ANALYSIS OF FUNCTIONAL MAGNETIC RESONANCE IMAGING DATA USING SPM2:

MODELLING AND RESULTS ASSESSMENT

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ACKNOWLEDGEMENTS

Information contained herein has been compiled from my own SPM2 experience at Toronto Western Research Institute, that of others in the Functional Imaging Research and Evaluation (FIRE) group at the University Health Network, the SPM email list (http://www.fil.ion.ucl.ac.uk/spm/) and helpful websites (such as that of Kalina Christoff, http://www-psych.stanford.edu/~kalina/SPM99). Also, thanks to our over-worked but ever-helpful physicist, Adrian Crawley, for all his help.

FIRST LEVEL SPM MODEL ESTIMATION (FIXED EFFECTS; BLOCK / EVENT-RELATED)

17. Timing files for efMRI

- Before estimating your models, create files listing event onsets in Excel (save in a tab delimited format), Notepad or using the "cat" function in a UNIX terminal
- Create a timing file for each condition for each subject. Place these in the each subject's directory
- List all event onsets in one column
- Unlike SPM99, these onsets can now be in either **scans** (i.e., volume acquisition; so if the TR is 2 seconds, every 2 seconds represents the onset of a new scan), with zero seconds being scan 0, or in **seconds**.
- Your first few scans may have already been dropped from you set of scans before you started preprocessing (to allow for scanner equilibrium). If this is the case, you should adjust your timing files accordingly (e.g., if you dropped 3 scans what was your fourth scan was preprocessed as your first scan) scan. You can check if they have been dropped by comparing the number of swauf*.img files you have in each subject directory to the number of TRs you collected during scanning.

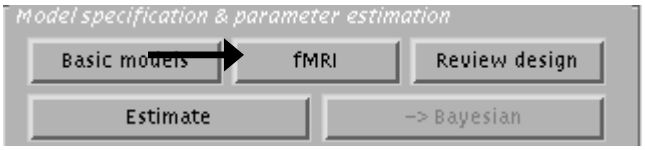
18. Fixed effects, event-related model for an individual subject

In this example, we are modelling 3 conditions: specific autobiographical memories (amsp), sentence completion (sent) and size discrimination (size)

- Files needed: scans (**swauf*.img**); timing files (***.txt**)
- Make sure your working directory is the subject's directory (result files will be written here). If it is, change your working directory selecting **Utilities** (from the main menu), **CD**

Step 1: Specify Design

- Select **fMRI** from the main menu



- Specify design or data? Select **design**
- Interscan Interval: Enter TR in secs, e.g., ***2***
- Scans per session: ***242*** *(Note: enter a value for each session/subject being entered into the analysis; you will then be prompted to enter information for this number of sessions; e.g., for three subjects enter **242 242 242**)*
  NB: This is how you specify how many subjects you are modeling
- Specify design in: **scans** or **seconds** (Select option that corresponds to your timefiles)
- Hemodynamic basis function: **hrf**
- Model interactions (Volterra): **No**

Session 1

- Enter number of conditions (trials): ***3***

- Are the conditions replicated? **Y**
  (Note: This question will only come up if you have more than one run for the subject you are analyzing. Select N if for this subject there are different conditions across runs)
- name for condition/trial 1?: ***amsp*** *(i.e., specific AMs)*
  name for condition/trial 2?: ***sent*** *(i.e., sentence completion)*
  name for condirion/trial3?: ***size*** *(i.e., size discrimination)*

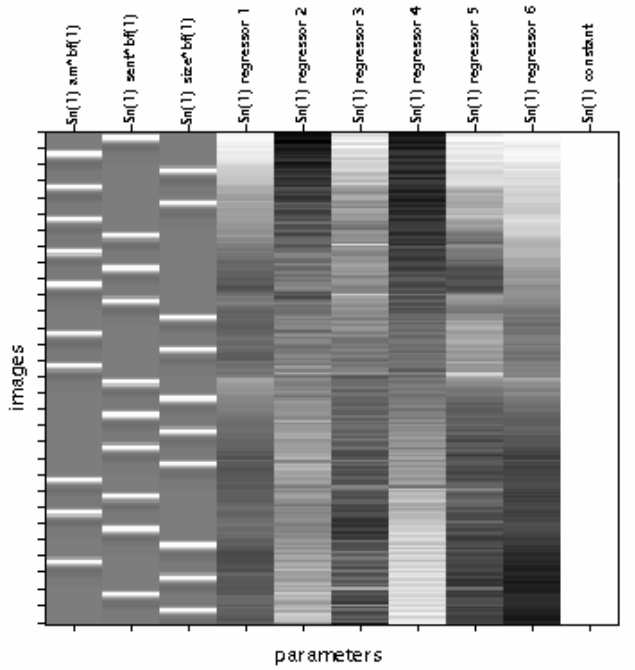
- Vector of onsets (scans) amsp**:** Type in onsets for amsp (condition 1), or if you have a timing file, right click on area outside of the entry box, select "**load text file**" from menu, and select the appropriate **timing textfile**
- Duration[s]: For block designs, enter duration of each block; for events, enter 0
- Parametric modulation: none / time / other? Select **none**
  (unless performing a parametric modulation; see section 19)

- Vector of onsets (scans) sent**:** **load textfile** of timings for sent (condition 2)
- Duration[s]: Enter durations
- Parametric modulation: **None**

- Vector of onsets (scans) size**:** **load textfile** of timings for size (condition 3)
- Duration[s]: Enter durations
- Parametric modulation: **None**

- User specified regressors: **Select 1**, then load **realign_param.txt** file
  *Allows you to add motion parameters into the model as regressors; if not select **0***
  ***Note if **Realign and Unwarp** has been used at preprocessing, you may not want to include motion parameters as regressors*

