6/10/2022

* Look into the rationale for censoring the previous TR if a TR has too much motion? – this is automatically implemented by AFNI’s AFNIproc. Is it necessary?
* Do we need to include an exclusion criteria for root‐mean‐square realignment estimates (RMS movement) exceeding 1.5 mm for the entire session? (or run?)
  + <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3895106/>
* Do motion exclusion by BLOCK
  + Instead of including good runs, include good blocks (e.g., if no more than 3 TRs are censored within the block (i.e., at least 6/9 good TRs)
    - ~~First step will be generating a spreadsheet that shows how many good TR’s each child has for each condition per run~~
  + In analyses, can control for the # of blocks in each condition
* How many runs/blocks of conditions do we need? Is 2 okay, or do we need 3?
  + Kathleen says push through preliminary results with at least 2 runs (20 or 25%) for the first 2 aims of the grant
  + Alaina suggests running the analyses with only the 55 with at least 3 good runs as well, just to be sure its similar
* ~~Once I get the onsets changed, we can share the data with steve – after next week~~

6/20/2022

* Convert coordinates between the pediatric template and MNI to define location of clusters
  + <http://nist.mni.mcgill.ca/pediatric-atlases-4-5-18-5y/> see “Comparing different ages”
* ~~Rerun first-level analyses with 1s onset adjustment to account for going from fMRIprep to AFNI~~
* ~~Run AFNI’s 3dREMLfit for REML estimation of the temporal auto-correlation structure~~
  + necessary for running Mixed Effects Meta Analysis (3dMEMA) and Linear Mixed-Effects Modeling (3dlme) in AFNI
* Run Risk\*ED\*PS analyses with 3dMEMA
* Examine relationships between neural responses and portion size effect
  + Estimate fixed effects individual slopes (Alaina)
  + Whole-brain analyses
    - <https://afni.nimh.nih.gov/pub/dist/edu/latest/afni_handouts/afni24_GroupAna.pdf>
* Control for motion in group analyses? – motion might differ between risk groups

7/6/2022

* Currently re-running first-level analyses that:
  + Adjust onsets by 1s to account for fMRIprep slice timing correction
  + Run 3dREMLfit
  + When this is done – rerun group-level analyses, implement analyses with 3dMEMA
* Update on rationale for censoring the previous TR: have yet to find any
  + Instead of censoring previous TR, could drop threshold to .9 as recommended by <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3895106/> but only censor affected TR
    - What would the sample size look like with this protocol?
    - Can run analyses with this protocol and compare results
* Update on motion by block
  + Wrote a script that generates a table that says which says how many TRs are good for each block (condition) per person, by run
  + Next steps:
    - Generate new onset files based on motion-by-block
      * Can loop through above table: for each person, for each condition (column), [open orig\_onset file for condition], for each run (row), if the # of good TRs is < threshold, change the value in orig\_onsets to \*
    - Figure out what analyses will look like since some people will have some good conditions and not others

3dLME example that could account for some subjects having enough good blocks for some conditions, but not all

Analysis: Risk\*ED\*PS

Two within-subject factor (ED: high, low; PS: large, small)

One between-subjects factor (risk group: high, low)

Analysis: Risk\*ED\*PS

One within-subject factor (EDcontrast: LargeHigh-Low SmallHigh-Low)

One between-subjects factor (risk group: high, low)

Analysis: Risk\*PS

One within-subject factor (ED: high, low; PS: large, small)

One between-subjects factor (risk group: high, low)

* Whole brain and ROI approaches?

