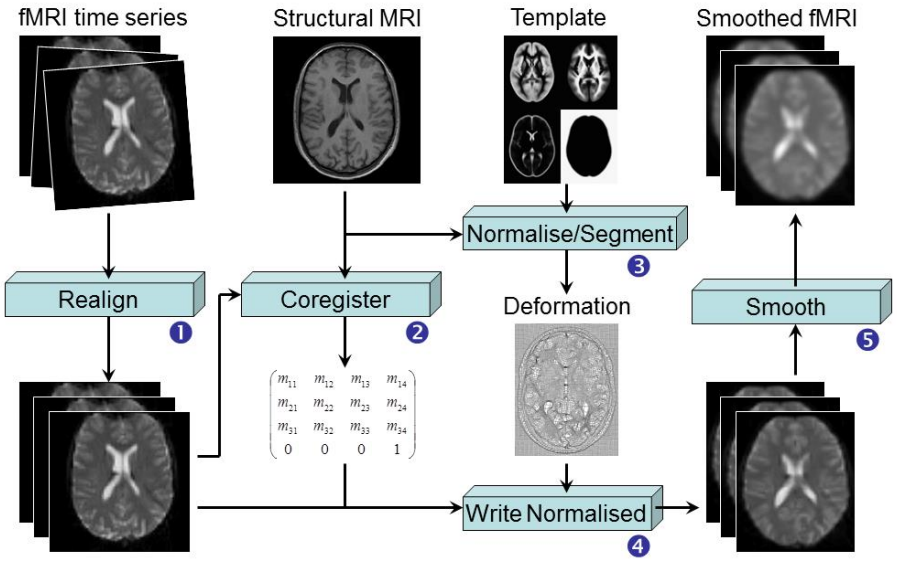
Chicago SPM Workshop: Session 1

The dataset we are going to use is part of an fMRI experiment from Henson et al, Cerebral Cortex, 2002. It consists of data from one of the participants of the experiment, stored in two directories:

- *functional*: 351 T_2^*-weighed scans from a single subject, single session (NIfTI files `sM03953_0005_*.nii`). Images were acquired using continuous EPI with TR=2s and 24 descending slices (64x64 3x3 mm^2), 3mm thick with a 1.5mm gap.

- *structural*: T_1 anatomical scan of the same subject (NIfTI file `sM03953_0007.nii`), 256x256x108 data array (1x1x1.5 mm^3).

In this practical session, we are going to spatially preprocess these data in preparation for their statistical analysis. The aim is to obtain a set of images corrected for movement, normalised to MNI space and smoothed with a sensible kernel size for single subject analysis.



Steps are as follow:

- Using the "Display" button, **display** the structural image. We want to change to origin of the image such that it is close to the anterior commissure (AC). Move the crosshair close to AC (around voxel coordinate [112 131 53]) and click on "**Set origin**" followed by a click on "**Reorient**" to apply the change to the image on disk (no need to save the reorientation matrix).

- **Reorient** the functional images using the same principle. To do so, display one of the 351 EPI images and move the crosshair close to AC again (around voxel coordinate [33 36 9]). Click on “Set origin” followed by a click on “Reorient” where, importantly, you, this time, select the 351 scan to apply the same reorientation to all the images.

- **Check the alignment** of the functional and structural data: click on the “**CheckReg**” and select two images: the structural image and one of the functional images. Then right-click on the functional image and choose “**Contour**”, “Display onto”, “all but current”.

- **Realign** the functional images to correct for movement. Click on “**Realign (Est & Res)**” and, in the batch interface, add a “Session” under “Data” and select the 351 functional images in their acquisition order. Under “Reslice Options”, “Resliced images”, choose “Mean Image Only”. You can assess the amount of movement in the dataset by doing a right-click on “Session” and select “**Preview**”.

- **Coregister** the structural image with the mean functional. Click on “**Coregister (Estimate)**”, and, select the newly created mean functional, `meansM03953_0005_0006.nii`, as the “Reference image”, and the structural image as the “Source image”.

- **Normalise** the structural image using unified segmentation. Click on “**Segment**” and, under “Volumes”, select the structural scan. Change default values for “Save Bias Corrected” to be “Save Bias Corrected”, and for “Deformation Fields” to be “Forward”.

- **Apply the deformation** estimated in the Segment step using “**Normalise (Write)**” to the functional images. Under “Data”, “Subject”, select `y_sM03953_0007.nii` as “Deformation Field” and all the functional images for “Images to Write”. Change the voxel size to be [3 3 3].

- Repeat the “**Normalise (Write)**” step, this time with bias corrected structural image `msM03953_0007.nii` and a voxel size of [1 1 1].

- **Smooth** the normalised functional images with a Gaussian kernel of FWHM 8x8x8 mm. Click on “Smooth” and select the 351 files with prefix “`w`”.

- *Optional*: Use “**ImCalc**” to perform **skull stripping**. ImCalc allows to perform algebraic manipulations on a set of images. Use a thresholded version of the sum of the grey and white matter probability maps to mask out the bias corrected structural scan. To do so, select the bias corrected structural image in subject space and the tissue probability maps with prefix “`c1`” and “`c2`” as “Input Images”. Enter “`brain.nii`” as “Output Filename”. The expression will be something like “i1.*((i2+i3)>0.1)”.