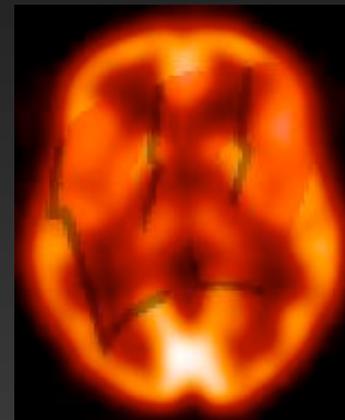


Coregistration

With your host, Terry Oakes

Waisman Laboratory for Functional Brain Imaging
University of Wisconsin-Madison

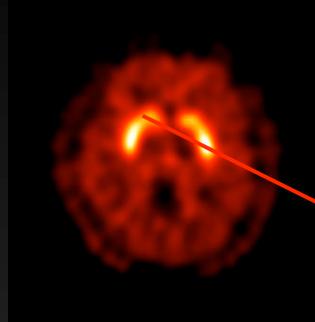


http://brainimaging.waisman.wisc.edu/~oakes/teaching/Coregistration_lecture.pdf
troakes@wisc.edu

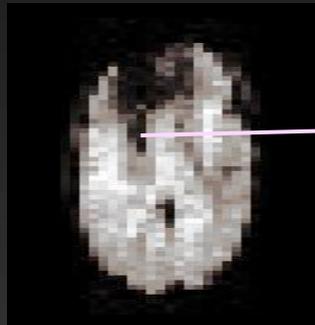
Why Coregister?



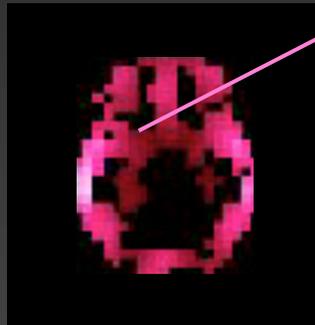
PET: concentration of radioactivity (mCi/cc brain tissue)



fMRI: paramagnetic signal from deoxygenated hemoglobin (~volts)



EEG: electrical signal strength (volts)

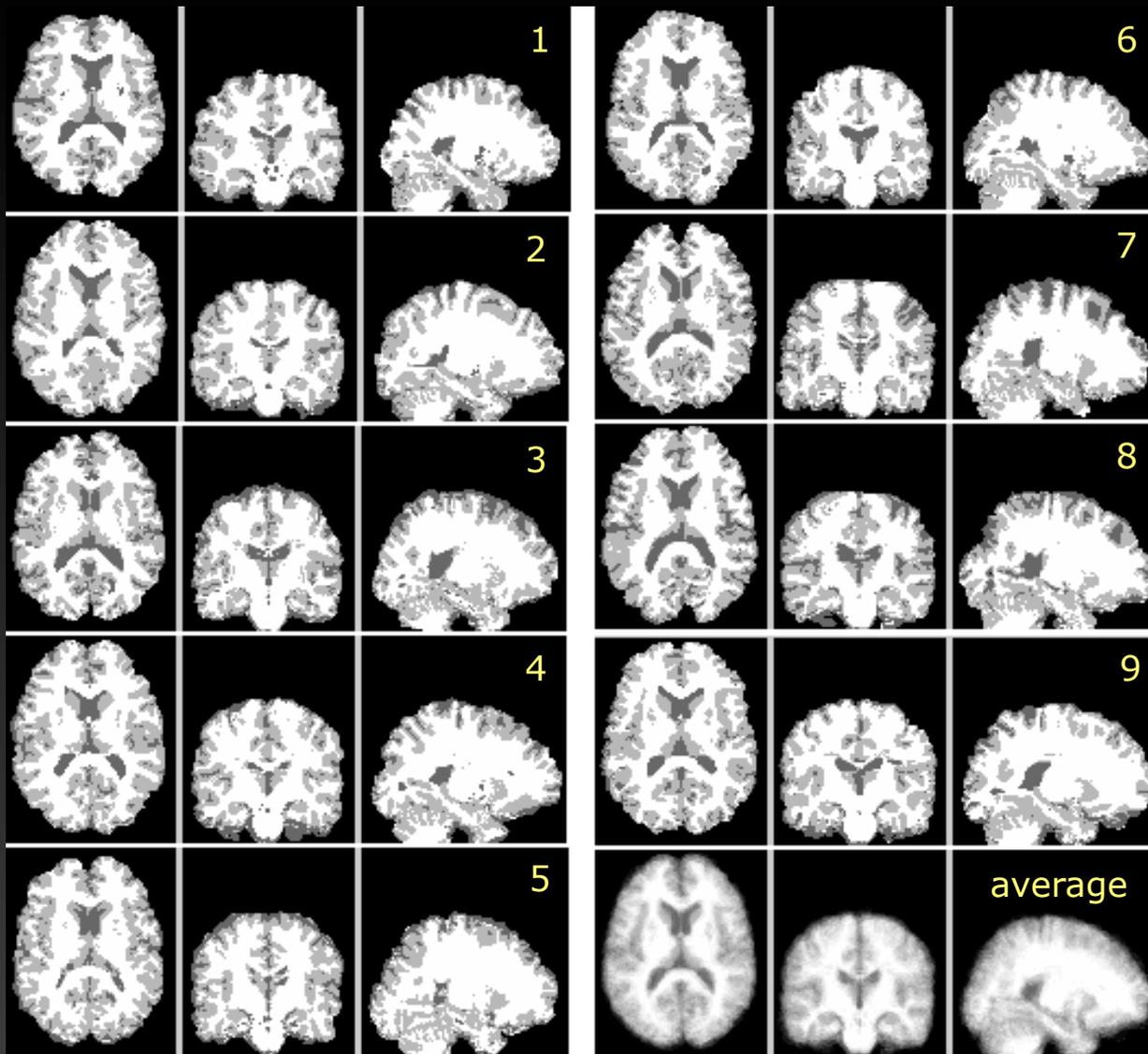


Parametric Images: Associating a parameter of interest with locations (voxels) throughout the brain.



MRI: T1-weighted paramagnetic spin realignment (~volts)

Why Coregister?



Within-subject:

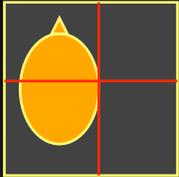
- Pixels have same size.
- Comparison with known locations.
- Assignment of standard names.

Inter-subject:

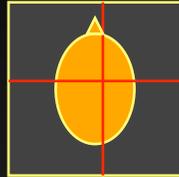
- Voxelwise categorization of data points.
- Common reference frame: (MNI, Talairach).

Types of Transform

Object

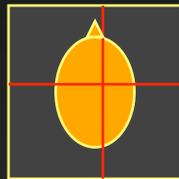


Target



Transform

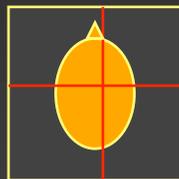
Translation



Rotation



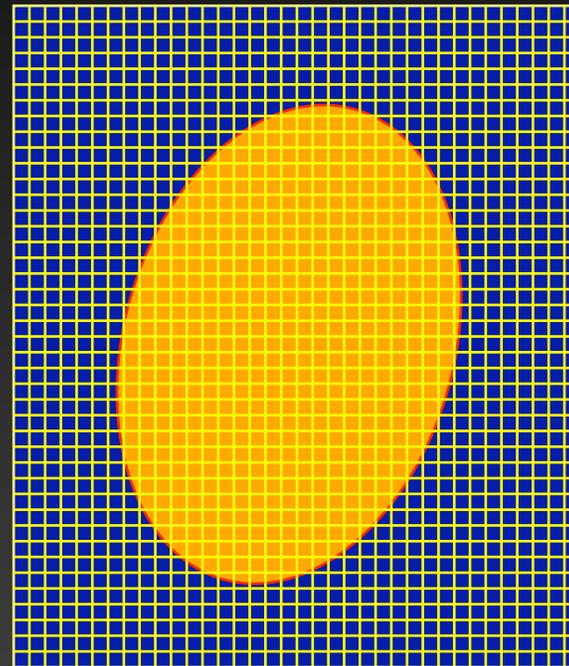
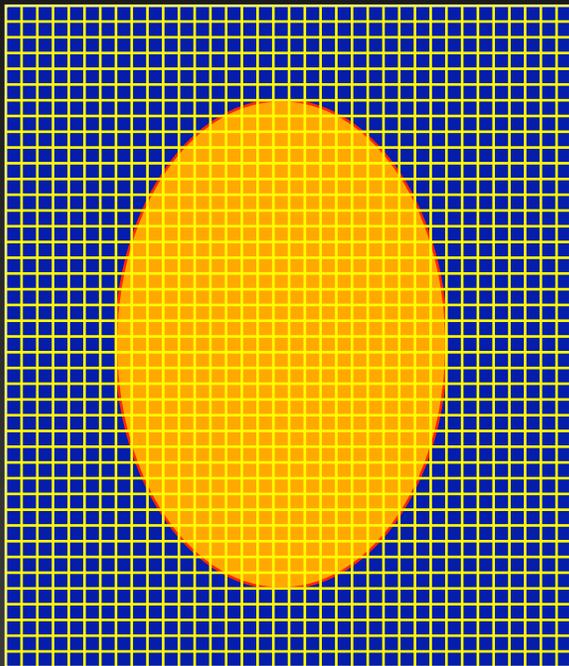
Zoom (x-dimension)



Skew (x-dimension)

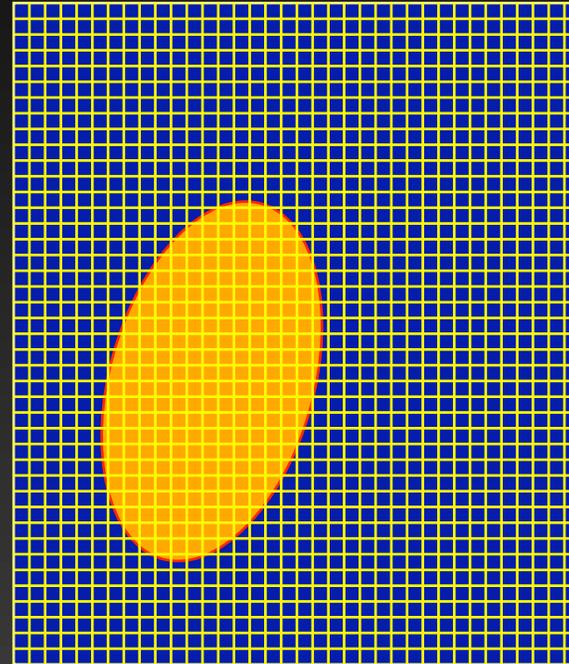
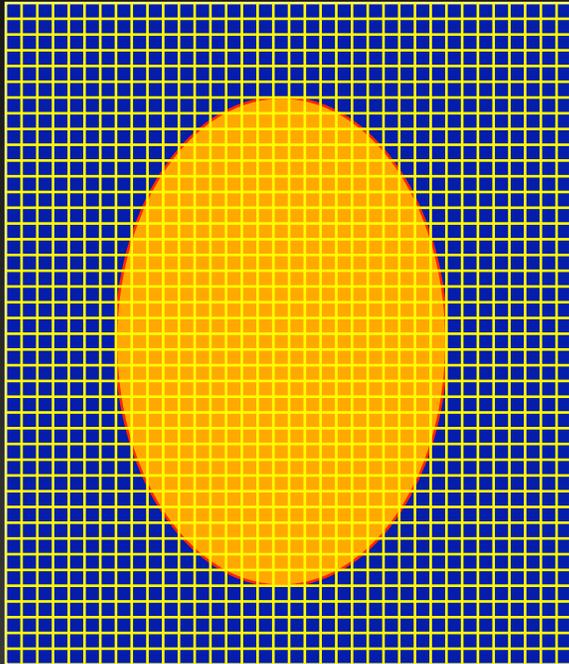
Types of Transforms: 1

Same shape, different orientation



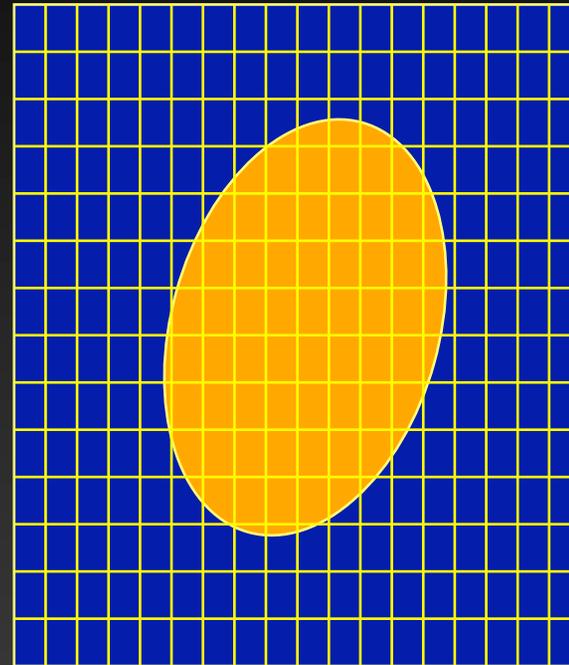
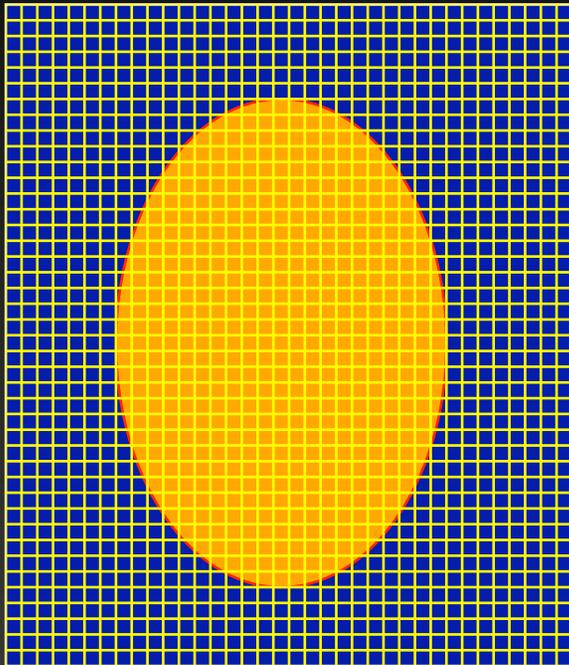
Types of Transforms: 2

Different shape, different orientation



Types of Transforms: 3

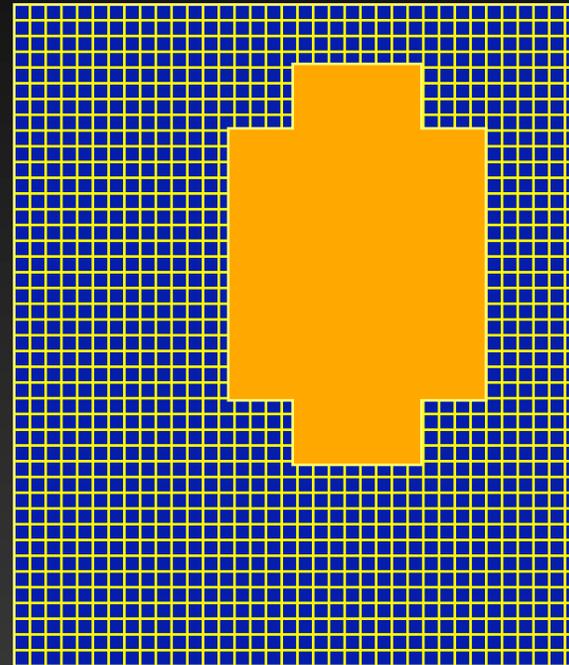
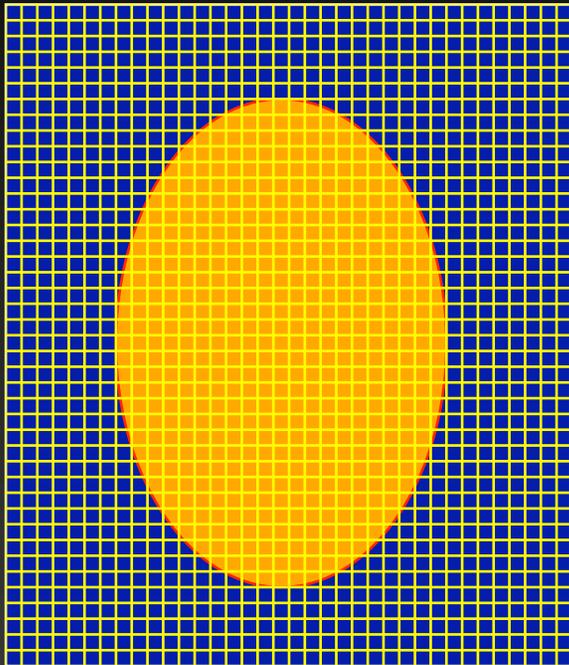
Different pixel size



