Image processing

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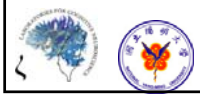
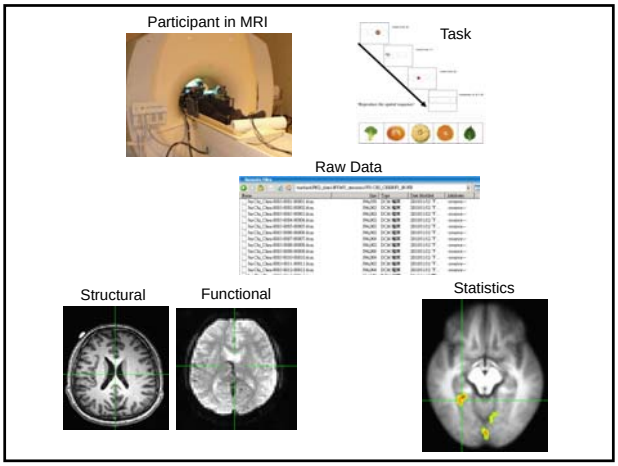
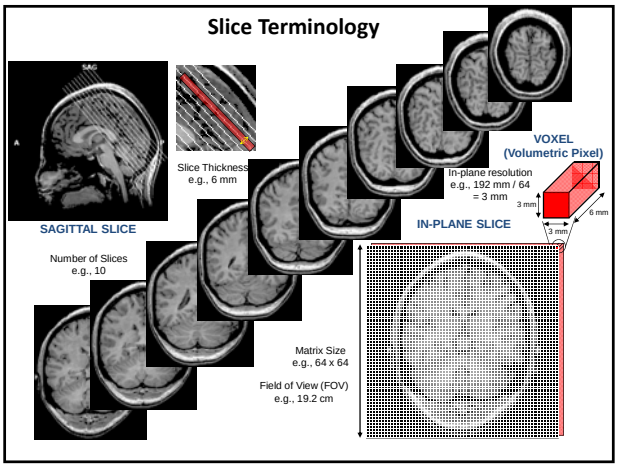


