Chapter 31

Auditory fMRI data

This experiment was conducted by Geraint Rees under the direction of Karl Friston and the FIL methods group. The purpose was to explore equipment and techniques in the early days of our fMRI experience. As such, it has not been formally written up, and is freely available for personal education and evaluation purposes.

This data set was the first ever collected and analysed in the Functional Imaging Laboratory (FIL) and is known locally as the mother of all experiments (MoAE).

This data set comprises whole brain BOLD/EPI images acquired on a modified 2T Siemens MAGNETOM Vision system. Each acquisition consisted of 64 contiguous slices ($64\times64\times64$ $3\times3\times3$ mm^3 voxels). Acquisition took 6.05s, with the scan to scan repeat time (TR) set arbitrarily to 7s.

96 acquisitions were made (TR=7s) from a single subject, in blocks of 6, giving 16 42s blocks. The condition for successive blocks alternated between rest and auditory stimulation, starting with rest. Auditory stimulation was bi-syllabic words presented binaurally at a rate of 60 per minute. The functional data starts at acquisition 4, image `fM00223_004.{hdr,img}`, and are stored in folder `fM00223`. Due to T1 effects it is advisable to discard the first few scans (there were no "dummy" lead-in scans). A structural image was also acquired: `sM00223_002.{hdr,img}`, stored in folder `sM00223`. These images are stored in Analyze format (now superseded by the NIfTI format, but SPM reads natively both formats and always saves images as NIfTI) and are available from the SPM site [1].

To analyse the data, first create a new directory DIR, eg. `C:\data\auditory`, in which to place the results of your analysis. Then create 3 subdirectories (i) `dummy`, (ii) `jobs` and (iii) `classical`. As the analysis proceeds these directories will be filled with dummy scans, job-specification files, design matrices and models estimated using classical inference.

Start up MATLAB enter your `jobs` directory and type `spm fmri` at the MATLAB prompt. SPM will then open in fMRI mode with three windows (see Figure 31.1): (1) the top-left or "Menu" window, (2) the bottom-left or "Interactive" window and (3) the right-hand or "Graphics" window. Analysis then takes place in three major stages (i) spatial pre-processing, (ii) model specification, review and estimation and (iii) inference. These stages organise the buttons in SPM's Menu window.

31.1 Preamble (dummy scans)

To avoid T1 effects in the initial scans of an fMRI time series we recommend discarding the first few scans. To make this example simple, we'll discard the first complete cycle (12 scans, `04-15`), leaving 84 scans, image files `16-99`. This is best done by moving these files to a different directory, `dummy`, that we created earlier.

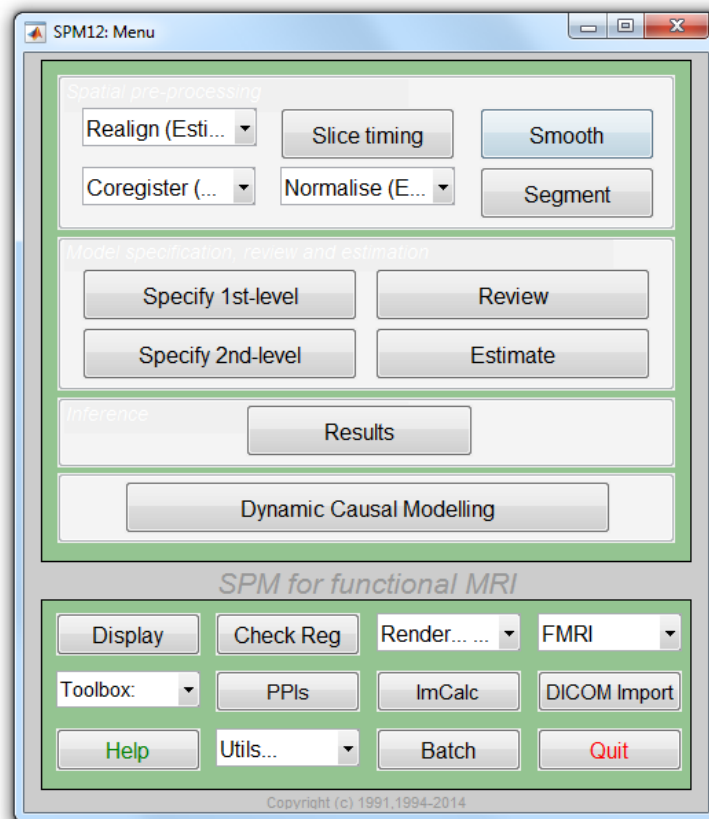[1] Auditory fMRI dataset: http://www.fil.ion.ucl.ac.uk/spm/data/auditory/

Figure 31.1: *The SPM base window comprises three sections i) spatial pre-processing, (ii) model specification, review and estimation and (iii) inference.*

31.2 Spatial pre-processing

31.2.1 Realignment

Under the spatial pre-processing section of the SPM Menu window select REALIGN (EST & RES) from the REALIGN pulldown menu. This will call up a realignment job specification in the batch editor. Then

- Highlight "Data", select "New Session", then highlight the newly created "Session" option.

