TEMPLATES AND ATLASES

Fig. 1.

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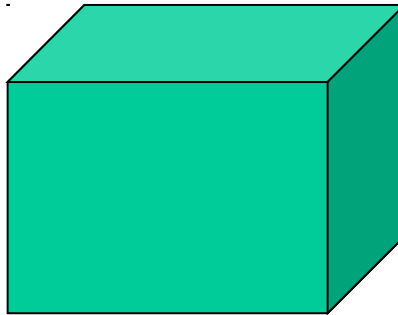
Ex: TT_N27+tlrc, MNI_EPI+tlrc, TT_ICBM452+tlrc.
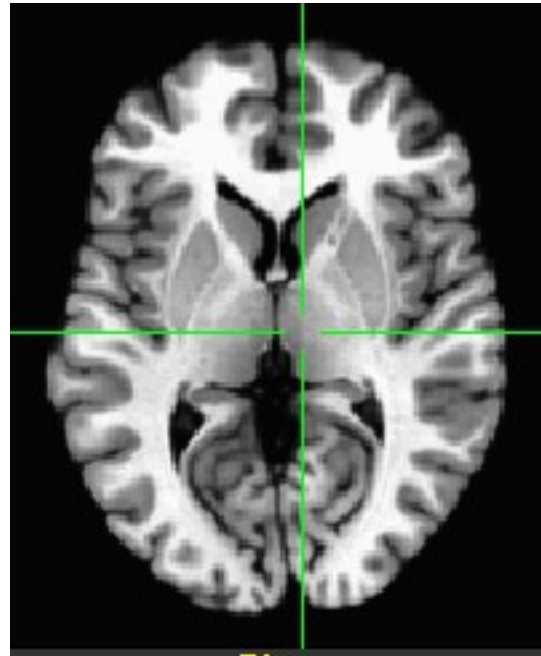
TT_N27+tlrc

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).

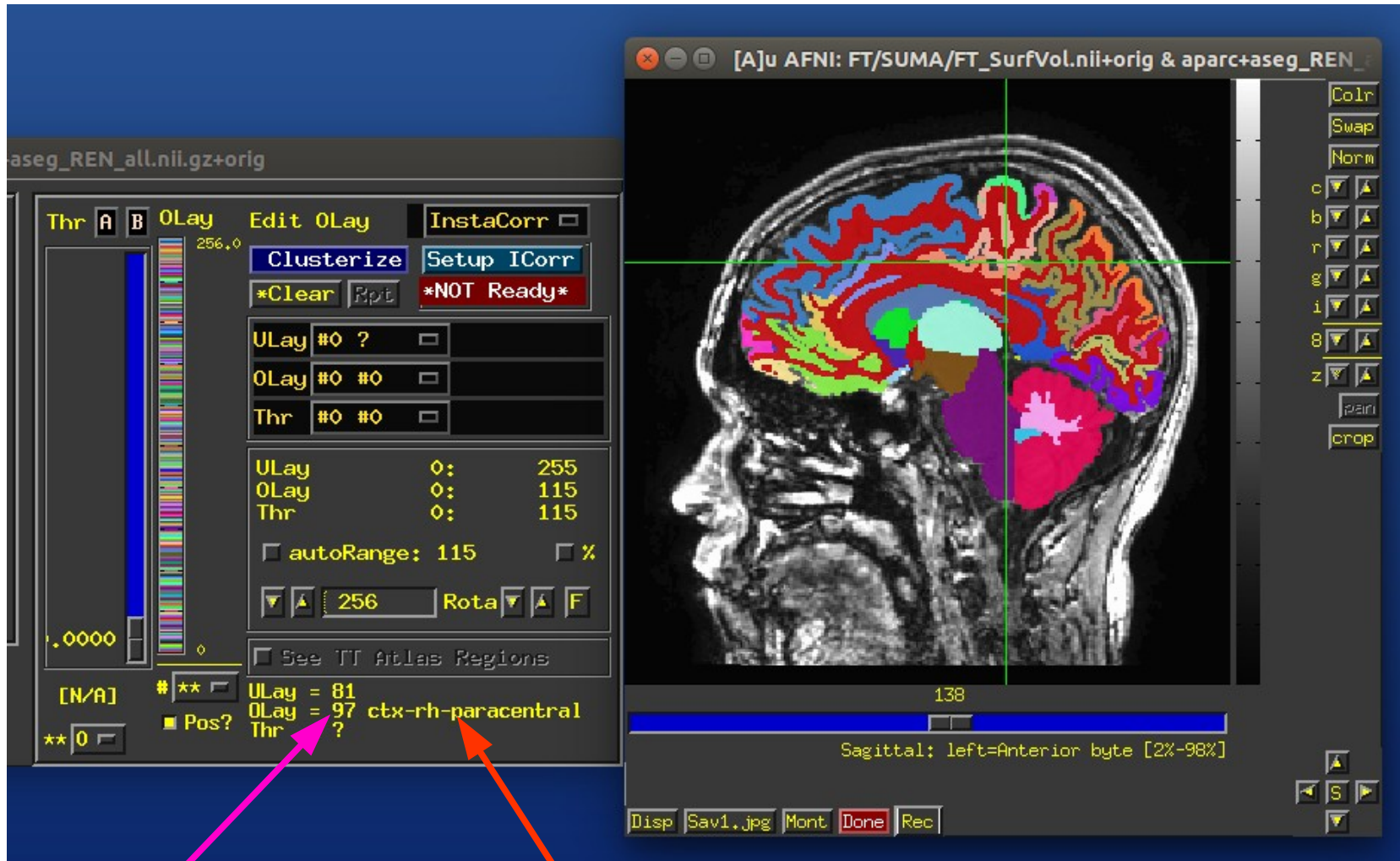*Ex*: TTatlas+tlrc, TT_N27_EZ_ML+tlrc, my_roidset+orig.
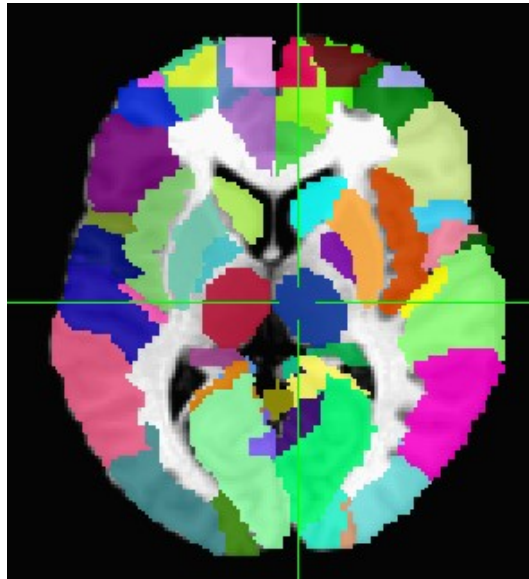
TT_N27_EZ_ML+tlrc

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

Definitions

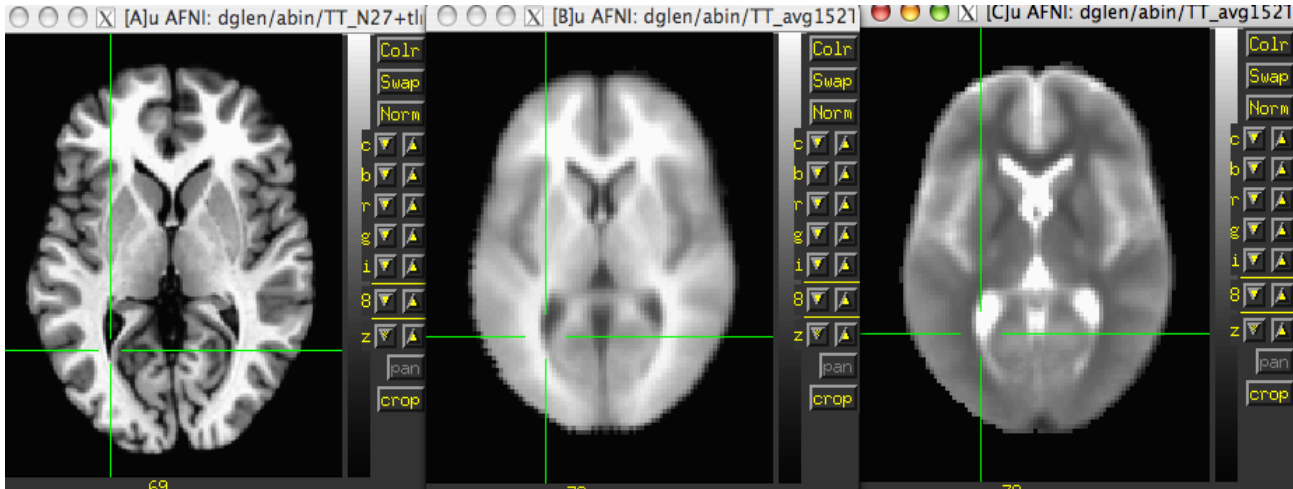## Atlas (or general ROI) label in GUI

integer value of ROI   associated string label

Templates included with AFNI
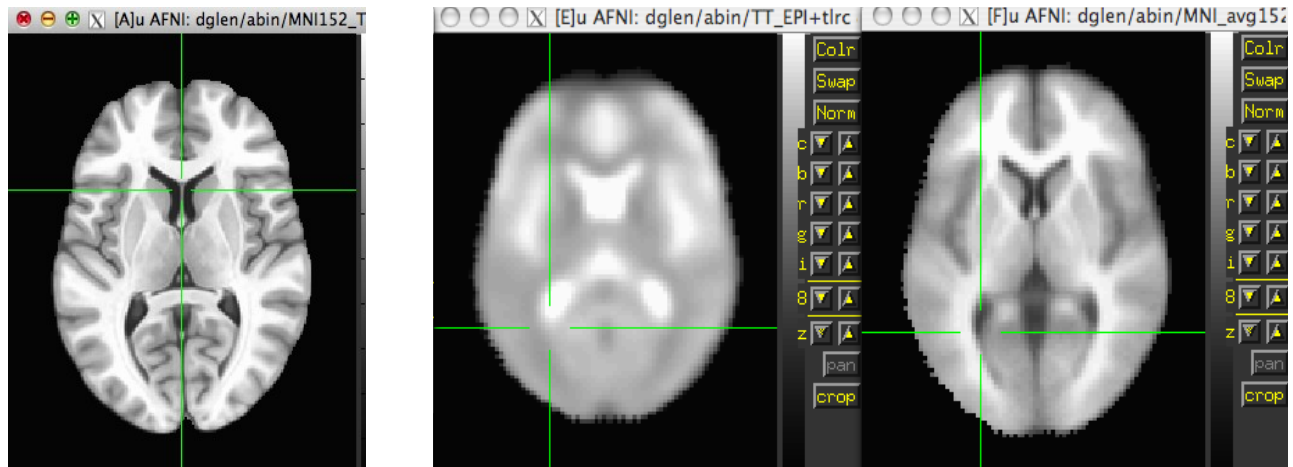
After default AFNI installation, these templates (and others) would be in **~/abin/:**

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".)

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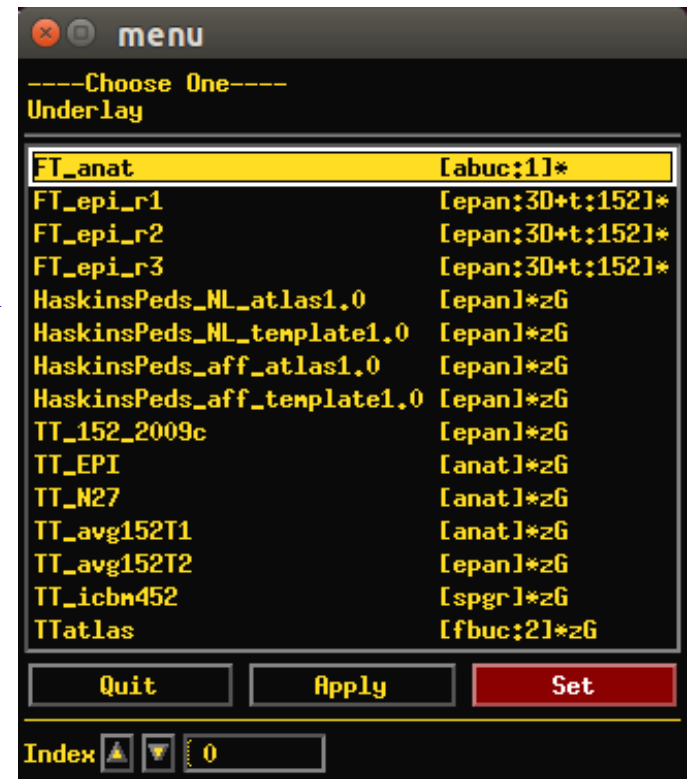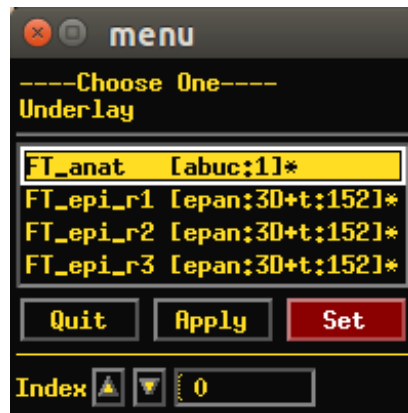
```
AFNI_GLOBAL_SESSION = /home/nmandela/abin
```

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
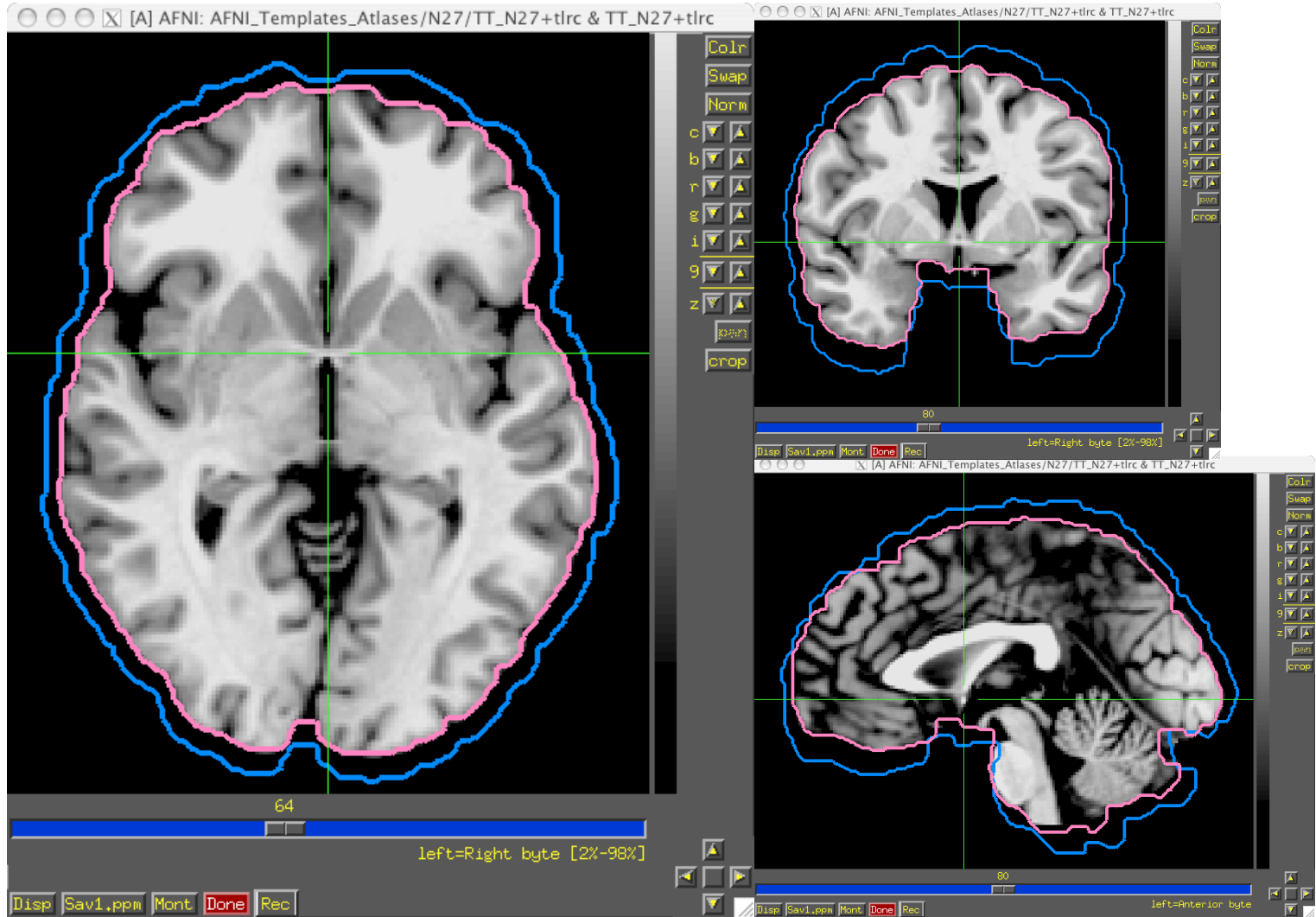- Lower threshold for multiple comparison adjustments

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

TLRC, MNI, and MNI-Anat

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`)

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...
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- 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_Qwarpar**
        - **And now/soon make_template_dask.py**

