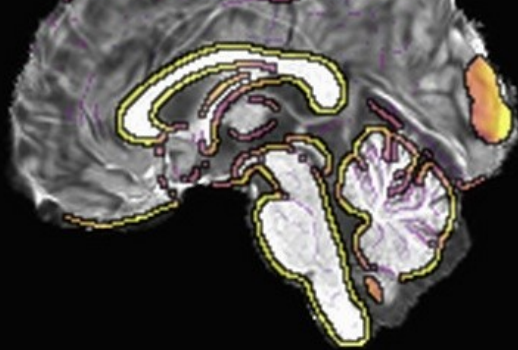
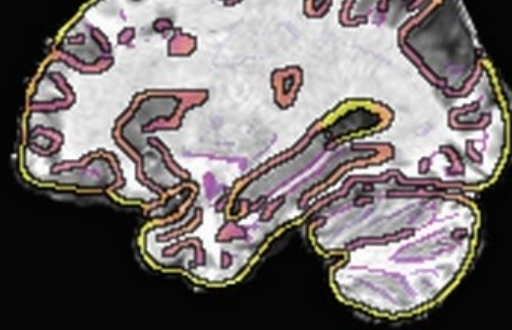


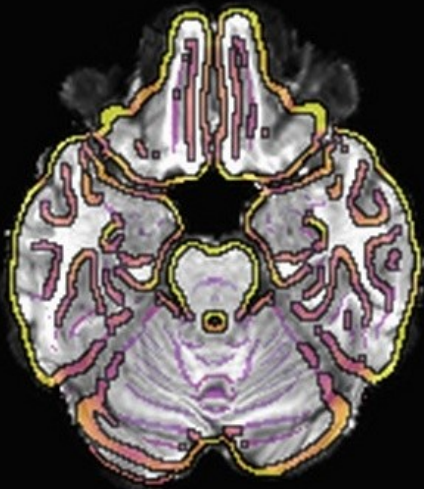
23I



95



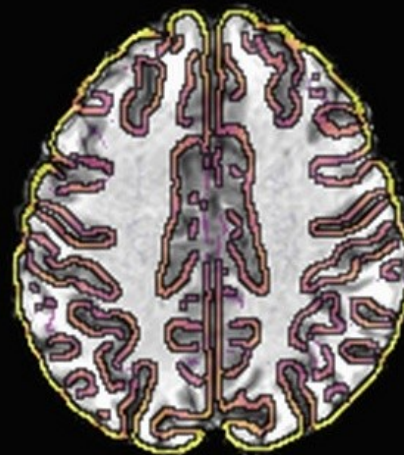
41S



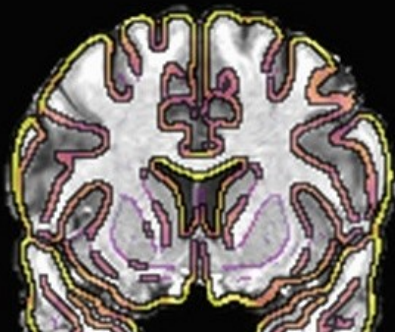
10A



22P



54P



Alignment

## Abbrevs used here

abbrev	= abbreviation
AKA	= also known as
anat	= anatomical
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
subj	= subject
vol	= volume
vox	= voxel(s)
xyz	= physical coordinates (units of mm)

## Alignment and its purpose(s)

- **Alignment (AKA registration):** bringing separate objects into the same space so that each location (e.g., voxel) within one object corresponds to the same location in the other
  - note: other software might refer to this process as “normalization,” but not in AFNI; too many things can be “normalized” (e.g., a vol’s brightness), so it is not descriptive enough on its own.

## Alignment and its purpose(s)

- **Alignment (AKA registration):** bringing separate objects into the same space so that each location (e.g., voxel) within one object corresponds to the same location in the other
- Common types of alignment
  - ✧ **EPI-EPI:** align a subject's EPI vols across time (to a selected ref EPI)
    - for motion “correction” (= “reduction” or “mitigation”)
  - ✧ **EPI-anat:** align a subject's EPI with anatomical vol
    - to assign a location with a functional result
  - ✧ **anat-template:** register a subject's anatomical to a standard template
    - for group level alignment, also compare/use locations from lit.
    - can then utilize associated atlases (= maps of regions)
  - ✧ and more:
    - distortion correction (such as EPI distortion)
    - “axialize”: rotate brain to standardize slice viewing
    - quality control: check for left-right flipping
    - ....

## Mechanics of alignment

- Several different tools exist for alignment
  - choose based on properties of the images, what type of distortion/diff is present, and the **type** of desired alignment
- Some important questions about each alignment:
  - what is the **purpose** (e.g., undo distortion, or just overlay good volumes)?
  - are we aligning data from the same or different **subjects**?
  - do the data sets have similar or different **appearance** (both have bright CSF? or opposite tissue contrast?)
  - do both data sets have whole brain coverage? do both data sets have skull on or off?
- important concepts for selecting parameters include: contrast, smoothness, detail, resolution, field of view (FOV), concatenation, source/base dsets, grid
- NB: `afni_proc.py` will take care of *many* of these details for FMRI processing (so use it!), but it is still good to have some familiarity with them!

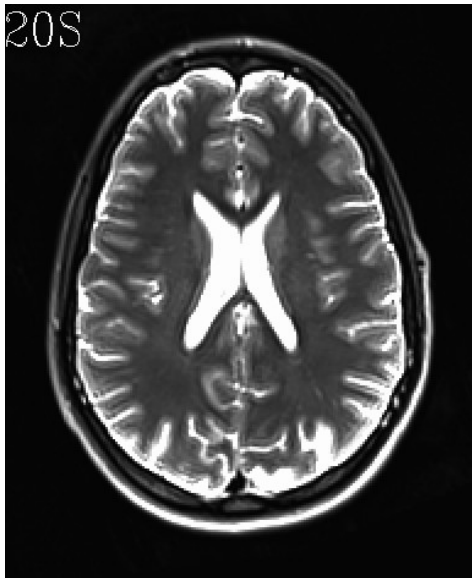
*We highlight some alignment/registration programs in this presentation.*

*See the complete list on the AFNI website:*

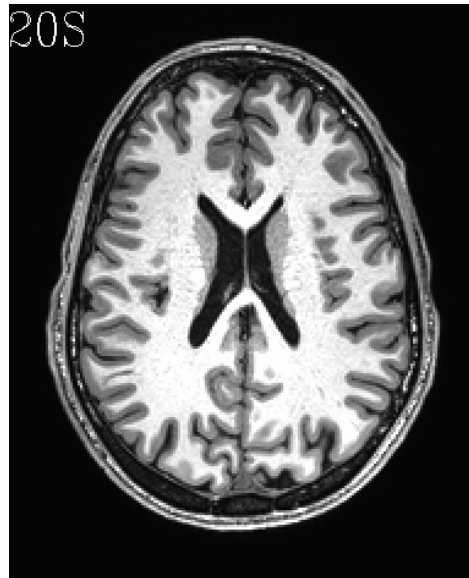
[https://afni.nimh.nih.gov/pub/dist/doc/html/doc/educational/classified\\_progs.html#align-register-warp-axialize-spatially](https://afni.nimh.nih.gov/pub/dist/doc/html/doc/educational/classified_progs.html#align-register-warp-axialize-spatially)

## Alignment concepts: tissue contrast

- Do the vols have similar or different tissue contrast?



A) T2w



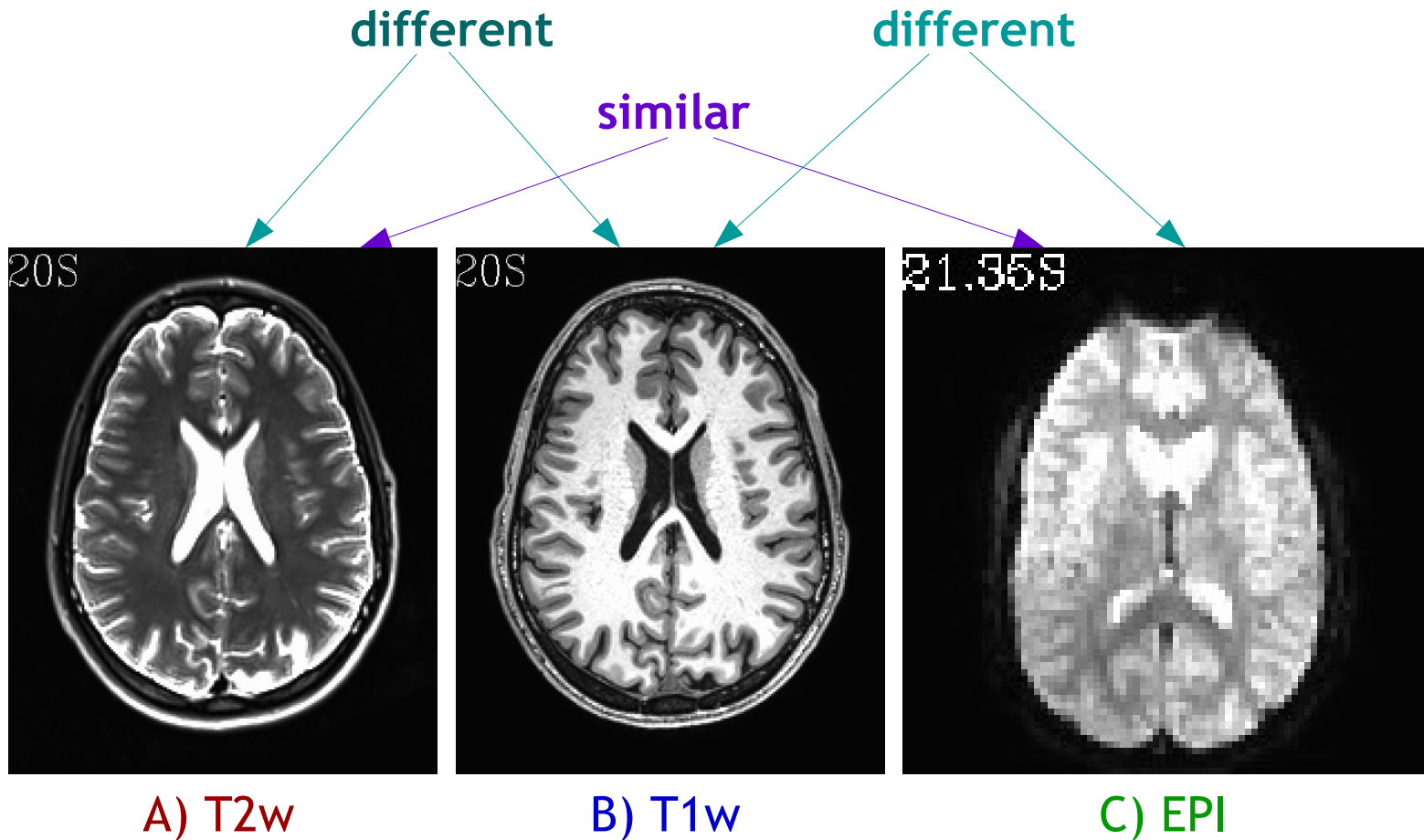
B) T1w



C) EPI

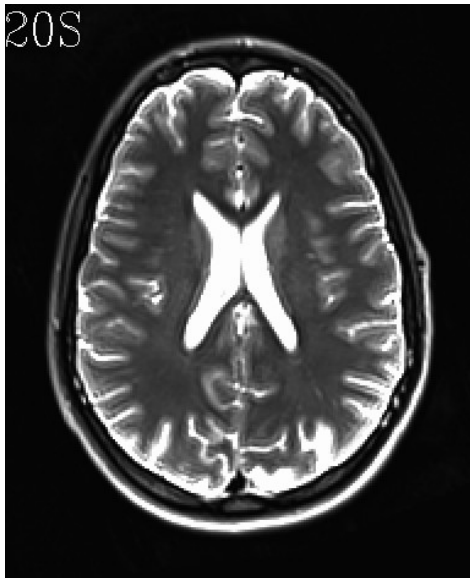
## Alignment concepts: tissue contrast

- Do the vols have similar or different tissue contrast?  
→ *determines what cost function we use (see slides 25-27).*

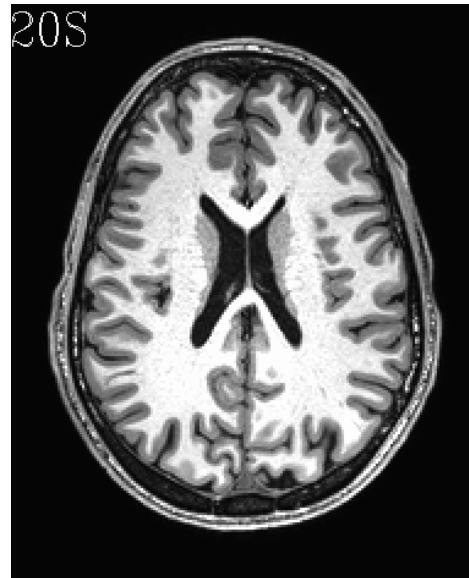


## Alignment concepts: spatial resolution

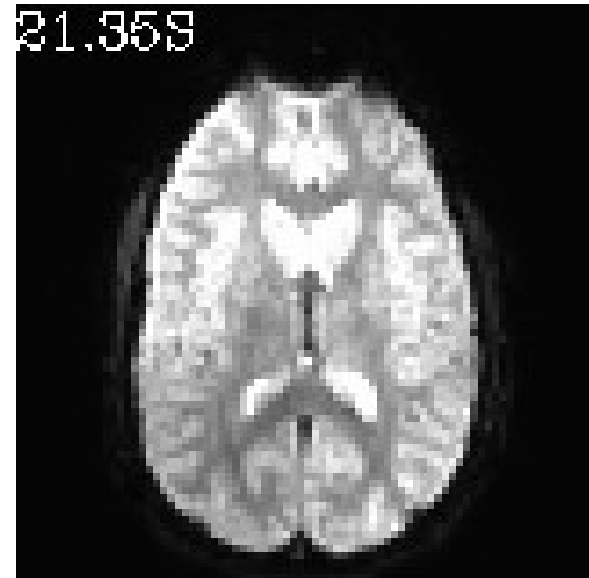
- What kind of resolution do vols have (high/low)?



A) T2w



B) T1w



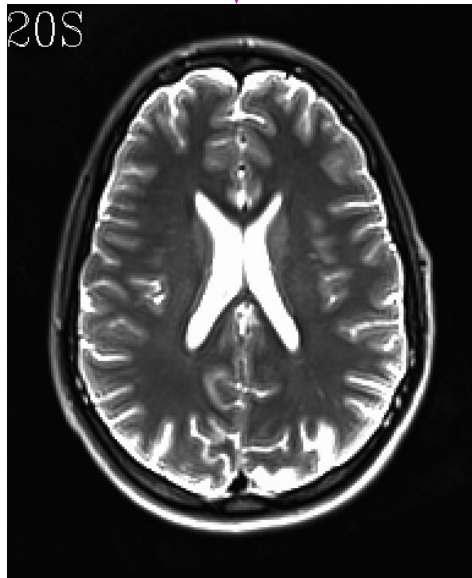
C) EPI



## Alignment concepts: spatial resolution

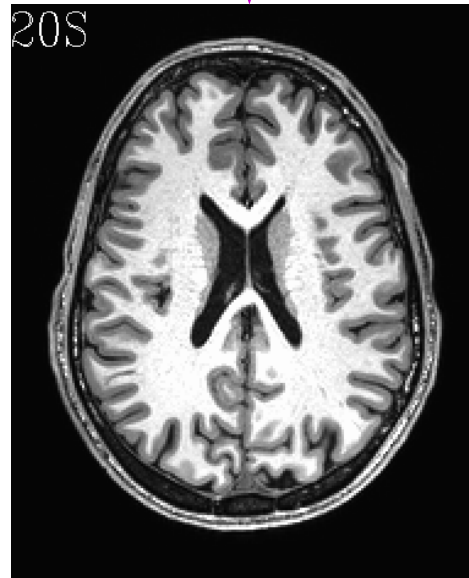
- What kind of resolution do vols have (high/low)?  
→ *affects how we choose which vol is “source” (to-be-warped) and which is “base” (=target) and level of warping*

high res



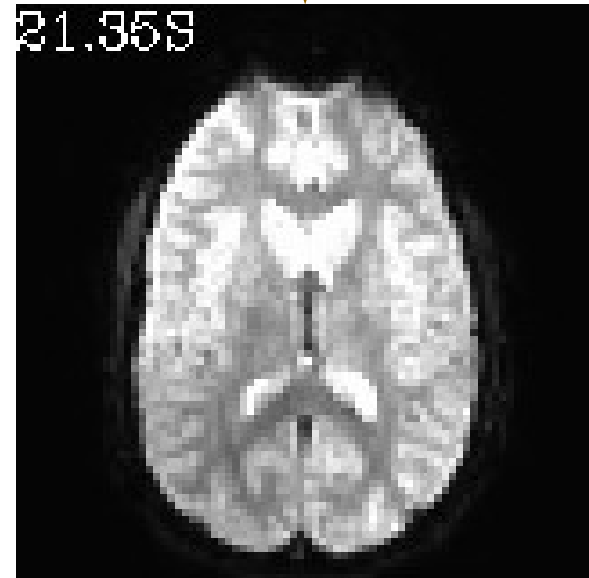
A) T2w

high res



B) T1w

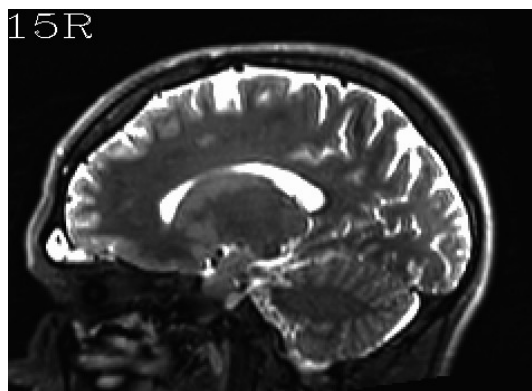
low res



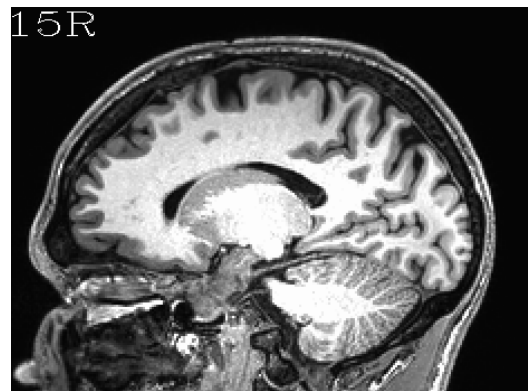
C) EPI

## Alignment concepts: field of view (FOV) coverage

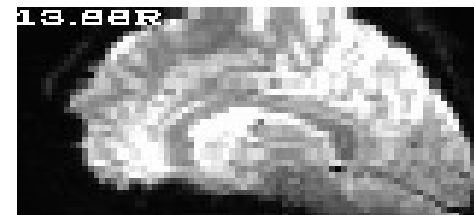
- What kind of coverage does the FOV have? Does it include the whole brain?



