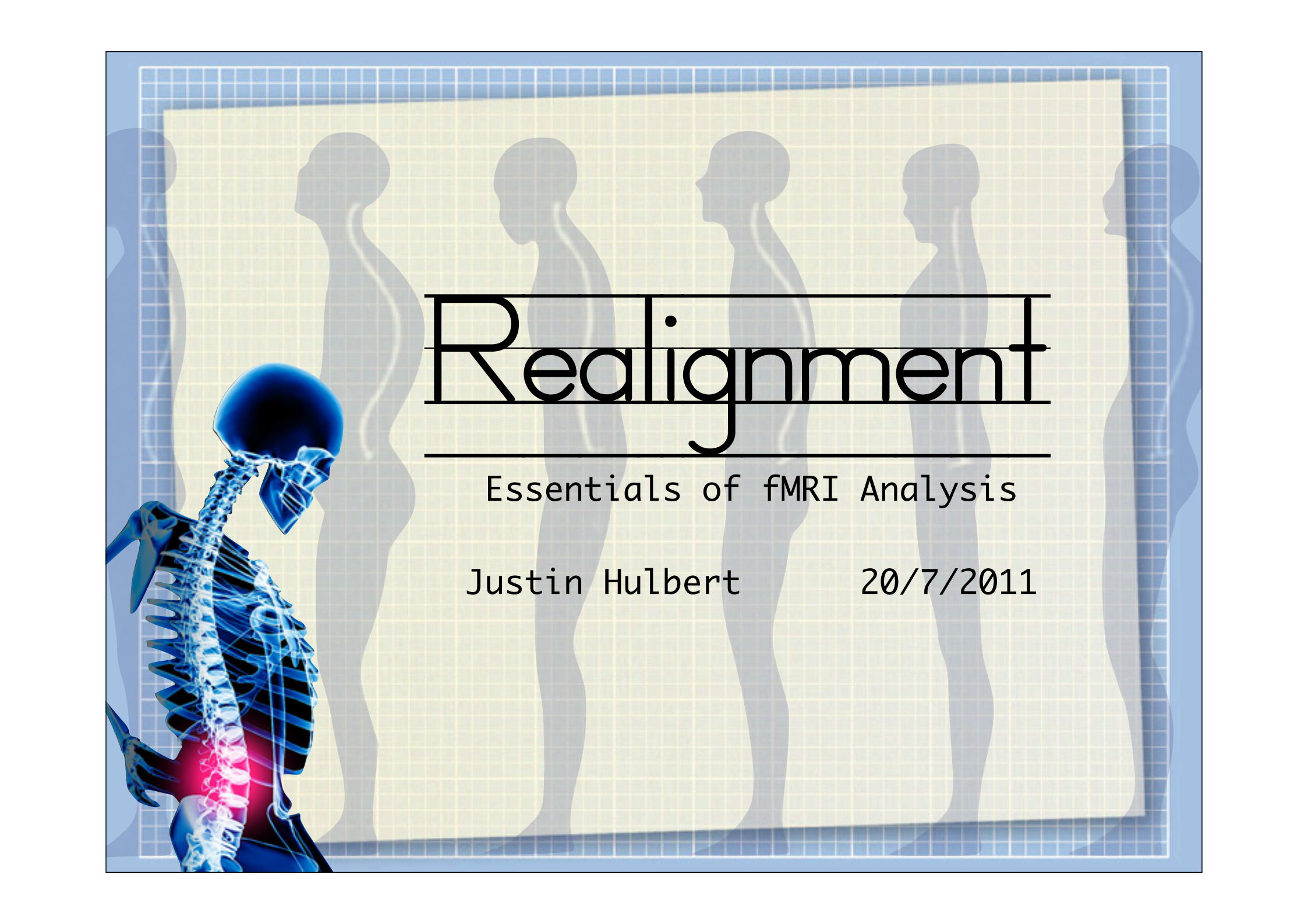


Realignment

Essentials of fMRI Analysis

Justin Hulbert

20/7/2011



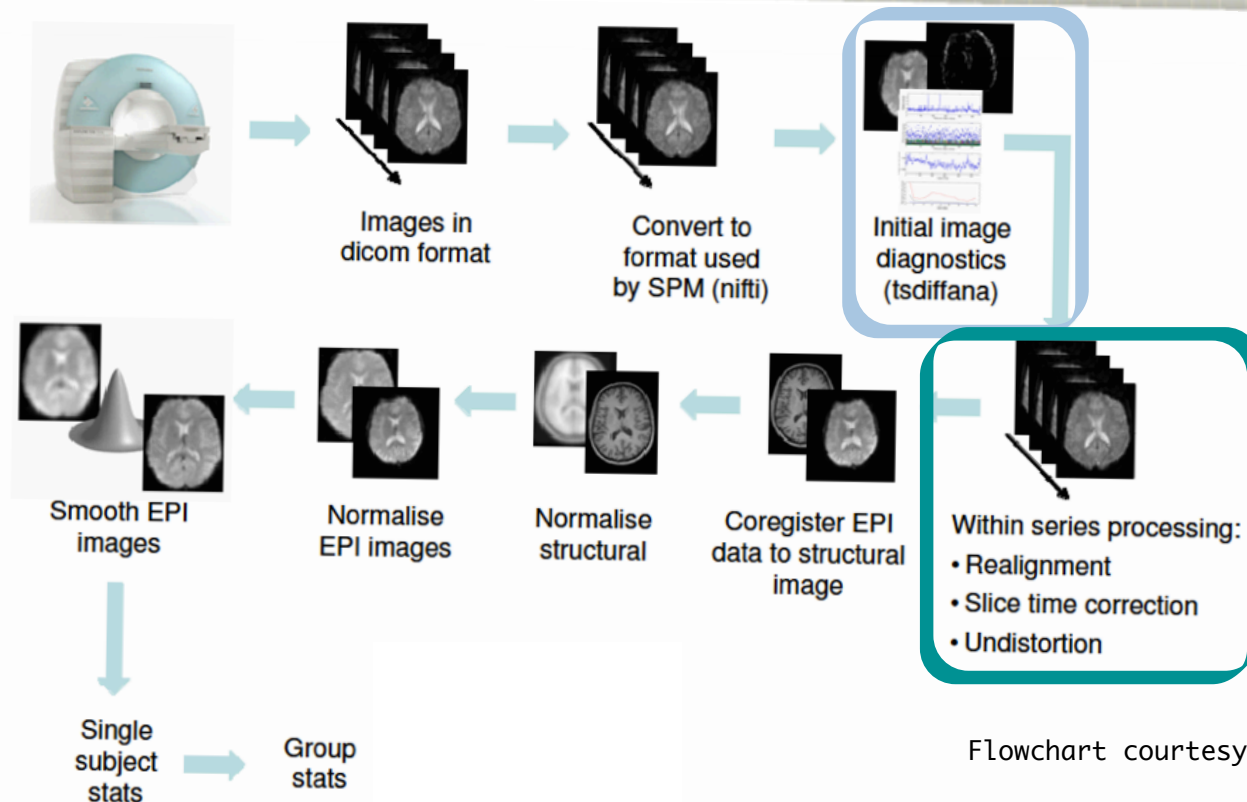
Realignment

Essentials of fMRI Analysis

Justin H.

