Belyk's Abridged guide to SPM12 — Command line

0. Organize data
   a. Make a well nested folder hierarchy. E.g.
      i. MyProject
         1. Subject1
            a. anat
            b. bold1
            c. bold2…
         2. Subject2…

   b. Convert images to 4D nifty (.nii) files
      i. Download MRIcron
      ii. Launch dcm2gui utility
      iii. Set format to FSL/SPM8 4D NifTi
      iv. Drag & drop or File -> dcm to nii, wait…
      v. Give more sensible filenames. My script assumes filenames like anat.nii, bold.1.nii, bold2.nii etcetera. It's useful if each subject has files with identical names that are organized into separate folders
      vi. In matlab bold1.nii,1 contains the first volume… ,2 the second…

   c. Some useful packages to download
      i. Add these to the spm12/toolbox folder
      ii. [Anatomy:](#) Make ROIs from probabilistic cytoarchitecture maps
      iii. [SnPM](#): Permutation tests and clusterwise thresholding.

   d. Launch SPM
      i. Open MATLAB
      ii. Change MATLAB directory to spm12 installation
      iii. >>addpath D:\Michel\Phonotopy\spm12 (…or wherever)
      iv. >>spm (to launch the GUI)
      v. Click fMRI

Pre-processing

0. **Re-origin** anatomical scans so the anterior commissure is near 0,0,0 and the brain is more or less facing straight forward. This part has to be done manually and is kind of a pain. Later coregistration and normalization steps depend strongly on this being done well. Use the SPM12 GUI.
    a. Click Display->browse for anatomical
    b. Click Add overlay->browse for first volume of each functional run
    c. Check that these images start more or less coregistered
    d. Remove overlay
    e. Rotate anatomical to roughly the usual orientation by typing values into the pitch (x-rotation), roll (y-rotation), yaw (z-rotation) fields (units in radians because dumb).
    f. Move crosshair to the anterior commissure (AC)
    g. Note values in mm field
    h. Type these values in the fields below with the sign inverted (i.e. * -1)
    i. Enter
    j. Type 0 0 0 in top mm field
    k. Enter
    l. Origin (check that crosshairs snaps to the AC)
    m. Reorient image->select anat.nii,1 and all volumes of all functional runs
        i. Might need to set the filter field to 1:no_vols_per_run
        ii. You are prompted to save a matrix. This is optional.
    n. Use Add Overlay to confirm that functional runs line up with anat.nii
    o. I know this sucks… but take your time anyway. Having to do it all over again sucks harder.
    p. Repeat for each subject

1. Look at **preproc**.m
    a. There are some things at the top that you should change
        i. *subjects:* this contains the ID for each of your subjects. These should be identical to the names of each subject's folder.
        ii. *runs:* The names of folders containing functional runs within each subject folder. Also give the nifty files for those runs the same name as the folder.
        iii. *Skip_runs:* If some runs for some subjects are missing you should list them here. The format is 'subjectrun' all one word.
        iv. *n_volumes*: The number of volumes per functional run. This is needed because sometimes you have to do a thing to every volume within a run.
        v. *basepath***:** The filepath to the top-level folder for the analysis. In the example above this would be 'user/MATLAB/MyProject/' make sure this file architecture is somewhere that MATLAB can find it.

b. I've saved some of the commands that SPM uses in the GUI as various "jobs". If we load these jobs into MATLAB we see that they are objects of class struct. They contain a function and all of the settings that it needs. Importantly, we can edit some of these settings through the command line, things like filenames. The basic idea behind this script is to point these jobs at a certain set of files, execute them, then point them towards another set of files and execute them again, until we run out of a data. This script should come with some .mat files with names like "realign", "coregister" etc. Put these somewhere that MATLAB can find them. It's possible that you might need to create your versions of these files with presets that are closer to the needs for your experiment. You can do this by setting up individual steps in the GUI and saving them as .mat files.

c. This is more or less what the script does
  i. *Segment* anat.nii
    - This produces a set of images for the different kinds of tissue in the scan.
    - It also makes a deformation field (y_anat.nii) that we need later to normalize our scans to the MNI template.
  ii. *Normalize* anat.nii
    - Apply the deformation field to transform into mni space. Saves as wanat.nii
  iii. Loop through the next steps for each functional run
  iv. *Realign*
    - Correct for head movement.. Align each volume in functional runs with the first volume of the run. Saves movement parameters in rp_bold1.txt (for example).
  v. *Coregister*
    - Line up functional runs with anatomical run. Really this coregisters the first functional volume to the anatomical, then applies the same transformation to the remaining volumes. If realignment went well, then this approach should be fine.
  vi. *Normalize* bold.nii
    - Apply deformation field to all volumes of functional runs. If realignment and coregistration worked well then this should be fine.
 vii. *Spatial smoothing*
    - I have not implemented this yet.

2. **Manually check registration**
   a. Check Reg ->browse for images
   Or...
   b. Display->browse for wanat.nii
   c. Add Overlay->browse for wbolds.nii

    d. If everything lines up, then move on to analysis. If not you have some trouble shooting to do. Maybe check that something didn't go wrong at the *re-origin* step.

First-Level Analysis

1. Look at **ffx**.m
    a. You need to set some things, just like in the preproc script
    b. Runs separate general linear models for each subject. Parameter estimates from this analysis are inputs to the group level random effects analysis.
    c. This outputs a file called SPM.mat is every subject folder, which contains the design matrix for each subject. It also outputs a map of beta values for each condition in the same folder.
    d. This will have clumsy file names. With X conditions of interests
        i.   beta0001 through beta000X = conditions of interest in run 1
        ii. beta000[X+1] through beta000[X+6] = motion correction
        iii. beta000[X+7] through beta000[2X+7] = conditions in run 2
        iv. etc...
        v.   The final beta*.nii files are intercepts and of little interest.
    e. In the fMRI GUI click Review and browse for one of these SPM.mat files to have a gander at the design matrix.