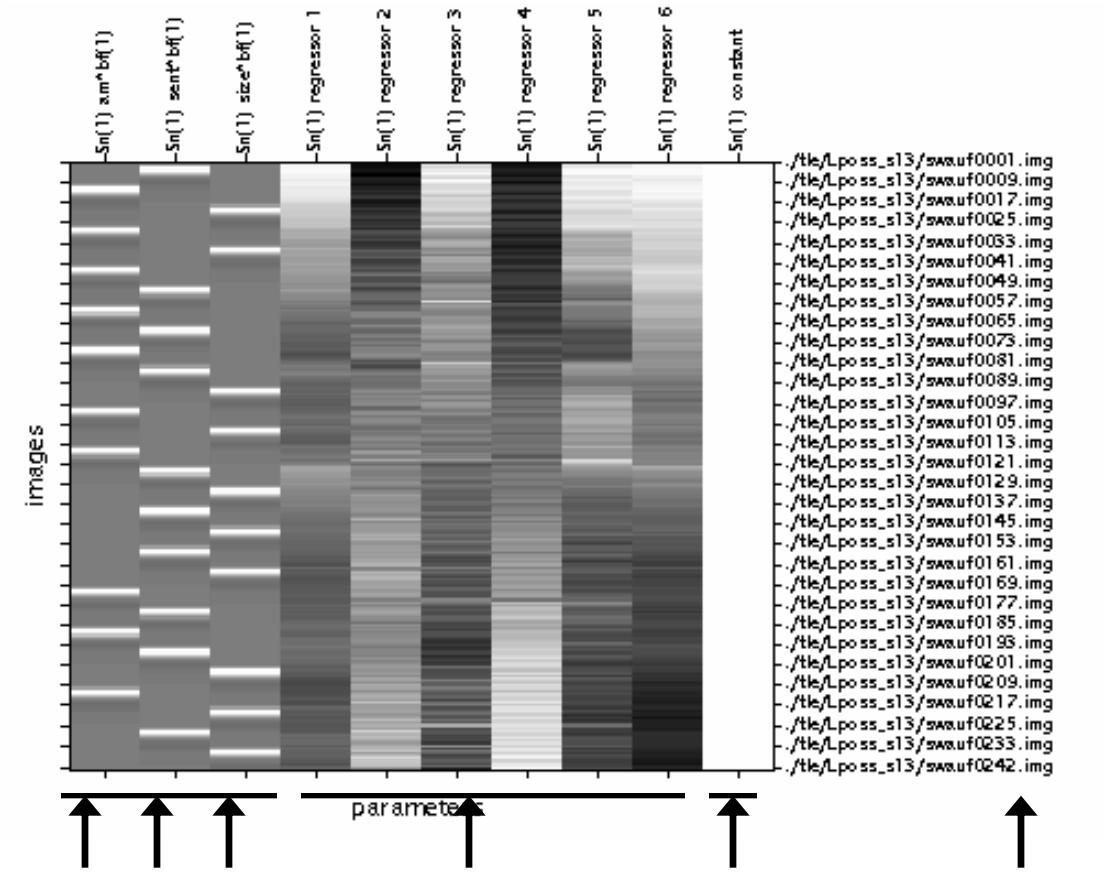
- **Outputs**: **SPM.mat, SPM_fMRIDesMtx.mat** (contains design parameters – onsets, number of conditions, names of conditions, etc; No data/scans assigned; this can be applied to another subject, select to only estimate a specified model and use this file)



Step 2: Specify Data

- Select **fMRI** from the main menu

- Specify design or data? Select **data**
- Select appropriate **SPM.mat**
- Select scans for session 1: Select **swauf*.img**
- Remove global effects? Select **None**
- *If you select 'scale' the value in each voxels for a given swauf*.img will be divided by the global brain mean value for this swauf*.img.. Global scaling can beneficial, since it reduces intersubject variability and improves the sensitivity at the group level of analysis. However, it relies on the assumption that the global brain mean does not correlate with the task. If this assumption is violated, applying global scaling can cause large areas of the brain to appear as activated, in some case almost entire slices.* ***Global scaling should be applied only with extreme caution****.*
- Temporal autocorrelation options: High-pass filter? **Specify** and enter cutoff values.
- *Do not accept the default (unlike SPM99, this is a standard default, not one calculated on the basis of your data). To determine values for each subject using the script* ***SPMhpcutoff;*** *This script (written by A.P. Crawley; email donnad@psych.utoronto.ca for code) uses your timefiles to calculate values to be entered*
  High-pass filtering filters out the low-frequency components of your signal. High-pass filtering is usually beneficial, since the low-frequency components in the fMRI signal contain much more noise than the high-frequency components.
  Note about Low-Pass Filtering*: Unlike SPM99, you will not have the option to select a low-pass filter as noise has been whitened by SPM2. Note though this may cause some differences between SPM99 & SPM2, as low-pass filtering in the former decreases number of df whereas the automatic correction by SPM2 does not result in a change in df (thus, at the same p-value with more df in SPM2, your activations may be more extensive).*
- Correct for serial correlations?: **None**
  This has the same theoretical goal as temporal smoothing, but also makes statistical inferences overly conservative. Only choose if you haven't specified a low-pass filter.
- **Outputs**: **Y.mad** (file containing the raw data, directly entered from the swauf*.img files; contains values for only those voxels that survived the upper F threshold during the analysis**;** **xCon.mat** (file containing info you will enter (next) about the contrasts)



These 3 columns represent the 3 modeled conditions (amsp, sent, size)

These 6 columns represent the 6 realignment parameters entered as a user-specified regressor

This final blank column represents the "contrast" or implicit baseline & includes all events which have not been explicitly modeled.

All the scans for the subject (note, this was not present in the design matrix after Step 1)

Step 3: Statistical Estimation

- Select **Estimate** from the main menu

- Statistical estimation should begin

FIRST LEVEL SPM MODEL ESTIMATION (FIXED EFFECTS, EVENT-RELATED)

19. Parametric Modulation Analysis

Note that this is basically the same as the standard fixed effects analysis protocol, except for the parametric modulation step when specifying the design (Step 1). In this example, we are modeling specific AMs and entering detail as a covariate of interest in our parametric modulation, and also recency as a nuisance covariate that we want to take into account.

- For each covariate, create a textfile for each subject in each condition that contains a column of the parameters for each event in that condition (e.g., ***detail.txt, recency.txt***). Save in the subject's directory.
- Create a directory for this analysis (e.g., ***PM_Detail_Recency***)
- Change directory so this is your PWD (**Utilities, CD**)

Step 1: Specify Design

- Select **fMRI** from the main menu

- Specify design or data? Select **design**
- Interscan Interval: Enter TR in secs, e.g., ***2***
- Scans per session: ***242*** *(Note: enter a value for each session/subject being entered into the analysis; you will then be prompted to enter information for this number of sessions; e.g., for three subjects enter **242 242 242**)*
  NB: This is how you specify how many subjects you are modeling
- Specify design in: **scans** or **seconds** (Select option that corresponds to your timefiles)
- Hemodynamic basis function: **hrf**
- Model interactions (Volterra): **No**

