

SPM fMRI data analysis: from using public data, to analyse it, make figures, export and share your results

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Start

The SPM software is available on the web (<http://www.fil.ion.ucl.ac.uk/spm/>) and should be already present in the Matlab path. Launch Matlab and type spm in the Matlab command window and select fMRI. If this doesn't work, check that this is present in your Matlab path (Home >> Set Path >> Add Folder >> select the spm12 folder and save).

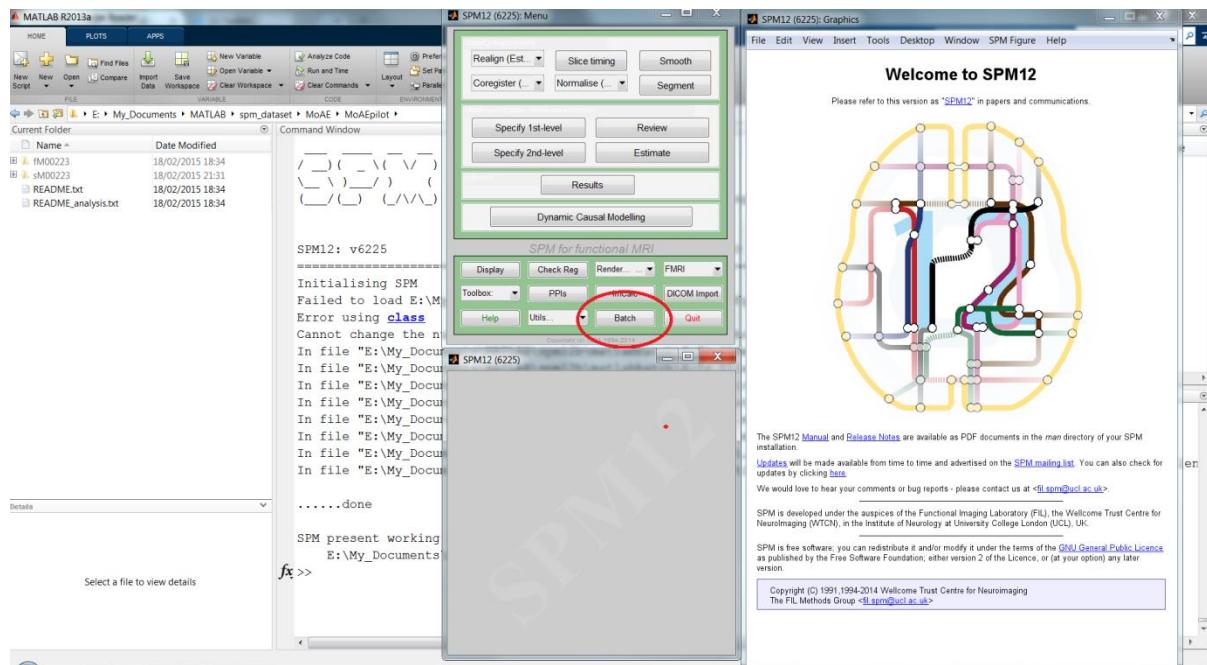


Figure 1. overview of SPM GUI

1st level data processing and analysis

The data

The data that we use to learn pre-processing and the 1st level analysis, are from Wakeman & Henson 2015. A multi-subject, multi-modal human neuroimaging dataset. Scientific Data, 2. <http://www.nature.com/articles/sdata20151>. Only the fMRI data are here – and to make it more manageable only raw data from 2 subjects are available along with some pre-processed data.

The experiment

19 people were watching photographs of faces (cross 400 to 600ms followed by faces 800 to 1000ms), 1700ms ISI. Three types of faces: famous, non-famous, scrambled and 50% are repeated, either immediately or delayed. The task was to judge the symmetry of each face.

Data were collected in Cambridge on a 3T Siemens Tim Trio with one high resolution (1mm³) T1 image (MPRAGE), 9 functional run (210 EPI volumes per run, TR 2000, 3.3*3.75*4.05mm, interleaved acquisition, starting at the bottom of the brain), and corresponding Field Map EPI sequences.

The Brain Imaging Data Structure

BIDS (<http://bids.neuroimaging.io/>) is a simple standard which allows to organize and describe neuroimaging experiment and data (<http://www.nature.com/articles/sdata201644>). Wakeman & Henson (2015) are presented using that format, and **we will explore this a little, since this is how you should also store your data and prepare them for sharing**. On the drive the data are stored with each 'subject' at the folder root, along with meta-data.

README.txt

Multi-subject, multi-modal (fMRI+MEG+EEG) neuroimaging dataset on face recognition in BIDS format

===== These data are provided freely for research purposes only (as part of their Award of the BioMag2010 Data Competition).

See README.txt in parent directory for full information about the data.

The T1, BOLD and T2* fieldmaps are in BIDS format in each of 16 subject directories. In future, hope to add FLASH, DTI and MEG+EEG data in (developing) BIDS format.

The "Scripts" directory contains an Automatic Analysis pipeline (<https://github.com/rhodricusack/automaticanalysis/wiki>) that analyses fMRI data from start to finish. Note that this analysis includes slightly different preprocessing to that in SPM12 scripts directory in parent directory (and in SPM manual chapter): the AA pipeline includes unwarping from fieldmaps, slice-time correction and only a canonical HRF.

Any questions, please contact rik.henson@mrc-cbu.cam.ac.uk.

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dataset_description.json

```
{  
    "Name": "A multi-subject, multi-modal human neuroimaging dataset: fMRI, EEG and MEG data  
on face processing",  
    "BIDSVersion": "1.0.0rc1",  
    "License": " Creative Commons Attribution 4.0 International License",  
    "Authors": "DanielGWakeman, TiborAuer, RichardNHenson",  
    "Acknowledgements": "UK Medical Research Council and Elekta Ltd",  
    "HowToAcknowledge": " Daniel Wakeman and Richard Henson. Wakeman, D. G. & Henson, R. N. A  
multi-subject, multi-modal human neuroimaging dataset. Sci. Data 2:150001 doi:  
10.1038/sdata.2015.1 (2015).",  
    "Funding": "UK Medical Research Council (MC_A060_5PR10) and Elekta Ltd",  
    "ReferencesAndLinks": " Wakeman, D. G. & Henson, R. N. A multi-subject, multi-modal human  
neuroimaging dataset. Sci. Data 2:150001 doi: 10.1038/sdata.2015.1 (2015)",  
    "DatasetDOI": " OpenfMRI ds000117 (2014). ftp://ftp.mrc-  
cbu.cam.ac.uk/personal/rik.henson/wakemandg_hensonrn/"  
}
```

```
participant.tsv
```

```
participant_id age sex group
1 31 1 control
2 25 1 control
3 30 1 control
4 26 2 control
5 23 2 control
6 26 1 control
7 31 2 control
8 26 1 control
9 29 1 control
10 23 1 control
11 24 2 control
12 24 2 control
13 25 2 control
14 24 2 control
15 30 1 control
16 25 1 control
```

Inside each subject, we have folders for anatomical, functional and field map data. Each time, we have the data in nifti (.nii.gz) format along with meta-data. That structure is simple to follow and accommodate most modalities (check the website for details on how to organize DTI, MEEG, PET, etc). The metadata allow users to obtain very quickly all the information needed to analyses the data.

Browse from within Matlab to the data directory ('fMRI') and in command window, type:

```
meta = spm_BIDS
```

```
meta =
```

```
struct with fields:
```

```
    dir: 'F:\fmri'
    descr: [1x1 struct]
    sessions: {}
    subjects: [1x16 struct]
    tasks: {}
    scans: [0x0 struct]
    sess: [0x0 struct]
    participants: []
```

Note that BIDS follow the following naming convention: a subject come to the scanner for a 'session'. A longitudinal study would therefore have multiple sessions. Within a session, subject can have multiple 'runs'.

Typically, but not always, sessions are modelled separately but the pre-processing follow dedicated longitudinal pipelines (see <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3117465/>). Similarly, if you have different tasks, they are modelled separately. By contrast, all runs from a given task are modelled together. In the SPM interface, runs are called sessions.

```

meta.subjects(3).func(1)

    struct with fields:

        filename: 'sub-Sub03_task-facerecognition_run-01_bold.nii.gz'
        task: 'facerecognition'
        acq: ''
        rec: ''
        run: 'run-01'
        meta: [1x1 struct]
        events: [1x1 struct]
        physio: []

```

```
meta.subjects(3).func(1).meta
```

```

    struct with fields:

        RepetitionTime: 2
        EchoTime: 0.0300
        FlipAngle: 78
        SliceTiming: [33x1 double]
        EffectiveEchoSpacing: 5.1000e-04
        PhaseEncodingDirection: 'j-'
        TaskName: 'facerecognition'

```

Preparing data

Because fMRI data analyses are hierarchical, we process 1st within subject and then between subjects. *It is thus essential to replicate exactly the pre-processing and statistics for each subject.* Fortunately, SPM has a pipeline engine (**SPM batch**) which allows specifying what to do.

Because SPM is open, and we have the ‘meta’ structure with all the needed information, we can fill up the batch simply using that variable.

After opening the batch (figure 1), click **Basic IO** → **File/Dir operation** → **File Operations** → **Gunzip Files**. Under **‘File Set’**, input the data of subject anatomical data. **Basic IO** → **File/Dir operation** → **Dir Operations** → **Make directory**. Inside subject 3/func (parent directory), create a ‘run1’ folder. **Basic IO** → **File/Dir operation** → **File Operations** → **Gunzip Files**. Under **‘File Set’**, input the data of subject functional data run 1. Use ‘dependency’ for the output directory (figure 2). Repeat the operation for run2.

SPM works fine with 4D nifti files, but not zipped ones.

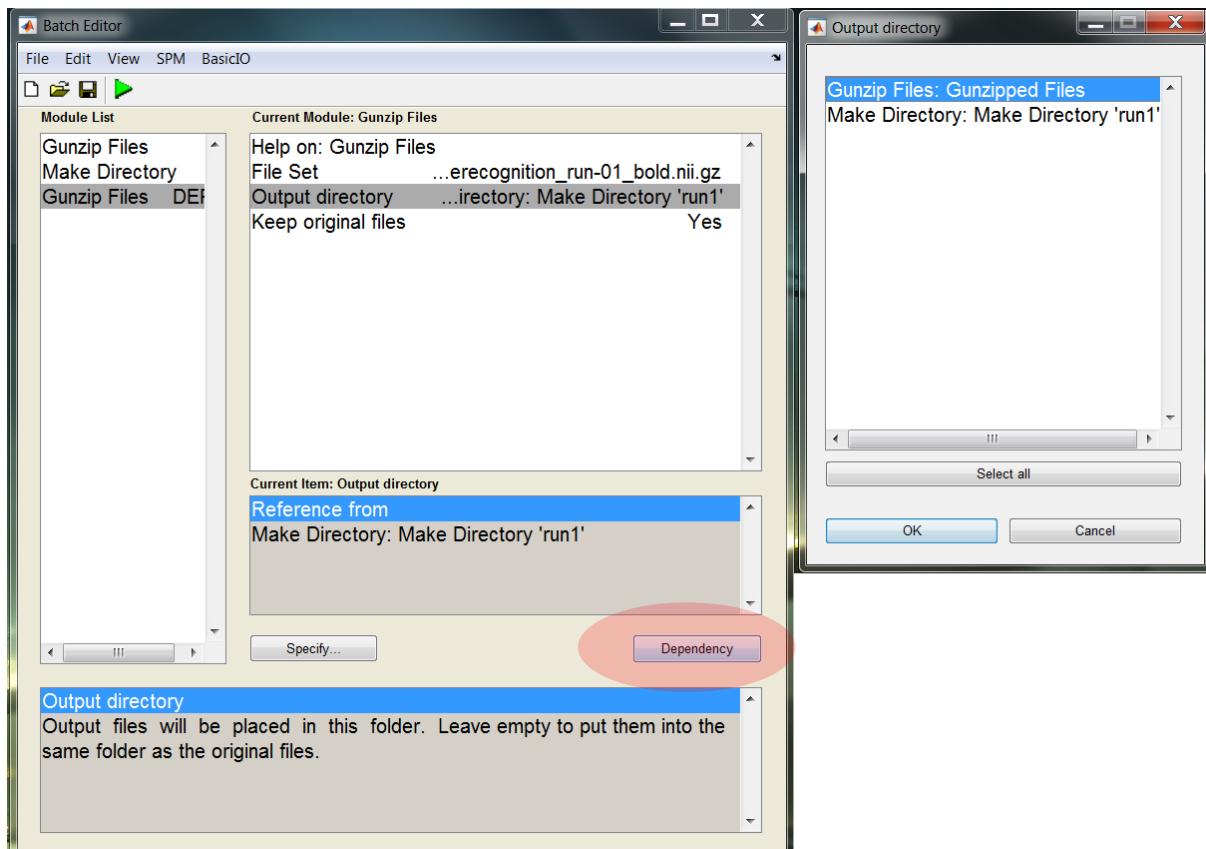


Figure 2. Unzip anatomical and functional data.

Build the pipeline for subject 3

The ‘standard’ preprocessing pipeline is

- 1 – slice timing correction of EPI data
- 2 – realignment of EPI data (write mean only)
- 3 – coregister T1 to mean EPI
- 4 – segment the coregistered T1
- 5 – normalize EPI data (and possibly T1)
- 6 – smooth
- 7 – stats modelling and estimation

SPM >> Temporal >> Slice Timing.

Click on ‘Data’ and select ‘New Session’ twice, since we have 2 runs. Highlight a ‘session’ and change the range of files to 1:999 (see figure 3) and select images – repeat for the next run.

