

**\*\*CREATED FOR SPM5, update 665, plus additional updates available here:  
[http://www.mrc-cbu.cam.ac.uk/~rh01/spm\\_eeg\\_updates\\_beyond\\_665.tar.gz](http://www.mrc-cbu.cam.ac.uk/~rh01/spm_eeg_updates_beyond_665.tar.gz) \*\***

## **Chapter 32**

# **Multimodal dataset: Localising face-evoked responses using MEG, EEG, sMRI and fMRI**

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(basic preprocessing of EEG/MEG, ECD for EEG, WMM for MEG, fMRI analysis)

Second draft, R. Henson, 28/11/06, [rik.henson@mrc-cbu.cam.ac.uk](mailto:rik.henson@mrc-cbu.cam.ac.uk)  
(added TF analysis, 2D/3D SPMs, robust averaging, WMM images)

### **32.1 Overview**

This dataset contains EEG, MEG, functional MRI and structural MRI data on the same subject within the same paradigm, which allows a basic comparison of faces versus scrambled faces.

It can be used to demonstrate, for example, 3D source reconstruction of various electrophysiological measures of face perception, such as the "N170" evoked response (ERP) recorded with EEG, or the analogous "M170" evoked field (ERF) recorded with MEG. These localisations are informed by the anatomy of the brain (from the structural MRI) and possibly by functional activation in the same paradigm (from the functional MRI).

The demonstration below involves localising the N170 using an equivalent current dipole (ECD) method, and the M170 using a distributed source method (called an "imaging" solution in SPM) analogous to "weighted minimum L2-norm". The data can also be used to explore further effects, e.g. induced effects (Friston et al, 2006), effects at different latencies, or the effects of adding fMRI constraints on the localisation.

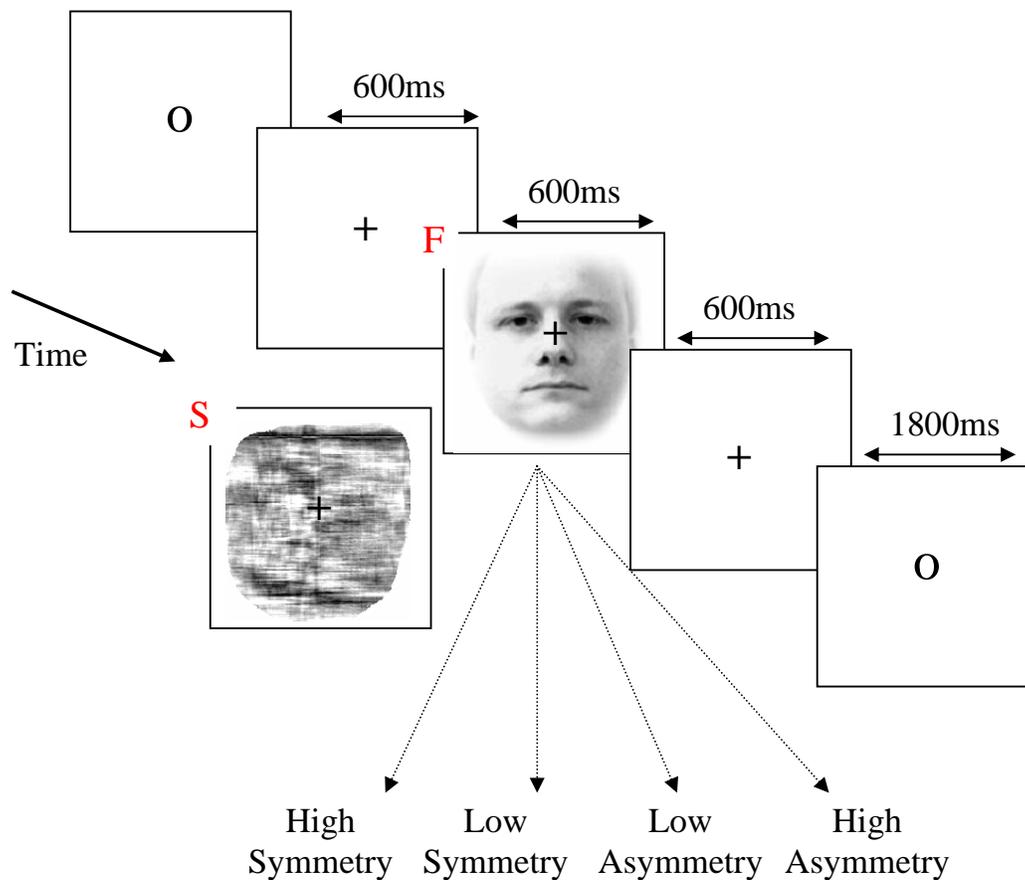
The EEG data were acquired on a 128 channel ActiveTwo system; the MEG data were acquired on a 151 channel CTF Omega system; the sMRI data were acquired using a phased-array headcoil on a Siemens Sonata 1.5T; the fMRI data were acquired using a gradient-echo EPI sequence on the Sonata. The dataset also includes data from a Polhemus digitizer, which are used to coregister the EEG and the MEG data with the structural MRI.

Some related analyses of these data are reported in Henson et al (2005a, 2005b, submitted), Kiebel & Friston (2004) and Friston et al (2006).

The analysis below is best done in Matlab7, but all mat files should be in a format readable by Matlab6.5.

### 32.2 Paradigm and Data

The basic paradigm involves randomised presentation of at least 86 faces and 86 scrambled faces (Figure 32.1), based on Phase 1 of a previous study by Henson et al (2003). The scrambled faces were created by 2D Fourier transformation, random phase permutation, inverse transformation and outline-masking of each face. Thus faces and scrambled faces are closely matched for low-level visual properties such as spatial frequency power density. Half the faces were famous, but this factor is collapsed in the current analyses. Each face required a four-way, left-right symmetry judgment (mean RTs over a second; judgments roughly orthogonal to conditions; reasons for this task are explained in Henson et al, 2003). The subject was instructed not to blink while the fixation cross was present on the screen.



**Figure 32.1:** One trial in the experimental paradigm: Trials involved either a Face (F) or Scrambled face (S).

#### 32.2.1. Structural MRI

The T1-weighted structural MRI of a young male was acquired on a 1.5T Siemens Sonata via an MDEFT sequence with resolution  $1 \times 1 \times 1 \text{ mm}^3$  voxels, using a whole-

body coil for RF transmission and an 8-element phased array head coil for signal reception.

The images are in Analyze format in the `sMRI` sub-directory, consisting of two files:

```
sMRI/sMRI .img  
sMRI/sMRI .hdr
```

The structural was manually-positioned to match roughly Talairach space, with the origin close to the Anterior Commissure, which produced the associated SPM Matlab file:

```
sMRI/sMRI .mat
```

The approximate position of 3 fiducials within this MRI space - the nasion, and the left and right peri-auricular points - are stored in the file:

```
sMRI/smri_fids.mat
```

These were identified manually (based on anatomy) and are used to define the MRI space relative to the EEG and MEG spaces, which need to be coregistered (see below). It doesn't matter that the positions are approximate, because more precise coregistration is done via digitised surfaces of the scalp ("head shape functions") that were created using the Polhemus 3D digitizer.

### 32.2.2 EEG data

The EEG data were acquired on a 128-channel ActiveTwo system, sampled at 2048 Hz (subsequently downsampled to 200Hz to reduce filesize), plus electrodes on left earlobe, right earlobe, and two bipolar channels to measure HEOG and VEOG. The data were referenced to the average of the left and right earlobes (for consistency with Henson et al, 2003). The 128 scalp channels are named: 32 A (Back), 32 B (Right), 32 C (Front) and 32 D (Left).

The original data were converted into SPM M/EEG format and epoched from -200ms to +600ms post-stimulus (baseline-corrected from -200 to 0ms), ie 161 samples:

```
EEG/e_eeg.mat  
EEG/e_eeg.dat
```

(using the "`bdf_setup.mat`" channel template provided with SPM5 in the `EEGtemplates` sub-directory).

Other details about the data can be examined by typing:

```
D = spm_eeg_ldata
```

and selecting the `e_meg.mat` file. This will show the contents of the structure "D" that is loaded into the Matlab workspace, the various fields of which can be explored. Note that the data values themselves are memory-mapped from the `e_eeg.dat` file

to the field `D.data` (e.g, `D.data(1,2,3)` returns the field strength in the first sensor at the second sample point during the third trial).

You will see that there are 344 events (`D.Nevents`), consisting of 172 faces (event code 1) and 172 scrambled faces (event code 2), which are randomly intermixed (see `D.events.code`).<sup>1</sup> If you type `D.channels.name`, you will see the order and the names of the channels.

The EEG data also contains a Polhemus sub-directory with the following files:

```
EEG/Polhemus/eeg_fids.mat
EEG/Polhemus/eeg_sens_loc.mat
EEG/Polhemus/eeg_hsf.mat
```

All files contain matrices, the three columns of which code location in a right-handed 3D space, the axes of which conform to the Talairach space, i.e, the first column is x (left-right), the second is y (anterior-posterior) and the third is z (inferior-superior). The units are mm.

The `eeg_fids.mat` file contains the position of 3 fiducial markers that were placed approximately on the nasion and peri-auricular points and digitised by the Polhemus digitizer. The digitizer was also used to locate the position of each electrode (in the `eeg_sens_loc.mat` file), and to trace out many points along the surface of the subject's scalp and nose (the "head shape function" in the `eeg_hsf.mat` file). Later, we will coregister the fiducial points and the head shape to map the electrode positions in the "Polhemus space" to the "MRI space".

### 32.2.3 MEG data

The MEG data were acquired on a 151 channel CTF Omega system, using second-order axial gradiometers sampled at 625 Hz (subsequently downsampled to 200Hz to reduce filesize). The original data were converted into SPM MEEG format and epoched from -200ms to +600ms post-stimulus (i.e, baseline-corrected from -200ms to 0ms), ie 161 samples:

```
MEG/e_meg.mat
MEG/e_meg.dat
```

These channel template for these data is also provided:

```
MEG/CTF151_setup.mat
```

(which may need to be copied to the EEGtemplates sub-directory of your local SPM5 installation directory, if not already there).

The MEG data also contains a Polhemus sub-directory with the following files:

---

<sup>1</sup> These data were actually concatenated from two separate runs on the same subject (using `spm_eeg_merge`), which is why there are twice as many events as with the MEG and fMRI data.

```
MEG/Polhemus/meg_fids.mat
MEG/Polhemus/meg_sens_loc.mat
MEG/Polhemus/meg_sens_or.mat
MEG/Polhemus/meg_hsf.mat
```

which are analogous to the corresponding MEG files described in the previous section.<sup>2</sup> More specifically, the `meg_fids.mat` contains the position of 3 "locator coils", positioned *close* to the fiducials<sup>3</sup>, the locations of which are measured by the CTF machine, and used to define the coordinates (in "CTF space") for the location of the 151 sensors (in the `meg_sens_loc.mat` file) and their (axial gradiometer) orientations (`meg_sens_or.mat`). The same three locator coils were digitised by a Polhemus digitizer outside the MEG machine, together with the head shape, to define the "Polhemus space". Subsequently, the fiducials in the Polhemus space were coregistered with the fiducials in the CTF space, and the resulting rigid-body transformation applied to the Polhemus head shape. Thus the coordinates in all four files above are in alignment in the CTF space, which will subsequently be transformed into the "MRI space".

### 32.2.4 fMRI data

The fMRI data were acquired using a Trajectory-Based Reconstruction (TBR) gradient-echo EPI sequence (Josephs et al, 2000) on a 1.5T Sonata. There were 32, 3mm slices of  $3 \times 3 \text{ mm}^2$  pixels, acquired in a sequential descending order with a TR of 2.88s. There are 215 images in the 'Scans' sub-directory (5 initial dummy scans have been removed), each consisting of an Analyze image and header file:

```
fMRI/Scans/fM*.img
fMRI/Scans/fM*.hdr
```

Also provided are the onsets of faces and scrambled faces (in units of scans) in the Matlab file:

```
fMRI/onsets.mat
```

and the SPM "Job" files (see Section 32.6):

```
fMRI/realign_job.mat
fMRI/slicetime_job.mat
fMRI/smooth_job.mat
fMRI/stats_job.mat
```

## 32.3 Getting Started

You need to start SPM5 and toggle "EEG" as the modality (bottom-right of SPM main window), or start SPM5 with "spm eeg".

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<sup>2</sup> These matrices are transformations from the original CTF / Polhemus files - in which x codes anterior-posterior and y codes left-right - i.e, a 90 degree clockwise rotation about the z-axis.

<sup>3</sup> Unlike the MRI and EEG data, these fiducials were not precisely the nasion and peri-auricular points. However, given that the coregistration of the MEG and MRI data is based mainly on the headshape (see later), this inaccuracy in the MEG fiducials does not matter.

You will also need to 1) copy the MEG template file (`CTF151_setup.mat`) to the `EEGtemplates` sub-directory within your SPM5 installation directory, if it is not already there (see Section 32.2.3 above), and 2) ensure this `EEGtemplates` directory is on your Matlab path.

## 32.4 EEG analysis

### 32.4.1 Preprocessing the EEG data

- Change directory to the EEG subdirectory (either in Matlab, or via the "CD" option in the SPM "Utils" menu)
- Press 'Artefacts', select the '`e_eeg.mat`' file, press 'no' to the 'read own artefact list?' question, 'no' to 'robust average?', 'yes' to 'threshold channels?', and enter 200 for the threshold

This will detect trials in which the signal recorded at any of the channels exceeds 200 microvolts (relative to pre-stimulus baseline). These trials will be marked as artefacts. Most of these artefacts occur on the VEOG channel, and reflect blinks during the critical timewindow.<sup>4</sup> The procedure will also detect channels in which there are a large number of artefacts (which may reflect problems specific to those electrodes, allowing them to be removed from subsequent analyses).

