Scripting 1st Level Analysis

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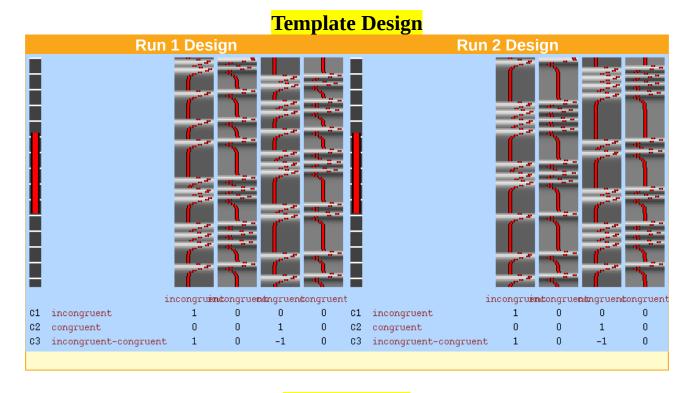
Make_FSL_Timings.sh:

```
#!/bin/bash
#Check whether the file subjList.txt exists; if not, create it
if [!-f subjList.txt]; then
    ls -d sub-?? > subjList.txt
#Loop over all subjects and format timing files into FSL format
for subj in `cat subjList.txt`; do
     cd $subj/func #Navigate to the subject's func directory, which contains the timing
files
     #Extract the onset times for the incongruent and congruent trials for each run. NOTE:
This script only extracts the trials in which the subject made a correct response. Accuracy
is nearly 100% for all subjects, but as an exercise the student can modify this to extract the
incorrect trials as well.
     cat ${subj}_task-flanker_run-1_events.tsv | awk '{if ($3=="incongruent_correct")
{print $1, $2, "1"}}' > incongruent_run1.txt
     cat ${subj}_task-flanker_run-1_events.tsv | awk '{if ($3=="congruent_correct")
{print $1, $2, "1"}}' > congruent_run1.txt
     cat ${subj}_task-flanker_run-2_events.tsv | awk '{if ($3=="incongruent_correct")
{print $1, $2, "1"}}' > incongruent_run2.txt
     cat ${subj}_task-flanker_run-2_events.tsv | awk '{if ($3=="congruent_correct")
{print $1, $2, "1"}}' > congruent_run2.txt
    cd ../..
done
```

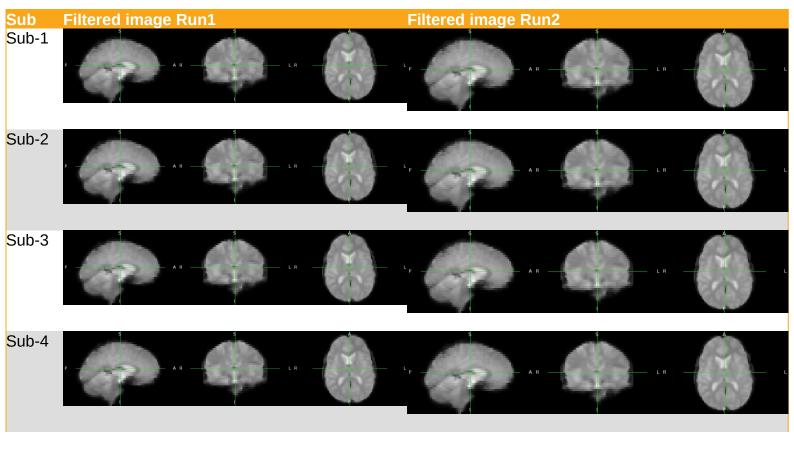
run_1stLevel_Analysis.sh:

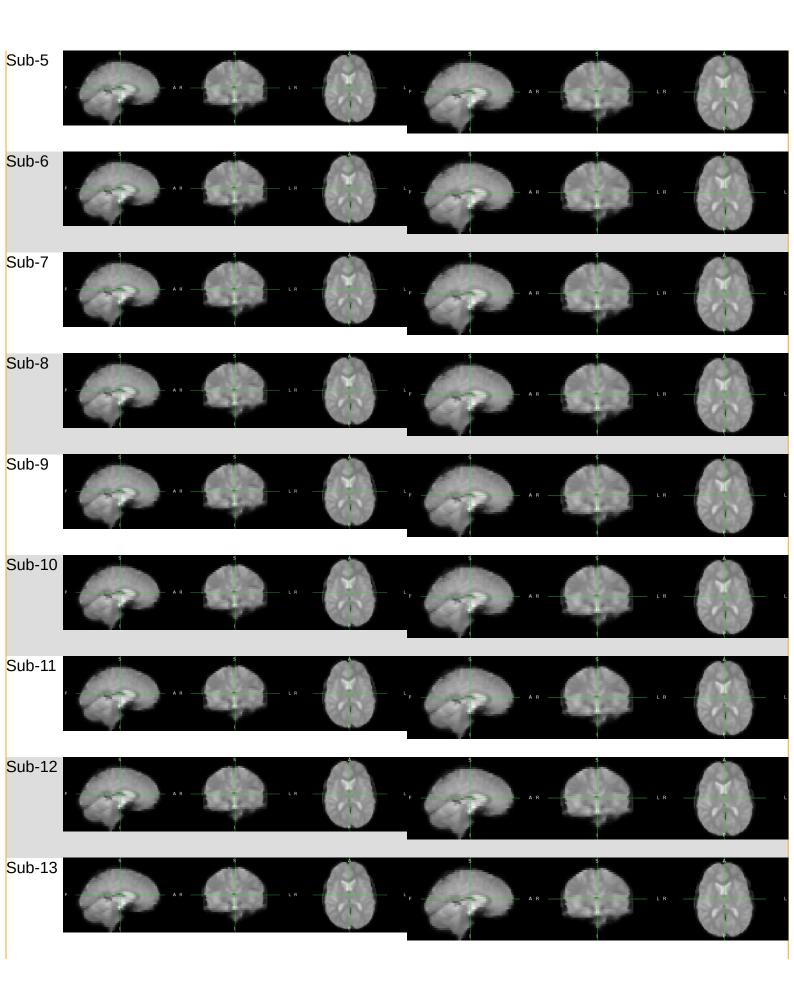
cd .. done echo

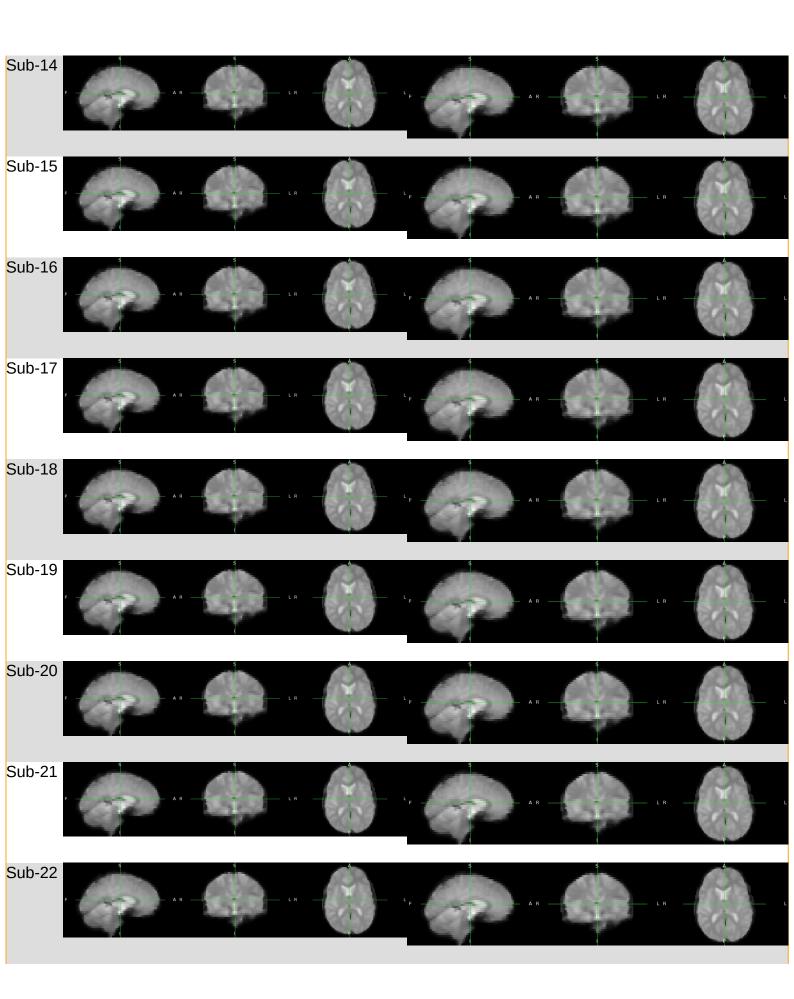
#!/bin/bash # Generate the subject list to make modifying this script # to run just a subset of subjects easier. for id in `seq -w 1 26`; do subj="sub-\$id" echo "===> Starting processing of \$subj" echo cd \$subi # If the brain mask doesn't exist, create it if [!-f anat/\${subj}_T1w_brain_f02.nii.gz]; then echo "Skull-stripped brain not found, using bet with a fractional intensity threshold of 0.2" # Note: This fractional intensity appears to work well for most of the subjects in the # Flanker dataset. You may want to change it if you modify this script for your own study. bet2 anat/\${subj}_T1w.nii.gz \ anat/\${subj}_T1w_brain_f02.nii.gz -f 0.2 fi # Copy the design files into the subject directory, and then # change "sub-08" to the current subject number cp ../design_run1.fsf . cp ../design_run2.fsf . # Note that we are using the | character to delimit the patterns # instead of the usual / character because there are / characters # in the pattern. sed -i " "s|sub-08|\${subj}|g" \ design_run1.fsf sed -i " "s|sub-08|\${subj}|g" \ design_run2.fsf # Now everything is set up to run feat echo "===> Starting feat for run 1" feat design_run1.fsf echo "===> Starting feat for run 2" feat design run2.fsf echo # Go back to the directory containing all of the subjects, and repeat the loop

