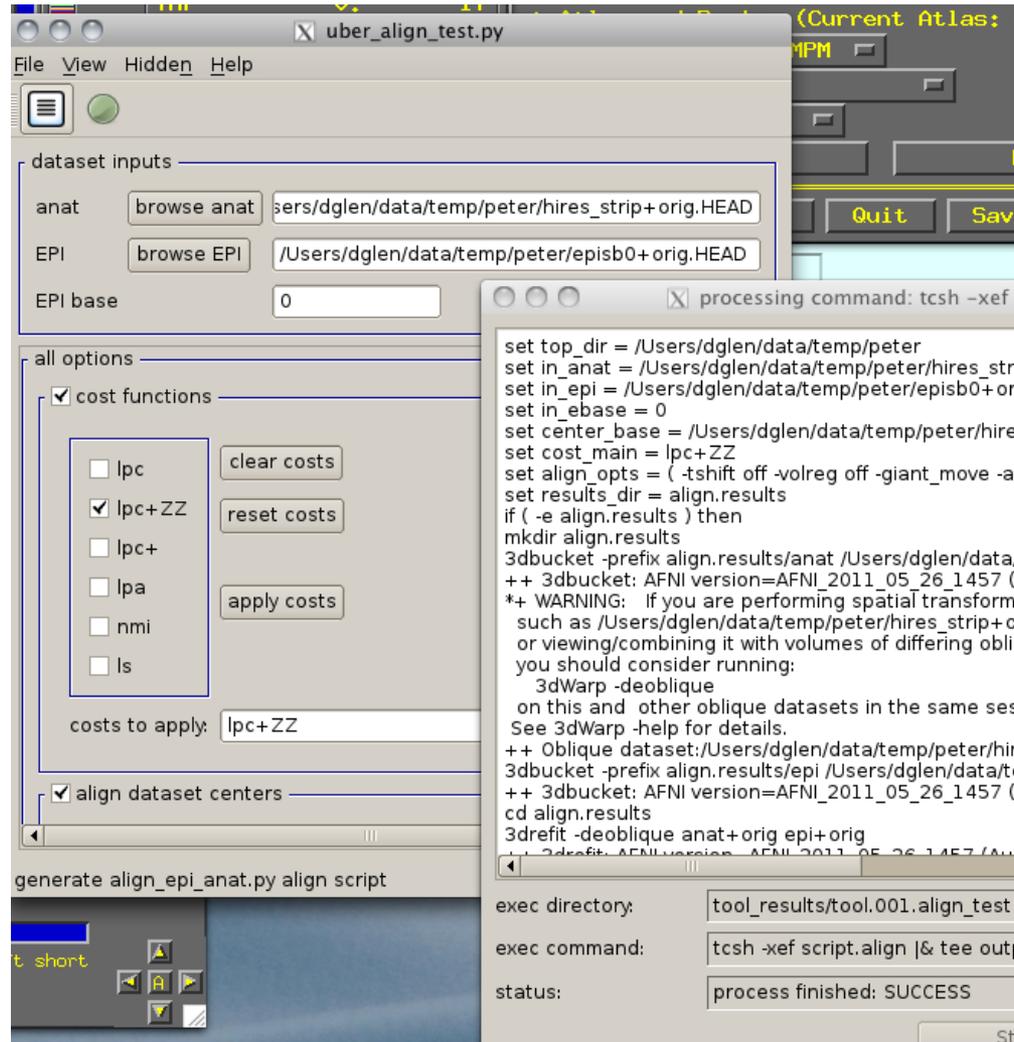


```
#!/bin/tcsh
# align_times.csh
set basedset = 14_pre+orig
foreach timedset ( 14_*hr+orig.HEAD)
  align_epi_anat.py -prep_off -anat $timedset -epi $basedset \
  -epi_base 0 -anat_has_skull no -epi_strip None -suffix _edge2prep \
  -cost lpa -overwrite -edge -rat_align
end
3dTcat -prefix 14_timealigned_edge 14_pre+orig. 14*edge2prep+orig.HEAD
```

Data from Der-Yow Chen (NINDS)

# uber\_align\_test.py

- select input data
- set options
- create script
- run script



## afni\_proc.py – alignment handling

- Single script to do all the processing of a typical fMRI pipeline including motion correction (3dvolreg), alignment (align\_epi\_anat.py)
- combines transformations when possible
- from example 6 in afni\_proc.py's prodigious help:

```
afni_proc.py -subj_id sb23.e6.align \
             -dsets sb23/epi_r??+orig.HEAD \
             -do_block align tlrc \
             -copy_anat sb23/sb23_mpra+orig \
             -tcat_remove_first_trs 3 \
             -volreg_align_to last \
             -volreg_align_e2a \
             -volreg_tlrc_warp \
```

...

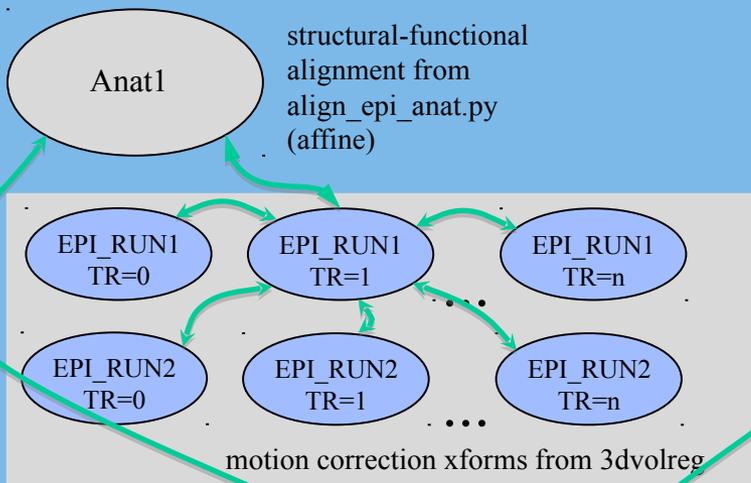
To process in orig space, remove -volreg\_tlrc\_warp.

To apply manual tlrc transformation, use -volreg\_tlrc\_adwarp.

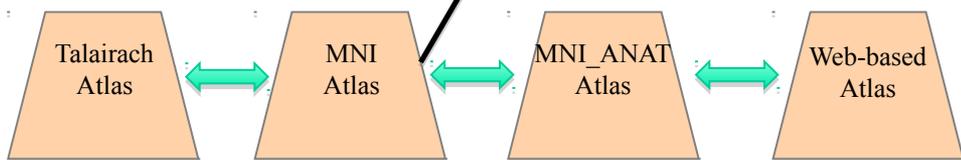
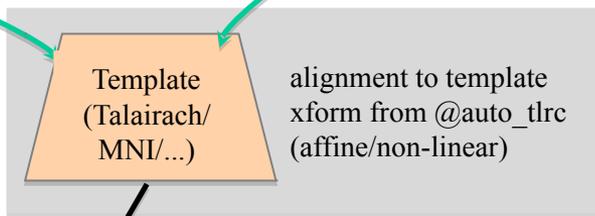
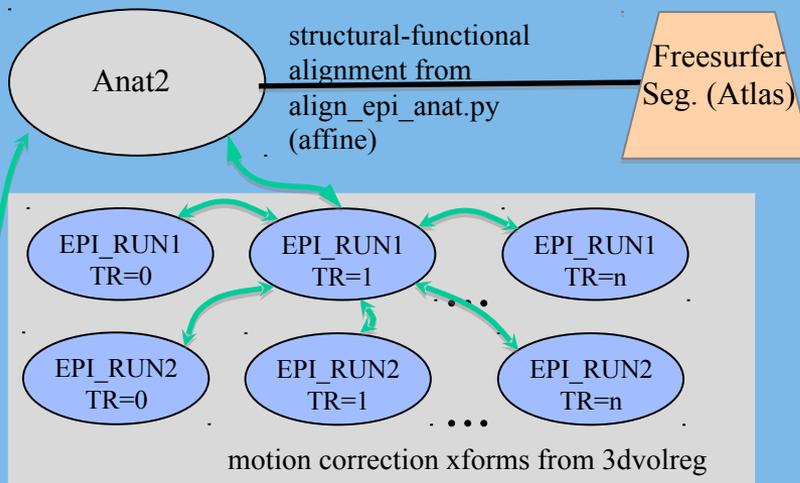
To process as anat aligned to EPI, remove -volreg\_align\_e2a.

# Transformation Chains Example

## Session 1

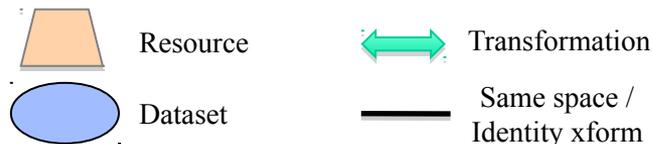


## Session 2



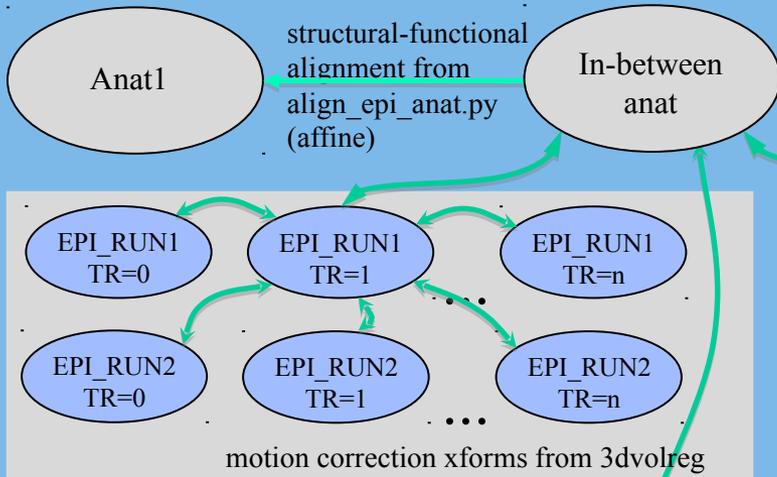
Known or User-defined transformations

Atlas information available to any space through shortest chain of xforms

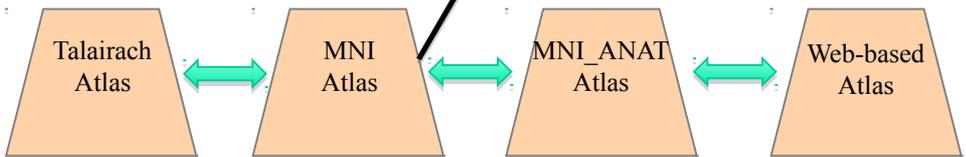
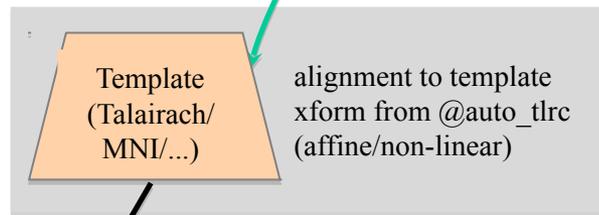
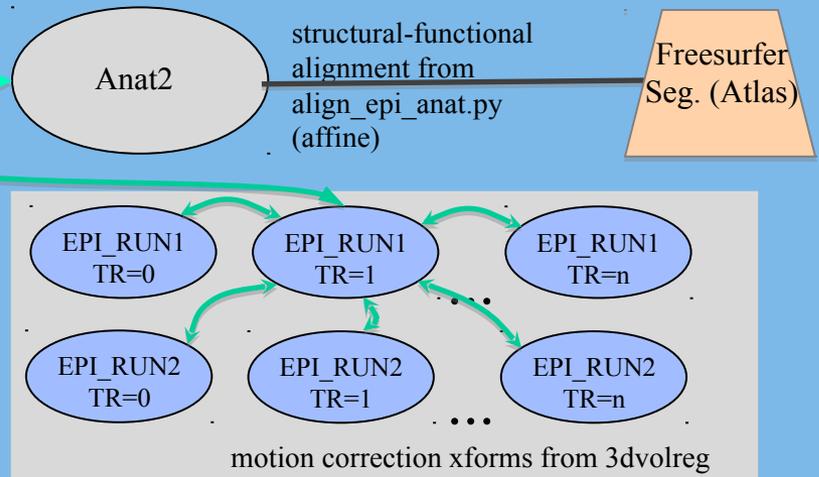


# Alignment across two sessions

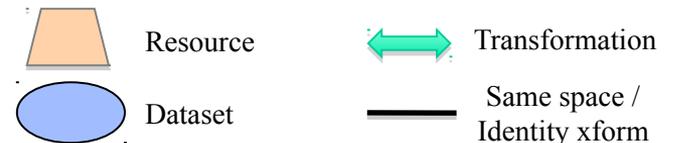
## Session 1



## Session 2



Atlas information available to any space through shortest chain of xforms



Known or User-defined transformations

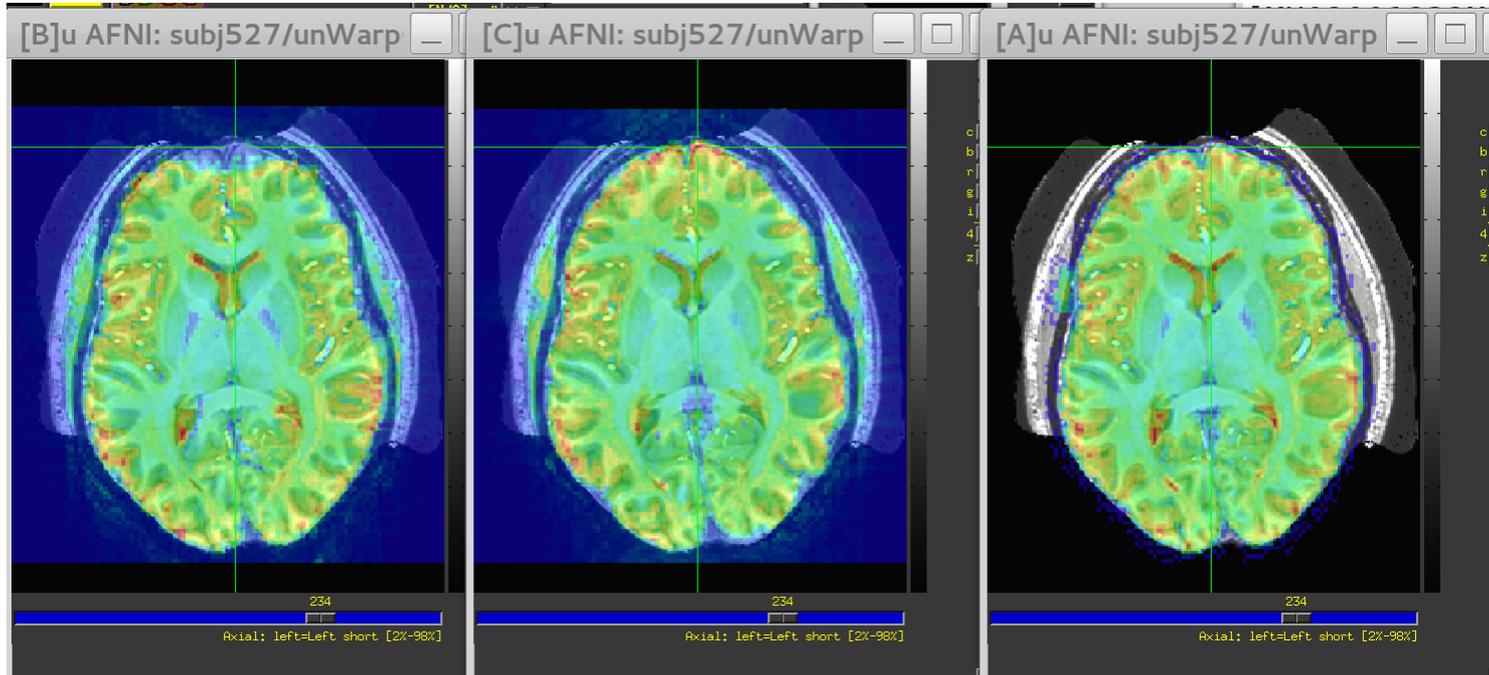
<http://afni.nimh.nih.gov/sscc/dglen/alignmentacross2sessions>

## Nonlinear Warping

### 3dQwarp

- $I_{\text{new}}(\mathbf{x}) = I_{\text{old}}(\mathbf{W}(\mathbf{x}))$ 
    - ✧ where  $\mathbf{W}(\mathbf{x})$  depends on a *lot* of parameters (1000-50000+)
    - ✧ Method: Incremental transformation with Hermite cubic polynomials over finer and finer 3D patches. Output is both aligned dataset and the warp and the inverse warp deformations in Dx,Dy,Dz
    - ★ Better alignment of anatomical volumes to template space
      - ☐ Then carry the functional results to template space for better group analyses?
      - ☐ As an aid to brain segmentation and atlas-ing accuracy?
    - ★ Pre- and post-surgical alignment, EPI distortion correction
  - Related programs and scripts:
    - ✧ *3dNwarpApply, 3dNwarpCat, 3dNwarpCalc, 3dNwarpAdjust, 3dNwarpFuncs*
    - ✧ *auto\_warp.py, afni\_proc.py*
- UnwarpEPI.py - blipup-blipdown script (Vinai Roopchansingh)*

# Blip-up/down distortion correction



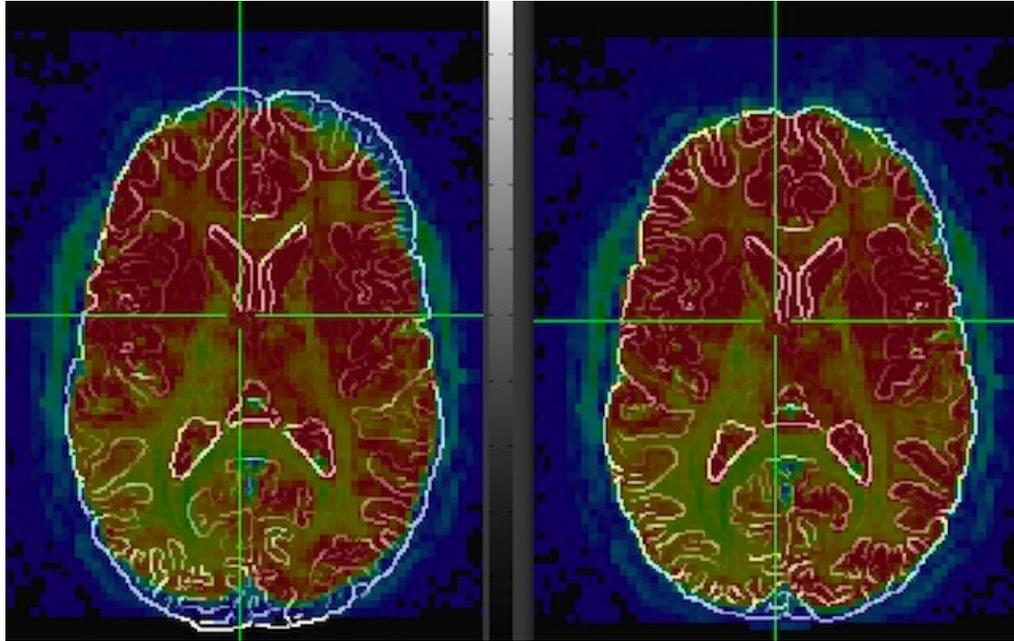
Data  
courtesy of  
Sam Torrisi,  
NIMH

Blip-up  
(uncorrected)

Blip-down

Corrected

## Left and Right - flipping



```
align_epi_anat.py -anat anat+orig -epi epi_r1+orig -epi_base 0 \  
-giant_move -check_flip
```

The output will include this warning if the data is flipped:

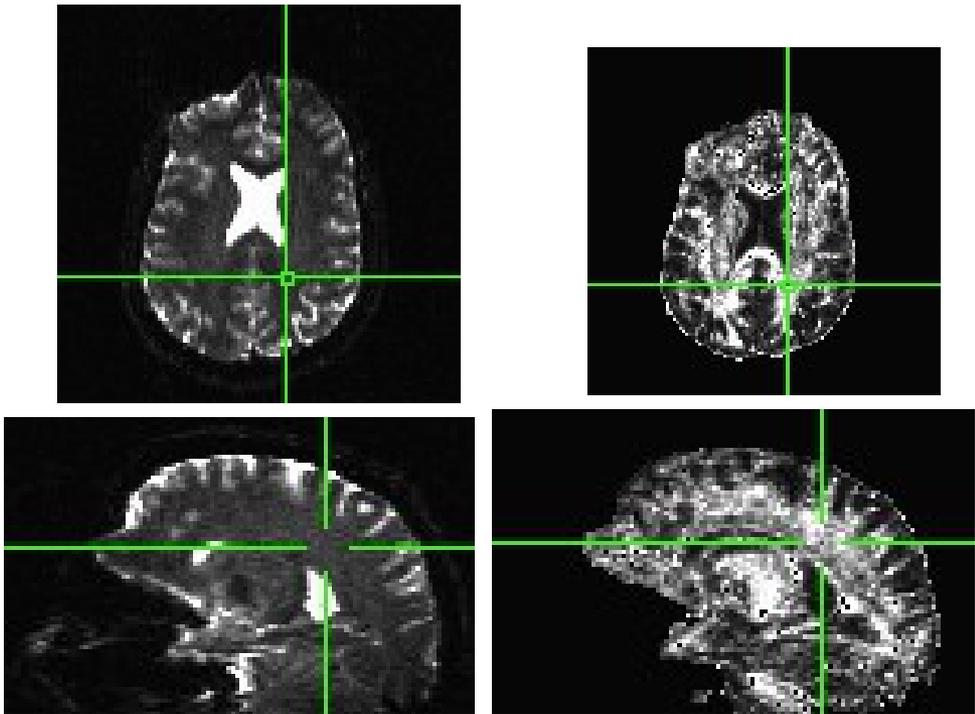
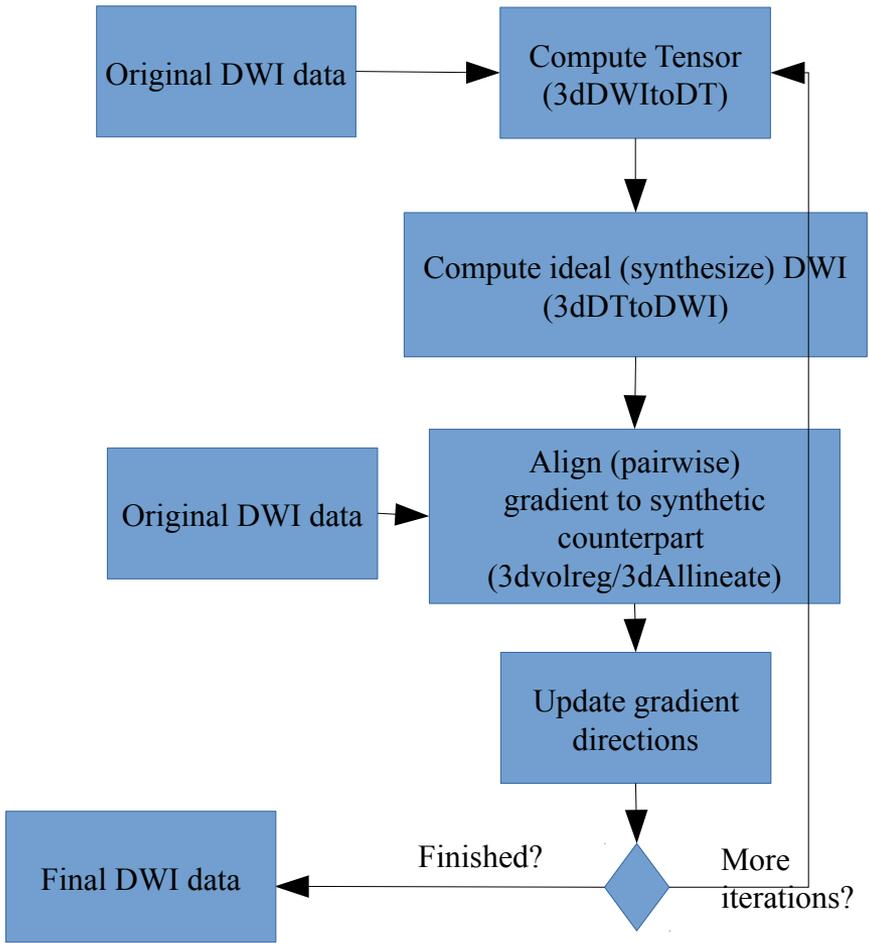
**WARNING: \*\*\*\*\* flipped data aligns better than original data**

**Check for left - right flipping in the GUI \*\*\*\*\***

If everything is okay, this message appears instead:

**Data does not need flipping**

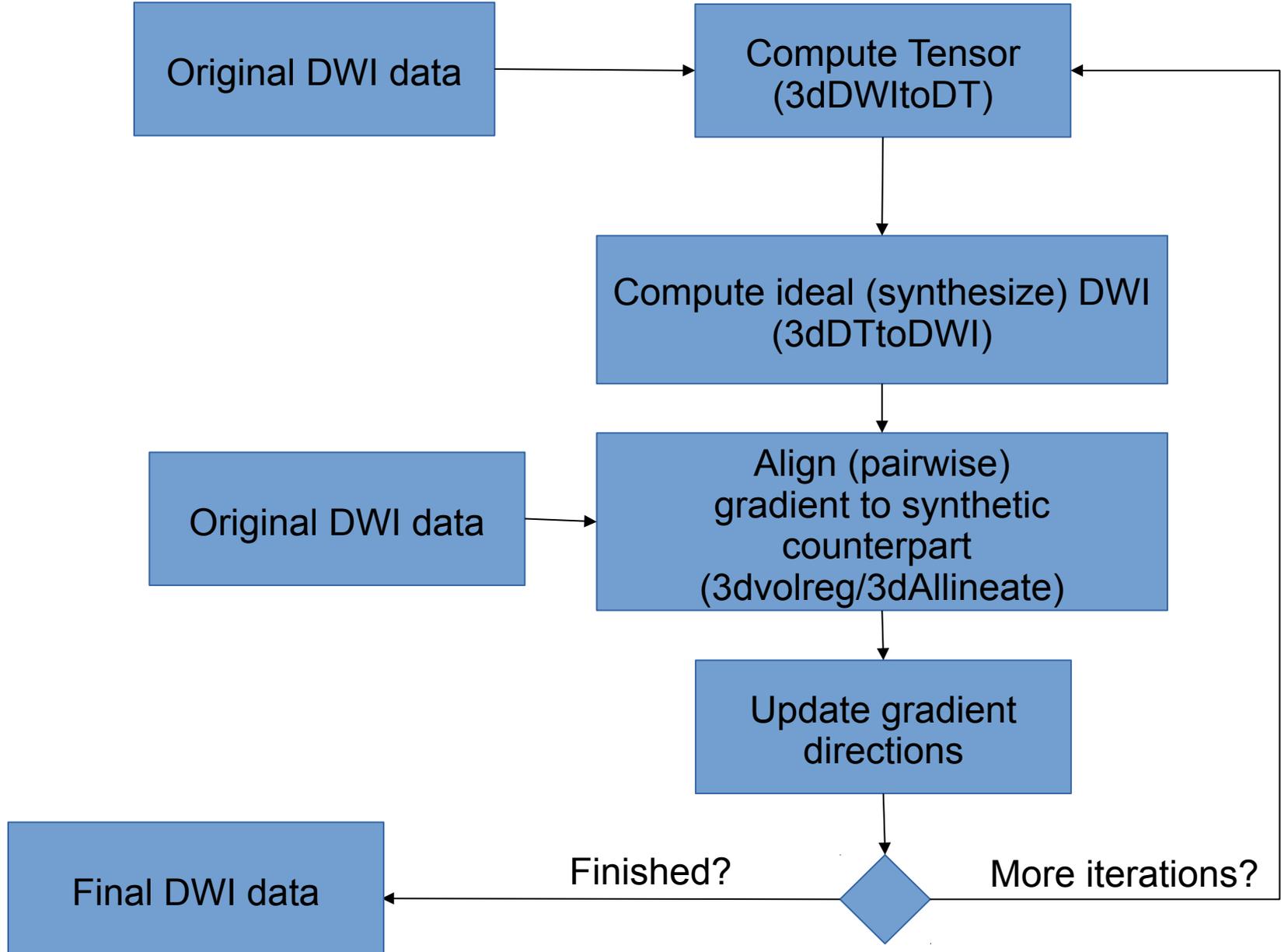
### DWI Motion Correction



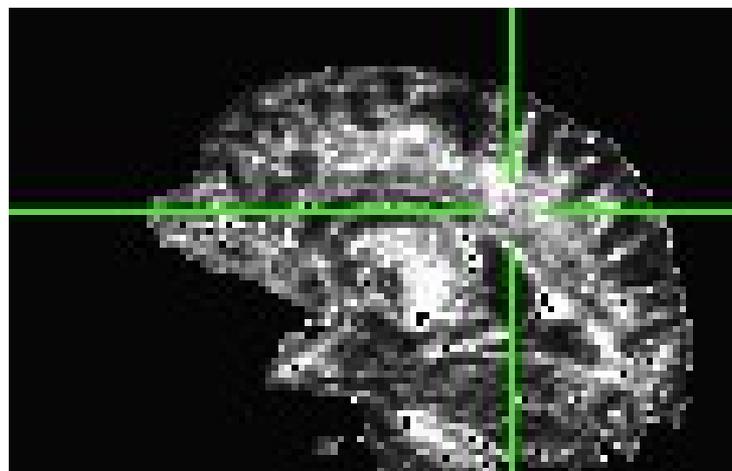
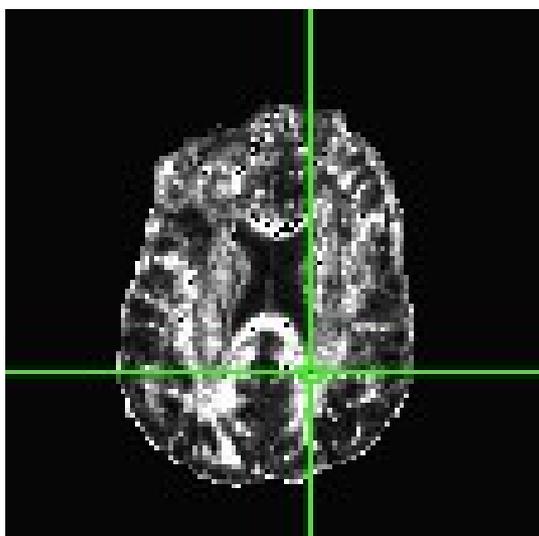
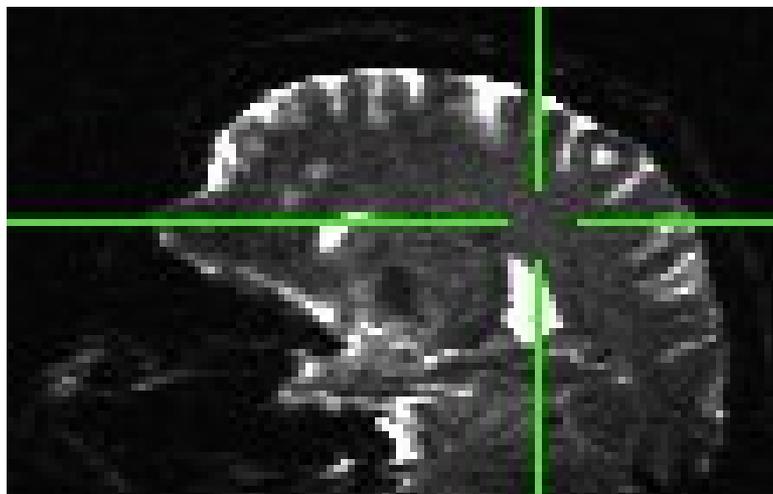
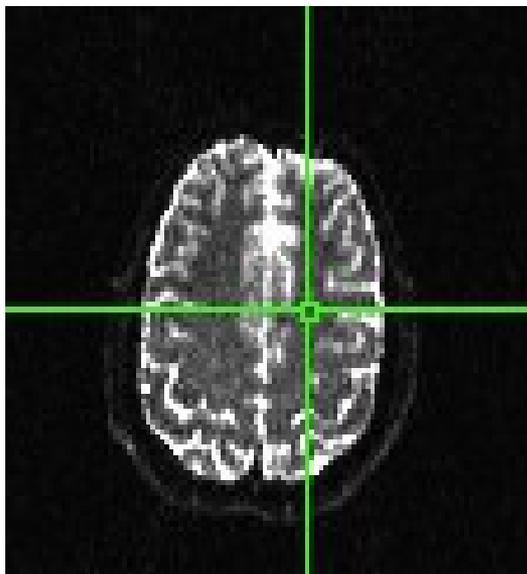
Original motion

FA maps with iteration

# Method overview



## DWI Motion Correction



# ATLASES

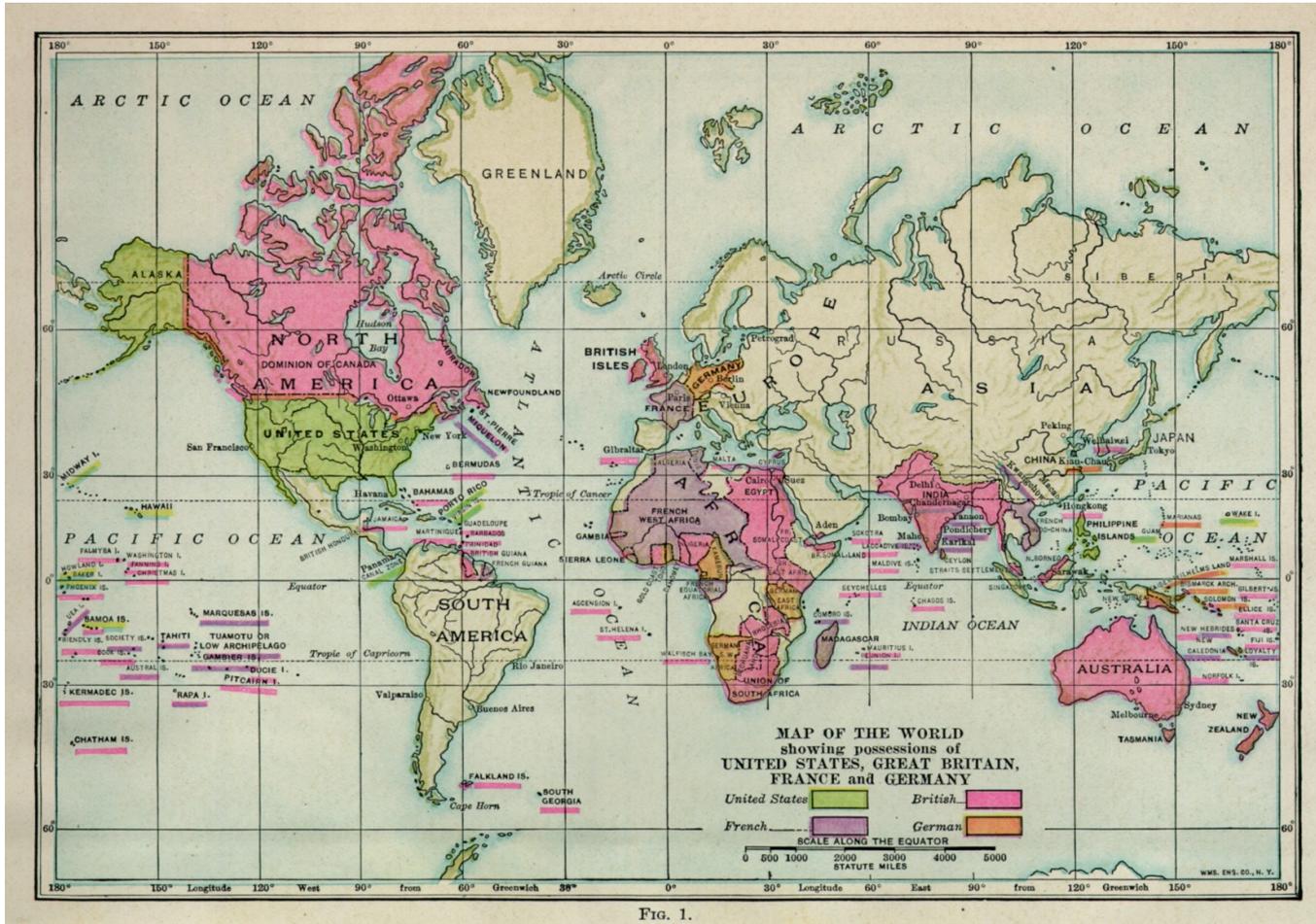
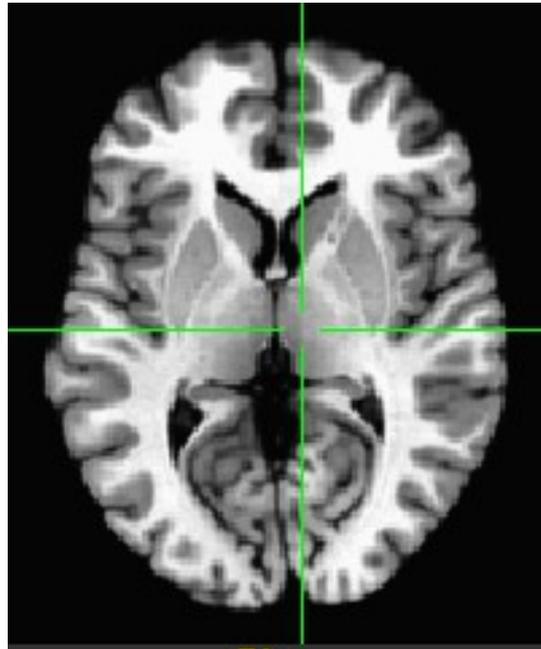


FIG. 1.

## ATLAS DEFINITIONS

**Template** - a reference dataset used for matching shapes.

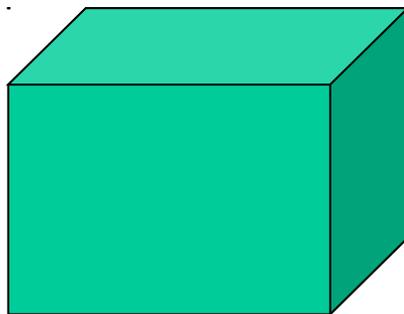
Examples: TT\_N27+tlrc, MNI\_EPI+tlrc, TT\_ICBM452+tlrc.



TT\_N27+tlrc

## ATLAS DEFINITIONS

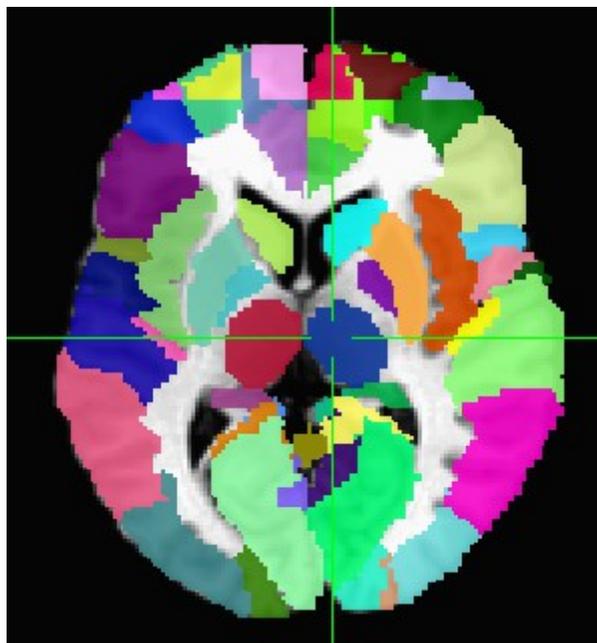
**Template Space** -  $x,y,z$  coordinate system shared by many datasets (the basic shoebox) Examples: TLRC (Talairach-Tourneaux), MNI, MNI\_ANAT, ORIG.



## ATLAS DEFINITIONS

**Atlas** - segmentation info.

Examples: TTatlas+tlrc, TT\_N27\_EZ\_ML+tlrc, roidset+orig.



TT\_N27\_EZ\_ML+tlrc

## Registration To Standard Spaces

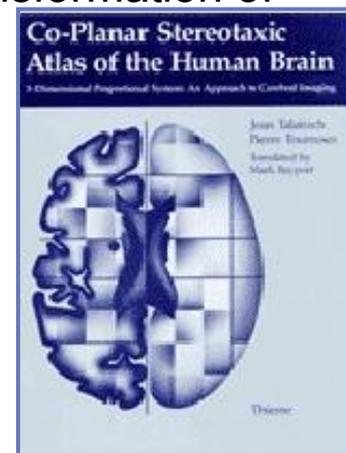
### Transforming Datasets to Talairach-Tournoux Coordinates

- The original purpose of AFNI (*circa* 1994 A.D.) was to perform the transformation of datasets to Talairach-Tournoux (stereotaxic) coordinates
- The transformation can be manual, or automatic
- In manual mode, you must mark various anatomical locations, defined in

Jean Talairach and Pierre Tournoux

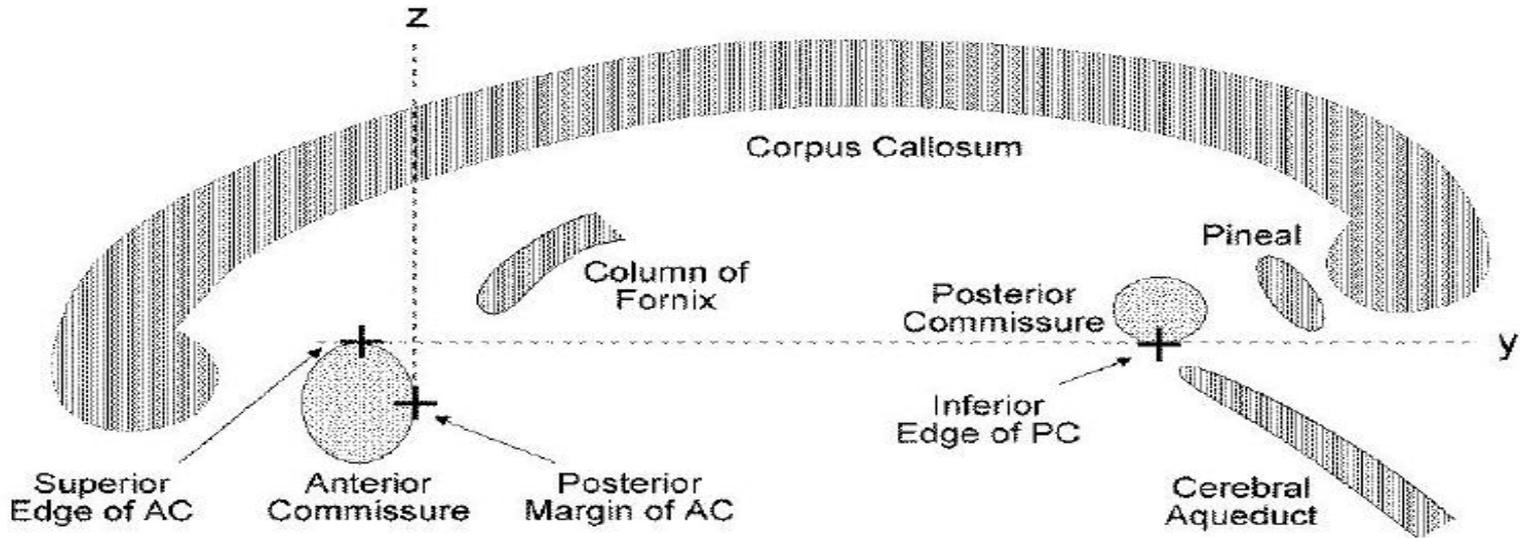
“Co-Planar Stereotaxic Atlas of the Human Brain”

