**The effect 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 subject (to run on many participants at once). The result is a file which includes, for each subject, 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-002\_task-cond1\_run-1\_design.fsf*” is an example for a level-1 FEAT design template of one scan (cond1) of one subject (002).
5. **05\_change\_reg\_files\_cond.sh**: This script performs the “[mumford workaround](https://www.youtube.com/watch?v=U3tG7JMEf7M&t=200s&ab_channel=mumfordbrainstats)”, 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 (needs to be done 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 subjects’ 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.

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 subjects’ 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). For each contrast of interest (US vs. baseline / CS+ vs. CS-), one file shows the higher-level contrast of parent > alone (i.e., increased activation during parental presence), and a second file shows the higher-level contrast of alone > parent (i.e., decreased activation during parental presence).