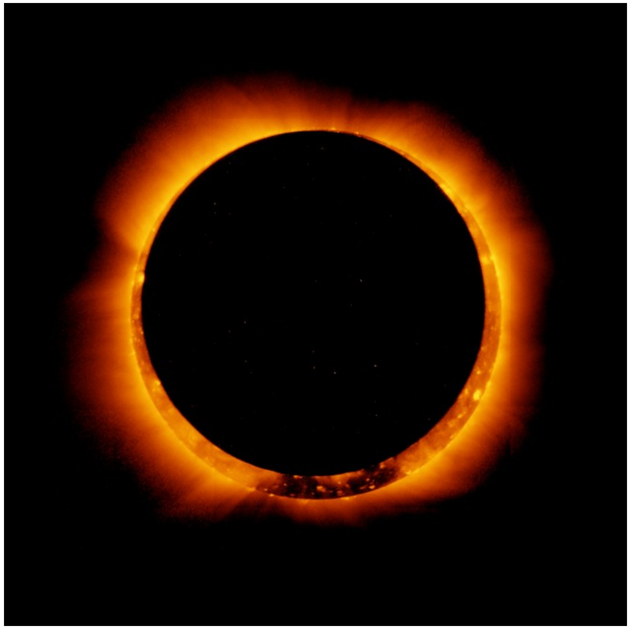
Alignment and Atlases



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 <u>nonlinearly</u> 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)

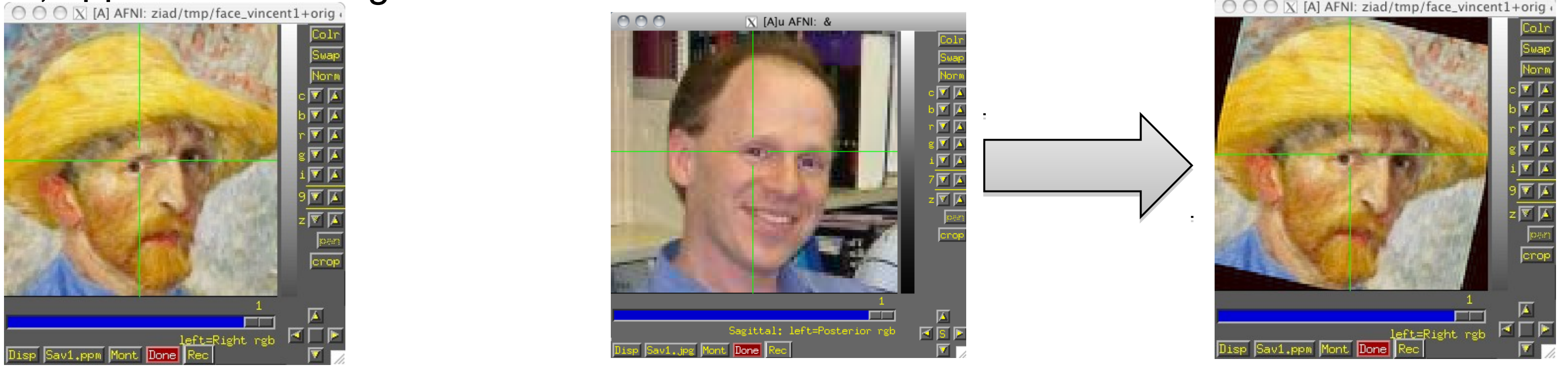
- Align partial data to roughly the right part of the brain
- **Nudge plug-in** - visually align two volumes
- rotate by known amount between volumes
- ◇ **3drotate** – moves (shifts and rotates) volumes
- ◇ **3dWarp** – make oblique, deoblique to match another dataset
- Put centers of data from outside 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 **J(x)** and target (or source) image **I(x)**, find a geometrical transformation **T[x]** so that $\mathbf{I}(\mathbf{T}[\mathbf{x}]) \approx \mathbf{J}(\mathbf{x})$
  - **T[x]** will depend on some parameters
    - Goal is to find the parameters that make the transformed **I** a ‘best fit’ to **J**
  - To register an entire time series, each volume $\mathbf{I}_n(\mathbf{x})$ is aligned to **J(x)** with its own transformation $\mathbf{T}_n[\mathbf{x}]$, for $n = 0, 1, \ldots$
    - Result is time series $\mathbf{I}_n(\mathbf{T}_n[\mathbf{x}])$ for n=0, 1, …
    - User must choose base image **J(x)**

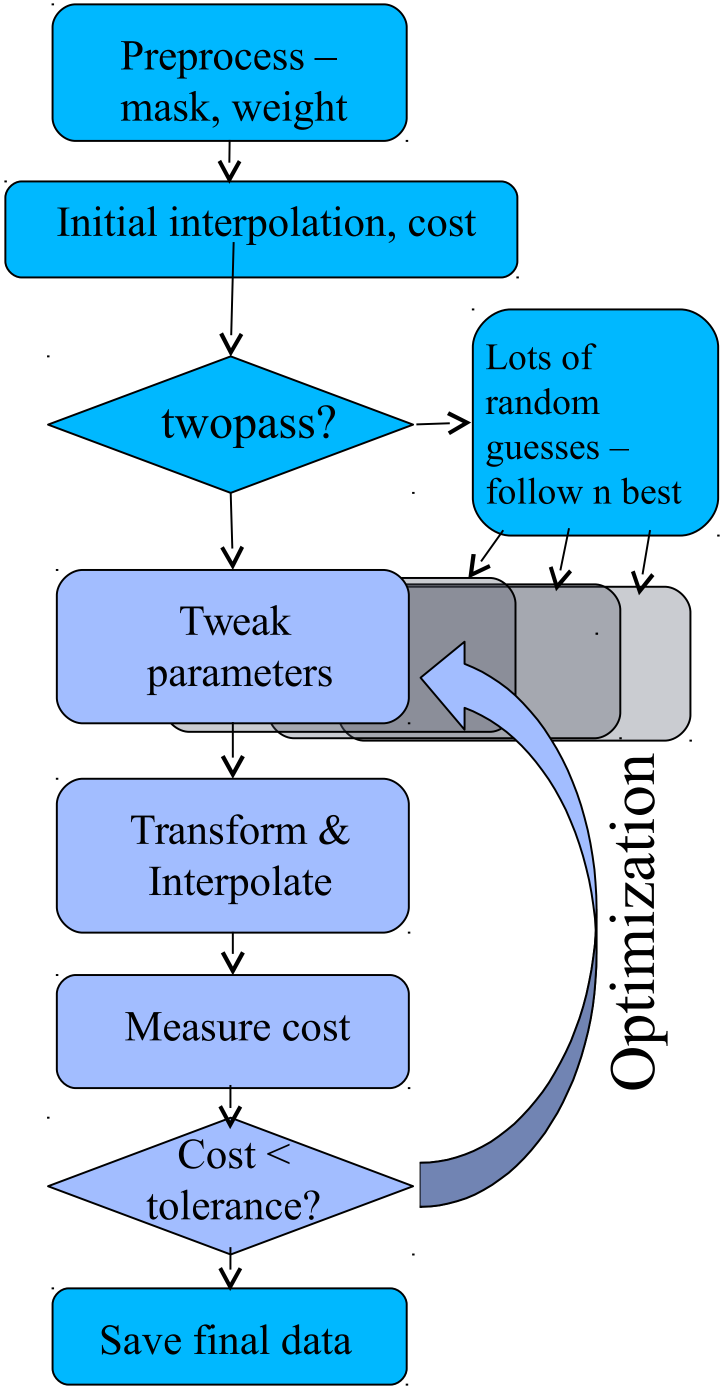
- Most image registration methods make 3 algorithmic choices:
  - How to measure mismatch **E** (for error) between **I(T[x])** and **J(x)**?
    - **Or** … How to measure goodness of fit between **I(T[x])** and **J(x)**?
      - **E**(parameters) ≡ **–Goodness**(parameters)
  - How to adjust parameters 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…

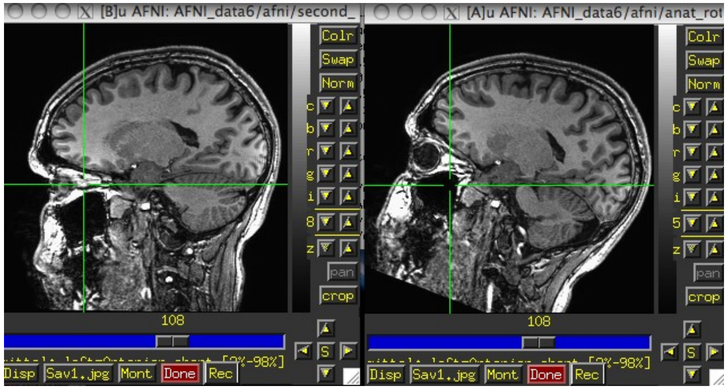


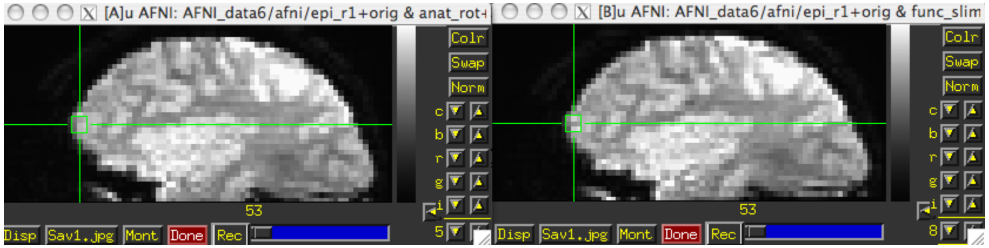
Alignment process - overview

- 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 = $\Sigma_x w(x) \cdot \{I(T[x]) - J(x)\}^2$
    - 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.

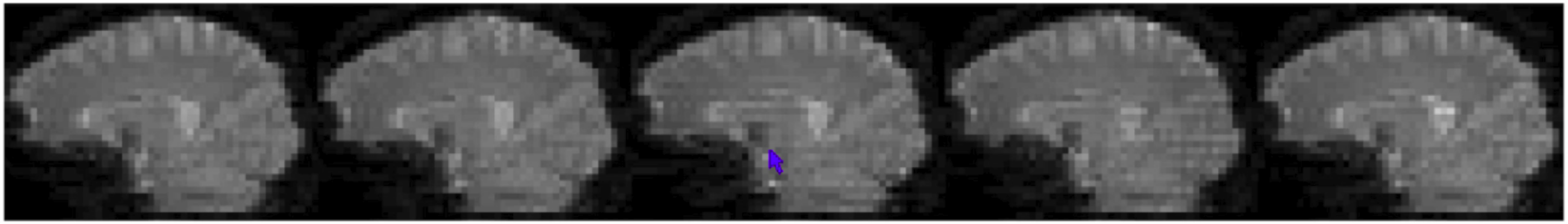


Image courtesy of Jonathan Power, NIMH

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

- 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 7th 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) :

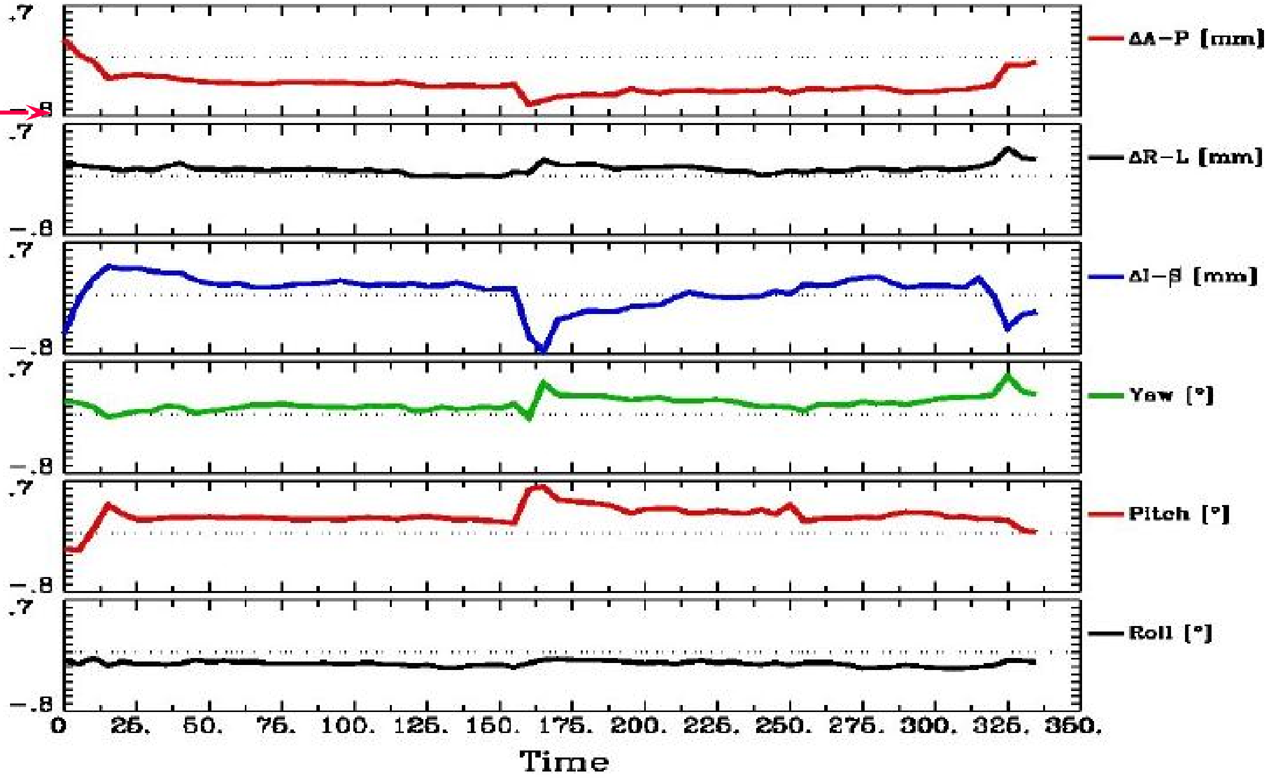
```
3dvolreg -base 3 -cubic -prefix epi_r1_vrt -1Dfile vr_dfile.1D epi_r1+orig
1dplot -volreg vr_dfile.1D &
```

- 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
```



About A-P

About R-L
Typical

About I-S

- Note motion peaks at time ≈ 160s: subject jerked head up at that time

"Fixing Motion"

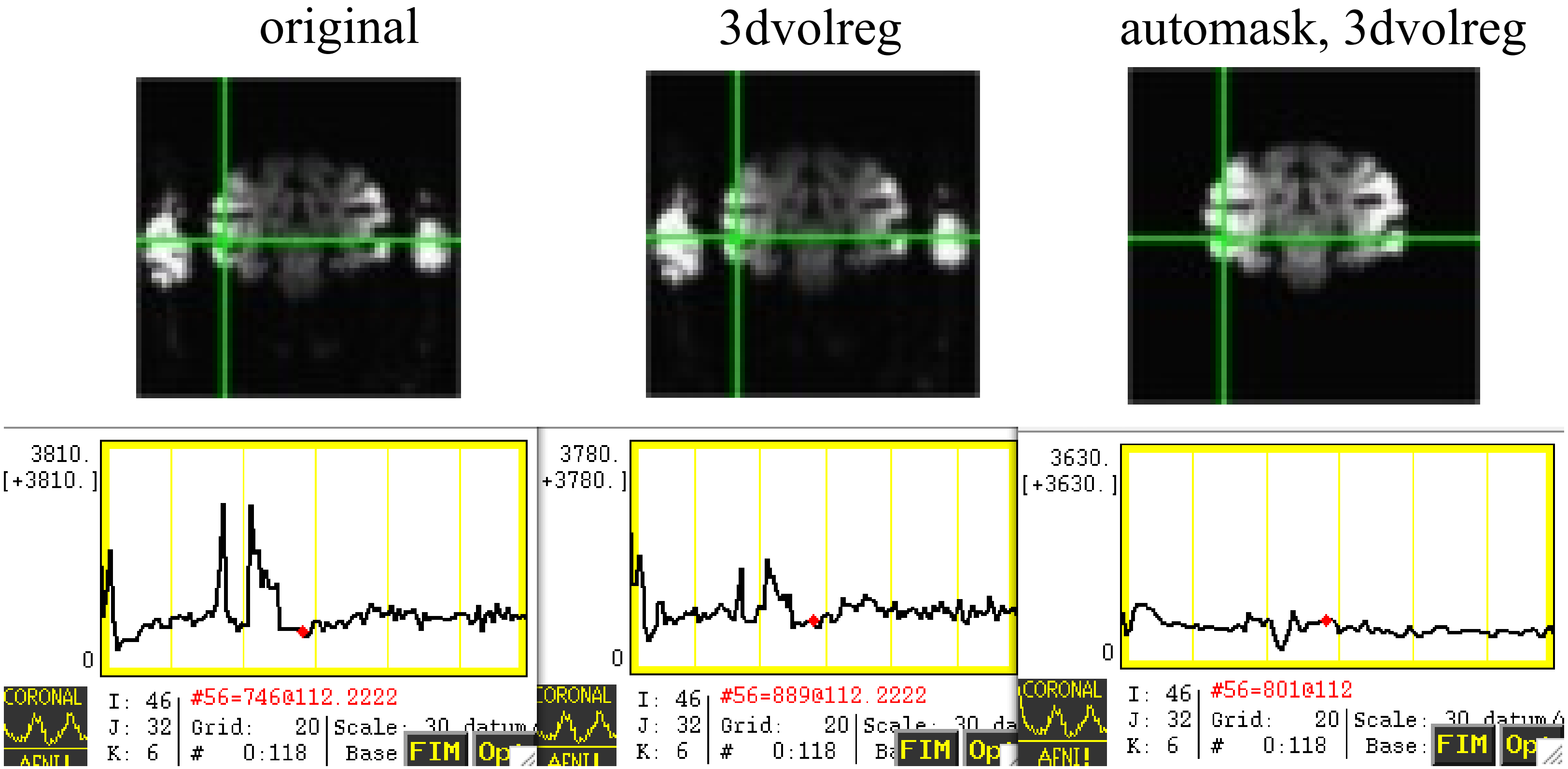
- Motion occurs over slices and not volumes and moves data off original grid
- "Regressing out" – motion parameters, derivatives, displacement, euclidean norm of derivatives (summary parameters)
- Censoring ("scrubbing", "sweeping under the mat",...)
- Experimental design – kids, monkeys, juice, talking, 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

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]
  - **corrratio_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

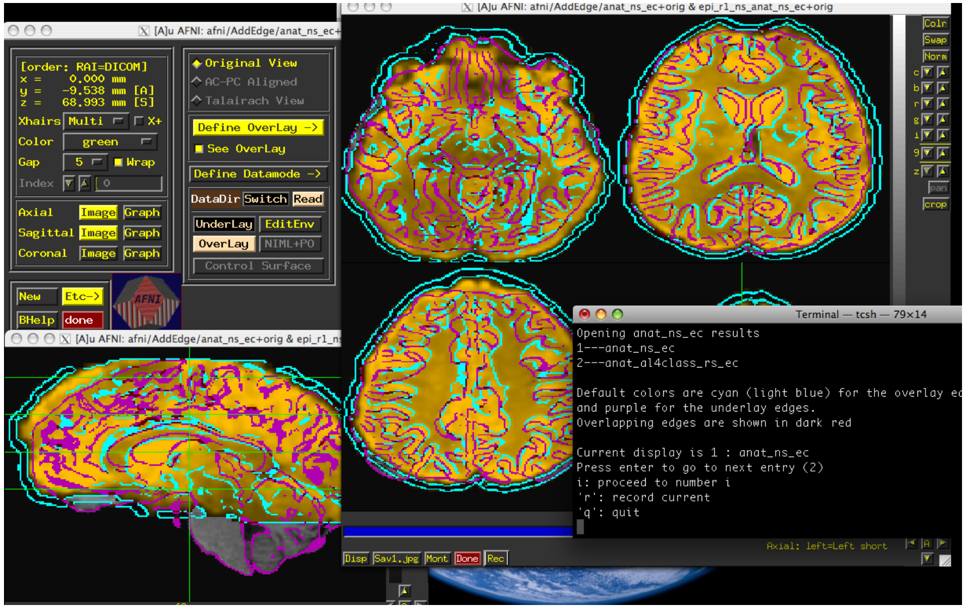
- Simple Example:

```
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

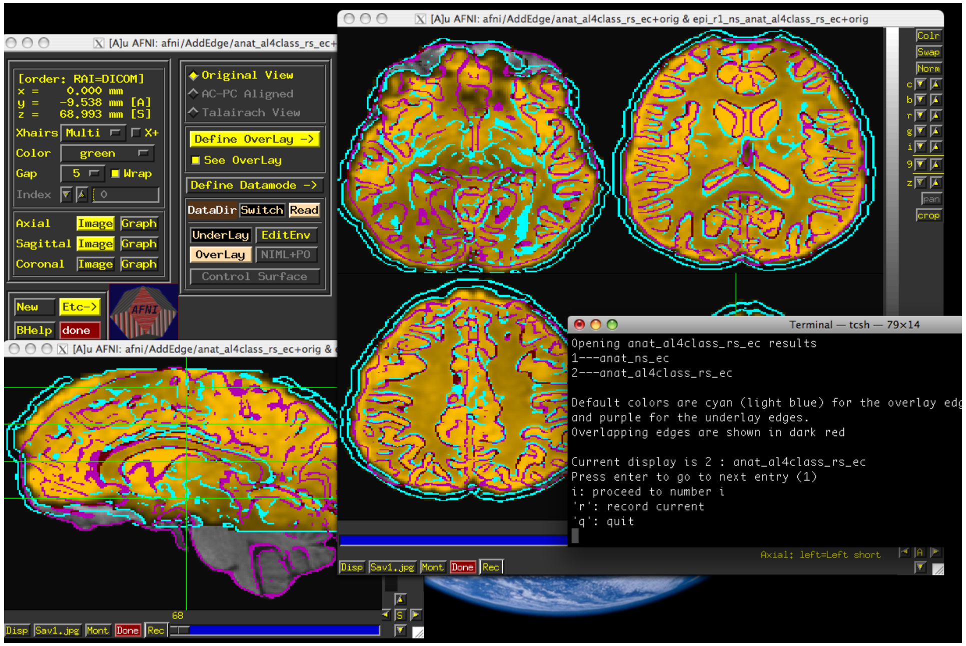


```
[order: RAI=DICOM]
x =     0.000 mm
y =    -9.538 mm [A]
z =    68.993 mm [S]
Xhairs Multi   X+
Color   green
Gap   5   Wrap
Index
```

Terminal — tcsh — 79×14

```
Opening anat_ns_ec results
1---anat_ns_ec
2---anat_al4class_rs_ec

Default colors are cyan (light blue) for the overlay ed
and purple for the underlay edges.
Overlapping edges are shown in dark red

Current display is 1 : anat_ns_ec
Press enter to go to next entry (2)
i: proceed to number i
'r': record current
'q': quit
```

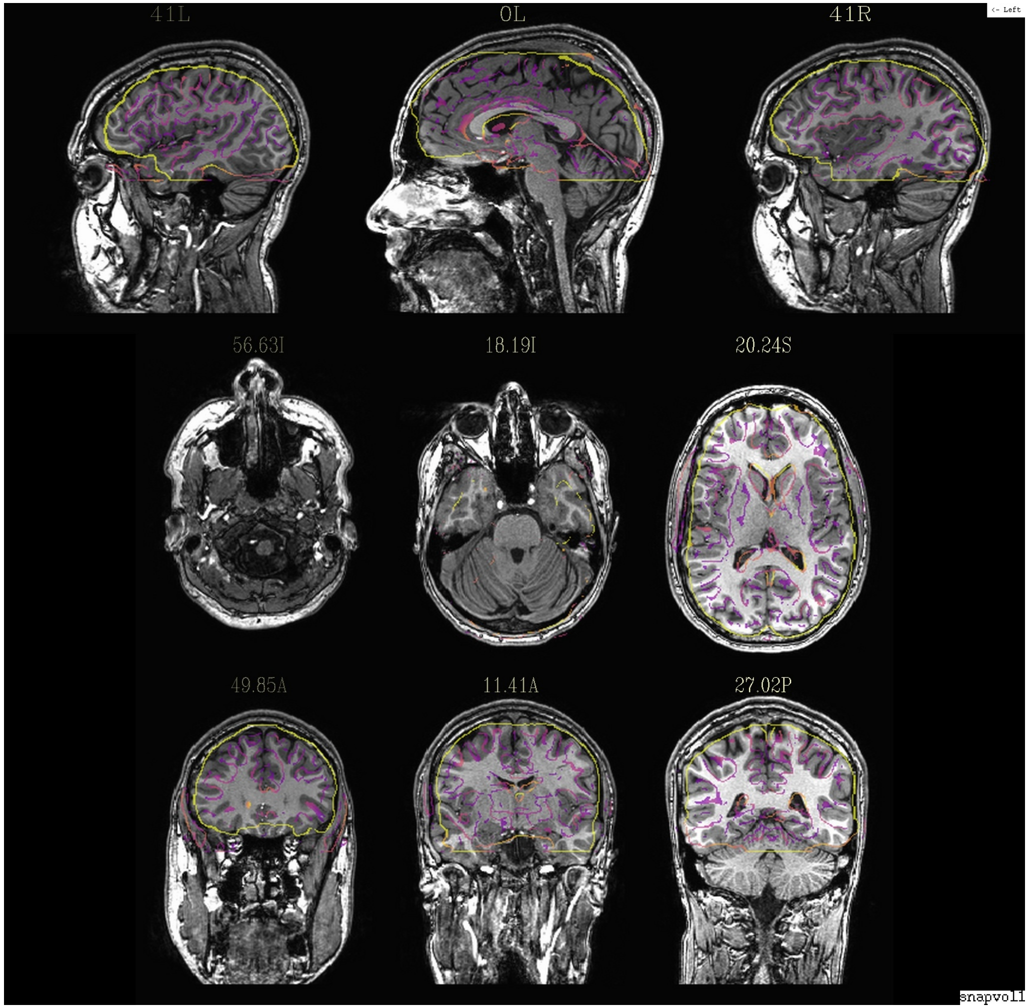
After



```
[order: RAI=DICOM]
x =     0.000 mm
y =    -9.538 mm [A]
z =    68.993 mm [S]
Xhairs Multi   X+
Color   green
Gap   5   Wrap
Index
```

Terminal — tcsh — 79×14

```
Opening anat_al4class_rs_ec results
1---anat_ns_ec
2---anat_al4class_rs_ec

Default colors are cyan (light blue) for the overlay edg
and purple for the underlay edges.
Overlapping edges are shown in dark red

Current display is 2 : anat_al4class_rs_ec
Press enter to go to next entry (1)
i: proceed to number i
'r': record current
'q': quit
```



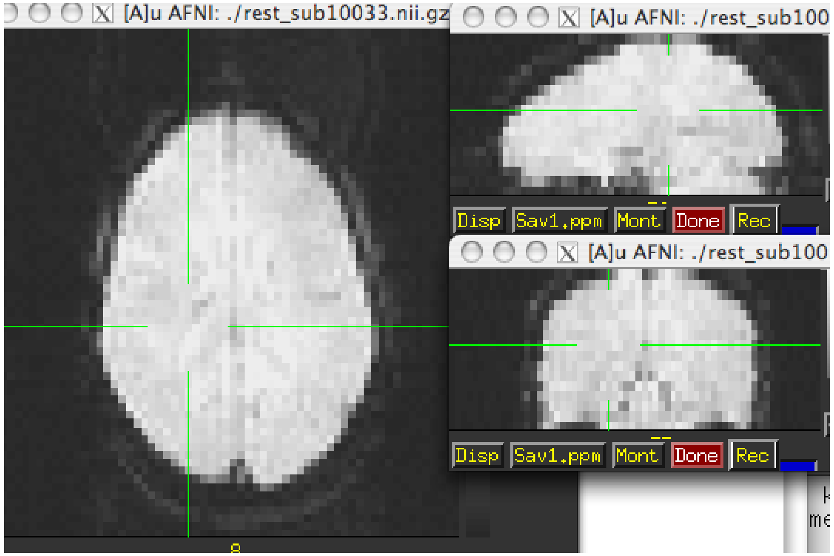
```
@snapshot_volreg anat+orig. epi_r1+orig edges.jpg
aiv edges.jpg
```