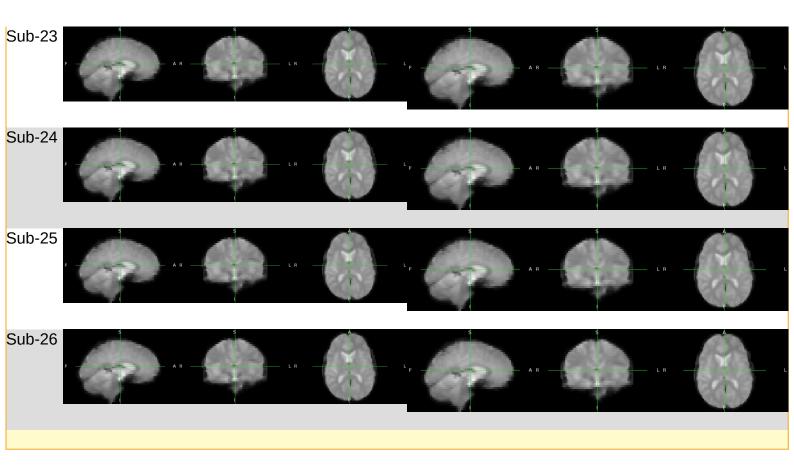


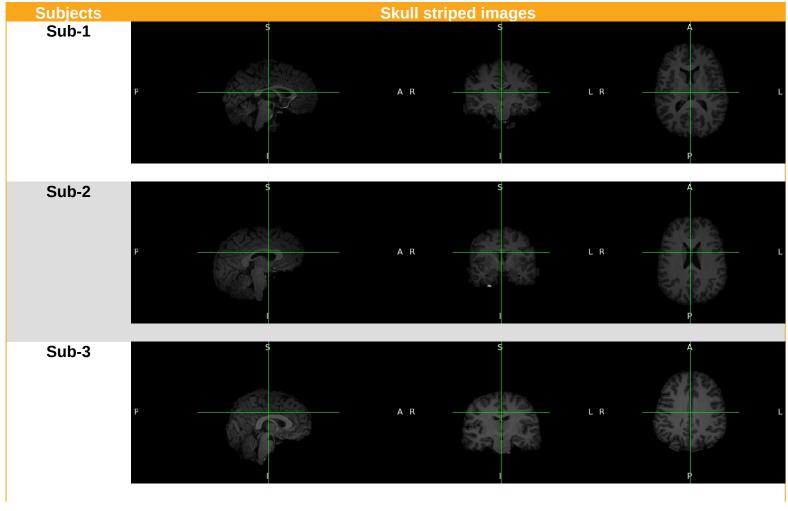
Preprocessing

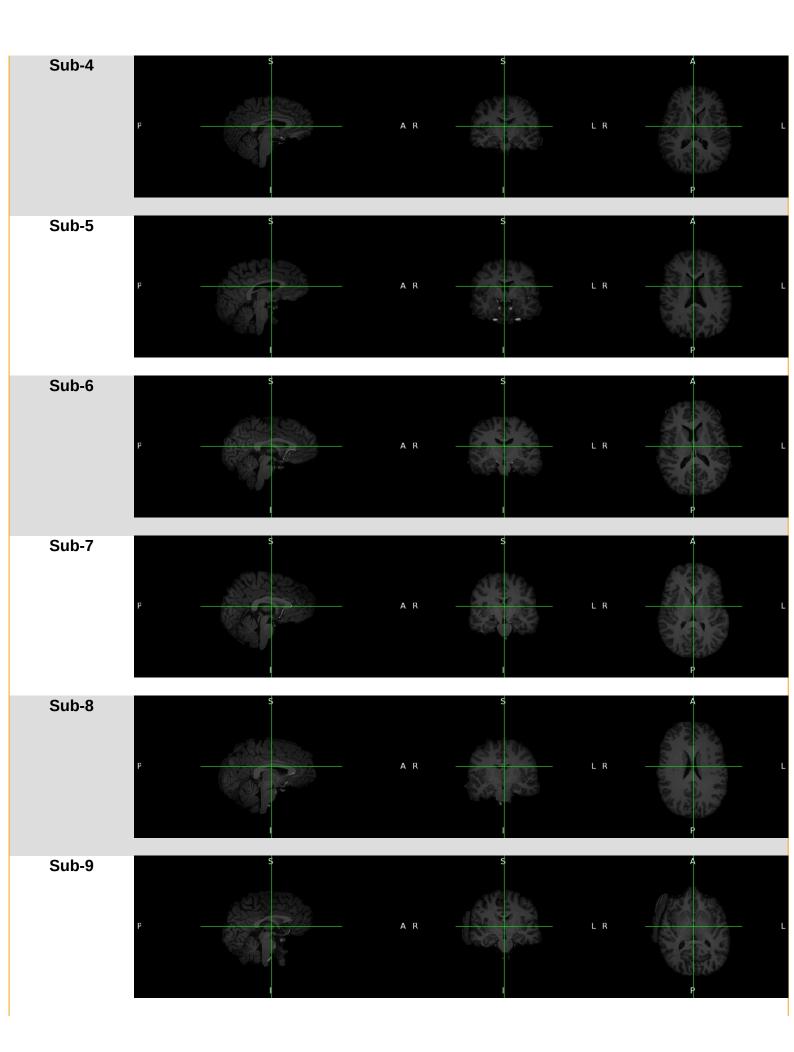


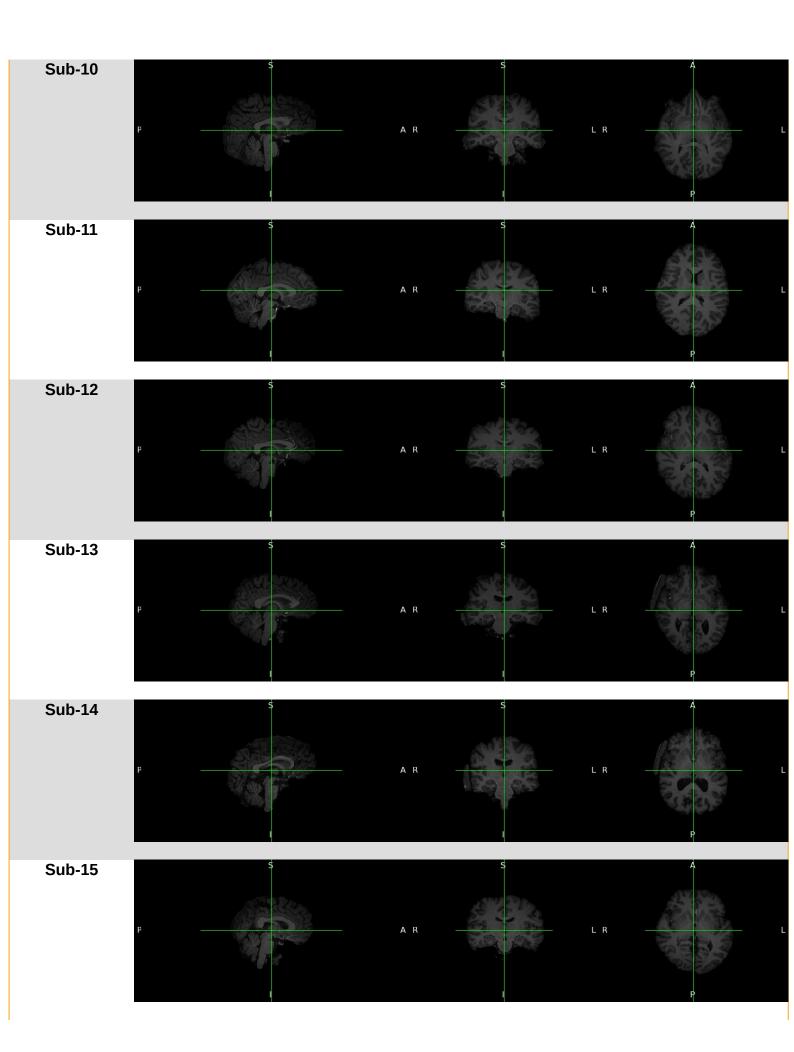