Session 1

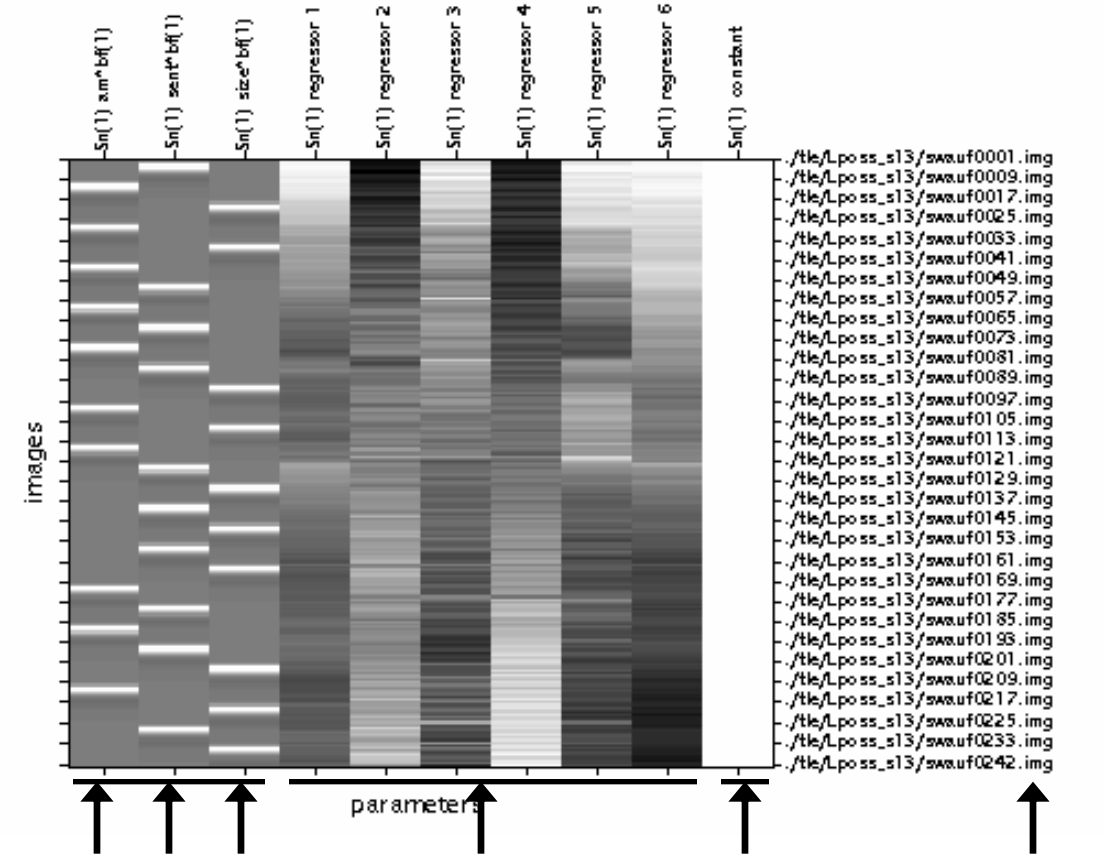
- Enter number of conditions (trials): ***1***
- Are the conditions replicated? **Y**
  (Note: This question will only come up if you have more than one run for the subject you are analyzing. Select N if for this subject there are different conditions across runs)
- name for condition/trial 1?: ***amsp*** *(i.e., specific AMs)*
- Vector of onsets (scans) amsp**:** Type in onsets for amsp (condition 1), or if you have a timing file, right click on area outside of the entry box, select "**load text file**" from menu, and select the appropriate **timing textfile**
- Duration[s]: For block designs, enter ***duration*** of each block; for events, enter ***0***

Parametric modulation step:

- Parametric modulation: Select **other**
- Expansion: linear / exponen / polynom: Select the function you wish to test, e.g., **Linear**
- Name of parameter: ***Detail_recency***
- Which trials? 1: Enter ***1 1***

*(If you have 1 parameter, **enter 1** only once. By **entering 1 twice**, you will be prompted twice to enter a set of parameters for condition 1. If, for example, you have modeled 2 conditions and have 3 parameters, enter **1 1 1 2 2 2**)*

- [10] Parameters for amsp: Using right click, **Load text file,** load textfile for first parameter
  (The "10" is prompting you to enter a number of parameters same as number of events or blocks in that condition)
- [10] Parameters for amsp: Using right click, **Load text file,** load textfile for second parameter
- User specified regressors: **Select 1**, then load **realign_param.txt** file
  Allows you to add motion parameters into the model as regressors; if not select 0
- **Outputs**: **SPM.mat, SPM_fMRIDesMtx.mat** (contains design parameters – onsets, number of conditions, names of conditions, etc; No data/scans assigned; this can be applied to another subject, select to only estimate a specified model and use this file)



Column 1 represents the condition modeled (amsp), and columns 2 & 3 represent the parametric covariates (detail & recency)

These 6 columns represent the 6 realignment parameters entered as a user-specified regressor

This final blank column represents the "contrast" or implicit baseline & includes all events which have not been explicitly modeled.

All the scans for the subject (note, this was not present in the design matrix after Step 1

Note: Specifying contrasts in this instance is different; please read Section 21.

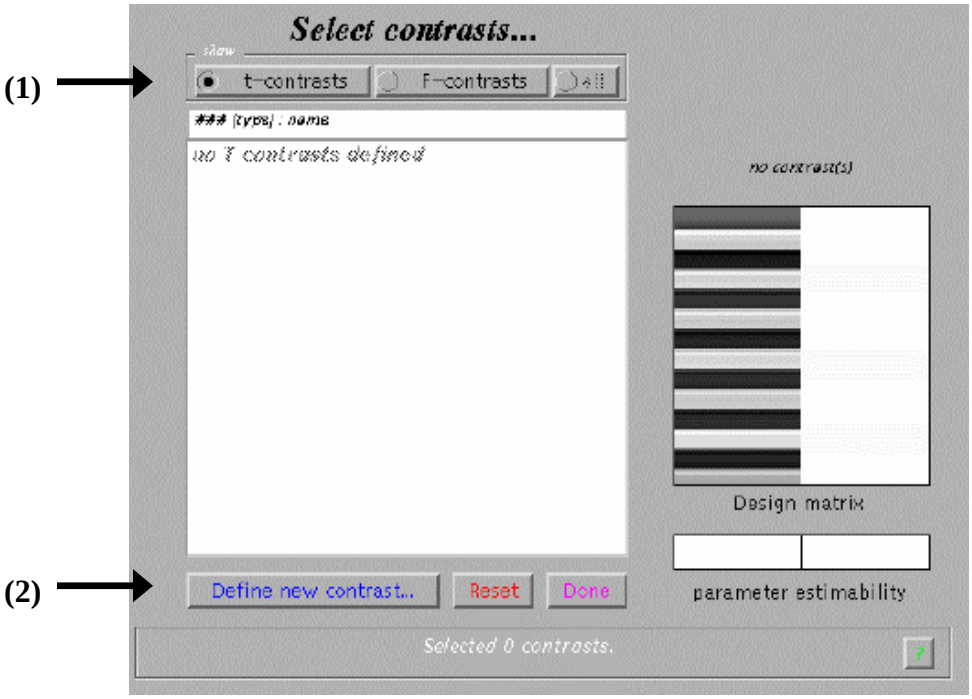
Steps 2 & 3 - Specify Data & Estimate: See Section 18

RESULTS: DEFINING CONTRASTS

20. Results: Defining contrasts for fixed effects models

- Select **Results** from main menu

- Select **SPM.mat** file (for an individual subject, or from the group analysis)



- In SPM contrast manager: Select **t-contrasts (1)**
  Select **Define new contrast (2)**
- Type in name of contrast, then the contrast values, e.g. ***1 1 -1 -1 0 0 0 0 0 0 1 1 -1 -1 0 0 0 0 0 0***
- *Determining your contrasts: note that each column represents a condition for each subject (in the order you specified them in the model), followed by the next condition for that subject, followed by the six motion parameters*
  e.g., S1cond1, S1cond2, S1cond3, S1cond4, S1motion1, S1motion2, S1motion3, S1motion4 S1motion5, S1motion6, S2cond1, S2cond2, S2cond3, S2cond4, S2motion1, S2motion2, S2motion3, S2motion4 S2motion5, S2motion6 …etc
  Thus, to contrast cond1 + cond2 against cond3 + cond 4, enter the following:
  1 1 -1 -1 0 0 0 0 0 0 …. for all subjects (i.e., 1 1 -1 -1 0 0 0 0 0 0 1 1 -1 -1 0 0 0 0 0 0 etc)
  Note, zeros are added for motion parameters; they are considered in the model in that other variables are othoganilized to these.
- Click **Submit**
- Check the design matrix on the right, to see if the contrast is what you want. If so, click **OK**
- The contrast will appear in the contrast manager window.