Alignment Visualization in AFNI

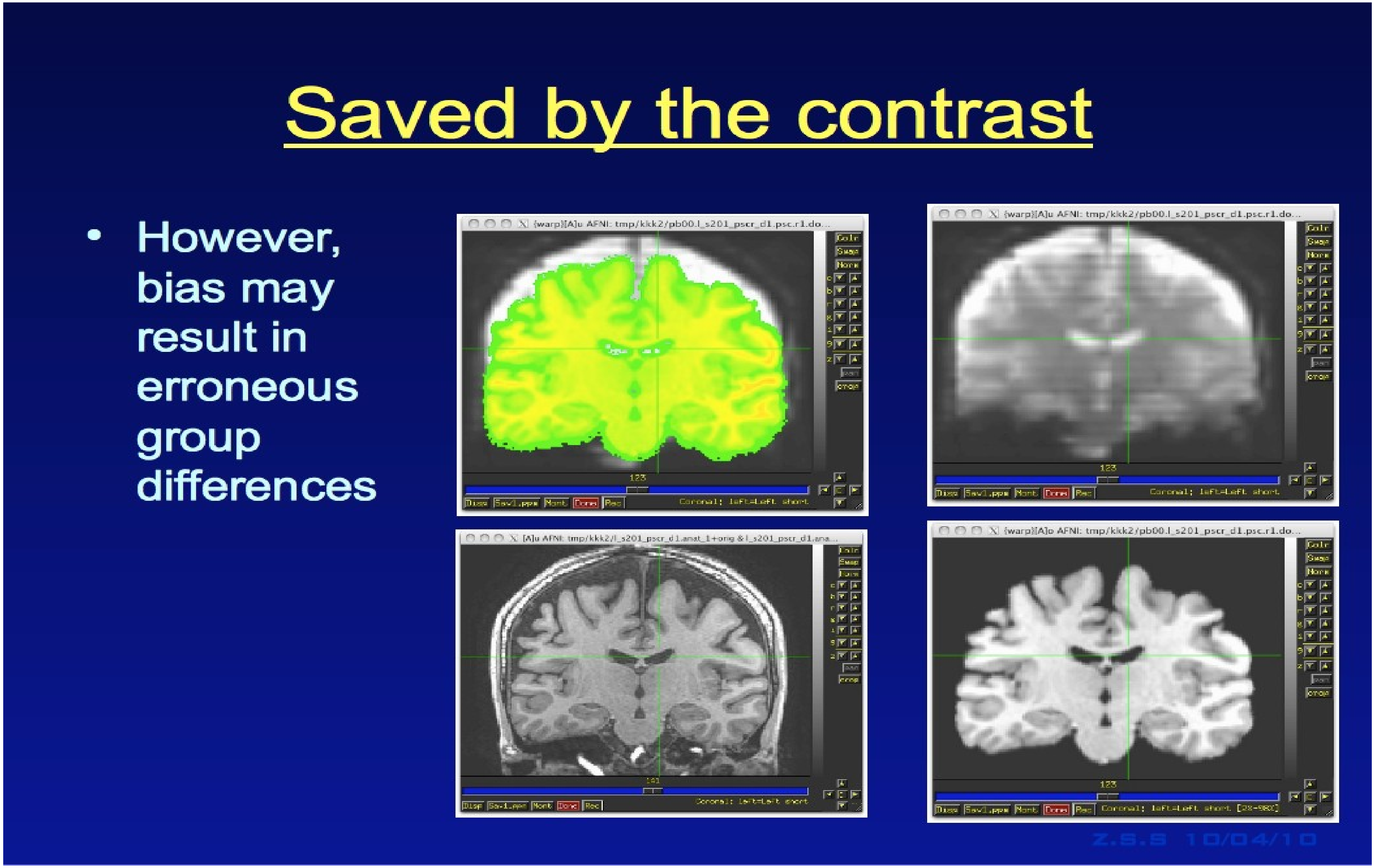
- Graph and image – travel through time for motion correction or for a thousand datasets in a row.
- Multiple controllers and crosshairs – up to ten datasets at a time, quick and rough.
- Overlay display – opacity control, thresholding. A single pair – good for different or similar datasets.
- Overlay 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



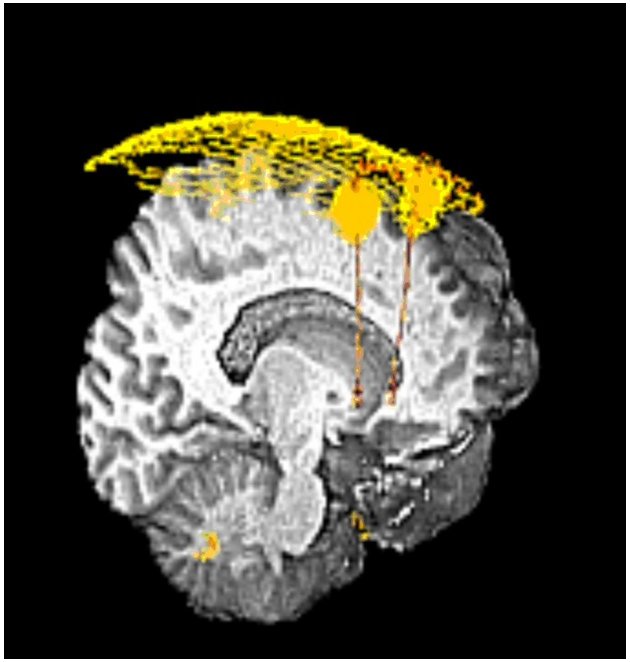
Saved by the contrast

- However, bias may result in erroneous group differences

Z.S.S 10/04/10

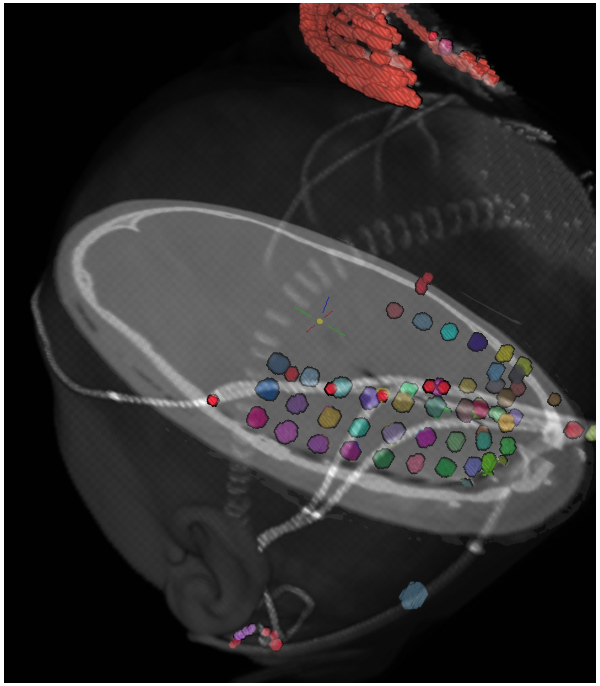
Alignment –special cases

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



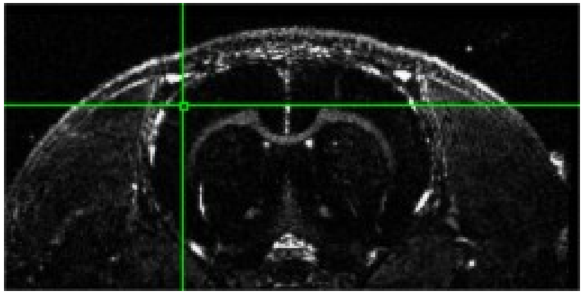
Dataset courtesy of Justin Rajendra,
(Formerly at Emory, Now in our group.
Woohoo!)
Also see @Install_DBSproc for DBS with
CT and DTI processing
(S. Horovitz)

ECOG – align CT with electrodes
to pre-surgical MRI

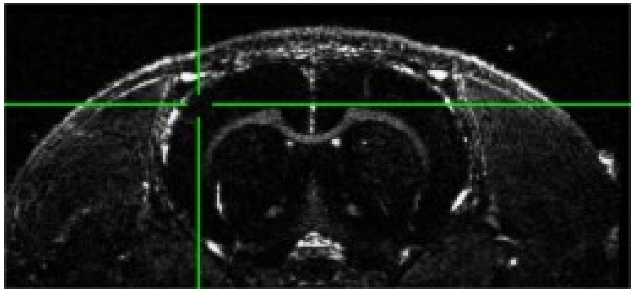


Dataset courtesy of Anna Gaglianese
(University of Utrecht, Netherlands)

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)

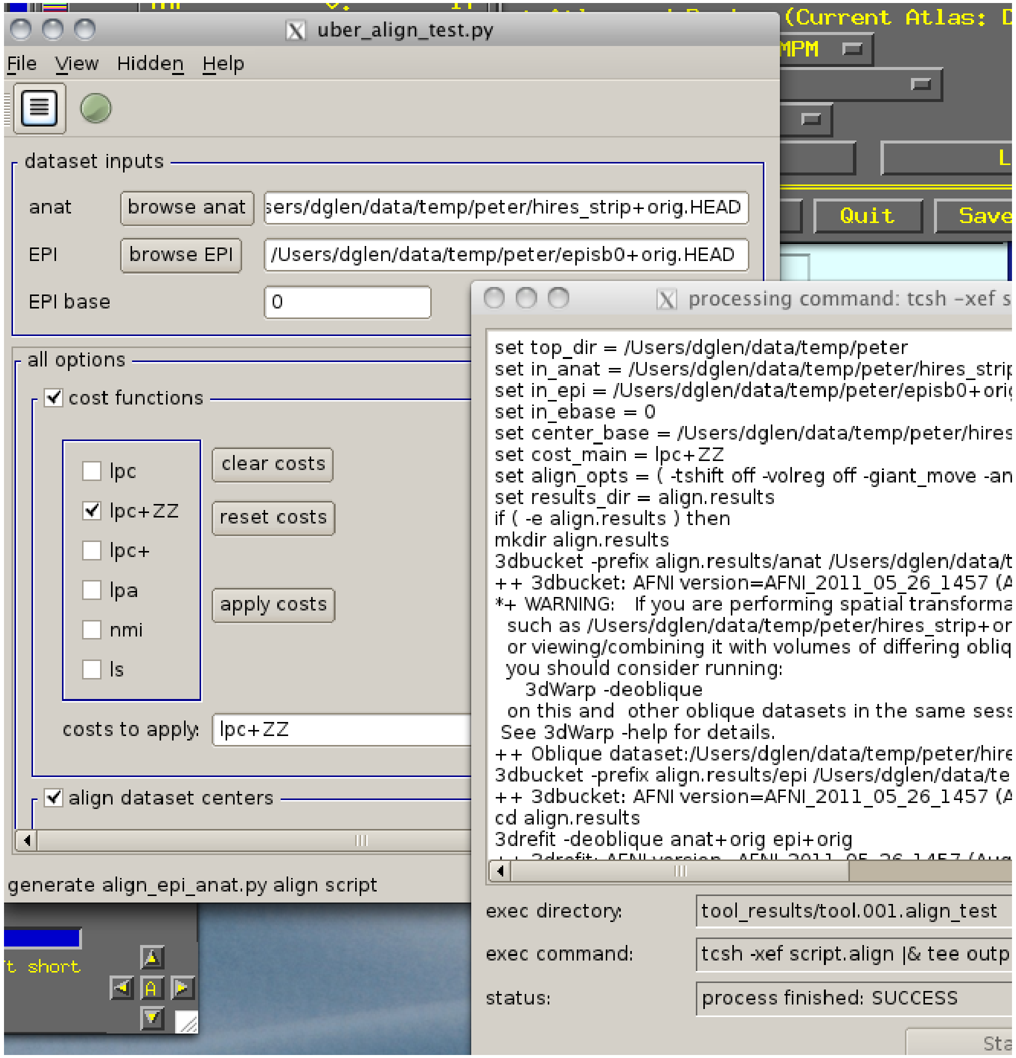
uber_align_test.py

select input data

set options

create script

run script



anat: /sers/dglen/data/temp/peter/hires_strip+orig.HEAD

EPI: /Users/dglen/data/temp/peter/episb0+orig.HEAD

EPI base: 0

☑ cost functions

☐ lpc
☑ lpc+ZZ
☐ lpc+
☐ lpa
☐ nmi
☐ ls

costs to apply: lpc+ZZ

☑ align dataset centers

```
set top_dir = /Users/dglen/data/temp/peter
set in_anat = /Users/dglen/data/temp/peter/hires_stri
set in_epi = /Users/dglen/data/temp/peter/episb0+ori
set in_ebase = 0
set center_base = /Users/dglen/data/temp/peter/hires
set cost_main = lpc+ZZ
set align_opts = ( -tshift off -volreg off -giant_move -an
set results_dir = align.results
if ( -e align.results ) then
mkdir align.results
3dbucket -prefix align.results/anat /Users/dglen/data/t
++ 3dbucket: AFNI version=AFNI_2011_05_26_1457 (
*+ WARNING:   If you are performing spatial transforma
  such as /Users/dglen/data/temp/peter/hires_strip+or
  or viewing/combining it with volumes of differing obliq
  you should consider running:
     3dWarp -deoblique
  on this and  other oblique datasets in the same sess
 See 3dWarp -help for details.
++ Oblique dataset:/Users/dglen/data/temp/peter/hire
3dbucket -prefix align.results/epi /Users/dglen/data/te
++ 3dbucket: AFNI version=AFNI_2011_05_26_1457 (
cd align.results
3drefit -deoblique anat+orig epi+orig
```

exec directory: tool_results/tool.001.align_test

exec command: tcsh -xef script.align |& tee outp

status: process finished: SUCCESS

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:

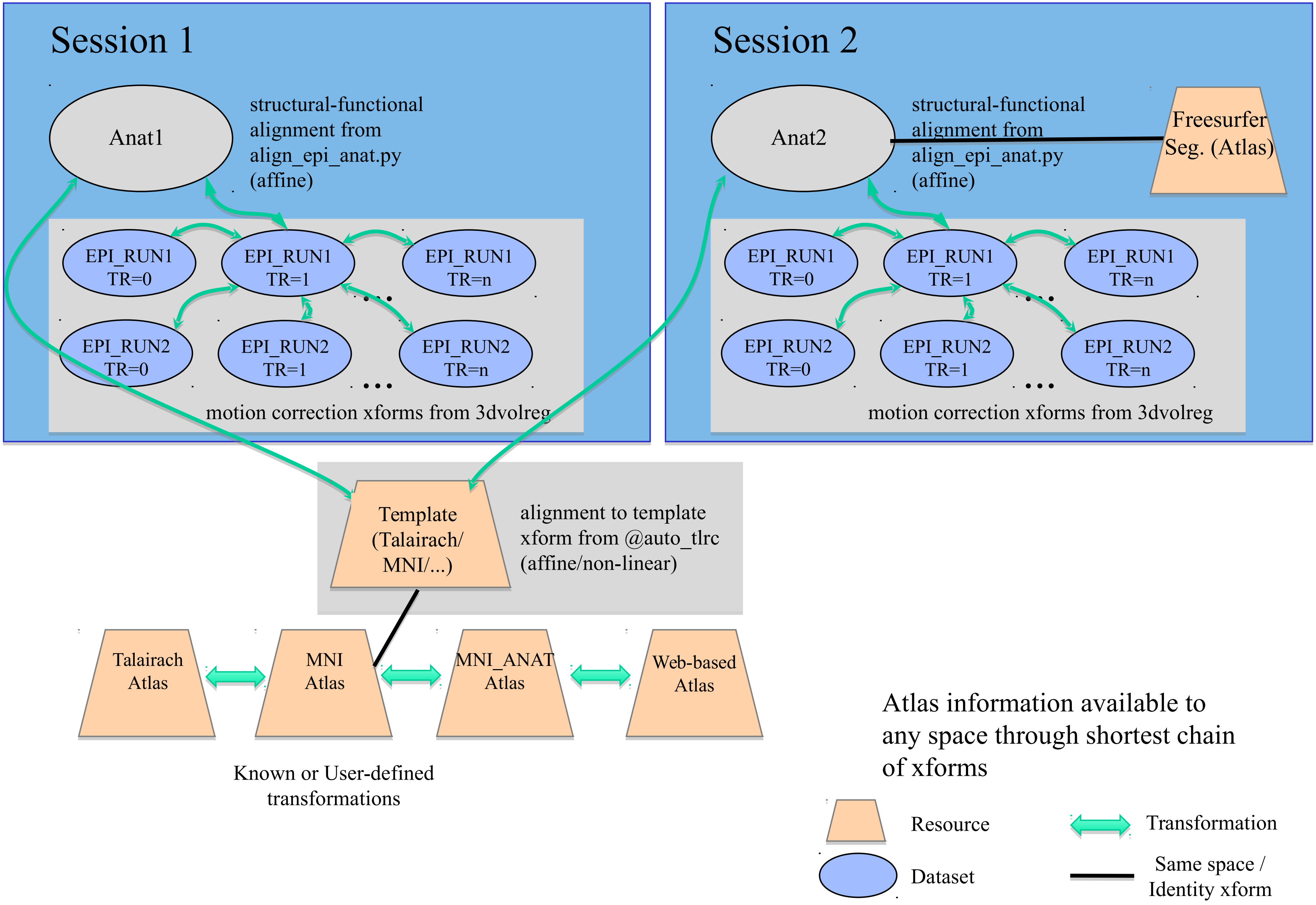
```
afni_proc.py -subj_id sb23.e6.align    \
        -dsets sb23/epi_r??+orig.HEAD  \
        -do_block align tlrc           \
        -copy_anat sb23/sb23_mpra+orig \
        -tcat_remove_first_trs 3       \
        -volreg_align_to last          \
        -volreg_align_e2a              \
        -volreg_tlrc_warp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

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

Anat1

structural-functional alignment from align_epi_anat.py (affine)

EPI_RUN1 TR=0

EPI_RUN1 TR=1

EPI_RUN1 TR=n

EPI_RUN2 TR=0

EPI_RUN2 TR=1

EPI_RUN2 TR=n

...

motion correction xforms from 3dvolreg

Session 2

Anat2

structural-functional alignment from align_epi_anat.py (affine)

Freesurfer Seg. (Atlas)

EPI_RUN1 TR=0

EPI_RUN1 TR=1

EPI_RUN1 TR=n

EPI_RUN2 TR=0

EPI_RUN2 TR=1

EPI_RUN2 TR=n

...

motion correction xforms from 3dvolreg

Template (Talairach/ MNI/...)

alignment to template xform from @auto_tlrc (affine/non-linear)

Talairach Atlas

MNI Atlas

MNI_ANAT Atlas

Web-based Atlas

Known or User-defined transformations

Atlas information available to any space through shortest chain of xforms

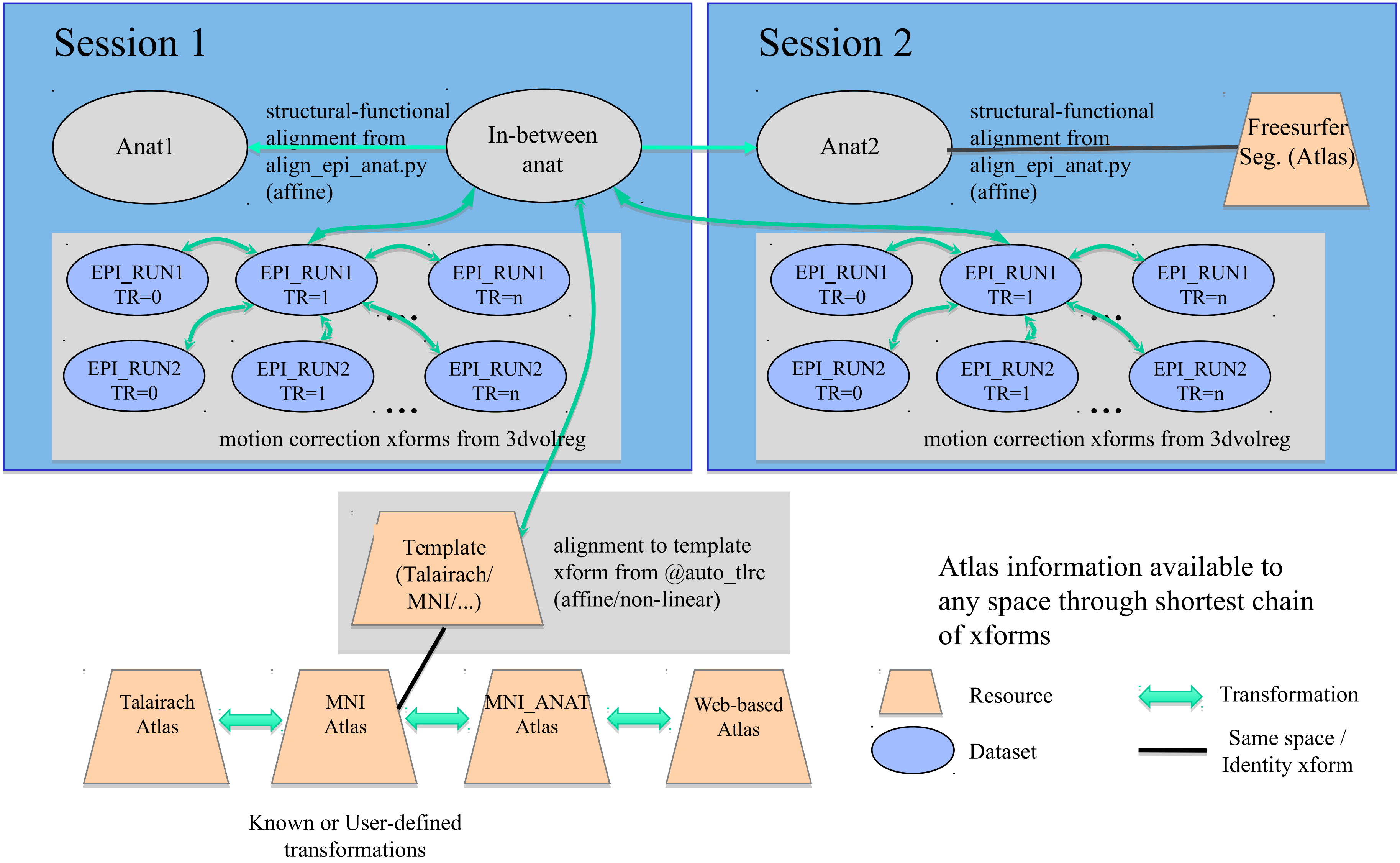
Resource

Transformation

Dataset

Same space / Identity xform

Alignment across two sessions



Session 1

Anat1

structural-functional alignment from align_epi_anat.py (affine)

In-between anat

EPI_RUN1 TR=0

EPI_RUN1 TR=1

EPI_RUN1 TR=n

EPI_RUN2 TR=0

EPI_RUN2 TR=1

EPI_RUN2 TR=n

motion correction xforms from 3dvolreg

Session 2

Anat2

structural-functional alignment from align_epi_anat.py (affine)

Freesurfer Seg. (Atlas)

EPI_RUN1 TR=0

EPI_RUN1 TR=1

EPI_RUN1 TR=n

EPI_RUN2 TR=0

EPI_RUN2 TR=1

EPI_RUN2 TR=n

motion correction xforms from 3dvolreg

Template (Talairach/ MNI/...)

alignment to template xform from @auto_tlrc (affine/non-linear)

Talairach Atlas

MNI Atlas

MNI_ANAT Atlas

Web-based Atlas

Known or User-defined transformations

Atlas information available to any space through shortest chain of xforms

Resource

Dataset

Transformation

Same space / Identity xform

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

Nonlinear Warping

3dQwarp

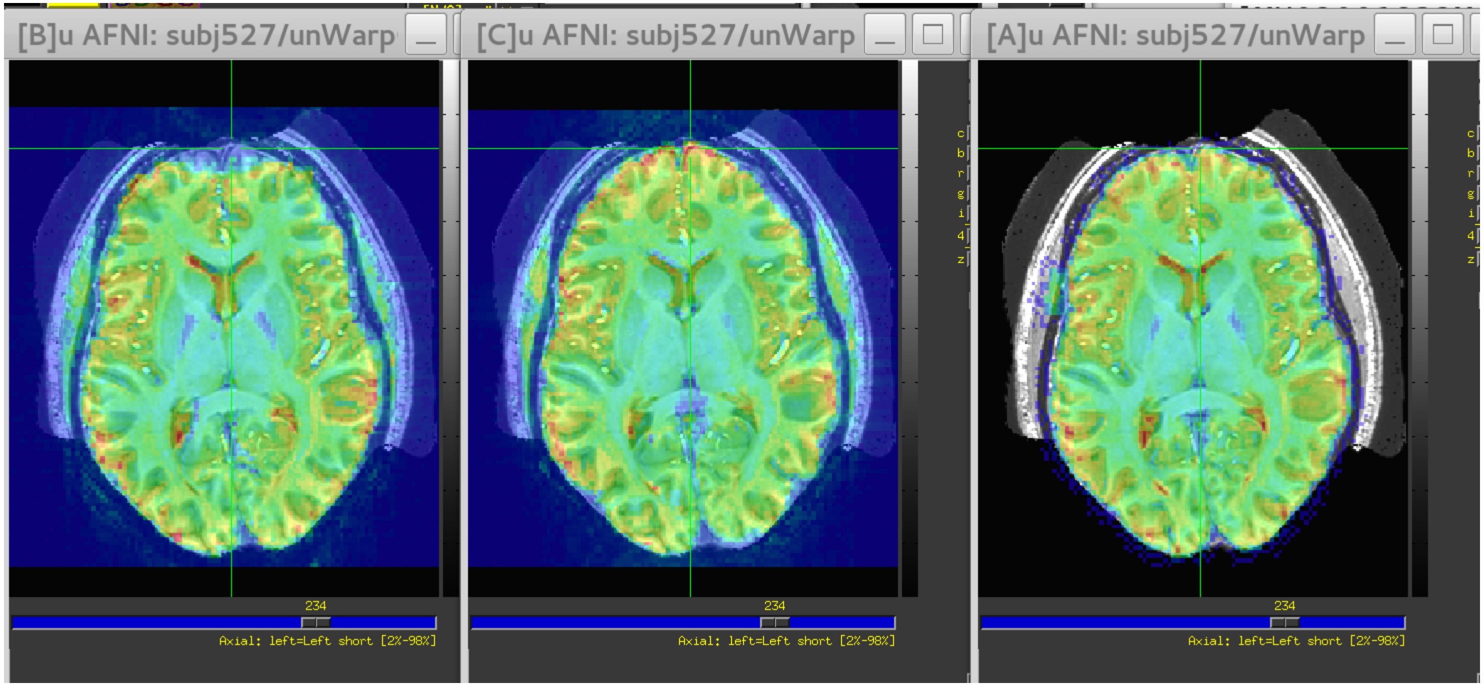
- $I_{\text{new}}(\mathbf{x}) = I_{\text{old}}(\ \mathbf{W}(\mathbf{x})\ )$
  - ◇ where **W**(**x**) depends on a ***lot*** of parameters (1000-50000+)
  - ◇ Method: Incremental transformation with Hermite cubic polynomials over finer and finer 3D patches. Output is both aligned dataset and the warp 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



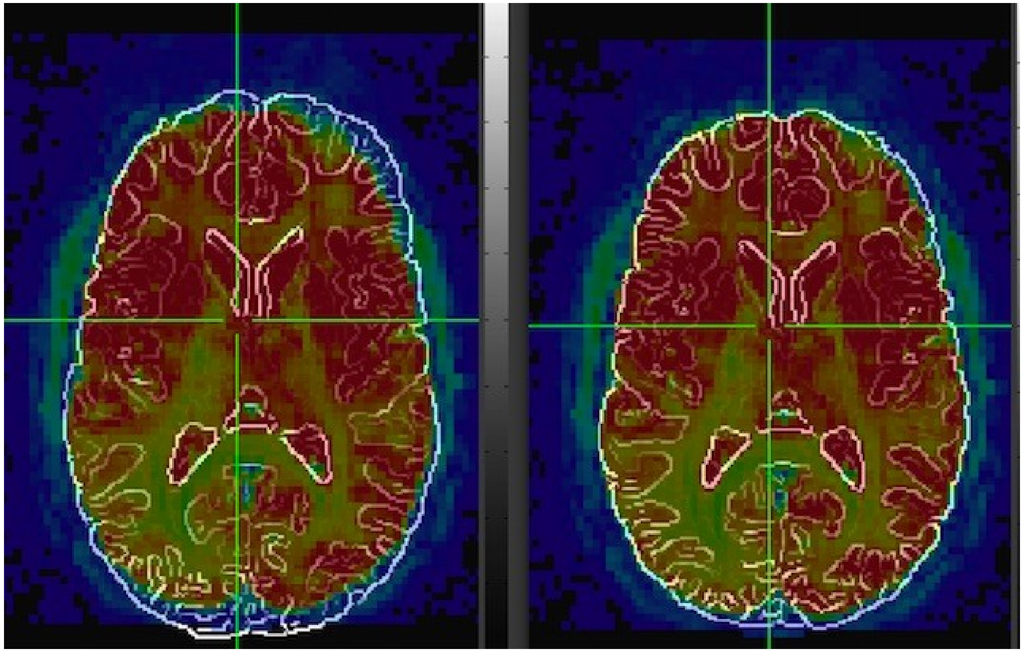
Data
courtesy of
Sam Torrisi,
NIMH

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
```