Trading Spaces

How to transform data to a standard template space

- **@SSwarper** – skullstrip and align data to some select standard spaces
- **auto_warp.py** -combination affine and nonlinear alignment to a template
- **@auto_tlrc** – affine alignment to a template
- Manual talairach
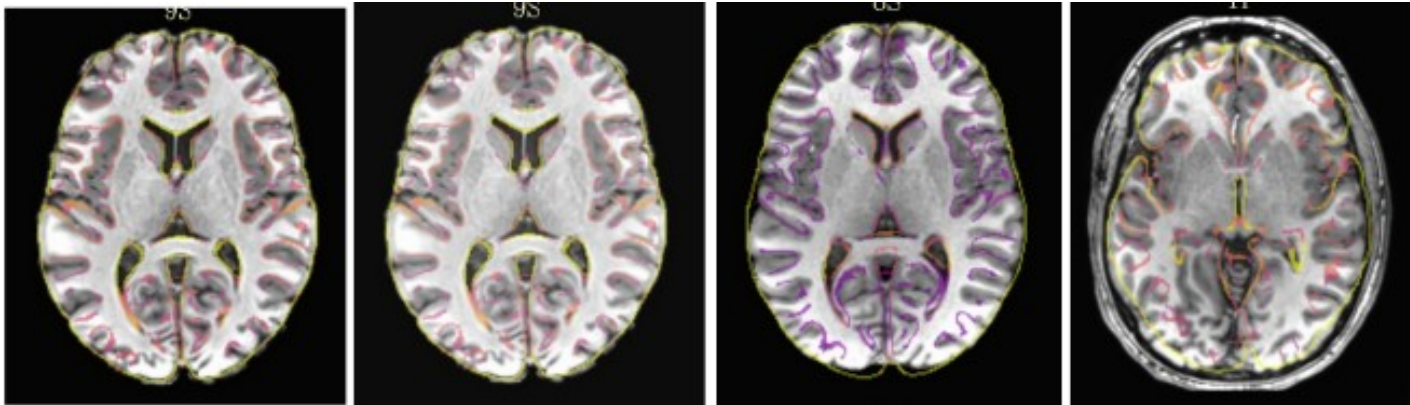
Trading Spaces

afni_proc.py options
tlrc block before volreg!
-volreg_tlrc_warp
-tlrc_base $tpath/$btemplate   (runs @auto_tlrc)
-tlrc_NL_warp (runs auto_warp.py)

For @SSwarper output, add these:
-copy_anat anatSS.${subj}.nii   \
-anat_has_skull no   \
-tlrc_NL_warp   \
-tlrc_NL_warped_dsets   \
          anatQQ.${subj}.nii   \
          anatQQ.${subj}.aff12.1D \
          anatQQ.${subj}_WARP.nii

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
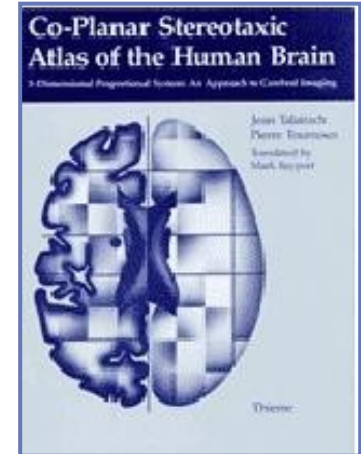
  ◇ Marking is best done on a high-resolution T1-weighted structural MRI volume
- In automatic mode, you need to choose a template to which your data are aligned. Different templates are made available with AFNI's distribution. You can also use your own templates.
- Transformation carries over to all other (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**

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).
  - ◇ <u>Differences from Manual Transformation</u>:
    - ➡ 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 Commisure (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 →
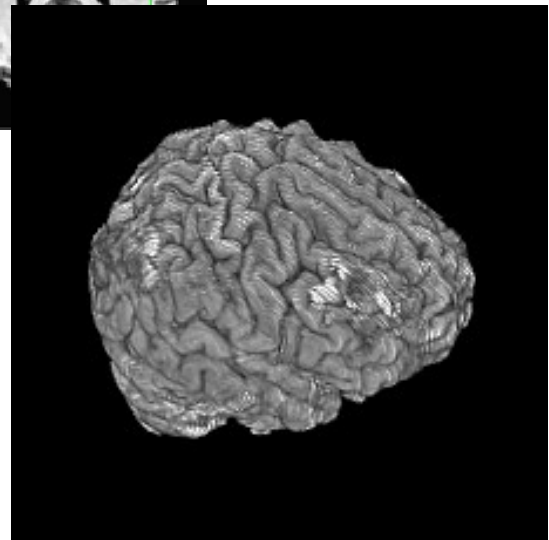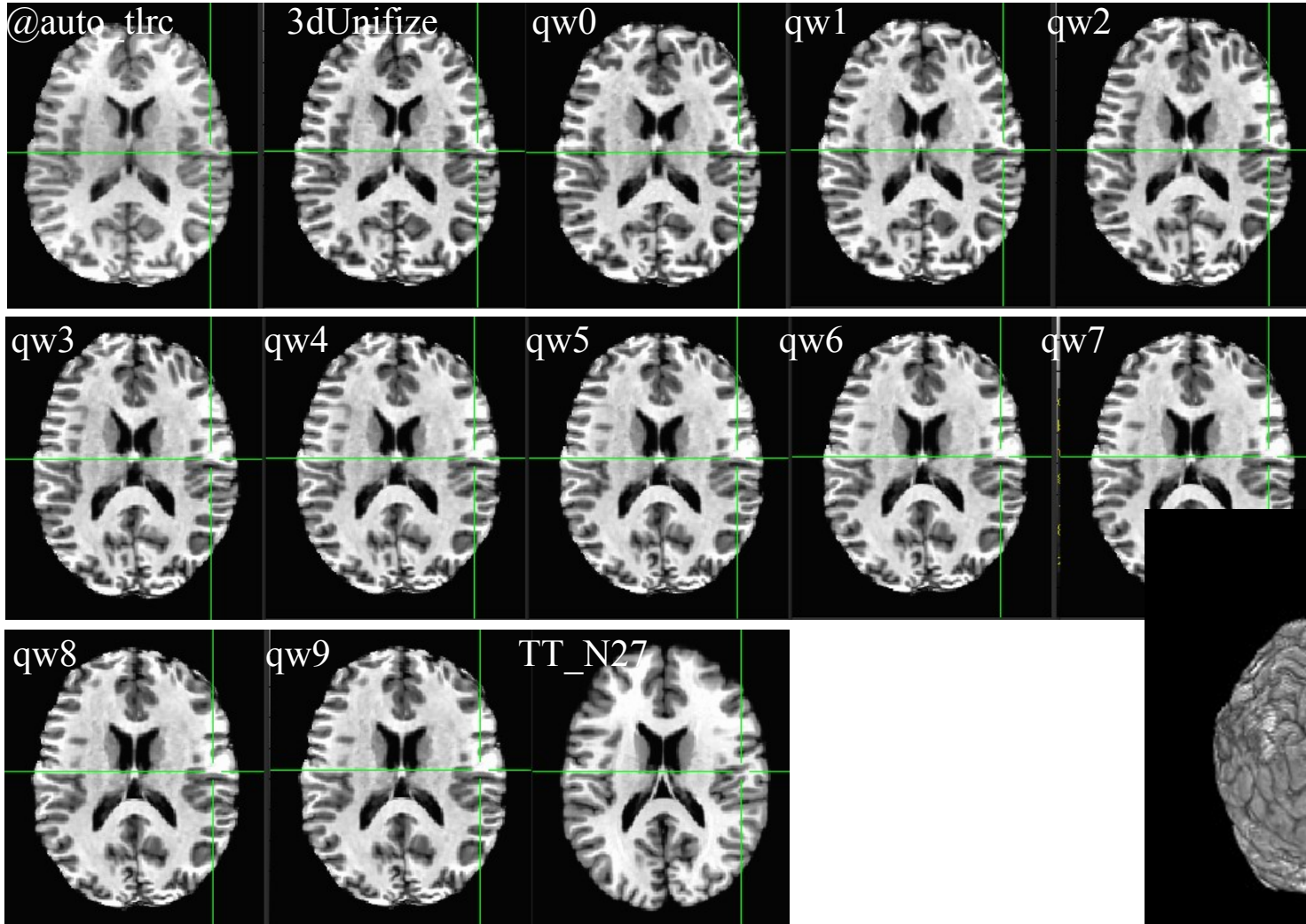
Nonlinear alignment to template

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/htmldoc/
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
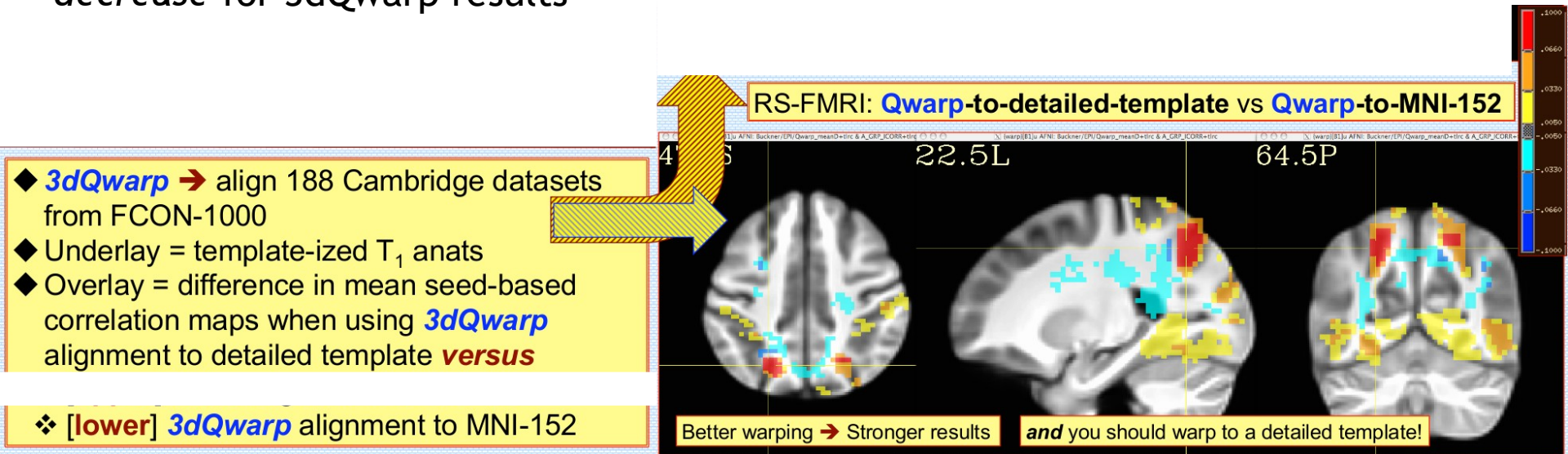 - better method would have higher corr in GM networks and lower corr in WM.

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

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

47.5S   22.5L   64.5P

Seed = Left Precuneus

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

◆ *3dQwarp* ➜ align 188 Cambridge datasets from FCON-1000
◆ Underlay = template-ized T_1 anats
◆ Overlay = difference in mean seed-based correlation maps when using *3dQwarp* alignment to detailed template *versus*
❖ [**upper**] affine alignment to MNI-152

(Cox & Glen, 2013, OHBM)

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.

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Can compare: <u>using detailed vs non-detailed template for nonlinear alignment</u>
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◆ *3dQwarp* ➔ align 188 Cambridge datasets
  from FCON-1000
◆ Underlay = template-ized T$_1$ anats
◆ Overlay = difference in mean seed-based
  correlation maps when using *3dQwarp*
  alignment to detailed template *versus*

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

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

Better warping ➔ Stronger results   *and* you should warp to a detailed template!

(Cox & Glen, 2013, OHBM)

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.

ANTS, DARTEL and FNIRT run with default settings *(Cox & Glen, 2013, OHBM)*

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/SPM   FNIRT/FSL   3dQwarp
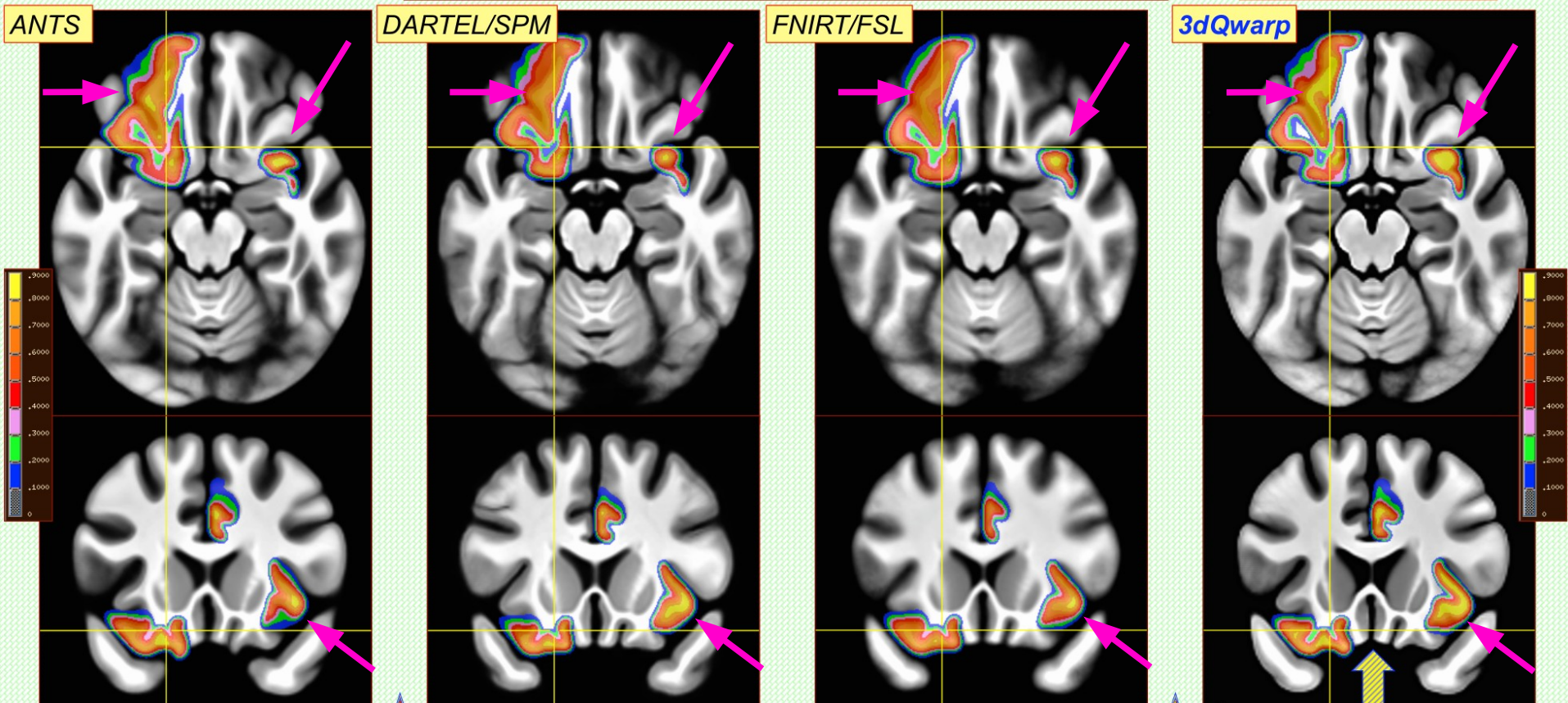
ANTS, DARTEL and FNIRT run with default settings   *(Cox & Glen, 2013, OHBM)*

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)

RS-FMRI: **Qwarp** vs **Affine** registration (188 datasets)

47.5S   22.5L   64.5P

Seed = Left Precuneus

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

22.5L   64.5P

Better warping → Stronger results   *and* you should warp to a detailed template!
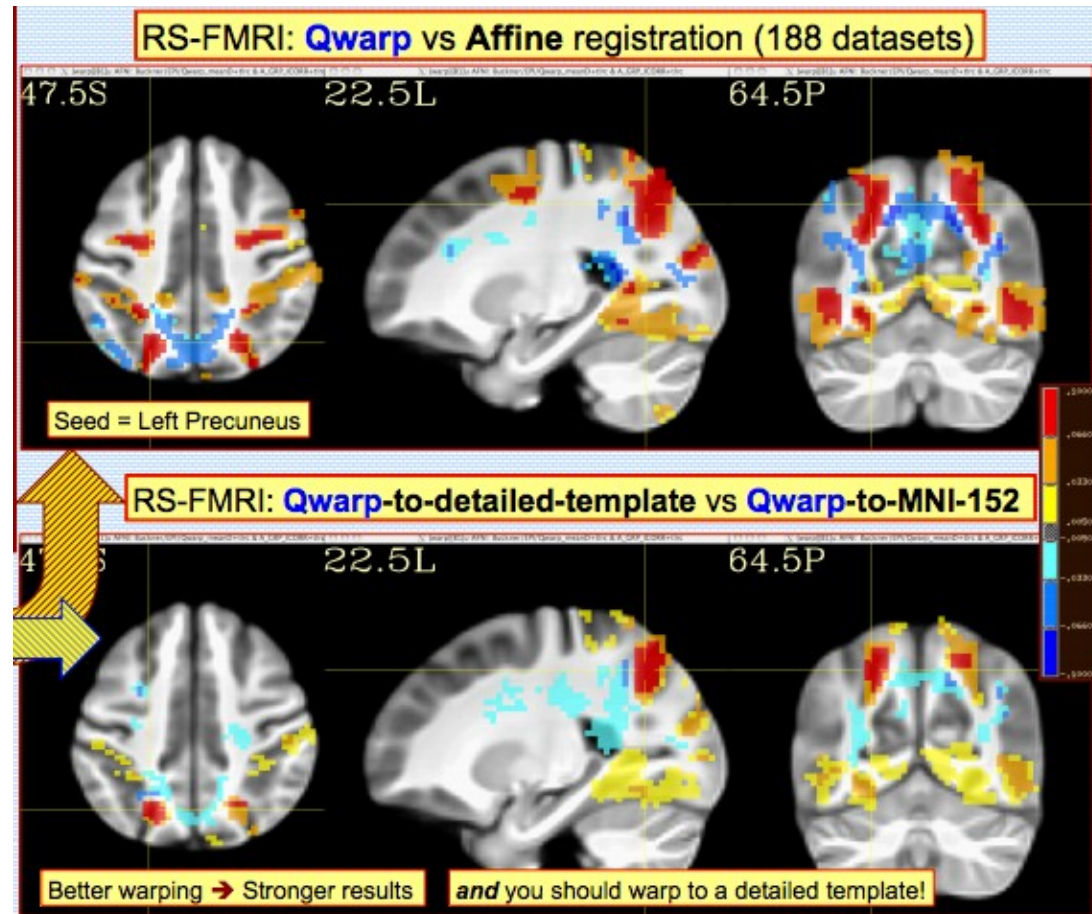
(Cox & Glen, 2013, OHBM)

Going where the atlases live

AFNI binary directory for datasets and configuration

AFNI_atlas_spaces.niml describe the distributed atlases

CustomAtlases.niml and SessionAtlases.niml allow for more
  atlases and templates

Saving the Environment

AFNI_ATLAS_LIST "CA_ML_18_MNI,DKD_Desai_MPM"
    "ALL"
AFNI_TEMPLATE_SPACE_LIST "MNI,TLRC"
AFNI_ATLAS_COLORS CA_ML_18_MNI
AFNI_SUPP_ATLAS_DIR ~/MyAtlases
AFNI_WHEREAMI_DEC_PLACES 2
AFNI_WHEREAMI_MAX_SEARCH_RAD 3