- Press "Select Files" and use the SPM file selector to choose all of the functional images eg. ("`fM000*.img`"). There should be 84 files.

- Press "Resliced images" in the "Reslice Options" and select "Mean Image Only".

- Save the job file as eg. `DIR\jobs\realign.mat`.

- Press the `RUN` button in the batch editor (green arrow).

This will run the realign job which will estimate the 6 parameter (rigid body) spatial transformation that will align the times series of images and will modify the header of the input images (`*.hdr`), such that they reflect the relative orientation of the data after correction for movement artefacts. SPM will then plot the estimated time series of translations and rotations shown in Figure 31.2. These data are also saved to a file eg. `rp_fM00223_016.txt`, so that these variables can be later used as regressors when fitting GLMs. This allows movements effects to be discounted when looking for brain activations.

SPM will also create a mean image eg. `meanfM00223_016.img` which will be used in the next step of spatial processing - coregistration.

31.2.2 Coregistration

Select COREGISTER (ESTIMATE) from the COREGISTER pulldown. This will call up the specification of a coregistration job in the batch editor.

- Highlight "Reference Image" and then select the mean fMRI scan from realignment eg. `meanfM00223_016.img`.

- Highlight "Source Image" and then select the structural image eg. `sM00223_002.img`.

- Press the Save button and save the job as `DIR\jobs\coregister.mat`.

- Then press the `RUN` button.

SPM will then implement a coregistration between the structural and functional data that maximises the mutual information. The image in figure 31.3 should then appear in the Graphics window. SPM will have changed the header of the source file which in this case is the structural image `sM00223_002.hdr`.

The CHECK REG facility is useful here, to check the results of coregistration. Press the CHECK REG button in the lower section of the Menu window and then select the "Reference" and "Source" Images specified above ie `meanfM00223_016.img` and `sM00223_002.img`. SPM will then produce an image like that shown in Figure 31.4 in the Graphics window. You can then use your mouse to navigate these images to confirm that there is an anatomical correspondence.

