

30.3 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 30.8.

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 30.8. If you select “Explore” then “Session 1” then “listening”, SPM will produce the plots shown in Figure 30.9.

If you select the second item on the “Design” tab, “Design Orthogonality”, SPM will produce the plot shown in Figure 30.10. 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 30.10 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.

30.3.1 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.

30.4 Inference

After estimation:

- Press “Results”.
- Select the `SPM.mat` file created in the last section.

This will invoke the contrast manager.

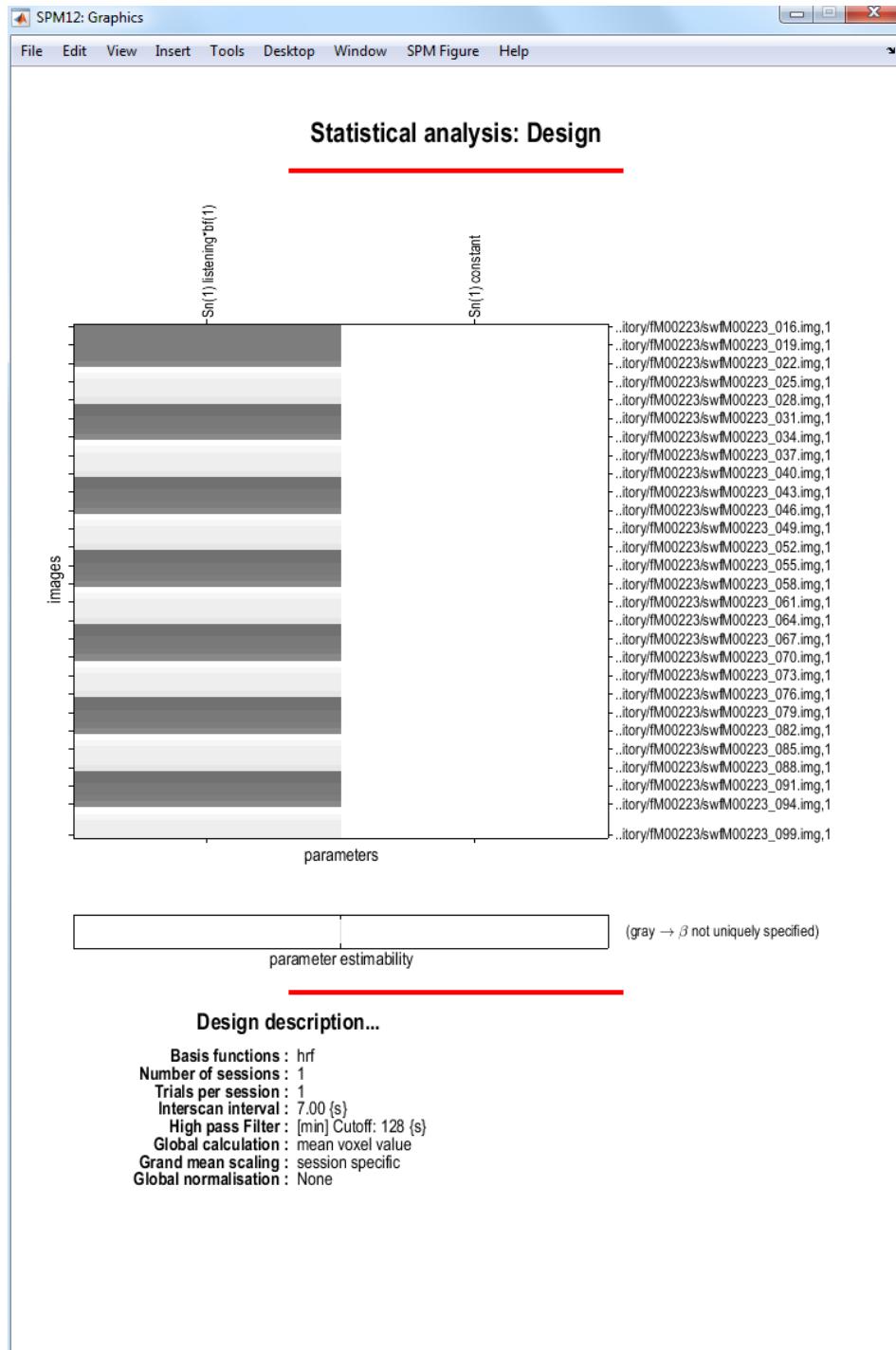


Figure 30.8: *Design matrix*: The filenames on the right-hand side of the design matrix indicate the scan associated with each row.

