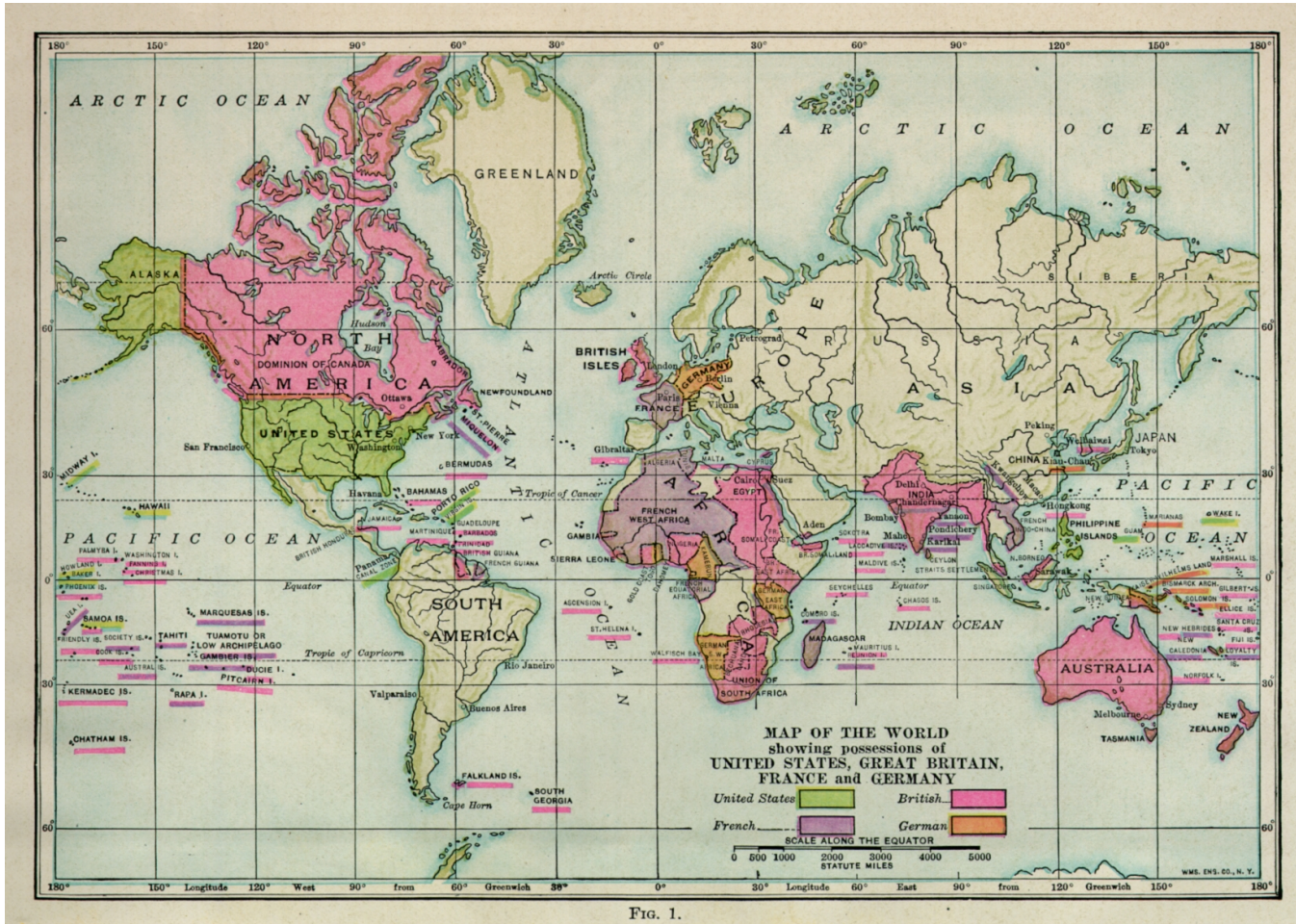


TEMPLATES AND ATLASES



Abbrevs used here

abbrev	= abbreviation
AKA	= also known as
anat	= anatomical
corr	= correlation
diff	= difference
dset	= dataset
e.g.	= exempli gratia (= “for example”)
EPI	= echo planar image
Ex	= example
FOV	= field of view
i.e.	= id est (= “that is”)
ijk	= coordinate indices (integer)
NB	= nota bene (= “note well”)
phys	= physics or physical
ref	= reference
ROI	= region of interest
subj	= subject
vol	= volume
vox	= voxel(s)
xyz	= physical coordinates (units of mm)

Definitions

Template

A reference dataset (typically whole brain) used for matching shapes, reporting coordinates of results, etc.

Ex: TT_N27+tlrc, MNI_EPI+tlrc, TT_ICBM452+tlrc.



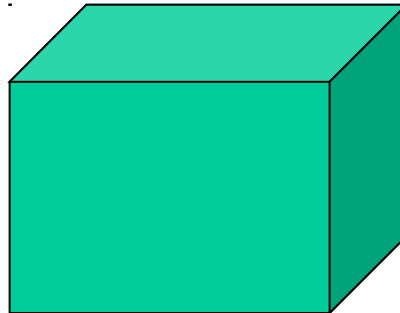
TT_N27+tlrc

Definitions

Template Space

An (x, y, z) coordinate system shared by many datasets in alignment with a template.

Ex: TLRC (Talairach-Tourneaux), MNI, MNI_ANAT, ORIG.



To see what “space” a dset is in, type:

```
3dinfo -space DSET_NAME
```

Definitions

A note on AFNI usage of “tlrc”:

The “+tlrc” extension in a dataset’s name is used to denote that the volume in question is in a standardized space; it does not always mean that the standard space in question is the Talairach-Tournoux one, specifically-- it could be MNI, pediatric template, macaque, ...

Hopefully the context makes things clear.

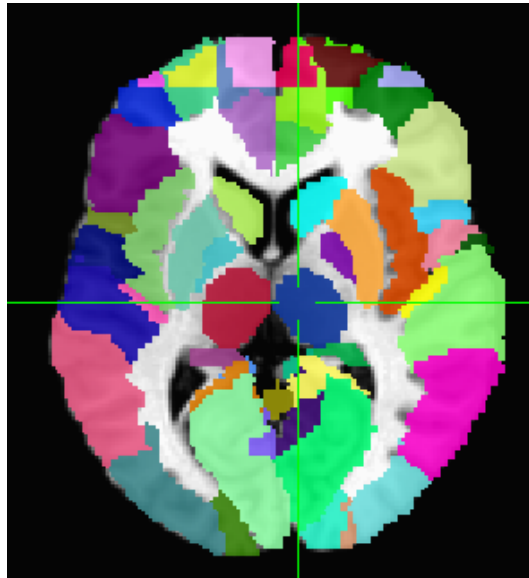
(Typically, there are so many templates for a given space now-- MNI, for example, has several templates-- that one really has to specify the full file name of a template to be able to refer to it unambiguously, anyways.)

Definitions

Atlas

A dset containing segmentation or parcellation information. It can be considered a “map” of ROIs: each ROI is defined as a set of voxels with a certain integer value (and a string label can be attached to each ROI).

Ex: TTatlas+tlrc, TT_N27_EZ_ML+tlrc, my_roidset+orig.

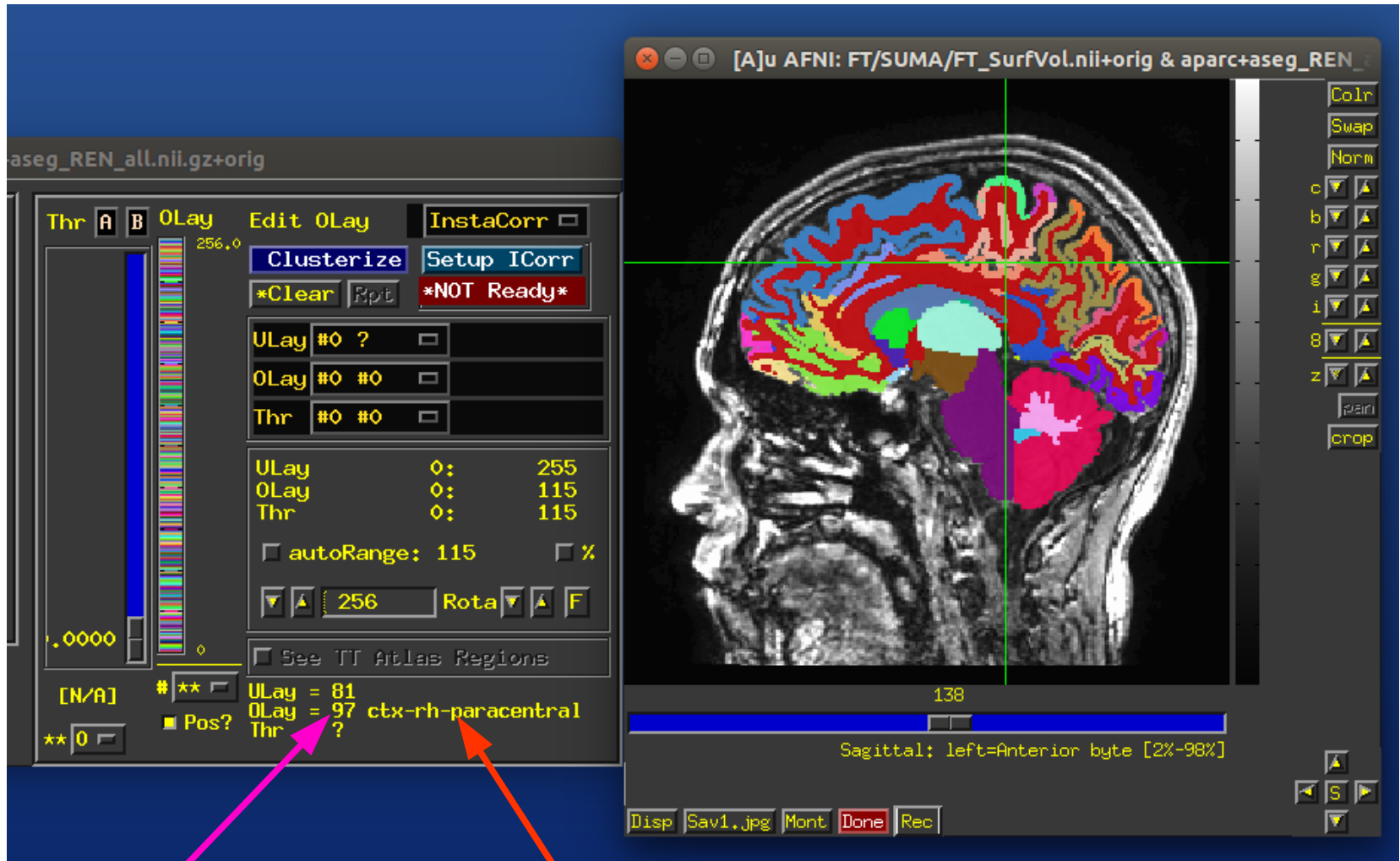


TT_N27_EZ_ML+tlrc

See more description about templates+atlases (including making your own) on the AFNI website:
https://afni.nimh.nih.gov/pub/dist/doc/html/doc/template_atlas/framework.html

Definitions

Atlas (or general ROI) label in GUI

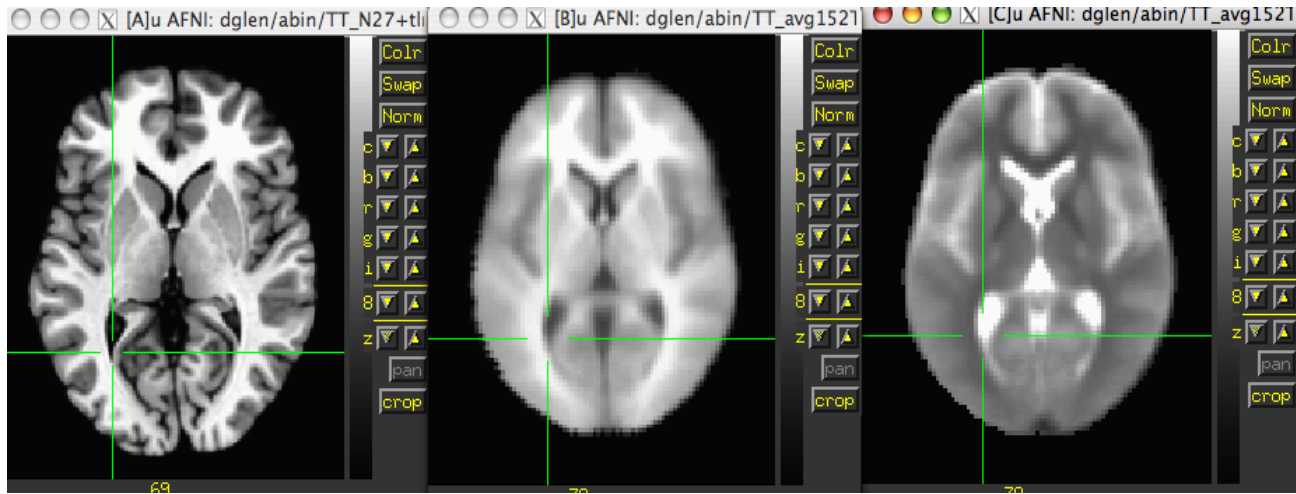


integer value of ROI

associated string label

Templates included with AFNI

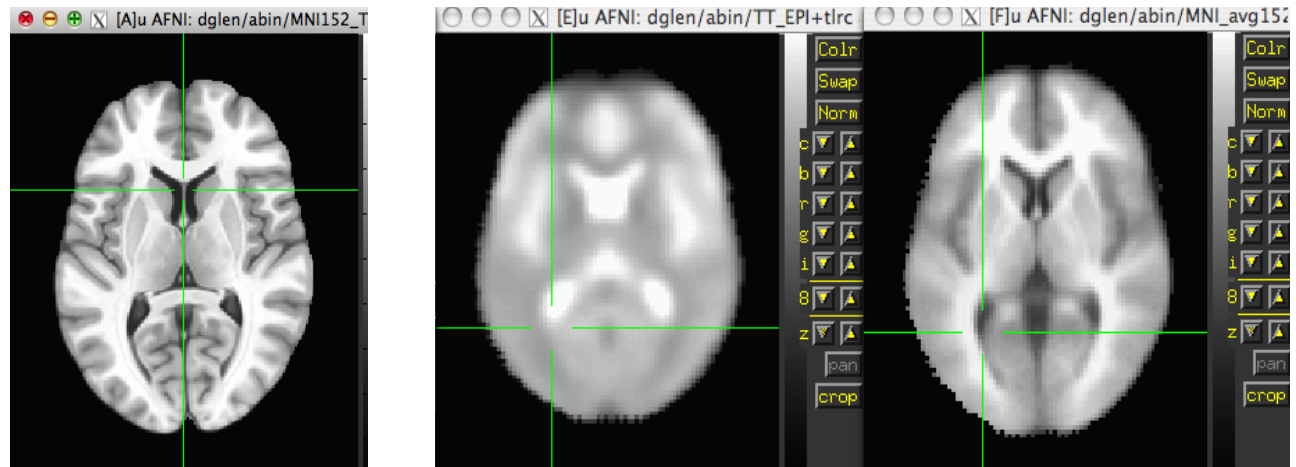
After default AFNI installation, these templates (and others) would be in ~/abini/:



TT_N27

TT_avg152T1

TT_avg152T2



MNI152_T1_2009c

TT_EPI

MNI_avg152T1

And a quick question: what important properties does each dset here have?

Templates included with AFNI

A helpful note on viewing templates (or any dsets) **each time** you open up the AFNI GUI, regardless of directory!

Set the **AFNI_GLOBAL_SESSION** variable in your `~/.afnirc` file, e.g.,:

```
AFNI_GLOBAL_SESSION = /home/nmandela/abin
```

All dsets there will appear in your “Underlay” or “Overlay” menu in the AFNI GUI. (Use full path of directory, no “~” or “\$HOME”.)

Templates included with AFNI

A helpful note on viewing templates (or any dsets) each time you open up the AFNI GUI, regardless of directory!

Set the **AFNI_GLOBAL_SESSION** variable in your `~/.afnirc` file, e.g.,:

```
AFNI_GLOBAL_SESSION = /home/nmandela/abin
```

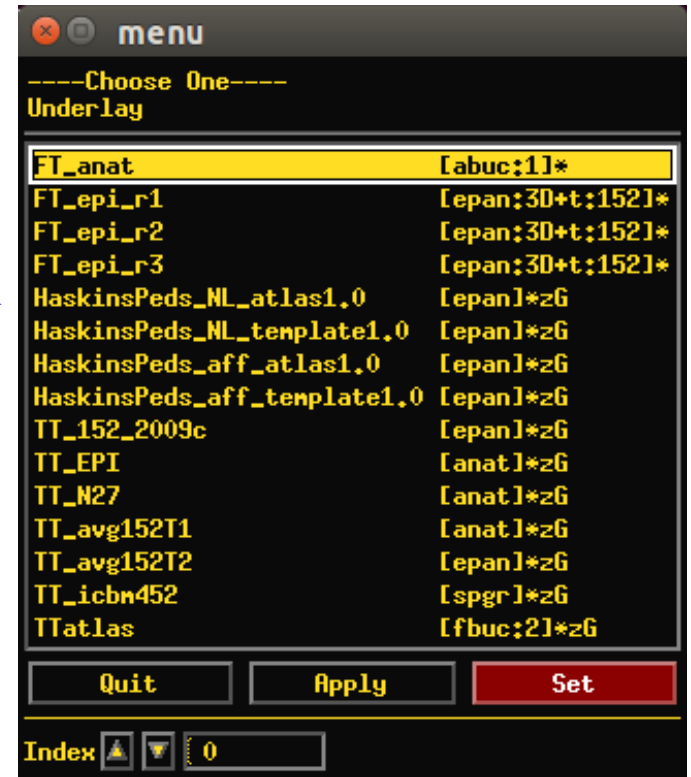
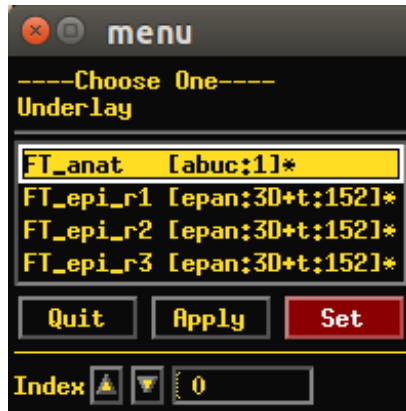
All dsets there will appear in your “Underlay” or “Overlay” menu in the AFNI GUI. (Use full path of directory, no “~” or “\$HOME”.)