2. **Define Fixed Effects Contrasts.** You'll need these before moving to group analyses.
    a. Click *Results*->Browse for SPM.mat saved in previous step
    b. Define new contrast
        i.   Give a sensible name
        ii. Provide contrast weights, examples below

        - **1 0 0 0**   to test if first condition is greater than zero
        - **1, -1,0,0**   to contrast the first two of four conditions
        - **-1,-1,1,1**   to contrast the first two against last two
        - Note: weight motion parameters and intercepts as 0
        - Note: with multiple runs this could be quite long
        - Eg. for two runs: **1 0 0 0** *0 0 0 0 0 0* **1 0 0 0** *0 0 0 0 0 0* <u>0 0</u>
        - (**condition params,** *motion params*, <u>intercepts</u>)
        iii. Submit, Ok, Repeat for all contrasts. Done.
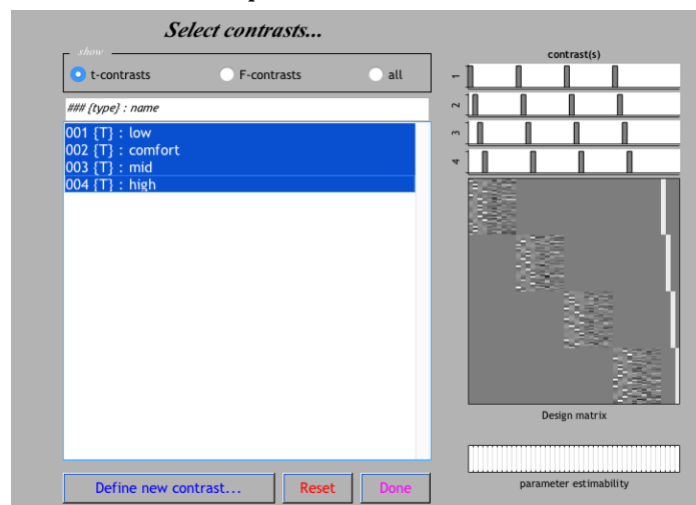
       iv. I see no convenient way of scripting this. Maybe saving the contrast vectors somewhere so you can at least copy/paste might reduce error and make this less of a nuisance.

       v. Select *one* of the contrasts - > Done

      vi. Answer questions about what thresholds you want to apply.

     vii. This opens a glass brain and cluster tables, but most importantly it saves images for each contrast that you specified (e.g., con001.nii, con002.nii, that you need later.

c. Look at FFX contrasts

       i. Overlays->sections->browse for wanat.nii (shows heatmap)

      ii. Contrasts->Change Contrast-> select a different one

     iii. Hot tip: click near a blob -> current cluster to get peak voxels.

Random-Effects Analysis

This is mostly painless so we'll GUI it.

1. Specify 2nd-level
   a. Directory <- where to send results, best make a new folder
   b. Design <- chose the kind of analysis. If like most studies you only test within subjects hypotheses and you've already run your ffx contrasts for each participant then things become easy. Choose *One-sample T*.
   c. Scans <- browse for contrast images from each subject (e.g., con001.nii).
   d. Run (green flag)
   e. Outputs SPM.mat file. Do not rename this.
   f. Close window.
   g. Estimate->run
2. Repeat for each contrast.
3. Result->browse for folder/SPM.mat
   a. This may ask you to define a contrast. If you're just doing a one-sample t the contrast vector can just be: 1.
   b. Done
   c. Answer thresholding questions
   d. An inclusive mask from the grey matter of the MNI template would be a good idea here. Can make one using the segment tool.

ROI

Install MarsBar toolbox separately.

1. ROI from functional contrasts
   a. Toolbox->Marsbar->ROI definition-> get SPM clusters->browse for a SPM.mat file
   b. Answer questions to set your thresholds as described above.
   c. Click Whole brain to see a cluster table

   d. Click a coordinate in cluster table to select it.
   e. Write ROI(s)->write one cluster->give sensible name
   f. ROI definition->View->Browse for .mat file just saved
   g. ROI definition->Export...
   h. Export ROI9s) to:..->image->browse for .mat again
   i. Space for ROI image...->base space for ROI->browse for directory

2. Extract Beta values from ROI.
   a. Toolbox->Marsbar->ROI definition->View
   b. Design...->set design from file->browse for SPM.mat file for the
      contrast that you want. *If you choose your RFX analysis this will give
      you betas from each participant at this ROI.*
   c. Data...-> Extract ROI data (full option)->browse for all ROI files (.mat)
   d. Use SPM design->Yes
   e. Images from->SPM design
   f. Scaling from->Raw->0 (for raw beta values)
   g. Results...->Estimate
   h. Results...->Save results to file (makes a .mat file)
   i. In SPM cmd
      • >load("filename.mat")
      • >SPM.marsY.Y
      • This prints a matrix with one column per ROI and one row per
        subject. Resave this to a more useful .csv file.
      • >csvwrite("filename.csv", SPM.marsY.Y)

Results Montage

 I like looking at a 5-by-6 array of axial slices with my blobs. This gives a nice balance of printing at a large enough scale and covering the whole brain without skipping *too many* slices between images.

Results->Browse for SPM.mat->select a contrast
Render->Slice Overlay-> wanat.nii-> Structural with blobs->axial-> -60:5:80