- Select the contrast you want to display, and click **Done**.
  (if more than one contrast is selected, the conjunction between them will be computed and displayed)
- Mask with other contrast(s): **No**
  Note, if you select Yes, you will prompted to select another contrast from the same SPM.mat file for inclusive masking (displays everything in contrast A plus voxels activated by contrast B and not activated by contrast A) or exclusive masking (displays voxels activated by contrast A that are also activated by contrast B).
- P-value adjustment: **FWE** (Apply family-wise error correction for multiple comparisons) or **None** (uncorrected)
- Threshold {T or p value}: Enter desired ***p-value***
- Extent threshold {voxels}: Enter the min number of voxels that a cluster should have in order to be displayed. For the least conservative estimate, enter 0.
- **Outputs**: **con*.img** (i.e., an image for the contrast) and **spmT*.img** (i.e., an image coding every voxel with its t-value) is created for each contrast. The con*.img can be entered in a random effects analysis.

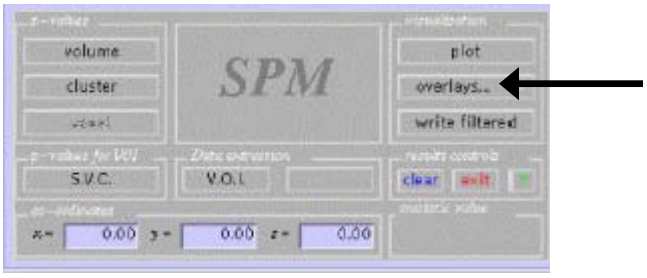
21. Results: Defining contrasts for parametric modulation models

- Select **Results** from main menu
- Select **SPM.mat** file (for an individual subject, or from the group analysis)
- In SPM contrast manager: Select **t-contrasts**
- Select **Define new contrast**
- Type in name of contrast, then the contrast values, e.g. ***1 1 -1 -1 0 0 0 0 0 0 1 1 -1 -1 0 0 0 0 0 0***
- *Determining your contrasts: note that in this instance, the first column for each subject represents the effect of the modeled condition, followed by the parametric effect of parameter 1 (e.g., detail), parameter 2 (e.g., recency), and the six motion parameters*
  e.g., S1cond1, S1detail, S1recency, S1motion1, S1motion2, S1motion3, S1motion4 S1motion5, S1motion6, S2cond1, S2detail, S2recency, S2motion1, S2motion2, S2motion3, S2motion4 S2motion5, S2motion6 …etc
  Thus, to look at the positive parametric effect of parameter 1 (orthogonal to parameter 2), enter the following:
  0 1 0 0 0 0 0 0 0 …. for all subjects.
  To look at the negative parametric effect of parameter 1, enter: 0 -1 0 0 0 0 0 0 etc
  To look at the positive parametric effect of parameter 2, enter: 0 0 1 0 0 0 0 0 0 etc
- Click **Submit**
- Check the design matrix on the right, to see if the contrast is what you want. If so, click **OK**
- The contrast will appear in the contrast manager window.
- Select the contrast you want to display, and click **Done**.
- Mask with other contrast(s): **No**
- P-value adjustment: **FWE** (Apply family-wise error correction for multiple comparisons) or **None** (uncorrected)
- Threshold {T or p value}: Enter desired p-value
- Extent threshold {voxels}: Enter the min number of voxels that a cluster should have in order to be displayed. For the least conservative estimate, enter 0.
- **Outputs**: **con*.img** (i.e., an image for the contrast) and **spmT*.img** (i.e., an image coding every voxel with its t-value) is created for each contrast. The con*.img can be entered in a random effects analysis.

SPM RESULTS: OVERLAYS

22. Results: Overlaying on anatomical scans

- Once you select a contrast to display, the results will appear on a glass brain.
- To overlay these activations on a anatomical scan: Select **Overlays, Sections**

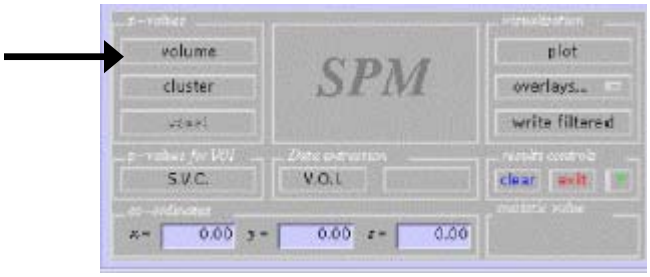


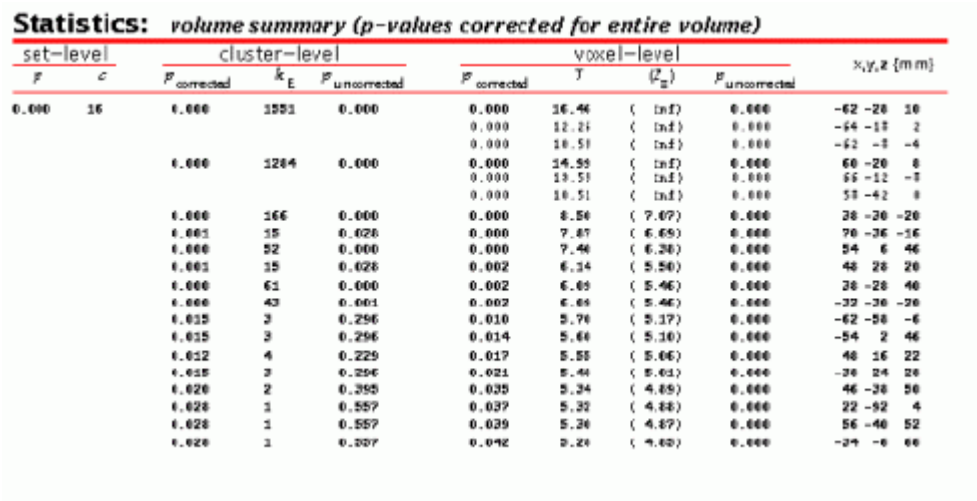
- Select the anatomical image, e.g., **single_subj_T1.img** (located users/crawley/spm99/canonical directory)
- Image will be displayed
- To remove crosshairs: in the matlab window, type the following command line: ***spm_orthviews xhairs off*** and ***spm_orthviews xhairs on*** to reinstate them
- To save the images: either use the Print Screen function on your computer and paste it into a picture-editing programme; or before selecting the contrast, change the defaults for Printing (select Defaults from main menu; defaults for printing; print to file; other format; tif)
- Additionally, you can render the image on a 3D brain by selecting: **Overlays, Render**

SPM RESULTS: CO-ORDINATES

23. Results: Extracting co-ordinates to a textfile

- To display a table of local maxima below the glass brain, select **Volume** from the main menu





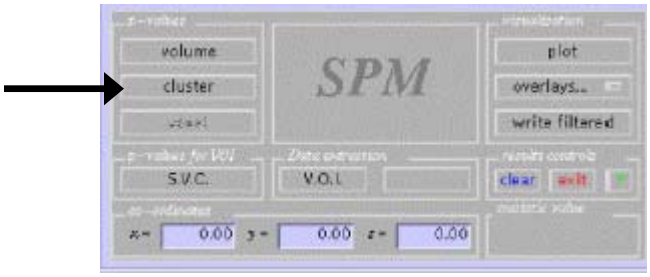
- By clicking on co-ordinate in the table, the pointer on the glass brain will move to coordinate
- By default, the local maxima listed in the table are 8mm apart. To change this, and the number of local maxima listed for each cluster, type the following command line in matlab:
  d=5 *(d being distance between each local maxima)*
  m=6 *(m being the number of maxima listed for each cluster)*
  title='Extended list of local maxima'
  tabData=spm_list('list', SPM, VOL, d, m, title, hReg)
- To save table of co-ordinates and z-scores etc: print into matlab (right click on table, select **print**).
- Once in matlab, you can copy this to Notepad (if working in windows) or to a terminal window where you have begun a "cat" process (to create a txt file).
- Note co-ordinates are MNI and must be converted to TAL before localization.
- First, open your txt file in Excel, copy the list of co-ordinates to another Excel spreadsheet and make sure everything looks okay.