Ex: then open AFNI GUI in some directory, say:

```
~/AFNI_data6/FT_analysis/FT/
```

after →

before →



Standard spaces

Reasons to use a standard template space:

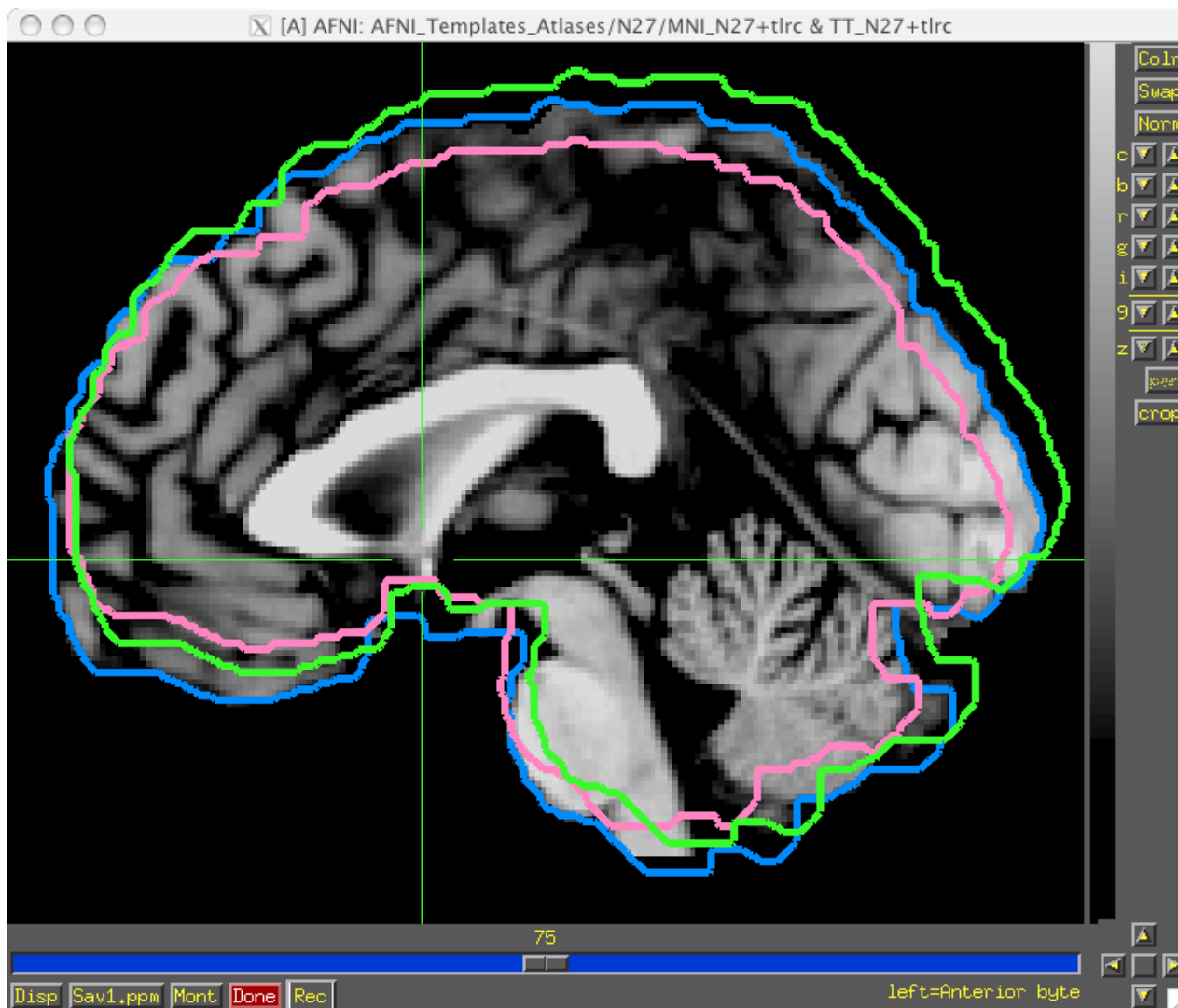
- Compare across subjects and groups easily for every voxel in the brain
- Standardize coordinates with others
- Know where a voxel is automatically from an atlas
- Mostly automated and no specific ROI drawing required

Reasons not to 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

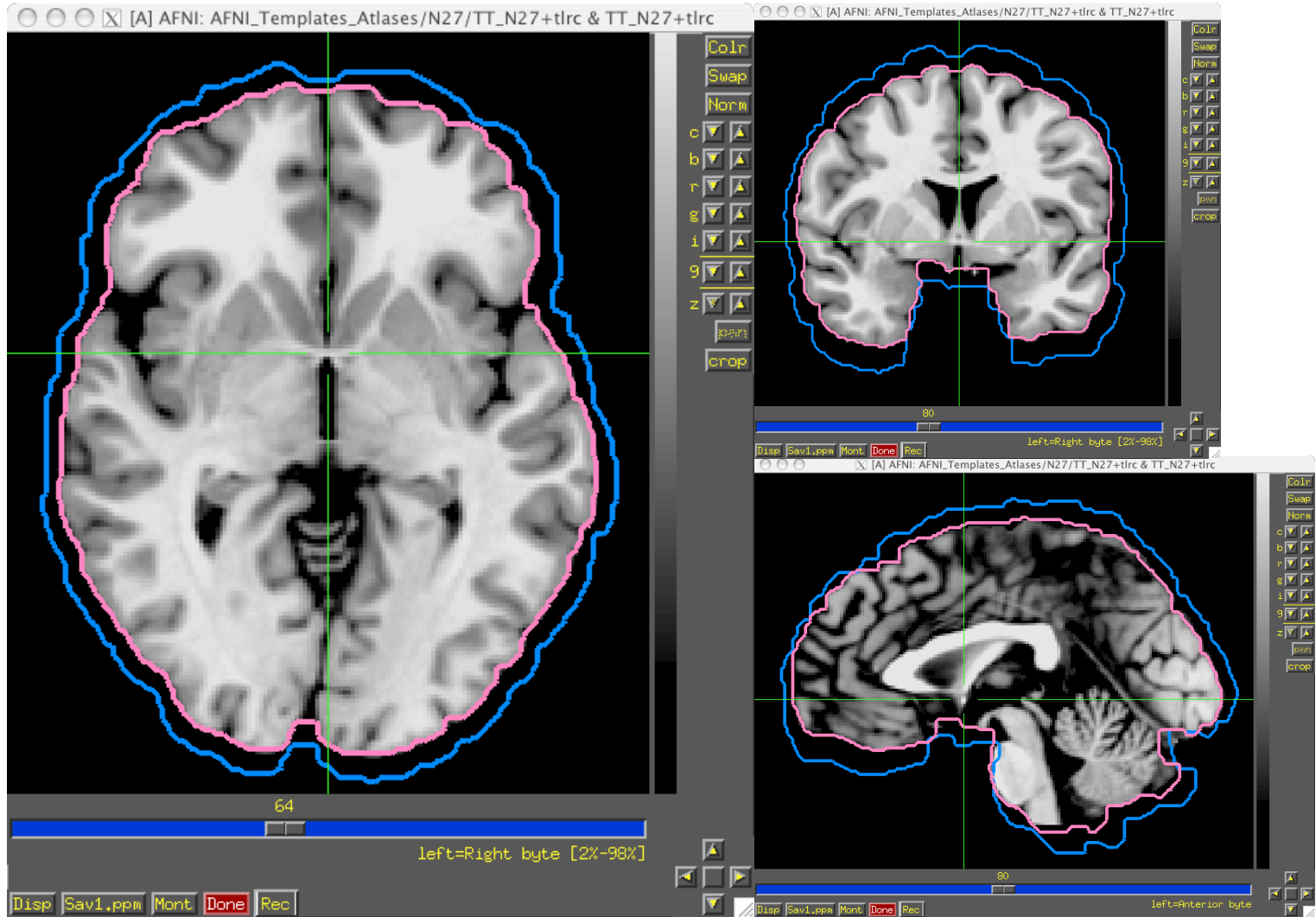
Template spaces differ in origin

TLRC, MNI, and MNI-Anat



Template spaces differ in size

The **MNI** brain is larger than the **TLRC** brain.



From space to space

For going between TLRC and MNI:

Approximate equation

→ used by **whereami** and **3dWarp**

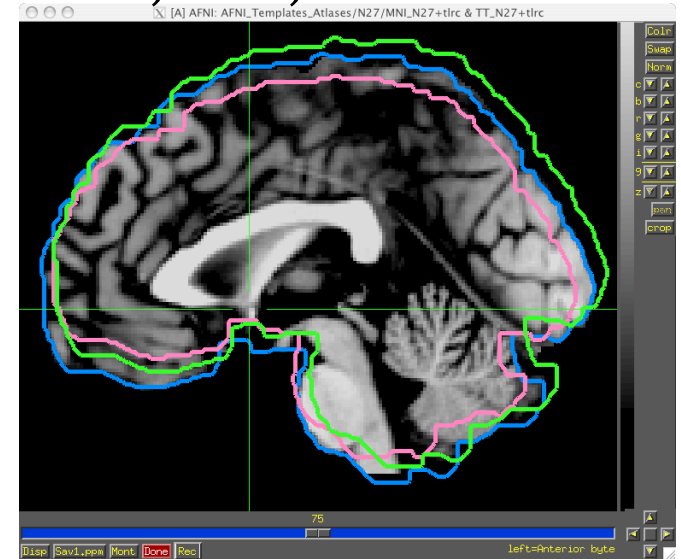
A manual TLRC transformation of MNI template to TLRC space

→ used by **whereami** (as precursor to MNI Anat.), based on N27 template

Multiple space coordinates reported in **whereami** output

(**AFNI_ATLAS_TEMPLATE_SPACE_LIST**)

TLRC, MNI, and MNI-Anat



For going between MNI and MNI Anat (Eickhoff et al., 2005):

$MNI + (0, 4, 5) = MNI\ Anat.$ (in RAI coordinate system)

Going between TLRC and MNI Anat (as practiced in whereami):

Go from TLRC (TT_N27) to MNI via manual transform of N27 template

Add (0, 4, 5)

Choosing a template

Try to pick a template that...

- is similar to the subject group: neonates, pediatric, young adults, elderly, macaque, rabbit...
- is of the same modality and coverage as your data sets
- has a relevant atlas segmentation.

Choosing a template

Try to pick a template that...

- is similar to the subject group: neonates, pediatric, young adults, elderly, macaque, rabbit...
- is of the same modality and coverage as your data sets
- has a relevant atlas segmentation.

You can also make your own template (and maybe an atlas too):

- Individual or group template
 - Group: average or iterative (discussed more later)
- Scripts/commands exist in AFNI
 - Ex. Haskins pediatric atlas
 - ➔ several methods tested
 - ➔ best approach: *iterative nonlinear alignment*
 - @toMNI_Awarp, @toMNI_Qwarp

Registration To Standard Spaces

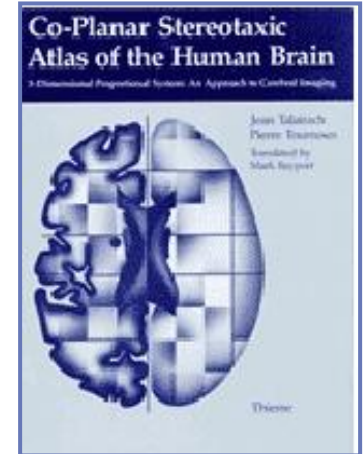
Transforming Datasets to Talairach-Tournoux Coordinates

- 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 `t03d` 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`

Automatic Talairach transform (affine) with `@auto_tlrc`

- In the olden days, people would spend a lot of time transforming data to standard space by hand (see Supplement slides for how to perform the Manual TLRC transform using the AFNI GUI by setting AC-PC landmarks).
- Here, we describe how to perform a TLRC transform *automatically* using AFNI's `@auto_tlrc` (used by `afni_proc.py` for linear affine alignment to standard space).
 - ◇ 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.
 - The Anterior Commissure (AC) center is no longer at $xyz = (0,0,0)$, and the 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 (just be consistent in your group analysis).
 - It is easy + automatic. Just check final results to make sure nothing went seriously awry.

@auto_tlrc example

- To run in AFNI_data6/afni/
Transform the subj anat to a template space (output: **anat_TT+tlrc**):

```
@auto_tlrc          \  
-base TT_N27+tlrc  \  
-suffix _TT        \  
-input anat+orig
```

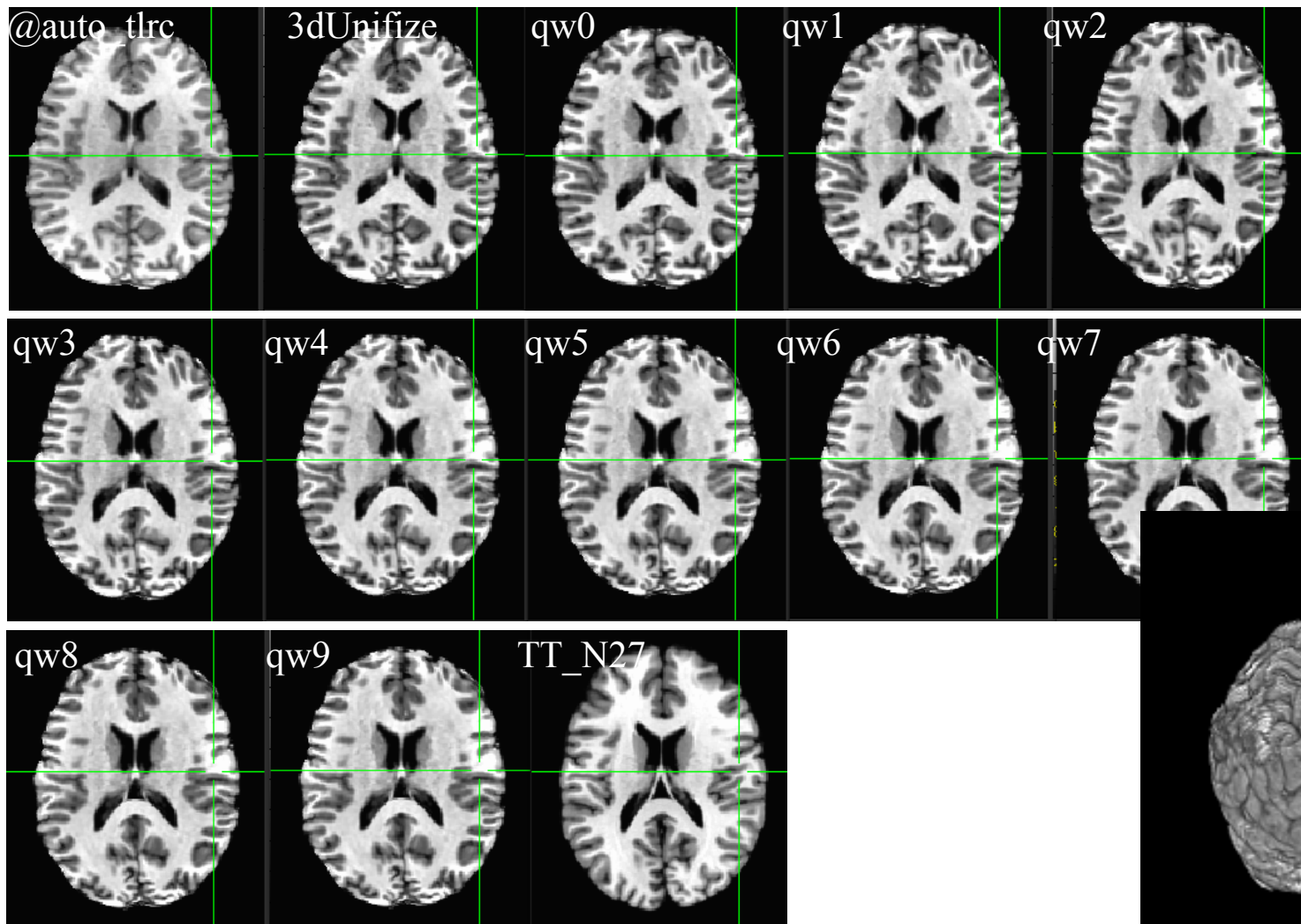
- Then apply the transform stored in **anat_TT+tlrc**'s header to a "follower dset" (here, func data), specifying output resolution at 3 mm (output: **func_slim_TT+tlrc**):

```
@auto_tlrc          \  
-apar anat_TT+tlrc  \  
-input func_slim+orig \  
-suffix _TT        \  
-dxyz 3
```

- Instead of **TT_N27**, you could also use the **icbm452**, or the mni's **avg152T1** template, or any other template you like (see **@auto_tlrc -help** for a few good words on templates)

Nonlinear alignment to template

3dQwarp, through multiple levels of refinement →



Nonlinear alignment to template

Multiple nonlinear alignment tools in AFNI

3dQwarp: the standard nonlinear workhorse

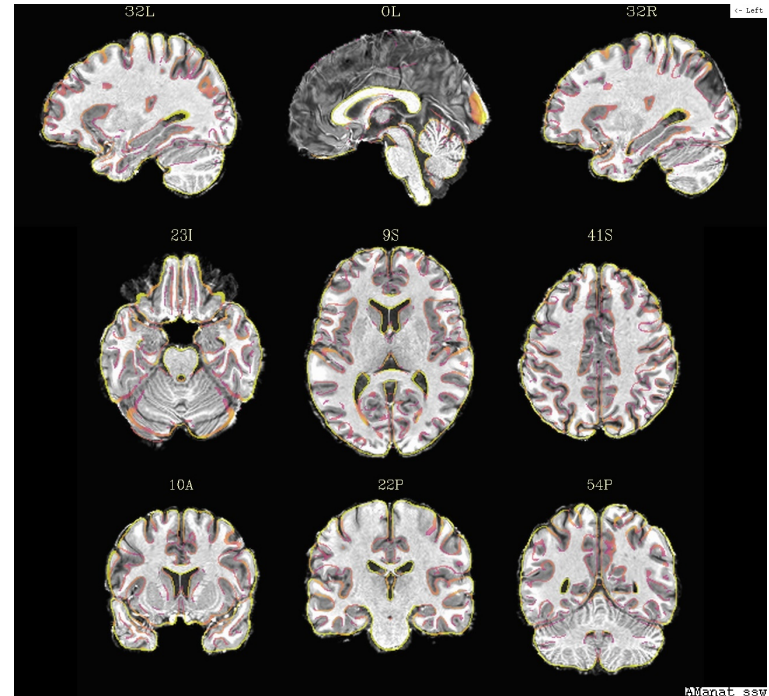
auto_warp.py: wrapper for alignment functionality, ~simpler syntax
(@auto_tlrc + 3dQwarp together)

```
Ex: auto_warp.py -base MNI152_T1_2009c+tlrc. \
      -suffix _awarp -input strip+orig.
```

@SSwarper: skull stripping and alignment in one-- and bonus automatic QC images →

+ @SSwarper uses a multi-volume base; several exist for standard templates already, and more can be made-- see full description for these online:

https://afni.nimh.nih.gov/pub/dist/doc/html/doc/template_atlas/sswarper_base.html



Measuring quality of alignment

Can compare: nonlinear alignment vs affine alignment

- + Estimate warp from subject anat to template for a group of subjects
- + Apply warp when processing fMRI data (here, resting state)
- + Check changes in seed-based correlation maps between results
 - better method would have higher corr in GM networks and lower corr in WM.

