Subject Classification

Prepare excel file

- In the folder subjectclassification.zip you can find two excel files. This files are examples of the excel file that you'll have to make yourself.
- The excel file should have two columns in Sheet1:
    - Column 1: the subjectIDs for how your folders are named
    - Column 2: the group to which the subject belongs
- Save this excel file with the .xls-extension

Options

This script comes with several options:

- GUI or not
    - To adjust the variables and parameters for what you want to do, you can either work with a gui or adjust the variables in the script itself.
    - I recommend that if you are using this script for the first time, use the GUI. Once you are familiar with the different variables that are used in the script and if you have some matlab experience, you can adjust the variables in the script itself.
- Functional or anatomical data:
    - You can do the analysis on the functional or anatomical data that you have of subjects.
    - In both cases, only the voxels that are included by your masks will be used.
    - If you opt for the anatomical analysis, PLEASE DO THIS:
        - make a separate folder with all the wr-anatomical files of the subjects. Make sure that the name of the wr-anatomical files is the following: wrC1.nii where C1 is the SubjectID that corresponds to the subjectID in your excelfile).
- Subject confusion:
    - Sometimes you might want to track how often subjects are confused with the other group than the one they belong. You might want to correlate this "confusion" to behavioral measures.
    - If you want to get the subject confusion results, this is possible if you select this option.
- Random permutations:
    - To test the statistical significance of subject classification, you must perform a random permutation test.
    - However, this takes some time, so only do this when you finally know what you want to do with this script.
- Classification or generalization:
    - You can either train and test on the same two groups (classification).
    - Or you can do a generalization (train and test on different groups).

All the results of all the analysis will be saved in the result directory of you choosing as a mat-file and a summary will be written away to an excel file.
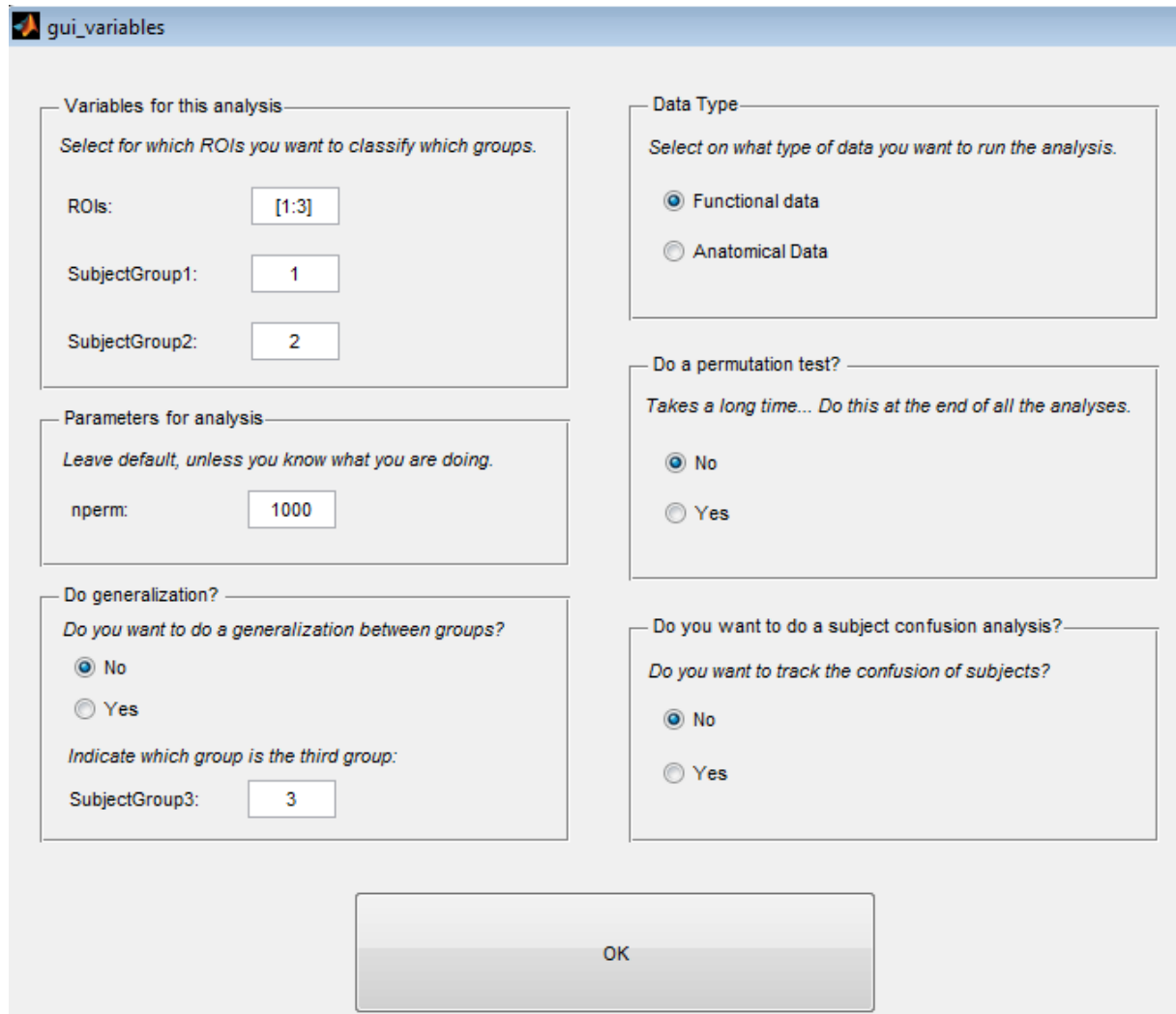
Working with the GUI