Types of Transforms: 4

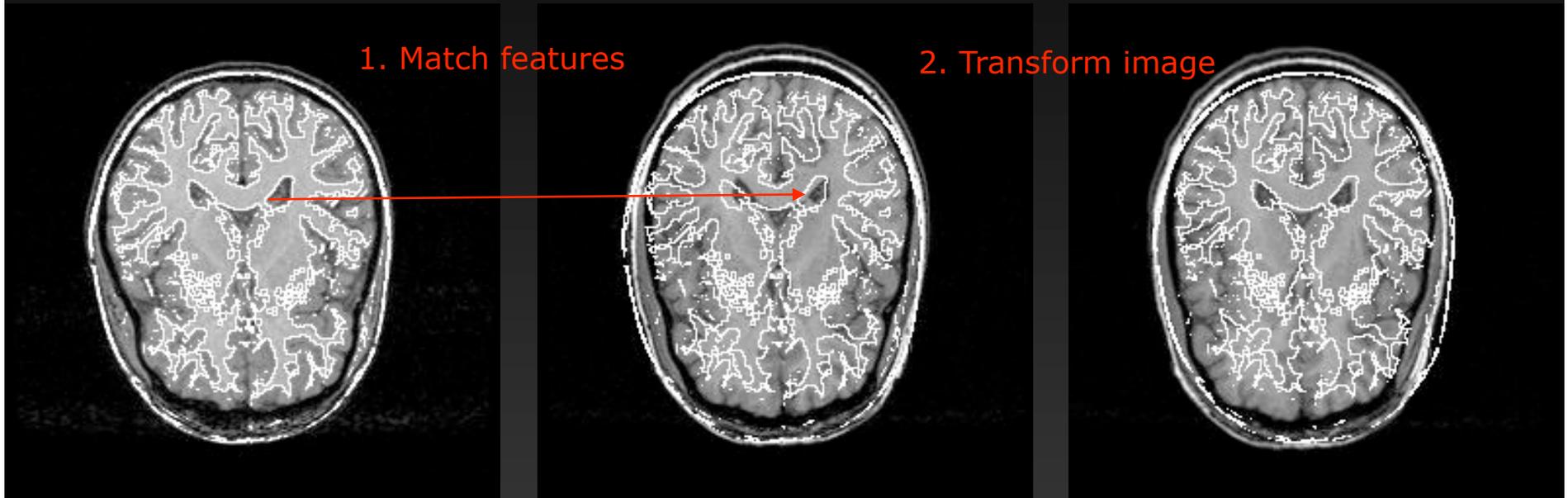
Different shape

- local stretching required
- affine, nonlinear, or higher-order fit



A Two-Step Process

1. Determine the transform parameters
2. Apply the transform (reslice)



Subject 1

(with contour at GM/WM boundary overlaid)

Subject 2: original

(with contour from Subject 1 overlaid)

Subject 2: transformed

(with same contour from Subject 1 overlaid)

Alignment Ingredients

- Cost Function

- A data reduction technique to compare 2 images
- Examples:
 - least squares
 - mutual information

- Optimization method

- efficient search through parameter space
- find global minima, avoid local minima
- Examples:
 - Gradient descent
 - Powell
 - Amoeba
 - Levenberg-Marquardt

- Interpolation algorithm

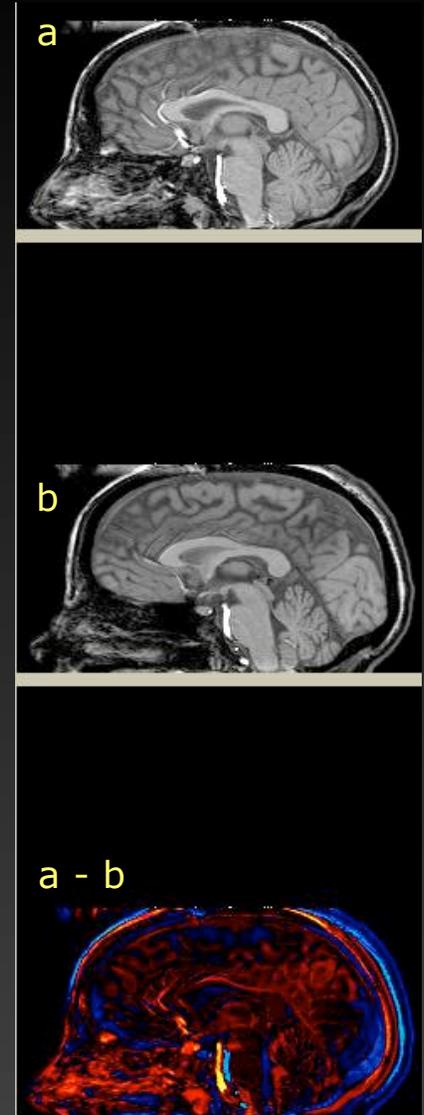
- can limit accuracy of cost function
- Examples:
 - trilinear
 - sinc and related (FFT, chirp, B-spline)

Cost Function

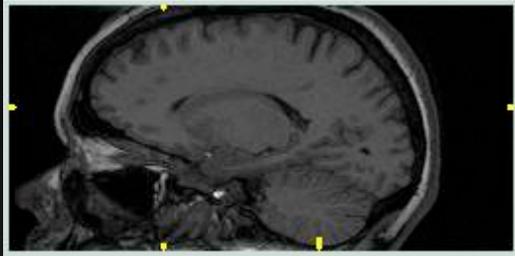
1. By Eye
2. Matching landmarks or fiducial markers
3. Surface Matching
 - a. Pelizzari's "head-in-hat"
4. Volume Matching
 - a. subtraction
 - b. ratio
 - c. least squares
 - d. mutual information

Example cost function:

$$c = \sum_i \{ A(v_i) - B(v_i) \} / N$$



Mutual Information Cost Function

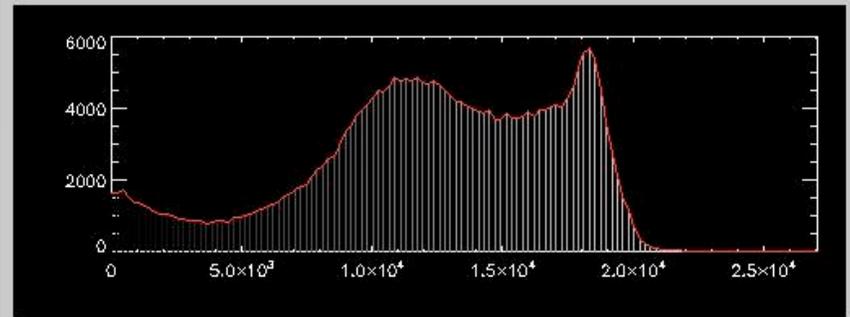


Minimize the function for joint entropy:

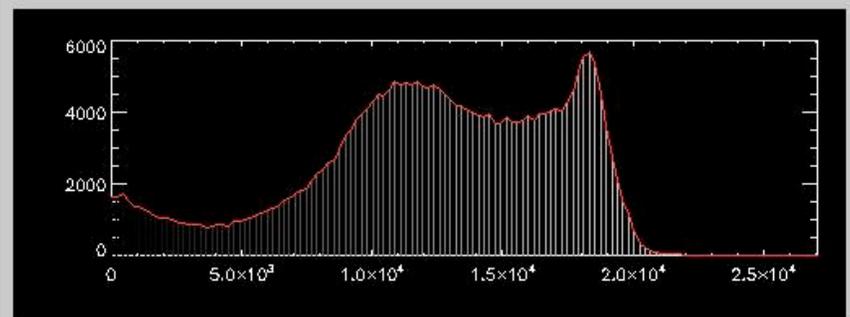
$$\sum_x \sum_y p(x,y) \frac{\log(p(x,y))}{p(x)p(y)}$$



Menu



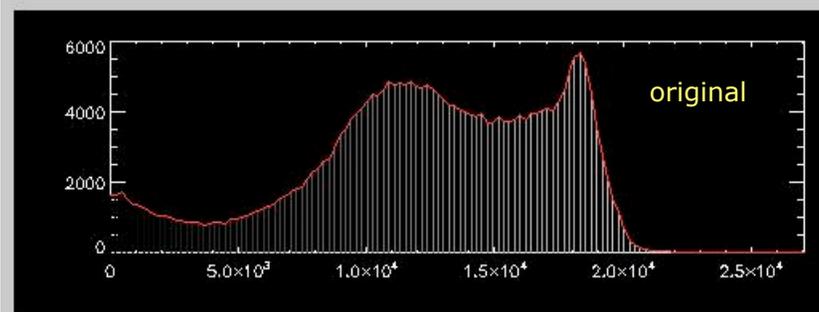
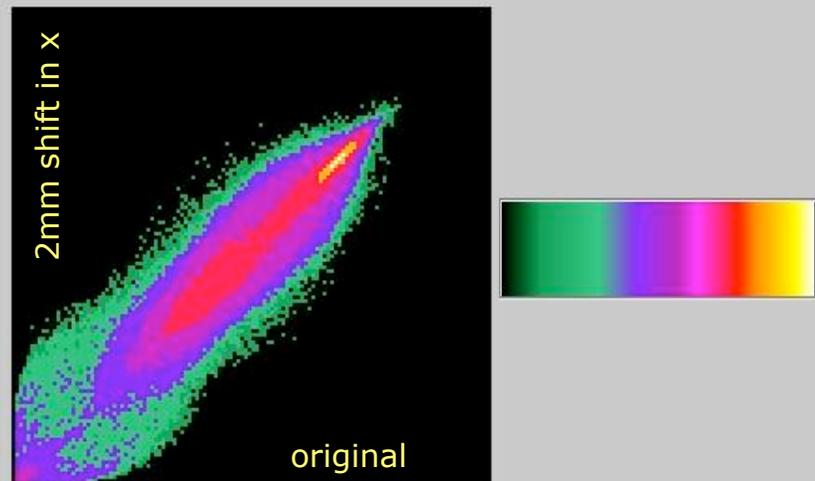
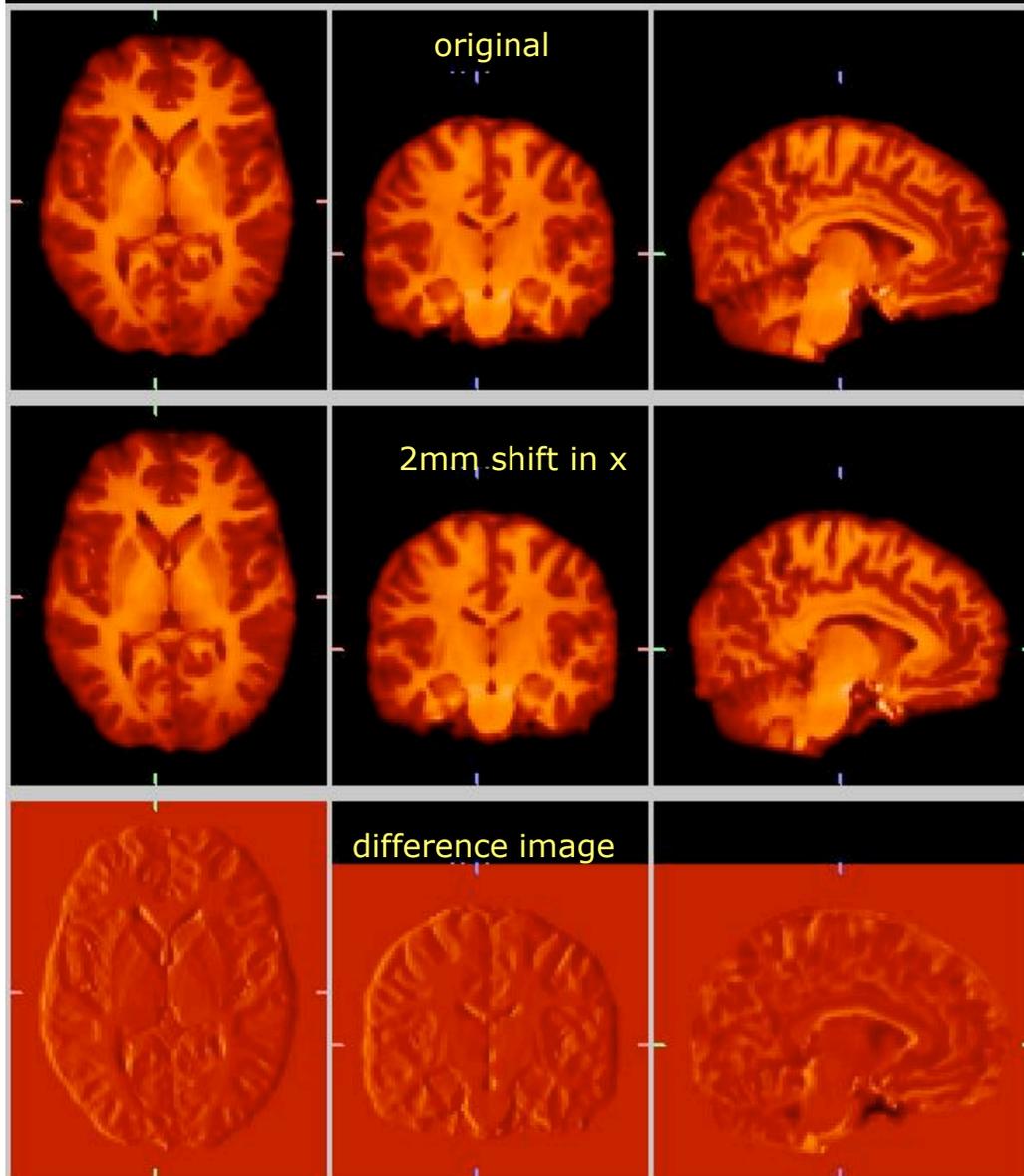
Y-Axis log



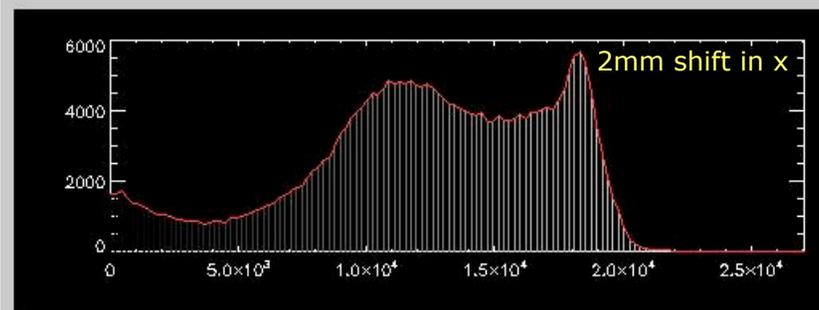
Y-Axis log

Use selected voxels:

Mutual Information



Y-Axis log [Lop Top](#) [Help](#)

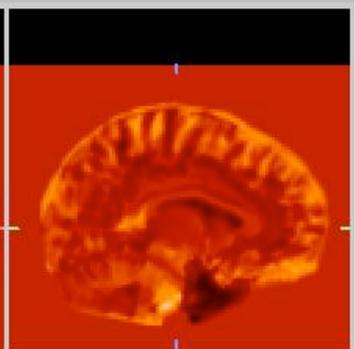
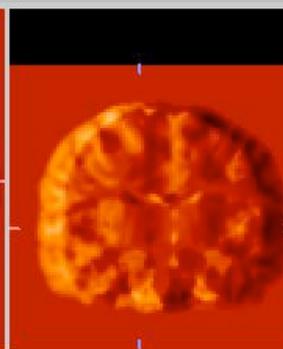
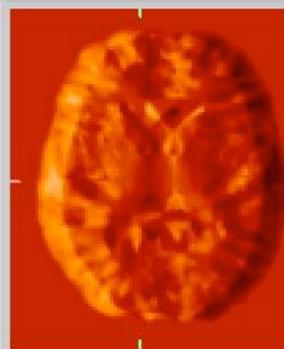
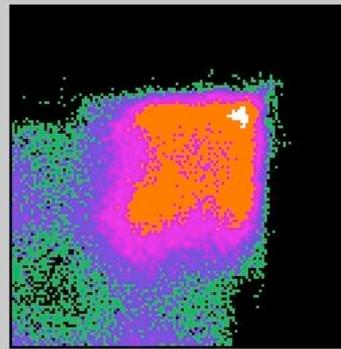


Y-Axis log [Lop Top](#) [Help](#)