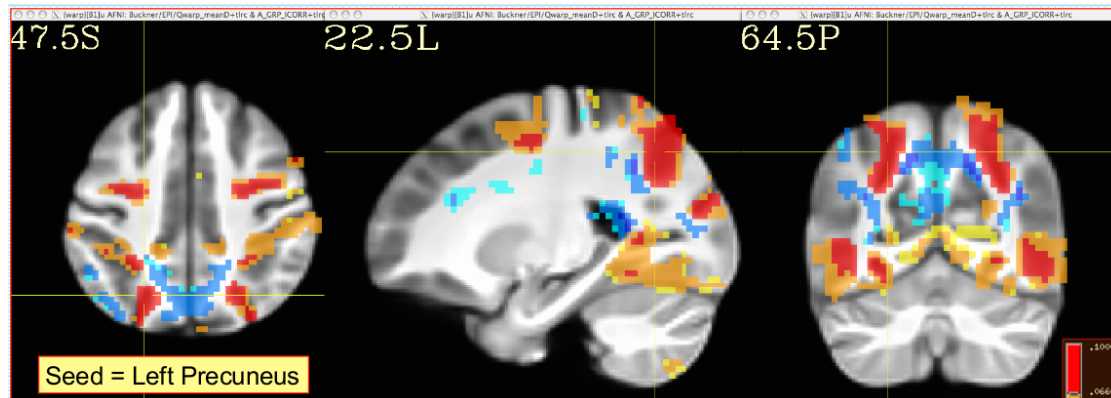
Measuring quality of alignment

Can compare: nonlinear alignment vs affine alignment

- + Estimate warp from subject anat to template for a group of subjects
- + Apply warp when processing fMRI data (here, resting state)
- + Check changes in seed-based correlation maps between results
 - better method would have higher corr in GM networks and lower corr in WM.

red: [0.066, 0.100] corr increase for 3dQwarp results

blue: [0.066, 0.100] corr decrease for 3dQwarp results



RS-FMRI: **Qwarp-to-detailed-template** vs **Qwarp-to-MNI-152**

- ◆ **3dQwarp** → align 188 Cambridge datasets from FCON-1000
- ◆ Underlay = template-ized T₁ anats
- ◆ Overlay = difference in mean seed-based correlation maps when using **3dQwarp** alignment to detailed template **versus**
 - ❖ **[upper]** affine alignment to MNI-152

Measuring quality of alignment

Can compare: using detailed vs non-detailed template for nonlinear alignment

- + Estimate warp from subject anat to template for a group of subjects
- + Apply warp when processing fMRI data (here, resting state)
- + Check changes in seed-based correlation maps between results
 - better method would have higher corr in GM networks and lower corr in WM.

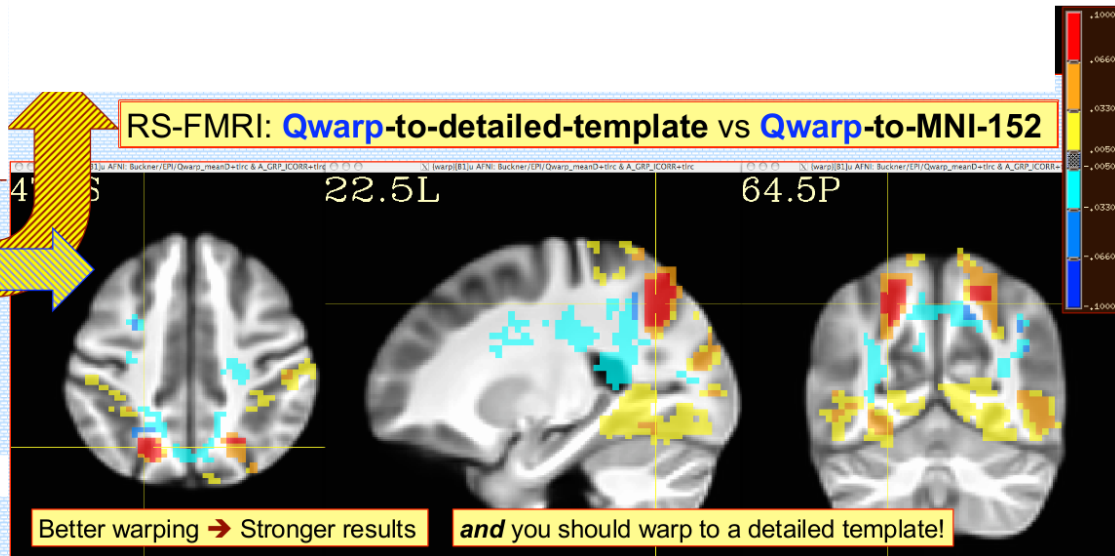
Measuring quality of alignment

Can compare: using detailed vs non-detailed template for nonlinear alignment

- + Estimate warp from subject anat to template for a group of subjects
- + Apply warp when processing fMRI data (here, resting state)
- + Check changes in seed-based correlation maps between results
 - better method would have higher corr in GM networks and lower corr in WM.

red: [0.066, 0.100] corr
increase for 3dQwarp results

blue: [0.066, 0.100] corr
decrease for 3dQwarp results



◆ **3dQwarp** → align 188 Cambridge datasets from FCON-1000

◆ Underlay = template-ized T₁ anats

◆ Overlay = difference in mean seed-based correlation maps when using **3dQwarp** alignment to detailed template **versus**

❖ [**lower**] **3dQwarp** alignment to MNI-152

Measuring quality of alignment

Can compare 3dQwarp with other available nonlinear alignment tools

- + For a group of subjects, estimate warp from anat to template
- + Apply warp to labeled ROIs, and measure % overlap in results.

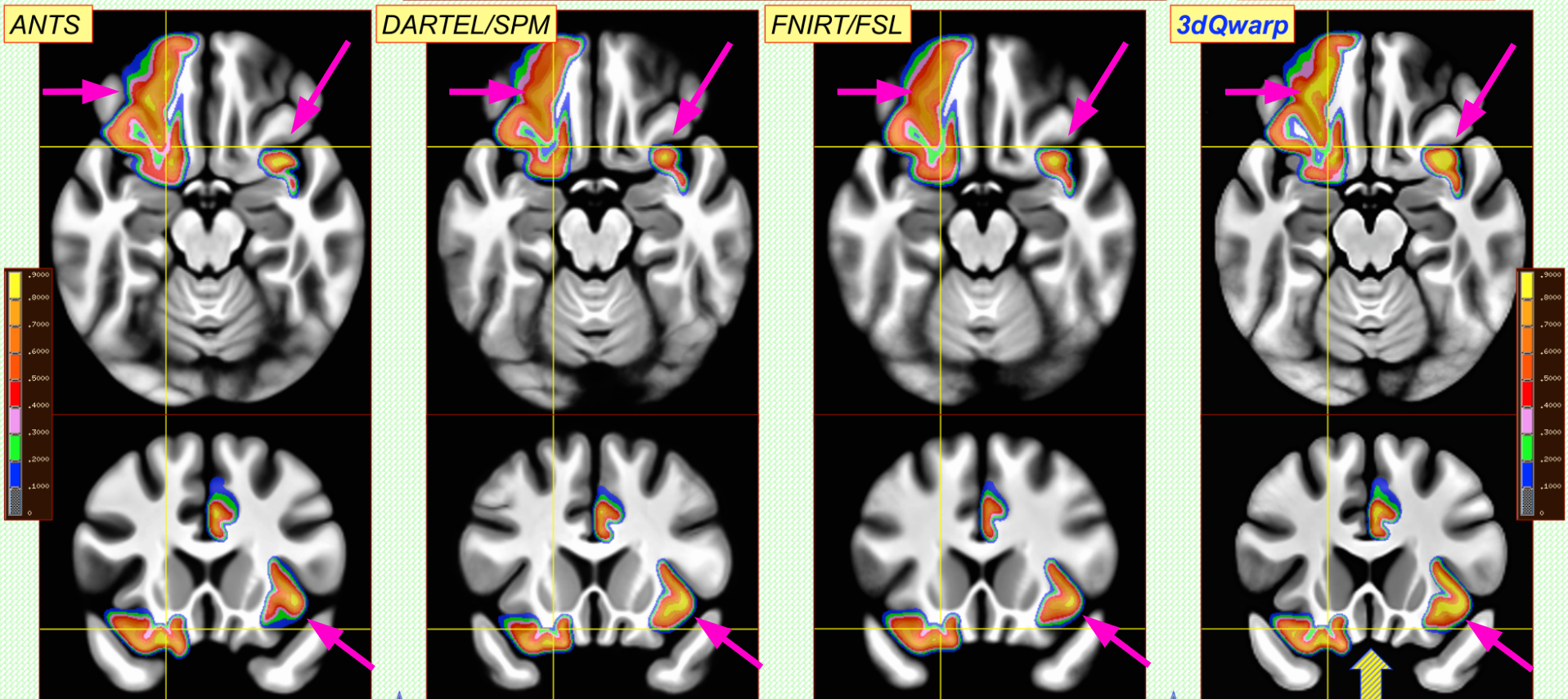
Measuring quality of alignment

Can compare 3dQwarp with other available nonlinear alignment tools

- + For a group of subjects, estimate warp from anat to template
- + Apply warp to labeled ROIs, and measure % overlap in results. (Yellow: >90% overlap)

Align MindBoggle 101 T₁ Datasets to Separate Template:
Overlap Probability Maps for 3 of the Labeled Regions

LH: lateral orbital frontal
RH: caudal anterior cingulate
RH: insula



ANTS, DARTEL and FNIRT run with default settings

(Cox & Glen, 2013, OHBM)

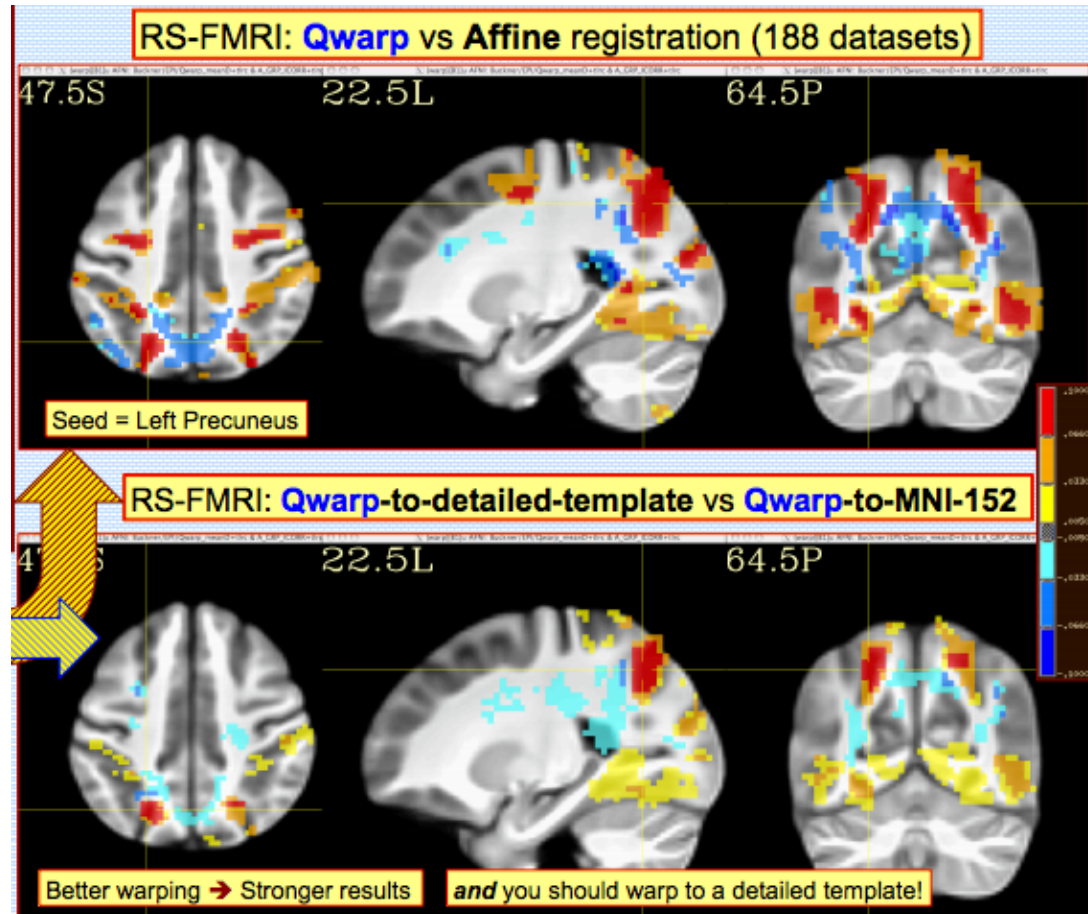
Nonlinear alignment to standard space

Advantages

- Better spatial correspondence across data
→ consistent data reinforces across group
- Final data matches template (reporting coordinates, etc.)

Disadvantages

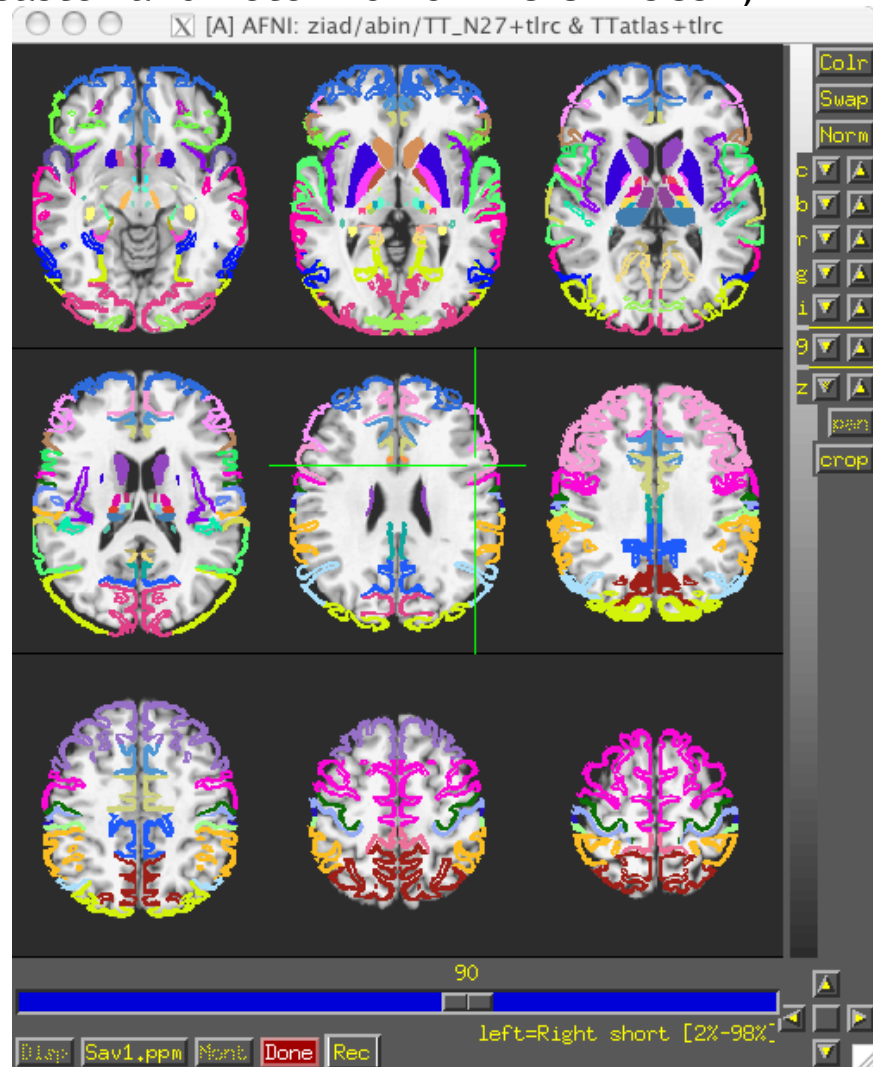
- Individual data is distorted
- Aligned data matches template. Choose template carefully
- Skullstripping must be done much more carefully
→ note that @SSwarper actually *combines* nonlinear warping with skullstripping, so benefit now!
- Processing time much slower (but... such is life)



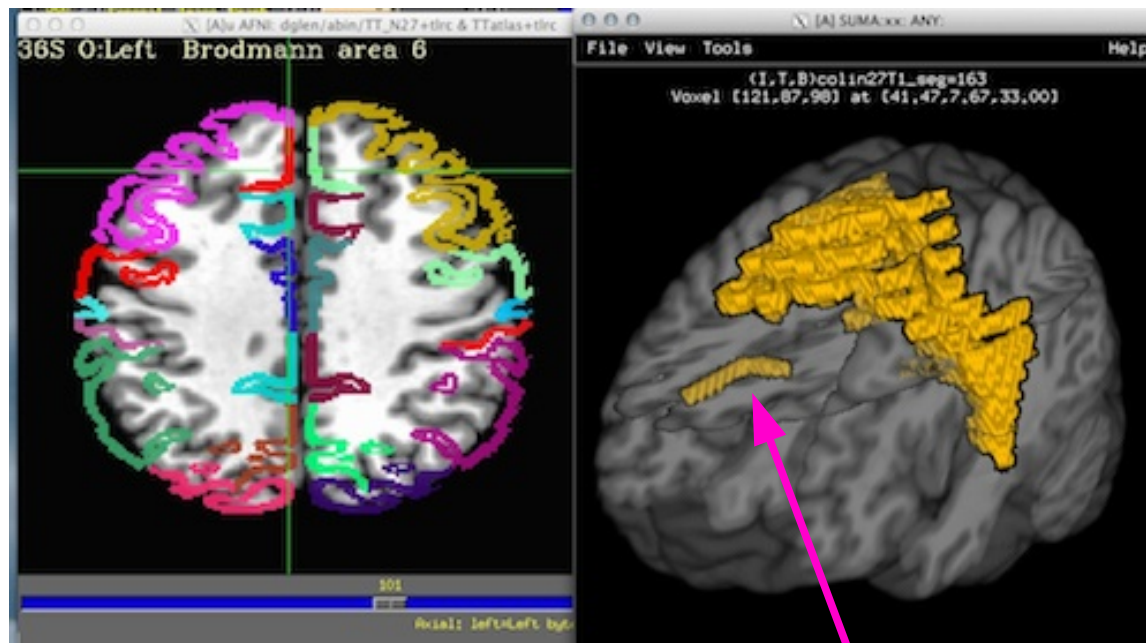
(Cox & Glen, 2013, OHBM)

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)