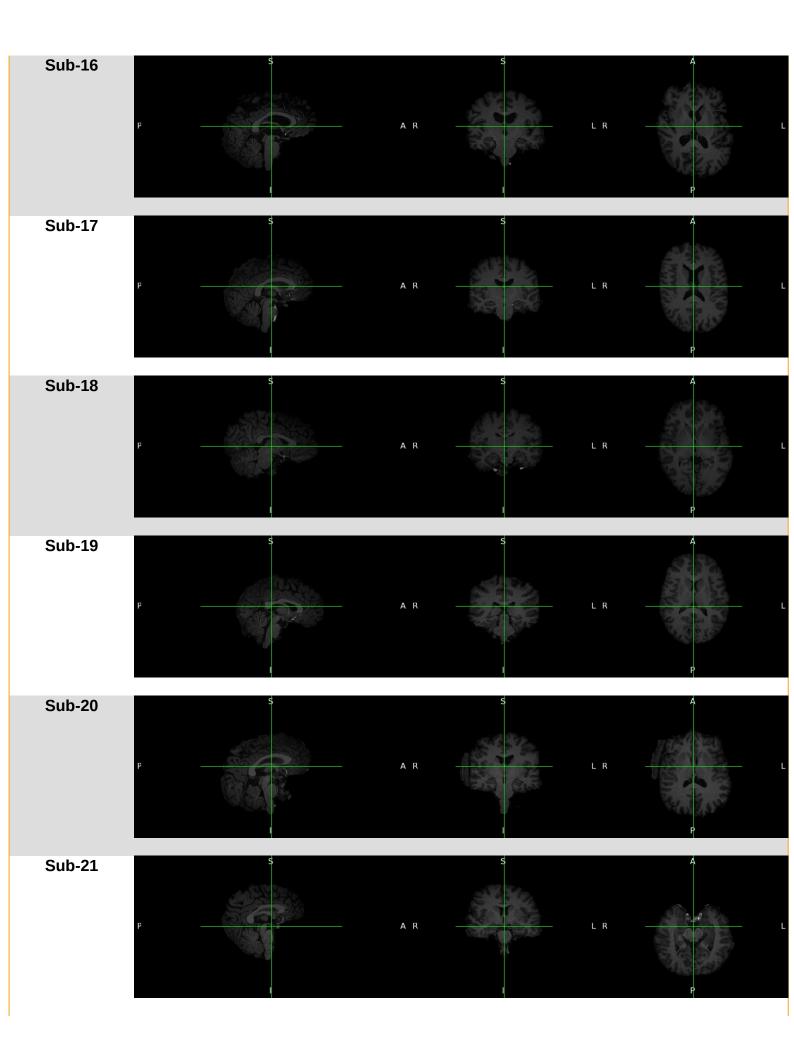


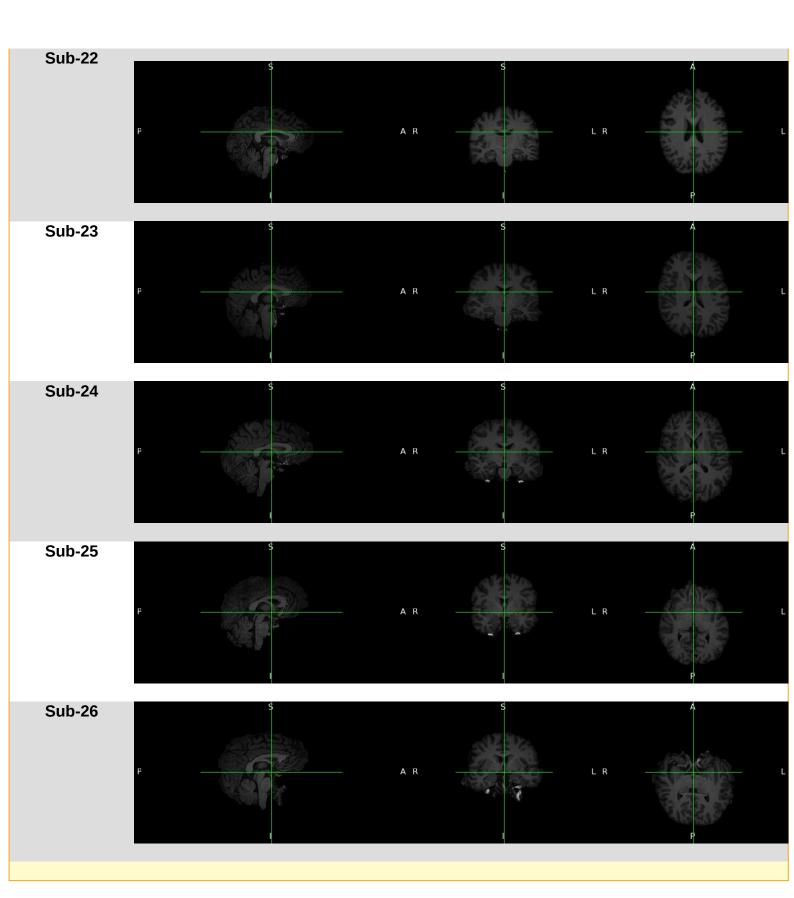




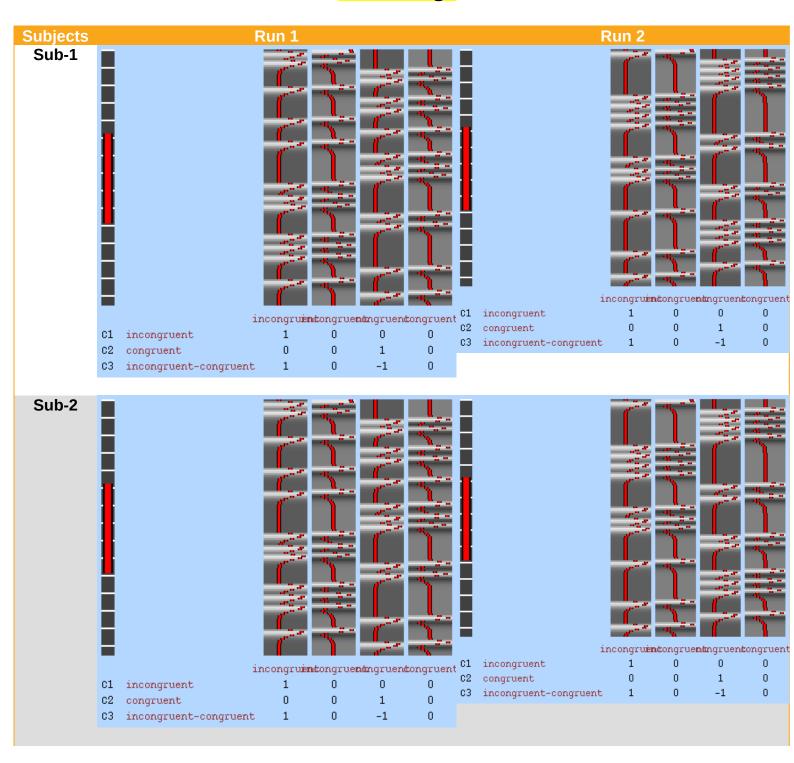


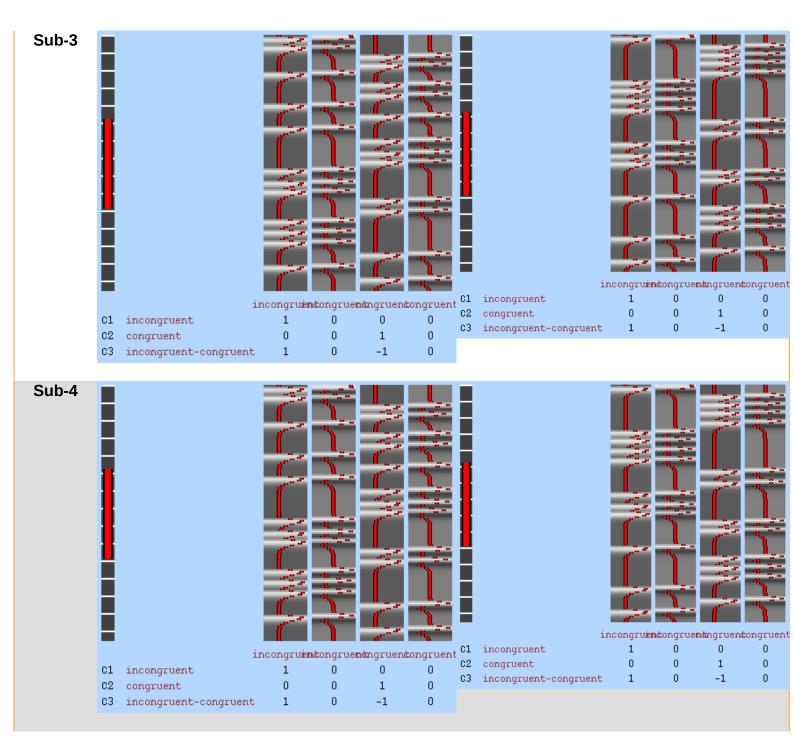


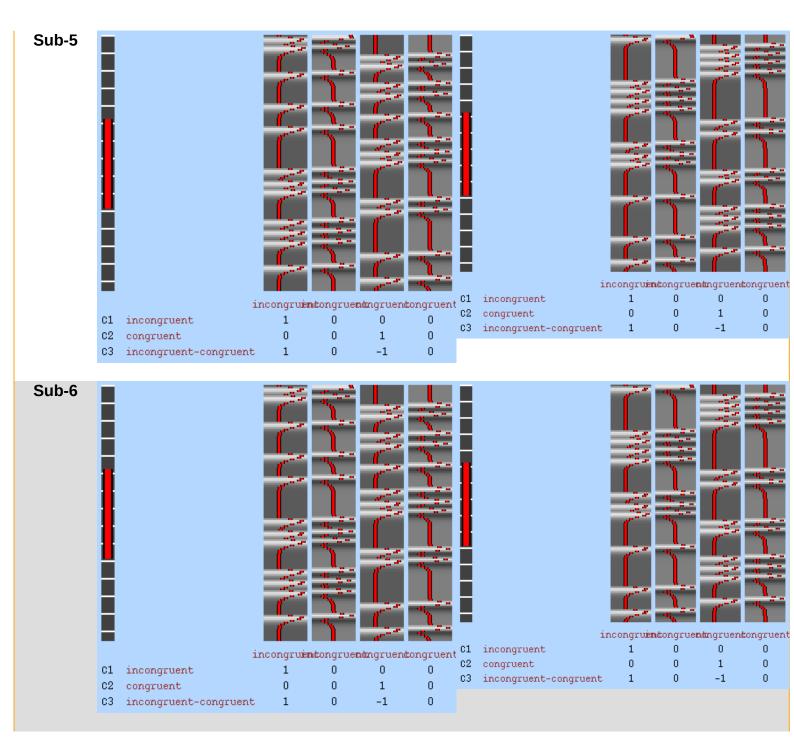