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)
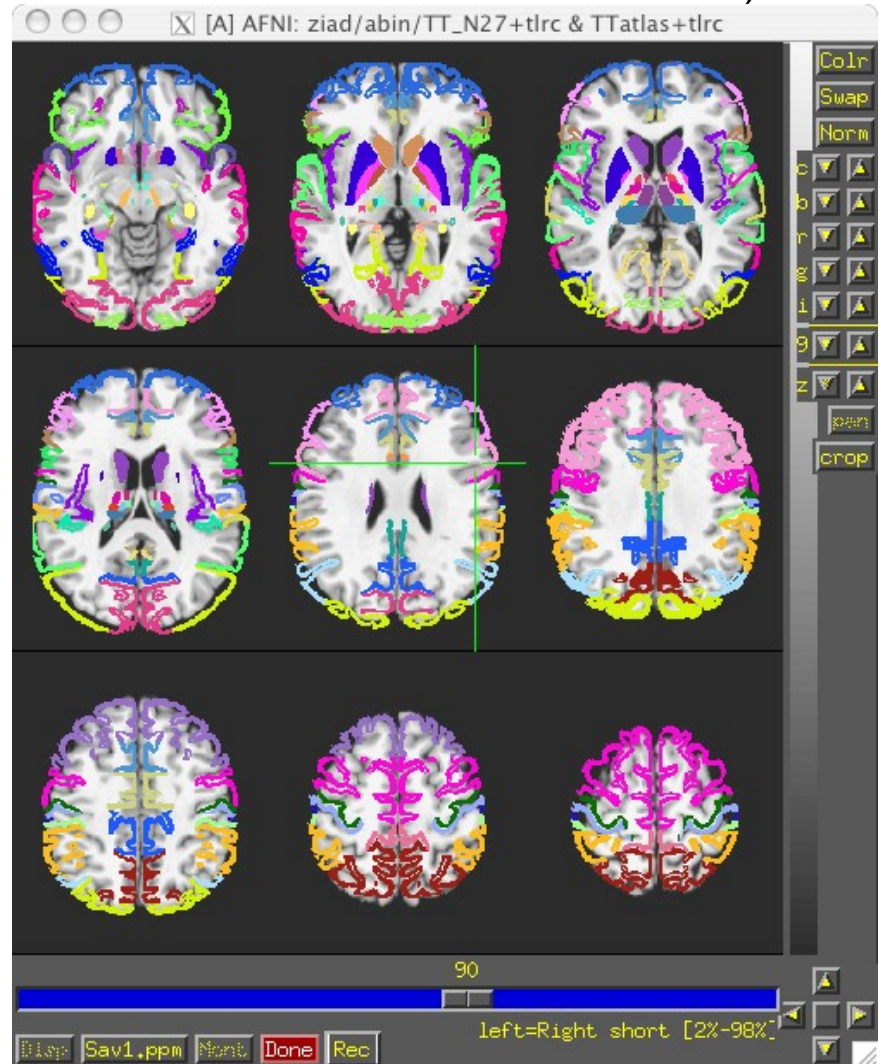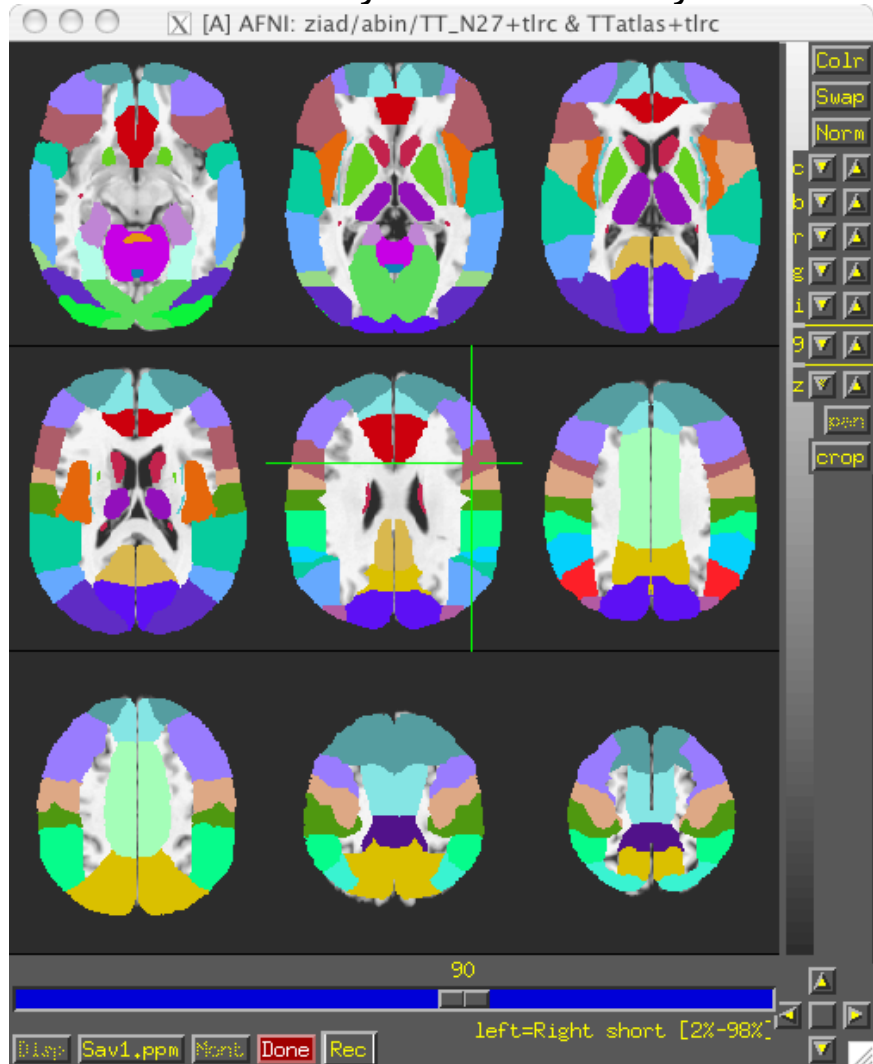
Caution: Talairach Daemon (TT_Daemon) problems
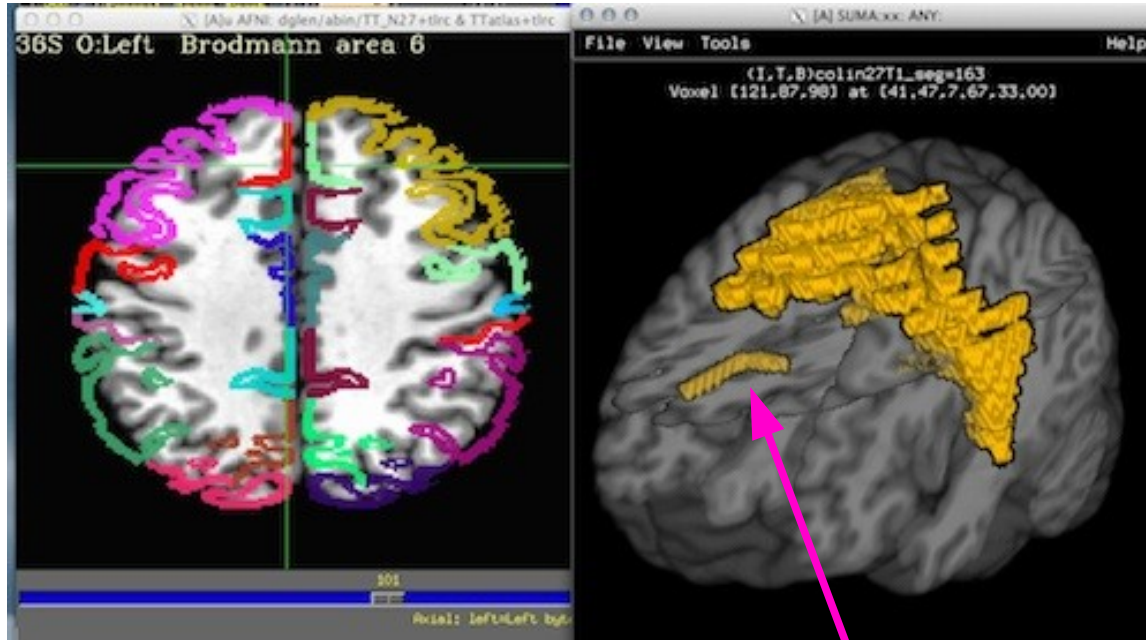
This piece is labeled as BA 6, but is really another part.

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
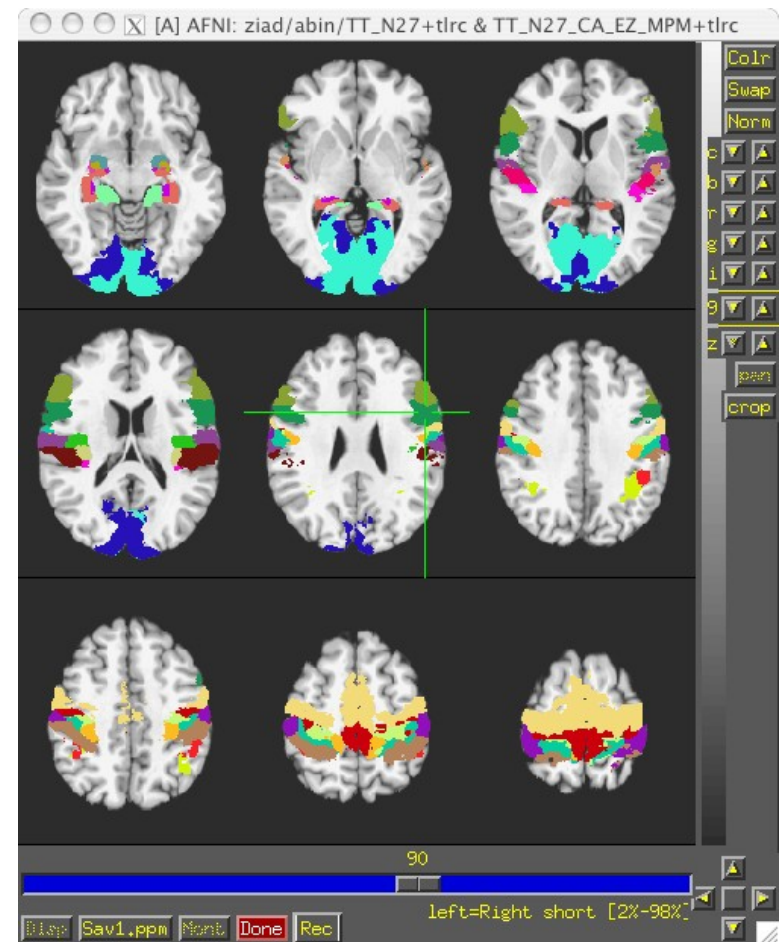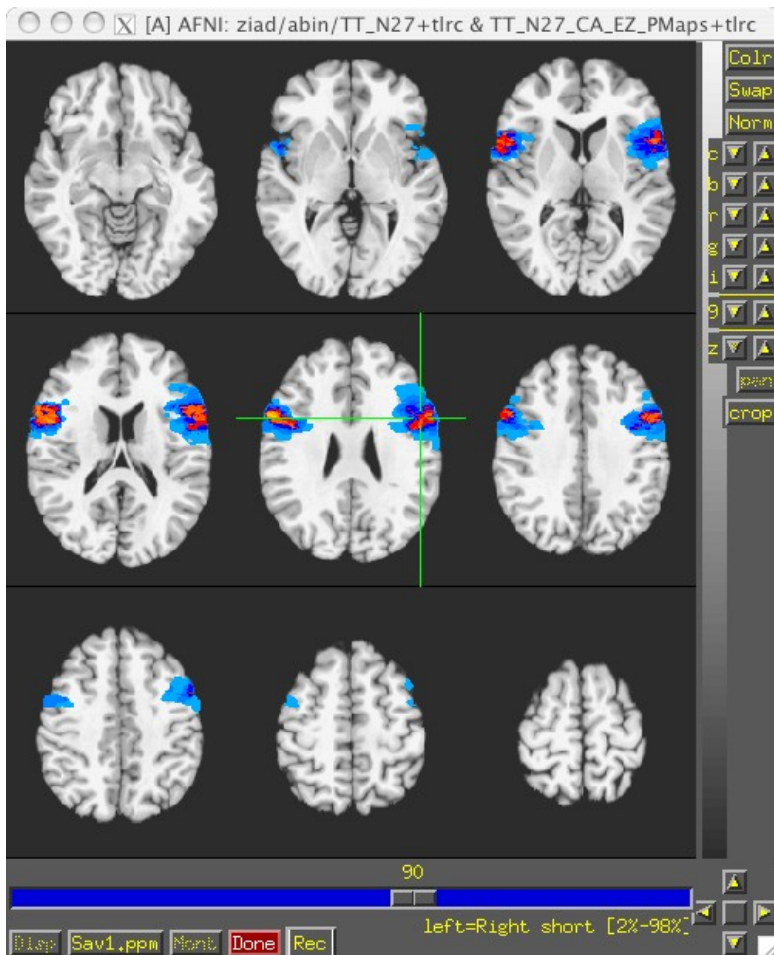
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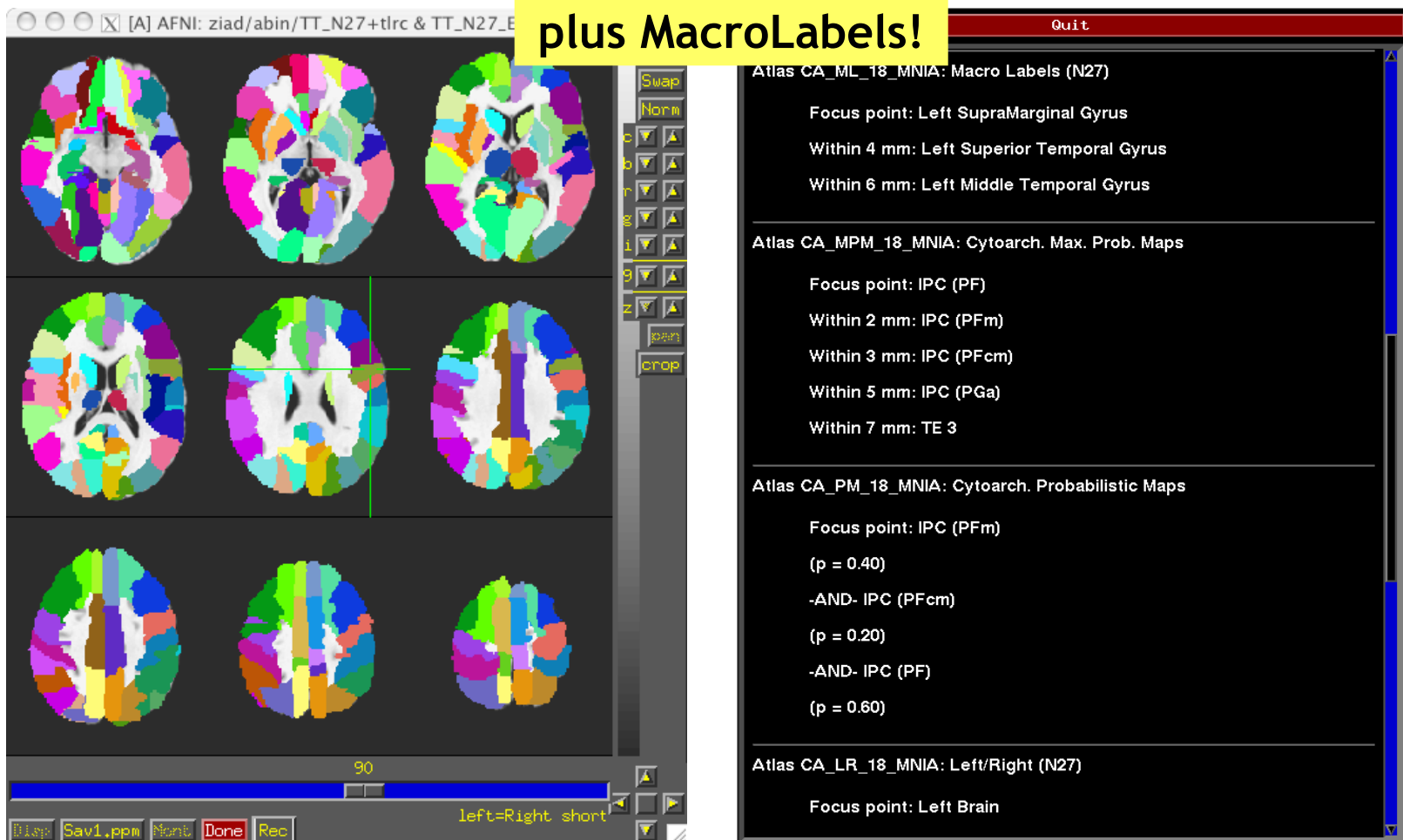
Atlases distributed with AFNI: Desai PMaps and MPMs