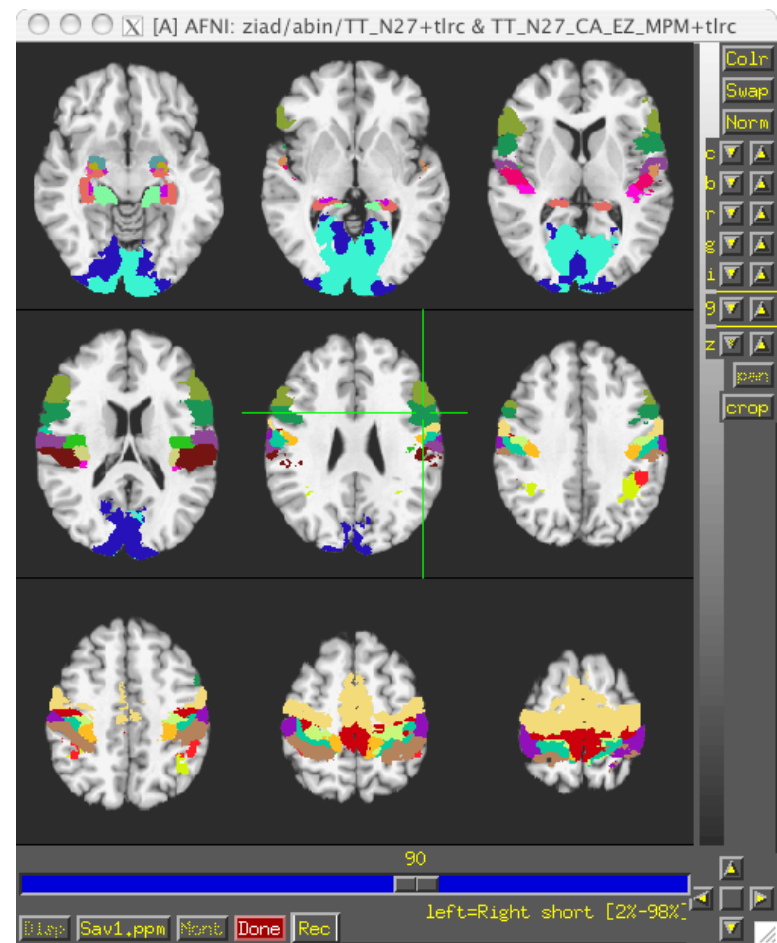
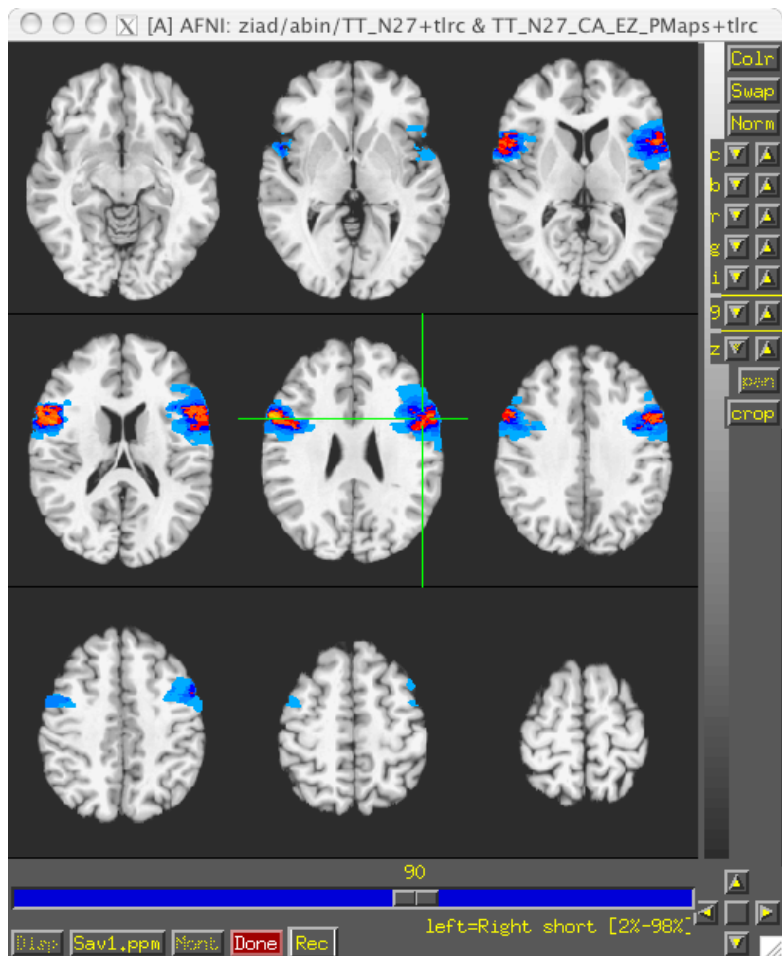
Caution: Talairach Daemon (TT_Daemon) problems



This piece is labeled as BA 6,
but is really another part.

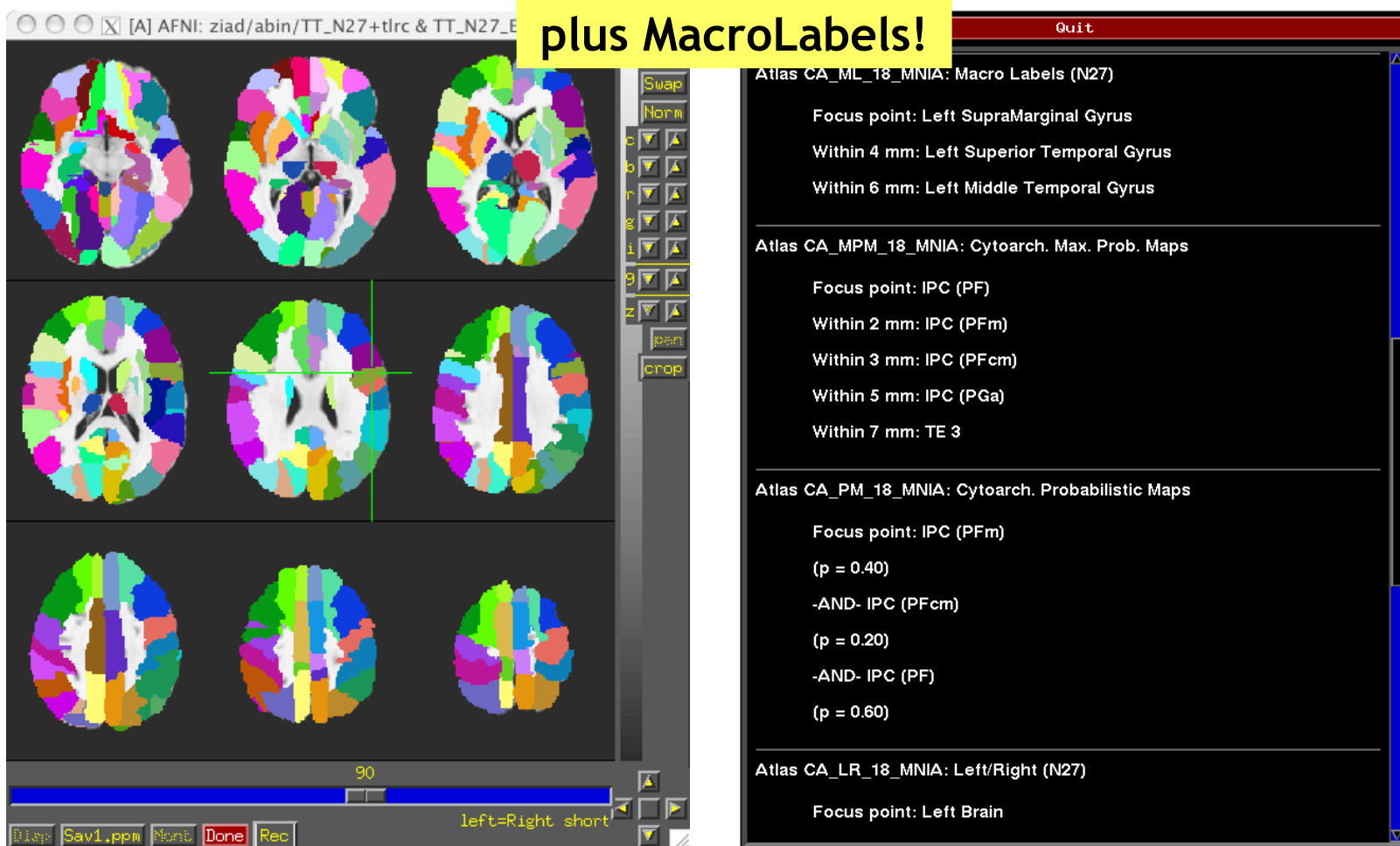
Atlases distributed with AFNI: “Anatomy Toolbox”

- 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
 - ◊ Probabilistic maps and max. probability maps generously contributed by K. Amunts, S. Eickhoff, and K. Zilles of IME, Julich, Germany



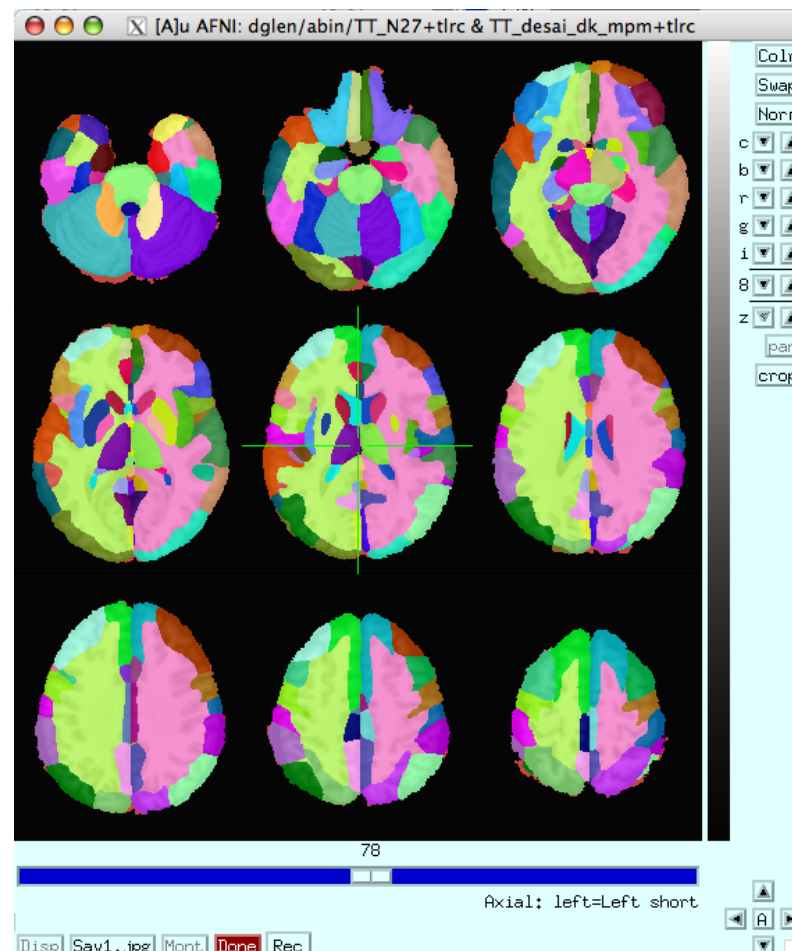
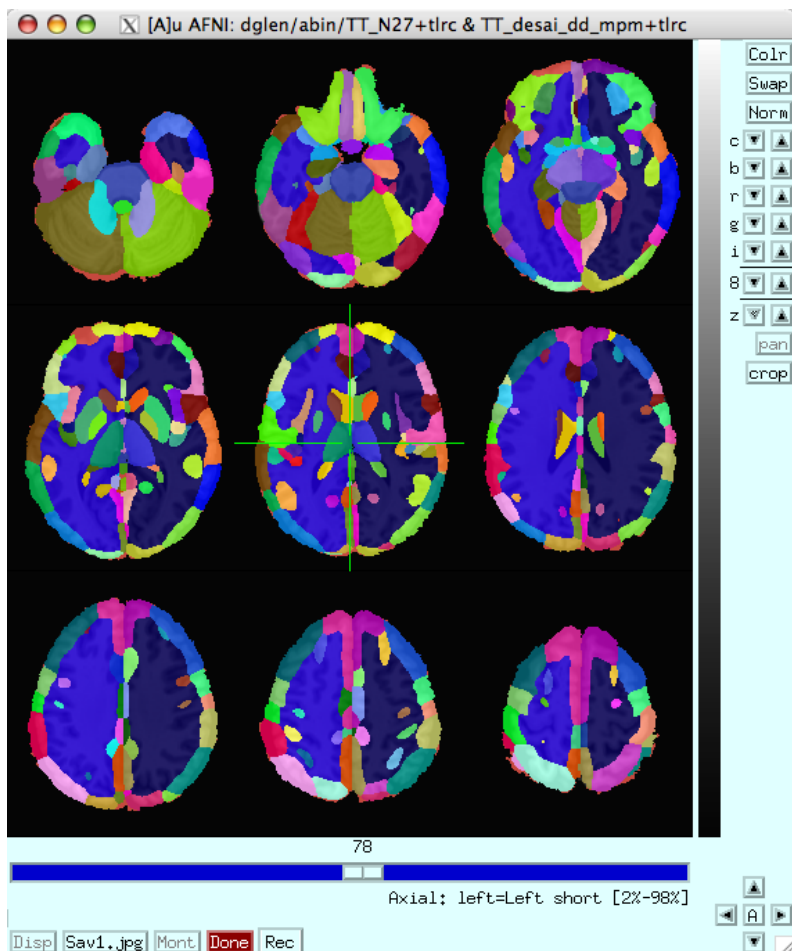
Atlases distributed with AFNI: “Anatomy Toolbox”

- 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
 - ◊ Probabilistic maps and max. probability maps generously contributed by K. Amunts, S. Eickhoff, and K. 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



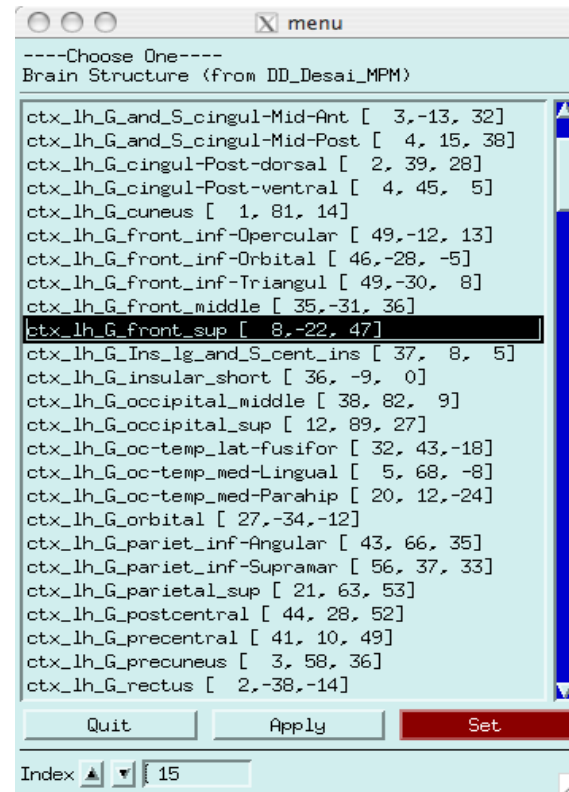
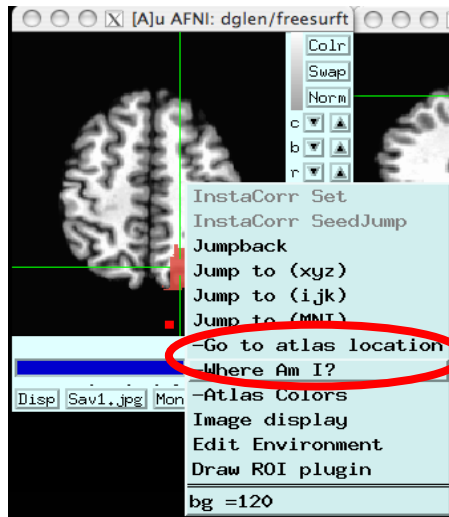
Using atlases in AFNI GUI

- Some fun and useful things to do with `+tlrc` datasets are on the 2D slice viewer.
Ex: can be run in `~/AFNI_data6/afni/`

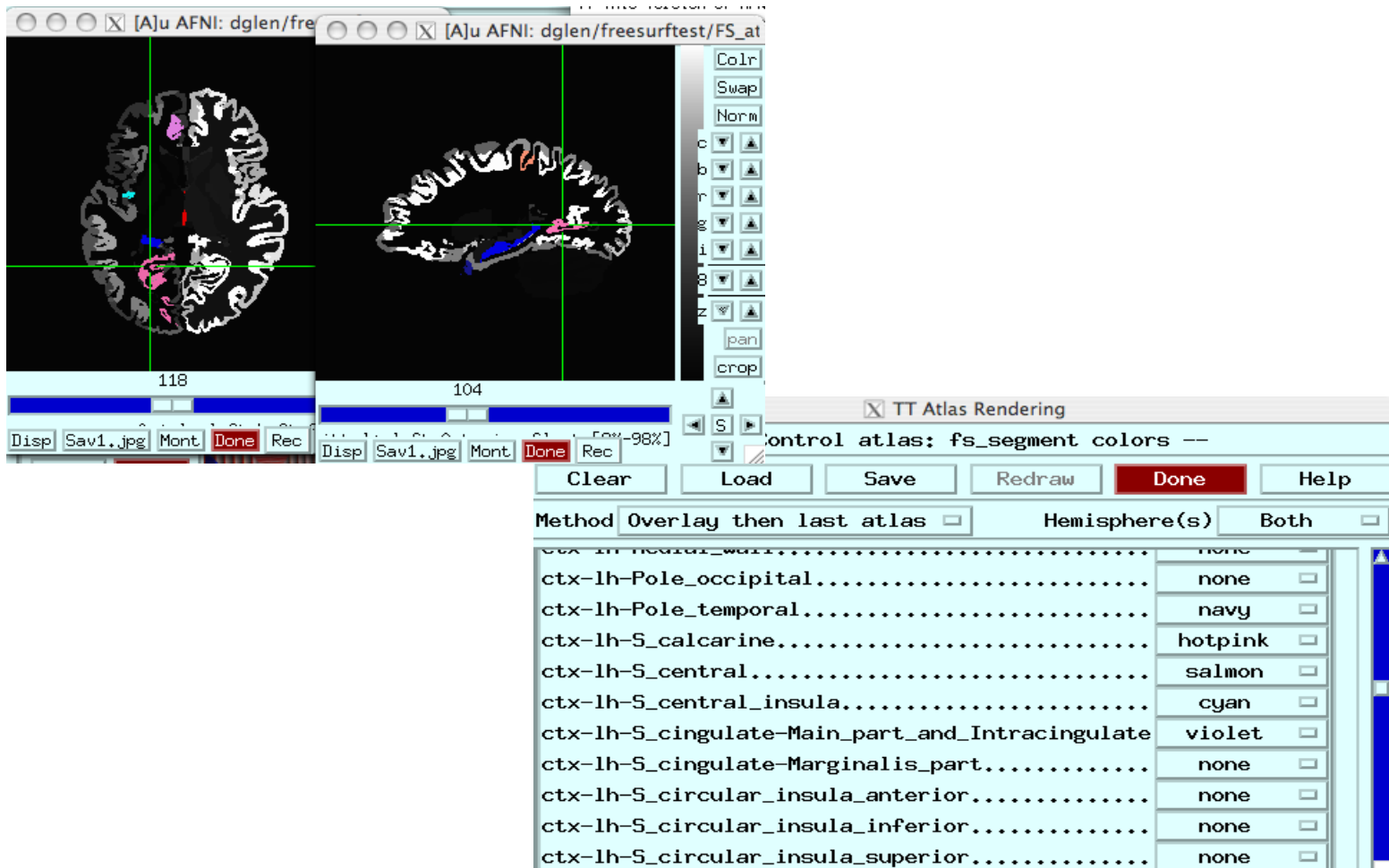
1) Right click to get menu:

- ◇ [\[Go to Atlas Location\]](#)

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



◇ [Atlas colors]



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

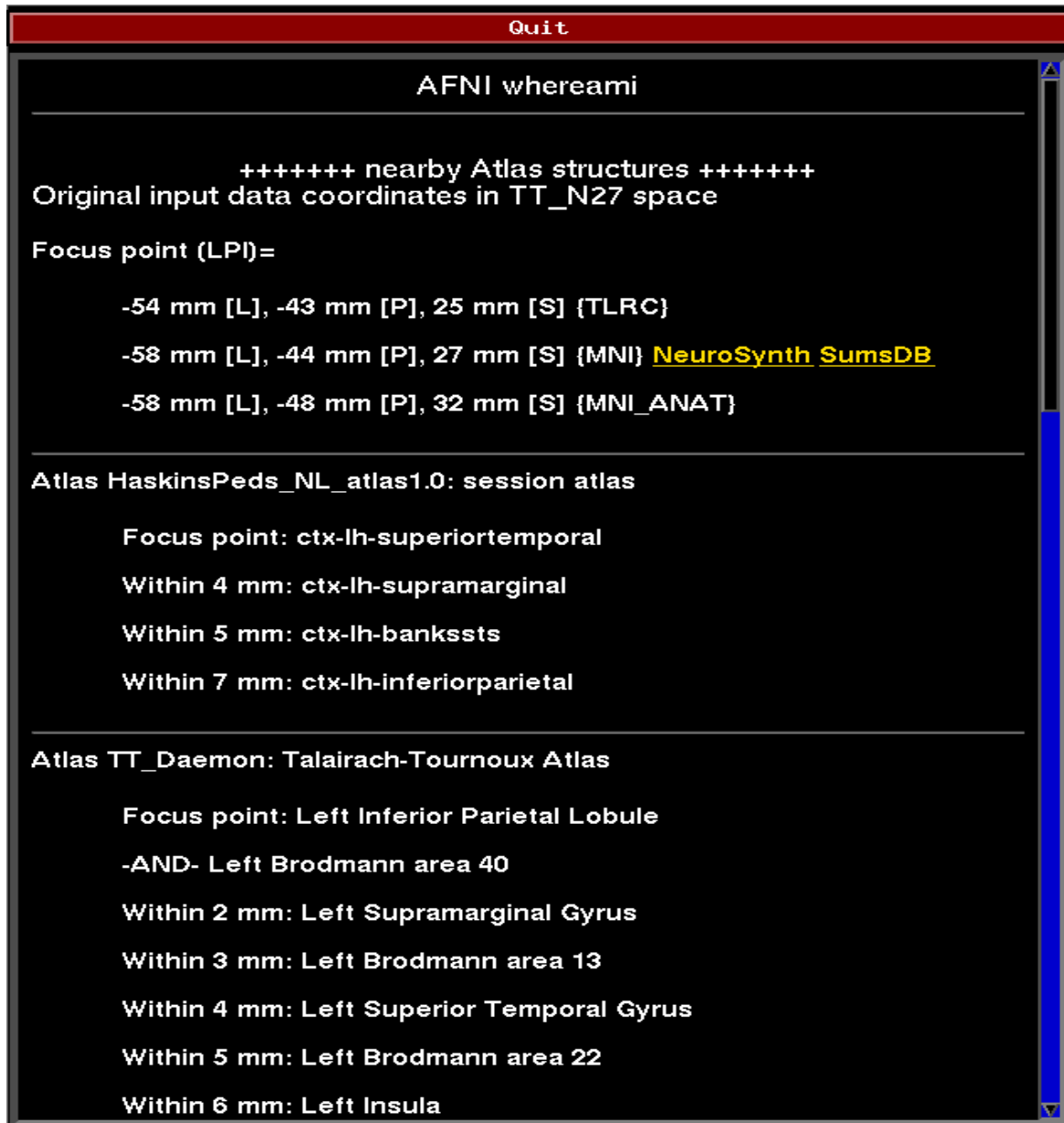
◇ [\[Where am I?\]](#)

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 on the command line

whereami can combine usefully with 3dClusterize:

- 1) 3dClusterize finds cluster volumes, and
- 2) whereami provides detailed info like overlap with atlas regions

Ex: can be run in ~/AFNI_data6/afni/

```
# Threshold the index-0 vol (an F-stat) at >9.5 and
# find clusters with >=1000 voxels
```

```
3dClusterize -1sided RIGHT 9.5 \
  -clust_nvox 1000 -NN 1 \
  -inset func_slim+orig -ithr 0 -idat 0 \
  > clusts.1D
```

```
# Use the center of mass coords in
# cols [1,2,3] to show location according
# to several atlases (TT, MNI, etc.); also
# shows nearby structures
```

```
whereami \
  -coord_file \
  clusts.1D' [1,2,3]' \
  -tab | more
```

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

Original input data coordinates in TLRC space

Focus point (LPI)          Coord.Space
  0 mm [L],   0 mm [P],   0 mm [S]  {Unknown}
  2 mm [R],  -60 mm [P],   9 mm [S]  {TT_N27}
  2 mm [R],  -60 mm [P],   9 mm [S]  {TT_avg}

Atlas      Within  Label          Prob.  Code
TT_Daemon  0.0    Right Posterior Cingulate  MPM    20
TT_Daemon  2.0    Right Cuneus              MPM    40
TT_Daemon  3.0    Left Posterior Cingulate  MPM    220
TT_Daemon  4.0    Left Cuneus               MPM    240
TT_Daemon  6.0    Right Lingual Gyrus      MPM    32
CA_N27_ML  0.0    Right Calcarine Gyrus    ---    44
CA_N27_ML  1.0    Left Calcarine Gyrus     ---    43
CA_N27_ML  1.0    Left Lingual Gyrus       ---    47
CA_N27_ML  2.0    Right Lingual Gyrus      ---    48
CA_N27_ML  5.0    Cerebellar Vermis (4/5)  ---    111
CA_N27_MPM 0.0    Area 17                  ---    181
CA_N27_MPM 3.0    Area 18                  ---    240
CA_N27_PM  0.0    Area 17                  0.60   38
CA_N27_PM  0.0    Area 18                  0.30   67
```

whereami on the command line

whereami can also report the overlap of ROIs with atlases

Ex: can be run in ~/AFNI_data6/afni/

Quick way to make test ROI a sphere at a given location)

echo -14 66 23 > tmp.txt

3dUndump

-xyz

-prefix tmproi.nii.gz

-master anat+tlrc

-datum byte

-srad 9.5

tmp.txt

\
\
\
\
\
\

report overlap

**whereami **

-omask tmproi.nii.gz



```

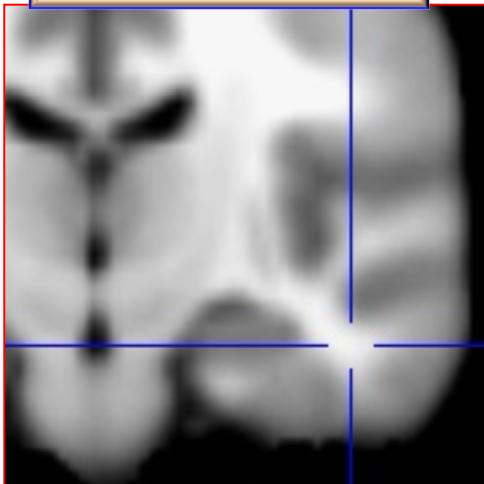
++ Input coordinates orientation set by default rules to RAI
++ In ordered mode ...
++ Have 2 unique values of:
  0  1
++ Skipping unique value of 0
++ =====
++ Processing unique value of 1
++   3695 voxels in ROI
++   3695 voxels in atlas-resampled mask
Intersection of ROI (valued 1) with atlas TT_Daemon (sb0):
  63.3 % overlap with Right Precuneus, code 45
  17.6 % overlap with Right Cuneus, code 40
  7.9 % overlap with Right Posterior Cingulate, code 20
  ----
  88.8 % of cluster accounted for.

Intersection of ROI (valued 1) with atlas TT_Daemon (sb1):
  29.7 % overlap with Right Brodmann area 31, code 107
  10.2 % overlap with Right Brodmann area 18, code 95
  3.2 % overlap with Right Brodmann area 7, code 87

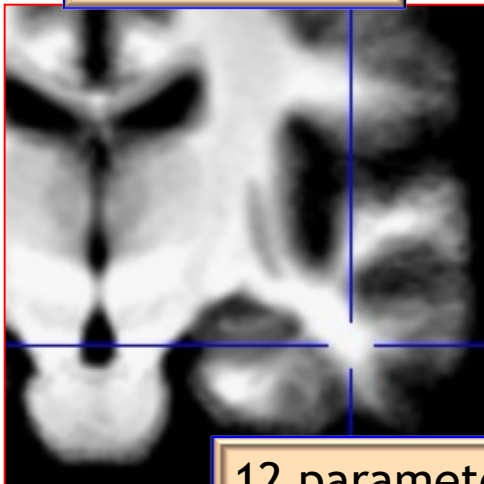
```

Make your own template

MNI 152 template



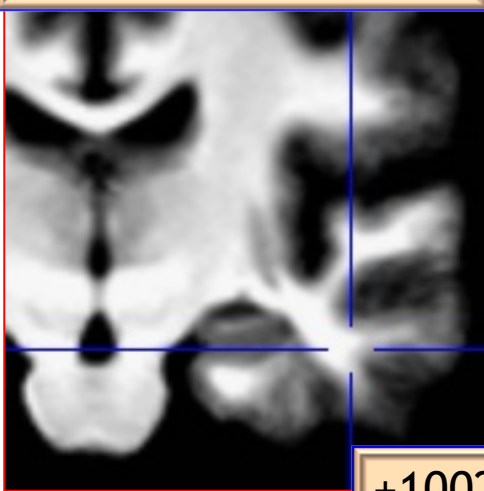
Linear = Affine



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

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/
```

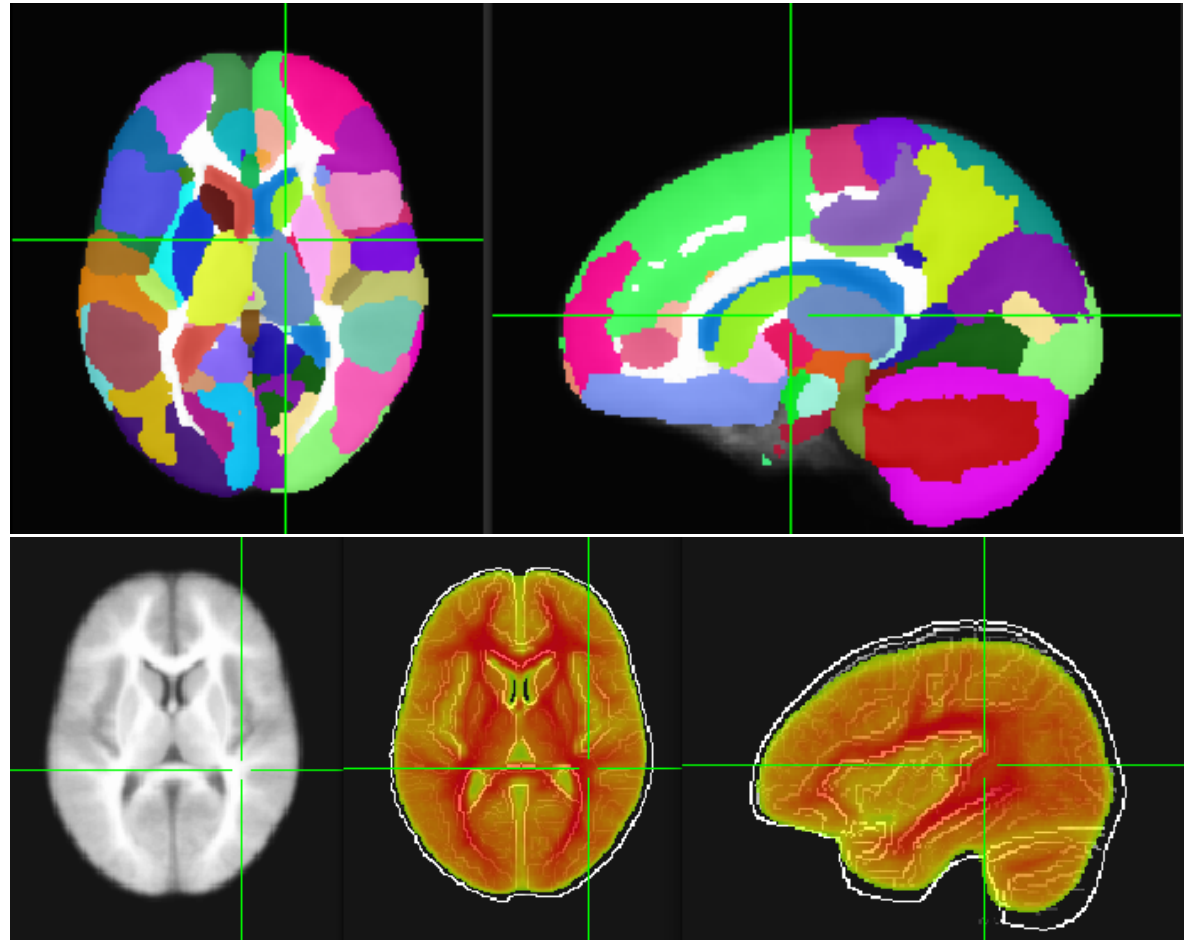
Then:

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

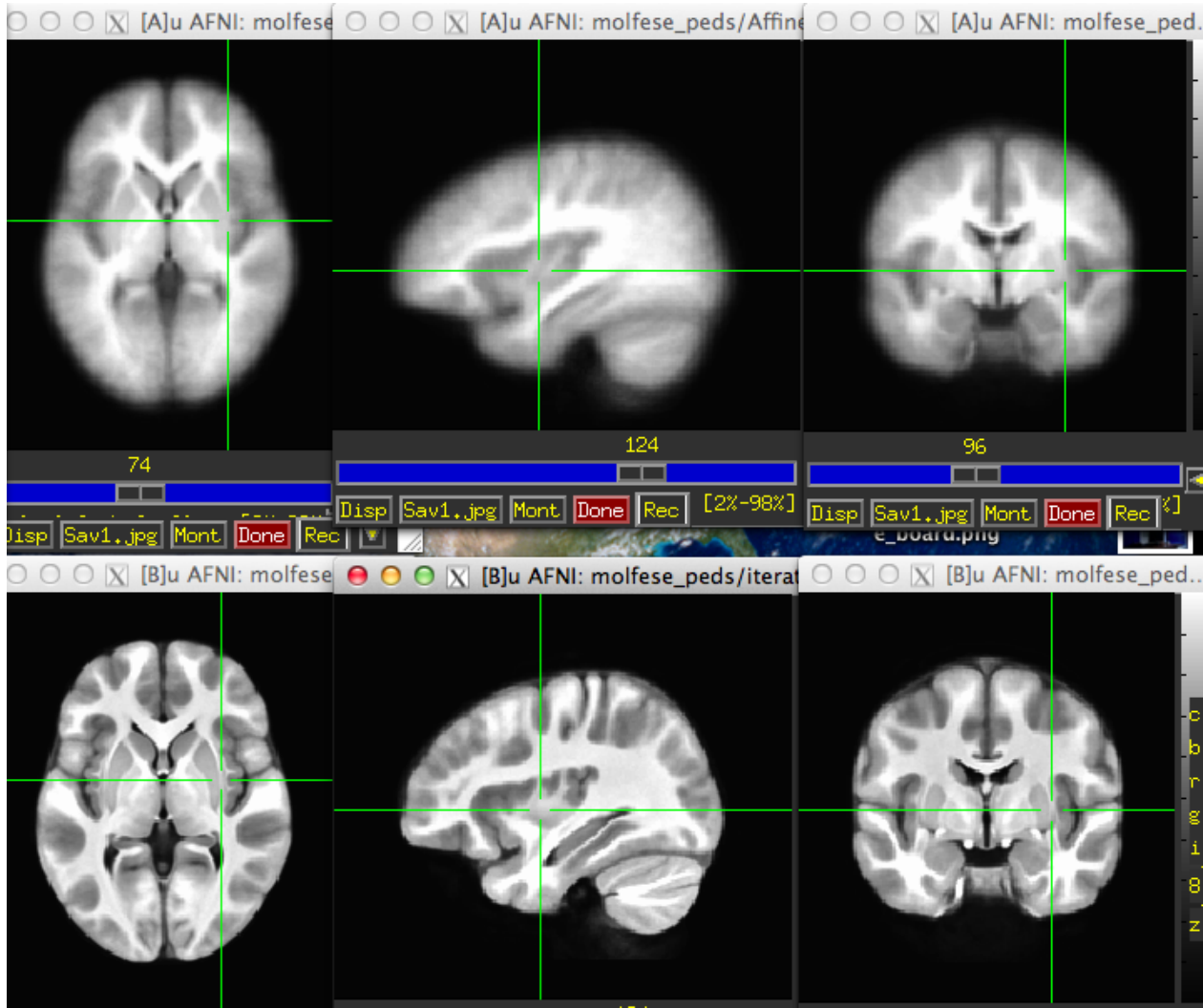
In ~/MyCustomAtlases/ you will now find atlas_for_all.nii along along with a modified CustomAtlases.niml file.