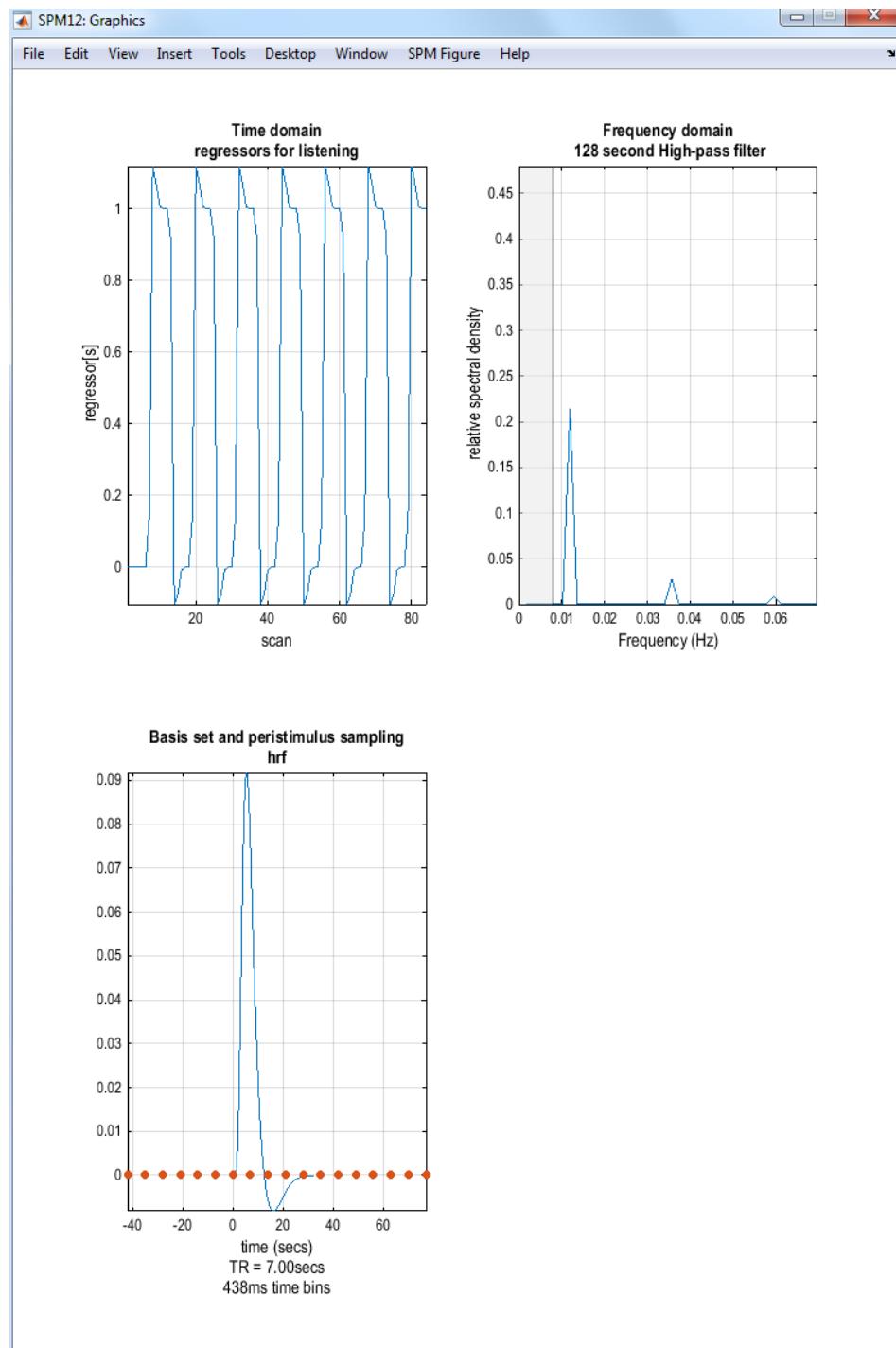


Figure 30.9: *Exploring the design matrix in Figure 30.8:* This shows the time series of the “listening” regressor (top left), a frequency domain plot of the “listening” regressor (top right) and the basis function used to convert assumed neuronal activity into hemodynamic activity. In this model we used the default option - the canonical basis function. The frequency domain plot shows that the frequency content of the “listening” regressor is 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).