- Atlases generated with typical AFNI pipeline using *@auto_tlrc* and FreeSurfer segmentation across multiple subjects
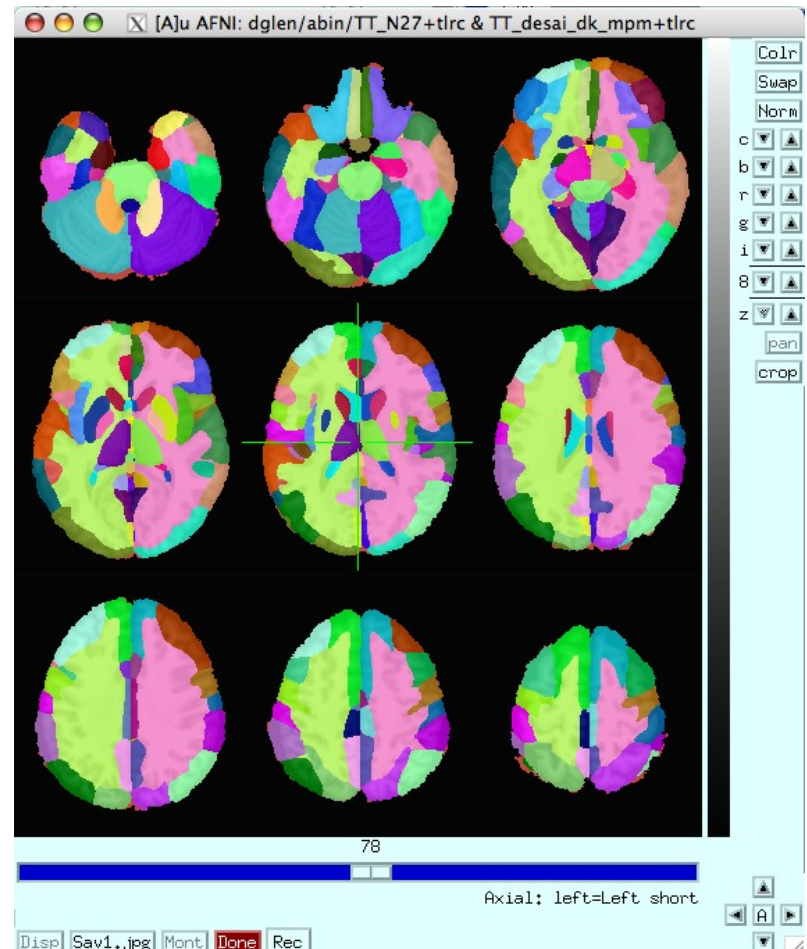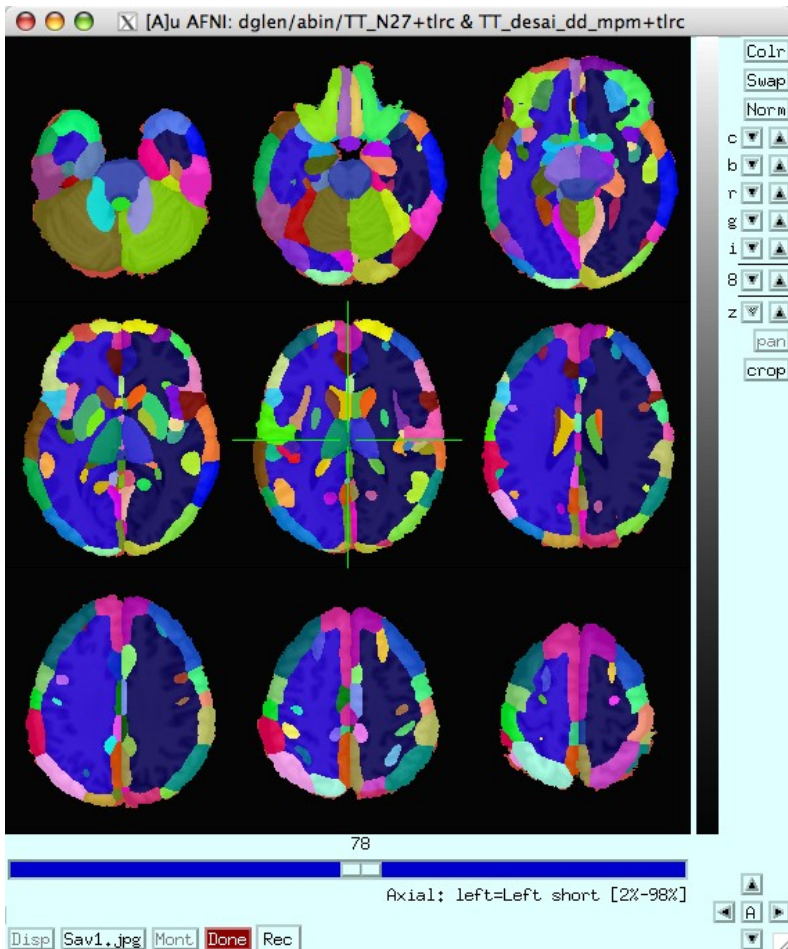
Using atlases in AFNI GUI

- 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.
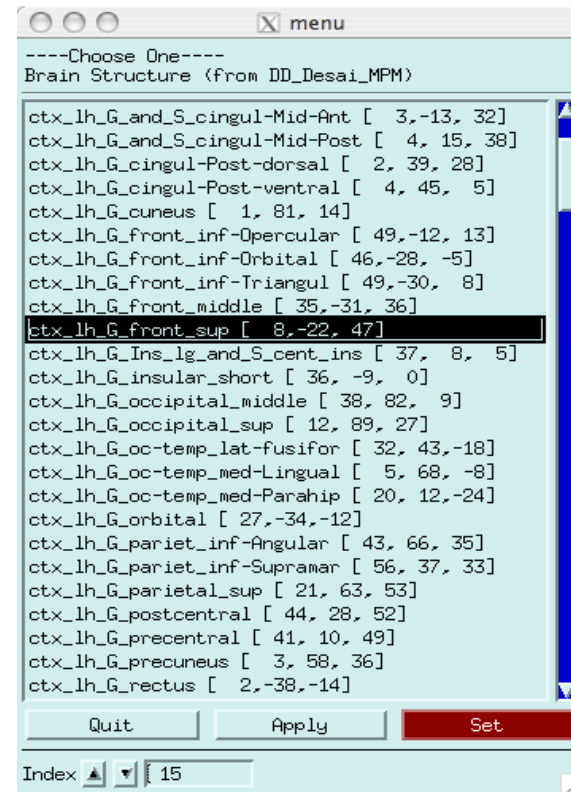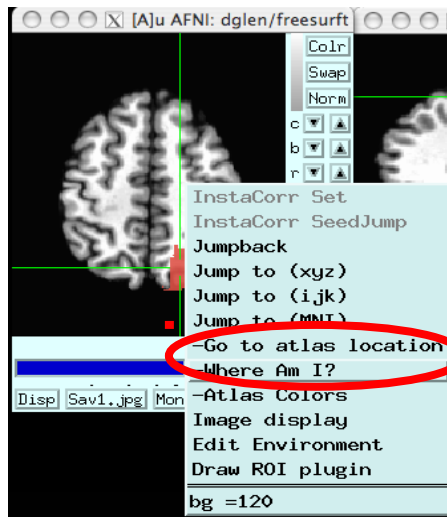
⬦ **[Atlas colors]**
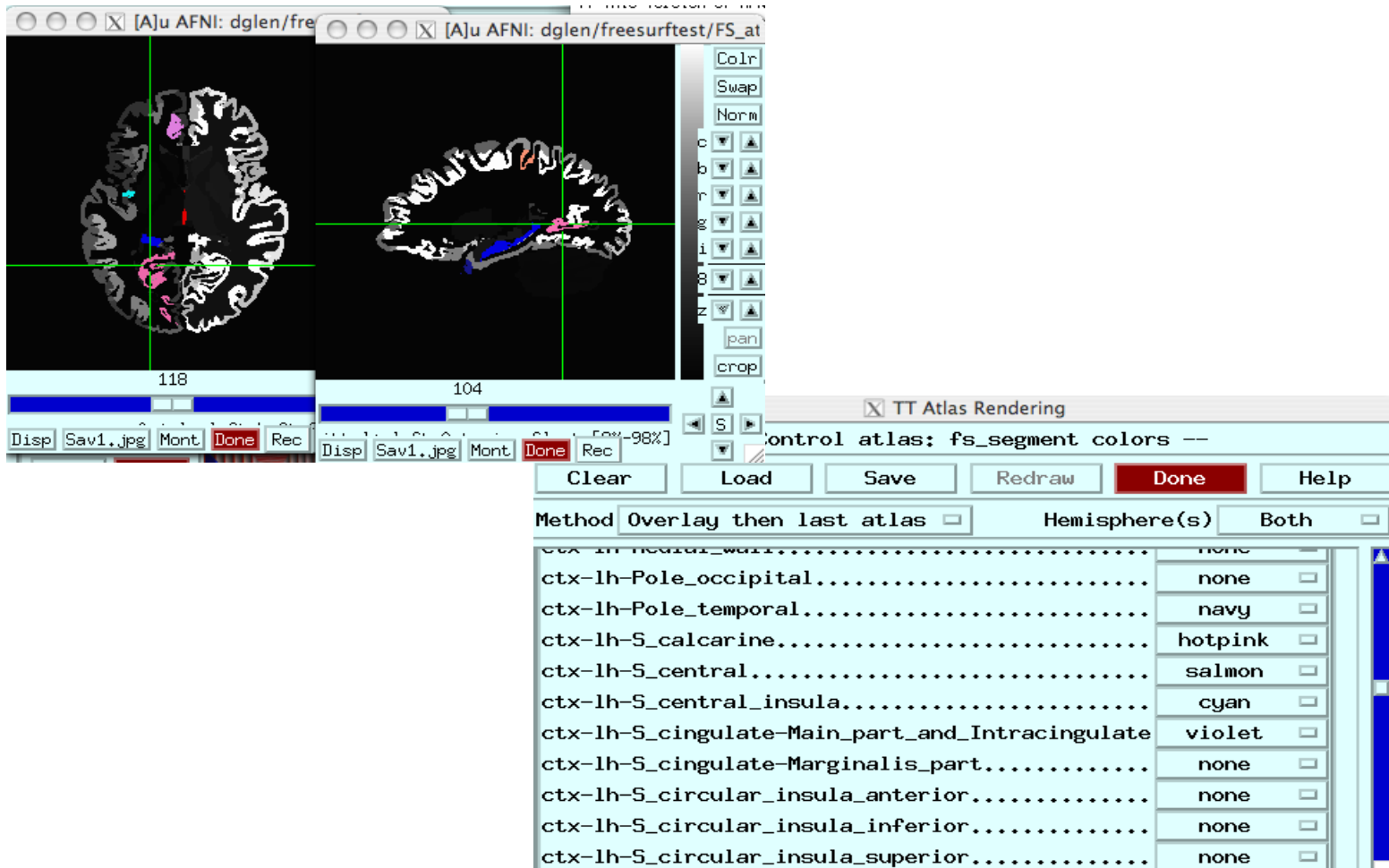
Lets you show atlas regions over your own data (works only in `+tlrc`).

◇ **[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
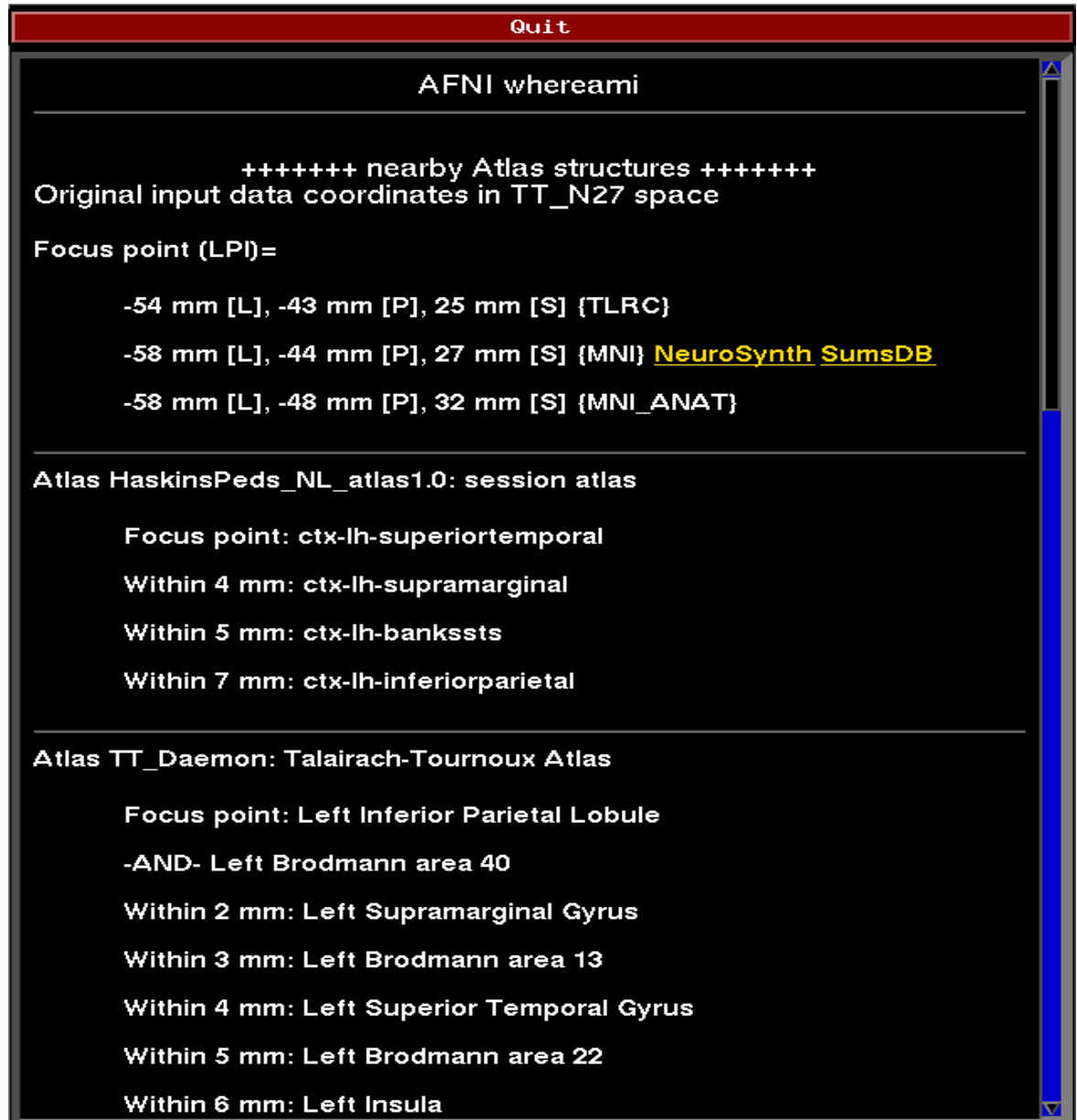
whereami on the command line

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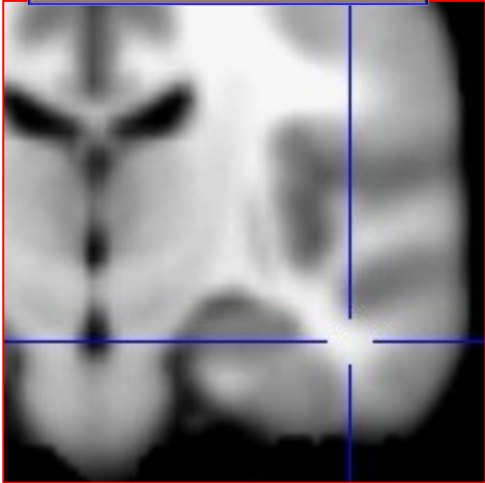
Linear = Affine
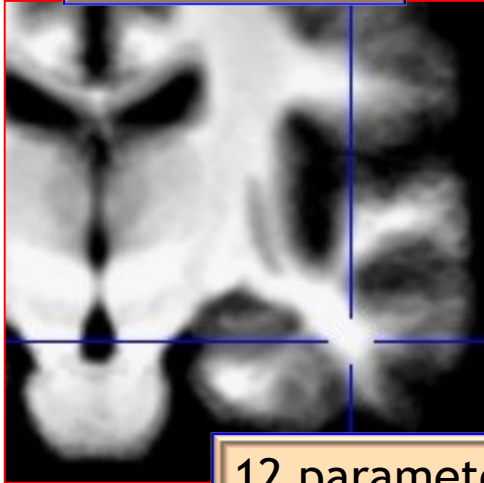
```
@toMNI_Awarp
@toMNI_Qwarpar
```
Averages of 21
3 Tesla brain volumes
with varied
levels of refinement in
the nonlinear warping
(smaller patch=more refinement)

12 parameters

Nonlinear: Patch=101
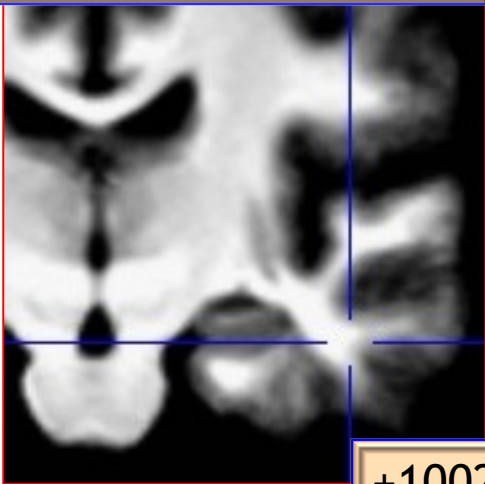
Nonlinear: Patch=49
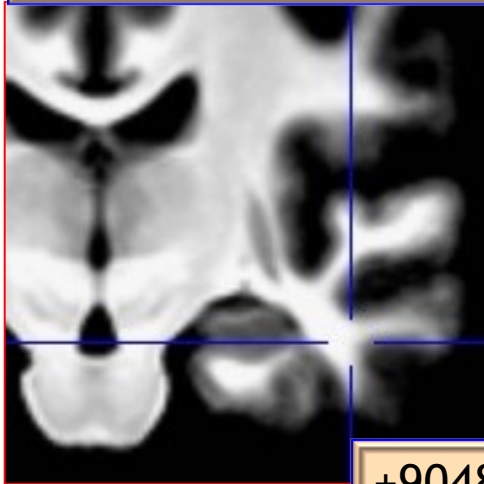
Nonlinear: Patch=23

+1002

+9048

+70008

Make your own template - faster, easier!

make_template_dask.py - Dask parallelization - 10, 100 or 1000 subjects on a cluster, server or PC
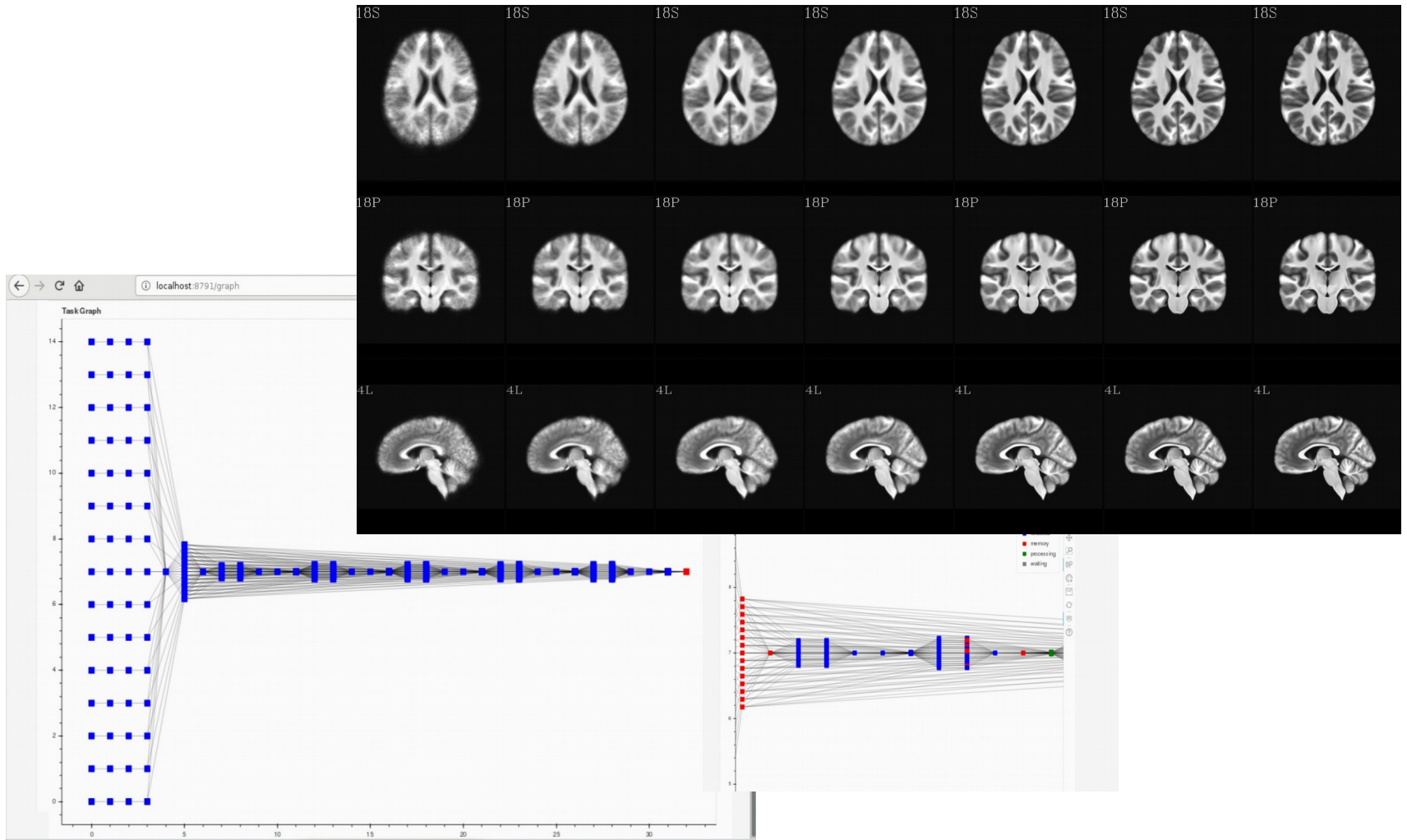
Make your own atlas!