Haskins Pediatric Atlas

- 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



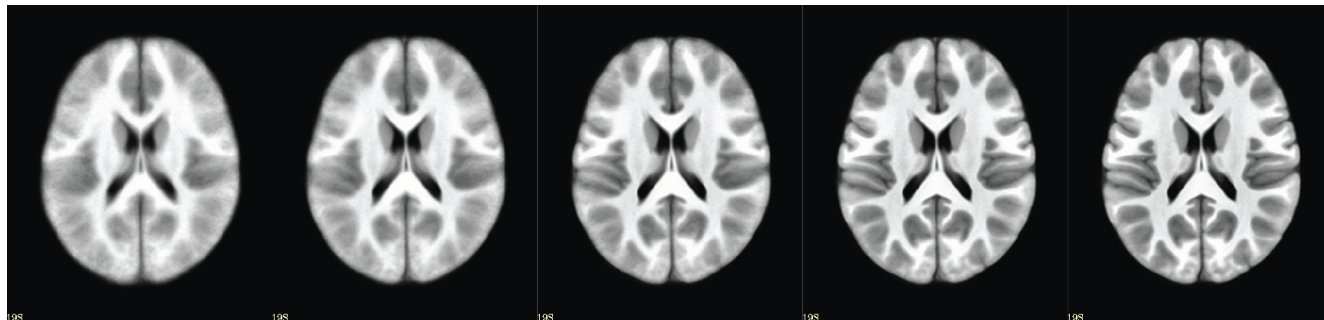
Haskins Pediatric Atlas: the templates



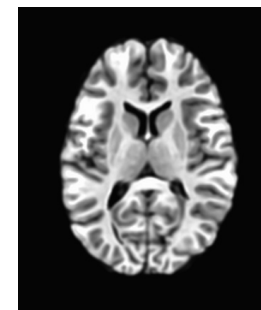
Affine Group

Nonlinear Group I - iterative

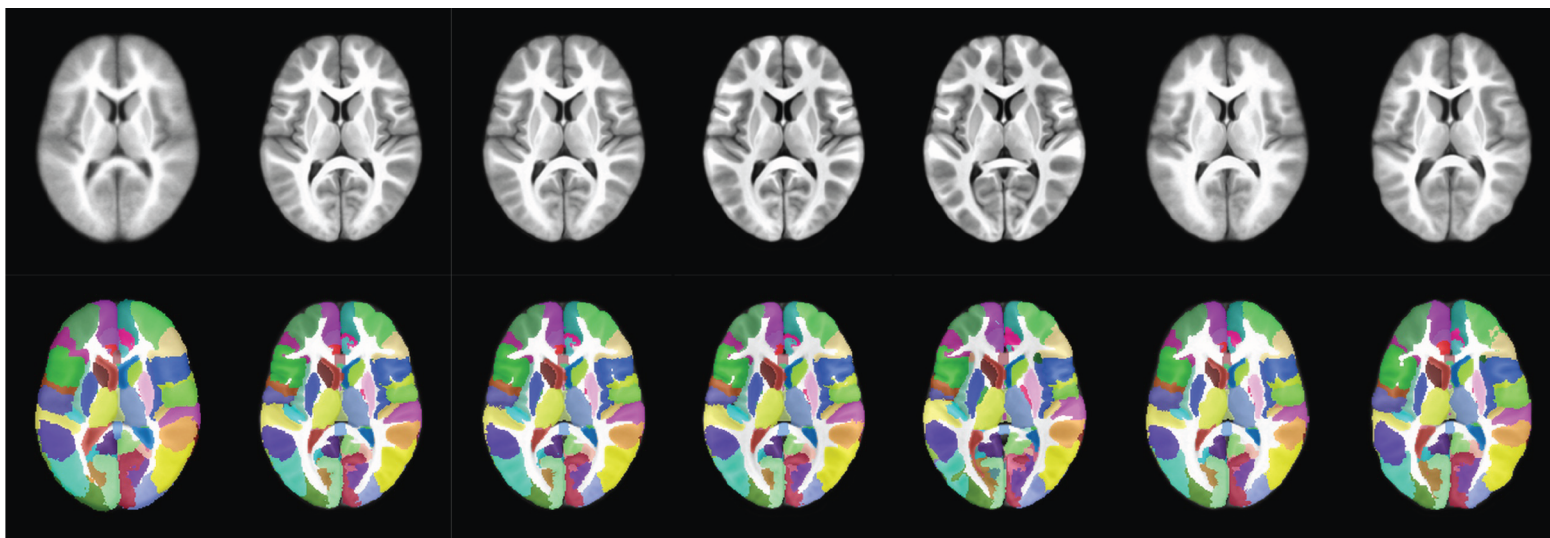
ALTERNATIVE ATLAS CREATION TECHNIQUES: ITERATIVE AND TYPICAL METHODS



Iterative nonlinear alignment to affine template with progressively smaller patch sizes



**“Typical”
Brain**



Affine

Affine
Iterative

Typical
Iterative

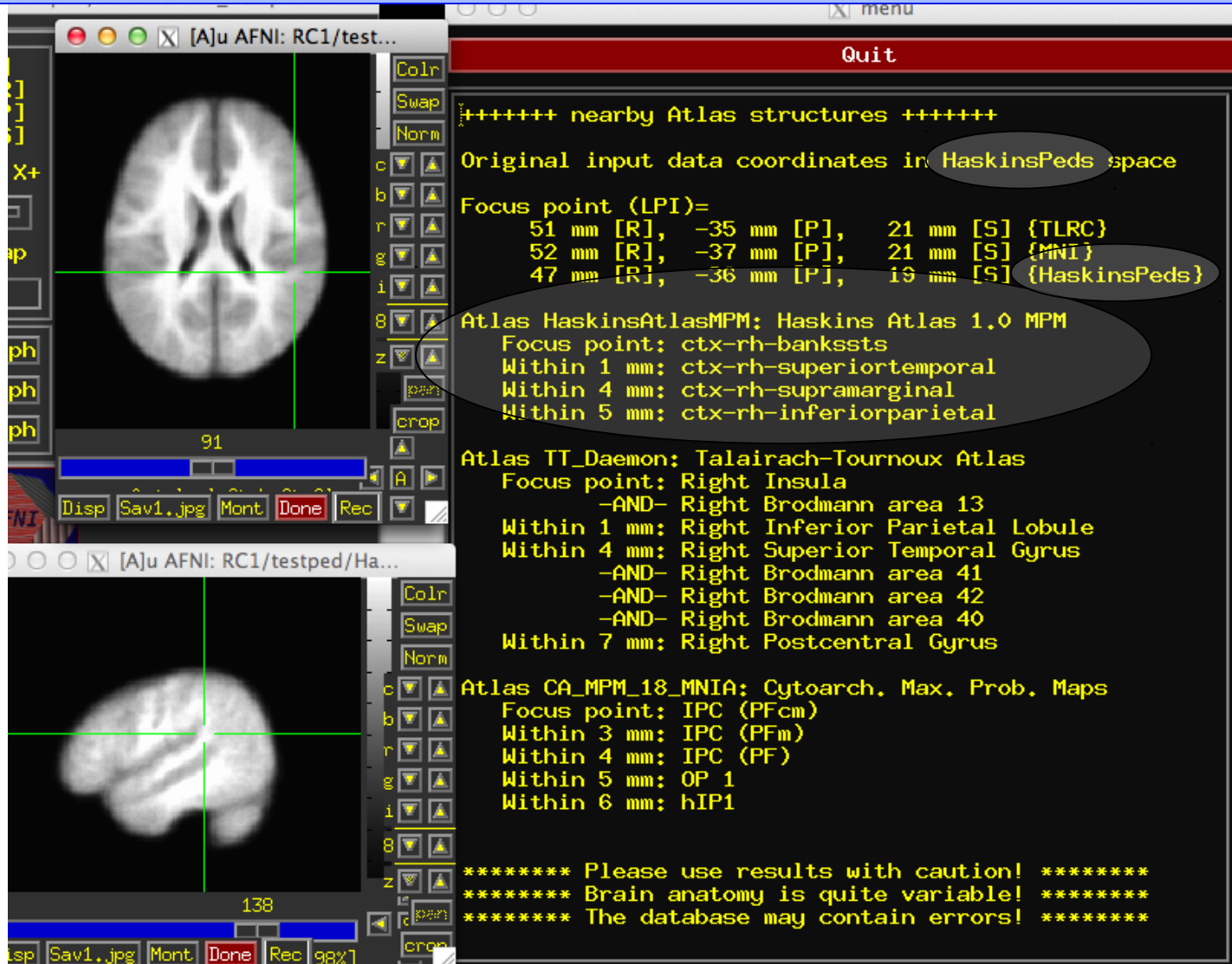
MNI
Iterative

Nonlinear
to MNI

Nonlinear
to Affine

Nonlinear
to Typical

Haskins Pediatric Atlas



The screenshot displays the AFNI software interface. On the left, two axial brain MRI slices are shown with green crosshairs. The top slice is labeled '91' and the bottom slice is labeled '138'. 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). Below the slices are buttons for 'Disp', 'Sav1.jpg', 'Mont', 'Done', and 'Rec'. On the right side of the screen, a text window titled 'Quit' contains 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

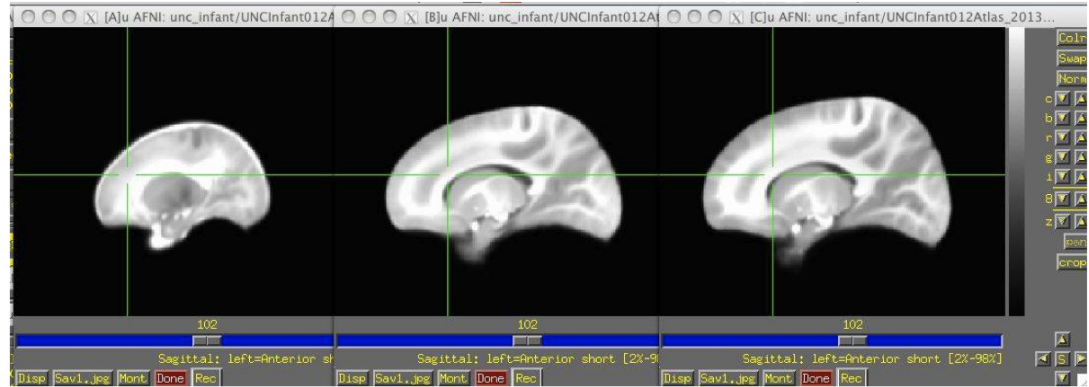
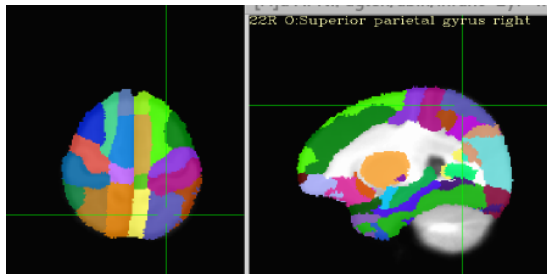
Atlas TT_Daemon: Talairach-Tournoux Atlas
Focus point: Right Insula
-AND- Right Brodmann area 13
Within 1 mm: Right Inferior Parietal Lobule
Within 4 mm: Right Superior Temporal Gyrus
-AND- Right Brodmann area 41
-AND- Right Brodmann area 42
-AND- Right Brodmann area 40
Within 7 mm: Right Postcentral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

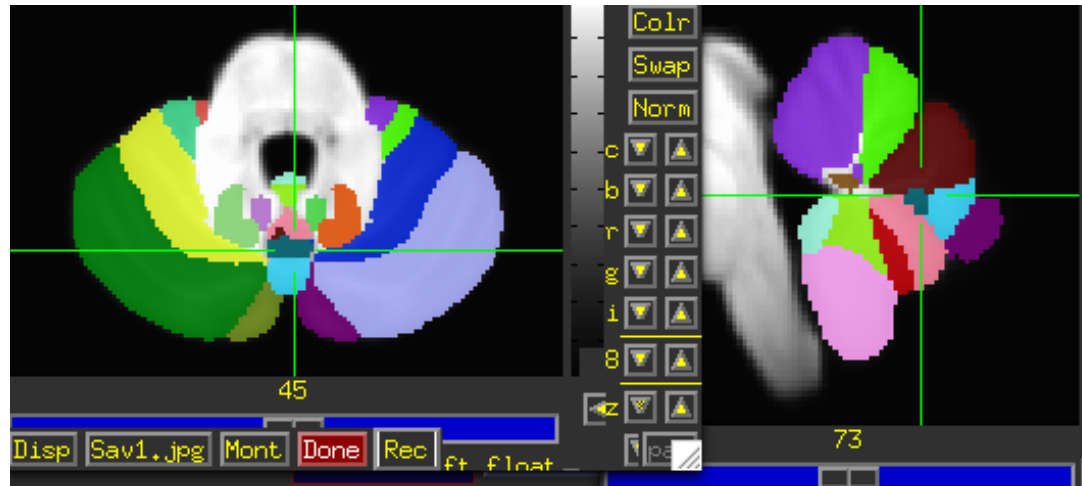
Atlases and Templates Available!

- 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

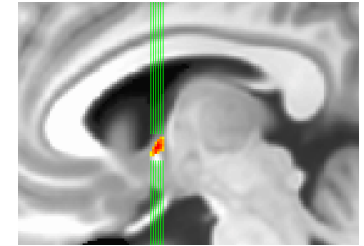
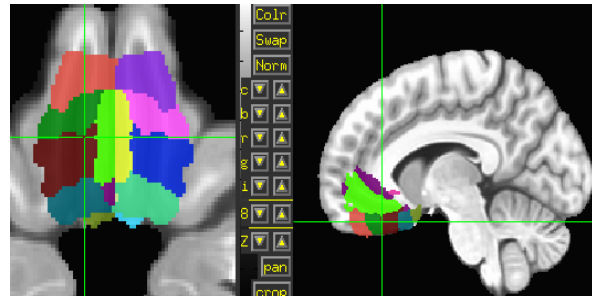


More Atlases and Templates Available!

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?

The screenshot shows the AFNI software interface with several windows open. On the left, there are three brain slices: a coronal view, a sagittal view, and a coronal view with colored atlas regions. In the center, there is a terminal window displaying the following text:

```

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

```

On the right, there is another terminal window showing the command-line output for the atlas structure:

```

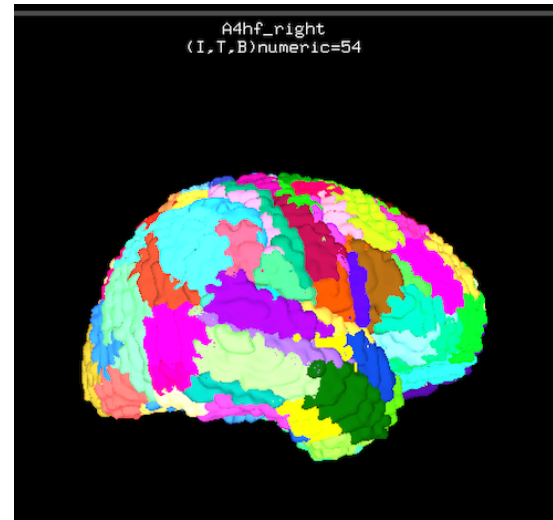
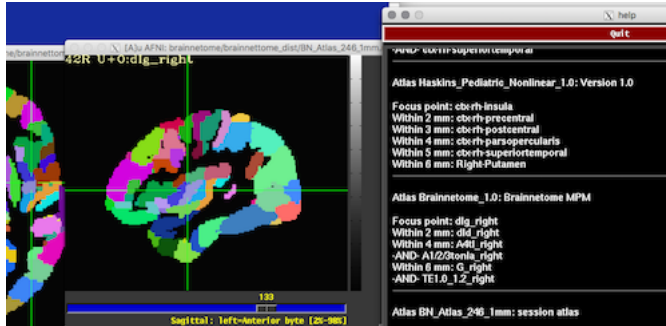
cornu_ammonis_1
(I,T,B)numeric=98

```

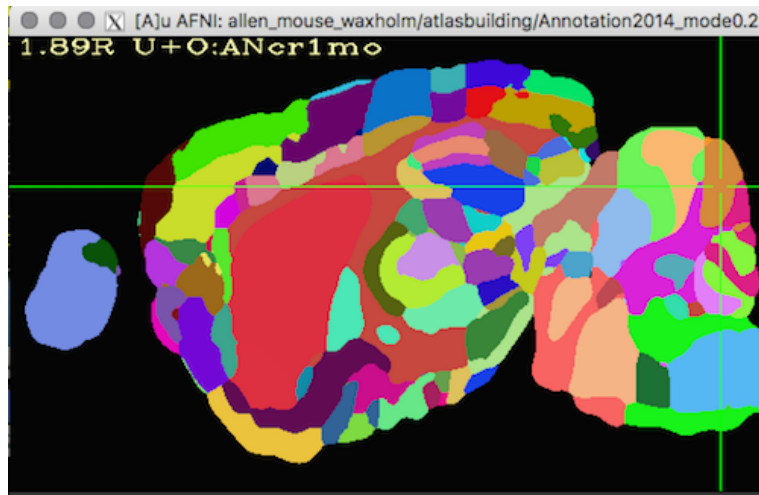
At the bottom right, there is a 3D rendering of the brain with colored atlas regions overlaid, showing the dentate gyrus and cornu ammonis structures in various colors (green, yellow, orange, red, purple, blue, cyan).

Even More Atlases and Templates Available!

Brainnetome



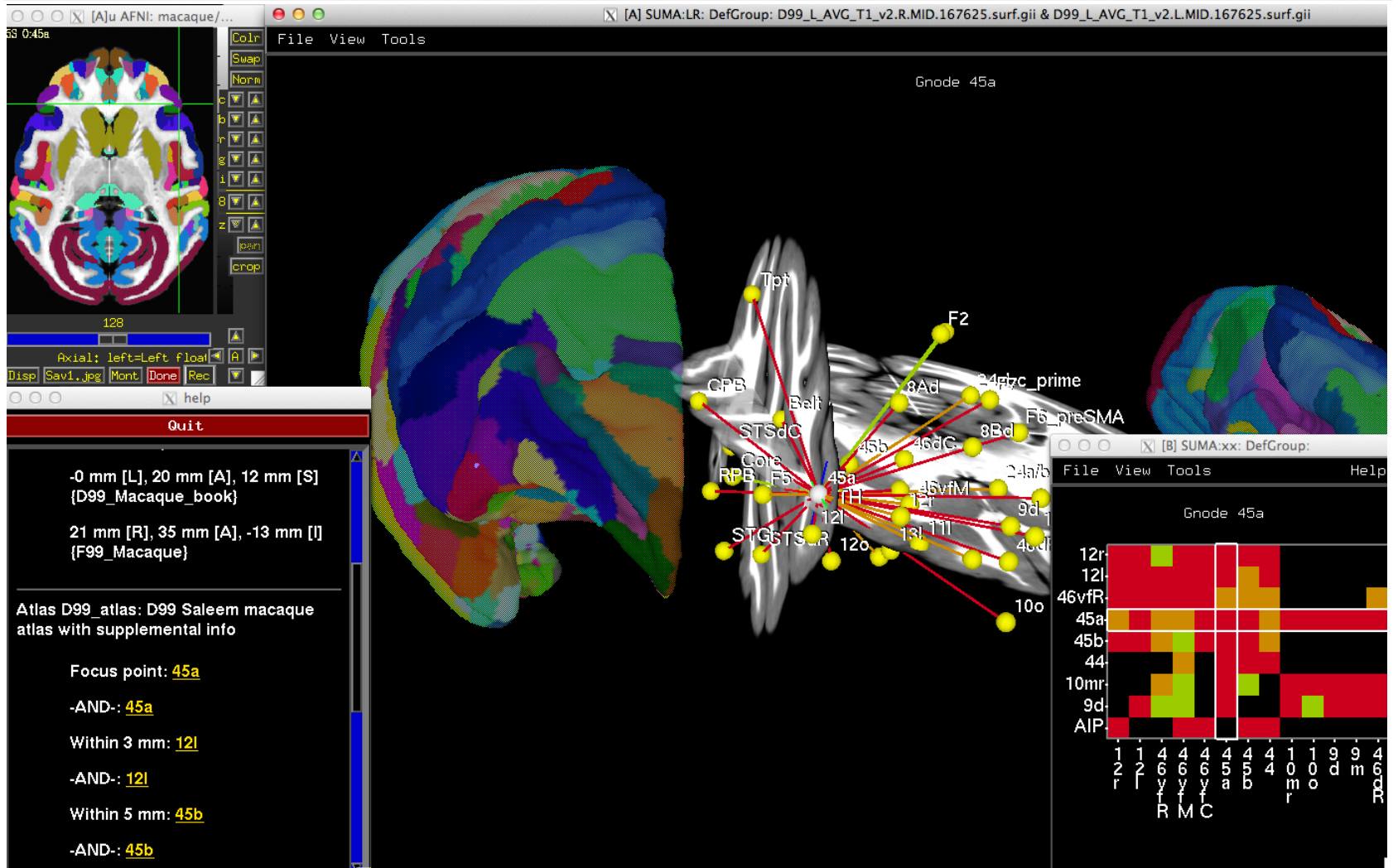
Allen Mouse Brain



All of these are user requests or contributions!