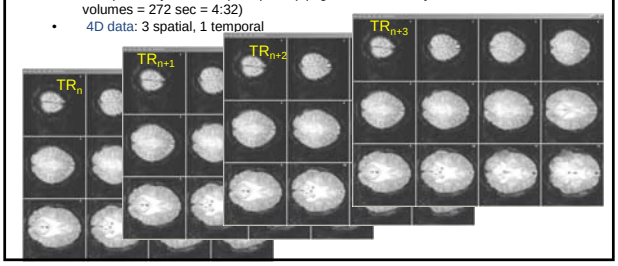


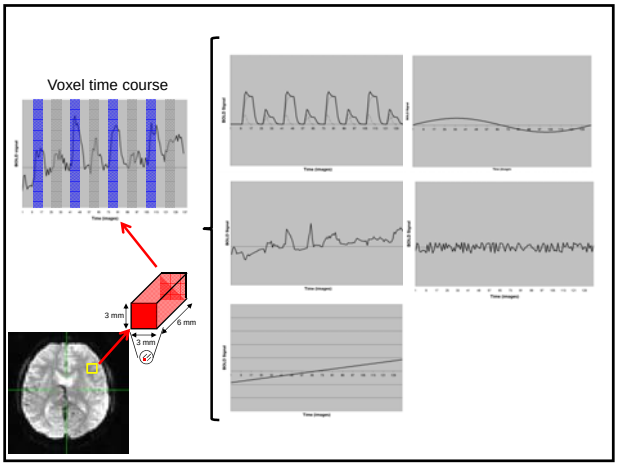


fMRI Experiment Stages: Functionals

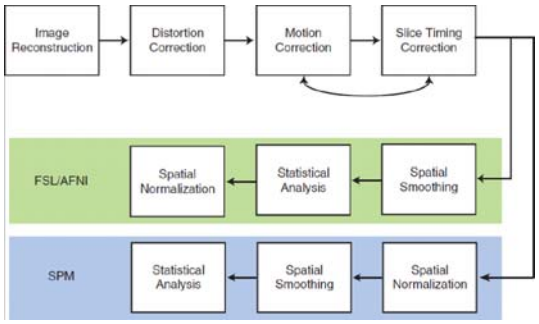
Take functional (T2*) images

- images are indirectly related to neural activity
- usually low resolution images (3 x 3 x 6 mm)
- all slices at one time = a volume (sometimes also called an image)
- sample many volumes (time points) (e.g., 1 volume every 2 seconds for 136 volumes = 272 sec = 4:32)
- 4D data: 3 spatial, 1 temporal





Flow of Data Analysis



Talk Outline

1. Slice Timing
2. Realignment
3. Co-registration
4. Normalisation
5. Smoothing

Talk Outline

1. **Slice Timing**
2. Realignment
3. Coregistration
4. Normalisation
5. Smoothing

Henri Lartigue

slit-sca

exposed last

exposed first

slit-sca

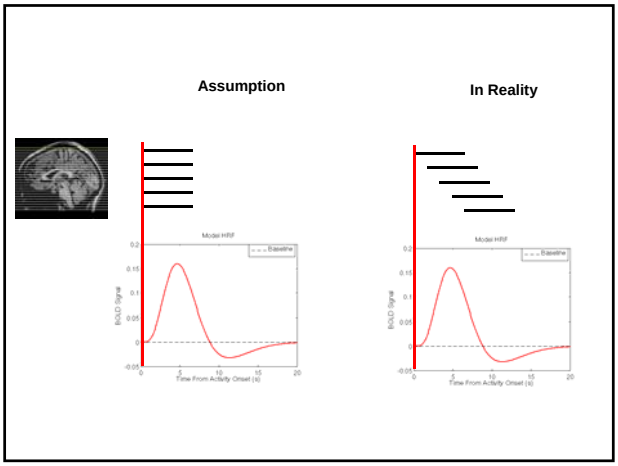
exposed last

exposed first

slit-sca

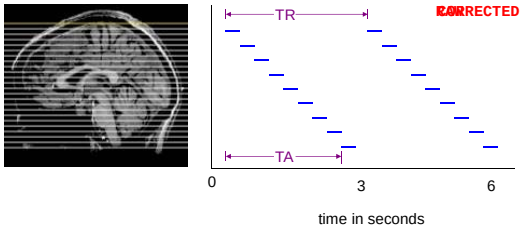
exposed last

exposed first

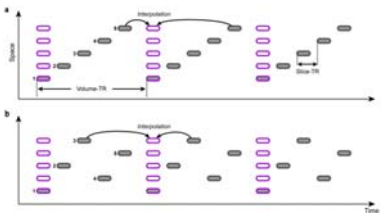


Slice Timing

SPM assumes each scan is 'instantaneous'



Interpolation



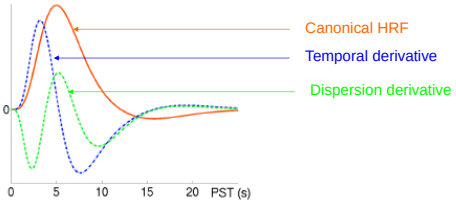
Slice timing

Only needed if:

- Temporal dynamics of evoked responses are important and if
- TR is sufficiently small to permit interpolation (<3 seconds)

- BioPhysical latency is on the order of seconds
- Usually unnecessary if latency differences are modelled in SPM analysis "proper" using temporal derivatives.

HRF and Its Derivatives



Slice timing

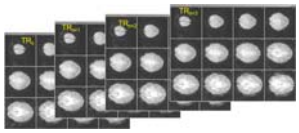
Output:

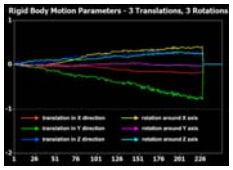
`afilename.hdr`
`afilename.img`
`afilename.mat`

Talk Outline

1. Slice Timing
2. **Realignment**
3. Coregistration
4. Normalisation
5. Smoothing

Subject motion: front line defence





Realignment of subject motion

Why bother?