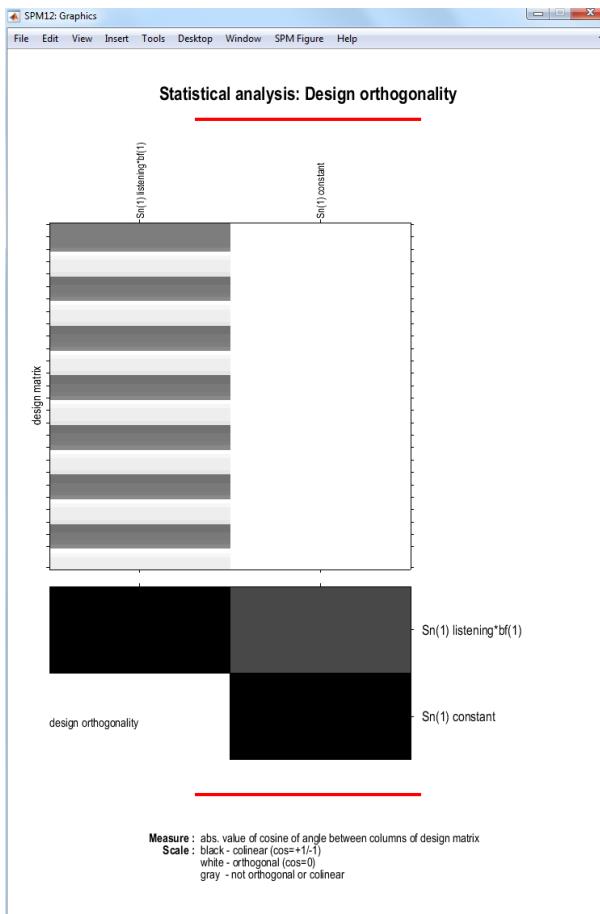


Figure 30.10: *Design Orthogonality*: The description above the first column in the design matrix $\text{Sn}(1)\text{Listening}^*\text{bf}(1)$ means that this column refers to the first session of data (in this analysis there is only 1 session), the name of this condition/trial is ‘listening’ and the trial information has been convolved with the first basis function (the canonical hemodynamic response). The constant regressor for session 1 is referred to as $\text{Sn}(1)\text{Constant}$. The orthogonality matrix at the bottom indicates a degree of collinearity between regressors.