A) T2w



B) T1w

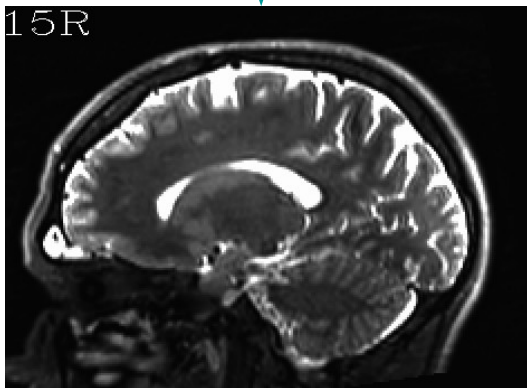


C) EPI

## Alignment concepts: field of view (FOV) coverage

- What kind of coverage does the FOV have? Does it include the whole brain?  
→ *might need extra options, affects how we view quality of alignment, and we might just expect some alignment problems*

whole brain FOV



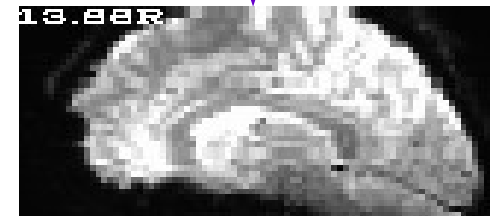
A) T2w

whole brain FOV



B) T1w

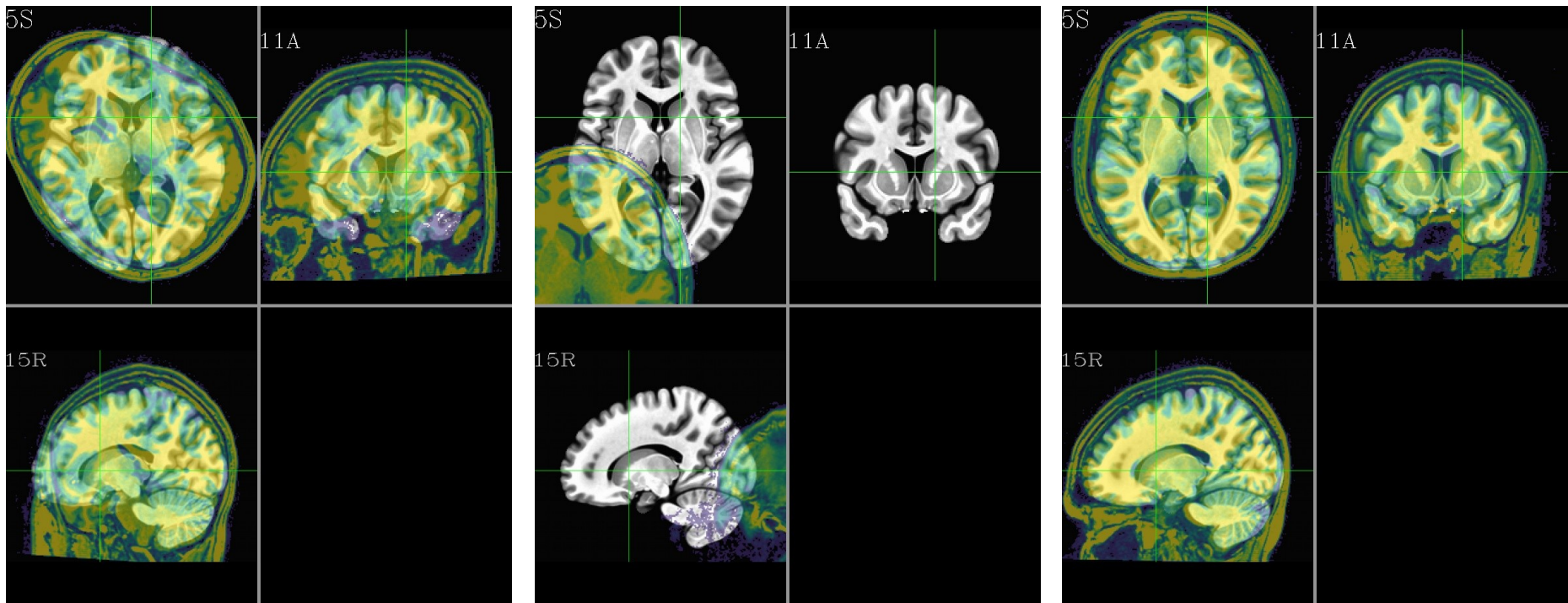
cut-off FOV  
(both sup cortex  
and cerebellum)



C) EPI

## Alignment concepts: dset overlap

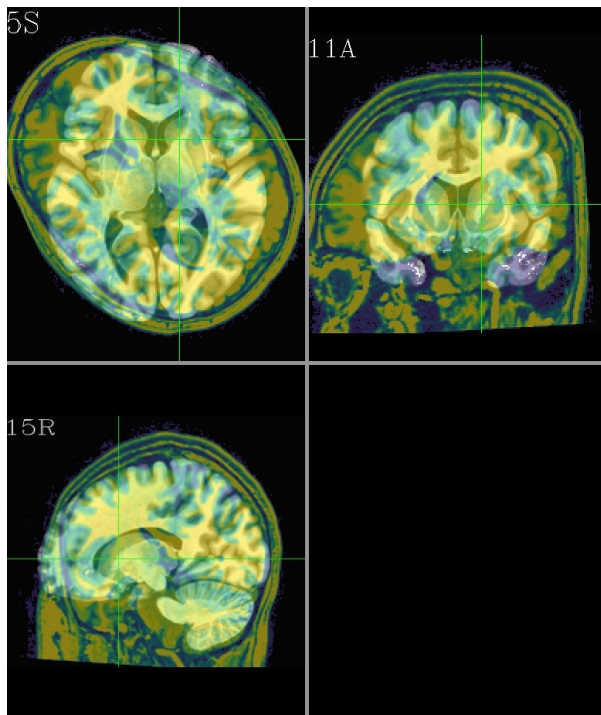
- How far apart are the “source” and “base” dsets? Do they overlap in the GUI?



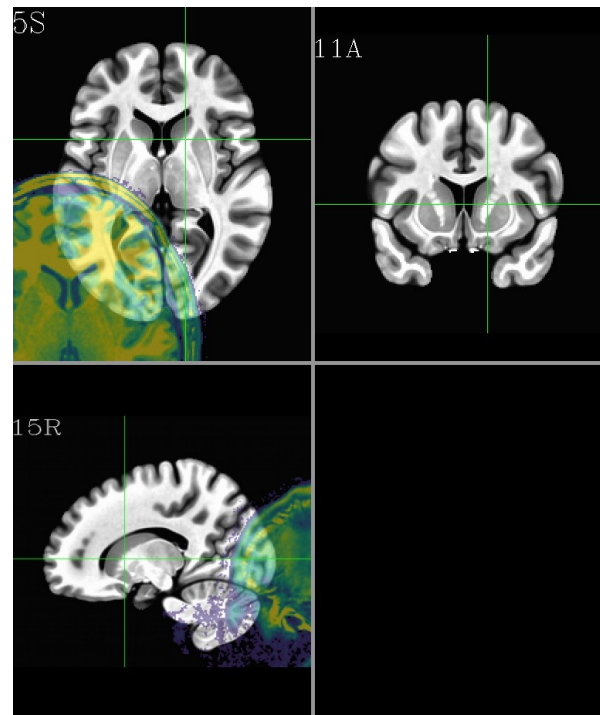
## Alignment concepts: dset overlap

- How far apart are the “source” and “base” dsets? Do they overlap in the GUI?  
→ *large differences in location, rotation, size, etc. can make alignment tricky. The greater the overlap/similarity of the dsets, the better the alignment prospects.*

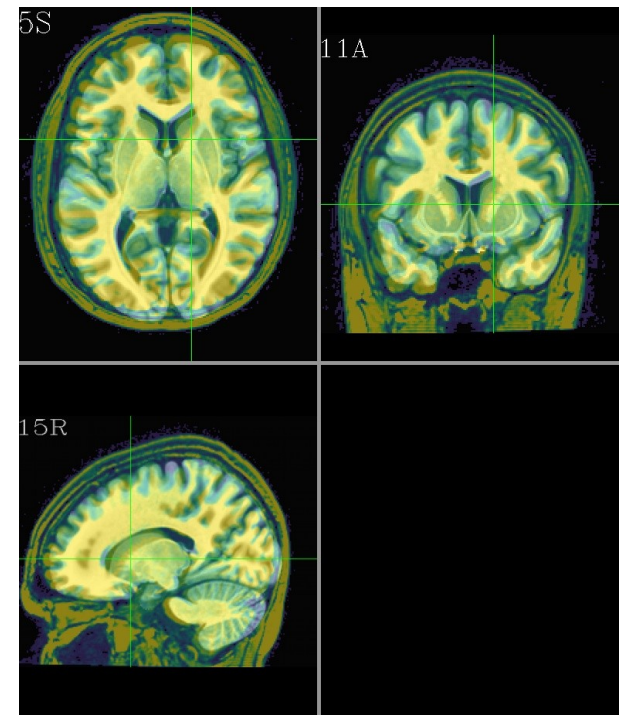
*large rotation!*



*large translation!*



*pretty darn close*



- To deal with large relative differences, one might need to use additional preprocessing steps or options for the alignment programs. [See S1 at end of slides for image script.]

## How is alignment transformation calculated?

- The fundamental aspects are the same across the tools:  
Take two images, a base (=reference) and source (=to be adjusted)
  - 1) quantify “how similar” they are,
  - 2) if they are “similar enough,” then stop;  
otherwise, tweak/perturb the source image,
  - 3) quantify “how similar” the new source and base are, ... [repeat]

## How is alignment transformation calculated?

- The fundamental aspects are the same across the tools:  
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  - 1) quantify “how similar” they are,
  - 2) if they are “similar enough,” then stop;  
otherwise, tweak/perturb the source image,
  - 3) quantify “how similar” the new source and base are, ... [repeat]
- To *quantify how similar dsets are*, we need a **cost function**
  - the **cost function** is how we take values from both dsets and make an overall assessment of a desired property; different functions yield different alignments
  - For example, could:
    - reward similarity or when peak values line up (e.g., for matching contrasts)
    - reward when *anti*-peaks line up (e.g., for opposite contrasts)

## Cost functions in AFNI

- There are *many* cost functions in AFNI, from historical development/evolution but there are just a few we now recommend (from 3dAllineate's help):

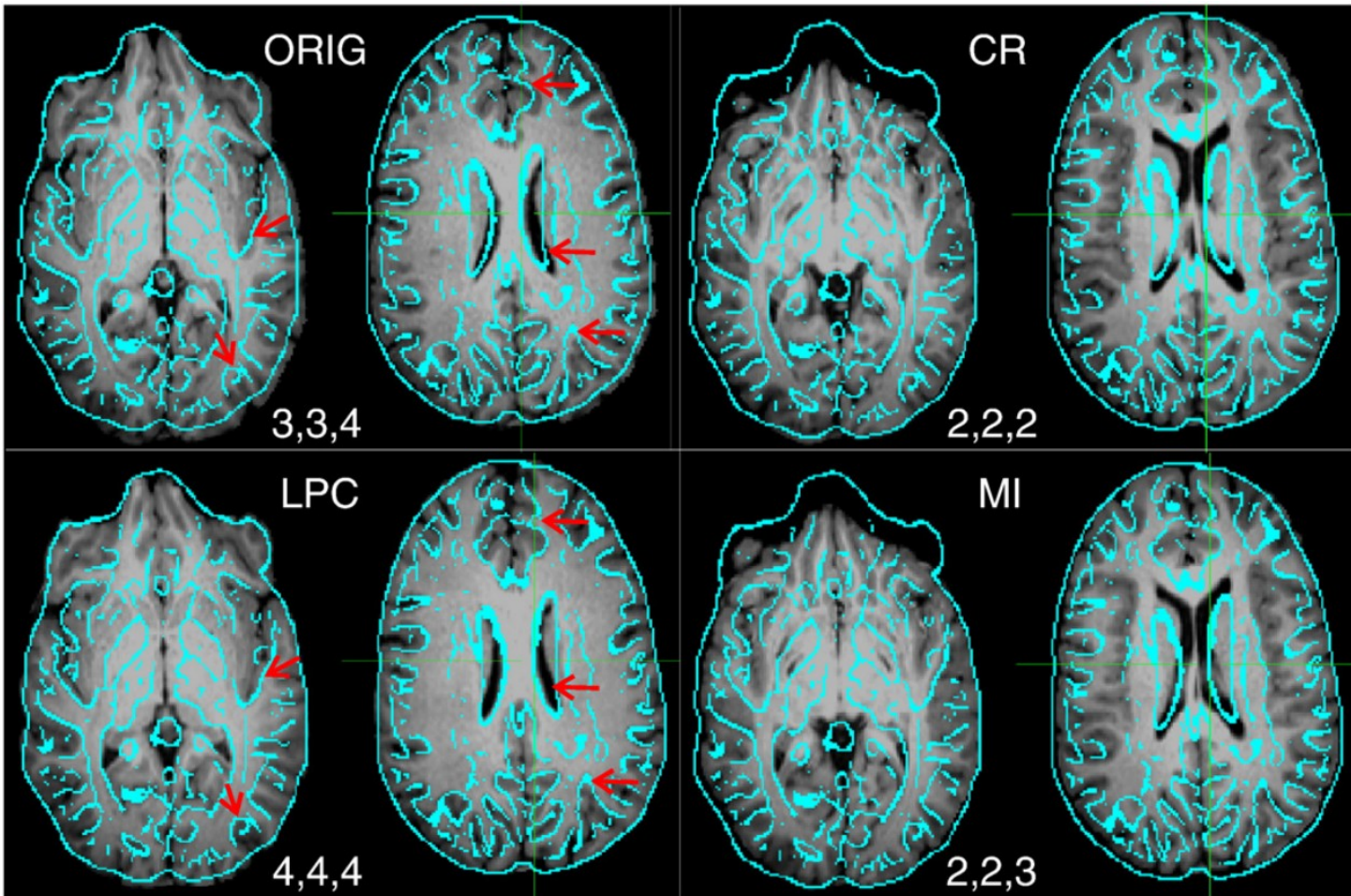
```
ls  :: 1 - abs(Pearson correlation coefficient)
sp  :: 1 - abs(Spearman correlation coefficient)
mi  :: - Mutual Information = H(base,source)-H(base)-H(source)
crM :: 1 - abs[ CR(base,source) * CR(source,base) ]
nmi :: 1/Normalized MI = H(base,source)/[H(base)+H(source)]
je  :: H(base,source) = joint entropy of image pair
hel :: - Hellinger distance(base,source)
crA :: 1 - abs[ CR(base,source) + CR(source,base) ]
crU :: CR(source,base) = Var(source|base) / Var(source)
lss :: Pearson correlation coefficient between image pair
lpc :: nonlinear average of Pearson cc over local neighborhoods
lpa :: 1 - abs(lpc)
lpc+:: lpc + hel + mi + nmi + crA + overlap
ncd :: mutual compressibility (via zlib) -- doesn't work yet
```

- “lpa” is basic choice for vols with *similar* contrast
- “lpc” is basic choice for vols with *differing/opposite* contrast
  - and “lpc+ZZ” might be even better for awkward cases: robuster, but slower
- (“ls” is okay for simple EPI-EPI alignment in 3dvolreg)



## Cost functions in AFNI

- “lpc” in action, EPI-to-anat (olay: edges from same EPI slice; ulay: matched anat):



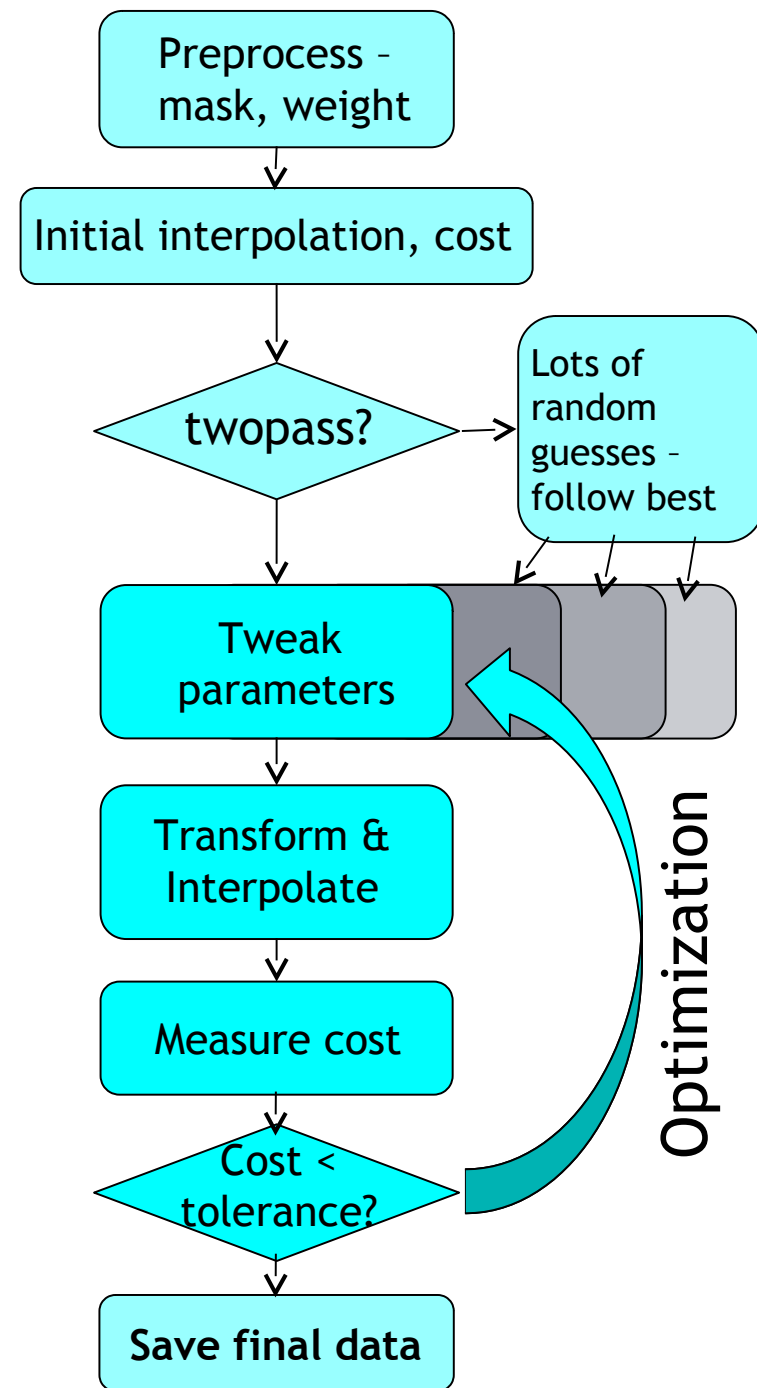
ZS Saad, DR Glen, G Chen, MS Beauchamp, R Desai, RW Cox (2009). A new method for improving functional-to-structural MRI alignment using local Pearson correlation. *NeuroImage* 44: 839-848.

## How is alignment transformation calculated?

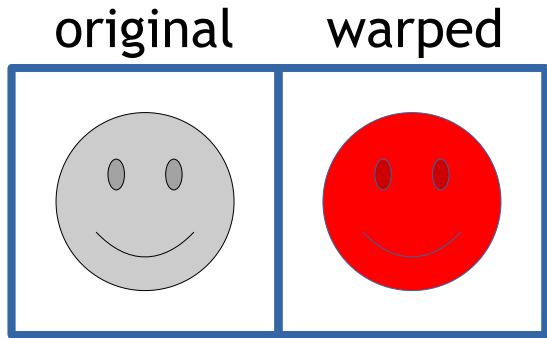
- The fundamental aspects are the same across the tools:  
Take two images, a base (=reference) and source (=to be adjusted)
  - 1) quantify “how similar” they are,
  - 2) if they are “similar enough,” then stop;  
otherwise, tweak/perturb the source image,
  - 3) quantify “how similar” the new source and base are, ... [repeat]
- To *quantify how similar dsets are*, we need a **cost function**
  - the **cost function** is how we take values from both dsets and make an overall assessment of a desired property; different functions yield different alignments
  - For example, could:
    - reward similarity or when peak values line up (e.g., for matching contrasts)
    - reward when *anti*-peaks line up (e.g., for opposite contrasts)
- To *tweak/perturb the source*, we need to know what kind of parameters to change
  - rotations, translations, shear, scaling, higher order (determined by **degrees of freedom**)
  - and whether we are matching entire FOV or smaller pieces (family: **linear/affine or nonlinear**)

## View inside *alignment* process

- **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

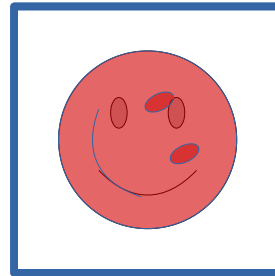


# Types of warps: Linear affine (average FOV fit)

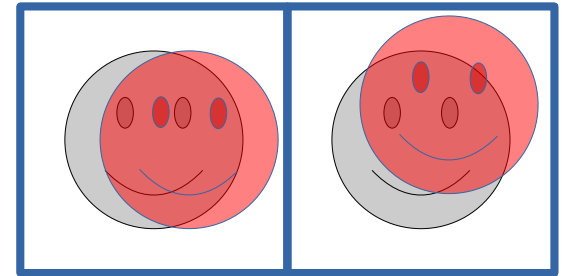


## Parameters (applied globally)

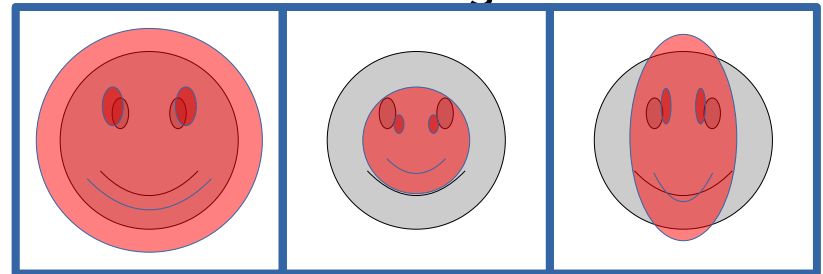
rotation



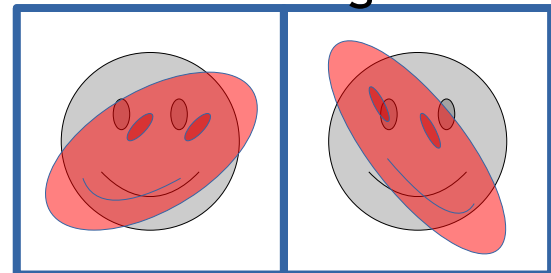
translation



scaling



shearing



There are four parameters in the linear affine family of warps:

*rotation*

*translation*

*shearing*

*scaling*

In 3D alignment, each parameter has three **degrees of freedom (DOFs)**:

+ rigid body (AKA “solid body”)

6 DOF = 3 transl + 3 rot

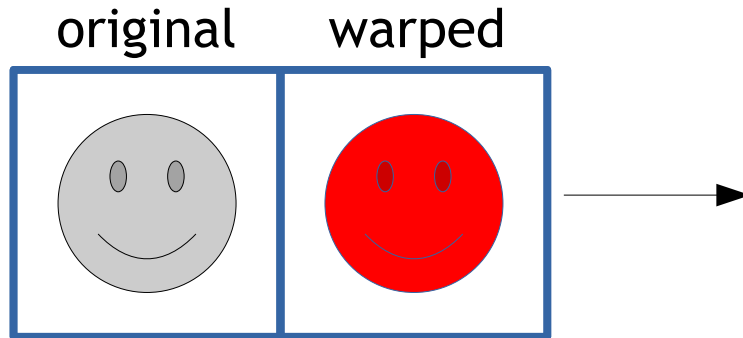
Ex: *3dvolreg*

+ linear affine

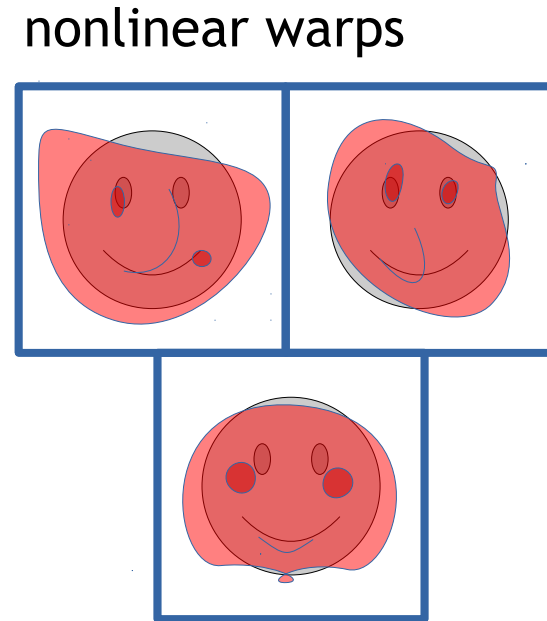
12 DOF = 3\*(transl + rot + scale + shear)

Ex: *3dAllineate*, *align\_epi\_anat.py*

## Types of warps: nonlinear (patch refinement)



Parameters (applied *locally*)



In nonlinear warping, a first pass is done with simpler *global* alignment, and then the matching is refined *locally* in “patches” down to a certain length scale.

