28/11/2005 Jaclyn Billington

GUIDE TO SPM2 PRE-PROCESSING

This is a general guide for those carrying out SPM2 analysis and first level analysis (on the Cambridge WBIC network).

Red reflects filenames/ folder which change depending on you study/ series number etc.

Basics .... page 2

Preprocessing .... page 3

Getting Data from WBIC

3d -4d convert

Getting Structurals and Phasemaps

Using the VNC server

Tsdiffana

Slice timing .... page 5

Reorientation .... page 6

Realignment .... page 8

Unditortion .... page 8

Skull Strip .... page 9

Coregister .... page 10

Smoothing .... page 11

Obtaining Contrasts .... page 12

Batch Scripting Contrasts .... page 15

PUTTY

Download Putty

http://www.chiark.greenend.org.uk/~sgtatham/putty/

The address for the wbic is gate0.wbic.cam.ac.uk. This can be saved.

Click on putty icon

Highlight <gate0> and click on load

Log in <username>

Password <********>

Type <ssh psych6> press return

Type password – return

NAVIGATING THE SERVER USEFUL UNIX PROMPTS!

<pwd> Tells you where you are in the directory

<ls> Tells you what is in the directory

<…..*> * is a wild card, will take you to a directory that starts with what is typed before.

<cd ..> Go up on directory

<rm ……> Remove file, will ask you for confirmation

<rm –fr ……> Will remove all file without asking you for confirmation. CAREFUL!

<mkdir ….> makes folder

<cp –fr ….. /…/…/> copied all to directory you state

<chmod u+x ……> gives permissions to files stated

<gunzip ….> unzips file

<ls –a …..> searches for file with a particular name/prefix/suffix

Ctrl <c> Will get you out of trouble, bring prompt command back

Pressing "Tab" will fill in rest of directory name.

mv <old filename> <new filename> To copy a file to a new name.

http://www.sscnet.ucla.edu/ssc/software/unix.htm

GETTING DATA FROM THE WBIC and 4d to 3d convert

To download reconstructed data type
<pvconv.pl /pvCache/pvuser/nmr/Wwbic no*/ -series series_no –verbose>
or
<pvconv.pl /pvCache/pvuser/nmr/Wwbic no*/ -series series_no –recono 2 –verbose>
for those reconstructed more than once!

Series number is obtained from your scan log.

(Note: if the subject has been scanned more than once you will not be able to use the *wildcard. Have to use full subject name. Check out this in the nmr directory.
<ls -1 Wbic no*> while in the nmr directory. Will give you a .xxx extention after the wbic number that you have permission to)

If the subject has been scanned several times see which one you have access to
<ls -1 Wbic no*> while in the nmr directory. Will give you a .xxx as well as wbic number.

Converting 4d images to 3d images

Make a directory for time series 3dfiles <mkdir 3dfiles>
While in directory above 3dfiles
<ana4dto3d –m –v Wwbic no_series no.img
/home/username/study_dir/individual_dir/3dfiles
or
<ana4dto3d –m –v –d22 Wwbic no_series no.img /home/username/study_dir/
individual_dir /3dfiles
to delete you initial X number of files that correspond to time before stimuli onset (the –d command allows you to do this)

GETTING STURCTURALS

From home username <mkdir structurals>

Store all your structurals in one simple directory at same level as individual directories.

<pvconv.pl /pvCache/pvuser/nmr/Wwbic no*/ -series spgr series no –verbose

Again see you log to find out series number.

Can drag to computer via WinSCP.

COPYING PHASEMAPS TO YOUR DIRECTORY

Create a folder named phasemaps in the appropriate individual directory

<mkdir phasemaps>

Go to where the data is stored

<cd pvCache/pvuser/nmr/Wwbic no.*>

When in the folder copy your fieldmap series

<cp –fr 7 /home/username/study_dir/individual_dir /phasemaps

Wait a while

USING THE VNC VIEWER

Click on listen mode in the start up menu/ desktop

Open putty exe as before Log in with user name and PsychX

<vncserver –depth 24 –geometry 1200x900>

Will give you a session ID number "log file is /home/username/.vnc/psych6:3.log"

Make a note of the :3 number

<exit> <exit>

Open putty again: click on load gate0 then click on tunnels

Source port type 5903

Destination port <psych6:5903> click add

Click on "enableX11 for loading"

Click on Open

Log in to Psych6 etc as normal

Then double click on the VNC server icon in the tool bar

Type you session number (03) and password.