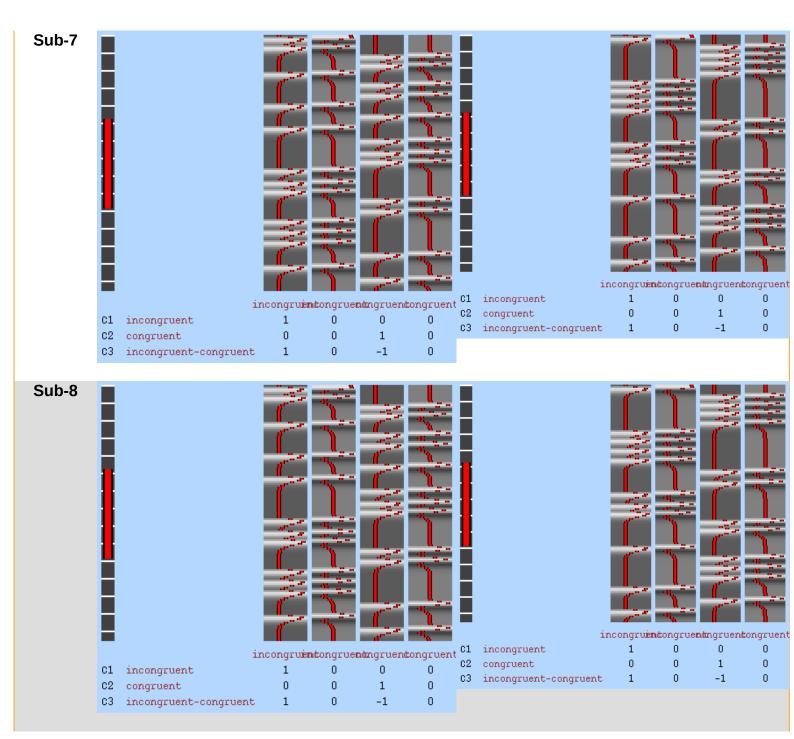


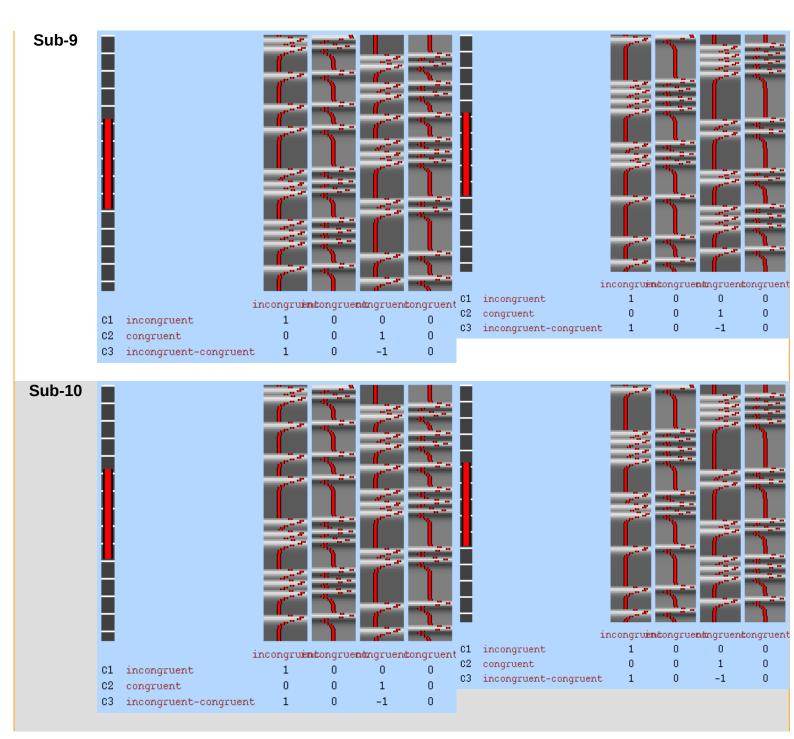
GLM Design

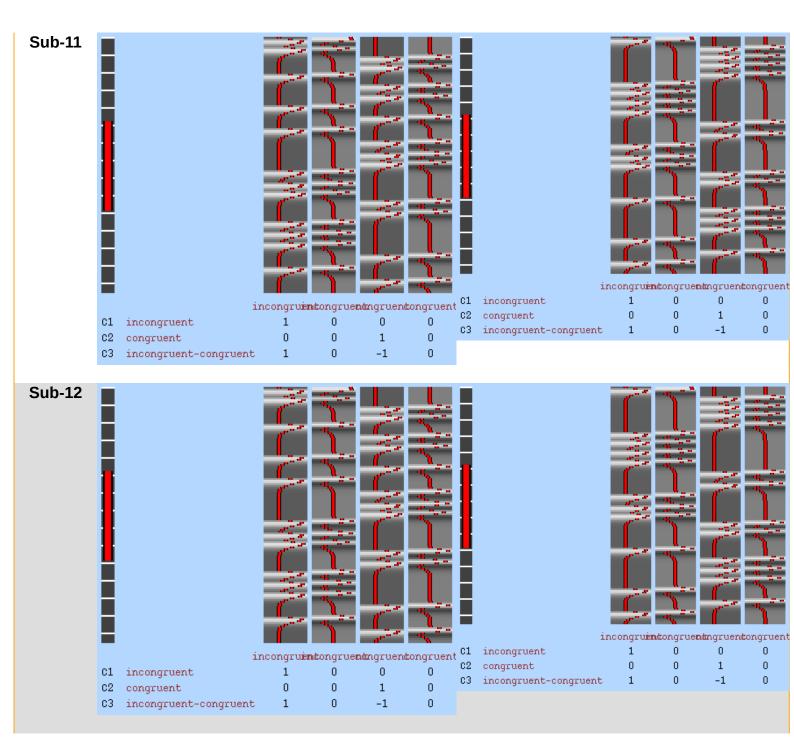


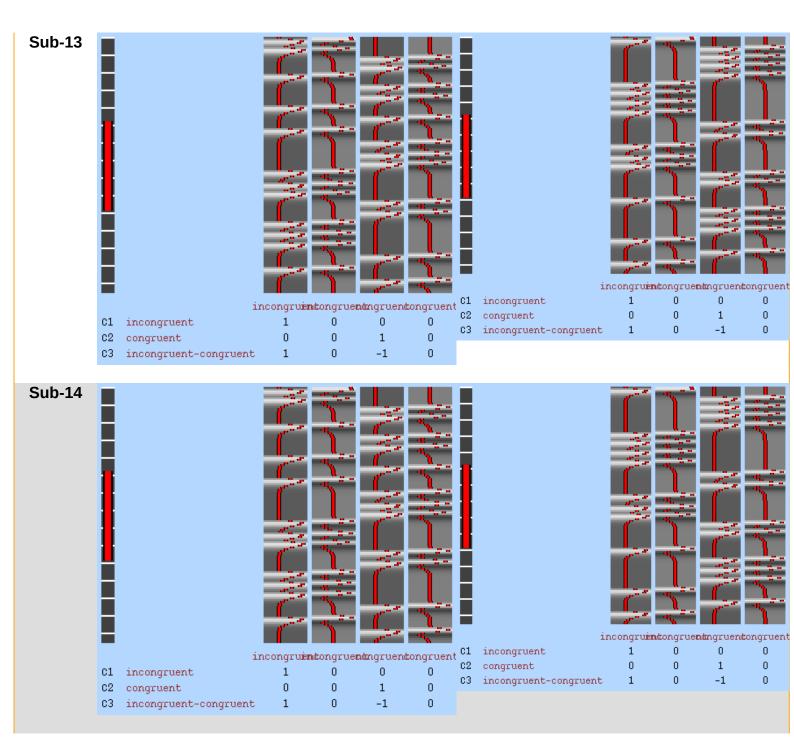


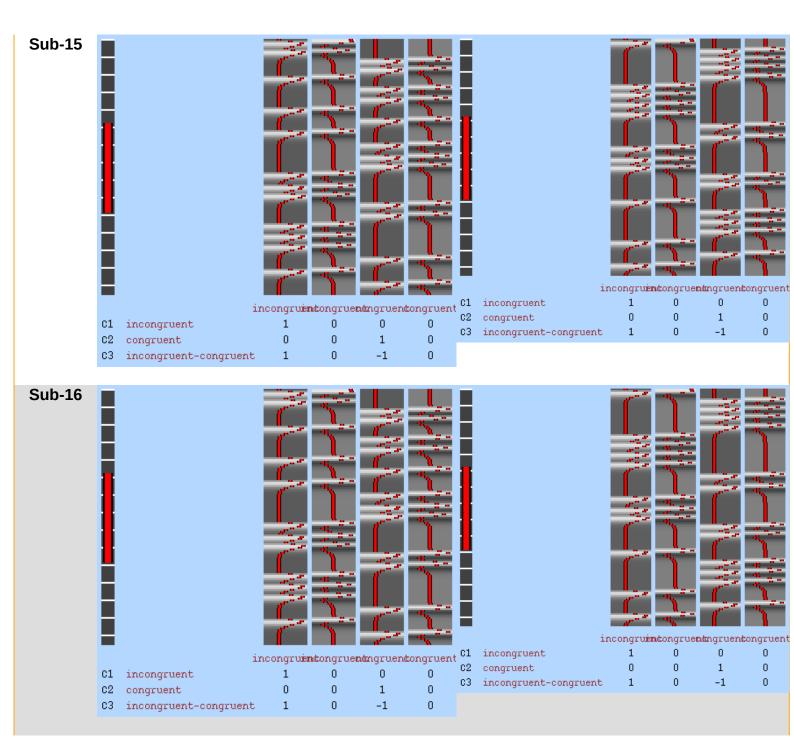


