

## 31.2 Modelling categorical responses

Before setting up the design matrix we must first load the Stimulus Onsets Times (SOTs) 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.<sup>6</sup>

- At the MATLAB command prompt type `load sots`

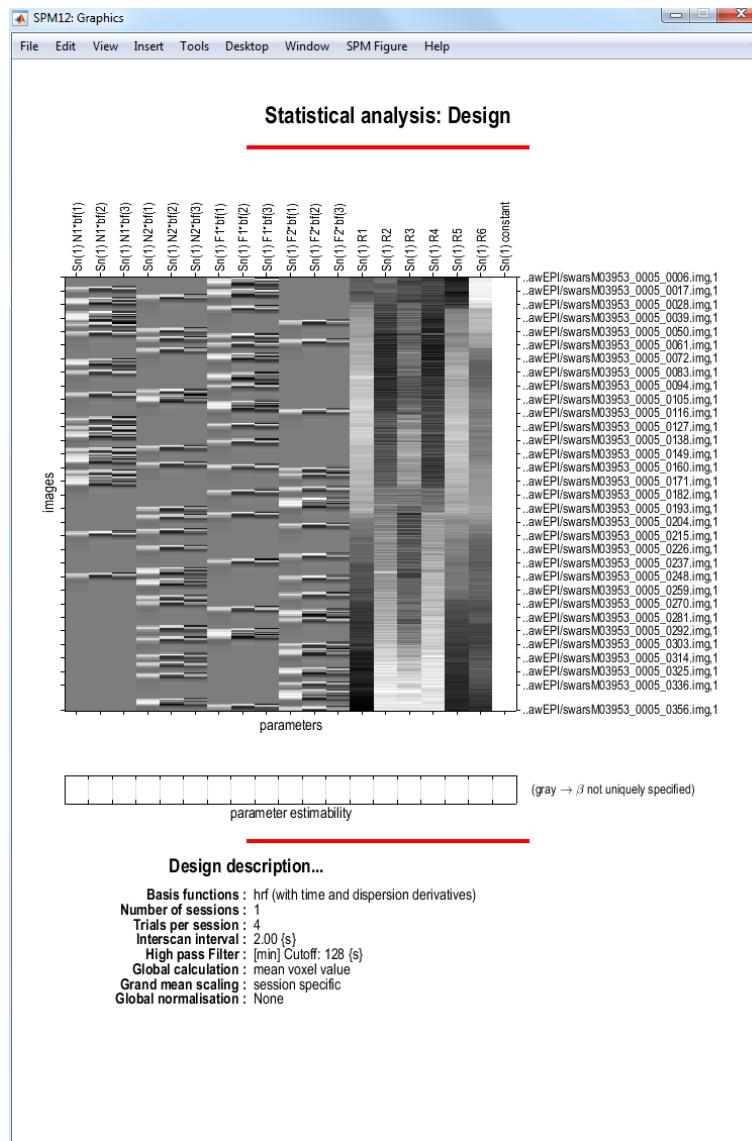
Now press the SPECIFY 1ST-LEVEL button. This will call up the specification of a fMRI specification job in the batch editor window. Then

- For “Directory”, select the “categorical” folder you created earlier,
- In the “Timing parameters” 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”.
- 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”<sup>7</sup>.
- Open the newly created “Condition” option. Highlight “Name” and enter “N1”. Highlight “Onsets” and enter `sot{1}`. Highlight “Durations” and enter 0.
- Highlight “Conditions” 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 “Conditions” 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 “Conditions” 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 realignment parameter file `rp_sM03953_0005_0006.txt` file that was saved during the realignment preprocessing step in the folder containing the fMRI data<sup>8</sup>.

<sup>6</sup>Unlike previous analyses of these data in SPM99 and SPM2, we will not bother with extra event-types for the (rare) error trials.

<sup>7</sup>It 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.