There are many more DOFs used here, and one can match more features-- but details also matter more (e.g., skullstripping)

### + nonlinear warping

12 DOF initially + hundreds (or thousands) more DOFs in refinement steps

Ex: *3dQwarp*, *@SSwarper*, *@animal\_warper*, *auto\_warp.py*

## Types of warps: example case “rigid”

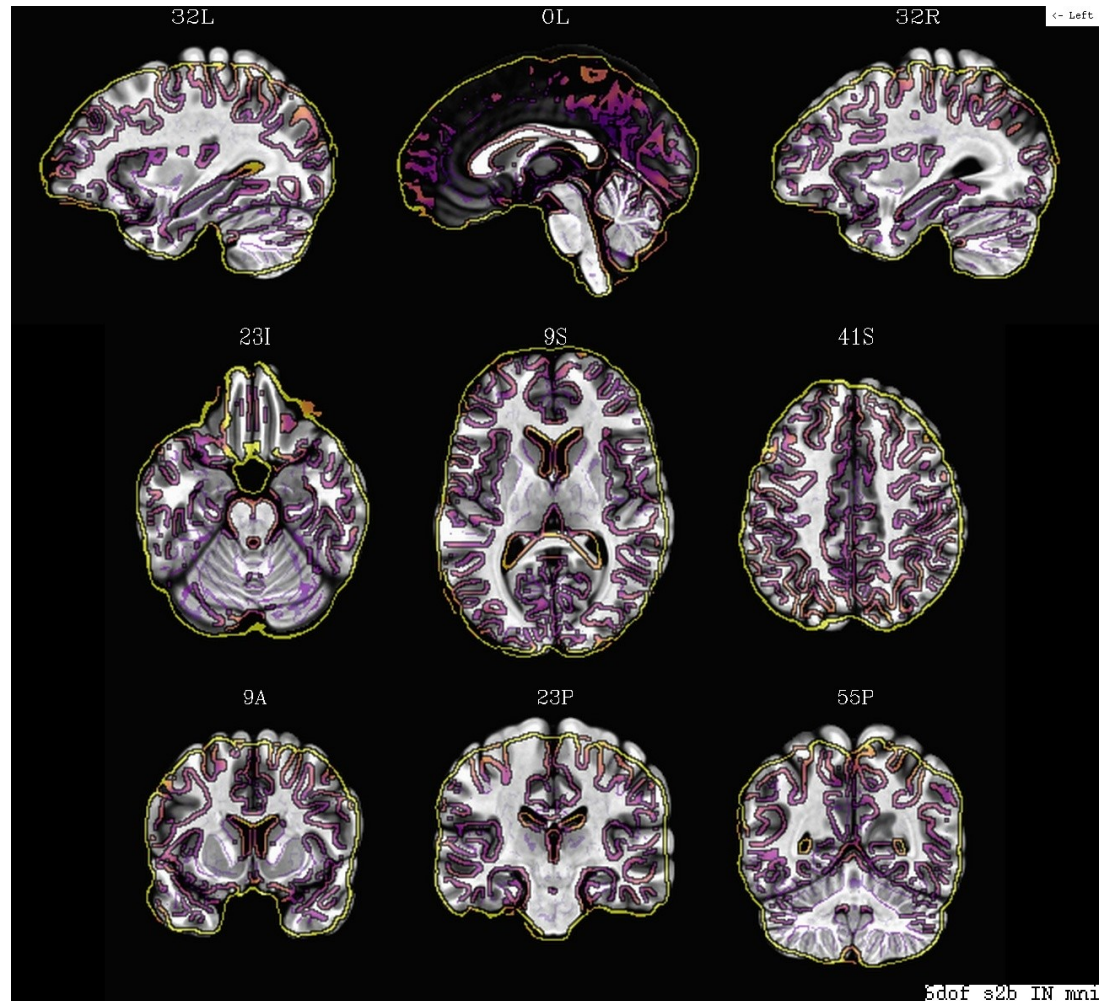
ulay: base template

olay: warped dset (6DOF, linear, “rigid body”)

Compare alignment with  
overlying edges of warped  
source dset on base template

“Base” volume in this case is  
MNI template; “source” is  
typical subject anat vol.

Overall fit: **OK**, some major  
parts align, but brain shapes  
are (and remain) different.



PLOT: @snapshot\_volreg TEMPLATE\_VOL WARPED\_VOL

# Types of warps: example case “linear affine”

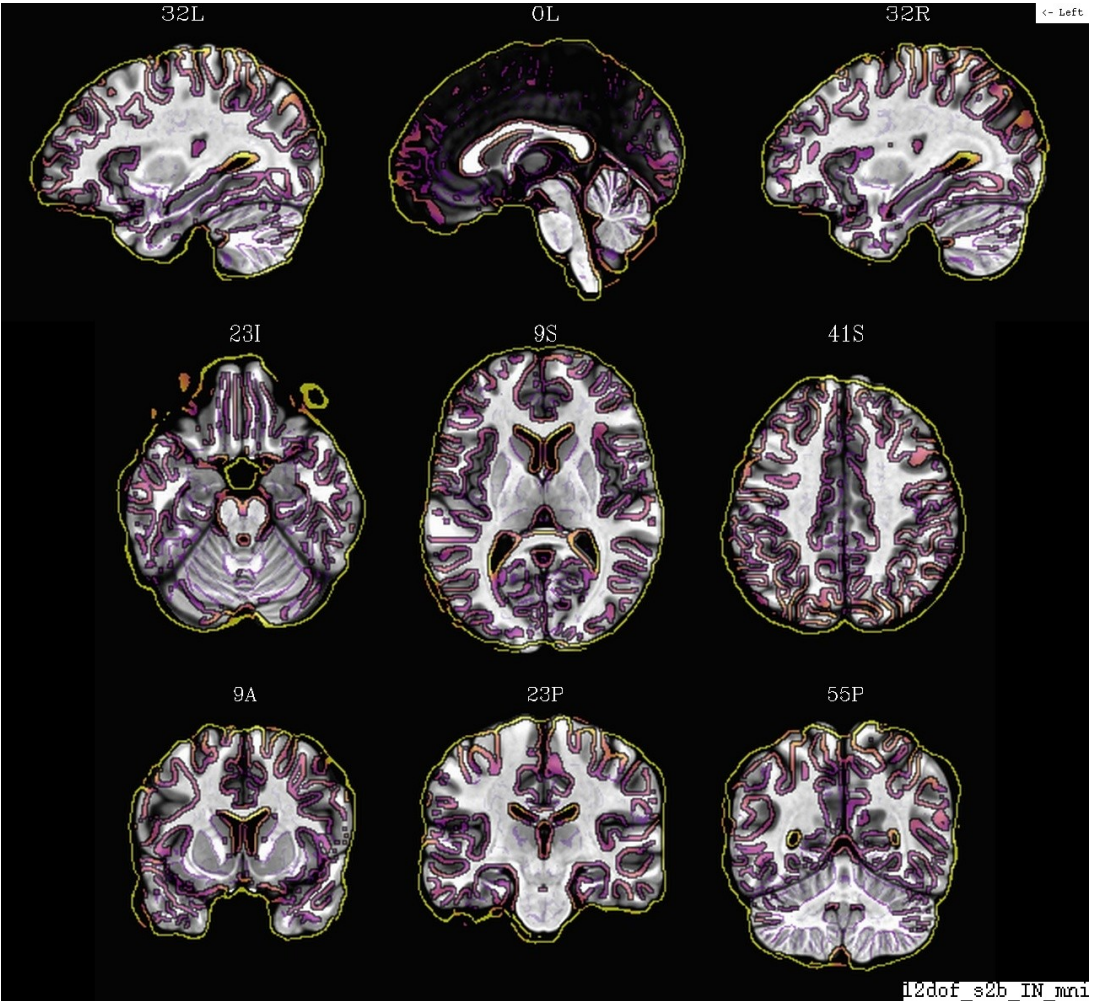
Compare alignment with overlaying edges of warped source dset on base template

“Base” volume in this case is MNI template; “source” is typical subject anat vol.

Overall fit: **Good, general shape and many sulci/gyri match, but not all and many are approximate.**

Bonus Type - **rigid equivalent**  
6-parameters extracted.  
"Axializing" subjects to template of different size

blue: base template  
red: warped dset (12DOF, affine)



PLOT: @snapshot\_volreg TEMPLATE\_VOL WARPED\_VOL

## Types of warps: example case “nonlinear”

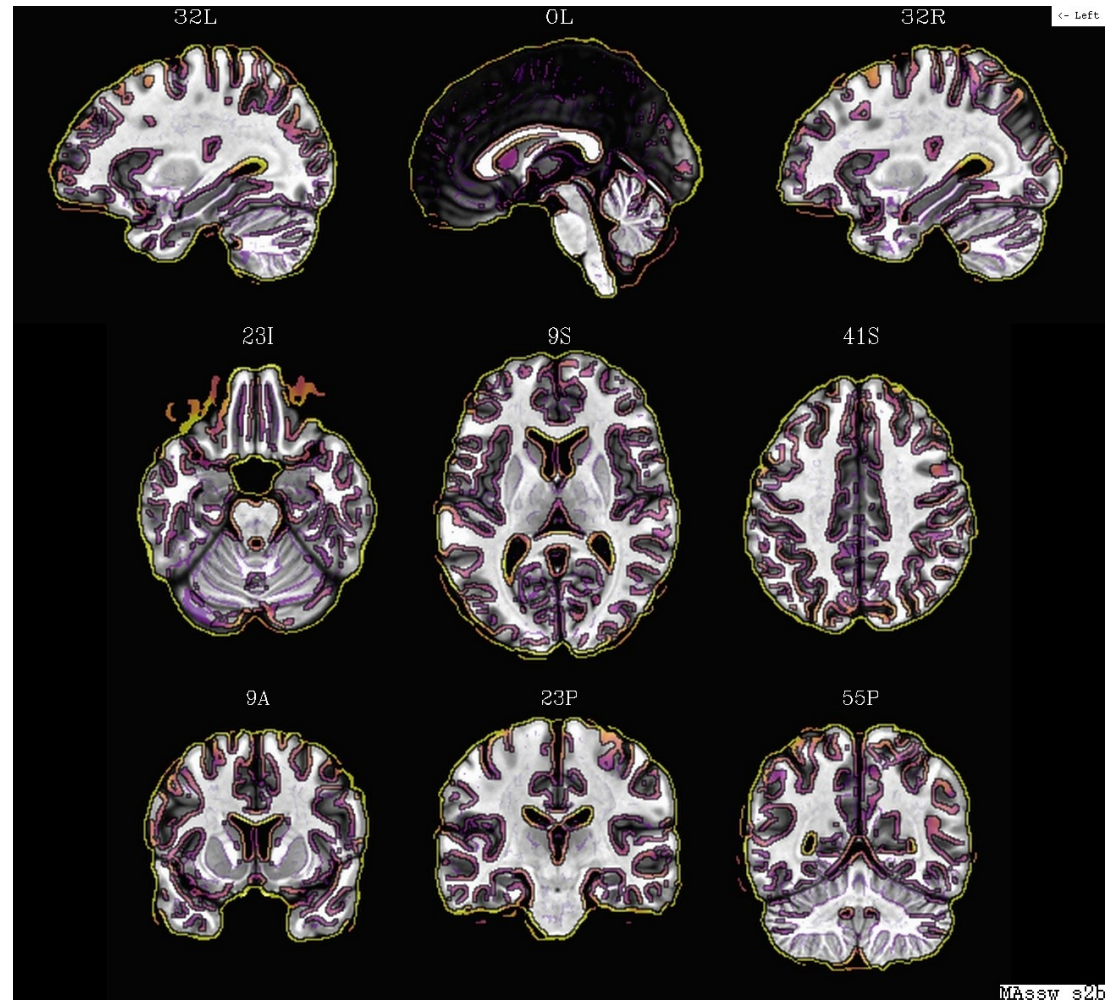
ulay: base template

olay: warped dset (nonlinear, @SSwarper)

Compare alignment with  
overlying edges of warped  
source dset on base template

“Base” volume in this case is  
MNI template; “source” is  
typical subject anat vol.

Overall fit: **Very good, nearly  
all sulci/gyri match closely  
throughout.**

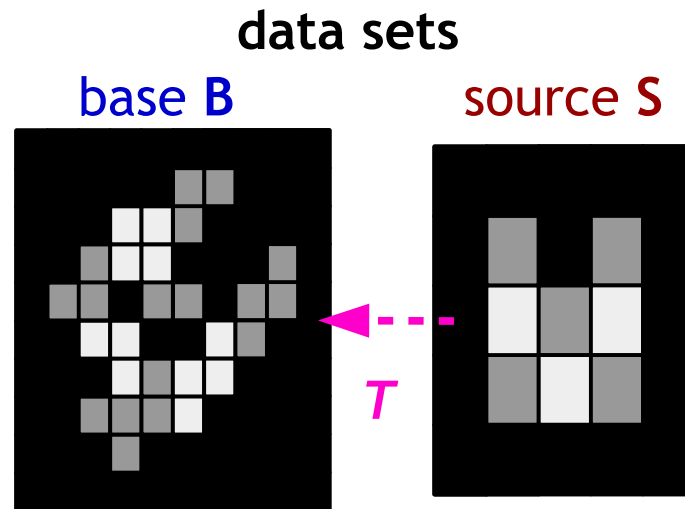


PLOT: @snapshot\_volreg TEMPLATE\_VOL WARPED\_VOL



## Transformation and mapping

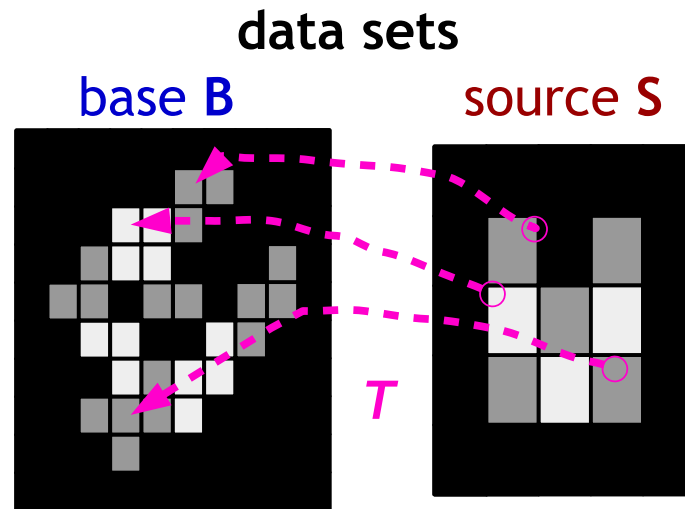
- What is a transformation (or warp)?
  - *It is a rule for mapping information from a source dset  $S$  onto a base  $B$ 's grid. It says where a given spot  $(x_B, y_B, z_B)$  in  $B$  pulls information from in  $S$ .*



For alignment, we want a transform  $T$ , such that  $B' = T(S)$  is similar to  $B$ .

## Transformation and mapping

- What is a transformation (or warp)?
  - *It is a rule for mapping information from a source dset  $S$  onto a base  $B$ 's grid. It says where a given spot  $(x_B, y_B, z_B)$  in  $B$  pulls information from in  $S$ .*



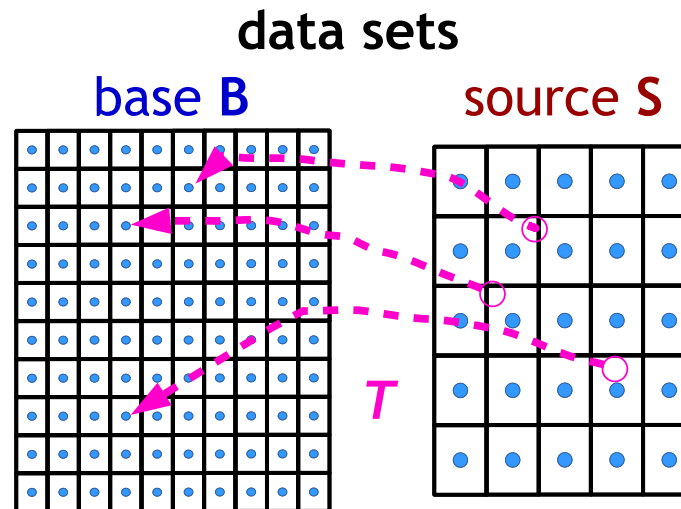
For alignment, we want a transform  $T$ , such that  $B' = T(S)$  is similar to  $B$ .

We choose how much warping  $T$  is allowed to do: match FOV average or refine over smaller patches; and how much “freedom” of movement.

Goal: maximize structure matching, and minimize smoothing.

## Transformation and mapping

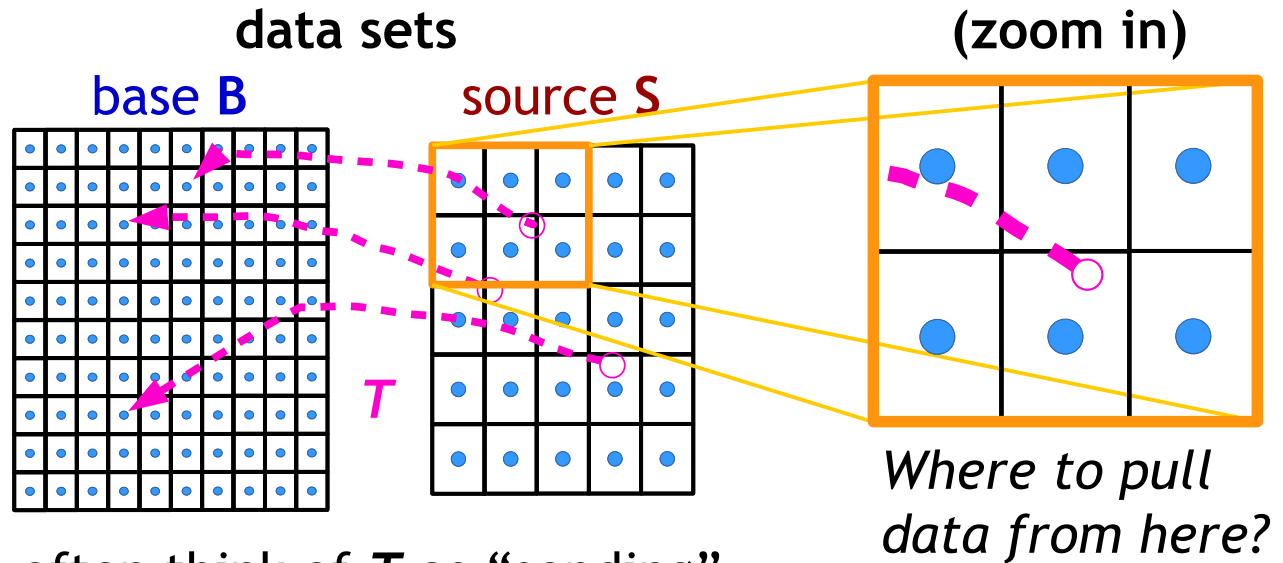
- What is a transformation (or warp)?
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We often think of  $T$  as “sending” values from  $S$  to  $B$ , but actually we start from a point in  $B$  and ask, “Where do I get my value from in  $S$ ?”