20/7/2011

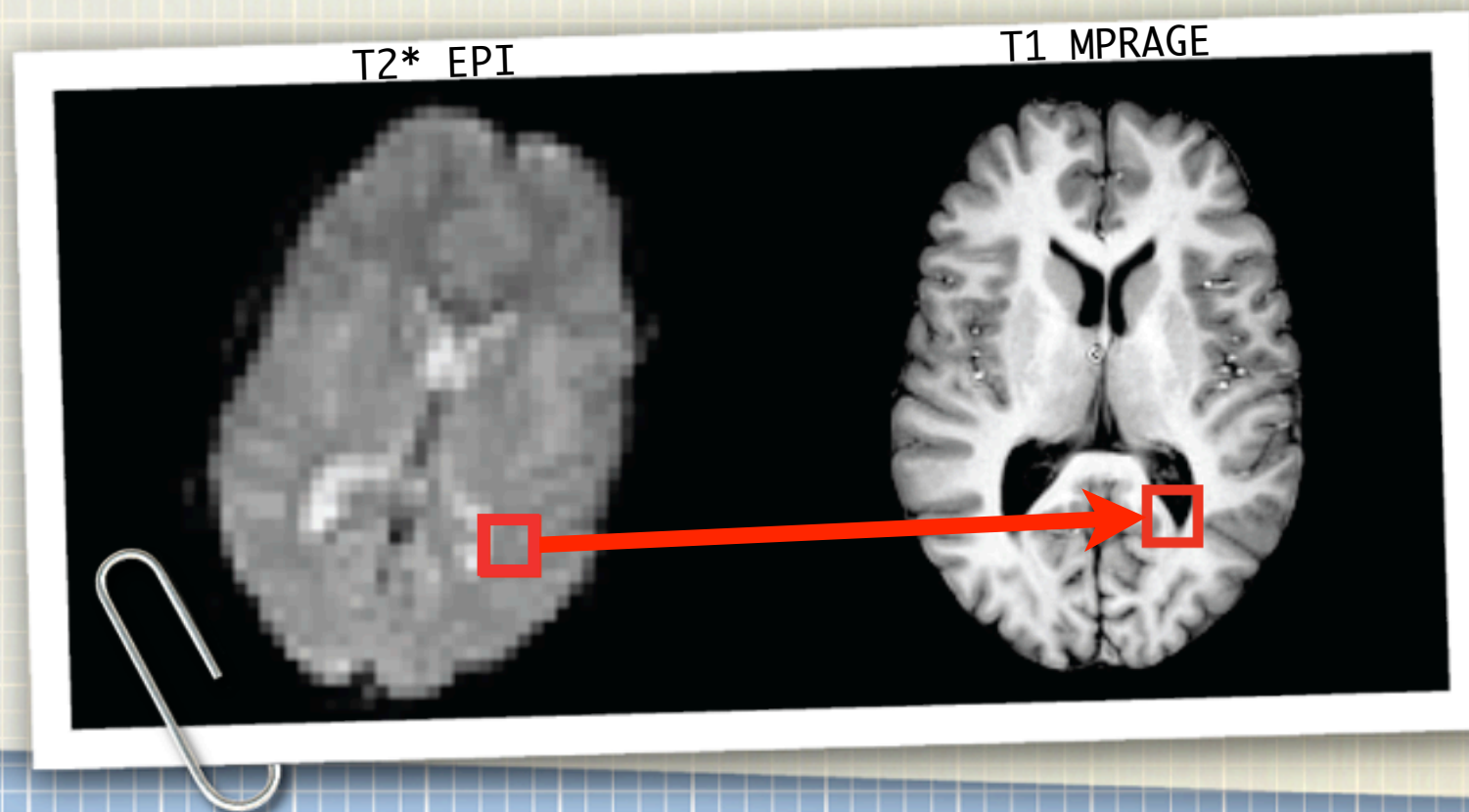
Data Analysis: A Birdseye View



Flowchart courtesy Russell Thompson

Where Is My Mind?

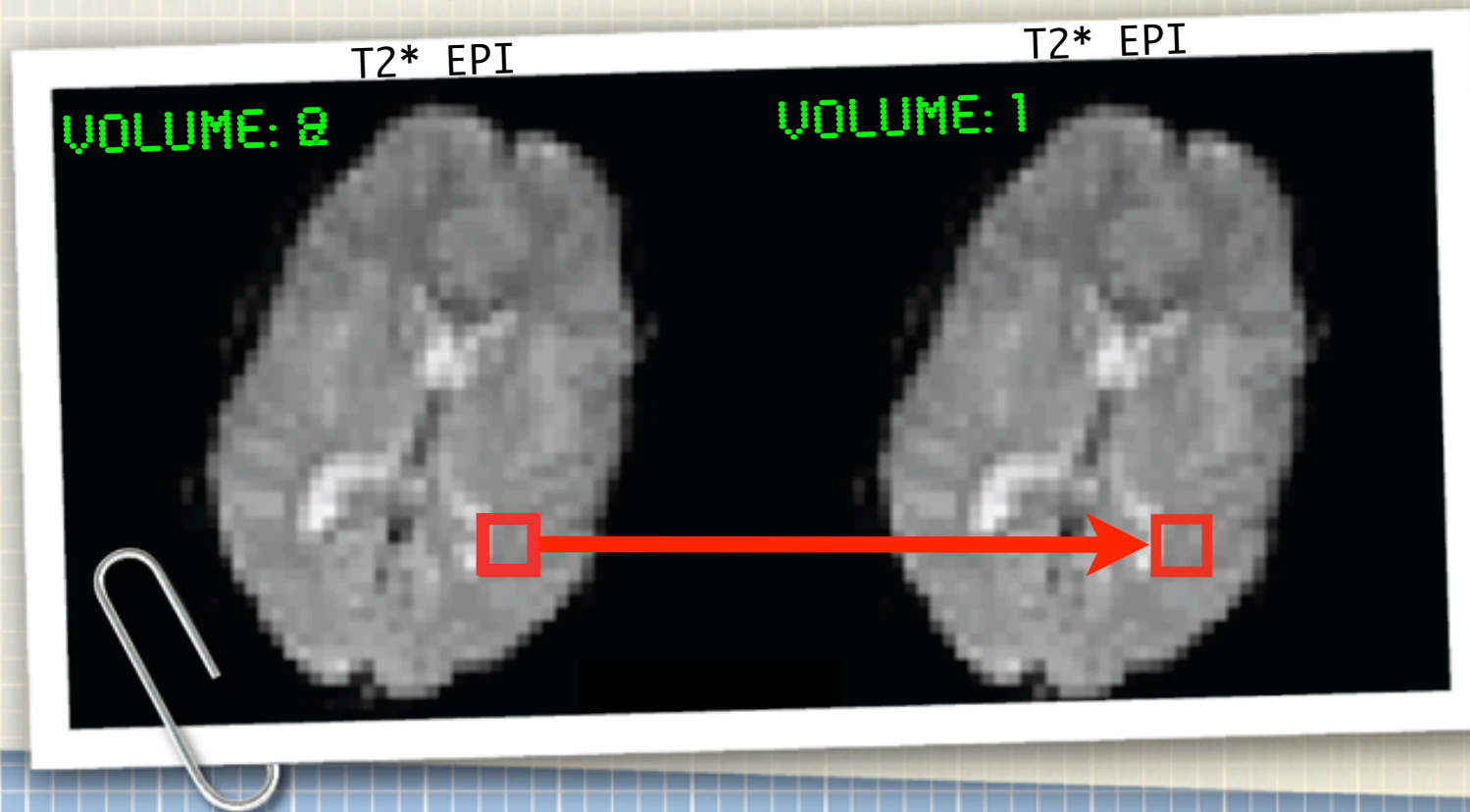
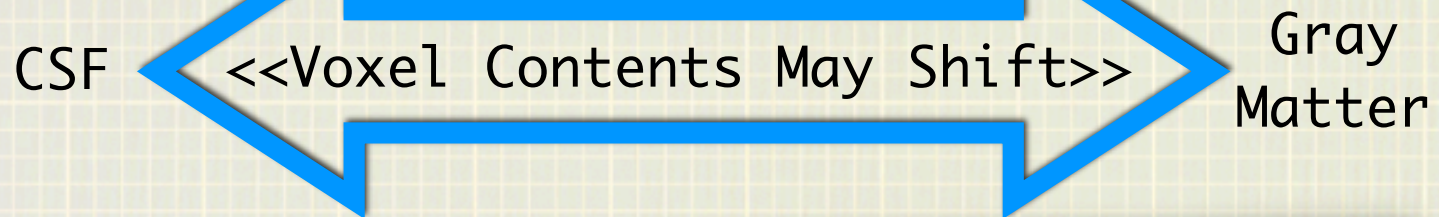
Co-Registration: Aligning two images of different modalities from the same individual





**THE
REALIGNMENT
ZONE**

The Problem



The Goal: Compare Like to Like

Remove movement arti[e]facts in fMRI time-series

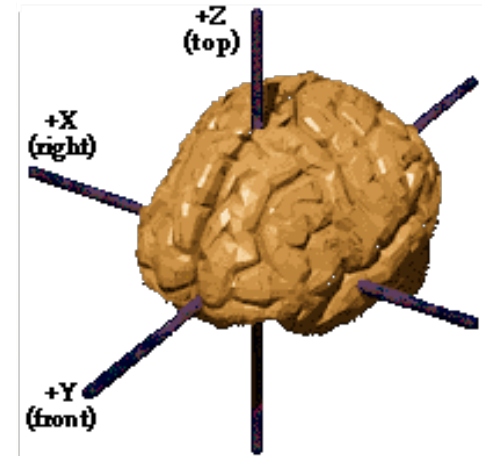
- ▶ Increases SNR by reducing residual noise
- ▶ Reduces likelihood of false positive due to task-correlated motion
 - ▶ But can hurt sensitivity to real effects



Six Rigid Body Transformation

Parameters:

3 Flavours of Translation



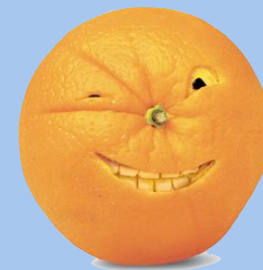
Side-to-Side

Translation in X



Front-to-Back

Translation in Y
(Different than Zoom)