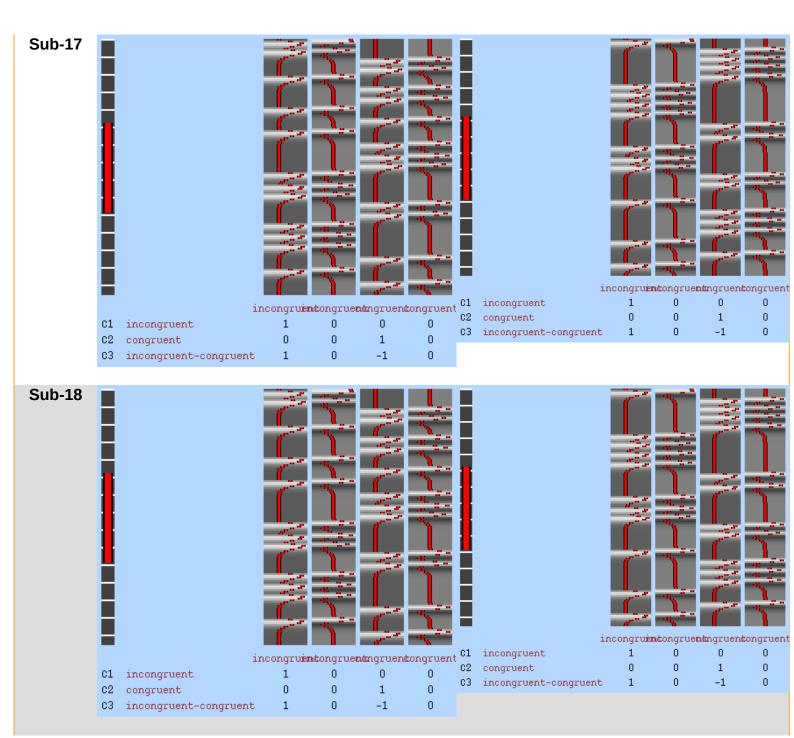


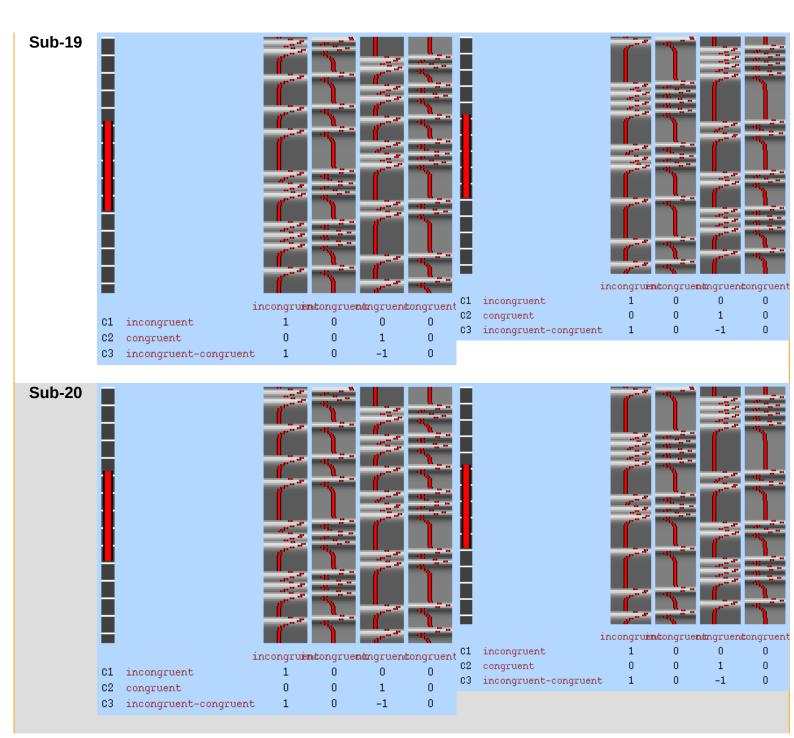


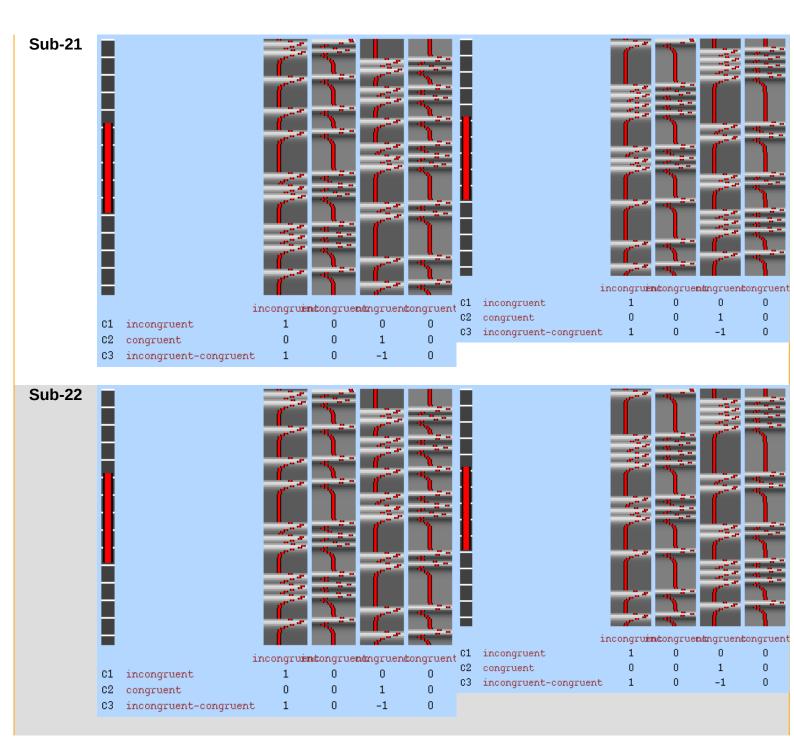


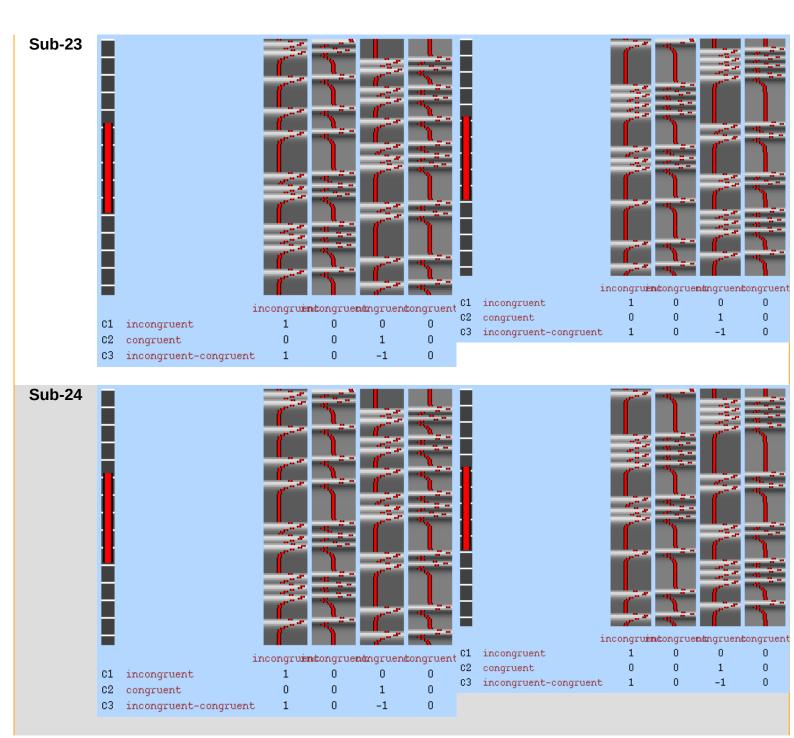


