

Chapter 26

Face data

As a third and more sophisticated example, consider the data from a repetition priming experiment performed using event-related fMRI. Briefly, this is a 2x2 factorial study with factors ‘fame’ and ‘repetition’ where famous and non-famous faces were presented twice against a checkerboard baseline (for more details, see [33]). The subject was asked to make fame judgements by making key presses. There are thus four event-types of interest; first and second presentations of famous and non-famous faces, which we denote N1, N2, F1 and F2. The experimental stimuli and timings of events are shown in Figures 26.1 and 26.2.

Images were acquired using continuous Echo-Planar Imaging (EPI) with TE=40ms, TR=2s and 24 descending slices ($64 \times 64 \times 3 \text{mm}^2$), 3mm thick with a 1.5mm gap. The data archive is available from http://www.fil.ion.ucl.ac.uk/spm/data/face_rep_SPM5.html. This contains 351 Analyse format functional images `sM03953_0005_*.img` of dimension $64 \times 64 \times 24$ with $3 \text{mm} \times 3 \text{mm} \times 4.5 \text{mm}$ voxels. A structural image is also provided `sM03953_0007.img` also in Analyse format.

To analyse the data, first create a new directory DIR eg. `c:\home\wpenny\fmri_analysis\face-rep\all`, in which to place the results of your analysis. Then create 4 subdirectories (i) `jobs`, (ii) `categorical`, (iii) `parametric` and (iv) `bayesian`. As the analysis proceeds these directories will be filled with job-specification files, design matrices and models estimated using classical or Bayesian methods.

As well as the classical/Bayesian distinction we will show how this data can be analysed from a parametric as well as a categorical perspective. We will look at the main effects of fame and repetition and in the parametric analysis we will look at responses as a function of ‘lag’, that is, the number of faces intervening between repetition of a specific face.

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 (1) the top-left or ‘command’ 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 base window.

26.1 Spatial pre-processing

26.1.1 Display

Display eg. the first functional image using the ‘Display’ button. Note orbitofrontal and inferior temporal drop-out and ghosting. This can be seen more clearly by selecting ‘brighten if necessary’ from the ‘Effects’ tab at the top of the graphics window.

26.1.2 Realignment

Under the spatial pre-processing section of the SPM base window select ‘Realign’ from the ‘Realign’ pulldown menu. This will call up a realignment job specification in the graphics window. Then

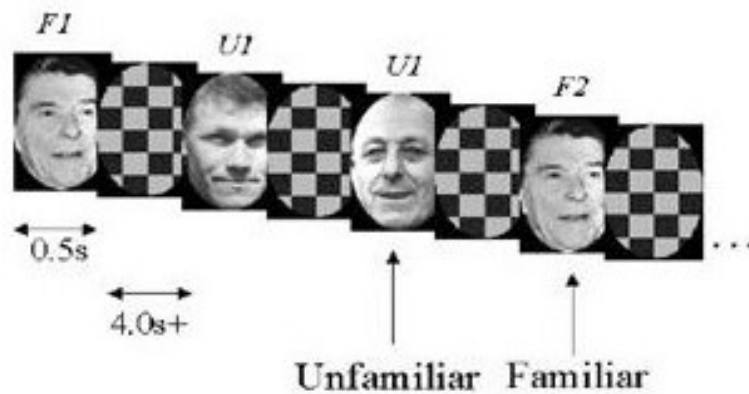


Figure 26.1: *Face repetition paradigm.* There were 2 presentations of 26 Famous and 26 Nonfamous Greyscale photographs, for 0.5s each, randomly intermixed. The minimal Stimulus Onset Asynchrony (SOA)=4.5s, with probability 2/3 (ie 1/3 null events). The subject made one of two right finger key presses denoting whether or not the subject thought the face was famous.

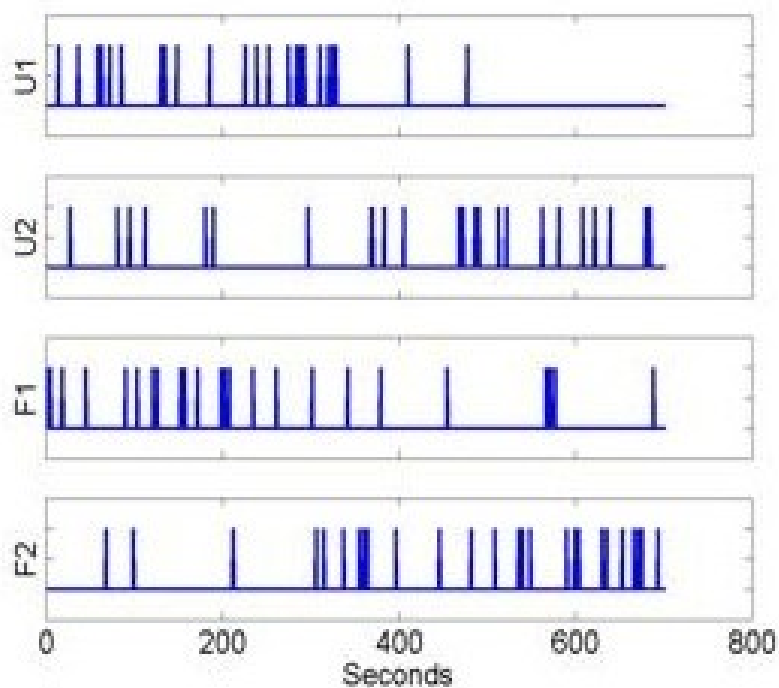


Figure 26.2: *Time series of events.*

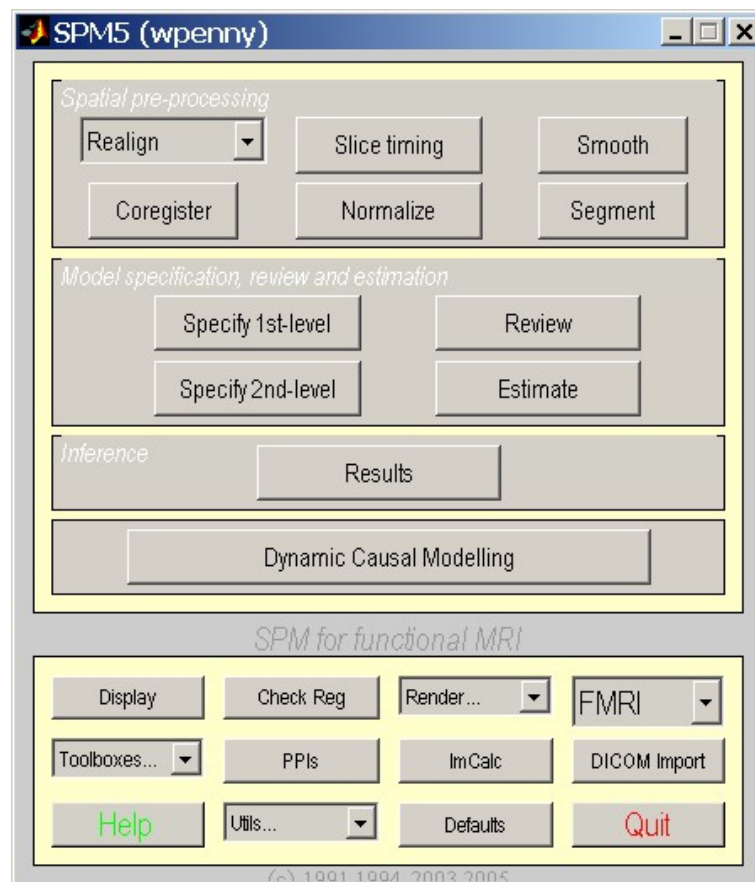


Figure 26.3: The SPM base window comprises three sections *i*) spatial pre-processing, *(ii)* model specification, review and estimation and *(iii)* inference.

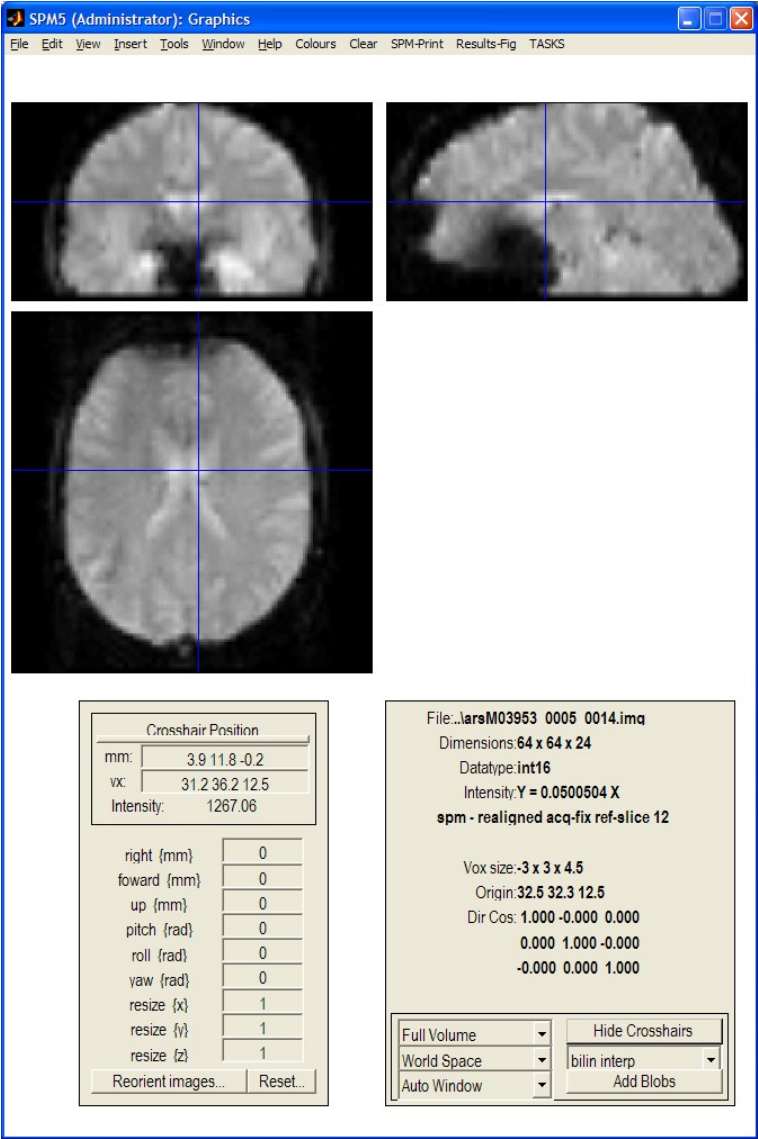


Figure 26.4: Signal dropout in EPI images.