Ready to start spm2! At the matlab promt type >>spm2 and when you have finished type >>quit

When have finished using Matlab remember to exit

In UNIX type <vncserver –kill :session id

To check what your session id is type <ps aux | grep Xvnc>

OBTAINING TIME SERIES GRAPHS

You need to have downloaded Tsdiffana scripts for this and have them in a file (such as "my_matlab_scripts" in your home space. These can be downloaded from http://www.mrc-cbu.cam.ac.uk/Imaging/Common/diagnostics.shtml

Also be in the right file (3dfiles) before starting spm2 FOR EACH ONE

Should have the >> prompt

<addpath /home/username/my_matlab_scripts>

<tsdiffana>

Select the appropriate image i.e. your Wwbic no.img EPI series files

Write difference images? Click no

Click on the SPM print option at top of screen/ right click on the page to save (and to save anything else you do in future.

NOTE: CBU default is slice timing first. Arguments to say that realign first is better with linear acquisition (1,2,3,4...) and slice timing better with interleaved acquisition (1,3,5....)

SLICETIMING

Click on fMRI option and then Slice timing

Number of subject is 1

Select the entire time series in the 3dfiles folder, usually prefix by a W.

Enter acquisition order. This is interleaved so is 1-21, 2-20 Or variation.

Reference slice the central slice position

TR (this is the time taken to acquire a whole brain, 21 slices) 1.10053

TA (This is the slice repetition time = TR-CBU trigger pulse length/Total Number of slices * Total number of slices -1)

1.10053 – 50 / 21 *20 = 1

You can find this by opening your brkhrd file

Make a cup of tea (or ten) and when finished "quit"

All file should be prefixed with an "a" after this (aWxxxx*.)

REORIENTING

Start up spm2 in VNC in viewer mode again. Go to /3dfiles.

Click “display”

Select the first image (will be prefixed with “a” if slicetiming has been done first)

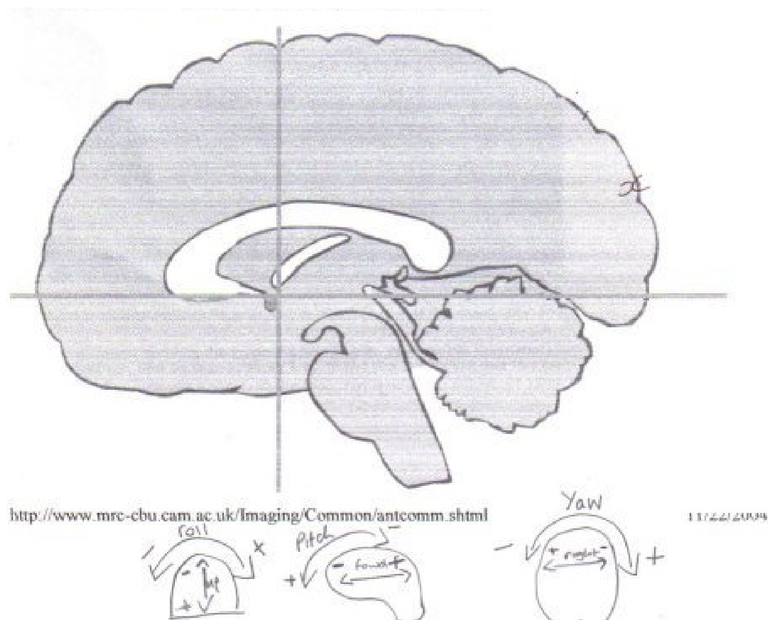
Don’t click on the actual image, change the up/ right/ yaw/ roll/ pitch at the bottom.

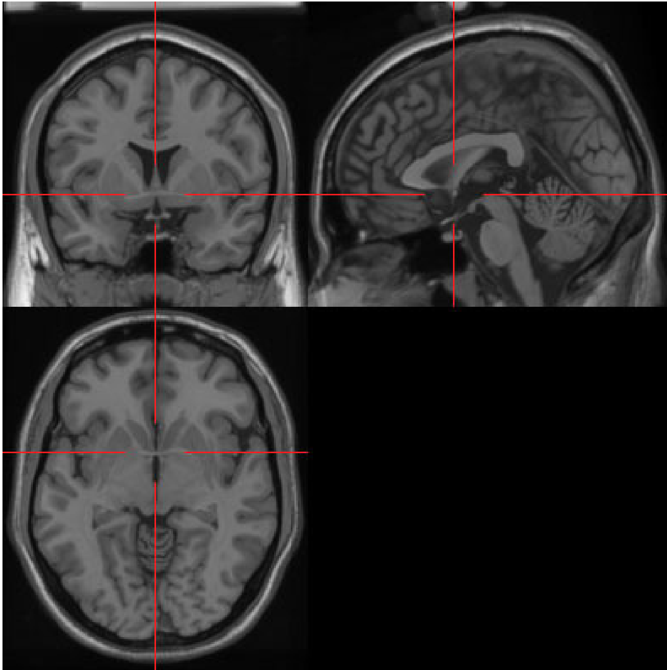
Get the cross hair to align with the ant comm.