Figure 30.11: *The contrast manager*

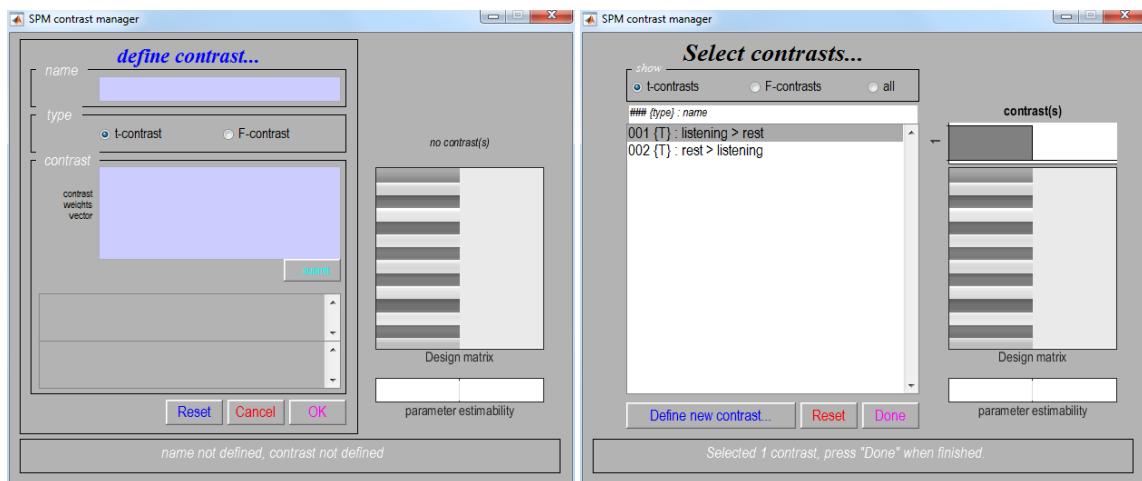


Figure 30.12: Left: A contrast is entered by specifying the numeric values in the lower window and the name in the upper window. Right: After contrasts have been specified they can be selected.

30.4.1 Contrast manager

The contrast manager displays the design matrix (surfable) in the right panel and lists specified contrasts in the left panel. Either “t-contrast” or “F-contrast” can be selected. To examine statistical results for condition effects

- Select “Define new contrast”

One sided main effects for the listening condition (i.e., a one-sided t-test) can be specified (in this example) as “1” (listening > rest) and “-1” (rest > listening). SPM will accept estimable contrasts only. Accepted contrasts are displayed at the bottom of the contrast manager window in green, incorrect ones are displayed in red. To view a contrast

- Select the contrast name e.g., “listening > rest”.
- Press “Done”.

30.4.2 Masking

You will then be prompted with

- *Apply masking ? [none/contrast/image].*
- “Specify none”.

Masking implies selecting voxels specified by other contrasts. If “yes”, SPM will prompt for (one or more) masking contrasts, the significance level of the mask (default $p = 0.05$ uncorrected), and will ask whether an inclusive or exclusive mask should be used. Exclusive will remove all voxels which reach the default level of significance in the masking contrast, inclusive will remove all voxels which do not reach the default level of significance in the masking contrast. Masking does not affect p -values of the “target” contrast, it only includes or excludes voxels.

30.4.3 Thresholds

You will then be prompted with

- *p value adjustment to control: [FWE/none].*
 - Select “FWE”.
- *p value(family-wise error).*

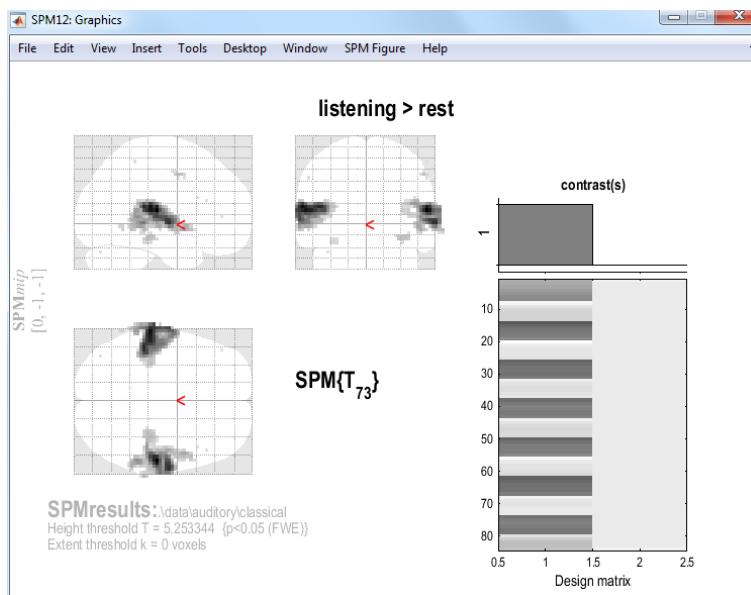


Figure 30.13: *SPM showing bilateral activation of auditory cortex.*

- Accept the default value, 0.05.

A Family Wise Error (FWE) is a false positive anywhere in the SPM. Now, imagine repeating your experiment many times and producing SPMs. The proportion of SPMs containing FWEs is the FWE rate. A value of 0.05 implies that on average 1 in 20 SPMs contains one or more false positives somewhere in the image.