Thieme Medical Publishers, New York, 1988



- ✧ Marking is best done on a high-resolution T1-weighted structural MRI volume
- In automatic mode, you need to choose a template to which your data are aligned. Different templates are made available with AFNI's distribution. You can also use your own templates.
- Transformation carries over to all other (follower) datasets in the same directory
  - ✧ This is where the importance of getting the relative spatial placement of datasets done correctly in  $t \rightarrow 3d$  really matters
  - ✧ You can then write follower datasets, typically functional or EPI timeseries, to disk in Talairach coordinates
    - ❓ Purpose: voxel-wise comparison with other subjects
    - ❓ May want to blur volumes a little before comparisons, to allow for residual anatomic variability: AFNI programs [3dmerge](#) or [3dBlurToFWHM](#)

- Hidden in GUI - right click on “DataDir” or set AFNI\_ENABLE\_MARKERS to YES in .AFNIRC
- Manual Transformation proceeds in two stages:
  1. Alignment of AC-PC and I-S axes (to `+acpc` coordinates)
  2. Scaling to Talairach-Tournoux Atlas brain size (to `+tlrc` coordinates)
- Stage 1: Alignment to `+acpc` coordinates:
  - ✧ Anterior commissure (AC) and posterior commissure (PC) are aligned to be the y-axis
  - ✧ The longitudinal (inter-hemispheric or mid-sagittal) fissure is aligned to be the yz-plane, thus defining the z-axis
  - ✧ The axis perpendicular to these is the x-axis (right-left)
  - ✧ Five markers that you must place using the [[Define Markers](#)] control panel:
    - AC superior edge = top middle of anterior commissure
    - AC posterior margin = rear middle of anterior commissure
    - PC inferior edge = bottom middle of posterior commissure
    - First mid-sag point = some point in the mid-sagittal plane
    - Another mid-sag point = some other point in the mid-sagittal plane
  - ✧ This procedure tries to follow the Atlas as precisely as possible
    - ❓ Even at the cost of confusion to the user (e.g., you)



**Click Define Markers to open the "markers" panel**

**Select which marker you are editing**

**Press this IN to create or change markers**

**Color of "primary" (selected) marker**

**Color of "secondary" (not selected) markers**

**Size of markers (pixels)**

**Size of gap in markers**

**Clear (unset) primary marker**

**Set primary marker to current focus location**

**Carry out transformation to +acpc coordinates**

**Perform "quality" check on markers (after all 5 are set)**

◆ Original View  
◆ AC-PC Aligned  
◆ Talairach View

**Define Markers**  
■ See Markers

Define Overlay  
■ See Overlay

Define Datamode

Switch Session  
Switch UnderLay  
Switch Overlay  
Control Surface

◆ AC superior edge  
◆ AC posterior margin  
◆ PC inferior edge  
◆ First mid-sag pt  
◆ Another mid-sag pt

Allow edits

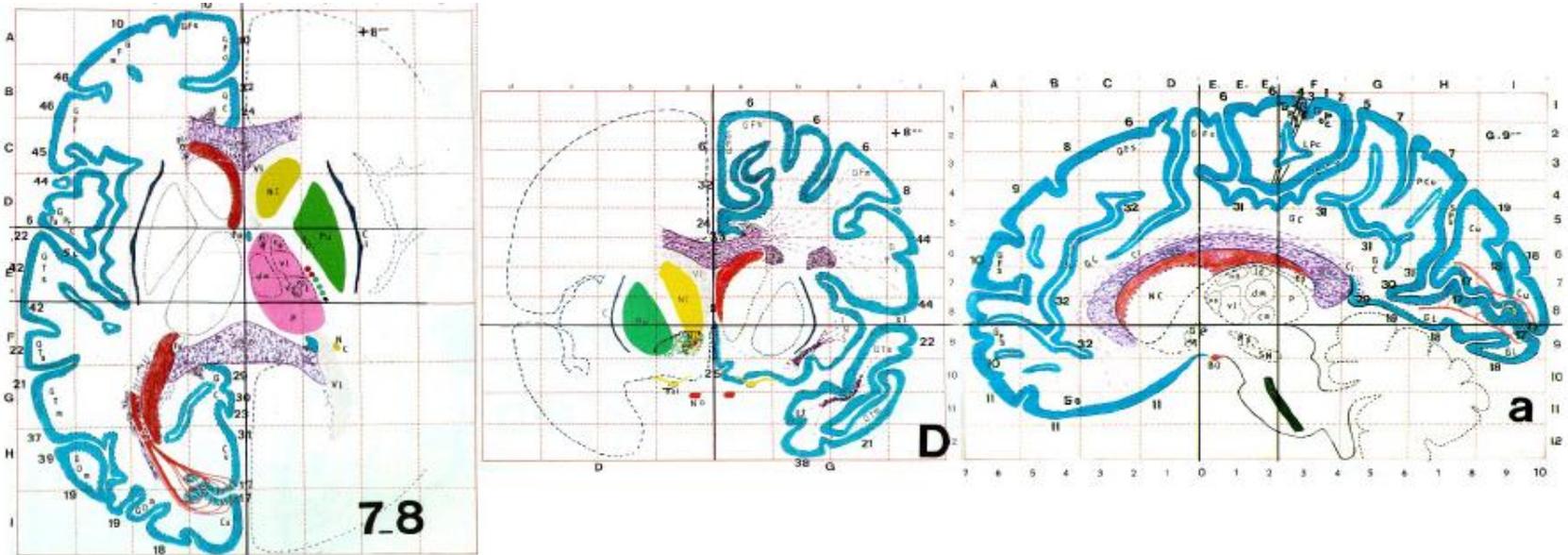
Pcolor   
Scolor   
Size   
Gap

Set Clear Quality?

Transform Data  
■ Big Talairach Box?

**Stage 2: Scaling to Talairach-Tournoux (+tlrc) coordinates:**

- Once the AC-PC landmarks are set and we are in ACPC view, we now stretch/shrink the brain to fit the Talairach-Tournoux Atlas brain size (sample TT Atlas pages shown below, just for fun)

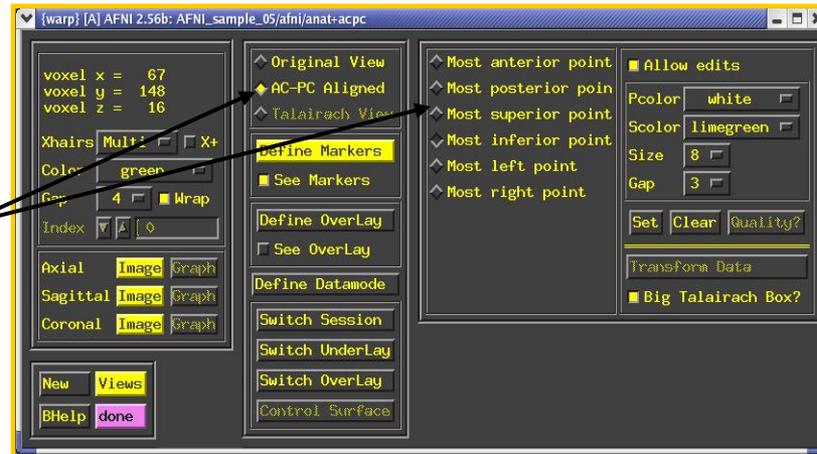


Most anterior to AC	70 mm		
AC to PC	23 mm		
PC to most posterior	79 mm		
Most inferior to AC	42 mm		
AC to most superior	74 mm	Length of cerebrum	172mm
AC to left (or right)	68 mm	Width of cerebrum	136mm

- Selecting the Talairach-Tournoux markers for the bounding box:

- ✧ There are 12 sub-regions to be scaled (3 A-P x 2 I-S x 2 L-R)
- ✧ To enable this, the transformed +acpc dataset gets its own set of markers
  - ☑ Click on the [\[AC-PC Aligned\]](#) button to view our volume in ac-pc coordinates
  - ☑ Select the [\[Define Markers\]](#) control panel
- ✧ A new set of six Talairach markers will appear and the user now sets the bounding box markers (see Appendix C for details):

Talairach markers appear only when the AC-PC view is highlighted

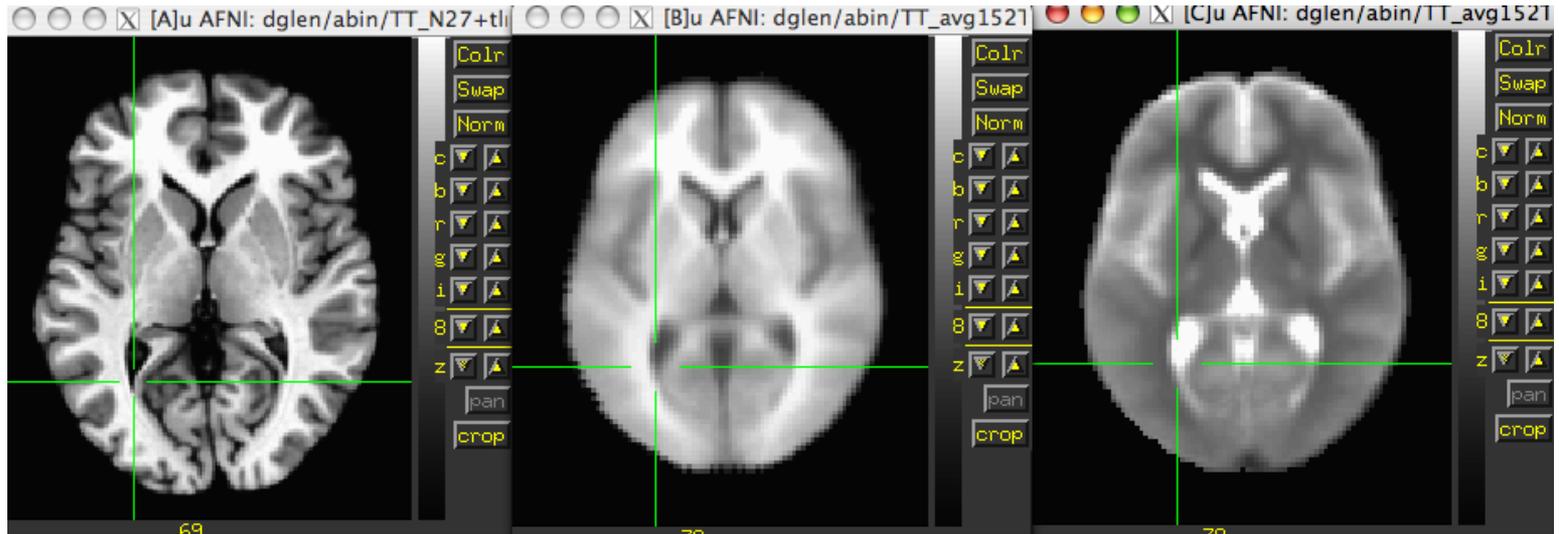


- ✧ Once all the markers are set, and the quality tests passed. Pressing [\[Transform Data\]](#) will write new **header** containing the Talairach transformations (see Appendix C for details)
  - ☑ Recall: With AFNI, spatial transformations are stored in the header of the output

- Is manual selection of AC-PC and Talairach markers bringing you down? You can now perform a TLRC transform **automatically** using an AFNI script called @auto\_tlrc.
  - ✧ Differences from Manual Transformation:
    - ❑ Instead of setting ac-pc landmarks and volume boundaries by hand, the anatomical volume is warped (using 12-parameter affine transform) to a template volume in TLRC space.
    - ❑ Anterior Commissure (AC) center no longer at 0,0,0 and size of brain box is that of the template you use.
      - ❑ For various reasons, some good and some bad, templates adopted by the neuroimaging community are not all of the same size. Be mindful when using various atlases or comparing standard-space coordinates.
    - ❑ You, the user, can choose from various templates for reference but be consistent in your group analysis.
    - ❑ Easy, automatic. Just check final results to make sure nothing went seriously awry. AFNI is perfect but your data is not.

- ✧ Templates in @auto\_tlrc that the user can choose from:
  - **TT\_N27+tlrc:**
    - AKA “Colin brain”. One subject (Colin) scanned 27 times and averaged. (www.loni.ucla.edu, www.bic.mni.mcgill.ca)
    - Has a full set of FreeSurfer (surfer.nmr.mgh.harvard.edu) surface models that can be used in SUMA (*link*).
    - Is the template for cytoarchitectonic atlases (www.fz-juelich.de/ime/spm\_anatomy\_toolbox)
      - For improved alignment with cytoarchitectonic atlases, I recommend using the TT\_N27 template because the atlases were created for it. In the future, we might provide atlases registered to other templates.
  - **TT\_icbm452+tlrc:**
    - International Consortium for Brain Mapping template, average volume of 452 normal brains. (www.loni.ucla.edu, www.bic.mni.mcgill.ca)
  - **TT\_avg152T1+tlrc:**
    - Montreal Neurological Institute (www.bic.mni.mcgill.ca) template, average volume of 152 normal brains.
  - **TT\_EPI+tlrc:**
    - EPI template from spm2, masked as TT\_avg152T1. TT\_avg152 and TT\_EPI volumes are based on those in SPM's distribution. (www.fil.ion.ucl.ac.uk/spm/)
  - **MNI152\_T1\_2009c+tlrc:**
    - MNI's 152 nonlinear asymmetric template

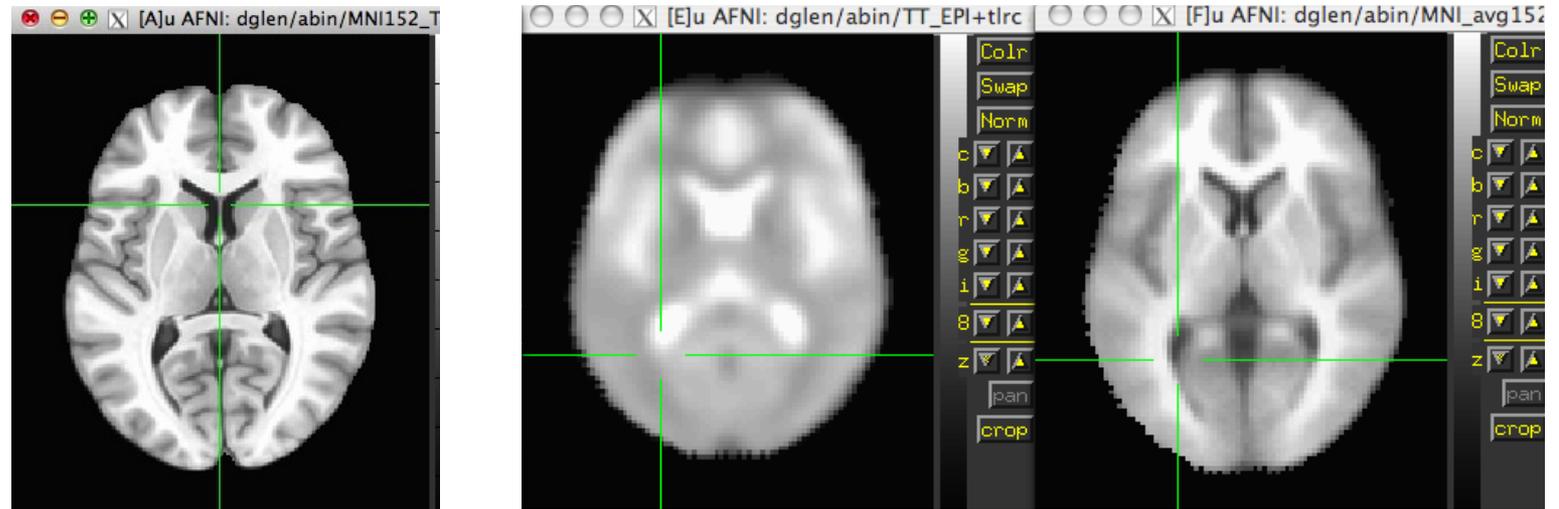
# Templates included with AFNI



TT\_N27

TT\_avg152T1

TT\_avg152T2



MNI152\_T1\_2009c

TT\_EPI

MNI\_avg152T1

## Steps performed by @auto\_tlrc

- For warping a volume to a template (Usage mode 1):
  1. Pad the input data set to avoid clipping errors from shifts and rotations
  2. Strip skull (if needed)
  3. Resample to resolution and size of TLRC template
  4. Perform 12-parameter affine registration using **3dWarpDrive**

*Many more steps are performed in actuality, to fix up various pesky little artifacts. Read the script if you are interested.*
- ✧ Typically this steps involves a high-res anatomical to an anatomical template
  - ❑ Example: @auto\_tlrc -base TT\_N27+tlrc. -input anat+orig. -suffix NONE
- ✧ One could also warp an EPI volume to an EPI template.
  - ❑ If you are using an EPI time series as input. You must choose one sub-brick to input. The script will make a copy of that sub-brick and will create a warped version of that copy.

## Applying a transform to follower datasets

- Say we have a collection of datasets that are in alignment with each other. One of these datasets is aligned to a template and the same transform is now to be applied to the other *follower* datasets
- For Talairach transforms there are a few methods:
  - ✧ Method 1: Manually using the AFNI interface (see Appendix C)
  - ✧ Method 2: With program `adwarp`

```
adwarp -apar anat+tlrc -dpar func+orig
```

    - ❑ The result will be: `func+tlrc.HEAD` and `func+tlrc.BRIK`
  - ✧ Method 3: With `@auto_tlrc` script in mode 2
    - ❑ ONLY when `-apar` dataset was created by `@auto_tlrc`
    - ❑ `@auto_tlrc -apar SubjectHighRes+tlrc. \`
    - ❑ `-input Subject_EPI+orig. -dxyz 3`
    - ❑ (the output is named `Subject_EPI_at+TLRC`, by default)
- Why bother saving transformed datasets to disk anyway?
  - ✧ Datasets without `.BRIK` files are of limited use, only for display of slice images

## @auto\_tlrc Example

---

- Transforming the high-resolution anatomical:
  - ✧ (If you are also trying the manual transform on workshop data, start with a fresh directory with no +tlrc datasets )

```
@auto_tlrc          \  
-base TT_N27+tlrc  \  
-suffix NONE      \  
-input anat+orig
```

Output:  
anat+tlrc

- Transforming the function (“follower datasets”), setting the resolution at 2 mm:

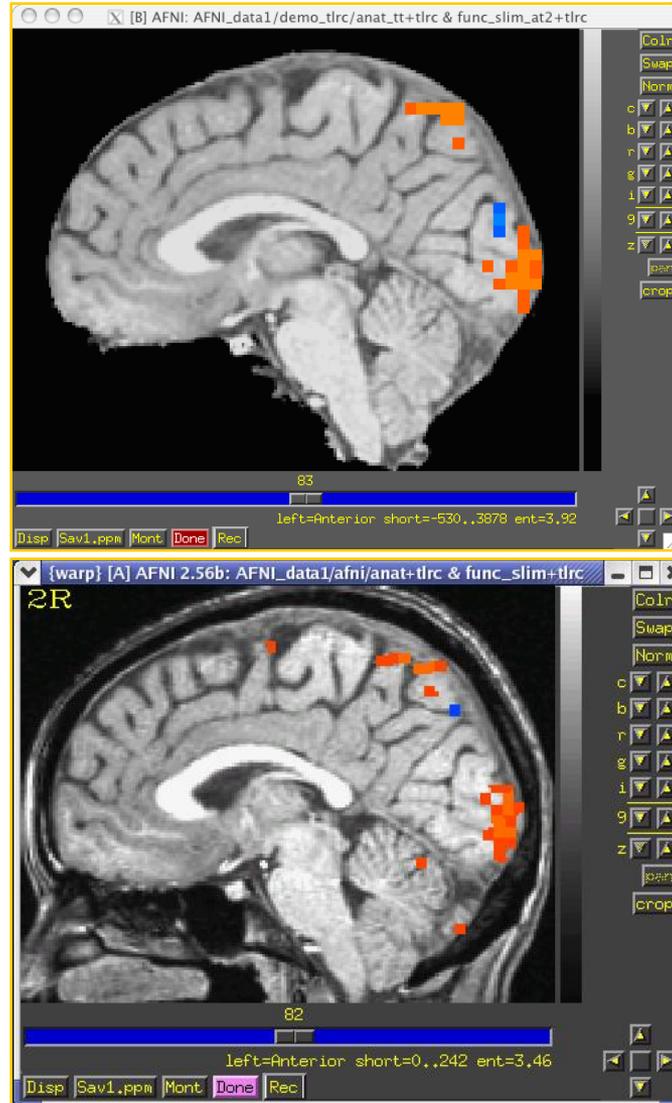
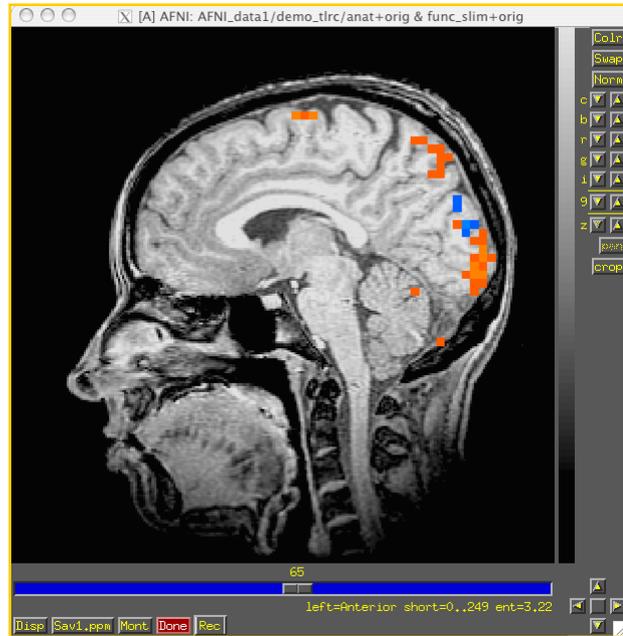
```
@auto_tlrc          \  
-apar anat+tlrc    \  
-input func_slim+orig \  
-suffix NONE      \  
-dxyz 2
```

Output:  
func\_slim+tlrc

- You could also use the **icbm452** or the mni’s **avg152T1** template instead of **N27** or any other template you like (see @auto\_tlrc -help for a few good words on templates)