Top-to-Bottom

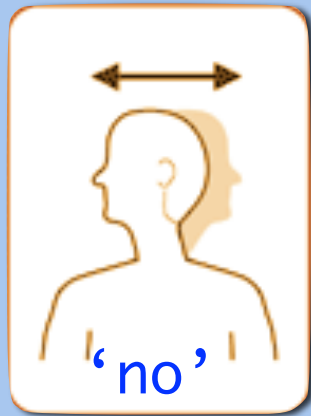
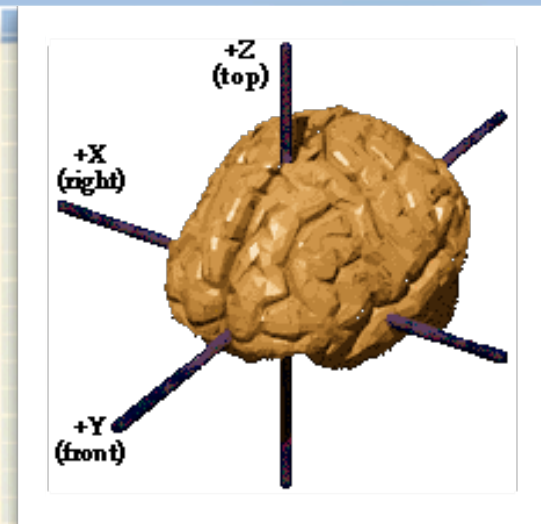
Translation in Z [Z]



Six Rigid Body Transformation

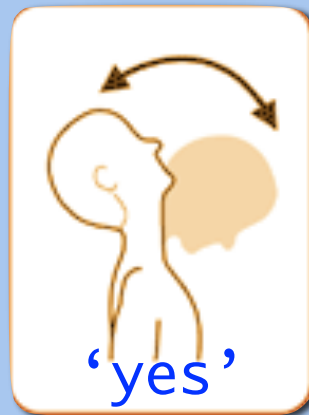
Parameters:

3 Flavours of Rotation



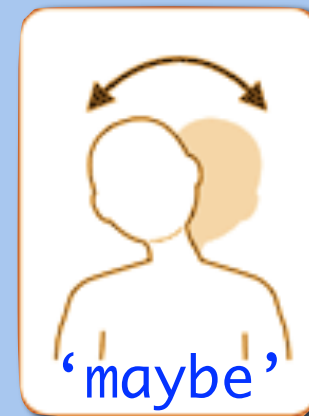
Yaw

Rotation around Z [Z]



Pitch

Rotation around X



Roll

Rotation around Y



Solutions*

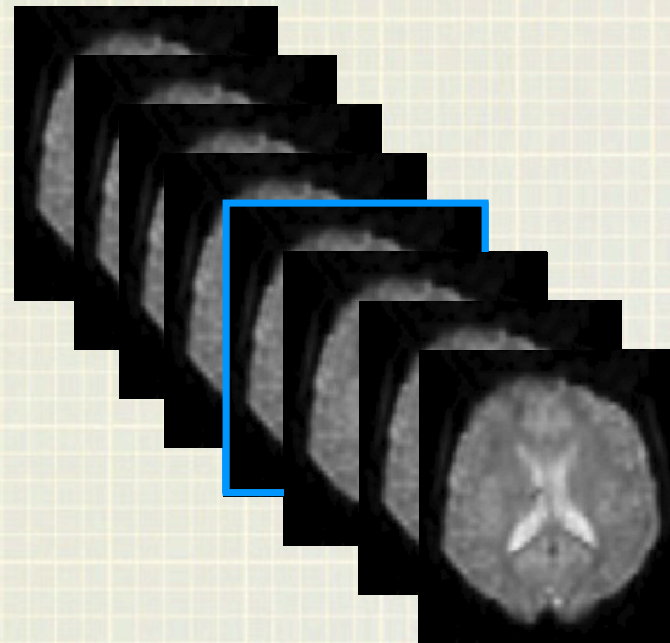
- 1) Prevention
 - a. Comfortably lock down
 - ▶ Padding, bite bar,...
 - b. Instructions
 - ▶ Lie still!
 - ▶ Don't talk b/t runs!
 - ▶ Minimiz[s]e swallowing!
 - c. Design
 - a. Keep scan time reasonable
- 2) Realignment (Motion Correction)
 - a. Prospective Movement Correction (PACE)
 - ▶ Only rec. for real-time
 - b. Offline pre-processing
 - c. Include motion parameters
- 3) Reject bad data



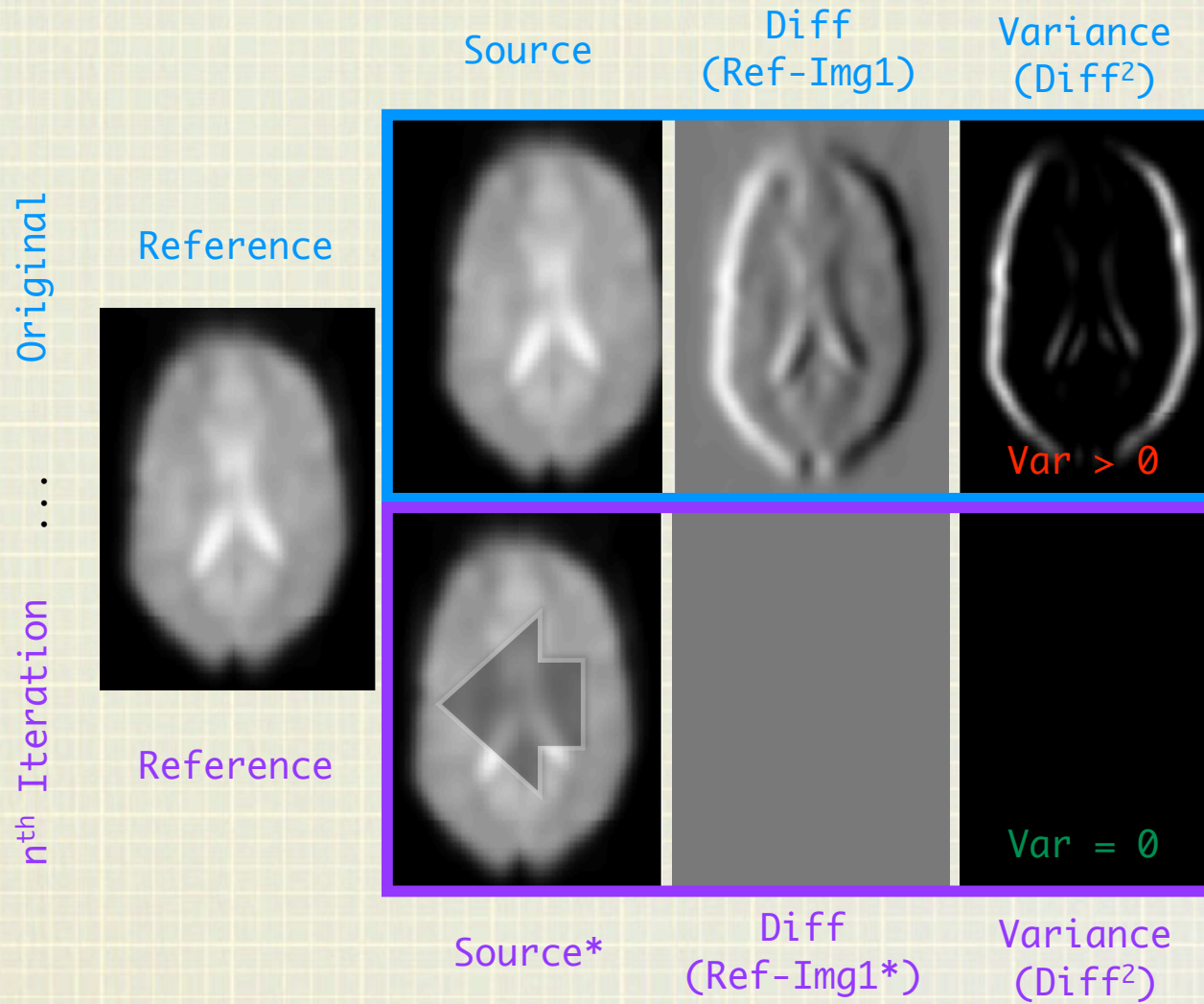
*nothing's perfect

DIY: Realignment

1. Choose a reference image
 - Not necessarily the very first (dummy scans)
 - Should be representative & reasonably close in time to the structural
2. Registration
 - Estimate the 6 transformation parameters b/t each image & reference
 - Minimiz[s]e variance
3. Apply transformation (re-slice)
 - Re-sample each imaging according to the transformation parameters
 - *NOT necessary now for every image if later normaliz[s]ing