• Subsequent analysis assumes that voxel = bit of brain
(e.g. Subtraction and averaging)

•Haemodynamic response is small compared to signal from movement

•Increase sensitivity of t-test (movement contributes to variance)

Realignment of subject motion

When to do it?

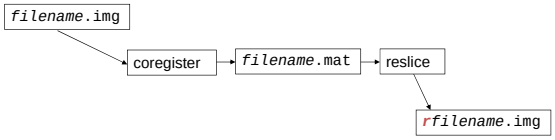
• Must be done before Normalization

• Can be either before or after slice time correction (disadvantages to both options)

• For interleaved acquisitions it's recommended to slice time correct first

• For sequential acquisitions it's recommended to realign first

Realignment of subject motion

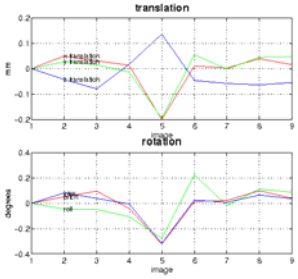


Realignment

Realignment involves:

1. "coregister" - Estimate 6 parameters (3x translations, 3x rotations) of an affine rigid body transform.

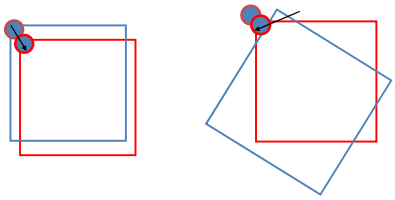
Aim: minimize COST FUNCTION computed between each successive scan and a reference scan



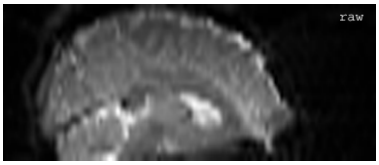
Realignment

Realignment involves:

2. "reslice" Apply transformation by re-sampling the data

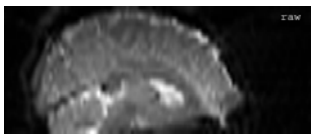


EPI undistortion



- EPI images are distorted relative to the structural scans
- Bigger magnet = more distortion

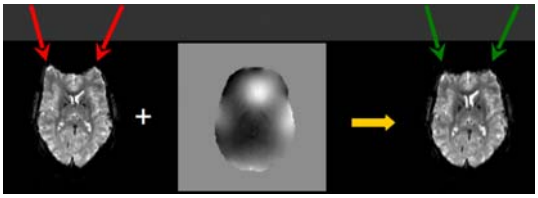
EPI undistortion



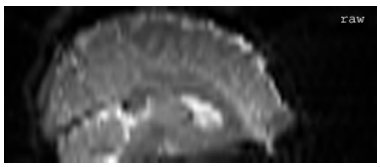
Different tissues have different magnetic susceptibilities

Magnetic field warps at tissue boundaries

But the field gradient encodes position!



EPI undistortion



- It is possible to directly measure the magnetic field across the head, and then use this information to undistort the EPI images after reconstruction.

EPI undistortion

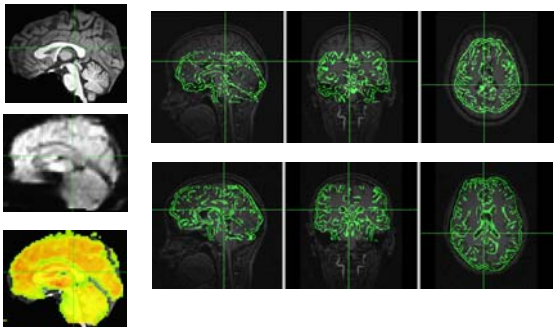
new feature in SPM2:

Talk Outline

1. Slice Timing
2. Realignment
3. **Coregistration**
4. Normalisation
5. Smoothing

Coregistration

- Align different modalities (eg PET & MRI)
- Align functional (EPI) with structural (T1)
- Optimize parameters describing rigid body transformation to match functional with structural



Part 2

1. Slice Timing
2. Realignment
3. Coregistration
4. Normalisation
5. Smoothing

Normalisation and smoothing

- The story so far…
  - fMRI time data set
  - Movement between scans has been corrected for (realignment)
  - Functional data has been overlaid onto the high resolution anatomical data (co-registration)
- What next…?