31.2.3 Segmentation

Press the SEGMENT button. This will call up the specification of a segmentation job in the batch editor. Highlight the "Volumes" field and then select the subject's registered anatomical image eg. `sM00223_002.img`. Highlight "Save Bias Corrected" and select "Save Bias Corrected". Highlight "Deformation Fields" the bottom of the list and select "Forward". Save the job file as `segment.mat` and then press `RUN`. SPM will segment the structural image using the default tissue probability maps as priors [9].
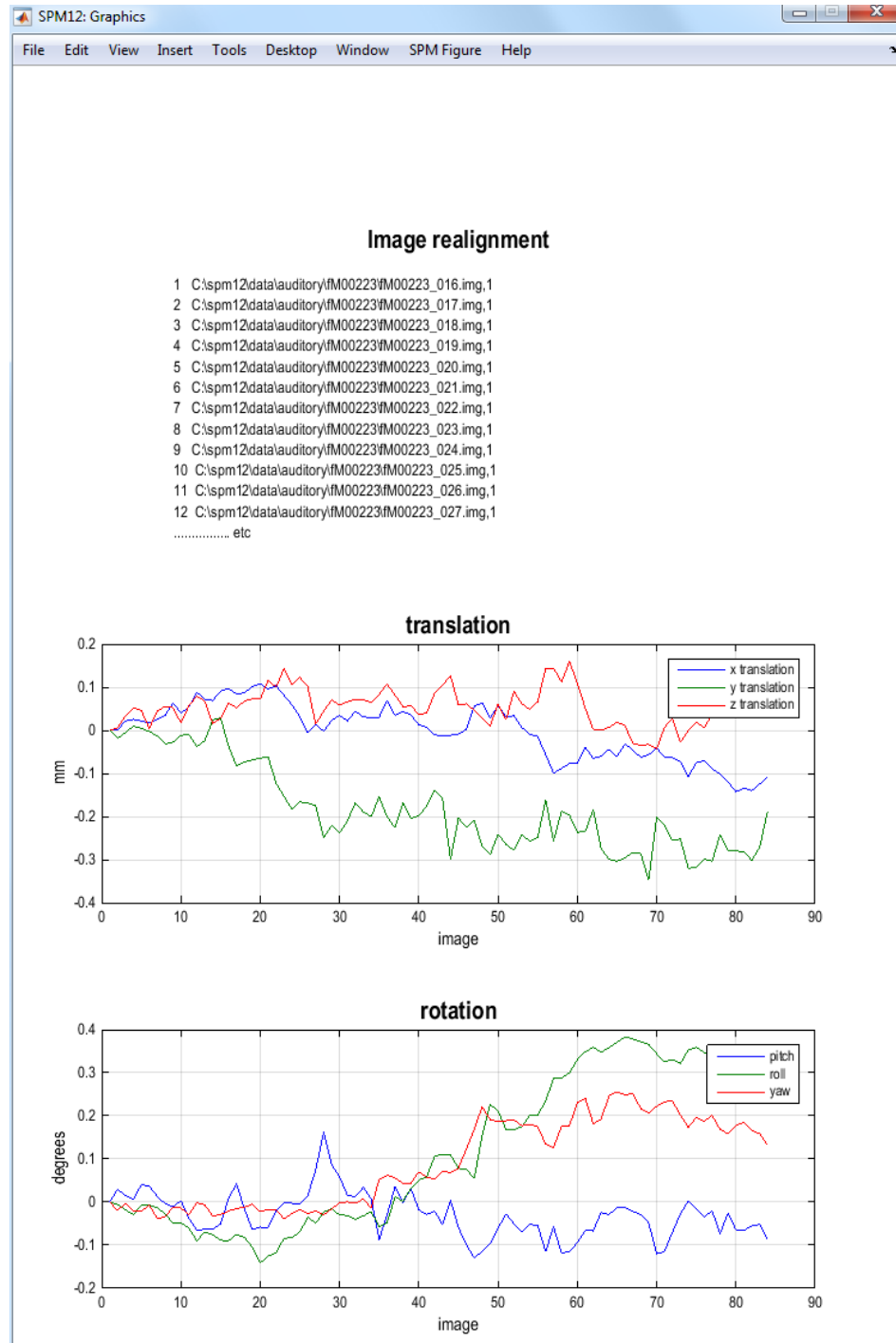
Figure 31.2: *Realignment of Auditory data.*
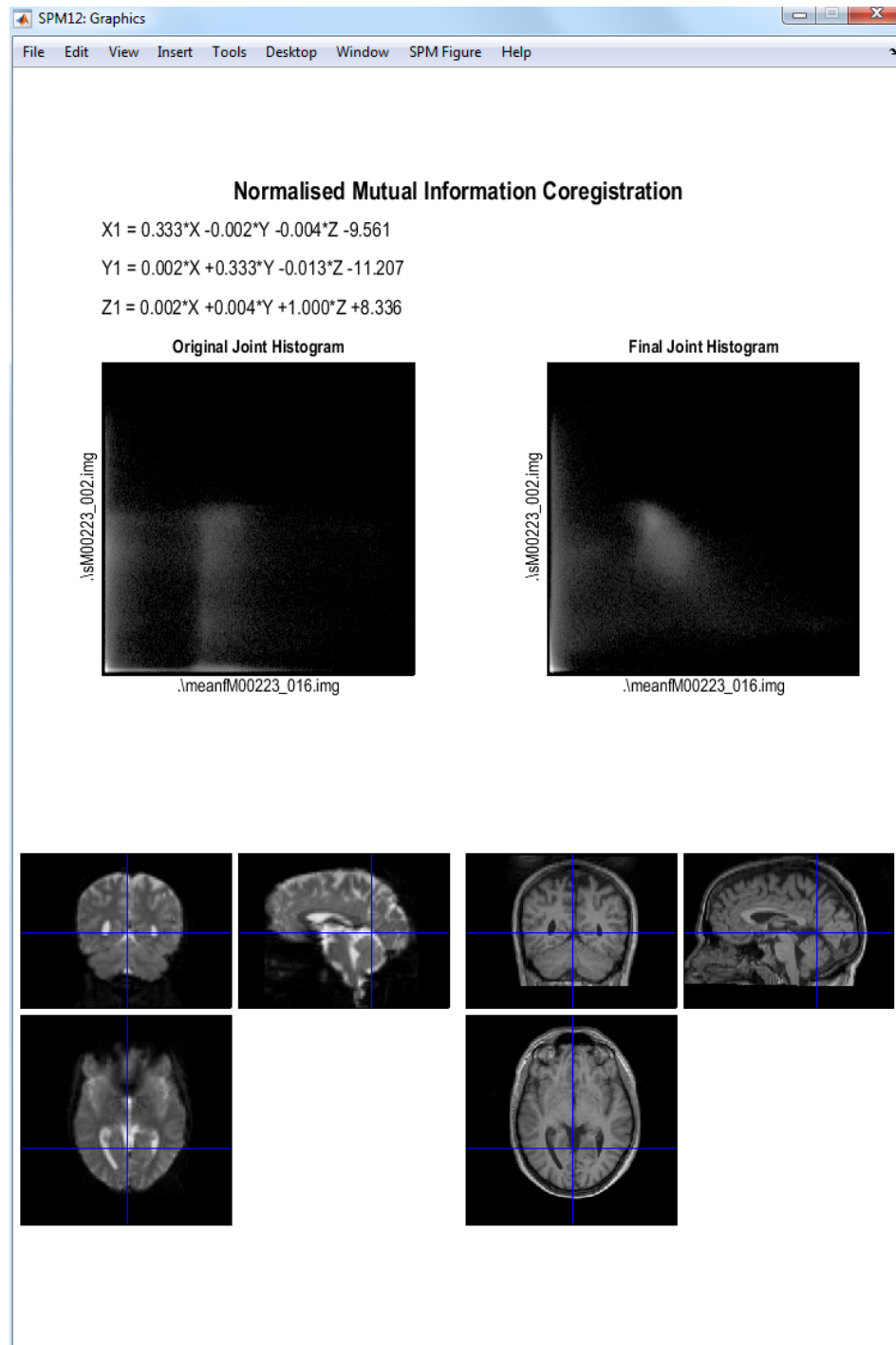
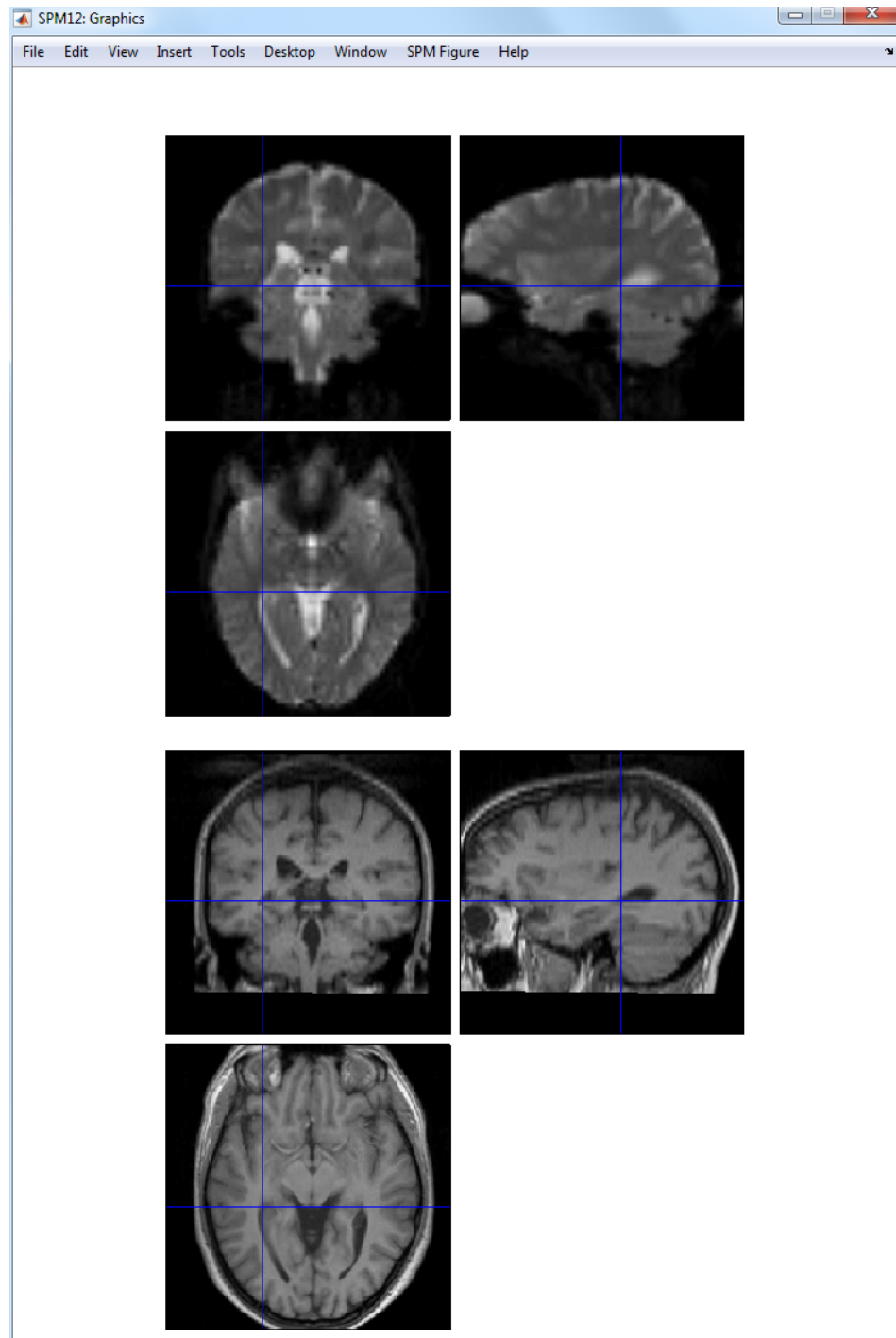Figure 31.3: *Mutual Information Coregistration of Auditory data.*