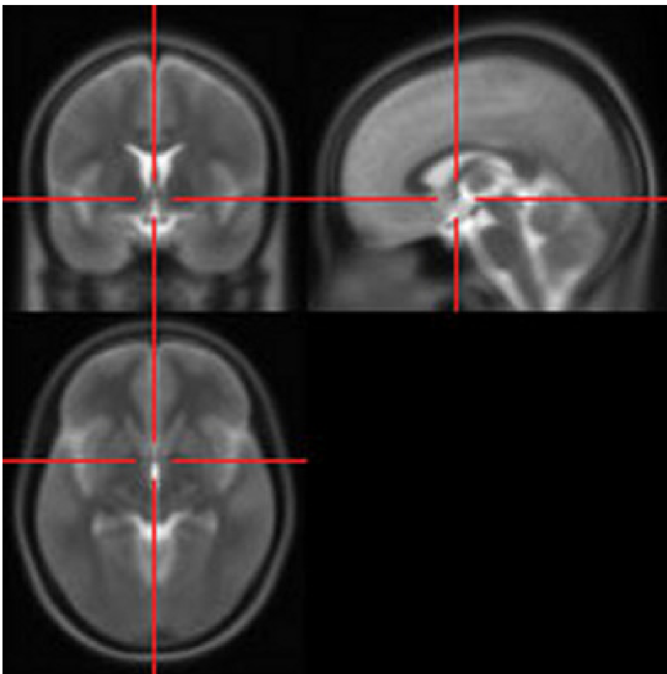
See http://www.mrc-cbu.cam.ac.uk/Imaging/Common/antcomm.shtml

Or http://www.med.harvard.edu/AANLIB/home.html

Examples from here below







Courtesy of mrc-cbu imaging website.

Once correct click on “reorient images” make a note of the changes you have made. Pick the file to reorient, these will the epi files still prefixed with an “aW*”

CAREFUL not to click on the screen and mess up the location of the cross while the program is running!!!!

REALIGNMENT

Start spm2 using VNC viewer mode.
Make sure you are in the right folder i.e. your 3dfiles for the subject you are working on.
<spm2>
Click on “fMRI time series”
Click on “Realign and Unwarp”
Number of subjects? <1>
Number of sessions? <1>
Select all aW*.img files in 3dfiles folder (they should be prefixed with an a if they have been slice timed)
Choose “all”
Choose “all images +mean”
Make a cup of tea
Once realignment finished don’t forget to click SPM print.
Files are created in your directory that are prefixed with “aW”

UNDISTORTION

Using Rhodri’s undistortion program. See Rhodri’s pages.

Then <ref_reco_2.2 phasemaps 7> When in directory above phasemaps
Start VNC server

At spm2 prompt type
<addpath /home/username/my_matlab_scripts>
For this to work while using the WBIC system you need to have the following file saved in “my_matlab_scripts” ; “fieldmap_undistortv3b” (tweaked version of Rhodri’s v), “brkmat3.m”, “fieldmap_newprepro.m”.
<fieldmap_undistort_v3b>
UPDATED can now type (fieldmap_undist_v3> instead at the spm2 prompt.
Choose “do not accept defaults”
Start at “reco”
Choose “New MultiEcho Fieldmaps”
Choose all the * defaults for the rest and the default numerical values given”

Choose directory for processed phasemaps “7” in this case
Choose raw number fieldmap directory “7”
Choose EPI header file: this will be your .brkhdr file
Choose EPI to coregister to: this will be the mean EPI generated after realignment “meanaWwbic no._07_0023.img”
Choose EPI’s you wish to undistort: this is the all the individual EPI scans and the mean “534 aWwbic no._07_0023.img” and “umeanaWwbic no._07_0023.img”
Wait a while! Mean should have “uaW*” prefix after this process.