- Select ‘New Realign:Estimate and Reslice’
- Open the newly created ‘Realign:Estimate and Reslice’ option.
- Highlight data, select ‘New Session’, then highlight the newly created ‘Session’ option.
- Select ‘Specify Files’ and use the SPM file selector to choose all of your functional images eg. `sM03953_0005_*.img`.
- Save the job file as eg. `DIR/jobs/realign.mat`.
- Press the RUN button in the graphics window.

This will run the realign job which will write realigned images into the directory where the functional images are. These new images will be prefixed with the letter ‘r’. SPM will then plot the estimated time series of translations and rotations shown in Figure 26.5. These data, the realignment parameters, are also saved to a file eg. `rp_sM03953_0005_0006.txt`, so that these variables can be used as regressors when fitting GLMs. To prepare for this copy the file into the `DIR\jobs\` directory and rename it `moveparams.txt`. This allows movements effects to be discounted when looking for brain activations.

SPM will also create a mean image eg. `meansM03953_0005_0006.img` which will be used in the next step of spatial processing - coregistration.

26.1.3 Slice timing correction

Press the ‘Slice timing’ button. This will call up the specification of a slice timing job in the graphics window. Note that these data consist of $N=24$ axial slices acquired continuously with a $TR=2s$ (ie $TA = TR - TR/N$, where TA is the time between the onset of the first and last slice of one volume, and the TR is the time between the onset of the first slice of one volume and the first slice of next volume) and in a descending order (ie, most superior slice was sampled first). The data however are ordered within the file such that the first slice (slice number 1) is the most inferior slice, making the slice acquisition order `[24 23 22 ... 1]`.

- Open the ‘Slice Timing’ option
- Highlight ‘Data’ and select ‘New Sessions’
- Highlight the newly create ‘Sessions’ option, ‘Specify Files’ and select the 351 realigned functional images using the filter `^r.*`.
- Select ‘Number of Slices’ and enter 24
- Select TR and enter 2
- Select TA and enter 1.92 (or $2 - 2/24$)
- Select ‘Slice order’ and enter `24:-1:1`
- Select ‘Reference Slice’, and enter 12
- Save the job as `slice_timing.mat` and press ‘Run’

SPM will write slice-time corrected files with the prefix ‘a’ in the functional data directory.

26.1.4 Coregistration

Press the ‘Coreg’ button. This will call up the specification of a coregistration job in the graphics window.

- Select New ”Coreg:Estimate”
- Double-click on the newly created Coreg:Estimate
- Highlight ‘Reference Image’ and then select the mean functional image `meansM03953_0005_0006.img`

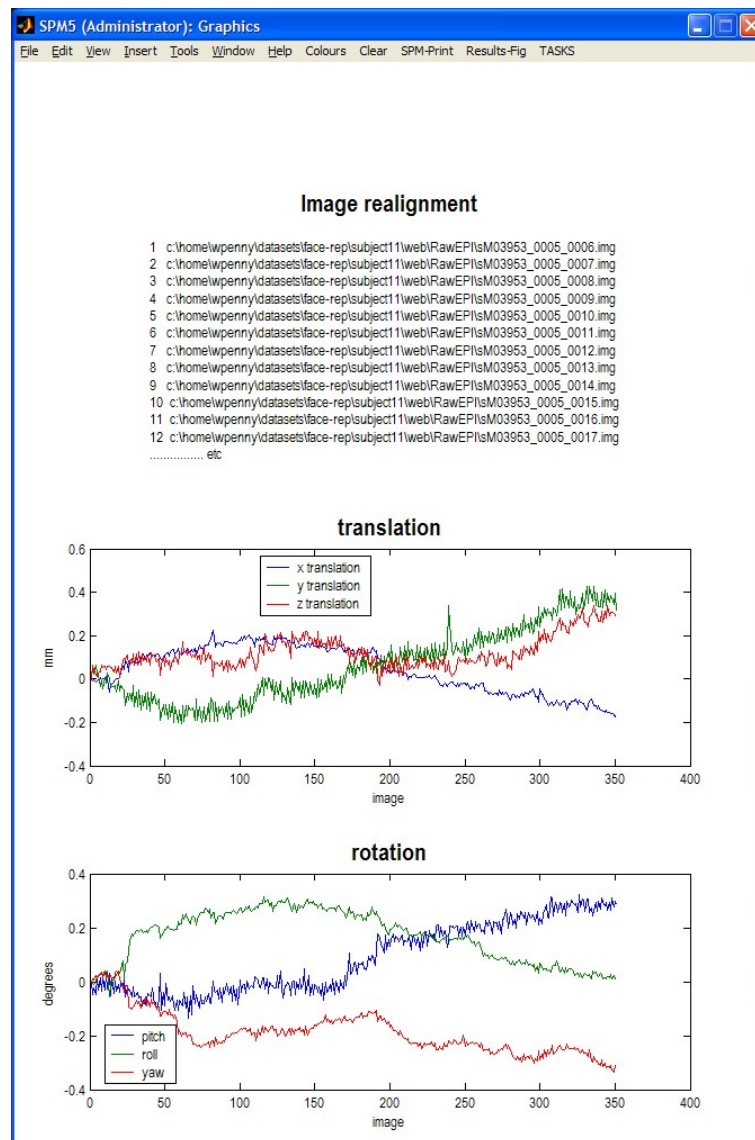


Figure 26.5: *Realignment of face data. Movement less than the size of a voxel, which for this data set is 3mm, is not considered problematic.*

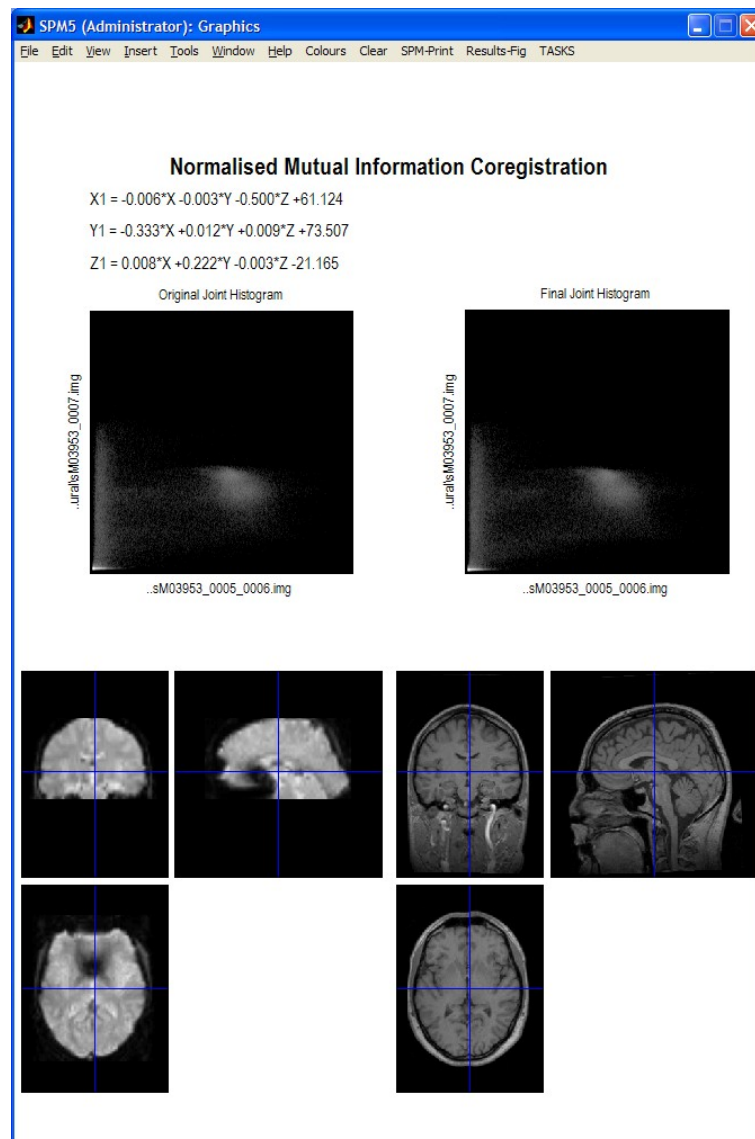


Figure 26.6: *Mutual Information Coeregistration of Face data.*

- Highlight ‘Source Image’ and then select the structural image eg. `sM03953_0007.img`.
- Press the Save button and save the job as `coreg.job`
- Then press RUN

SPM will then implement a coregistration between the structural and functional data that maximises the mutual information. The image in figure 26.6 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 `sM03953_0007.img`.