<sup>8</sup>It 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 31.9: **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 2<sup>9</sup>.
- 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 the Run button.

SPM will then write an **SPM.mat** file to the DIR/categorical directory. It will also plot the design matrix, as shown in Figure 31.9.

<sup>9</sup>The order of naming these factors is important - the factor to be specified first is the one that “changes slowest” ie. 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.

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 31.9. If you select "Explore" then "Session 1" then "N1", SPM will produce the plots shown in Figure 31.10.

### 31.2.1 Estimate

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

- 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 button.

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

### 31.2.2 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 31.11.

- 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'.
- *Apply masking ? [None/Contrast/Image]*
- Specify None.
- *p value adjustment to control: [FWE/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 31.12.

### 31.2.3 Statistical tables

To get a summary of local maxima, press the "whole brain" 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 31.12

The columns in volume table show, from right to left:

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

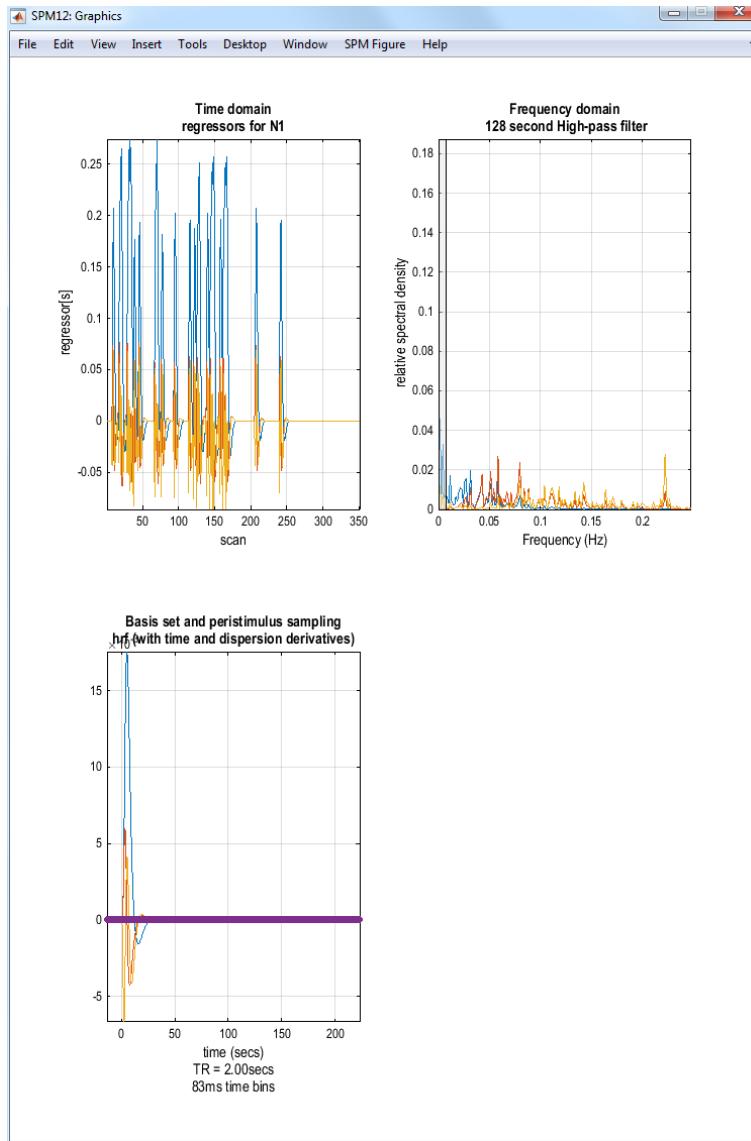


Figure 31.10: **Exploring the design matrix in Figure 31.9.** This shows the time series of the “N1” regressor (top left), the three basis functions used to convert assumed neuronal activity into hemodynamic activity (bottom left), and a frequency domain plot of the three regressors for the basis functions 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).