Talk Outline

1. Slice Timing
2. Realignment
3. Coregistration
4. **Normalisation**
5. Smoothing

Normalisation

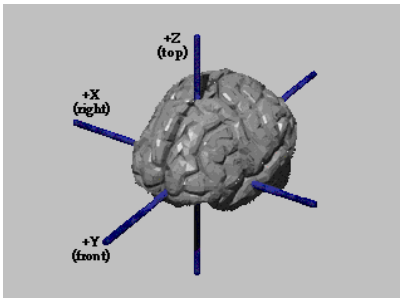
What do we want from fMRI?

1. Analysis within subject data
2. Analysis between subjects

But how do we compare 2 different brains?

Squash the subjects data into a common 3D brain space.

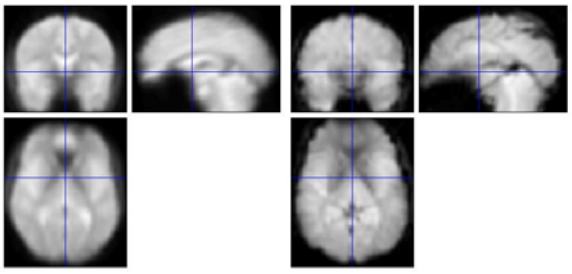
The Talairach brain template[1]



[1]Talairach and Tournoux, 1988

How is the data warped?

- Either anatomical scan or functional data is used to estimate *warping parameters*, using one of the following models:
  - 12 parameter affine transformation
  - Low frequency basis spatial functions
  - Vector field specifying the mapping for each voxel



Template Normalised Image

Problems with normalisation

- Structural alignment does not mean functional alignment
- Differences in gyral anatomy and physiology lead to non-perfect fit
- Strict warping to template will create non-existent features
- Brain pathology may confuse the normalising procedure

Talk Outline

1. Slice Timing
2. Realignment
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5. **Smoothing**

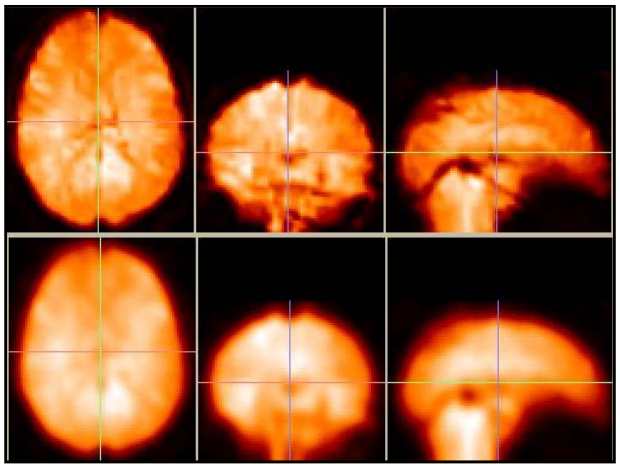
Smoothing

How?

Intensity value of a voxel is replaced by a weighted average of the neighbouring voxels

Why smooth?

1. Render the errors more normal in their distribution (I.e. Gaussian)
2. For inter-subject analyses
3. Increase signal-noise ratio



Summary

1. Realignment - (adjust for movement between slices)
2. Co-registration - (link functional scans to anatomical scan)
3. Normalisation - (warp functional data into template space)
4. Smoothing - (to increase signal to noise ratio)