What do you need?

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



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)

+32mm rostral to EBZ

f f f
R M C

15R 0:46v

Mapping the digital atlas onto different macaques MRI

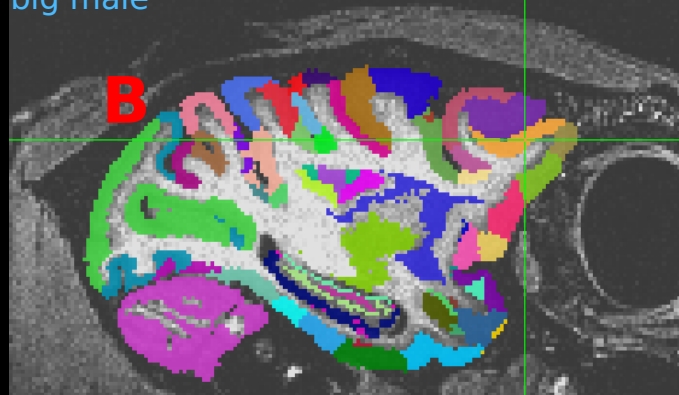
D99 - Digital atlas



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

14.25R 0:46v

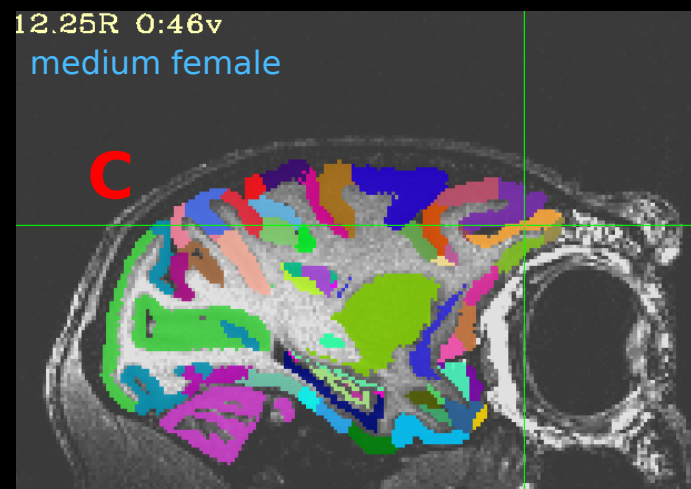
big male



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

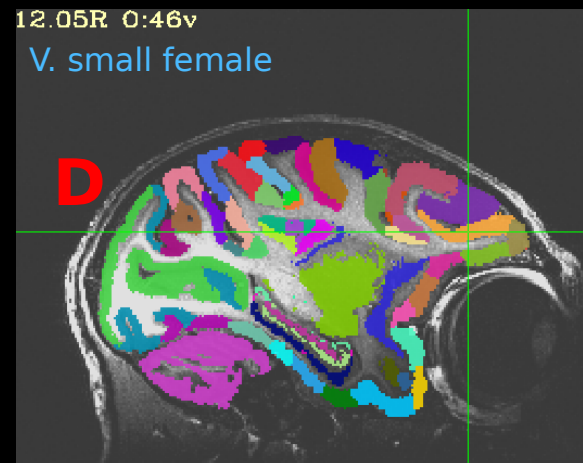
12.25R 0:46v

medium female



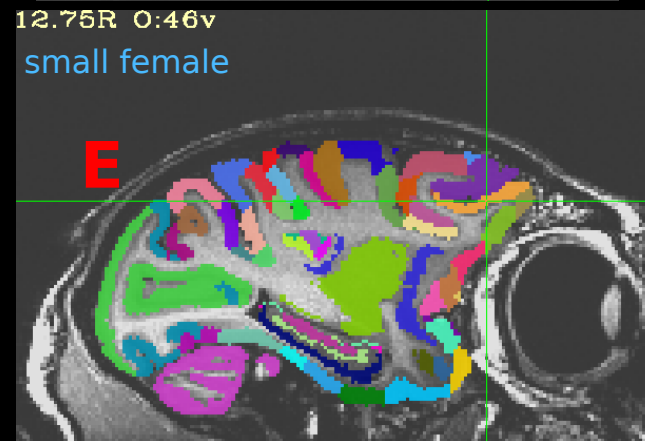
12.05R 0:46v

V. small female



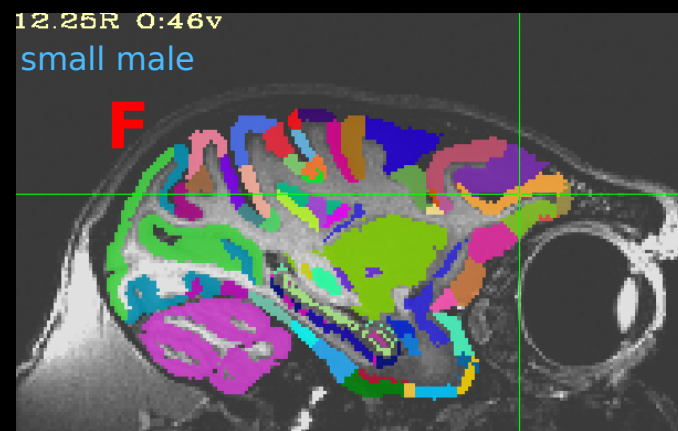
12.75R 0:46v

small female



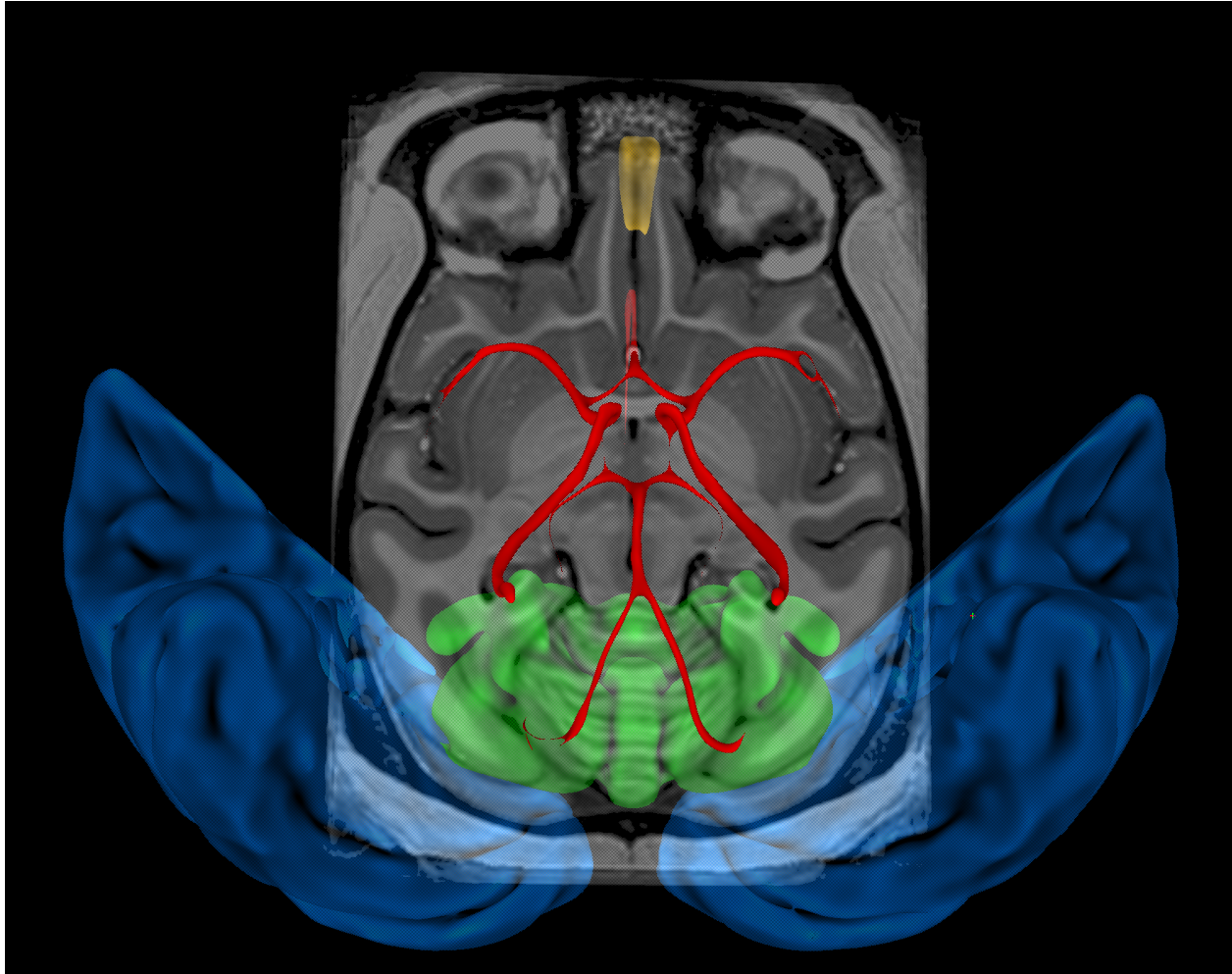
12.25R 0:46v

small male



NMT (NIH Macaque Template)

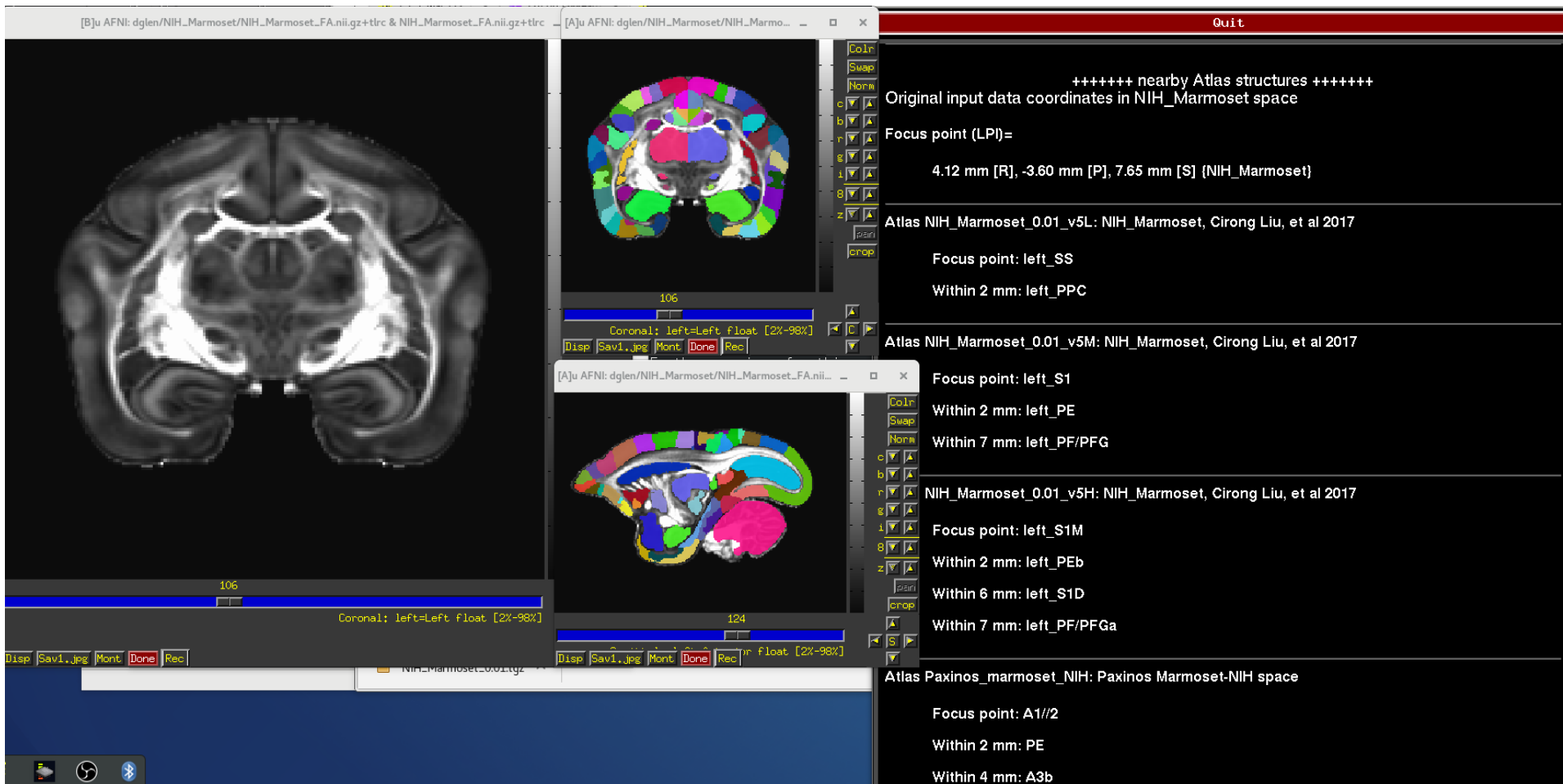
Group template from 31 macaques (+ surfaces, GM/WM/CSF segmentation)



(Seidlitz, et al., 2017)

NIH Marmoset Template

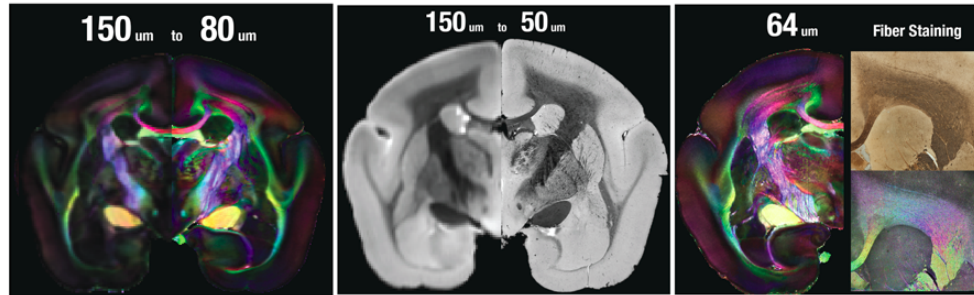
Individual marmoset template - 150um resolution



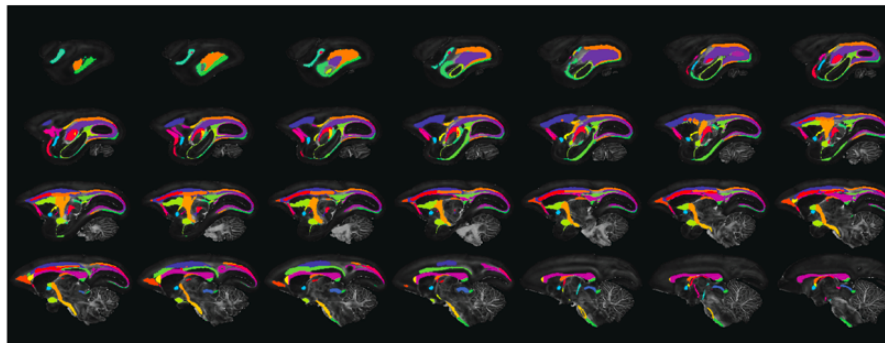
(Liu, Ye, Yen, Newman, Glen, Leopold, Silva, 2018)

2018: *improved* NIH Marmoset Template

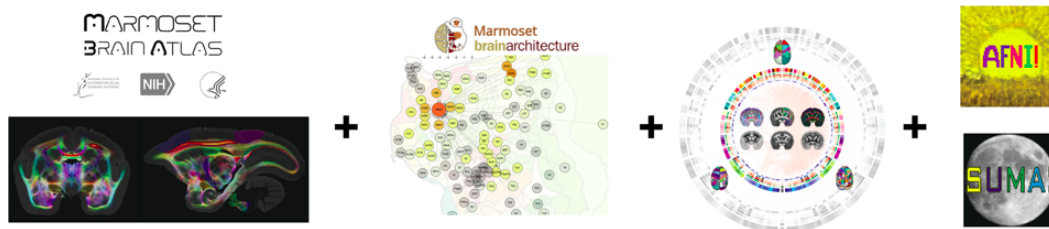
Better Data



Detailed labels



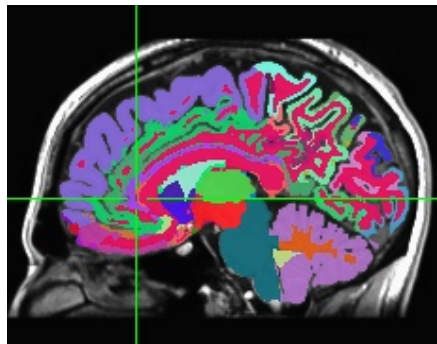
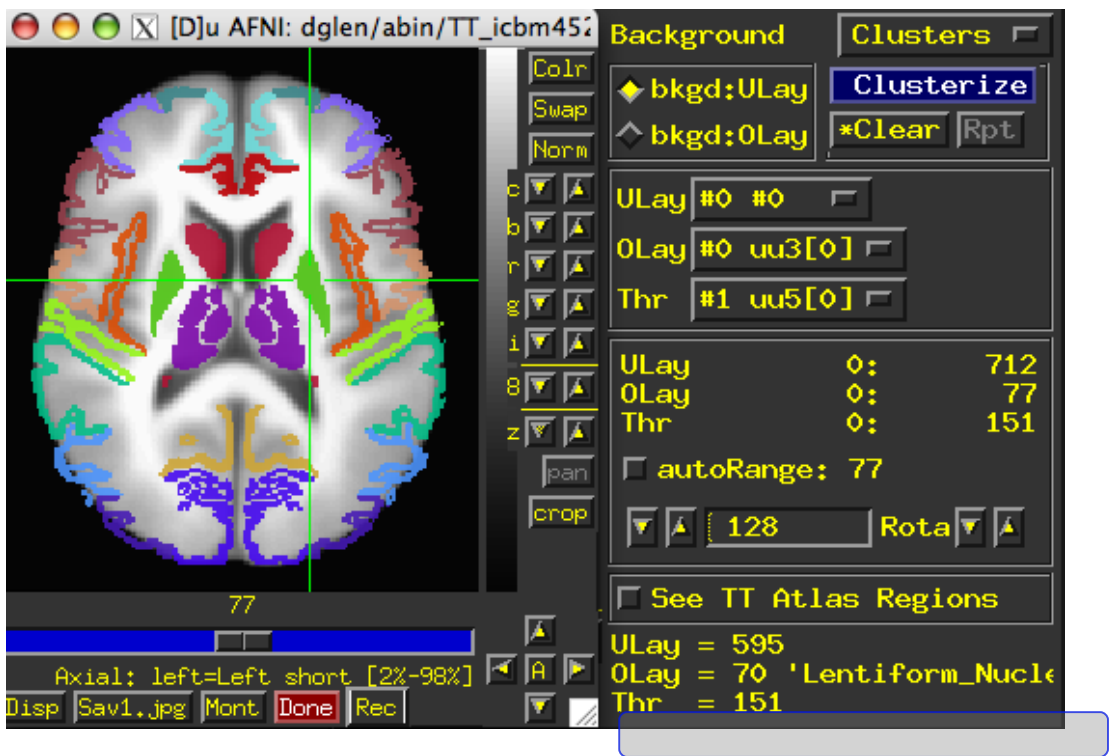
Support with tracing data, connectome and atlas utilities



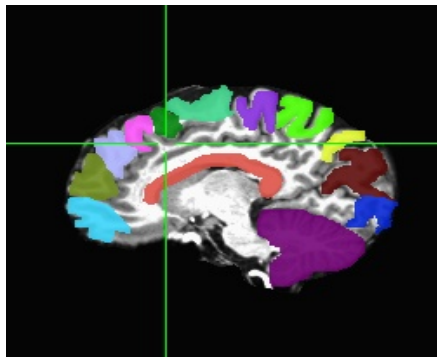
(Liu et al., 2018, SfN)

Individual Subjects

@SUMA_MakeSpecFS - atlasizes too!