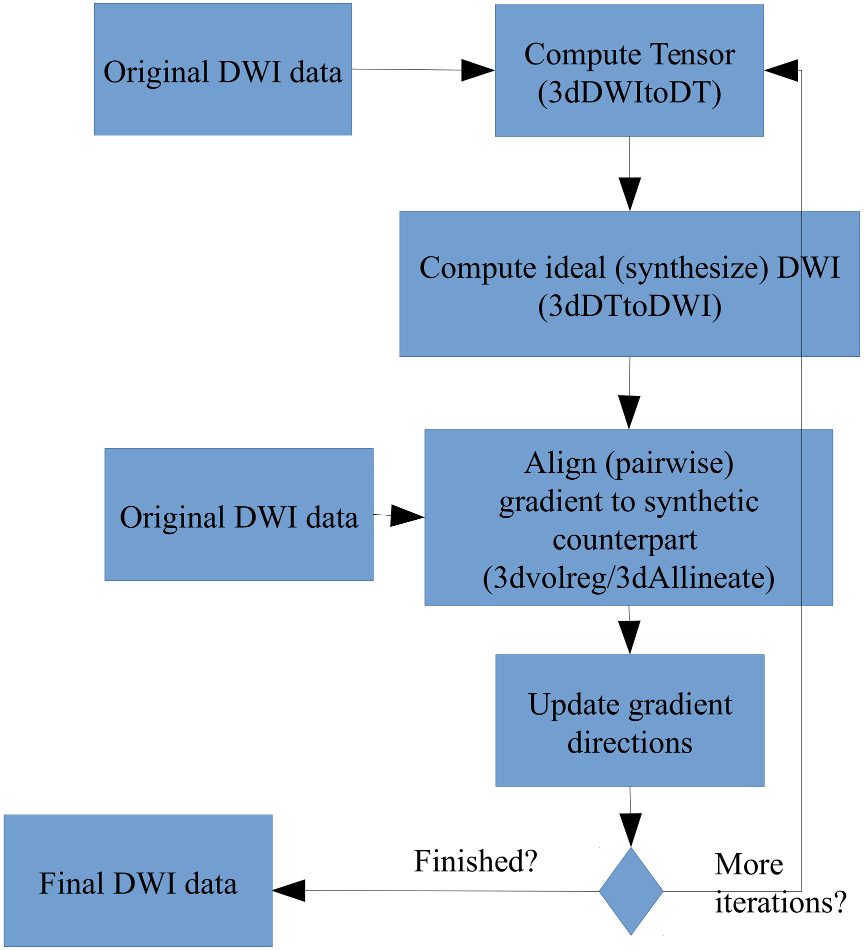
The output will include this warning if the data is flipped:

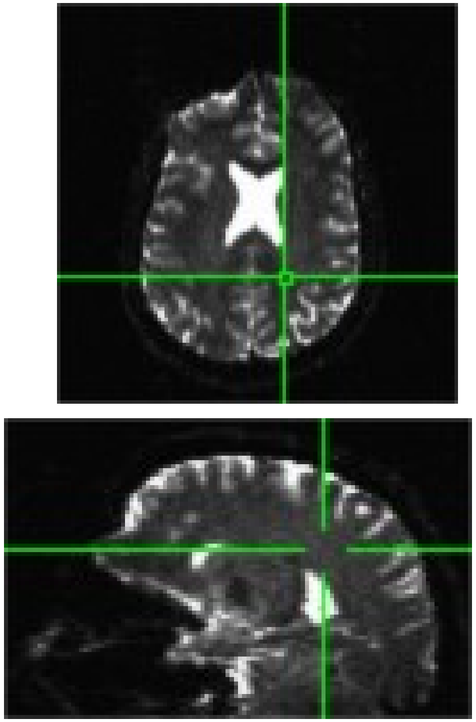
```
WARNING: ************ flipped data aligns better than original data
Check for left - right flipping in the GUI *************************
```

If everything is okay, this message appears instead:

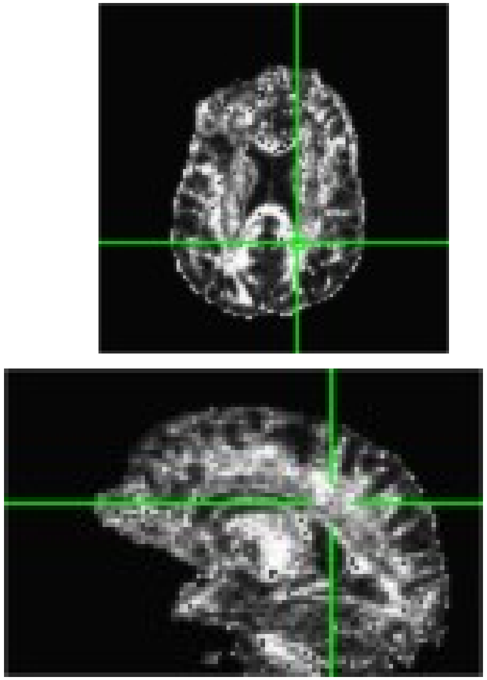
```
Data does not need flipping
```

DWI Motion Correction



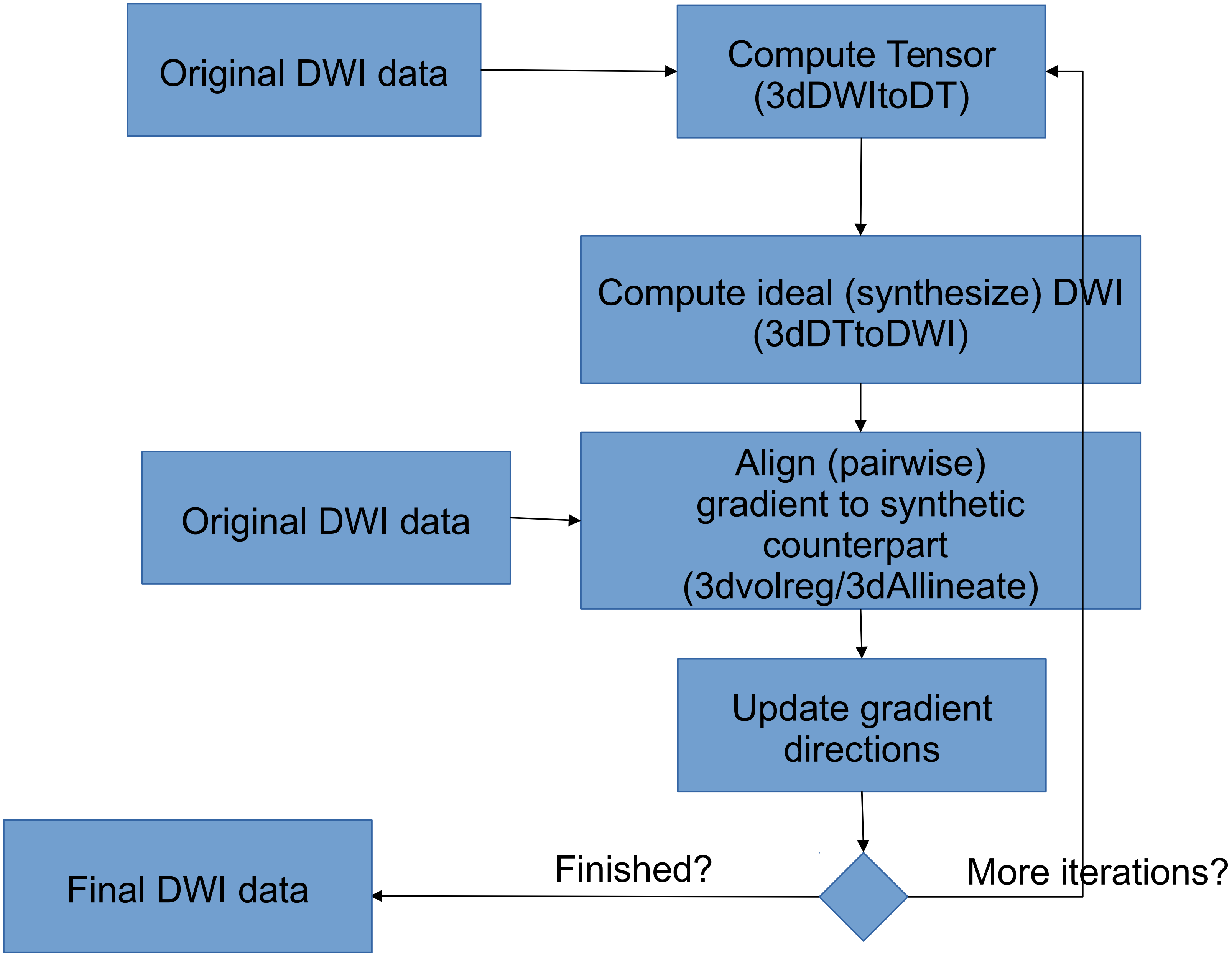


Original motion



FA maps with iteration

Method overview



Original DWI data

Compute Tensor
(3dDWItoDT)

Compute ideal (synthesize) DWI
(3dDTtoDWI)

Original DWI data

Align (pairwise)
gradient to synthetic
counterpart
(3dvolreg/3dAllineate)

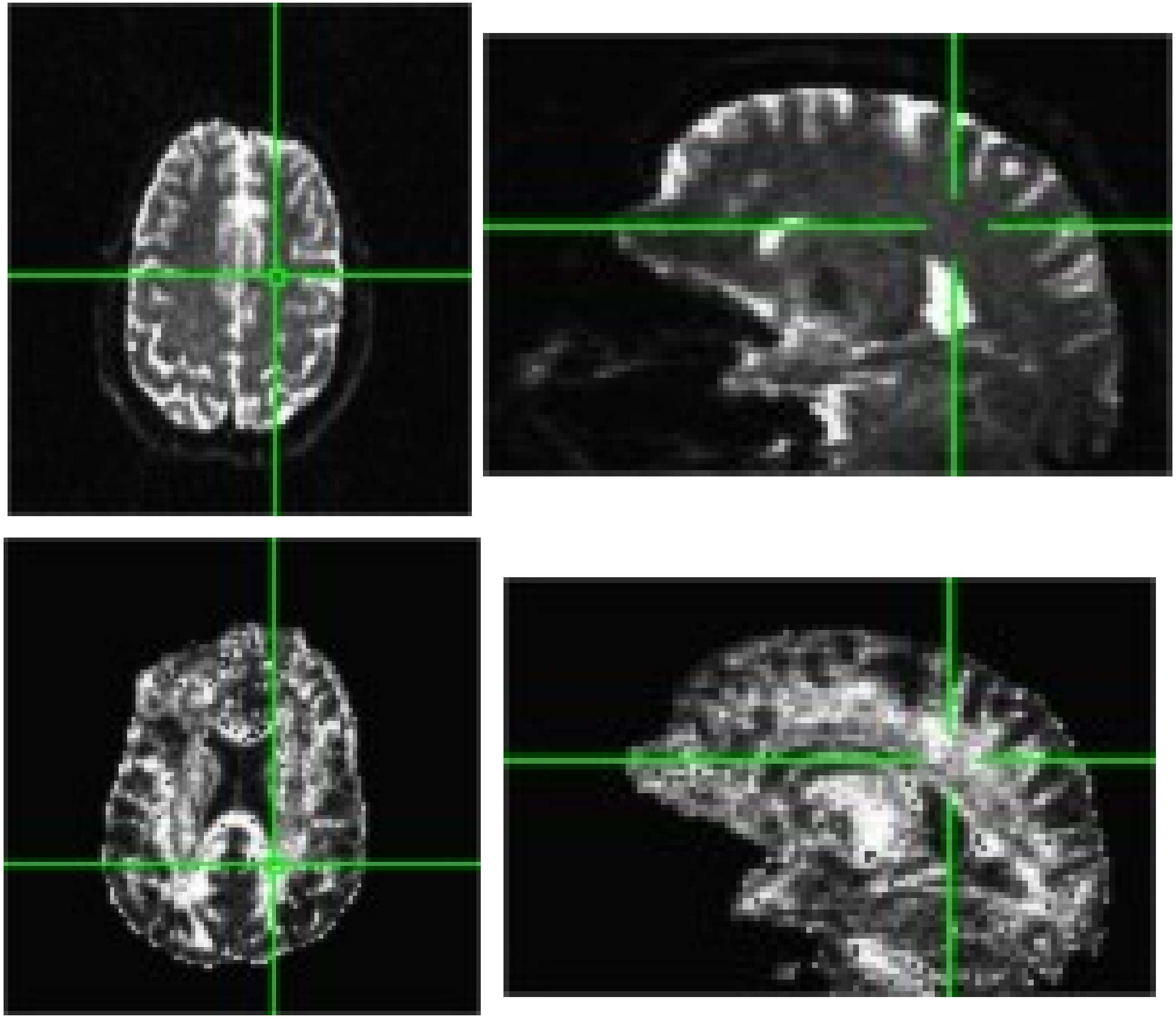
Update gradient
directions

Final DWI data

Finished?

More iterations?

DWI Motion Correction



ATLASES

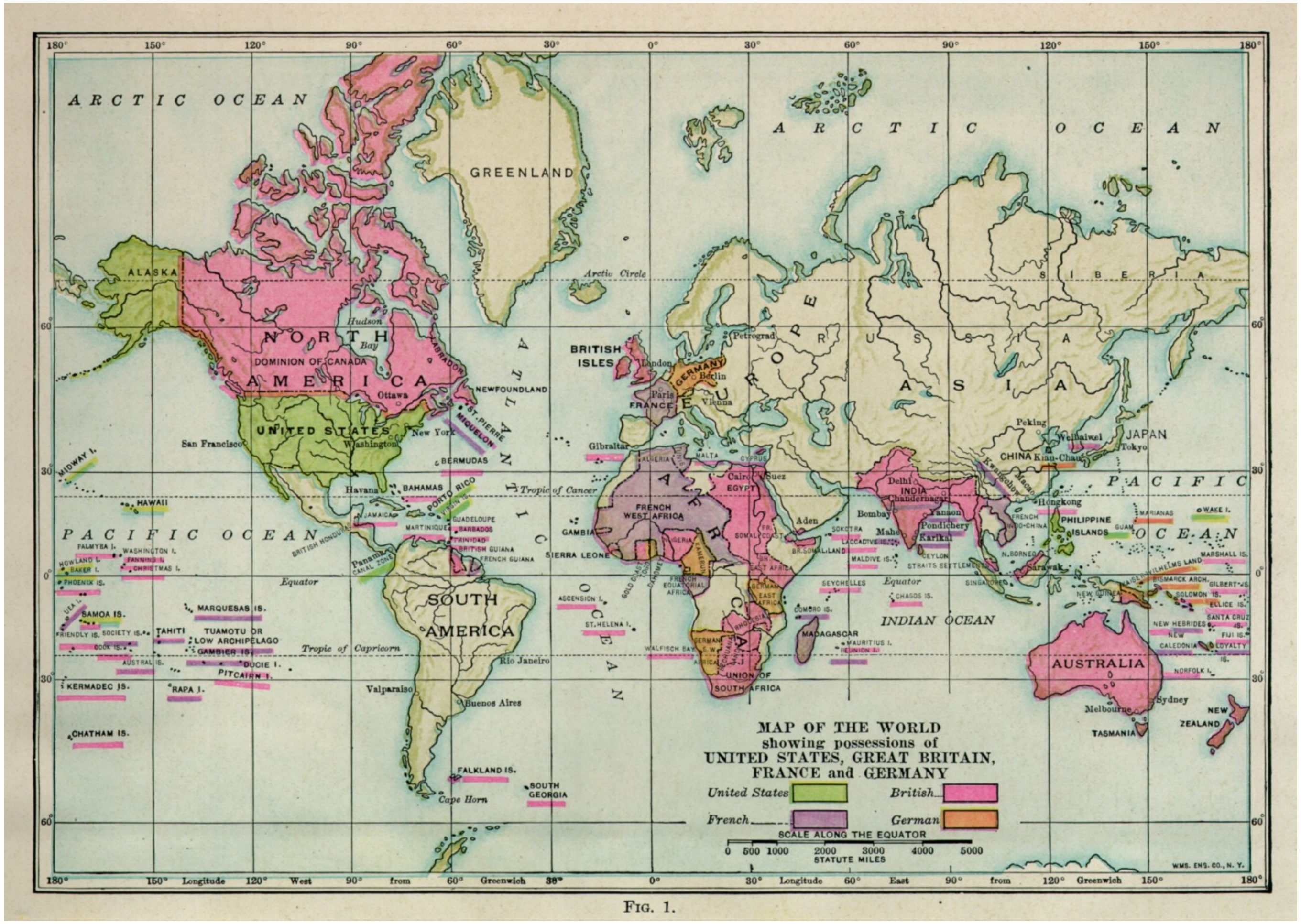
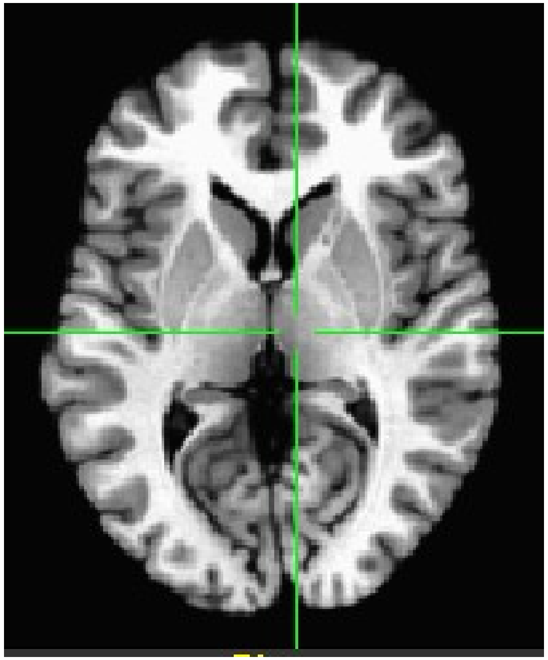


FIG. 1.

ATLAS DEFINITIONS

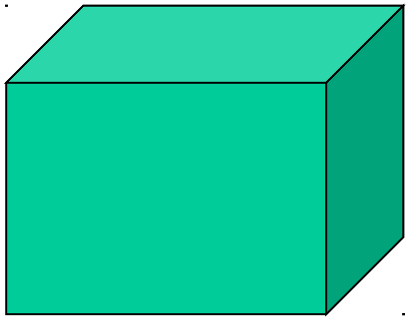
Template - a reference dataset used for matching shapes.
Examples: TT_N27+tlrc, MNI_EPI+tlrc, TT_ICBM452+tlrc.



TT_N27+tlrc

ATLAS DEFINITIONS

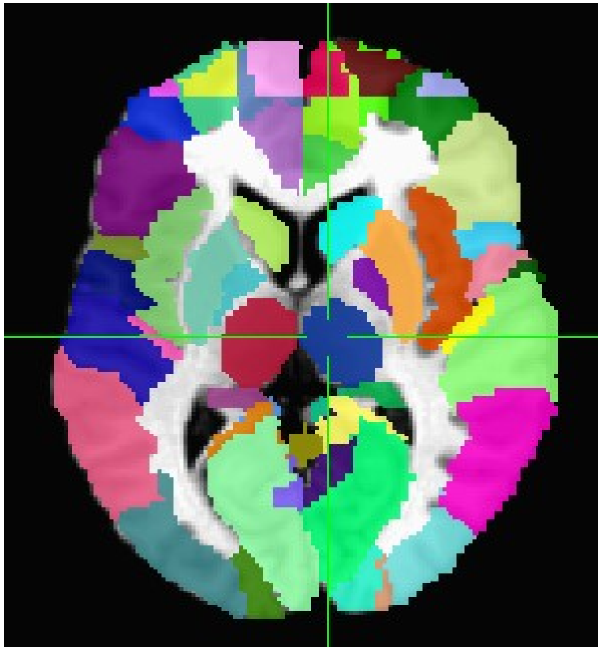
Template Space - x,y,z coordinate system shared by many datasets (the basic shoebox) Examples: TLRC (Talairach-Tourneaux), MNI, MNI_ANAT, ORIG.



ATLAS DEFINITIONS

Atlas - segmentation info.

Examples: TTatlas+tlrc, TT_N27_EZ_ML+tlrc, roidset+orig.



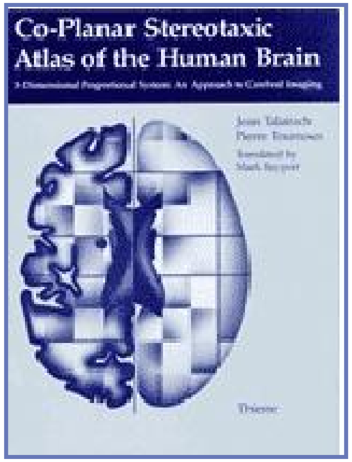
TT_N27_EZ_ML+tlrc

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 `to3d` 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:

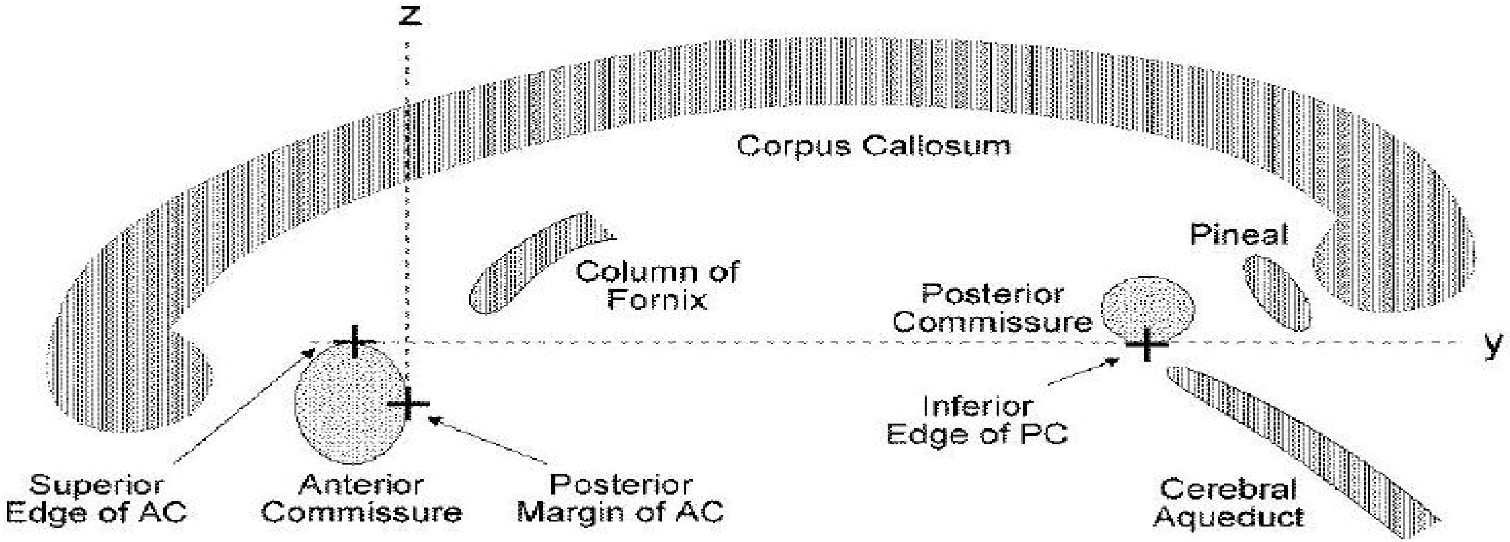
    `AC superior edge` = top middle of anterior commissure

    `AC posterior margin` = rear middle of anterior commissure

    `PC inferior edge` = bottom middle of posterior commissure

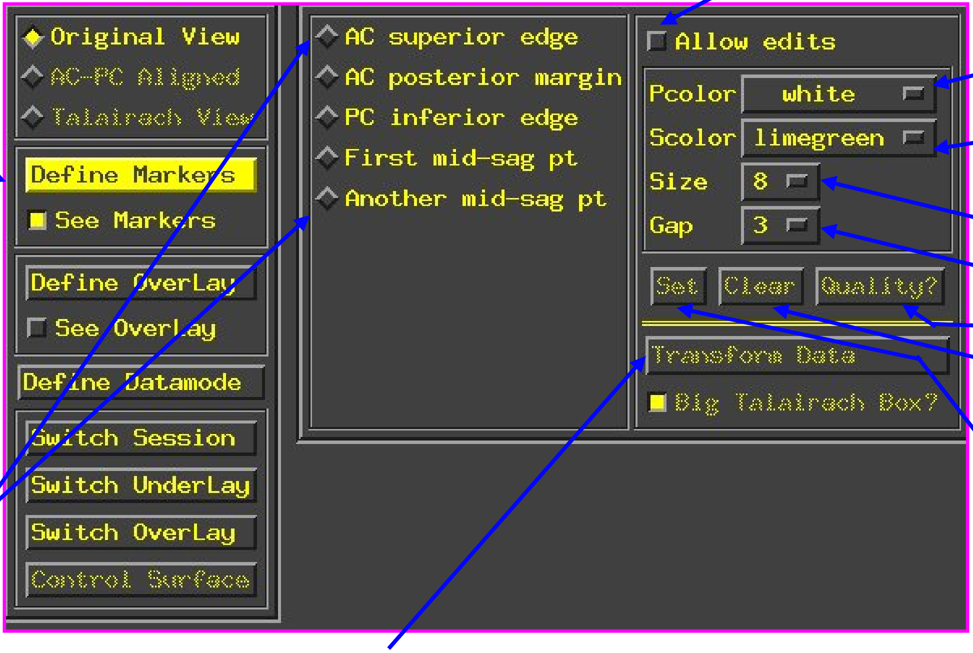
    `First mid-sag point` = some point in the mid-sagittal plane

    `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)



Press this IN to create or change markers

Click **Define Markers** to open the “markers” panel



Pcolor white

Scolor limegreen

Size 8

Gap 3

Color of “primary” (selected) marker

Color of “secondary” (not selected) markers

Size of markers (pixels)