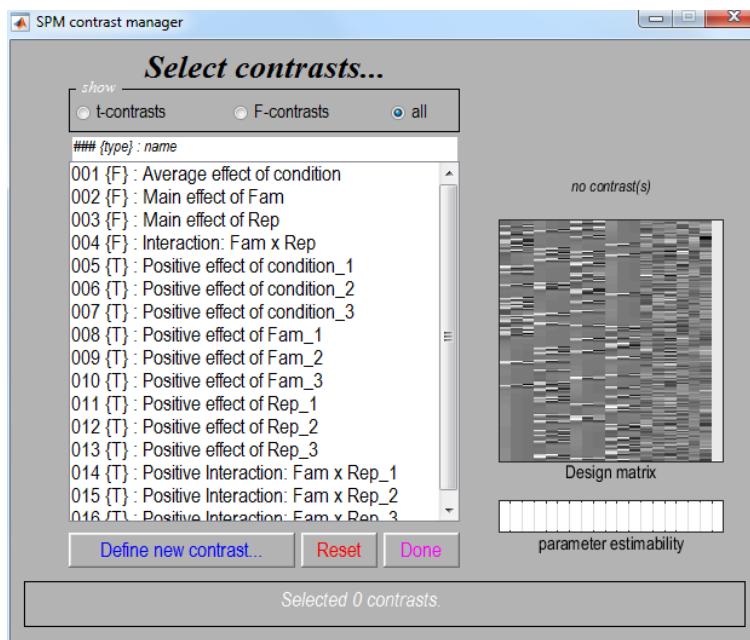


Figure 31.11: *Contrast Manager* containing default contrasts for categorical design.

- **set-level:** the chance (*p*) of finding this (*c*) or a greater number of clusters in the search volume.

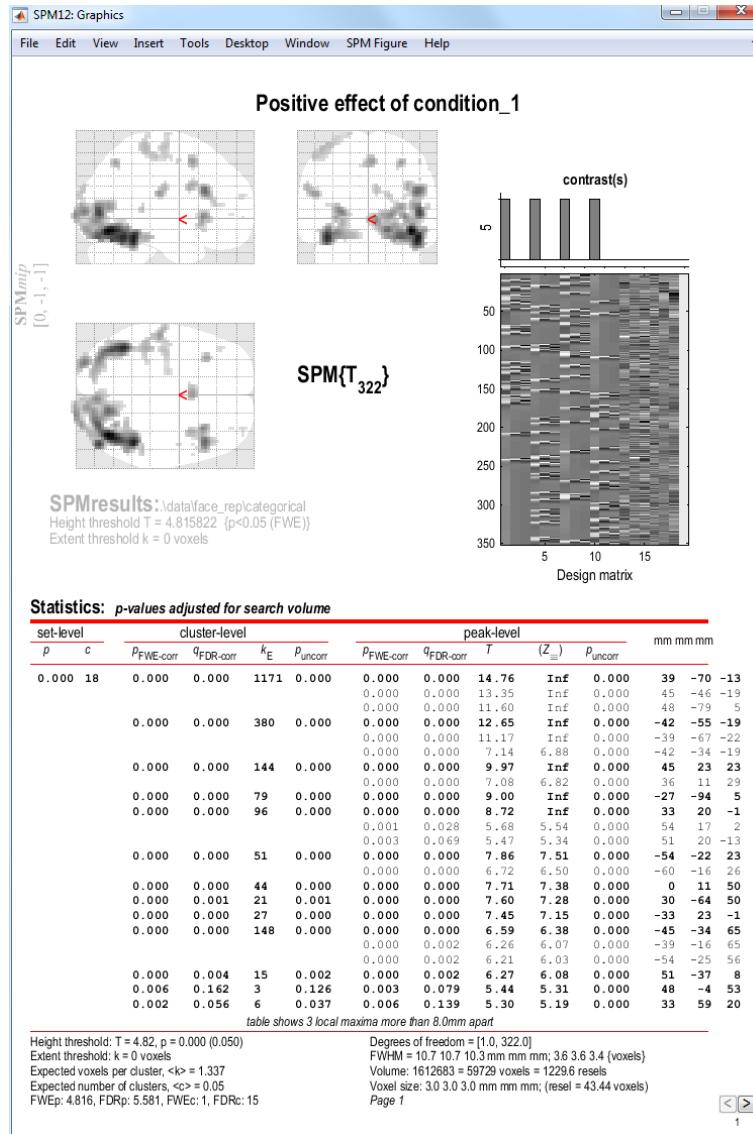
Right-click on the MIP and select “goto global maximum”. The cursor will move to [39 -70 -14]. You can view this activation on the subject’s normalised, bias-corrected structural (*wmsM03953\_0007img*), which gives best anatomical precision, or on the normalised mean functional (*wmeansM03953\_0005\_0006.nii*), 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).