SKULL STRIP

Go to the file with your stucturals stored in it.
Start spm2
Click on “display”
Choose appropriate .img file: the one in your structurals folder.
Click “world space” the “voxel space”
Click on where you want the bottom and top plane and make a note of these Y values in the voxel box (the y value is the middle one)
Return to matlab window
Type <addpath /home/username/my_matlab_scripts>
<trim_img>
select the structural you just displayed and type in the co ordinates you attained before.
Direction in which to trim? Select Y
The bottom value is the highest y value, the top value is the lowest.
NOTE. The mat files will now be useless as it is in a different orientation.

Will have a structural file with a “tb” prefix. Click “check reg” and open the tb structural and the mean undistorted epi to see if it matches with the mean epi, as in the 3 views are in the same place for both the images. Adjust the image using the spm display utility so it more or less matched the template with the anterior commissures at 0 0 0. Use the reorienting coordinates to do this. You will have a new mat file.

Go back to matlab screen and type <bet> to do a skull strip

Select the tb structural file you just trimmed and accept a fraction threshold of 0.5 (more towards one is there is too much skull and more towards zero if too much has been stripped).
Should have an ss_tb file do a "check reg" command again to match against the mean epi.

COREGISTER

Go to 3dfiles before starting spm2
Not using resliced images for this study so….
Number of subjects 1
Click on "coregister" and "coregister only" for which option.
umeana epi is target image
ss_tb structural image is the source image
tb structural is selected for other image

Good idea to co register and resliced if you do not have fieldmaps. As the EPI mask would be created in MRIcro by comparing slices of the resliced structural ss_tb* and the mean pre-processed image.
http://www.mrc-cbu.cam.ac.uk/Imaging/Common/epimasking.shtml

NORMALISING

Click on "Normalise"
Select "determine parameters and write normalised"
Select the skull stipped the template image "sbrain_avg_152T1_smp2.img"
Select the "ss_tb_Wbic no_07_0*.img" file for the source file.
Select the "uuaWbic no_07_0*IMAGE" and the "umeanuaWbic no_07_ .img" file for the images to write.

Click done
Wait a while.
Should have epi's with wuaWxxxxx.img prefix and a wumenaWxxxx.img file after this process.

SMOOTHING

Click on “smooth”

Choose “8mm” FWHM of the Guassian kernel

Select your normalised epis “wuWbic no_05_ua*IMAGE

Should generate swuua* images.

SPM Note: Obtaining contrasts

See batch script section for faster version….

Specifying the Design

Click on the "fMRI" button on the GUI

Select "design"

Enter inter scan interval 1.1 (the TR or time to acquire a volume).

Enter number of volumes, if doing individual analysis only enter it once (if doing all enter it x amount of times).

Specify design: select "scans" if block design or "secs" if event

Specify Basis Set: select "hrf" is block design or "hrf (with time derivative) if event design (More complex basis sets may be better if there is an expected HRF shape or for capturing differences in response between sets).

Model Interactions: NO

Enter number of conditions/ trials

Then enter name of first condition "cond1"

Enter vector of onset: for this you need to have created a .txt file in your directory with the onsets. This file should be one line long with a single space separating each vector. (in seconds if you have selected this previously) Type "spm_load" and then select this file.

Enter duration of events (default will be one if you don't enter anything).

In SPM block design is simply an event with a long duration.

For Parametric Modulation choose "none" Any other option is for when you think your design events may have different weightings.

For user specified repressors select "none"

You should have a SPM.mat file in your directory now this has been done.

Entering the Data

Click on fMRI and select "data"

Select the "SPM.mat" file that has just been created

Select the pre-processed epi's "swuuaWXXX_XX*.img"

Remove global effects; choose “none” to avoid using proportional scaling on your data.
High pass filter: choose “specify” and then remain with the default of 128.
Correcting for serial correlations: select the default of AR(1) to stop SPM auto correlating you data. Necessary to look at fixed effects (single subject p values).

Estimating the Design

Click on “estimate”
Select the “SPM.mat file”

Contrasts

Click on “Results”
Select “SPM.mat” file
For F contrasts and basic activation select condition and click “done”
Mask with other contrasts “no”
ROA analysis “no”
Name of comparison “ XXXXX”
P value adjustment to control pick “PWE” to change it. Pick “none” to choose 0.0001
Voxels: default 0 or pick more.
Can alter p value and voxel number.
Can click on activated regions to find out co-ordinates or click on co-ordinates and arrow should move to activated region.