Size of gap in markers

Clear (unset) primary marker

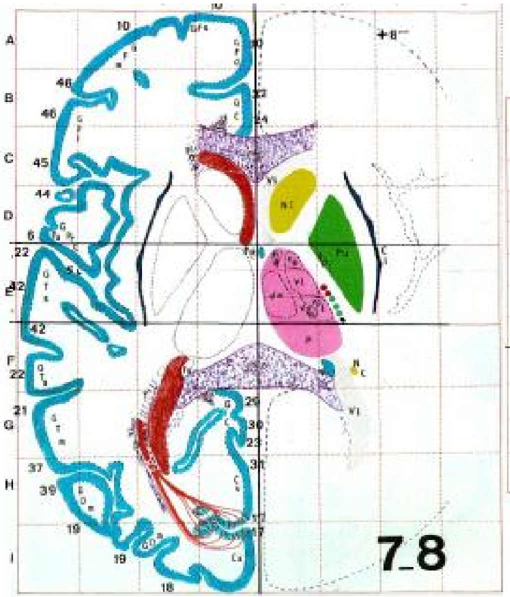
Set primary marker to current focus location

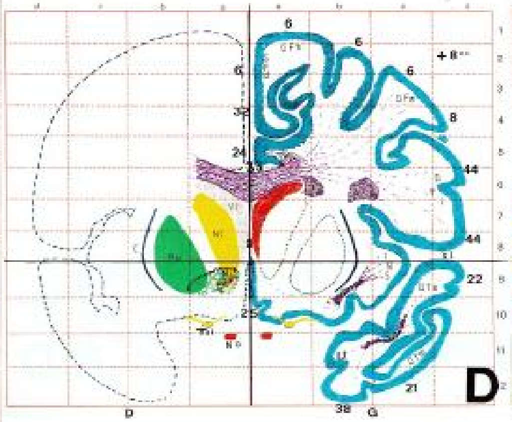
Select which marker you are editing

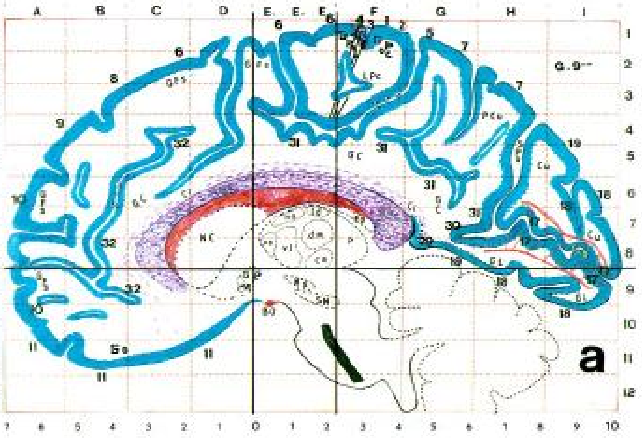
Carry out transformation to +acpc coordinates

Perform “quality” check on markers (after all 5 are set)

- **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)



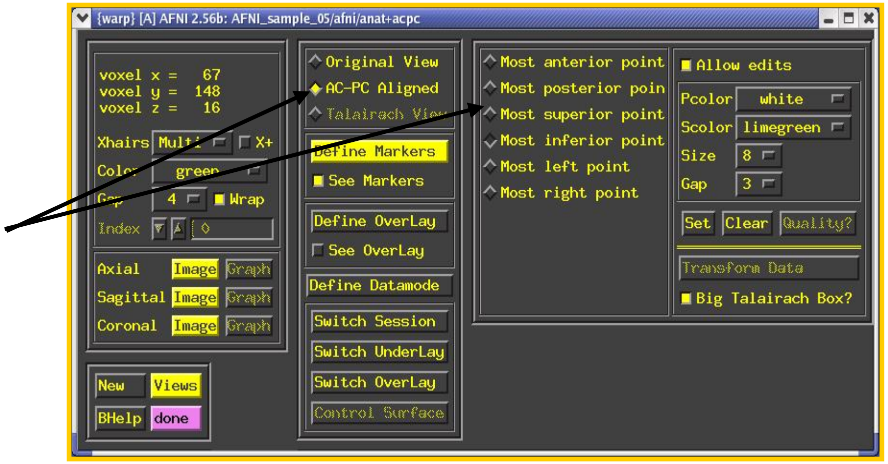




Most anterior to AC	70 mm
AC to PC	23 mm
PC to most posterior	79 mm
Most inferior to AC	42 mm
AC to most superior	74 mm
AC to left (or right)	68 mm

Length of cerebrum	172mm
Width of cerebrum	136mm
Height of cerebrum	116mm

- **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):



{warp} [A] AFNI 2.56b: AFNI_sample_05/afni/anat+acpc

voxel x = 67
voxel y = 148
voxel z = 16

Xhairs Multi
Color green
Gap 4
Index 0

Pcolor white
Scolor limegreen
Size 8
Gap 3

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

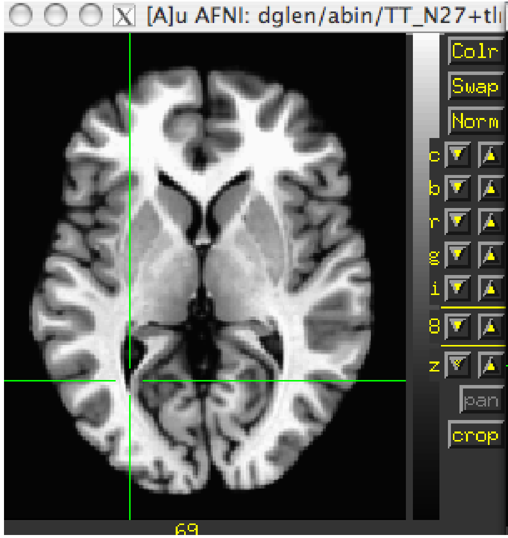
- Once all the markers are set, and the quality tests passed. Pressing **[Transform Data]** will write new ***header*** containing the Talairach transformations (see Appendix C for details)
  - Recall: With AFNI, spatial transformations are stored in the header of the output

Automatic Talairach Transformation with @auto_tlrc

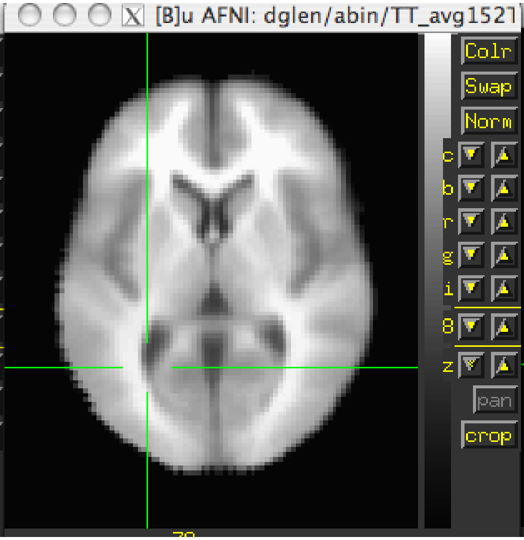
- Is manual selection of AC-PC and Talairach markers bringing you down? You can now perform a TLRC transform ***automatically*** using an AFNI script called **`@auto_tlrc`**.
  - Differences from Manual Transformation:
    - Instead of setting ac-pc landmarks and volume boundaries by hand, the anatomical volume is warped (using 12-parameter affine transform) to a template volume in TLRC space.
    - Anterior Commisure (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 (l*ink*).
    - 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

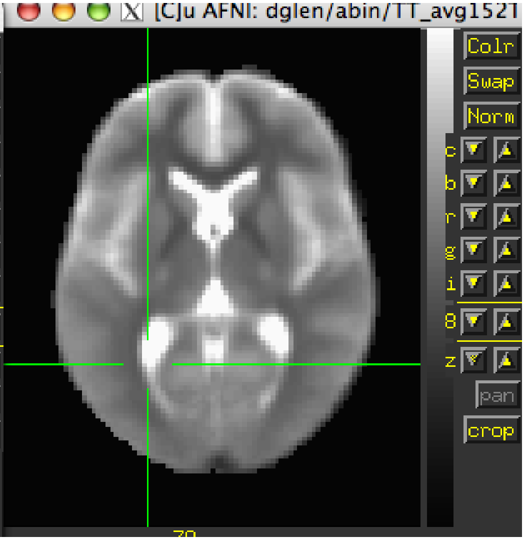
Templates included with AFNI



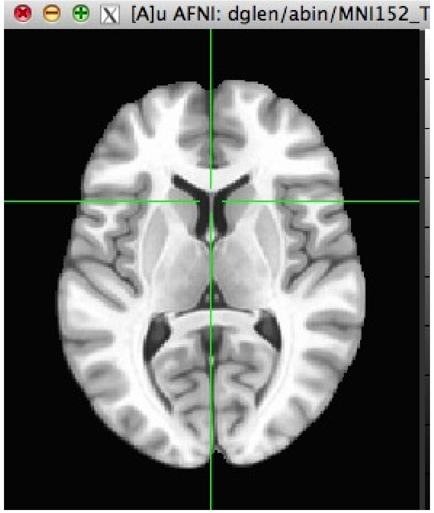
TT_N27



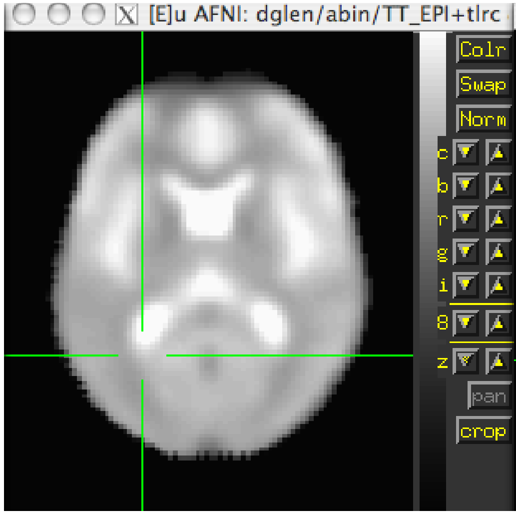
TT_avg152T1



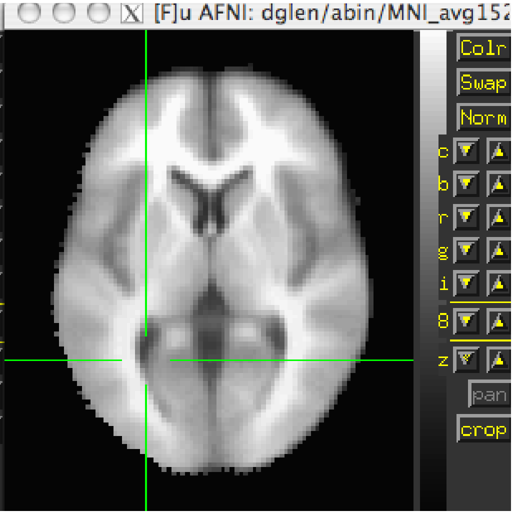
TT_avg152T2



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:

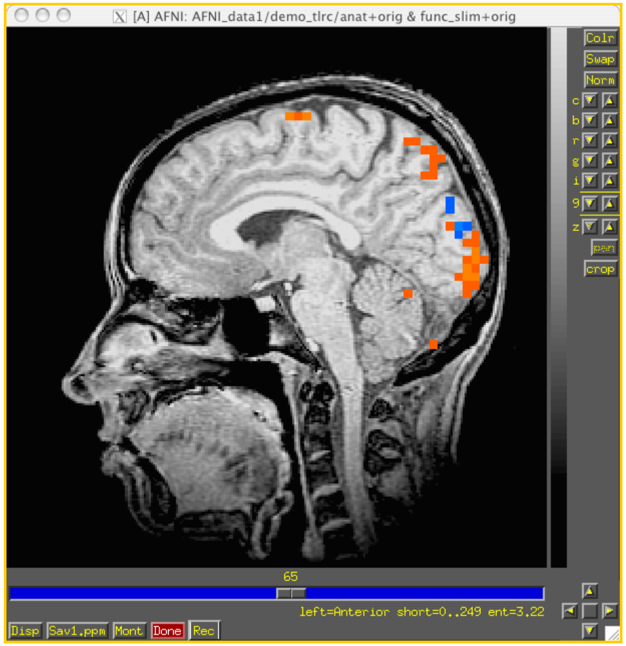
```
@auto_tlrc                          \
 -apar anat+tlrc                 \
 -input func_slim+orig           \
 -suffix NONE                    \
 -dxyz  2
```

Output:
`func_slim+tlrc`

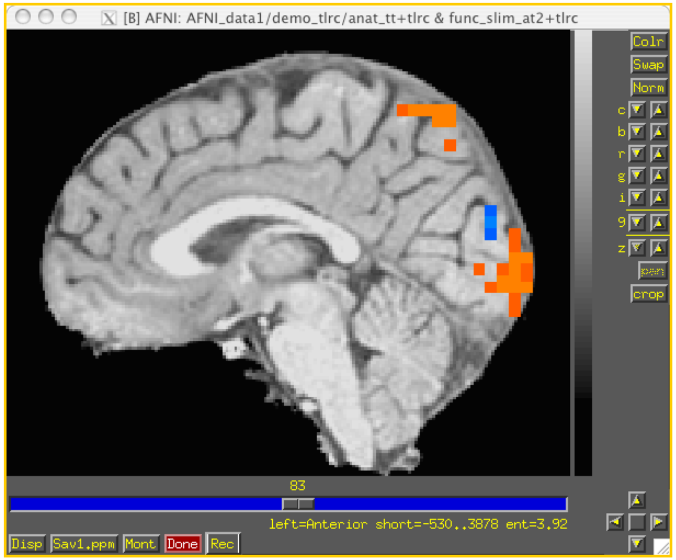
- You could also use the **icbm452** or the mni's **avg152T1** template instead of **N27** or any other template you like (see @auto_tlrc -help for a few good words on templates)

@auto_tlrc Results are Comparable to Manual TLRC:

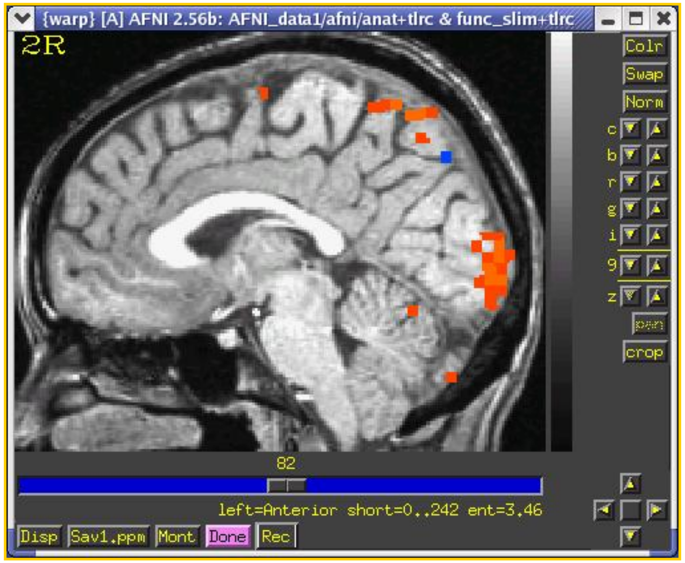
Original



@auto_tlrc



Manual



Standard Spaces

Why use a standard template space?

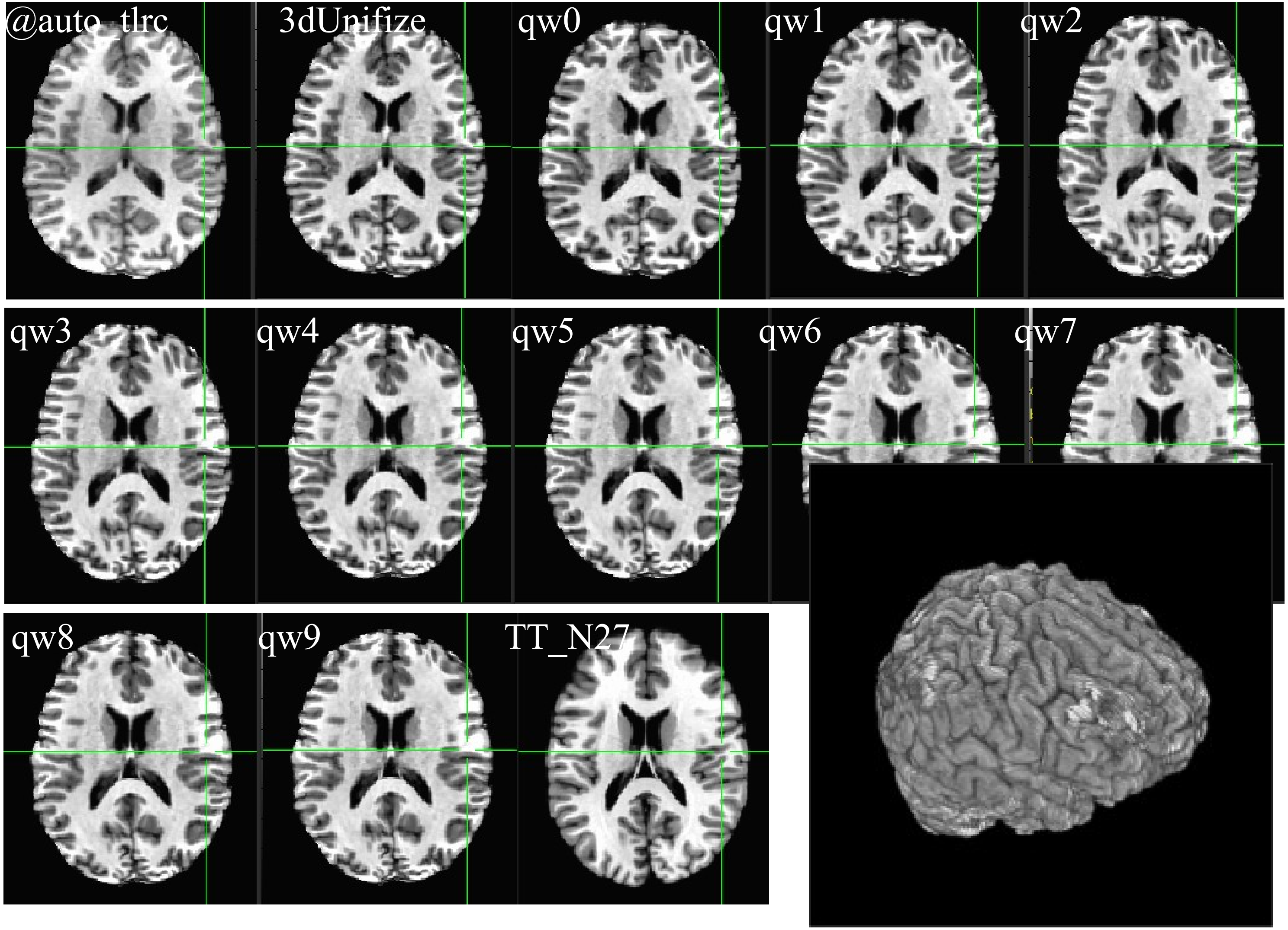
- Compare across subjects and groups easily for every voxel in the brain
- Standardize coordinates with others
- Know where a voxel is automatically from an atlas
- Mostly automated and no specific ROI drawing required

Why <u>not</u> 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 →



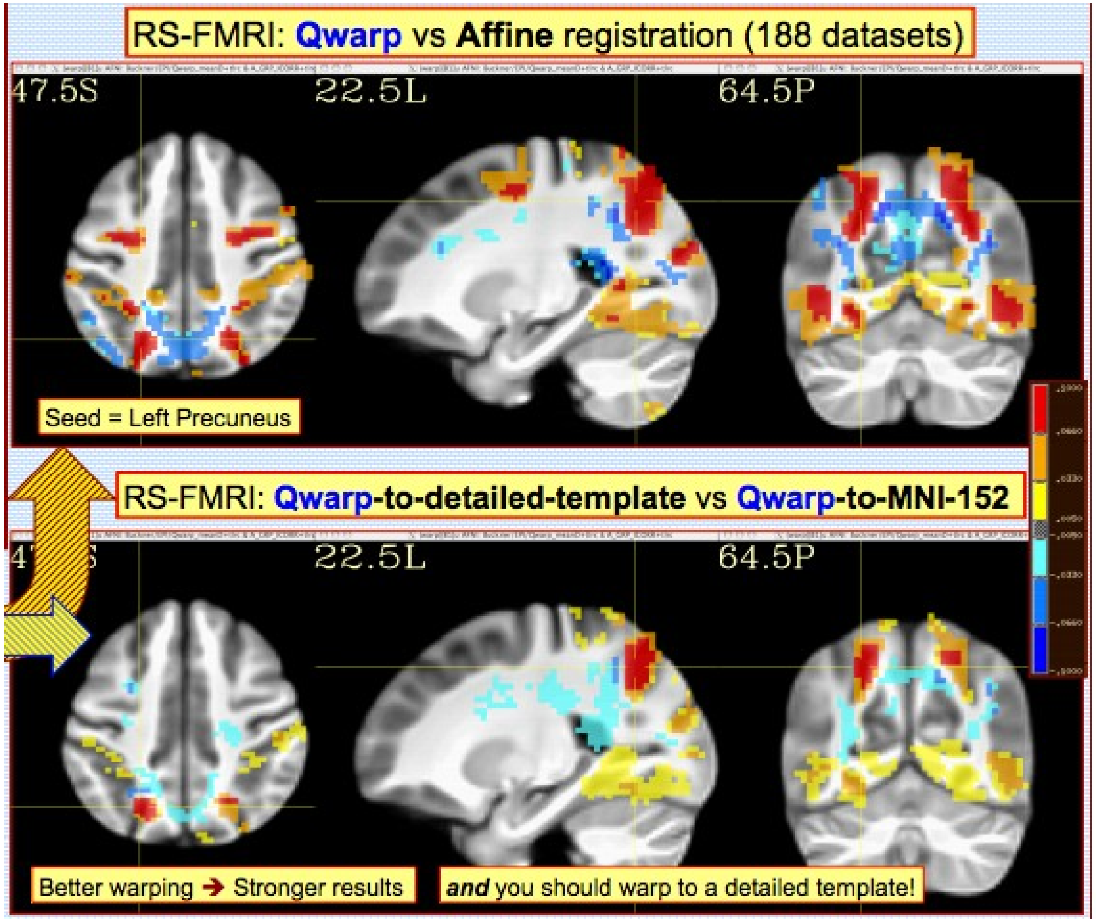
Nonlinear alignment

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



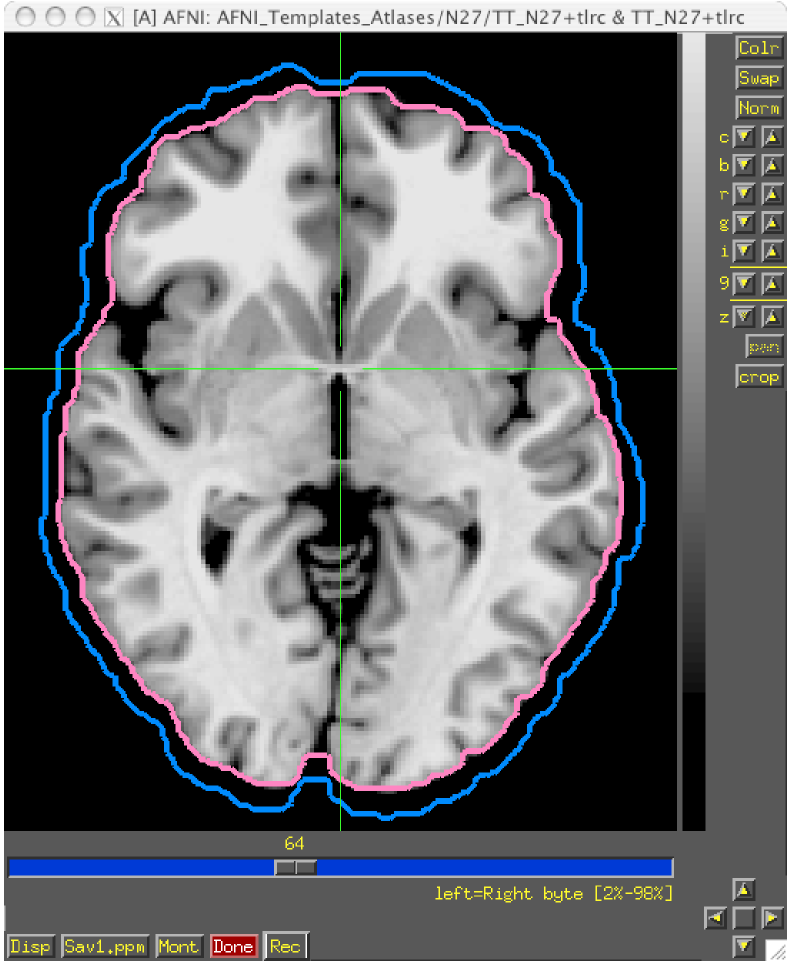
Comparing data

- 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

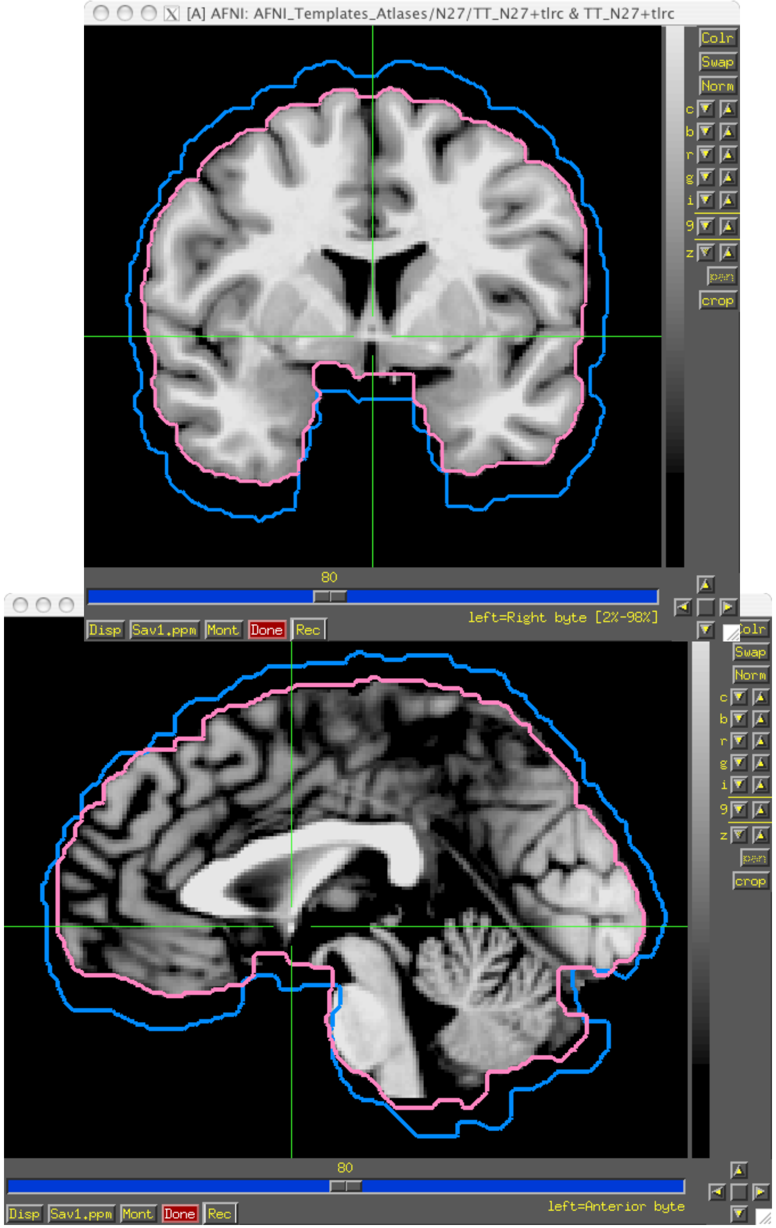
Choosing a template

- 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_Qwarpar

Atlas/Template Spaces Differ In Size

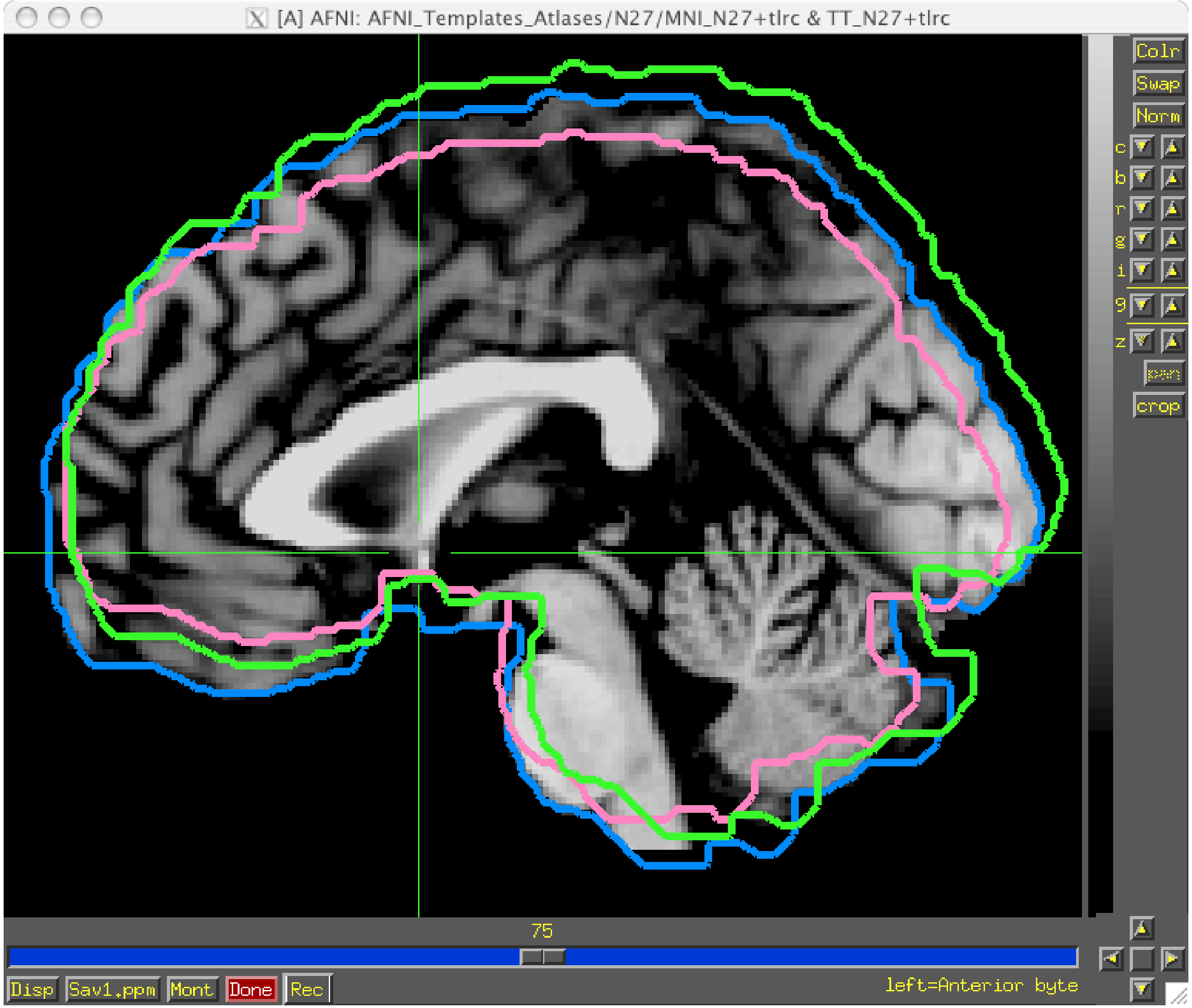


MNI is larger than TLRC space.