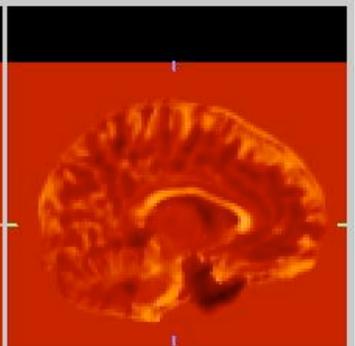
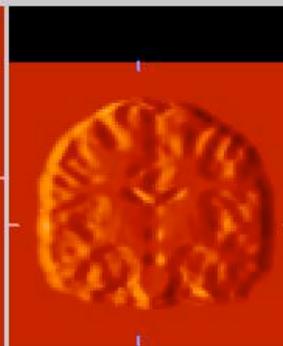
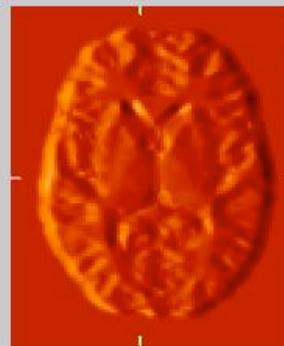
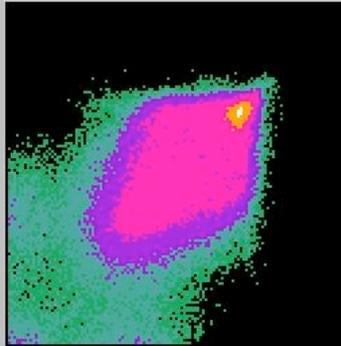
Use selected voxels: [Replace current VOI](#) [Quit](#)

Mutual Information

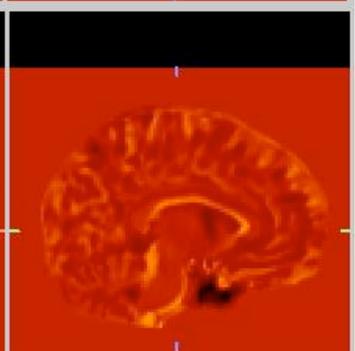
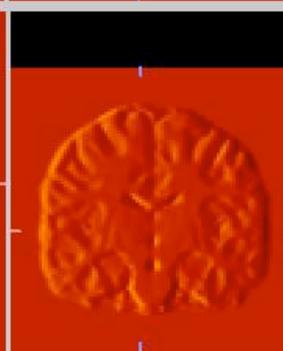
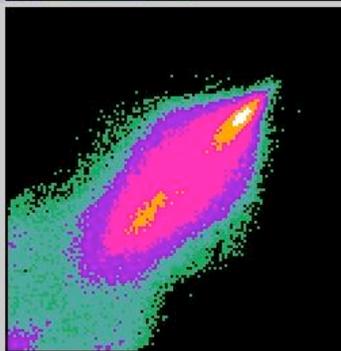
16 mm x-shift



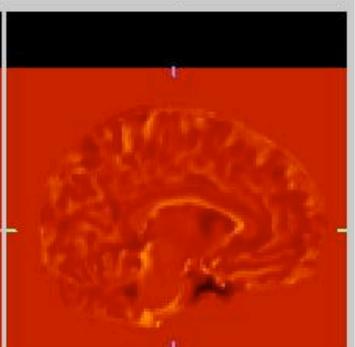
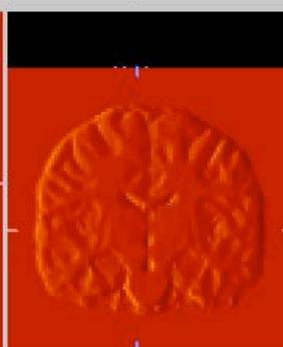
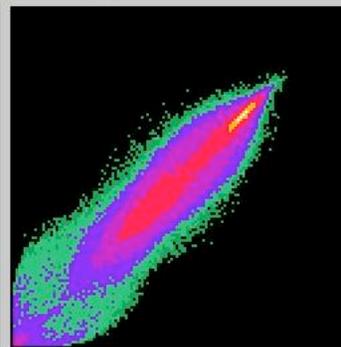
8 mm x-shift

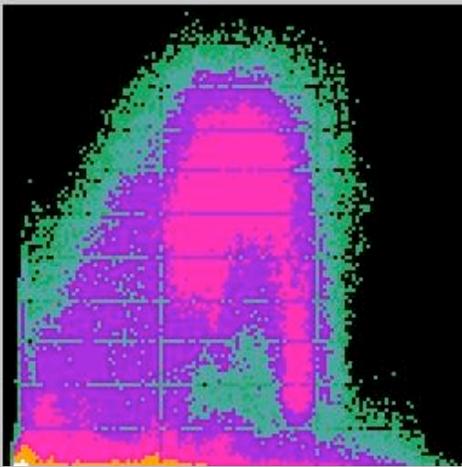


4 mm x-shift

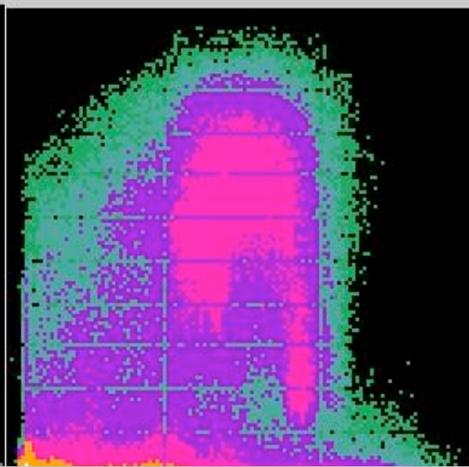


2 mm x-shift

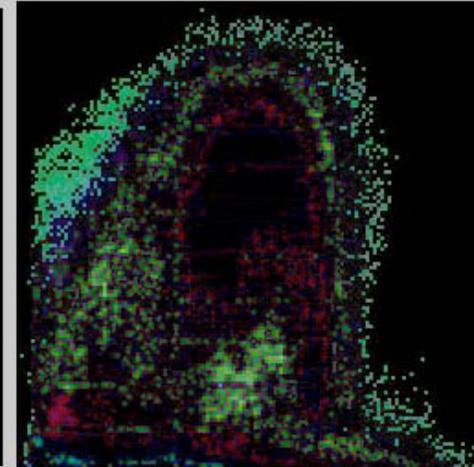




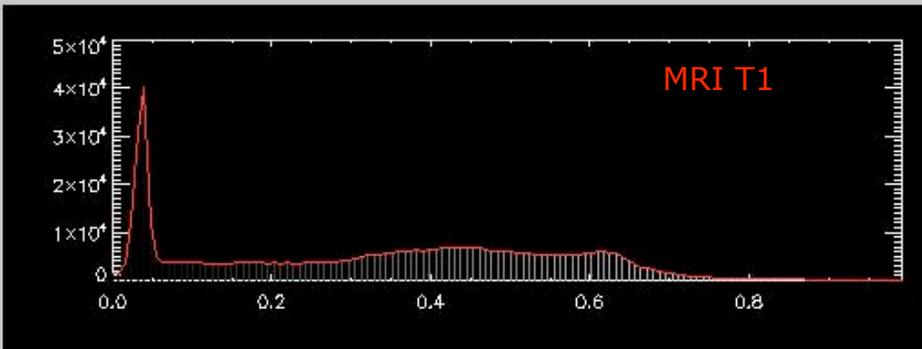
coregistered



PET 4mm x shift

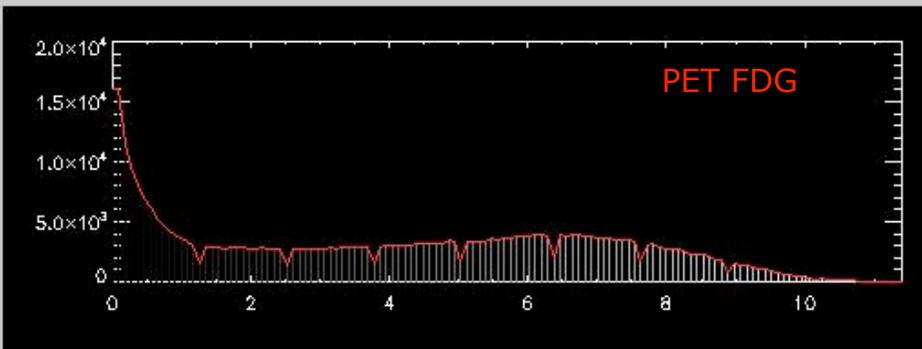


Histogram difference image



MRI T1

Y-Axis log [Log Top](#) [Help](#)



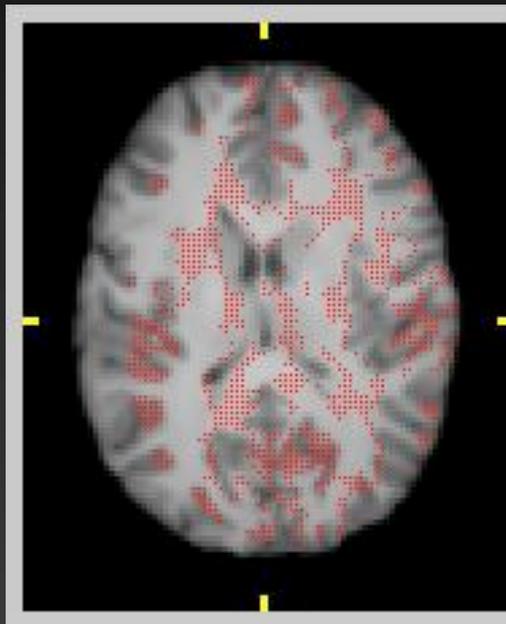
PET FDG

Multimodal Joint Histogram

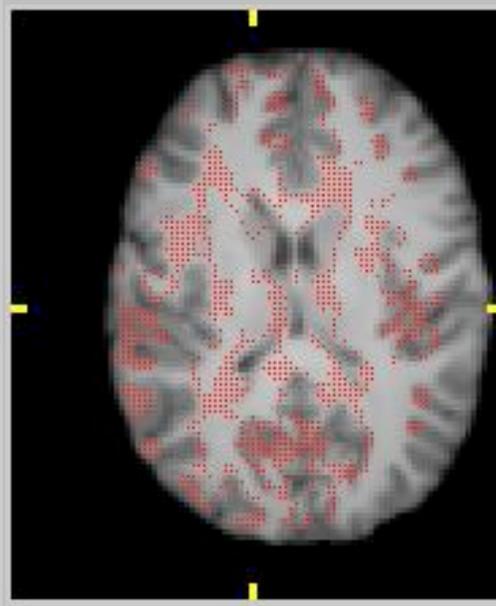
- Not necessarily symmetric about line of unity
- Need an objective cost function: "by eye" inadequate here.

Optimization Method

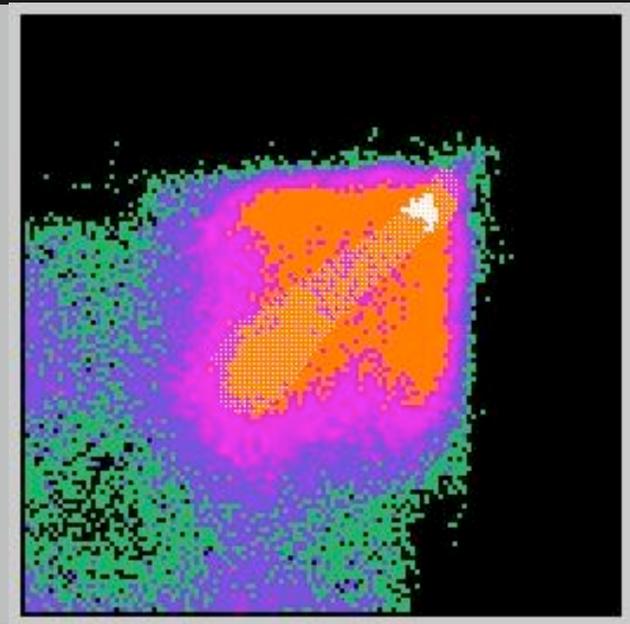
- Efficient search through parameter space
 - Avoid searching entire parameter space, concentrate on lucrative subspace.
- Find global minima, avoid local minima
 - Need to search a large enough region of parameter space.
 - Multiple-scale or decreasing coarseness.



original



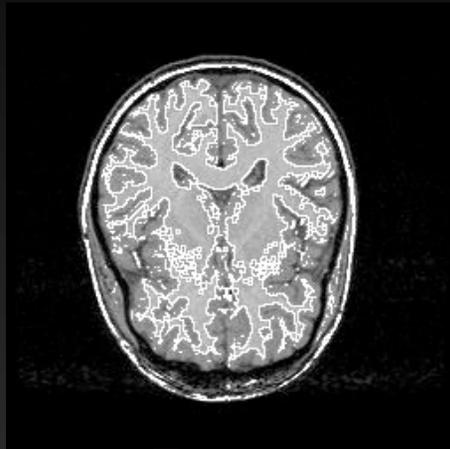
16mm x shift



joint histogram

Determining the Transform: Iterative Methods

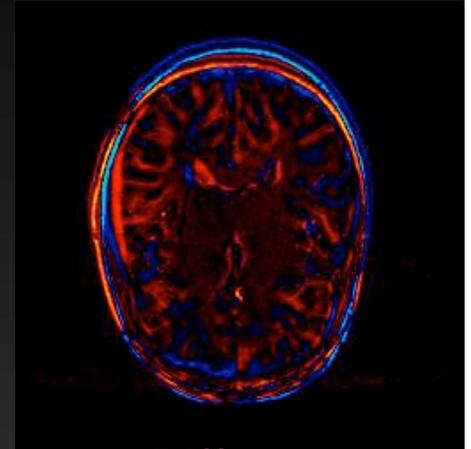
1. Compare object to target using Cost Function



Target



Object



Difference

2. Evaluate Cost Function

3. Store current transform if Cost Function minimized

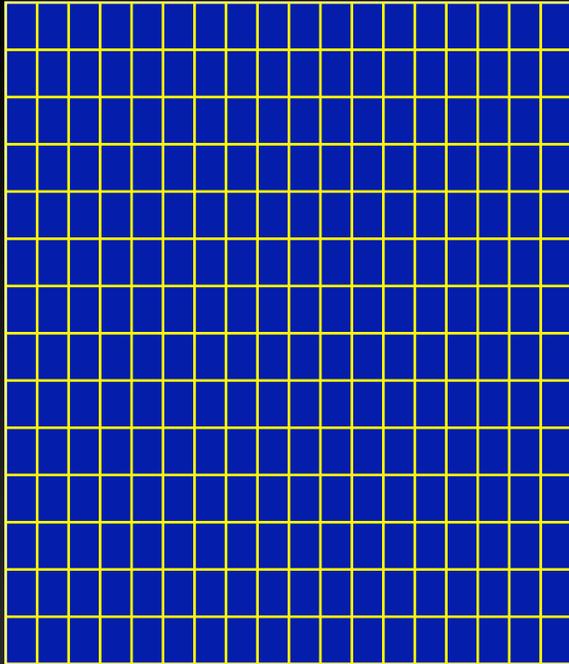
4. Try new parameters (via Optimization method)

5. From the top...

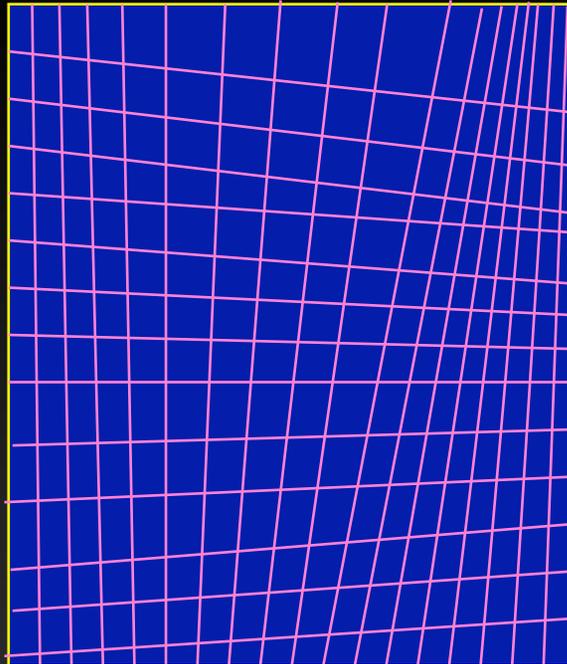
Apply the Transform

1. Shift, Rotate, Zoom.
2. Transformation matrix
3. Vector field

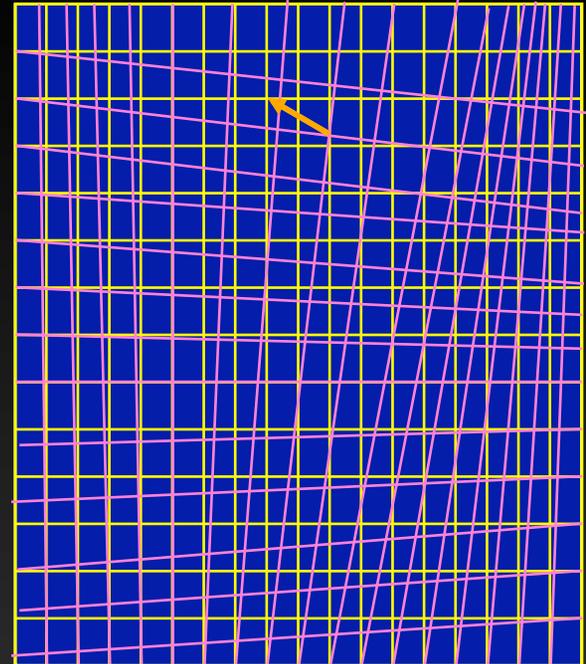
Vector Field Transform



Target



Object



Overlay

At every location (voxel), a X, Y ($, Z$) vector is stored that tells the magnitude and direction of movement required to match the object to the target image.