Figure 31.4: *Checking registration of functional and "registered" structural data.*

SPM will create gray and white matter images and bias-field corrected structural image. These can be viewed using the CHECKREG facility as described in the previous section. Figure 31.5 shows the gray matter image, `c1sM0023_002.nii` along with the original structural. Figure 31.6 shows the structural and bias-corrected image, `msM0023_002.nii`.

SPM will also write a deformation field, file `y_sM00223_002.nii` in the original structural directory. It contains 3 volumes to encode the x, y and z coordinates. Given that the structural and functional data are in alignment, this can be used to spatially normalise the functional data.

31.2.4 Normalise

Select NORMALISE (WRITE) from the NORMALISE pulldown menu. This will call up the specification of a normalise job in the batch editor.

- Highlight "Data", select New "Subject",

- Highlight "Deformation Field" and select the `y_sM00223_002.nii` file that you created in the previous section,

- Highlight "Images to Write" and select all of the realigned functional images `fM000*.img`. You can right click over the listed files, choose "Select all" and press "Done".

- In the "Writing Options", change "Voxel sizes" from [2 2 2] to [3 3 3]. This step is not strictly necessary: it will write images out at a resolution closer to that at which they were acquired.

- Press "Save", save the job as `normalise_functional.mat` and then press the RUN button.

SPM will then write spatially normalised files to the functional data directory. These files have the prefix `w`.

If you wish to superimpose a subject's functional activations on their own anatomy[2] you will also need to apply the spatial normalisation parameters to their (bias-corrected) anatomical image. To do this

- Select NORMALISE (WRITE), highlight "Data", select "New Subject".

- Highlight "Deformation Field", select the `y_sM00223_002.nii` file that you created in the previous section, press "Done".

- Highlight "Images to Write", select the bias-corrected structural eg. `msM00223_002.nii`, press "Done".

- Open "Writing Options", select voxel sizes and change the default [2 2 2] to [1 1 3] which corresponds to the original resolution of the images.

- Save the job as `normalise_structural.mat` and press the RUN button.

31.2.5 Smoothing

Press the SMOOTH button. This will call up the specification of a smooth job in the batch editor.

- Select "Images to Smooth" and then select the spatially normalised files created in the last section eg. `wf*.img`. This can be done efficiently by changing the filter in the SPM file selector to `^wf.*`. SPM will then only list those files beginning with letters `wf` ie. those that have been spatially normalised.

- Highlight "FWHM" and change [8 8 8] to [6 6 6]. This will smooth the data by 6mm in each direction.

- Save the job as `smooth.mat` and press the Run button.

An example of functional image and its smoothed version is displayed on Figure 31.7.