# Transformation and mapping

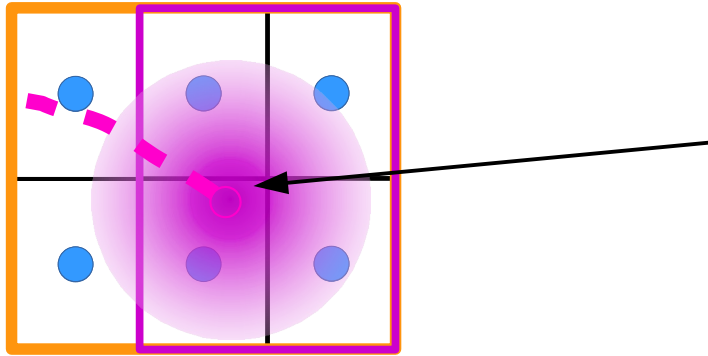
- What is a transformation (or warp)?  
→ It is a rule for mapping information from a source dset  $S$  onto a base  $B$ 's grid. It says where a given spot  $(x_B, y_B, z_B)$  in  $B$  pulls information from in  $S$ .



We often think of  $T$  as “sending” values from  $S$  to  $B$ , but actually we start from a point in  $B$  and ask, “Where do I get my value from in  $S$ ?”

# Mapping and Interpolation

*Where exactly to pull data from?  
Choose with interpolation (or resampling) mode*



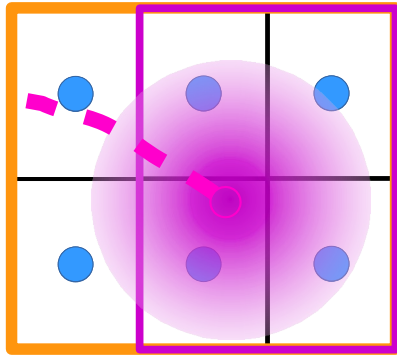
Basic case:  
the location to pull data “from”  
is not directly on a centroid, so  
we interpolate with a weighted  
average-- here a cubic spline  
(in 3D)

**Cu** = “cubic Lagrange  
polynomial”  
→ decent interp (bit  
of smoothing)

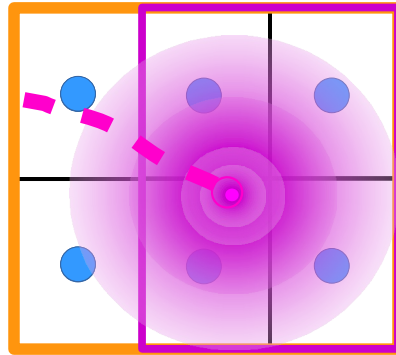
1D vers: 

# Mapping and Interpolation

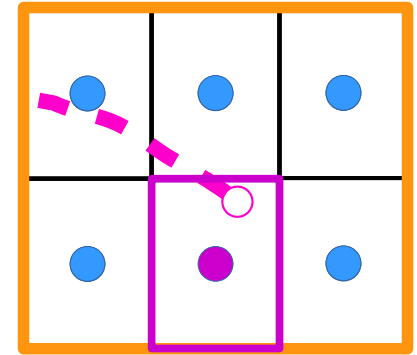
*Where exactly to pull data from?  
Choose with interpolation (or resampling) mode*



**Cu** = “cubic Lagrange polynomial”  
→ decent interp (bit of smoothing)

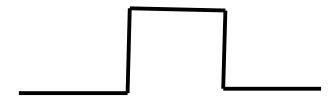


**wsinc5** = “sinc function”  
→ preserve edges and sharpness (some ringing)



**NN** = “nearest neighbor”  
→ preserve int values (atlases!)

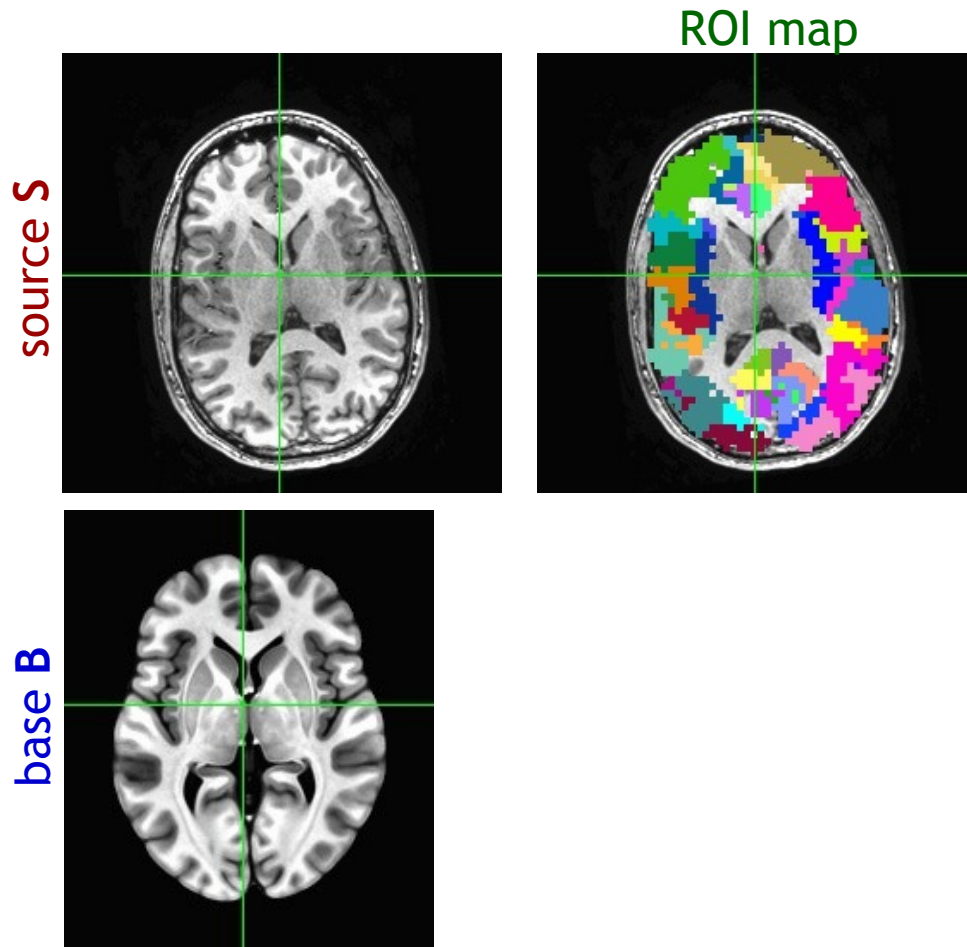
1D vers:



*(There are other modes, such as linear **Li**, etc.; see program help files.)*

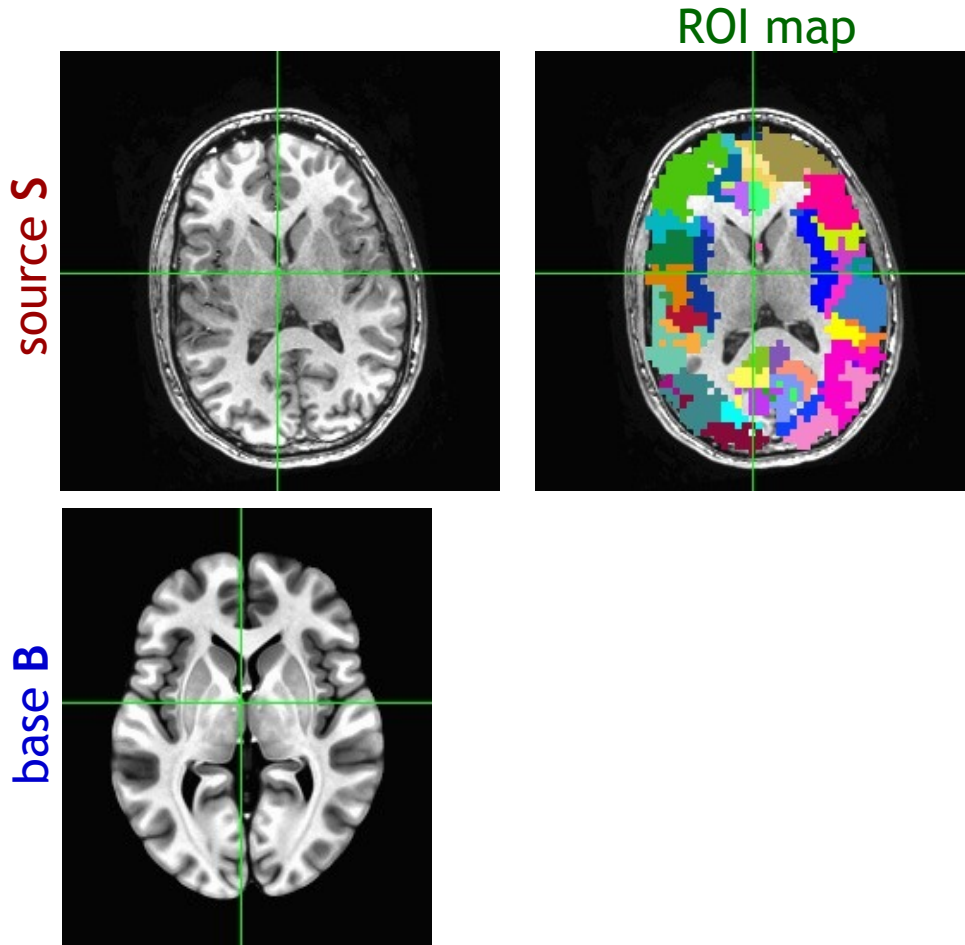
## Applying transformations: moving ROIs

- How can we move ROIs between spaces?



## Applying transformations: moving ROIs

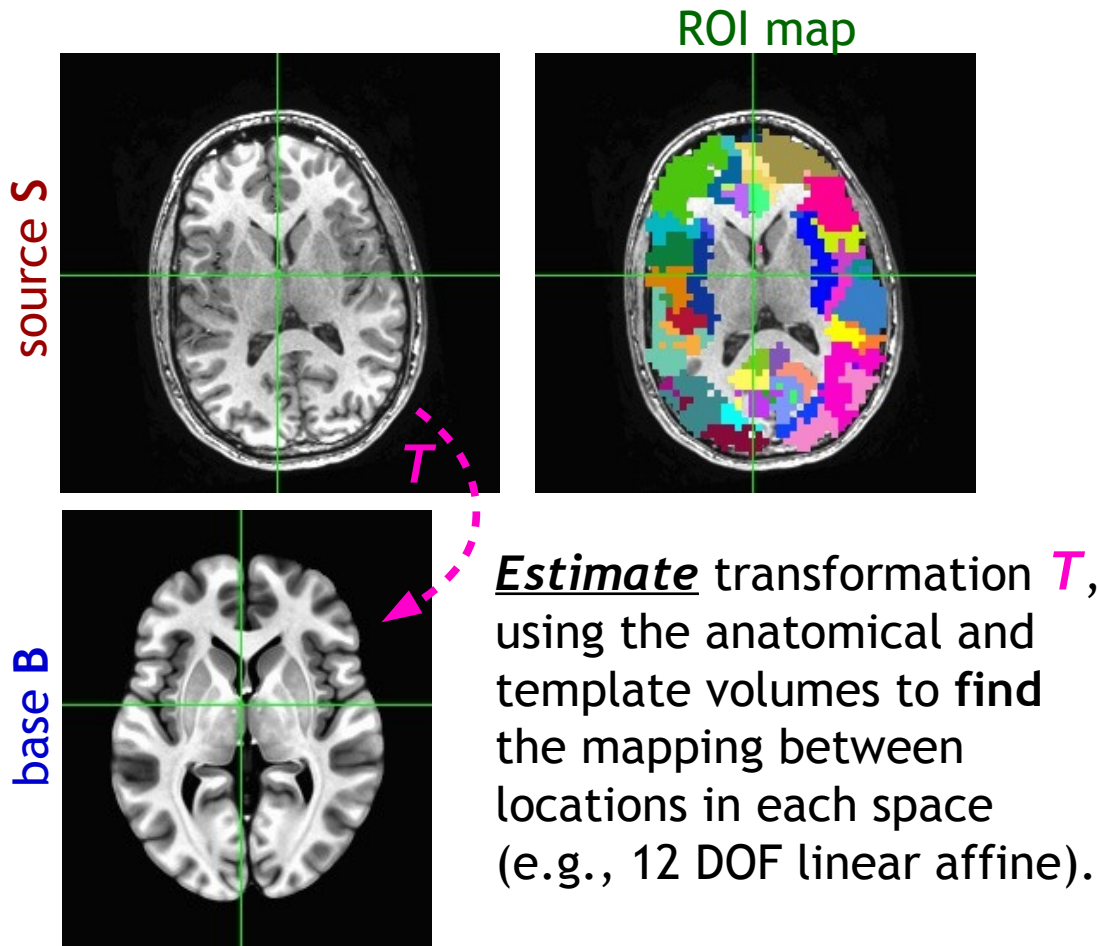
- How can we move ROIs between spaces?  
→ *Once we have the mapping  $T$  from  $S$  to  $B$ , we can apply it to other datasets-- like an atlas, a map of ROIs, and more.*





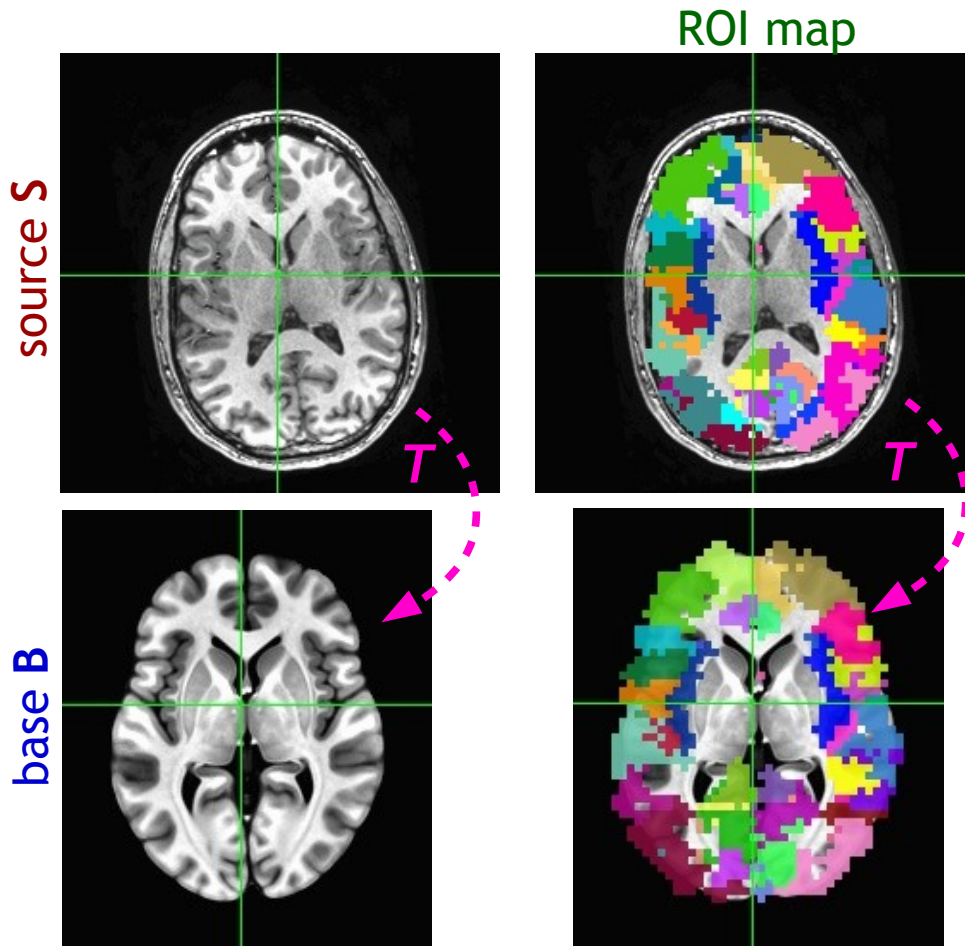
## Applying transformations: moving ROIs

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## Applying transformations: moving ROIs

- How can we move ROIs between spaces?  
→ *Once we have the mapping  $T$  from  $S$  to  $B$ , we can **apply** it to other datasets-- like an atlas, a map of ROIs, and more.*



Apply transformation  $T$  to the ROI map.

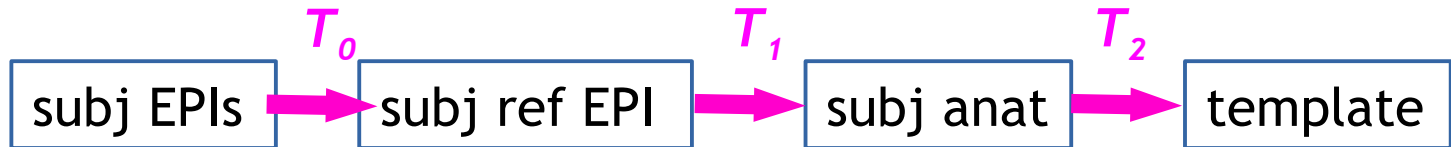
We also include an option to make the interpolation be “NN” (nearest neighbor) in order to avoid smoothing of ROIs: ints stay ints, so the ROIs keep their identity.

## Concatenating transforms

- Note: as observed earlier, any alignment/warping/interpolation/resampling leads to *smoothing* of data.
- Therefore, when mapping data through several spaces (EPI → anat → template), we **DON'T** want to regrid at each step; we *concatenate the transforms into a single one, and then have to only regrid once!*

## Concatenating transforms

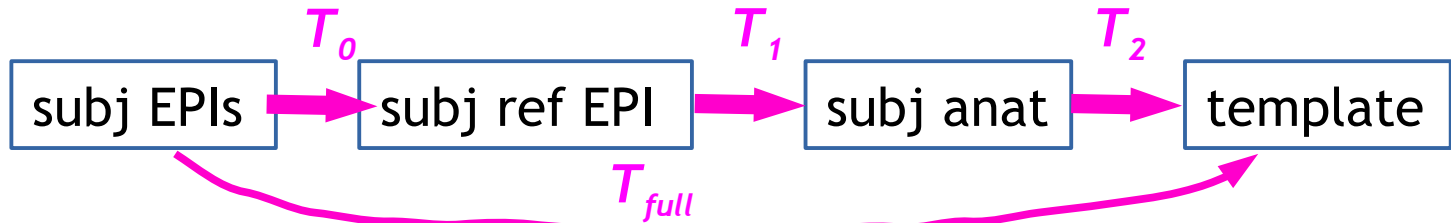
- Note: as observed earlier, any alignment/warping/interpolation/resampling leads to *smoothing* of data.
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- So, calculate individual transforms, such as within EPI (e.g., 3dvolreg), EPI-anat (e.g., align\_epi\_anat.py) and anat-template (e.g. @SSwarper):



- but **DON'T** apply  $T_0$  to make a new dset, and then apply  $T_1$  to that, etc.

## Concatenating transforms

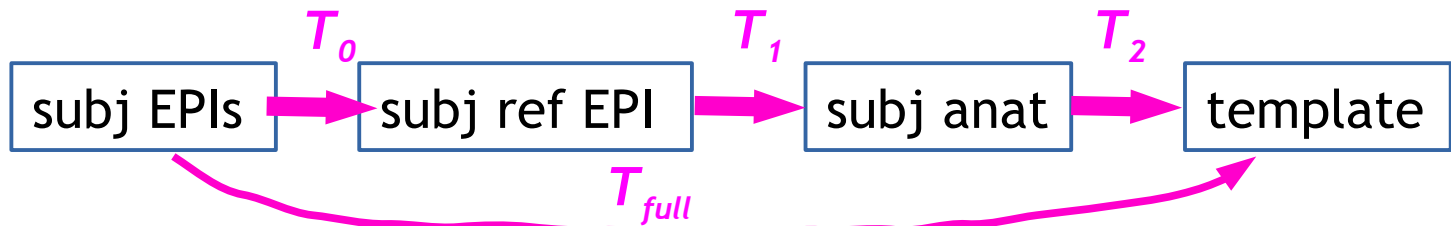
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- **DO** concatenate  $T_0$ ,  $T_1$ , and  $T_2$  to make  $T_{full}$ , and then apply  $T_{full}$  to the EPIs to send the data to the template space in a single step (i.e., only one regridding)

## Concatenating transforms

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- sidenote: probably don't upsample the EPI data a lot, e.g., from 3.5mm to 2mm iso
  - cannot “create” higher resolution information, no matter how it *looks*
  - just makes larger datasets, more processing time, more disk space, etc.