- 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

- 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
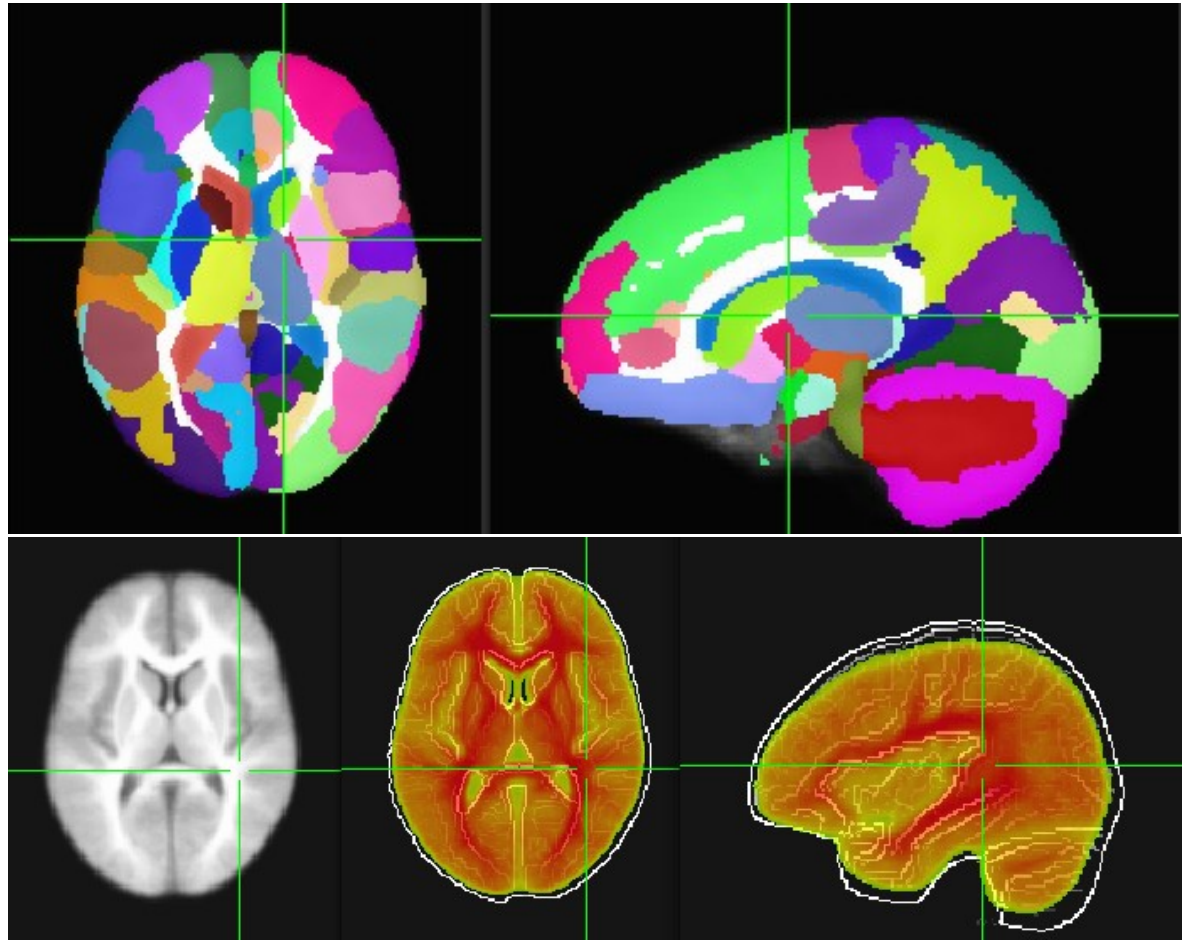
Haskins Pediatric Atlas: the templates

Affine Group

Nonlinear Group I – iterative

ALTERNATIVE ATLAS CREATION TECHNIQUES: ITERATIVE AND TYPICAL METHODS
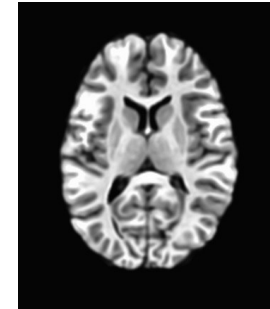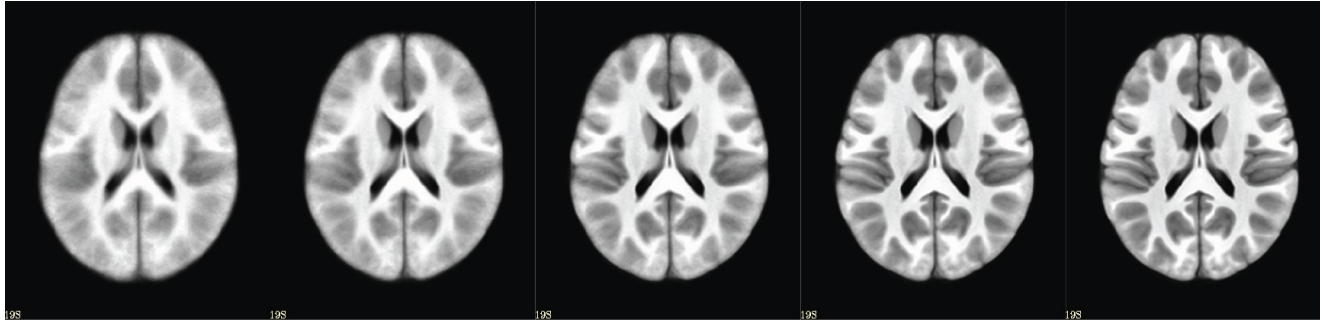
Iterative nonlinear alignment to affine template with progressively smaller patch sizes

"Typical" Brain
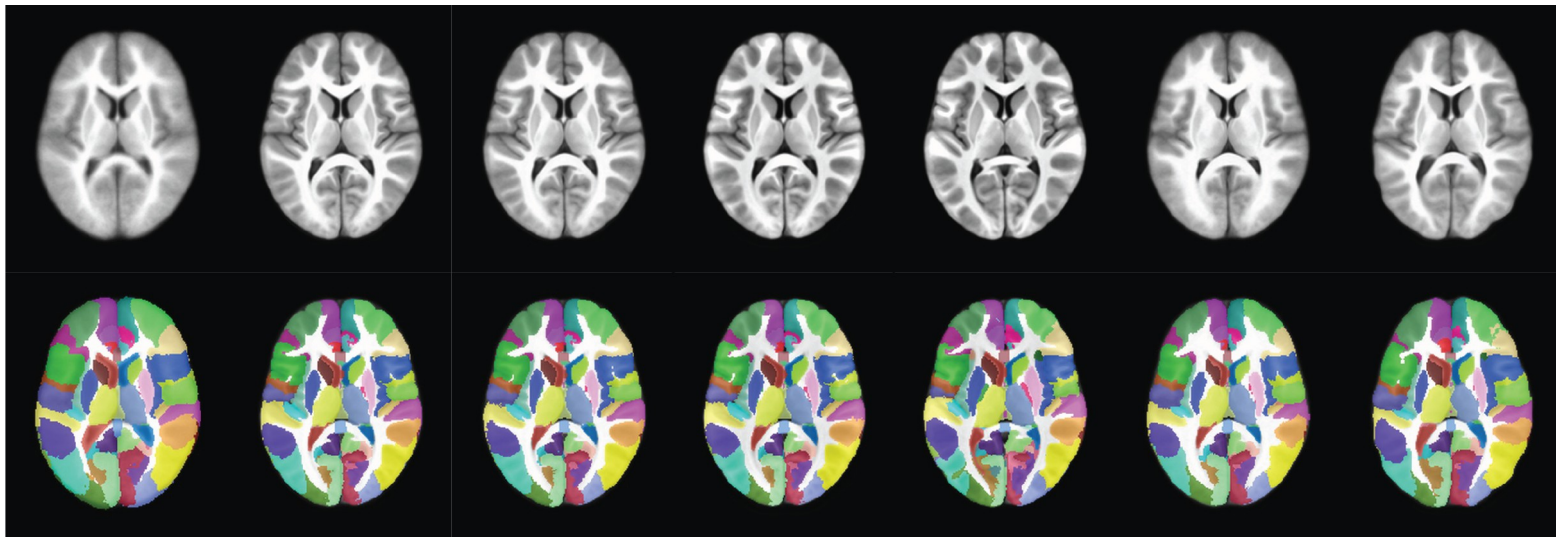
| Affine | Affine Iterative | Typical Iterative | MNI Iterative | Nonlinear to MNI | Nonlinear to Affine | Nonlinear to Typical |
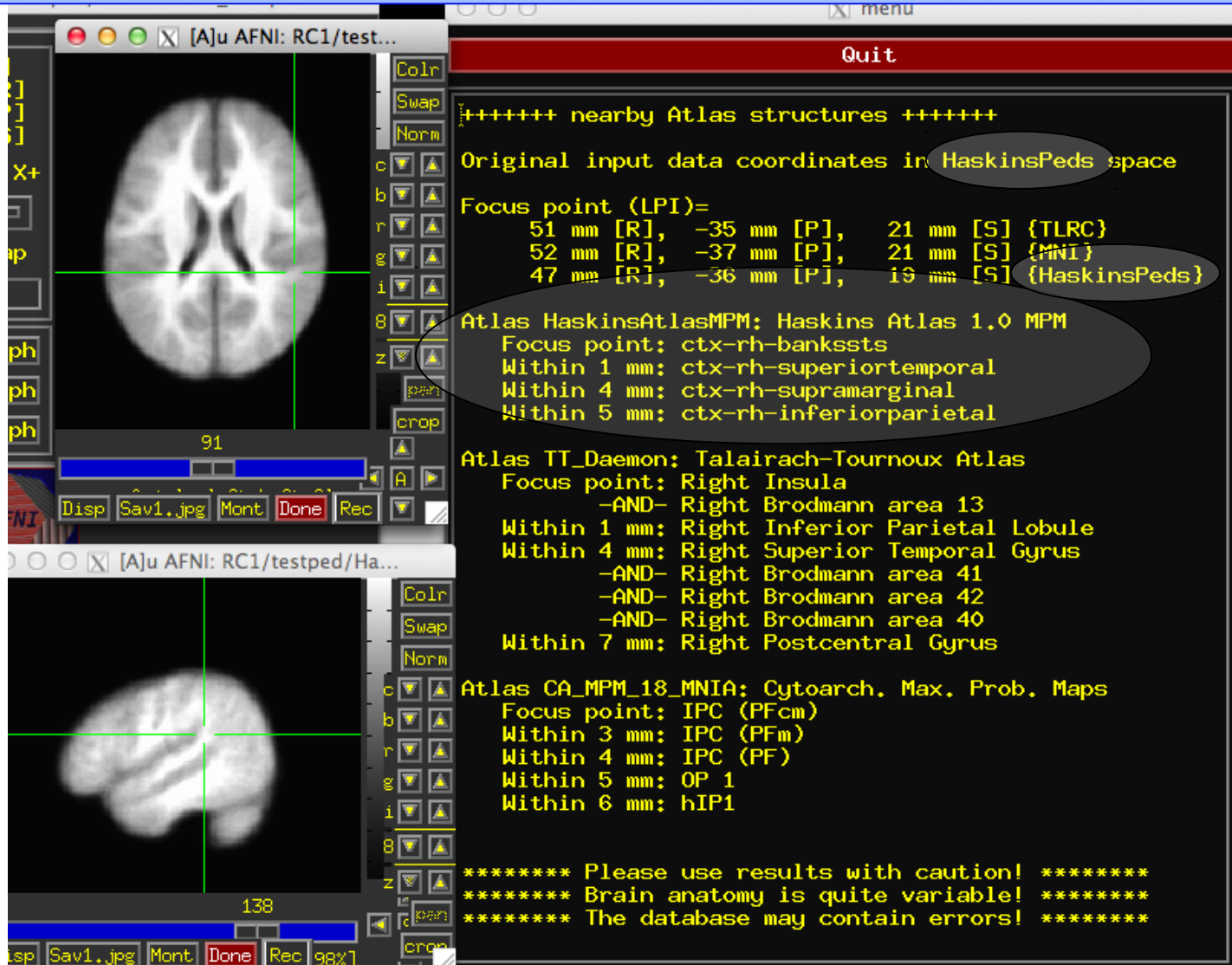
Haskins Pediatric Atlas

Templates and Atlases across Species in AFNI

Atlases and Templates Available!

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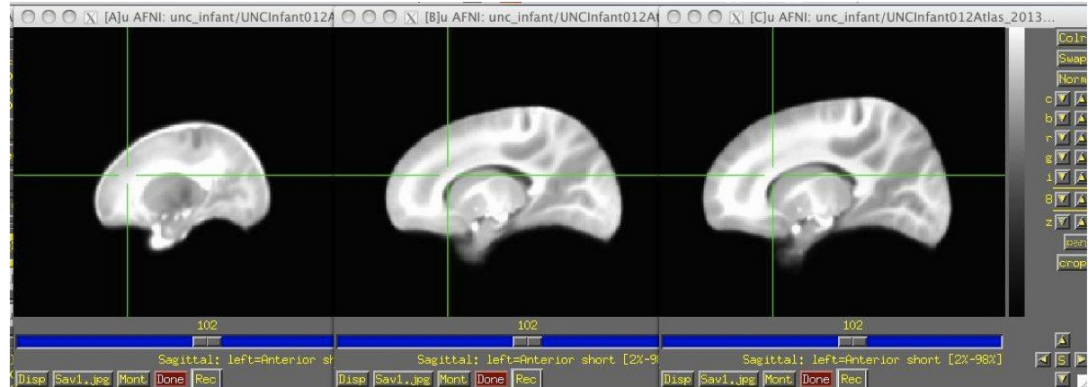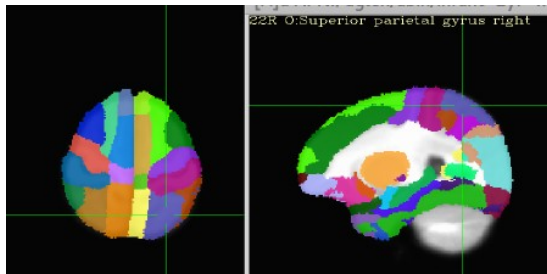
UNC infant templates and atlases – neonate, 1 yr, 2 yr old

- Cerebellum atlas and templates – Jorn Diedrichsen,UCL,UK contribution
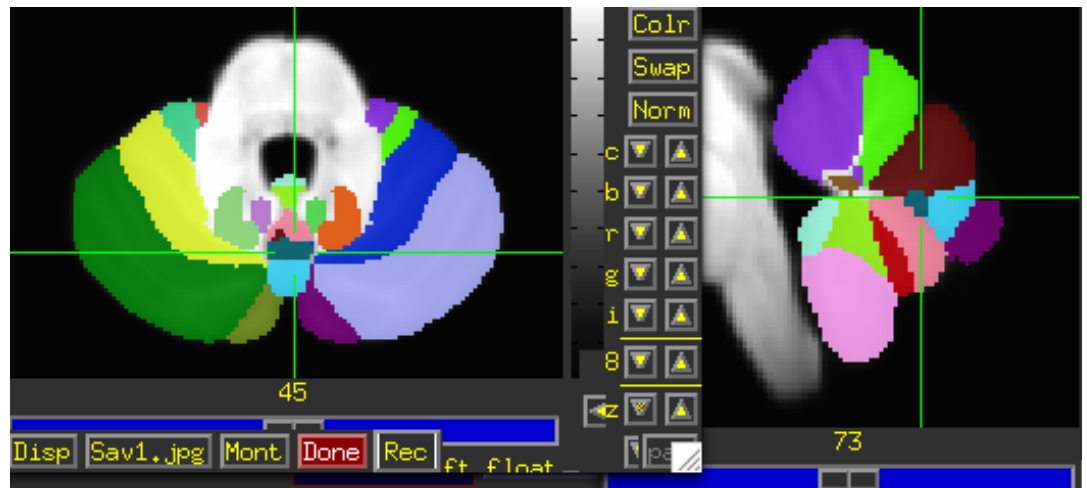
More Atlases and Templates Available!

