fMRI

Preprocessing

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Contents

* **Preliminaries**
  * Rigid-body and affine transformations
  * Optimisation and objective functions
  * Transformations and interpolation

* Within-subject: Realignment
* Within-subject: EPI Distortion Correction
* Within-subject: Coregistration
* Between-subject: Normalise/Segment
* Between-subject: Dartel
* Between-subject: Smoothing
Image registration

Most “preprocessing” involves aligning images together.

Two components:

• **Registration** - i.e. Optimise the parameters that describe spatial transformations between the images.

• **Transformation** - i.e. Re-sample according to the determined transformation parameters.
Rigid-body transformations

* Assume that brain of the same subject doesn’t change shape or size in the scanner.
  * Head can move, but remains the same shape and size.
  * Some exceptions:
    * Image distortions.
    * Brain slops about slightly because of gravity.
    * Brain growth or atrophy over time.

* If the subject’s head moves, we need to correct the images.
  * Do this by image registration.
2D affine transforms

* Translations by $t_x$ and $t_y$
  * $x_1 = x_0 + t_x$
  * $y_1 = y_0 + t_y$

* Rotation around the origin by $\Theta$ radians
  * $x_1 = \cos(\Theta) x_0 + \sin(\Theta) y_0$
  * $y_1 = -\sin(\Theta) x_0 + \cos(\Theta) y_0$

* Zooms by $s_x$ and $s_y$
  * $x_1 = s_x x_0$
  * $y_1 = s_y y_0$

*Shear
  * $x_1 = x_0 + h y_0$
  * $y_1 = y_0$
2D affine transforms

* Translations by \( t_x \) and \( t_y \)
  * \( x_1 = 1 \ x_0 + 0 \ y_0 + t_x \)
  * \( y_1 = 0 \ x_0 + 1 \ y_0 + t_y \)

* Rotation around the origin by \( \Theta \) radians
  * \( x_1 = \cos(\Theta) \ x_0 + \sin(\Theta) \ y_0 + 0 \)
  * \( y_1 = -\sin(\Theta) \ x_0 + \cos(\Theta) \ y_0 + 0 \)

* Zooms by \( s_x \) and \( s_y \):
  * \( x_1 = s_x \ x_0 + 0 \ y_0 + 0 \)
  * \( y_1 = 0 \ x_0 + s_y \ y_0 + 0 \)

* Shear
  * \( x_1 = 1 \ x_0 + h \ y_0 + 0 \)
  * \( y_1 = 0 \ x_0 + 1 \ y_0 + 0 \)
3D rigid-body transformations

* A 3D rigid body transform is defined by:
  * 3 translations - in X, Y & Z directions
  * 3 rotations - about X, Y & Z axes
* The order of the operations matters

\[
\begin{pmatrix}
1 & 0 & 0 & X_{\text{trans}} \\
0 & 1 & 0 & Y_{\text{trans}} \\
0 & 0 & 1 & Z_{\text{trans}} \\
0 & 0 & 0 & 1
\end{pmatrix}
\times
\begin{pmatrix}
1 & 0 & 0 & 0 \\
0 & \cos \Phi & \sin \Phi & 0 \\
0 & -\sin \Phi & \cos \Phi & 0 \\
0 & 0 & 0 & 1
\end{pmatrix}
\times
\begin{pmatrix}
\cos \Theta & 0 & \sin \Theta & 0 \\
0 & 1 & 0 & 0 \\
-\sin \Theta & 0 & \cos \Theta & 0 \\
0 & 0 & 0 & 1
\end{pmatrix}
\times
\begin{pmatrix}
\cos \Omega & \sin \Omega & 0 & 0 \\
-\sin \Omega & \cos \Omega & 0 & 0 \\
0 & 0 & 1 & 0 \\
0 & 0 & 0 & 1
\end{pmatrix}
\]

Translations  
Pitch about x axis  
Roll about y axis  
Yaw about z axis
Voxel-to-world transforms

* Affine transform associated with each image
  * Maps from voxels \((x=1..n_x, y=1..n_y, z=1..n_z)\) to some world co-ordinate system. e.g.,
    * Scanner co-ordinates - images from DICOM toolbox
    * T&T/MNI coordinates - spatially normalised

* Registering image B (source) to image A (target) will update B’s voxel-to-world mapping
  * Mapping from voxels in A to voxels in B is by
    * A-to-world using \(M_A\), then world-to-B using \(M_B^{-1}\)
    * \(M_B^{-1} M_A\)
Optimisation

* Image registration is done by optimisation.
* Optimisation involves finding some “best” parameters according to an “objective function”, which is either minimised or maximised.
* The “objective function” is often related to a probability based on some model.
Optimisation

* Because registration only finds a local optimum, some manual reorienting of the images may be needed before doing anything else in SPM.