Now highlight ‘Number of Slices’, click ‘Specify’ and input `length(meta.subjects(3).func(1).meta.SliceTiming)` i.e. 33. Next, highlight ‘TR’ and input `meta.subjects(3).func(1).meta.RepetitionTime` i.e. 2. Next, highlight ‘TA’, and input the proposed formula `2-(2/33)` i.e. 1.93. Next, highlight ‘Slice Order’ and input `meta.subjects(3).func(1).meta.SliceTiming`, which is here the actual time of acquisition of each slice. Finally, highlight ‘Reference Slice’ and chose the middle of the temporal sequence, i.e. either slice 2 or 33 (check in Slice Order, which one is closest to 1sec).

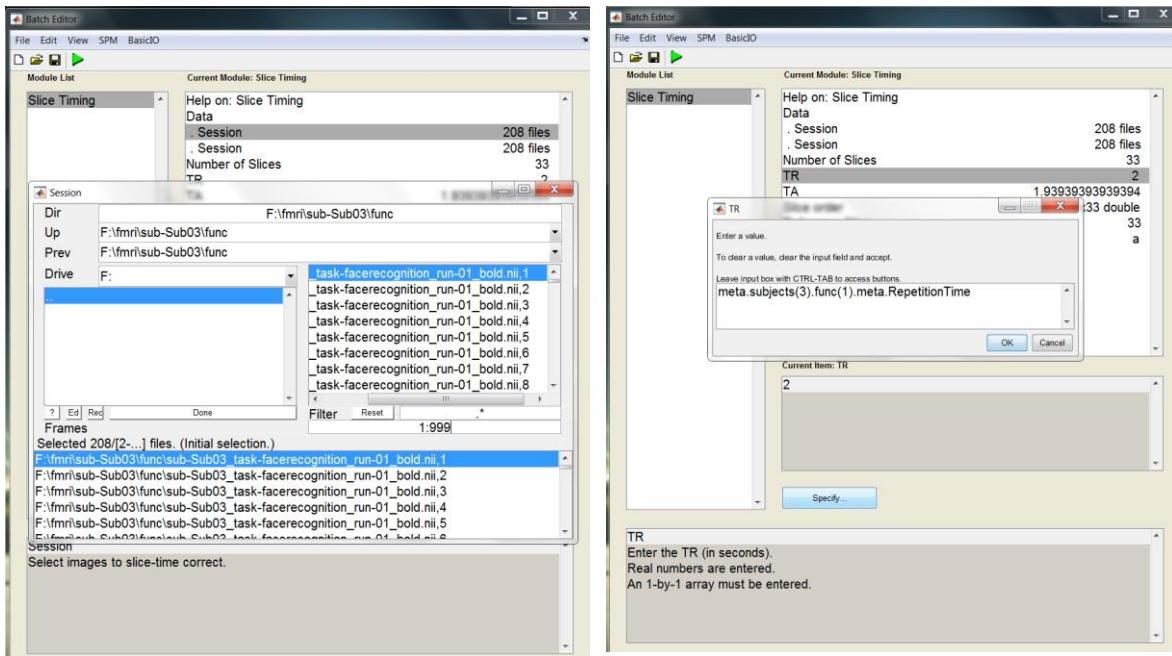


Figure 3. Slice Timing

SPM >> Spatial >> Realign >> Realign: Estimate & Reslice

Click on “Data” and select “New Session” (twice), then highlight the newly created “Session” option and Press “Select Files” and use the Dependency to choose the slice timed functional images (repeat for the second run). Finally, in the Reslice Options panel, select “Resliced images” and select “Mean Image Only”.

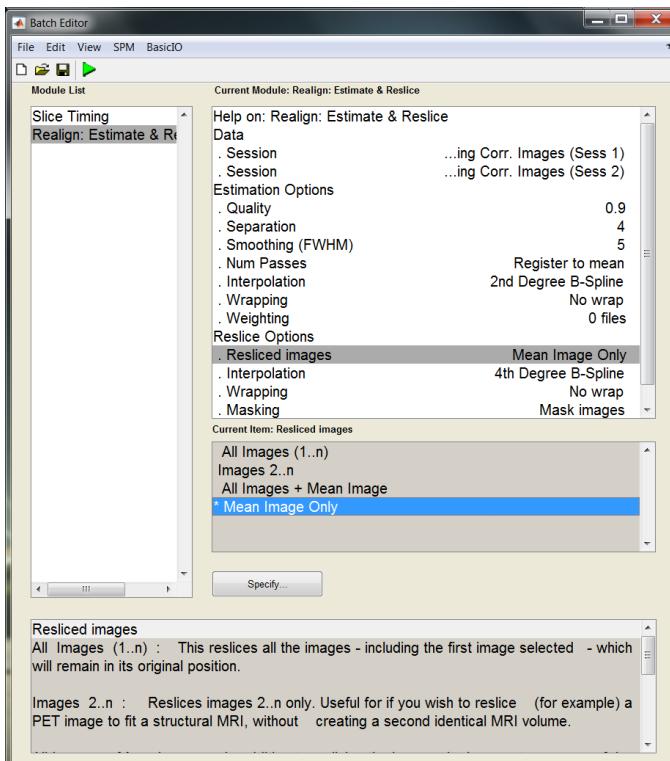


Figure 4. Realignment.

Since images are made of a header and of the image (values) themselves, SPM will compute how to move (translate/rotate) each image and store the transformation to apply in the header. SPM will also create a mean image which will be used in the next step of spatial processing - coregistration. The computed motion corrections are also saved to a `rp_XXXXXX.txt` file which will be used later as regressors for the statistics. This allows movements artefacts to be discounted when looking for brain activations.

SPM >> Spatial >> Coregister >> Coregister: Estimate

The next step, is to Normalize the EPI data. This is achieved by 1 – coregistering the structural image (T1) to the mean EPI data, then 2 – segmenting the coregistered T1 and derive the normalization parameters, and 3 – apply the normalization parameters to the EPI data.

- Highlight “Reference Image” – that is the image that remains the same, i.e. the mean EPI image. Click “dependency” in the batch interface and select the ‘Mean Image’ from the realign module.
- Highlight “Source Image” and then select the structural image.

At this stage, it is good to check that the mean EPI and T1 are well coregistered – this can again be achieved with the batch **SPM >> Util >> Check Registration**. Again use the dependency button to select the mean EPI and coregistered T1 image. Finally, we want to print that figure – **SPM >> Util >> Print**. Change the filename and format to pdf.

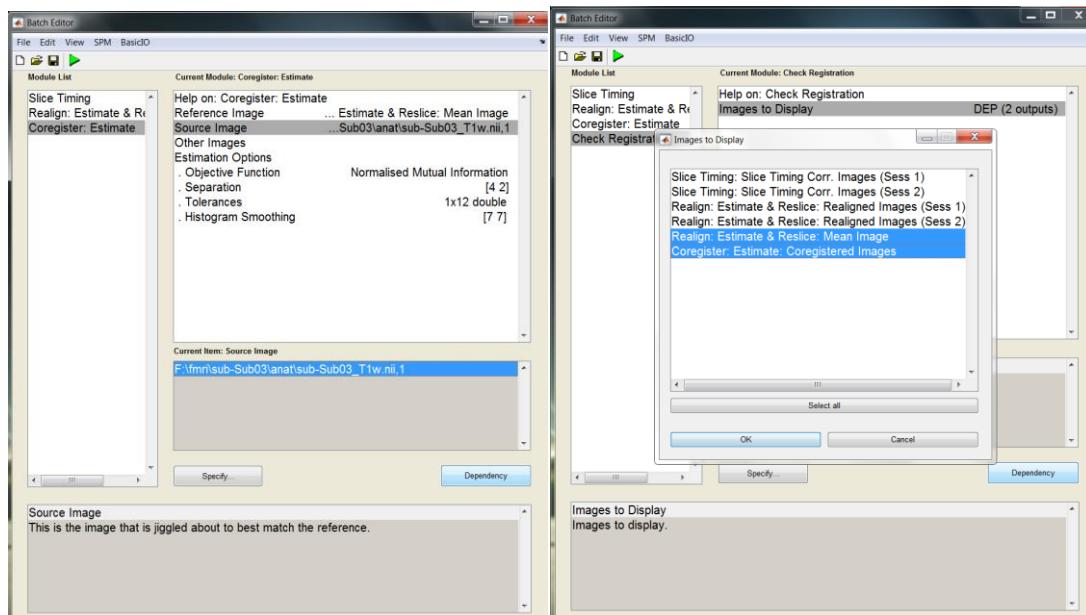


Figure 5. Coregistration + quick quality check.

SPM >> Spatial >> Segment

In Data >> Channel: (1) Highlight “Volumes” and select the subject's registered (anatomical) image using the dependency button (Figure 6, left) . (2) Highlight “Save Bias Corrected” and select “Save Bias Corrected”.

In Warping and MRF (at the bottom), Highlight “Deformation Fields” and select “Forward” (Figure 6 - right)

As above, you can check the result using **SPM >> Util >> Check Registration** and select the segment c1 (gray) and c2 (white) and print a figure. **SPM >> Util >> Print**. Change the filename and format to pdf.

SPM >> Spatial >> Normalise >> Write

We can simply use the deformation field obtained from the coregistered T1 and apply it to the EPI data. Highlight Data – and create a new subject (three times). In the subject, use the dependency button to select the forward deformation field. Similarly, use the dependency button to select the bias corrected anatomical or the EPI images (each run separately – Figure 7, left).

SPM >> Spatial >> Smooth

Images to Smooth: Use the dependency button to select the EPI normalized images (Figure 7, right) and change the kernel size (FWHM) to [6 6 6]. Do it separately for each run.

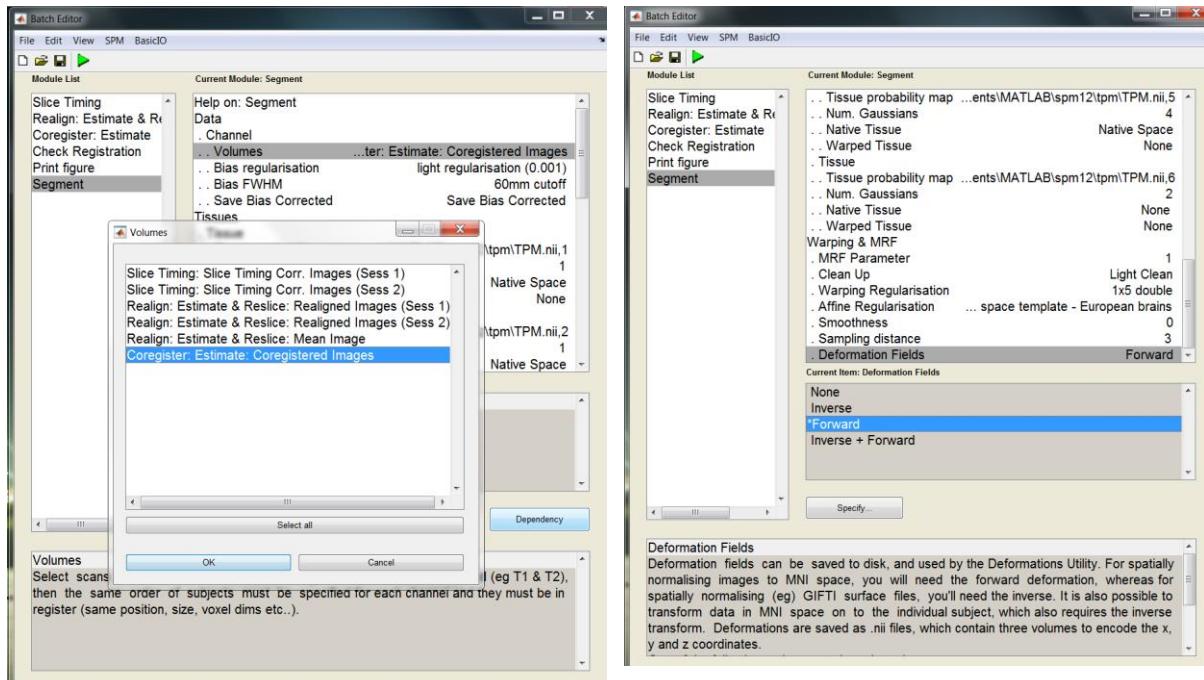


Figure 6. Segmentation

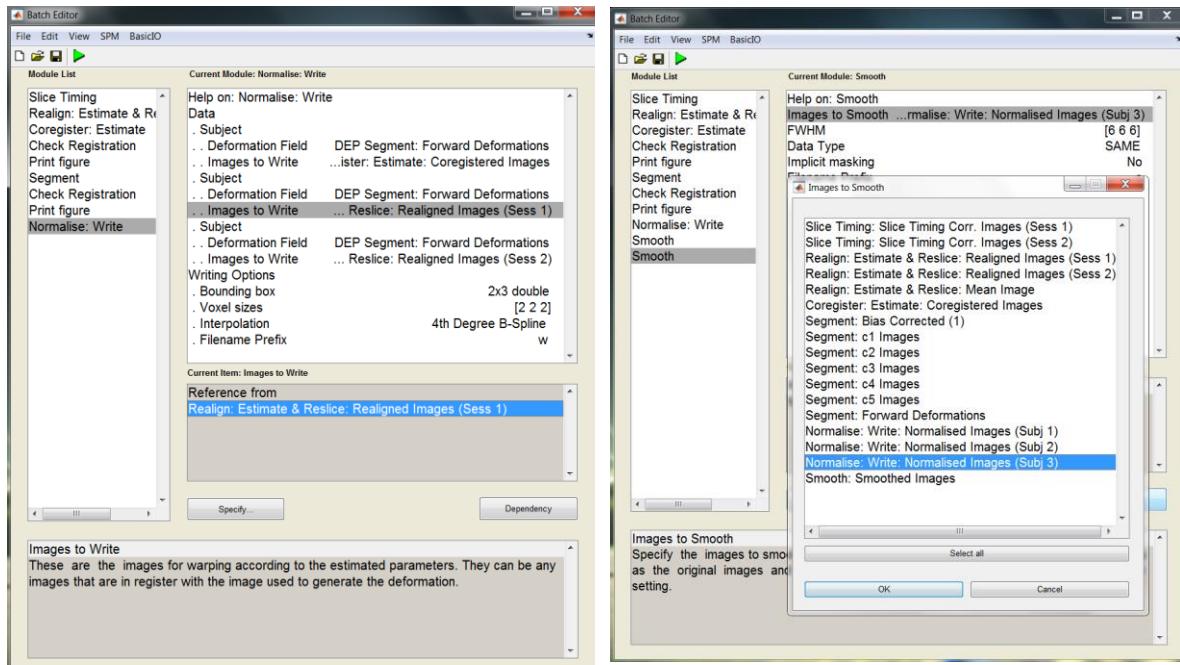


Figure 7. Normalise and Smooth

This marks the end of data pre-processing. The next step is statistical modelling.