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

BNST – Torrisi, NIMH
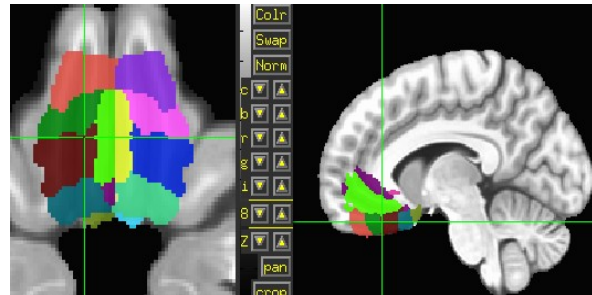
All of these are user requests or contributions!
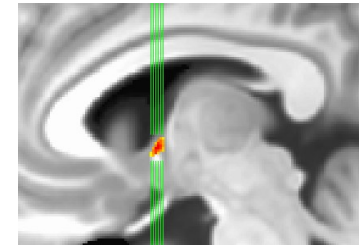
What do you need?

Even More Atlases and Templates Available!

Brainnetome
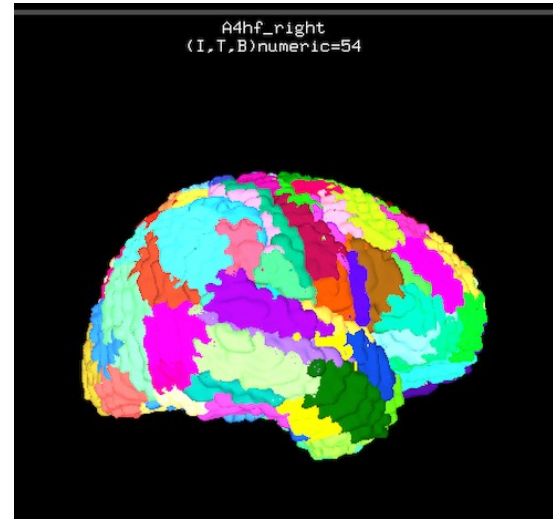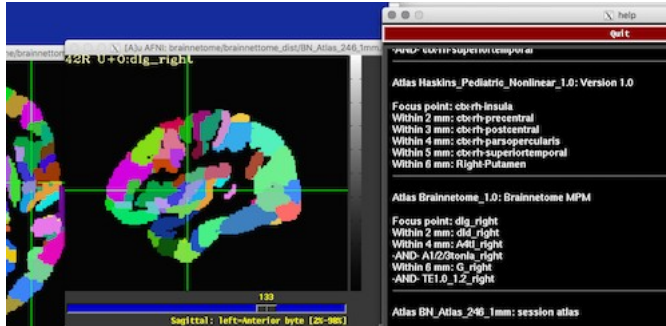
Allen Mouse Brain
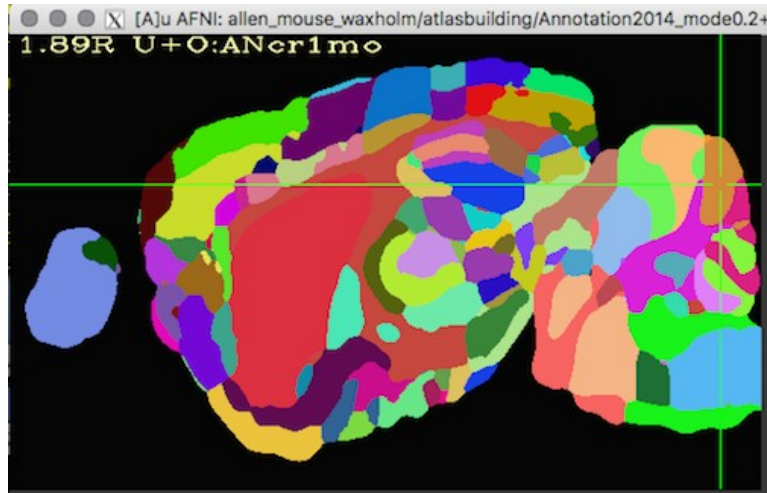
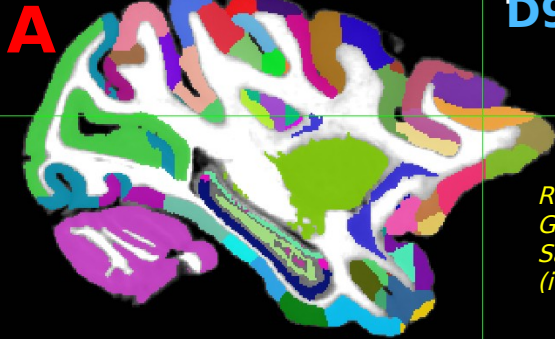**All of these are user requests or contributions!**

What do you need?

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

Saleem macaque atlas – MRI, surfaces, connections, supplemental webpages (in development)
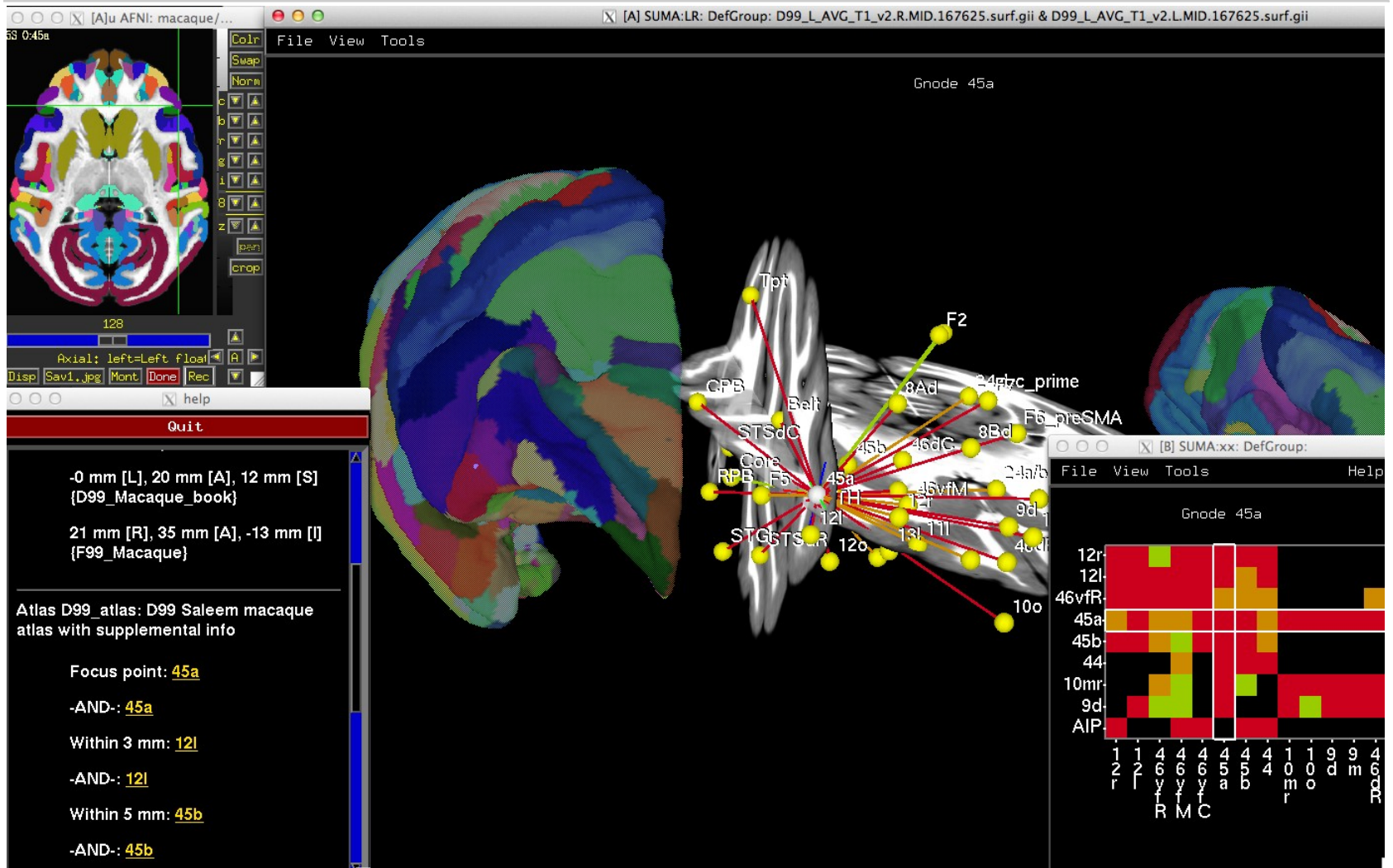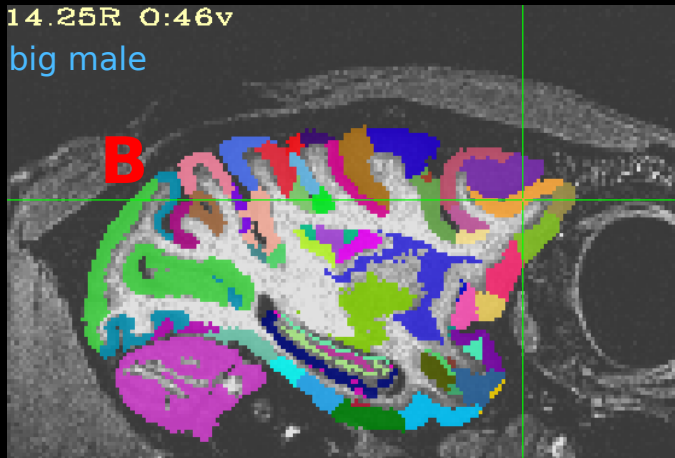
Mapping the digital atlas onto different macaques MRI

D99 – Digital atlas

A

15R 0:46v

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

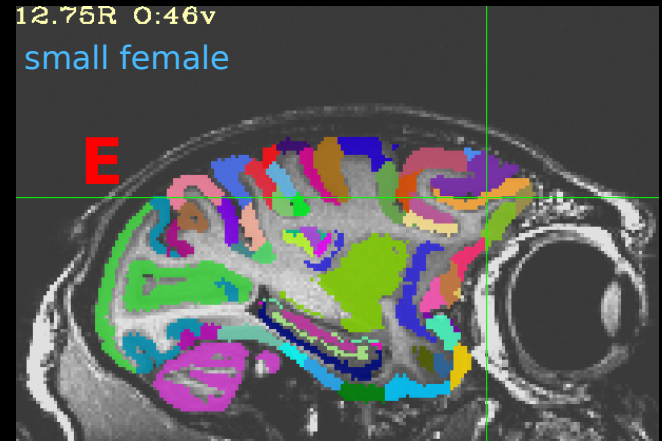**Spatial transformation of the atlas segmentation to each macaque's native space**

B

14.25R 0:46v
big male

C

12.25R 0:46v
medium female

D

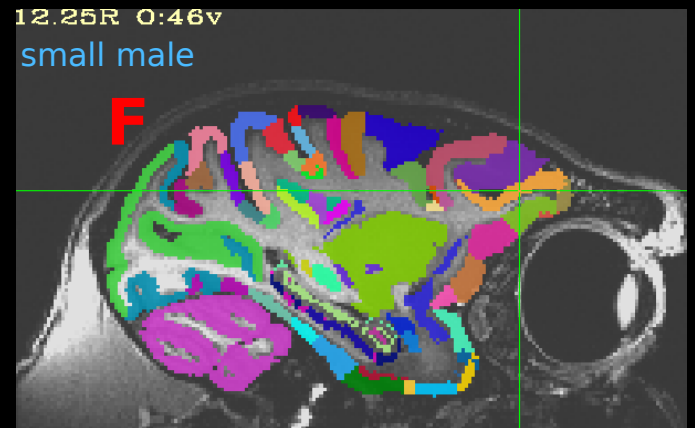12.05R 0:46v
V. small female

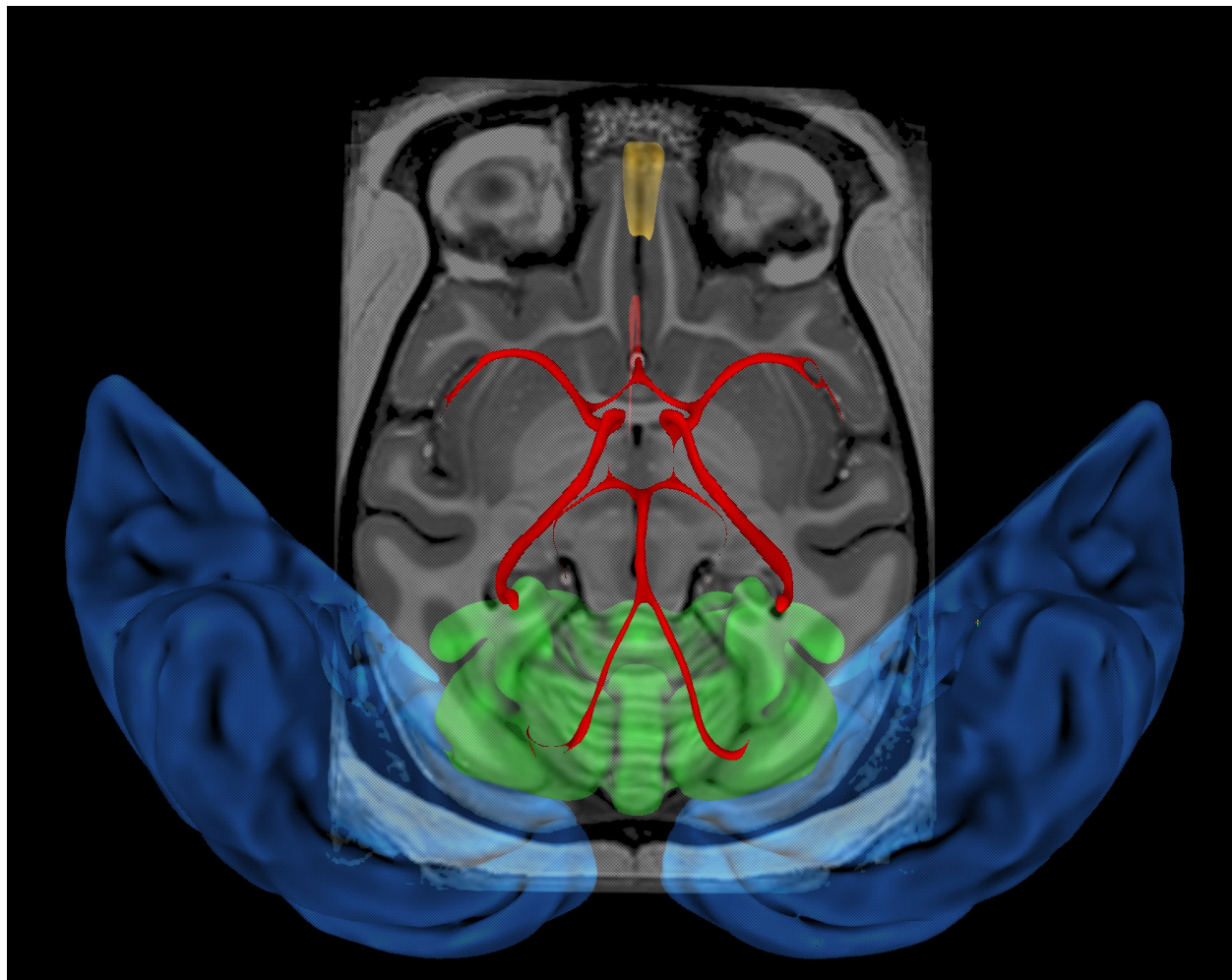**E**

12.75R 0:46v
small female

F
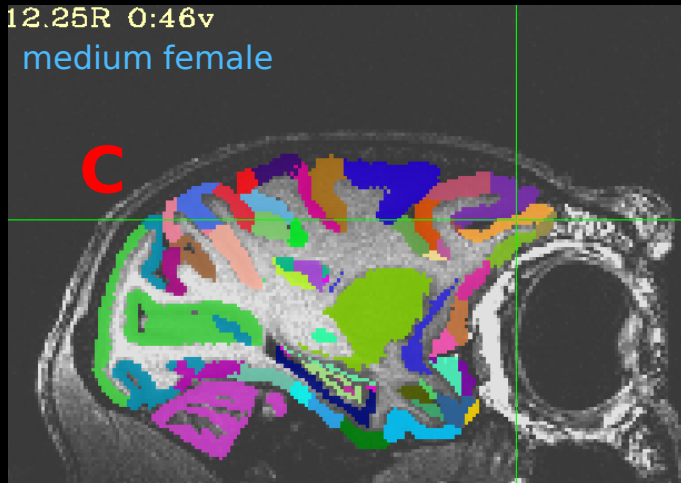
12.25R 0:46v
small male
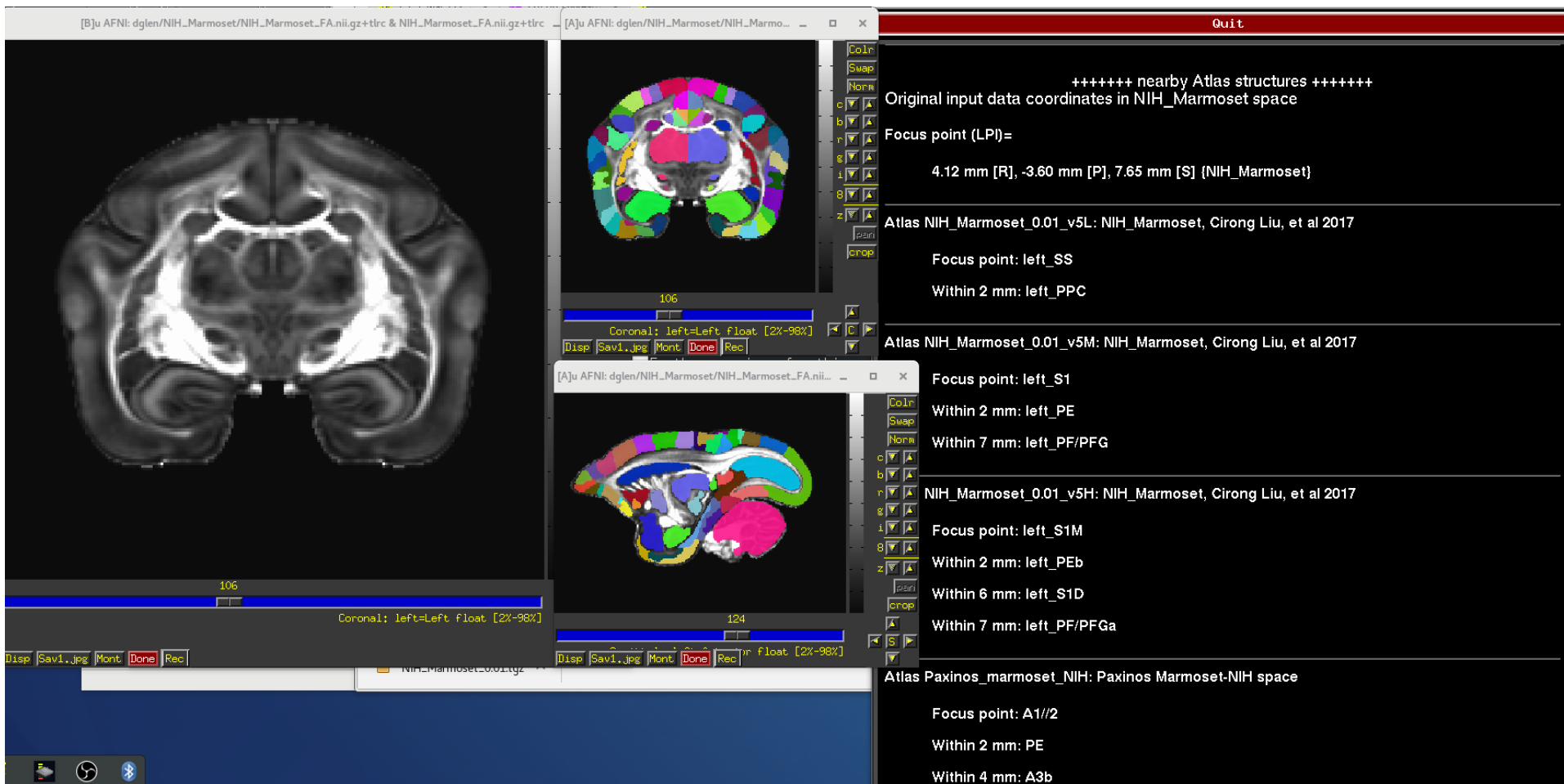
NMT (NIH Macaque Template)