24. Results: Converting co-ordinates from MNI to TAL space

- Copy just the list of co-ordinates to another spreadsheet. Save as a **tab-delimited** textfile, e.g., ***contrastA-B_MNI.txt***.
- Open textfile of MNI co-ordinates in a terminal window (i.e. view file using "more" command)
- To convert co-ordinates, a programme called **mni2tal** is used
  Download from: http://www.mrc-cbu.cam.ac.uk/Imaging/mnispace.html
- In the Matlab window type,
  mni2tal([x y z
  x y z
  x y z])
  Note, x y z represents the MNI co-ordinates you should copy and paste over from the textfile open in your terminal window.
- Save output (TAL co-ordinates) as a textfile by pasting into the terminal window where you have started a "cat" process (to create a textfile)
- To make this file compatible for programmes such as **Talairach Daemon** *(see Section 33)*, open the textfile in Excel, make sure negative signs are in appropriate columns (sometimes they are attached to the end of the value in front); reduce to **no decimal places**; save as a **tab-delimited** textfile

25. Results: Listing local maxima for a cluster

- To display a table of local maxima for a specified cluster, place pointer on cluster on glass brain.
- Select **Cluster** from the main menu



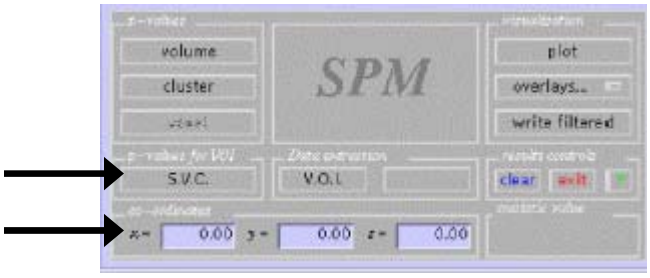
- Follow guidelines above to print table to a textfile.

SPM RESULTS: SMALL VOLUME CORRECTIONS

26. Results: Small Volume Corrections

Corrects statistics for an ROI rather than the whole brain volume.

- In order to list a table of statistics where p-values are corrected for a small volume rather than the whole brain, place pointer on glass brain in area of interest
- Place pointer at appropriate voxel on glass brain (or enter co-ordinates)
- Select S.V.C.



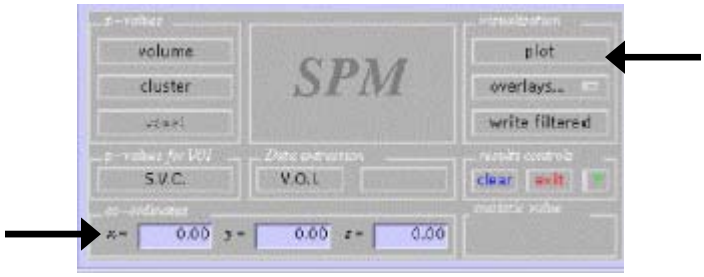
- Search volume: Sphere *(centered on selected voxel)*, box *(at selected voxel)*, nearest cluster, image
- If you selected **Sphere**, radius of spherical ROI (mm): Enter ***radius*** in mm
- If you selected **Box**, box dimensions [k l m] (mm): Enter ***box dimensions***
- If you selected **nearest cluster**, this will be computed
- If you selected **image**, choose a mask image (e.g., created in MARINA): **mask*.img**
- Table will be printed, listing local maxima at 4mm apart.
- To save as a textfile, follow guidelines in Section 23.

SPM RESULTS: PLOTS

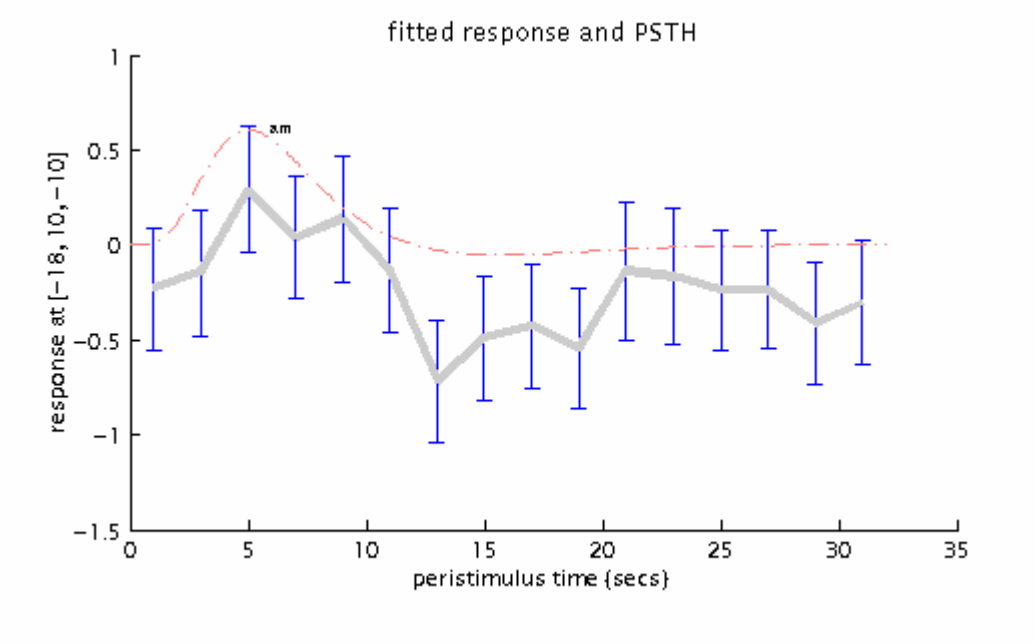
27. Results: Plotting Timecourses for Peak Voxel

Note: this can only be done with fixed effects analysis as these contain the actual data (for RFX we input con.imgs rather than swauf*.imgs). The example here is a group fixed-effects analysis, thus you are asked if you want to average over sessions.*

- Place pointer at appropriate voxel on glass brain (or enter co-ordinates)
- To plot the mean signal over the timecourse of the event (PSTH), select **plot**



- Select **Event/epoch-related responses**
- Average over sessions? ***Y*** *(to include all subjects; to select certain sessions, enter* ***N)***
- Which trial or conditions?: ***amsp? sent? size?*** Specify the condition you wish to examine
  Note: at present this allows you to plot only one condition unlike SPM99.
- Plot in terms of: Select **Fitted response and PSTH**
- You will get the graph below