### 31.2.4 F-contrasts

To assess the main effect of repeating faces, as characterised by both the hrf *and* its derivatives, an F-contrats is required. 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 31.13. Press “Done”.
- *Apply masking ? [None/Contrast/Image]*.
- Specify “Contrast”.
- Select contrast 5 - **Positive effect of condition\_1** (the T-contrast of activation versus baseline, collapsed across conditions, that we evaluated above)

Figure 31.12: *MIP and Volume table for Canonical HRF: Faces > Baseline.*

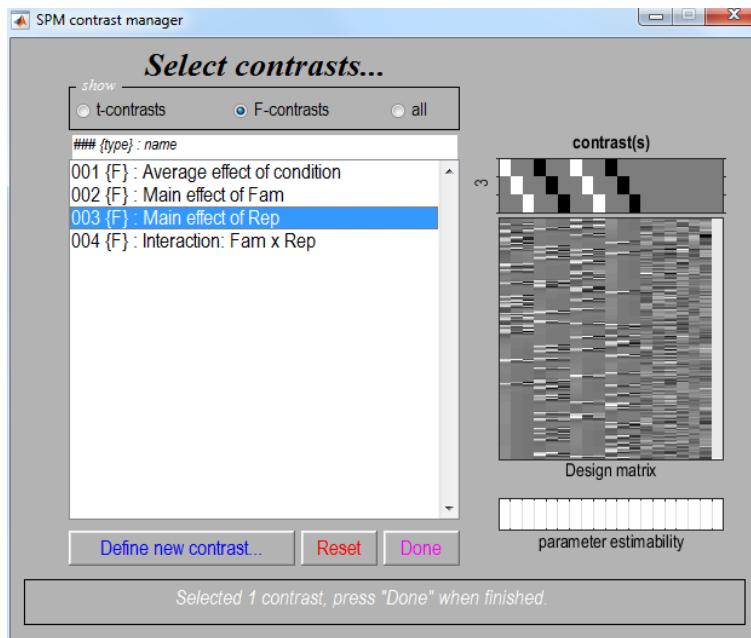


Figure 31.13: Contrast manager showing selection of the first contrast “Main effect of Rep” (repetition: F1 and N1 vs F2 and N2)

- uncorrected mask p-value ?
- Change to 0.001
- nature of mask?
- Select ‘inclusive’
- p value adjustment to control: [FWE/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 31.14.

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). Select “goto global max”, which is in right ventral temporal cortex [42 -64 -8].

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 Interactive window, and 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 31.14.