If you choose the “none” option above this corresponds to making statistical inferences at the “voxel level”. These use “uncorrected” p values, whereas FWE thresholds are said to use “corrected” p -values. SPM’s default uncorrected p -value is $p=0.001$. This means that the probability of a false positive at each voxel is 0.001. So if, you have 50,000 voxels you can expect $50,000 \times 0.001 = 50$ false positives in each SPM.

You will then be prompted with

- *Extent Threshold {voxels} [0].*

- Accept the default value, “0”.

Entering a value k here will produce SPMs with clusters containing at least k voxels. SPM will then produce the SPM shown in Figure 30.13.

30.4.4 Files

A number of files are written to the working directory at this time. Images containing weighted parameter estimates are saved as `con_0001.nii`, `con_0002.nii`, etc. in the working directory. Images of T-statistics are saved as `spmT_0001.nii`, `spmT_0002.nii` etc., also in the working directory.

30.4.5 Maximum Intensity Projections

SPM displays a Maximum Intensity Projection (MIP) of the statistical map in the Graphics window. The MIP is projected on a glass brain in three orthogonal planes. The MIP is surfable: right-clicking in the MIP will activate a pulldown menu, left-clicking on the red cursor will allow it to be dragged to a new position.

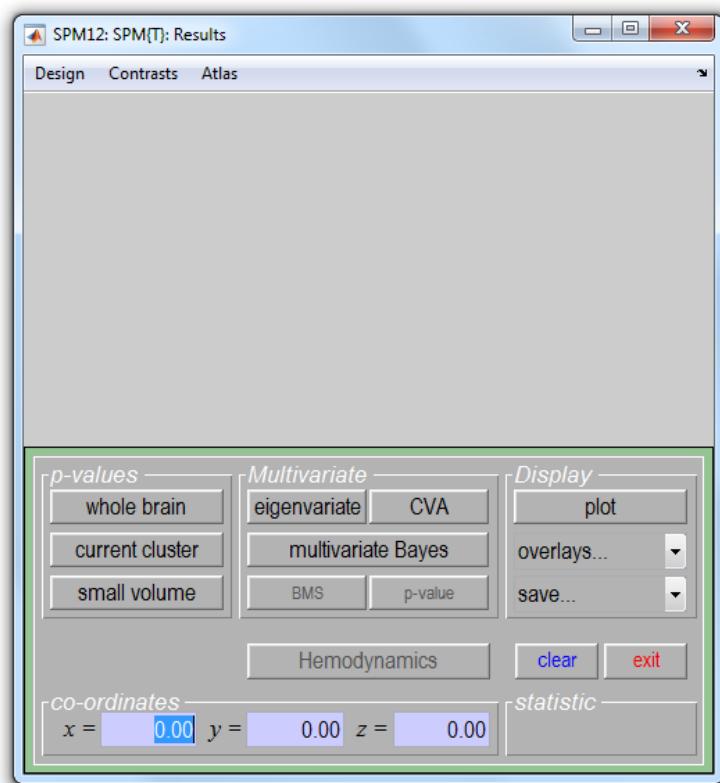


Figure 30.14: *SPM's Interactive window during results assessment. The “p-values” section is used to produce tables of statistical information. The visualisation section is used to plot responses at a voxel or to visual activations overlaid on anatomical images. The “Multivariate” section, ie. the “eigenvariate” button, is used to extract data for subsequent analyses such as assessment of PsychoPhysiological Interactions (PPIs) or Dynamic Causal Models (DCMs).*