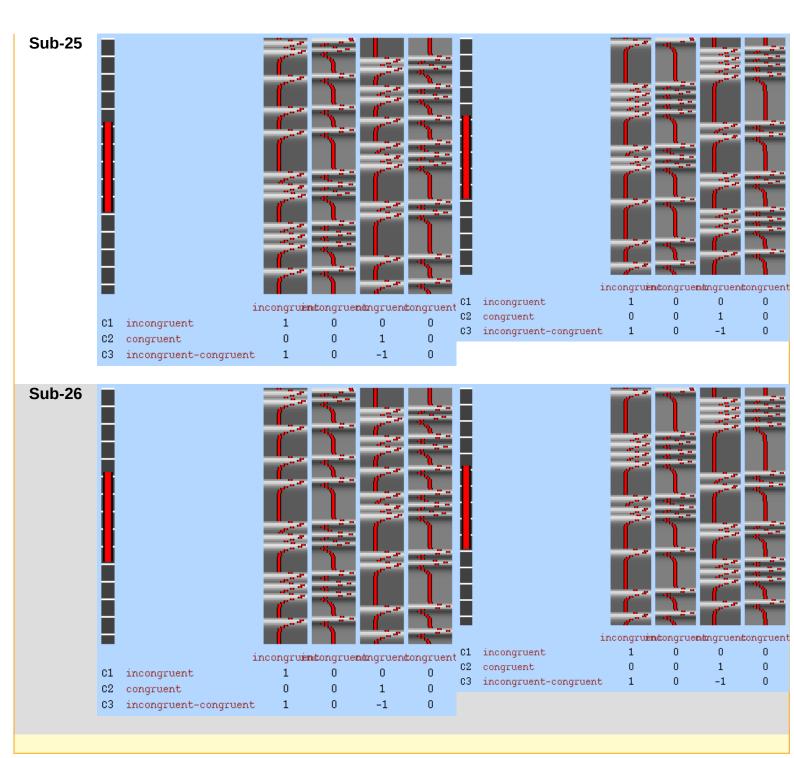












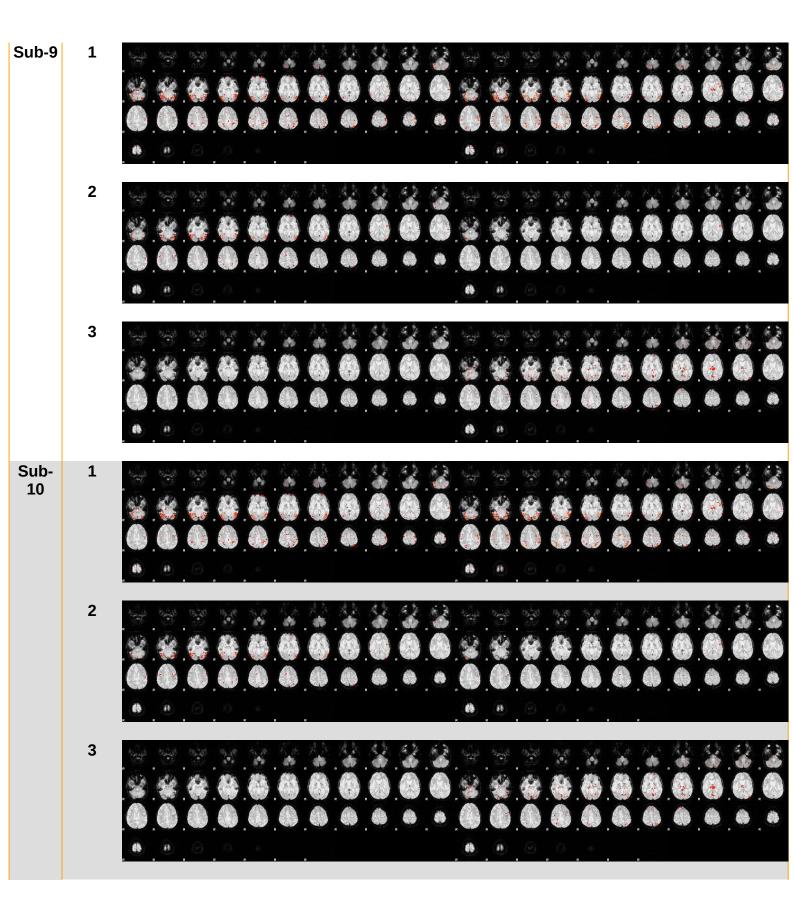
GLM Z-stats 1,2 and 3

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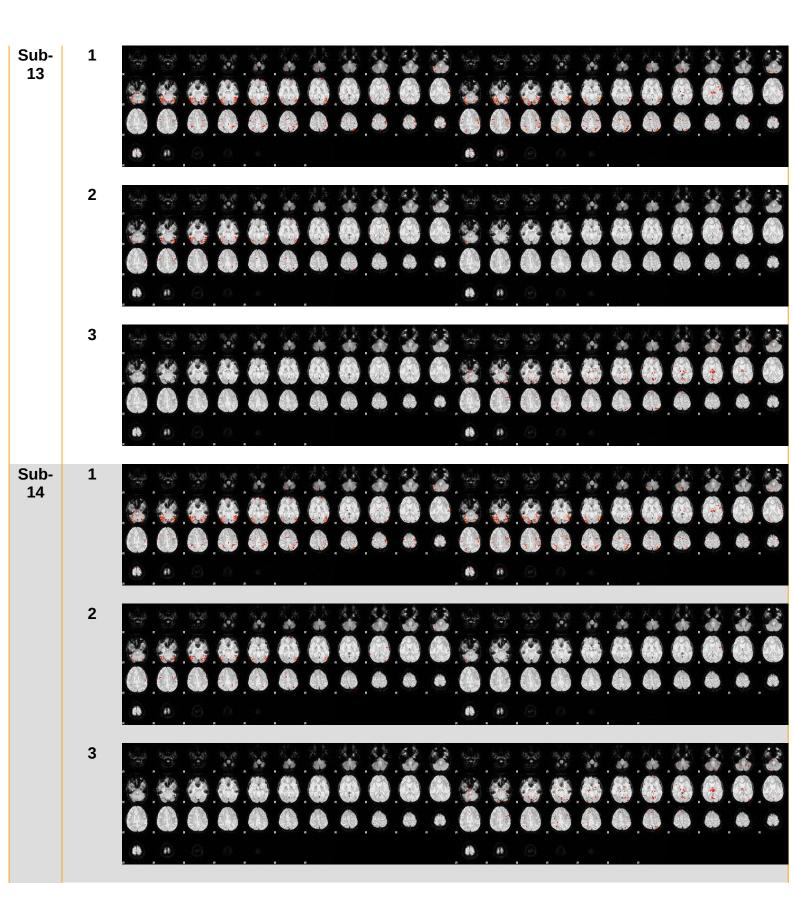