## Some warping guidelines

### Warping guidelines

- + For most EPI-EPI alignment, **ls** cost function (via **3dvolreg**) is fine
  - for blip up-down EPI, there are nonlinear warping opts (**lpa** cost)
  - always check subj motion profiles and censoring
- + For all other warping, look to **lpa** (similar contrast) and **lpc** or **lpc+ZZ** (differing contrasts)
- + Use nonlinear warping when aligning anat data between different subjects (including subject to reference)
  - consider **@SSwarper** for combined nonlinear warping + skullstripping
  - can input results directly into **afni\_proc.py**
  - lots of templates are fine, but use one with good detail as base
- + Calculate all warps in a chain individually, then *concatenate* them into one before applying, to reduce smoothing (less regridding steps)
- + Use **afni\_proc.py** when processing FMRI data
  - concatenation and other tiny details are managed *automatically*

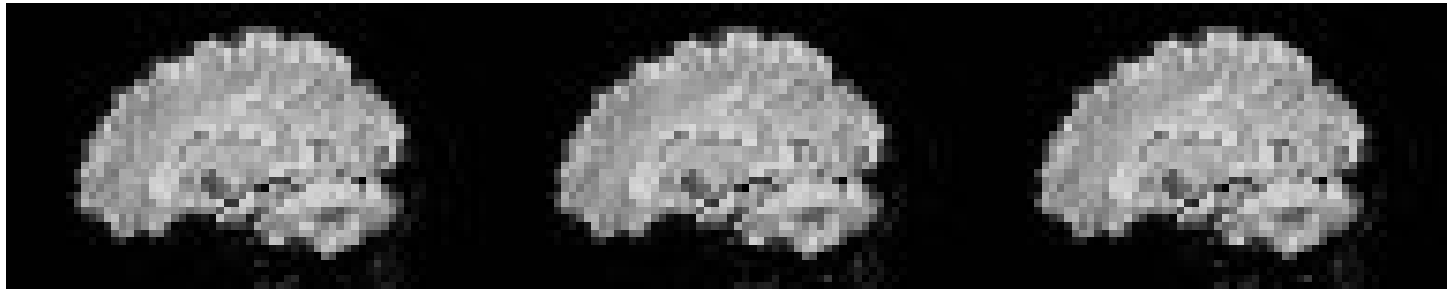
Considerations for:  
**within EPI (EPI-EPI) alignment**



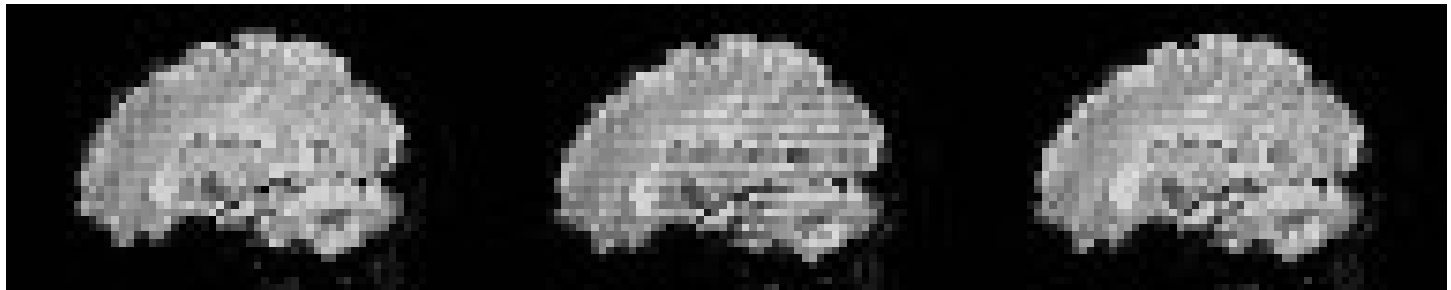
# EPI time series: motion

EPI vols: standard, interleave acquisition

without motion

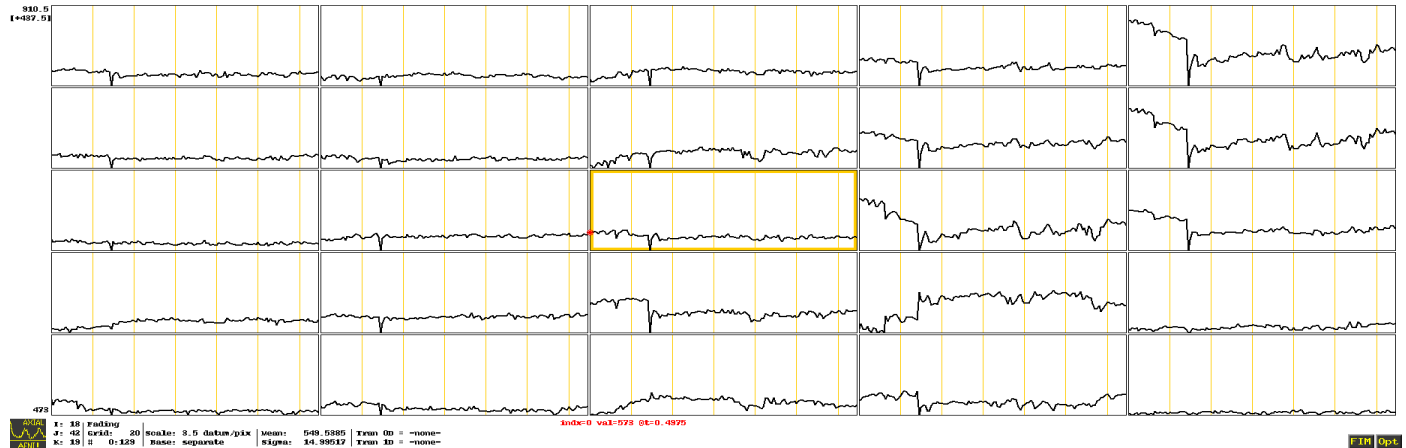


with motion



## EPI time series

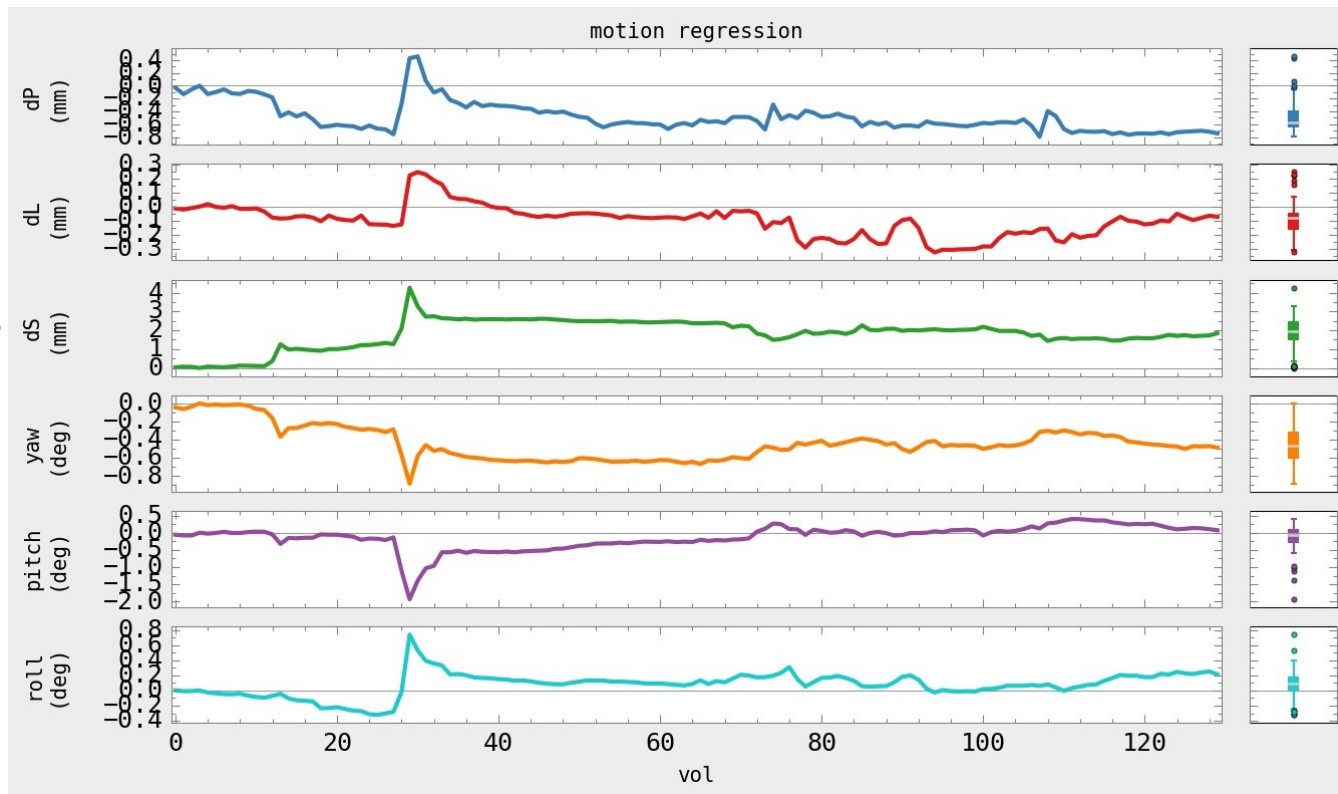
- + see the motion effect(s)?
- + see differences between voxels?



# EPI time series: motion

Main tool: `3dvolreg` (often via `afni_proc.py`). Use EPI-EPI alignment to:

- 1) estimate motion “time series” (rigid body params: rot + transl) and
- 2) use these “time series” as regressors and as censoring criteria



```
PLOT: 1dplot.py -sepscl -boxplot_on -reverse_order -ylabels VOLREG -xlabel vol \  
-title "motion regression" -prefix OUTPUT_NAME -infiles MOT_EST_VR.1D
```

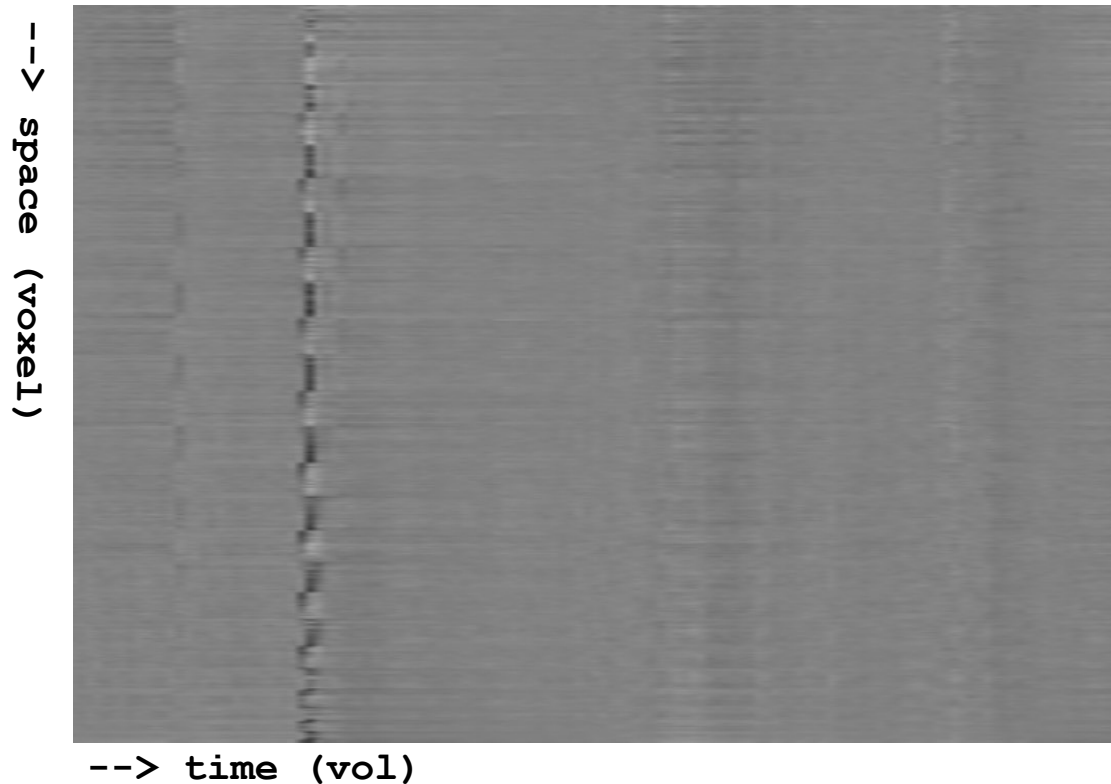
## EPI time series: motion

Can visualize motion's effects in time series as a (normalized) “grayplot”:

+ each row is one time series (values translated to grayscale)

+ each col is one instant/volume in time

Probably large outlier fractions where motion occurs (→ *censoring*)



PLOT: 3dGrayplot -mask mask+orig. -input FILE\_TIMESERIES -prefix OUTPUT\_NAME

## EPI time series: censoring

Typically two measures to detect and censor motion

- **enorm** (Euclidean norm): based on 3dvolreg's motion parameter estimates
  - suprathreshold enorm leads to censoring multiple vols

For each [i]th volume, use the derivatives of motion profiles to calc enorm:

$$\text{enorm}_i = \left( \Delta dP_i^2 + \Delta dL_i^2 + \Delta dS_i^2 + \Delta \text{yaw}_i^2 + \Delta \text{pitch}_i^2 + \Delta \text{roll}_i^2 \right)^{0.5}$$

... which is to say, where there are bigger changes in motion due to either translation, rotation or both, the **enorm** value is larger.

- Enorm has units of ~mm (for human head radius, approx. 1deg ~1mm).  
Can threshold with a preset value, e.g., 0.2 (~mm); since enorm is based on a derivative (difference), two volumes get censored for suprathreshold values.

*Ex. calculation from output of 3dvolreg:*

```
1d_tool.py \
  -infile VOLREG_OUTPUT.1D -set_nruns 1 \
  -derivative -collapse_cols euclidean_norm \
  -write ENORM_OUTPUT
```

## EPI time series: censoring

Typically two measures to detect and censor motion

- **enorm** (Euclidean norm): based on 3dvolreg's motion parameter estimates
  - suprathreshold enorm leads to censoring multiple vols
- **outliers**: based on outliers from time series trends (total fraction in volume)

For each [i]th volume, count how many voxels have an outlier; record fraction:

$$\text{outlier\_frac}_i = (\# \text{ vox with outlier})_i / (\# \text{ vox in automask})$$

- Outlier frac has no units; just has a range [0, 1].

Can threshold with a preset value, e.g., 0.05. Only one volume gets censored for suprathreshold values.

*Ex. calculation from unprocessed data set:*

```
3dToutcount
```

```
-automask -fraction -polort 3 -legendre
```

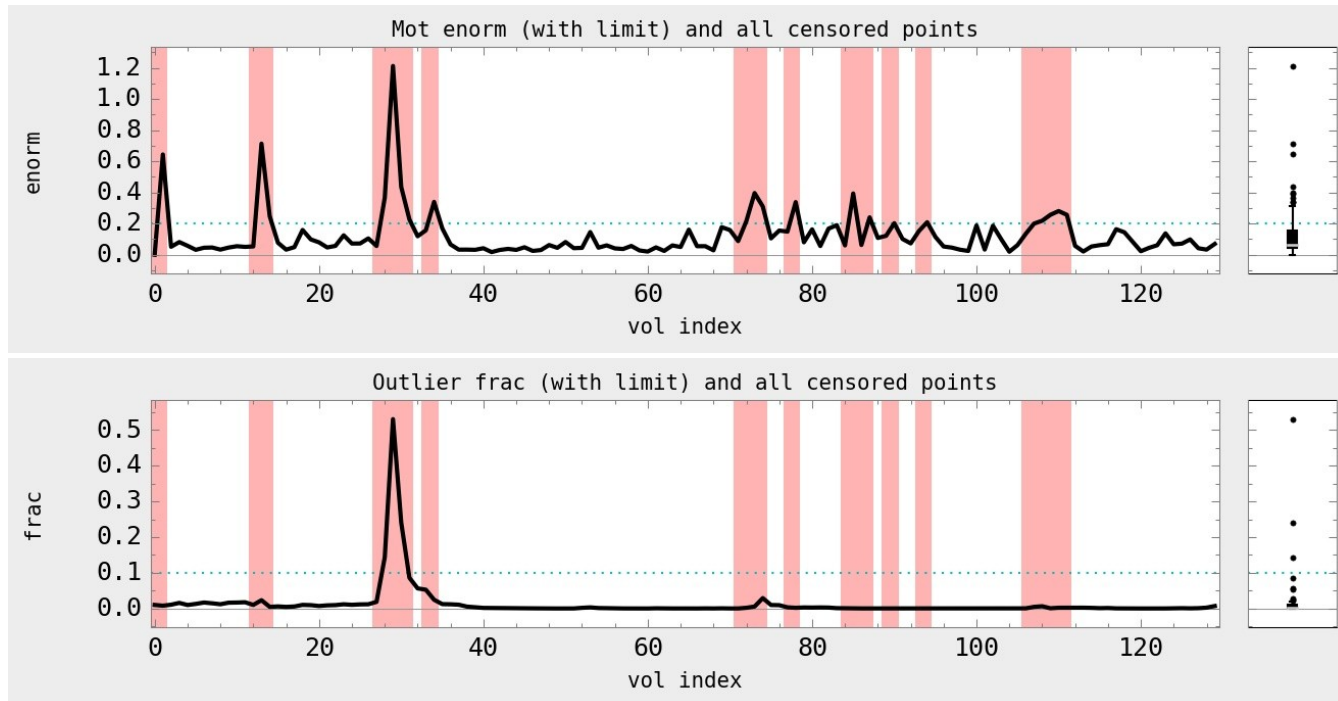
```
DSET > OUTLIER_FRAC.1D
```

```
\  
\
```

## EPI time series: censoring

Typically two measures to detect and censor motion

- **enorm** (Euclidean norm): based on 3dvolreg's motion parameter estimates
  - suprathreshold enorm leads to censoring multiple vols
- **outliers**: based on outliers from time series trends (total fraction in volume)



PLOT (for motion-enorm, and similar for outlier frac):

```
1dplot.py -boxplot_on -reverse_order -infile MOT_ENORM.1D -censor_hline VAL \
-censor_files CEN_FILE.1D -xlabel "vol index" -ylabels "enorm" \
-title "Mot enorm (with limit) and all censored points" -prefix OUT_MOT.jpg
```

## Example: 3dvolreg

Can run the following in “AFNI\_data6/afni/”:

```
3dvolreg -base 3 -cubic -zpad 1 \
        -1Dfile dfile_vr.1D \
        -1Dmatrix_save mat_vr.aff12.1D \
        -prefix epi_r1_vrt \
        epi_r1+orig
```

- `epi_r1+orig`: (last entry) input time series to align
- `-base 3`: select brick [3] of input `epi_r1+orig` dset as reference vol  
(NB: in `afni_proc.py`, one can select the ref vol to be the one with fewest outliers, with keyword: `MIN_OUTLIERS`)
- `-cubic`: use cubic polynomial interpolation
- `-zpad 1`: put (intermed) layer of zeros around base vol, helps if large rotations exist
- `-1Dfile ...`: save motion estimates as columns of numbers in text (1D) file
- `-1Dmatrix_save ...`: save motion params (12 DOF in matrix form) to text (1D) file
- `-prefix ...`: save motion-corrected vol to new 4D volumetric dset

... and a quick view of motion estimates:

```
1dplot -volreg dfile_vr.1D &
```

## Example: 3dvolreg (cont'd)

... and a quick calculation of 'enorm' (= Euclidean norm) and possible censoring (see "1d\_tool.py -help" for description of opts here):

```
1d_tool.py -infile dfile_vr.1D      \  
          -set_nruns 1              \  
          -show_censor_count        \  
          -censor_prev_TR           \  
          -censor_motion 0.3 SUBJ
```

... with a quick view of *those* results (with censorline fanciness):

```
ldplot -one SUBJ_enorm.1D "1D: 152@0.3" &
```

and to see the (command line-usable) string of indices to be censored:

```
cat SUBJ_CENSORTR.txt
```

or pro-level fanciness combining the previous two:

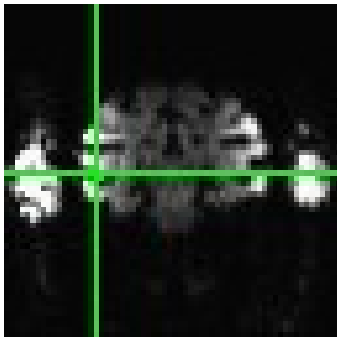
```
ldplot -one `cat SUBJ_CENSORTR.txt` SUBJ_enorm.1D "1D: 152@0.3" &
```



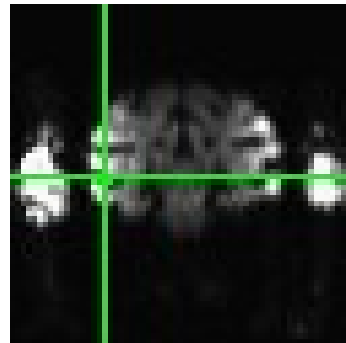
# Motion correction: caveats

- Alignment *cannot* fix motion; use motion pars as regressors (helps more, not total).
- Motion correction → volume alignment → regriding → smoothing.
- Check in the AFNI GUI to be sure the “corrected” data is not “bouncing” around
- **Example:** Monkey sips juice at stimulus time, and large jaw muscles move. If the muscles are not masked, then motion correction may track muscles, not brain.