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

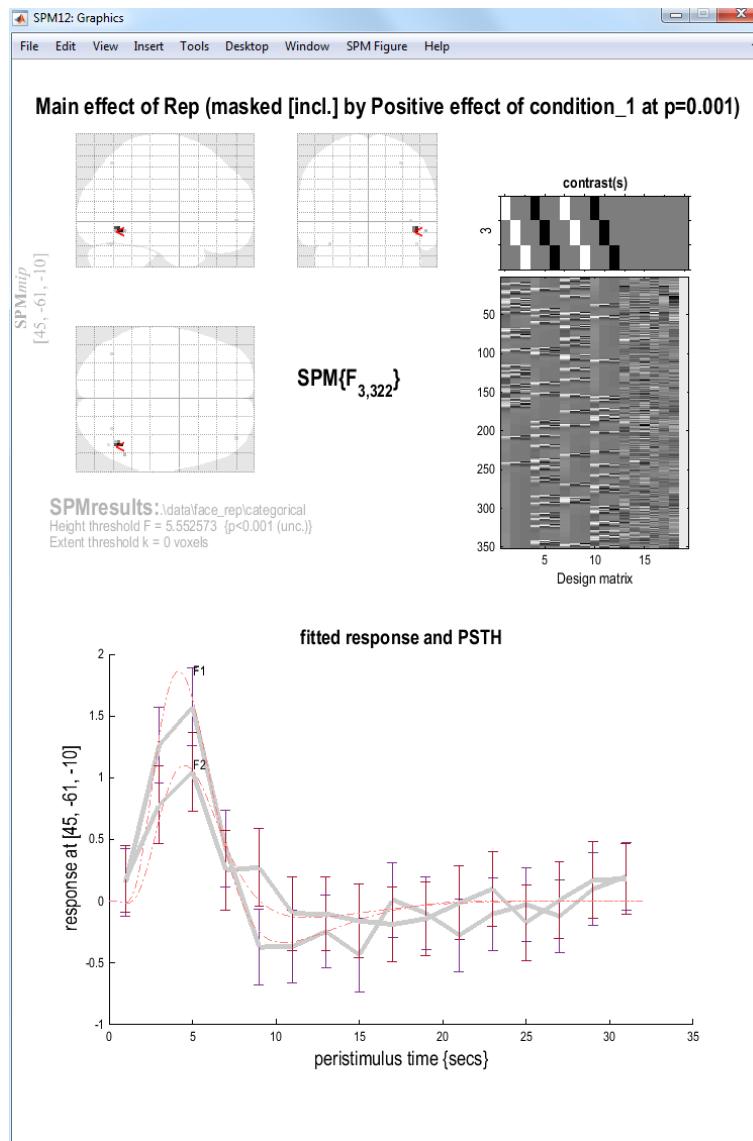


Figure 31.14: MIP for Main effect of Rep, masked inclusively with Canonical HRF: Faces > Baseline at  $p < .001$  uncorrected. Shown below are the best-fitting responses and peri-stimulus histograms (PSTH) for F1 and F2.

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], 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.

### 31.2.5 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 “Apply masking?” (none), “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.nii**).

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 31.15). (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.

## 31.3 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 sot`. 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 batch editor window. Then

- Press “Load” and select the **categorical\_spec.mat** job file you created earlier.
- Open “Conditions” and then open the second “Condition”.
- Highlight “Parametric Modulations”, select “New Parameter”.
- 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”.