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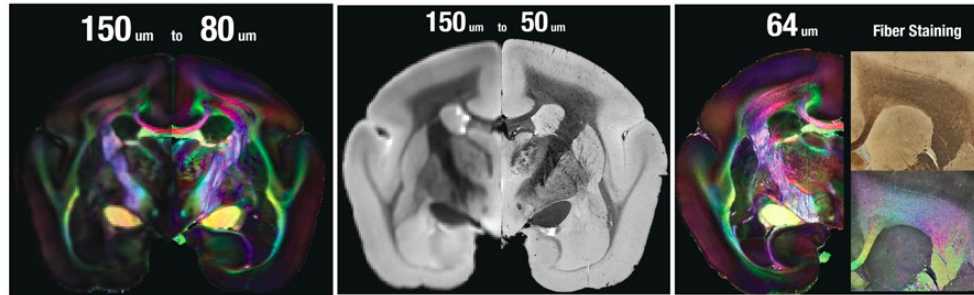

(Seidlitz, et al., 2017)

NIH Marmoset Template

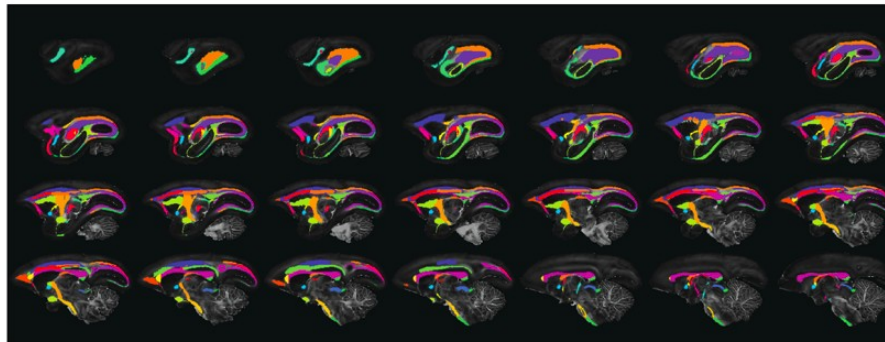## Individual marmoset template - **150um** resolution

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

2018: *improved* NIH Marmoset Template

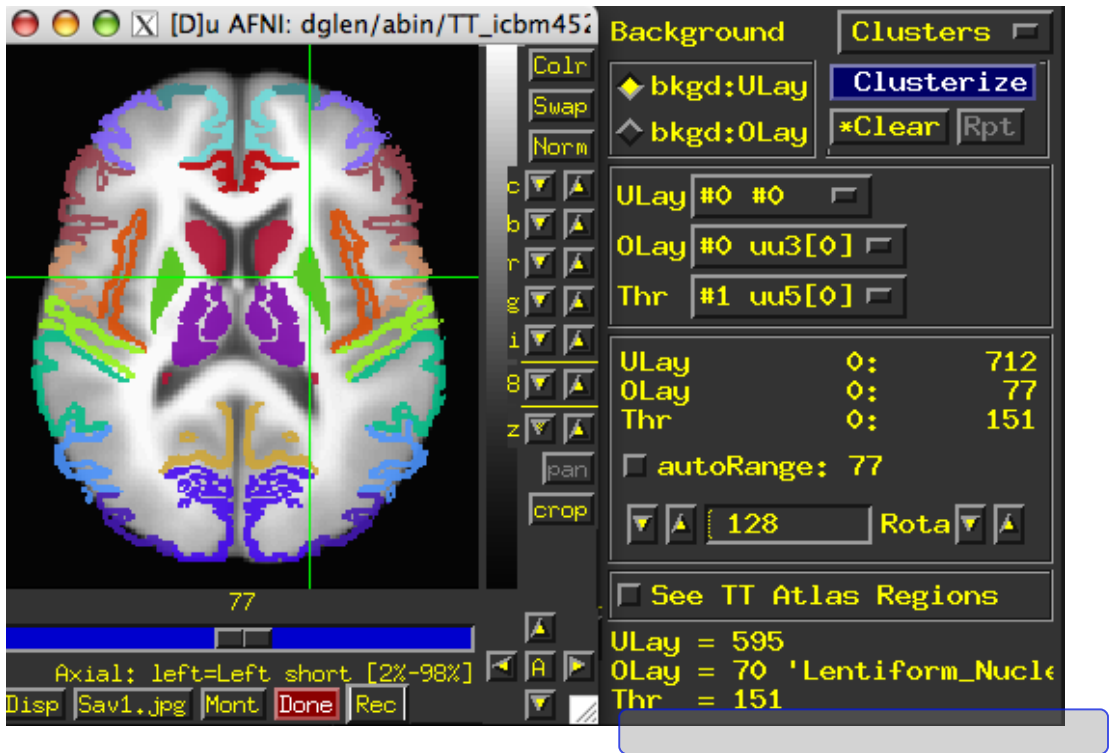## Better Data

Detailed labels

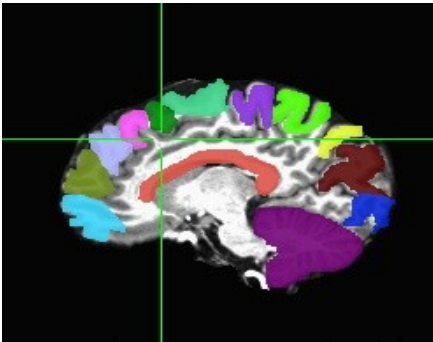## Support with tracing data, connectome and atlas utilities

(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.**

In Development

- New templates and template spaces – fully supported in AFNI
  - ◇ macaque
  - ◇ rat, mouse, (zebrafish?)
  - ◇ human
    - toddler, elderly, Indian
- Extra information about atlas structures – long names, web links, ….
- HAWG standardized format – atlases for everyone!

HCP Atlas -
Glasser →
Megan Robinson
and Mike
Beauchamp
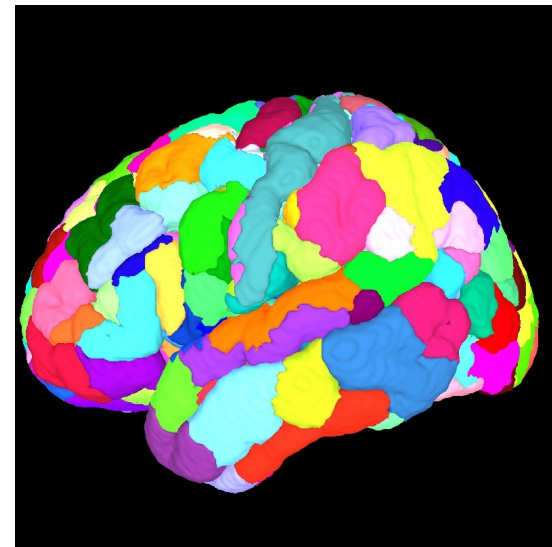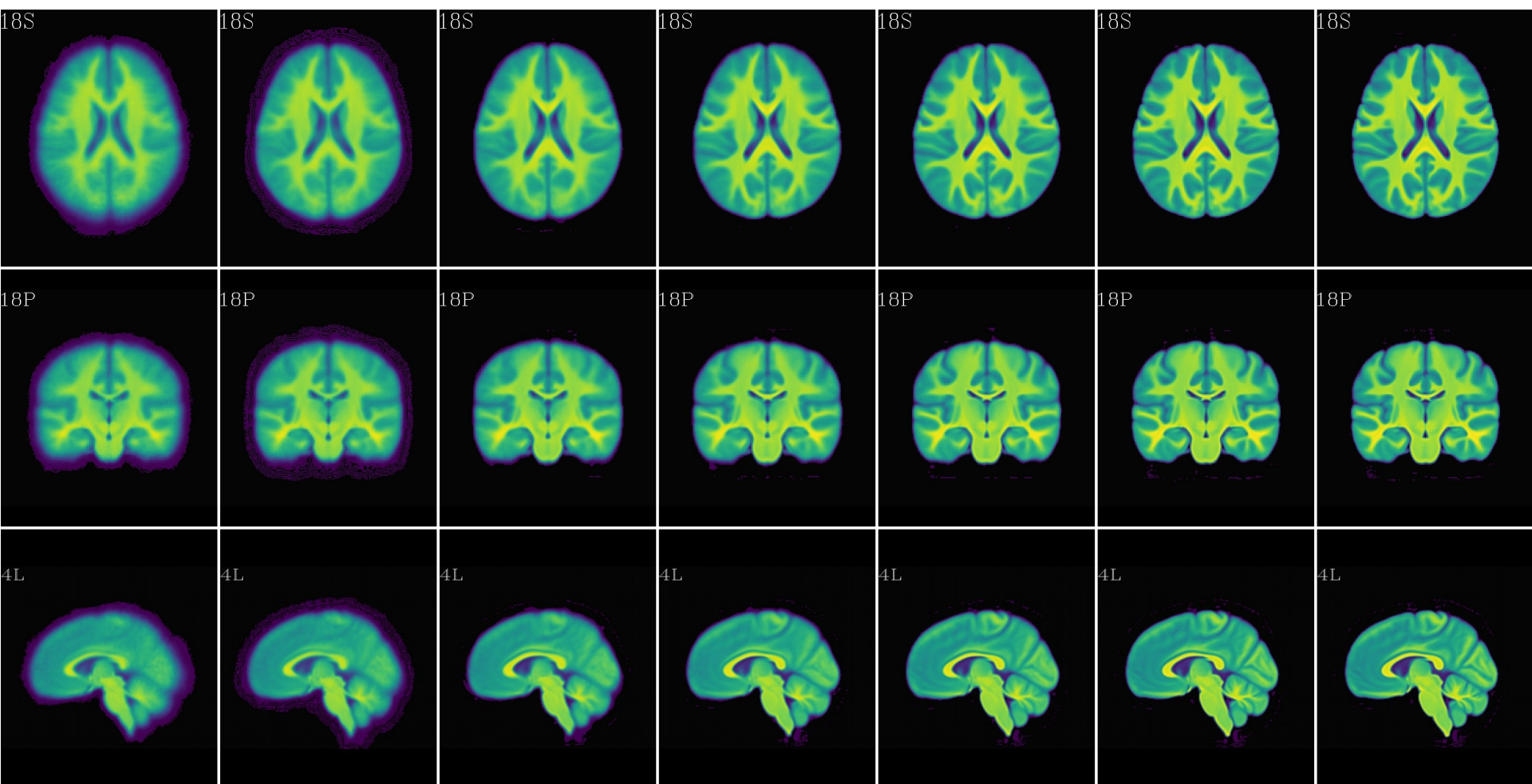
Indian Brain Template C2: IBT
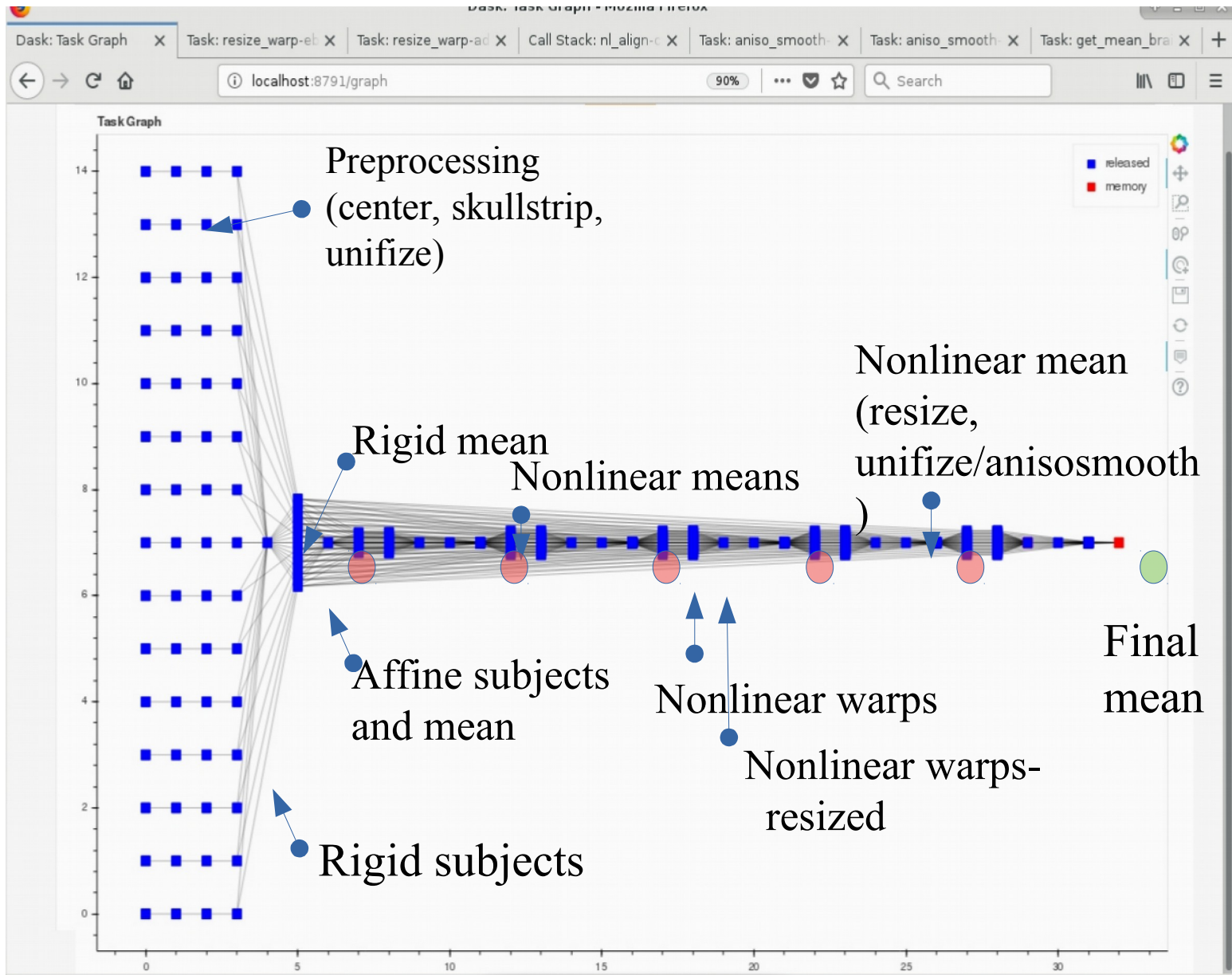
Dask Template task graph

Upcoming atlases

- Eickhoff-Zilles 2.2 cytoarchitectonic atlas

Version 2.2 vs Version 1.8

Upcoming atlases

- Jurgen Mai Human Brain Atlas - Brodmann Areas!