FreeSurfer segmentation



Manual segmentation

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

Web-based atlases

Several presently available (probably a growing number):
NeuroSynth, LinkrBrain, BrainMap.org, Allen Brain, ...

The collage illustrates the workflow from web-based atlas search to local software visualization. On the left, the AFNI software interface shows a brain slice with a focus point and a list of nearby anatomical structures. The central SumsDB website displays search results for coordinates, listing various brain regions and their coordinates. The right side shows the Neurosynth website interface, including a search bar for coordinates (26, 38, -6) and resulting brain connectivity maps.

foci_id	name	original x	original y	original z	flirt x	flirt y	flirt z
106081	Christensen_CC07	33	36	-9	30.2	3	26.1
99935	Downing_CC06	24	37	3	26.1	3	26.1
95817	Noguchi_CC05	32	44	-8	30.7	4	26.1
95087	Honey_CC05	24	36	-8	22.2	3	26.1
89538	LaBar_CC03	19	34	-4	19.9	3	26.1
77651	Ullén_JN08	26	39	-12	24.5	3	26.1
77635	Ullén_JN08	26	39	-10	25.1	3	26.1
77429	Pochon_JN08	30	40	-12	28.5	3	26.1
77316	Plailly_JN08	19	34	-9	18.9	3	26.1
76942	Petrovic_JN08b	24	36	-10	22.1	3	26.1

set each of the following environment variables in ~/.afnirc to YES:

AFNI_WEBBY_WAMI
AFNI_NEUROSYNTH

Web-based atlases

LinkrBrain - coordinates

The screenshot displays the AFNI software interface with several windows open. The main window shows a brain scan with a cluster of voxels highlighted in red and yellow. 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 SaveTabl Clust SaveMsk WamI Done

Aux.Dset From To Mean Scat.1D Clear

[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

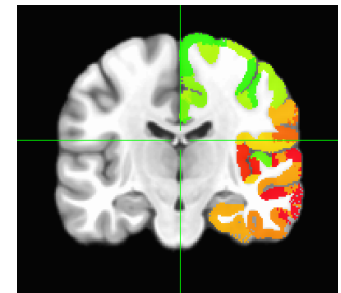
Query of coordinates to linkrbrain.org correlations

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!



HCP atlas -
Glasser →
Megan Robinson
and Mike
Beauchamp

Supplements

extra stuff

S1: Labeltables

Reading/creating labeltables

The text or string description of each ROI can be added to a dset by creating a “labeltable” that is either added to a file’s header or is a separate file pointed to in the header.

To view a labeltable on a dset:



3dinfo -labeltable DSET_NAME

```
<VALUE_LABEL_DTABLE
  ni_type="2*String"
  ni_dimen="118" >
  "4" "Left-Inf-Lat-Vent"
  "10" "Left-Pallidum"
  "79" "ctx-lh-transversetemporal"
  "88" "ctx-rh-inferiorparietal"
  "97" "ctx-rh-paracentral"
  "5" "Left-Cerebellum-White-Matter"
  "11" "3rd-Ventricle"
  "20" "Left-choroid-plexus"
  "89" "ctx-rh-inferiortemporal"
  "98" "ctx-rh-parsopercularis"
```

S1: Labeltables

Reading/creating labeltables

The text or string description of each ROI can be added to a dset by creating a “labeltable” that is either added to a file’s header or is a separate file pointed to in the header.

To view a labeltable on a dset:



```
3dinfo -labeltable DSET_NAME
```

To make a labeltable and attach it to a file:

```
@MakeLabelTable \
  -lab_file LABEL_FILE 1 0 \
  -labeltable OUTPUT_LT \
  -dset DSET_NAME
```

```
<VALUE_LABEL_DTABLE
  ni_type="2*String"
  ni_dimen="118" >
  "4" "Left-Inf-Lat-Vent"
  "10" "Left-Pallidum"
  "79" "ctx-lh-transversetemporal"
  "88" "ctx-rh-inferiorparietal"
  "97" "ctx-rh-paracentral"
  "5" "Left-Cerebellum-White-Matter"
  "11" "3rd-Ventricle"
  "20" "Left-choroid-plexus"
  "89" "ctx-rh-inferiortemporal"
  "98" "ctx-rh-parsopercularis"
```

where LABEL_FILE contains one column of integer keys and one column of string values; OUTPUT_LT is the name for the created new table; and DSET_NAME is the dset it gets attached to.

S2: Manual transform to Talairach space using AFNI GUI

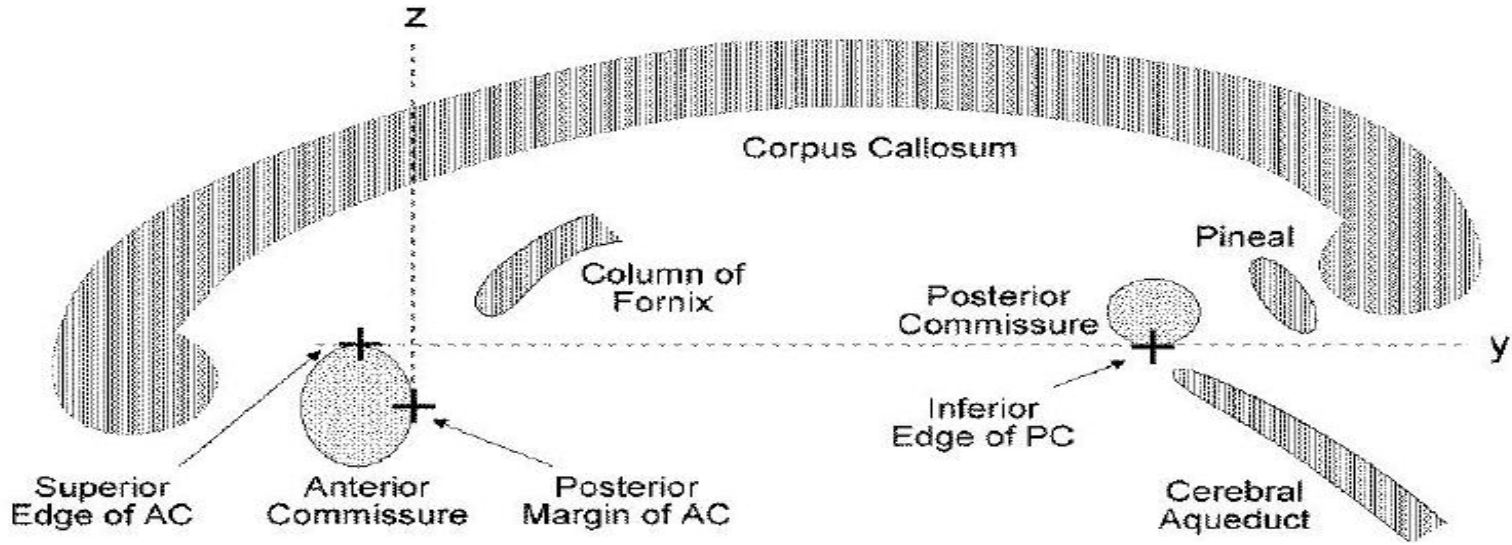
To start, right click on “DataDir” in the GUI or set AFNI_ENABLE_MARKERS to YES in ~/.afnirc.

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

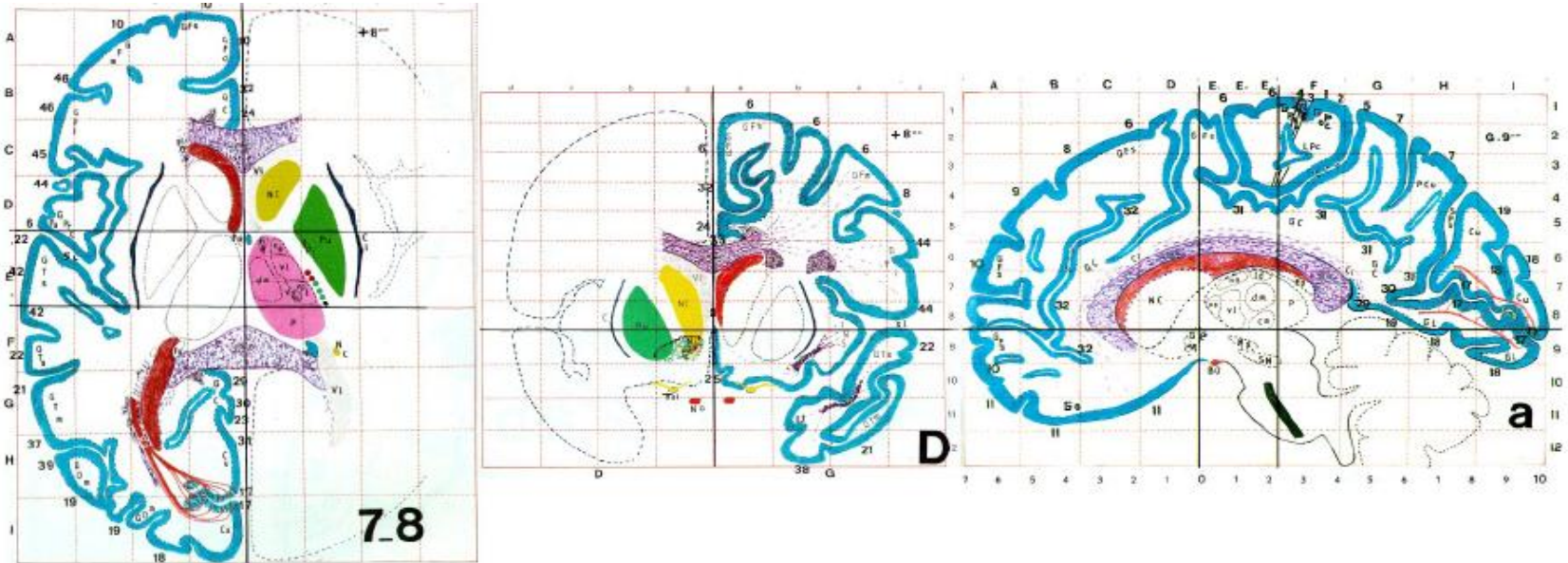
Carry out transformation to +acpc coordinates

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

<ul style="list-style-type: none"> ◆ Original View ◆ AC-PC Aligned ◆ Talairach View <li style="background-color: yellow;">Define Markers ■ See Markers Define Overlay ■ See Overlay Define Datamode Switch Session Switch UnderLay Switch Overlay Control Surface 	<ul style="list-style-type: none"> ◆ AC superior edge ◆ AC posterior margin ◆ PC inferior edge ◆ First mid-sag pt ◆ Another mid-sag pt 	<input type="checkbox"/> Allow edits Pcolor <input type="text" value="white"/> Scolor <input type="text" value="limegreen"/> Size <input type="text" value="8"/> Gap <input type="text" value="3"/> Set Clear Quality? <hr/> Transform Data <input type="checkbox"/> Big Talairach Box?
---	---	--

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

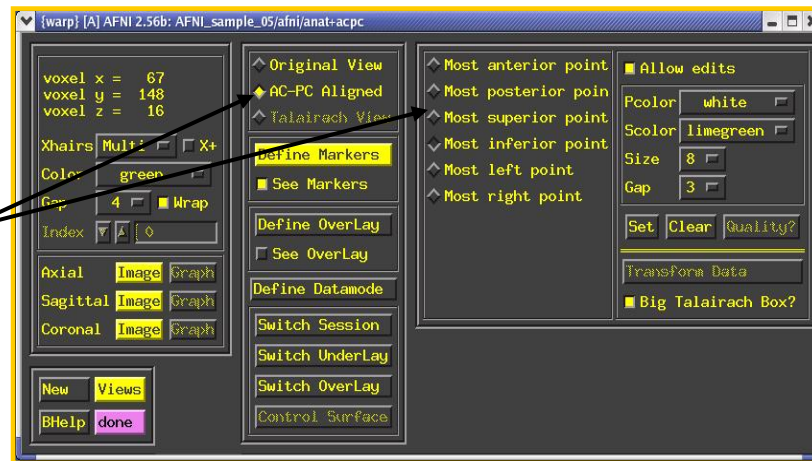
- ◇ Once the AC-PC landmarks are set and we are in ACPC view, we now stretch/shrink the brain to fit the Talairach-Tournoux Atlas brain size (sample TT Atlas pages shown below, just for fun)



• 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

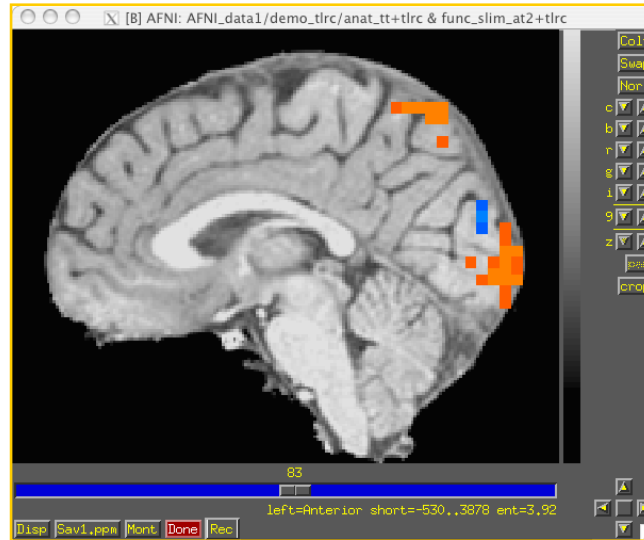
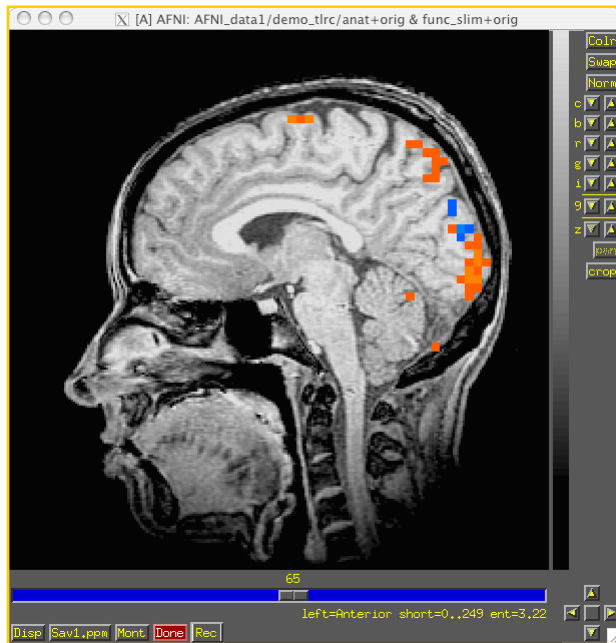


- ◇ Once all the markers are set, and the quality tests passed. Pressing [\[Transform Data\]](#) will write new **header** containing the Talairach transformations (see Appendix C for details)
 - Recall: With AFNI, spatial transformations are stored in the header of the output

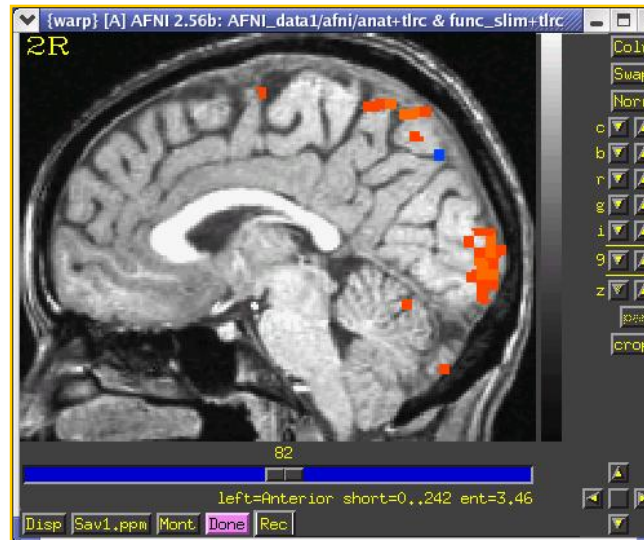
@auto_tlrc Results are Comparable to Manual TLRCing

Comparison of results from “follower” func dsets: similar reduction in spurious voxels with high correlation.

Original



@auto_tlrc



Manual