In this case, the Matlab window will show:

```
There isn't a bad channel.  
45 rejected trials: [5 38 76 82 83 86 87 88 89 90 92  
93 94 96 98 99 100 101 104 105 106 107 108 112 117 118  
119 120 122 124 126 130 137 139 159 173 221 266 268 279  
281 292 293 298 326]
```

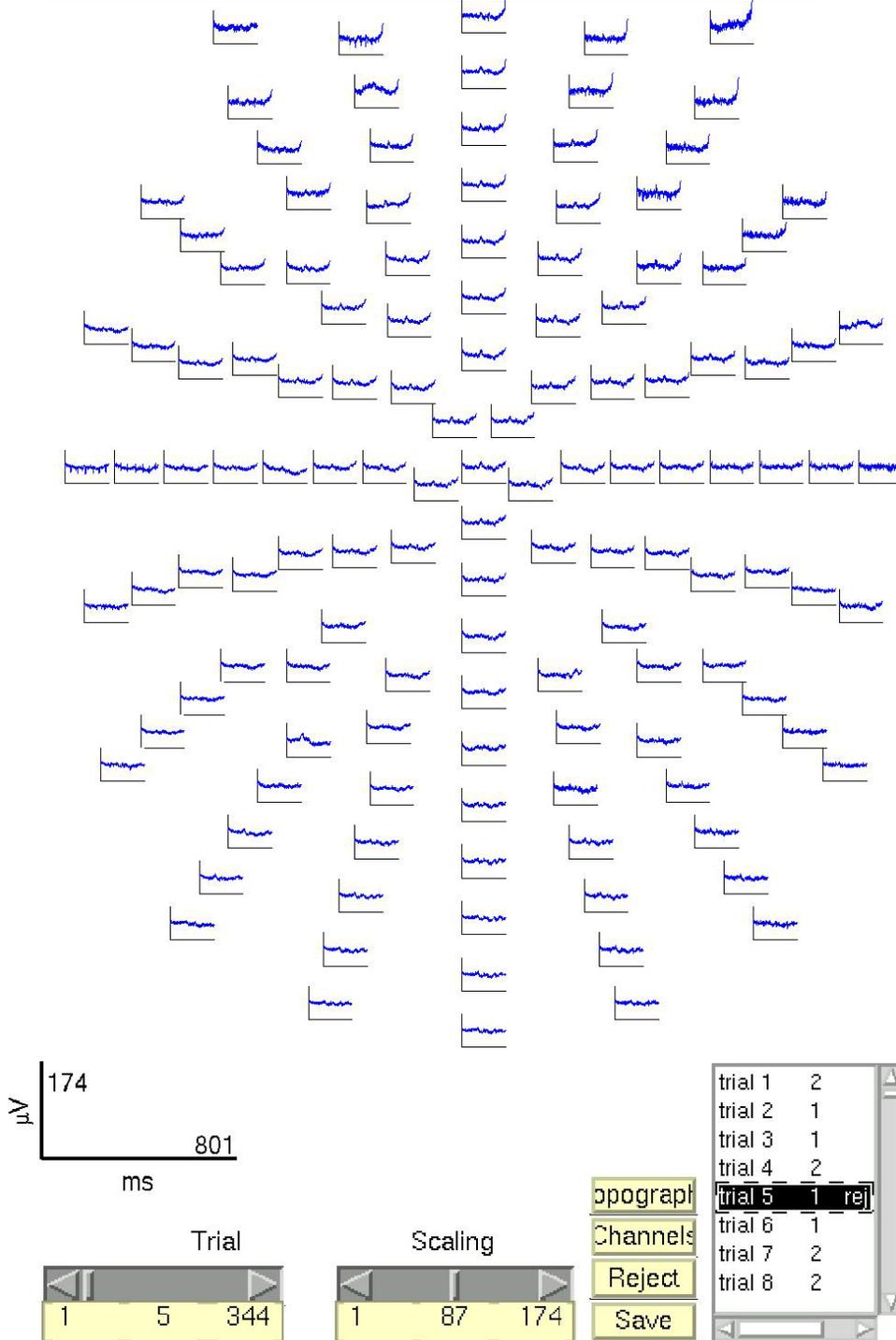
(leaving 299 valid trials). A new file will also be created, `ae_eeg.mat` (in which these artefacts are coded in the fields `D.events.reject` and `D.channels.thresholded`).

At this point, you may want to look at the data. Press "Display: M/EEG", and select the `ae_eeg.mat` file. After a short delay, the Graphics window should show the mean ERP (for trial 1) at each of the 130 channels (as in Figure 32.2). You can click on one of the channels (e.g. VEOG, on the top right of the display) to get a new window with the data for that channel expanded. You can alter the scaling or trial number using the sliders on the bottom of the Graphics window, or select a subset of channels to display by pressing the 'Channels' button.

---

<sup>4</sup> Channel-specific thresholds can be used by entering 130 thresholds, one per EEG/EOG channel, with a value of `Inf` for those channels that you do not want to threshold.

/imaging/rh01/SPMCourse/SPM5/MultiModal/Test/EEG/ae



**Figure 32.2** SPM Display window for trial 5 for all 128 EEG plus 2 EOG channels (top left and top right) in ae\_eeg.mat. Trial 5 is marked as an artefact because the VEOG channel (top right) exceeds the user-specified threshold of 200uV, most likely reflecting the onset of a blink towards the end of the epoch.

### 32.4.2 Basic ERPs

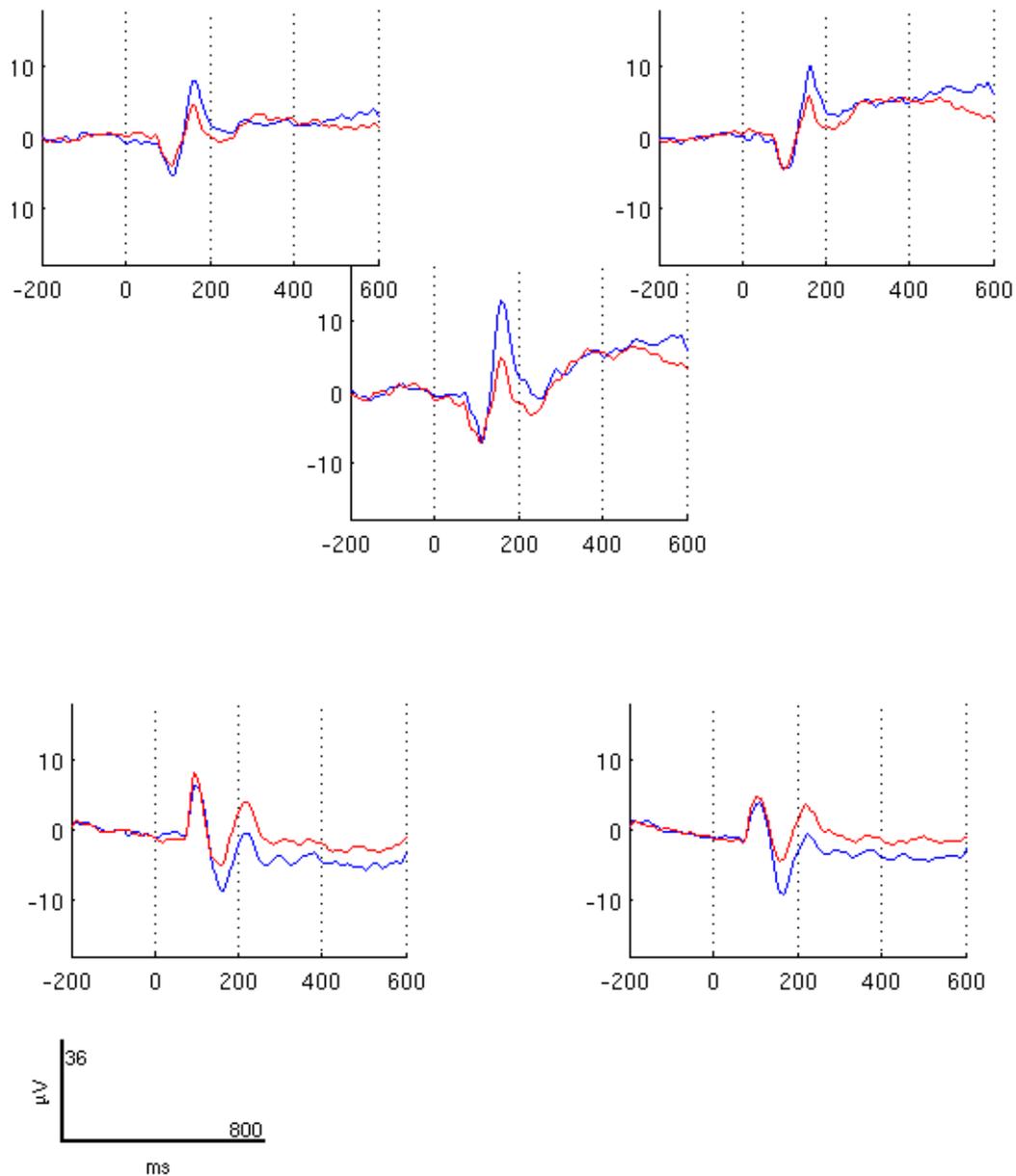
- Press the 'Averaging' button and select the `ae_eeg.mat` file. After a few moments, the matlab window will echo:

```
ae_eeg.mat: Number of replications per contrast:  
average 1: 151 trials, average 2: 148 trials
```

(artefact trials are excluded from averaging) and a new file will be created in the MEG directory called `mae_eeg.mat` ("m" for "mean").

- Press the 'Filtering' button, select the `mae_eeg.mat` file, select 'lowpass', and enter 40 (Hz) as the cutoff. This smooths the data to 40Hz, producing the file `fmae_eeg.mat` (using zero-phase-shift forward and reverse digital filtering with a 5th-order Butterworth filter)

You can display the mean ERPs using the "Display: M/EEG" menu option again. Once you have done so, press the "channels" button in the Graphics window, then "Deselect all", and then click only, eg channels 'd7', 'a12', 'b12' and 'c7'. (You can save these selections as a file, and use this file to display only a subset of channels in future). After pressing "ok", you will now only see these 5 channels (which will also make the display much faster!). Once you hold SHIFT and select trial-type 2, you should see something like Figure 32.3.

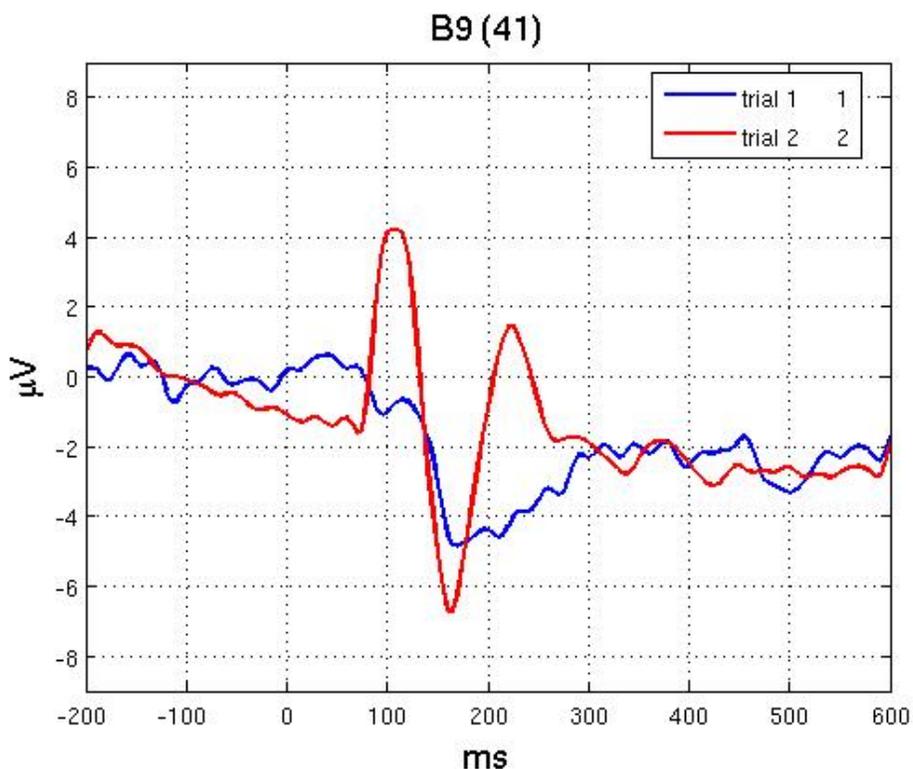


**Figure 32.3** SPM Display window for smoothed, average ERPs for faces (blue) and scrambled faces (red) for 5 selected channels in `fmae_eeg.mat`.

- Select "Contrast" from the "Other..." pulldown menu on the SPM window (or type `spm_eeg_weight_epochs` in the Matlab window). This function creates linear contrasts of ERPs/ERFs. Select the `fmae_eeg.mat` file, and enter `[1 -1; 1/2 1/2]` as the contrasts. This will create new file

mfmae\_eeg.mat, in which the first trial-type is now the differential ERP between faces and scrambled faces, and the second trial-type is the average ERP for faces and scrambled faces.

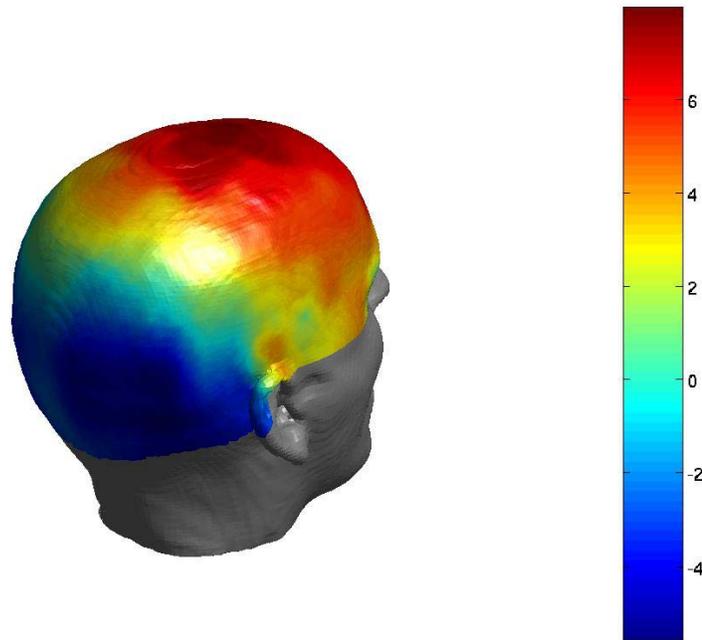
To look at the differential ERP, again press 'Display: M/EEG', and select the mfmae\_eeg.mat file. After a short delay, the Graphics window should show the ERP for each channel (for trial-type 1). Hold SHIFT and select trial-type 2 to see both conditions superimposed. Then click on one of the channels (e.g. 'B9' on the bottom right of the display) to get a new window with the data for that channel expanded, as in Figure 32.4.