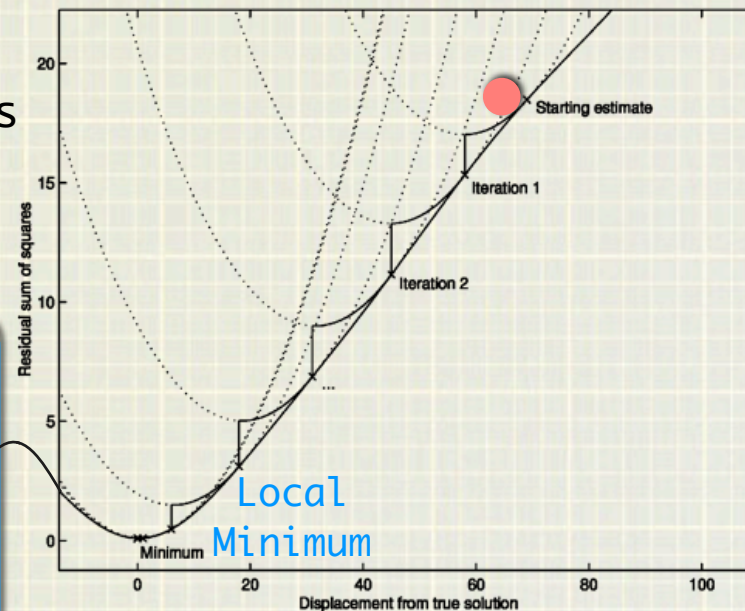
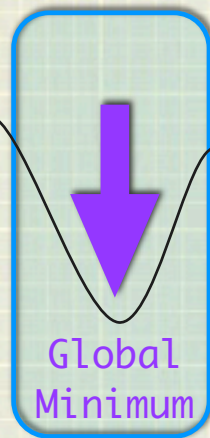


Optimiz[ing] the Cost Function



Gauss-Newton Algorithm

- Provides a systematic way of modifying the parameters at each iteration
- Attempts to minimize the mean of squared difference between two images
- Minimum is estimated by fitting a quadratic at each iteration
- We slowly build up a full transformation matrix out of this



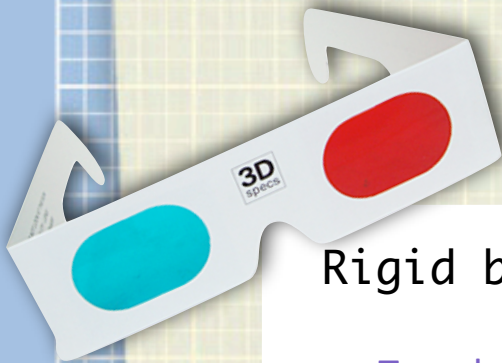
(I) Registration



Affine transformations can be represented in matrix form:

Transformation
(mapping) Parameters

$$\begin{array}{c} \text{New} \end{array}
 \begin{bmatrix} x_1 \\ y_1 \\ z_1 \\ 1 \end{bmatrix}
 =
 \begin{bmatrix} m_{11} & m_{12} & m_{13} & m_{14} \\ m_{21} & m_{22} & m_{23} & m_{24} \\ m_{31} & m_{32} & m_{33} & m_{34} \\ 0 & 0 & 0 & 1 \end{bmatrix}
 \times
 \begin{array}{c} \text{Original} \end{array}
 \begin{bmatrix} x_0 \\ y_0 \\ z_0 \\ 1 \end{bmatrix}$$



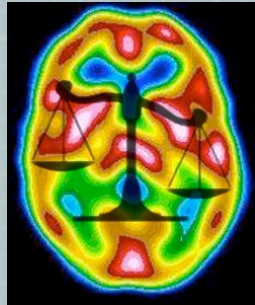
Rigid body transformations parameterized by:

Translations	Pitch about X axis	Roll about Y axis	Yaw about Z axis
$ \begin{pmatrix} 1 & 0 & 0 & X_{\text{trans}} \\ 0 & 1 & 0 & Y_{\text{trans}} \\ 0 & 0 & 1 & Z_{\text{trans}} \\ 0 & 0 & 0 & 1 \end{pmatrix} $	$ \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & \cos(\Phi) & \sin(\Phi) & 0 \\ 0 & -\sin(\Phi) & \cos(\Phi) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} $	$ \begin{pmatrix} \cos(\Theta) & 0 & \sin(\Theta) & 0 \\ 0 & 1 & 0 & 0 \\ -\sin(\Theta) & 0 & \cos(\Theta) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} $	$ \begin{pmatrix} \cos(\Omega) & \sin(\Omega) & 0 & 0 \\ -\sin(\Omega) & \cos(\Omega) & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} $

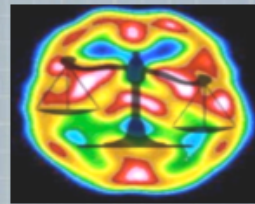
<<SPM does not care about the order of transformations, at least

Order of Operations

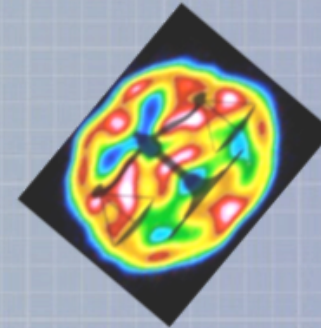
Original



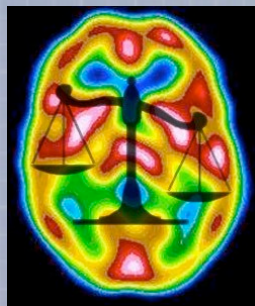
50° around Y



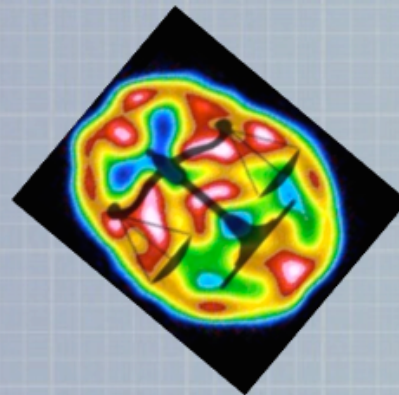
50° around Z



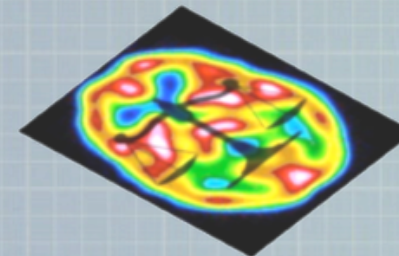
Original



50° around Z

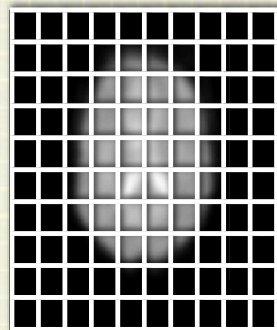


50° around Y

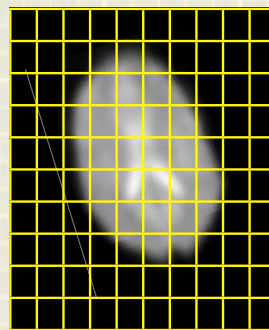


(2) Transformation (Reslicing)

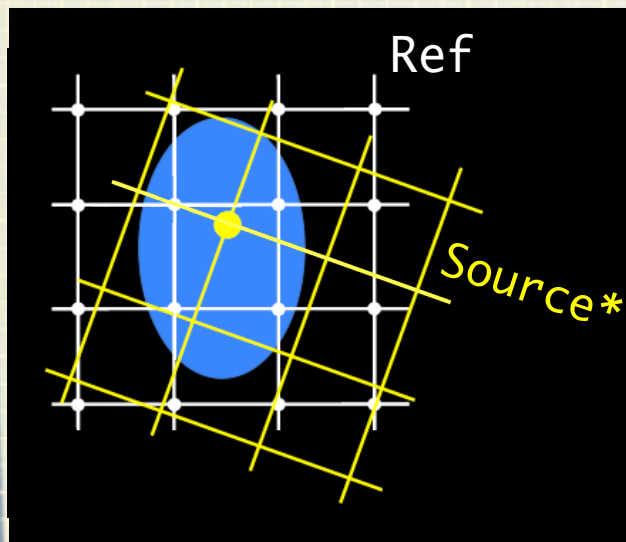
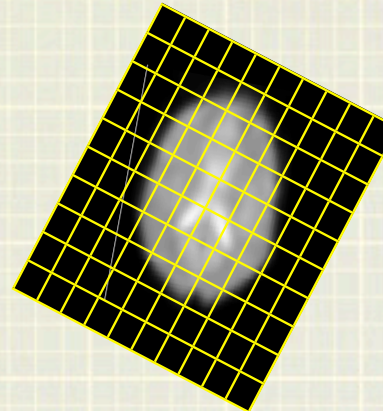
Reference



Source

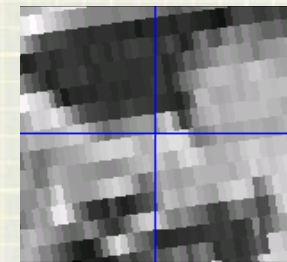


Source*

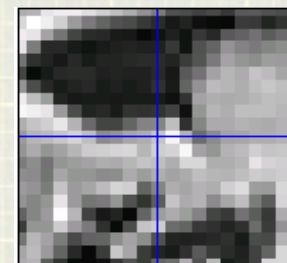


- Transform according to the estimated parameters & resample to match the reference grid
- To do this, we need estimate intensity values between grid points
- So...interpolate!