An MNI-space image from spm12/canonical directory.
Objective functions

* Intra-modal
  * Mean squared difference (minimise)
  * Normalised cross correlation (maximise)

* Inter-modal (or intra-modal)
  * Mutual information (maximise)
  * Normalised mutual information (maximise)
  * Entropy correlation coefficient (maximise)
Simple interpolation

* Nearest neighbour
  * Take the value of the closest voxel

* Tri-linear
  * Just a weighted average of the neighbouring voxels
    * \( f_5 = f_1 x_2 + f_2 x_1 \)
    * \( f_6 = f_3 x_2 + f_4 x_1 \)
    * \( f_7 = f_5 y_2 + f_6 y_1 \)
B-spline interpolation

A continuous function is represented by a linear combination of basis functions.

B-splines are piecewise polynomials.

2D B-spline basis functions of degrees 0, 1, 2 and 3.

Nearest neighbour and trilinear interpolation are the same as B-spline interpolation with degrees 0 and 1.
Pre-processing overview

- fMRI time-series
- Motion/Distortion Correct
- Coregister

Anatomical MRI

Template

- Estimate Spatial Norm
- Spatially normalised

Deformation

Smoothed

Smooth

Spatially normalised

Statistics or whatever
Contents

* Preliminaries

* **Within-subject: Realignment**
  * Realignment by minimising mean-squared difference
  * Residual artifacts

* Within-subject: Realignment

* Within-subject: EPI Distortion Correction

* Within-subject: Coregistration

* Between-subject: Normalise/Segment

* Between-subject: Dartel

* Between-subject: Smoothing
Mean-squared difference

- Minimising mean-squared difference works for intra-modal registration (realignment)
- Simple relationship between intensities in one image, versus those in the other
  - Assumes normally distributed differences
Motion estimates

"Browse" option from Check Reg allows fMRI time series to be shown as a movie.
Residual errors from aligned fMRI

* Re-sampling can introduce interpolation errors
  * especially tri-linear interpolation
* Gaps between slices can cause aliasing artefacts
* Slices are not acquired simultaneously
  * rapid movements not accounted for by rigid body model
* Image artefacts may not move according to a rigid body model
  * image distortion
  * image dropout
  * Nyquist ghost
* BOLD signal changes influence the estimated motion.
* Functions of the estimated motion parameters can be modelled as confounds in subsequent analyses
Contents

* Preliminaries
* Within-subject: Realignment
* **Within-subject: EPI Distortion Correction**
  * FieldMap Toolbox
  * Movement by distortion interaction
* Within-subject: Coregistration
* Between-subject: Normalise/Segment
* Between-subject: Dartel
* Between-subject: Smoothing
EPI distortion

* Magnetic susceptibility differs among tissues.
* Greatest difference is between air and tissue.
* Subject disrupts $B_0$ field, rendering it inhomogeneous
* Distortions in phase-encode direction
FieldMap toolbox

* Computes a voxel-displacement map (VDM) from fieldmap scans.

* Used to correct distortions in EPI.
Phase unwrapping

* Phase of complex data used.
* \(-\pi/2 < \text{phase} < \pi/2\)
* Phase-unwrapping needed.
  * Part that is most likely to go wrong.
  * Phase is poorly defined when magnitude is small relative to noise.
Movement-by-distortion interaction

Original position

After rotation

Original position

After rotation
Realign & Unwarp
Correcting for distortion changes

Estimate movement parameters.

Estimate reference from mean of all scans.

Estimate new distortion fields for each image:
- estimate rate of change of field with respect to the current estimate of movement parameters in pitch and roll.

\[ \Delta \varphi \quad \Delta \theta \]

\[ \partial B_0 / \partial \varphi \quad \partial B_0 / \partial \theta \]

Unwarp time series.

Andersson et al, 2001
Contents

* Preliminaries
* Within-subject: Realignment
* Within-subject: EPI Distortion Correction

* **Within-subject: Coregistration**
  * Coregistration by maximising mutual information
* Between-subject: Normalise/Segment
* Between-subject: Dartel
* Smoothing
Coregistration

• Inter-modal registration.
• Match images from same subject but different modalities:
  – anatomical localisation of single subject activations
  – achieve more precise spatial normalisation of functional image using anatomical image.
Coregistration maximises Mutual Information