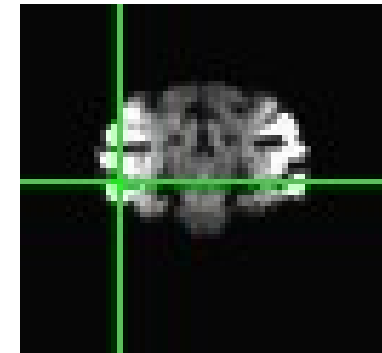
original



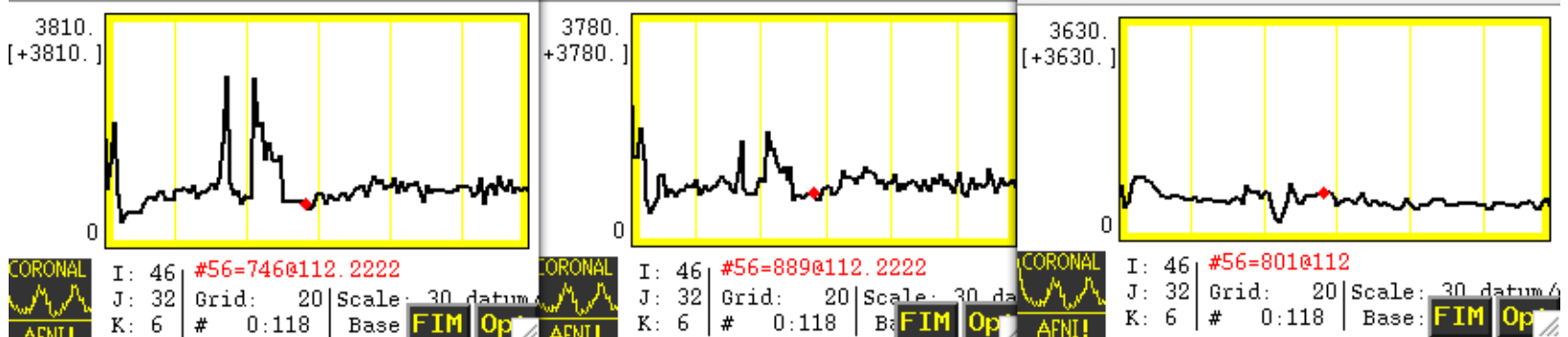
3dvolreg



automask, 3dvolreg



[movies →]



## “Fixing” Motion

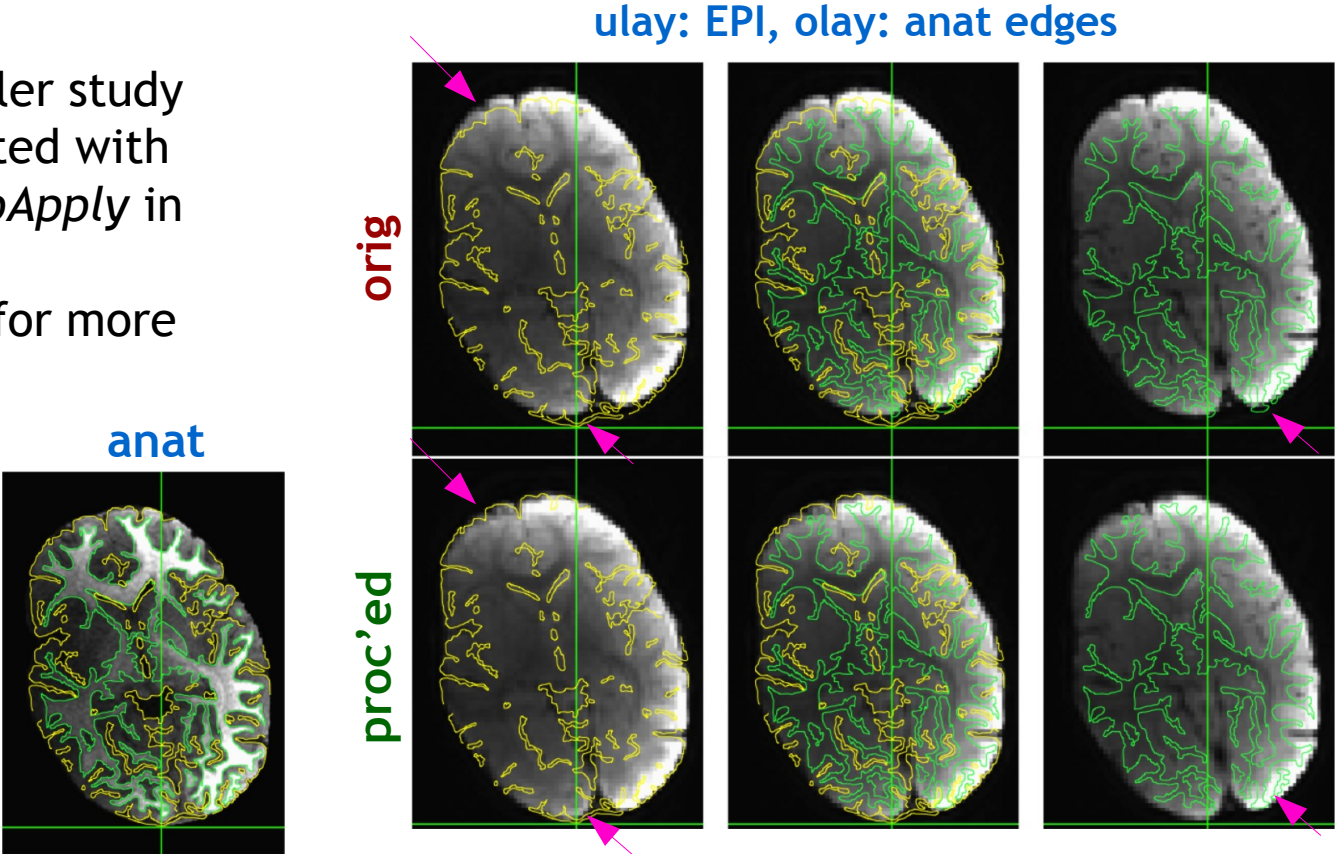
- Motion occurs over slices and not volumes and moves data off original grid
- “Regressing out” - motion parameters, derivatives, displacement, euclidean norm of derivatives (summary parameters)
- Censoring (“scrubbing”, “sweeping under the mat”,...)
- Experimental design - kids, monkeys, juice, talking,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

# EPI distortion correction in EPI data (1/2)

- Data acquired with an EPI sequence has distortions due to B0 inhomogeneity
- One way to correct: acquire data with opposite phase encoding (PE) to help “undo” the warping (AKA, “blip up, blip down” acquisitions)
- 1) Align opposite PE dsets nonlinearly. 2) Apply “half” warp to est. undistorted dset.

### Example

- + EPI dset from toddler study
- + Unwarping calculated with *3dQwarp+3dNwarpApply* in *afni\_proc.py*.
- + [Watch this space for more scripts/tools]

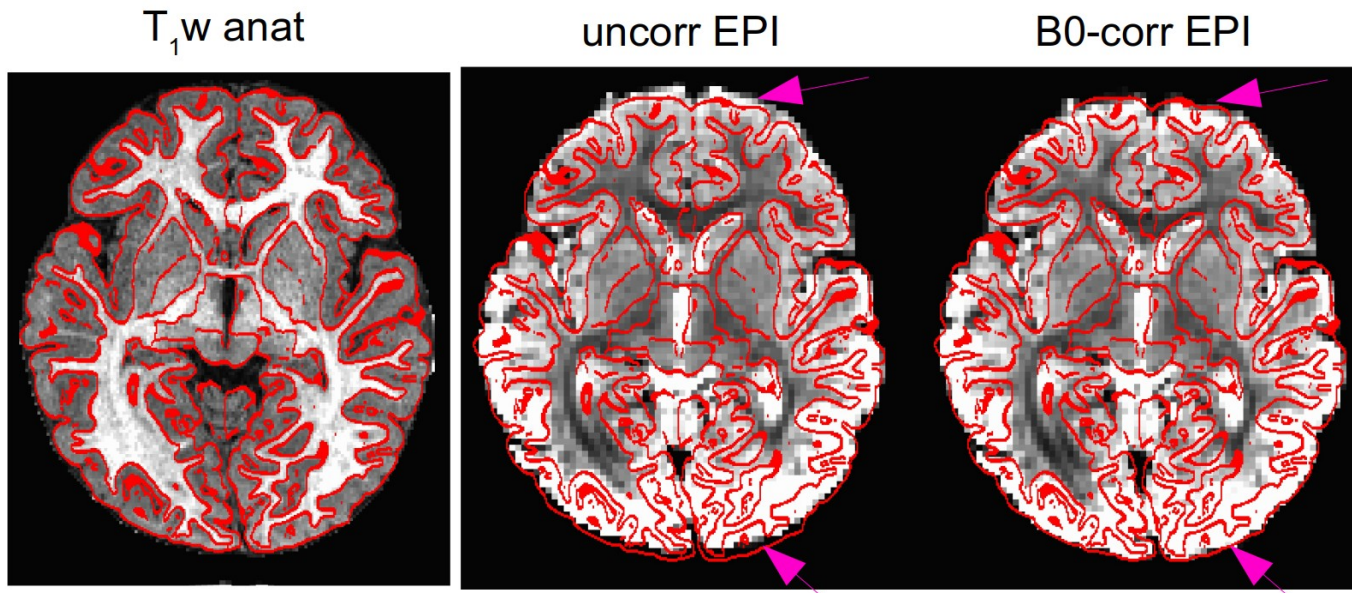


## EPI distortion correction in EPI data (2/2)

- New tool in AFNI for B0 (phase dset) correction: `epi_b0_correct.py`
  - Also put together by Vinai Roopchansingh, uses `3dNwarpApply`
  - can be integrated in `afni_proc.py`

### Example

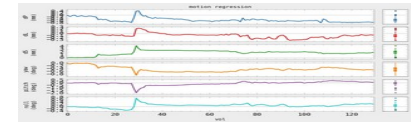
- + EPI dset from toddler study (Roopchansingh et al., in prep)
- + compare outlines of anatomical tissues (red) with EPI structures before and after correction



## EPI alignment: general comments

### Comments on motion “correction” (= reduction) in EPI

- One **cannot** fully “correct” effects of motion
  - intravol motion *can’t* be corrected, but bad cases will likely be **censored** (e.g., via outlier count, enorm vals)
  - motion parameter estimation+regression is useful, but won’t totally account for motion variance
- Motion is probably a bigger problem in resting state (and naturalistic) FMRI than in task-based, because there aren’t beta weights to focus on
- In general, global signal regression is **not** recommended (Saad et al., 2012; Gotts et al. 2013; Murphy et al. 2009)
- **GCOR** parameter might be one way to include motion information on group level, esp. for rs-fMRI (Saad et al. 2013; Gotts et al. 2013)
- Dealing with motion requires planning **before** scanning (make subjects comfortable, practice scanner, study design)
- Work must always be done to show that motion differences between groups is not driving effects



Considerations for:  
**EPI-anatomical alignment**

## Affine alignment

Main tool: `align_epi_anat.py` (often via `afni_proc.py`), and `3dAllineate`.

- 1) align EPI to anatomical of same subject; assumes no major/nonlinear distortions.
- 2) can check for left-right flipping in EPI/anat (e.g., bad header info)

### `align_epi_anat.py`

- + Combines deoblique, motion correction, alignment and talairach transformations into a single transformation.
- + Can also perform slice timing correction and applies transformations to “child” datasets.
- + “lpc” or “lpc+ZZ” cost function to align vols with opposite contrast (e.g., T1w and EPI)

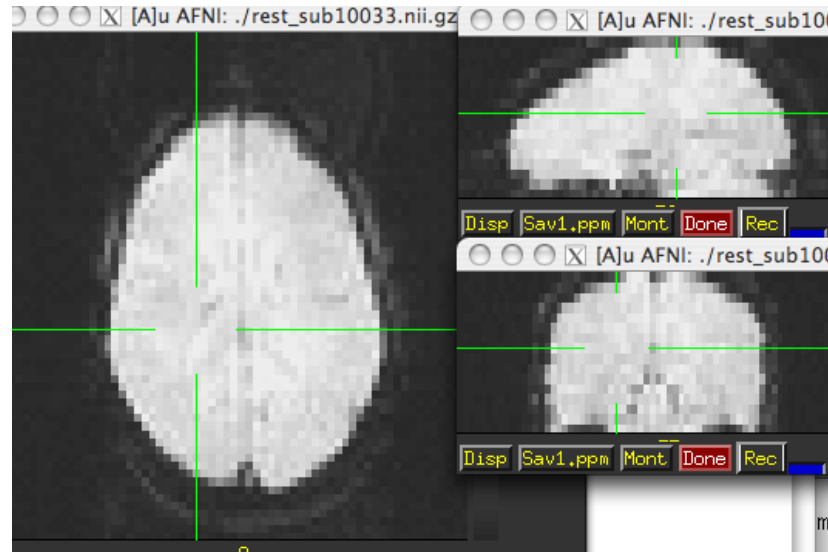
## Alignment strategies with align\_epi\_anat.py

Defaults work usually (>90% - FCON1000)

Examples of problems and → solutions to try:

- Far off start → “-big\_move”, “-giant\_move”, “-ginormous\_move”
- Poor contrast → “-cost lpa”, “-cost nmi”, “-cost lpc+ZZ”
- Poor non-uniformity → “-edge”, “-cost lpa”

Non-standard dsets: stroke/MS lesions, tumors, monkeys, rats, multi-modality (CT/PET/DTI/...), something else? → see us, post on Message Board

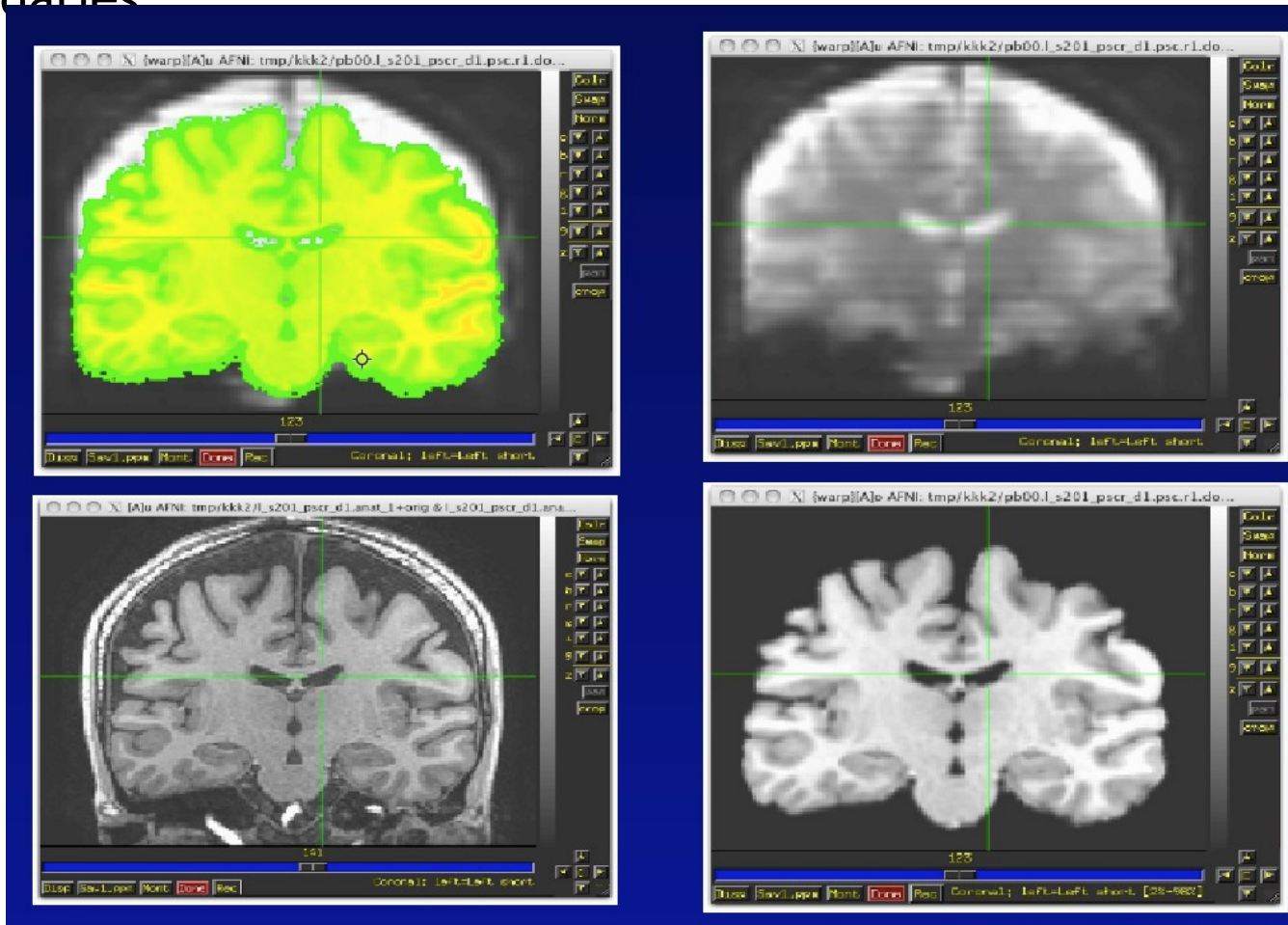




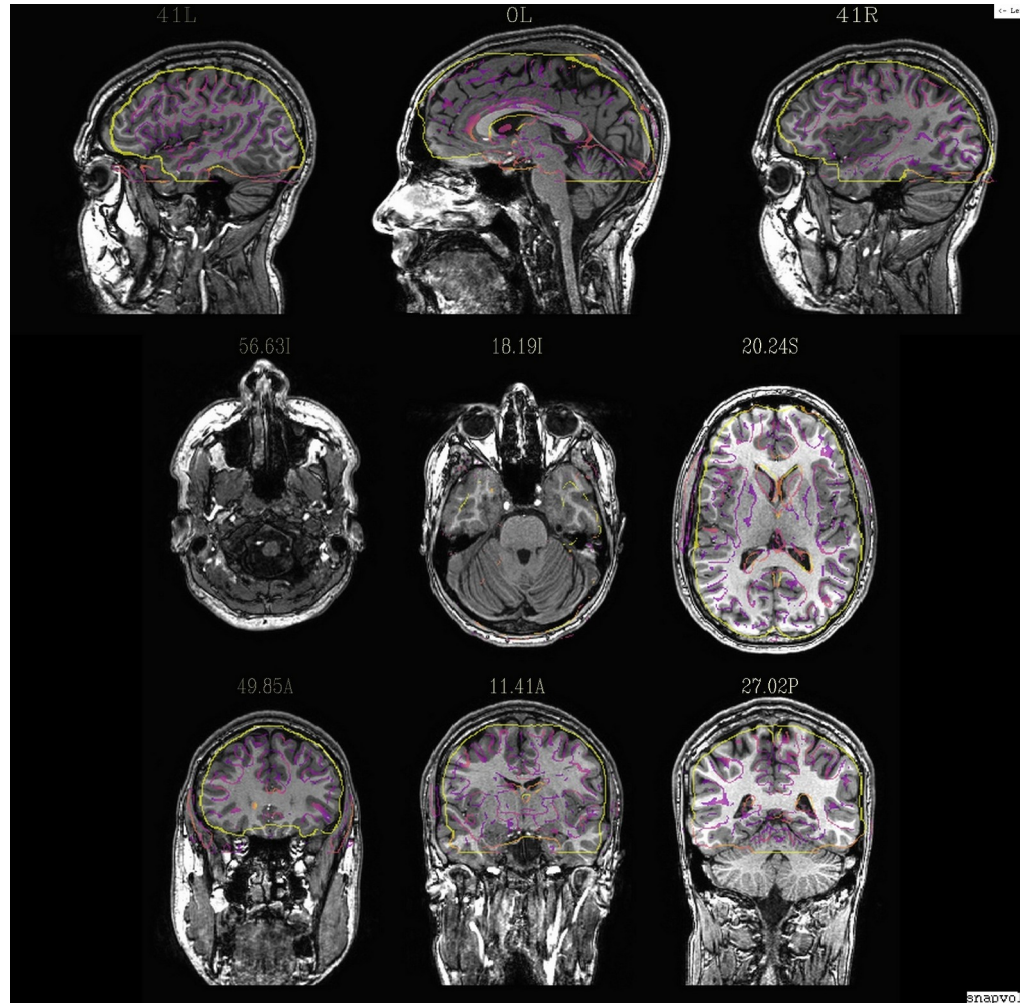
## Checking alignment: what to look for

It's what's on the *inside* that counts!