Reoriented



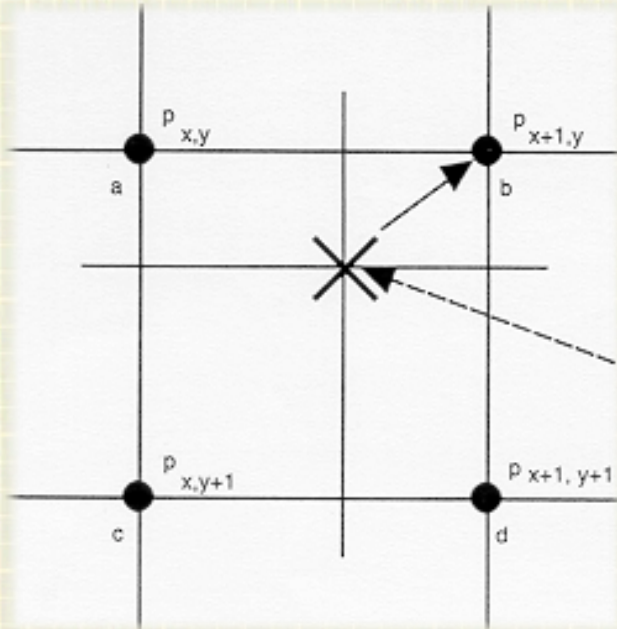
Re-sliced





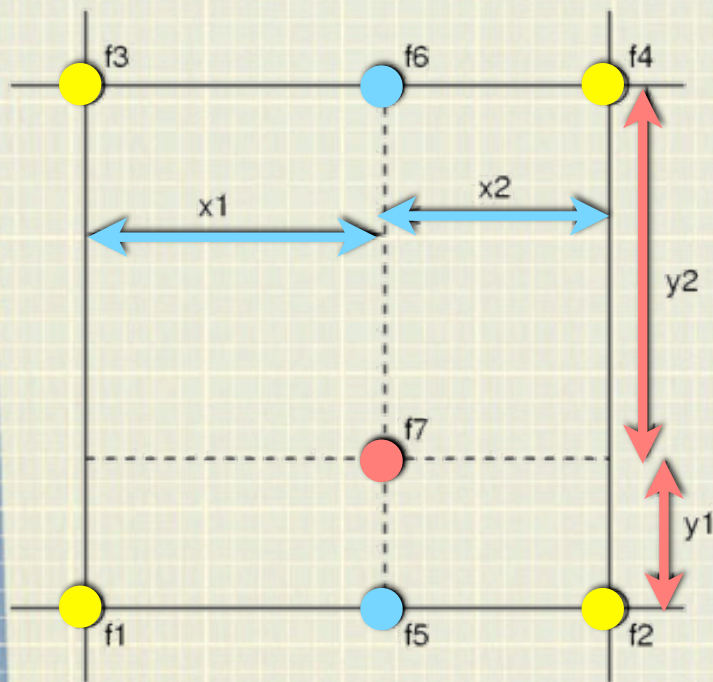
Nearest Neighbour

(Zero-Order Hold)



- Takes value of closest voxel
- Original voxel intensities preserved
- Very fast
- But...image is degraded considerably
- “Blocky” images

Trilinear Interpolation (First-Order Hold)



Represented in 2D for
illustration

○ Takes the weighted average of the neighboring voxels

○ $f_5 = f_1x_2 + f_2x_1$

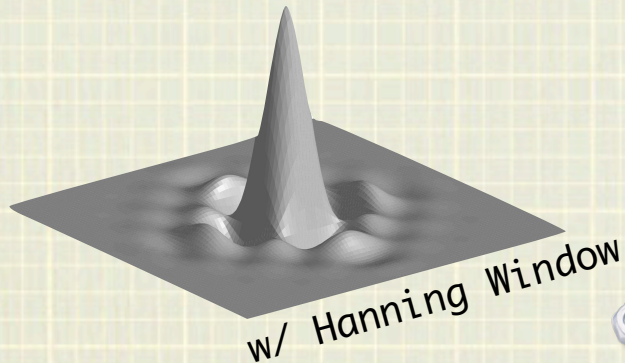
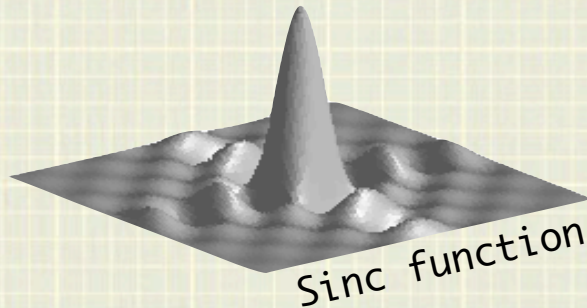
○ $f_6 = f_3x_2 + f_4x_1$

○ $f_7 = f_5y_2 + f_6y_1$

○ Slower but less blocky than nearest neighbor

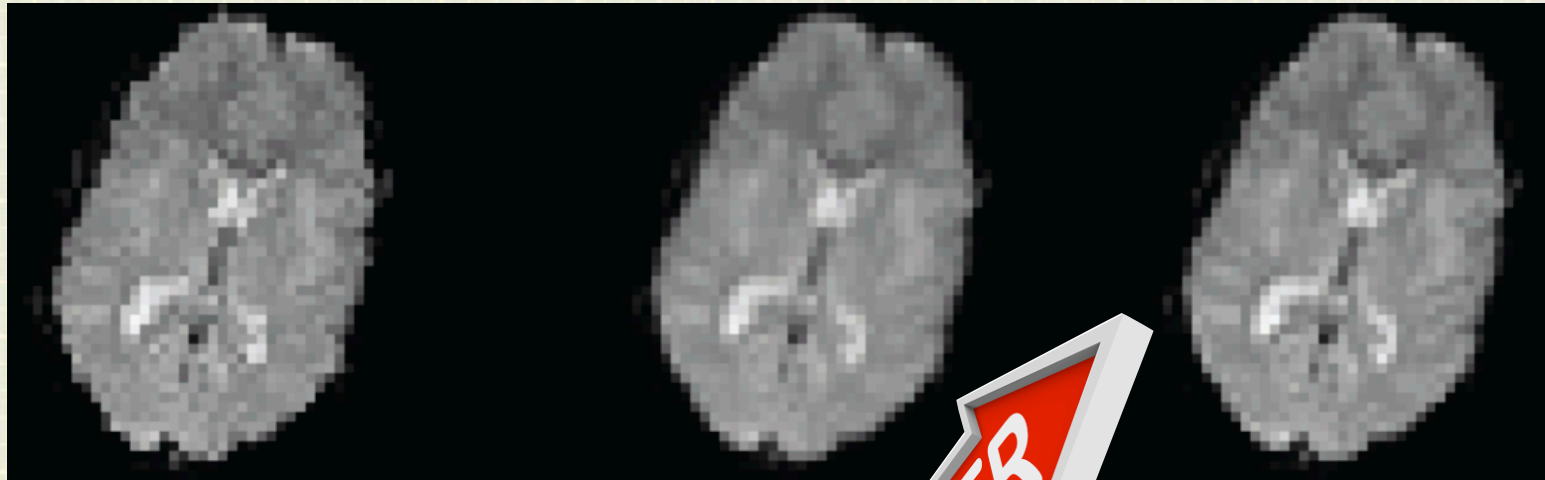
○ Loses some high frequency information (smoothing)

Windowed Sinc Interpolation



- Sinc interpolation gives results closest to a Fourier interpolation (which is ideal) but in real space
- Convolve sinc function centered on the point to be resampled
- Theoretically, every voxel in sample is used, but an approx. using subset of near neighbors speeds things up
 - Hence the 'window'
- Greatly reduces artifacts, but S-L-O-W
- Interpolation performed on each dimension sequentially

Results of Interpolation



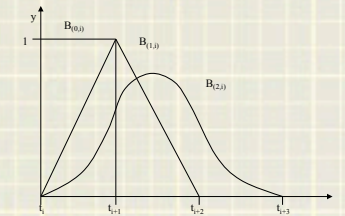
Nearest Neighbor

Trilinear

Sinc

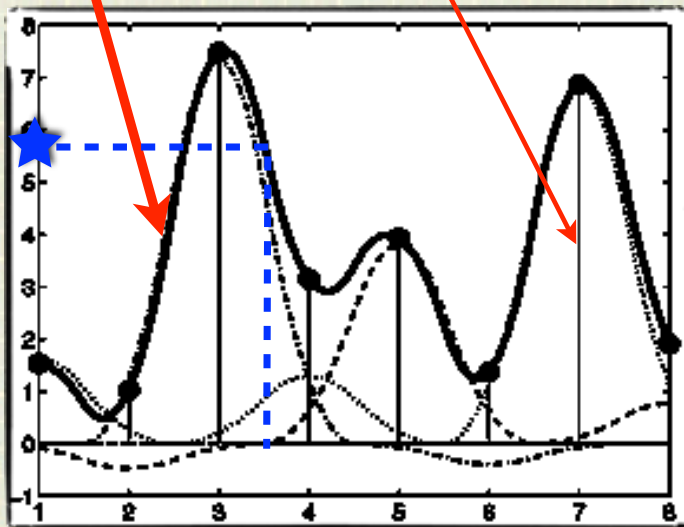


B[asis]-splines



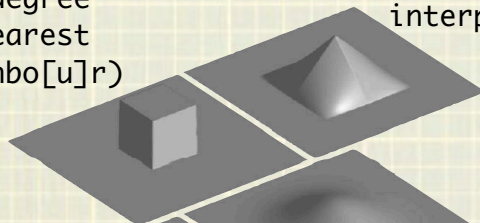
Smoothed Interpolated Function

Measured Voxel Value



1st degree
(bilinear/
trilinear
interpolation)