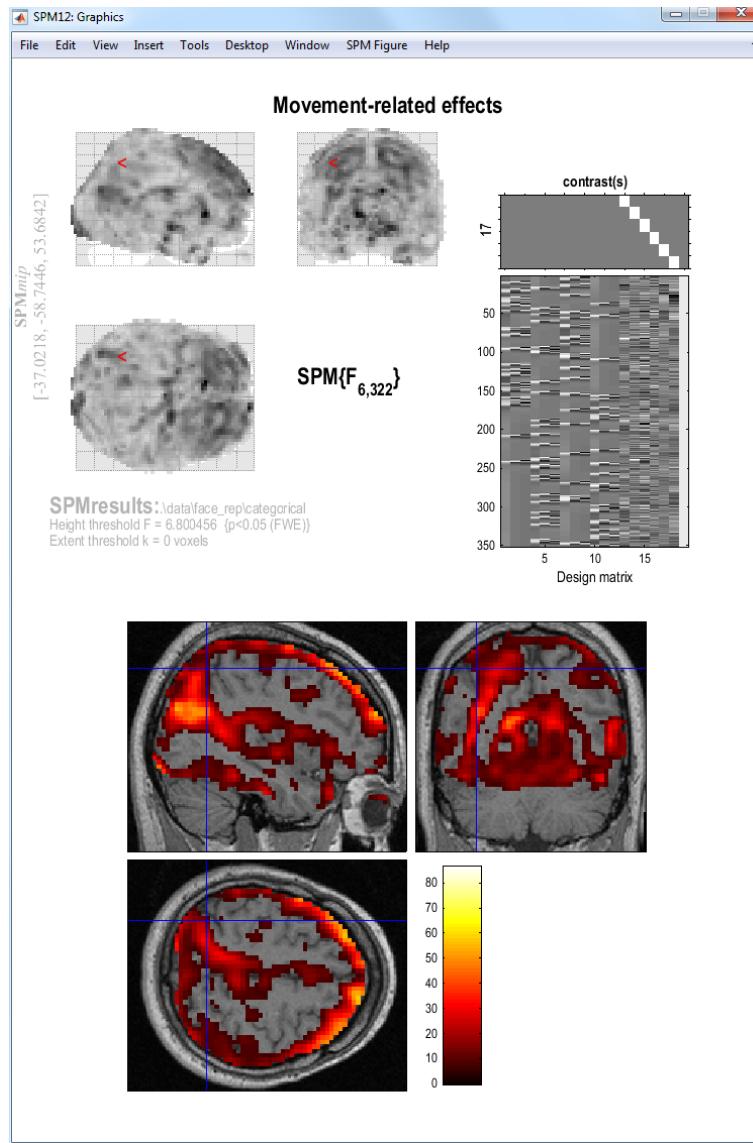


Figure 31.15: *Movement-related activations.* These spurious ‘activations’ are due to residual movement of the head during scanning. These effects occur at tissue boundaries and boundaries between brain and non-brain, as this is where contrast differences are greatest. Including these regressors in the design matrix means these effects cannot be falsely attributed to neuronal activity.

- 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 the Run button.

This should produce the design matrix shown in Figure 31.16.

### 31.3.1 Estimate

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

- 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 the Run button.

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

### 31.3.2 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.
- *Apply masking ? [None/Contrast/Image]*
- Specify “Contrast”.
- Select the “Positive Effect of Condition 1” T contrast.
- Change to an 0.05 uncorrected mask p-value.
- Nature of Mask ? inclusive.
- *p value adjustment to control: [FWE/none]*
- Select None
- *Threshold {F or p value}*
- Accept the default value, 0.001
- *Extent threshold {voxels} [0]*
- Accept the default value, 0.

Figure 31.17 shows the MIP and an overlay of this parametric effect using overlays, sections and selecting the `wmsM03953_0007.nii` image. The effect is plotted in the time domain in figure 31.18. This was obtained by