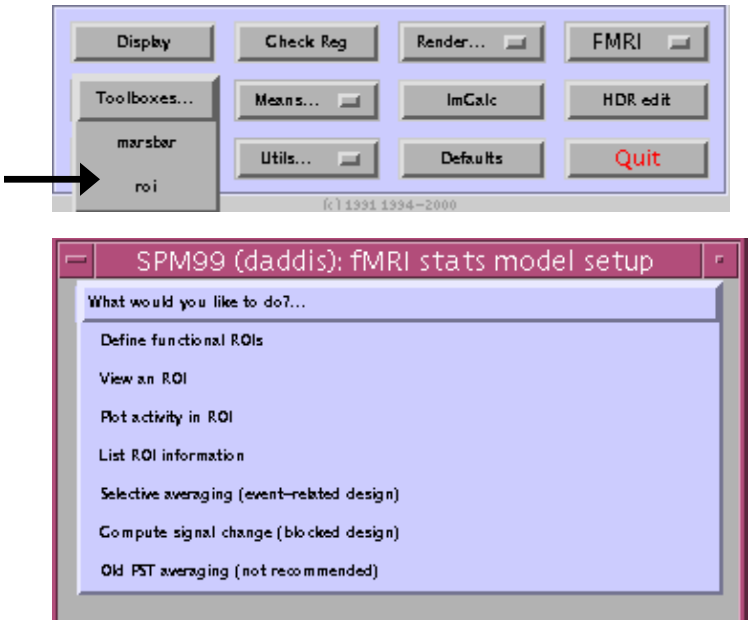


- Note, if you want to change the x-axis (i.e., the amount of time it covers), use the attributes button, and enter the limits for the x-axis (e.g., ***-4 20***)

28. Results: Plotting Timecourses for an ROI

I***Note: From SPM99 Manual. As yet, we haven't tried this toolbox with SPM2. Please check back****

- Install ROI toolbox (download from http://sourceforge.net/projects/spm-toolbox and save in your spm99/toolbox directory; note it must be unzipped and un-tarred)
- To plot the mean signal over the timecourse of the event averaged across an ROI, select **Toolboxes, ROI** from the main menu



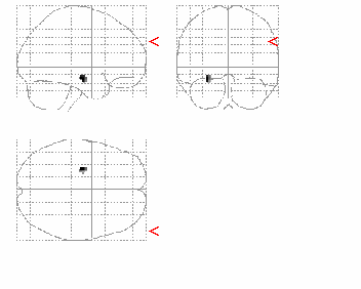
- Select **Define functional ROIs**
- Enter the ***radius*** of ROIs in mm *(i.e., radius of a sphere centred on each peak voxel across the brain)*
- Select **SPM.mat**
- Select the relevant contrast, threshold etc. In the Matlab window, ROIs will be calculated
- Outputs: **con*_clust#.img, con*_clust#.hdr, con*_clust#.tal**; *(Note * is the number assigned to this contrast by SPM when you originally defined this contrast; # is the number of that particular cluster; files will be created for each cluster in the brain)* **con*_roi.mat**

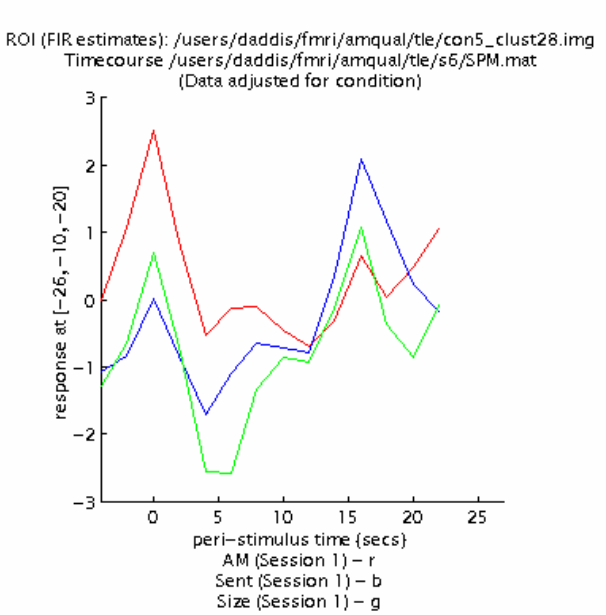
- Select **Toolboxes, ROI** from the main menu
- Select **View an ROI**
- Select anatomical image over which to superimpose cluster, e.g., **a.img**
- Select **con*_roi.mat**
- All clusters are listed according to their number and peak voxel in the SPM graphics window. Note down the number of each cluster you are interested in (this denotes the relevant con*_clust#.img)

To plot an ROI for one subject:

- Select **Toolboxes, ROI** from the main menu
- Select **Selective averaging**
- Select cluster image **con*_clust#.img** *(e.g., con5_clust28.img)*
- Select **SPM.mat**

- Adjustment: **by condition**
- **Select subject (sessions) and trials**
- y values for each voxel of the cluster are computed in matlab
- Displays the cluster on a glass brain, and a timecourse:





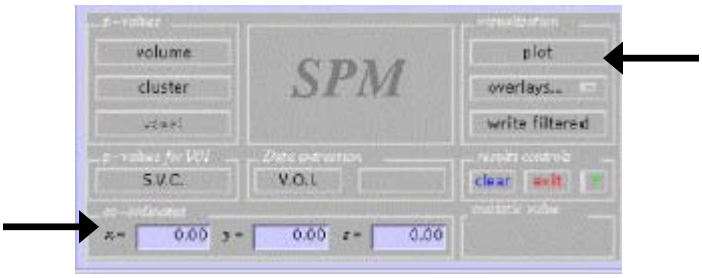
**To plot an ROI averaged across multiple subjects:

- Select **Toolboxes, ROI** from the main menu
- Select **Plot activity**
- Select cluster image **con*_clust#.img** *(e.g., con5_clust28.img)*
- Select **SPM.mat**
- Average across subjects? **Yes**
- y values for each voxel of the cluster are computed in matlab

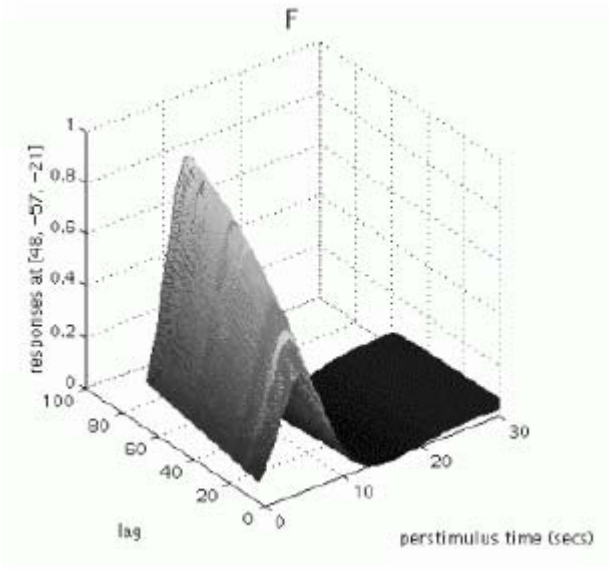
29. Results: 3D plots of parametric effects

Note: this option is appropriate if you have one parameter in your parametric modulation; when you have more than one, both effects will be plotted on the same 3D plot. Additionally, this feature can only plot the parametric effect of one subject per plot (i.e., you can't plot the average effect; see Section 28).

