The effects of parental presence on amygdala and mPFC activation during fear conditioning: An exploratory study

Walk through- OSF Repository

fMRI Scripts folder

The behavioral and ROI analyses for this paper were done in R using the main script "parenting_and_fear_learning_analyses.Rmd". The scripts for the fMRI pipeline are in the folder fmri_scripts, described below:

1. **01_run_one_participant_fmriprep_ignore_fmap_cond.sh**: the fMRIPrep pipeline used for the raw bids file preprocessing (need to run on a high computing cluster). Full description of the pipeline, as generated by fMRIPrep report, can be found in the paper's supplementary file.
2. **02_run_one_participant_confound_cond.sh**: This is a bash script that runs the R script "*create_confound_txtfile_lowdof_rm1st4TRs_cond.R*" on a high computing cluster. Before doing so, it changes the name of the fMRIPrep confound output file of each participant (to run on many participants at once). The result is a file which includes, for each participant, only the nuisance regressors that were included in the level-1analyses.
3. **03_run_one_participant_skulstrip_cond.sh**: This is a bash script that uses fslmaths to skull-strip the functional preprocessed data.
4. **04_run_one_participant_level1_cond.sh**: This is a bash script that run the level-1 FEAT analyses on a high computing cluster. The design.fsf file "*sub-104_task-cond1_run-1_design.fsf*" is an example for a level-1 FEAT design template of one scan (cond1) of one participant (104).
5. **05_change_reg_files_cond.sh**: This script performs the "[mumford workaround](#)", which is necessary when performing level-1 analyses in FSL with fMRIPrep preprocessed files, before doing higher level analyses.
6. **06_regenerate_examplefunc_file_cond1.sh**: This script reverts the mumford workaround for the purpose of performing ROI analyses (do this on a copied folder)
7. **07_creating_amygdala_nuclei_nooverlap_masks.sh**: This script uses fslmaths to create the amygdala ROI masks.
8. **08_extracting_mean_values_cond.sh**: This script organizes all the participants' mean BOLD activation in a given ROI under one file (the extraction of these values from the level-1 outputs was conducted using the FSL featquery gui panel).
9. **09_design_group_analysis.fsf**: This is the FSL FEAT template that was used for the whole-brain higher-level analysis. *Note*: 'cope1' is the file name of the specific contrast that was examined (US vs. baseline). For the second contrast of interest (CS+ vs. CS-), input files were 'cope2'.
10. **ROI_masks**: This folder contains the masks nifty files which were used for the ROI analyses. The screenshot '*resampling tool definitions_ROIs*' shows the options that were chosen to resample the masks to the MNI152Nlin6Asym template in fsl GUI.

Data folder

1. **classical_conditioning_behavior_data.csv**: Behavioral data from the classical conditioning 'Like' and 'Nervous' rating questions. Used in the main R script.
2. **classical_conditioning_parental_presence_data.csv**: parental context version information, needed for the analyses in the main R script.
3. **valid_fmri_participant_list.csv**: list of participants' numbers that were included in the fmri analyses. Needed for the ROI analyses in the main R script.
4. **Files with the prefix 'ROI_'**: mean BOLD activation values data. Each file contains data of one scan (cond1 or cond2) of one mask.

Output folder

This folder includes the non-thresholded whole-brain activation maps (zstats) from the whole-brain analyses (in the MNI152NLin6Asym standard space).

1. **zstat1_parent_higher_than_alone_CS+_vs_CS-.nii.gz**: whole-brain activation map for the CS+ vs. CS- contrast for parent > alone (i.e., increased activation during parental presence)
2. **zstat1_parent_higher_than_alone_US_vs_baseline.nii.gz**: whole-brain activation map for the US vs baseline contrast for parent > alone (i.e., increased activation during parental presence)
3. **zstat2_parent_lower_than_alone_CS+_vs_CS-.nii.gz**: whole-brain activation map for the CS+ vs. CS- contrast for alone > parent (i.e., decreased activation during parental presence)
4. **zstat2_parent_lower_than_alone_US_vs_baseline.nii.gz**: whole-brain activation map for the US vs baseline contrast for alone > parent (i.e., decreased activation during parental presence)