Basic IO → File/Dir operation → Dir Operations → Make directory. Inside subject 3 (parent directory), create a ‘stats’ folder.

SPM >> Stats >> fMRI model specification

Under ‘Directory’, use the dependency and choose the stats folder. Units for design is second, and interscan interval is `meta.subjects(3).func(1).meta.RepetitionTime`, i.e. 2. Microtime resolution is the resolution used to create the regressor convoluted by the hrf, which is then downsampled to the TR. A typical choice, is the number of volumes, `length(meta.subjects(3).func(1).meta.SliceTiming)` i.e. 33. Finally, how much in time should we start the regressor with regards to acquisition? Since the slice timing reference slice is the middle in time, everything temporally moved by half of the TR, that is the middle in time, i.e. set microtime onset to 16 or using the meta BIDS info, this is equal to `(floor(length(meta.subjects(3).func(1).meta.SliceTiming)/2))`.

Under ‘Data & Design’, click twice on ‘Subject/Session’ to model the 2 runs. ‘Scans’ can be selected using dependency (i.e. smooth images). Similarly, ‘multiple regressors’ are for regressors that will not be convoluted by the hrf ; and therefore ideal to input motion parameters (again using the dependency select ‘Realignment Param file’). At this stage, the batch should look like figure 8 (right).

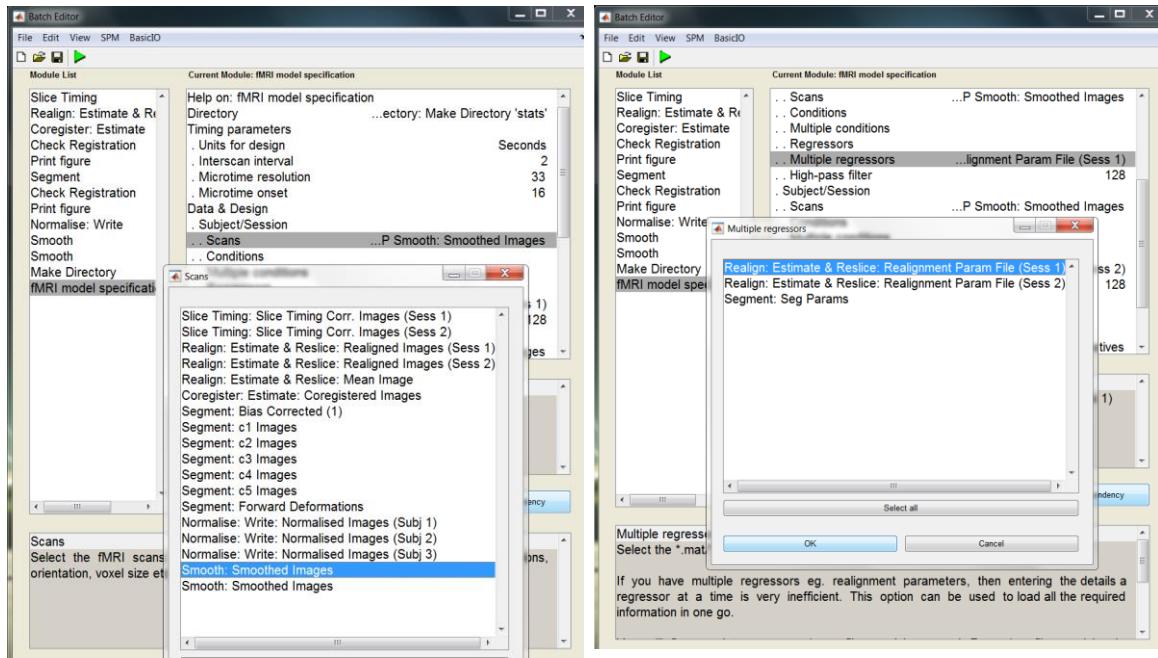


Figure 8. Setting up the statistical model

The last thing is to model each condition. We can find the details in `meta.subjects(3).func(n).events`. By querying events we can create a logical vector and get onsets and durations.

In the command window type:

```
FAMOUS = meta.subjects(3).func(1).events.trial_type(:,1) == 'F';
UNFAM = meta.subjects(3).func(1).events.trial_type(:,1) == 'U';
SCRAMBLED = meta.subjects(3).func(1).events.trial_type(:,1) == 'S';
```

Back to the batch, for the 1st run, i.e. under 'Subject/Session', create 3 conditions (click on 'New: Condition'). The first one, Name is Famous, Onset is `meta.subjects(3).func(1).events.onset(FAMOUS)`, duration is `meta.subjects(3).func(1).events.duration(FAMOUS)`. Repeat for unfamiliar and scrambled (figure 9). For the 2nd run, repeat the operation starting with

```
FAMOUS = meta.subjects(3).func(2).events.trial_type(:,1) == 'F';
UNFAM = meta.subjects(3).func(2).events.trial_type(:,1) == 'U';
SCRAMBLED = meta.subjects(3).func(2).events.trial_type(:,1) == 'S';
```

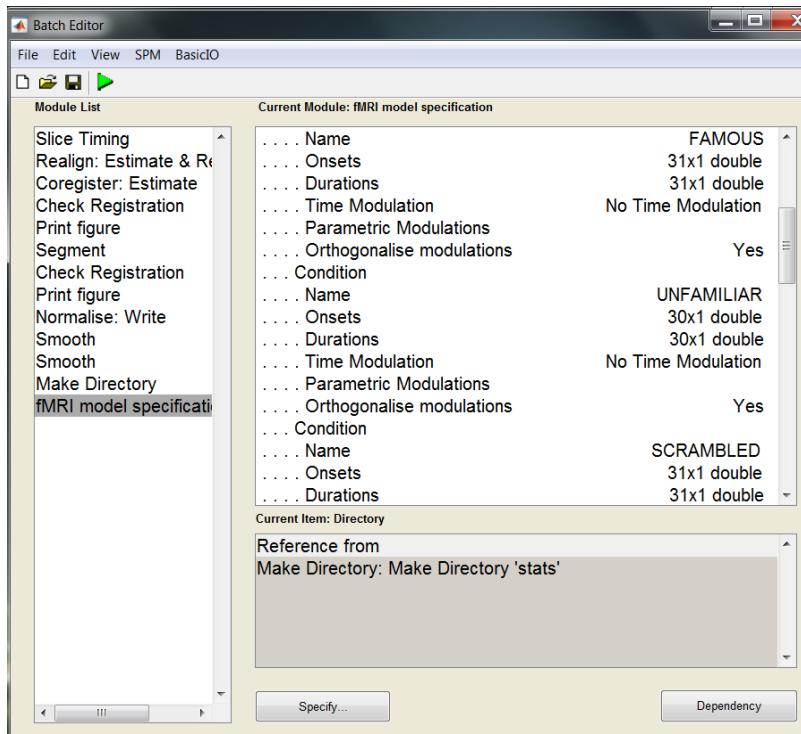


Figure 9. Entering conditions in the statistical model

SPM >> Stats >> Model estimation

Click Select SPM.mat, and use the dependency.

SPM >> Stats >> Contrast Manager

This the last step – we have set the model, estimated it, now we want a test to pull together the same conditions. Click Select SPM.mat, and use the dependency. Under 'Contrast Session', click New: T-contrast. Next fill in the detail: Name, Famous; Weights vector, 1 (for the 1st column in our design, SPM will fill the rest with 0); Replicate over Sessions, Replicate. Do the same for unfamiliar (Weights vector is now 0 1, the second column in the design matrix), and scrambled (Weights vector 0 0 1).

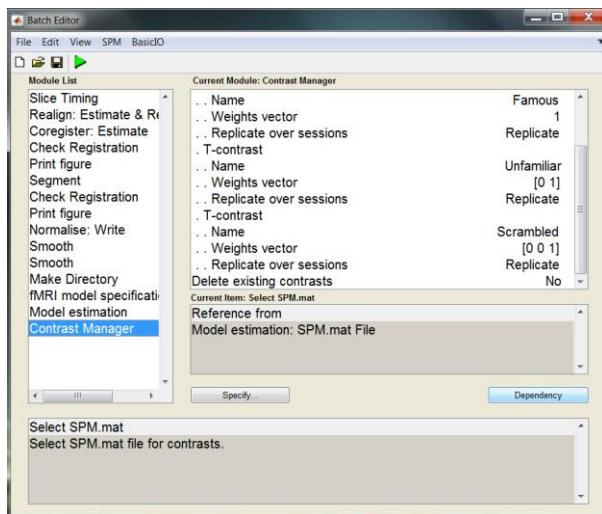


Figure 10. Entering contrasts

Now click on **File → Save Batch** (choose the name you want)

This will allow to reload the batch and process new subjects the exact same way (left as an exercise for the other subject available – think of what needs to be changed?)

Click the green arrow and wait for results.

Review pre-processed data

Mean and variance images

First we can check that the mean image is a good quality – too much blurring or distortion would indicate a problem. Another useful diagnostic image is the variance image. We can use the SPM image calculator to do that. On the main interface click on **ImCalc**.

In “*Input Images*”, enter normalized images of run 1 (as with slice timing, change the range of files to 1:999 and select all wst files of run1, this gives 208 3D files rather than a single 4D file, see figure 11). Set the “*Output Filename*” as mean. Choose the “*Output Directory*” (the func folder). In “*Expression*” type: mean(X). Importantly, to see all the files as X (a matrix), in “Options”, set “*Data Matrix*” to “Yes – read images into data matrix”. Press the green arrow.

Re-iterate the procedure with “*Output Filename*” as variance and “*Expression*” var(X).

On the main interface click on **CheckReg** and choose the mean EPI and the variance image (figure 11).

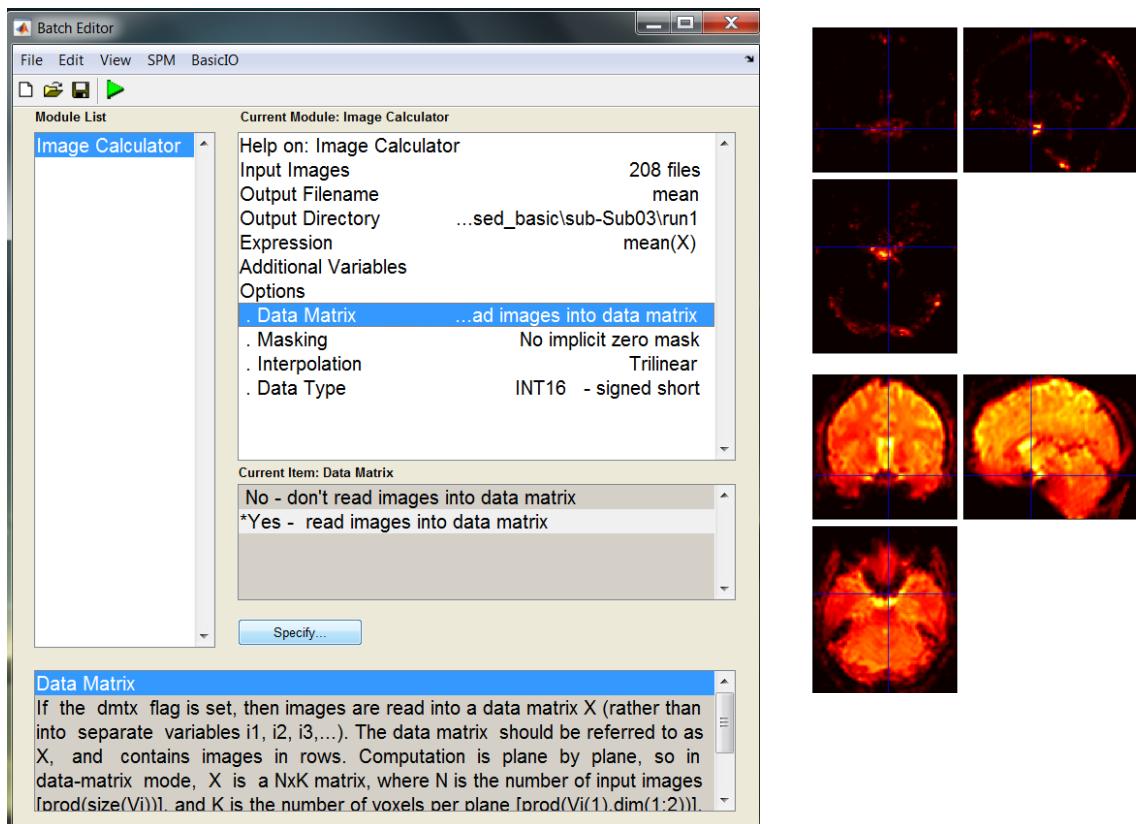


Figure 11. Computing the mean image using the image calculator (left) and visualization with check reg (right). Note that here the colour was changed (graphic window → SPM Figure → colours → colormap → hot)

Volume-series

Another good way to check the data are well realigned and normalized is to visualize the volumes one after the other as a movie. We can use again **CheckReg** → Select the swasub....run-01.nii. The 1st image is then displayed – right click on the figure and go to Browse. Select again but, as done earlier expand file from 1:999 to select all swasub... run-01.nii images. You can now browse the time series as there is a slider at the bottom of the graphical window (you can see it ‘flickers’ a little).