26.1.5 Segmentation

Press the ‘Segment’ button. This will call up the specification of a segmentation job in the graphics window. Highlight the Data field and then select the subjects coregistered anatomical image eg. `sM03953_0007.img`. 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. SPM will create, by default, gray and white matter images and bias-field corrected structural image. These can be

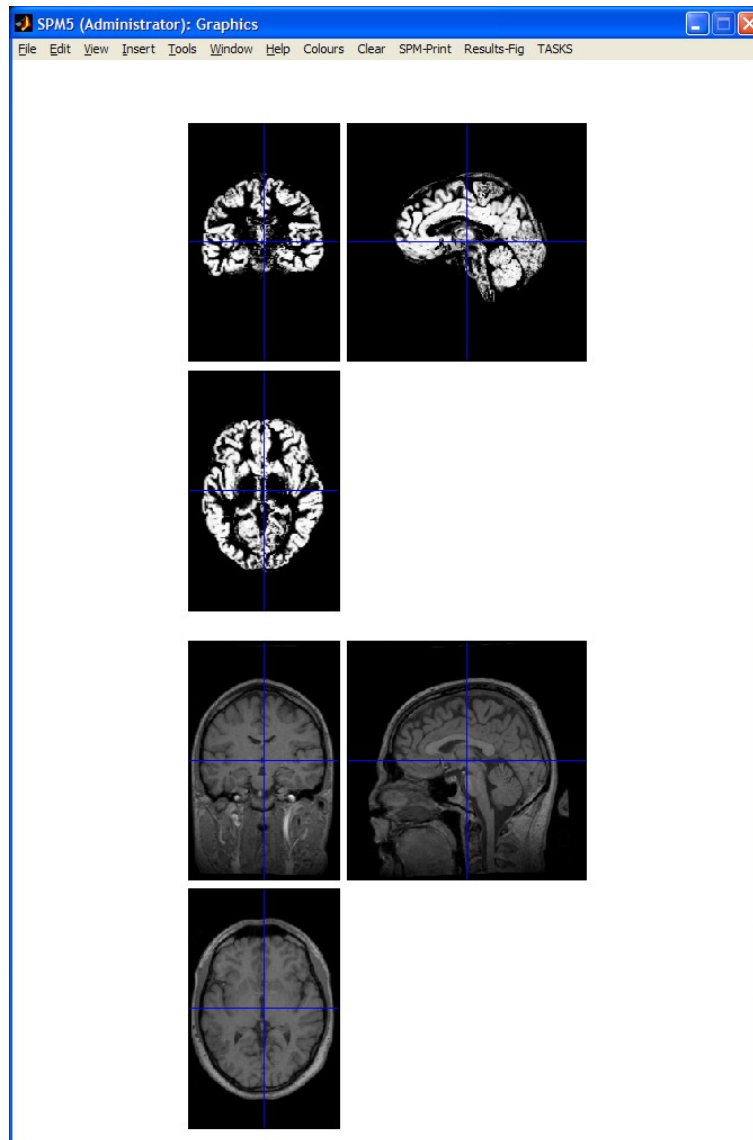


Figure 26.7: *Gray matter (top) produced by segmentation of structural image (below).*

viewed using the CheckReg facility as described in the previous section. Figure 26.7 shows the gray matter image, `c1sM03953_0007.img`, along with the original structural.¹

SPM will also write a spatial normalisation eg. `sM03953_0007_seg_sn.mat` file in the original structural directory. This will be used in the next section to normalise the functional data.

26.1.6 Normalize

Press the ‘Normalize’ button. This will call up the specification of a normalise job in the graphics window.

- Select a New “Normalise:Write” field. This allows previously estimated warps to be applied to a series of images.
- Highlight ‘Data’, select New “Subject”

¹Segmentation can sometimes fail if the source (structural) image is not close in orientation to the MNI templates. It is generally advisable to manually orient the structural to match the template (ie MNI space) as close as possible by using the ‘Display’ button, adjusting x/y/z/pitch/roll/yaw, and then pressing the ‘Reorient’ button.

- Open ‘Subject’, highlight ‘Parameter File’ and select the `sM03953_0007_seg_sn.mat` file that you created in the previous section
- Highlight images to write and select all of the slice-time corrected, realigned functional images ‘arsM*.img’. Note: This can be done efficiently by changing the filter in the SPM file selector to `^ar.*`. You can then right click over the listed files, choose ‘Select all’. You might also want to select the mean functional image created during realignment (which would not be affected by slice-time correction), i.e, the `meansM03953_0005_006.img`. Then press ‘Done’.
- Open ‘Writing Options’, and change ‘Voxel sizes’ from `[2,2,2]` to `[3,3,3]`.²
- Press ‘Save’, save the job as `normalise.mat` and then press ‘Run’.

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 anatomy³ you will also need to apply the spatial normalisation parameters to their (bias-corrected) anatomical image. To do this

- Press ‘Normalise’, select New ”Normalise:Write”
- Open ‘Normalise: Write’, highlight ‘Data’, select New ”Subject”
- Open ‘Subject’
- Highlight ‘Parameter File’, select the `sM03953_0007_seg_sn.mat` file that you created in the previous section, press ‘Done’.
- Highlight ‘Images to Write’, select the bias-corrected structural eg. `msM03953_0007.img`, press ‘Done’.
- Open ‘Writing Options’, select voxel sizes and change the default `[2 2 2]` to `[1 1 1]` which better matches the original resolution of the images `[1 1 1.5]`.
- Save the job as `norm_struct.mat` and press ‘Run’.

26.1.7 Smoothing

Press the ‘Smooth’ button⁴. This will call up the specification of a smooth job in the graphics window.

- Open ‘Smooth’, select ‘Images to Smooth’ and then select the spatially normalised files created in the last section eg. `war*.img`.
- Save the job as `smooth.mat` and press ‘Run’.

This will smooth the data by (the default) 8mm in each direction, the default smoothing kernel width.

²This step is not strictly necessary. It will write images out at a resolution closer to that at which they were acquired. This will speed up subsequent analysis and is necessary, for example, to make Bayesian fMRI analysis computationally efficient.

³Beginners may wish to skip this step, and instead just superimpose functional activations on an ‘canonical structural image’.

⁴The smoothing step is unnecessary if you are only interested in Bayesian analysis of your functional data.

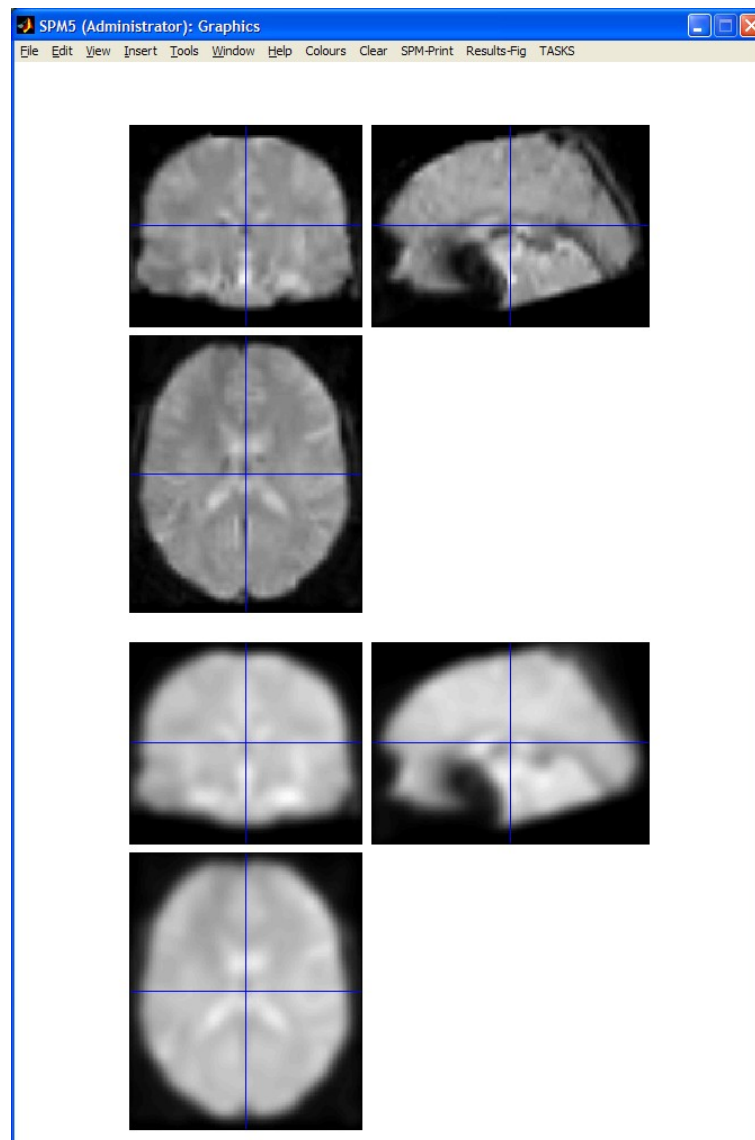


Figure 26.8: *Functional image (top) and 8mm-smoothed functional image (bottom). These images were plotted using SPM's 'CheckReg' facility.*

26.2 Modelling categorical responses

Before setting up the design matrix we must first load the Stimulus Onsets Times (SOTs) and movement parameters into matlab. SOTs are stored in the `sots.mat` file in a cell array such that eg. `sot{1}` contains stimulus onset times in TRs for event type 1, which is N1. Event-types 2,3 and 4 are N2, F1 and F2.⁵

- At the matlab command prompt type ‘load sots’
- Then type ‘load movepars.txt’