On line 40 of the script `SubjectClassification` adjust the following variable:
`what_to_use = 'gui';`

Now run the script. You'll get several windows popping up. The explanation of the windows, you can find in the next subsections of this document.

Variables of your choosing

- ROIs:
    - Select which masks you want to use. Keep the []!!!
    - There is an example folder of masks (ROIs) that I have included. Make sure that your masks are named as numbers.
    - The masks will be automatically coregistred to the right volume of your data.
- SubjectGroup1:
    - The number of the first group you want to compare.
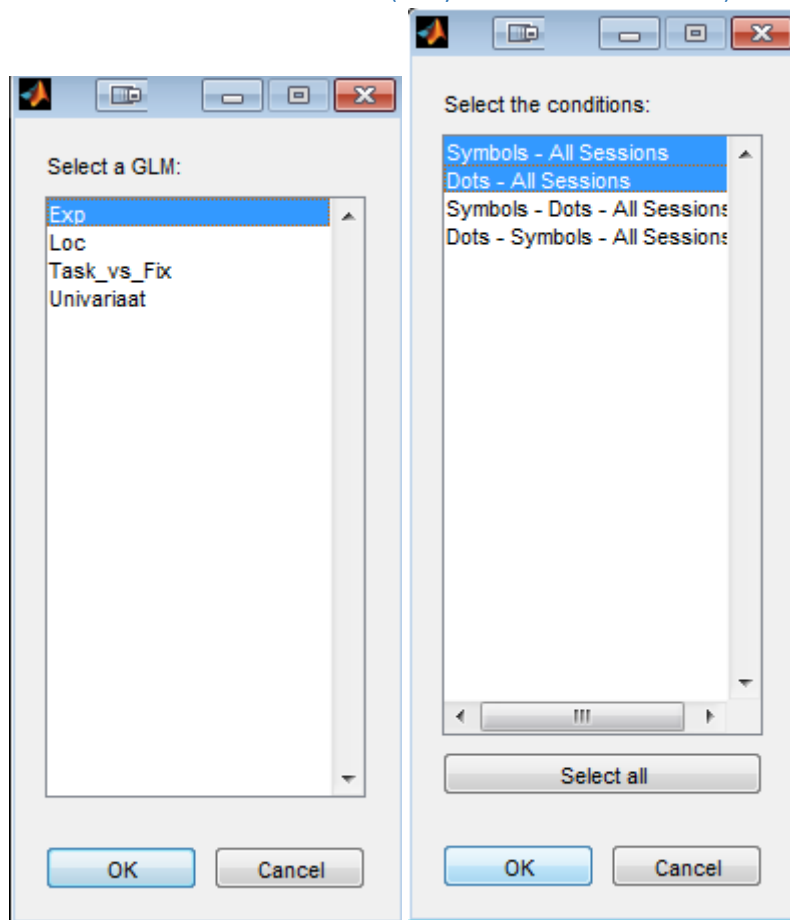   - This number should be in your excel-file (the second column).

- SubjectGroup2:
  - The number of the second group you want to compare.
  - This number should also be included in your excel-file (the second column).
- nperm:
  - How many random permutations do you want to do? I recommend to keep this at 1000.
  - If you have 1000 nperm's, you'll do a 1000 times 100 (= nrep) random permutation replications.
- Generalization:
  - If you want to do a generalization, click "Yes".
  - Generalization will happen as follows:
    - Direction 1: training SubjectGroup1 versus SubjectGroup2 ** testing SubjectGroup1 versus SubjectGroup3
    - Direction 2: training SubjectGroup1 versus SubjectGroup3 ** testing SubjectGroup1 versus SubjectGroup2
    - Accuracy: the average across both directions
  - Random permutations will happen as follows:
    - Again generalization in both directions, creating two random permutations distributions (for each direction one distribution)
    - A new distribution will be created by taking random nperm/2 elements from each distribution.
- Data type:
  - Select if you wish to use functional or anatomical data.
- Permutation test:
  - Select if you wish to do a random permutation
- Subject confusion:
  - Select if you want to keep track of the subject confusion.