Pros: Versatile, accomodates unusual fits.

Cons: Time- and space-consuming.

Transformation Matrix

4x4 Homogenous Coordinate Transformation Matrices

(from AIR documentation. See <http://bishop.loni.ucla.edu/AIR3/homogenous.html>)

Combines any 3-dimensional linear transform into a single matrix:

- translation
- rotation
- zoom
- perspective distortion

Provides an equation that dictates where the value contained in any (and every) voxel will be placed in the new output image.

$$\begin{pmatrix} T' x' \\ T' y' \\ T' z' \\ T' \end{pmatrix} = \begin{pmatrix} T'' a & T'' b & T'' c & T'' d \\ T'' e & T'' f & T'' g & T'' h \\ T'' i & T'' j & T'' k & T'' m \\ T'' n & T'' o & T'' p & T'' \end{pmatrix} * \begin{pmatrix} T x \\ T y \\ T z \\ T \end{pmatrix}$$

Transformation Matrix Operations

Translation

$$\begin{pmatrix} 1 & 0 & 0 & \text{x-shift} \\ 0 & 1 & 0 & \text{y-shift} \\ 0 & 0 & 1 & \text{z-shift} \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Rotation

$$\begin{pmatrix} (\cos\varphi\cos\theta + \sin\varphi\sin\theta\sin\phi) & (\sin\varphi\cos\theta - \cos\varphi\sin\theta\sin\phi) & (\cos\theta\sin\phi) & 0 \\ (-\sin\varphi\cos\theta) & (\cos\varphi\cos\theta) & (\sin\theta) & 0 \\ (\sin\varphi\sin\theta\cos\phi - \cos\varphi\sin\phi) & (-\cos\varphi\sin\theta\cos\phi - \sin\varphi\sin\phi) & (\cos\theta\cos\phi) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Zoom

$$\begin{pmatrix} \text{x-zoom} & 0 & 0 & 0 \\ 0 & \text{y-zoom} & 0 & 0 \\ 0 & 0 & \text{z-zoom} & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Perspective

$$\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 1/\text{xview} & 1/\text{yview} & 1/\text{zview} & 1 \end{pmatrix}$$

x-,y-,z-view
denote the coordinate
from which image
is viewed

Transform Software Implementation

```
*** Construct transform matrix: ***
;* Rotation: *
;* Translate image center to rotate about it: *
T3D, TRANSLATE=[FLOAT(-x_d)/2., FLOAT(-y_d)/2., FLOAT(-z_d)/2.], /RESET
T3D, ROTATE=[0, 0, crgm.p.rot.a]
T3D, ROTATE=[0, (-1.0)*crgm.p.rot.c, 0]
T3D, ROTATE=[crgm.p.rot.s, 0, 0]
T3D, TRANSLATE=[FLOAT(x_d)/2., FLOAT(y_d)/2., FLOAT(z_d)/2.]
rot_mat=!P.T

;* Translation (convert from mm to pixels): *
x_s = FLOAT(crgm.p.shift.x)/x_p
y_s = FLOAT(crgm.p.shift.y)/y_p
z_s = FLOAT(crgm.p.shift.z)/z_p
T3D, TRANSLATE=[x_s, y_s, z_s]*FLOAT(-1)

;* Zoom: *
;* If we zoom, translate image so original center is (again) at center: *
xt=FLOAT(x_d)/2.0 * (crgm.p.mag.x - 1.0)
yt=FLOAT(y_d)/2.0 * (crgm.p.mag.y - 1.0)
zt=FLOAT(z_d)/2.0 * (crgm.p.mag.z - 1.0)
T3D, TRANSLATE=[xt, yt, zt]
T3D, SCALE=[1.0/crgm.p.mag.x, 1.0/crgm.p.mag.y, 1.0/crgm.p.mag.z]

;* retrieve the transform matrix: *
mat_transform = !P.T

*** Apply transform to create new element locations: ***
new_coords = mat_uncubic # transpose(mat_transform) # mat_cubic # coord_triples

*** Apply transform to object data: ***
image_out = INTERPOLATE(img_orig, new_pts[0,*], new_pts[1,*], new_pts[2,*])
```

Spatial Transform Models

<u>Name</u>	<u>Parameters</u>
Rigid-body	6: translation + rotation
Global rescaling	7: trans + rot + zoom (xyz locked)
Traditional	9: trans + rot + zoom
Affine	12: trans + rot + zoom + perspective

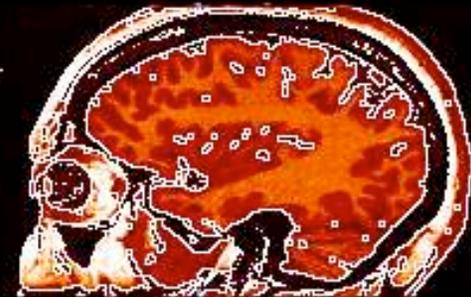
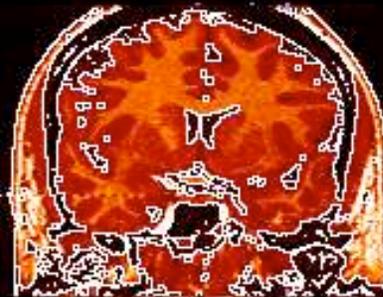
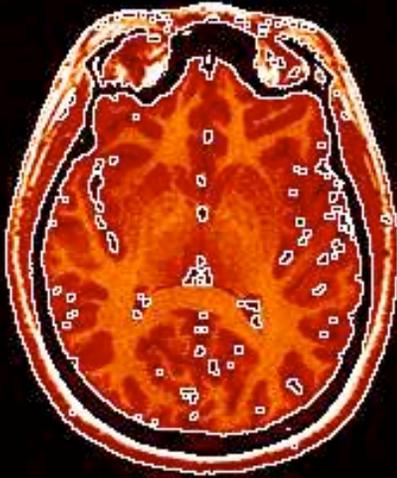
More is not always better!

Only use as many parameters as you need.
If you ask for more parameters to be fit,
they will be used,
at the expense of the correct parameters.

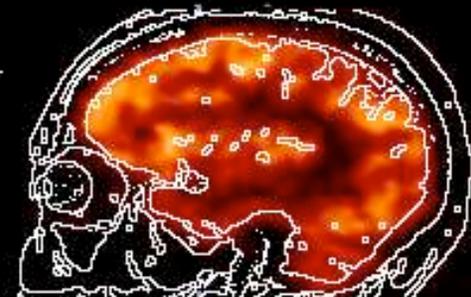
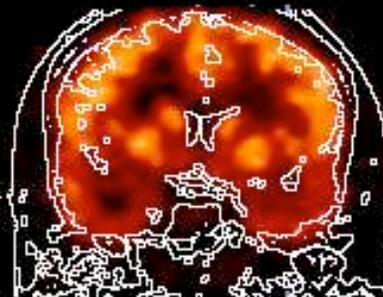
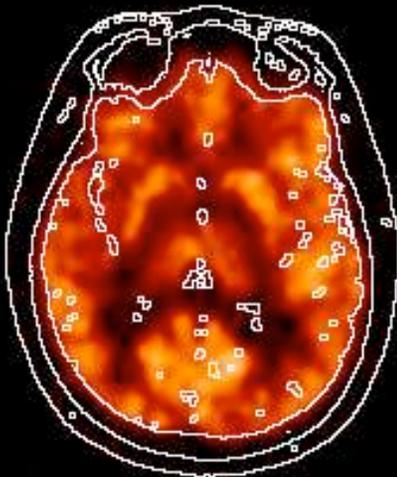
Within-subject coregistration

Rigid-body transform is most appropriate.

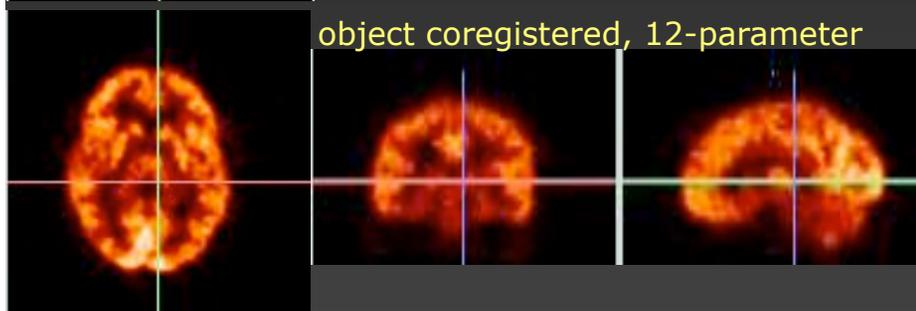
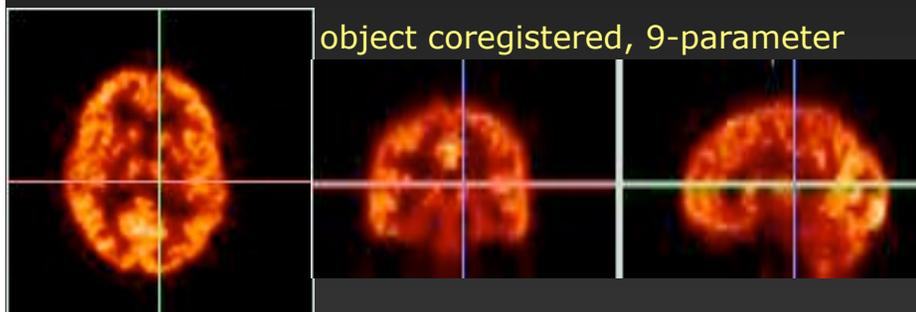
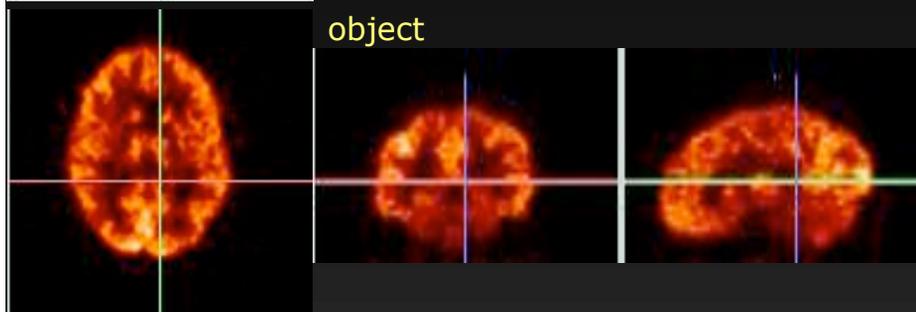
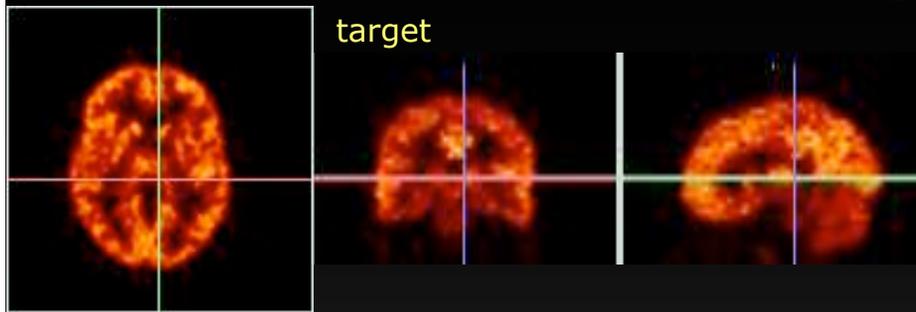
MRI



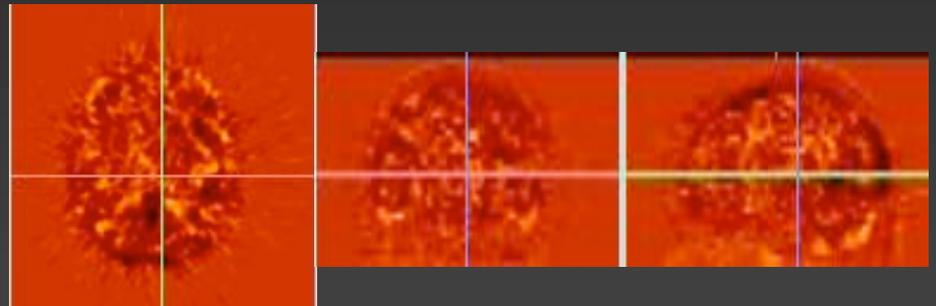
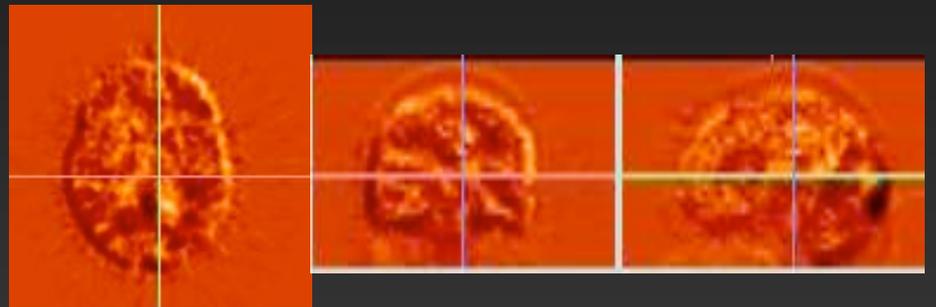
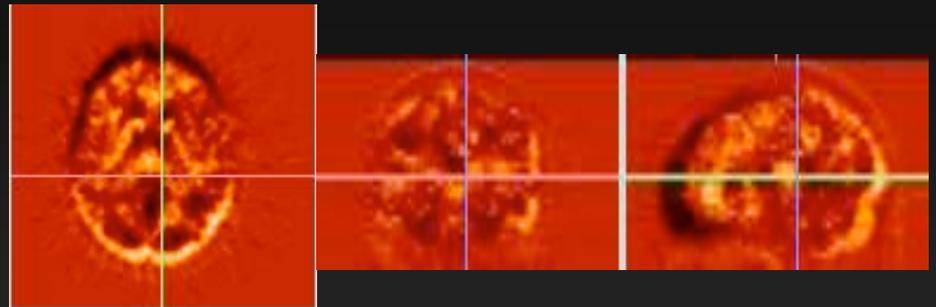
PET



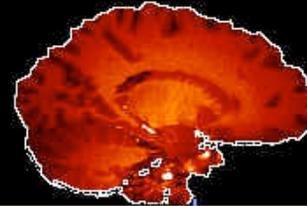
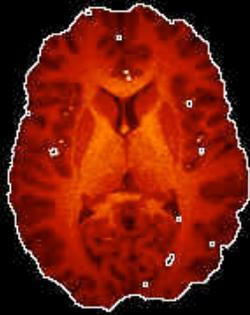
Inter-Subject Registration



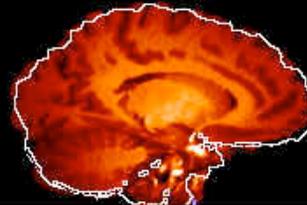
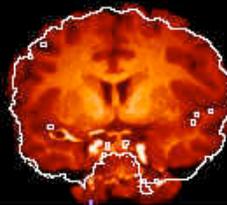
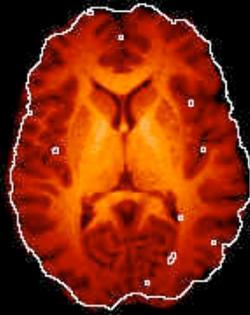
Difference Images



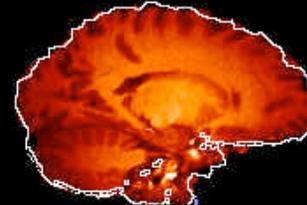
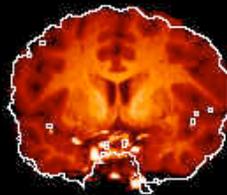
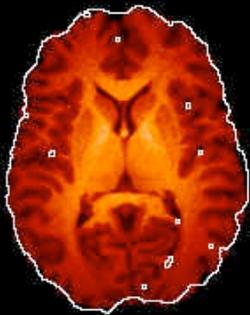
More parameters = more time