0 degree
(nearest
neighbo[u]r)

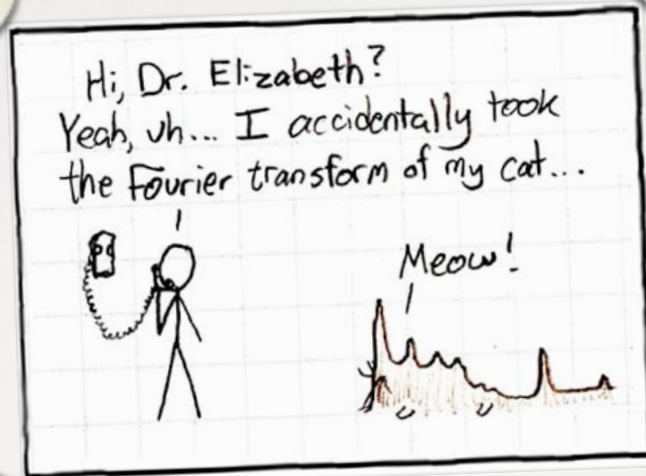


2nd degree

3rd degree

- A form of 'generalized interpolation'
- First transforms image into basis functions before applying local convolution
- Re-sampling involves computing linear combination of functions
- Done sequentially along each dimension
- Far more efficient than classical interpolation

Fourier Methods

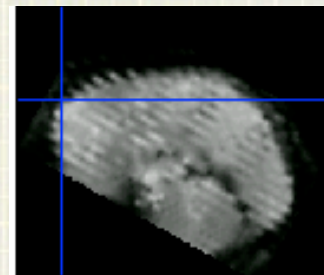


- Faster than higher-order interpolation
- Uses fast Fourier transforms
- Convolution performed rapidly in Fourier space
- However, can only handle translations (not really built for rotations currently)

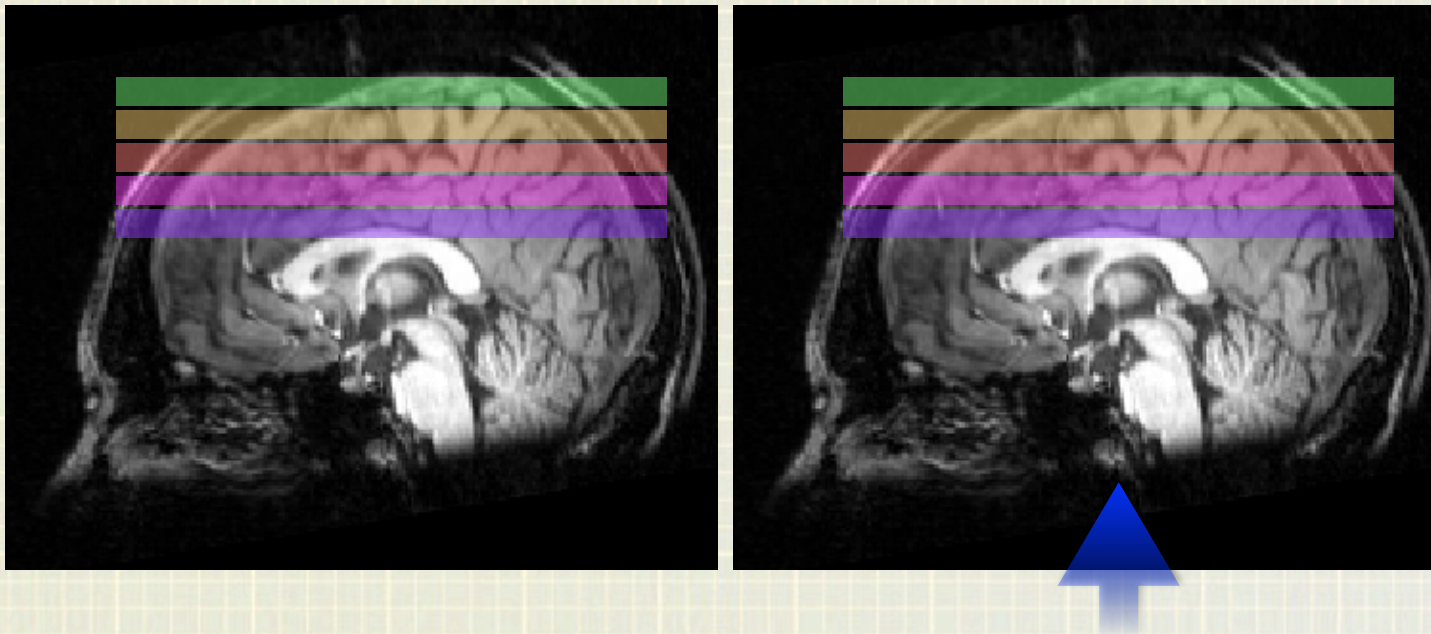
Residual Errors

- Post-realignment, still variance due to movement left over:
 - Can be due to shifts between and within slice acquisition
 - Interpolation arti[e]facts
 - Non-linear distortions due to inhomogeneities of magnetic field...
- Spin-history changes (@ their worst when acquired interleaved)
 - Residual magnetiz[s]ation effects of previous scans
 - Movement may make effective TR longer/shorter for some slices
- Adding motion parameters may help

Spin History
'Striping'



The Limits of Realignment



- 🔩 Make sure you have good coverage of ROI
- 🔩 If expect this problem, perhaps use PACE

SPM Walkthrough

1) Realign ("Est & Reslice")

2) Select images for each session. Don't include dummies; First should be 'good'

3) Speed (0.001) vs. Quality (1)

4) Separation (mm) b/t points sampled in ref (smaller = better, slower)

5) Use 1st image or run registration 2x

6) Higher degree = better, slower (uses more neighboring voxels)

7) Create 'Mean image only'*

8) Set interpolation degree (higher=slower/more neighbors)

SPM8 (Jh03): Menu

Batch Editor

File Edit View SPM BasicIO

Module List

Current Module: Realign: Estimate & Reslice

Help on: Realign: Estimate & Reslice

Data

Estimation Options

- . Quality 0.9
- . Separation 4
- . Smoothing (FWHM) 5
- . Num Passes
- . Interpolation 2nd Degree B-Spline
- . Wrapping No wrap
- . Weighting 0 files

Reslice Options

- . Resliced images All Images + Mean Image
- . Interpolation 4th Degree B-Spline
- . Wrapping No wrap
- . Masking Mask images
- . Filename Prefix r

Current Item: Data

New: Session

Edit Value

Data

Add new sessions for this subject. In the coregistration step, the sessions are first realigned to each other, by aligning the first scan from each session to the first scan of the first session. Then the images within each session are aligned to the first image of the session. The parameter estimation is performed this way because it is assumed (rightly or not) that there may be systematic differences in the images between sessions.

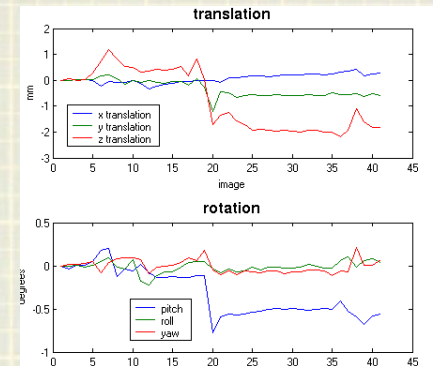
SPM8 (Jh03): Menu

*if NOT doing spatial normaliz[s]ation or need EPI undistortion, choose "All Images + Mean Image"