Cortex Surface

Amygdala

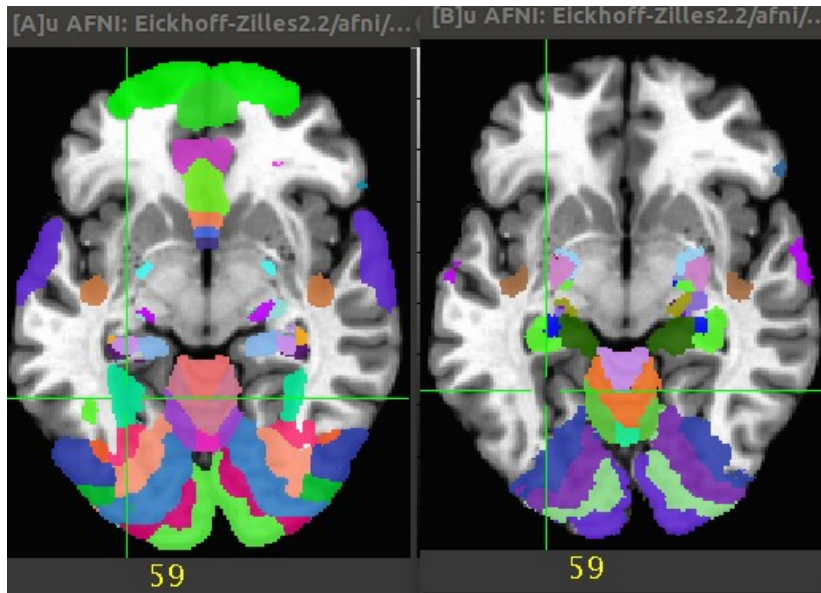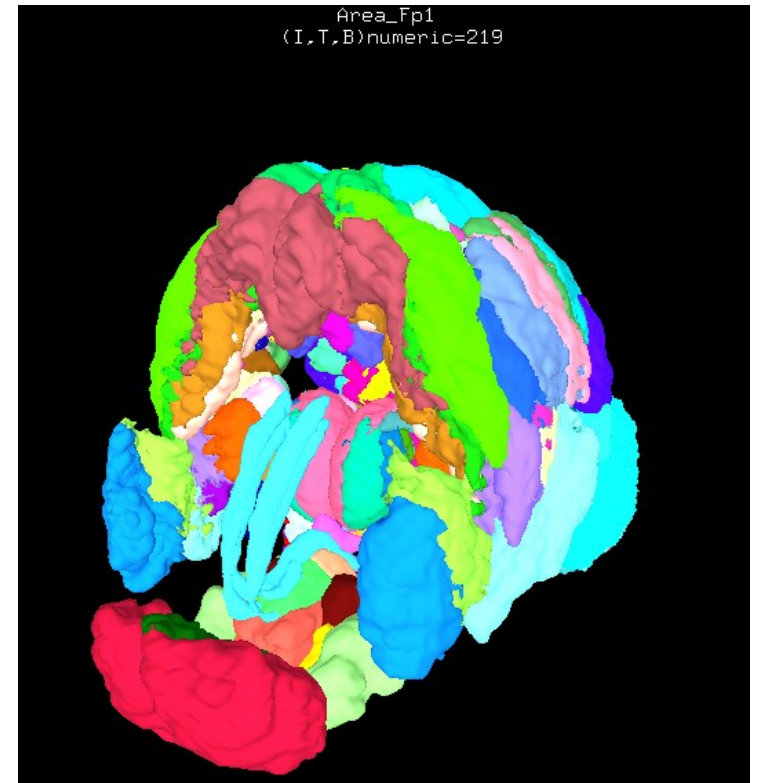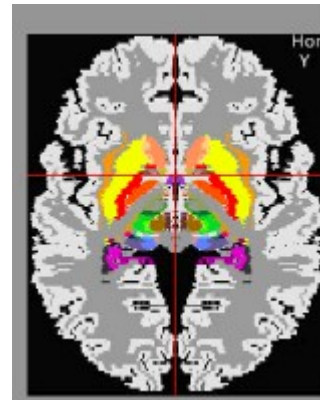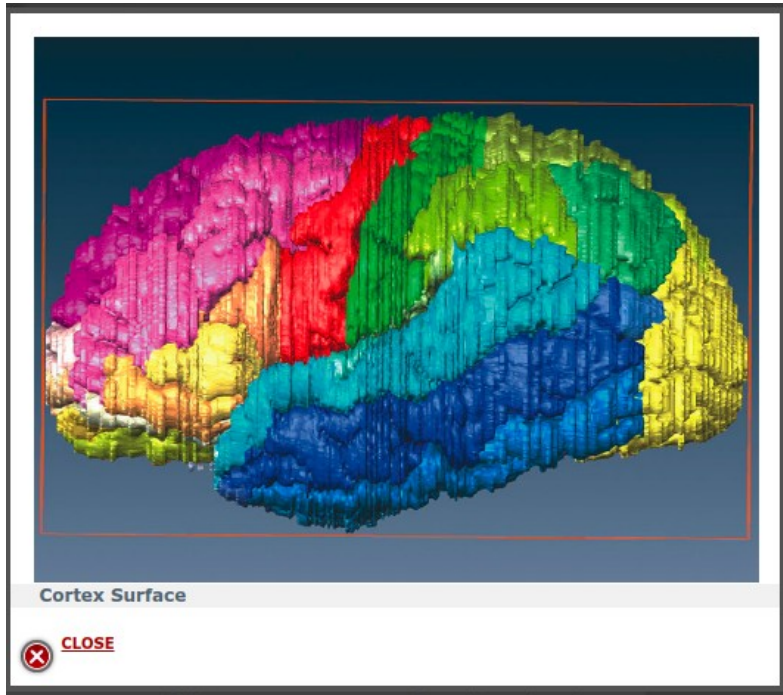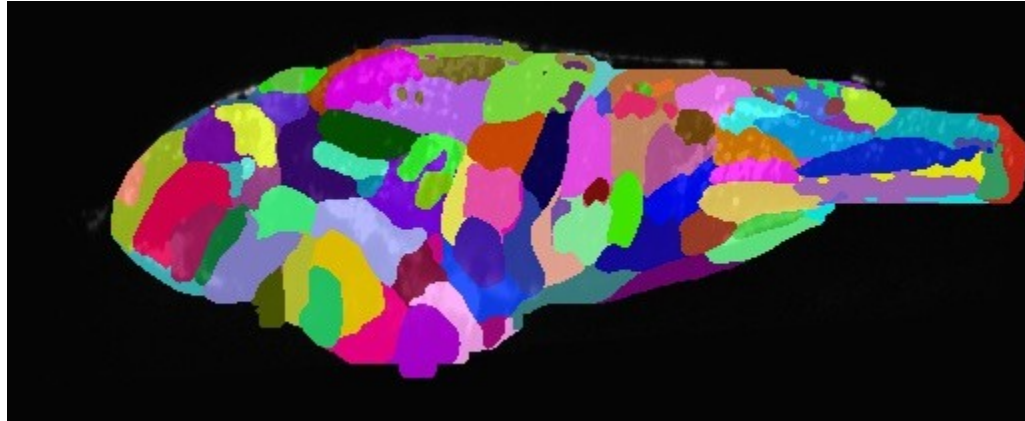Zebrafish atlas 2 micron data!
Harold Burgess, NIH

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"
```

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 "5" "Left-Cerebellum-White-Matter"
 "11" "3rd-Ventricle"
 "20" "Left-choroid-plexus"
 "89" "ctx-rh-inferiortemporal"
 "98" "ctx-rh-parsopercularis"
```

To make a labeltable and attach it to a file:

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

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.

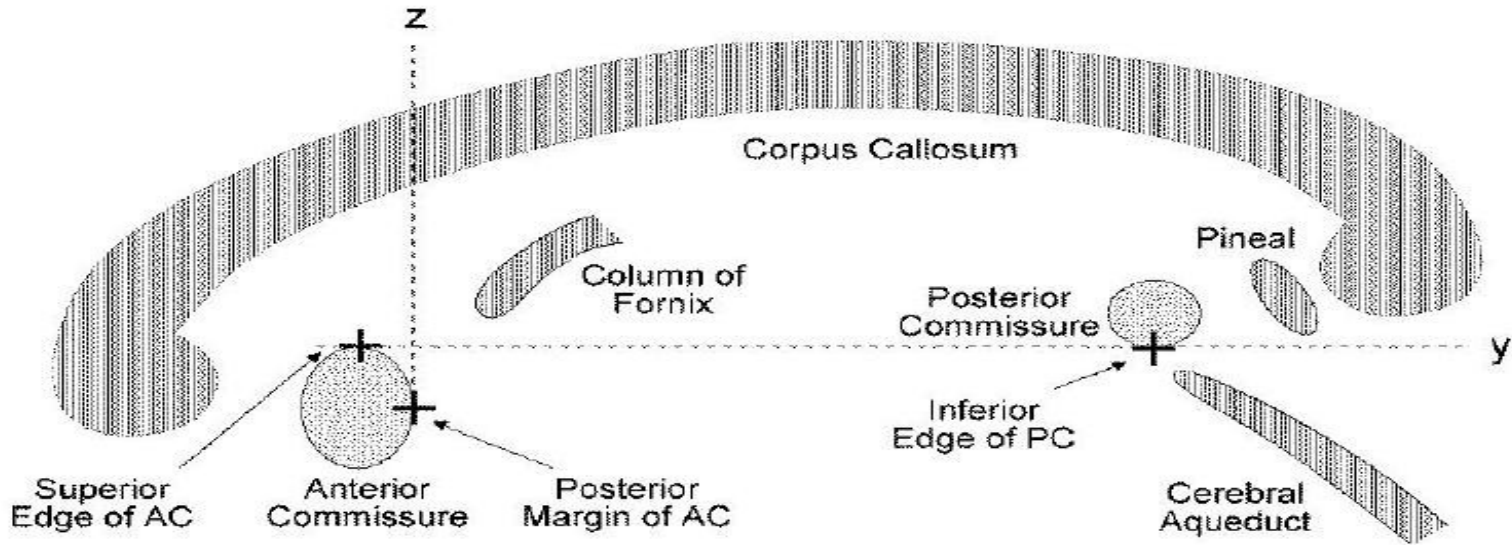# S2: Manual transform to Talairach space using AFNI GUI

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)

z

Corpus Callosum

Pineal

Column of
Fornix

Posterior
Commissure

Inferior
Edge of PC

y

Superior
Edge of AC

Anterior
Commissure

Posterior
Margin of AC

Cerebral
Aqueduct

Press this IN to create or change markers

◆ Original View
◇ AC-PC Aligned
◇ Talairach View

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

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

□ Allow edits

**Click <u>Define</u>
<u>Markers</u> to
open the
"markers"
panel**

Define Markers
■ See Markers

Pcolor   white   ☐
Scolor limegreen ☐
Size   8 ☐
Gap   3 ☐

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

Size of markers (pixels)
Size of gap in markers

Define OverLay
□ See Overlay

Set Clear Quality?

Transform Data
■ Big Talairach Box?

**Clear (unset)
primary marker**

Define Datamode

Switch Session
Switch UnderLay
Switch OverLay
Control Surface

**Select which
marker you
are editing**

**Set primary marker to
current focus location**

**Carry out transformation
to +acpc coordinates**

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

- **<u>Stage 2: Scaling to Talairach-Tournoux (+tlrc) coordinates</u>**:
    - ◇ 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)
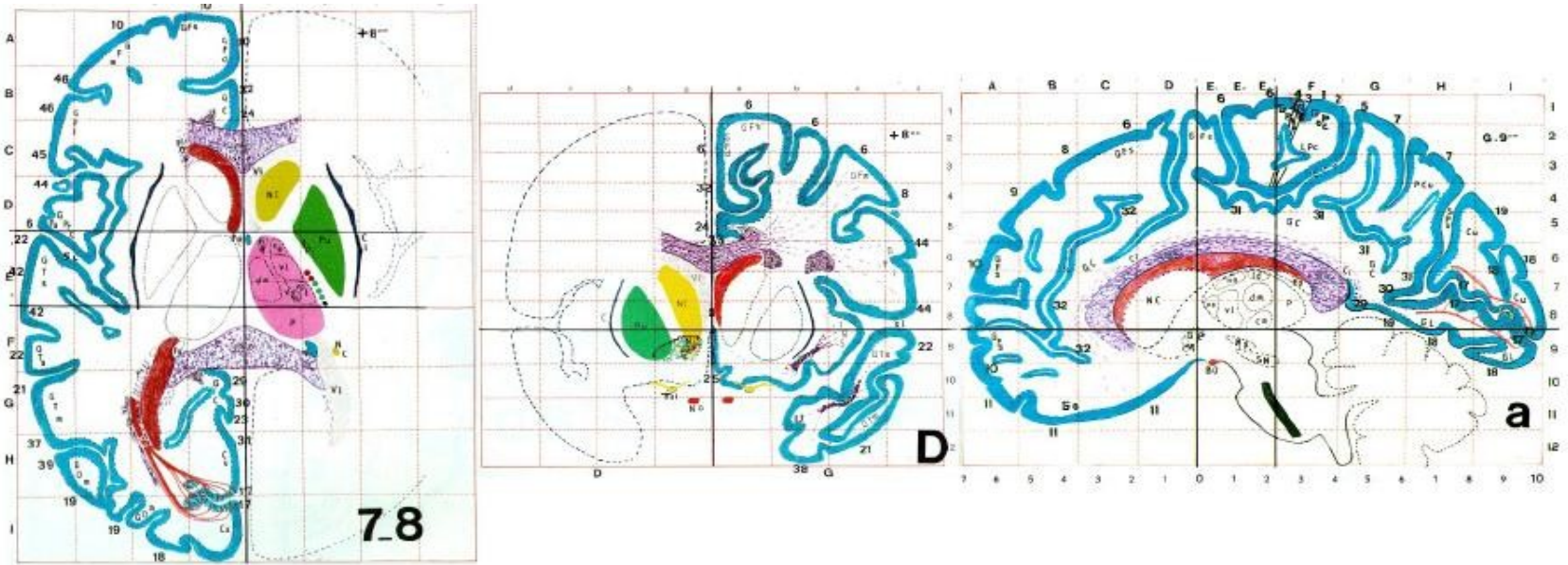
- **<u>Selecting the Talairach-Tournoux markers for the bounding box</u>**:
    - ◇ There are 12 sub-regions to be scaled (3 A-P x 2 I-S x 2 L-R)
    - ◇ To enable this, the transformed `+acpc` dataset gets its own set of markers
        - ➥ Click on the **[<u>AC-PC Aligned</u>]** button to view our volume in ac-pc coordinates
        - ⬚ Select the **[<u>Define Markers</u>]** 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):

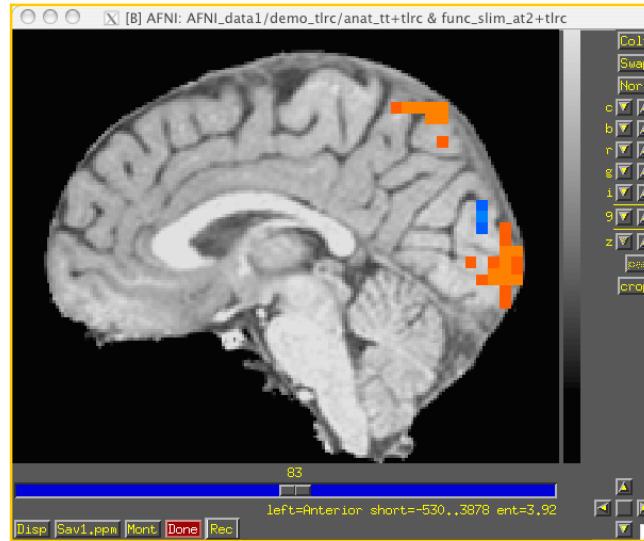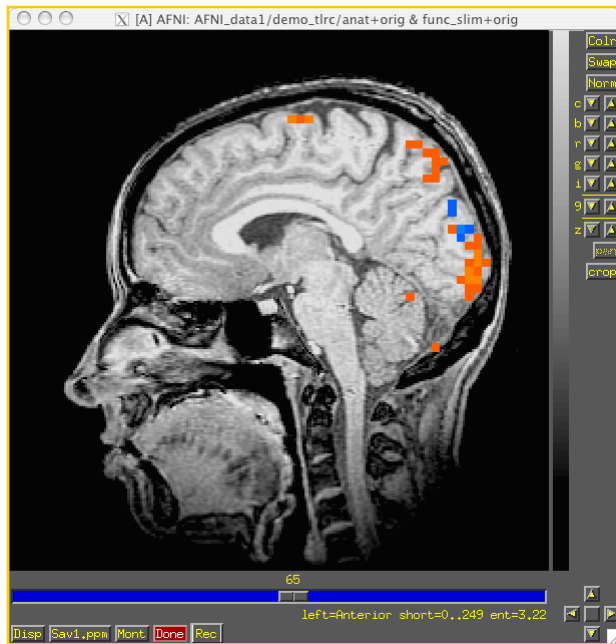**Talairach markers appear only when the AC-PC view is highlighted**
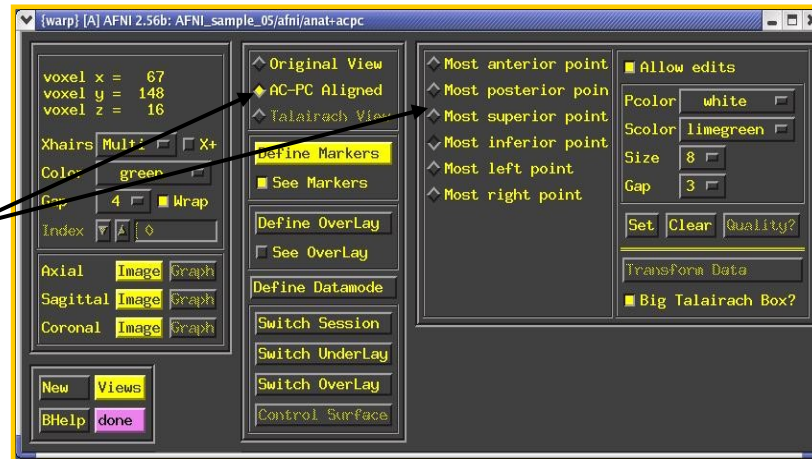
- ◇ Once all the markers are set, and the quality tests passed. Pressing **[<u>Transform Data</u>]** will write new *header* containing the Talairach transformations (see Appendix C for details)
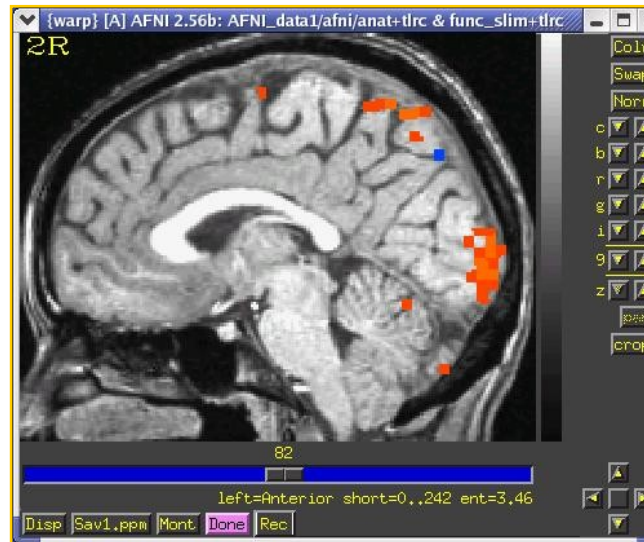   - ⬚ Recall: With AFNI, spatial transformations are stored in the header of the output

@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