- Place pointer at appropriate voxel on glass brain (or enter co-ordinates)
- To plot the parametric effect from an individual subject, select **<u>plot</u>**



- Select **<u>Plots of Parametric Responses</u>**
- Which session?: Enter ***subject number***
- Which effect?: Select desired ***effect*** from choices given



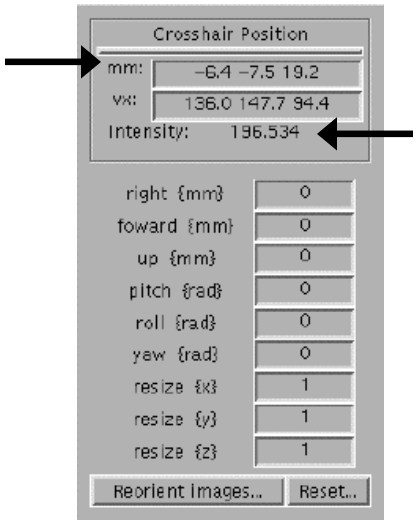
30. Results: Plots of group parametric effects

This requires use of a script written by A.P. Crawley (email donnad@psych.utoronto.ca for code) and allows you to plot the group parametric effect of the covariate of interest, orthogonal to nuisance covariates. First, however, it requires you define an additional contrast for the effect of the modelled condition.

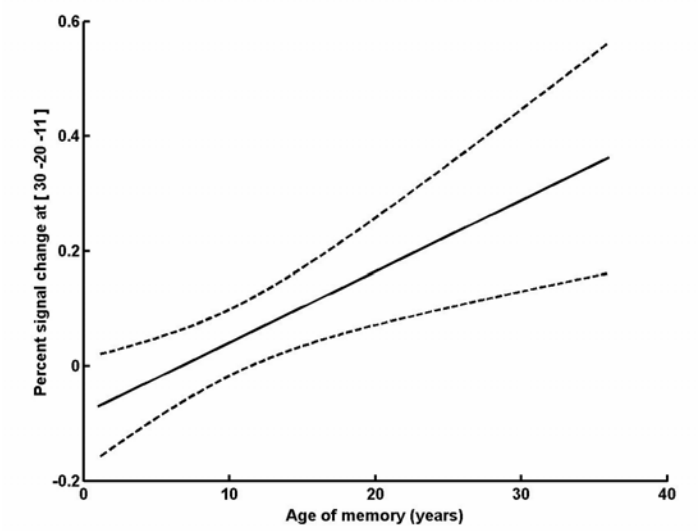
- Select **Results** from main menu
- Select **SPM.mat** file (e.g., from the group parametric modulation analysis)
- In SPM contrast manager: Select **t-contrasts**
- Select **Define new contrast**
- Type in name of contrast, then the contrast values, e.g. ***1 0 0 0 0 0 0 0 0***
- *Determining your contrasts: Remember, the first column for each subject represents the effect of the modeled condition, followed by the parametric effect of parameter 1 (e.g., detail), parameter 2 (e.g., recency), and the six motion parameters*
  e.g., S1cond1, S1detail, S1recency, S1motion1, S1motion2, S1motion3, S1motion4 S1motion5, S1motion6, S2cond1, S2detail, S2recency, S2motion1, S2motion2, S2motion3, S2motion4 S2motion5, S2motion6 …etc
  Thus, to create a contrast for the modeled condition, enter the following:
  1 0 0 0 0 0 0 0 0 …. for all subjects.
- Click **Submit**
- Check the design matrix on the right, to see if the contrast is what you want. If so, click **OK**
- The contrast will appear in the contrast manager window.
- Select the contrast you want to display, and click **Done**.
- Mask with other contrast(s): **No**
- Corrected height threshold: **Yes** (corrects for multiple comparisons) or **No** (uncorrected)
- Threshold {T or p value}: Enter desired ***p-value*** *(not overly important in this case)*
- Extent threshold {voxels}: Enter the min number of voxels that a cluster should have in order to be displayed. For the least conservative estimate, enter ***0***.

Obtaining values for pm_plot script

- Select **Display** from main menu
- Select the **con*.img** for the effect of the modeled condition (the contrast you just specified)
- Enter co-ordinates of voxel you wish to plot
- Note down the intensity value



- Repeat for the **con*.img** for the parameter of interest, and for the corresponding **spmT*.img**
- In a terminal window, type (name of script**)
- Enter these values into the script.



SECOND LEVEL SPM MODEL ESTIMATION (RANDOM EFFECTS)

31. Random effects model: One group

This analysis is second level as it takes the contrast images (con.img) created in your first analysis on each individual subject and runs a t-test on these.*

- Create a new results directory (e.g., ***RFX_am-con***)
- Decide which contrast **con*.img** files you need from each subject. Each is numbered according to the number that contrast was assigned by the contrast manager. If you're not sure, click Results, select the SPM.mat for that subject, and see which number each contrast has been assigned. If you entered all your contrasts in the same order for each subject when running your individuals analyses and there were no other con*.img files in their directories, then they should all have the same number.
- E.g., con009.img for each subject (e.g., am-con, the contrast between AM tasks and control tasks)

- Select **Basic Models** from the main menu

- Select design type: **One-sample t-test**
- Select images: Select the appropriate **con*.img** from each subject's directory
- Grand mean scaling?: **No**
- Explicitly mask images?: **No**
- Global Calculation?: **Omit**
- Estimate? **Now**

The estimation of this model is fairly fast, as you have inputted contrast images rather than actual data (i.e., swauf.img)*

32. Random effects model: Two groups (e.g., patients and controls)

- Select **Basic Models** from the main menu
- Select design type: **Two-sample t-test**
- Select images: Select the appropriate **con*.img** from directory of each Gp. 1 subject, then each Gp. 2 subject
- Groups: e.g., ***1 1 1 2 2 2***
  (Enter number for each subject in the order you selected the con.img files, denoting their group membership)*
- Threshold masking?: **None**
- Grand mean scaling?: **No**
- Explicitly mask images?: **No**
- Global Calculation?: **Omit**
- Estimate? **Now**

SPM RESULTS: RANDOM EFFECTS MODELS

33. Random effects model: One group

- Select **Results** from main menu
- Select **SPM.mat** file (for an individual subject, or from the group analysis)
- In SPM contrast manager: Select **t-contrasts**
- Select **Define new contrast**
- Type in name of contrast, then the contrast values, e.g. ***1***
- *Determining your contrasts: Note in this instance, you are testing whether the effect in the con*.img is different from zero. To test if it is greater than 0, simply enter 1 (or -1 to see if it is less than zero)*
- Click **Submit**
- Check the design matrix on the right, to see if the contrast is what you want. If so, click **OK**
- The contrast will appear in the contrast manager window.
- Select the contrast you want to display, and click **Done**.
- Mask with other contrast(s): **No**
- Corrected height threshold: **Yes** (corrects for multiple comparisons) or **No** (uncorrected)
- Threshold {T or p value}: Enter desired ***p-value***
- Extent threshold {voxels}: Enter the min number of voxels that a cluster should have in order to be displayed. For the least conservative estimate, enter ***0***.
- **Outputs**: **con*.img** (i.e., an image for the contrast) and **spmT*.img** (i.e., an image coding every voxel with its t-value) is created for each contrast. The con*.img can be entered in a random effects analysis.