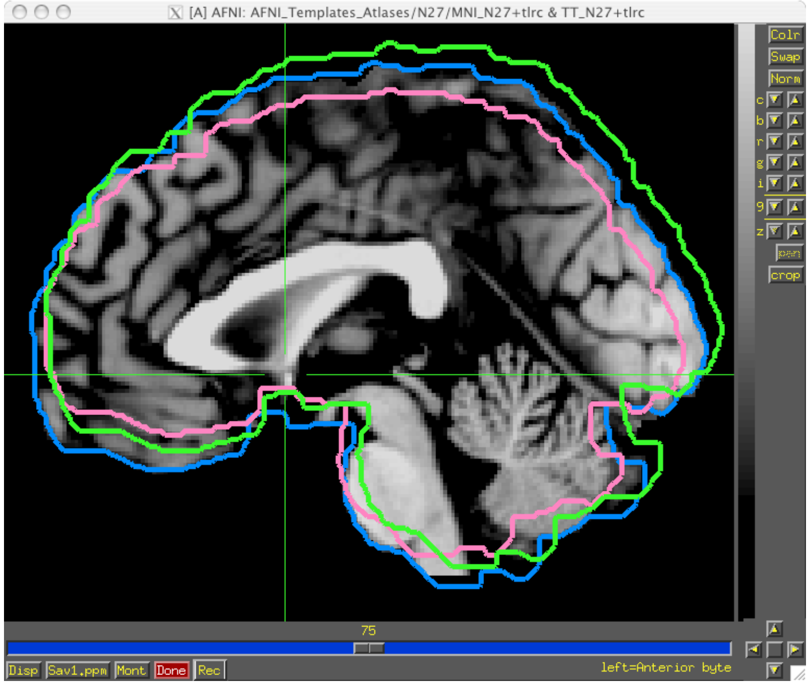
Atlas/Template Spaces Differ In Origin

TLRC
MNI
MNI-Anat.



From Space To Space

TLRC
MNI
MNI-Anat.



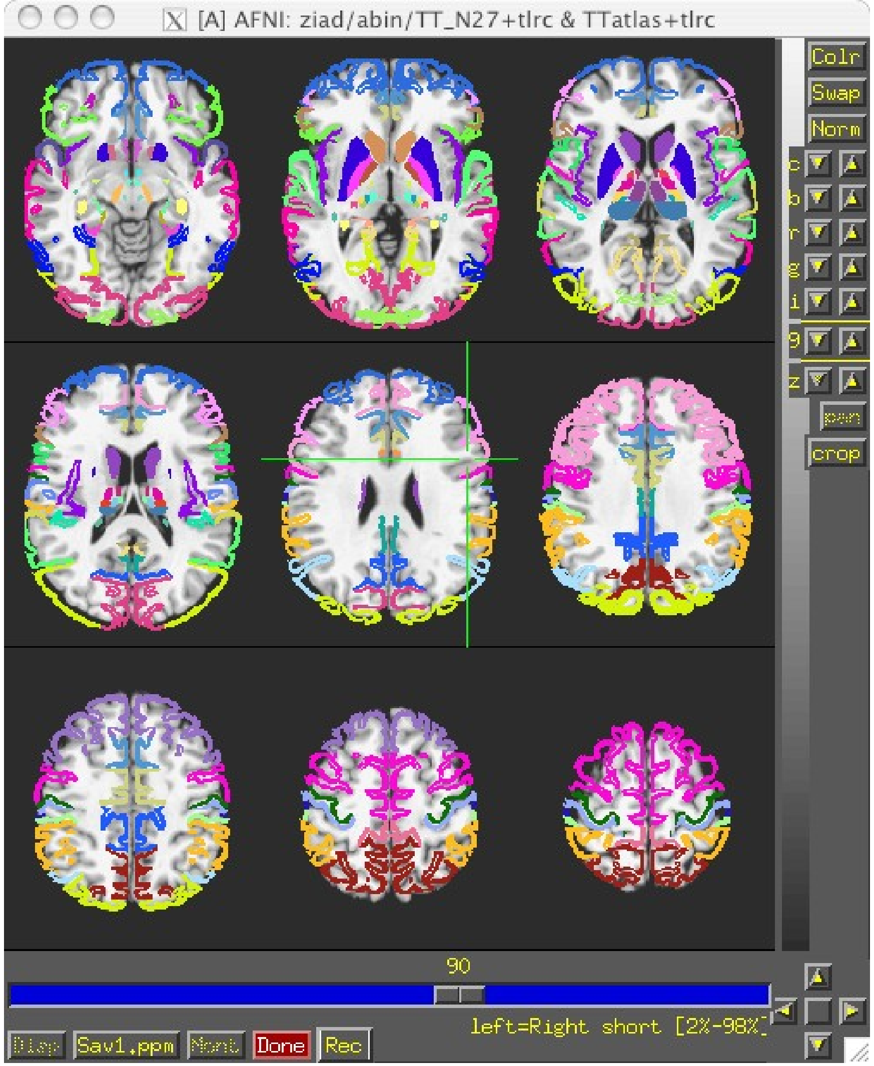
- Going between TLRC and MNI:
  - ◇ Approximate equation
    - ➥ used by **`whereami`** and **`3dWarp`**
  - ◇ Manual TLRC transformation of MNI template to TLRC space
    - ➥ used by **`whereami`** (as precursor to MNI Anat.), based on N27 template
  - ◇ Multiple space coordinates reported in whereami 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.

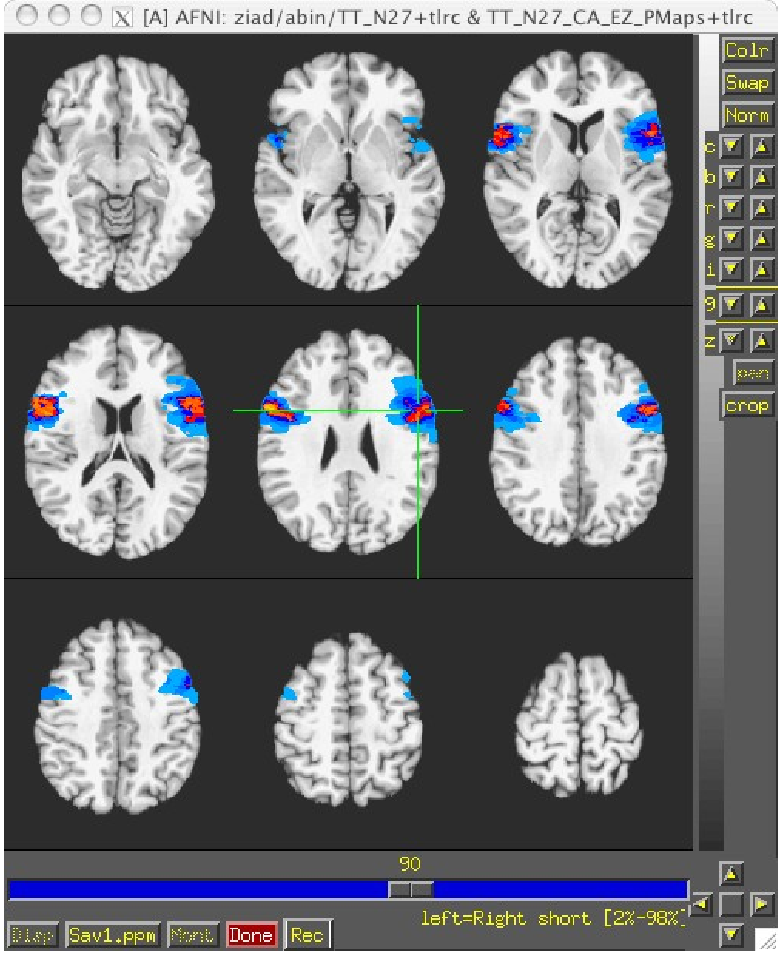
Atlases Distributed With AFNI
TT_Daemon

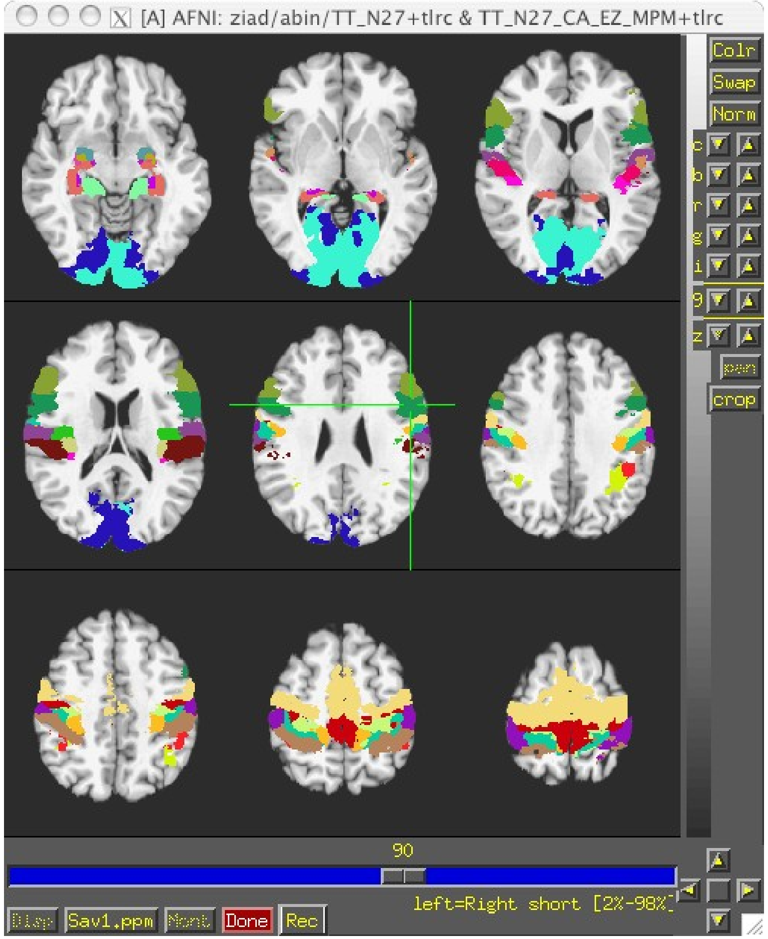
- TT_Daemon : Created by tracing Talairach and Tournoux brain illustrations.
  - ◇ Generously contributed by Jack Lancaster and Peter Fox of RIC UTHSCSA)



Atlases Distributed With AFNI
Anatomy Toolbox: Prob. Maps, Max. Prob. Maps

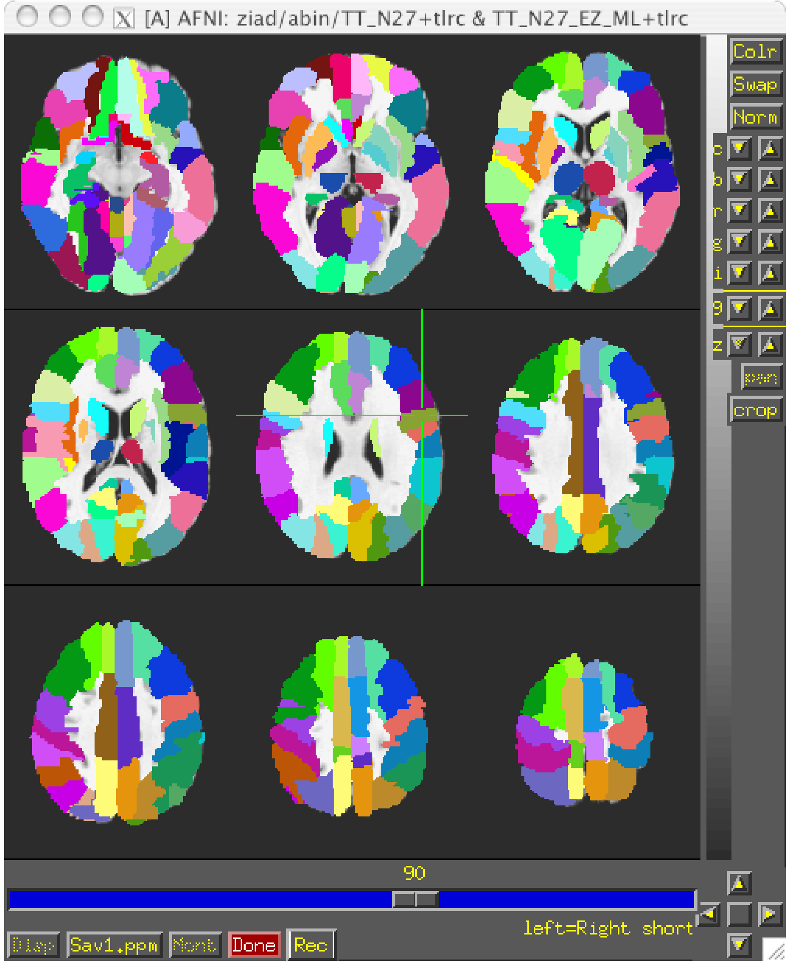
- CA_N27_MPM, CA_N27_ML, CA_N27_PM: Anatomy Toolbox's atlases with some created from cytoarchitectonic studies of 10 human post-mortem brains
  - Generously contributed by Simon Eickhoff, Katrin Amunts and Karl Zilles of IME, Julich, Germany

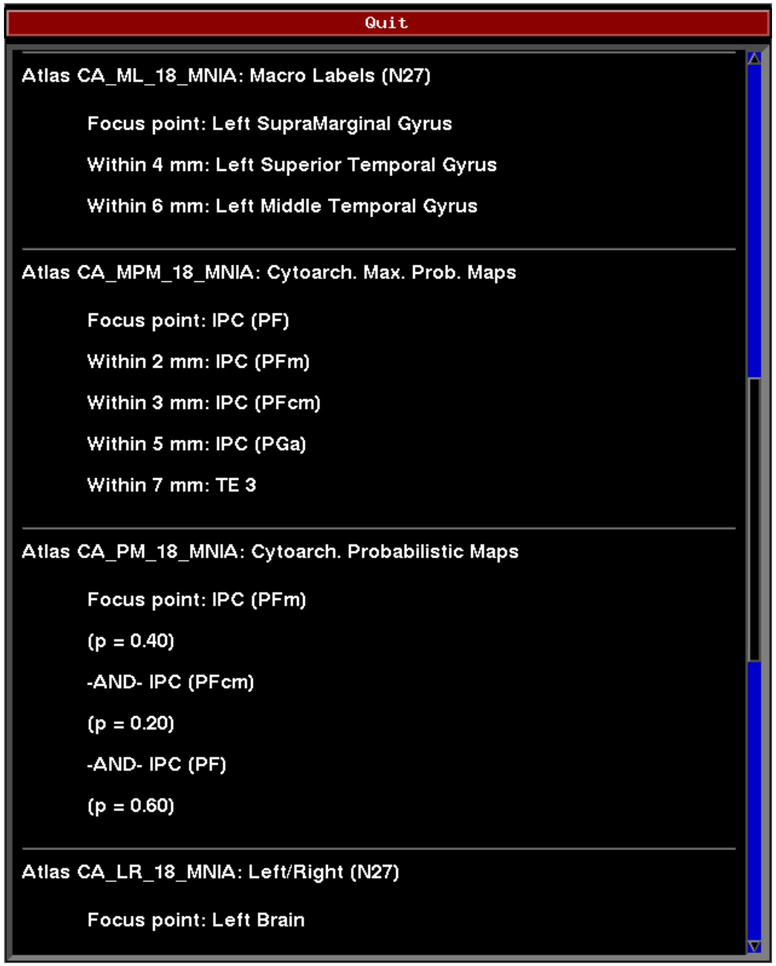




Atlases Distributed With AFNI:
Anatomy Toolbox: MacroLabels

- 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





Atlas CA_ML_18_MNIA: Macro Labels (N27)

Focus point: Left SupraMarginal Gyrus
Within 4 mm: Left Superior Temporal Gyrus
Within 6 mm: Left Middle Temporal Gyrus

Atlas CA_MPM_18_MNIA: Cytoarch. Max. Prob. Maps

Focus point: IPC (PF)
Within 2 mm: IPC (PFm)
Within 3 mm: IPC (PFcm)
Within 5 mm: IPC (PGa)
Within 7 mm: TE 3

Atlas CA_PM_18_MNIA: Cytoarch. Probabilistic Maps

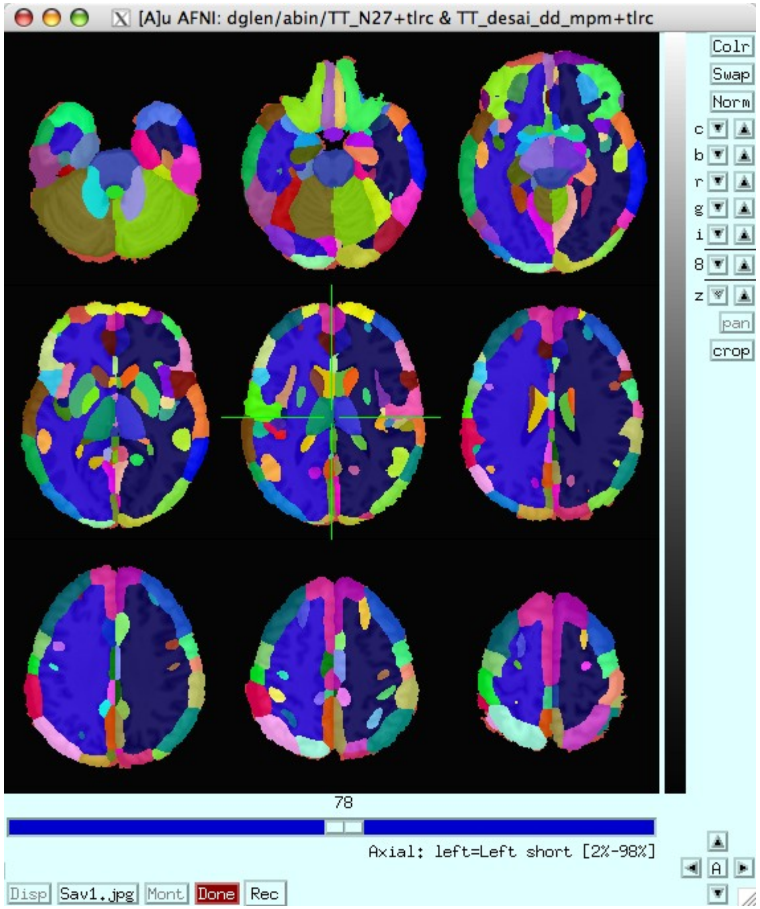
Focus point: IPC (PFm)
(p = 0.40)
-AND- IPC (PFcm)
(p = 0.20)
-AND- IPC (PF)
(p = 0.60)

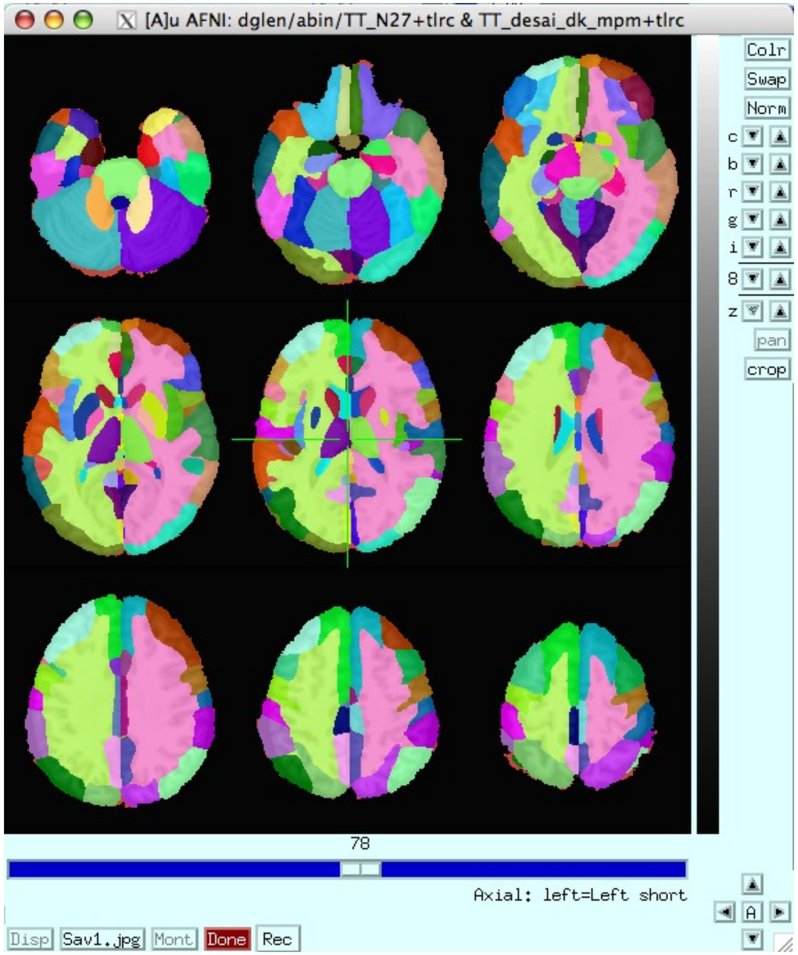
Atlas CA_LR_18_MNIA: Left/Right (N27)

Focus point: Left Brain

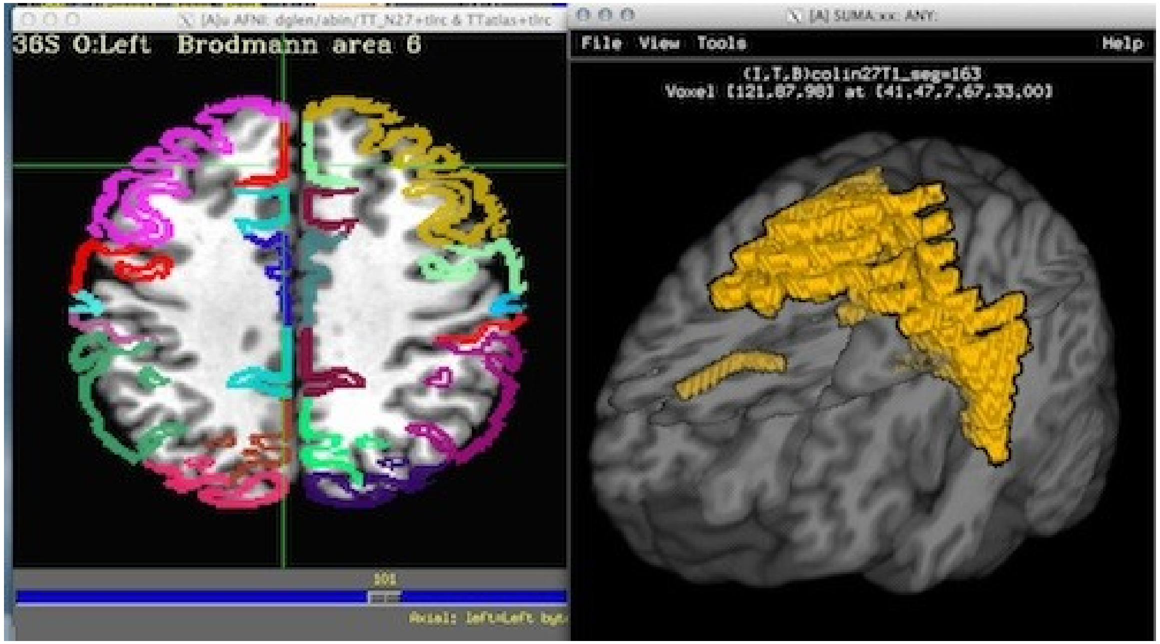
Atlases Distributed With AFNI: Desai PMaps and MPMs

- Atlases generated with typical AFNI pipeline using @auto_tlrc and FreeSurfer segmentation across multiple subjects