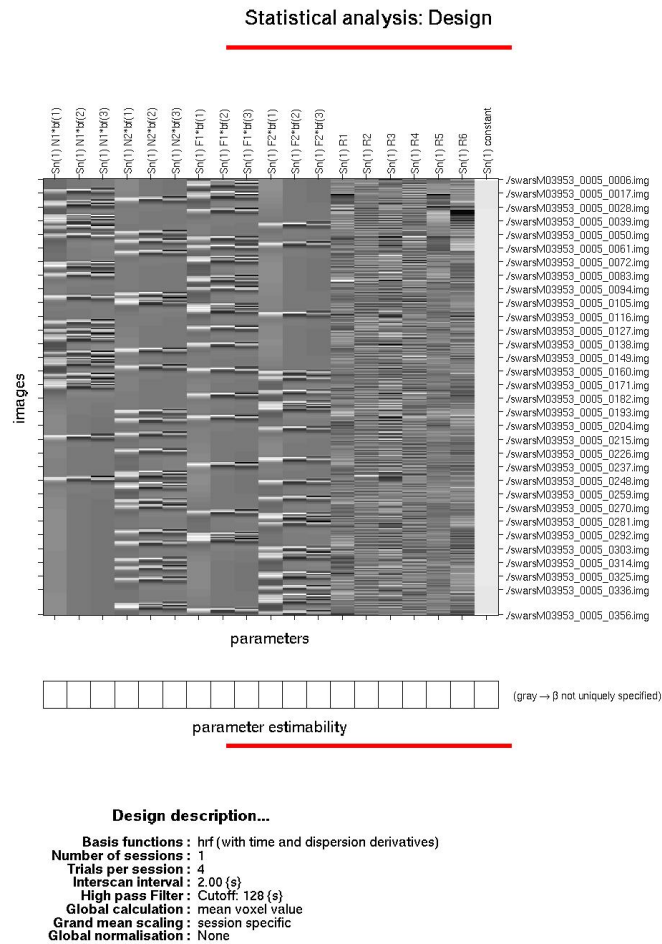
Now press the ‘Specify 1st-level’ button. This will call up the specification of a fMRI specification job in the graphics window. Then

- Open the fMRI model specification option
- Open the ‘Timing paramaters’ option
- Highlight ‘Units for design’ and select ‘Scans’
- Highlight ‘Interscan interval’ and enter 2
- Highlight ‘Microtime resolution’ and enter 24
- Highlight ‘Microtime onset’ and enter 12. These last two options make the creating of regressors commensurate with the slice-time correction we have applied to the data, given that there are 24 slices and that the reference slice to which the data were slice-time corrected was the 12th (middle slice in time).
- 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 351 smoothed, normalised, slice-time corrected, realigned functional images ie `swarsM.img`. These can be selected easily using the `~swar.*` filter, and select all. Then press ‘Done’.
- Highlight ‘Conditions’ and select ‘New condition’⁶
- Open the newly created ‘Condition’ option. Highlight ‘Name’ and enter ‘N1’. Highlight ‘Onsets’ and enter ‘sot{1}’. Highlight ‘Durations’ and enter 0.
- Highlight ‘Condition’ and select ‘Replicate condition’
- Open the newly created ‘Condition’ option (the lowest one). Highlight ‘Name’ and change to ‘N2’. Highlight ‘Onsets’ and enter ‘sot{2}’.
- Highlight ‘Condition’ and select ‘Replicate condition’
- Open the newly created ‘Condition’ option (the lowest one). Highlight ‘Name’ and change to ‘F1’. Highlight ‘Onsets’ and enter ‘sot{3}’.
- Highlight ‘Condition’ and select ‘Replicate condition’
- Open the newly created ‘Condition’ option (the lowest one). Highlight ‘Name’ and change to ‘F2’. Highlight ‘Onsets’ and enter ‘sot{4}’.
- Highlight ‘Multiple Regressors’ and select the `movepars.txt` file.⁷

⁵Unlike previous analyses of these data in SPM99 and SPM2, we will not bother with extra event-types for the (rare) error trials.

⁶It is also possible to enter information about all of the conditions in one go. This requires much less button pressing and can be implemented by highlighting the ‘Multiple conditions’ option and then selecting the `all-conditions.mat` file, which is also provided on the webpage.

⁷It is also possible to enter regressors one by one by highlighting ‘Regressors’ and selecting ‘New Regressor’ for each one. Here, we benefit from the fact that the realignment stage produced a text file with the correct number of rows (351) and columns (6) for SPM to add 6 regressors to model (linear) rigid-body movement effects.

Figure 26.9: *Design matrix.*

- Highlight ‘Factorial Design’, select ‘New Factor’, open the newly created ‘Factor’ option, highlight ‘Name’ and enter ‘Fam’, highlight ‘Levels’ and enter 2.
- Highlight ‘Factorial Design’, select ‘New Factor’, open the newly created ‘Factor’ option, highlight ‘Name’ and enter ‘Rep’, highlight ‘Levels’ and enter 2⁸.
- Open ‘Canonical HRF’ under ‘Basis Functions’. Select ‘Model derivatives’ and select ‘Time and Dispersion derivatives’.
- Highlight ‘Directory’ and select the `DIR/categorical` directory you created earlier.
- Save the job as `categorical_spec.mat` and press ‘RUN’

SPM will then write an `SPM.mat` file to the `DIR/categorical` directory. It will also plot the design matrix, as shown in Figure 26.9.

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

⁸The order of naming these factors is important - the factor to be specified first is the one that ‘changes slowest’ i.e. as we go through the list of conditions N1,N2,F1,F2 the factor ‘repetition’ changes every condition and the factor ‘fame’ changes every other condition. So ‘Fam’ changes slowest and is entered first.

window clicking on which produces a pulldown menu. If you select the first item ‘Design Matrix’ SPM will produce the image shown in Figure 26.9. If you select ‘Explore’ then ‘Session 1’ then ‘N1’, SPM will produce the plots shown in Figure 26.10.

26.2.1 Estimate

Press the ‘Estimate’ button. This will call up the specification of an fMRI estimation job in the graphics window. Then

- Open the ‘fMRI model estimation’ option
- Highlight the ‘Select SPM.mat’ option and then choose the SPM.mat file saved in the `DIR/categorical` directory
- Save the job as `categorical_est.job` and press Run

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

26.2.2 Inference for categorical design

Press ‘Results’ and select the SPM.mat file from `DIR\categorical`. This will again invoke the contrast manager. Because we specified that our model was using a ‘Factorial design’ a number of contrasts have been specified automatically, as shown in Figure 26.11.

- Select contrast number 5. This is a t-contrast **Positive effect of condition_1** This will show regions where the average effect of presenting faces is significantly positive, as modelled by the first regressor (hence the `_1`), the canonical HRF. Press ‘Done’.
- *Mask with other contrast ? [Yes/No]*
- Specify No.
- *Title for comparison ?*
- Enter ‘Canonical HRF: Faces > Baseline’
- *p value adjustment to control: [FWE/FDR/none]*
- Select FWE
- *Corrected p value(family-wise error)*
- Accept the default value, 0.05
- *Extent threshold {voxels} [0]*
- Accept the default value, 0

SPM will then produce the MIP shown in Figure 26.12.

26.2.3 Statistical tables

To get a summary of local maxima, press the ‘Volume’ button in the p-values section of the interactive window. This will list all clusters above the chosen level of significance as well as separate (>8mm apart) maxima within a cluster, with details of significance thresholds and search volume underneath, as shown in Figure 26.12 The columns in volume table show, from right to left:

- x, y, z (mm): coordinates in MNI space for each maximum
- voxel-level: the chance (p) of finding (under the null hypothesis) a voxel with this or a greater height (T- or Z-statistic), corrected (FWE or FDR)/ uncorrected for search volume.

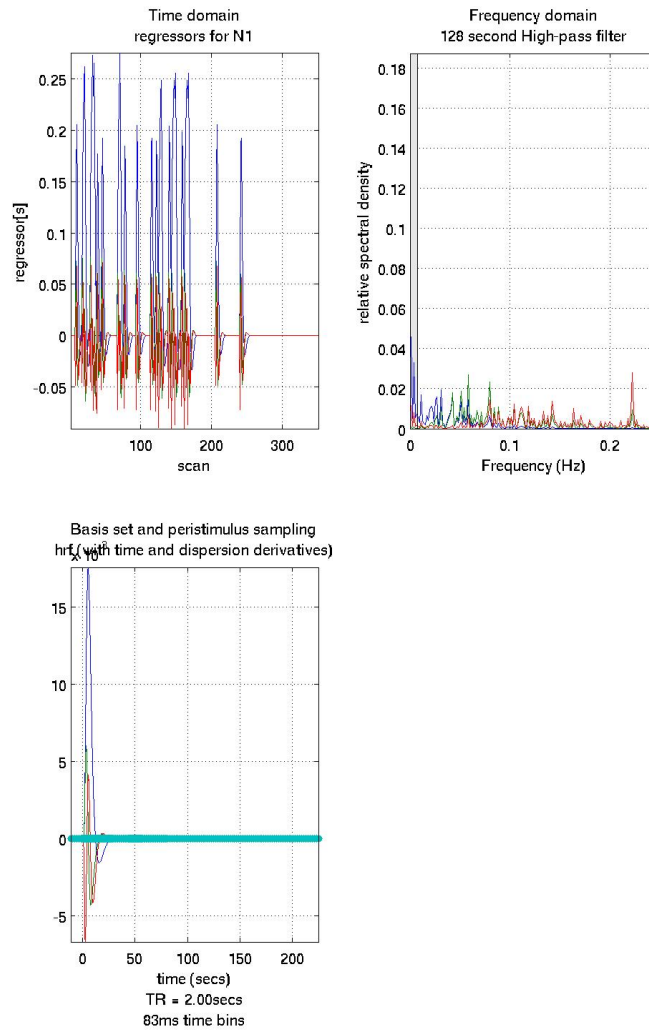


Figure 26.10: *Exploring the design matrix in Figure 26.9. This shows the time series of the ‘active’ regressor (top left), the three basis functions used to convert assumed neuronal activity into hemodynamic activity (bottom left), and a frequency domain plot of the three regressors for the basis functions in this condition (top right). The frequency domain plot shows that the frequency content of the ‘N1’ condition is generally above the set frequencies that are removed by the High Pass Filter (HPF) (these are shown in gray - in this model we accepted the default HPF cut-off of 128s or 0.008Hz).*