34. Random effects model: Two groups

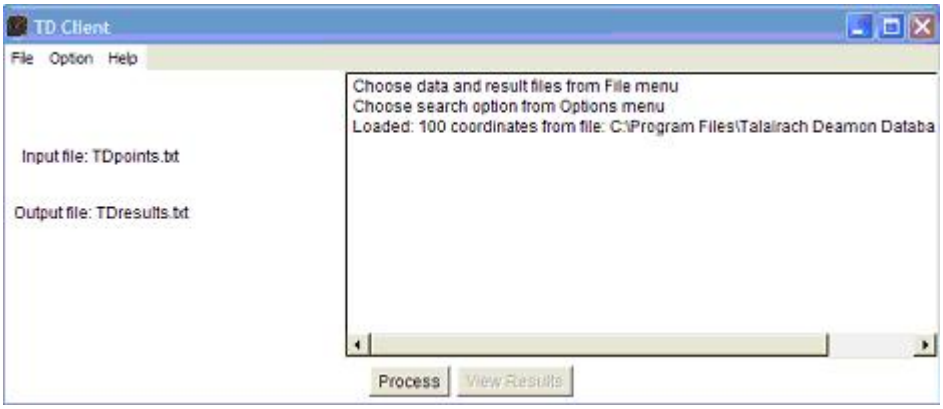
- Select **Results** from main menu
- Select **SPM.mat** file (for an individual subject, or from the group analysis)
- In SPM contrast manager: Select **t-contrasts**
- Select **Define new contrast**
- Type in name of contrast, then the contrast values, e.g. ***1 -1***
- *Determining your contrasts: Note that in this instance, you are testing whether the effect in the con*.img for patients is different from controls. To test if patients are greater than controls, enter 1 -1; to test if controls are greater than patients, enter -1 1*
- Click **Submit**
- Check the design matrix on the right, to see if the contrast is what you want. If so, click **OK**
- The contrast will appear in the contrast manager window.
- Select the contrast you want to display, and click **Done**.
- Mask with other contrast(s): **No**
- Corrected height threshold: **Yes** (corrects for multiple comparisons) or **No** (uncorrected)
- Threshold {T or p value}: Enter desired ***p-value***
- Extent threshold {voxels}: Enter the min number of voxels that a cluster should have in order to be displayed. For the least conservative estimate, enter ***0***.
- **Outputs**: **con*.img** (i.e., an image for the contrast) and **spmT*.img** (i.e., an image coding every voxel with its t-value) is created for each contrast. The con*.img can be entered in a random effects analysis.

LOCALISING MAXIMA: TALAIRACH DAEMON

35. Localising maxima: Talairach daemon

Download from: http://biad02.uthscsa.edu/RIC_WWW.data/Components/talairach/talairachdaemon.html
Note: the co-ordinates used at this stage should be converted to TAL using ***mni2tal***

- Co-ordinates: you should have created a textfile of Talairach co-ordinates, with all co-ordinates reduced to **zero decimal places**. If this file was created in Excel, it must have been saved as a **tab-delimited** text file (not a Unicode textfile)
- Run Talairach daemon database.



- To define the output you want, select **Option**.
- Choose either "assign a Talairach label" (default) or "search nearest gray matter"
- To load a file of co-ordinates, select **File**, **Choose data file**
- The number of co-ordinates successfully loaded will be printed in the window.
- If the number of co-ordinates it less than 100, you will be able to view the results in a window. If you have more than 100, you must specify an output file. Select **File**, **Choose Result file**
- Click **Process**
- Talairach labels for each co-ordinate will be assigned. Copy and paste into your spreadsheet of statistics outputted from SPM.

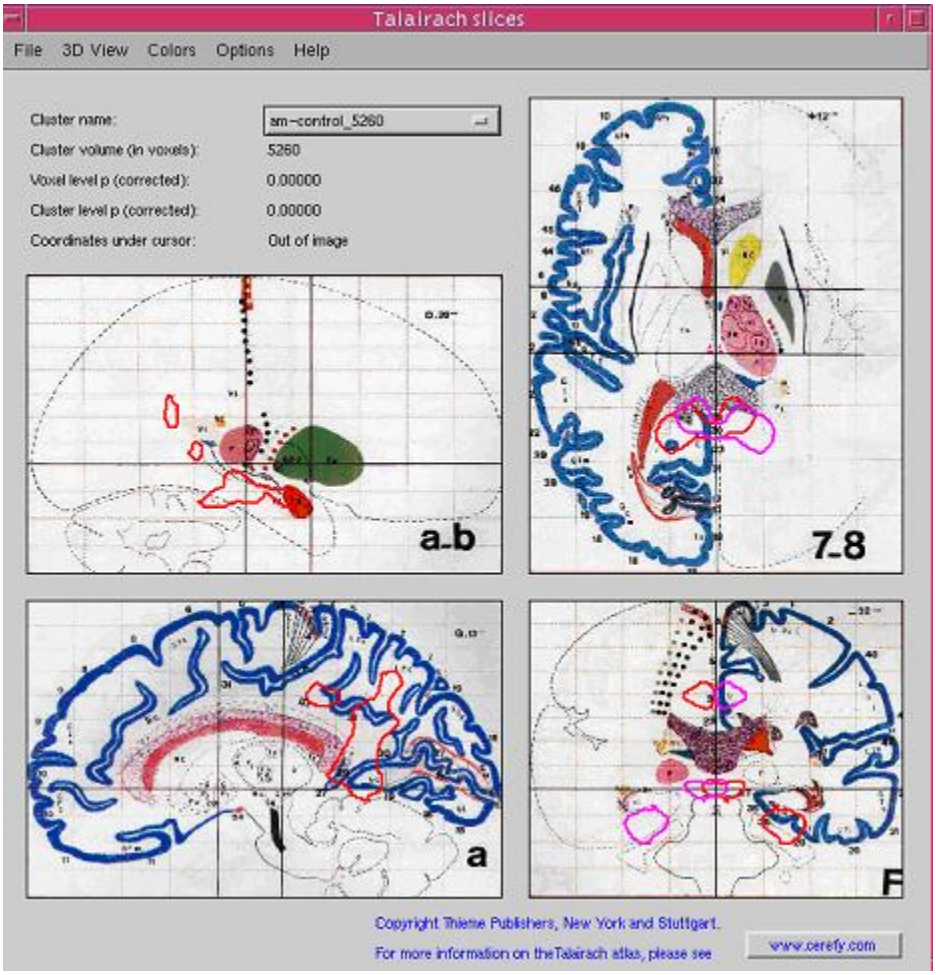
LOCALISING MAXIMA: TALAIRACH SPACE UTILITY (TSU)

36. Localising maxima: Talairach space utility

I***Note: From SPM99 Manual. As yet, we haven't tried this toolbox with SPM2. Please check back***

Download from: http://www.ihb.spb.ru/~pet_lab/TSU/TSUMain.html
Note this programme runs in the matlab window and uses some of the SPM windows.

- In matlab, open SPM in the desired working directory
- In the matlab window, type ***TSU***
- You will then be prompted through the SPM window to select the **SPM.mat** and **contrast** you wish to view results for.
- On TSU, all the significant clusters will be loaded, and you can view each overlayed on a Talairach atlas.
- Note, you can identify clusters by their cluster size (this is included in the table of local maxima from the SPM Results section)



APPENDIX: CODE

1. Changes to spm_graph.m

Purpose: to plot PTSH (timecourses) without fitted response or SE bars

- In section beginning at Line 459, titled ***case 'fitted response and PSTH'***, comment out the following lines:

```
errorbar(PST,PSTH,SEM,[':' COL(u)])
plot(x,Y,['-.' COL(u)])
```