>this requires reslicing, otherwise, not necessary to do at this stage



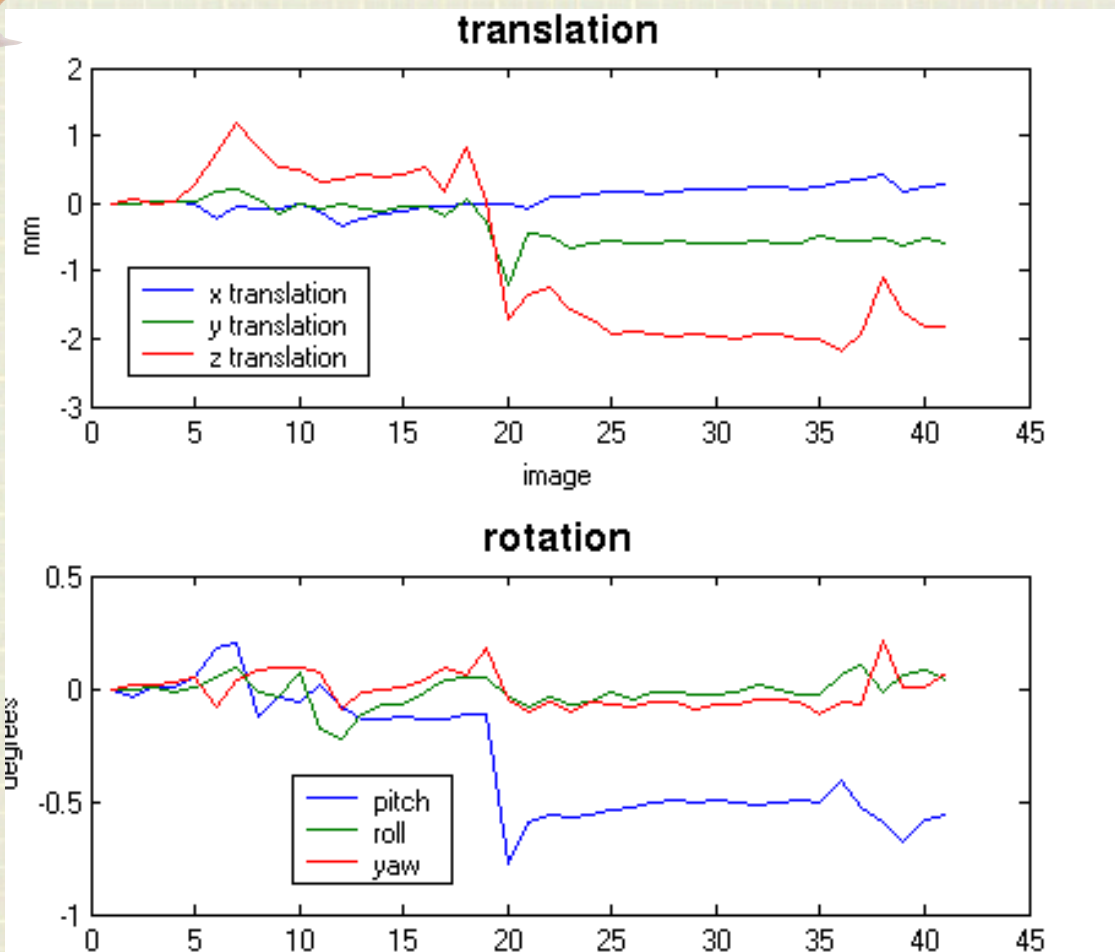
SPM Outputs



- `spm.ps`
- Graphs of the estimated motion
- `rp_[firstimage].txt`
- all realignment parameters to realign to the first image file
- Number of rows = number images in run
 - Need this for later stats & can be modeled as confounds
- `means*.nii`
- Mean of the realigned/resliced images, used in coregistration
- `r*.nii`
- Resliced images (only required if NOT doing spatial normalization or IF planning to apply EPI undistortion)

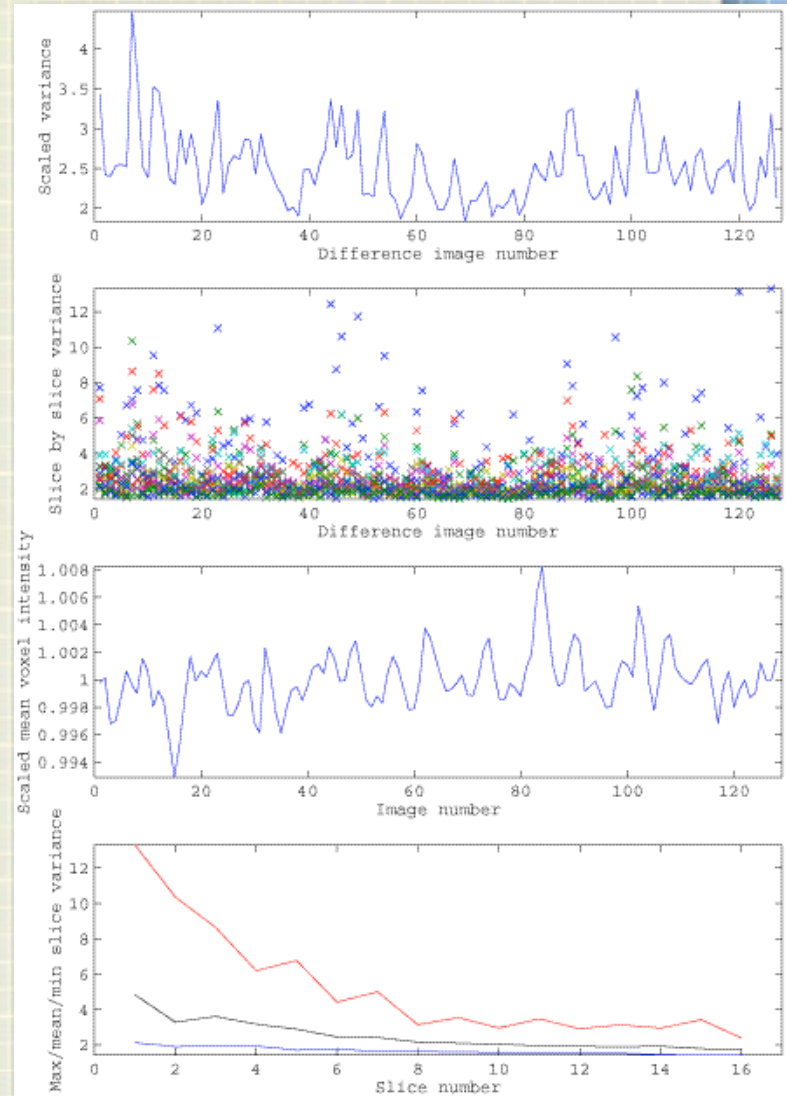


Estimated Motion



Tsdiffana: Typical Data

- Run before realignment
- Available to outsiders:
<http://imaging.mrc-cbu.cam.ac.uk/imaging/DataDiagnostics>
- `>>tsdiffana`
- Select files for one session & press “done”
- Say “no” when asked if should write difference images
- Writes mean, stdev, and slice-to-slice variance

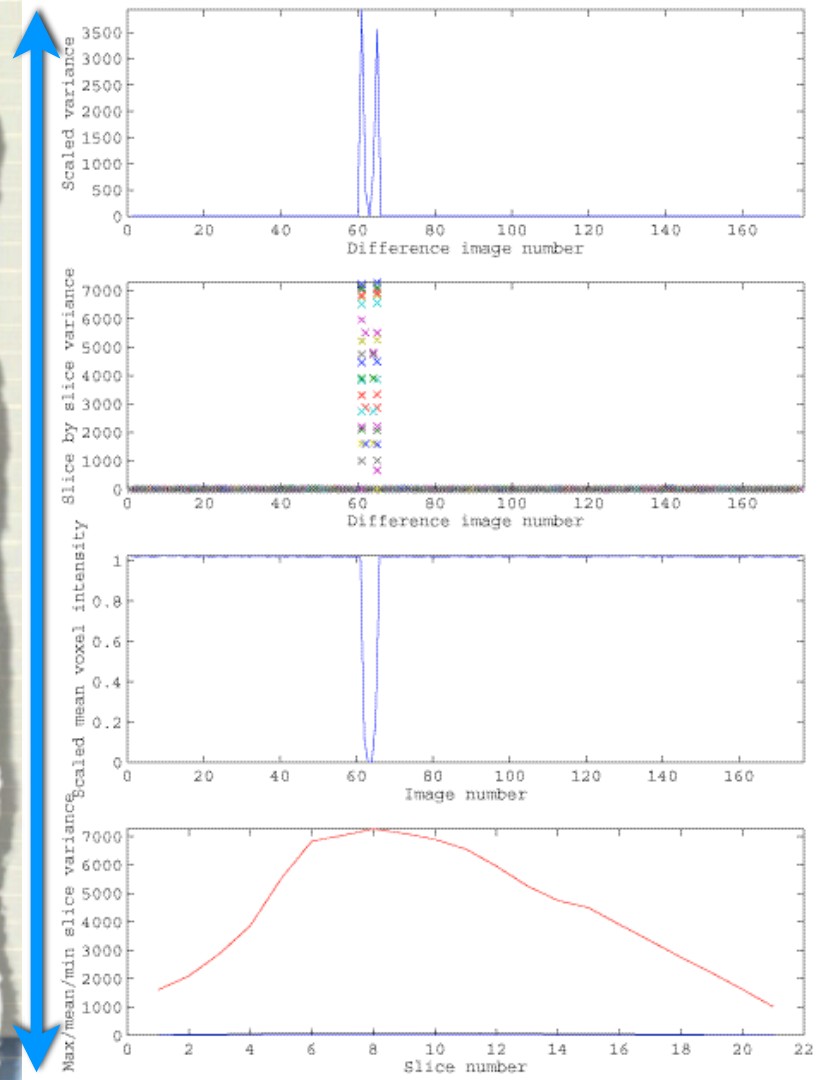
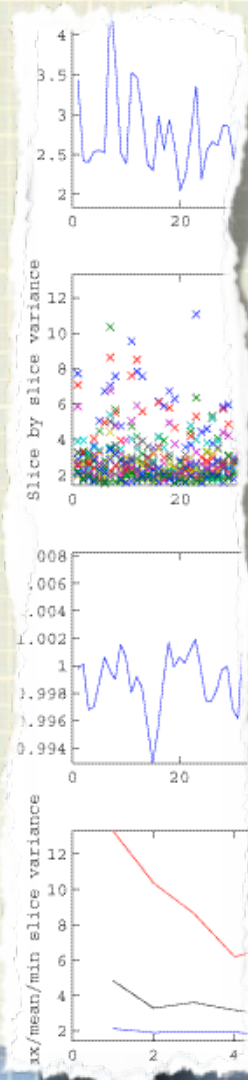


