

# Data pre-processing framework in SPM

Bogdan Draganski

# Outline

- Why do we need pre-processing?
- Overview
- Structural MRI pre-processing
- fMRI pre-processing

# Why do we need pre-processing?

#### What do we want?





- Inter-subject averaging
  - Increase sensitivity with more subjects
    - Fixed-effects analysis
  - Extrapolate findings to the population as a whole
    - Mixed-effects analysis
- Make results from different studies comparable by aligning them to standard space
  - e.g. The T&T convention, using the MNI template

## Movement





## Distortions



## Non-gaussian distribution











#### **Pre-processing Overview**







- MR Images are corrupted by smoothly varying intensity inhomogeneity caused by magnetic field imperfections and subject-field interactions
  - Would make intensity distribution spatially variable
- A smooth intensity **correction** can be modelled by a linear combination of DCT (discrete cosine transform) basis functions



#### Inhomogeneity correction

- Field inhomogeneity will disrupt intensity based segmentation
- Bias correction required



Estimate

 $T_1$ 







Tissue intensity distributions – T1w MRI









- Find the "best" parameters according to an "objective function" (minimised or maximised)
- Objective functions can often be related to a probabilistic model (Bayes -> MAP -> ML -> LSQ)







#### Segmentation results





Spatially normalised — BrainWeb phantoms (T1, T2, PD)

Tissue probability maps of GM<sup>7</sup> and WM

Cocosco, Kollokian, Kwan & Evans. "BrainWeb: Online Interface to a 3D MRI Simulated Brain Database". NeuroImage 5(4):S425 (1997)

#### Spatial normalisation





#### Affine registration

#### Non-linear registration



Without regularisation, the non-linear spatial normalisation can introduce unwanted deformation Template image Von-linear registration using

regularisation

(error = 302.7)

Affine registration (error = 472.1)

Non-linear registration without regularisation (error = 287.3)

#### **Spatial normalisation - Limitations**

- Seek to match functionally homologous regions, but...
  - No exact match between structure and function
  - Different cortices can have different folding patterns
  - Challenging high-dimensional optimisation
    - Many local optima
- Compromise
  - Correct relatively large-scale variability (sizes of structures)
  - Smooth over finer-scale residual differences



• Uses information from tissue probability maps (TPMs) and the intensities of voxels in the image to work out the probability of a voxel being GM, WM or CSF

#### Old Segmentation













#### New Segmentation





- If someone has atrophy, normalisation will stretch grey matter to make brain match healthy template
- This will reduce ability to detect differences





Analogy: as we blow up a balloon, the surface becomes thinner.

Likewise, as we expand a brain area it's volume is reduced.







**Modulated** 

## 

#### Modulation

- Multiplication of the warped (normalised) tissue intensities so that their regional or global volume is preserved
  - Can detect differences in completely registered areas
- Otherwise, we *preserve concentrations*, and are detecting *mesoscopic* effects that remain after approximate registration has removed the macroscopic effects
  - Flexible (not necessarily "perfect") registration may not leave any such differences



Native

intensity = tissue density

#### Unmodulated



1/3

1/3

2/3

Modulated

2/3



- Why would we deliberately blur the data?
  - Improves spatial overlap by blurring over minor anatomical differences and registration errors
  - Averaging neighbouring voxels suppresses noise
  - Increases sensitivity to effects of similar scale to kernel (matched filter theorem)
  - Makes data more normally distributed (central limit theorem)
  - Reduces the effective number of multiple comparisons
- How is it implemented?
  - Convolution with a 3D Gaussian kernel, of specified full-width at half-maximum (FWHM) in mm



- Smoothing kernel should match the shape and size of the expected effect
- Benefits
  - more "Gaussian distribution" of the data
  - Smooth out incorrect registration
- RFT requires FWHM > 3 voxels















12mm



#### **Global normalisation**



- Shape is really a multivariate concept
  - Dependencies among volumes in different regions
- SPM is mass univariate
  - Combining voxel-wise information with "global" integrated tissue volume provides a compromise



Above: (ii) is globally thicker, but locally thinner than (i) – either of these effects may be of interest to us.

Below: The two "cortices" on the right both have equal volume...



Figures from: *Voxel-based morphometry of the human brain*... Mechelli et al, 2005

# fMRI pre-processing

- Slice timing correction (optional)
- Realignment (Motion correction)
- Unwarping (Motion correction x B0 correction)
- Co-registration
  - Link functional scans to anatomical scan
- Spatial normalisation (unified segmentation)
  - Fitting images to a standard brain
- Smoothing
  - Increases signal-to-noise ratio and approximates a Gaussian distribution

#### **Pre-processing Overview**





#### Objectives Overview Structural Functional Outline

# Slice timing (optional)









# Slice timing (optional)



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# Realignment - motion correction Translation Rotation Ζ Yaw Roll





# **Realignment - motion correction**

Rigid body transformations parameterised by:

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		about X axis														
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Minimizing the squared difference (error) between the images



# **Realignment motion correction**

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# Unwarp

Fieldmap



#### Raw EPI

#### **Undistorted EPI**



#### Unwarp can estimate changes in distortion

#### from movement



- distortions in a reference image (FieldMap)
- subject motion parameters (that we obtain in realignment)
- change in deformation field with subject movement (estimated via iteration)

# Co-registration



# Normalized mutual information







Visual Image

Thermal Image



Chess Image after Registration Image after Fusion







functional and structural images in the same space

**Co-registration** 



# Spatial registration

Registration of structural images to a standard brain template (standard space)

→The obtained transformation (warping) parameters can be applied on co-registered fMRI data

 $\rightarrow$  Improved spatial normalization based on high resolution structural information



# Smoothing







# Smoothing









# LREN Laboratoire de Recherche en Neuro-Imagerie

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