Tgt
0 sec

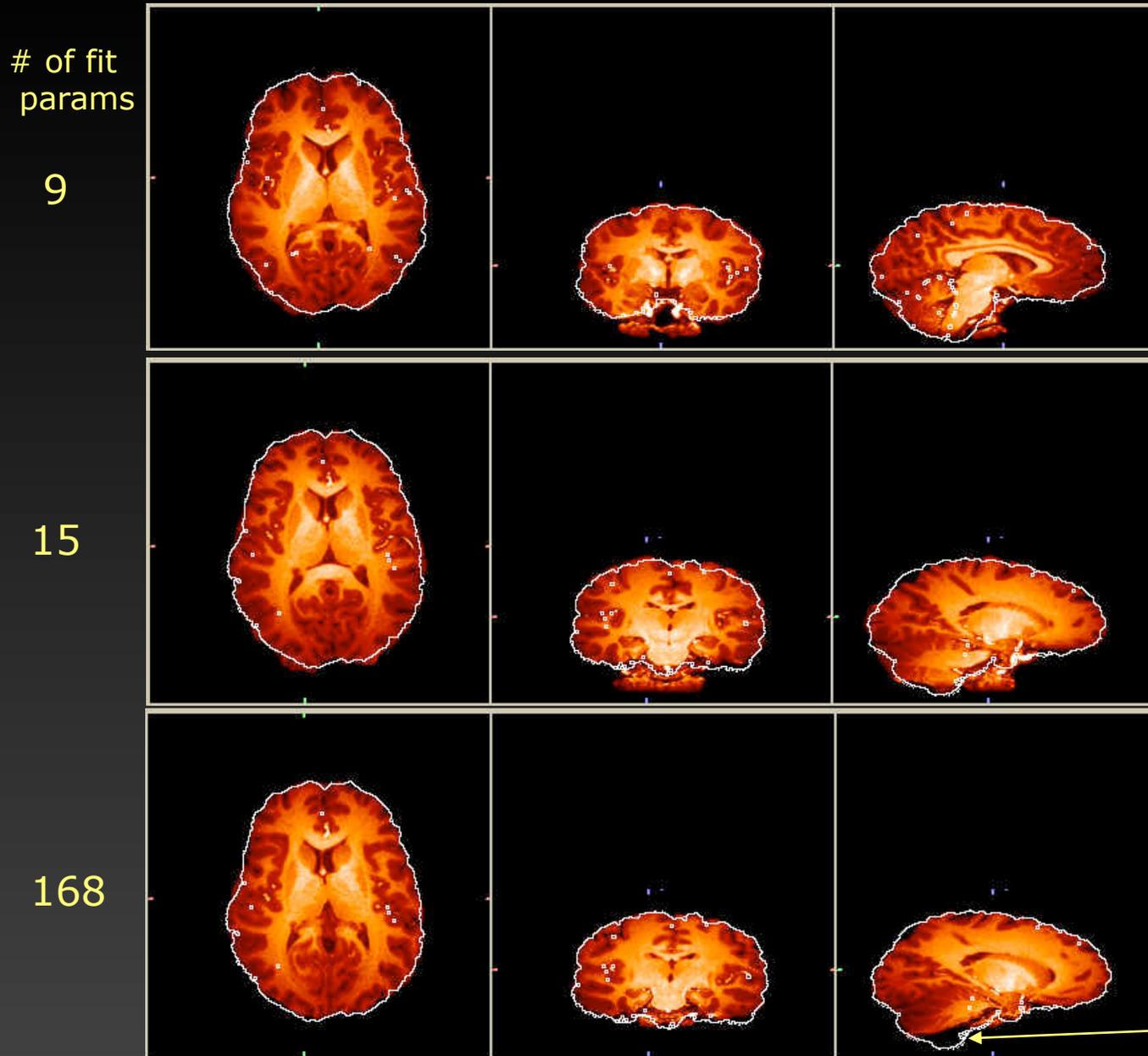


12 params
36 sec



168 params
775 sec

Increasing number of alignment parameters

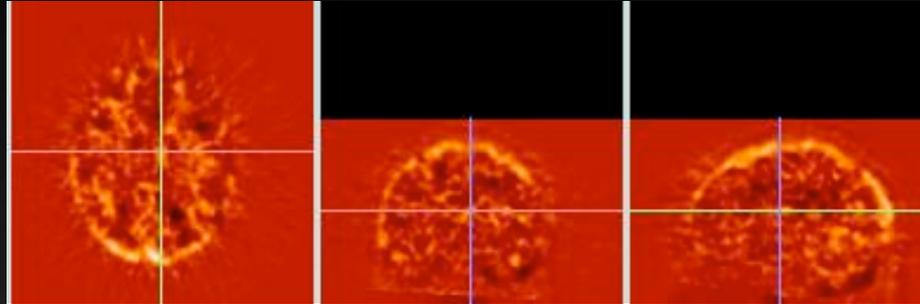


Fitting more parameters not always better!

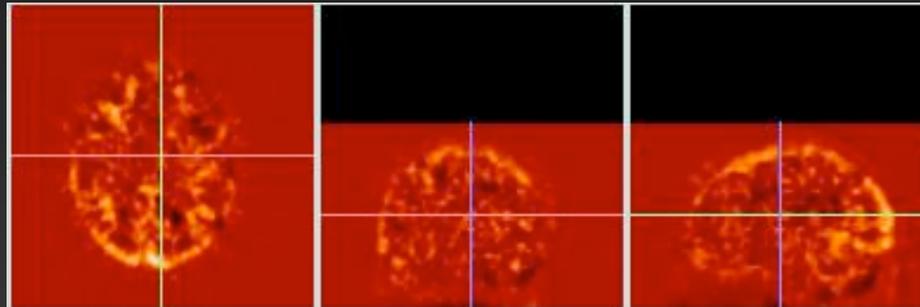
Distortion

Interpolation Methods

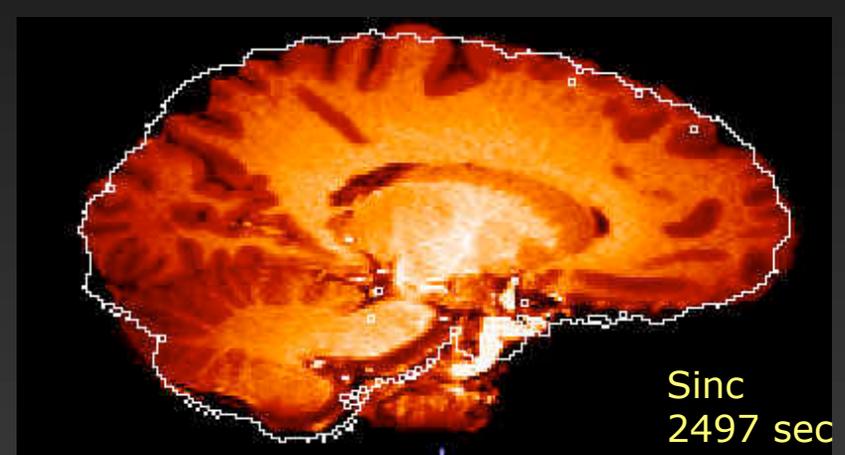
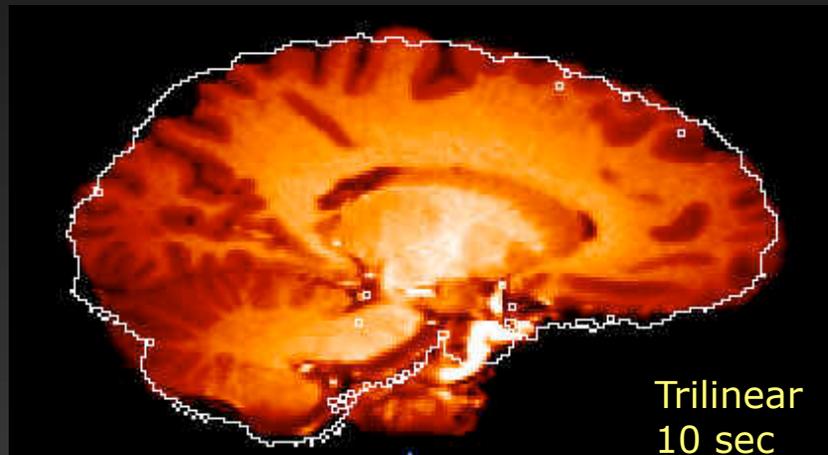
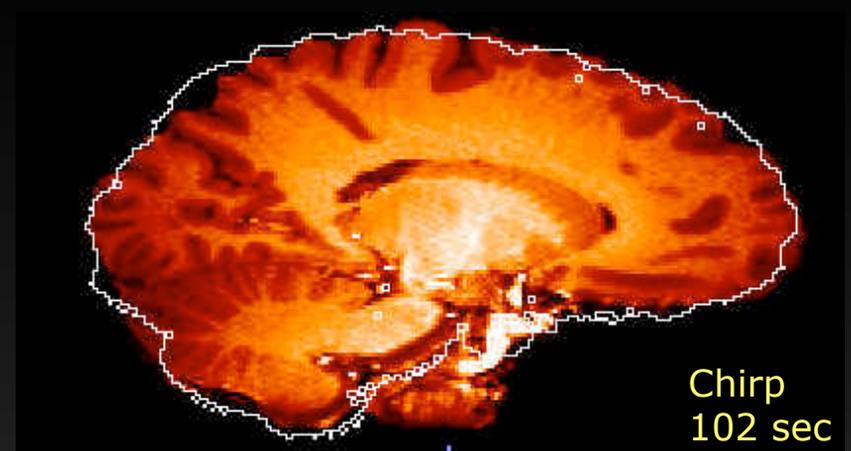
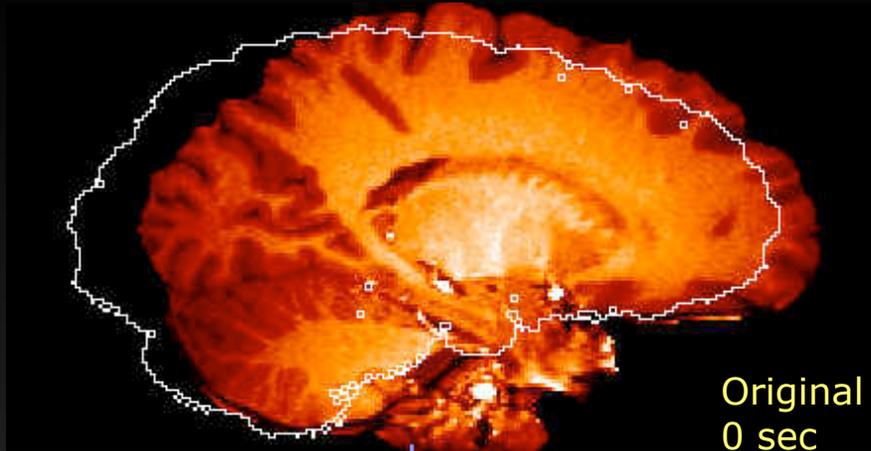
Trilinear



Sinc

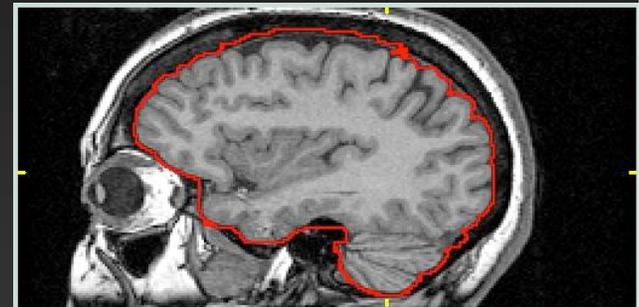
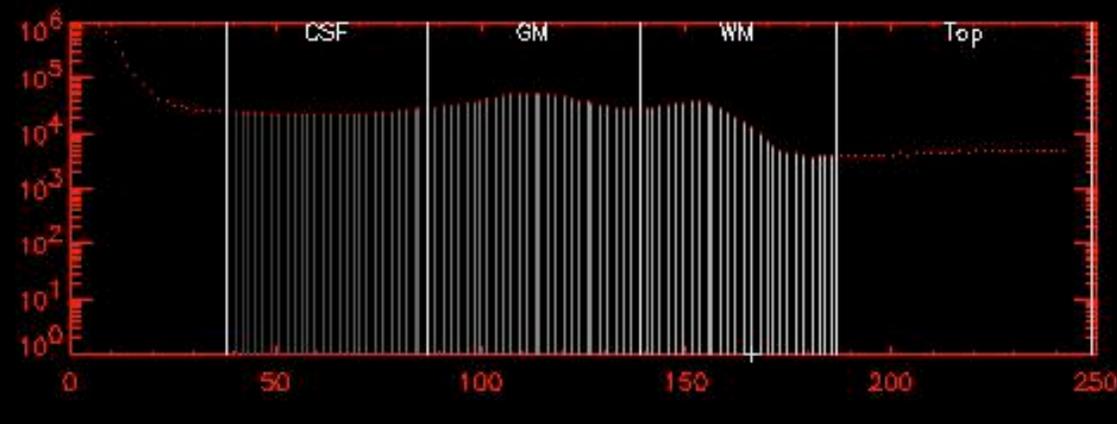
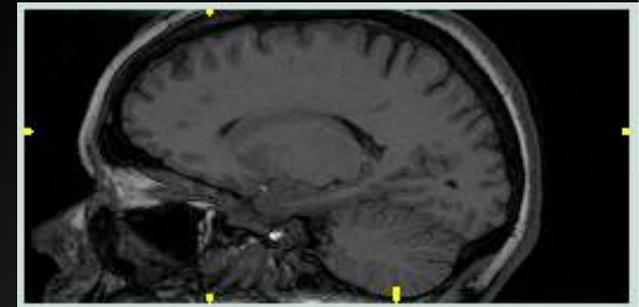
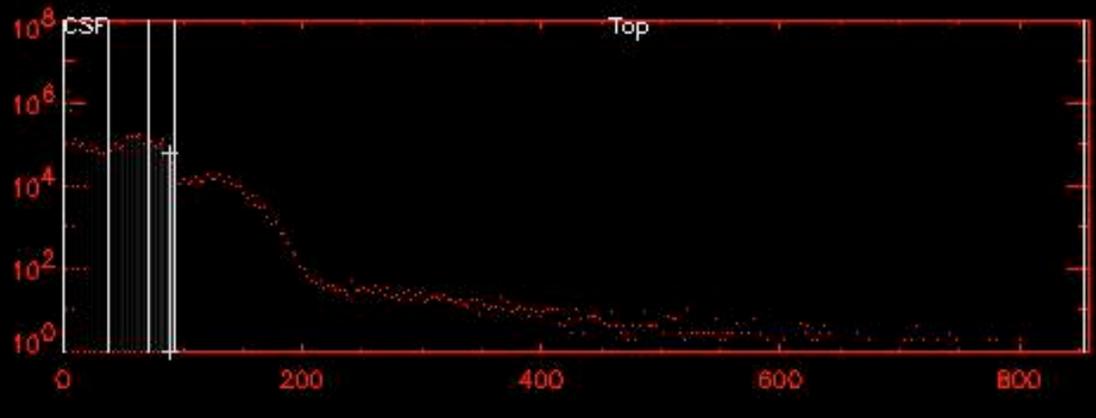


Interpolation methods where it matters...