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[2]Beginners may wish to skip this step, and instead just superimpose functional activations on an "average structural image".
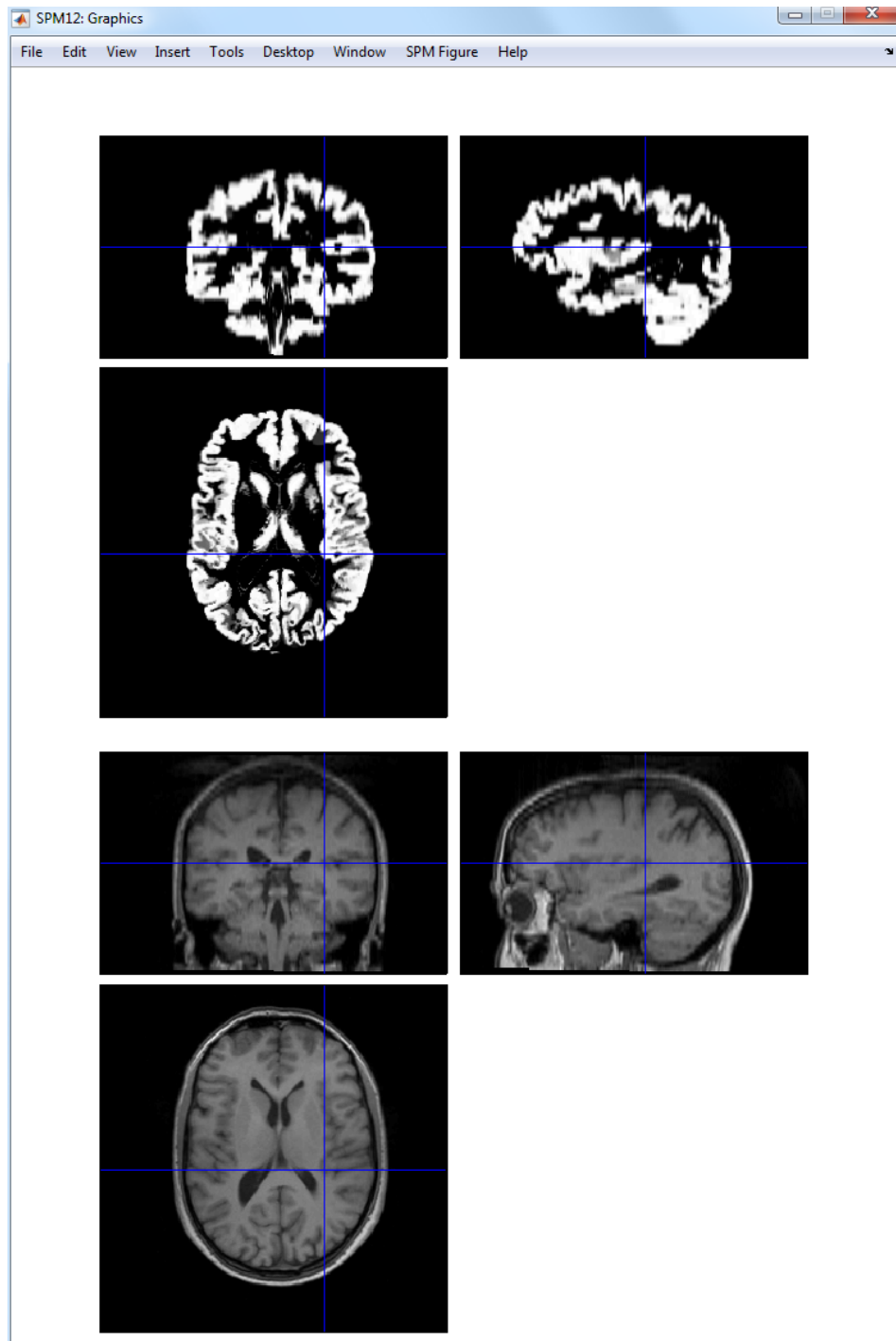
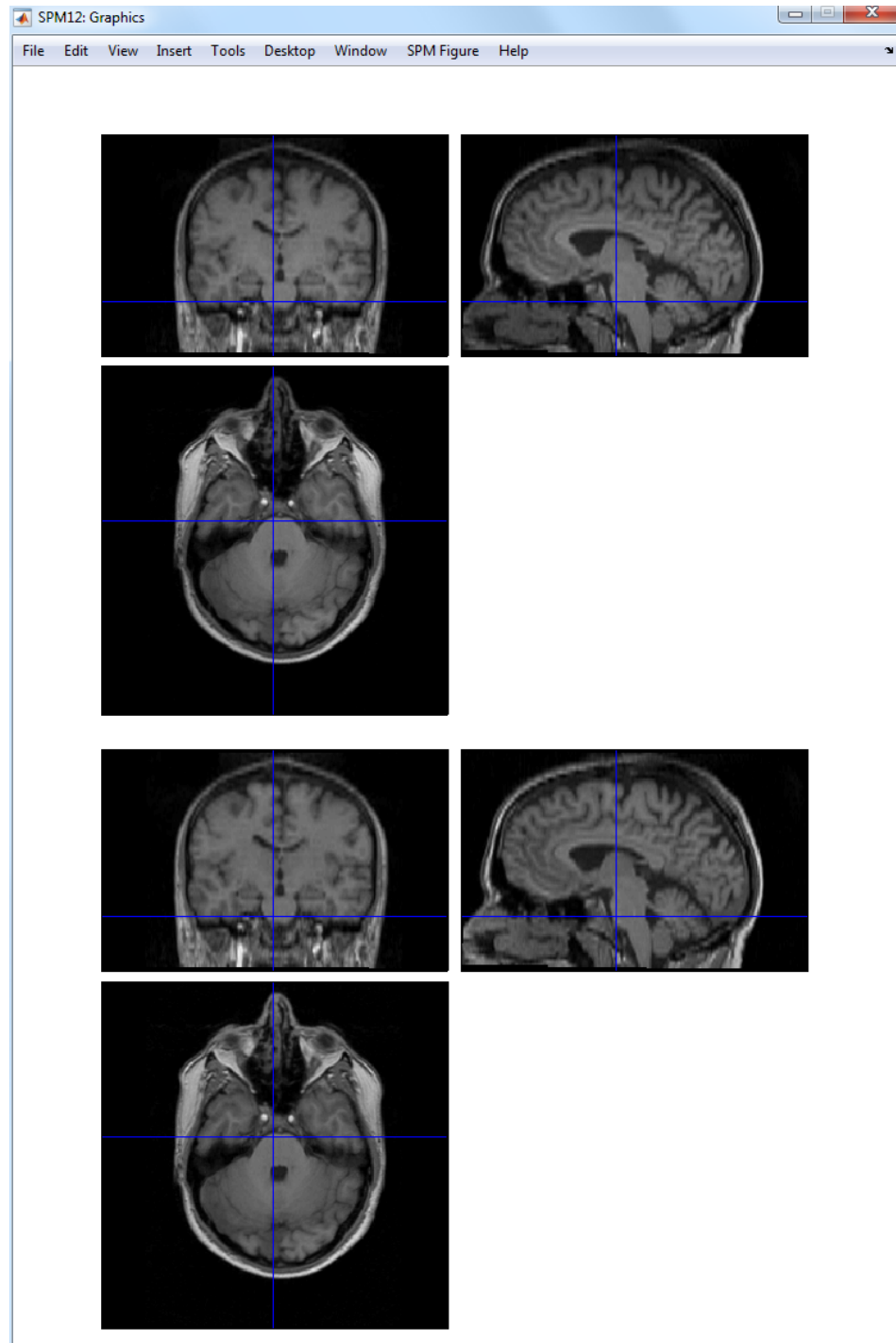Figure 31.5: *Gray matter image and "registered" structural image.*