Data Visualization (part 1)

Now that we have pre-process the data, done a little of quality control, we can check the results. Note that at the group level, only parameter estimates or contrasts are used, and therefore only the between-subjects variance matters. This implies that the presence or absence ‘significant’ activation at the subject level is meaningless.

Result table

We described in SPM/stats design matrix the periods of activations, and the results show where there are significant voxels (more on that tomorrow).

On the main GUI, click **Results** and select the SPM.mat from the stats directory. Next select a contrast, eg. Famous and follow the defaults (masking none, FWE correction at 0.05 and 0 for extent threshold). The result table shows for each cluster the size and peak significance (figure 12).

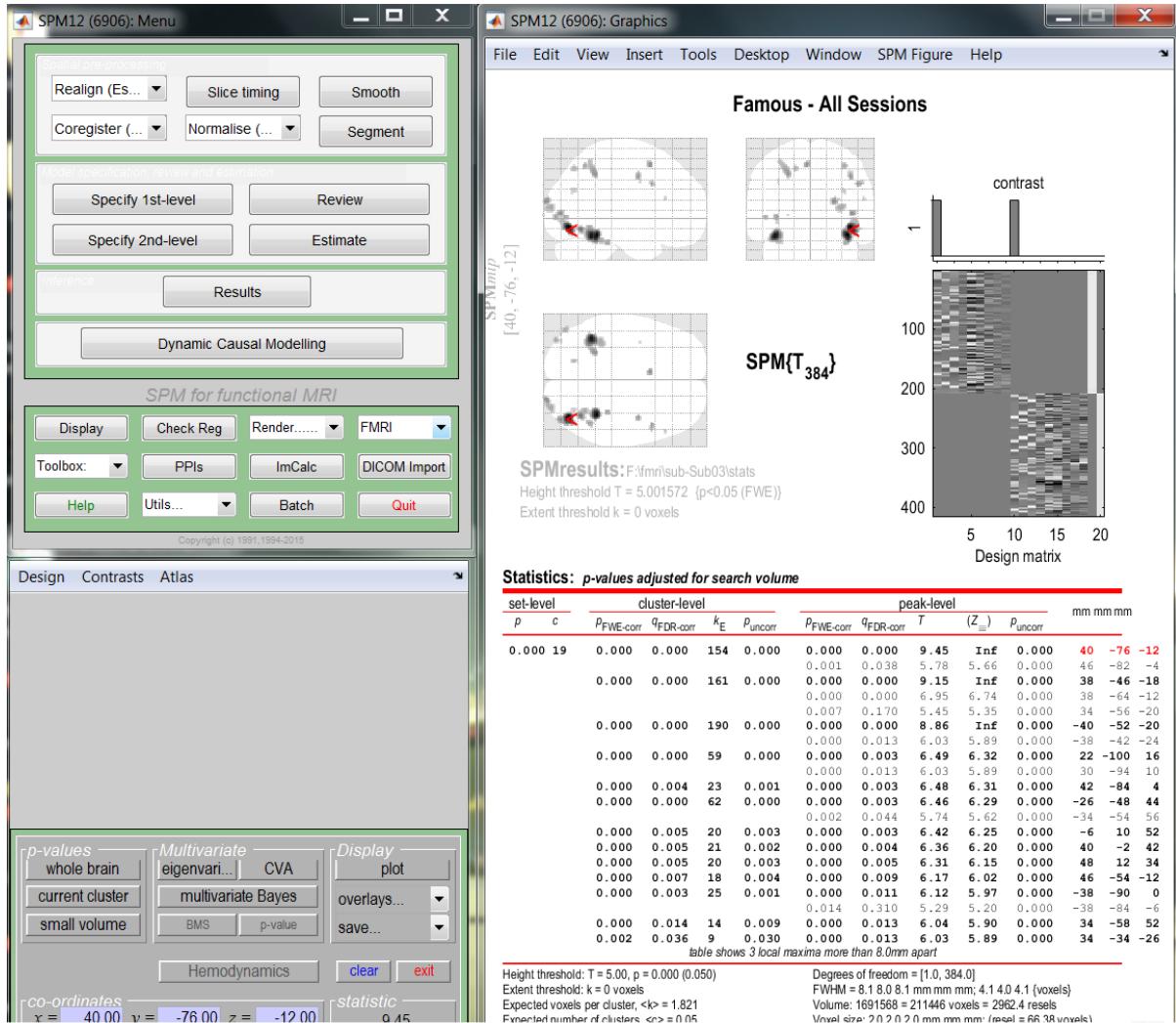


Figure 12. Results for the 'Famous' condition in subject 3.

If you right click on the result table (somewhere in the white toward the left side) – several options show up to save/print/export that table. Click on **export to NIDM**. Now check on the drive, a nidm folder was created and this can be used to share your results (mow on that tomorrow).

Another interesting tool, is to use automated labelling. In the result main interface, click on **Atlas >> Label using >> Neuromorphometrics**. Now selecting a coordinate in the table and right click shows labels. Be however careful with this as exact anatomy can be difficult – see 'In praise of tedious anatomy' (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1986635/>)

Display orthogonal views

There are three ways to look at orthogonal views. [1] The simplest, is to choose “overlays ...” and “sections”. In the selection, surf to the spm12/canonical directory and choose an image. (figure 13)

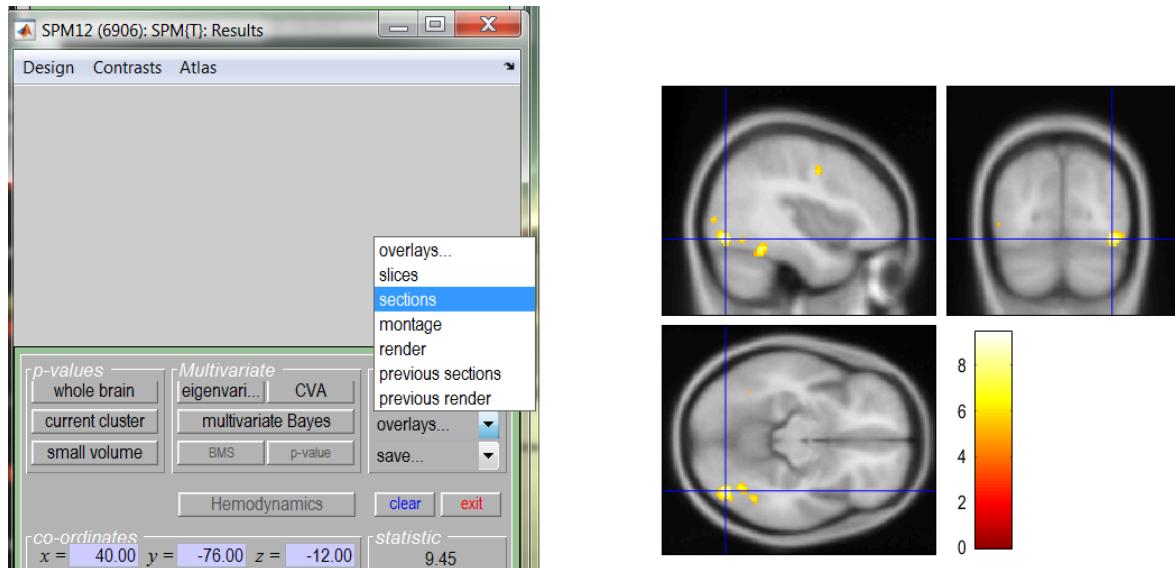


Figure 13. displaying results on orthogonal sections

The other option [2] is to click on “Display”, again choose an anatomical image from spm12/canonical – from the graphical window you can then select to “add overlay” – select the SPM.mat and proceed. You can however also directly add images. For instance, click results, and select Famous face, then click ‘save’ → ‘thresholded SPM’. Repeat with scrambled. Now we have two images on the drive, and we can use Display → add blobs → select those two images. (figure 13)

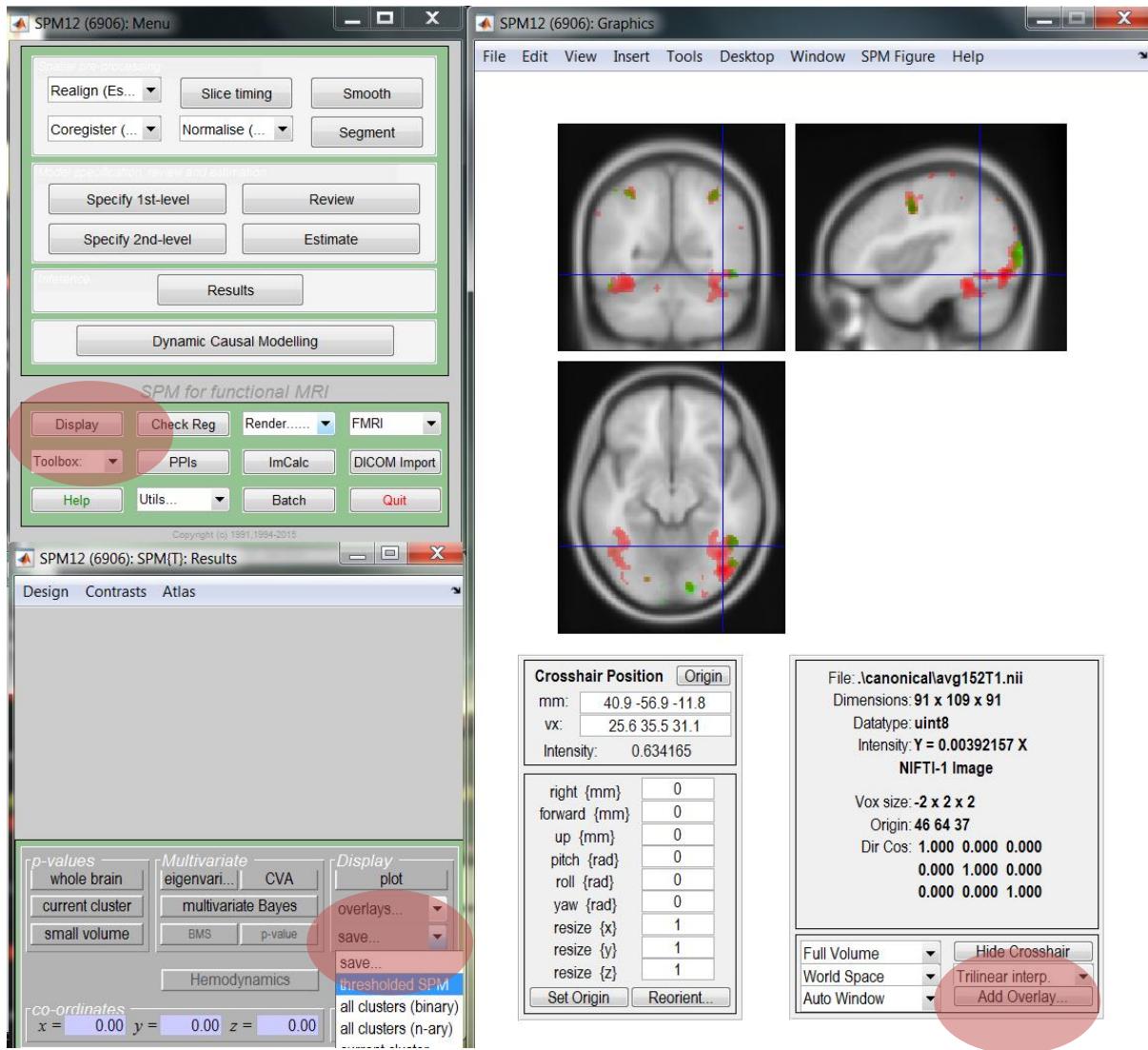


Figure 13. Using ‘Display’ to show multiple results (here famous and scrambled saved using a uncorrected statistical threshold of $p=0.001$)

Finally, it is also possible to add overlay [3] using CheckReg, which calls **spm_orthviews**. Select an anatomical image from spm12/canonical/ and once displayed, right click in the graphic window. Select an image to overlay (similar to display). Among others, it can be used to set the maximum of overlapped data and thus allows having the same colour scale for several contrasts.