Statistics: p-values adjusted for search volume											
set-level		cluster-level				peak-level					
p	c	$P_{FWE\text{-corr}}$	$q_{FDR\text{-corr}}$	k_E	P_{uncorr}	$P_{FWE\text{-corr}}$	$q_{FDR\text{-corr}}$	T	(Z_{adj})	P_{uncorr}	mm mm mm
0.000	12	0.000	0.000	425	0.000	0.000	0.000	17.09	Inf	0.000	57 -22 11
						0.000	0.000	14.42	Inf	0.000	66 -10 -1
						0.000	0.000	10.89	Inf	0.000	69 -19 11
		0.000	0.000	568	0.000	0.000	0.000	15.94	Inf	0.000	-63 -28 14
						0.000	0.000	14.68	Inf	0.000	-48 -34 14
						0.000	0.000	12.23	Inf	0.000	-66 -20 -2
		0.000	0.000	31	0.000	0.000	0.003	7.03	6.12	0.000	36 -28 -13
		0.000	0.001	12	0.000	0.000	0.004	6.90	6.03	0.000	54 -1 44
0.003	0.096	3	0.048	0.002	0.002	0.075	6.07	5.44	0.000	-63 -55 -7	
0.000	0.003	10	0.001	0.006	0.006	0.207	5.77	5.22	0.000	-33 -31 -19	
0.015	0.232	1	0.232	0.032	0.032	0.389	5.37	4.41	0.000	-39 -76 -28	
0.015	0.232	1	0.232	0.032	0.032	0.783	5.77	4.91	0.000	57 -56 -56	
0.015	0.232	1	0.232	0.042	0.042	0.923	5.30	4.86	0.000	-57 -1 41	
0.015	0.232	1	0.232	0.043	0.043	0.923	5.29	4.85	0.000	-45 41 5	
0.015	0.232	1	0.232	0.044	0.044	0.923	5.29	4.85	0.000	48 26 20	
0.015	0.232	1	0.232	0.050	0.099	5.25	4.82	0.000	45 17 23		

table shows 3 local maxima more than 8.0mm apart

High threshold: T = 5.25, p = 0.000 (0.050)
Extent threshold: k = 0 voxels
Expected voxels per cluster, <k> = 0.753
Expected number of clusters, <> = 0.07
FWEp: 5.253, FDRp: 6.320, FWEc: 1, FDRc: 10
Degree of freedom = 110.730
FWHM = 9.9 9.9 8.6 mm mm mm; 3.3 3.3 2.9 (voxels)
Volume: 1901367 = 70421 voxels = 19957 resels
Voxel size: 3.0 3.0 3.0 mm mm mm; (resel = 31.52 voxels)

Figure 30.15: Volume table for “listening > rest” effect. This table of values was created by pressing the SPM Figure > Results Table option at the top of the Graphics window and then pressing the “whole brain” button. This displays the table of results in a separate window.

30.4.6 Design matrix

SPM also displays the design matrix with the selected contrast. The design matrix is also surfable: right-clicking will show parameter names, left-clicking will show design matrix values for each scan.

In the SPM Interactive window (lower left panel) a button box appears with various options for displaying statistical results (p-values panel) and creating plots/overlays (visualisation panel). Clicking “Design” (upper left) will activate a pulldown menu as in the “Explore design” option.

30.4.7 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 30.15

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 (*k*) or a greater number of voxels, corrected (FWE or FDR)/ uncorrected for search volume.
- **set-level**: the chance (*p*) of finding this (*c*) or a greater number of clusters in the search volume.

It is also worth noting that:

- The table is surfable: clicking a row of cluster coordinates will move the pointer in the MIP to that cluster, clicking other numbers will display the exact value in the MATLAB window (e.g. 0.000 = 6.1971e-07).
- To inspect a specific cluster (e.g., in this example data set, the right auditory cortex), either move the cursor in the MIP (by left-clicking and dragging the cursor, or right-clicking the MIP background which will activate a pulldown menu).

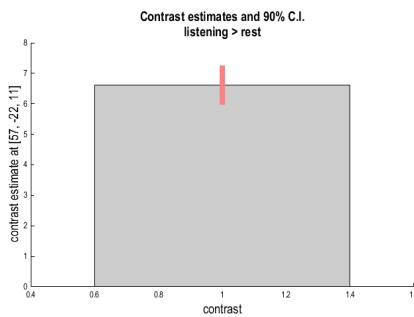


Figure 30.16: Estimated effect size.

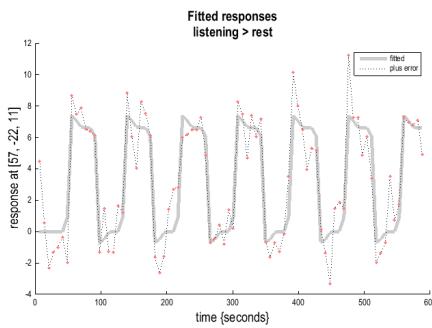


Figure 30.17: Fitted responses.

