

# More FMRI QC in AFNI: updates for afni\_proc.py's automatic HTML review Paul A. Taylor, Daniel R. Glen, Richard C. Reynolds Scientific and Statistical Computing Core, NIMH, NIH, USA

# FMRI processing is hard. AFNI's<sup>1</sup> afni\_proc.py makes QC easier. Here are new features in the QC HTML.

1) Check censoring both overall and per stimulus (for task-FMRI)

Motion censoring uses up degrees of freedom in data. Be careful to check overall, and for each stimulus type.

General censor fraction warnings
Done
Censored 6 of 450 total time points : 1.3%
Censor fraction warnings (per stim)
none
Max indiv stim censoring fraction : 2.5%
Censored 6 of 240 TRs of 'vis#0' stim : 2.5% Censored 0 of 239 TRs of 'aud#0' stim : 0.0%
General censor fraction warnings
medium
Censored 60 of 242 total time points : 24.8%
Censor fraction warnings (per stim)
mild
Max indiv stim censoring fraction : 24.1%
Censored 33 of 137 TRs of 'CONTROL#0' stim : 24.1% Censored 45 of 213 TRs of 'TASK#0' stim : 21.1%
General censor fraction warnings
severe
Censored 129 of 242 total time points : 53.3%
Censor fraction warnings (per stim)
medium
Max indiv stim censoring fraction : 51.2%
Censored 63 of 136 TRs of 'CONTROL#0' stim : 46.3% Censored 107 of 209 TRs of 'TASK#0' stim : 51.2%

Online tutorial: https://afni.nimh.nih.gov/pub/dist/doc/htmldoc/tutorials/apqc\_html/main\_toc.html

Contact: paul.taylor@nih.gov http://afni.nimh.nih.gov



### 2) For resting state, check seed-based correlation of some major networks.

For known standard spaces, seeds for 3 networks are pre-loaded: visual, auditory, and default mode.



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# 3) Check for left-right flips between EPI and anatomical volumes.

Surprisingly, this problem has been found in <u>a lot</u> of data<sup>2</sup> (in FCP, ABIDE, OpenFMRI,...). How can you be sure it isn't in yours? Check both quantitatively and visually!



[1] Cox RW. 1996. Comput Biomed Res 29:162-173 [2] Glen DR, et al. 2020. Front. Neuroinformatics 14.



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