* Used for between-modality registration
* Derived from joint histograms
* \( MI = \int_{ab} P(a,b) \log_2 \left[ \frac{P(a,b)}{P(a)P(b)} \right] \)
  * Related to entropy: \( MI = -H(a,b) + H(a) + H(b) \)
  * Where \( H(a) = -\int_a P(a) \log_2 P(a) \) and \( H(a,b) = -\int_a P(a,b) \log_2 P(a,b) \)
“Check Reg” to assess alignment

Check Reg allows contours from one image to be shown superimposed on another
EPI dropout and distortion
References


Pre-processing overview

fMRI time-series

Motion Correct

Anatomical MRI

Template

Spatially normalised

Smoothed

Statistics or whatever

Deformation

Coregister

Smooth

Spatially normalised

Template

Estimate Spatial Norm

Deformation

Template
Alternative pipeline

fMRI time-series

Motion Correct

Template

Deformation

Spatially normalised

Smoothed

Smooth

Statistics or whatever

Spatial Norm

Smoothed
Contents

* Preliminaries
* Within-subject: Realignment
* Within-subject: EPI Distortion Correction
* Coregistration
* **Between-subject: Normalise/Segment**
  
  Use segmentation routine for spatial normalisation
  * Gaussian mixture model
  * Intensity non-uniformity correction
  * Deformed tissue probability maps

* Between-subject: Dartel
* Between-subject: Smoothing
Spatial normalisation
* Brains of different subjects vary in shape and size.
* Need to bring them all into a common anatomical space.
  * Examine homologous regions across subjects
    * Improve anatomical specificity
    * Improve sensitivity
  * Report findings in a common anatomical space (eg MNI space)

* In SPM12, alignment is achieved by matching grey matter with grey matter and white matter with white matter.
  * With possible alignment of other tissues.
Normalise/Segment

* This is the same algorithm as for tissue segmentation.

* Combines:
  * Mixture of Gaussians (MOG)
  * Bias Correction Component
  * Warping (Non-linear Registration) Component
Spatial normalisation

* Default spatial normalisation in SPM12 estimates nonlinear warps that match tissue probability maps to the individual image.

* Spatial normalisation achieved using the inverse of this transform.
Segmentation

* Segmentation in SPM12 also estimates a spatial transformation that can be used for spatially normalising images.

* It uses a generative model, which involves:
  * Mixture of Gaussians (MOG)
  * Warping (Non-linear Registration) Component
  * Bias Correction Component
Image Intensity Distributions
(T1-weighted MRI)
Modelling tissue intensities

* Classification is based on a *Mixture of Gaussians* model (MOG), which represents the intensity probability density by a number of Gaussian distributions.
Tissue probability maps in SPM12

Includes additional non-brain tissue classes (bone, and soft tissue)
Modelling deformations
Modelling a bias field

A bias field is modelled as a linear combination of basis functions.

Corrupted image  Bias Field  Corrected image
Iterative optimisation scheme

Update tissue estimates

Update bias field estimates

Update deformation estimates

Converged?

Yes

No
Contents

* Preliminaries
* Within-subject: Realignment
* Within-subject: EPI Distortion Correction
* Within-subject: Coregistration
* Between-subject: Normalise/Segment
* **Between-subject: Dartel**
  * Velocity field parameterisation
  * Objective function
  * Template creation
  * Examples
* Between-subject: Smoothing
Dartel image registration

* Uses fast approximations
  * Deformation integrated using scaling and squaring
* Uses Levenberg-Marquardt optimiser
  * Multi-grid matrix solver
* Matches GM with GM, WM with WM etc
* Diffeomorphic registration takes about 30 mins per image pair (121×145×121 images).
Scaling and squaring example
Registration objective function

* Simultaneously minimize the sum of:
  * **Matching Term**
    * Drives the alignment of the images.
    * Multinomial assumption
  * **Regularisation term**
    * A measure of deformation roughness
    * Keeps the warps spatially smooth.

* A balance between the two terms.
Effect of different forms of regularisation
Simultaneous registration of GM to GM and WM to WM
Iteratively generated from 471 subjects

Began with rigidly aligned tissue probability maps
Grey matter average of 452 subjects – affine
Grey matter average of 471 subjects
Initial GM images
Aligned GM images
471 Subject Average
471 Subject Average
471 Subject Average
471 Subject Average
Evaluations of nonlinear registration algorithms
Contents

* Preliminaries
* Within-subject: Realignment
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* Within-subject: Coregistration
* Between-subject: Normalise/Segment
* Between-subject: Dartel
* **Between subject: Smoothing**
  * Compensating for inaccuracies in inter-subject alignment
**Smooth**

Blurring is done by *convolution*.

Each voxel after smoothing effectively becomes the result of applying a weighted region of interest (ROI).
Smooth
References