# @auto\_tlrc Results are Comparable to Manual TLRC:

Original



@auto\_tlrc

Manual

## Standard Spaces

### **Why use a standard template space?**

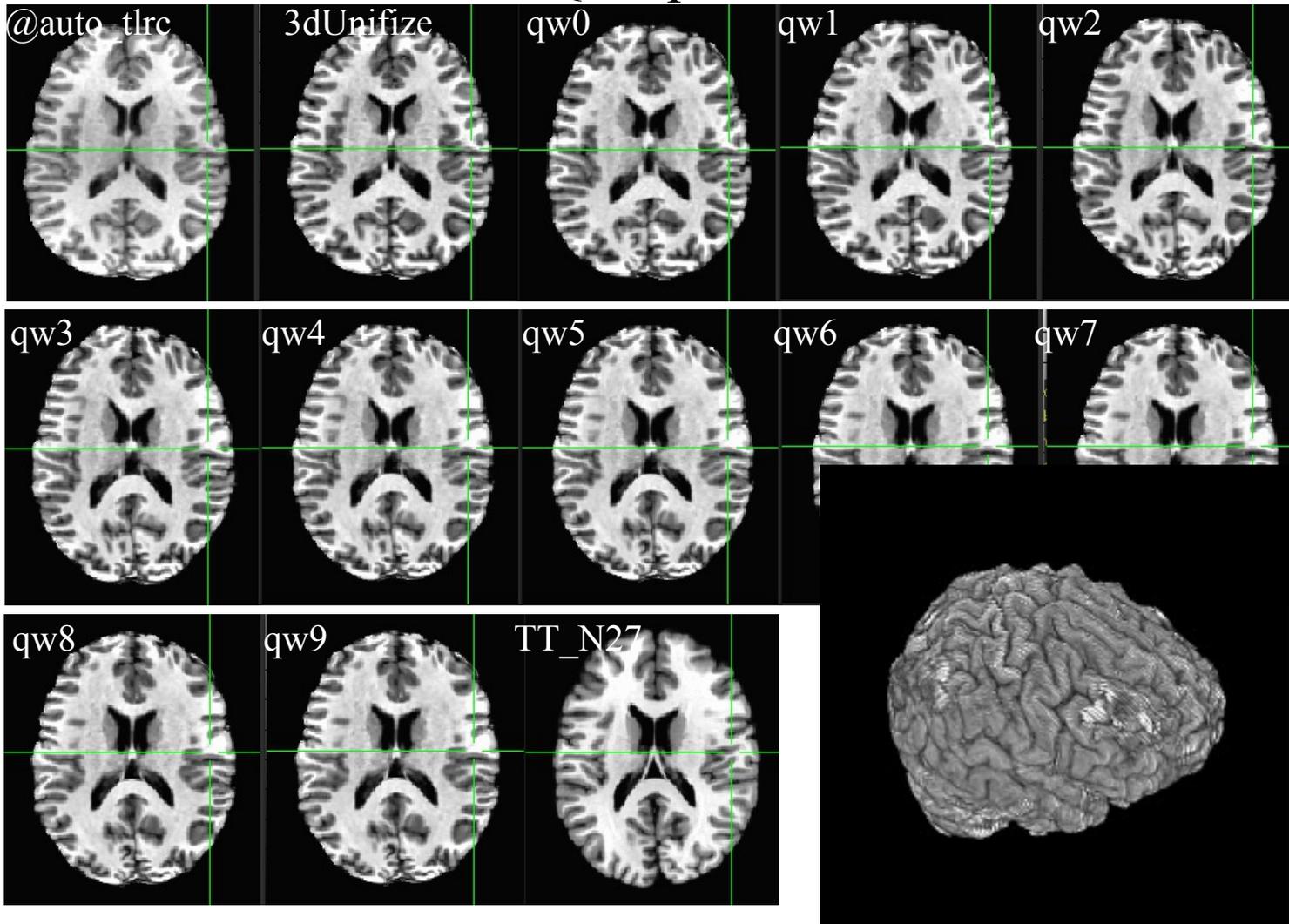
- Compare across subjects and groups easily for every voxel in the brain
- Standardize coordinates with others
- Know where a voxel is automatically from an atlas
- Mostly automated and no specific ROI drawing required

### **Why not use a standard template space?**

- Inconsistency among subjects
- Inconsistency among groups – elderly versus younger
- Use consistent anatomical ROIs with good anatomical knowledge
- Lower threshold for multiple comparison adjustments

# Nonlinear alignment to template

3dQwarp →



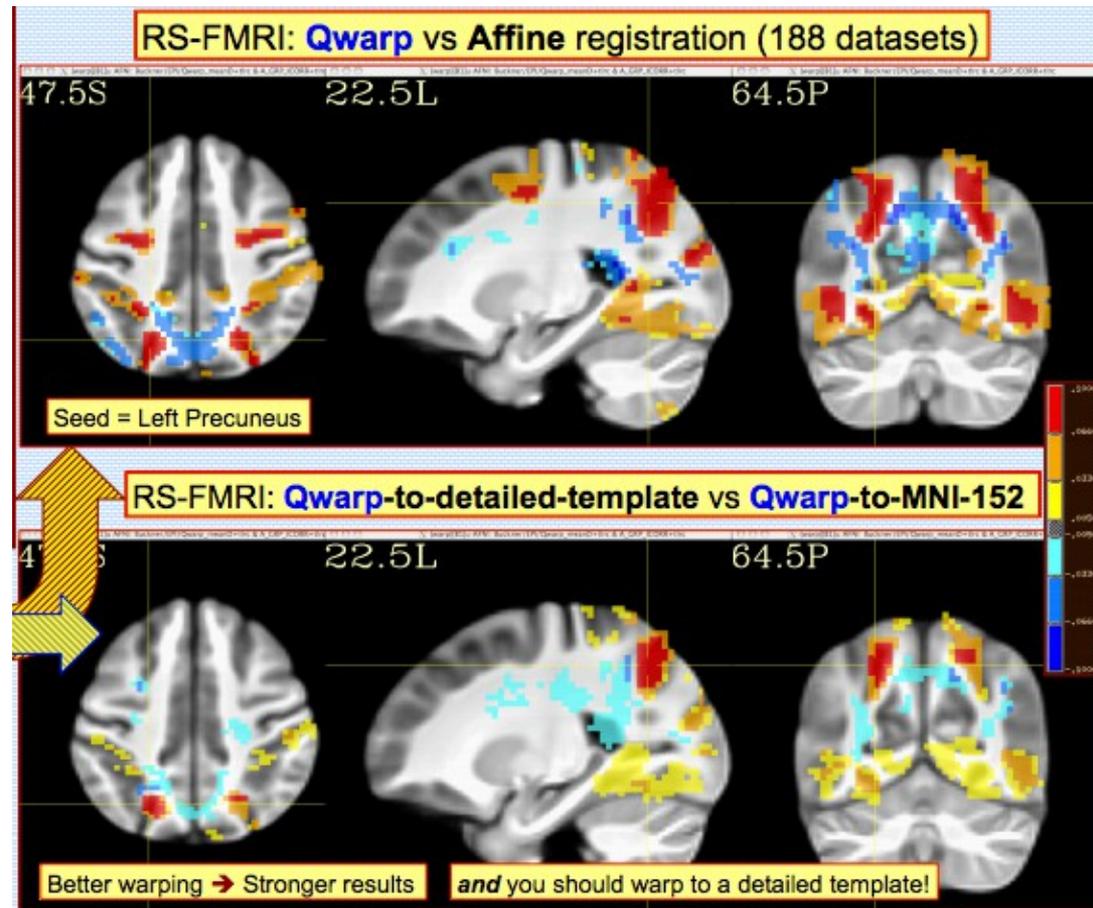
# Nonlinear alignment

## Advantages:

- Great alignment – better spatial correspondence across data →
- Aligned data matches template

## Disadvantages:

- Distortion of individual data
- Aligned data matches template. Choose template carefully
- End limits?
- Skullstripping must be done much more carefully
- Processing time much slower
- Not yet integrated into AFNI GUI for warp-on-demand



## Comparing data

- How can I compare regions/voxels across subjects and groups?

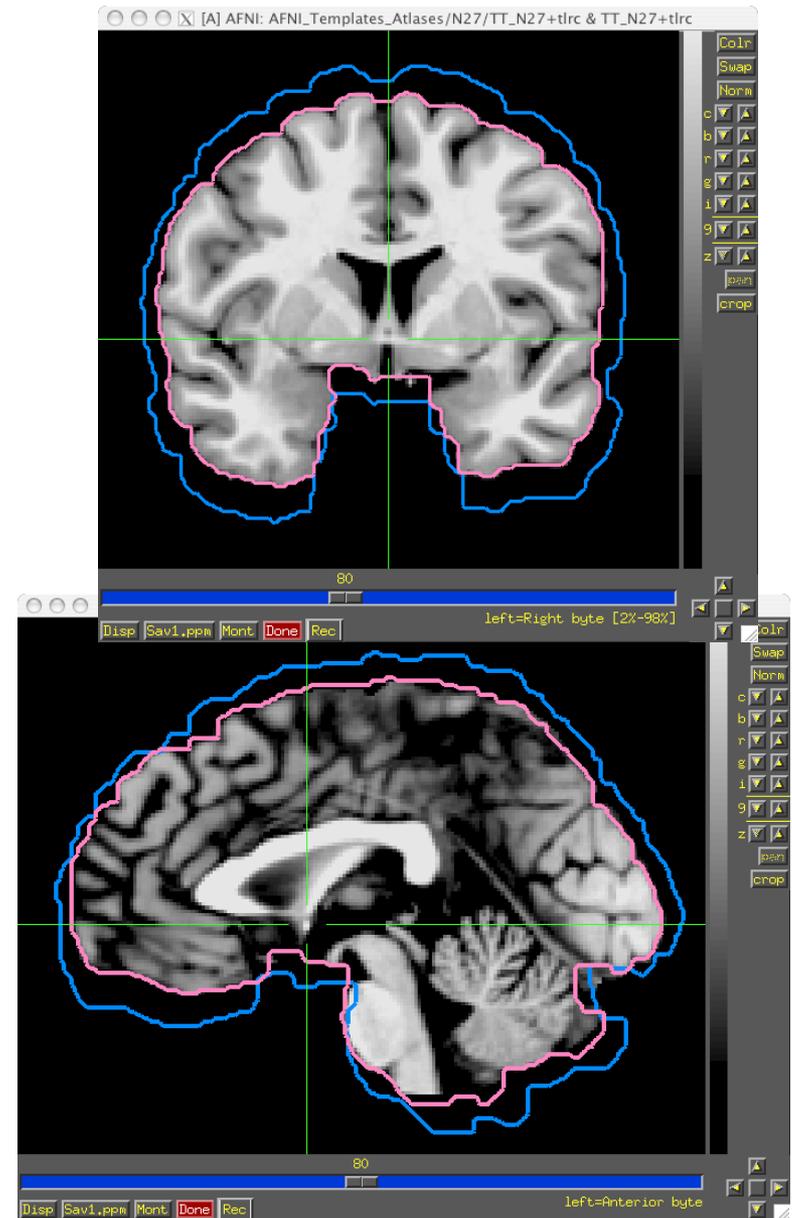
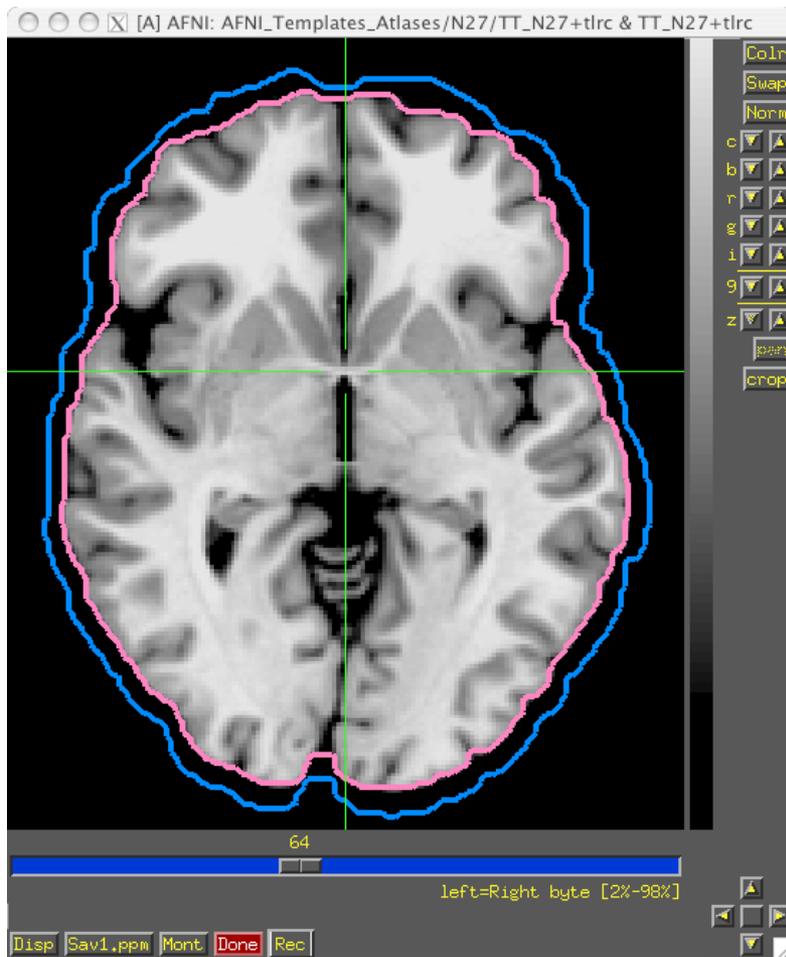
What works “best”?

- ✧ **@auto\_tlrc** – affine registration method to align individual subjects to a template
- ✧ **auto\_warp.py** – nonlinear alignment to template – better.
- ✧ **manual Talairach** – based on specific markers divides data up based on AC-PC line and brain enclosing boxes. Better for looking at medial structures.
- ✧ **3dTagalign** – place markers on specific corresponding points among datasets and align with affine transformation
- ✧ **ROI creation** – draw ROI’s (Draw Dataset plug-in) for each structure

## Choosing a template

- Similar to subject group – neonates, pediatric, young adults, elderly, macaque, rabbit...
- Same modality, similar coverage
- Relevant atlas segmentation
- Individual or group template
  - Group – average or iterative
- Make your own template (and maybe an atlas too)
  - ✧ Haskins pediatric atlas research
    - affine group averages
    - finding the most "typical" individual in group
    - nonlinear alignment to typical
    - iterative nonlinear alignment
    - @toMNI\_Awarp, @toMNI\_Qwarp

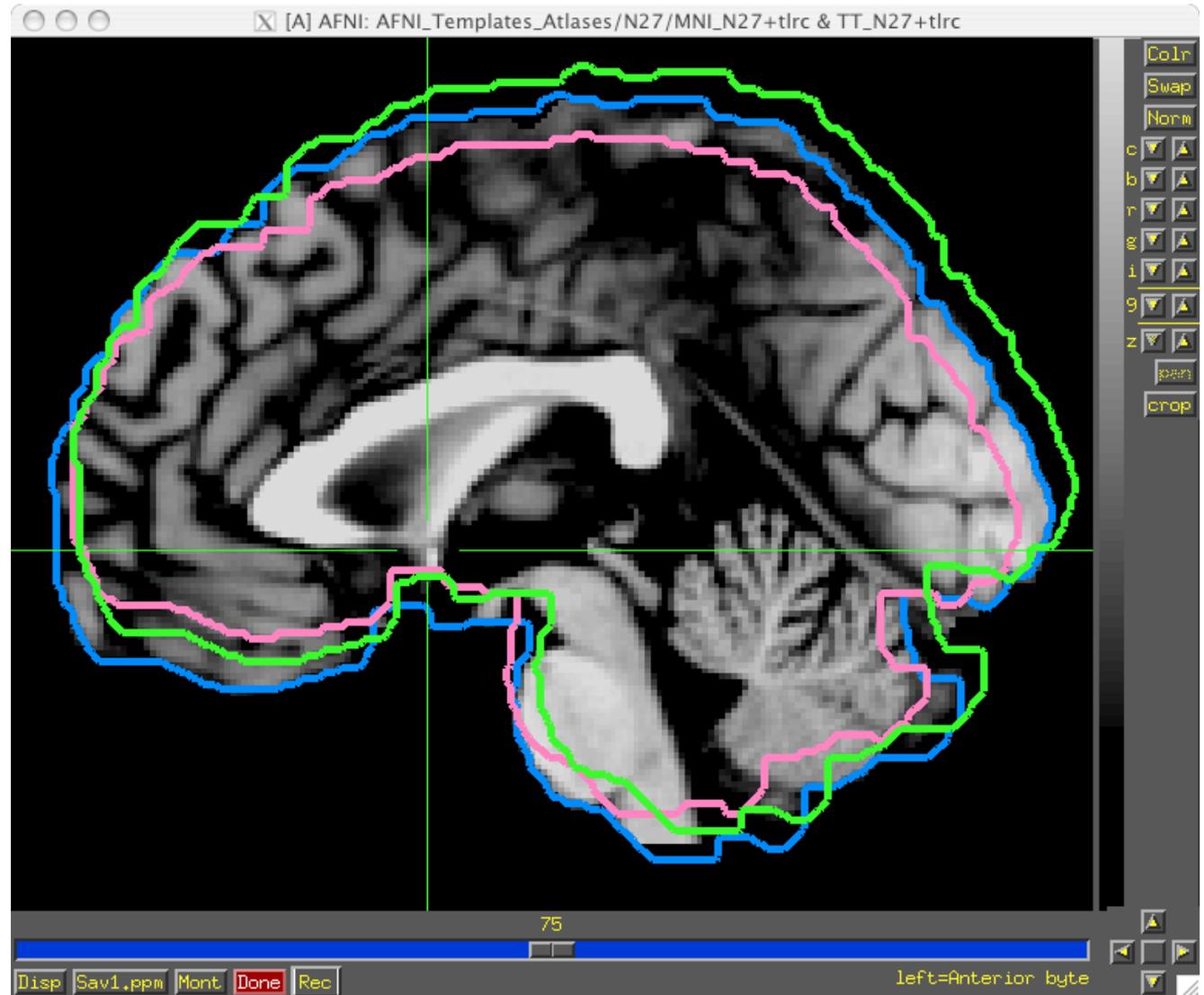
# Atlas/Template Spaces Differ In Size



MNI is larger than TLRC space.

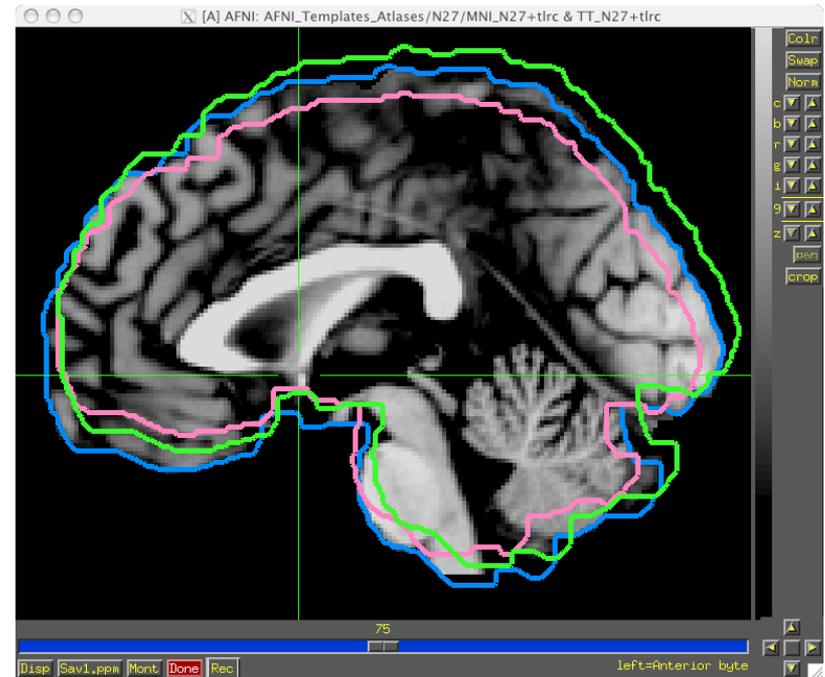
# Atlas/Template Spaces Differ In Origin

TLRC  
MNI  
MNI-Anat.



# From Space To Space

TLRC  
MNI  
MNI-Anat.