Do checkreg, select an anatomical image and type in the Matlab command window: `spm_orthviews('addtruecolourimage')` and select an spmT image, then at the SPM prompt, select a colormap e.g. parula ; move the mouse around (figure 14)

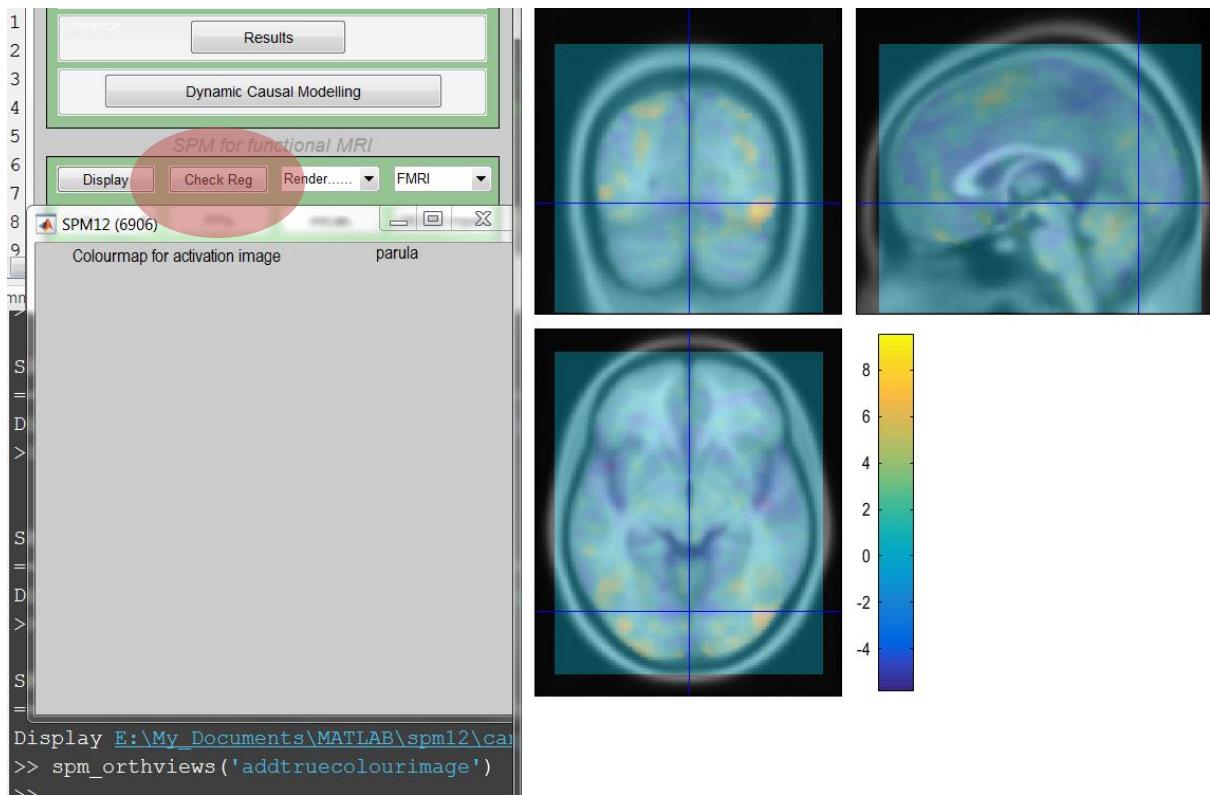


Figure 14. Using check reg to show an *spm_T* map

Display slices

As for orthogonal views, the simplest option is to choose “overlays ...” and “slices”. In the selection, surf to the spm12/canonical directory and choose an image. It will show 3 slices around the current position (below/at/above).

Alternatively, we can use **slover** (see help slover). From the Render dropdown menu select ‘slice overlay’ and choose an image from the spm12/canonical directory and from the stats directory choose the spmT_0001.nii – Choose "Structural" as the type for the structural image, and "Truecolour" as the type for the activation image. For the truecolour image, the routine asks for a colormap to use – change to actc or parula. To show blobs rather than a continuous image, choose ‘blobs’ rather than “Truecolour”. It is also possible to simply select a structural image and choose the option "Structural with SPM blobs".

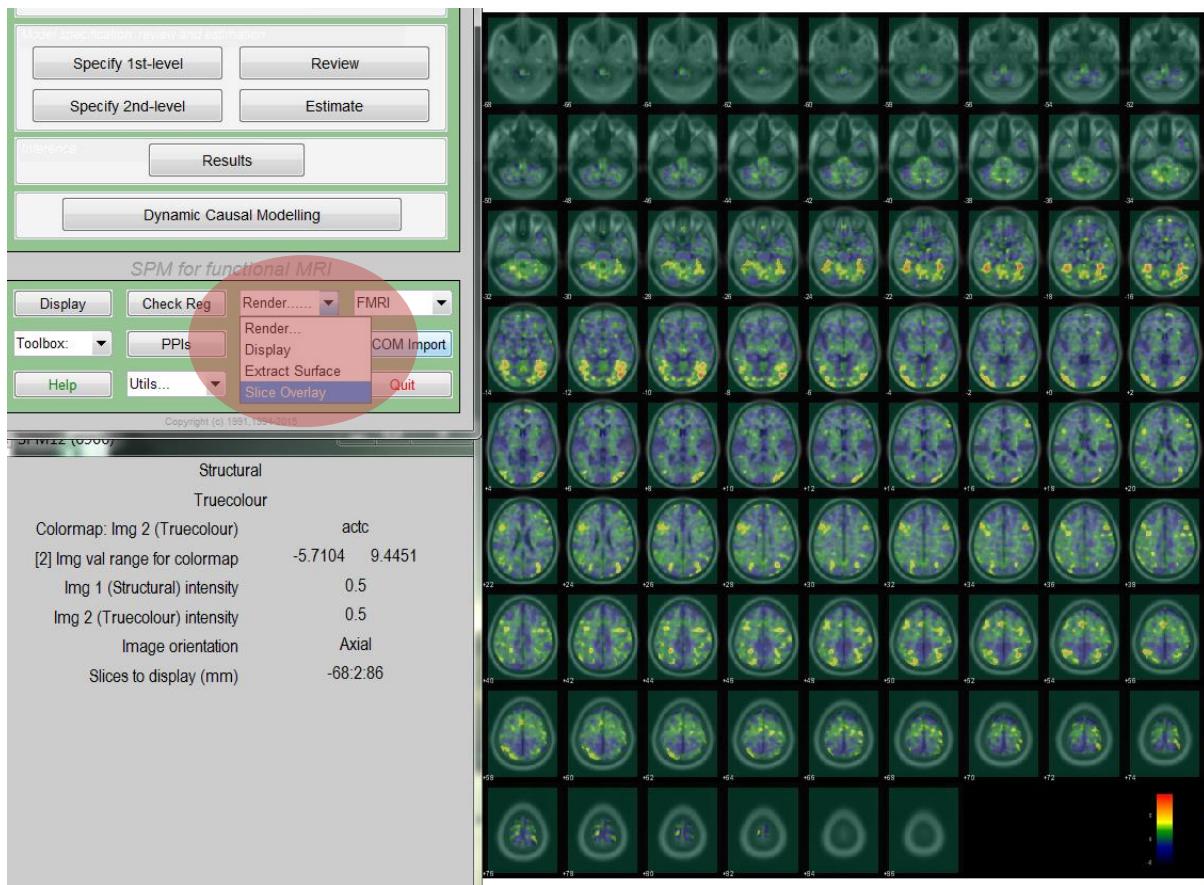


Figure 15. Using slover to show an spmT map

Group level analysis

fMRI data

The data to process can be downloaded on the SPM website and instructions to process them are in the SPM manual: \...\spm12\man

We are looking again at the face dataset (an older version of it). Importantly here we are using subjects' parameter estimates derived from the full repetition priming experiment: 2_2 factorial study with factors "fame" and "repetition" where famous and non-famous faces were presented twice against a checkerboard baseline. The subject was asked to make fame judgements by making key presses. There are thus four event-types of interest; 1st and 2nd presentations of famous and non-famous faces, which we denote N1, N2, F1 and F2.

Images were acquired using continuous Echo-Planar Imaging (EPI) with TE=40ms, TR=2s and 24 descending slices (64_64_3_3 mm³), 3mm thick with a 1.5mm gap. Because fMRI data analyses are hierarchical, we process 1st within subject and then between subject. We start here by the basic model and then we'll explore other possible way to analyse the data.

We skip altogether the preprocessing. Just one note here compared to the data we processed yesterday: usually slice timing is done 1st, because most of the time data are acquired using an interleaved acquisition that minimizes spin history effects. Realigning 1st such data may lead to align

data which are half a TR apart, hence slice timing first. Here data are acquired in sequential mode and thus realigning comes first.

A simple model - 1st level (subject)

We start with the pre-processed data 4D_preprocessed.nii (located in [...] \Data\spm_dataset\single_subject\func). Open SPM, click on batch, then proceed to set up the statistical model, evaluate it and prepare some contrast.

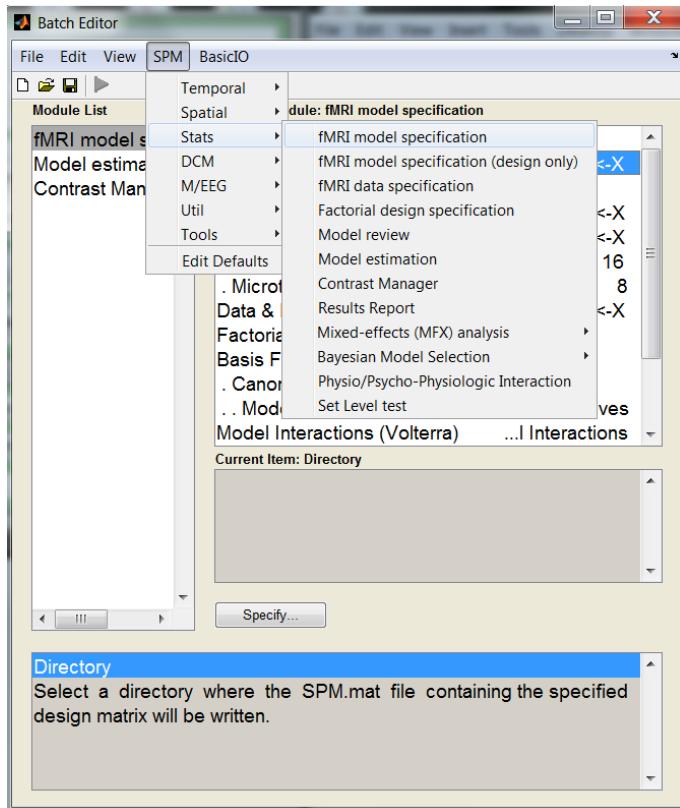


Figure 16. 1st level fMRI model specification

SPM >> Stats >> fMRI model specification

Setting up the design matrix, is simply describing when each condition occurs. To do so, we 1st have to load the timing information. While yesterday we used the BIDS info, here this is stored in the file sots.mat located in the func folder. In the Matlab command window, type load sots (or right click the file and load). As you can see this is a cell array and information per conditions are stored into separate cells (accessible with curly brackets {}): Non-Famous 1st presentation is stored in sot{1}, Non-Famous 2nd presentation is stored in sot{2}, Famous 1st presentation is stored in sot{3}, Famous 2nd presentation is stored in sot{4}.

In the batch fMRI model specification, proceed as follow (figure 17):

- For Directory, select the stats folder
- 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).

- "Data and Design" and select "New Subject/Session".

Highlight "Scans" and 1 – expand the number of volumes (1:999) and choose the 351 4D-preprocessed.nii images.

Highlight "Conditions" and click "New condition" 4 times (can replicate/delete in the middle menu).
 For the 1st Condition Highlight "Name" and enter "N1".

Highlight "Onsets" and enter sot{1}
 Highlight "Durations" and enter 0.

For the 2nd Condition Highlight "Name" and enter "N2".
 Highlight "Onsets" and enter sot{2}.

For the 3rd Condition Highlight "Name" and enter "F1".
 Highlight "Onsets" and enter sot{3}.

For the 4th Condition Highlight "Name" and enter "F2".
 Highlight "Onsets" and enter sot{4}.

Highlight "Multiple Regressors" and select the realignment parameter file rp sM03953 0005 0006.txt
 This file was saved during the realignment preprocessing step in the folder containing the fMRI data.

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.

SPM >> Stats >> model estimation

Highlight "Select SPM.mat" option and click on dependency to choose the SPM.mat

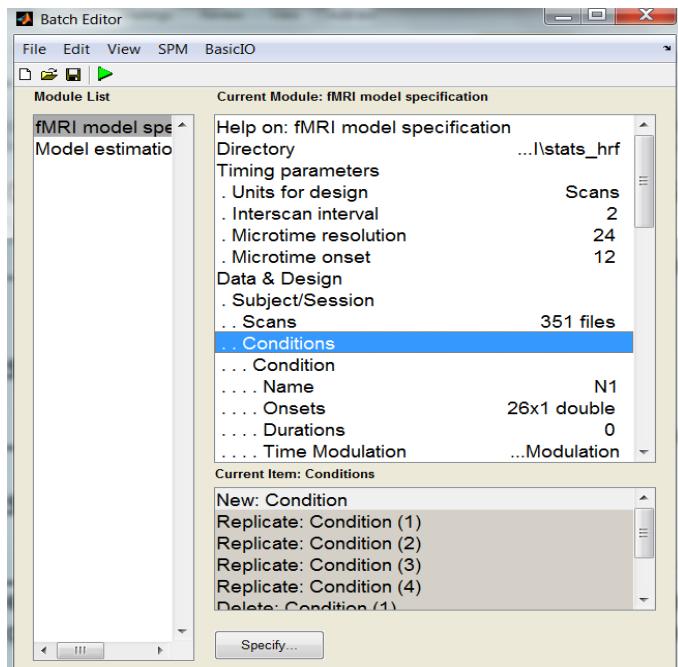
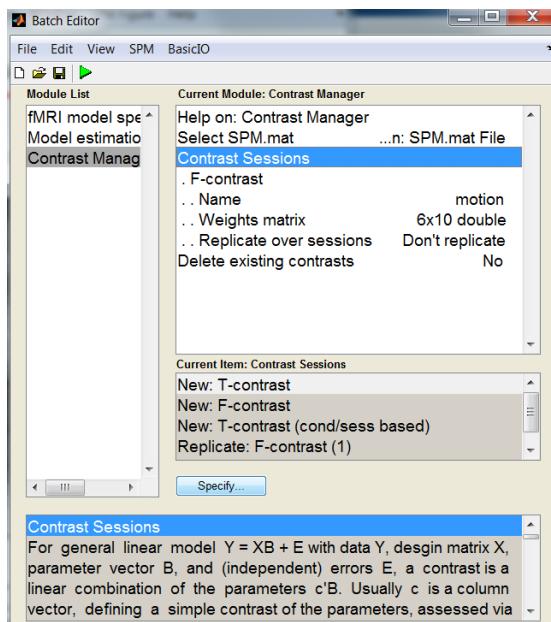


Figure 17. Specifying conditions

SPM >> Stats >> Contrast manager

Highlight “Select SPM.mat” option and click on dependency to choose the SPM.mat from estimation

Highlight “Contrast Sessions” and create a new F contrast: Name: “motion” Weight matrix: [zeros(6,4) eye(6)] (figure 18)



Weight matrix: [zeros(6,4) eye(6)]



Figure 18. Contrasts

Save the batch as categorical_spec.mat and press the Run (green triangle) button.