**Figure 32.4** Average (red) and differential (blue) ERPs for faces and scrambled faces at channel B9 in mfmae\_eeg.mat.

The red line shows the average ERP evoked by faces and scrambled faces (at this occipitotemporal channel). A P1 and N1 are clearly seen. The blue line shows the differential ERP between faces and scrambled faces. This is approx zero around the P1 latency, but negative around the N1 latency. The latter likely corresponds to the "N170" (Henson et al, 2003). It is this first trial-type (the difference wave) that we use to localise the M170 using equivalent current dipoles (ECDs) in Section 32.4.4.

To see the topography of the differential ERP, press the "topography" button in the main graphics window, enter 165ms for the latency, and select "3D", to produce Figure 32.5.



**Figure 32.5** 3D topography for faces minus scrambled faces at 165ms.

### 32.4.3 3D SPMs (Sensor Maps over Time)

One novel feature of SPM is the ability to use Random Field Theory to correct for multiple statistical comparisons across N-dimensional spaces. For example, a 2D space representing the scalp data can be constructed by flattening the sensor locations and interpolating between them to create an image of  $M \times M$  pixels (when  $M$  is user-specified, eg  $M=32$ ). This would allow one to identify locations where, for example, the ERP amplitude in two conditions at a given timepoint differed reliably across subjects, having corrected for the multiple t-tests performed across pixels. That correction uses Random Field Theory, which takes into account the spatial correlation across pixels (i.e, that the tests are not independent). This kind of analysis is described earlier in the SPM manual, where a 1st-level design is used to create the images for a given weighting across timepoints of an ERP/ERF, and a 2nd-level design can then be used to test these images across subjects.

Here, we will consider a 3D example, where the third dimension is time, and test across trials within the single subject. We first create 3D image for each trial of the two types, with dimensions  $M \times M \times S$ , where  $S=161$  is the number of samples. We then take these images into an unpaired t-test across trials (in a 2nd-level model) to compare faces versus scrambled faces. We can then use classical SPM to identify locations in space and time in which a reliable difference occurs, correcting across the multiple comparisons entailed. This would be appropriate if, for example, we had no a

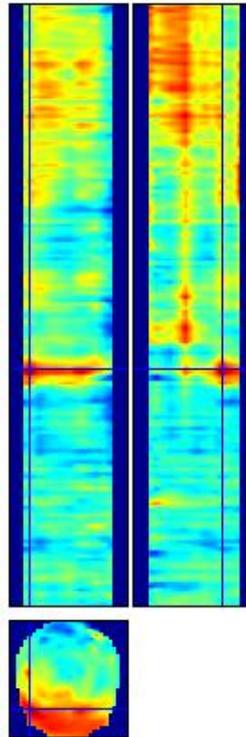
priori knowledge where or when the difference between faces and scrambled faces would emerge.<sup>5</sup>

- Type `spm_eeg_convertmat2ana3D` in the Matlab window, and select the `ae_eeg.mat` file. You will then be prompted for "output image dimensions", for which you can accept the default of 32 (leading to a 32x32 pixel space). It will also ask whether you want to interpolate or mask out bad channels, for which you can select interpolate (though it will make no difference here because there are no bad channels). Finally, it will ask for a pixel size, which is currently arbitrary, but you can change to 5 to make the subsequent graphics larger.

This will create a new directory called `ae_eeg`, which will itself contain two subdirectories, one for each `trialtype`. In each `trialtype` subdirectory there will be image and header files for each non-rejected trial of that type, e.g, `trial2.img/hdr`. You can press "Display: images" to view one of these images - it will have dimensions 32x32x161(x1), with the origin set at [16 16 40] (where 40 samples is 0ms), as in Figure 32.6.

---

<sup>5</sup> Note that the 2D location in sensor space for EEG will depend on the choice of reference channel.



Crosshair Position	
mm:	-47.9 -38.3 118.9
VX:	6.4 8.3 63.8
Intensity:	23.7841

right {mm}	0
foward {mm}	0
up {mm}	0
pitch {rad}	0
roll {rad}	0
yaw {rad}	0
resize {x}	1
resize {y}	1
resize {z}	1

File: <b>..eg/trialtype1/trial2.img</b>	
Dimensions: <b>32 x 32 x 161</b>	
Datatype: <b>float32</b>	
Intensity: <b>Y = 1 X</b>	
<b>NIFTI-1 Image</b>	
Vox size: <b>5 x 5 x 5</b>	
Origin: <b>16 16 40</b>	
Dir Cos: <b>1.000 0.000 0.000</b>	
<b>0.000 1.000 0.000</b>	
<b>0.000 0.000 1.000</b>	

Full Volume	Hide Crosshairs
World Space	bilin interp
Auto Window	Add Blobs

**Figure 32.6** 3D image for trial 2 of `ae_eeg.mat`. The bottom image is a square 2D x-y space interpolated from the flattened electrode locations (at one point in time). The two top images are sections through x and y respectively, now expressed over time (vertical (z) dimension). (Colormap changed to 'jet').

To perform statistics on these images, first create a new directory, eg. `mkdir XYTstats`.

- Then press the "specify 2nd level" button, select "two-sample t-test" (unpaired t-test), and define the images for "group 1" as all those in the subdirectory

"trialtype1" (using right mouse, and "select all") and the images for "group 2" as all those in the subdirectory "trialtype2". Finally, specify the new `XYZstats` directory as the output directory, and press "run".<sup>6</sup>

This will produce the design matrix for a two-sample t-test.

- The press "Estimate", and when it has finished, press "Results" and define a new F-contrast as [1 -1] (for help with these basic SPM functions, see elsewhere in the Manual). Keep the default contrast options, but threshold at  $p < .05$  FWE corrected for the whole "image". Then press "volume", and the Graphics window should now look like that in Figure 32.7 (ignore the outline of the brain in the MIP!).

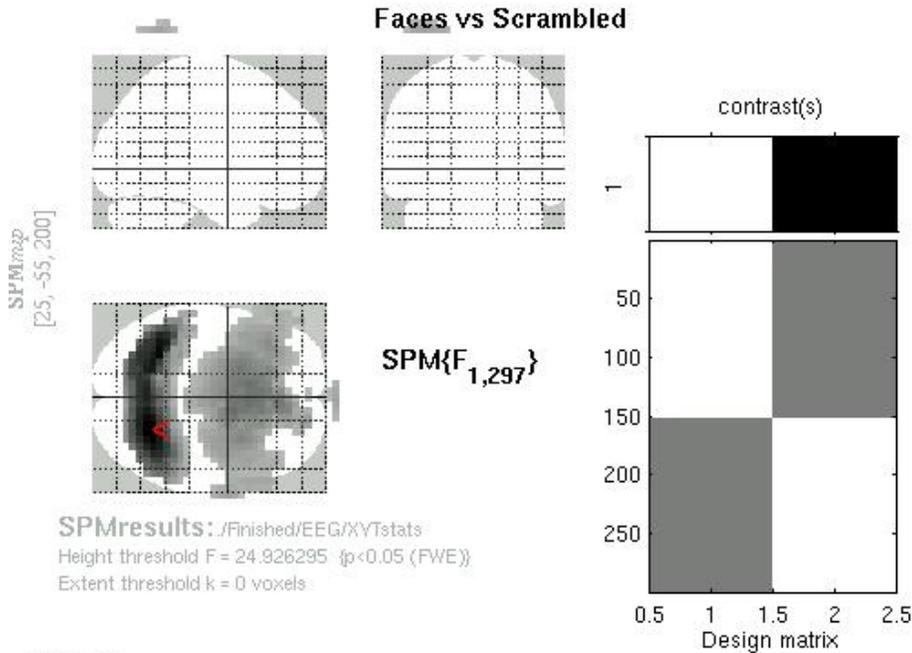
This will reveal "regions" within the 2D sensor space and within the -200ms to 600ms epoch in which faces and scrambled faces differ reliably, having corrected for multiple F-tests across pixels/time. There are a number of such regions, but we will concentrate on the first two (largest ones), with cluster maxima of [25 -55 200] and [10 5 160]. An F-test was used because the sign of the difference reflects the polarity of the ERP difference, which is not of primary interest (and depends on the choice of reference; see footnote 5). Indeed, if you plot the contrast of interest from the cluster maxima, you will see that the difference is negative for the first cluster (which is located posteriorly) but positive for the second cluster (which is more central, close to Cz). This is consistent with the polarity of the differences in Figure 32.3.<sup>7</sup>

If one had more constrained a priori knowledge about where and when the N170 would appear, one could perform an SVC based on, for example, a box around posterior channels and between 150 and 200ms poststimulus.

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<sup>6</sup> Note that we can use the default "nonsphericity" selections, i.e, that the two trial-types may have different variances, but are uncorrelated.

<sup>7</sup> With a reference similar to the current earlobes, the former likely corresponds to the "N170", while the latter likely corresponds to the "VPP" (though we have no evidence here for a dissociation between them).



**Statistics: p-values adjusted for search volume**

set-level		cluster-level			voxel-level					mm mm mm			
p	c	p <sub>corrected</sub>	k	E	p <sub>uncorrected</sub>	p <sub>FWE-corr</sub>	p <sub>FDR-corr</sub>	F	(Z <sub>≡</sub> )	p <sub>uncorrected</sub>			
0.000	10			3422	0.000	0.000	126.23	Inf	0.000	0.000	25	-55	200
					0.000	0.000	118.53	Inf	0.000	0.000	-30	-50	200
				2054	0.000	0.000	112.31	Inf	0.000	0.000	25	-55	215
					0.000	0.000	66.04	7.66	0.000	0.000	10	5	160
					0.000	0.000	65.23	7.58	0.000	0.000	0	15	170
				547	0.000	0.000	47.71	6.54	0.000	0.000	-40	-45	335
					0.000	0.000	45.97	6.39	0.000	0.000	-35	-45	320
					0.000	0.000	42.68	6.20	0.000	0.000	40	-45	395
				32	0.000	0.000	36.23	5.73	0.000	0.000	-40	-50	100
				32	0.001	0.000	35.63	5.69	0.000	0.000	0	80	170
					0.001	0.000	35.25	5.65	0.000	0.000	5	80	185
				58	0.004	0.000	31.30	5.33	0.000	0.000	45	-50	495
					0.004	0.000	31.15	5.31	0.000	0.000	45	-50	505
					0.010	0.000	28.70	5.10	0.000	0.000	50	-50	480
				4	0.027	0.000	26.45	4.89	0.000	0.000	70	0	175
					0.030	0.000	26.13	4.86	0.000	0.000	70	-10	170
				2	0.028	0.000	26.32	4.88	0.000	0.000	-55	50	185
				2	0.034	0.000	25.84	4.84	0.000	0.000	0	60	170
				1	0.041	0.000	25.42	4.80	0.000	0.000	-60	-25	320

table shows 3 local maxima more than 8.0mm apart

Height threshold: F = 24.93, p = 0.000 (0.050) (p < 0.05 FWE) (df freedom = [1.0, 297.0])  
 Extent threshold: k = 0 voxels, p = 1.000 (0.050) FWHM = 27.5 25.6 16.4 mm mm mm; 5.5 5.1 3.3 (voxels);  
 Expected voxels per cluster, <k> = 2.542 Volume: 15174250; 121394 voxels; 1204.2 resels  
 Expected number of clusters, <c> = 0.05 Voxel size: 5.0 5.0 5.0 mm mm mm; (resel = 92.08 voxels)  
 Expected false discovery rate, <= 0.00

**Figure 32.7** 3D sensor-time SPM{F} at p<.05 FWE corrected for the amplitude difference between face and scrambled face trials. Note that the brain outline in the MIP should be ignored. The x, y coordinates refer to arbitrary units in the 32x32 electrode plane (origin = [16 16]); the z coordinate refers to peristimulus time in ms (to the nearest sampling of 5ms).

**32.4.4 "ECD" reconstruction**

- Press the '3D source reconstruction' button, and select the `mfmee_eeg.mat` file and type a label (eg "N170") for this analysis.<sup>8</sup>
- Press the 'Meshes' button, and select the `smri.img` file within the sMRI sub-directory...

This will take some time while the MRI is segmented (and normalisation parameters determined). This will create the usual files, i.e, `c1/c2/c3smri.img/hdr`, for grey/white/CSF respectively, `msmri.img/hdr` for the attenuation-corrected image, and the normalisation and inverse normalisation parameters (`mri_vbm_sn_1.mat` and `smri_vbm_inv_sn_1.mat` respectively) in the sMRI directory (see Chapter 5 for further details).

This process will also create binary images of the skull inner-surface and the scalp, which are then used to create meshes (of 2002 vertices) for these surfaces, stored in the following files:

```

sMRI/smri_iskull.img
sMRI/smri_scalp.img
sMRI/smri_iskull_Mesh_2002.mat
sMRI/smri_scalp_Mesh_2002.mat

```

- .. after some time, you will be prompted for the number of vertices in your cortical mesh (3000 to 7000). Choosing 3000 for now will reduce computation (the actual number of vertices resulting will be 3004).

This will create the new files:

```

sMRI/smri_CortexMesh_3004.mat
sMRI/smri_CortexGeoDist_3004.mat

```

The former file contains a triangulated greymatter mesh consisting of (3004) vertices, (6000) faces, and (3004) normals to the surface at each vertex; the latter file codes the geodesic distance between the vertices (which is only relevant if you plan to use a smoothness constraint on your imaging solutions; see Section 32.5.4).