- Going between TLRC and MNI:
  - ✧ Approximate equation
    - ❑ used by **whereami** and **3dWarp**
  - ✧ Manual TLRC transformation of MNI template to TLRC space
    - ❑ used by **whereami** (as precursor to MNI Anat.), based on N27 template
  - ✧ Multiple space coordinates reported in whereami output (AFNI\_ATLAS\_TEMPLATE\_SPACE\_LIST)
- Going between MNI and MNI Anatomical (Eickhoff et al. Neuroimage 25, 2005):
  - ✧  $MNI + (0, 4, 5) = MNI\ Anat.$  (in RAI coordinate system)
- Going between TLRC and MNI Anatomical (as practiced in **whereami**):
  - ✧ Go from TLRC (TT\_N27) to MNI via manual xform of N27 template
  - ✧ Add (0, 4, 5)

## Atlases/Templates Use Different Coord. Systems

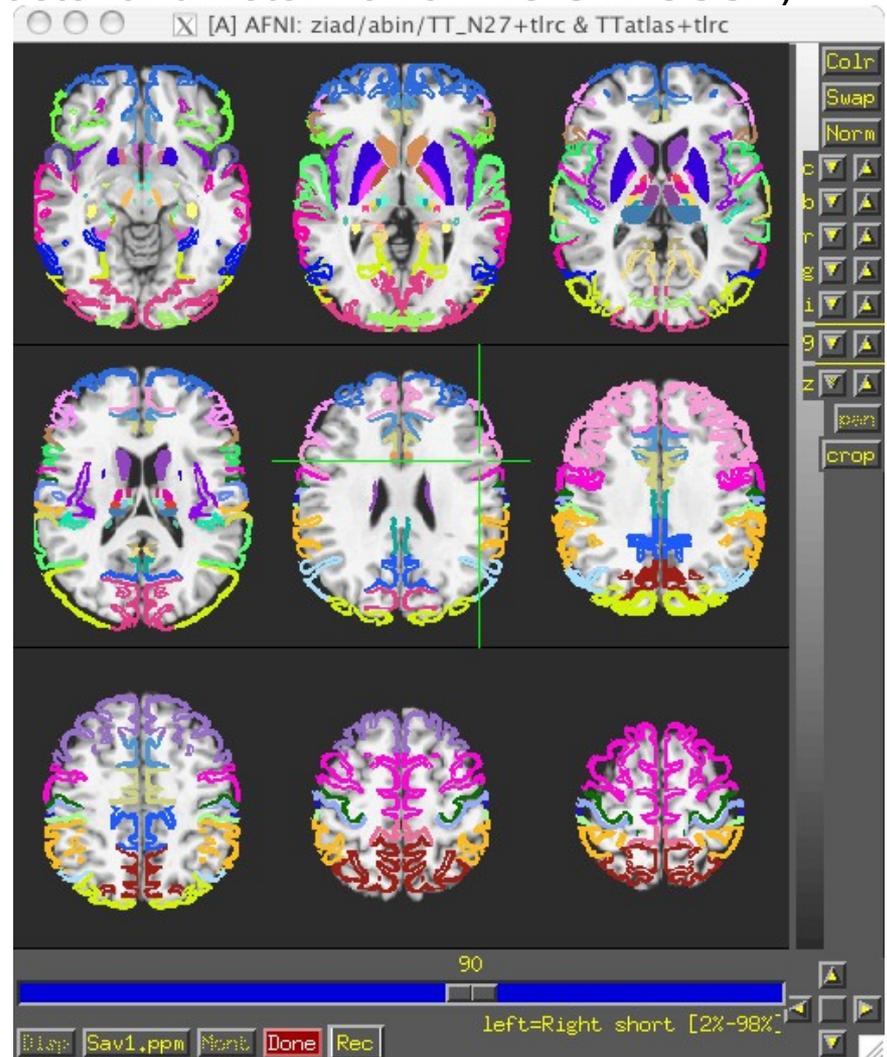
---

- There are 48 manners to specify XYZ coordinates
- Two most common are RAI/DICOM and LPI/SPM
- RAI means
  - ✧ X is Right-to-Left (from negative-to-positive)
  - ✧ Y is Anterior-to-Posterior (from negative-to-positive)
  - ✧ Z is Inferior-to-Superior (from negative-to-positive)
- LPI means
  - ✧ X is Left-to-Right (from negative-to-positive)
  - ✧ Y is Posterior-to-Inferior (from negative-to-positive)
  - ✧ Z is Inferior-to-Superior (from negative-to-positive)
- To go from RAI to LPI just flip the sign of the X and Y coordinates
  - ✧ Voxel -12, 24, 16 in RAI is the same as 12, -24, 16 in LPI
  - ✧ Voxel above would be in the Right, Posterior, Superior octant of the brain
- AFNI allows for all coordinate systems but default is RAI
  - ✧ Can use environment variable `AFNI_ORIENT` to change the default for AFNI *AND* other programs.
  - ✧ See `whereami -help` for more details.

# Atlases Distributed With AFNI

## TT\_Daemon

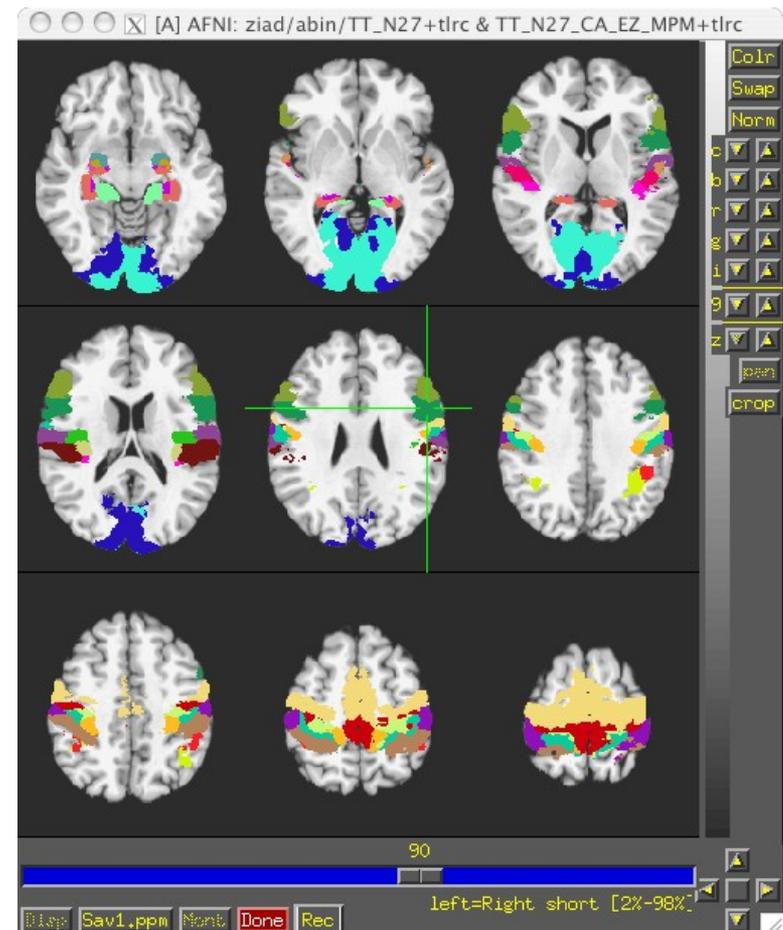
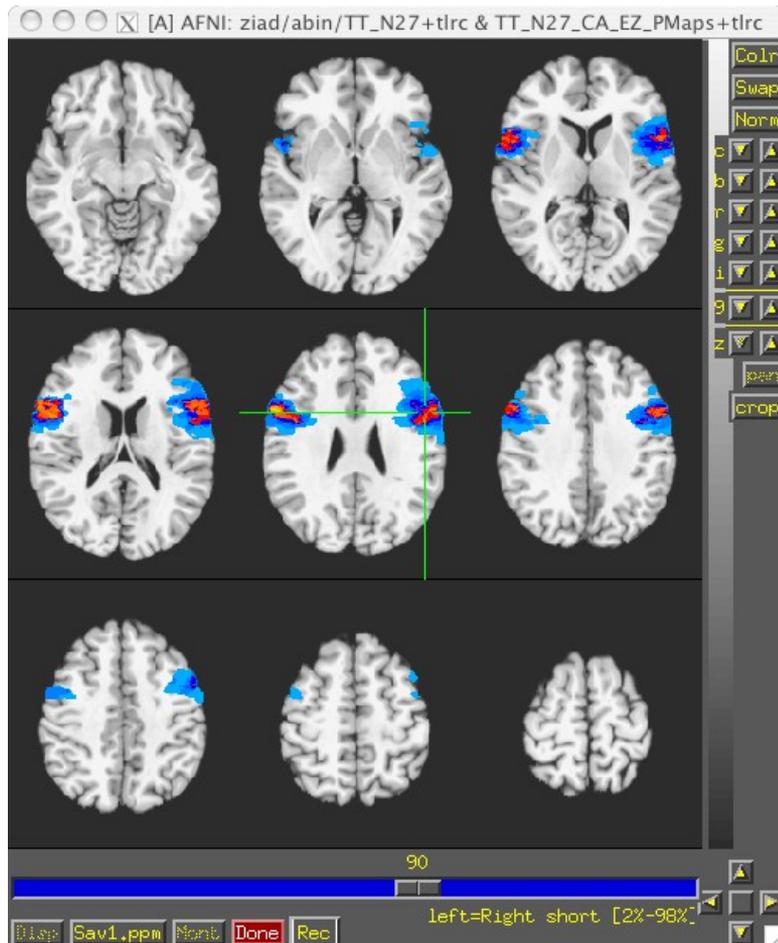
- TT\_Daemon : Created by tracing Talairach and Tournoux brain illustrations.
  - ✧ Generously contributed by Jack Lancaster and Peter Fox of RIC UTHSCSA)



# Atlases Distributed With AFNI

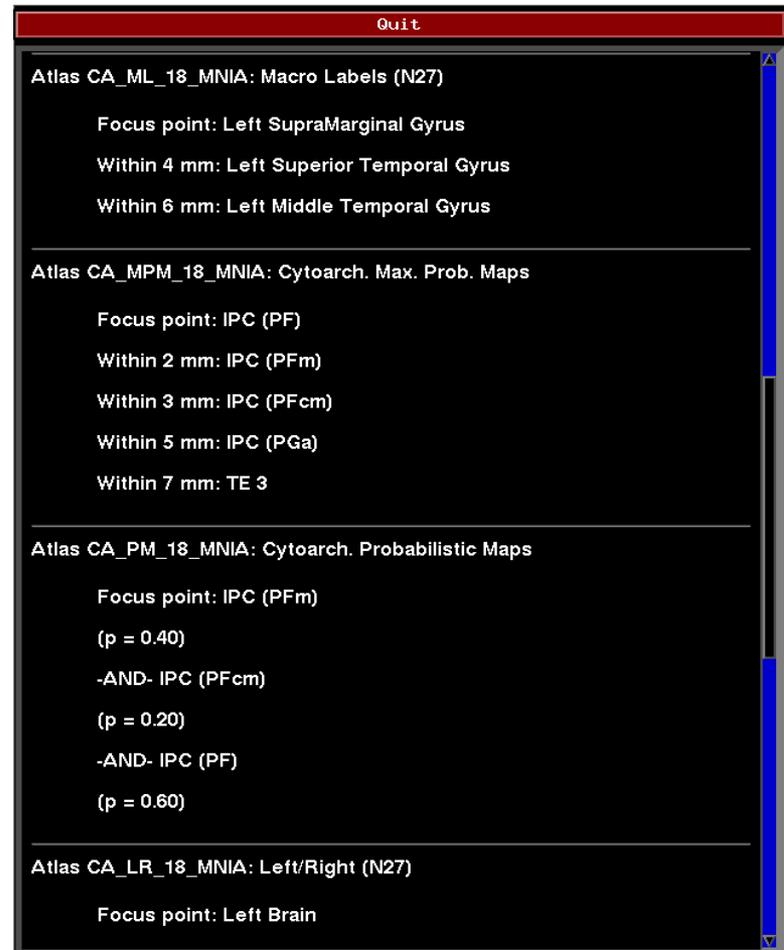
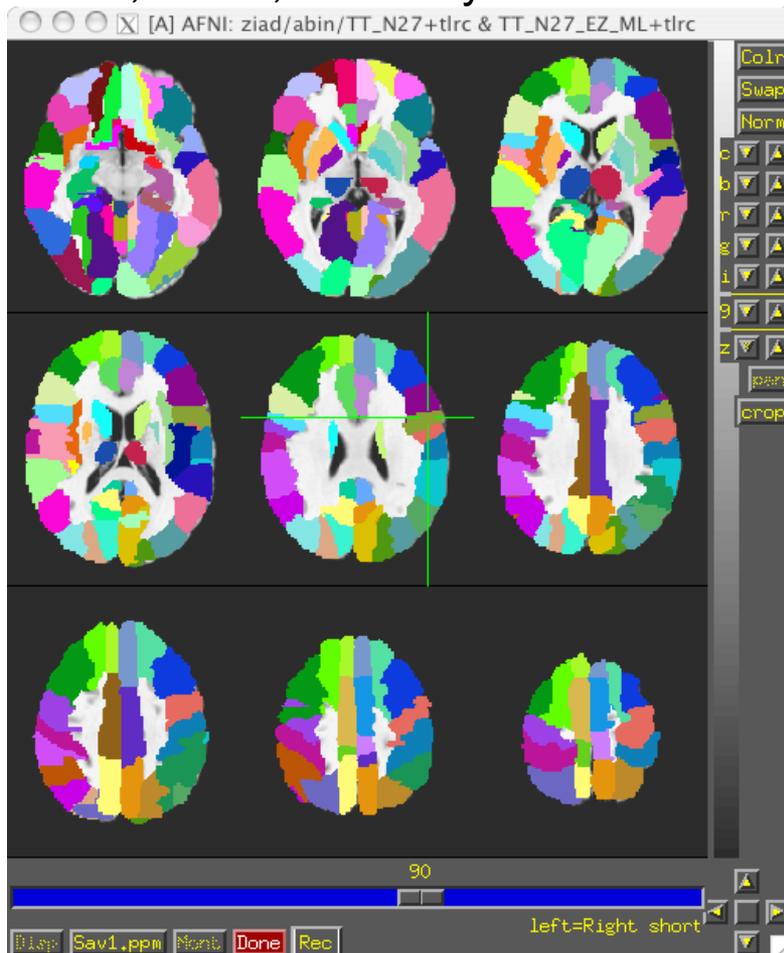
## Anatomy Toolbox: Prob. Maps, Max. Prob. Maps

- CA\_N27\_MPM, CA\_N27\_ML, CA\_N27\_PM: Anatomy Toolbox's atlases with some created from cytoarchitectonic studies of 10 human post-mortem brains
  - ✧ Generously contributed by Simon Eickhoff, Katrin Amunts and Karl Zilles of IME, Julich, Germany



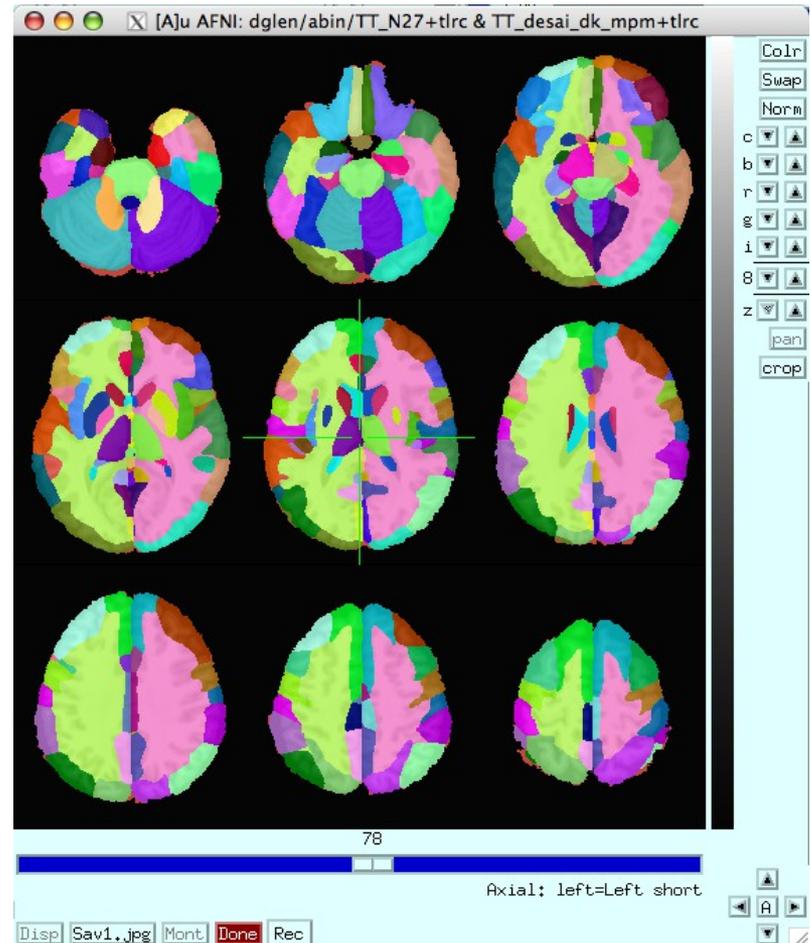
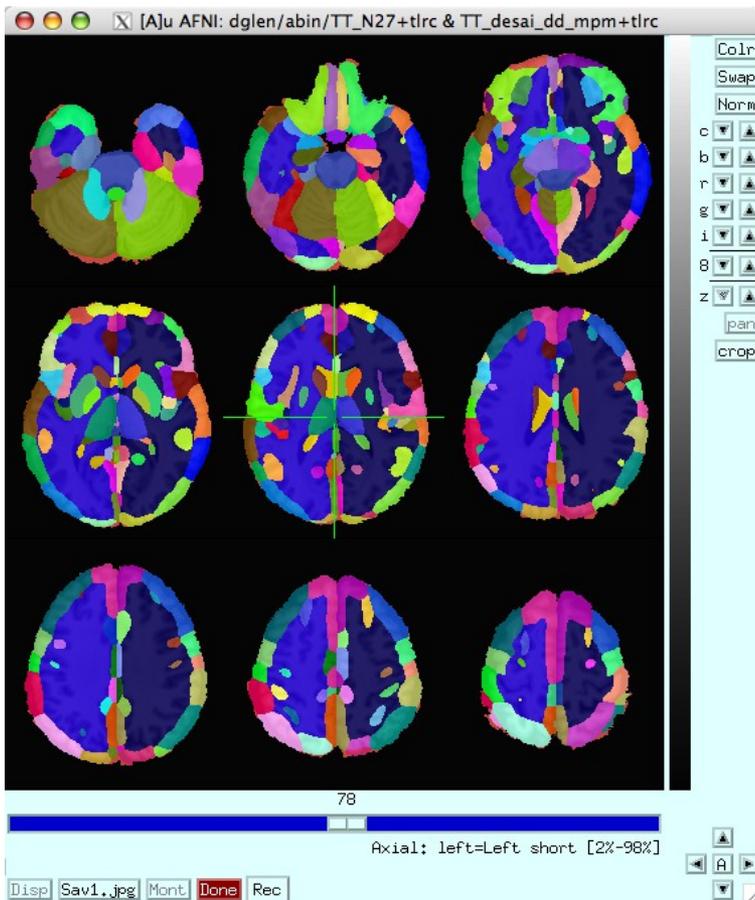
# Atlases Distributed With AFNI: Anatomy Toolbox: MacroLabels

- CA\_N27\_MPM, CA\_N27\_ML, CA\_N27\_PM: Anatomy Toolbox's atlases with some created from cytoarchitectonic studies of 10 human post-mortem brains
  - ✧ Generously contributed by Simon Eickhoff, Katrin Amunts and Karl Zilles of IME, Julich, Germany

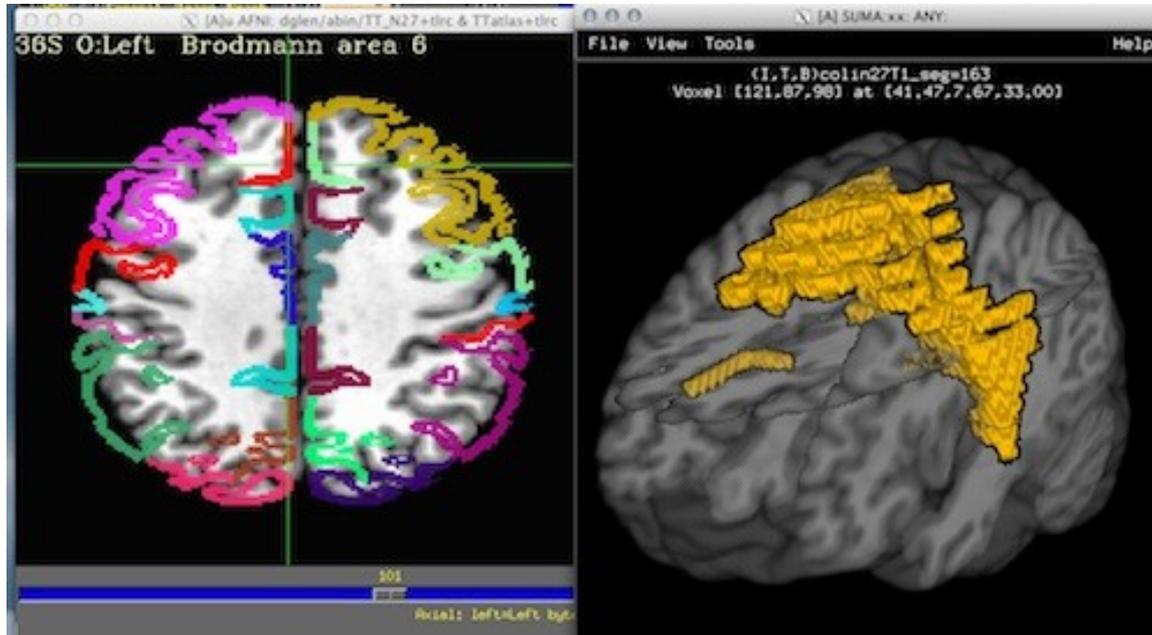


# Atlases Distributed With AFNI: Desai PMaps and MPMs

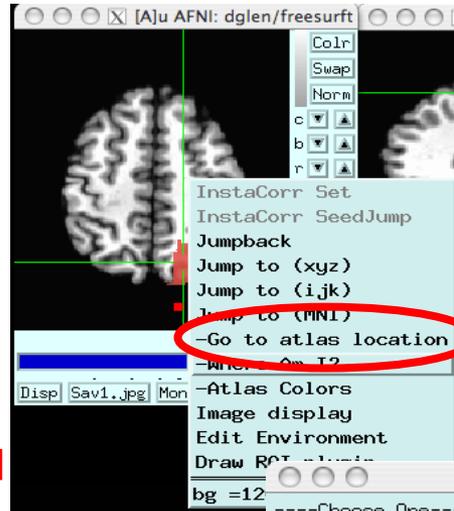
- Atlases generated with typical AFNI pipeline using @auto\_tlrc and FreeSurfer segmentation across multiple subjects