Figure 31.6: *Structural image (top) and bias-corrected structural image (bottom). Notice that the original structural is darker at the top than at the bottom. This non-uniformity has been removed in the bias-corrected image.*
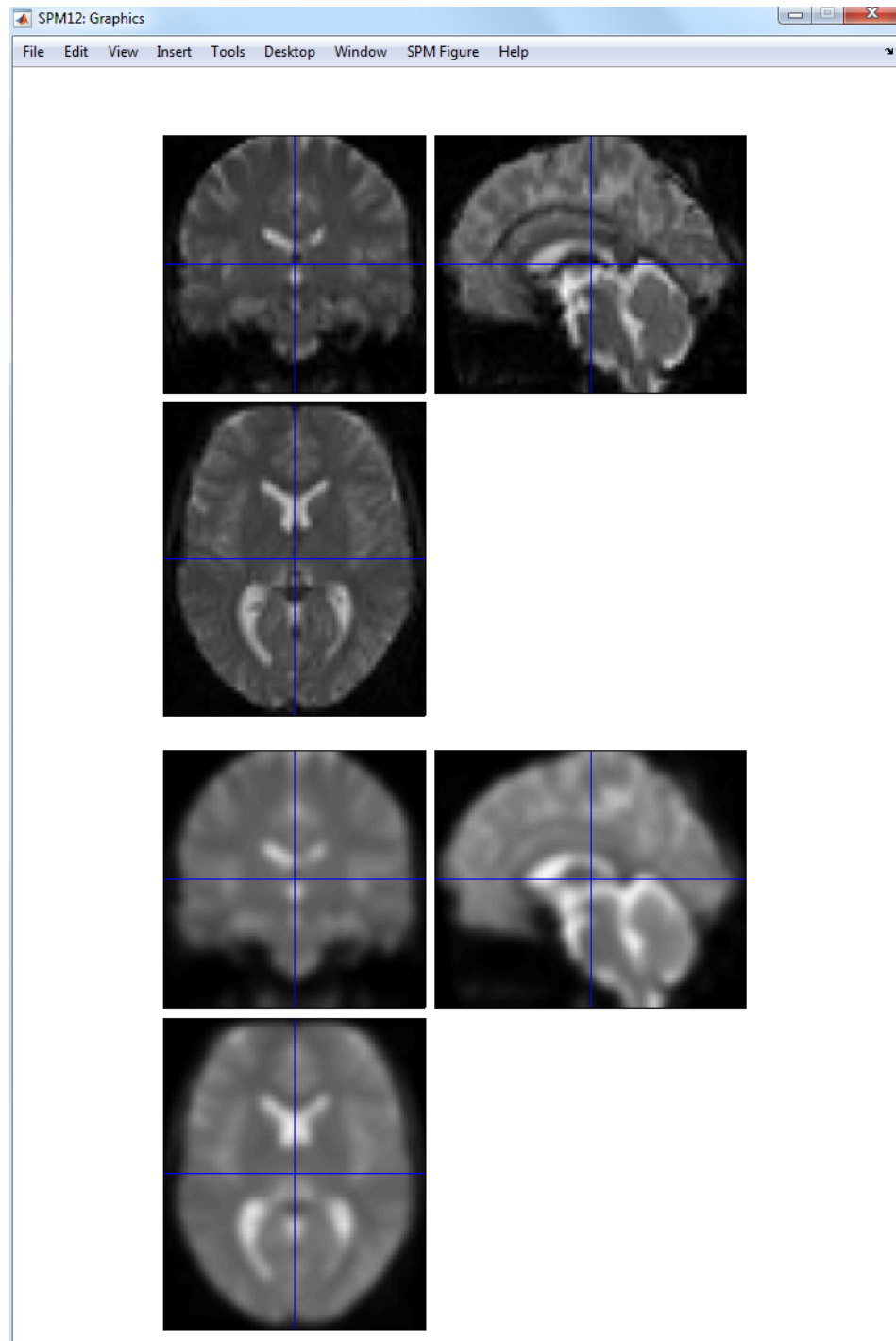
Figure 31.7: *Functional image (top) and 6mm-smoothed functional image (bottom). These images were obtained using SPM's "CheckReg" facility.*