→ match sulcal gyral patterns, ventricle location, tissue boundaries



## Checking alignment: edge-y view



```
CMD : @snapshot_volreg VOL_ULAY VOL_OLAY output.jpg  
view: aiv output.jpg
```

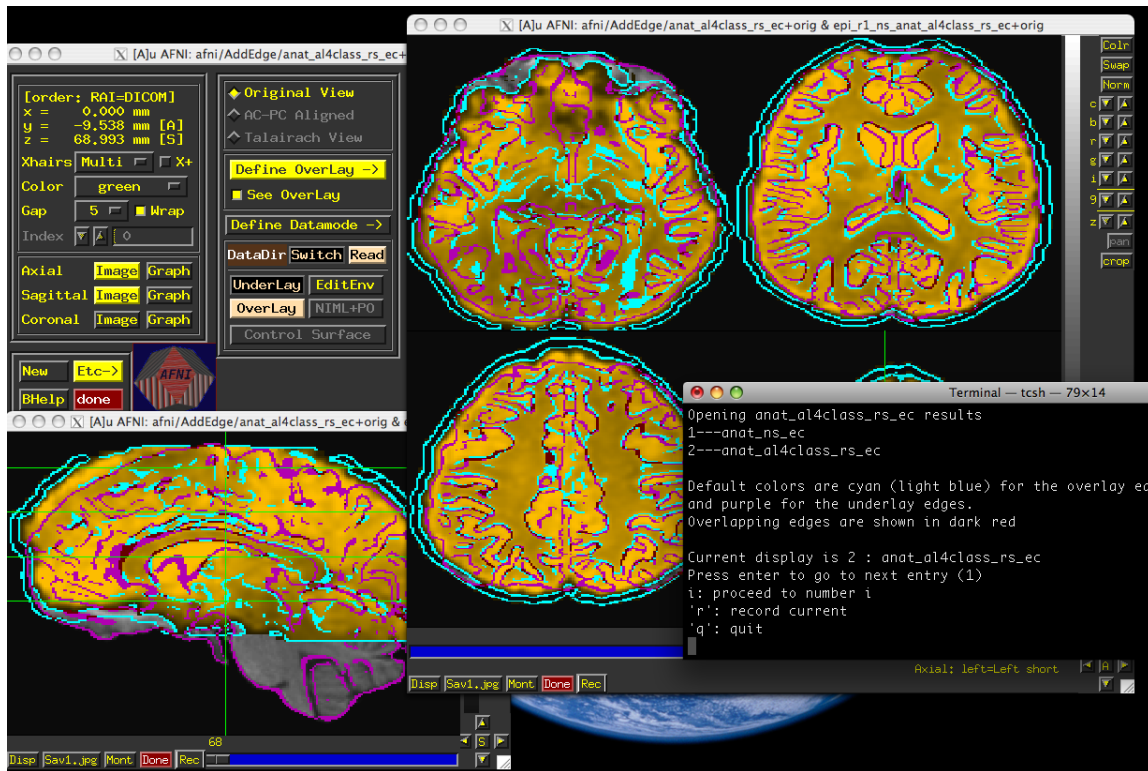
## Alignment visualization in AFNI

- **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.

# Affine alignment: auto-QC

Can run `align_epi_anat.py` with assistance for QCing alignment  
+ use “-AddEdge” option to view edge-highlights of dsets in AFNI GUI

## AFNI GUI with “@AddEdge” display settings



## Affine alignment: auto-QC

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+ use “-AddEdge” option to view edge-highlights of dsets in AFNI GUI

**Example to run in AFNI\_data6/afni/ (NB: takes a few mins in total):**

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

```
cd AddEdge
```

```
@AddEdge
```

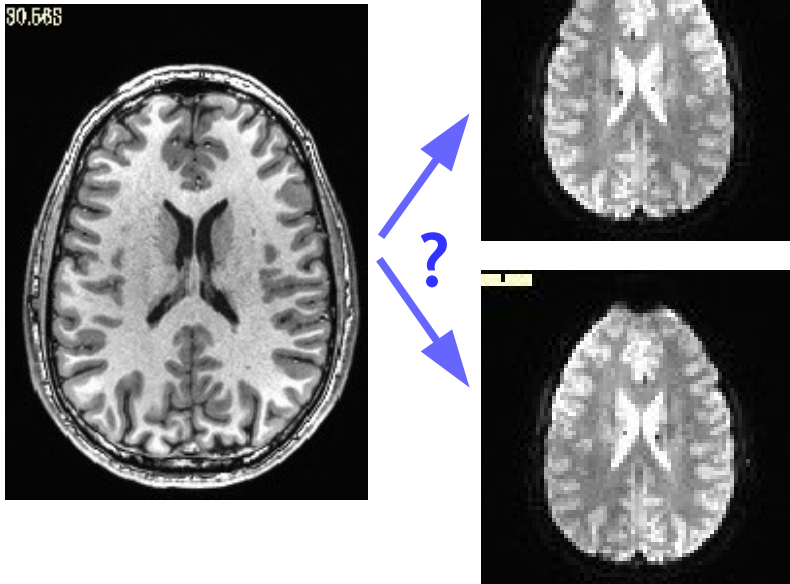
## Using alignment to check for left-right flipping

Check for dset header problems (esp. conversion software issues):

```
$ align_epi_anat -check_flip ...
```

```
$ afni_proc.py -check_flip ...
```

→ compare EPI $\leftrightarrow$ anatomical alignment cost results for both flipped and unflipped dsets.



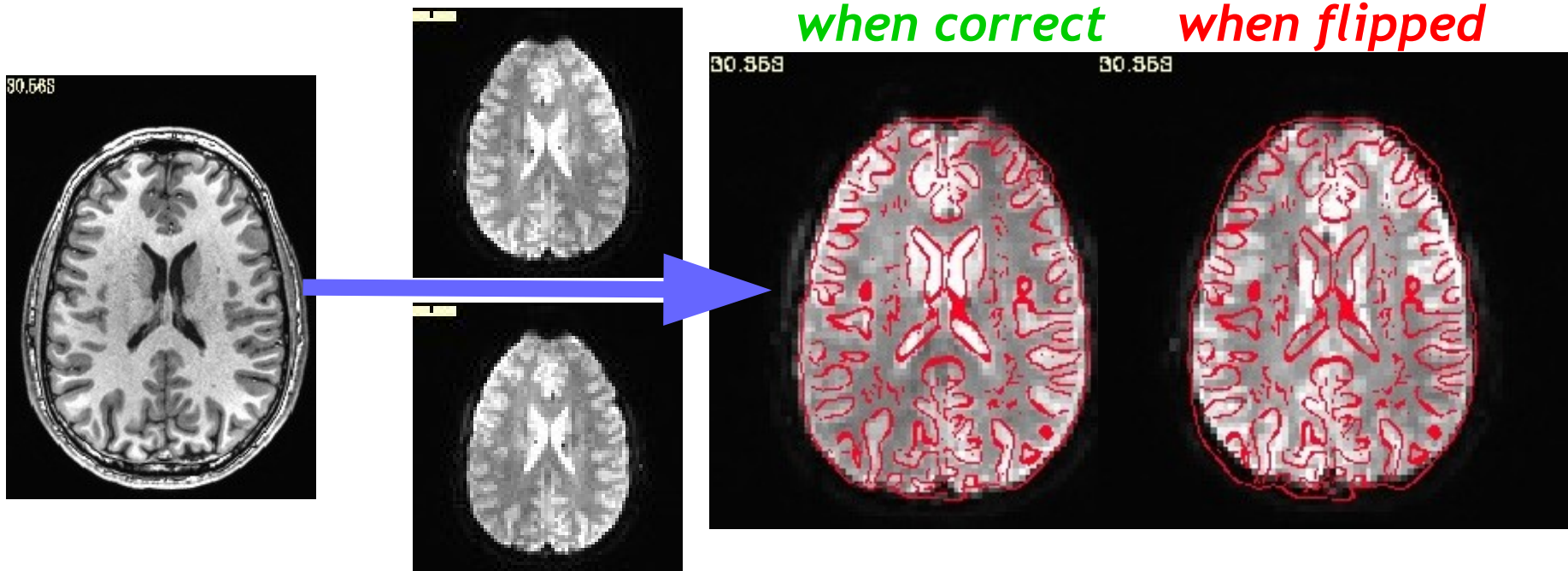
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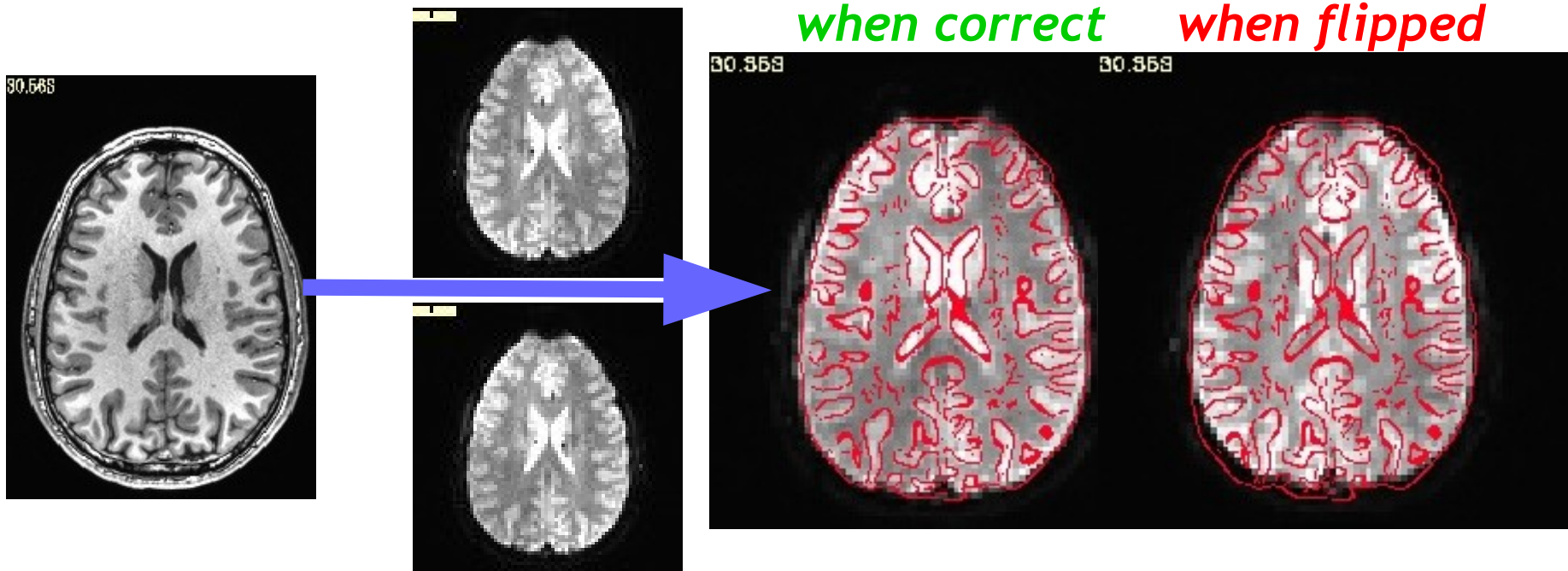
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(Has found systematic LR-flips in public FCP and OpenFMRI data sets.)