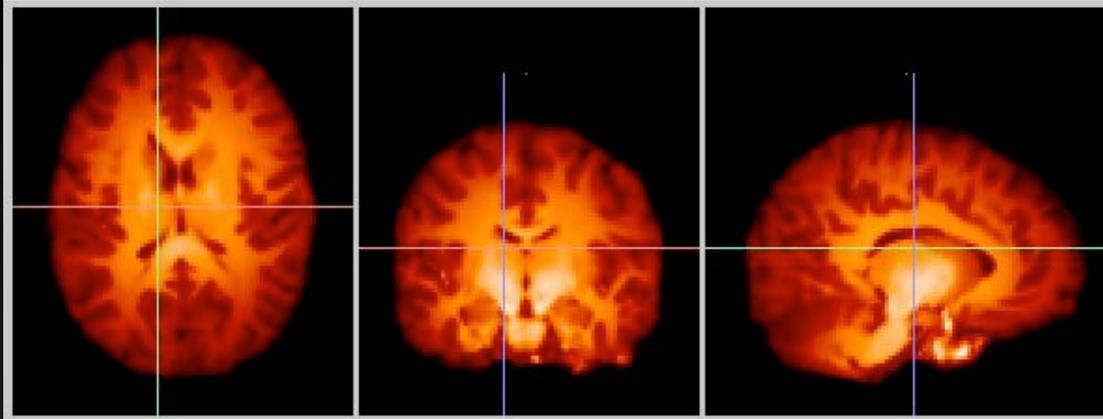
(AIR software)

Pre-processing: Range Scaling

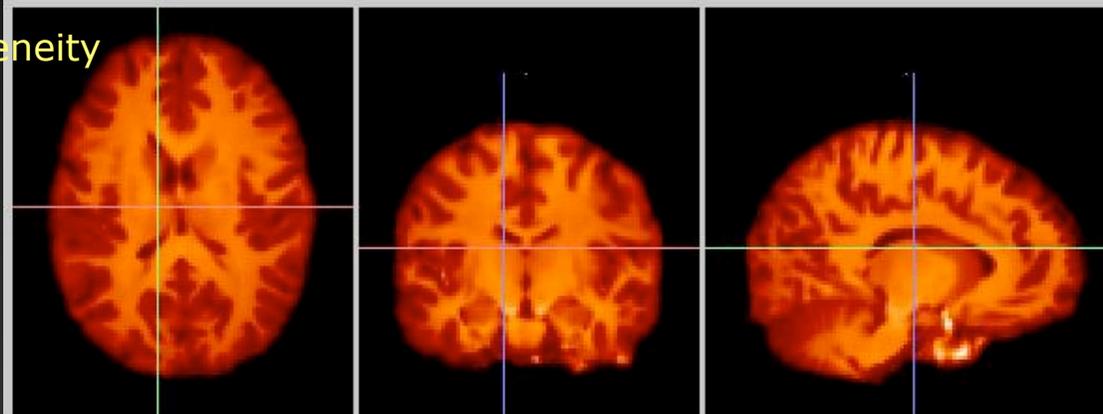


Pre-processing: inhomogeneity correction

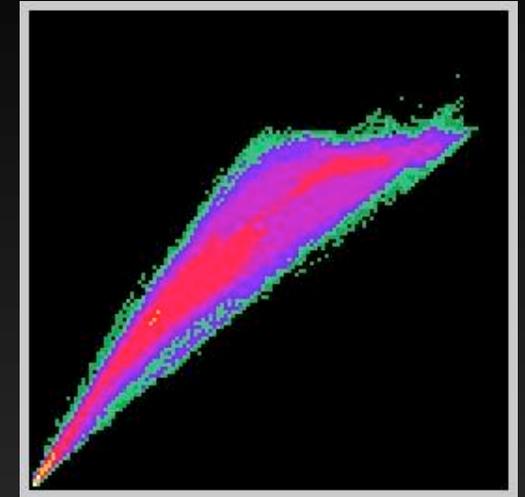
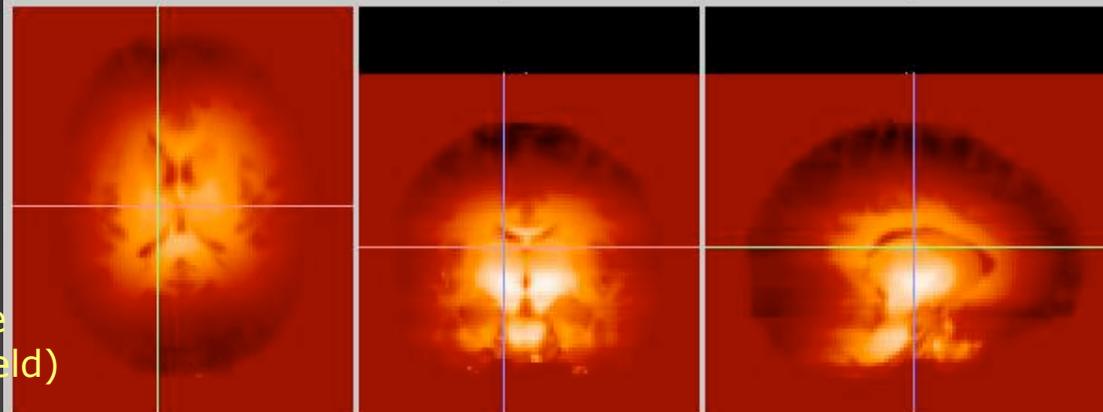
original



inhomogeneity corrected

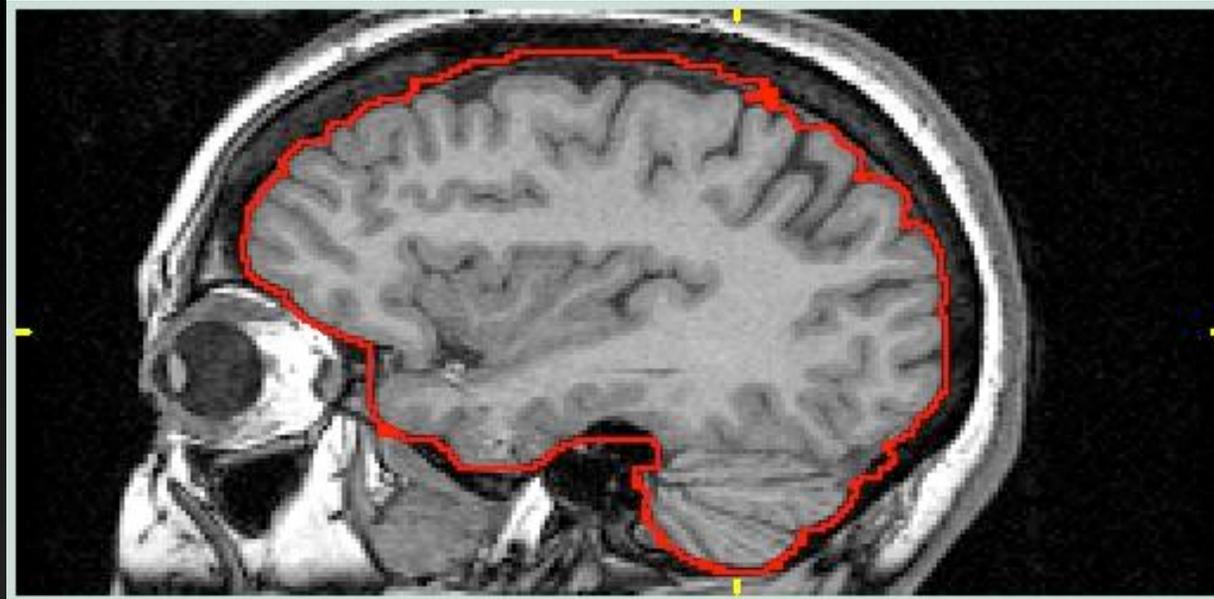


Difference
(\sim bias field)

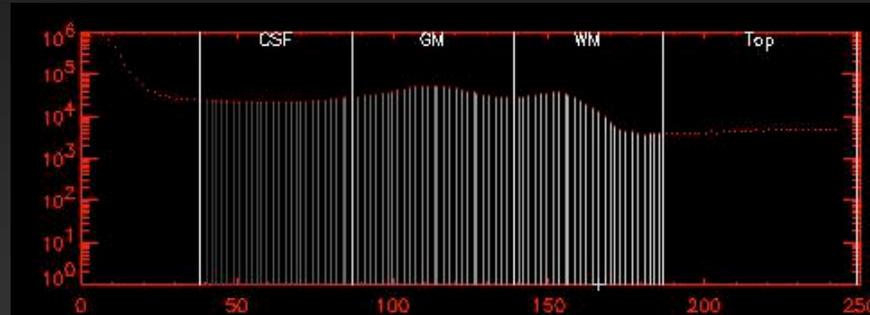


joint histogram

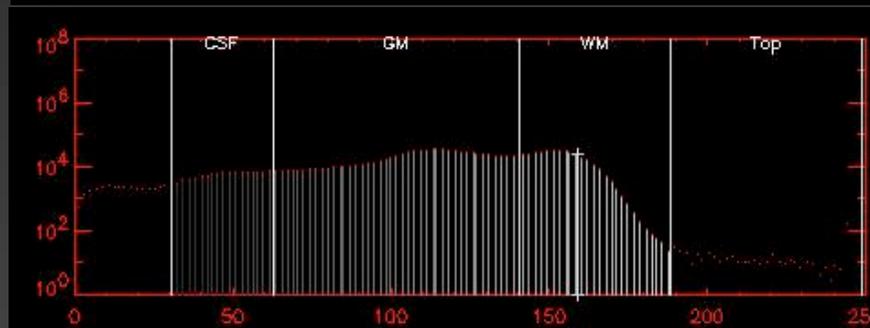
Pre-processing: skull-stripping



Original

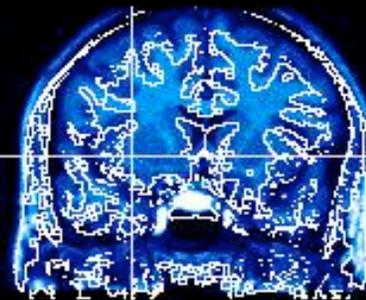
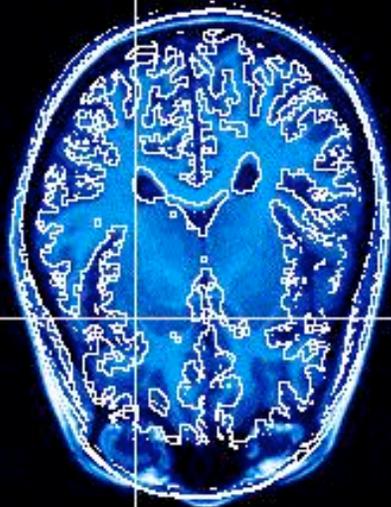
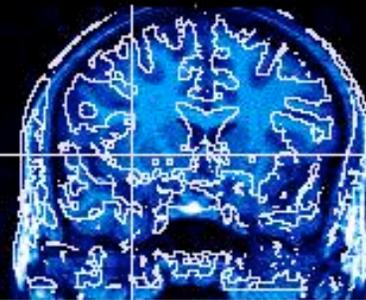


Skull-stripped

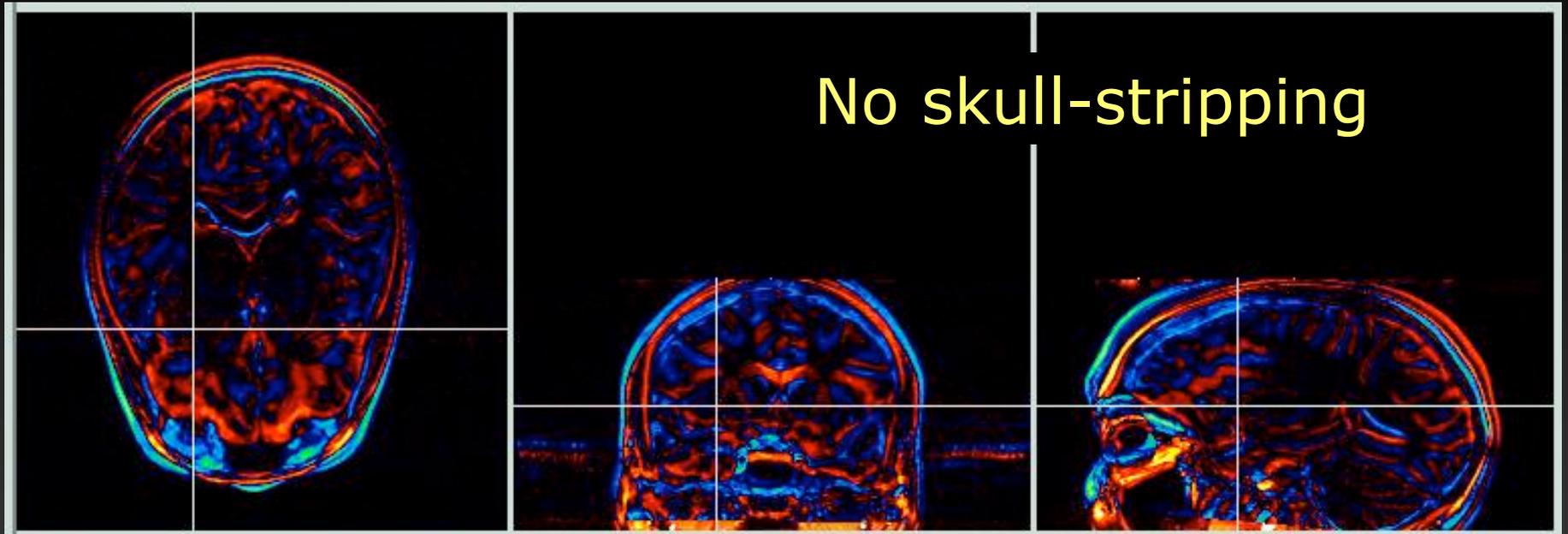


Inter-Subject Registration

No skull-stripping

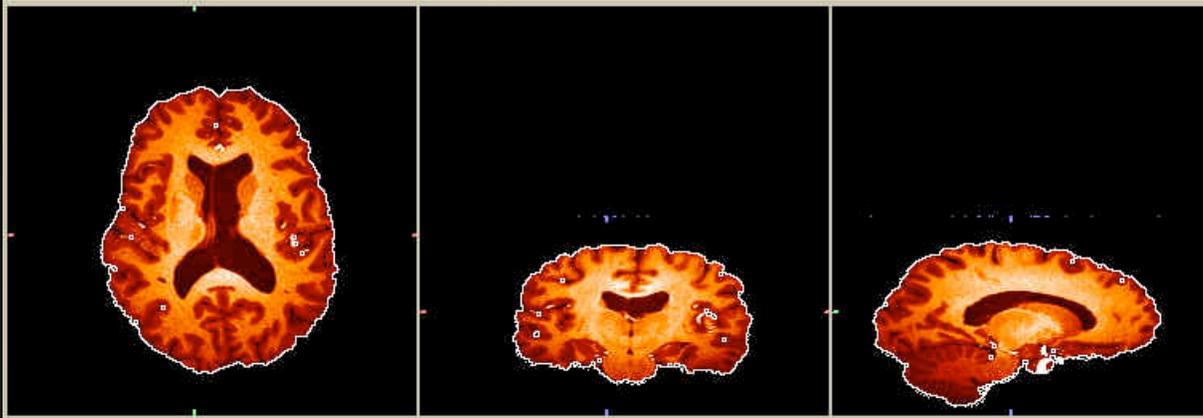


Inter-Subject Registration



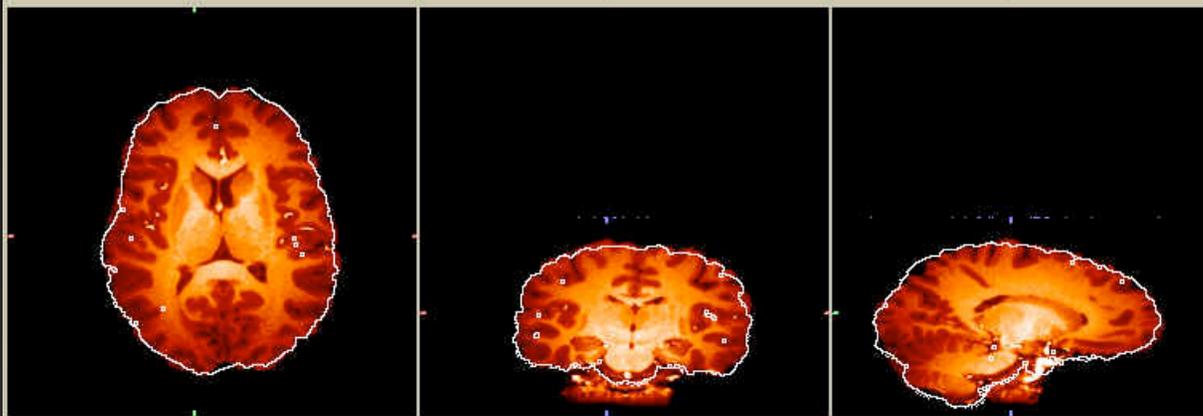
Inter-Subject Registration: Skull-stripped

Target



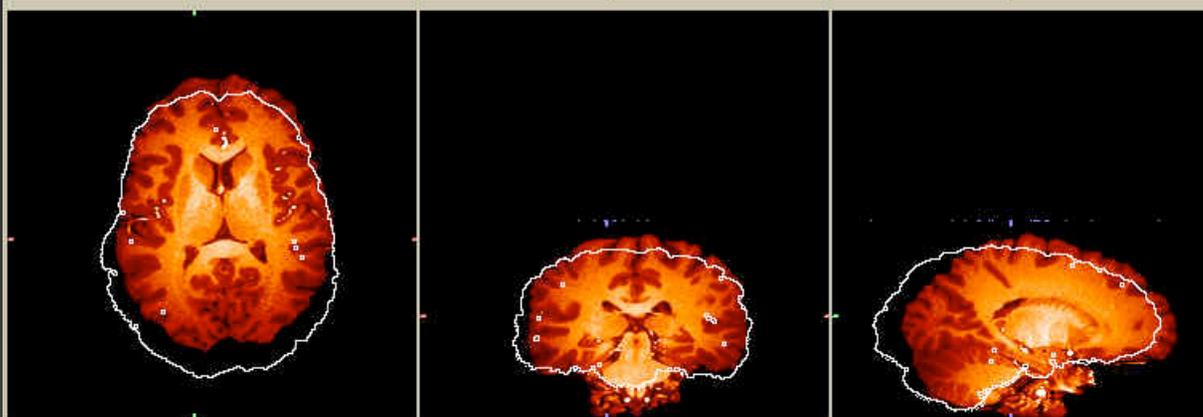
Note the large ventricles!