First image:
/cbu/imagers/data/matthew.brett/ER/010160/6/010160-m00_13_EPI_0011.img

tsdiffana: Problem Data

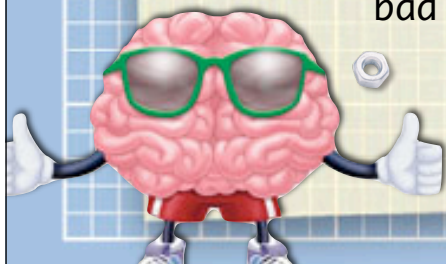
Here the gradient coil stopped working for a few volumes in the middle of the run

Notice
the
scale:



Rules of Thumb

- No simple rules to define 'too much' motion, but...
 - >2-3mm or 2 degrees (.38 radians) in any dimension, exclude subject (i.e., ~voxel size)
 - Ardekani et al. (2001) find SPM can handle up to 10mm summed across dimensions
 - If >.5 mm, consider including movement parameters (will eat up some DoFs, but typically have plenty)
 - Inside the brain, 1mm shifts can cause 3-5% signal change
 - At the edges, 3-5% change is caused by 1/20th of a pixel shift (~187 microns)!
- General points:
 - Rotational data harder to correct
 - Motion during scan session worse than in between
 - If motion correlated w/ task, can you redesign & rerun?
- Most researchers don't recommend removing/replacing/'fixing' bad slices/scans
 - But it is possible to come up with nuisance regressors for affected volumes (e.g. for epilepsy)

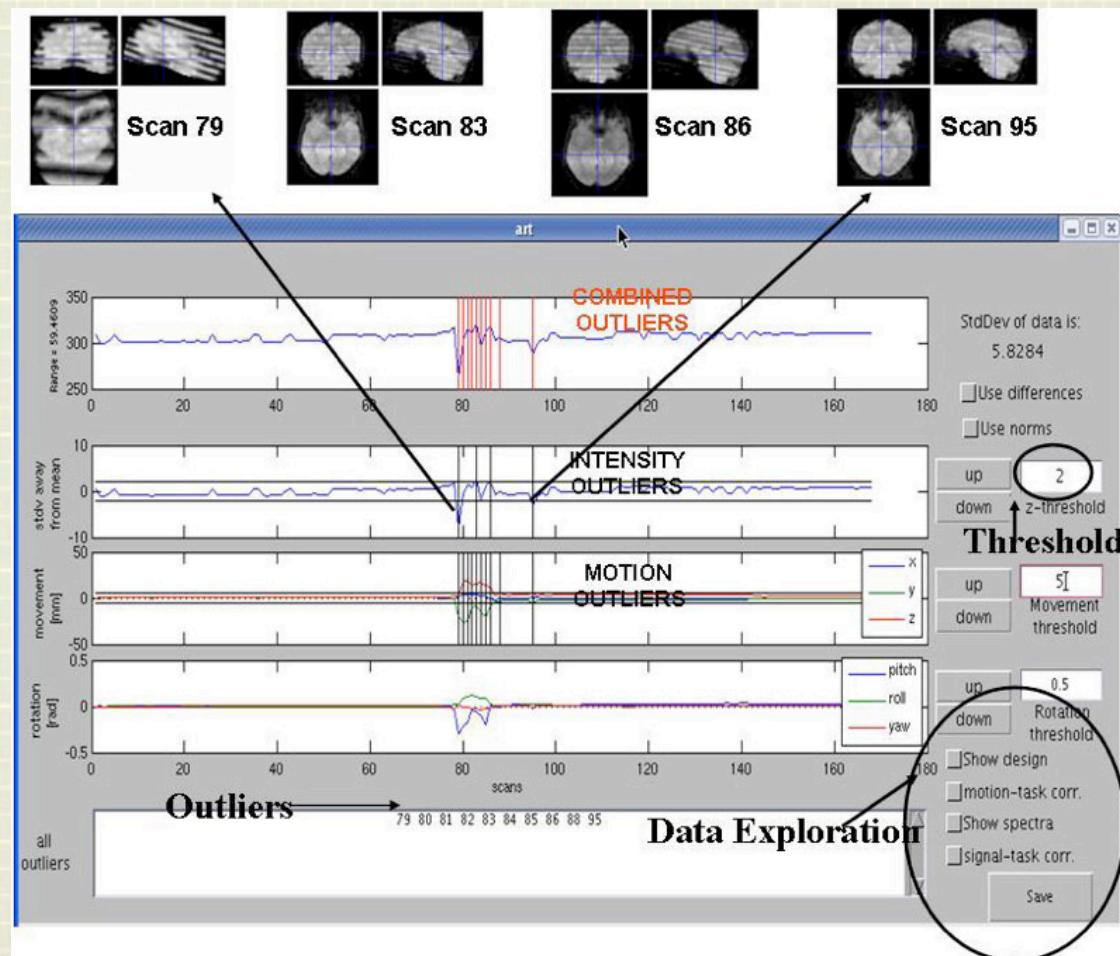


Slice Timing \Leftrightarrow Motion Correction?

- If you run slice timing correction 1st then abrupt movements between scans will cause it to interpolate between different brain regions :(
- If you run motion correction 1st, slices no longer necessarily correspond to acquisition order, so timing correction won't be appropriate :(
- Problem is worse if you have interleaved slice ordering, in which case you should run slice time correction 1st & select slice timing corrected images for realignment
- CBU acquires in sequence (down), and many prefer to run motion correction 1st under this system
- But whether this matters hasn't been investigated fully



Artifact Detection Toolbox (ART)

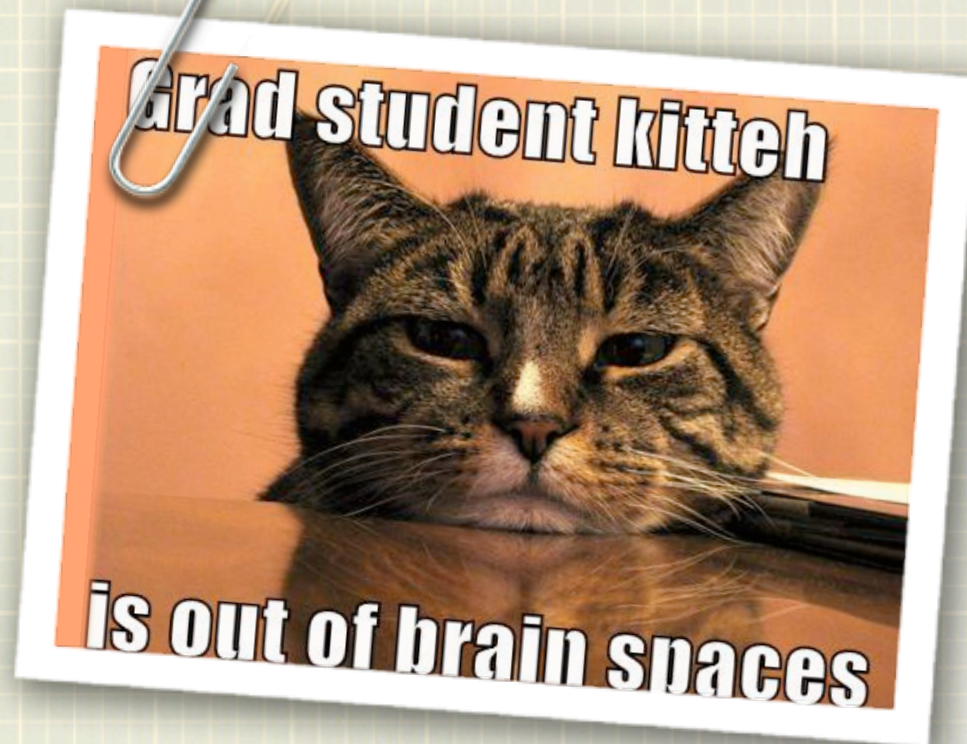


<http://web.mit.edu/swg/software.htm>

Acknowledgements

- SPM Methods for Dummies
 - www.fil.ion.ucl.ac.uk/spm/doc
- FSL Course
 - www.fmrib.ox.ac.uk/fslcourse
- CBU Imaging wiki
 - imaging.mrc-cbu.cam.ac.uk/imaging/CbuImaging
- Jody Culham's fMRI for Newbies
 - www.fmri4newbies.com
- Russell Thompson's fMRI Basics Course
- Florida's citrus growers





Warp Speed Ahead...