

Multiple ways to process multi-echo FMRI data with AFNI Richard C. Reynolds, Stephen J. Gotts, Adrian W. Gilmore, Daniel R. Glen, Paul A. Taylor

AFNI's afni_proc.py can flexibly set up analyses for: single- or multi-echo FMRI; with/without physio; with/without B0 correction; on a surface or in a volume; for rest- or task-modeling; etc...

Processing variations with afni_proc.py Here we present convenient ways to process multi-echo (ME) FMRI data using AFNI's [1] main tool for pipeline design at the Method 1: single echo with basic processing ("control"). single subject level, afni_proc.py. This includes: both Method 2: ME-FMRI with echos "optimally combined". Method 3: same as #2, but with added BO-correction. volumetric and surface analyses; integrating with TEDANA for ME-ICA [2] or "optimally combining" echos; and incorporating Method 4: same as #3, but also used TEDANA to create B0-distortion correction and cardiac/respiratory regressors. regressors of no interest for the regression model. Method 5: same as #4, but with surface analysis. (We also show single echo processing, for comparison.)

Standard (single echo) FMRI

- + a slice is acquired after a single, fixed echo time (TE)
- + images are essentially T2* weighted
- + echo spacing maximizes signal in GM; produces BOLD signal

Multi-echo FMRI (ME-FMRI)

- + multiple echos per volume
- + echos can be combined in various ways to identify+remove noise features [3,4]

Data details

This dataset was acquired using a GE 3T scanner at NIH in accord with IRB protocols (details in [5,6]). It includes a T1w anatomical volume: voxels=1x1x1 mm³; matrix=172x256x256. Six ME-FMRI runs were acquired for a naming task of visually-presented event stimuli: TR=2200ms; TE=12.5,27.6,42.7 ms; voxels=3.2x3.2x3.5 mm³; matrix=64x64x33; N=237 volumes (each run). One ME-FMRI resting state run (N=220 volumes) was acquired with the same parameters. A single-echo reverse encoded EPI set (N=10, TE=27.6ms) was acquired for BO-correction. Cardiac and respiratory data were collected for each scan.

Processing details

Here we perform various combinations of analyses for the large dataset available. Censoring at enorm=0.2 and outlier fraction=5% was performed in all cases. For surface analyses FreeSurfer v7 [7] was first run to estimate surfaces from the T1w anatomical; results were converted to NIFTI volumes and standard mesh surfaces for use in SUMA [8,9]. For all volumetric analyses, AFNI's @SSwarper calculated nonlinear alignment to MNI space, and warps were applied within afni_proc.py; also, a blur of 5mm was used. In some volumetric cases, BO-distortion correction was also used, via nonlinear alignment of opposite-phase encoded EPIs.

> Acknowledgments: Research funded by the NIMH & NINDS Intramural Research Programs of the NIH, USA.

NIMH, NIH, USA | https://afni.nimh.nih.gov | contact: paul.taylor@nih.gov

We present 5 resting state processing examples to highlight the ease of implementing different analysis choices with afni_proc.py.

How hard is it to adapt afni_proc.py for each? Not very... Method $1 \rightarrow 2$:

+ add "combine" block, with lists of ME datasets and times: \${dsets_epi_me} -dsets_me_run \${me_times} -echo times -combine method

Method 2 → 3:

- + add the names of reverse-phase encoded (blip) datasets: -blip forward dset
 - -blip_reverse_dset

Method $3 \rightarrow 4$:

+ change the ME combination method and include an option: -combine method OC tedort -combine_tedort_reject_midk no

- Method 4 → 5:
- + change "tlrc" to "surf", and input surface datasets

Download this ME-FMRI Demo from AFNI You can (and should!) get the full Demo data+scripts. Run: @Install_AP_MULTI_DEM01

[1] Cox 1996. CBR 29:162-173, 1996.

[2] Kundu et al. 2012. NI 603:1759-1770. [3] Barth et al. 1999. MRI 17:321-329.

\${epi forward} \${epi_reverse}

[4] Posse et al. 1999. MRM 42:87-97. [5] Gilmore et al. 2019. Neuropsy 124:31-43. [6] Gotts et al. 2020. NI 205:116289.

Let's look at some seed-based correlation maps from each method, via the automatic QC HTML: DMN (seed in Ih-PCC) and Visual network (seed in rh-cort-vis).





Results tend to be similar, but ME methods show larger, more symmetric correlation patterns than single echo. Though, Method #4 shows high correlation in several areas of WM. You can test them all (and more) using afni_proc.py!

[7] Fischl et al. 2002. Neuron 333341-55. [8] Saad et al. 2004. IEEE-ISBI 1510-1513. [9] Argall et al. 2006. HBM 27(1):14-27.



#2412

DMN

Meth #5