Select the directories with which you'll work with
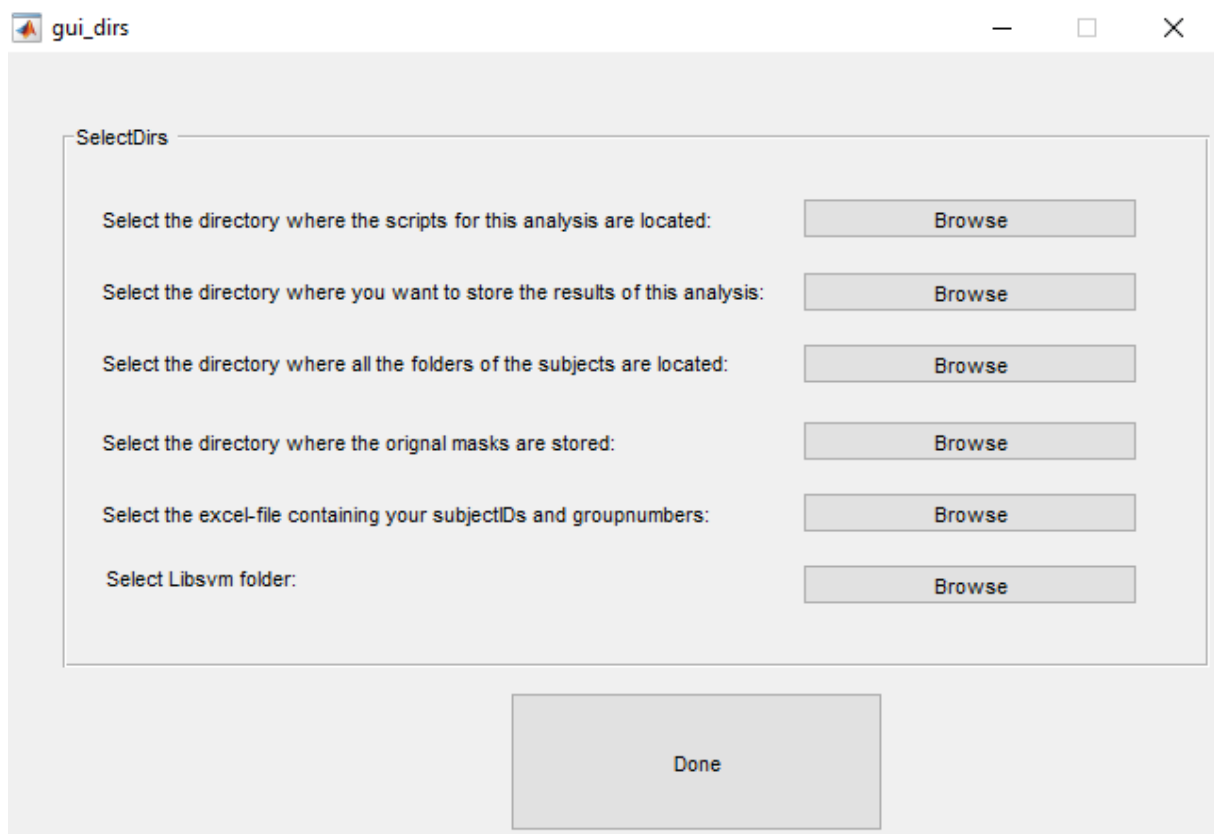
- Scripts:
  - o The directory where all the scripts that you need for this analysis are located.
- Results:
  - o The directory where you want to store the results to. Make sure you'll take each time another directory, otherwise your results will be overwritten.
- Folders of subjects:
  - o Functional data:
    - ▪ Take the directory where you have per subject one folder containing all the beta-values, spmT, spm.mat file.
    - ▪ If you have different GLMs per subject, it might be that you have several subfolders within the subject specific folder. This is not an issue, you'll get the opportunity to select which folder/glm you want to use in a next GUI.
  - o Anatomical data:
    - ▪ Take the directory containing the wrSubjectID.nii images for every subject.
- Original masks:
  - o The folder containing the masks aka ROIs.
- Excel-file:
  - o Select the excel-file containing the subjectIDs and group numbers.
- Libsvm:
  - o Select the folder containing the functions of libsvm (this folder is also included in the zipped-file you gotten from me).

Select GLM and conditions (only for functional data)

Select a GLM:

- Exp
- Loc
- Task_vs_Fix
- Univariaat

OK   Cancel

Select the conditions:

- Symbols – All Sessions
- Dots – All Sessions
- Symbols – Dots – All Sessions
- Dots – Symbols – All Sessions

Select all

OK   Cancel

- If you have different GLM's for every subject, select in the first folder the GLM you want to use.
- In the next window, select on which *contrasts* (spmT-files) you want to do the analysis.