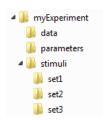
PREPARING AN EXPERIMENT

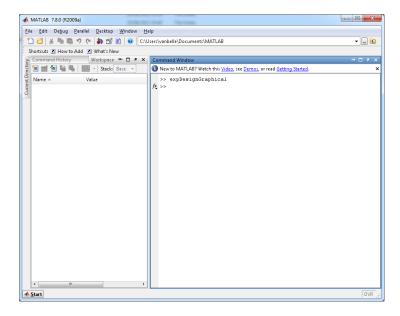
NEEDED: - expDesignGraphical.m

- expDesignGraphical.fig

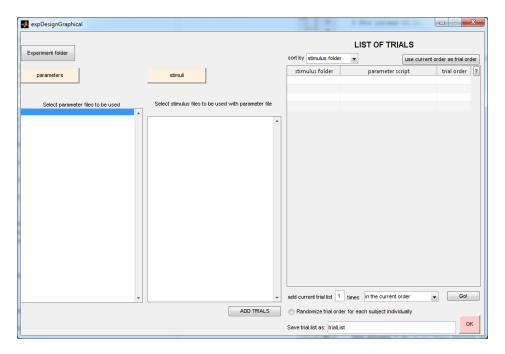
1. Create a folder with the following subfolders:



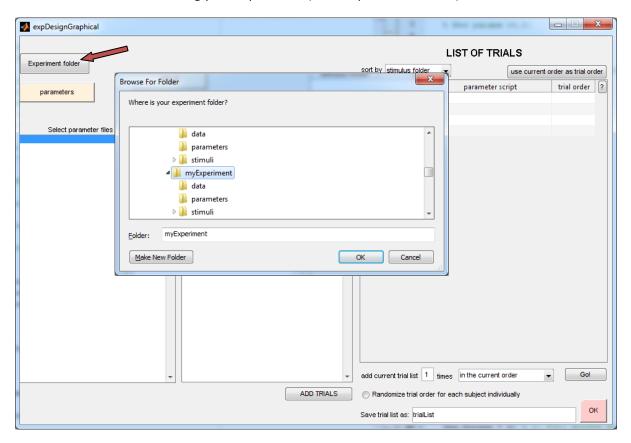
- data (empty for now)
- Parameters (contains sinstim_<paramterfilename>.m files)
- Stimuli (contains folders with stimuli, for each trial, stimuli will be picked from one of these folders in the way determined by the parameter file for that trial)
- 2. Run expDesignGraphical (through Matlab)



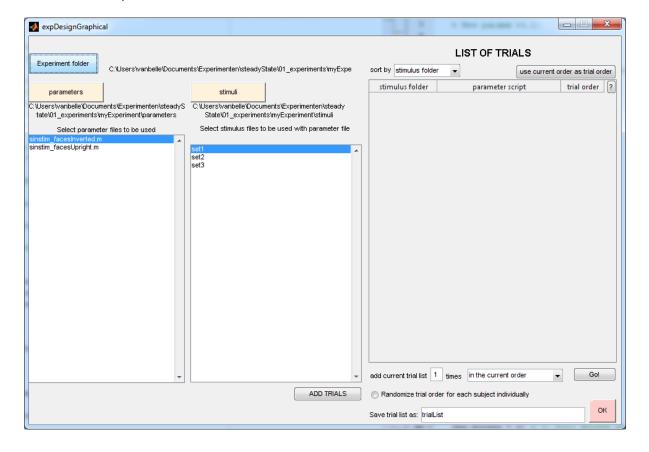
3. You should now get a graphical user interface that looks like this:



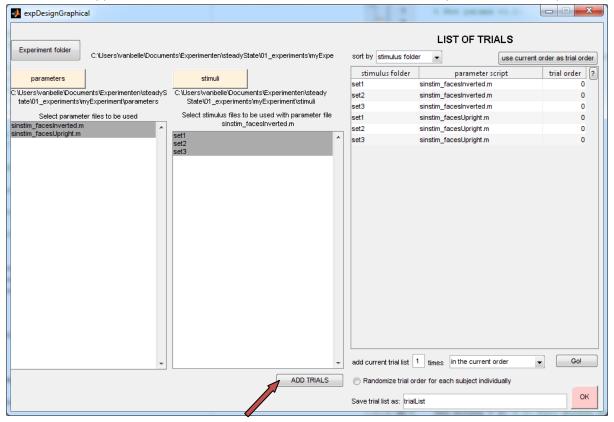
4. Select the folder containing your experiment (click 'Experiment folder'):



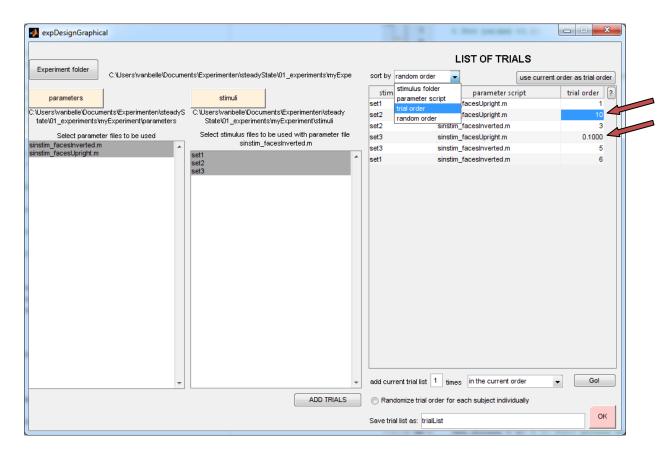
5. If your folder contains the correct subfolders, and the correct files, the parameter and stimulus field will be filled automatically:



6. Select the combinations of parameters and stimulus folders, and add them to the trial list. The selected combinations appear in the field with the list of trials. You can add as many combinations as you want.



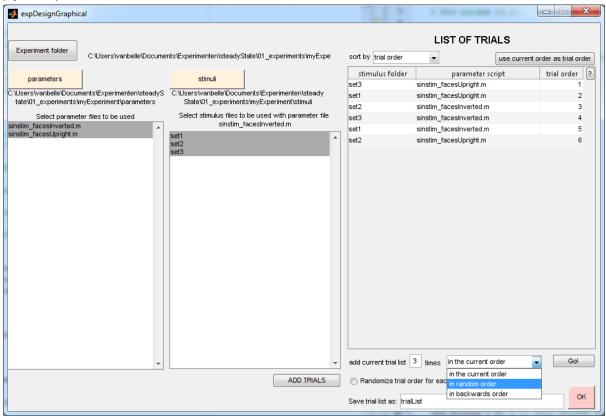
- 7. (optional) Change the order of the trials by
 - sorting the trials automatically using the 'sort by' menu
 - checking the radio button to randomize trial order for each subject individually. The list order is then created when running the actual experiment.
 - or by changing the trial order manually (just use any number indicating the position you would like the trial to be in, this can also be a decimal or negative number), and then sorting the trial based on trial order:



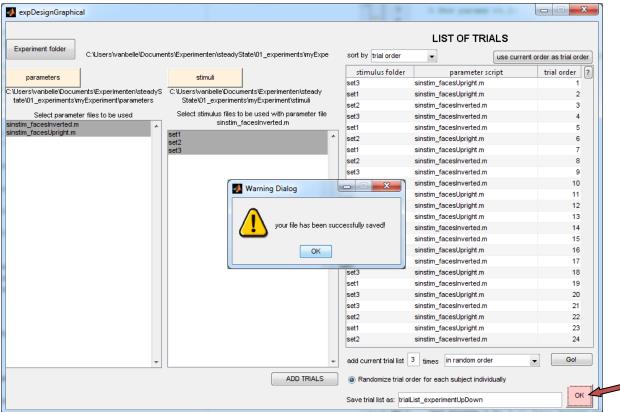
Clicking 'use current order as trial order' changes the values in the 'trial order' column from 1 -> the number of trials in the order they currently appear in the trial list.