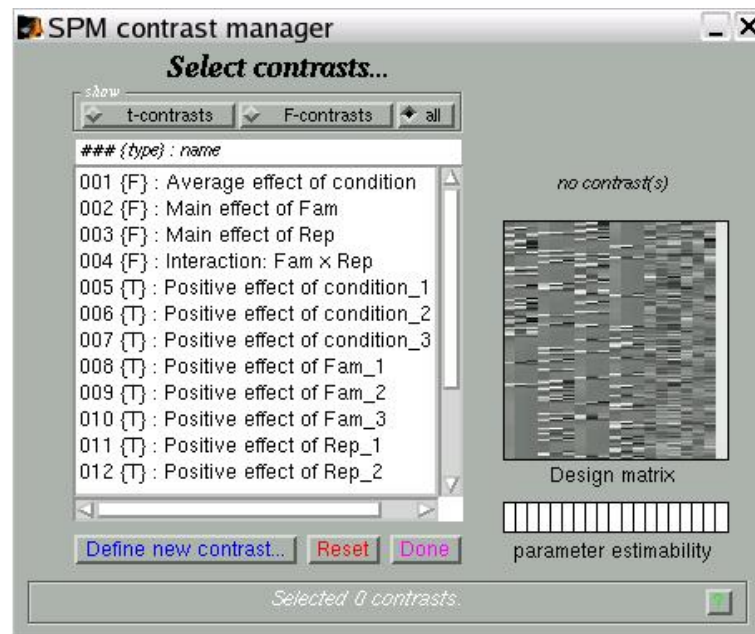


Figure 26.11: Contrast Manager containing default contrasts for categorical design.

- cluster-level: the chance (p) of finding a cluster with this many(ke) or a greater number of voxels, corrected / uncorrected for search volume
- set-level: the chance (p) of finding this (c) or a greater number of clusters in the search volume

Right-click on the MIP and select 'goto global maximum'. The cursor will move to (39 -72 -12). You can view this activation on the subject's normalised, attenuation-corrected structural ('wmsM03953_0007.img'), which gives best anatomical precision, or on the normalised mean functional (wmeansM03953_0005_0006.img), which is closer to the true data and spatial resolution (including distortions in the functional EPI data).

If you select 'plot' and choose 'Contrast of estimates and 90% C.I' (confidence interval), and select the 'Average effect of condition' contrast, you will see three bars corresponding to the parameter estimates for each basis function (summed across the 4 conditions). The BOLD impulse response in this voxel loads mainly on the canonical HRF, but also significantly (given that the error bars do not overlap zero) on the temporal and dispersion derivatives (see next Chapter).

26.2.4 F-contrasts

To assess the main effect of repeating faces, as characterised by both the hrf *and* its derivatives, . This is really asking whether repetition changes the *shape* of the impulse response (e.g. it might affect its latency but not peak amplitude), at least the range of shapes defined by the three basis functions. Because we have told SPM that we have a factorial design, this required contrast will have been created automatically - it is number 3.

- Press 'Results' and select the SPM.mat file in the DIR/categorical directory
- Select the 'F-contrast' toggle and the contrast number 3, as shown in Figure 26.13. Press 'Done'.
- Mask with other contrast ? [Yes/No]
- Specify Yes.

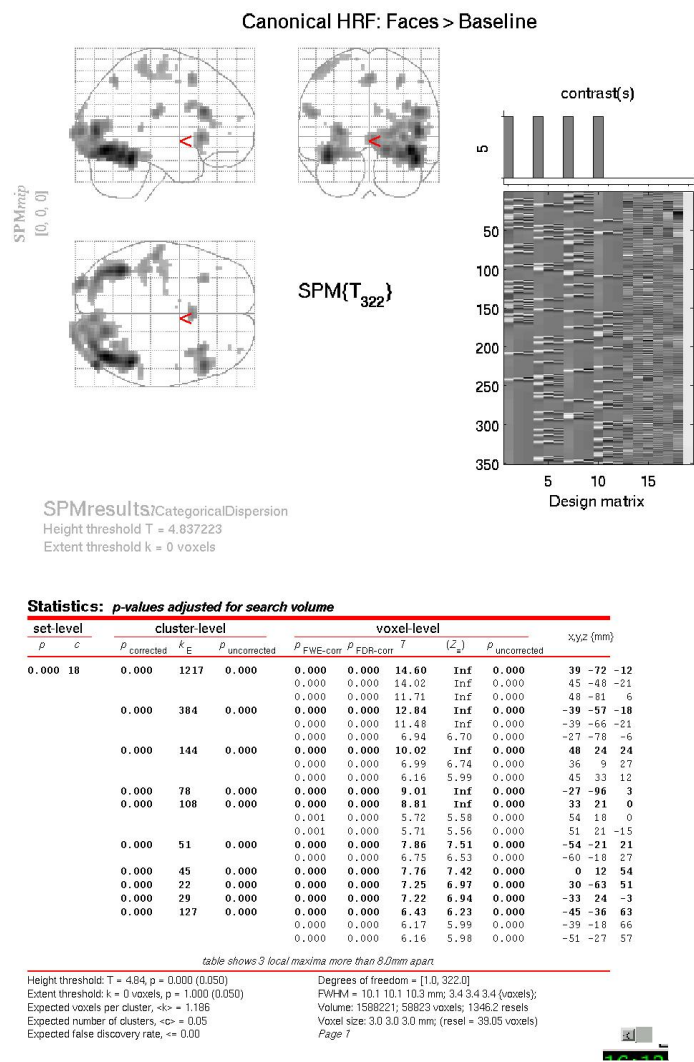


Figure 26.12: MIP and Volume table for Canonical HRF: Faces > Baseline.

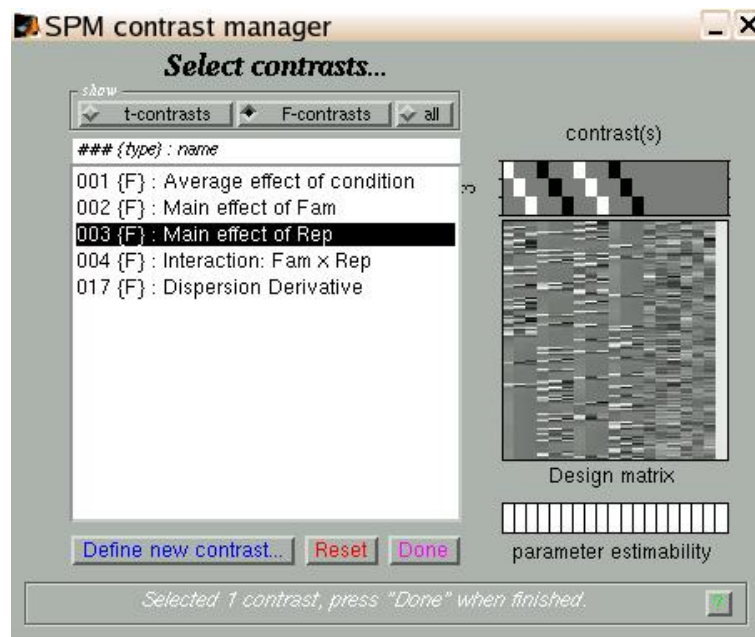


Figure 26.13: Contrast manager showing selection of the first contrast 'Main effect of Rep (repetition; F1 and N1 vs F2 and N2)'

- Select contrast 5 - Positive effect of condition 1 (the T-contrast of activation versus baseline, collapsed across conditions, that we evaluated above)
- *uncorrected mask p-value ?*
- Change to 0.001
- *nature of mask?*
- Select 'inclusive'
- *Title for comparison ?*
- Keep 'Main effect of Rep (masked with ...) '
- *p value adjustment to control: [FWE/FDR/none]*
- Select none
- *threshold (F or p value)*
- Accept the default value, 0.001
- *Extent threshold {voxels} [0]*
- Accept the default value, 0

A MIP should then appear, the top half of which should look like Figure 26.14.

Note that this contrast will identify regions showing any effect of repetition (e.g, decreased or increased amplitudes) *within* those regions showing activations (on the canonical HRF) to faces versus baseline (at $p < .05$ uncorrected). Only two small blobs will appear - one in right ventral temporal cortex (45 -60 -9).