Results

If all goes well, the statistical model has been build and estimated, as well as the new contrast. By default a series of contrasts would have been built as well to reflect the different effects.

Click on Review and select the SPM.mat. This shows the design matrix. The 1st four column show the 4 experimental conditions, the 6 following columns are the motion parameters (x y z translation and rotation) and the last column is the constant term. Left clicking on a column gives you the actual value on the current row whilst right clicking gives you the name (details are stored in the SPM.mat structure under SPM.xx). Under it, the vector ‘parameters estimability’ shows the unique contribution of each regressor to the model – the more gray the less unique (i.e. the more collinear).

Click on Design to further explore the modelling of each condition (figure 19). This plot the time course of the regressor (ie the values of a column in the design) but also its frequency along with the specified filter (here default is 128s ie 0.0078Hz) and finally the function used to model the vascular response.

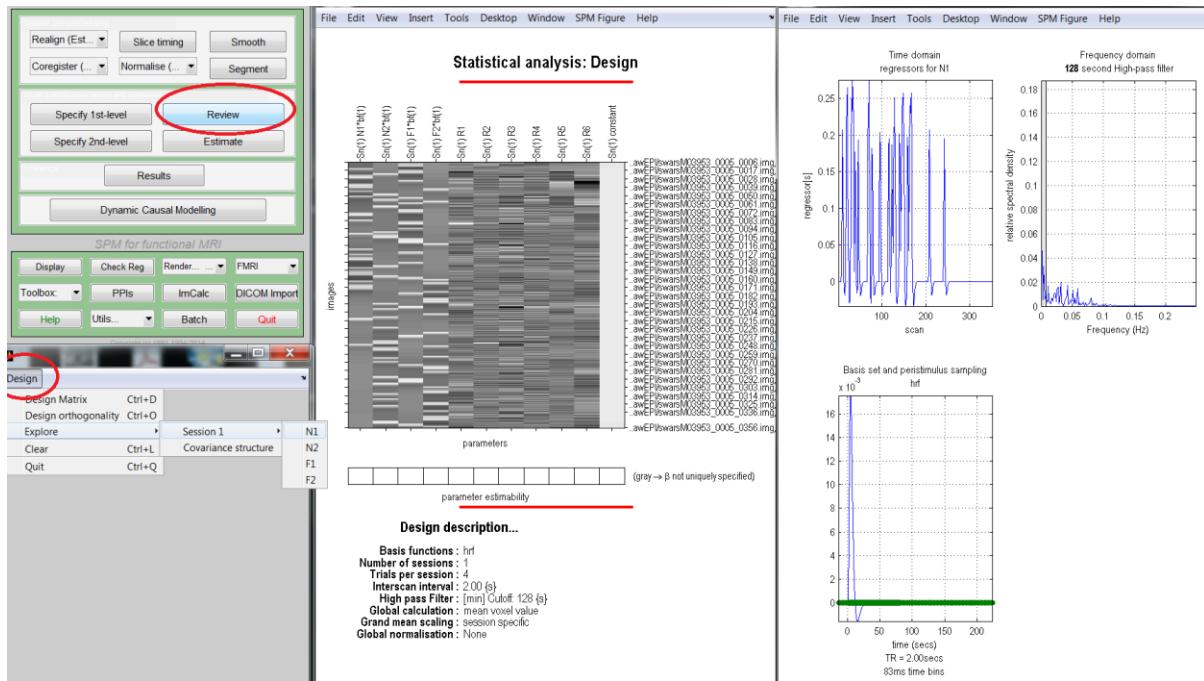


Figure 19: reviewing design

Click on Results and Select the SPM.mat. Choose the 5th contrast: Positive effect of condition_1. This shows the sum of positive activations for the 4 conditions. Then choose no masking, FWE p=0.01 k=0. Overlap on section choosing the wmsM*.nii file from the structural folder. You can also do a ‘slice overlay’ choosing an anatomical image and the spmT_0001.nii images with the ‘Truecolour’ option.

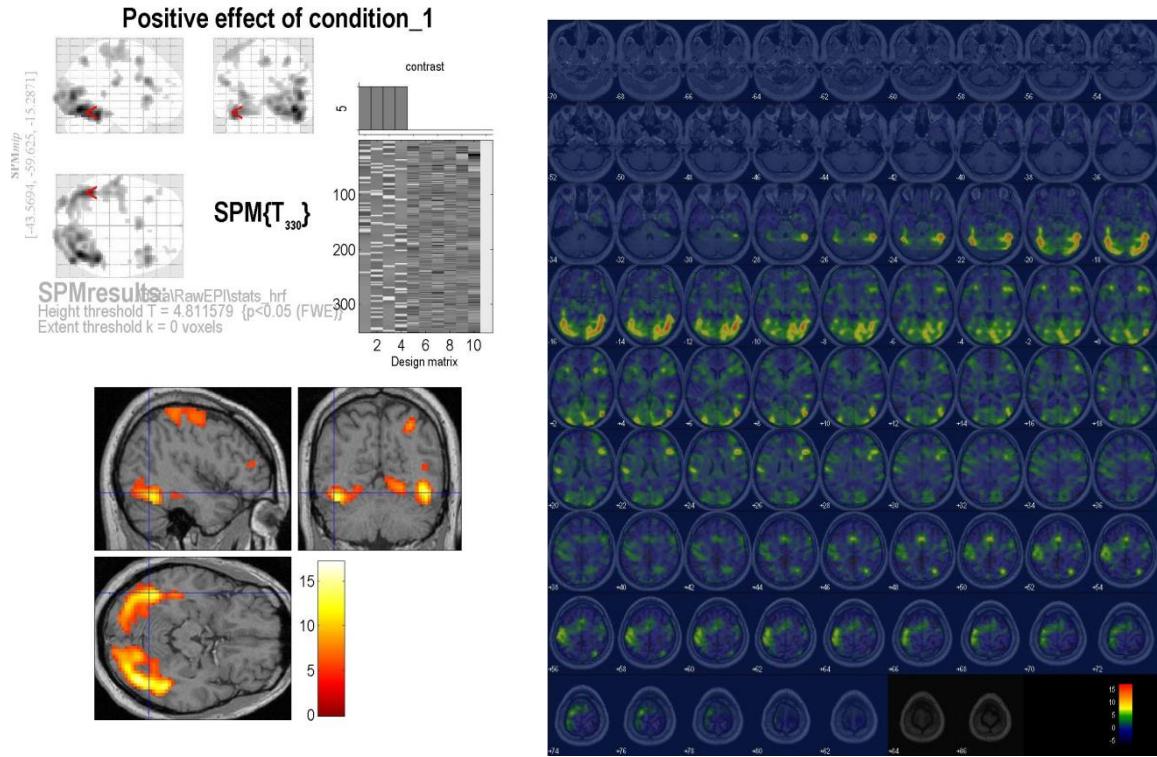


Figure 20: results for all faces > 0

Similarly, we can look at the effect of motion using the F contrast we created. Click on Contrast >> Change contrast >> motion

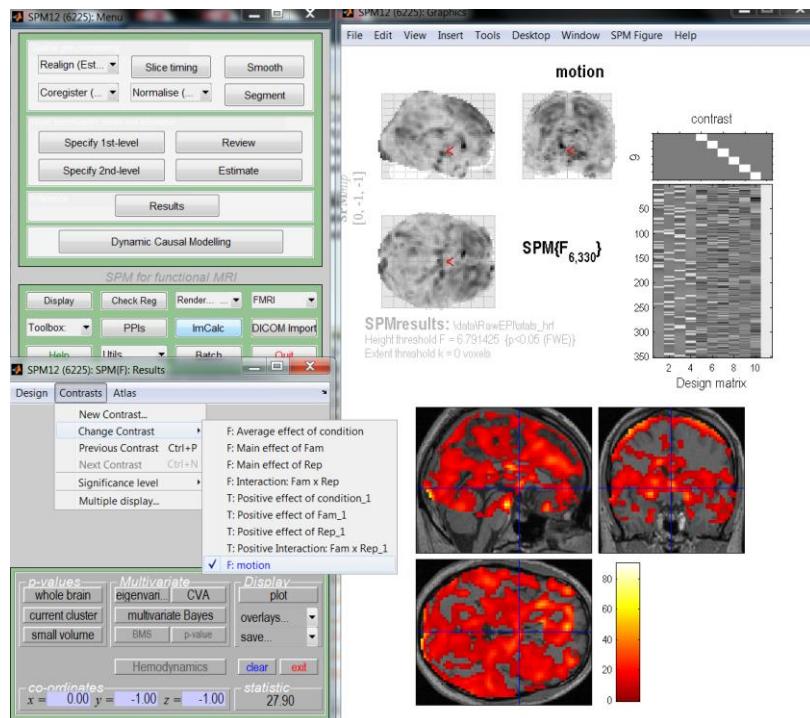


Figure 20: results for motion > 0

A simple model - 2nd level (group)

Once parameters have been estimated for each subject, we can combine these estimates at the group level. Since each subject has its own constant term modelling the overall level of activation, we allow random variations between subjects (subject is treated as a random variable). Here we use only the beta images or con images to assess the mean effect or the mean difference between effects, which constitute a random effect model.

In the above experiment, the real interest is to test the interaction. To do so, we need to compute the repeated-measure ANOVA entering the beta images 0001 (N1) 0002 (N2) 0003 (F1) and 0004 (F2). For simplicity, we will use here the contrast images corresponding to the main effect vs. baseline (move to the [...]\\Data\\spm_dataset\\canonical_con folder).

To 'see' where there are significant activations across subject for that contrast, all we need to do is to compute a one-sample t-test (i.e. is the mean activation > 0). Click on 2nd level – it will bring up the batch interface with the **Factorial module** loaded. In the batch interface, choose a directory for the stats, leave the Design to 'one sample t-test' and select the 12 con images (Figure 21). Add the **estimate module** and select the SPM.mat via dependency. Finally add the **contrast module**. Again, select the SPM.mat via dependency and add 2 contrasts: the 1st one with a weight [+1] and the 2nd one with a weight [-1]. Remember a contrast is a linear combination of parameters, i.e. for a subject $\text{con} = \text{beta_0001} + \text{beta_0002} + \text{beta_0003} + \text{beta_0004}$. When using a T-test, it only shows if that con is >0 given the error (between subjects) variance. But the con image itself is not positive or negative, and therefore, across subjects, the one sample t-test [+1] will test if >0 while [-1] will test if <0.

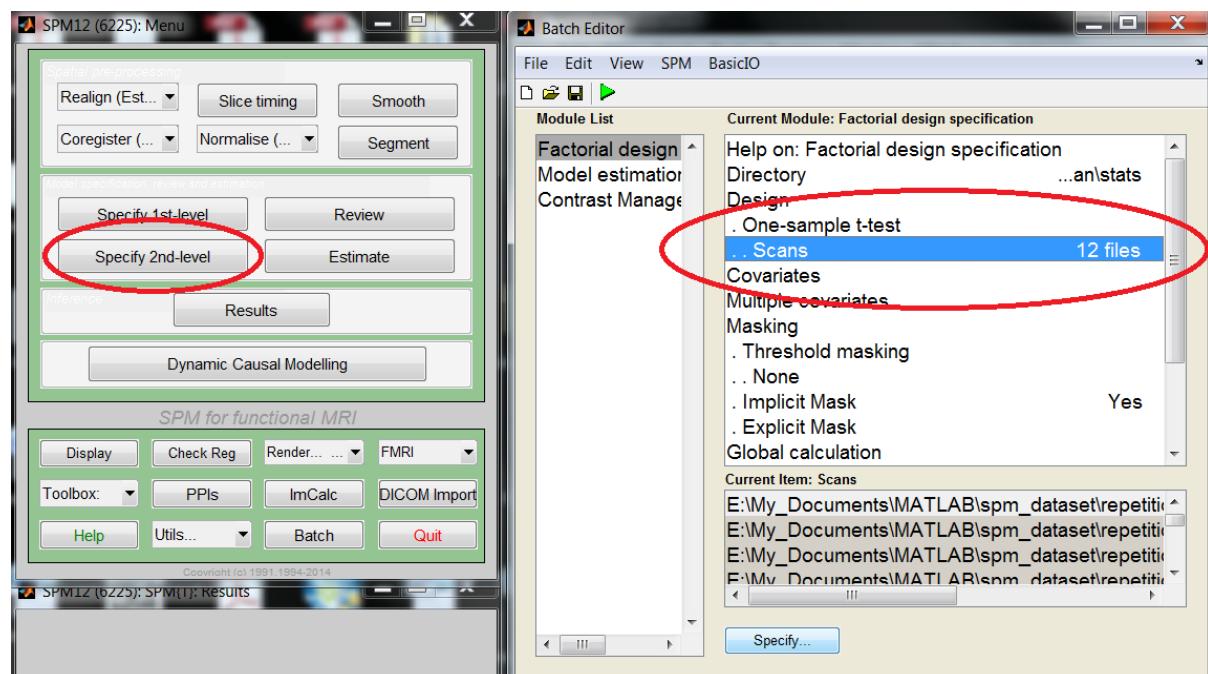


Figure 21. Setting up a one-sample t-test

Batch >> SPM >> Stats >> Results Report

Use the dependency to select the SPM.mat from contrasts.