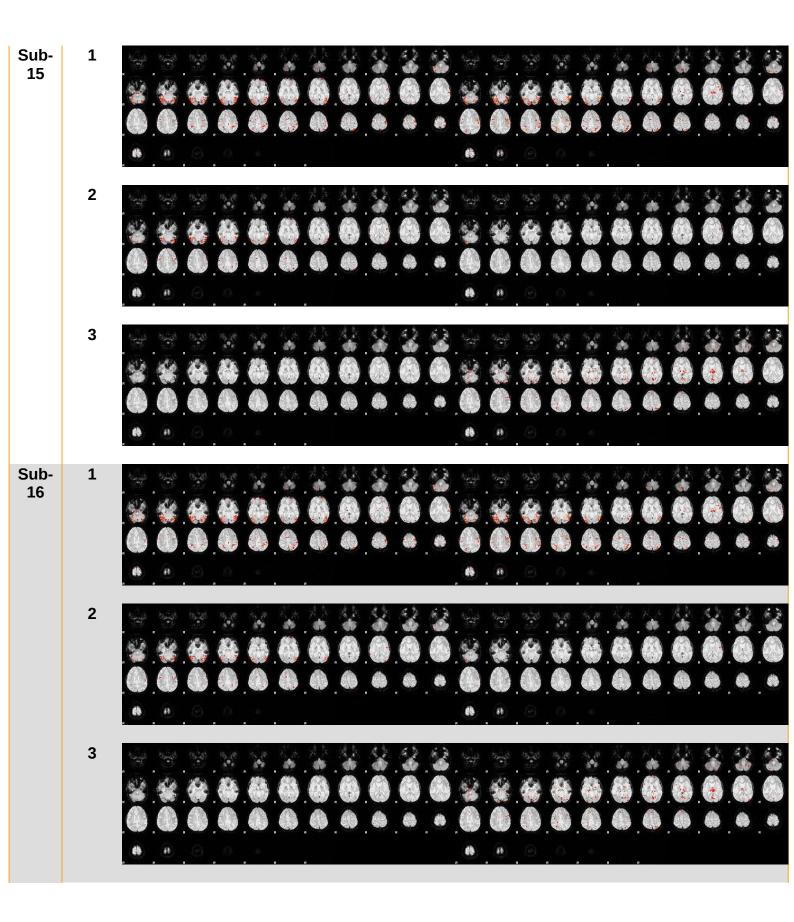


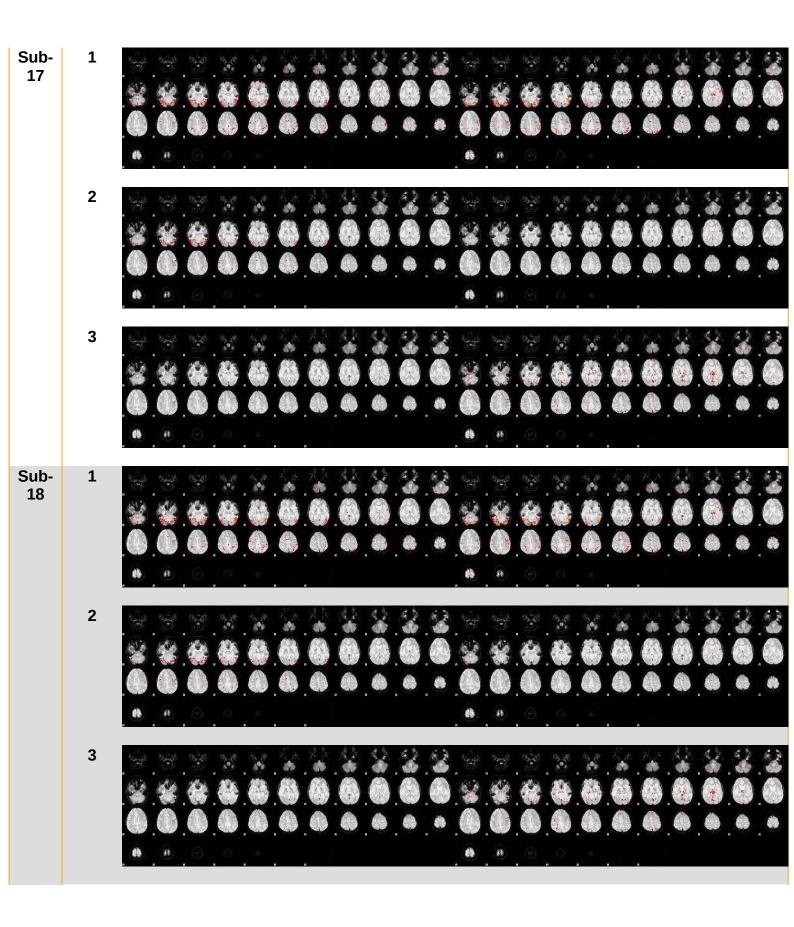


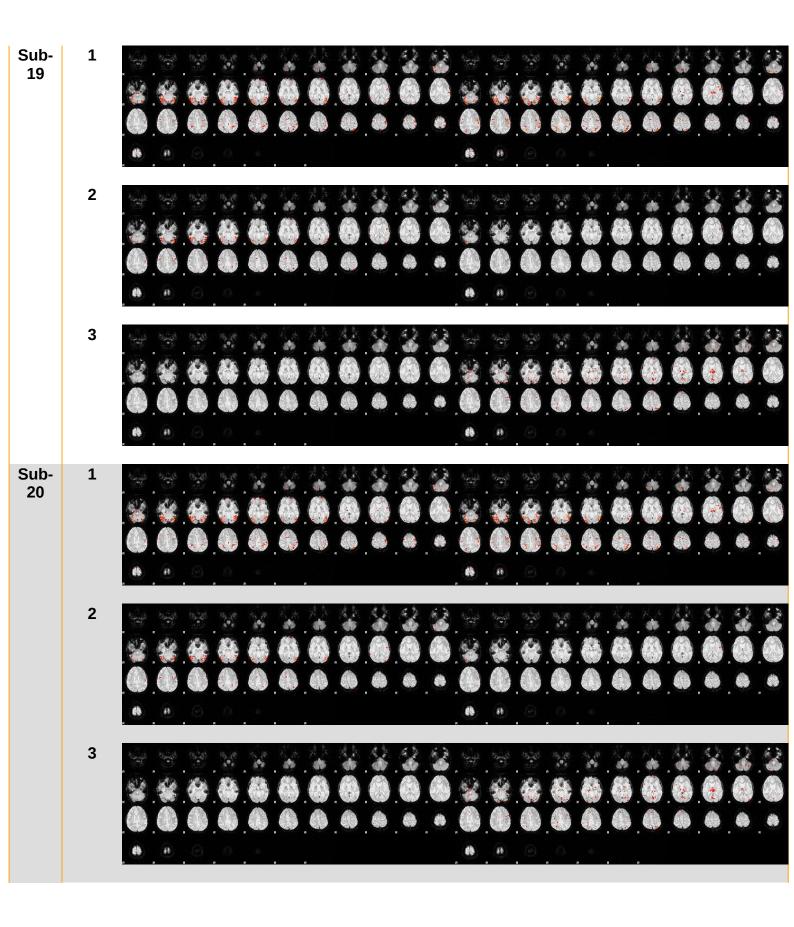


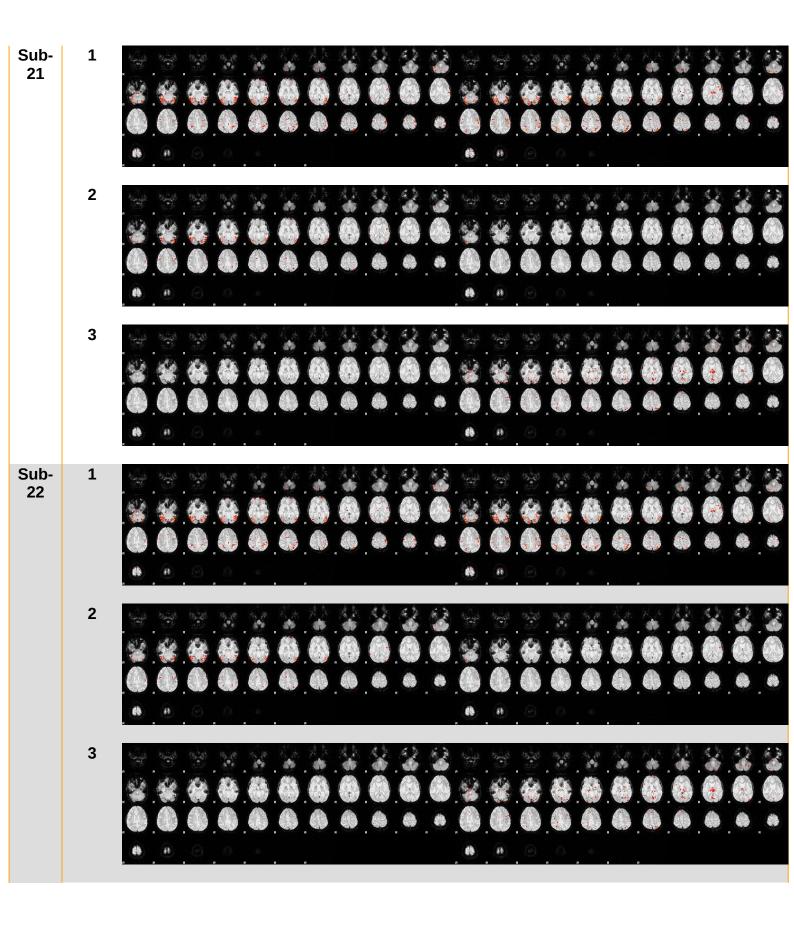