## Talairach Daemon (TT\_Daemon) problem

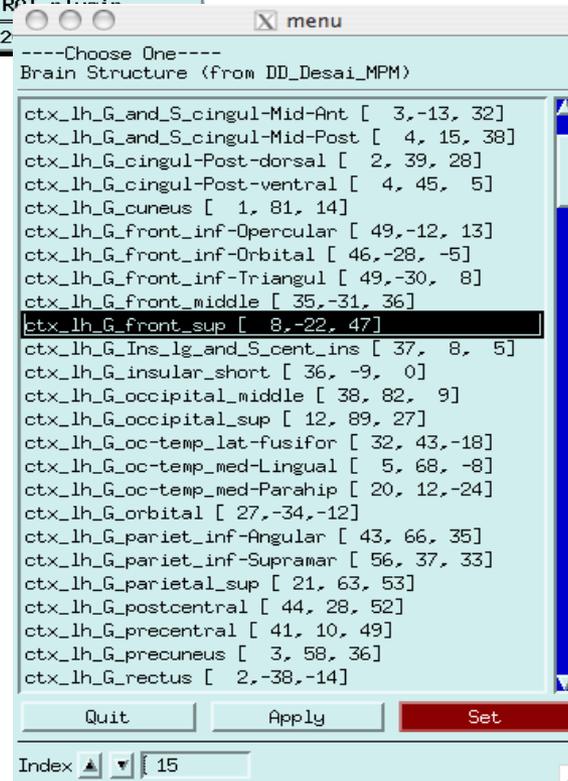


- Some fun and useful things to do with `+tlrc` datasets are on the 2D slice viewer  
Right click to get menu:



✧ [\[Go to Atlas Location\]](#)

Lets you jump to centroid of regions to current default atlas (set by `AFNI_ATLAS_COLORS`)  
Works in `+orig` too



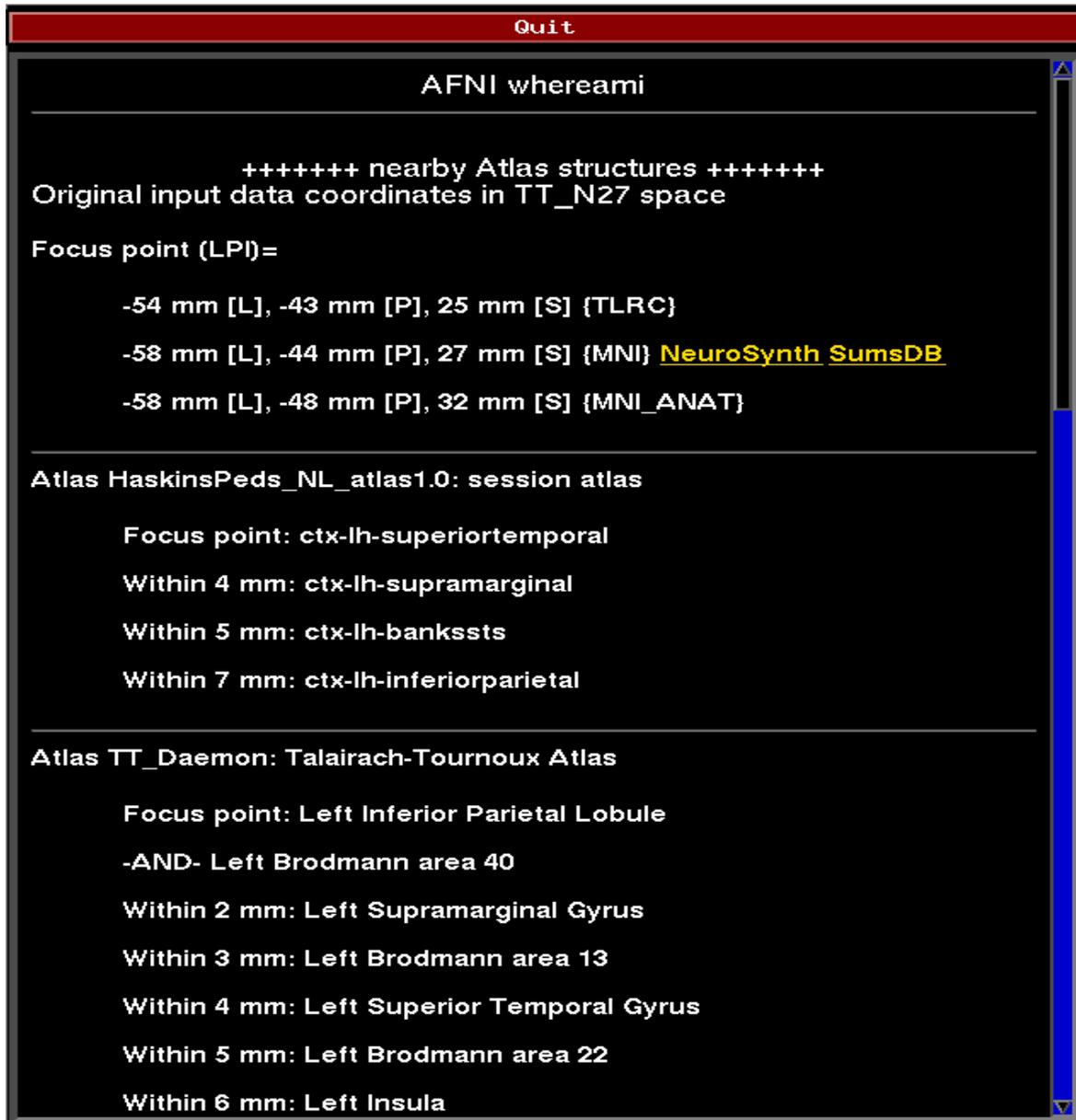
✧ [\[Where am I?\]](#)

Shows you where you are in various atlases and spaces

*(works in +orig too, if you have a transformed parent)*

For atlas installation, and much, much more, see help in command line version:

**whereami -help**



- **whereami** can provide the user with more detailed information regarding the output of **3dclust**
  - For instance, say you want more information regarding the center of mass voxels from each cluster (from the 3dclust output). I.e., where do they fall approximately within the atlases?

```
3dclust -dxyz=1 -lclip 9.5 1 1000 func_FullF+tlrc > clusts.1D
whereami -coord_file clusts.1D '[1,2,3]' -tab | less
```

Center of mass output, columns 1,2,3, from 3dclust output

```
++ Input coordinates orientation set by default rules to RAI
++ Input coordinates space set by default rules to TLRC
+++++++ nearby Atlas structures +++++++

Focus point (LPI)                               Coord.Space
 42 mm [R], -61 mm [P], -3 mm [I]                {T-T Atlas}
 43 mm [R], -63 mm [P], -7 mm [I]                {MNI Brain}
 45 mm [R], -69 mm [P],  2 mm [I]                {MNI Anat.}

Atlas      Within  Label                               Prob.  Code
TT_Daemon  3.0    Right Middle Occipital Gyrus  ---    33
TT_Daemon  3.0    Right Brodmann area 37        ---    113
TT_Daemon  4.0    Right Inferior Temporal Gyrus ---    29
TT_Daemon  4.0    Right Middle Temporal Gyrus  ---    35
TT_Daemon  6.0    Right Inferior Occipital Gyrus ---    28
TT_Daemon  7.0    Right Brodmann area 19        ---    96
CA_N27_MPM 4.0    hOC5 (V5 / MT+)              MPM    110
CA_N27_ML  0.0    Right Inferior Temporal Gyrus ---    90
CA_N27_ML  1.0    Right Middle Temporal Gyrus  ---    86
CA_N27_ML  5.0    Right Inferior Occipital Gyrus ---    54
CA_N27_ML  6.0    Right Middle Occipital Gyrus  ---    52

***** Please use results with caution! *****
***** Brain anatomy is quite variable! *****
***** The database may contain errors! *****
```

Shown: Cluster #1's coordinates according to various atlases (TT, MNI, etc), as well as the name of the anatomical structure that is located at or near these coordinates (which may vary by atlas)

etc...

- **whereami** can report on the overlap of ROIs with atlas-defined regions

**whereami -omask anat\_roi+tlrc**

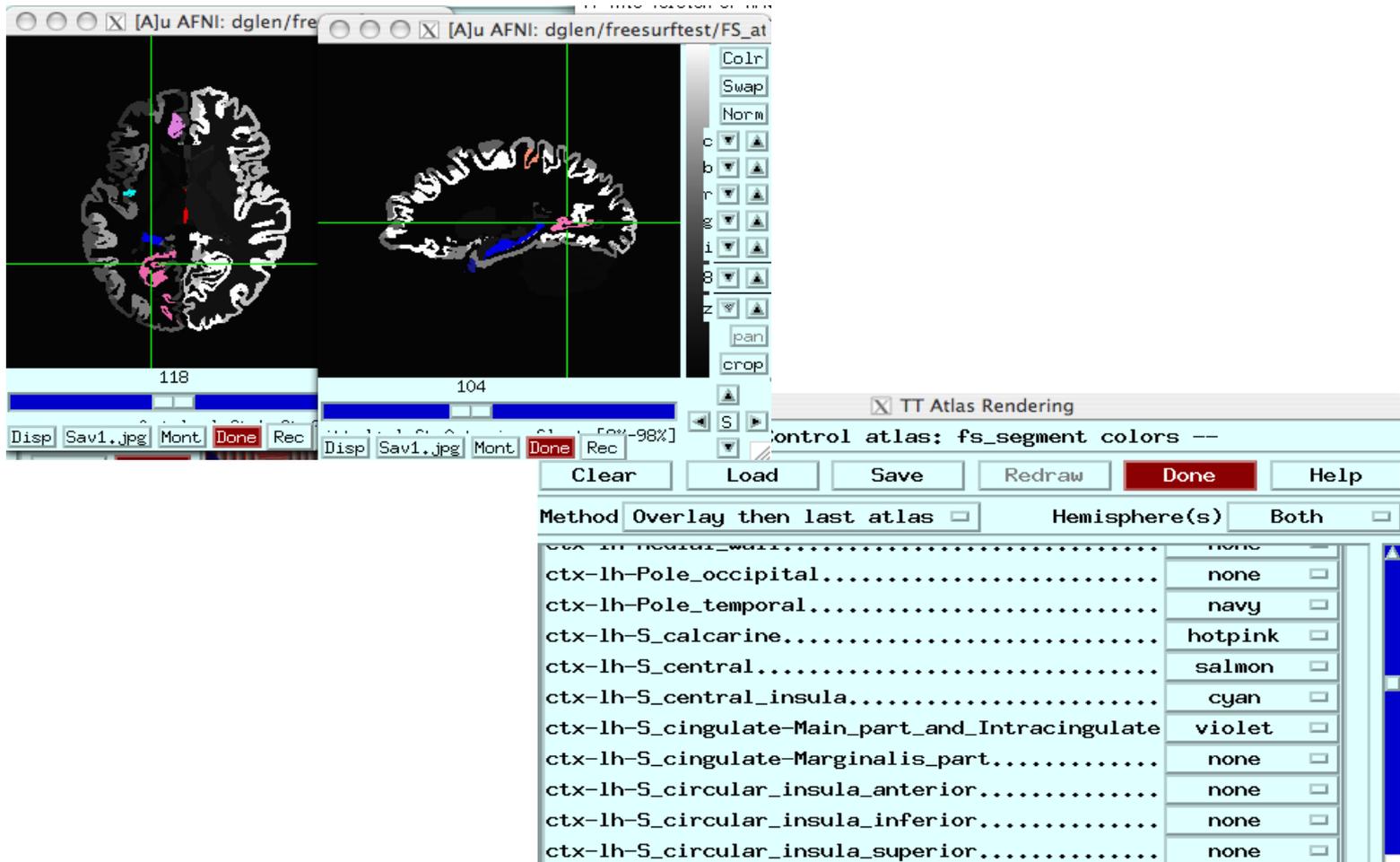
```
++ Input coordinates orientation set by default rules to RAI
++ Input coordinates space set by default rules to TLRC
++ In ordered mode ...
++ Have 2 unique values of:
  0  1
++ Skipping unique value of 0
++ Processing unique value of 1
++   195 voxels in ROI
++   195 voxels in atlas-resampled mask
Intersection of ROI (valued 1) with atlas TT_Daemon (sb0):
  89.2 % overlap with Middle Occipital Gyrus, code 33
  6.7 % overlap with Middle Temporal Gyrus, code 35
-----
  95.9 % of cluster accounted for.

Intersection of ROI (valued 1) with atlas TT_Daemon (sb1):
  19.5 % overlap with Brodmann area 37, code 113
  1.5 % overlap with Brodmann area 19, code 96
-----
  21.0 % of cluster accounted for.

++   195 voxels in atlas-resampled mask
Intersection of ROI (valued 1) with atlas CA_N27_MPM (sb0):
  1.5 % overlap with hOC5 (V5 / MT+), code 110
-----
  1.5 % of cluster accounted for.

++   195 voxels in atlas-resampled mask
Intersection of ROI (valued 1) with atlas CA_N27_ML (sb0):
  61.0 % overlap with Right Middle Occipital Gyrus, code 52
  20.0 % overlap with Right Middle Temporal Gyrus, code 86
-----
  81.0 % of cluster accounted for.
```

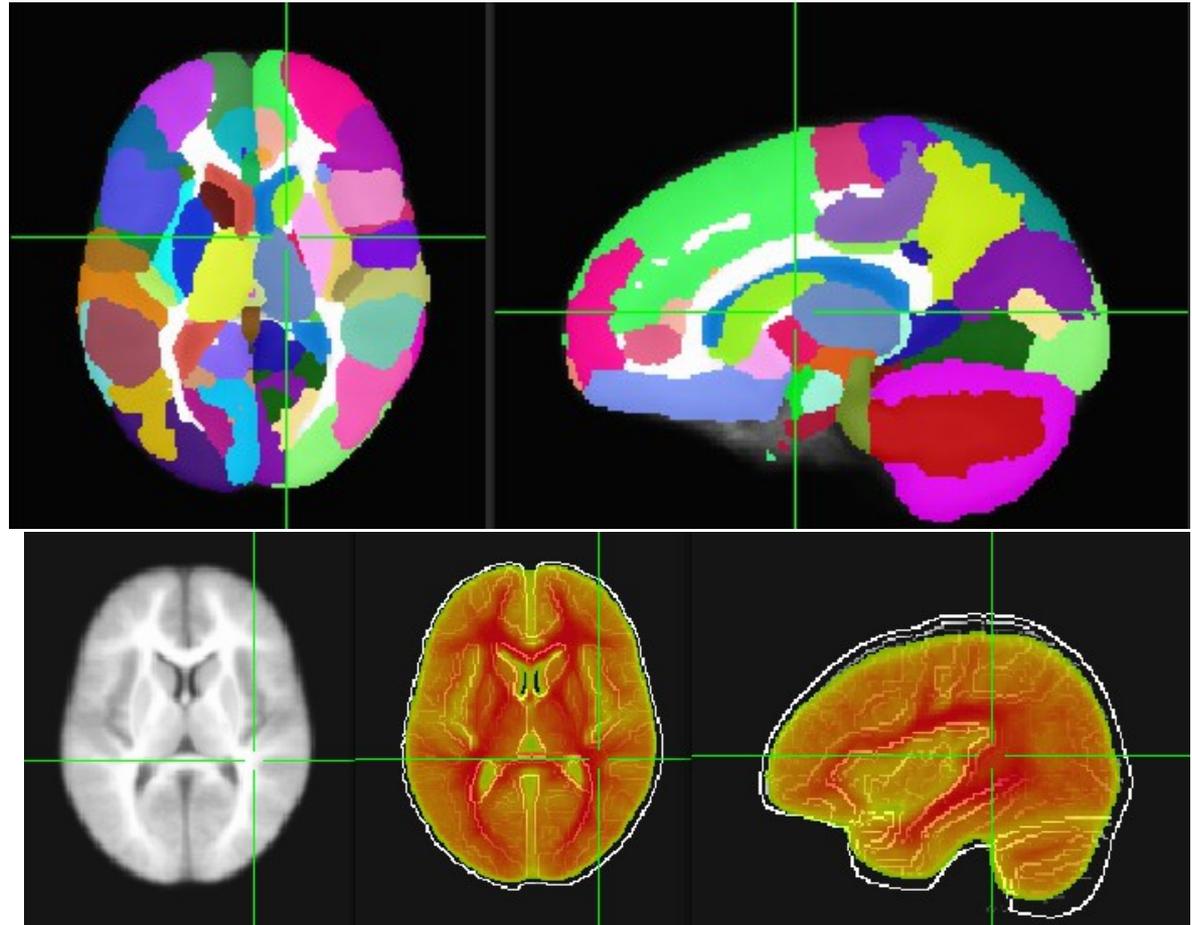
✧ [Atlas colors]



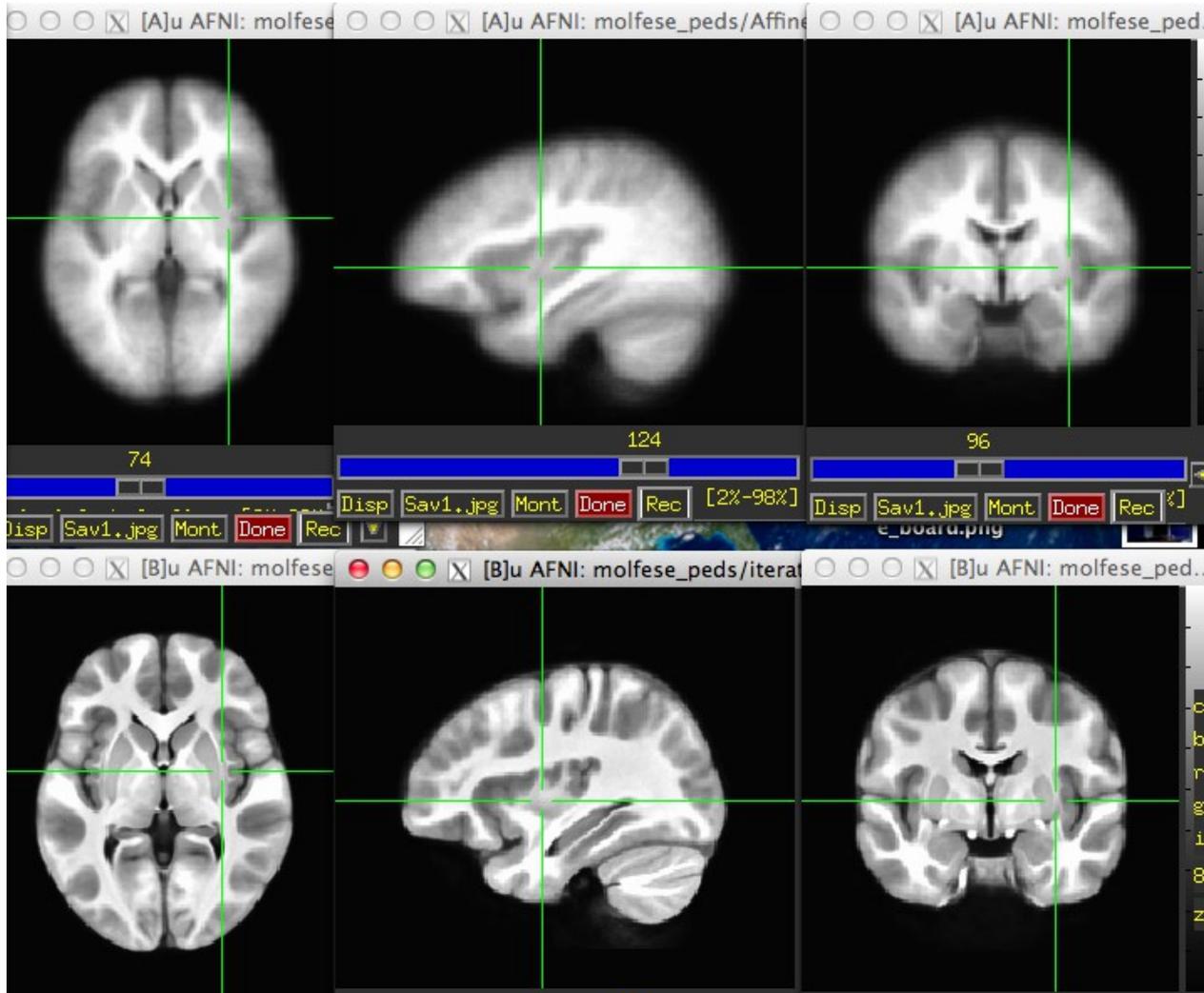
Lets you show atlas regions over your own data (works only in +tlrc).

## Haskins Pediatric Atlas

- Pediatric brain atlas and templates (7-12 years old) – Peter Molfese, (formerly Haskins Labs, now at NIH - woohoo!)
- Manually corrected segmentation from Freesurfer.
- Probabilistic, MPM and template
- ~75 subjects -> 500 (ages 6-13)
- Affine, nonlinear averages, ideal/typical subjects, outliers



# Haskins Pediatric Atlas - templates

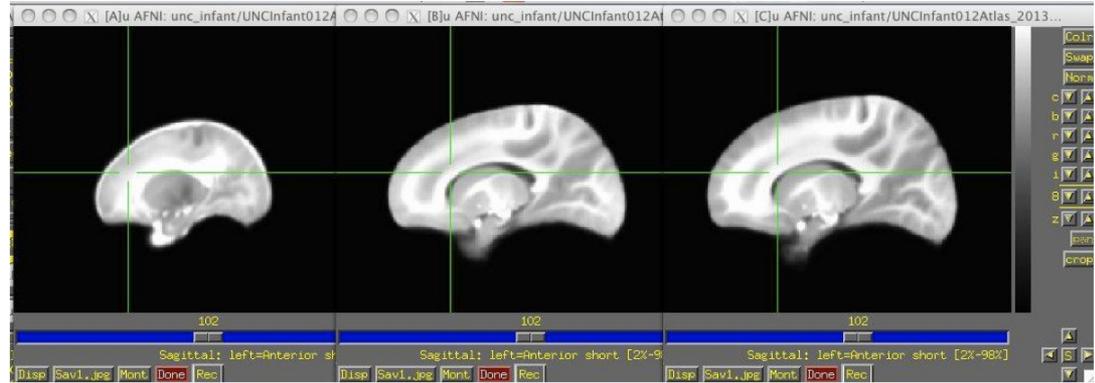
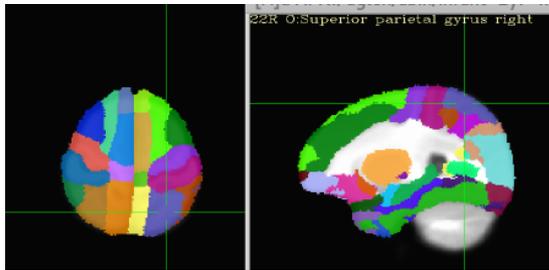


Affine Group

Nonlinear  
Group I –  
iterative

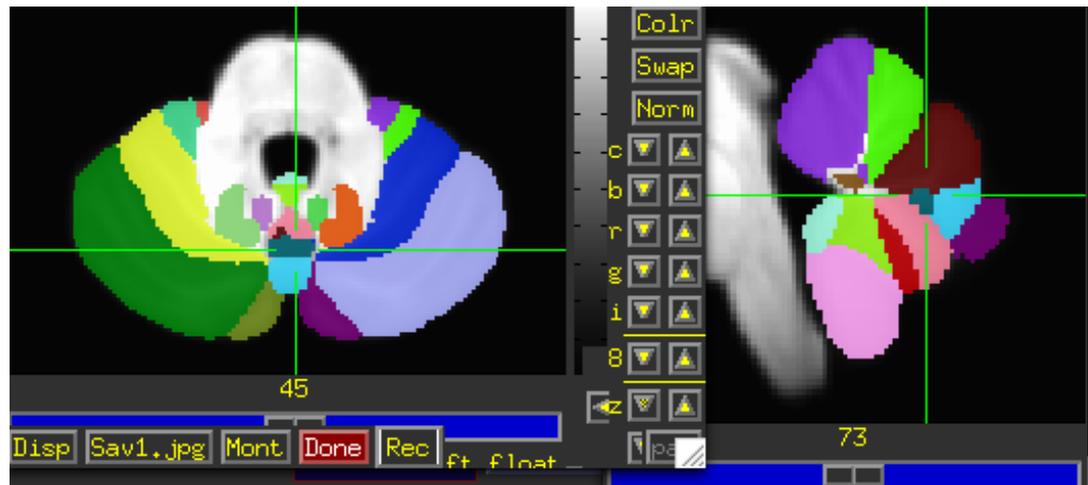
# Atlases and Templates Available!