If you press plot and select 'Event-related responses', then 'F1', then 'fitted response and PSTH', you will see the best fitting linear combination of the canonical HRF and its two derivatives (thin red line), plus the "selectively-averaged" data (peri-stimulus histogram, PSTH), based on an FIR refit (see next Chapter). If you then select the 'hold' button on the Input window, and

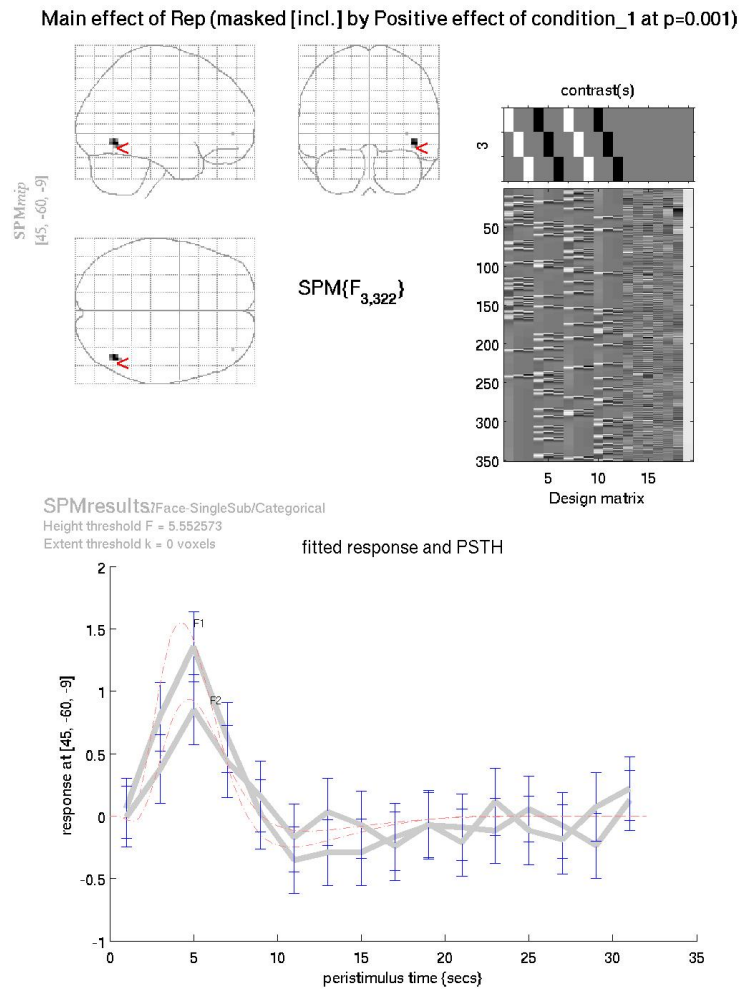


Figure 26.14: MIP for Main effect of Rep, masked inclusively with Canonical HRF: Faces > Baseline at $p<.001$ uncorrected. Shown below are the best-fitting responses and peri-stimulus histograms (PSTH) for F1 and F2.

then 'plot' and repeat the above process for the 'F2' rather than 'F1' condition, you will see two estimated event-related responses, in which repetition decreases the peak response (ie $F2 < F1$), as shown in Figure 26.14.

You can explore further F-contrasts, which are a powerful tool once you understand them. For example, the MIP produced by the 'Average effect of condition' F-contrast looks similar to the earlier T-contrast, but importantly shows the areas for which the sums across conditions of the parameter estimates for the canonical hrf *and/or* its temporal derivative *and/or* its dispersion derivative are different from zero (baseline). The first row of this F-contrast ($[1\ 0\ 0\ 1\ 0\ 0\ 1\ 0\ 0\ 1\ 0\ 0]$) is also a two-tailed version of the above T-contrast, ie testing for both activations and deactivations versus baseline. This also means that the F-contrasts $[1\ 0\ 0\ 1\ 0\ 0\ 1\ 0\ 0\ 1\ 0\ 0]$ and $[-1\ 0\ 0\ -1\ 0\ 0\ -1\ 0\ 0\ -1\ 0\ 0]$ are equivalent. Finally, note that an F- (or t-) contrast such as $[1\ 1\ 1\ 1\ 1\ 1\ 1\ 1\ 1\ 1\ 1\ 1]$, which tests whether the mean of the canonical hrf AND its derivatives for all conditions are different from (larger than) zero is not sensible. This is because the canonical hrf and its temporal derivative may cancel each other out while being significant in their own right. The basis functions are really quite different things, and need to represent separate rows in an F-contrast.

26.2.5 F-contrasts for testing effects of movement

To assess movement-related activation

- Press 'Results', select the SPM.mat file, select 'F-contrast' in the Contrast Manager. Specify e.g. 'Movement-related effects' (name) and in the 'contrasts weights matrix' window, or '1:12 19' in the 'columns for reduced design' window.
- Submit and select the contrast, specify 'mask with other contrasts?' (no), 'title for comparison' (accept default), 'corrected height threshold' (FWE), and 'corrected p-value' (accept default).
- When the MIP appears, select 'sections' from the 'overlays' pulldown menu, and select the normalised structural image (`wmsM03953_0007.img`)

You will see there is a lot of residual movement-related artifact in the data (despite spatial realignment), which tends to be concentrated near the boundaries of tissue types (eg the edge of the brain; see Figure 26.15). (Note how the MIP can be misleading in this respect, since though it appears that the whole brain is affected, this reflects the nature of the (X-ray like) projections onto each orthogonal view; displaying the same data as sections in 3D shows that not every voxel is suprathreshold.) Even though we are not interested in such artifact, by including the realignment parameters in our design matrix, we "covary out" (linear components) of subject movement, reducing the residual error, and hence improve our statistics for the effects of interest.

26.3 Modelling parametric responses

Before setting up the design matrix, we must first load into Matlab the Stimulus Onsets Times (SOTs), as before, and also the "Lags", which are specific to this experiment, and which will be used as parametric modulators. The Lags code, for each second presentation of a face (N2 and F2), the number of other faces intervening between this (repeated) presentation and its previous (first) presentation. Both SOTs and Lags are represented by Matlab cell arrays, stored in the `sots.mat` file.

- At the matlab command prompt type `load sots`. This loads the stimulus onset times and the lags (the latter in a cell array called `itemlag`).

Now press the 'Specify 1st-level' button. This will call up the specification of a fMRI specification job in the graphics window. Then

- Open the fMRI model specification option
- Press 'Load' and select the `categorical_spec.mat` job file you created earlier

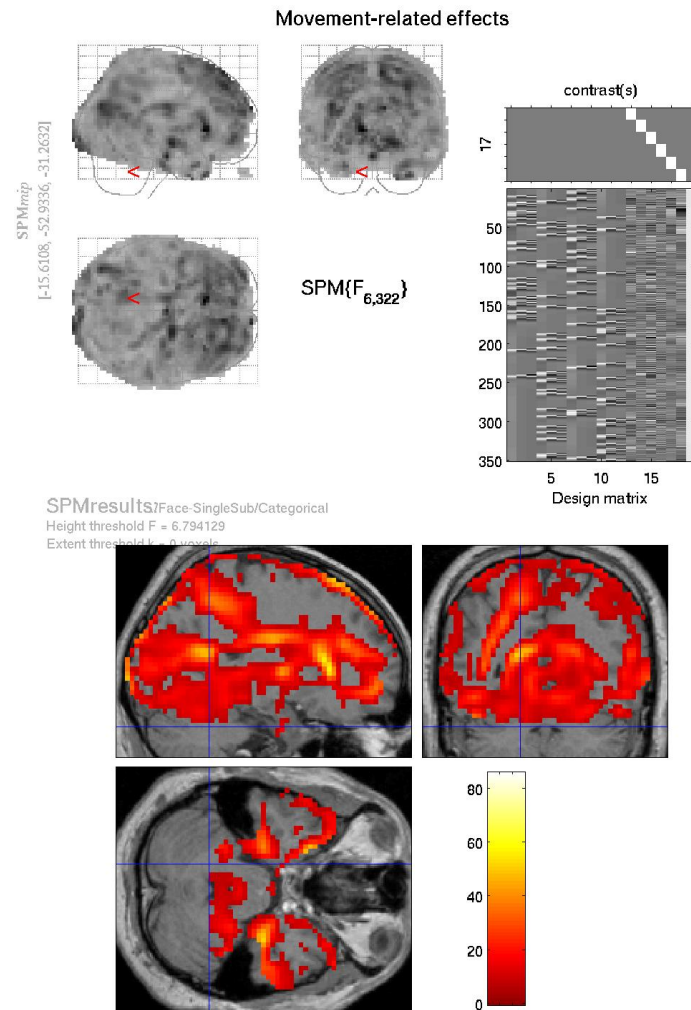


Figure 26.15: *Movement-related activations. These spurious ‘activations’ are due to residual movement of the head during scanning. These effects occur at tissue boundaries and boundaries between brain and non-brain, as this is where contrast differences are greatest. Including these regressors in the design matrix means these effects cannot be falsely attributed to neuronal activity.*

- Open ‘Conditions’ and then open the second ‘Condition’
- Highlight ‘Parametric Modulations’, select ‘New Parameter’ and open the newly created ‘Parameter’ option.
- Highlight ‘Name’ and enter ‘Lag’, highlight values and enter `itemlag{2}`, highlight polynomial expansion and ‘2nd order’.
- Now open the fourth ‘Condition’ under ‘Conditions’
- Highlight ‘Parametric Modulations’, select ‘New Parameter’ and open the newly created ‘Parameter’ option.
- Highlight ‘Name’ and enter ‘Lag’, highlight values and enter `itemlag{4}`, highlight polynomial expansion and ‘2nd order’.
- Open ‘Canonical HRF’ under ‘Basis Functions’, highlight ‘Model derivatives’ and select ‘No derivatives’ (to make the design matrix a bit simpler for present purposes!).
- Highlight ‘Directory’ and select `DIR/parametric` (having “unselected” the current definition of directory from the Categorical analysis)
- Save the job as `parametric_spec` and press ‘Run’

This should produce the design matrix shown in Figure 26.16.