Note that the cortical mesh (and the distances within the mesh) are not created directly from the segmented MRI (like the skull and scalp meshes), but rather are determined from a template cortical mesh in MNI space via inverse spatial normalisation (Mattout et al, in prep).

When meshing has finished, the cortex (blue), inner skull (red) and scalp (black) meshes will be shown in the Graphics window.

---

<sup>8</sup> Note that no new M/EEG files are created during each stage of the 3D reconstruction; rather, each step involves updating of the cell-array field `D.inv`, which will have one entry per analysis performed on that dataset (e.g, `D.inv{1}` in this case).

- Press the 'Coregister' button, select "& surface", respond "no" to the 'Read Polhemus?' question, and then select the following files in response to each prompt:

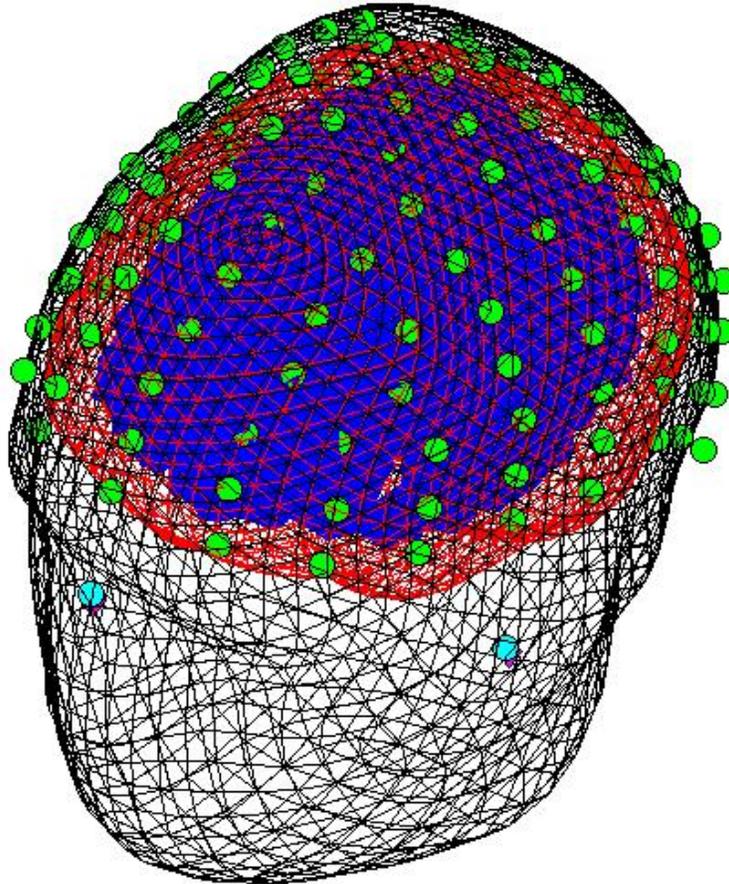
```
EEG/Polhemus/eeg_sens_loc.mat  
EEG/Polhemus/eeg_fids.mat  
sMRI/smri_fids.mat  
EEG/Polhemus/eeg_hsf.mat
```

This stage coregisters the EEG sensor positions with the structural MRI and cortical mesh, via an approximate matching of the fiducials in the two spaces, followed by a more accurate surface-matching routine that fits the head-shape function (measured by Polhemus) to the scalp that was created in the previous meshing stage via segmentation of the MRI. The following files will be produced:

```
EEG/eeg_fids_coreg.mat  
EEG/eeg_hsf_coreg.mat  
EEG/eeg_sens_loc_coreg.mat  
EEG/RegMat.mat
```

which contain the coregistered positions in MRI space (the final file contains the 4x4 matrix coding the rigid-body mapping from the EEG to MRI space).

A figure like that in Figure 32.8 will also be produced, which you can rotate with the mouse to check all sensors.



**Figure 32.8** Graphical output of Co-registration of EEG data, showing cortex (blue), inner skull (red) and scalp (black) meshes, electrode locations (green), and MRI/Polhemus fiducials (cyan/magneta).

- Press 'Forward Model', select 'ECD', and answer 'no' to the question "Use canonical model?" (because here we will create a forward model based on the individual's MRI (rather than a canonical MRI).

This will create a forward model (lead field matrix) based on "realistic spheres". This approach estimates the sphere that best-fits the scalp, and then deforms the cortex, inner skull and scalp meshes, and electrode positions, to fit this sphere (Spinelli et al, 2000). The forward model can then be calculated analytically, here using a 3-compartment spherical model for the cortex, skull and scalp (with assumed relative conductivities of [.33 .004 .33]). The estimated dipole locations within the brain can then be transformed back to the original space.

The Matlab window will also echo:

```
Scalp sphere will have centre : 0.07 -17.76 -9.67, and
radius R= 91.48
```

and another picture of the electrode positions on the head will be shown.

- Press 'Invert', select condition '1' (the difference between faces and scrambled faces, as created at the end of Section 32.4.2), [150 180] for the time window, '2' for the number of dipoles, '40' as the number of random seeds, select 'totally free orientation'.

This will take some time as each of 40 fits are performed, each with different initial random positions (seeds) for the two dipoles.

The Graphics window will show a number of dipoles. These are actually the first dipole from each of 5 "groups" of solutions. If you type in the Matlab window

```
D.inv{end}.inverse.resdip
```

you will see that the field 'n\_grp' (which should be [32 5 1 1 1]) indicates that, of the 40 random seeds, 5 "groups" of solutions were found, with the majority (32) conforming to the first group.

If you deselect all dipoles on the Graphics window (e.g, by pressing the 'solutions display' button, which will clear the current dipoles shown), then press button '1', which will show only Group 1 dipoles, and select 'all' from the 'Select dipole #' menu. This should produce the two dipoles from Group 1, as shown in Figure 32.9.

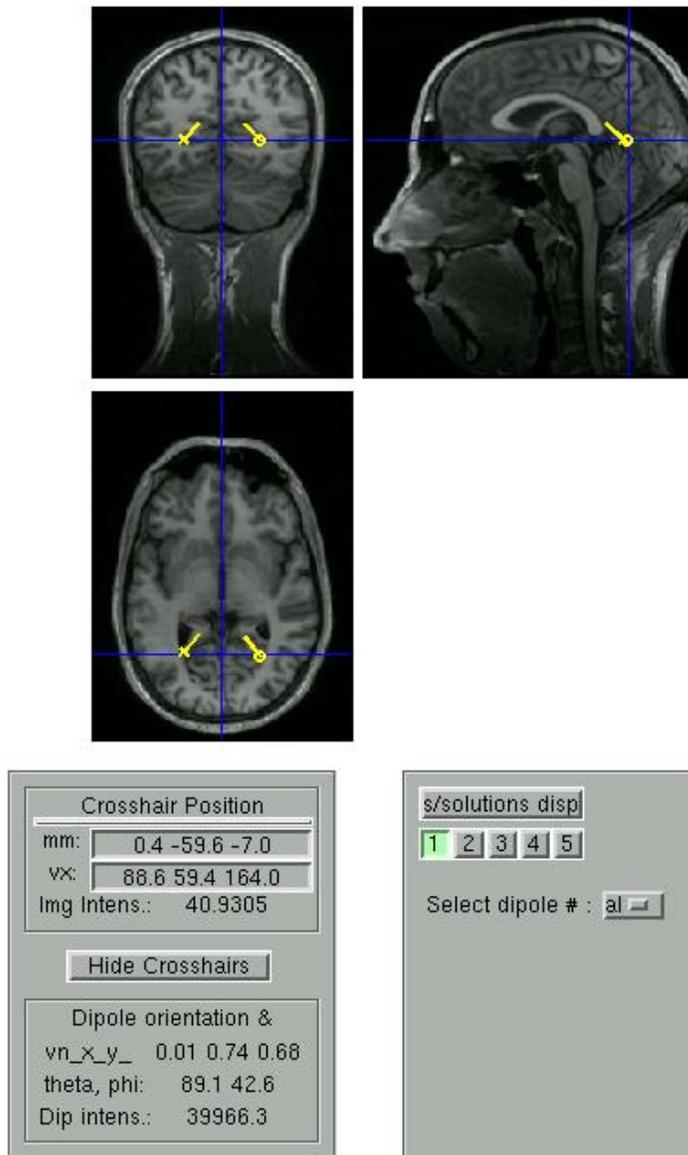
If you type in the Matlab window:

```
round(D.inv{end}.inverse.resdip.loc{1}')
```

you should get the answer:

```
26    -61    -7  
-26   -59    -7
```

These are the mean coordinates in the MRI space of the two dipoles from the first group of fits. Note that these are in the space of the subject's (unnormalised) MRI; not MNI space (though the axes do correspond, and the coordinates will not be far different, given that the origin of the subject's MRI space was manually positioned to match the Anterior Commissure). The field `D.inv{end}.inverse.resdip.varexpl(1)` also gives the proportion of variance explained (59% for Group 1).



**Figure 32.9** Most common result (32 of 40 random seeds) of fitting two dipoles to the 150-180ms latency region of the differential ERP between faces and scrambled faces (allowing dipole orientation to change freely throughout the latency region).

The precise location of these dipoles is difficult to ascertain, but they might correspond to the depth of the collateral sulcus, and are at least close to bilateral fusiform cortex. (These can be contrasted with the distributed solution of the MEG data in Figure 32.19, and the fMRI results in Figure 32.22, which show more posterior occipital and lateral temporal sources, and an orbitofrontal source). This illustrates the problem of fitting a distributed pattern of neural activity (as apparent in this case) with a small number of equivalent dipoles. These two dipoles do explain a some of the variance (~60%), but increasing their number might reveal additional sources in lateral temporal and orbitofrontal regions (though note that each dipole requires 7 degrees of freedom, and there are only 128 observations, which are likely to be spatially correlated).

## 32.5 MEG analysis

### 32.5.1 Preprocessing the MEG data

- Change directory to the MEG subdirectory (either in Matlab, or via the "CD" option in the SPM "Utils" menu)
- Press 'Artefacts', select the 'e\_meg.mat' file, press 'no' to the 'read own artefact list?' question, but 'yes' to 'robust average?' and select the default 'offset weighting function' (3) and default FWHM residual smoothing (20), and 'no' to 'threshold channels?'

This will take a while. The new file produced, ae\_meg.mat, will contain the same data, but a new field of "D.weights" will be created. These weights will be applied during the next step of averaging (see Kilner et al, in prep.):

- Press the 'Averaging' button and select the ae\_meg.mat file. After a few moments, the matlab window will echo:

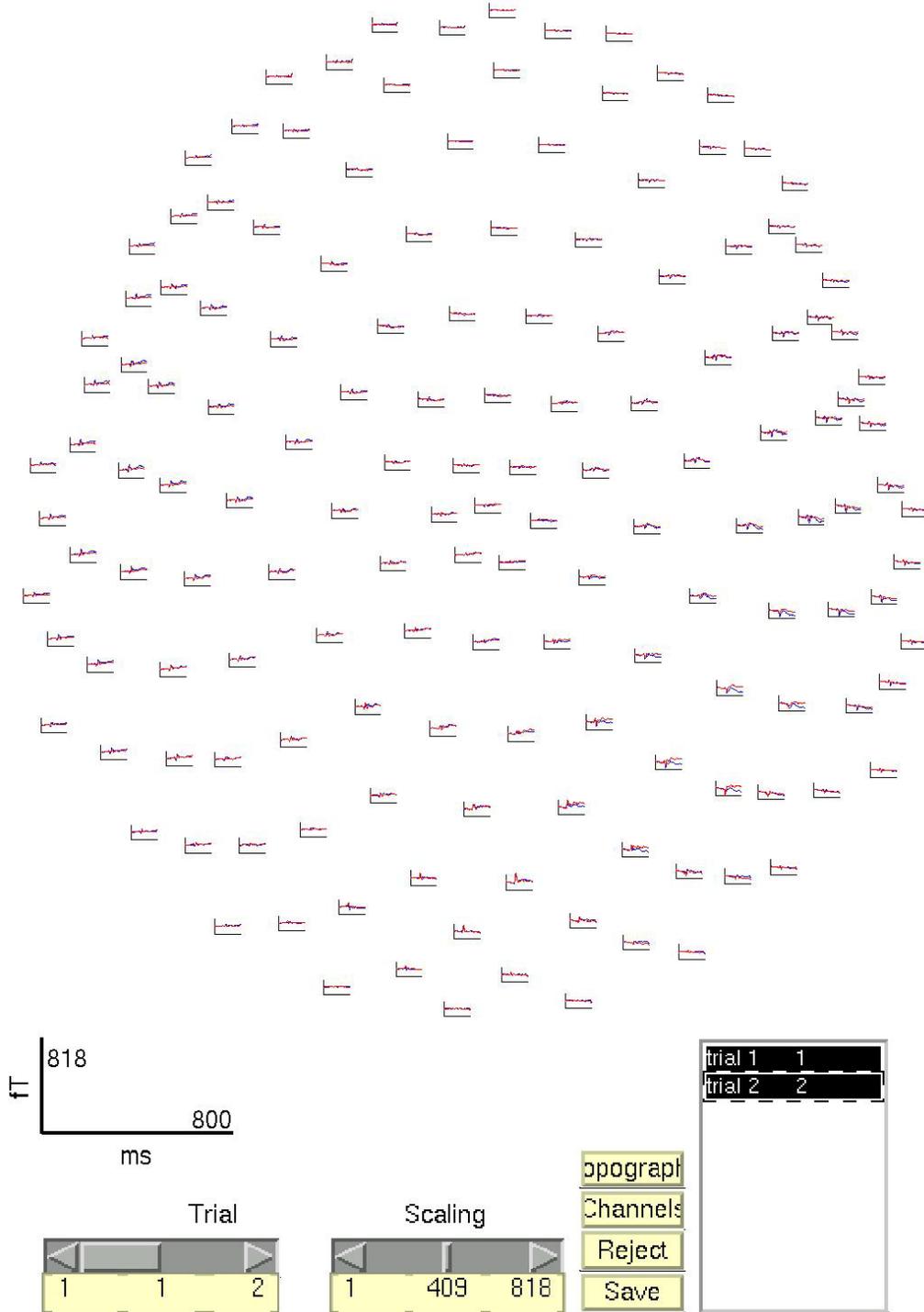
```
e_meg.mat: Number of replications per contrast:  
average 1: 86 trials, average 2: 86 trials
```

and a new file will be created in the MEG directory called mae\_meg.mat ("m" for "mean")

- Press the 'Filtering' button, select the mae\_eeg.mat file, select 'lowpass', and enter 40 (Hz) as the cutoff. This smooths the data to 40Hz, producing the file fmae\_eeg.mat.