Coregistered Object

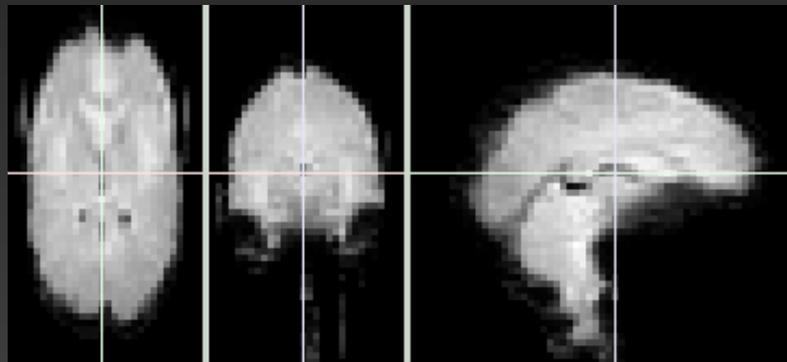
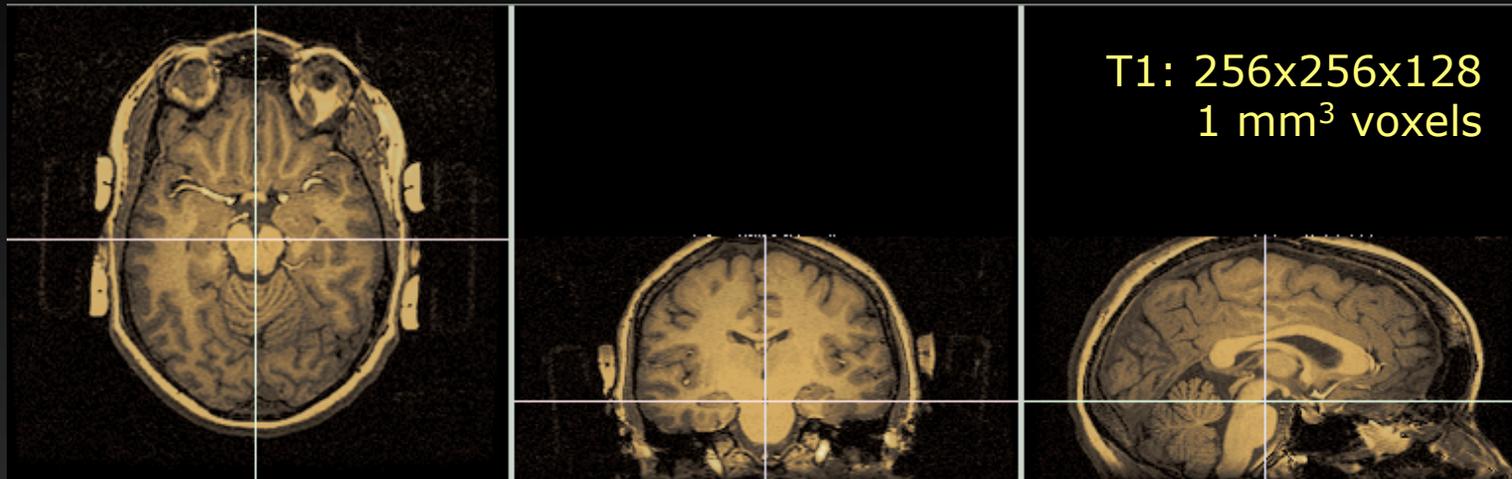


AIR:
12 parameters
Trilinear reslice
Align:163 sec
Reslice:9 sec

Original Object

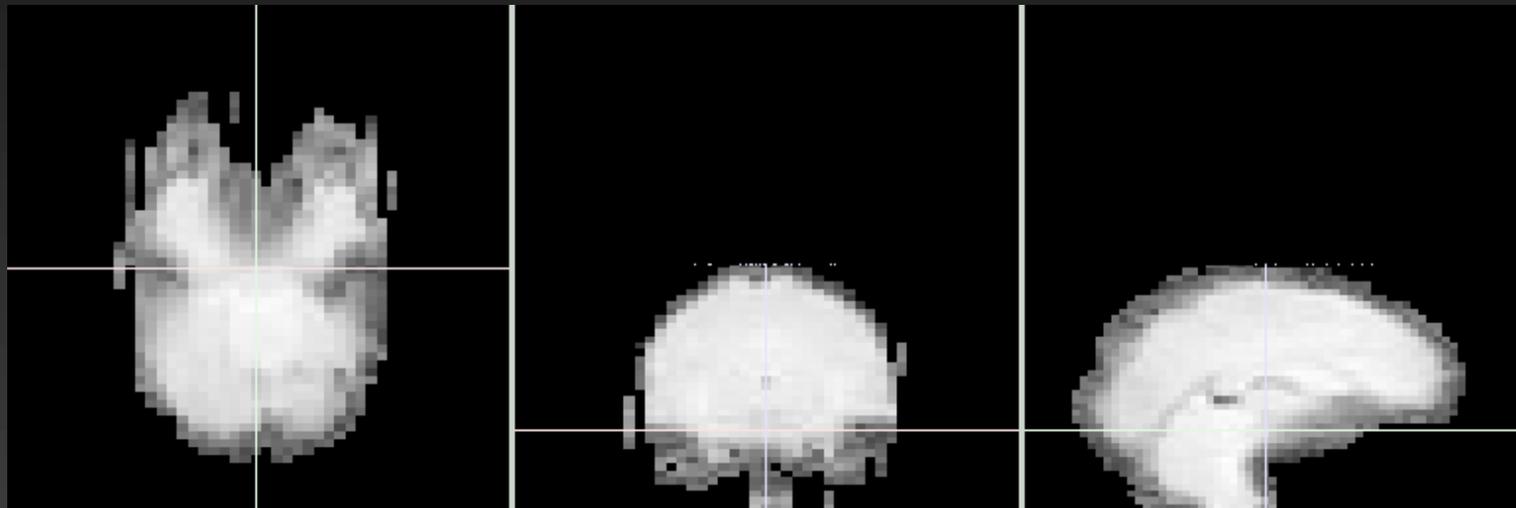
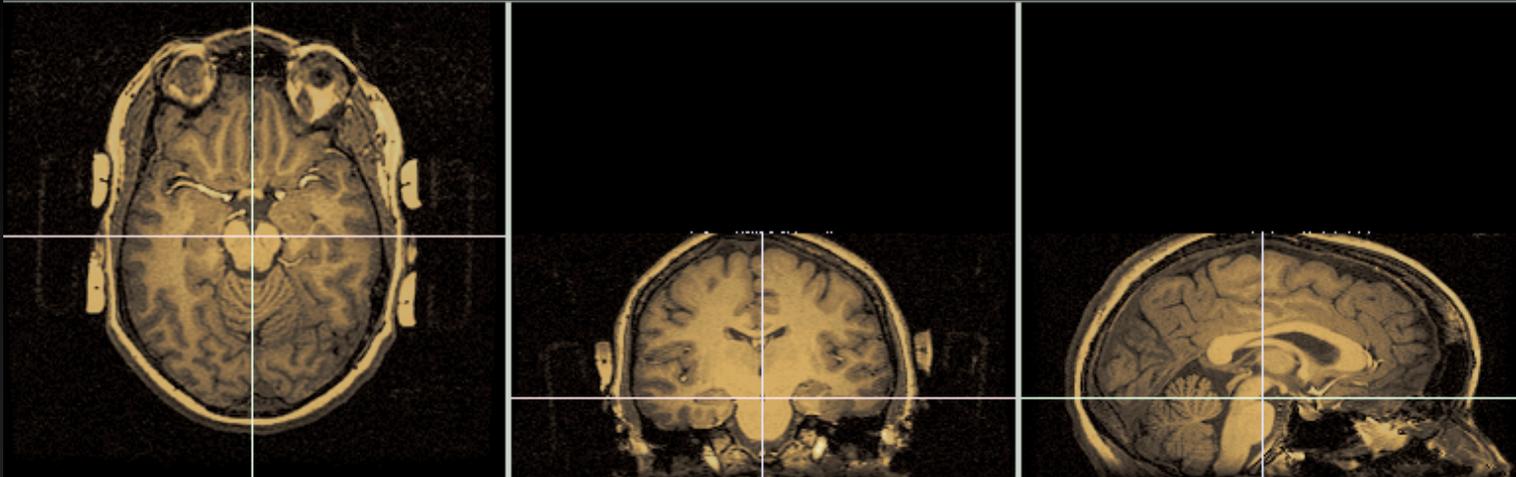


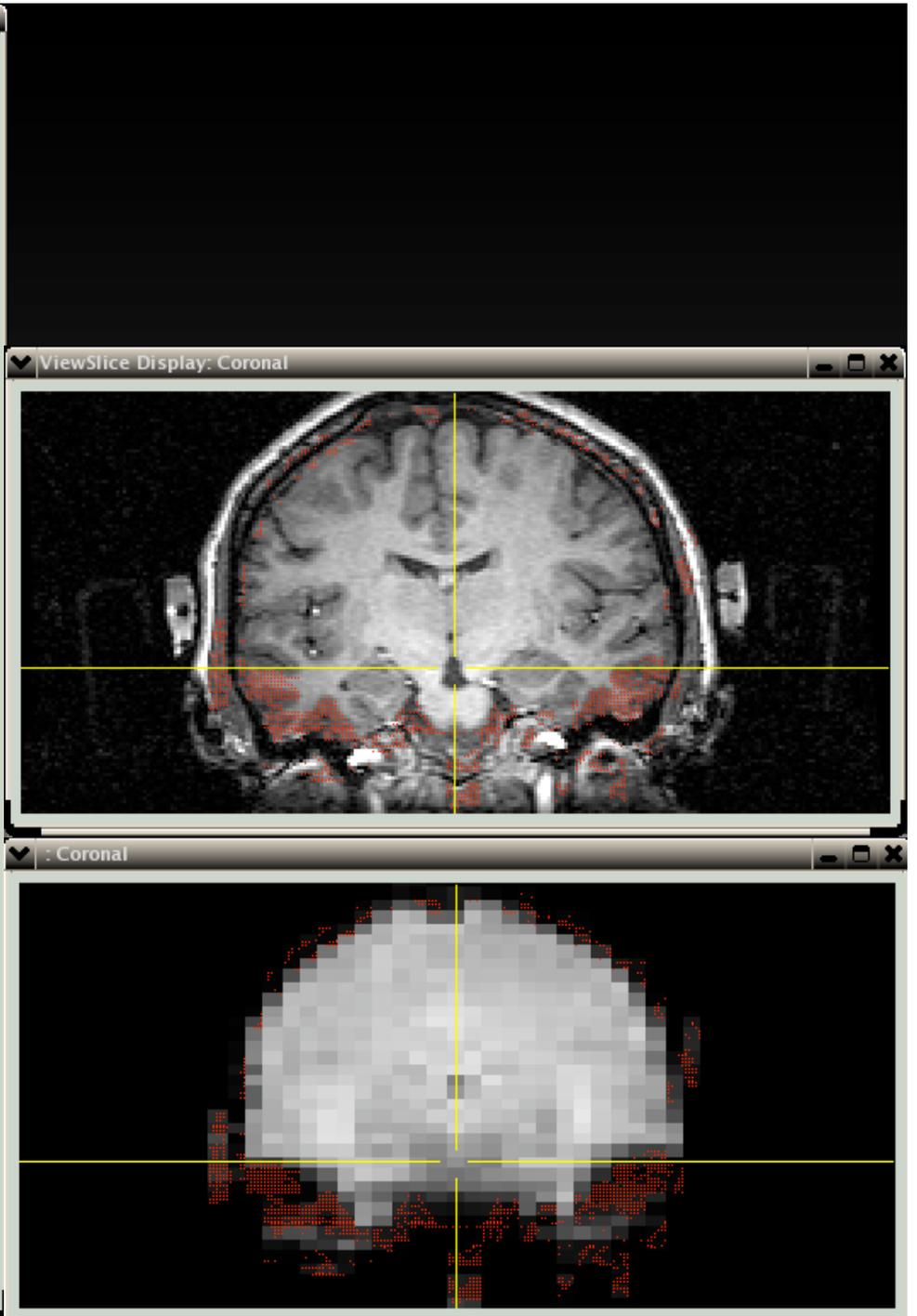
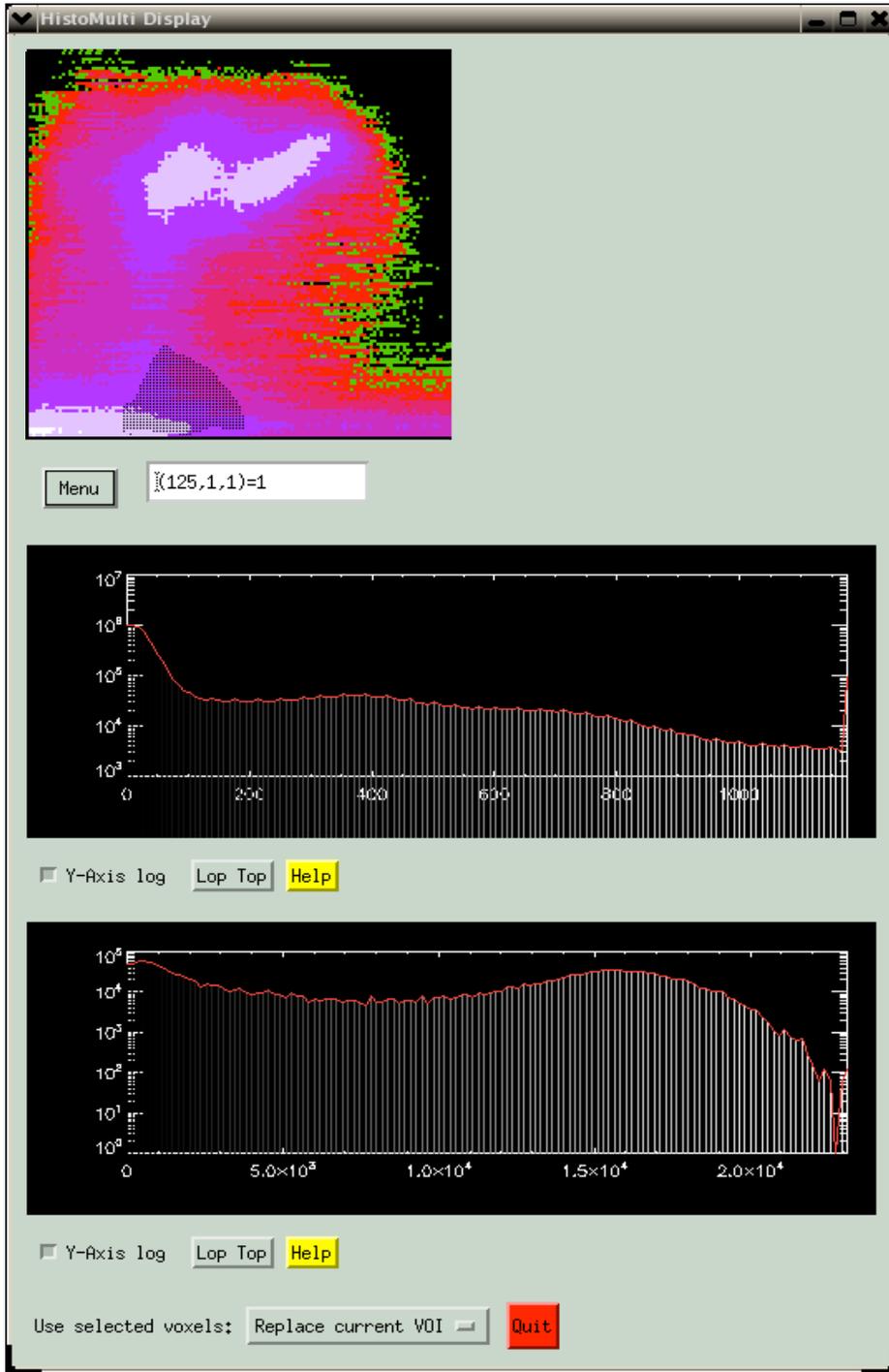
EPI registration