26.3.1 Estimate

Press the ‘Estimate’ button. This will call up the specification of an fMRI estimation job in the graphics window. Then

- Open the ‘fMRI model estimation’ option
- Highlight the ‘Select SPM.mat’ option and then choose the SPM.mat file saved in the `DIR/parametric` directory
- Save the job as `parametric_est.job` and press Run

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

26.3.2 Plotting parametric responses

We will look at the effect of lag (up to second order, ie using linear and quadratic terms) on the response to repeated Famous faces, within those regions generally activated by faces versus baseline. To do this

- Press ‘Results’ and select the SPM.mat file in the `DIR/parametric` directory
- Press ‘Define new contrast’, enter the name ‘Famous Lag’, press the ‘F-contrast’ radio button, enter ‘1:6 9:15’ in the ‘columns in reduced design’ window, press ‘submit’, ‘OK’ and ‘Done’.
- Select the ‘Famous Lag’ contrast.
- *Mask with other contrast ? [Yes/No]*
- Specify Yes.
- Select the ‘Positive Effect of Condition 1’ T contrast
- Change to an 0.05 uncorrected mask p-value
- Nature of Mask ? inclusive
- *Title for comparison ?*

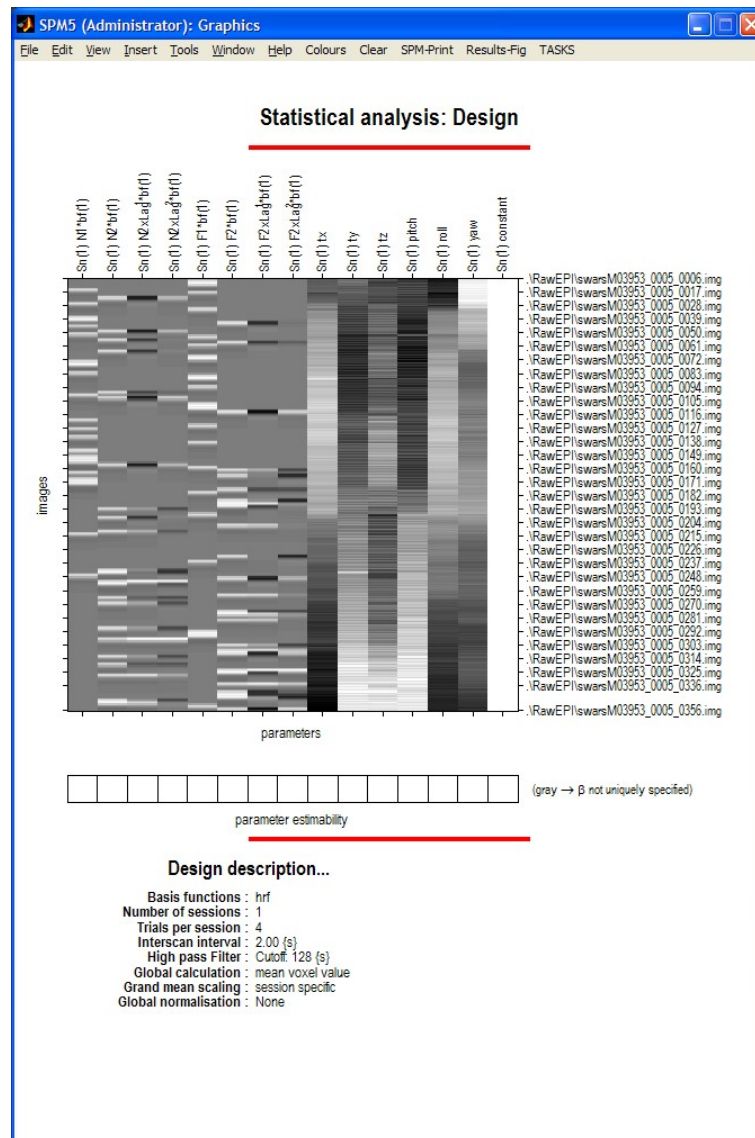


Figure 26.16: *Design matrix for testing repetition effects parametrically. Regressor 2 indicates the second occurrence of a nonfamous face. Regressor 3 modulates this linearly as a function of lag (ie. how many faces have been shown since that face was first presented), and regressor 4 modulates this quadratically as a function of lag. Regressors 6,7 and 8 play the same roles, but for famous faces.*

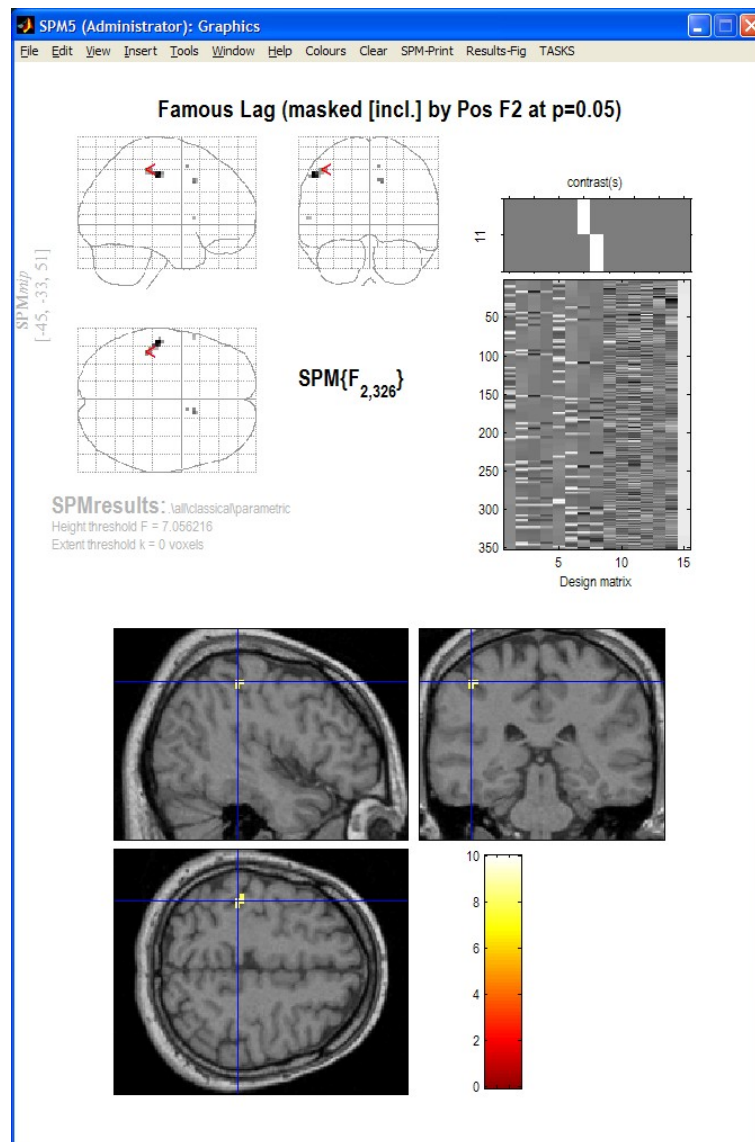


Figure 26.17: MIP and overlay of parametric lag effect in parietal cortex.

- Accept what is offered
- *p value adjustment to control:* $[FWE/FDR/none]$
- Select None
- *Threshold $\{F \text{ or } p \text{ value}\}$*
- Accept the default value, 0.001
- *Extent threshold $\{voxels\}$ $[0]$*
- Accept the default value, 0

Figure 26.17 shows the MIP and an overlay of this parametric effect using overlays, sections and selecting the `wmsM03953_0007.img` image. The effect is plotted in the time domain in figure 26.18. This was obtained by

- Right clicking on the MIP and selecting 'global maxima'

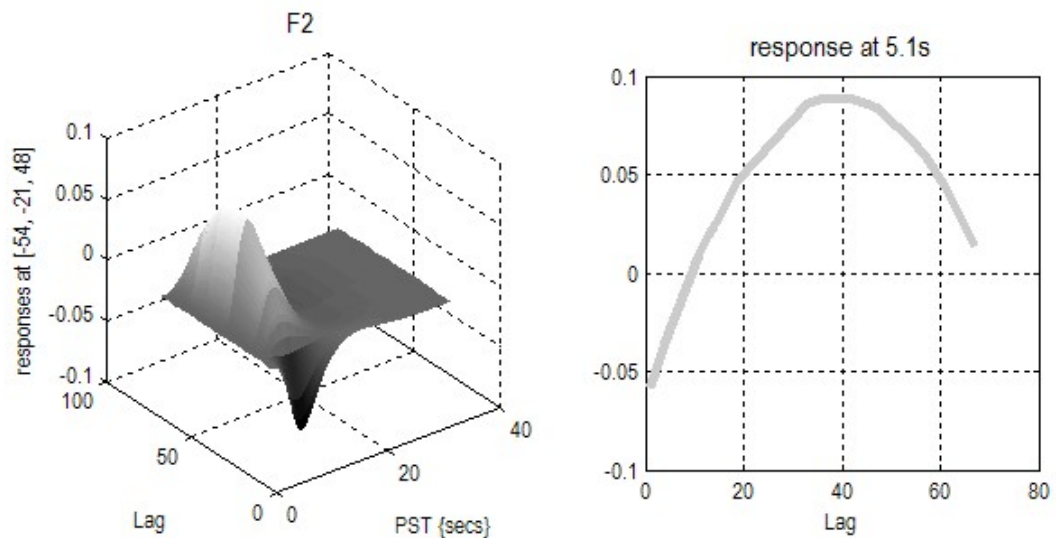


Figure 26.18: *Response as a function of lag.*

- Pressing Plot, and selecting ‘parametric responses’ from the pull-down menu
- Which effect ? select ‘F2’

This shows a quadratic effect of lag, in which the response appears negative for short-lags, but positive and maximal for lags of about 40 intervening faces (note that this is a very approximate fit, since there are not many trials, and is also confounded by time during the session, since longer lags necessarily occur later (for further discussion of this issue, see the SPM2 example analysis of these data on the webpage).

26.4 Bayesian analysis

26.4.1 Specification

Press the ‘Specify 1st-level’ button. This will call up an fMRI specification job in the graphics window. Then

- Open the fMRI model specification option
- Load the `categorical_spec.mat` job file created for the classical analysis
- Open ‘Subject/Session’, highlight ‘Scans’
- Deselect the smoothed functional images using the ‘unselect all’ option available from a right mouse click in the SPM file selector (bottom window)
- Select the unsmoothed functional images using the `~wa.*` filter and ‘select all’ option available from a right mouse click in the SPM file selector (top right window)

The Bayesian analysis uses a spatial prior where the spatial regularity in the signal is estimated from the data. It is therefore not necessary to create smoothed images if you are only going to do a Bayesian analysis.