As before, you can display these data by "Display: M/EEG" and selecting the fmae\_eeg.mat. Hold SHIFT and select trial-type 2 with the mouse in the bottom right of the window to see both conditions superimposed (as Figure 32.10).

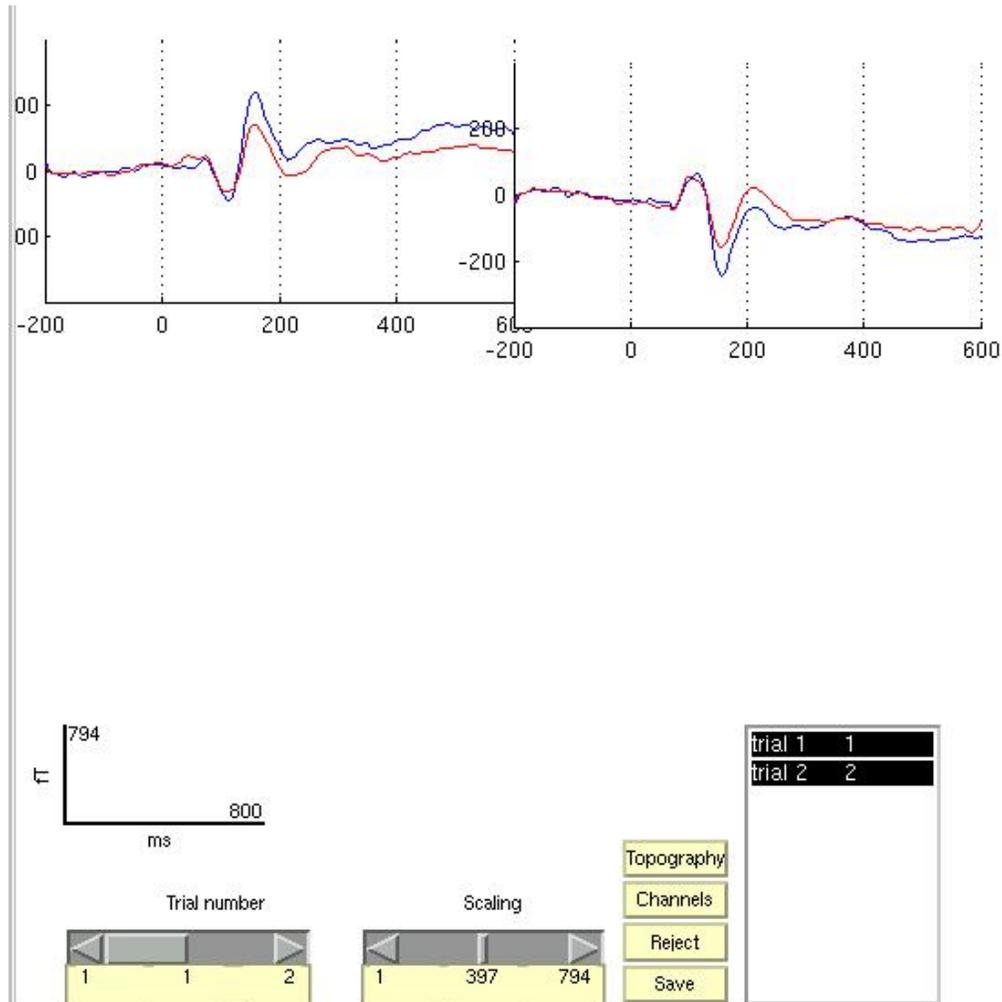
/imaging/rh01/SPMCourse/SPM5/MultiModal/Test/MEG/fm



**Figure 32.10** SPM Display window for mean, smoothed ERF (f\_mae\_meg.mat) for all 151 MEG channels.

You can also press this 'Channels' button and in the new window, "deselect" all the channels, then select MRT24 and MLT24 (e.g, from the channel names on the right),

and press 'ok'. (It will help if you save these selections as a file, which can be used later to display only a subset of channels). You will now only see these two channels in the SPM Graphics Window, which clearly show a difference between faces (trial-type 1, in blue) and scrambled faces (trial-type 2, in red) around approximately 170ms (the "M170"; Figure 32.11). The sign of this difference is reversed across left and right hemispheres, as is common for the axial components of the magnetic fields from tangential current sources.



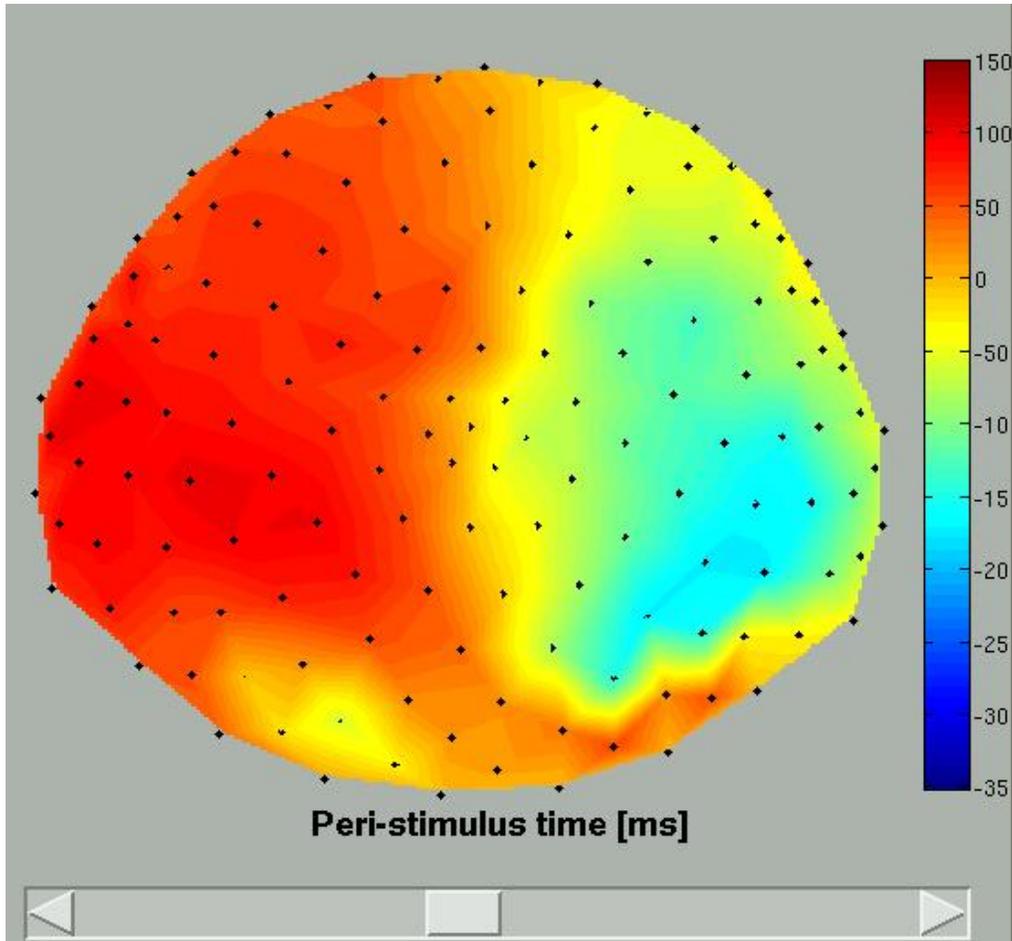
**Figure 32.11** Two selected MEG channels (MLT24 and MRT24).

- Select "Contrast" from the "Other..." pulldown menu on the SPM window (or type `spm_eeg_weight_epochs` in the Matlab window). This function creates linear contrasts of ERPs/ERFs. Select the `fmae_meg.mat` file, and enter  $[1 \ -1; \ 1/2 \ 1/2]$  as the contrasts. This will create new file `mfmae_meg.mat`, in which the first trial-type is now the differential ERF between faces and scrambled faces, and the second trial-type is the average ERF.

If you want to see the 2D topography of the differential ERF between faces and scrambled faces, you can Display the new file `mfmae_eeg.mat`, select trial-type 1,

press "Topography" and in the new window, select "2D" and 165ms as the timepoint (Figure 32.12). This will show a bilinear interpolation of the difference across the 151 channels.

You can move the slider left and right to see the development of the M170 over time.



**Figure 32.12** 2D topography of the ERF of faces minus scrambled faces at 165ms

We will use this file when we perform a distributed localisation of the evoked M170 in Section 32.5.4.

### 32.5.2 Time-Frequency Analysis

SPM uses Morlet wavelets to perform time-frequency analyses.

- Select the 'time-frequency' option under the 'Other' pull-down menu, and select the `e_meg.mat` file. SPM will then prompt you for the frequencies you wish to analyse, for which you can type [5:40] (Hz). To the question "remove baseline", press "no" (because for frequencies as low as 5Hz, one would need

a longer pre-stimulus baseline, to avoid edge-effects<sup>9</sup>). Later, we will compare two trial-types directly, and hence any pre-stimulus differences will become apparent. Change the default Morlet wavelet order (N) from 7 to 5. This factor effectively trades off frequency vs time resolution, with a lower order giving higher temporal resolution. You will then be prompted to select channels, for which you can highlight and delete the default option of all channels, and type just 66 (which corresponds to channel 'MLT34', as can be confirmed by typing `D.channels.names` in the Matlab window).<sup>10</sup>

This will produce two new files, `t1_e_eeg.mat` and `t2_e_eeg.mat`. The former contains the power at each frequency, time and channel; the latter contains the corresponding phase angles.

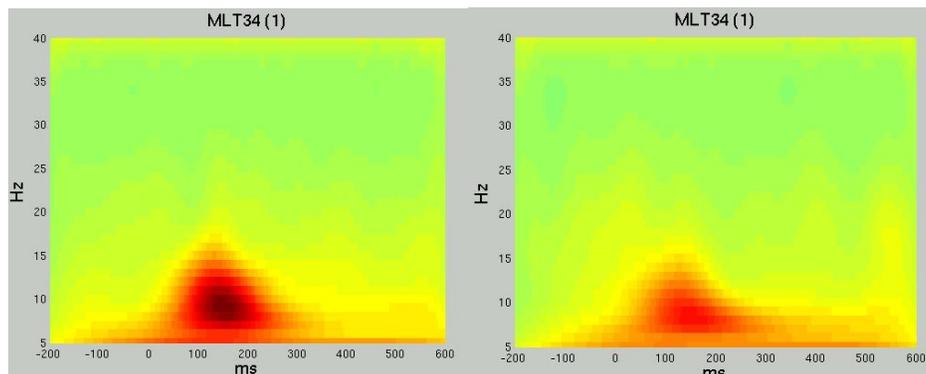
- Press the 'Averaging' button and select the `t1_e_meg.mat` file. After a few moments, the matlab window will echo:

```
e_meg.mat: Number of replications per contrast:
average 1: 86 trials, average 2: 86 trials
```

and a new file will be created in the MEG directory called `mt1_e_meg.mat`.

This contains the power spectrum averaged over all trials, and will include both "evoked" and "induced" power. Induced power is (high-frequency) power that is not phase-locked to the stimulus onset, which is therefore removed when averaging the amplitude of responses across trials (i.e, would be absent from a time-frequency analysis of the `mae_eeg.mat` file).

The power spectra for each trial-type can be displayed using the usual Display button and selecting the `mt1_e_eeg.mat` file. This will produce a plot of power as a function of frequency (y-axis) and time (x-axis) for Channel MLT34. If you use the "trial" slider to switch between trial(types) 1 and 2, you will see the greater power around 150ms and 10Hz for faces than scrambled faces (click on one channel to get scales for the axes, as in Figure 32.13). This corresponds to the M170 again.



<sup>9</sup> For example, for 5Hz, one would need at least  $N/2 \times 1000\text{ms}/5$ , where N is the order of the Morlet wavelets (i.e, number of cycles per Gaussian window), e.g, 600ms for a 6th-order wavelet.

<sup>10</sup> You can of course obtain time-frequency plots for every channel, but it will take longer (and result in a large file).

**Figure 32.13** Total power spectra for faces (left) and scrambled faces (right) for channel MLT34

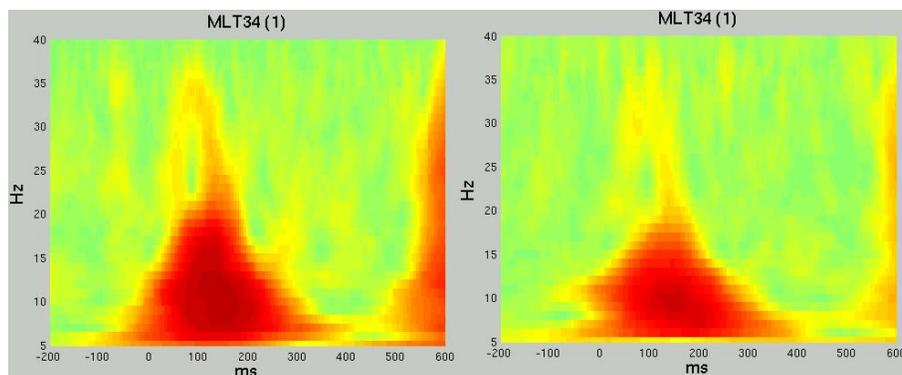
We can also look at evidence of phase-locking of ongoing oscillatory activity by averaging the phase angle information. This time, we do not take the straight (arithmetic) mean, since the data are phase angles, and this average is not particularly meaningful. Instead we calculate their vector mean (when converting the angles to vectors in Argand space), which corresponds to a "Phase-Locking Value" (PLV) which lies between 0 (no phase-locking across trials) to 1 (perfect phase-locking).