For comparisons…
Click on “define new contrasts”
Type in an obvious name.
In contrast box define the contrast you wish to look at.
For event related you need a number for condition and number for it’s time derivative.
Thus
0 0 0 0 -1 -1 1 1 0 0
would compare conditions 3 & 4 from a five condition paradigm (you are expecting more activation in condition 4 in this case)

For block design you need only type one number
0 0 -1 1 0
would compare conditions 3 & 4 from a five condition paradigm

click “submit” to see contrasts on design matrix
Click “ok”
Repeat selections as with looking at regions of activation.

To convert MNI to talairach type “mni2tal ([xx xx xx})

Batch Scripting

Batch scripting results

You need

Wrapper file (run contrast and model files)

Contrast file

Model file

Myv file with global specs.

Model File: adjustments…

Change name of myv file to specify (line17)

Change `SPM.xBF.name       = 'hrf (with time derivative)'; (line68)`

May need to change other aspects if you do not wish to have defaults.

Contrast File adjustments

Specify myv file (line3)

Specify contrasts….

```
SPM.xCon=spm_FcUtil('Set','abs>con','T','c',[-1 -1 0 0 1 1
0]',SPM.xX.xKXs);
SPM.xCon(2)=spm_FcUtil('Set','sym>con','T','c',[-1 -1 1 1 0 0
0]',SPM.xX.xKXs);
SPM.xCon(3)=spm_FcUtil('Set','abs>sym','T','c',[0 0 -1 -1 1 1
0]',SPM.xX.xKXs);
SPM.xCon(4)=spm_FcUtil('Set','sym>abs','T','c',[0 0 1 1 -1 -1
0]',SPM.xX.xKXs);
SPM.xCon(5)=spm_FcUtil('Set','con>abs','T','c',[1 1 0 0 -1 -1
0]',SPM.xX.xKXs);
SPM.xCon(6)=spm_FcUtil('Set','con>sym','T','c',[1 1 -1 -1 0 0
0]',SPM.xX.xKXs);
```

You need to change you names (here “sym>abs” etc.)

Change contrasts, you need a 0 or 1 for each condition*each run (this example also has time time derivatives). Also an extra 0 for each run as a constant…here only one run.

You myv file specifies all you design….an example.

```
% This file sets up various things specific to this
% analysis, and stores them in the global variable MYV,
% which is used by the other batch files.
% You don't have to do it this way of course, I just
% found it easier
```

```
global MYV

% Where the subjects' data directories are stored
MYV.root = '/home/your_dir/study_dir';

% The subject directory names
MYV.subjects = {'sub1','sub2','sub3',etc…};

% Session directories, assumed same for each subject
MYV.sesses = {'where_your_epi's_are'};
nsubs = length(MYV.subjects);
nsesses = length(MYV.sesses);
ntot = nsubs * nsesses;

% Prefixes to image names, to give a good filter for the filenames
% More recent data will have a W prefix, in which case you might
% want something like:
% MYV.prefixes = repmat({'W'}, 1, nsubs);

% TR for each subject.  Sometimes it's different for each subject
% but in this case it's the same
MYV.TRs = ones(1,nsubs) * your_TR;

% Time to acquire one slice of data - from Bruker header files
MYV.slicetime = 0.0500;


% Model stuff
% Condition names
MYV.cond_names = {'task1','task2','task3' etc};

% Files with condition information
% One file for each session. For is a cycle
sctr = 1;
conddir = fullfile(MYV.root, 'onsets' this is the file with your onsets
in. In_form /study_dir/onsets/subs/a text file);
for sb = 1:nsubs
          condfile_part = [MYV.subjects{sb}, '/your_onset_txt_file.txt'
should be in subject directory]
          end

MYV.cond_files{sctr} = fullfile(conddir, condfile_part)
     sctr = sctr + 1;
   end
end


% subdirectory name for analysis, will be created in each subject's
directory
MYV.ana_dir = 'contrast_bat_scp_results';
```

You text files (blah_blah_blah.txt) for you stimuli onsets should be in a separate file for each subject in a general onsets folder in you study directory. These should in the format.

Column one: condition (1,2,3 etc)

Column two: Duration (secs)

Column four: Onset (secs or scans) specify this in you model file.