Under Contrast query, add a new query and enter 1 entre Contrast(s)

Change Print results to NIDM (Neuroimaging Data Model) and fill up information requested. This last option means that the result of the contrast and related information are saved into a directory called nidm_001. The files generated can be used directly by other software like FSL, or data libraries like NeuroVault.

Results

Click results and select the SPM.mat and positive contrast – use FWE p=0.05. Results show that across all subjects, after correction for multiple comparisons, there significant activations in the fusiform regions (and SMA).

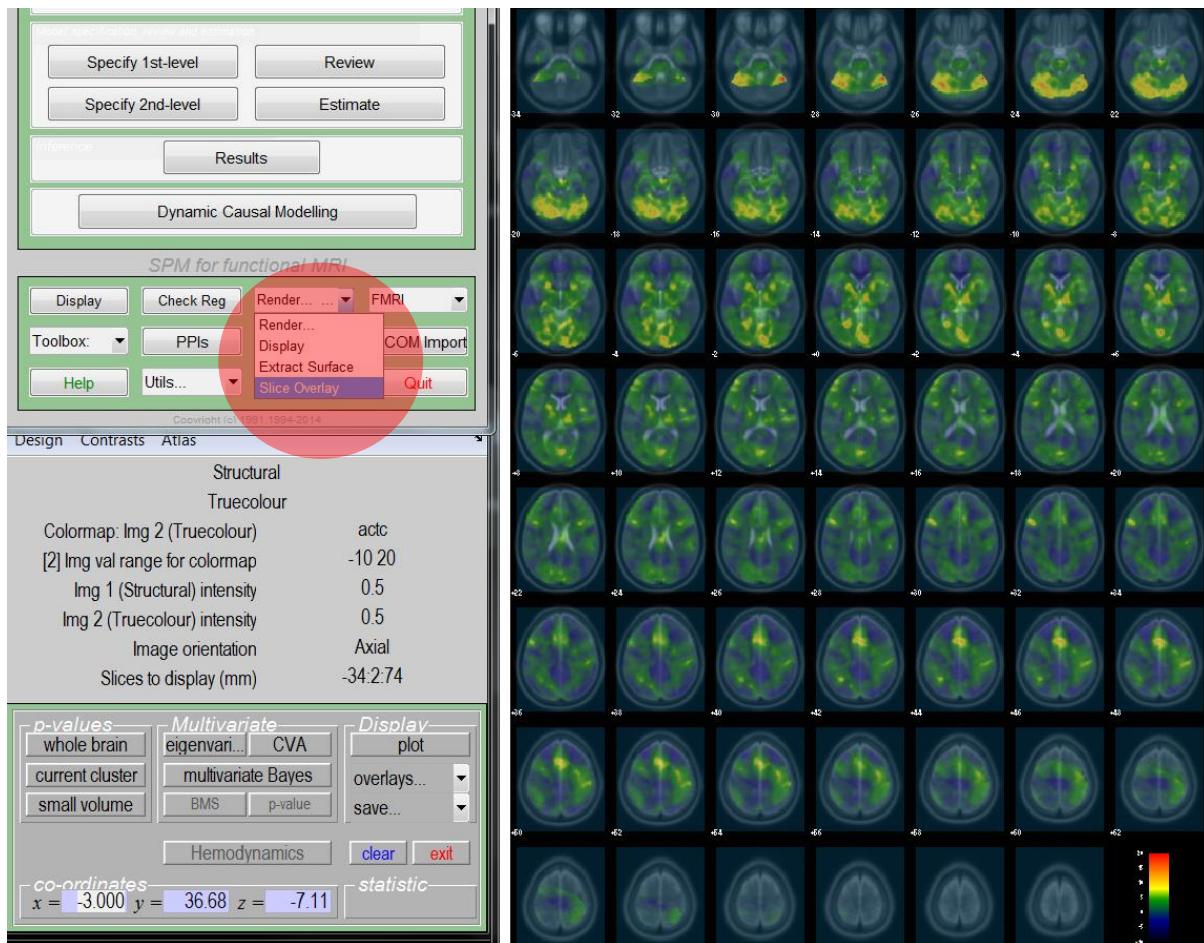


Figure 22. Results for the one sample t-test

Data Visualization (part 2)

Data plots

Using SPM, you can go on a coordinate and click the ‘plot’ button showing the average response. This however not satisfactory because 1) bar graphs hide the data dispersion (see ‘Beyond Bar and Line Graphs’ (<http://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.1002128>) and 2) this limits visualization to ‘activated areas’.

In a face experiment, like this one, many areas are expected to be activated – it would therefore be useful to report the average activations in those regions.

Step 1: generate a map of a priori locations. Go to neurosynth → meta-analysis → terms → faces; you can then download a map of where we can expect to see some activations (figure 23). This map is also available in the [...]\\Data\\spm_dataset\\canonical_con\\stats folder

Step 2: compare observed results to a priori regions – A) use results, select the activation contrast and save the thresholded SPM (no masking, no FEW correction, extend threshold 35 – this corresponds to cluster FDR < 0.05); B) use ‘Display’ to load the neurosynth map and the observed results (‘add blobs’); C) take note of ROI coordinates

Step 3: collect data for expected ROI (significant or not) which can then be reported

```
con_img = cell2mat(SPM.xY.P);
[Yright_moc, ~] = spm_summarise(con_img,struct('def','sphere',
'spec',8, 'xyz',[38 -82 -10]), @mean);
[Yleft_moc, ~] = spm_summarise(con_img,struct('def','sphere',
'spec',8, 'xyz',[-38 -82 -10]), @mean);
[Yright_fus, ~] = spm_summarise(con_img,struct('def','sphere',
'spec',8, 'xyz',[40 -52 -14]), @mean);
[Yleft_fus, ~] = spm_summarise(con_img,struct('def','sphere',
'spec',8, 'xyz',[-40 -52 -14]), @mean);
[Yleft_amyg, ~] = spm_summarise(con_img,struct('def','sphere',
'spec',8, 'xyz',[-24 -12 -14]), @mean);
[Yright_amyg, ~] = spm_summarise(con_img,struct('def','sphere',
'spec',8, 'xyz',[24 -12 -14]), @mean);
[Yright_thal, ~] = spm_summarise(con_img,struct('def','sphere',
'spec',8, 'xyz',[12 -32 -2]), @mean);
[Yleft_thal, ~] = spm_summarise(con_img,struct('def','sphere',
'spec',8, 'xyz',[-12 -32 -2]), @mean);
Data = [Yleft_moc Yright_moc Yleft_fus Yright_fus Yleft_amyg
Yright_amyg];
```

Step 4: make a figure and report results

```
figure; boxplot(Data);
h=findobj(gca,'tag','Outliers'); % Get handles for outlier lines.
set(h,'Marker','o'); % Change symbols for all the groups.
```

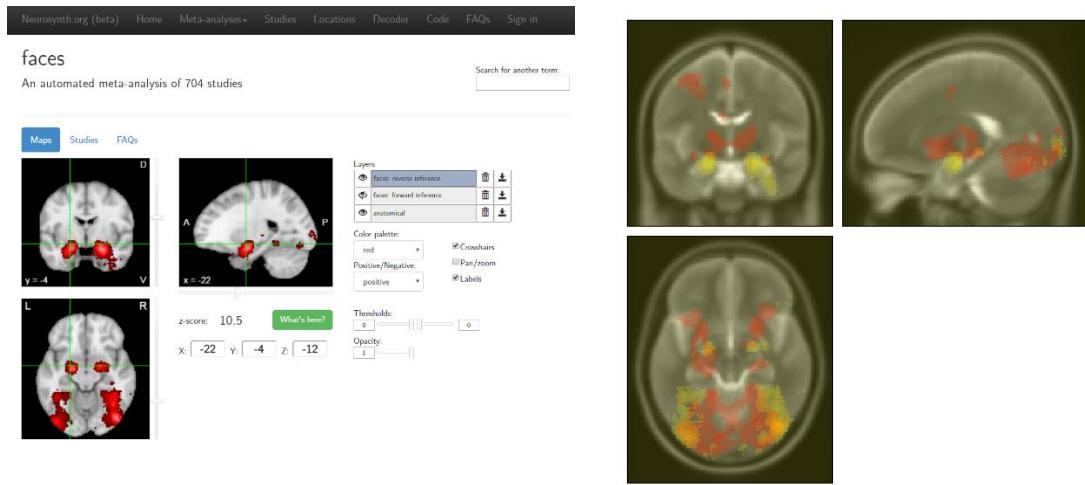


Figure 23. Neurosynth webpage for 'faces' (left) and intersection of the activation map (red) with the neurosynth one (right)

Volume and surface rendering

When the overall pattern of activation has to be shown, render are quite useful. The last type of display uses renders – these are objects that show a reconstruction of the cortical surface. You can create subject specific renders (see batch > SPM > tools > Rendering). Here we will use already made renders in the MNI space.

Click on results, select the positive contrast → no masking, no FEW correction, extend threshold 35 – this corresponds to cluster FDR < 0.05. Then click on overlays and select render. Volume rendering files are located in the spm12/rend folder (figure 24)

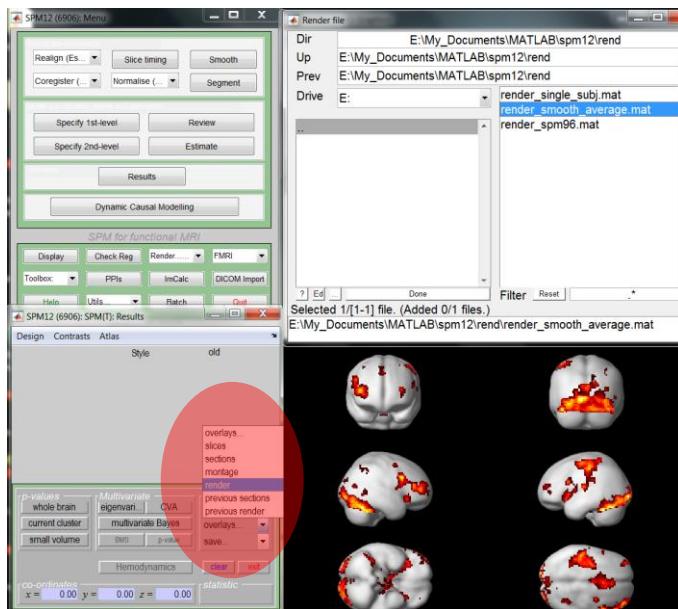


Figure 24. 'old' rendering the positive contrast on the smooth average.

SPM also does surface rendering. From the dropdown Render menu, select Display and select a .gii file from the spm12/canonical folder. For instance, select cortex_8196.gii and then select 1 set and the SPM.mat to show the positive. Once the cortical surface is displayed, right click on it and play (figure 25).

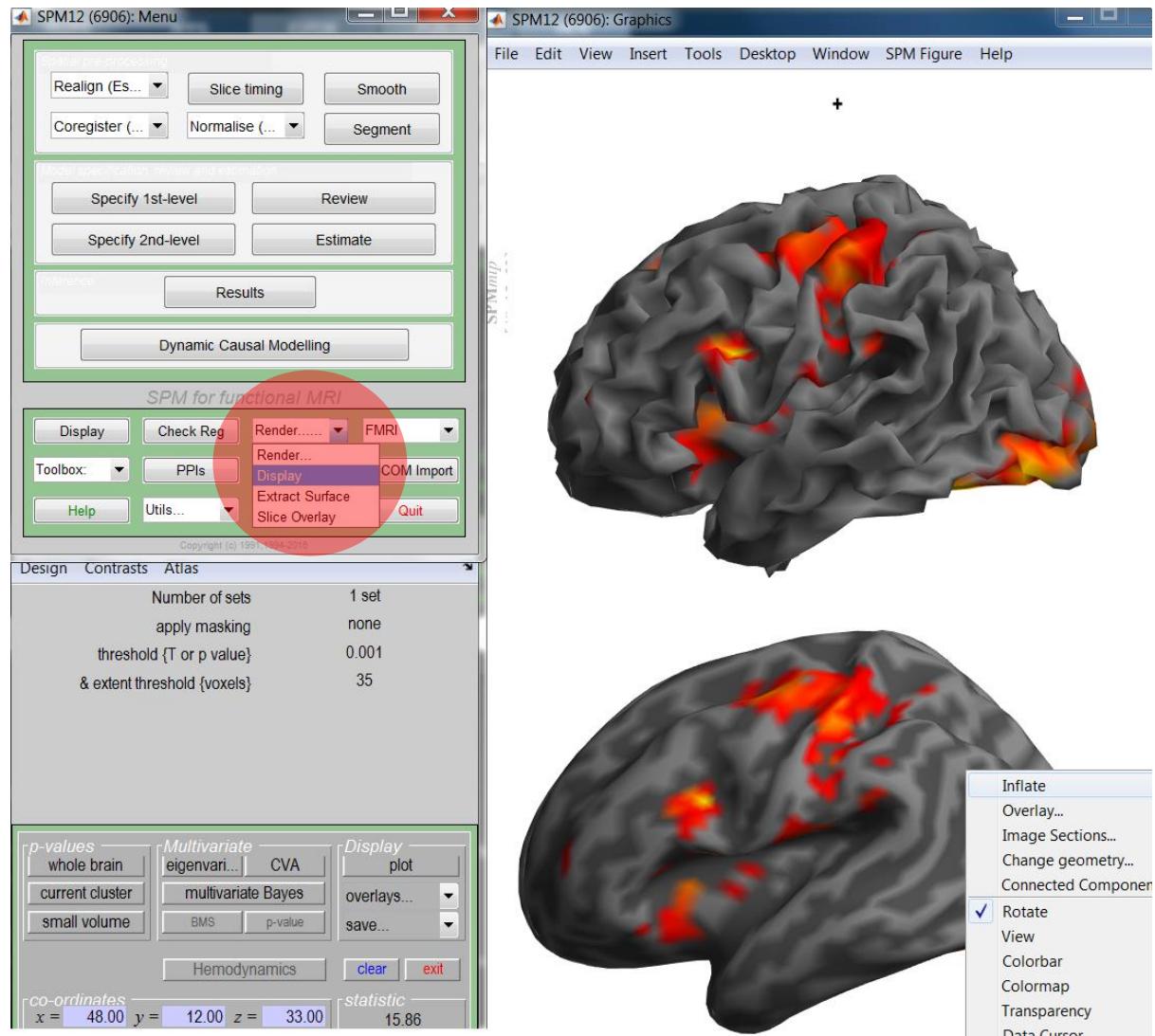


Figure 25. Surface rendering using SPM.