- Press the 'Averaging' button and select the `t2_e_meg.mat` file. This time you will be prompted for either a straight or a vector average, for which you should select "vector". After a few moments, the matlab window will echo:

```
e_meg.mat: Number of replications per contrast:  
average 1: 86 trials, average 2: 86 trials
```

and a new file will be created in the MEG directory called `mt2_e_meg.mat`.

If you now display the file `mt2_e_eeg.mat` file, you will see PLV as a function of frequency (y-axis) and time (x-axis) for Channel MLT34. Again, if you use the "trial" slider to switch between trial(types) 1 and 2, you will see greater phase-locking around 10Hz and 100ms for faces than scrambled faces, as in Figure 32.14. Together with the above power analysis, these data suggest that the M170 includes an increase both in power and in phase-locking of ongoing oscillatory activity in the alpha range (Henson et al, 2005b).



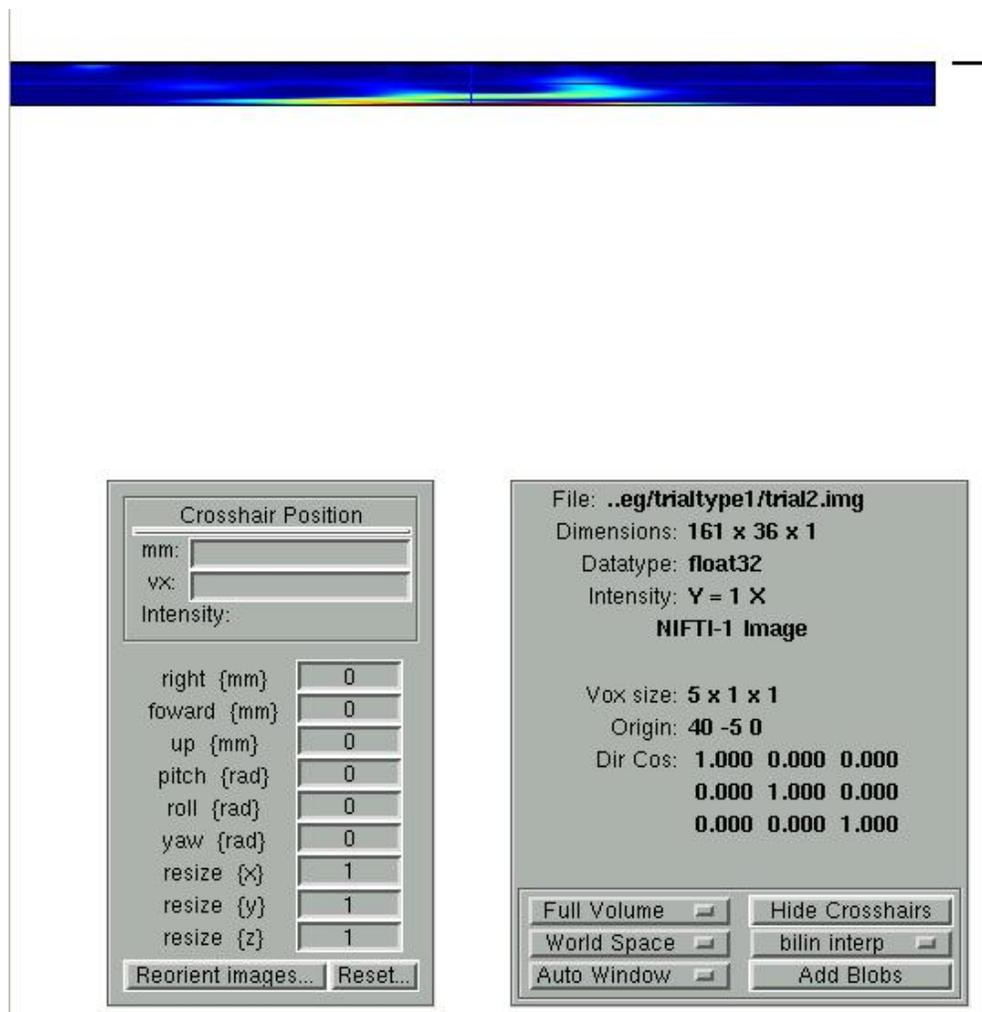
**Figure 32.14** Phase-Locking Values for faces (left) and scrambled faces (right) for channel MLT34

### 32.5.3 2D Time-Frequency SPMs

Analogous to Section 32.4.3, we can also use Random Field Theory to correct for multiple statistical comparisons across the 2-dimensional time-frequency space.

- `spm_eeg_convertmat2ana3Dtf` in the Matlab window, and select the `t1_e_eeg.mat` file.

This will create time-frequency images for each trial of the two types, with dimensions 161x36x1, as for the example shown in Figure 32.15 from pressing "Display: images" on the main SPM window.



**Figure 32.15** 3D image for trial 2 of `t1_e_eeg.mat`. The left section is through time (x) and frequency (y) (the right image is an y-z section, though there is only one value in z, i.e, it is really a 2D image).

As in Section 32.4.3, we then take these images into an unpaired t-test across trials to compare faces versus scrambled faces. We can then use classical SPM to identify times and frequencies in which a reliable difference occurs, correcting across the multiple comparisons entailed (Kilner et al, 2005).

- First create a new directory, eg. `mkdir TFstatsPow`.
- Then press the "specify 2nd level" button, select "two-sample t-test" (unpaired t-test), and define the images for "group 1" as all those in the subdirectory "trialtype1" (using right mouse, and "select all") and the images for "group 2" as all those in the subdirectory "trialtype2". Finally, specify the new

TFstatsPow directory as the output directory, and press "run". (Note that this will be faster if you saved and could load an SPM job file from Section 32.4.3).

This will produce the design matrix for a two-sample t-test.

- The press "Estimate", and when it has finished, press "Results" and define a new T-contrast as [1 -1]. Keep the default contrast options, but threshold at  $p < .001$  uncorrected for the whole "image". Then press "volume", and the Graphics window should now look like that in Figure 32.16.

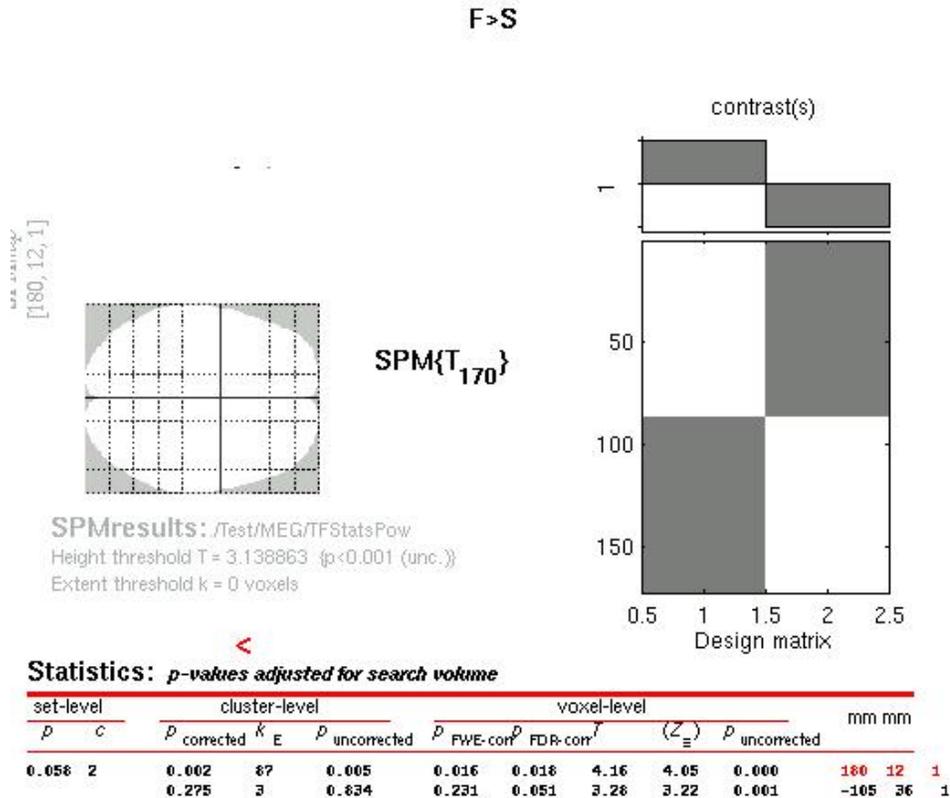


table shows 3 local maxima more than 8.0mm apart

Height threshold: T = 3.14, p = 0.001 (0.319) (p < 0.001 uncorrected) (degrees of freedom = [1.0, 170.0])  
Extent threshold: k = 0 voxels, p = 1.000 (0.319) FWHM = 51.4 7.6 mm mm ; 10.3 7.6 (voxels);  
Expected voxels per cluster, <k> = 16.564 Volume: 28980; 5796 voxels; 71.6 resels  
Expected number of clusters, <c> = 0.38 Voxel size: 5.0 1.0 mm mm ; (resel = 78.24 voxels)  
Expected false discovery rate, <= 0.06

**Figure 32.16** 2D time-frequency SPM{T} at  $p < .001$  uncorrected for the power difference between face and scrambled faces at Channel MLT34. Note that the brain outline in the MIP should be ignored. The x coordinates refer to time in ms; the y coordinates refer to frequency in Hz (the z-coordinate is always 1).

This will reveal "regions" within the 2D time-frequency space in which faces produce greater power than scrambled faces, having corrected for multiple T-tests across pixels. There are two such regions, but only the first survives correction for multiple comparisons, with a maximum of [180 12 1], ie 12 Hz and 180ms post-stimulus.

If you repeat the above time-frequency analysis on the `e_meg.mat` file, but this time keep every channel and answer 'yes' to the "average over channels?" question, and then repeat the above statistical analysis of power, you will notice that there is also a reliable decrease in induced high-frequency power (around 400ms and 35 Hz) for faces vs scrambled faces, which could also be source-localised.

### 32.5.4 "Imaging" reconstruction of evoked amplitude

Here we will demonstrate a distributed source reconstruction of the M170 differential ERF between faces and scrambled faces, using a grey-matter mesh extracted from the subject's MRI, and an L2-norm method in which multiple constraints on the solution can be imposed (Phillips et al, 2002; Mattout et al, 2005; Henson et al, submitted).

- Press the '3D source reconstruction' button, select the `mfmae_meg.mat` file, and enter a comment for the new analysis (eg, "M170").
- Press the 'Meshes' button, and press "yes" to the question "Use previous mesh?", since to avoid re-segmenting and creating meshes for the structural (as we did in Section 32.4.4), which takes some time, we can simply select the appropriate files. Thus, you will be prompted to select the files one by one:

```
sMRI/smri.img  
sMRI/smri_vbm_sn_1.mat  
sMRI/smri_vbm_inv_sn_1.mat  
sMRI/smri_CortexMesh_3004.mat  
sMRI/smri_CortexGeoDist_3004.mat  
sMRI/smri_iskull_Mesh_2002.mat  
sMRI/smri_scalp_Mesh_2002.mat
```

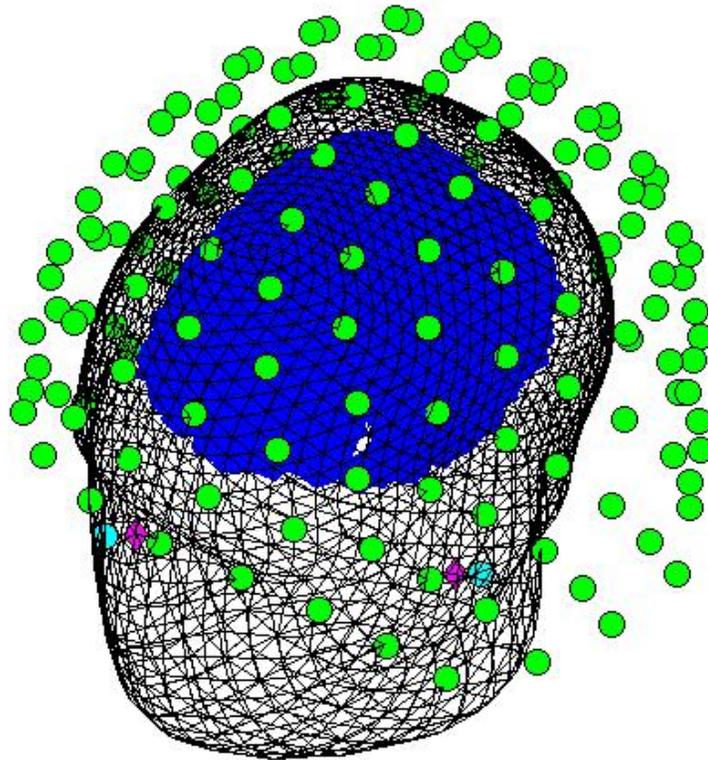
See Section 32.4.4 for more details on these files.

- Press the 'Coregister' button, select "& surface", respond "no" to the 'Read Polhemus?' question, and then select the following files in response to each prompt:

```
MEG/Polhemus/meg_sens_loc.mat  
MEG/Polhemus/meg_fids.mat  
sMRI/smri_fids.mat  
MEG/Polhemus/meg_sens_or.mat  
MEG/Polhemus/meg_hsf.mat
```

(like in Section 32.4.3, except now we also need to provide information about the orientation of each MEG sensor, as in the penultimate file here).

This stage coregisters the MEG sensor positions and orientations (in "MEG" space) with the structural MRI and solution mesh (in "MRI" space). This is done via an approximate matching of the fiducials in the two spaces, followed by a more accurate surface-matching routine that fits the head-shape function (in "MEG" space) to the scalp that was created in the previous meshing stage via segmentation of the MRI. The match will be shown in a window like that in Figure 32.17. (Note that the match of the MEG and MRI fiducials is poor because the MEG fiducials did not correspond exactly to the nasion and peri-auricular points (see footnote 3); this does not matter because the coregistration is dominated by the close fit of the digitized headshape to the scalp mesh).



