ANALYSIS OF FUNCTIONAL MAGNETIC RESONANCE IMAGING DATA USING SPM99:

VOXEL-BASED MORPHOMETRY

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SPM: VOXEL-BASED MORPHOMETRY

37. Voxel-Based Morphometry: Preparing anatomical images

Converting anatomical files for VBM

- ftp anatomical scans from E-Film or reload anatomical scans to your directory
- If scans are in dicom (*.dcm) format, convert to Analyze format using **dcmtoSPM** script in terminal window
- Are the files in the present working directory: ***Y***
- Are these dicom images: ***Y***
- Enter the file prefix, e.g., ***s66***

Preparing Headers

- Run ***matlab*** and ***SPM***
- Select **Defaults** from main menu
- Select defaults for **spatial normalization**
- Check that spatial normalisation parameters for parameter estimation are set to radiological
- Select **Header Edit** from main menu
- Image dimensions pixels: e.g., ***256 256 124*** (matrix size=256x256; number of slices=132)
- Voxel dimensions mm: (enter width, height, slice thickness) e.g., ***.78125 .78125 2.2***
  (n.b.: width = height = FOV/image dimension, e.g., 200/256 = .78125; note if there is spacing between slices, this should be added or subtracted from slice thickness)
- Datatype: ***uint16*** (for T1 weighted images)
- Apply to images: select the anatomical image (**a.img**)

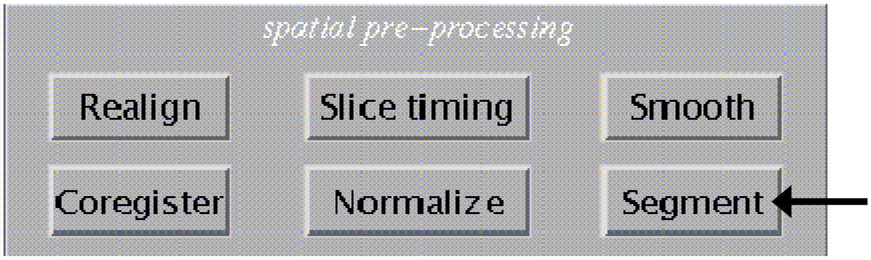
Reorienting images

- Select **Display** from main menu
- Resize y to ***-1***
- If the image is upside down, resize z to ***-1***
- Find AC, take down crosshair co-ordinates
- Put co-ordinates (with signs reversed) into table as translations right, fwd and up
- Check origin is at the AC by entering crosshair co-ordinates ***0 0 0***
- Click **re-orient** images to make AC the origin, select the anatomical (**a.img**) and click **okay** to flipping images

38. Voxel-Based Morphometry: The Good Method

Segmentation

- Select Segment from main menu



- Number of subjects: ***1***
- Select the MRI image to segment (**a.img**)
- Are these images spatially normalised? **No**
- Correct intensity inhomogeneities? Select "**a little**"
- Save inhomogeneity corrected images? **Yes**
- Outputs: creates **a_seg1.img** (grey matter), **a_seg2.img** (white matter) and **a_seg3img** (csf)

Extracting Brain

- Select **Render** from main menu

- Select **Xtract** Brain
- Select images: Select grey (**a_seg1.img**) and white (**a_seg2.img**) images
- Save extracted brain
- **Output**: creates **brain_a.img**

Creating grey_clean image

- Select **ImCalc** from main menu
- Select images (**a_seg1.img, a_seg2** and **brain_a.img**)
- Name output file (***grey_clean***)
- Enter formula to apply to images ***(i1./(i1 + i2 + eps).*i3***
- **Output:** creates **grey_clean.img**

Normalisation

- Select **Normalisation** from main menu
- Select "**determine and write parameters**"
- Number of subjects: ***1***
- Image to determine from: select **grey_clean.img**
- Image to write to: select **a.img**
- Template: Select **gray.img** (from directory: users/crawley/spm99/apriori)
- Interpolation?: Select **Sinc Interpolation**
- **Output**: creates **na.img**

Segmentation

- Select **Segment** from main menu
- Number of subjects: ***1***
- Select the MRI image to segment: **na.img**
- Are these images spatially normalised? **Yes**
- Correct intensity inhomogeneities? Select "**a little**"
- Save inhomogeneity corrected images? **Yes**
- **Output:** creates **na_seg1.img** (grey), **na_seg2.img** (white) and **na_seg3.img** (csf)

Extract Brain (creates brain_na.img)

- Select **Render**
- Select **Xtract** brain
- Select images: Select grey (n**a_seg1.img**) and white (n**a_seg2.img**) images
- Save extracted brain
- **Output**: creates **brain_na.img**

Creating a n_grey_clean image

- Select **ImCalc** from main menu
- Select images: **na_seg1.img**, **na_seg2.img** and **brain_na.img**
- Name output file: ***n_grey_clean***
- Enter formula: ***(i1./(i1 + i2 + eps).*i3***
- **Output:** creates **n_grey_clean.img**

Smoothing

- Select **Smooth** from main menu
- Select image to smooth: **n_grey_clean.img**
- Smoothing kernel: ***12mm***
- **Output:** creats **sn_grey_clean.img**

Modulation

- In matlab terminal, type: ***spm_modulate***
- Select **sn3d.mat** file (created during normalisation)
- Select image to modulate: **sn_grey_clean.img**
- **Output:** creates **msn_grey_clean.img**

39. Voxel-Based Morphometry: Model of differences between groups

- Select **Basic models** from main menu
- Select **two-sample t test**
- Select images Group 1: select **msn_grey_clean.img** files for subjects in Group 1
- Select images Group 2: select **msn_grey_clean.img** files for subjects in Group 2
- Grand mean scaling?: **No**
- Explicitly mask images?: **No**
- Global Calculation?: **Omit**
- Estimate? **Now**

40. Voxel-Based Morphometry: Model of correlation between structure and performance

- Select **Basic models** from main menu
- Select **Simple Regression (correlation)** (if one variable; if more, select **Multiple Regression**)
- Select images: select **msn_grey_clean.img** files for subjects
- Covariate: Right click, select **Load text file**, and load textfile of behavioural scores
- Name covariate: e.g., ***memory_scores***
- Grand mean scaling?: **No**
- Explicitly mask images?: **No**
- Global Calculation?: **Omit**
- Estimate? **Now**