- Alternatively, click the cluster coordinates in the volume table, or type the coordinates in the co-ordinates section of the Interactive window.

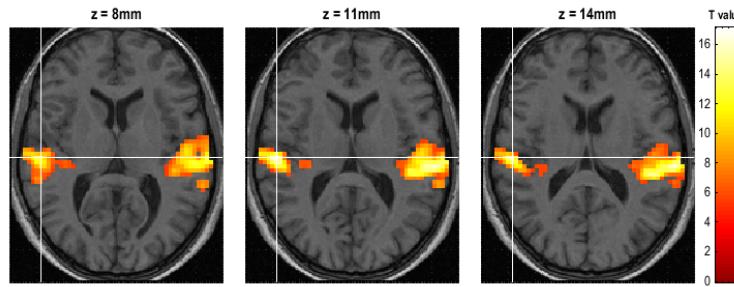
It is also possible to produce tables of statistical information for a single cluster of interest rather than for the whole volume. Firstly, select the relevant cluster in the MIP and then press the “current cluster” button in the *p*-values section of the Interactive window. This will show coordinates and voxel-level statistics for local maxima (>4mm apart) in the selected cluster. This table is also surfable.

30.4.8 Plotting responses at a voxel

A voxel can be chosen with coordinates corresponding to those in the Interactive window. The responses at this voxel can then be plotted using the “Plot” button in the visualisation section of the Interactive window. This will provide you with five further options:

1. Contrast estimates and 90% CI: SPM will prompt for a specific contrast (e.g., listening>rest). The plot will show effect size and 90% confidence intervals. See eg. Figure 30.16.
2. Fitted responses: Plots adjusted data and fitted response across session/subject. SPM will prompt for a specific contrast and provides the option to choose different ordinates (“an explanatory variable”, “scan or time”, or “user specified”). If “scan or time”, the plot will show adjusted or fitted data with errors added as shown in Figure 30.17.
3. Event-related responses: Plots adjusted data and fitted response across peri-stimulus time.
4. Parametric responses.
5. Volterra kernels.

For plotting event-related responses SPM provides three options

Figure 30.18: *Slices*.

1. Fitted response and PSTH (peri-stimulus time histogram): plots mean regressor(s) (ie. averaged over session) and mean signal +/- SE for each peri-stimulus time bin.
2. Fitted response and 90% CI: plots mean regressor(s) along with a 90% confidence interval.
3. Fitted response and adjusted data: plots regressor(s) and individual data (note that in this example the data are shown in columns due to the fixed TR/ISI relationship).

Its worth noting that

- The values for the fitted response across session/subject for the selected plot can be displayed and accessed in the MATLAB window by typing “Y”. Typing “y” will display the adjusted data.
- “Adjusted” data = adjusted for confounds (e.g., global flow) and high- and low pass filtering.