- Infant brain atlas and templates – neonate, 1-year, 2-year.  
Contributed by Feng Shi, UNC



UNC infant templates and atlases – neonate, 1 yr, 2 yr old

- Cerebellum atlas and templates –  
Jorn Diedrichsen, UCL, UK  
contribution

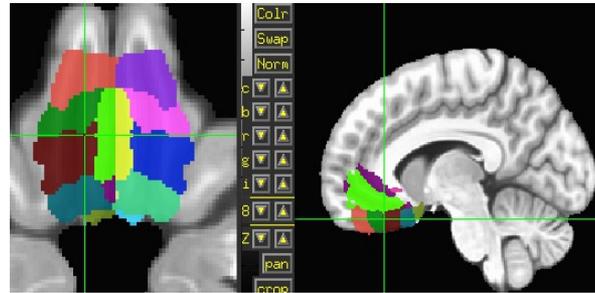


# More Atlases and Templates Available!

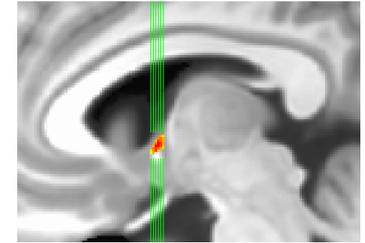
Ventromedial Prefrontal Cortex (vmPFC, Scott Mackey)

Waxholm Rat Atlas - Papp, et al.  
Rat brain templates in Paxinos space – Karolinska Institute, Woo Hyun Shim MGH contributions

BNST – Torrisi, NIMH



All of these are user requests or contributions!  
*What do you need?*



AFNI whereami

```

+++++++ nearby Atlas structures ++++++
Original input data coordinates in waxholm_rat space
Focus point (LP)=
4.258 mm [R], -5.078 mm [P], 3.828 mm [S] (waxholm_rat)

Atlas waxholm_rat: Waxholm V2.0
Focus point: dentate_gyrus
Within 6 mm: cornu_ammonis_3
-AND- cornu_ammonis_1
  
```

# Saleem macaque atlas – MRI, surfaces, connections, supplemental webpages

The screenshot displays the SUMA software interface for a macaque brain atlas. The main window shows a 3D brain model with a network graph overlaid. The graph has a central node labeled '45a' connected to various other nodes, including '12l', '12r', '45b', '45c', '46dC', '8Ad', '8Bd', 'F5\_preSMA', 'F2', 'Tpt', 'CpB', 'Balt', 'STSDC', 'Core', 'RPB', 'F5', '12l', '12r', 'STGSTS\_R', '12o', '13l', '11l', '10o', '46d', '24a/b', '9d', '46d', '10o'. The interface includes a menu bar (File, View, Tools), a toolbar with buttons like 'Swap', 'Norm', 'c', 'b', 'r', 'g', 'i', '8', 'p', 'crop', and a status bar showing 'Gnode 45a'. A secondary window in the bottom right shows a connectivity matrix for 'Gnode 45a'.

**Connectivity Matrix (Gnode 45a):**

	12r	12l	46vfR	45a	45b	44	10mr	9d	10o
12r	Red	Green	Red	Red	Red	Red	Red	Red	Red
12l	Red	Red	Red	Red	Red	Red	Red	Red	Red
46vfR	Red	Red	Red	Red	Red	Red	Red	Red	Red
45a	Red	Red	Red	Red	Red	Red	Red	Red	Red
45b	Red	Red	Red	Red	Red	Red	Red	Red	Red
44	Red	Red	Red	Red	Red	Red	Red	Red	Red
10mr	Red	Red	Red	Red	Red	Red	Red	Red	Red
9d	Red	Red	Red	Red	Red	Red	Red	Red	Red
AIP	Red	Red	Red	Red	Red	Red	Red	Red	Red

**Coordinate Information:**

- 0 mm [L], 20 mm [A], 12 mm [S] {D99\_Macaque\_book}
- 21 mm [R], 35 mm [A], -13 mm [I] {F99\_Macaque}

**Atlas Information:**

Atlas D99\_atlas: D99 Saleem macaque atlas with supplemental info

**Focus point: 45a**

**-AND-: 45a**

**Within 3 mm: 12l**

**-AND-: 12l**

**Within 5 mm: 45b**

**-AND-: 45b**

# Saleem macaque atlas – MRI, surfaces, connections, supplemental webpages (in development)

2.1. VLPFC (area 45a) – Macaque Atlas Web-based Information docs 1.0.1 documentation – Mozilla Firefox

file:///home/dglen/macaqueatlas/html/macaque/ROI\_45a.html

Macaque Atlas Web-based Information docs 1.0.1 documentation » 2. Atlas Regions Information » previous | next | index

## 2.1. VLPFC (area 45a) ¶

VLPFC (area 45a) Area 45 is found in the caudal aspect of the convexity, back to the inferior limb of the arcuate sulcus ( *Walker, 1940* ). Based on the comparative cytoarchitectonic analysis in both human and nonhuman primates, *Petrides and Pandya (1999, 2002)* have subdivided this area into 45a and 45b, on the convexity rostral to the arcuate sulcus and in the rostroventral bank of the sulcus, respectively (see also *Gerbella et al., 2010*, for the architectonic analysis of these areas ).

### 2.1.1. Images

#### VLPFC (area 45a)

EBZ

EBZ

+32mm  
rostral to EBZ

f f f  
R M C

Atlas D99\_atlas: D99 Saleem macaque atlas with supplemental info

Focus point: [45a](#)

-AND-: [45a](#)

Within 3 mm: [12l](#)

-AND-: [12l](#)

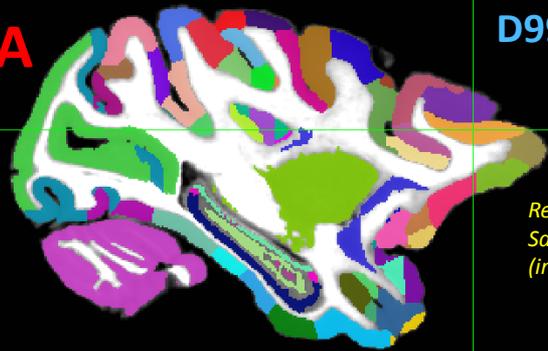
Within 5 mm: [45b](#)

-AND-: [45b](#)

15R 0:46v

# Mapping the digital atlas onto different macaques MRI

**A**



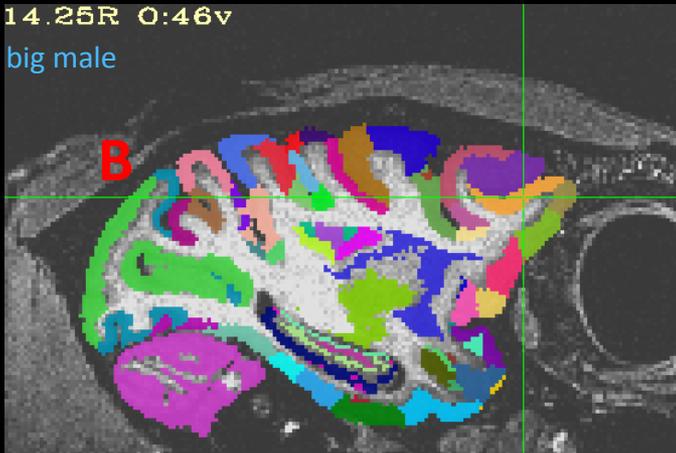
**D99 – Digital atlas**

*Reveley, Gruslys, Ye, Samaha, Glen,  
Saad, Seth, Leopold, and Saleem  
(in preparation)*

14.25R 0:46v

big male

**B**

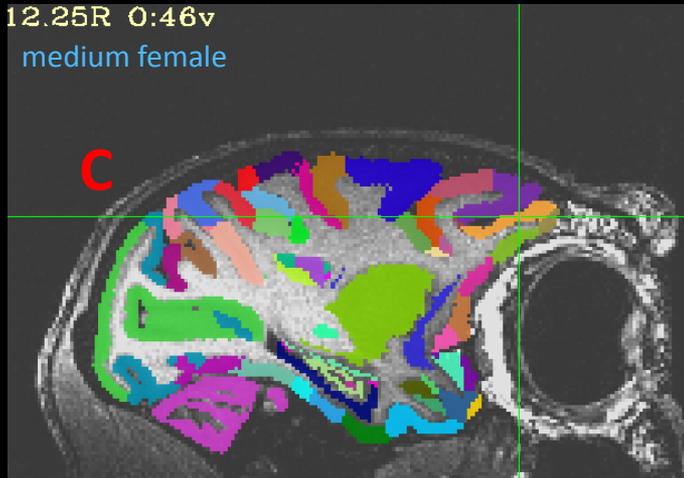


Spatial transformation of the atlas segmentation to each macaque's native space

12.25R 0:46v

medium female

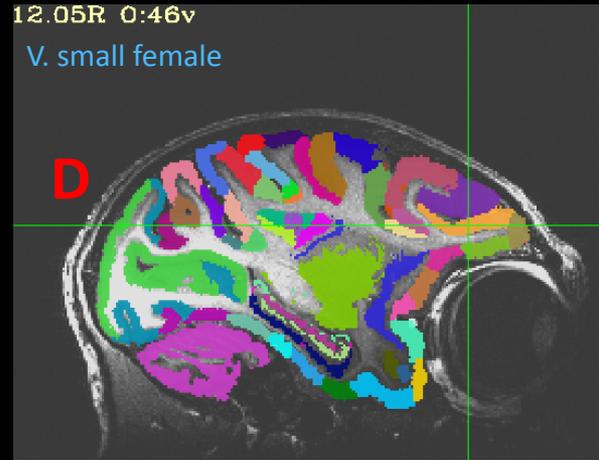
**C**



12.05R 0:46v

V. small female

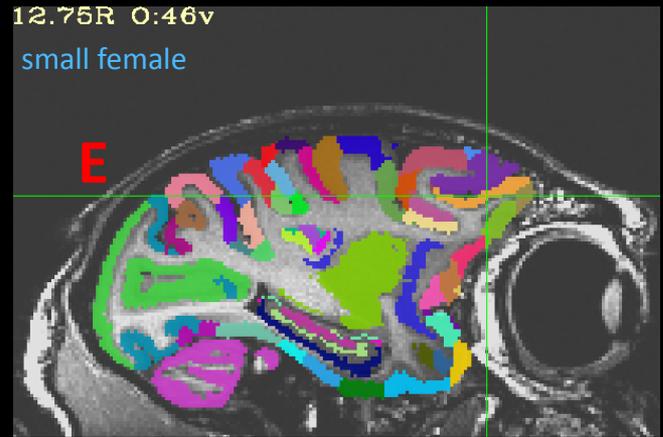
**D**



12.75R 0:46v

small female

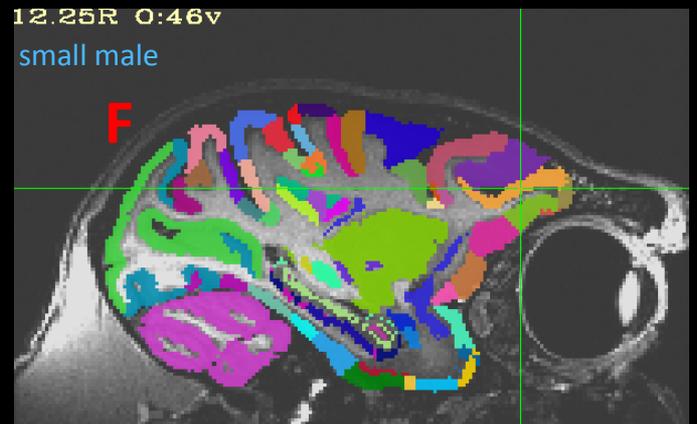
**E**



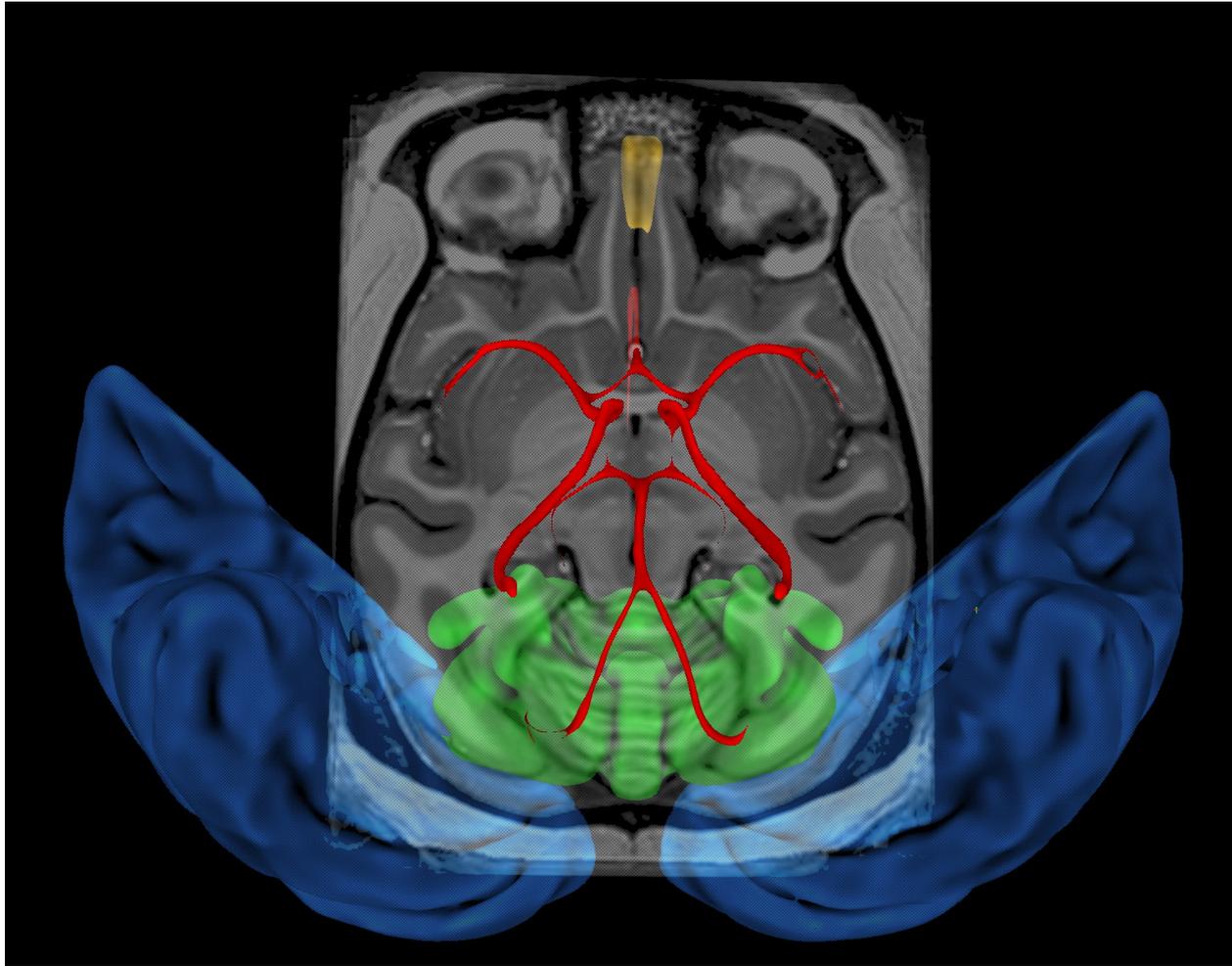
12.25R 0:46v

small male

**F**



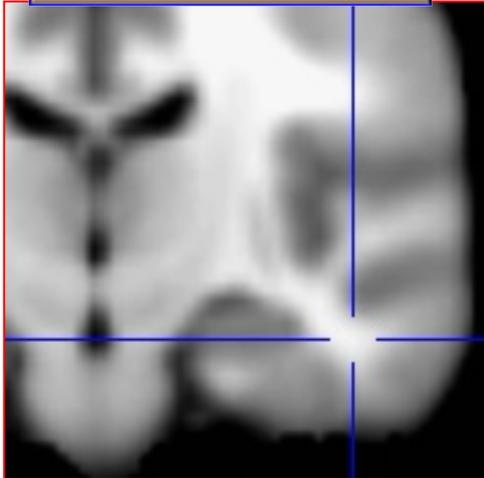
NMT (NIH Macaque Template) – Group template from 31 macaques, surfaces, GM/WM/CSF segmentation



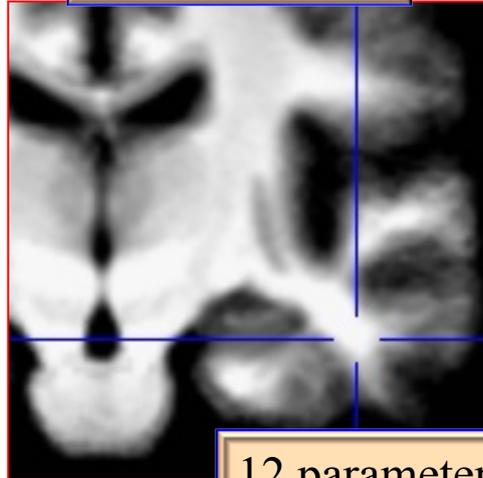
Submitted - with Adam Messinger, Caleb Sponheim, Jakob Seidlitz, Kadharbatcha Saleem,...