To randomize / delete only a subset of trials: select them and **right click** on them. A pop up menu will then appear with the two options.

8. (optional) add the current trial list X times in a certain order



9. Save the current trial list to a file that will later be used to run the experiment. Give the file a name that indicates which experiment it contains. order' column!

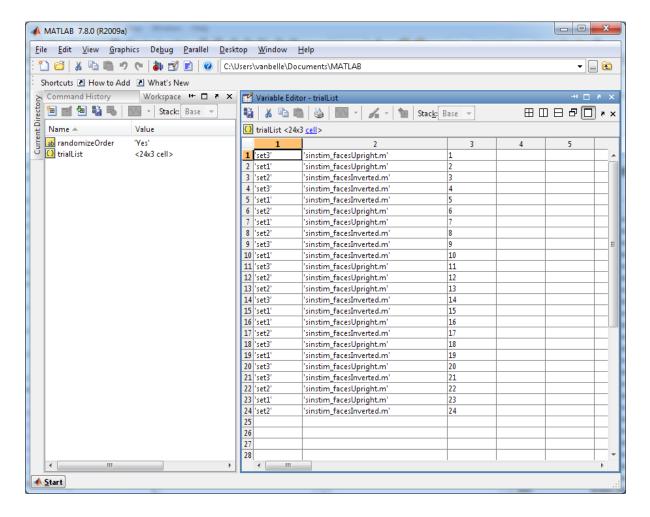


NOTE: trials will be saved in the order they appear in the list of trials. This does not necessarily correspond to the value in the 'trial

10. Your trial list (a .mat file) should now be saved in your experiment folder



This is what it contains: (you can see the content by opening the file through Matlab and then double clicking the variable name in the workspace)



- randomizeOrder: 'Yes' or 'No': indicates whether the trial order should be randomized for each subject individually (corresponds with the value of the checkbox in expDesignGraphical)
- trialList: cell variable containing one line per trial, containing stimulus folder, parameter file and trial order. Note that the last column is not used for running the experiment)