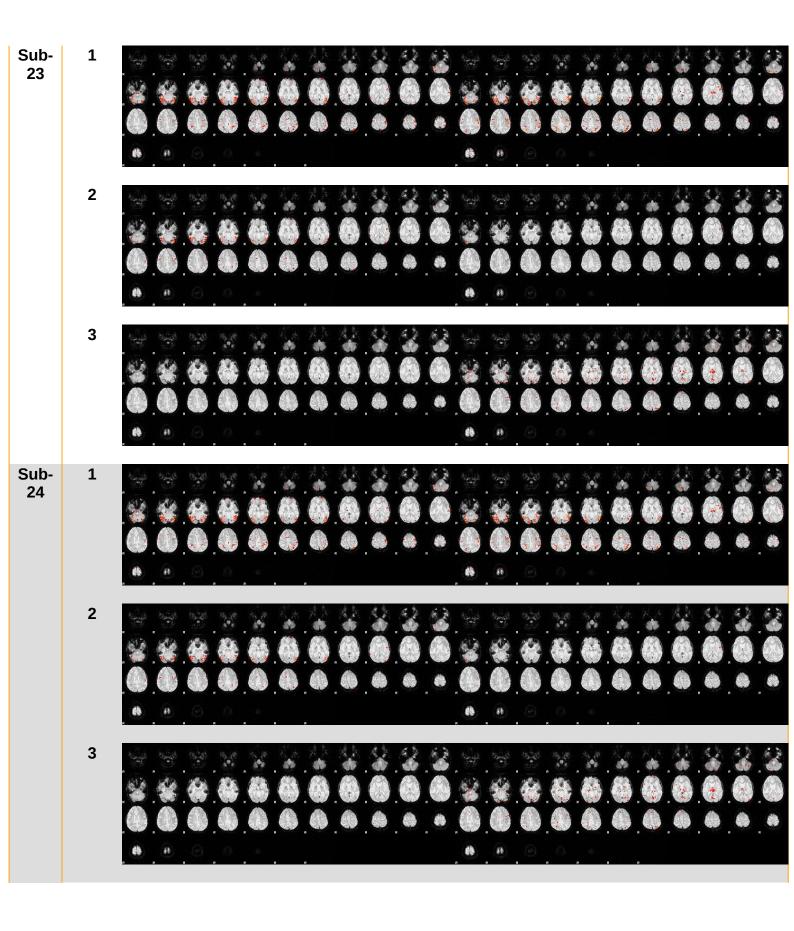


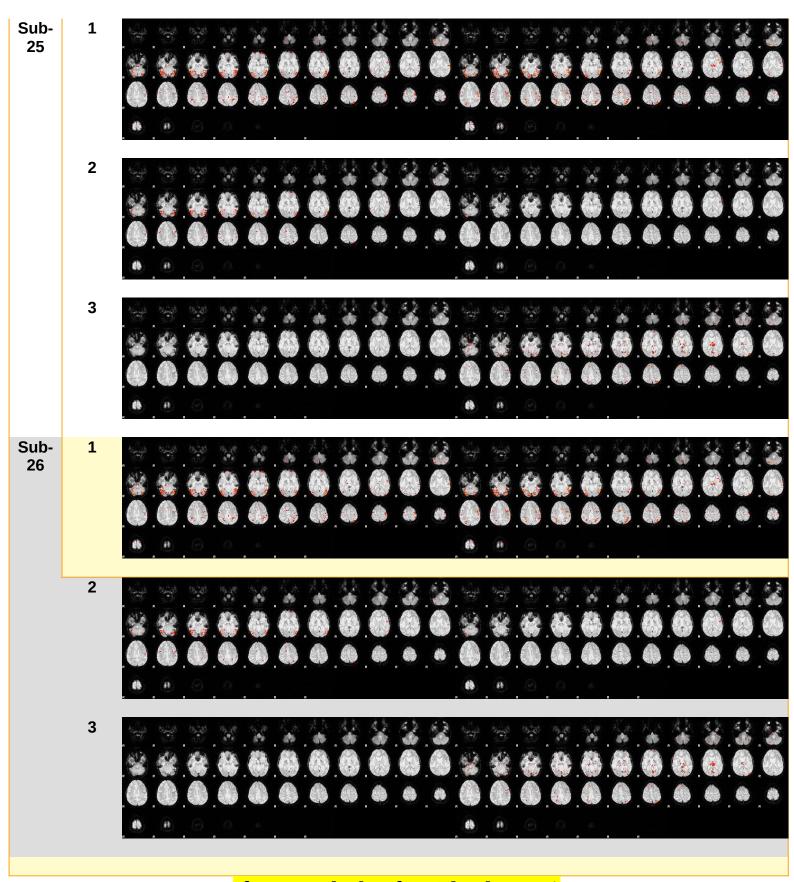












If you reached so far, Thank you:) attached with the report all full sized images for better resolution.