Sharing and Viewing on the web with Neurovault

Once you have finished with your analysis and are ready for publication, best is to upload your maps to neurovault (<http://neurovault.org/>). Sharing raw stats map is good practice (see OHBM COBIDAS report <http://biorxiv.org/content/early/2016/07/10/054262>) as it allows to assess which region are ‘activated’ or not using various thresholds and if there is spatial selectivity (is your significant blob top of a huge mountain or is it really just that blob).

Neurovault also comes with visualization tools (figure 26), a decoding tools (via neurosynth) and power analysis (via neuropower). Note is the next release of SPM – right clicking on the result table will take you to neurovault directly (providing you have a login).

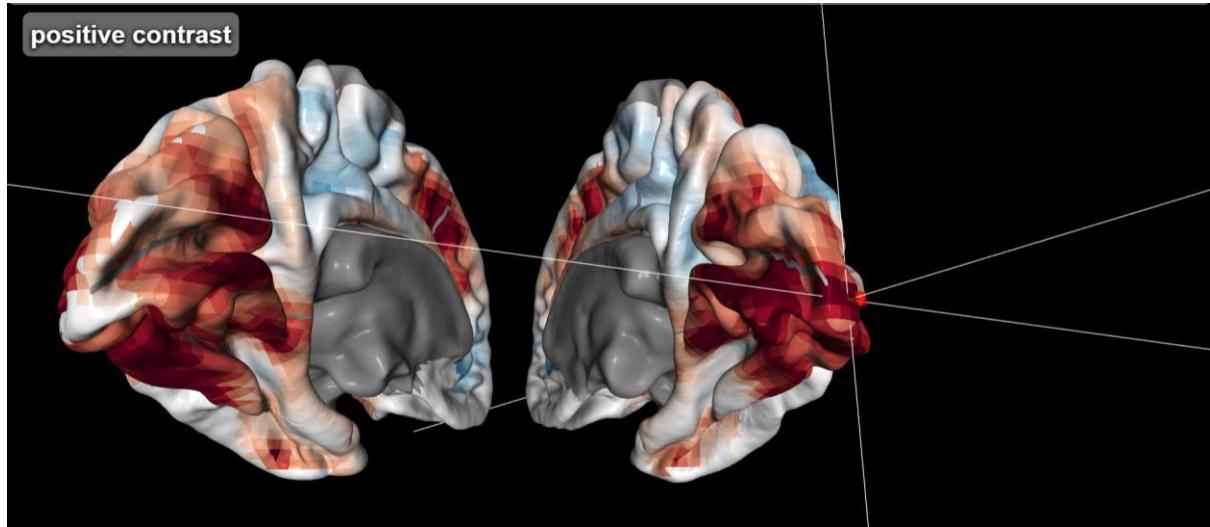


Figure 26. Surface rendering using NeuroVault.

A better model - 1st level (subject)

One problem with the previous model is that we assumed a fixed shape of the hemodynamic response. Studies on the topic have shown that the shape changes (i) with stimuli/conditions, (ii) across regions of the brain within a given subject, and (iii) between subjects. One way to accommodate such variation is to use basis functions of the hrf, i.e. use the derivatives.

The 1st derivative (red) is the difference from 1 time point to the next of the hrf. It thus indicates the rate of change, and any loading of a condition will indicate either an earlier response (+ beta) or a delayed response (- beta). The 2nd derivative (green) is the difference from 1 time point to the next of the 1st derivative. It thus indicates how much it spreads, and any loading of a condition will indicate either a larger response (+ beta) or sharper response (- beta).

Going back to the single subject do: **Batch >> load categorical_spec.mat.** We here use the same model as before, but change from a single hrf to 'Time and Dispersion derivatives' (under 'Basis Function'). Remember as well to change the working directory. Then *delete the contrast module* and finally press the green arrow to run and estimate the new model.

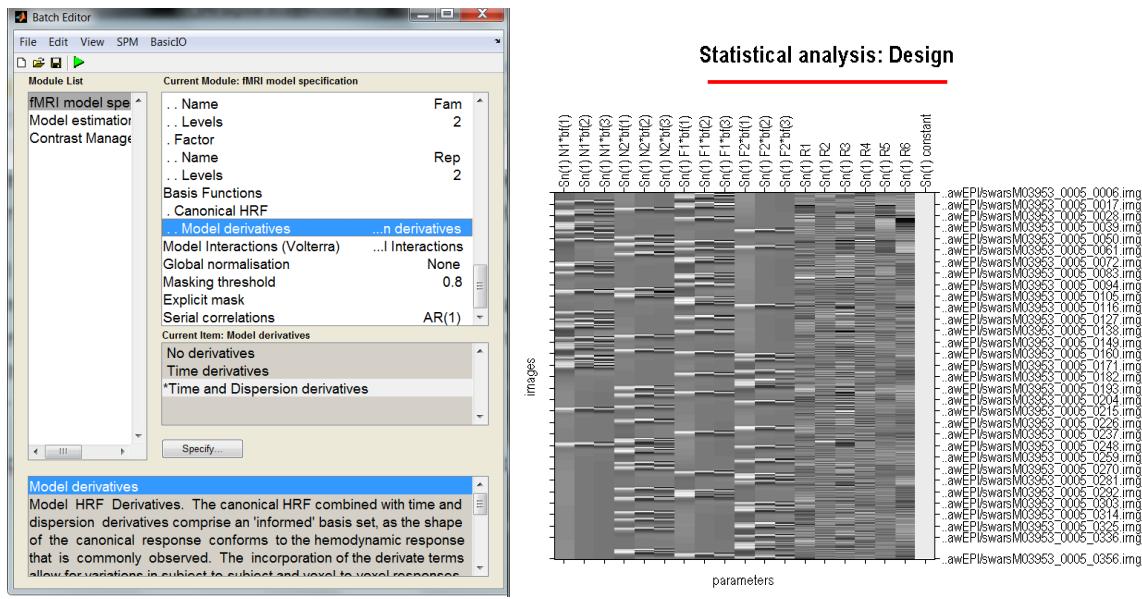


Figure 27. 1st level design matrix with derivatives.

Display an anatomical image and add the 3 contrasts: positive effect of condition 1 (hrf) , positive effect of condition 2 (time derivative), positive effect of condition 3 (dispersion derivative). Each time threshold at FWE p=0.05. We can see clearly that in the fusiform regions, there is a strong loading of the time derivative, which leads to underestimate the strength of the response using the hrf model alone.

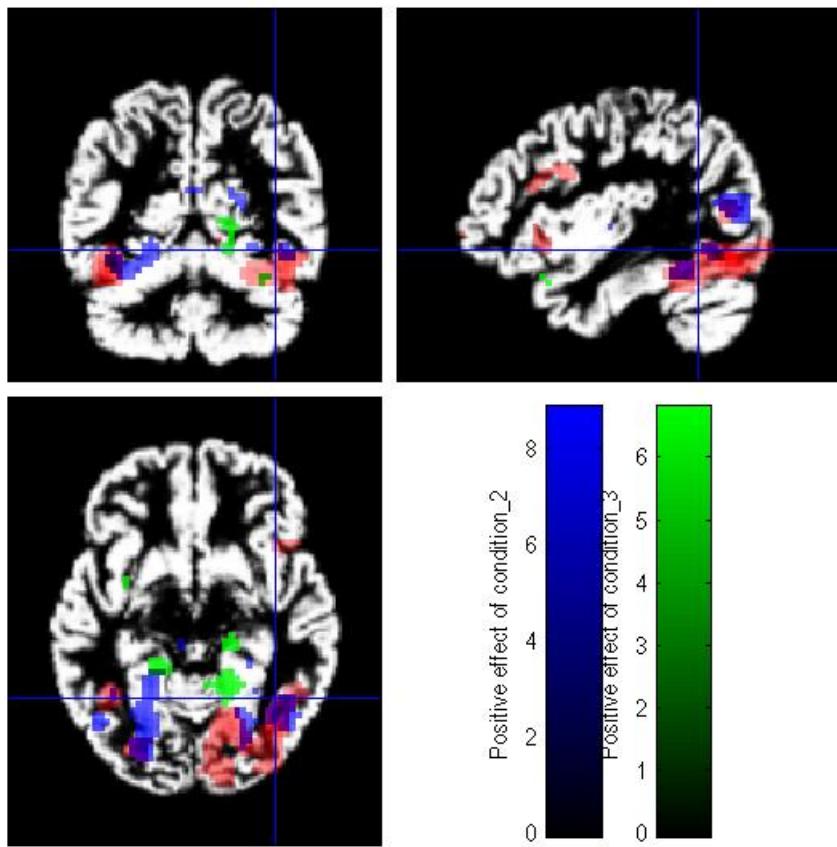


Figure 28 Results for one subject showing the hrf and derivatives.

A better model - 2nd level (group)

We can replicate the analysis done using the one sample t-test either by combining the beta parameter estimates or taking each parameter into an ANOVA. The issue here is that we cannot simply add the hrf, time and dispersion using a contrast because they reflect different properties of the response (see Pernet 2014 Front Neurosci. for how to combine them) – it would like adding percentage correct and reaction times together. Using an ANOVA model, we can however, look at the relative contribution of each parameter across all subjects.

3 contrast images per subject are thus taken to the 2nd-level. These are

- _ con 0003.img (canonical HRF, subject 1)
- _ con 0004.img (canonical HRF, subject 2)
- _ ...
- _ con 0014.img (canonical HRF, subject 12)
- _ con 0015.img (temporal derivative, subject 1)
- _ con 0016.img (temporal derivative, subject 2)
- _ ...
- _ con 0026.img (temporal derivative, subject 12)
- _ con 0027.img (dispersion derivative, subject 1)
- _ con 0028.img (dispersion derivative, subject 2)
- _ ...
- _ con 0038.img (dispersion derivative, subject 12)
- _ ...

Batch >> SPM >> Stats >> Factorial Design Specification

Select a new directory and change the design to Full factorial.

Under "Factor", type in "Basis" for Name and enter 3 under "Levels".

Highlight "Independence" and select "No". SPM will then take into account possible correlations between these repeated measures

Highlight "Cells", and create 2 new cells (3 cells in total).

For the 1st cell, set "Levels" to 1, and enter the canonical contrast images under scans (ie contrast images numbered 0003 to 0014).

For the 2nd cell, set "Levels" to 2, and enter the temporal derivative contrast images under scans (ie contrast images numbered 0015 to 0026).

For the 3rd cell, set "Levels" to 3, and enter the dispersion derivative contrast images under scans (ie contrast images numbered 0027 to 0038).

Batch >> SPM >> Stats >> Model estimation

Use the dependency to select the SPM.mat

Batch >> SPM >> Stats >> Contrast manager

Use the dependency to select the SPM.mat from estimation.

Create a new F contrast (name 'all') with weights eye(3).

Results

Use Display (choose an anatomical in spm12/canonical) to superimpose the results from the 2 different analyses: hrf only results and informed basis set (the last contrast created). We can see clearly the overall activation pattern is much wider – indicating that many voxels across subjects and earlier/later and/or wider/narrower responses.



Figure 29 Comparison of the simple and complex models.

One issue, is that some voxels can be noisy and it thus advisable to only consider voxels where there is some activation – to be understood as masking by a contrast $T [1 0 0]$ (hrf only) and use a lenient threshold like $p=0.05$ uncorrected. Click on **Results >> SPM.mat >> Define New Contrast >> title HRF and weight [1 0 0] >> Done**. Then evaluate. Redo the same to **create the F contrasts [0 1 0] (time derive) and [0 0 1] (dispersion)**.

Again use Display or CheckReg to superimpose the 3 contrasts – but mask the F contrasts of the derivatives by the T contrast of hrf. Finally surf to a region showing some differences and click on **Plot >> Contrast Estimates and 90% CI >> All**

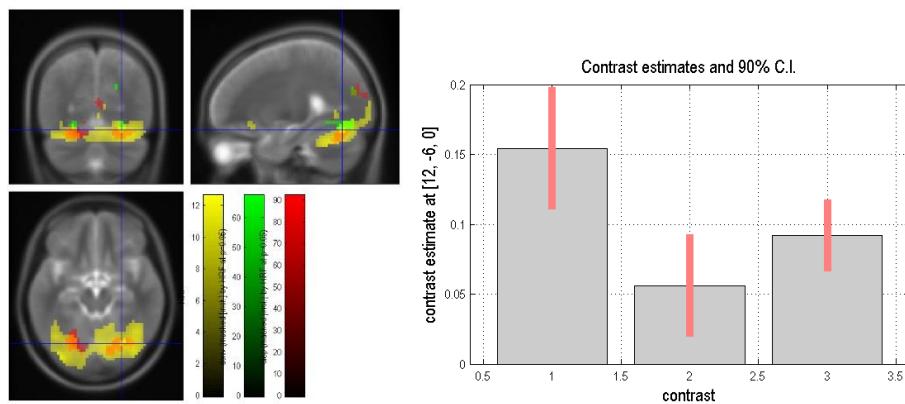


Figure 30 Results for the group showing the hrf and derivatives.