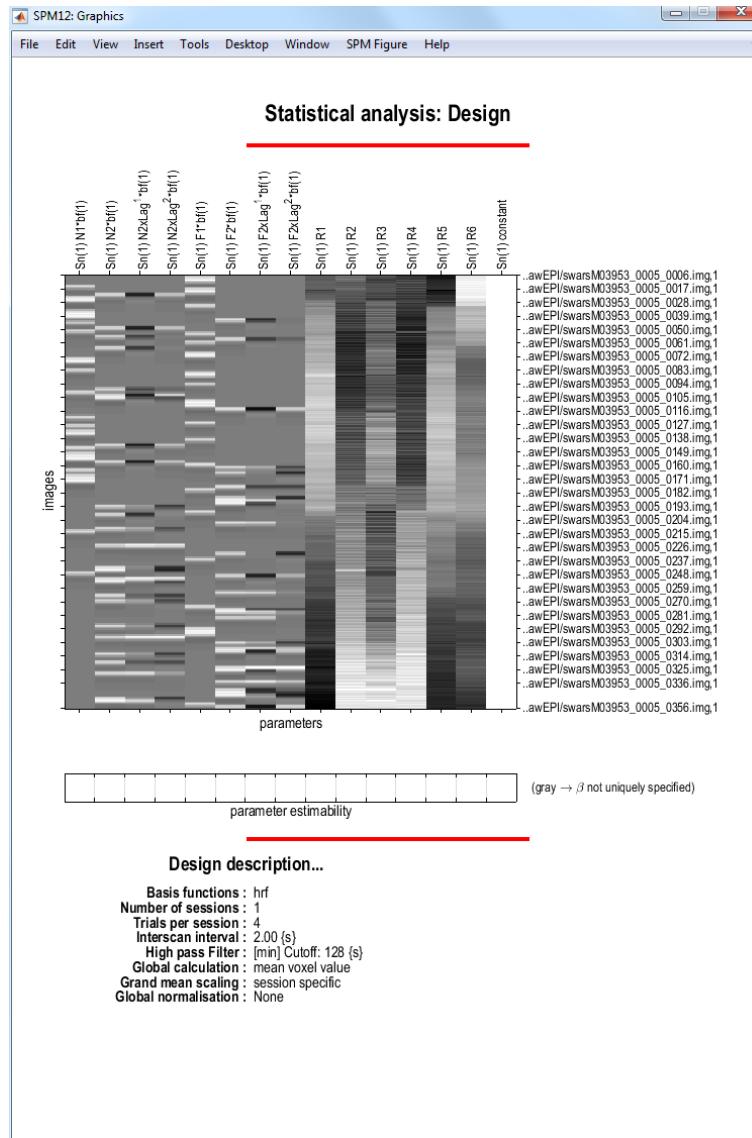


Figure 31.16: **Design matrix for testing repetition effects parametrically.** Regressor 2 indicates the second occurrence of a nonfamous face. Regressor 3 modulates this linearly as a function of lag (ie. how many faces have been shown since that face was first presented), and regressor 4 modulates this quadratically as a function of lag. Regressors 6,7 and 8 play the same roles, but for famous faces.