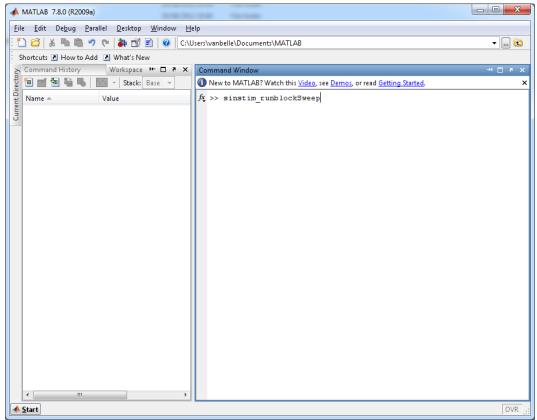
RUNNING AN EXPERIMENT

NEEDED: - sinstim_runBlockSweep

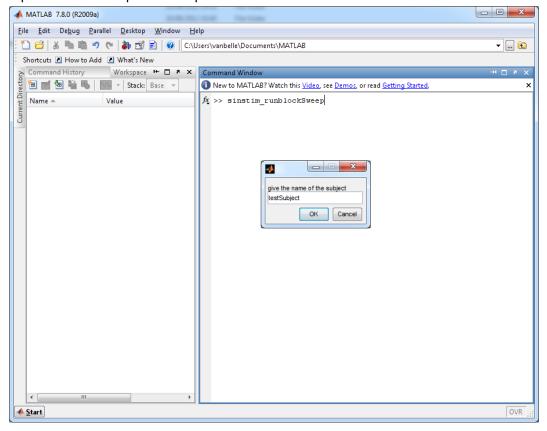
- psychtoolbox

- Ben's toolbox: sinstim, bentools, glab

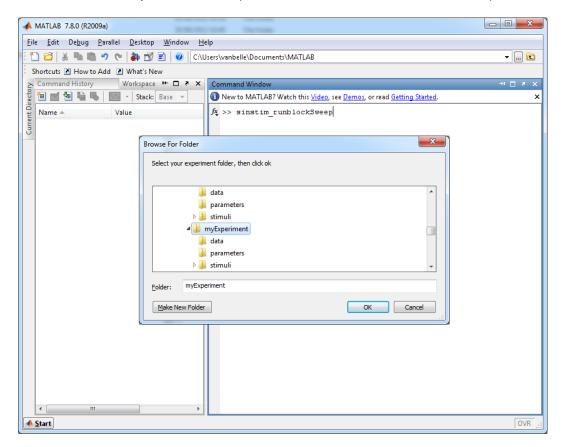
1. Run sinstim_runBlockSweep (through Matlab)



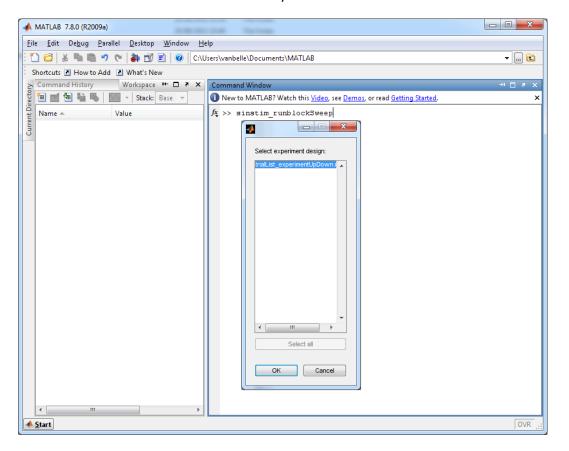
2. Enter the subject ID. Do not use an ID that has already been used for another subject in the same experiment. Avoid spaces and special characters.



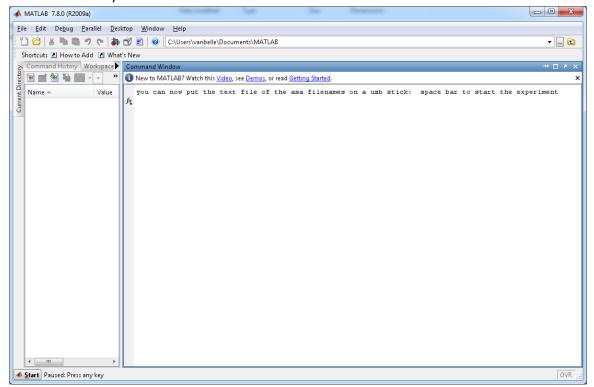
3. Select the experiment folder (= the folder in which the trial list is saved)



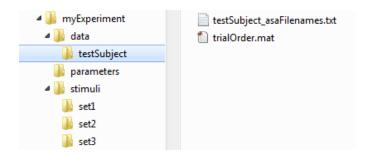
4. Select the .mat file with the trial list you would like to use for this session



5. In the matlab command window, a message will appear, saying that you can now put the file with the trial order on a usb key.

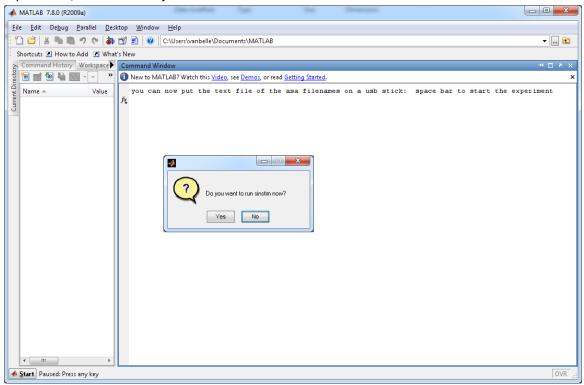


The file that is important is the text file named <subjectID>_asaFilenames.txt that has been created in a folder named after the subject ID, in the data folder. This file contains the names of the output files in the order in which the trials will appear.