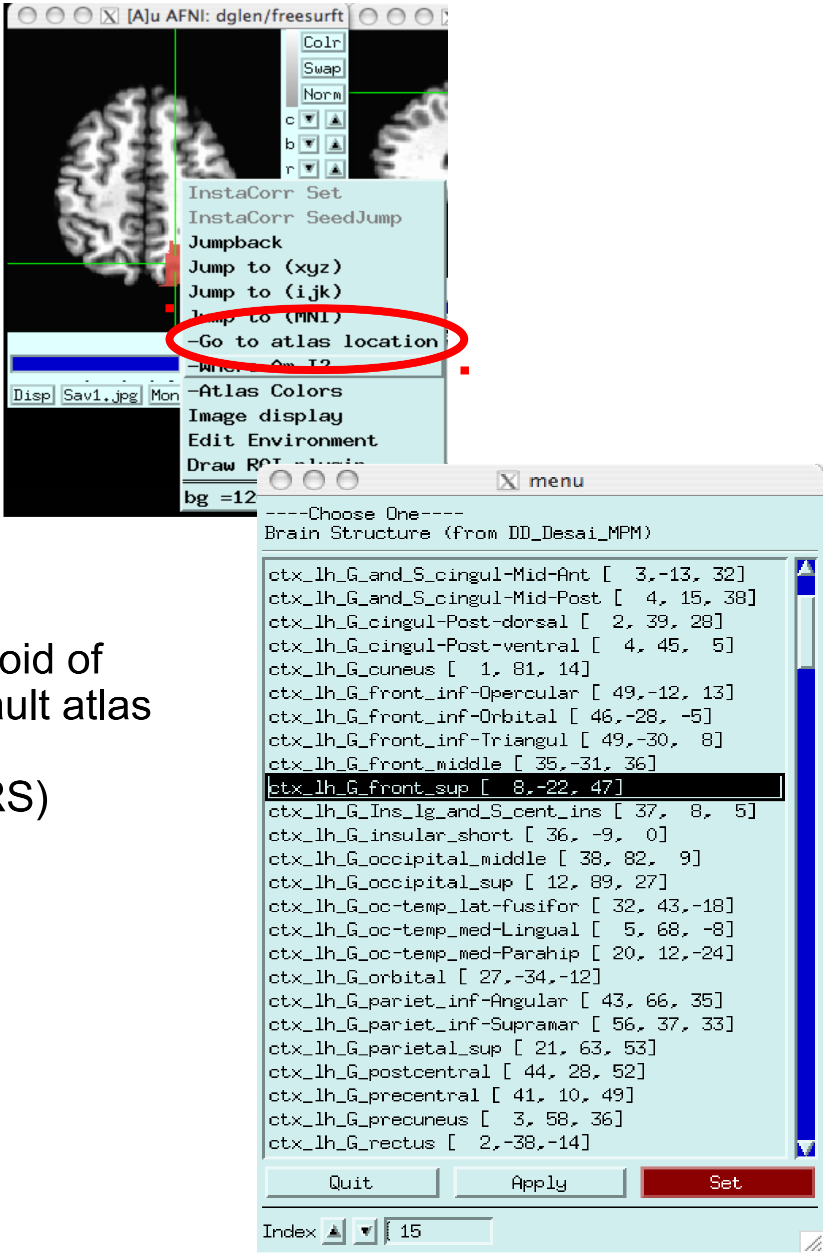
Talairach Daemon (TT_Daemon) problem



```
36S O:Left  Brodmann area 6
```

```
(I,T,B)colin27T1_seg=163
Voxel (121,87,98) at (41.47,7.67,33.00)
```

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



```
----Choose One----
Brain Structure (from DD_Desai_MPM)
ctx_lh_G_and_S_cingul-Mid-Ant [  3,-13, 32]
ctx_lh_G_and_S_cingul-Mid-Post [  4, 15, 38]
ctx_lh_G_cingul-Post-dorsal [  2, 39, 28]
ctx_lh_G_cingul-Post-ventral [  4, 45,  5]
ctx_lh_G_cuneus [  1, 81, 14]
ctx_lh_G_front_inf-Opercular [ 49,-12, 13]
ctx_lh_G_front_inf-Orbital [ 46,-28, -5]
ctx_lh_G_front_inf-Triangul [ 49,-30,  8]
ctx_lh_G_front_middle [ 35,-31, 36]
ctx_lh_G_front_sup [  8,-22, 47]
ctx_lh_G_Ins_lg_and_S_cent_ins [ 37,  8,  5]
ctx_lh_G_insular_short [ 36, -9,  0]
ctx_lh_G_occipital_middle [ 38, 82,  9]
ctx_lh_G_occipital_sup [ 12, 89, 27]
ctx_lh_G_oc-temp_lat-fusifor [ 32, 43,-18]
ctx_lh_G_oc-temp_med-Lingual [  5, 68, -8]
ctx_lh_G_oc-temp_med-Parahip [ 20, 12,-24]
ctx_lh_G_orbital [ 27,-34,-12]
ctx_lh_G_pariet_inf-Angular [ 43, 66, 35]
ctx_lh_G_pariet_inf-Supramar [ 56, 37, 33]
ctx_lh_G_parietal_sup [ 21, 63, 53]
ctx_lh_G_postcentral [ 44, 28, 52]
ctx_lh_G_precentral [ 41, 10, 49]
ctx_lh_G_precuneus [  3, 58, 36]
ctx_lh_G_rectus [  2,-38,-14]
```

◇ **[Go to Atlas Location]**

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

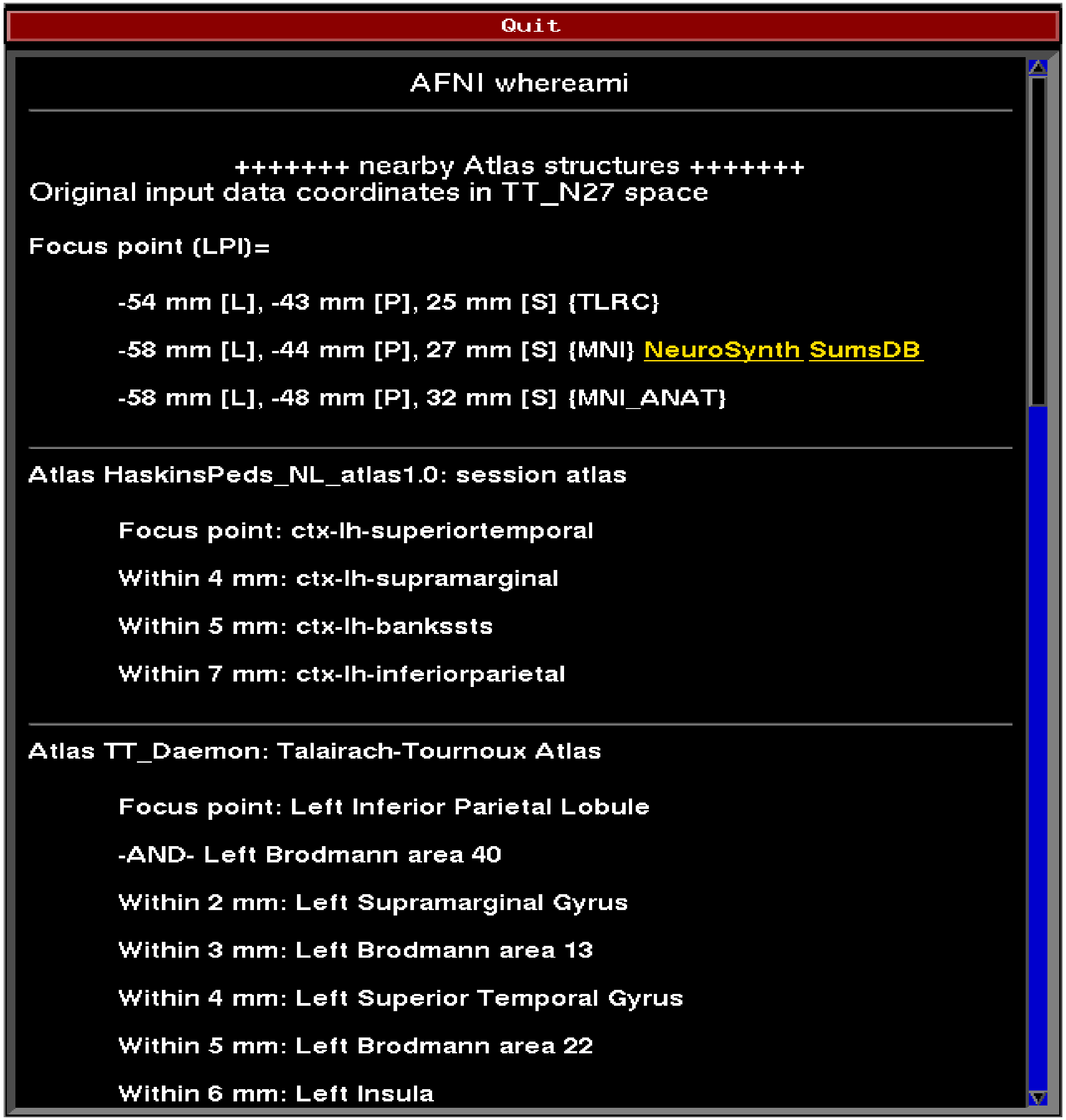
- [Where am I?]

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`

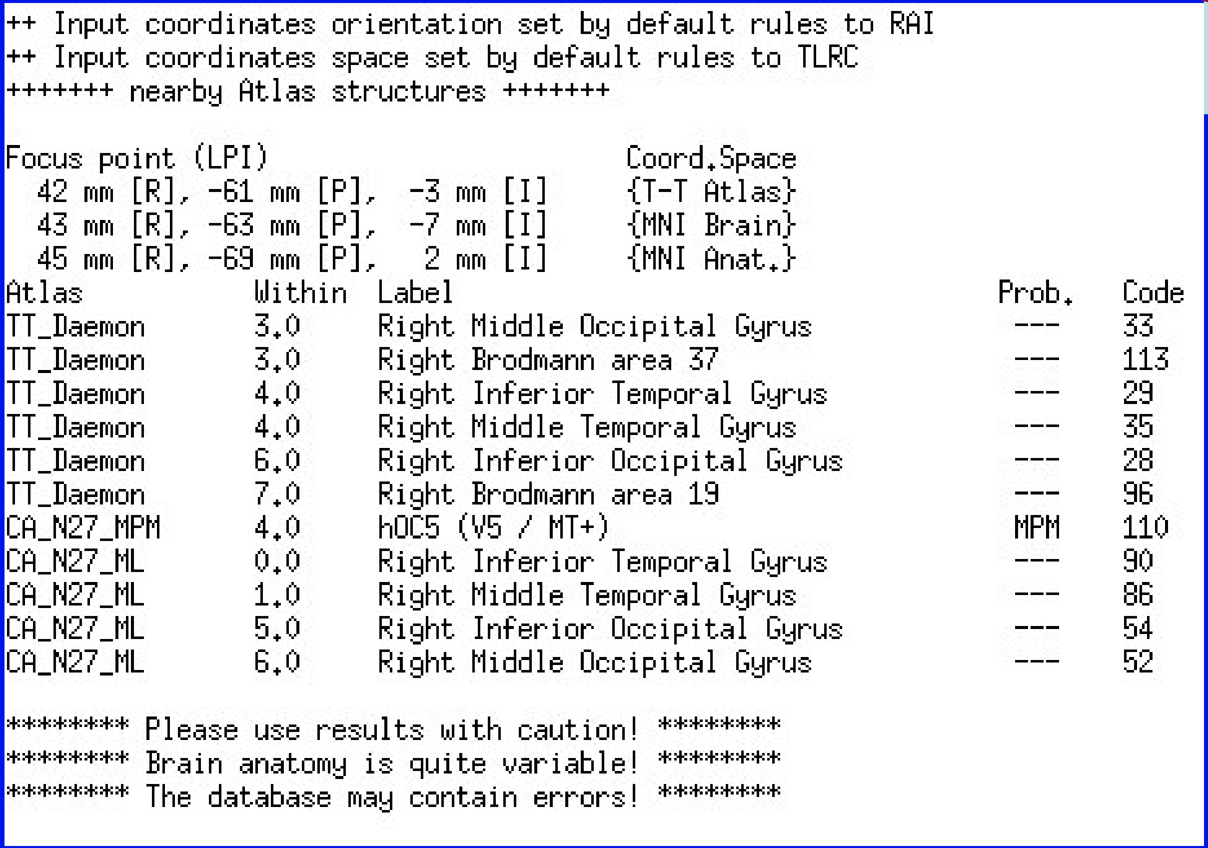


```
AFNI whereami

+++++++ nearby Atlas structures +++++++
Original input data coordinates in TT_N27 space

Focus point (LPI)=

   -54 mm [L], -43 mm [P], 25 mm [S] {TLRC}

   -58 mm [L], -44 mm [P], 27 mm [S] {MNI} NeuroSynth SumsDB

   -58 mm [L], -48 mm [P], 32 mm [S] {MNI_ANAT}

Atlas HaskinsPeds_NL_atlas1.0: session atlas

   Focus point: ctx-lh-superiortemporal

   Within 4 mm: ctx-lh-supramarginal

   Within 5 mm: ctx-lh-bankssts

   Within 7 mm: ctx-lh-inferiorparietal

Atlas TT_Daemon: Talairach-Tournoux Atlas

   Focus point: Left Inferior Parietal Lobule

   -AND- Left Brodmann area 40

   Within 2 mm: Left Supramarginal Gyrus

   Within 3 mm: Left Brodmann area 13

   Within 4 mm: Left Superior Temporal Gyrus

   Within 5 mm: Left Brodmann area 22

   Within 6 mm: Left Insula
```

- **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 -1clip 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



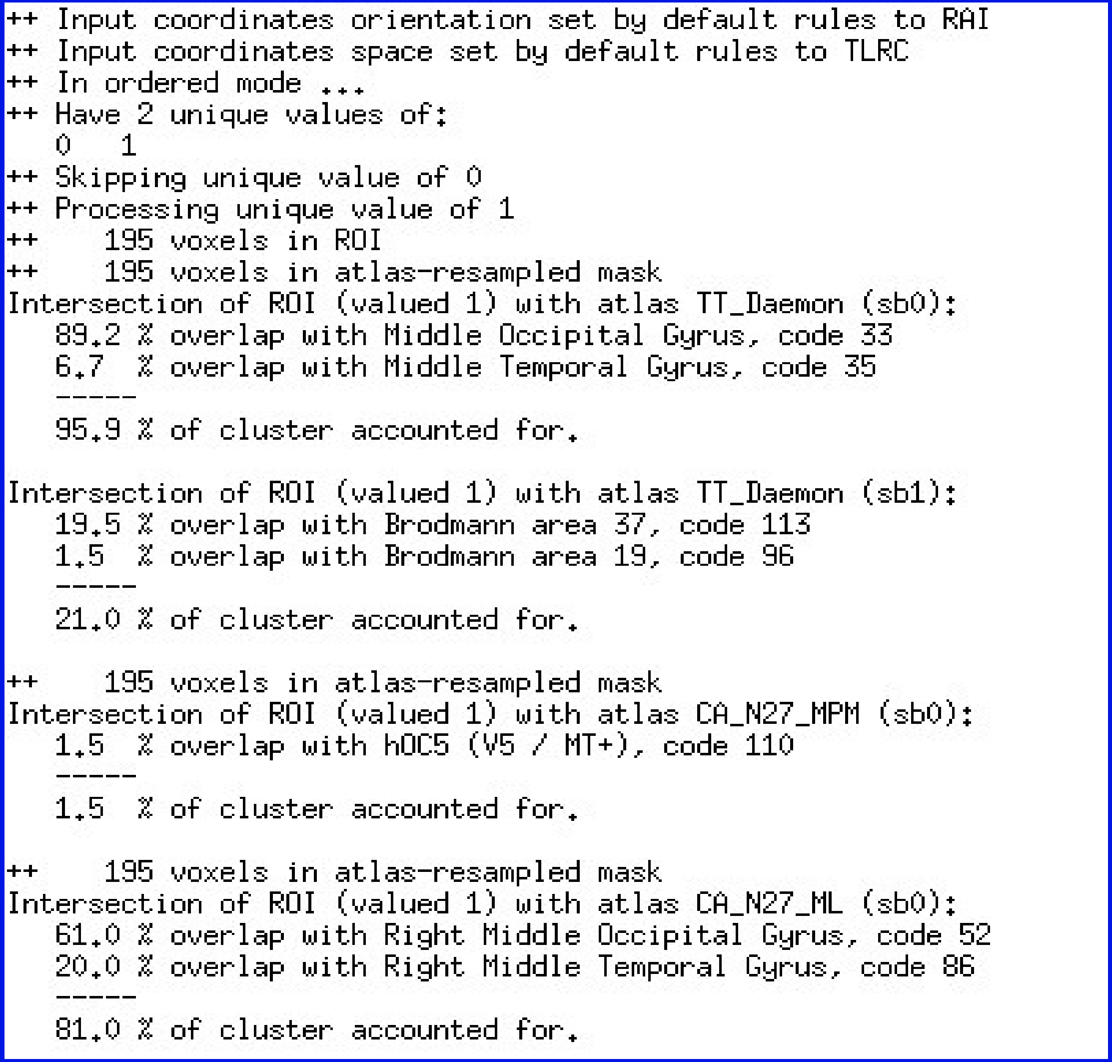
```
++ Input coordinates orientation set by default rules to RAI
++ Input coordinates space set by default rules to TLRC
+++++++ nearby Atlas structures +++++++

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! ********
```

etc…

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)

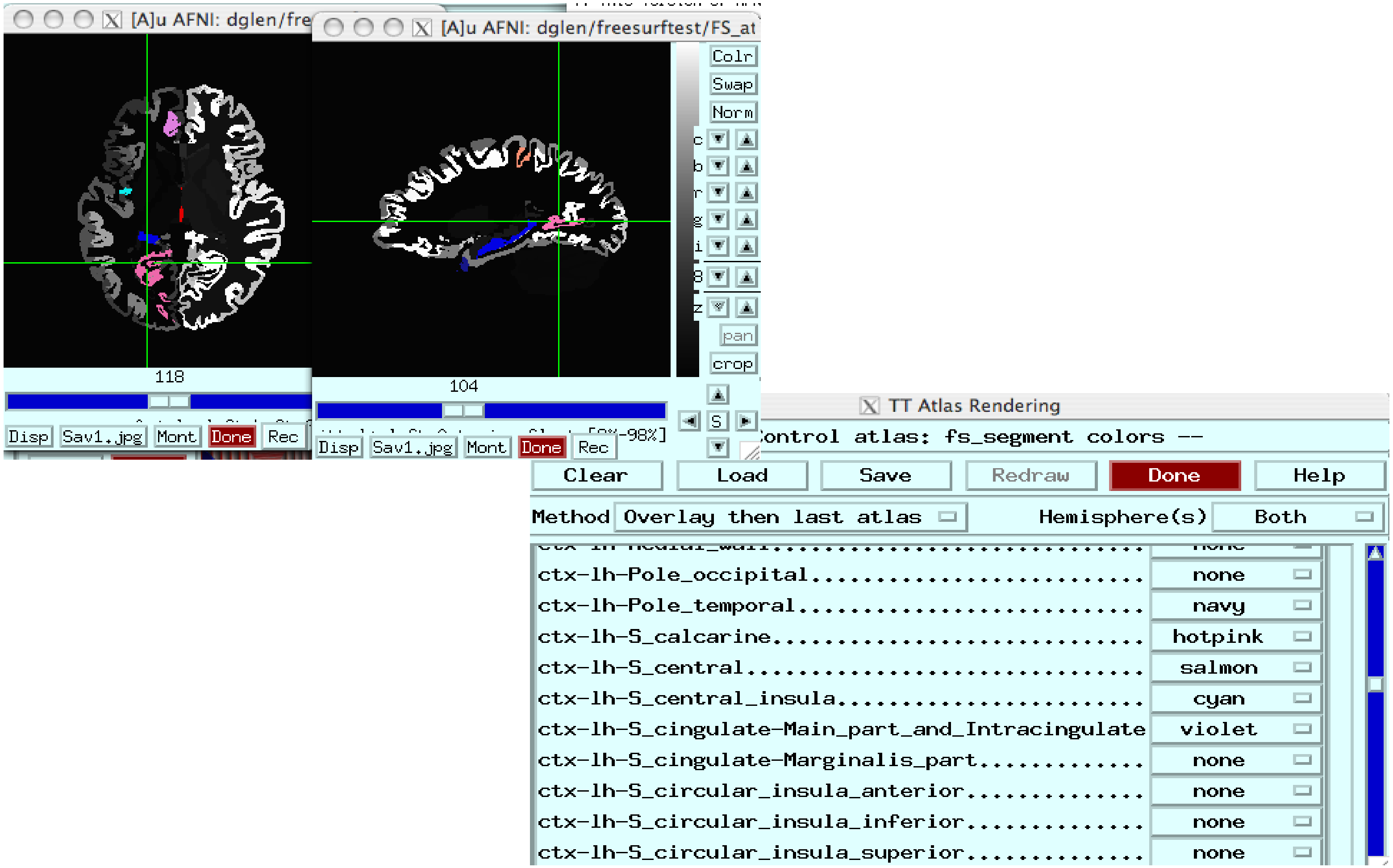
- **`whereami`** can report on the overlap of ROIs with atlas-defined regions

`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]**



ontrol atlas: fs_segment colors --

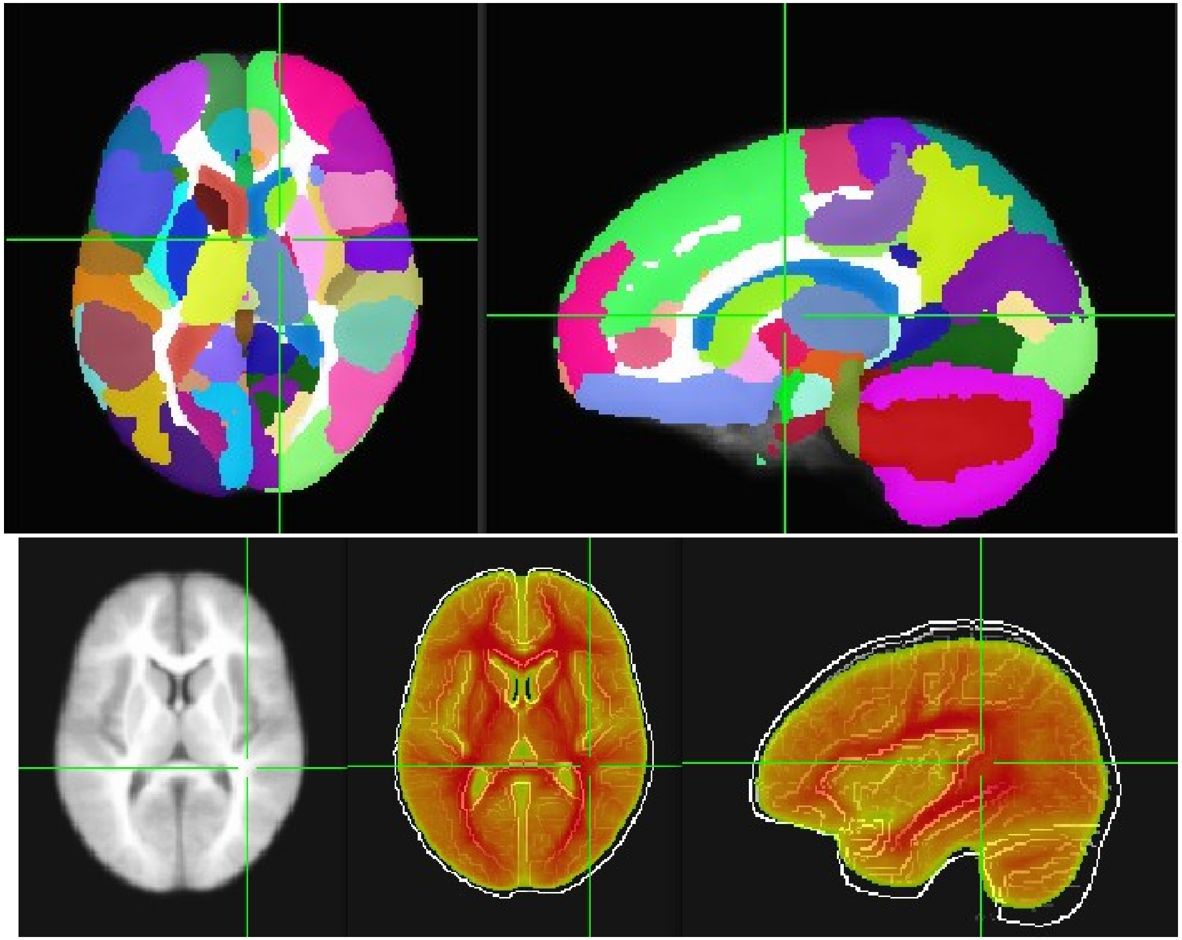
Method Overlay then last atlas   Hemisphere(s) Both

ctx-lh-Pole_occipital..........................	none
ctx-lh-Pole_temporal...........................	navy
ctx-lh-S_calcarine.............................	hotpink
ctx-lh-S_central...............................	salmon
ctx-lh-S_central_insula........................	cyan
ctx-lh-S_cingulate-Main_part_and_Intracingulate	violet
ctx-lh-S_cingulate-Marginalis_part.............	none
ctx-lh-S_circular_insula_anterior..............	none
ctx-lh-S_circular_insula_inferior..............	none
ctx-lh-S_circular_insula_superior..............	none

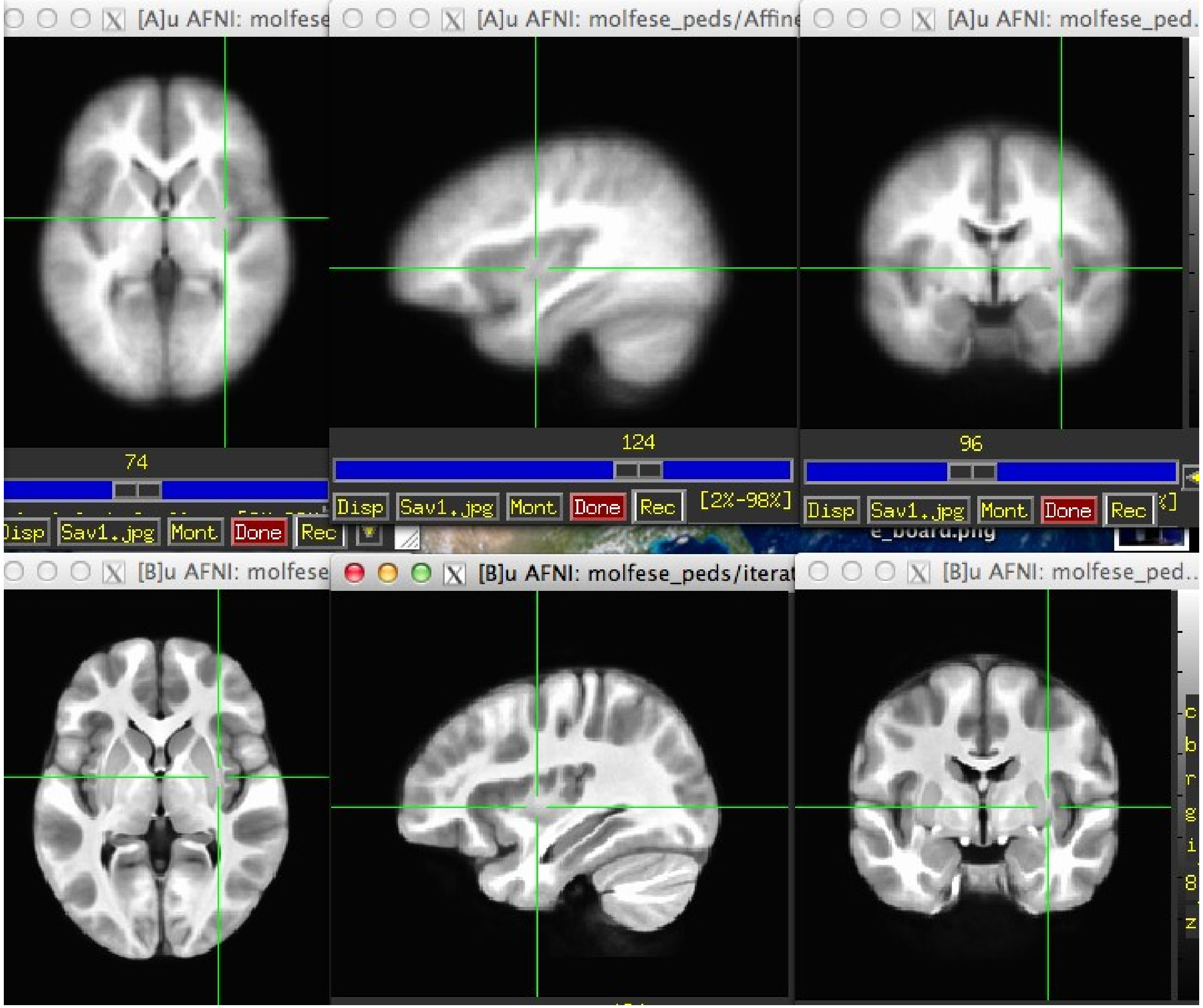
Lets you show atlas regions over your own data (works only in `+tlrc`).