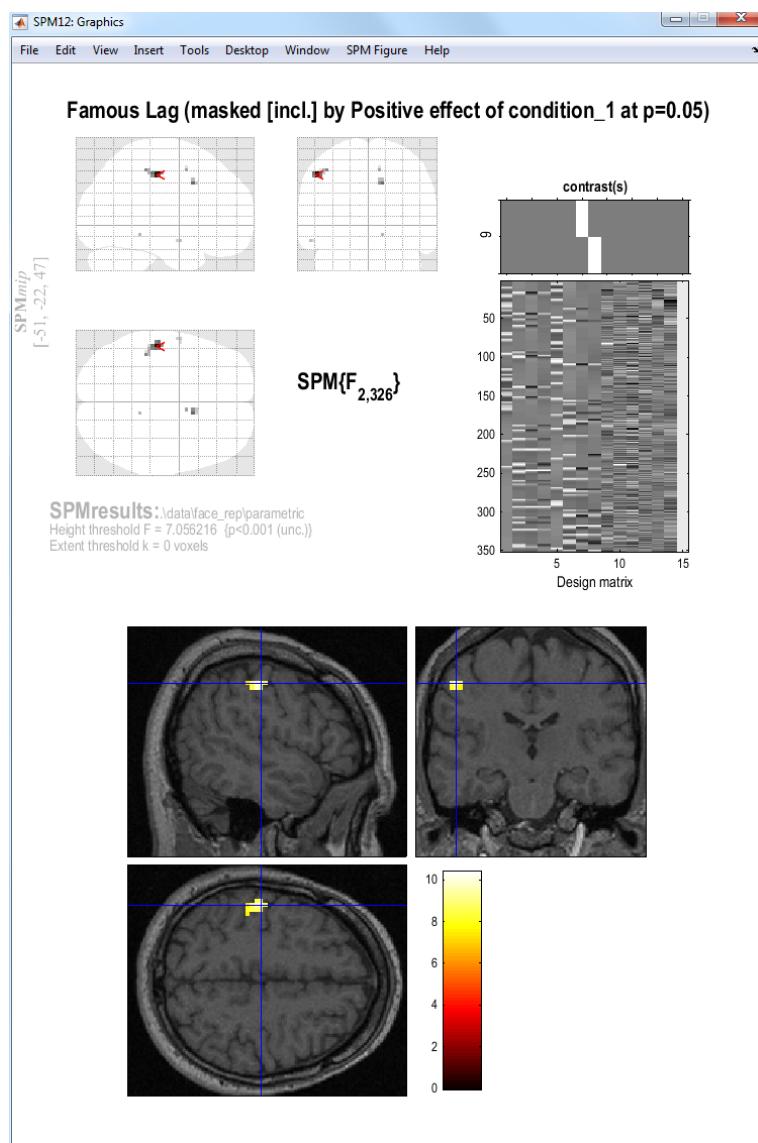


Figure 31.17: MIP and overlay of parametric lag effect in parietal cortex.

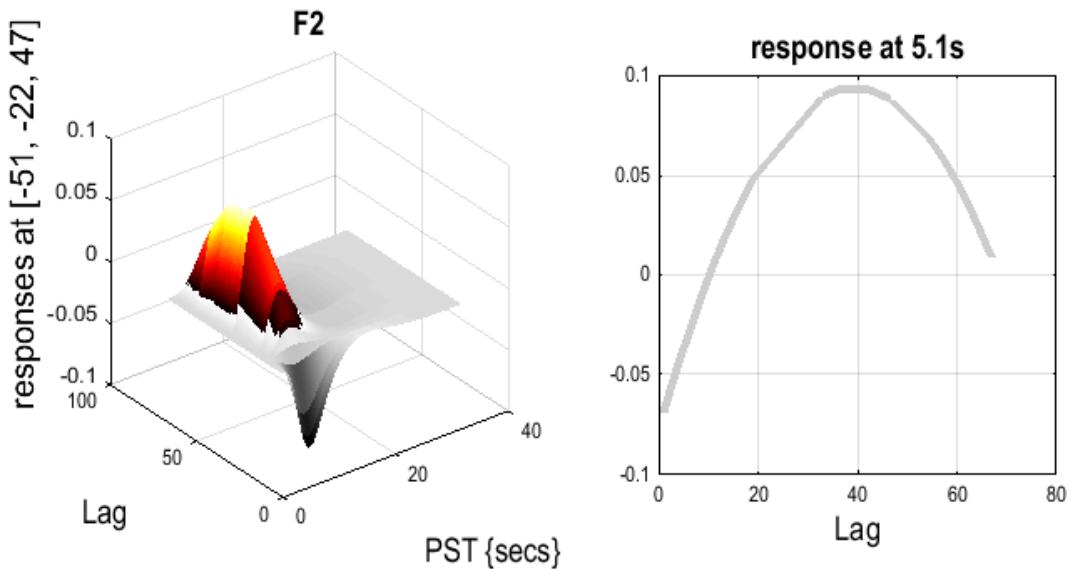


Figure 31.18: *Response as a function of lag.*

- Right clicking on the MIP and selecting “global maxima”.
- 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).

## 31.4 Bayesian analysis

### 31.4.1 Specification

Press the SPECIFY 1ST-LEVEL button. This will call up an fMRI specification job in the batch editor window. Then

- 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).