31.3 Model specification, review and estimation

Press the "Specify 1st-level" button. This will call up the specification of an fMRI specification job in the batch editor. Then

- Open the "Timing parameters" option.

- Highlight "Units for design" and select "Scans".

- Highlight "Interscan interval" and enter 7. That's the TR in seconds.

- Highlight "Data and Design" and select "New Subject/Session". Then open the newly created "Subject/Session" option.

- Highlight "Scans" and use SPM's file selector to choose the 84 smoothed, normalised functional images ie `swfM00223_016.img` to `swfM00223_099.img`. These can be selected easily using the `^sw.*'` filter, and select all. Then press "Done".

- Highlight "Condition" and select "New condition".

- Open the newly created "Condition" option. Highlight "Name" and enter "listening". Highlight "Onsets" and enter "6:12:84". Highlight "Durations" and enter "6".

- Highlight "Directory" and select the `DIR/classical` directory you created earlier.

- Save the job as `specify.mat` and press the `Run` button.

SPM will then write an `SPM.mat` file to the `DIR/classical` directory. It will also plot the design matrix, as shown in Figure 31.8.

At this stage it is advisable to check your model specification using SPM's review facility which is accessed via the "Review" button. This brings up a "design" tab on the interactive window clicking on which produces a pulldown menu. If you select the first item "Design Matrix" SPM will produce the image shown in Figure 31.8. If you select "Explore" then "Session 1" then "listening", SPM will produce the plots shown in Figure 31.9.

If you select the second item on the "Design" tab, "Design Orthogonality", SPM will produce the plot shown in Figure 31.10. Columns x_1 and x_2 are orthogonal if the inner product $x_1^T x_2 = 0$. The inner product can also be written $x_1^T x_2 = |x_1||x_2|cos\theta$ where $|x|$ denotes the length of x and θ is the angle between the two vectors. So, the vectors will be orthogonal if $cos\theta = 0$. The upper-diagonal elements in the matrix at the bottom of figure 31.10 plot $cos\theta$ for each pair of columns in the design matrix. Here we have a single entry. A degree of non-orthogonality or collinearity is indicated by the gray shading.

31.3.1 Estimate

Press the ESTIMATE button. This will call up the specification of an fMRI estimation job in the batch editor. Then

- Highlight the "Select SPM.mat" option and then choose the `SPM.mat` file saved in the `classical` subdirectory.

- Save the job as `estimate.mat` and press the `Run` button.

SPM will write a number of files into the selected directory including an `SPM.mat` file.

31.4 Inference

After estimation:

- Press "Results".

- Select the `SPM.mat` file created in the last section.

This will invoke the contrast manager.