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

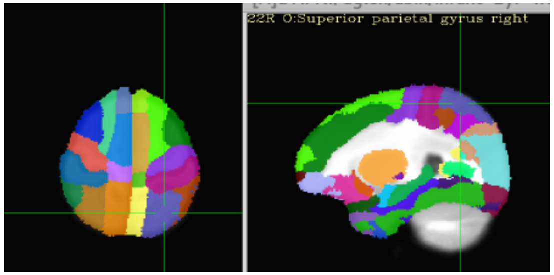


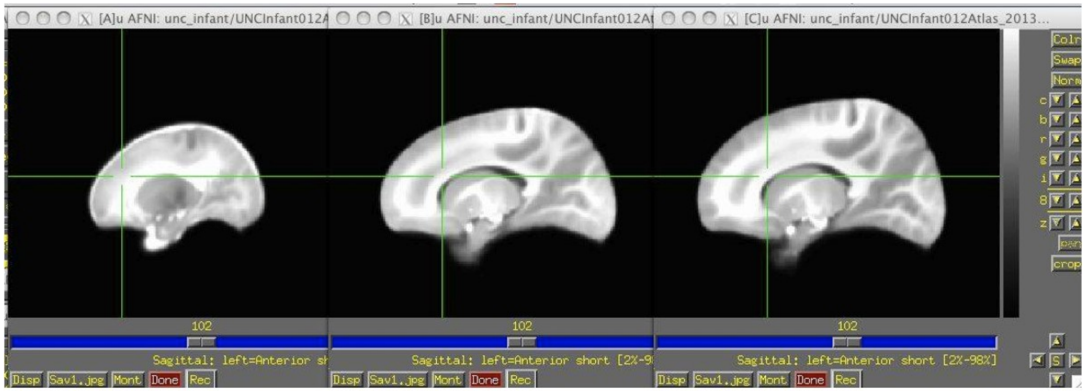
Affine Group

Nonlinear Group I – iterative

Atlases and Templates Available!

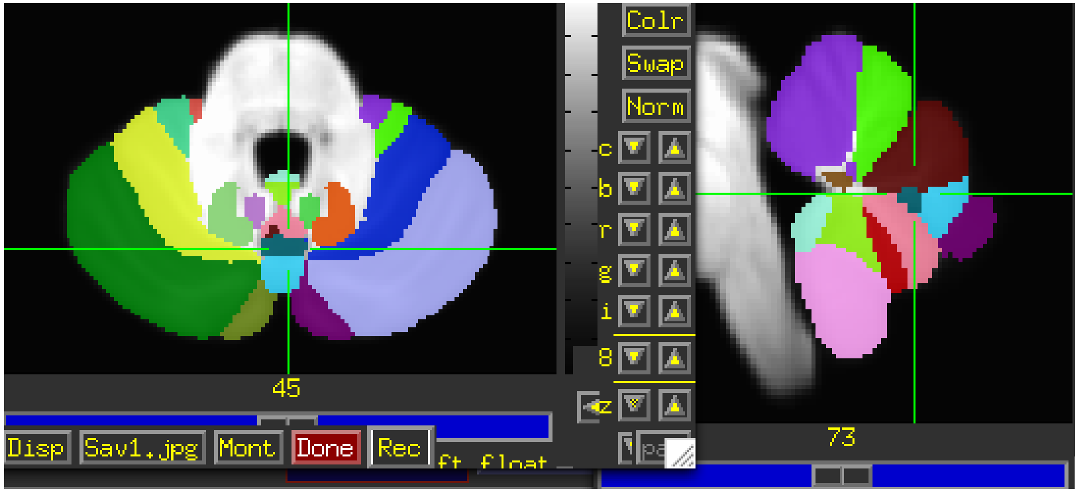
- Infant brain atlas and templates – neonate, 1-year, 2-year. Contributed by Feng Shi, UNC





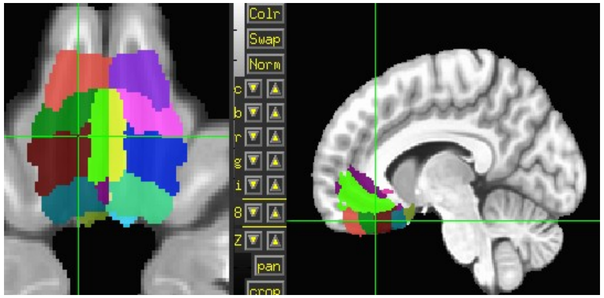
UNC infant templates and atlases – neonate, 1 yr, 2 yr old

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



More Atlases and Templates Available!

Ventromedial Prefrontral Cortex (vmPFC, Scott Mackey)



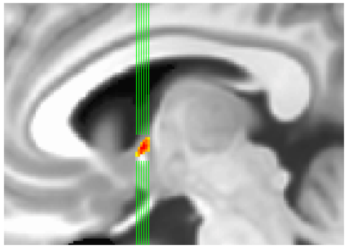
Waxholm Rat Atlas - Papp, et al.

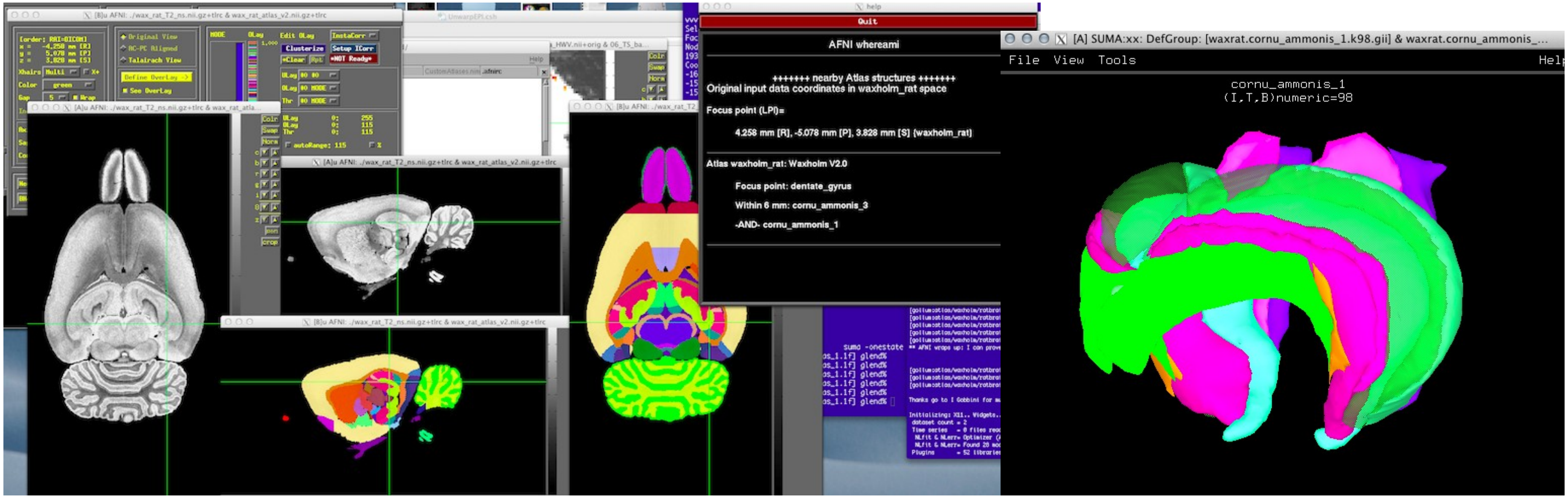
Rat brain templates in Paxinos space – Karolinska Institute, Woo Hyun Shim MGH contributions

All of these are user requests or contributions!

What do you need?

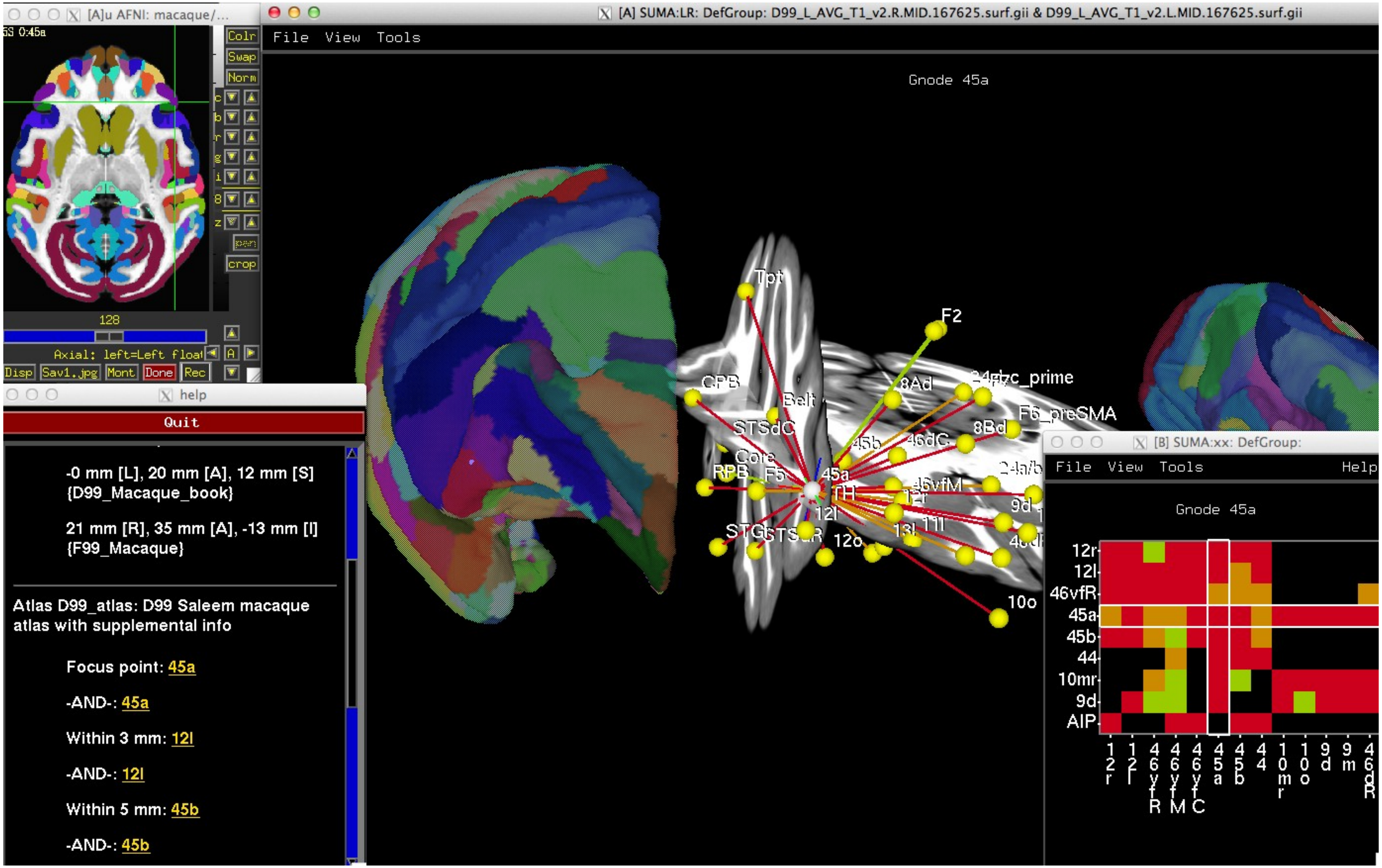
BNST – Torrisi, NIMH





```
AFNI whereami

+++++++ nearby Atlas structures +++++++
Original input data coordinates in waxholm_rat space

Focus point (LPI)=

     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



-0 mm [L], 20 mm [A], 12 mm [S]
{D99_Macaque_book}

21 mm [R], 35 mm [A], -13 mm [I]
{F99_Macaque}

Atlas D99_atlas: D99 Saleem macaque atlas with supplemental info

Focus point: 45a

-AND-: 45a

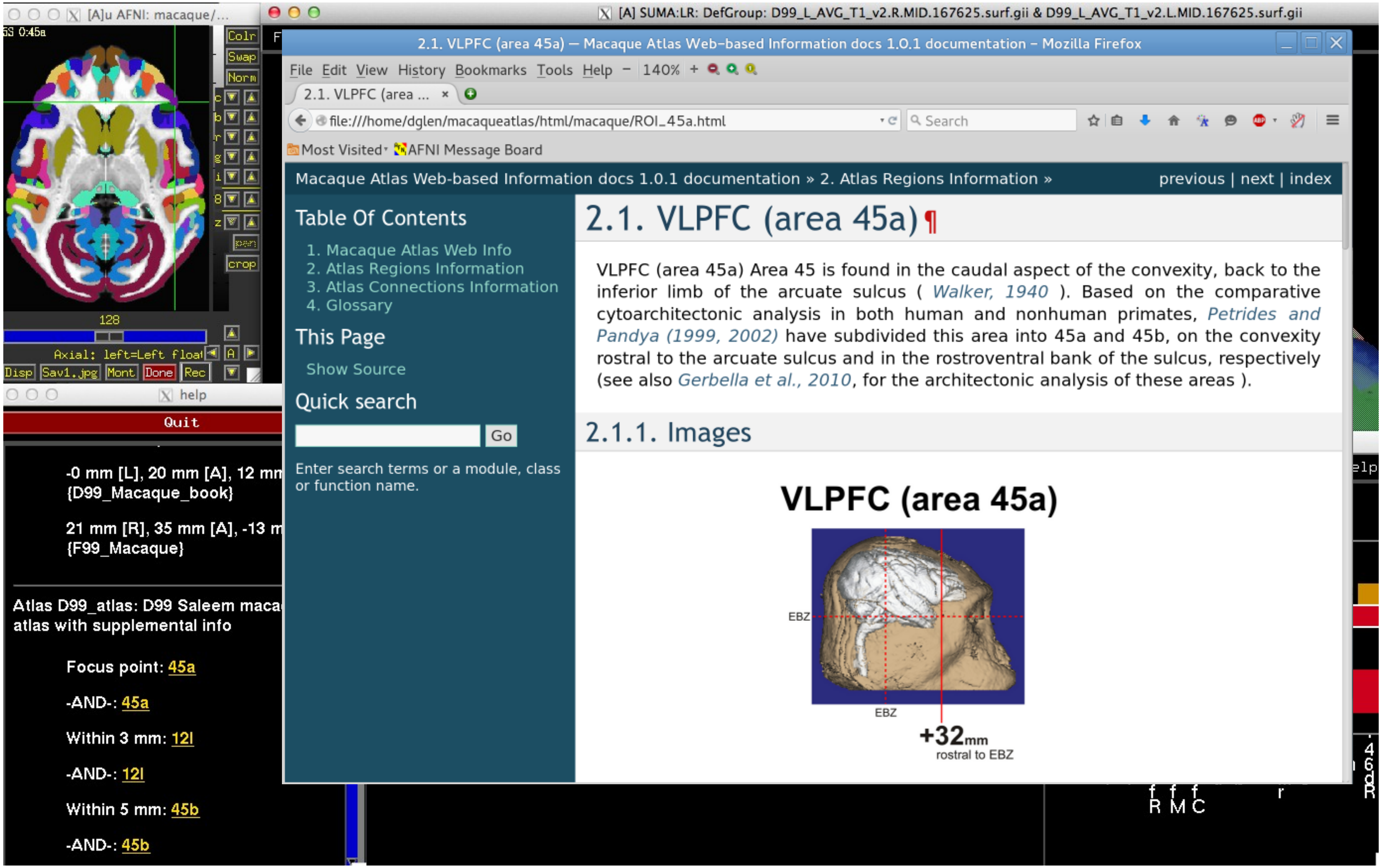
Within 3 mm: 12l

-AND-: 12l

Within 5 mm: 45b

-AND-: 45b

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



-0 mm [L], 20 mm [A], 12 m
{D99_Macaque_book}

21 mm [R], 35 mm [A], -13 m
{F99_Macaque}

Atlas D99_atlas: D99 Saleem maca
atlas with supplemental info

Focus point: 45a

-AND-: 45a

Within 3 mm: 12l

-AND-: 12l

Within 5 mm: 45b

-AND-: 45b

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3. Atlas Connections Information
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Enter search terms or a module, class or function name.

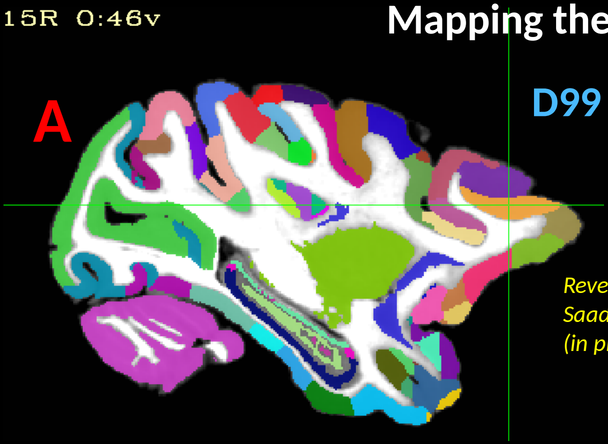
2.1. VLPFC (area 45a)

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

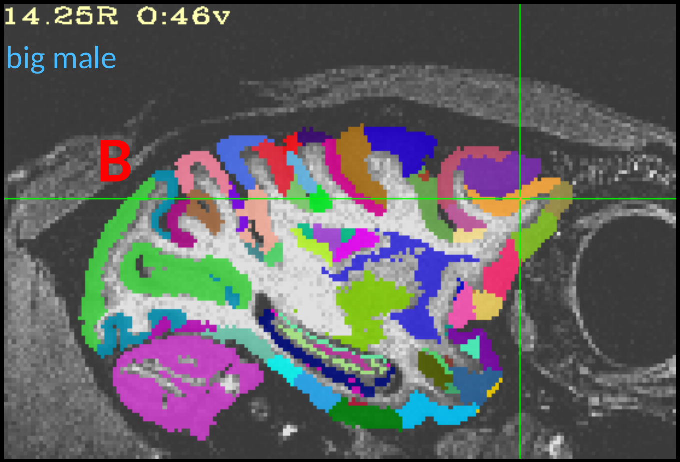
VLPFC (area 45a)

Mapping the digital atlas onto different macaques MRI

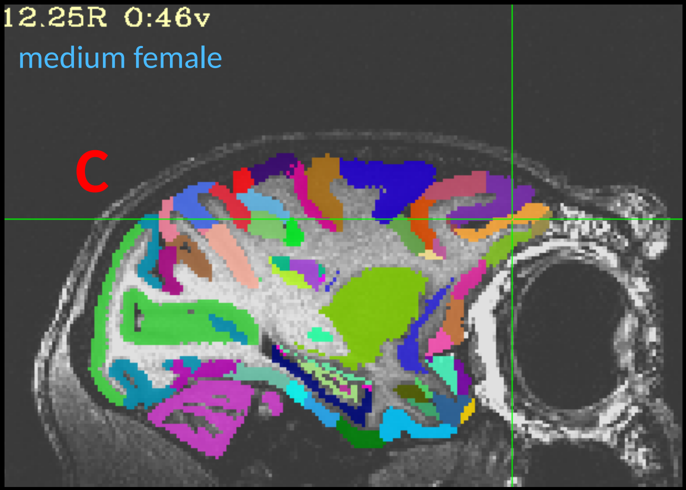


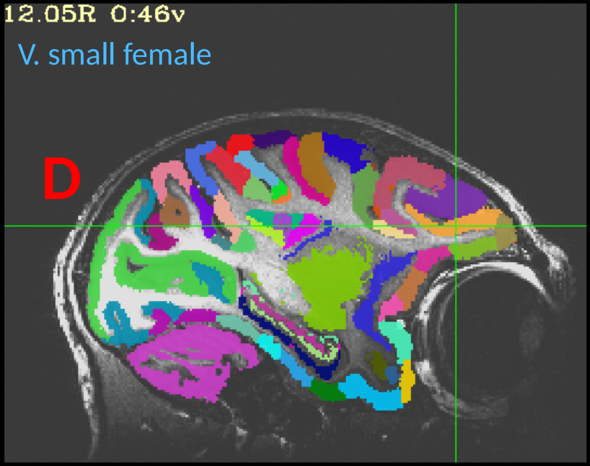
D99 – Digital atlas

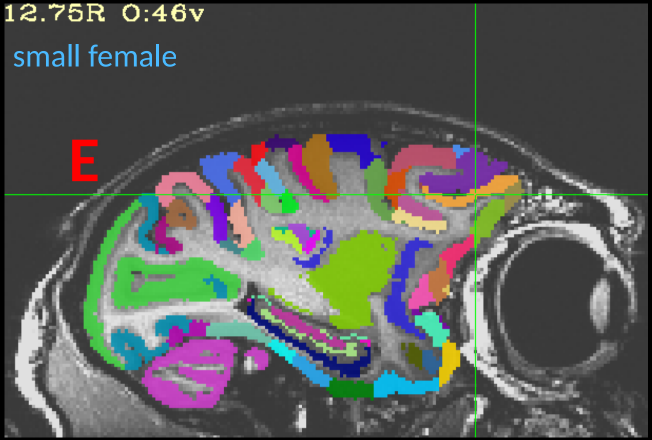
Reveley, Gruslys, Ye, Samaha, Glen, Saad, Seth, Leopold, and Saleem (in preparation)

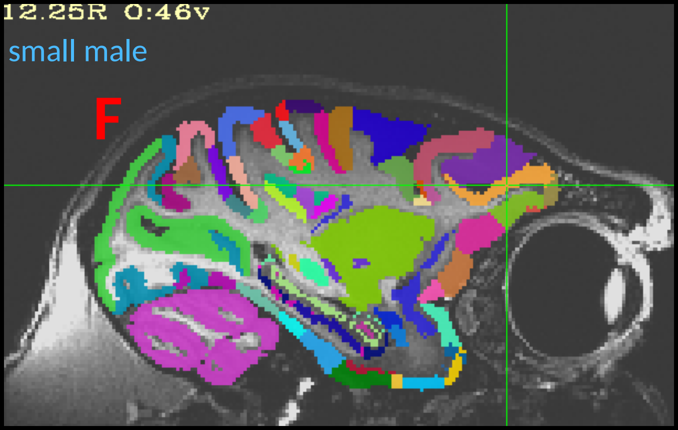


Spatial transformation of the atlas segmentation to each macaque's native space

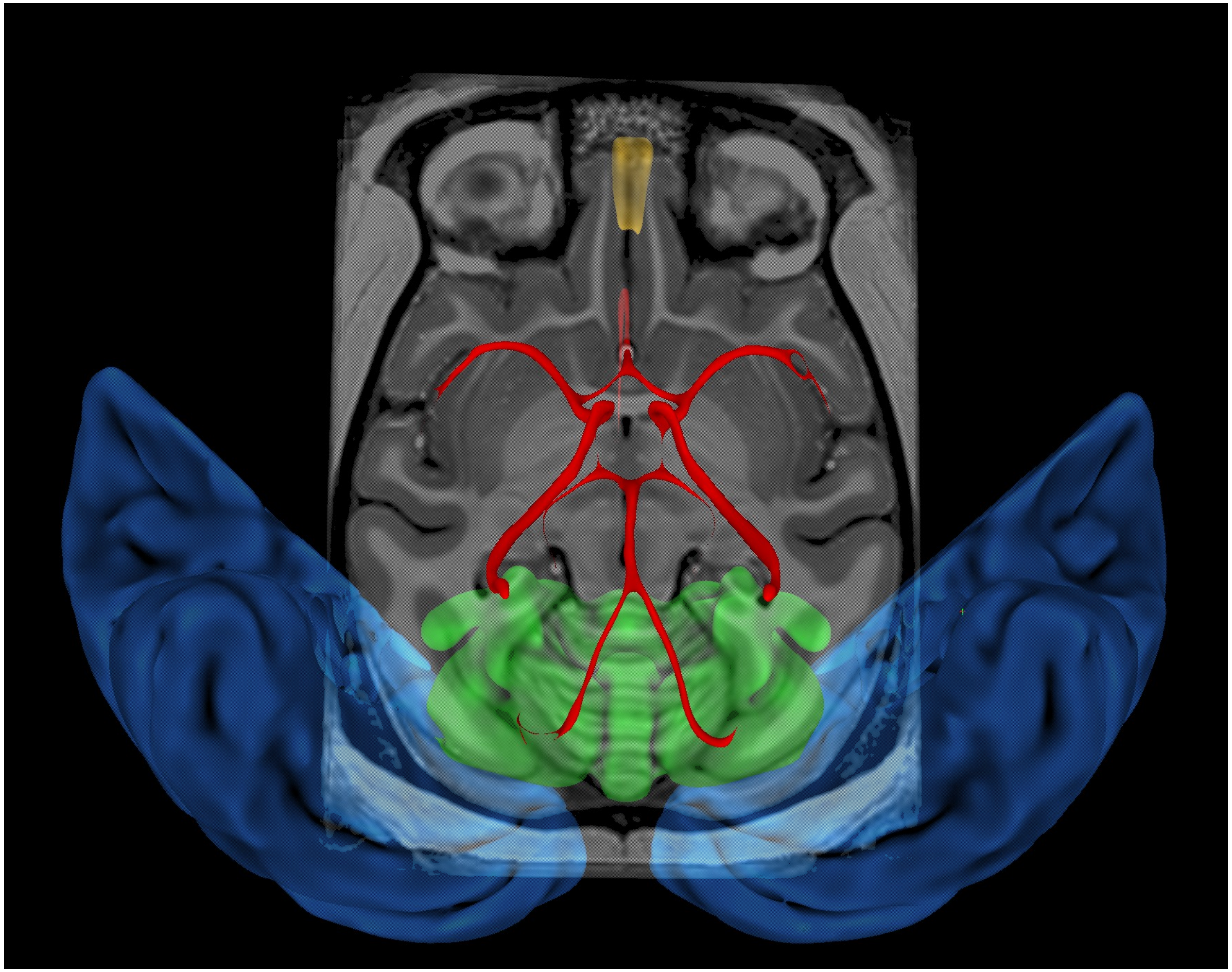








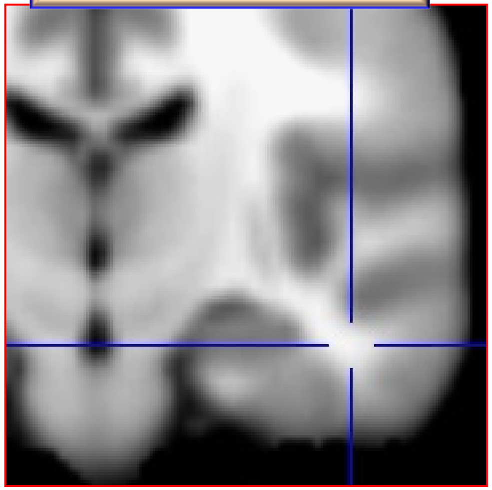
NMT (NIH Macaque Template) – Group template from 31 macaques, surfaces, GM/WM/CSF segmentation



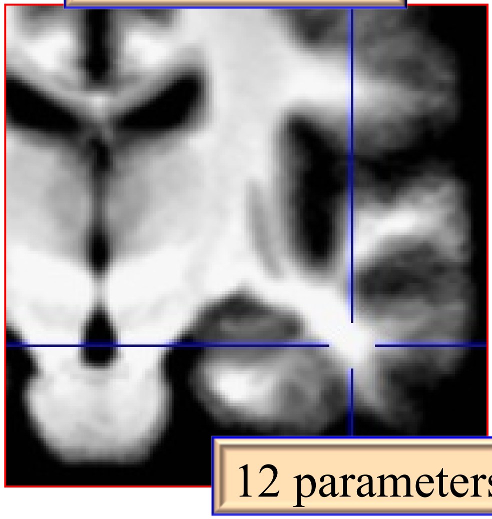
Submitted - with Adam Messinger, Caleb Sponheim, Jakob Seidlitz, Kadharbatcha Saleem,...

Make your own template

MNI 152 template



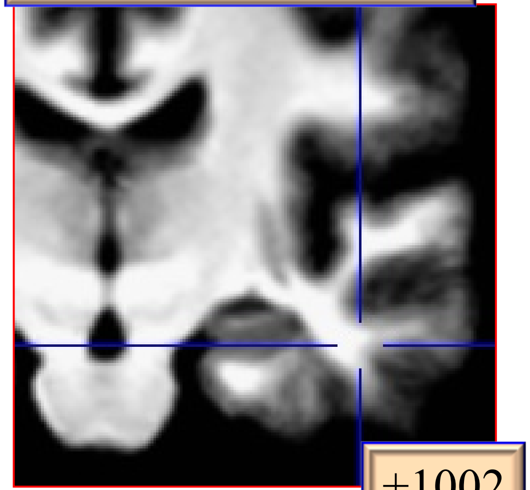
Linear = Affine



12 parameters

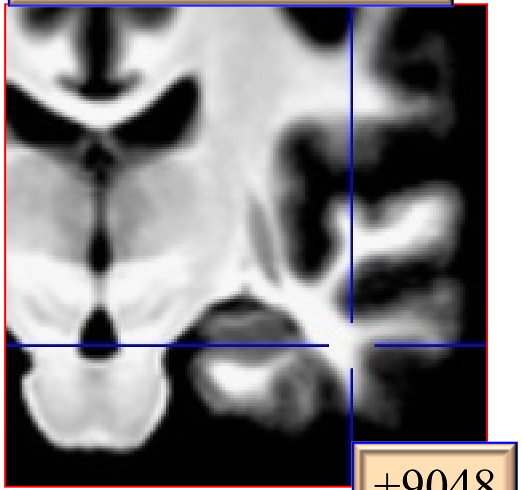
@toMNI_Awarp
@toMNI_Qwarpar
Averages of 21
3 Tesla brain volumes
with varied
levels of refinement in
the nonlinear warping
(smaller patch=more refinement)

Nonlinear: Patch=101



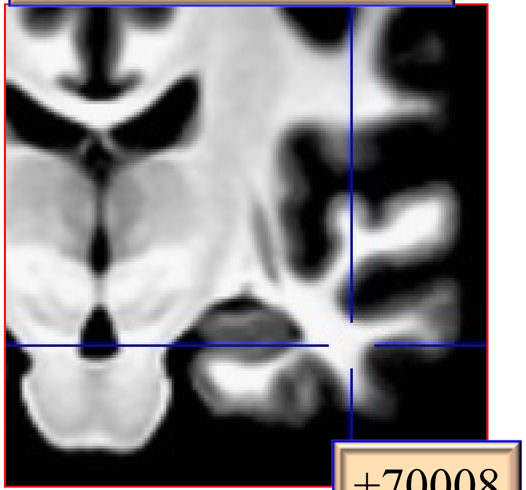
+1002

Nonlinear: Patch=49



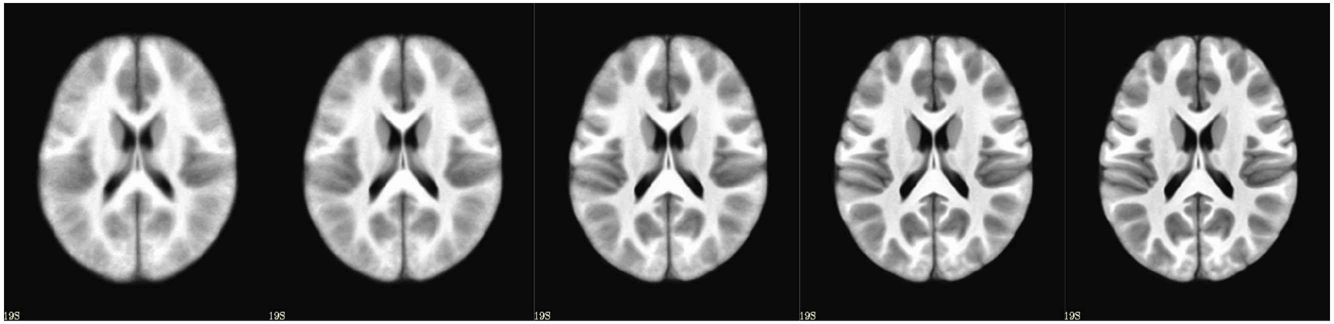
+9048

Nonlinear: Patch=23

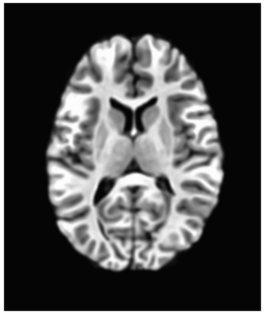


+70008

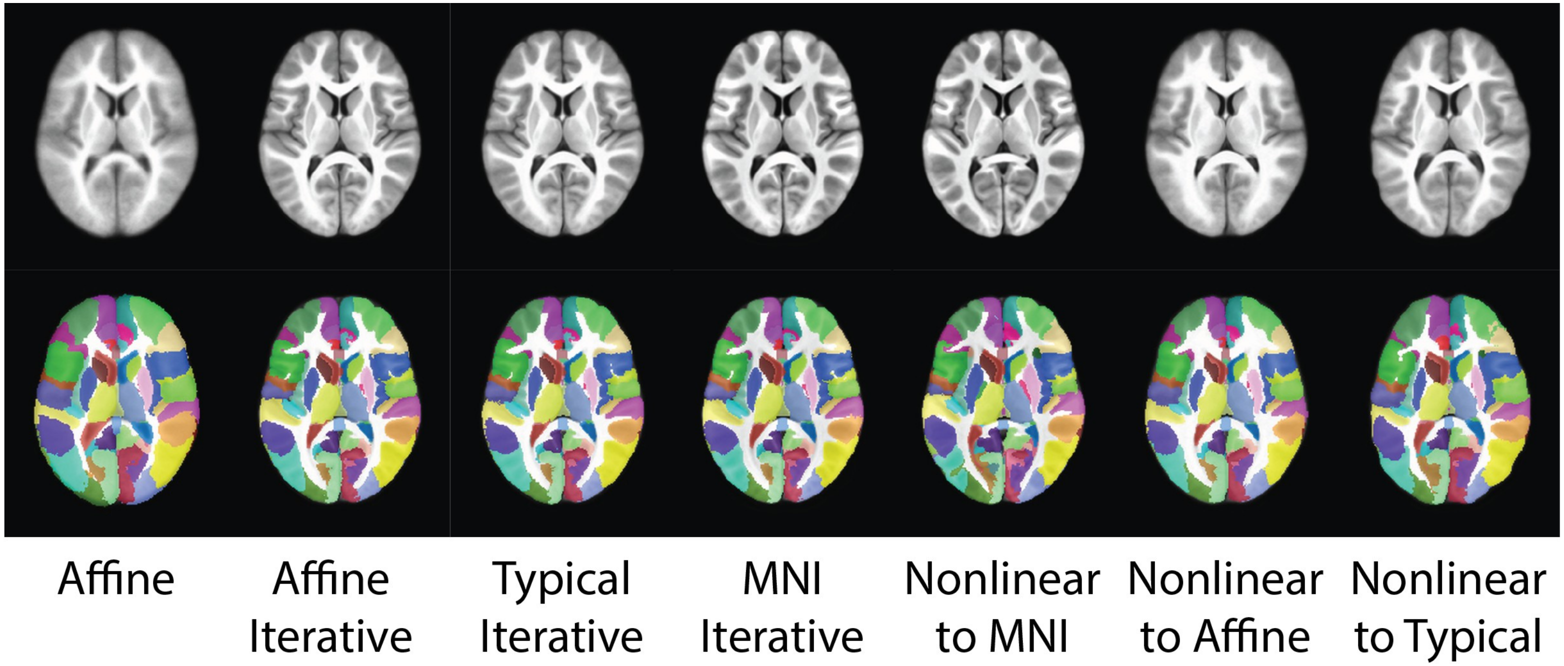
ALTERNATIVE ATLAS CREATION TECHNIQUES: ITERATIVE AND TYPICAL METHODS



Iterative nonlinear alignment to affine template with progressively smaller patch sizes



“Typical” Brain



Make your own atlas!

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

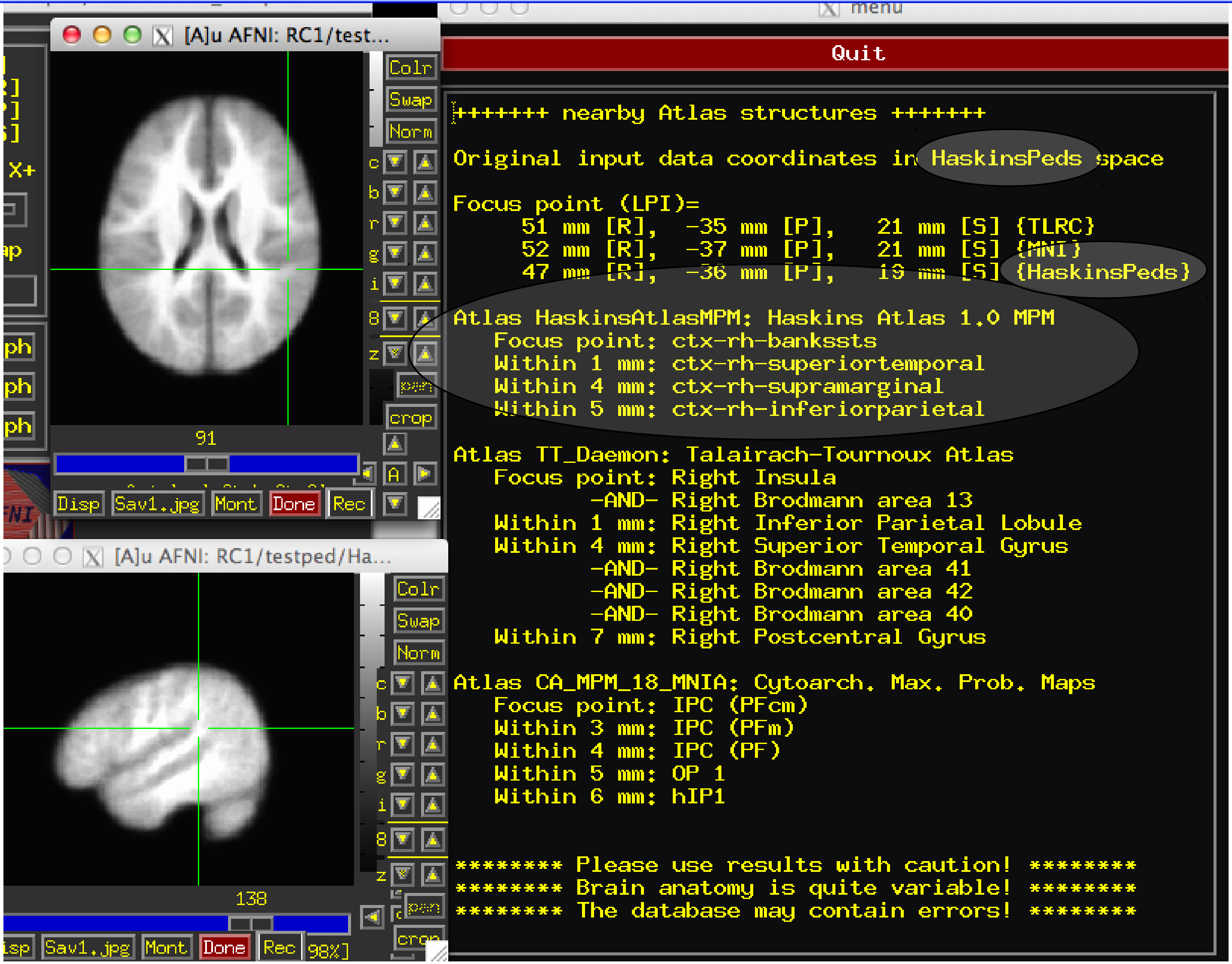
```
@AfniEnv -set AFNI_SUPP_ATLAS_DIR ~/MyCustomAtlases/
```

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.

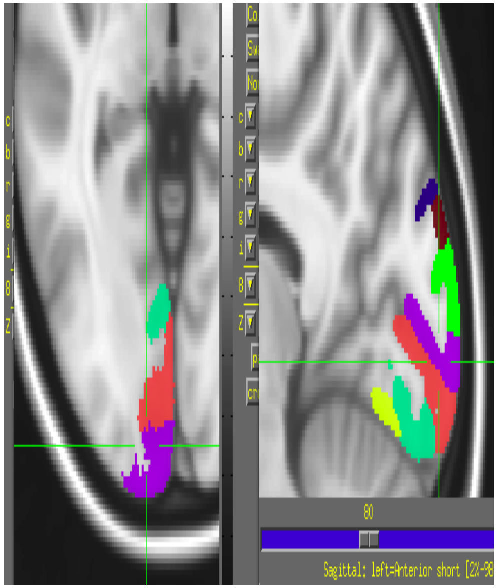
Haskins Pediatric Atlas



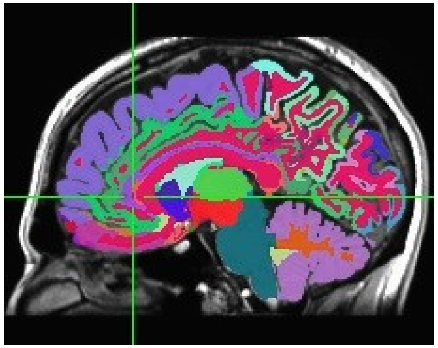
```
+++++++ nearby Atlas structures +++++++

