fMRI statistics instructions

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You will not be able to run the analysis correctly without knowledge of fMRI statistics. For an introduction, read the relevant chapters in the Huettel and Poldrack books and suitable web tutorials.

Prerequisites

- The script assumes you followed our preprocessing pipeline.

Specifying and estimating a GLM

1) Set up the parameters in the firstlevel_batch.m:

    - A number for this GLM analysis – this is useful if you run several GLMs, as the script will generate a numbered stats folder for each analysis.

    - The directory that contains your onset files. As described in the script intro, this can either be a subfolder per subject or one folder with onset files for all subjects. See comments in the script for naming suggestions. Depending on which option you choose, you will need to comment/uncomment code in lines 89-94.

    - The first run that should be part of this GLM analysis.

    - The number of functional runs that belong to the this statistical analysis. If you acquired different tasks that should not be analysed in a single GLM, you need to run several GLMs where you adjust the starting run index and number of runs.
      Example: Assume you want to have two GLMs – the first one to analyse runs 1-3 and the second one to analyse runs 4-5. You run one GLM with start_sess = 1 and n_sess = 3 and the second one with start_sess = 4 and n_sess = 2.

    - The name template for your directories (functional runs and stats directory)

    - Your scanning parameters (TR, slice number, reference slice used in preprocessing script)

    - The timing units used in your onset files

    - The name of the movement regressors file – if you include physio regressors, the physio regressors should be appended to the movement parameters (rp_*) for each run, i.e. one single file with both types of regressors for each run.

2) Run the script. As always, it makes sense to check everything thoroughly for the first subject(s). If you want to set up a design matrix and check it without having to wait until the estimation is finished, you can enter estimate = 0 in the first section of the script.

Suggestion: If you're comfortable with running the script as a function, you can change it so that the GLM number is an input to the function when you call it from the command line. (Only if no other parameters such as the run number change across GLM versions.)

Specifying first-level contrasts

1) Set up the basic parameters in the contrast_batch.m:

   - The number of the GLM analysis you want to create contrasts for

   - The name template for your stats directory

2) Set up the contrasts you need. This depends a lot on your paradigm and will vary!

   - For example, you may have a different number of regressors for each subject and each run. In this case, it is best to write a script that takes the different numbers into account when generating the regressors. For this, you would need to include a loop in the script that loops across subjects and loads the individual contrasts.

   - In a standard design, all conditions are present in each run. If this is not the case, you probably need to include weights in your contrast based on the number of runs for the respective condition (see SPM manual / contrast GUI interface).

   - If you have a standard design, you can enter your contrasts as shown in the two examples in the script.
     . If the contrasts are identical for each session, you can enter the contrast vector for one run and select "repl" so that SPM will replicate this for each run.
     . If the contrasts are not identical across runs, you will need to enter the full contrast vector and select "none".

   For all contrasts, it is very important that you **know the number of columns in your design matrix for each run**. This includes the basic regressors and the parametric modulators. Your contrast vector should have the same length. If it is too short, SPM will pad the right with zeros, but will not show an error message. This means that if you forget e.g. a parametric modulator, your contrasts may shift to the wrong columns without you noticing! Review the design in the GUI and/or the .mat file to check. (However, if the contrast vector is too long you will get an error message. This can be **useful for testing** whether you have the correct length – add a 0 and check whether you get an error message. It's best to do this **in the GUI before setting up the script**. There is a per-session variable at the end of the design matrix, so you will need a few extra zeros for the number of runs if you choose not to replicate across sessions.)

   NOTE: You will need to select the contrasts by number for the second-level model. If you have different numbers of contrasts for individual subjects, it will be hard to keep track of which contrast number corresponds to a particular contrast for a given subject. Therefore, it is best to set up the contrasts **identically for all subjects**. If you want to try out versions for your contrasts, you can either use the pilot subject for this, or you need to make sure that you change the part of the script that asks whether you want to delete existing contrasts, so that unwanted contrasts are deleted when needed. In any case, check whether con_000x is really identical for all subjects / whether all subjects have an identical number of contrasts and the same sequence of contrasts before running the second-level statistics.

3) Choose whether you want SPM to print the results table for each subject. If yes, choose the alpha threshold, cluster extent, etc. (lines 71ff). It will do this for all contrasts without including the contrast name, so if you want to have a look at the postscript file, you can use the page numbers for orientation – it will start with page 1 for each new contrast.

4) If you want, you can run art_summary (second dark green button in the toolbox, *Summarize* …) to check the quality of your subjects' results.

Specifying a second-level model

First create a folder for the second-level stats for this GLM model. Then use the GUI batch: SPM -> Stats -> Factorial design specification. For standard designs, run a one-sample t-test. As scans, enter corresponding contrast images for each subject by using regexp filters (e.g. con_0001). You can usually leave the defaults for all the other options.

You can easily create your own batch script by selecting "save batch and script" from the menu (make sure that all the inputs are empty, i.e. have an <-X). It creates a skript skeleton with the name you enter, plus a jobman file with the name and a _job suffix. You then need to enter a bit of code in the batch skeleton to loop through your subjects and fill in the empty fields.