**Figure 32.17** Graphical output of registration of MEG and sMRI data, showing cortex (blue) and scalp (black) meshes, sensor locations (green), and MRI and Polhemus fiducials (cyan/magenta).

The resulting new files are also created:

```
MEG/meg_fids_coreg.mat  
MEG/meg_sens_loc_coreg.mat  
MEG/meg_sens_or_coreg.mat
```

MEG/RegMat.mat

- Press the 'Forward Model' button. This assumes the sensors lie on a single best-fitting sphere, which allows analytical computation of the forward model (lead field) that maps each "dipole" in the cortical mesh to each sensor, assuming that the orientation of the dipole at each vertex is normal to the surface of the mesh at that point. This stage uses BrainStorm functions, (<http://neuroimage.usc.edu/ResearchMEGEEGBrainStorm.html>). The Matlab window will output:

```
Scalp best fitting sphere computed (in 9 iterations)

-----
Head modeling begins
Channel count for current computation:
151 MEG Channels

Computing the Image Gain Matrices (this may take a while). . .
Computing Gain Matrix for the CD Model
Computing Cortical Gain Vectors. . . Block # 1 of 1
Computing Gain Matrix for the CD Model -> DONE
Saved in:
smri_BSTGainMatrix.bin
Writing Cortical Image Support HeadModel file:
smri_bstchannelfile.matheadmodelSurfGrid_CD.mat
-> DONE
```

This stage outputs the following files in the MEG directory:

```
smri_bstchannelfile.matheadmodelSurfGrid_CD.mat
smri_BSTGainMatrix.bin
smri_BSTGainMatrix_xyz.bin
smri_BSTChannelFile.mat
smri_SPMgainmatrix_1.mat
smri_SPMgainmatrix_pca_1.mat
smri_tesselation.mat
```

- Press 'Invert.', select 'evoked', enter [1 0] for the contrast<sup>11</sup>, [150 180] for the timewindow...

...at this point, a number of possible covariance constraints can be placed at both the sensor level and the source level (the latter being equivalent to priors in a two-level Parametric Empirical Bayesian context; Phillips et al, 2002; Mattout et al, 2005b; Henson et al, submitted). Here we will stick with emulating a classic "weighted minimum norm" solution to the inverse problem, which corresponds to selecting 'iid (1st-level)' for the sensor-level components (corresponding to the assumption that the noise is independent and identically distributed (IID) across sensors), and 'minimum norm' for the source-level components (equivalent to an IID assumption about the sources). Then press 'no' for the question about user-specified covariance constraints<sup>12</sup>. The Matlab window will then echo:

```
ReML Iteration      : 1      ...1.191429e+04
ReML Iteration      : 2      ...1.166241e+04
```

<sup>11</sup> The [1 0] contrast on the `mfae_meg.mat` file is equivalent to a [1 -1] contrast on the `fmae_meg.mat` file.

<sup>12</sup> These user-specified constraints could come from, for example, fMRI data on the same subject (Section 32.6), though procedures will need to be developed that map SPM{F} images to the mesh (this will be a future development).

```

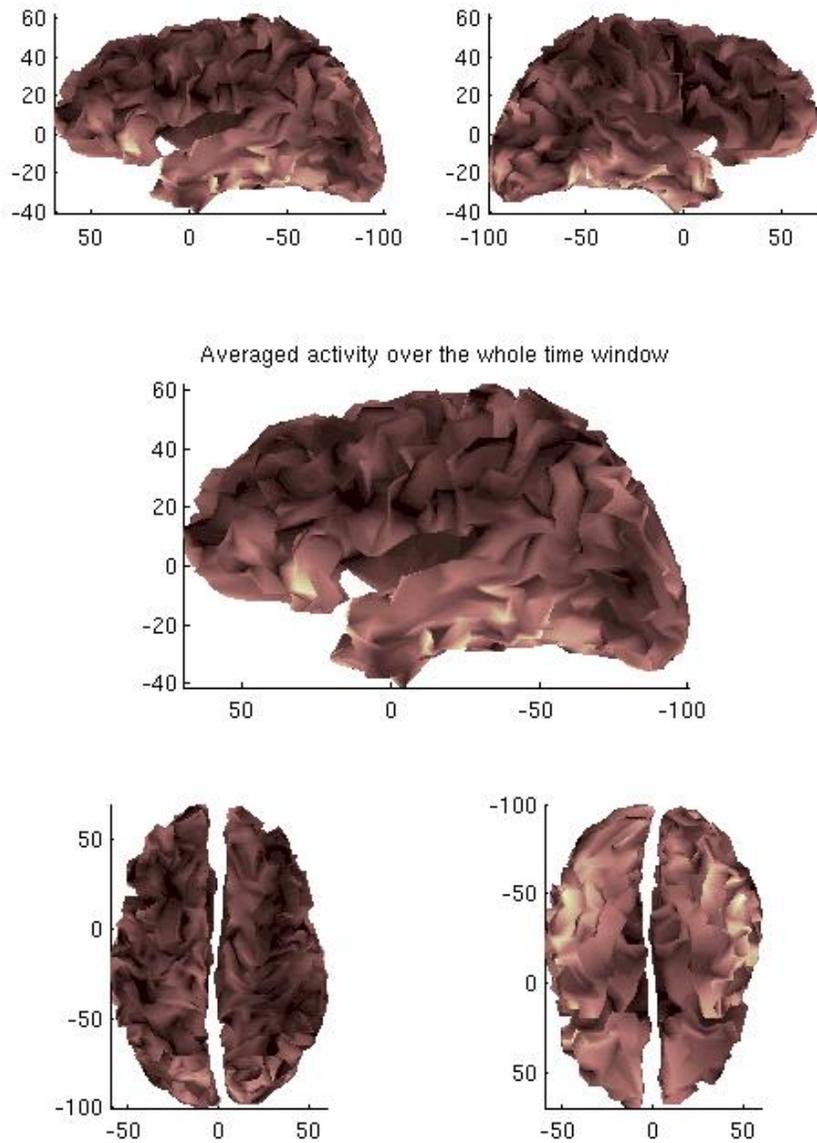
ReML Iteration      : 3      ...1.108131e+04
ReML Iteration      : 4      ...9.871567e+03
ReML Iteration      : 5      ...7.518794e+03
ReML Iteration      : 6      ...3.856499e+03
ReML Iteration      : 7      ...7.933406e+02
ReML Iteration      : 8      ...2.875161e+01
ReML Iteration      : 9      ...5.391859e-01
ReML Iteration      : 10     ...3.823624e-02

Model Log-Evidence: 100496.6694
Noise covariance hyperparameters: 1.0561e-05
Source covariance hyperparameters: 0.00027619

```

Here, ReML has been used to estimate the hyperparameters (analogous to the degree of regularisation) for the sensor-level and source-level component. The hyperparameters are estimated using the whole epoch. The absolute value of the source estimates (parameters) at each mesh vertex, averaged across the 150-180ms timewindow of interest, will appear in the Graphics window, as in Figure 32.18. The source estimates are also stored (as the variable J) in the file:

```
mfmae_meg_remlmat_150_180ms_evoked.mat
```



**Figure 32.18** Graphical output of a weighted minimum norm estimation of the differential ERF between faces and scrambled faces between 150-180ms.

- Select 'visualisation' from the 'other' pull-down option, and a new window will be produced that shows the absolute value of the estimated current at each vertex within the cortical mesh. This figure can be rotated with the cursor to see all parts of the cortex (using the Rotate3D matlab option)...

Note the activity in bilateral ventral occipital/temporal cortex and inferior prefrontal cortex. These agree reasonably well with the fMRI data on this subject (Section 32.6), and from the fMRI data from a group of 18 subjects (Henson et al, 2003).

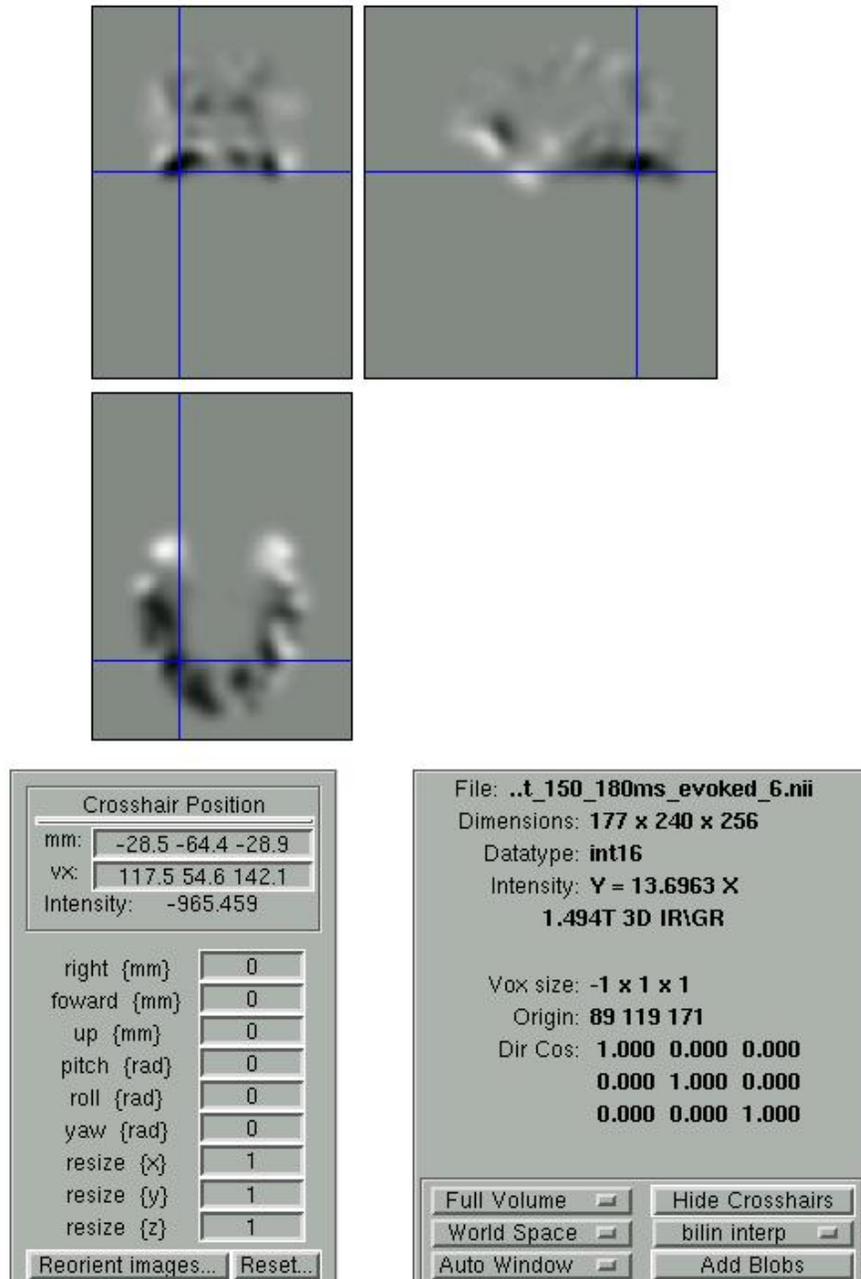
You can also convert this solution to an image, by typing in the Matlab window:

```
spm_eeg_inv_Mesh2Voxels
```

and selecting the `mfae_meg.mat` file. This will create two new images:

```
mfae_meg_relmag_150_180ms_evoked_1.nii  
smfae_meg_relmag_150_180ms_evoked_1.nii
```

(the second simply being a smoothed version of the first, using a 12mm FWHM isotropic Gaussian). You can then view one of these images with the normal SPM "Display:image" option (as in Figure 32.19), and locate the coordinates of "hotspots" (these coordinates will of course be in the native space of the MRI, but can be converted to MNI coordinates using the spatial normalisation parameters). Note that these images contain the signed rather than absolute source estimates, where the sign depends on the orientation of the current (which depends on the normal to the mesh surface estimated at each vertex).



**Figure 32.19** Display of the smoothed 3D image of the weighted minimum norm estimation of the differential evoked response between faces and scrambled faces between 150-180ms.

You can play with other combinations of constraints. Each combination corresponds to a different model, and these models can be compared using the 'Model Log-Evidence' that is output in the Matlab window. (Alternatively, you can include all possible constraints, and use their hyperparameters to infer the best model, Henson et al, submitted).

You can also try to localise evoked and/or induced power, rather than evoked amplitude (see Friston et al, 2006). This will be a future extension to this chapter.

## 32.6 fMRI analysis

Only the main characteristics of the fMRI analysis are described below; for a more detailed demonstration of fMRI analysis, see Chapter 29.

Note that all the job files for each stage of preprocessing and analysis are also provided:

```
fMRI/realign_job.mat  
fMRI/slicetime_job.mat  
fMRI/smooth_job.mat  
fMRI/stats_job.mat
```

These can be loaded and run, though of course the location of the files and the output directory will need to be changed.