- Press ‘Done’

- Highlight ‘Directory’ and select the DIR/`bayesian` directory you created earlier (you will first need to deselect the DIR/`categorical` directory).
- Save the job as `specify_bayesian.mat` and press ‘Run’

26.4.2 Estimation

Press the ‘Estimate’ button. This will call up the specification of an fMRI estimation job in the graphics window. Then

- Open the ‘fMRI model estimation’ option
- Highlight the ‘Select SPM.mat’ option and then choose the SPM.mat file saved in the DIR/`bayesian` subdirectory
- Highlight ‘Method’ and select the ‘Choose Bayesian 1st-level’ option.
- Save the job as `estimate_bayesian.job` and press Run

SPM will write a number of files into the output directory including

- An SPM.mat file.
- Images `Cbeta_k.img` where k indexes the k th estimated regression coefficient. These file-names are prefixed with a ‘C’ indicating that these are the mean values of the ‘Conditional’ or ‘Posterior’ density.
- Images of error bars/standard deviations on the regression coefficients `SDbeta_k.img`.
- An image of the standard deviation of the error `Sess1_SDerror.img`.
- An image `mask.img` indicating which voxels were included in the analysis.
- Images `Sess1_AR_p.img` where p indexes the p th AR coefficient. See eg. Figure 26.19.
- Images `con_i.img` and `con_sd_i.img` which are the mean and standard deviation of the i th pre-defined contrast.

26.4.3 Inference

After estimation, we can make a posterior inference using a PPM. Basically, we identify regions in which we have a high probability (level of confidence) that the response exceeds a particular size (eg, % signal change). This is quite different from the classical inferences above, where we look for low probabilities of the null hypothesis that the size of the response is zero.

To determine a particular response size (“size threshold”) in units of PEAK % signal change, we first need to do a bit of calculation concerning the scaling of the parameter estimates. The parameter estimates themselves have arbitrary scaling, since they depend on the scaling of the regressors. The scaling of the regressors in the present examples depends on the scaling of the basis functions. To determine this scaling, load the “SPM.mat” file and type in Matlab `sf = max(SPM.xBF.bf(:,1))/SPM.xBF.dt` (alternatively, press “Design:Explore:Session 1” and select any of the conditions, then read off the peak height of the canonical HRF basis function (bottom left)).

Then, if you want a size threshold of 1% peak signal change, the value you need to enter for the PPM threshold (ie the number in the units of the parameter estimates) is $1/sf$ (which should be 4.75 in the present case).⁹

Finally, if we want to ask where is there a signal greater than 1% (with a certain confidence) to faces versus baseline, we need to create a new contrast that takes the AVERAGE of the parameter estimates for the canonical HRF across the four conditions (N1 to F2), rather than the default **Positive effect of condition_1** contrast, which actually calculates the SUM of the parameter estimates for the canonical HRF across conditions (the average vs sum makes no difference for the classical statistics).

⁹Strictly speaking, this is the peak height of the canonical component of the best fitting BOLD impulse response: the peak of the complete fit would need to take into account all three basis functions and their parameter estimates.

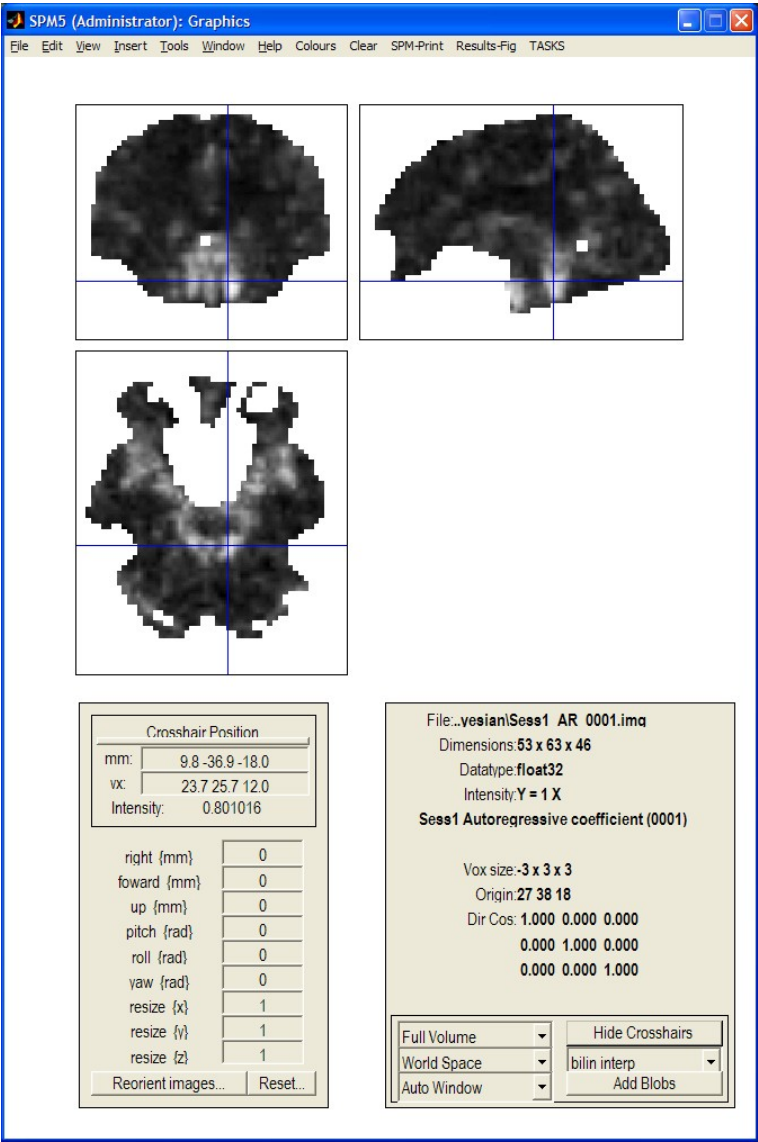


Figure 26.19: Bayesian analysis: Estimated $AR(1)$ coefficient image indicating heterogeneity near the circle of Willis

- Press ‘Results’
- Select the `SPM.mat` file created in the last section
- Press ‘Define new contrast’, enter the name ‘AVERAGE Canonical HRF: Faces > Baseline’, press the ‘T-contrast’ radio button, enter the contrast ‘[1 0 0 1 0 0 1 0 0 1 0 0]/4’, press ‘submit’, ‘OK’ and ‘Done’.
- *Mask with other contrast ? [Yes/No]*
- Specify No
- *Title for comparison*
- Enter ‘AVERAGE Canonical HRF: Faces > Baseline’
- *Effect size threshold for PPM*
- Enter the value
- *Posterior probability threshold for PPM*
- Enter the value 0.95
- *Extent threshold [0]*
- Accept the default value
- *Plot effect size [Yes/No]*
- Select the default ‘Yes’

SPM will then plot a map of effect sizes at voxels where it is 95% sure that the effect size is greater than 1% of the global mean. Then use overlays, sections, select the normalised structural image created earlier and move the cursor to the activation in the left hemisphere. This should create the plot shown in Figure 26.20

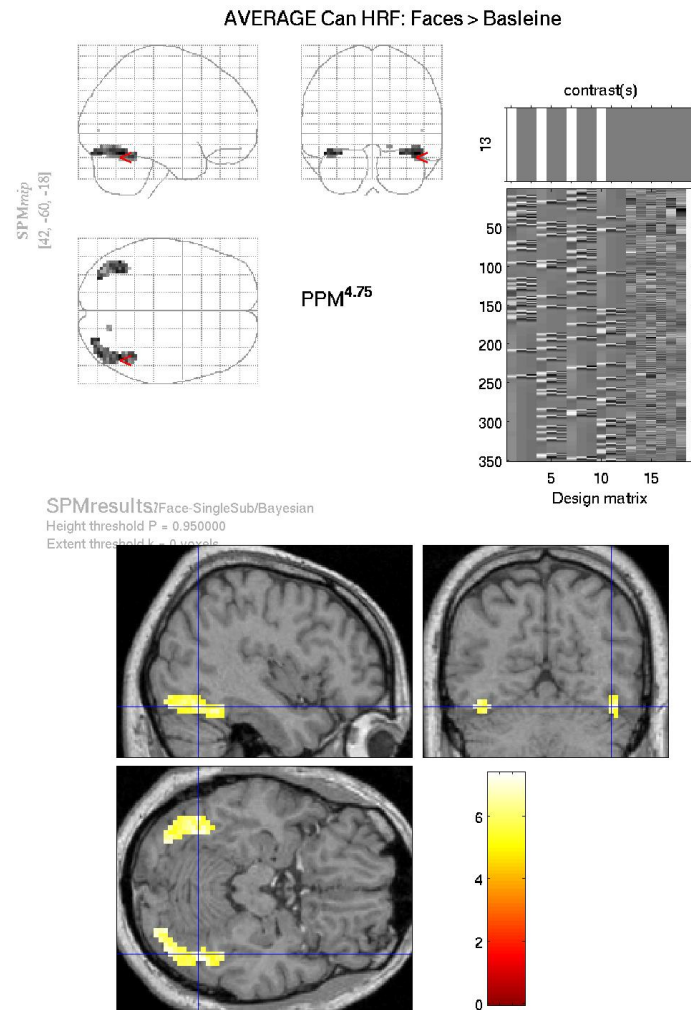


Figure 26.20: *Bayesian analysis: MIP and overlay of effect sizes at voxels where PPM is 95% sure that the effect size is greater than 1% of the global mean. The cursor is at the location $x = 42, y = -60, z = -18\text{mm}$*