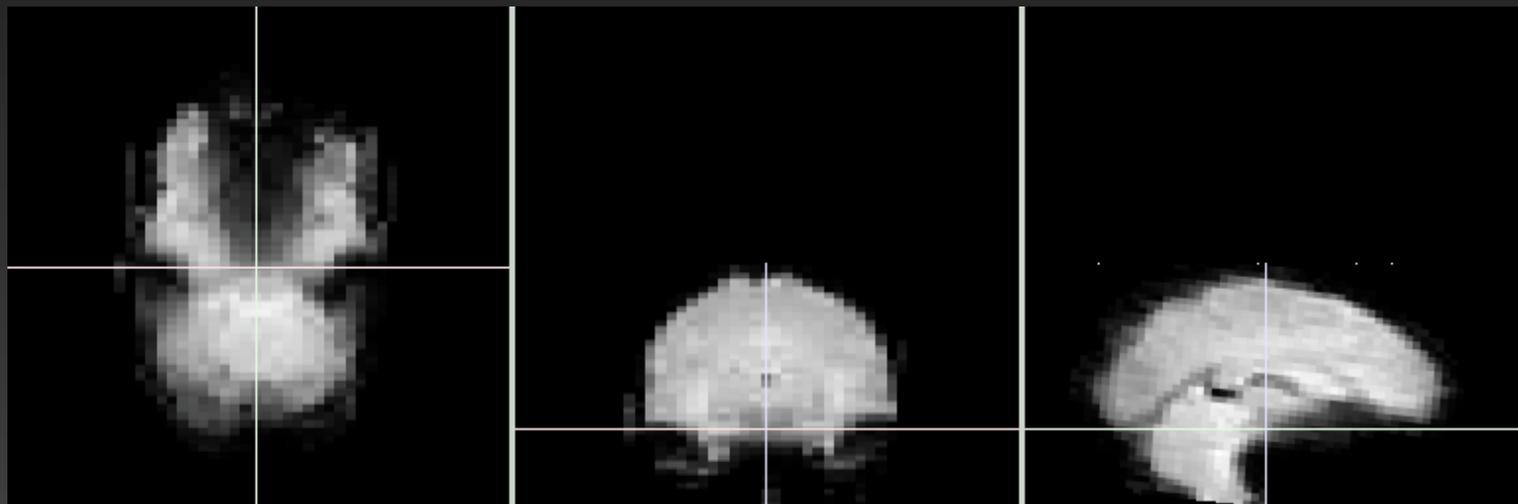
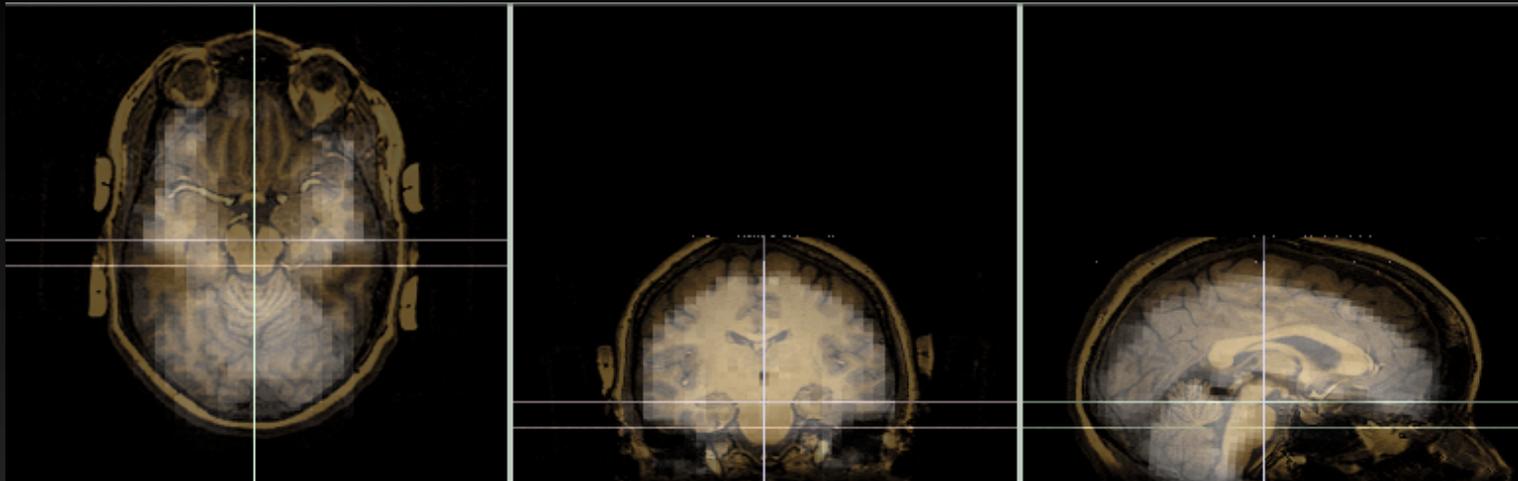
EPI: 64x64x30
5.0 x 3.0 x 3.0 mm voxels

EPI dropout (susceptibility) artifact

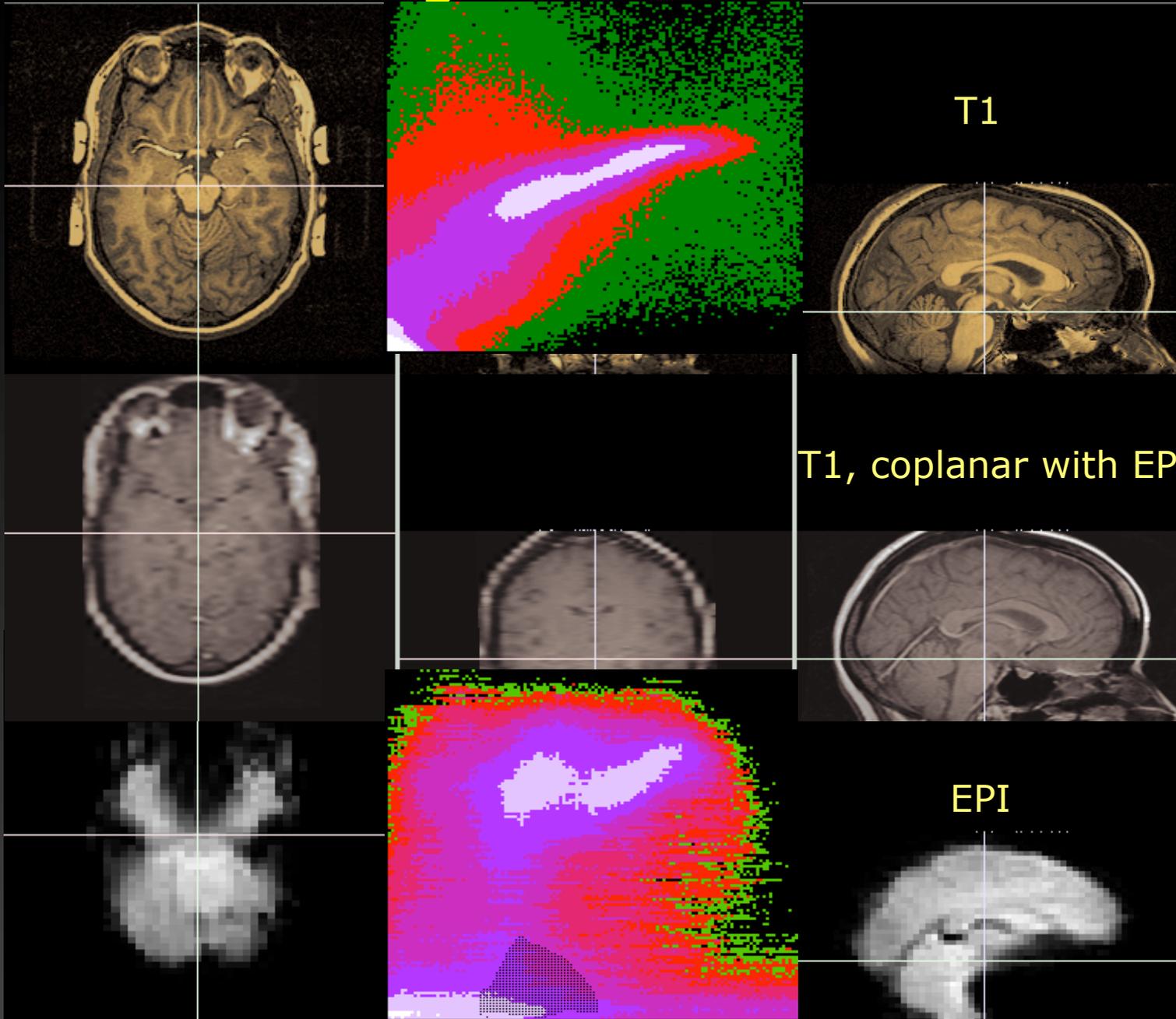




EPI registration



EPI registration solution



register

assume
no
movement

Adjusting functional activations using anatomical information

Functional Activations

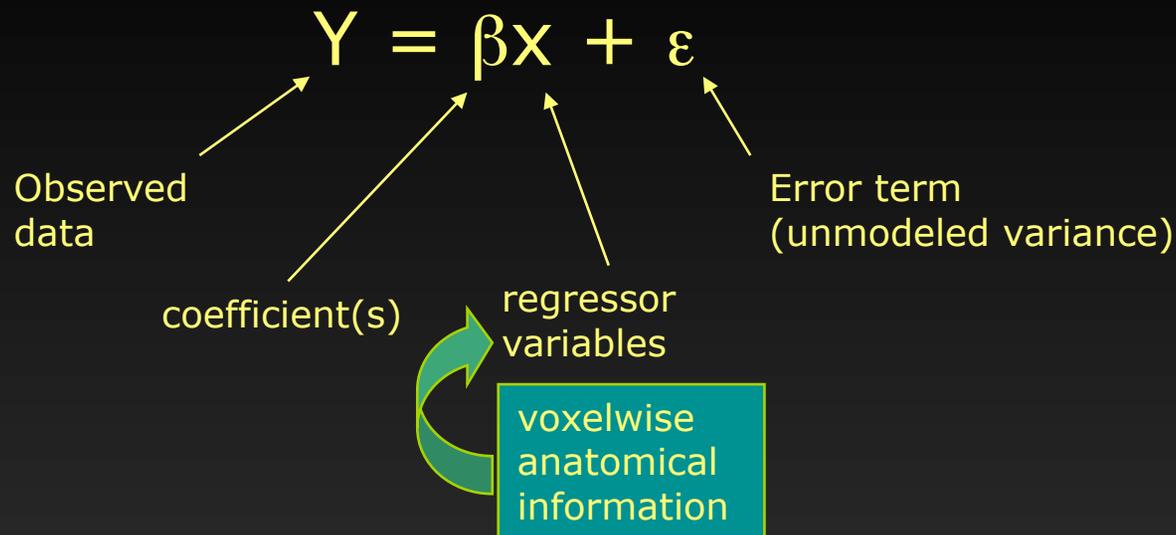
1. Difference in a specific metabolic process which influences measured signal.
2. Difference in tissue composition within a supposedly homogenous structure.
3. Misregistration of a structure to the target template.
4. Partial volume effect (PVE), a special case of spatial blurring.

VBM Activations

1. Differences in the tissue component of a structure (e.g. more WM in the thalamus).
2. Misregistration: underlying differences in structure shape not removed by the coregistration process.



General Linear Model



statistical parametric map

$$t = \text{effect} / \text{variance} \sim \beta / \epsilon$$

Does NOT ask, "Where is the effect large?", but rather "Where is the effect statistically reliable?"

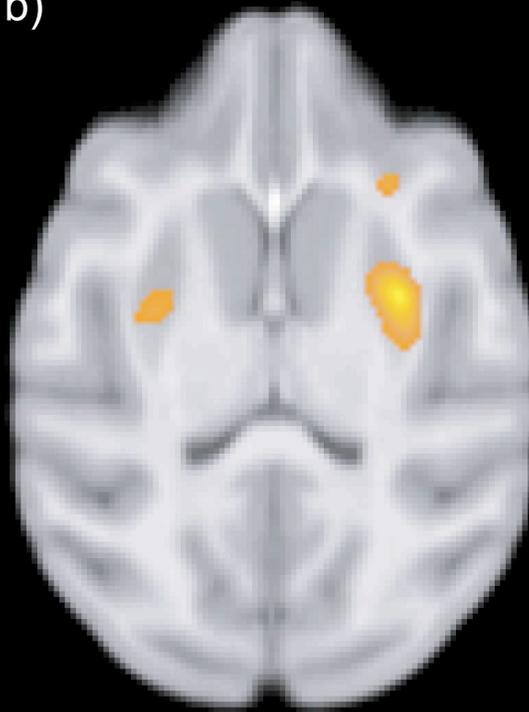
PET FDG rhesus

1a)



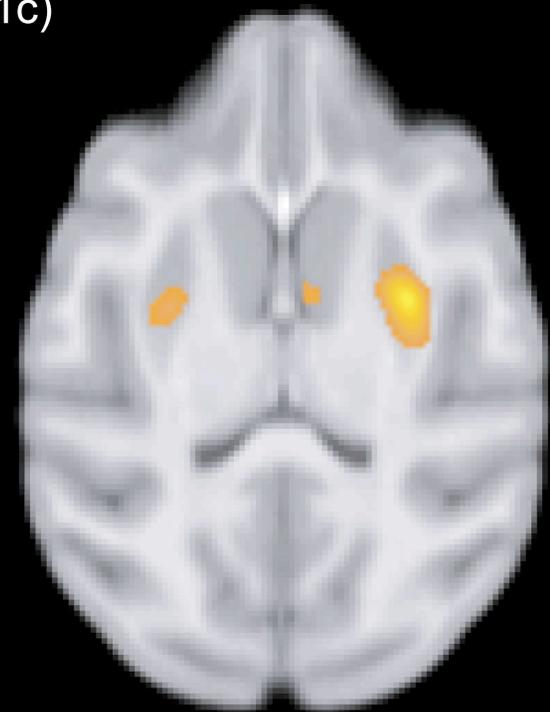
GMP Difference Clusters

1b)



Functional Activation Clusters

1c)

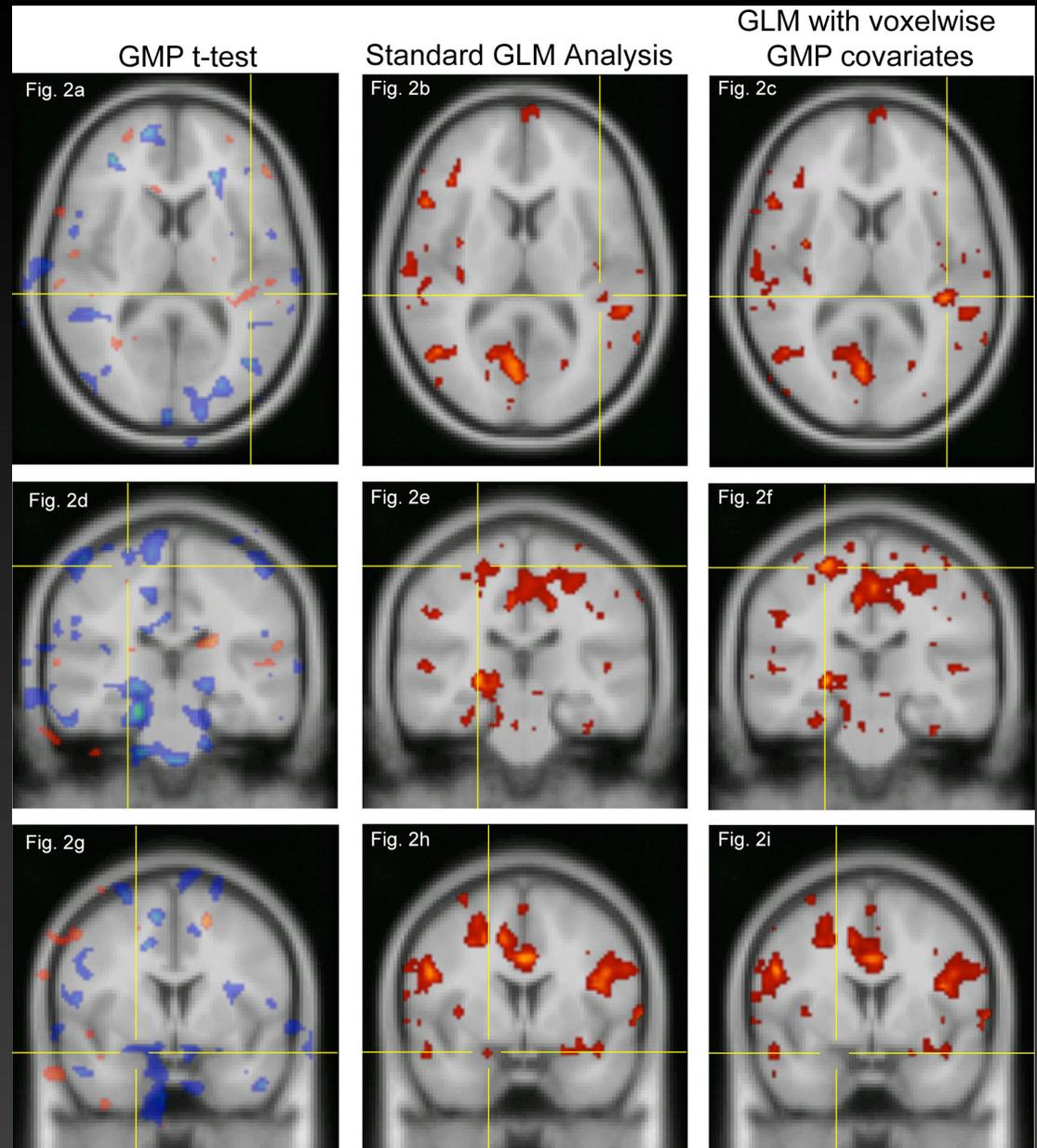


Functional Activation Clusters
After Covarying for GMP

Human fMRI

Functional activation increases
In both size and magnitude.

Functional activation decreases
(falls below statistical threshold).



Inter-Subject Registration Gone Awry

or, why visual inspection is important