### 32.6.1 Preprocessing the fMRI data

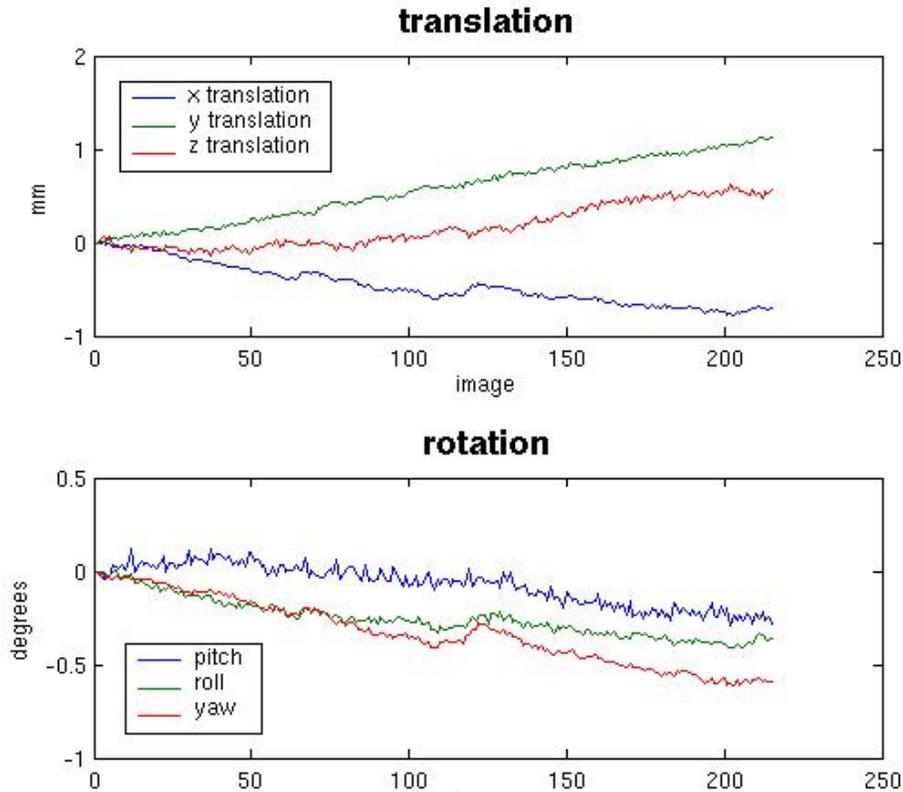
- Toggle the modality from EEG to fMRI, and change directory to the fMRI subdirectory (either in Matlab, or via the "CD" option in the SPM "Utils" menu)
- Select 'Realign' from the 'Realign & Unwarp' menu, click on 'Data', and select 'New Session'. Double-click on the new Session branch, and click on the 'Images' button, click on the 'specify files' and select all 215 `fM*.img` files in the Scan directory (using the right mouse to 'select all', assuming the filter is set to `^f.*img`).

Realignment will produce a `spm*.ps` postscript file in the current directory, which shows the estimated movement (like in Figure 32.14). Importantly, the resliced images will be output as `rfM*.img` files. A mean image will also be written:

```
meanfMS02554-0003-000006.img
```

as will the movement parameters in the text file:

```
rp_fMS02554-0003-000006.txt
```



**Figure 32.20** Movement parameters from Realignment of the fMRI data.

- Press the 'slice-timing' button, select the functional images (filter set to '^rf.\*' to avoid the mean image), enter 2.88 as the TR,  $2.88 \times 31/32$  as the TA, the slice-order as [1:32] (since the first slice in the file is the top slice, and this was the first slice acquired in the descending sequence), and the reference slice to 16. This will write out 215 images `arfM*.img`, in which the data have been interpolated to match the acquisition time of the middle slice (in space and time, given the sequential acquisition).
- Press the 'smooth' button and keep the default 10x10x10mm smoothing. This will produce 215 spatially-smoothed images `sarfM*.img`.

Note that we will not normalise these images, in order to compare them with the MEG and EEG source reconstructions, which are in the native MRI space.

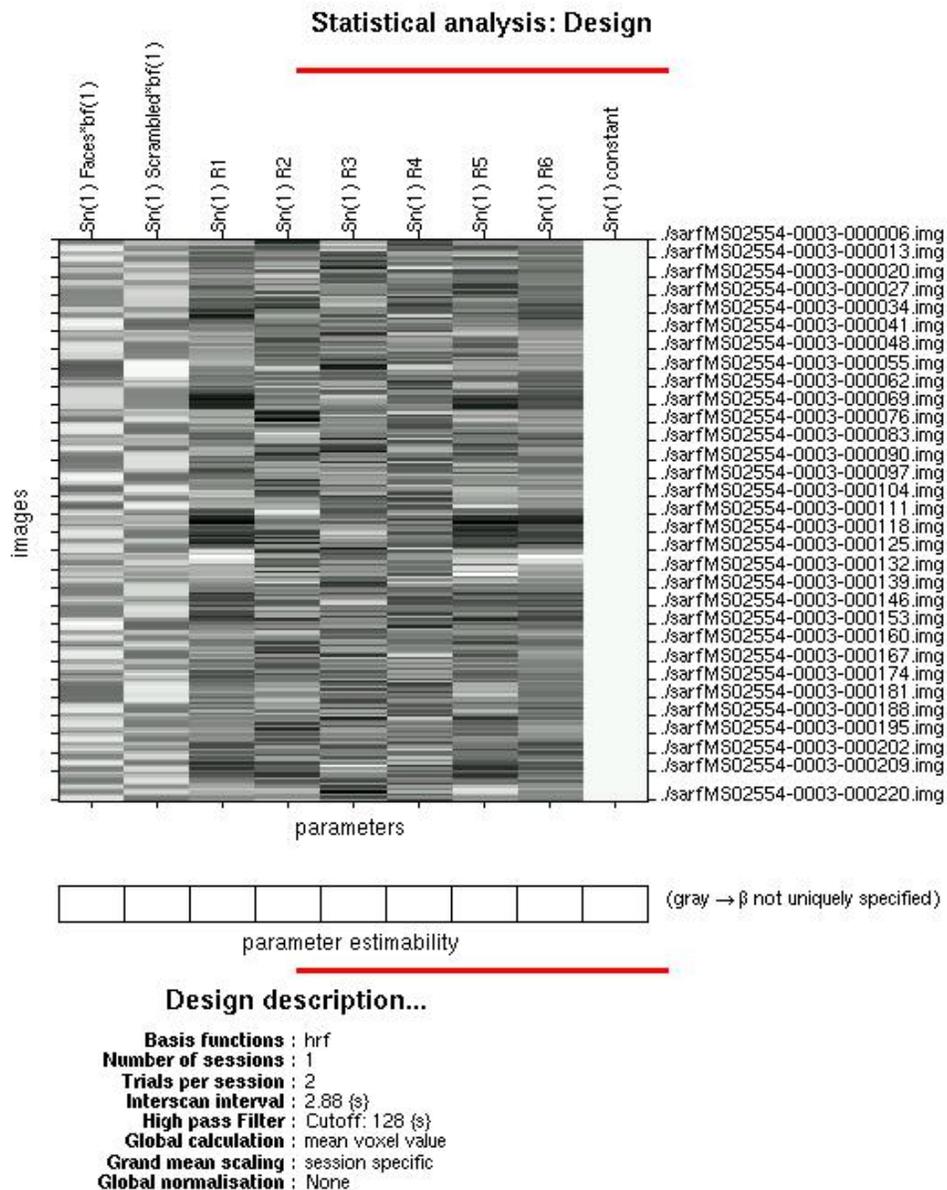
### 32.6.2 Statistical analysis of fMRI data

- Load the `onsets.mat` file provided into the Matlab workspace
- Press the 'specify 1st-level' button, change the microtime onset from 1 to 8, select the 215 '`sarfM*.img`' images, define two new conditions - condition 1 called "faces" with onsets set to `onsets{1}` and condition 2

called "scrambled faces" with onsets set to `onsets{2}` (all duration 0) - select the `rp_fMS02554-0003-000006.txt` file as 'Multiple Regressors' (to covary out some of the residual movement-related effects), and select the `fMRI/Stats` as the output directory (loading and editing the `stats_job.mat` file provided will save a lot of time here!). Keep the rest of the parameters (e.g. use of a canonical HRF basis function) at their default settings.

This will produce a design matrix like that in Figure 32.15, which is stored in the file:

`fMRI/Stats/SPM.mat`

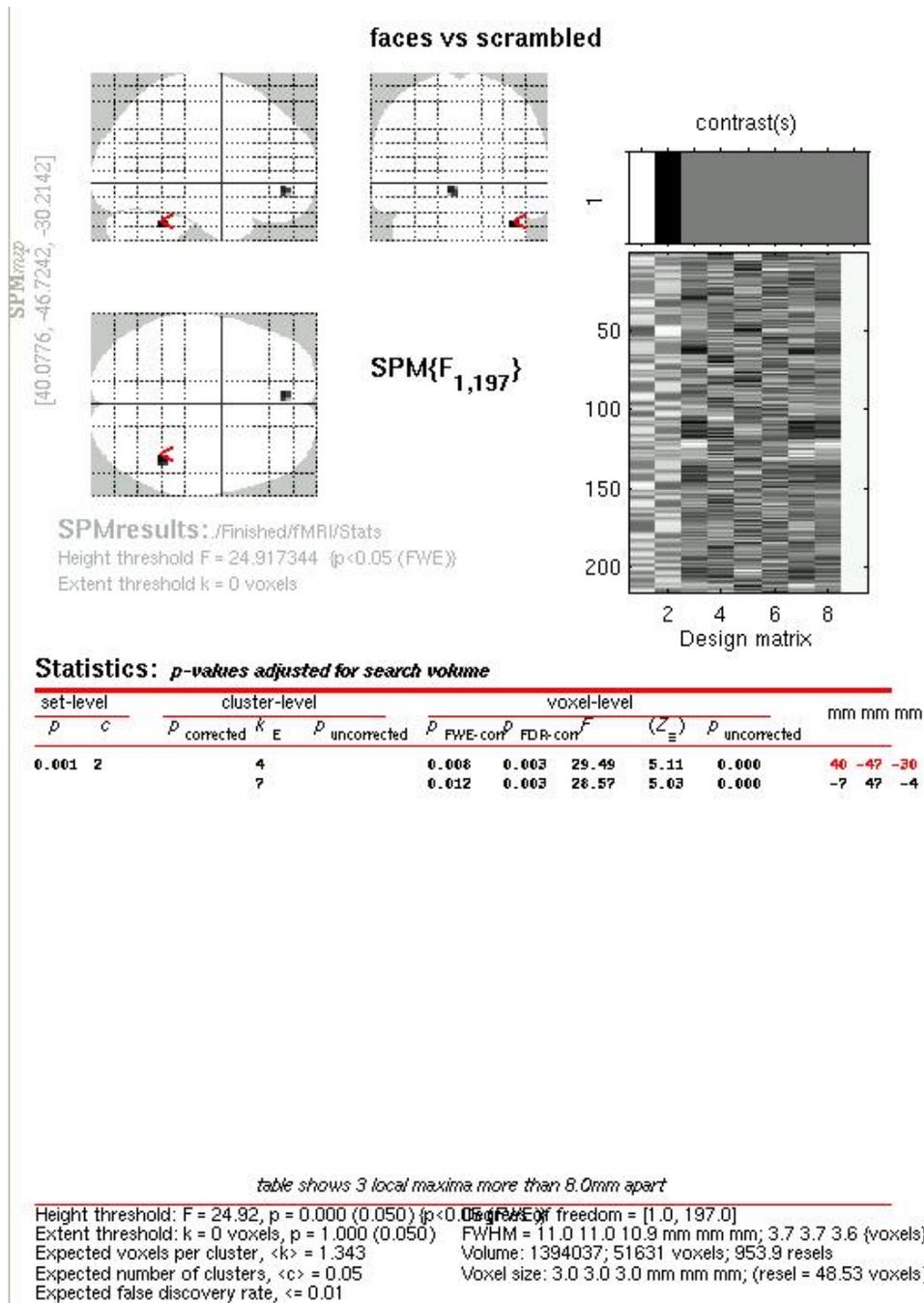


**Figure 32.21** Design matrix for the fMRI analysis.

- Then estimate the parameters of the design matrix by pressing the 'Estimate' button and selecting the SPM.mat file
- Finally, to see the regions that respond differentially between faces and scrambled faces, press 'Results' and define a new F-contrast (called, e.g, 'Faces - Scrambled') by typing the contrast weights [1 -1].

This will identify regions in which the parameter estimate for the canonical HRF differs reliably between faces and scrambled faces. This could include regions that show both a "greater" relative response for faces, and regions that show a "greater" relative response for scrambled faces (such a two-tailed test is used because we do not know the precise relationship between haemodynamic changes measured by fMRI and the synchronous current changes measured by EEG/MEG).

If the resulting  $SPM\{F\}$  is thresholded at  $p < .05$  FWE corrected, the resulting MIP and table of values should be like that in Figure 32.16. Only two regions survive correction: right fusiform and orbitofrontal cortex (note coordinates refer to native MRI space; not MNI space). These can be displayed on the (attenuation-corrected) structural `msmri.nii`. They are a subset of the regions identified by the same contrast in a group of 18 subjects in Henson et al (2003). At a lower threshold (e.g,  $p < .01$  uncorrected), one can see additional activation in left fusiform, as well as other regions.



**Figure 32.22** SPM{F} for faces vs scrambled faces. Note that the coordinates are in the MRI native space (no normalisation performed) so bear a close, but not exact, relationship with MNI coordinates (affecting brain outline in MIP too).

There is some agreement between these fMRI effects and the localised EEG/MEG effects around the 170ms latency - eg in orbitofrontal and right fusiform - though of course the EEG dipoles were bilateral, and there were more extensive posterior occipitotemporal effects in the source-localised MEG data. Note of course that the fMRI data may include differences between faces and scrambled faces that occur at

latencies other than the M170 (e.g, later), or differences in "induced" high-frequency M/EEG power that is not phase-locked to stimulus onset (Henson et al, 2005b).

One could use these "hotspots" to seed ECDs in Section 32.4.4, or use the whole unthresholded F-image as a continuous prior within the PEB L2-norm method in Section 32.5.4. Probably better still, one could take a number of regions after thresholding the SPM{F}, and enter each as a separate prior on the PEB L2-norm method (this way, different regions can be up-weighted or down-weighted as a function of whether they are likely to be active during the critical timewindow being localised).

### **32.7 Possible extensions:**

1. Use fMRI results as priors on distributed source solutions
2. Get localisation of induced power to work
3. Create general function for writing 3D images from mat files, eg where user prompted for dimensions (to replace above calls to "spm\_eeg\_convertmat2ana3D" and "spm\_eeg\_convertmat2ana3Dtf")
4. update spm\_mip to handle 2D/3D images with no brain overlay, and correct scaling

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