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

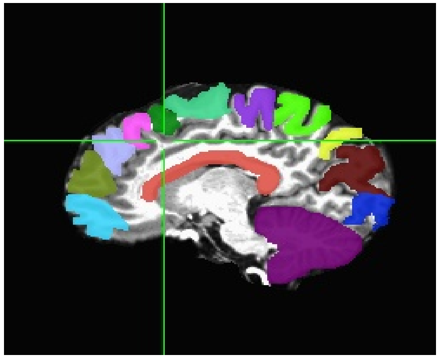
- Eickhoff-Zilles 2.2 cytoarchitectonic atlases
- DTI fiber atlas – Susumo Mori
- Princeton Visual Field Map, Kastner, et al.



Individual Subjects

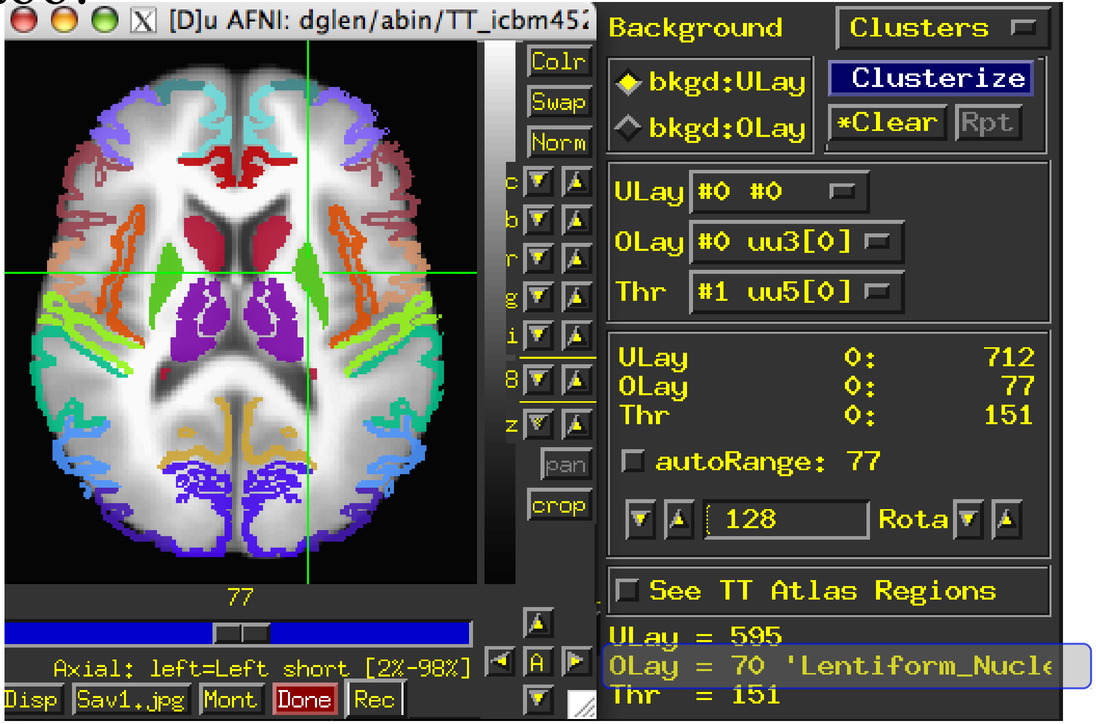


FreeSurfer segmentation



Manual segmentation

@SUMA_MakeSpecFS – atlasizes too!



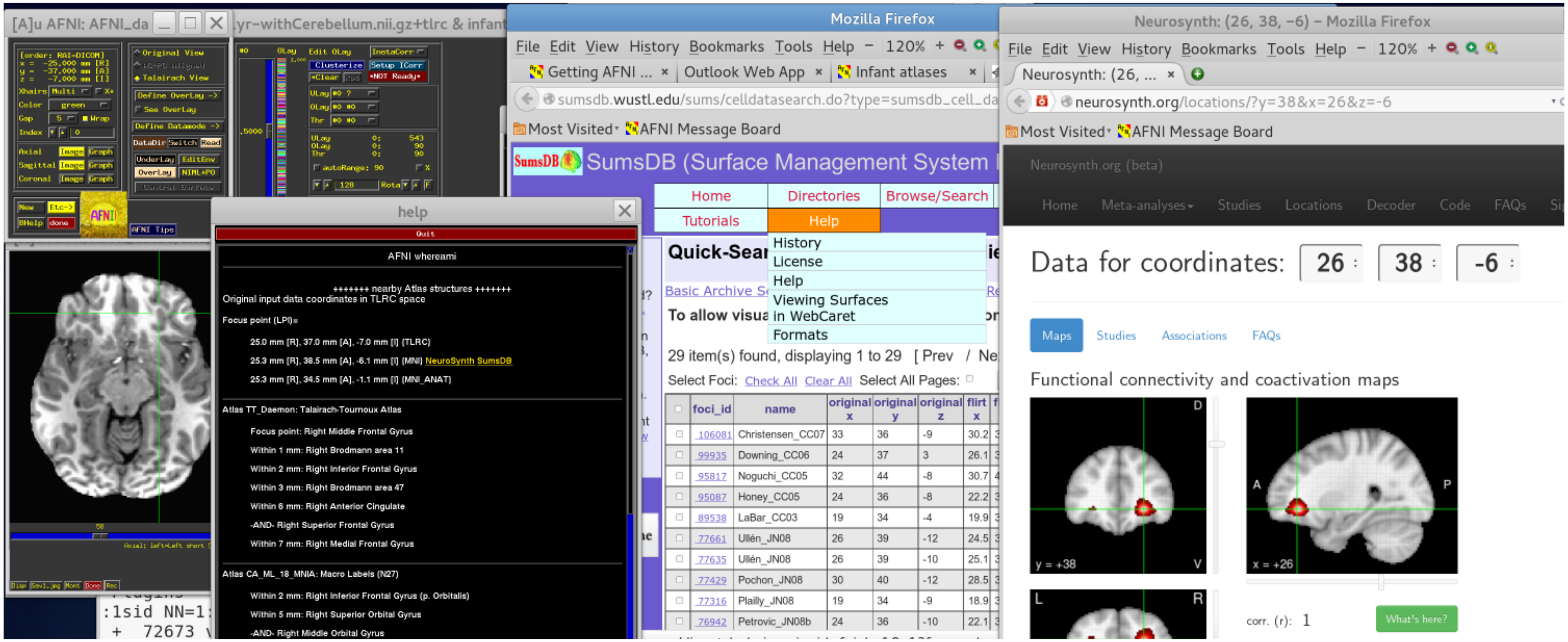
```
ULay        0:     712
OLay        0:      77
Thr         0:     151
```

```
ULay = 595
OLay = 70 'Lentiform_Nucle
Thr  = 151
```

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

Web-based atlases

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



```
AFNI whereami

+++++++ nearby Atlas 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], -6.1 mm [I] {MNI} NeuroSynth SumsDB
    25.3 mm [R], 34.5 mm [A], -1.1 mm [I] {MNI_ANAT}

Atlas TT_Daemon: Talairach-Tournoux 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 (N27)

    Within 2 mm: Right Inferior Frontal Gyrus (p. Orbitalis)
    Within 5 mm: Right Superior Orbital Gyrus
    -AND- Right Middle Orbital Gyrus
```

To allow visua

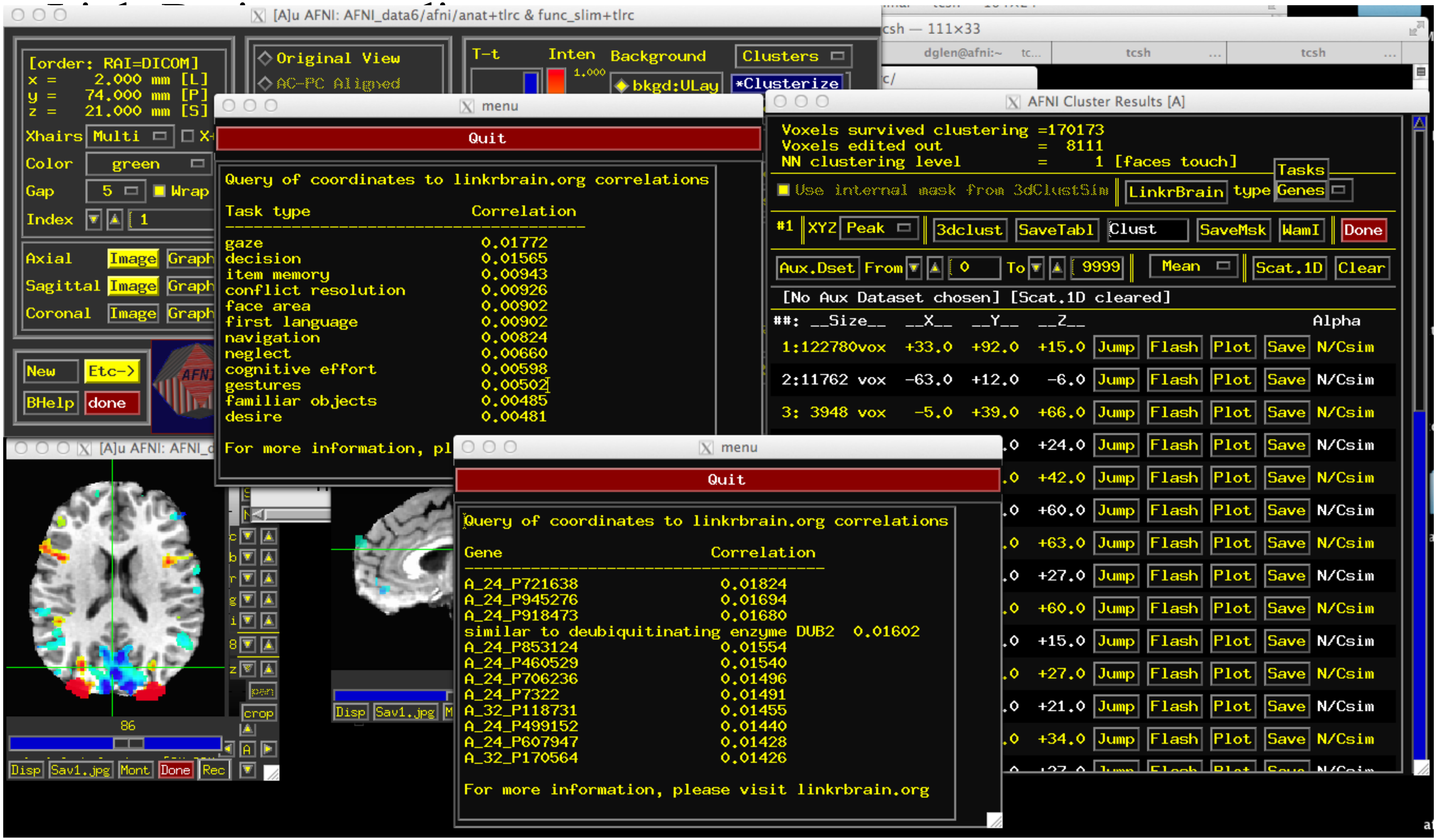
29 item(s) found, displaying 1 to 29 [Prev / Ne

Select Foci: Check All Clear All Select All Pages: ☐

☐	foci_id	name	original x	original y	original z	flirt x
☐	106081	Christensen_CC07	33	36	-9	30.2
☐	99935	Downing_CC06	24	37	3	26.1
☐	95817	Noguchi_CC05	32	44	-8	30.7
☐	95087	Honey_CC05	24	36	-8	22.2
☐	89538	LaBar_CC03	19	34	-4	19.9
☐	77661	Ullén_JN08	26	39	-12	24.5
☐	77635	Ullén_JN08	26	39	-10	25.1
☐	77429	Pochon_JN08	30	40	-12	28.5
☐	77316	Plailly_JN08	19	34	-9	18.9
☐	76942	Petrovic_JN08b	24	36	-10	22.1

set AFNI_WEBBY_WAMI to YES and AFNI_NEUROSYNTH to YES

Web-based atlases



```
[order: RAI=DICOM]
x =    2.000 mm [L]
y =   74.000 mm [P]
z =   21.000 mm [S]
```

```
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

For more information, pl
```

```
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

For more information, please visit linkrbrain.org
```

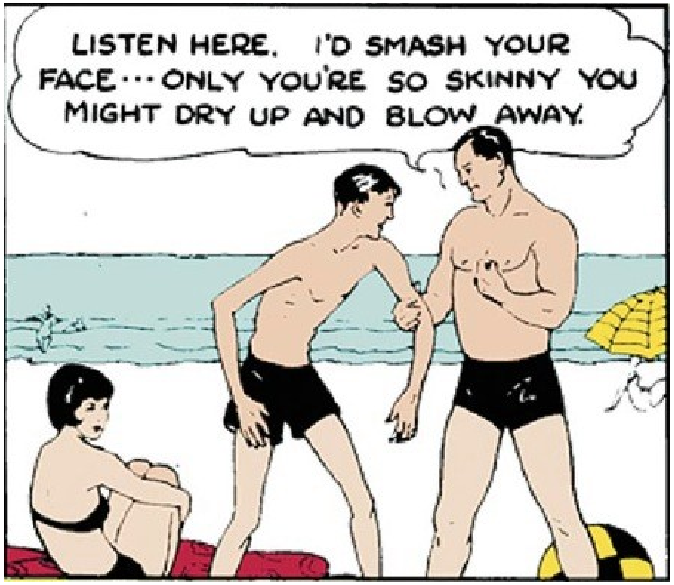
```
Voxels survived clustering =170173
Voxels edited out          =   8111
NN clustering level        =      1 [faces touch]

[No Aux Dataset chosen] [Scat.1D cleared]
##: __Size__  __X__  __Y__  __Z__                              Alpha
 1:122780vox  +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
```

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