# Make your own template

MNI 152 template



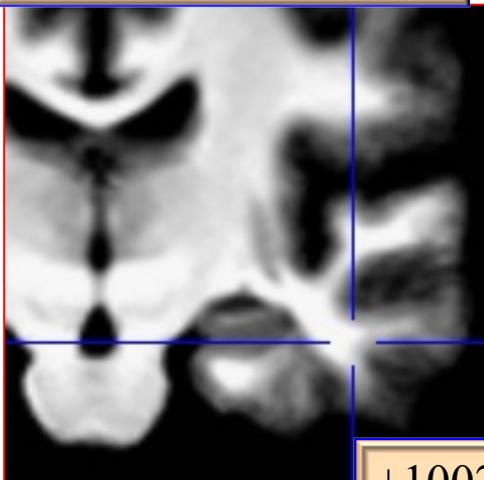
Linear = Affine



12 parameters

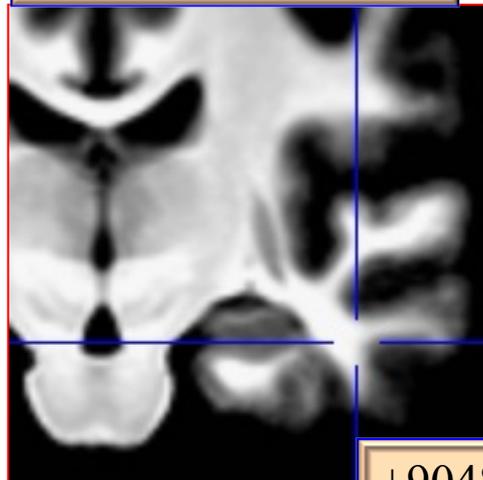
@toMNI\_Awarp  
@toMNI\_Qwarp  
Averages of 21  
3 Tesla brain volumes  
with varied  
levels of refinement in  
the nonlinear warping  
(smaller patch=more refinement)

Nonlinear: Patch=101



+1002

Nonlinear: Patch=49



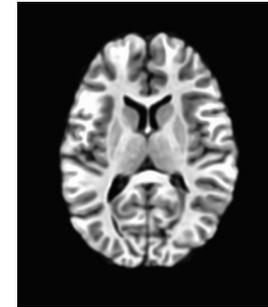
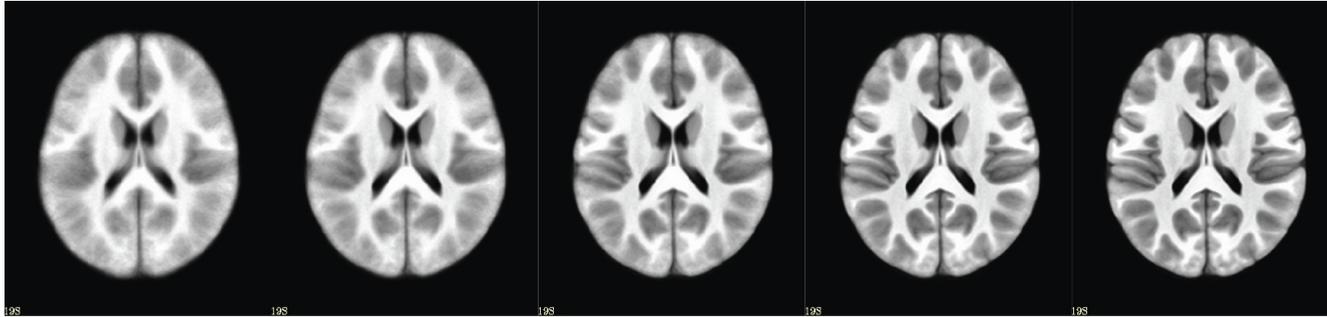
+9048

Nonlinear: Patch=23



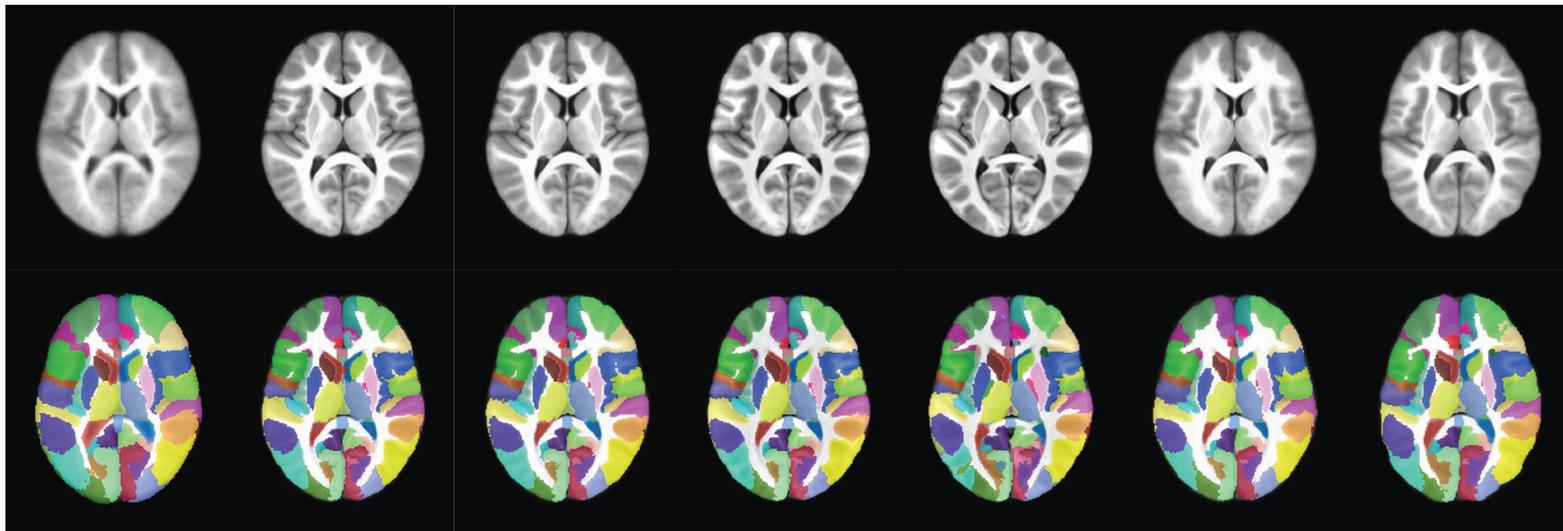
+70008

## ALTERNATIVE ATLAS CREATION TECHNIQUES: ITERATIVE AND TYPICAL METHODS



Iterative nonlinear alignment to affine template with progressively smaller patch sizes

**“Typical”  
Brain**



Affine

Affine  
Iterative

Typical  
Iterative

MNI  
Iterative

Nonlinear  
to MNI

Nonlinear  
to Affine

Nonlinear  
to Typical

## Make your own atlas!

- New atlases – easy and fun. Make your own!
  - ✧ make available in AFNI GUI and whereami and to other user

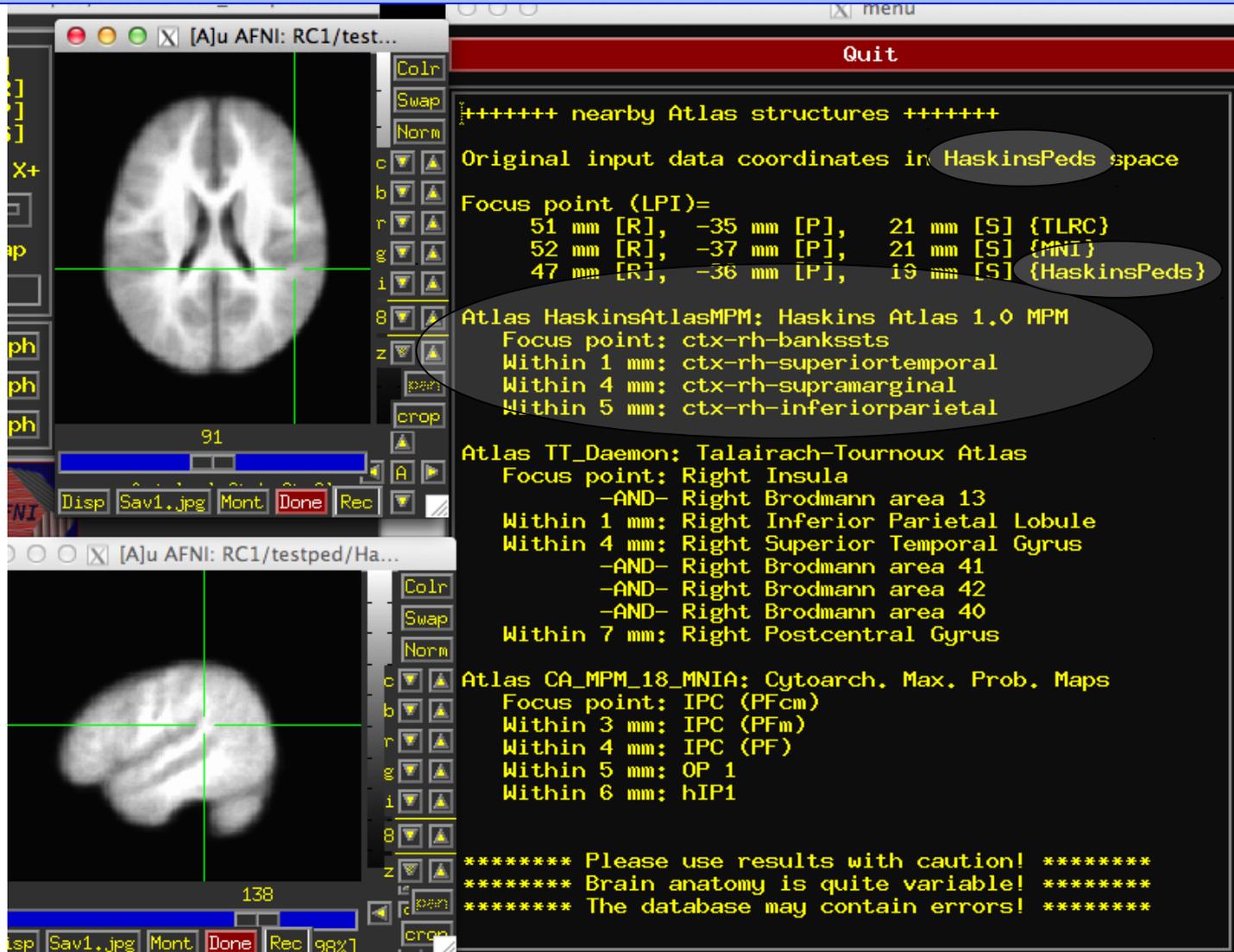
```
@AfnEnv -set AFNI_SUPP_ATLAS_DIR ~/MyCustomAtlases/
```

Then:

```
@Atlasize -space MNI -dset atlas_for_all.nii \  
          -lab_file keys.txt 1 0 -atlas_type G
```

In ~/MyCustomAtlases/ you will now find atlas\_for\_all.nii along along with a modified CustomAtlases.niml file.

# Haskins Pediatric Atlas



The screenshot displays the AFNI software interface. On the left, two axial brain MRI slices are shown. The top slice is labeled '91' and the bottom slice is labeled '138'. Both slices have a green crosshair indicating the current focus point. To the right of the slices is a control panel with buttons for 'Colr', 'Swap', 'Norm', and directional arrows (c, b, r, g, i, 8, z) for slice navigation. Below the slices are buttons for 'Disp', 'Sav1.jpg', 'Mont', 'Done', and 'Rec'. On the right side of the screen, a terminal window titled 'Quit' displays the following text:

```
+++++++ nearby Atlas structures +++++++
Original input data coordinates in HaskinsPeds space
Focus point (LPI)=
  51 mm [R], -35 mm [P],  21 mm [S] {TLRC}
  52 mm [R], -37 mm [P],  21 mm [S] {MNI}
  47 mm [R], -36 mm [P],  19 mm [S] {HaskinsPeds}

Atlas HaskinsAtlasMPM: Haskins Atlas 1.0 MPM
Focus point: ctx-rh-bankssts
Within 1 mm: ctx-rh-superiortemporal
Within 4 mm: ctx-rh-supramarginal
Within 5 mm: ctx-rh-inferiorparietal

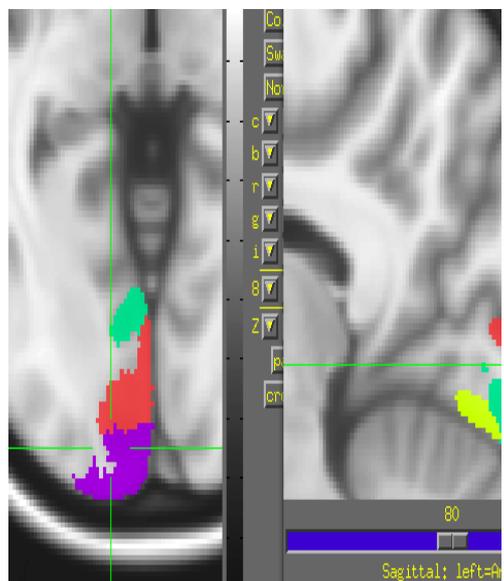
Atlas TT_Daemon: Talairach-Tournoux Atlas
Focus point: Right Insula
-AND- Right Brodmann area 13
Within 1 mm: Right Inferior Parietal Lobule
Within 4 mm: Right Superior Temporal Gyrus
-AND- Right Brodmann area 41
-AND- Right Brodmann area 42
-AND- Right Brodmann area 40
Within 7 mm: Right Postcentral Gyrus

Atlas CA_MPM_18_MNIA: Cytoarch. Max. Prob. Maps
Focus point: IPC (PFcm)
Within 3 mm: IPC (PFm)
Within 4 mm: IPC (PF)
Within 5 mm: OP 1
Within 6 mm: hIP1

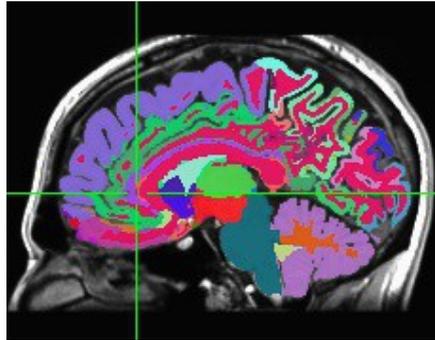
***** Please use results with caution! *****
***** Brain anatomy is quite variable! *****
***** The database may contain errors! *****
```

## Upcoming atlases

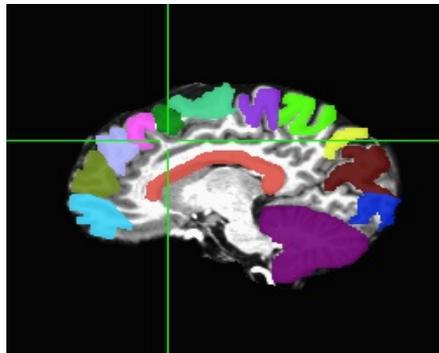
- Eickhoff-Zilles 2.2 cytoarchitectonic atlases
- DTI fiber atlas – Susumo Mori
- Princeton Visual Field Map, Kastner, et al.



# Individual Subjects

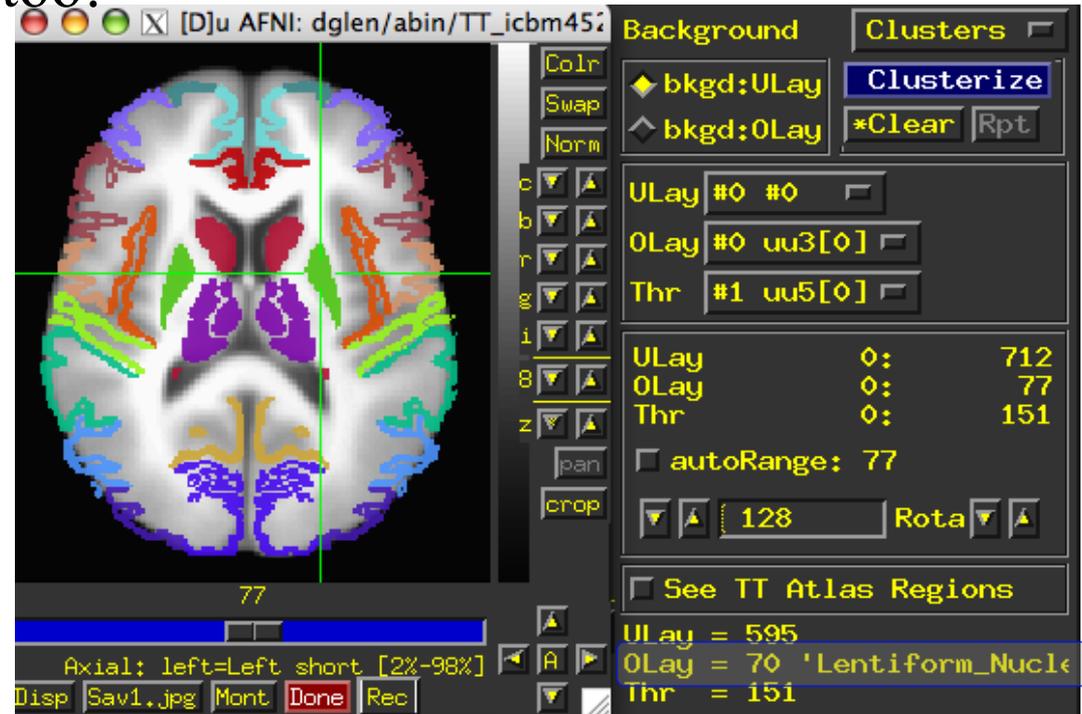


FreeSurfer segmentation



Manual segmentation

@SUMA\_MakeSpecFS – atlasizes too!



Overlay panel shows structure name.  
Now FreeSurfer segmentation can also be used in whereami

# NeuroSynth, LinkrBrain, BrainMap.org, Allen Brain, ...

The image displays three main components related to neuroimaging atlases:

- AFNI Software:** A screenshot of the AFNI (Analysis of Functional NeuroImages) interface. It shows a 3D brain volume with a red focus point. A text window titled "AFNI whereami" lists nearby anatomical structures:
  - Original input data coordinates in TLRC space
  - Focus point (LPI): 25.0 mm [R], 37.0 mm [A], -7.0 mm [I] (TLRC)
  - 25.3 mm [R], 38.5 mm [A], -8.1 mm [I] (MNI) [NeuroSynth](#) [SumsDB](#)
  - 25.3 mm [R], 34.5 mm [A], -1.1 mm [I] (MNI) (ANAT)
  - Atlas TT\_Daemon: Talairach-Tournoix Atlas
    - Focus point: Right Middle Frontal Gyrus
    - Within 1 mm: Right Brodmann area 11
    - Within 2 mm: Right Inferior Frontal Gyrus
    - Within 3 mm: Right Brodmann area 47
    - Within 6 mm: Right Anterior Cingulate
    - AND- Right Superior Frontal Gyrus
    - Within 7 mm: Right Medial Frontal Gyrus
  - Atlas CA\_ML\_18\_MNIA: Macro Labels (1827)
    - Within 2 mm: Right Inferior Frontal Gyrus (p. Orbitalis)
    - Within 5 mm: Right Superior Orbital Gyrus
    - AND- Right Middle Orbital Gyrus

- SumsDB Website:** A screenshot of the SumsDB (Surface Management System) website. It features a search bar and a table of search results:
 

foci_id	name	original x	original y	original z	flirt x	flirt y	flirt z
<a href="#">.106081</a>	Christensen_CC07	33	36	-9	30.2	3	30.2
<a href="#">.99935</a>	Downing_CC06	24	37	3	26.1	3	26.1
<a href="#">.95817</a>	Noguchi_CC05	32	44	-8	30.7	4	30.7
<a href="#">.95087</a>	Honey_CC05	24	36	-8	22.2	3	22.2
<a href="#">.89538</a>	LaBar_CC03	19	34	-4	19.9	3	19.9
<a href="#">.77661</a>	Ullén_JN08	26	39	-12	24.5	3	24.5
<a href="#">.77635</a>	Ullén_JN08	26	39	-10	25.1	3	25.1
<a href="#">.77429</a>	Pochon_JN08	30	40	-12	28.5	3	28.5
<a href="#">.77316</a>	Plailly_JN08	19	34	-9	18.9	3	18.9
<a href="#">.76942</a>	Petrovic_JN08b	24	36	-10	22.1	3	22.1
- NeuroSynth Website:** A screenshot of the NeuroSynth website showing a search interface. The search criteria are coordinates: 26 : 38 : -6 :. Below the search bar, there are tabs for "Maps", "Studies", "Associations", and "FAQs". The main content area displays "Functional connectivity and coactivation maps" with two brain slice visualizations. The first slice is labeled "y = +38" and the second "x = +26". A correlation value "corr. (r): 1" is shown, along with a "What's here?" button.

set AFNI\_WEBBY\_WAMI to YES and AFNI\_NEUROSYNTH to YES

# Web-based atlases

The screenshot displays the AFNI software interface with several windows open. The main window shows brain scan data with a color-coded cluster overlay. A 'Query of coordinates to linkrbrain.org correlations' window is open, showing a list of task types and their correlations. Another window shows 'AFNI Cluster Results' with a table of cluster statistics and coordinates. A third window shows a 'Query of coordinates to linkrbrain.org correlations' window with a list of genes and their correlations.

**Query of coordinates to linkrbrain.org correlations**

Task type	Correlation
gaze	0.01772
decision	0.01565
item memory	0.00943
conflict resolution	0.00926
face area	0.00902
first language	0.00902
navigation	0.00824
neglect	0.00660
cognitive effort	0.00598
gestures	0.00502
familiar objects	0.00485
desire	0.00481

**AFNI Cluster Results [A]**

Voxels survived clustering = 170173  
Voxels edited out = 8111  
NN clustering level = 1 [faces touch]

Use internal mask from 3dClustSim  LinkrBrain type Genes

#1 | XYZ Peak  | 3dclust SaveTab Clust SaveMsk WamI Done

Aux.Dset From  0 To  9999 | Mean  Scat.1D Clear

[No Aux Dataset chosen] [Scat.1D cleared]

##:	Size	X	Y	Z	Alpha
1:	122780 vox	+33.0	+92.0	+15.0	Jump Flash Plot Save N/Csim
2:	11762 vox	-63.0	+12.0	-6.0	Jump Flash Plot Save N/Csim
3:	3948 vox	-5.0	+39.0	+66.0	Jump Flash Plot Save N/Csim

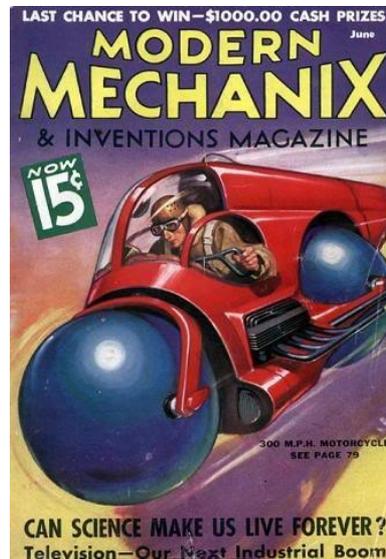
**Query of coordinates to linkrbrain.org correlations**

Gene	Correlation
A_24_P721638	0.01824
A_24_P945276	0.01694
A_24_P918473	0.01680
similar to deubiquitinating enzyme DUB2	0.01602
A_24_P853124	0.01554
A_24_P460529	0.01540
A_24_P706236	0.01496
A_24_P7322	0.01491
A_32_P118731	0.01455
A_24_P499152	0.01440
A_24_P607947	0.01428
A_32_P170564	0.01426

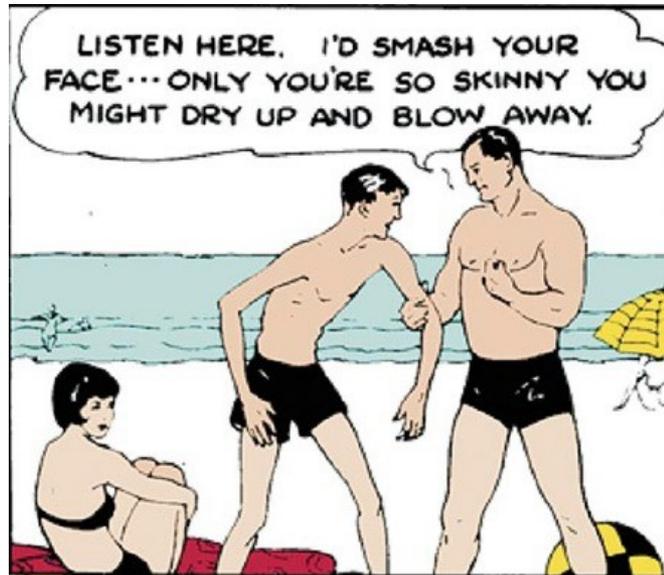
set AFNI\_LINKRBRAIN to YES

## In Development

- New templates and template spaces – fully supported in AFNI
  - ✧ macaque
  - ✧ rat, mouse, human
  - ✧ pediatric, ...
- On-the-fly transformations through all available template spaces
- Extra information about atlas structures
- HAWG standardized format – atlases for everyone!



## Atlas Conclusions and Questions



Charles Atlas