30.4.9 Overlays

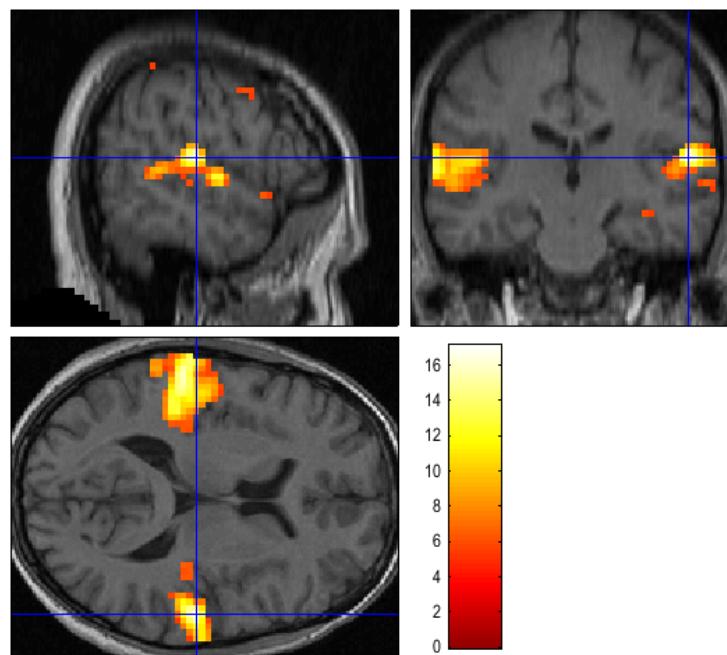
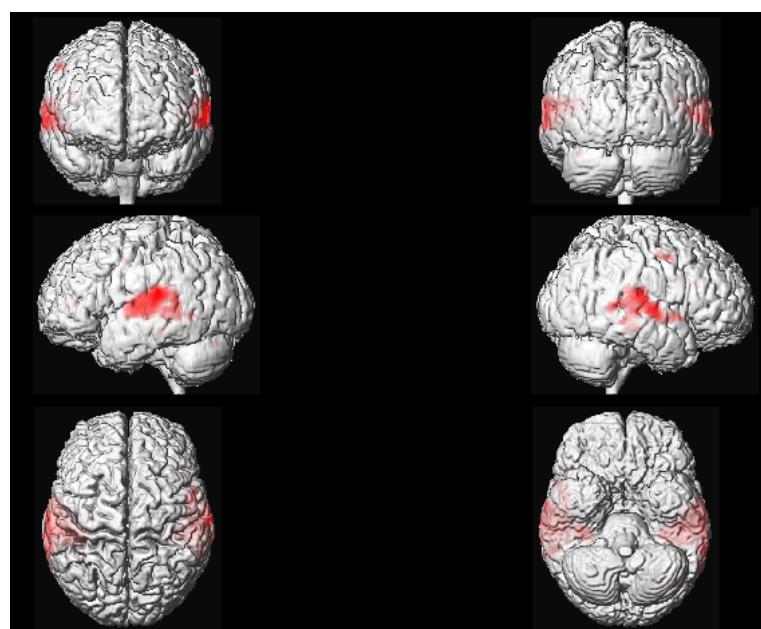
The visualisation section of the Interactive window also provides an overlay facility for anatomical visualisation of clusters of activation. Pressing “Overlays” will activate a pulldown menu with several options including:

1. **Slices**: overlay on three adjacent (2mm) transaxial slices. SPM will prompt for an image for rendering. This could be a canonical image (see `spm_templates.man`) or an individual T1/mean EPI image for single-subject analyses. Beware that the left-right convention in the display of that option will depend on how your data are actually stored on disk.
2. **Sections**: overlay on three intersecting (sagittal, coronal, axial) slices. These renderings are surfable: clicking the images will move the crosshair.
3. **Render**: overlay on a volume rendered brain.

Thresholded SPMs can be saved as NIfTI image files in the working directory by using the “Save” button in the Interactive window. In Figures 30.18, 30.19 and 30.20 the ‘listening > rest’ activation has been superimposed on the spatially normalised, bias-corrected anatomical image `wmsM00223_002.nii` created earlier.

For the “Render” option we first created a rendering for this subject. This was implemented by

- “Normalise (Write)” the two images `c1sM00223_002.nii` and `c2sM00223_002.nii` using the “Deformation Field” `y_sM00223_002.nii` and a voxel size of [1 1 1].
- Selecting “Extract Surface” from the “Render” pulldown menu.
- Selecting the gray and white matter images `wc1sM00223_002.nii` and `wc2sM00223_002.nii` created in the first step.
- Saving the results using the default options (Rendering and Surface).

Figure 30.19: *Sections*.Figure 30.20: *Render*.

Render (Acrobat Reader required)

Figure 30.21: *3D Rendering using canonical mesh.*

SPM plots the rendered anatomical image in the graphics window and saves it as `render_wc1sM00223_002.mat`. The surface image is saved as `surf_wc1sM00223_002.mat`.

It is also possible to project and display the results on a surface mesh, we are going to use here one of the canonical mesh distributed with SPM (in MNI space). Press “Overlays” and choose “Render”, then go in the `canonical` folder of your SPM installation and select file `cortex_20484.surf.gii` (this is a surface mesh stored using the GIfTI format) and you will obtain a figure similar to [30.21](#).