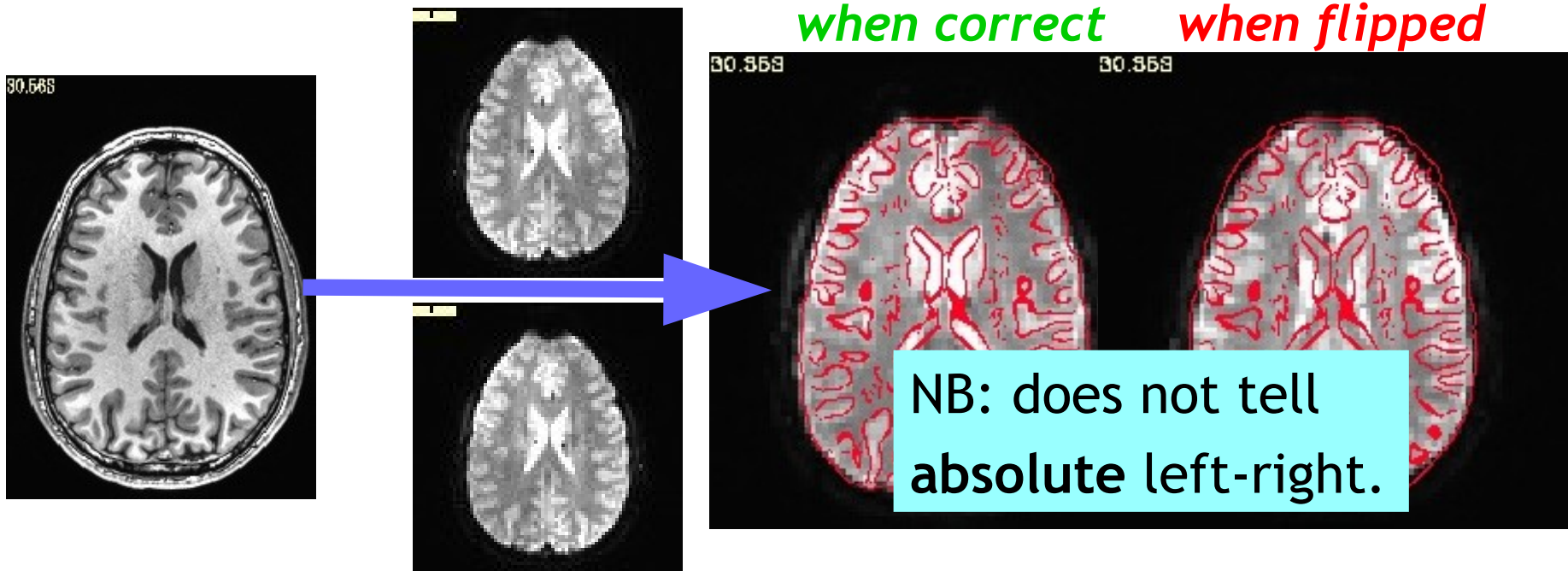
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```

```
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```

→ compare EPI $\leftrightarrow$ anatomical alignment cost results for both flipped and unflipped dsets.








(Has found systematic LR-flips in public FCP and OpenfMRI data sets.)

## Using alignment to check for left-right flipping

Read more about it here:

<https://www.medrxiv.org/content/10.1101/19009787v1>

### **Beware (surprisingly common) left-right flips in your MRI data: an efficient and robust method to check using AFNI**

 Daniel R Glen,  Paul A Taylor,  Bradley Buchsbaum,  Robert W Cox,  Richard C Reynolds

doi: <https://doi.org/10.1101/19009787>

**This article is a preprint and has not been peer-reviewed [what does this mean?]. It reports new medical research that has yet to be evaluated and so should *not* be used to guide clinical practice.**

**Abstract**

Info/History

Metrics

 Preview PDF

#### **Abstract**

Knowing the difference between left and right is generally assumed throughout the brain MRI research community. However, we note rather widespread occurrences of left-right orientation errors in MRI open database repositories where volumes have contained systematic left-right flips due to having incorrect or missing file header information. Here we present a simple method in AFNI for determining the consistency of left and right within a subject's acquired volumes; the method contains both a quantitative evaluation as well as a visualizable verification. We test the

Considerations for:  
**anatomical-template alignment**

## Registration to a template: nonlinear warps

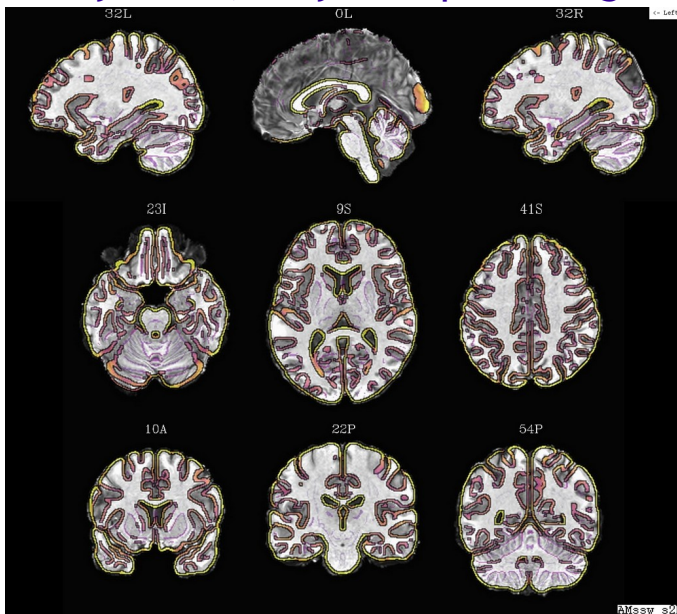
- Main tools: `3dQwarp`, `@SSwarper` (skull-strip & align), `auto_warp.py`
  - for animal dsets: `@animal_warper` (skullstrip & align, too)
- In general, one should use a nonlinear warp for all registration between different subjects (if the resolution/detail is high enough)
- Choosing a template similar/relevant to your subject group helps a lot
  - e.g., use a pediatric template for a study of children
- With nonlinear warping,
  - one wants a detailed template to latch onto
  - details of the source dset (like skullstripping) matter
    - e.g., small bits of skull left on can lead to odd warping
- Nonlinear warping is slooow, but parallelized for speedup on multi-core machines
  - set an environment variable for specifying number of CPUs:
    - `# for tcsh script or ~/.cshrc file:`  
`set OMP_NUM_THREADS = 7`
    - `# for bash script or ~/.bashrc file:`  
`export OMP_NUM_THREADS=7`
  - check setting (yours or default) in terminal with “`3dQwarp -hview`”

## @SSwarper: skull-strip and nonlinear warp

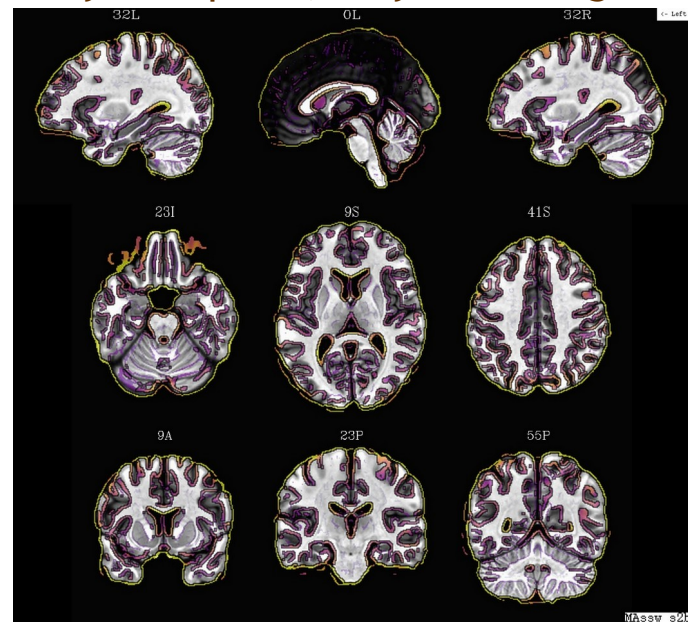
- @SSwarper does two jobs for the prices of one!
  - 1) Remove the skull of the subject's anatomical in native space,
  - 2) Estimate the nonlinear warp to a standard space template

*Call now and receive a bonus set of QC images of the alignment:*

ulay: anat, olay: template edges



ulay: template, olay: anat edges



- Presently, @SSwarper is the recommended tool for skullstripping (and maybe/probably for nonlinear warping, as well)
- Results can be passed directly to afni\_proc.py (see “@SSwarper -help”).

## 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.

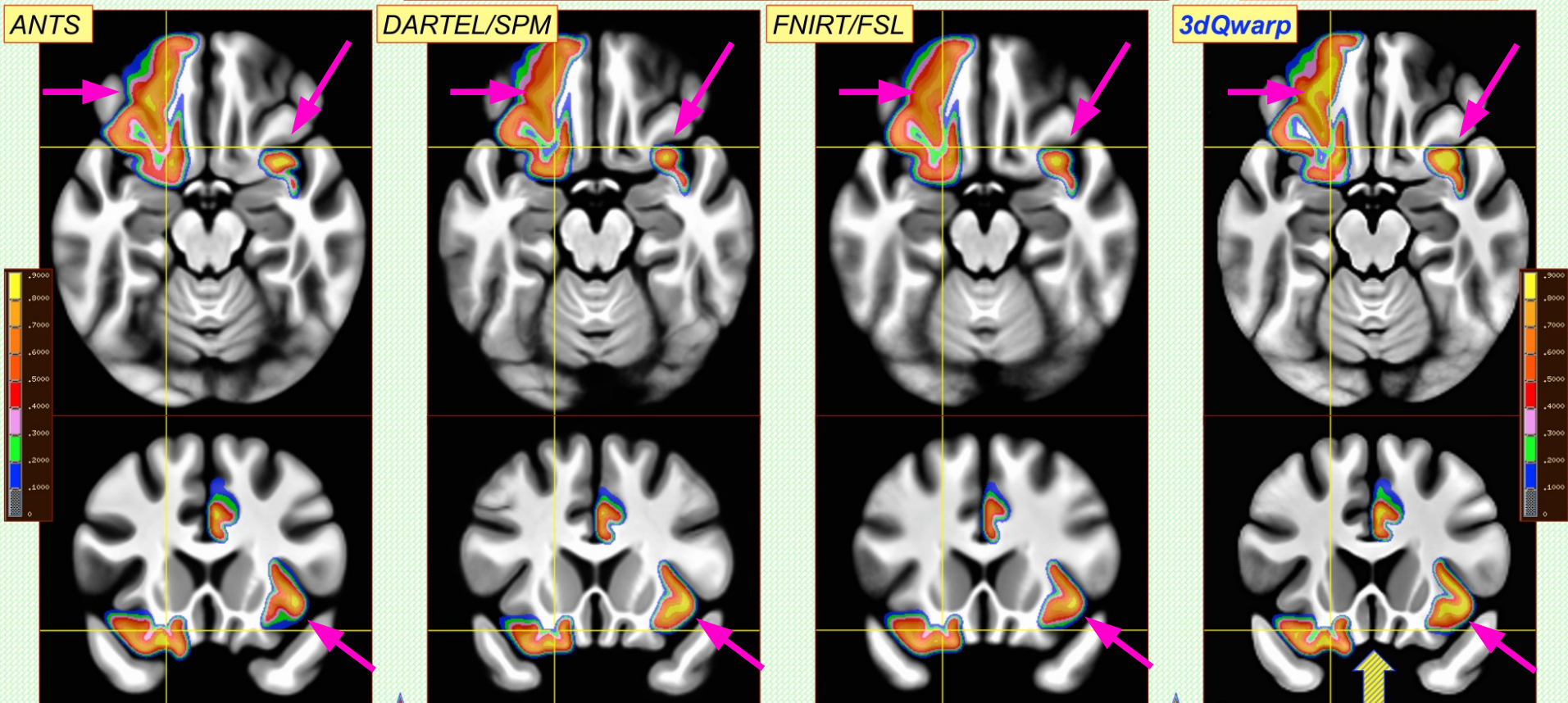
# Measuring quality of alignment

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 T<sub>1</sub> 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

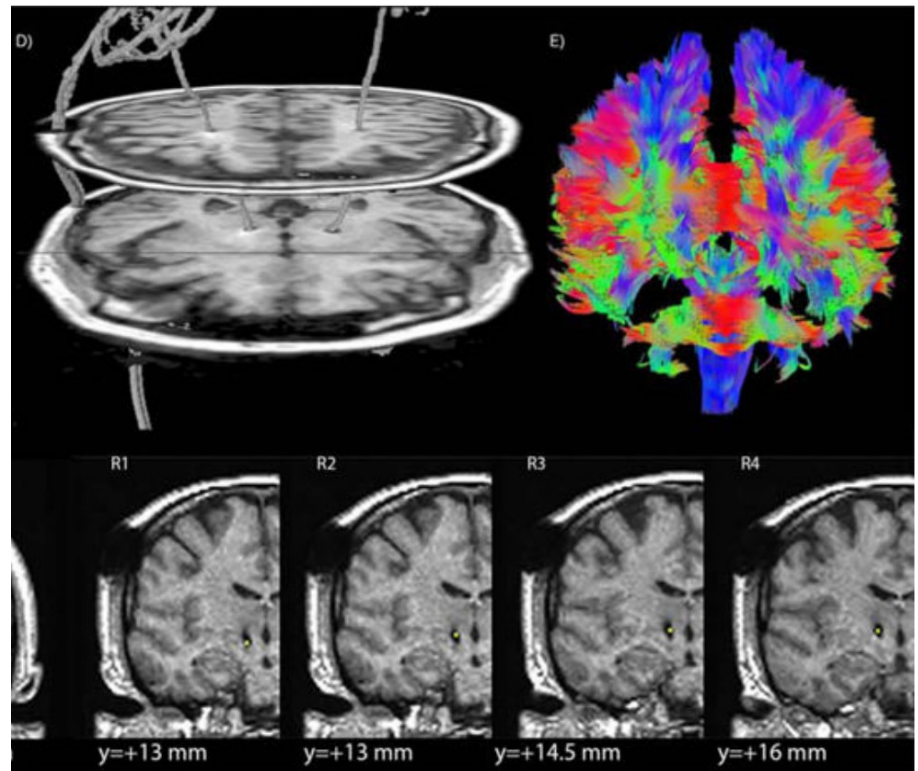
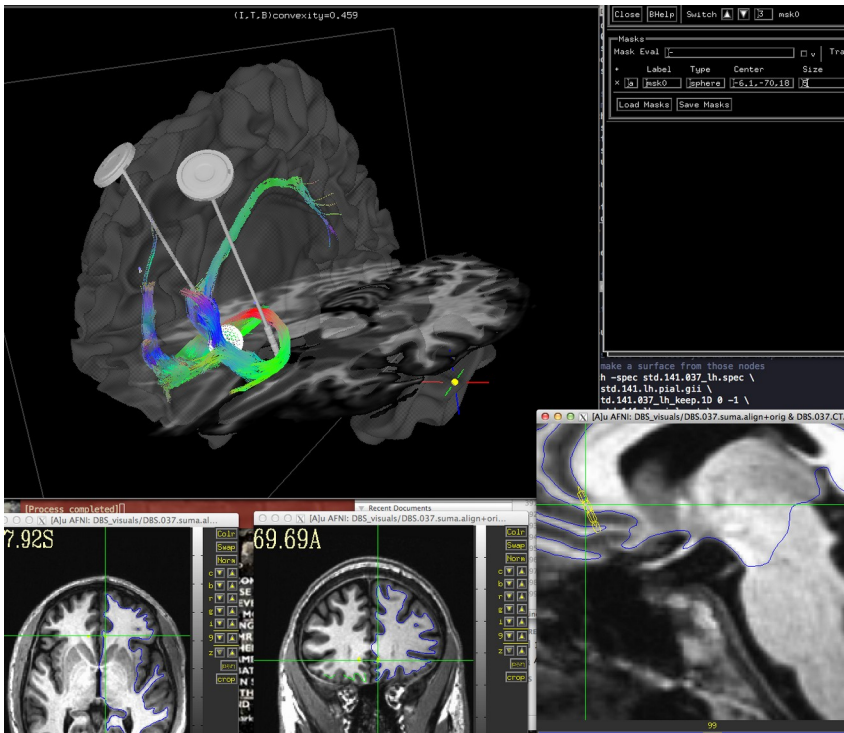
(Cox & Glen, 2013, OHBM)

other types of alignments  
that are possible in AFNI



## Alignment with non-MRI data

DBS - align CT with electrodes to pre-surgical MRI, PET (and sometimes DWI)

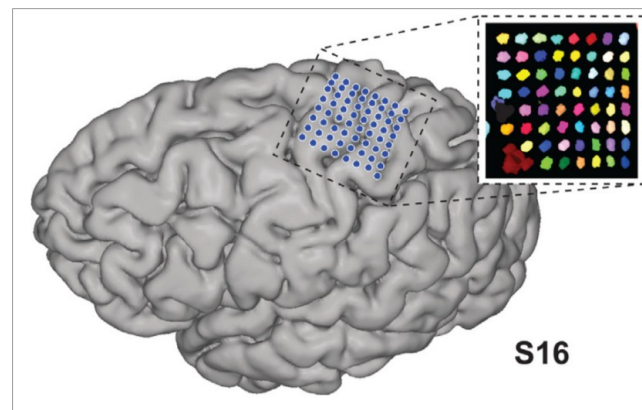
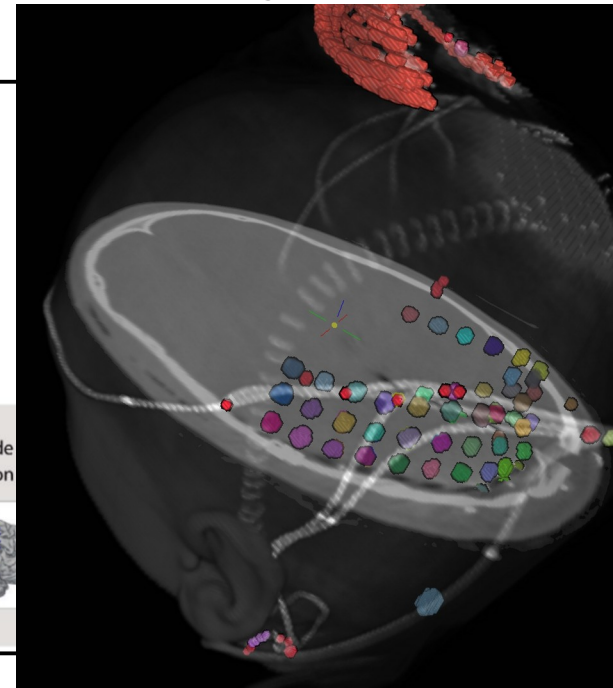
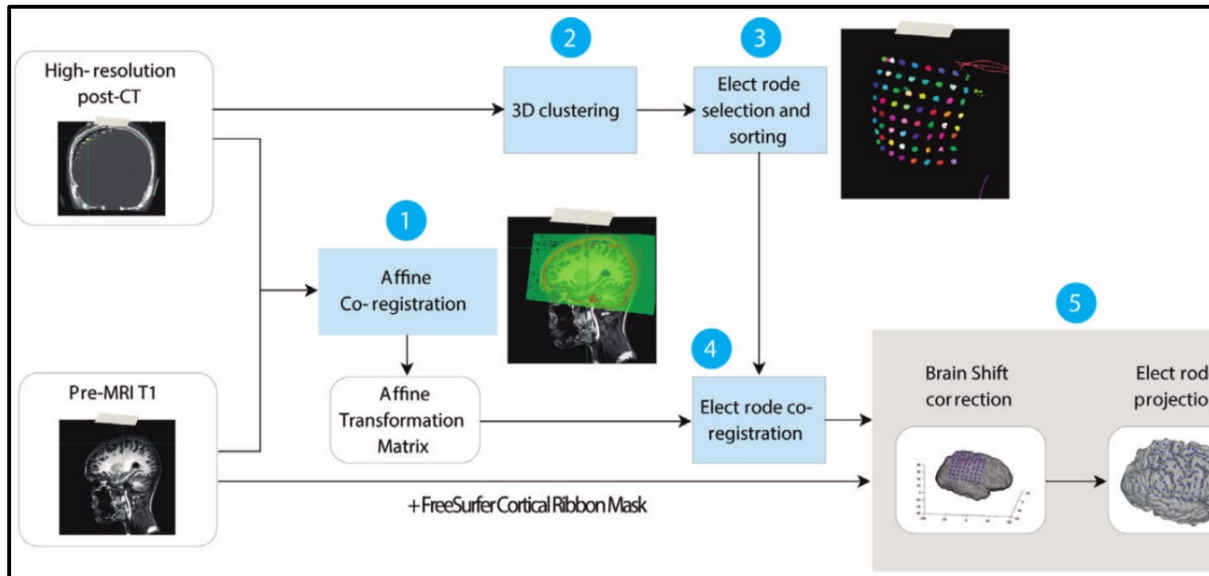


Dset courtesy of Justin Rajendra (now in AFNI group!) and Helen Mayberg.

Lauro et al. (2016). And check out [@Install\\_DBSPROC](#) for demo on DBS processing with CT and DTI processing in AFNI (with Silvina Horovitz).

# Alignment with non-MRI data

ECOG - align post-op CT with electrodes to pre-surgical MRI, view grids in 2D (AFNI slices) and 3D (SUMA surfaces).



Branco et al. (2018):  
*ALICE toolbox using AFNI+SUMA.*

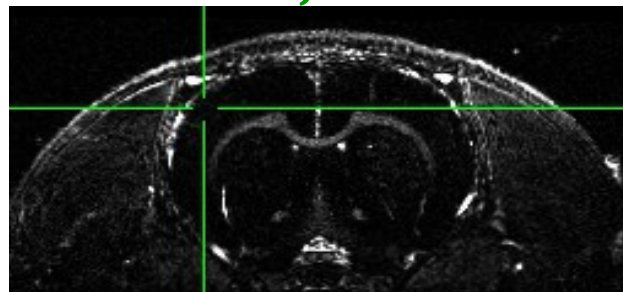
## Alignment with non-human data: rats

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

*before*



*after*

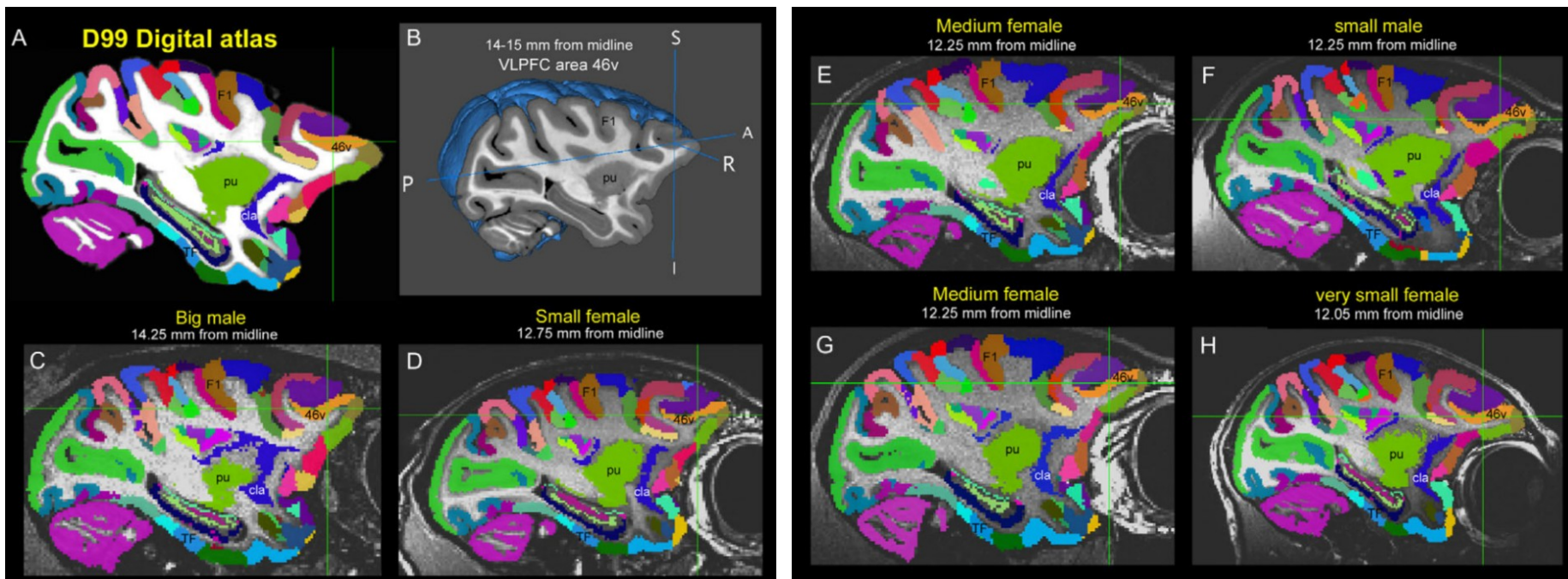


[movies→]

```
#!/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
```

## Alignment with non-human data: macaques

Align new D99 template (Reveley et al. 2017) to individual subjects



See here for alignment scripts and more:

- + Demo with scripts (e.g., *macaque\_align.csh*): @Install\_D99\_macaque
- + <https://github.com/jms290/NMT> (e.g., *NMT\_subject\_align.csh*)

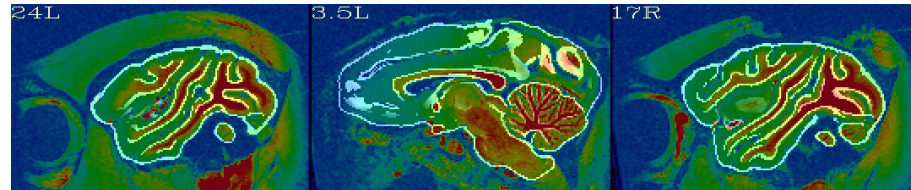
*For questions on non-human alignment, contact D. Glen in AFNI group (email, Message Board).*

## Alignment with non-human data: macaques

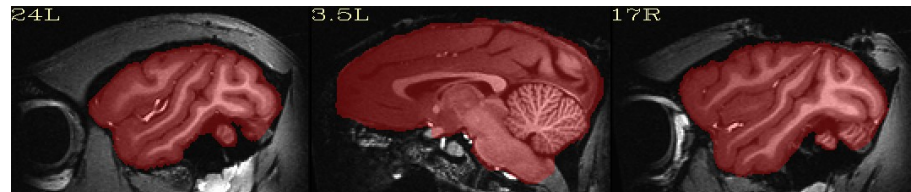
**New** macaque FMRI demo with `afni_proc.py` (@Install\_MACAQUE\_DEMO)

- 1) Uses new `@animal_warper` program in AFNI for nonlinear alignment
- 2) `afni_proc.py` generates pipeline with stats modeling + automatic QC

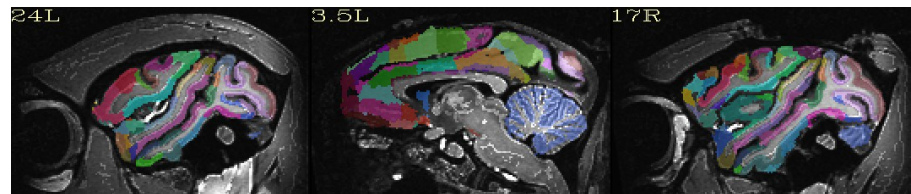
**align:** template (white lines)  
to orig anatomical (color)



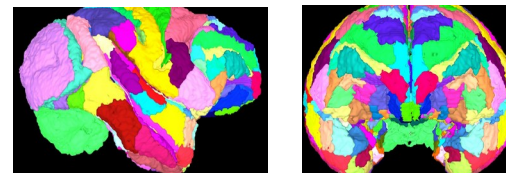
**skullstrip:** focus on brain  
(red) from tissue



**map atlas:** map D99 atlas  
locations to anatomy



**Bonus:** *SUMA surfaces*



## Conclusions

Lots of details and concepts to keep in mind:

+ what are the volume contrasts? resolutions? FOV? overlaps? ...?

**Always** visually check results of alignments

+ some scripts/commands make images automatically

+ the AFNI GUI has many useful features to check u/vlay/o/vlay

+ you can build your own image-making commands (@chauffeur\_afni)

For FMRI: ***afni\_proc.py is your new best friend***

+ many features of alignment are taken care of for you, for free!

+ you can also learn more alignment tips by reading the AP script

# Supplements

extra stuff

# S1: script for @chauffeur\_afni + imcat

```
#!/bin/tcsh
# Image-generating script for "Alignment concepts: dset overlap" slide; might be useful.
set odir = . # output dir: here
set lcol = ( 150 150 150 ) # grey gaps in imcat cmd
set refv = MNI152_2009_template_SSW.nii.gz # refvol, ulay

foreach ff ( `ls mni_match*gz` )
  # base name of vol, and make a list of all prefixes for later
  set ibase = `3dinfo -prefix_noext "${ff}"`
  set cpref = img0_${ibase}

  # Make a montage of the zeroth brick of each image
  @chauffeur_afni \
  -ulay ${refv} \
  -olay $ff \
  -thr_olay 14 \
  -set_subbricks 0 -1 -1 \
  -prefix $odir/${cpref} \
  -pbar_posonly \
  -opacity 5 \
  -func_range 110 \
  -cbar Viridis \
  -montx 1 -monty 1 \
  -set_dicom_xyz -15 -11 5 \
  -set_xhairs MULTI \
  -label_mode 1 -label_size 3 \
  -do_clean \

  # Glue together in 2x2 square, with empty matrix element zero-filled
  imcat \
  -echo_edu \
  -gap 5 \
  -gap_col $lcol \
  -nx 2 \
  -ny 2 \
  -zero_wrap \
  -prefix $odir/ALL_subj_${ibase}.jpg \
  $odir/${cpref}*
end
```