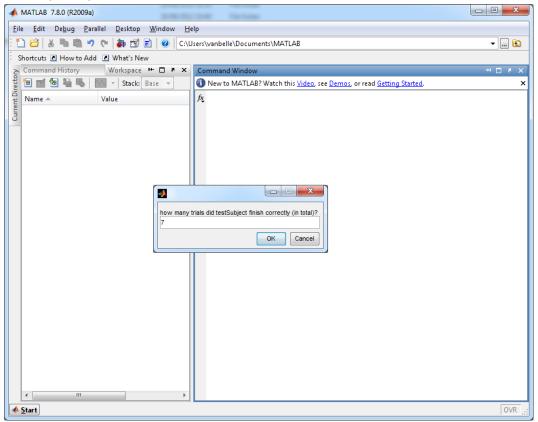
You can copy this file to a usb key, and use it for copy-pasting the names for the output in ASA. When done so, make sure the Matlab window is selected (left click somewhere in the command window) and push the space bar.

6. A question dialog appears asking whether you want to run sinstim now. You can either immediately start the experiment, or use the subject data at a later moment in time.



Upon starting sinstim, the experiment window will appear and the first trial will start.

If you entered a subject ID that already existed, the program will ask how many trials the subject finished correctly, and proceed from there.



- 7. After each trial, you have to hit a key to initiate the next trial. There are three possibilities:
 - $n = \underline{n}ext trial$
 - r = repeat trial (careful when naming the ASA output file!)
 - $-q = \underline{q}$ uit block of trials (all data are stored, the rest of the experiment can always be finished later)

ANALYZING THE DATA

NEEDED: - automatisationGoedele_v01.m

- automatisationGoedele_v01.fig

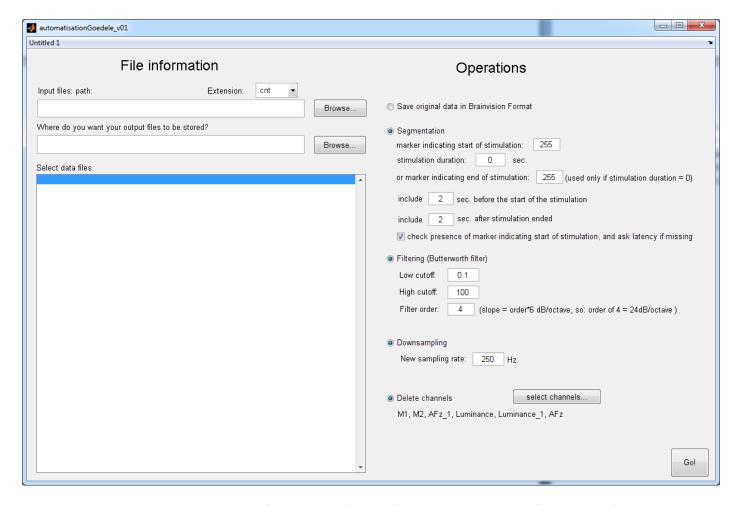
- channelNames.mat

- channelLocationsGoedele.loc

- toolbox: erplab 2.0.0.1, eeglab with anteepimport1.09

Run automatisationGoedele_v01.m to get the graphical interface.

This program allows you to import datafiles with eeg data directly from the cnt-format to a txt format that can be imported into Letswave. Along with the format change, you can segment, filter, downsample, and/or delete channels.



Once processed, the data are stored in a folder called 'preproc' in the selected output folder in .txt format, together with a file called 'reportAnalyses.txt' that contains the information you need for importing the data into Letswave.