

# A multi-echo fMRI processing demo including TEDANA in afni\_proc.py pipelines

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## Introduction

Multi-echo (ME) acquisitions are increasingly popular in fMRI. Acquiring multiple echos per time point (typically 3-5) provides useful information for noise reduction and SNR increase, compared to standard single echo (SE).

There are several methods/tools for combining the echos. It is nice to test them systematically within a coherent processing framework, like with AFNI's<sup>1</sup> afni\_proc.py. In fact, afni\_proc.py has previously implemented a ME processing block and several ME combination/denoising methods, including from Posse et al. (1999)<sup>2</sup>, Kundu et al. (2011)<sup>3</sup>, and the recent TEDANA of DuPre et al. (2021)<sup>4</sup>.

Here we describe updates to these in AFNI's "APMULTI" demo, particularly with TEDANA (whose QC report is now included in afni\_proc.py's own QC HTML). The demo also incorporates nonlinear alignment, physio regressors, blip up/down correction, and/or surface-based analysis.

## Methods

The demo contains several afni\_proc.py commands for comparison: one SE example and eight ME examples. The following ME-fMRI methods (with and without smoothing applied) are investigated:

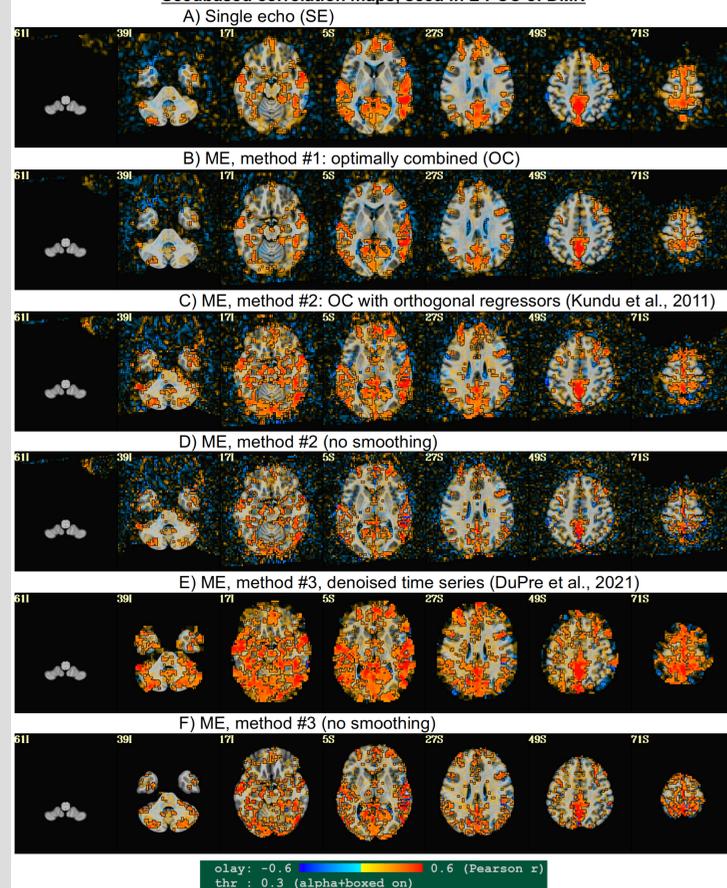
- 1) optimally combining (OC) across echoes;
- 2) OC with passing the orthogonal regressors from tedana (from Kundu et al.);
- 3) using TEDANA-denoised time series (DuPre et al.)

The data used in the APMULTI demo has been described previously<sup>5,6,7</sup>. **Data:** Briefly, it includes a standard T1w anatomical volume (1mm isotropic voxels) and one ME-fMRI resting state run with: TR=2200ms; TE=12.5, 27.6, 42.7 ms; voxels=3.2x3.2x3.5 mm<sup>3</sup>; matrix=64x64x33; N=220 volumes. A single-echo reverse encoded EPI set (N=10, TE=27.6ms) was acquired for B0-correction. Cardiac and respiratory data were collected.

**Processing:** Using AFNI (v21.3.11) nonlinear alignment from anatomical to MNI standard space was estimated with @SSwarper, and slicewise physiological regressors were estimated with RetroTS.py. Anatomical surfaces and parcellations were estimated with FreeSurfer<sup>8</sup>, v7. Outputs from these steps were variously incorporated in afni\_proc.py commands.

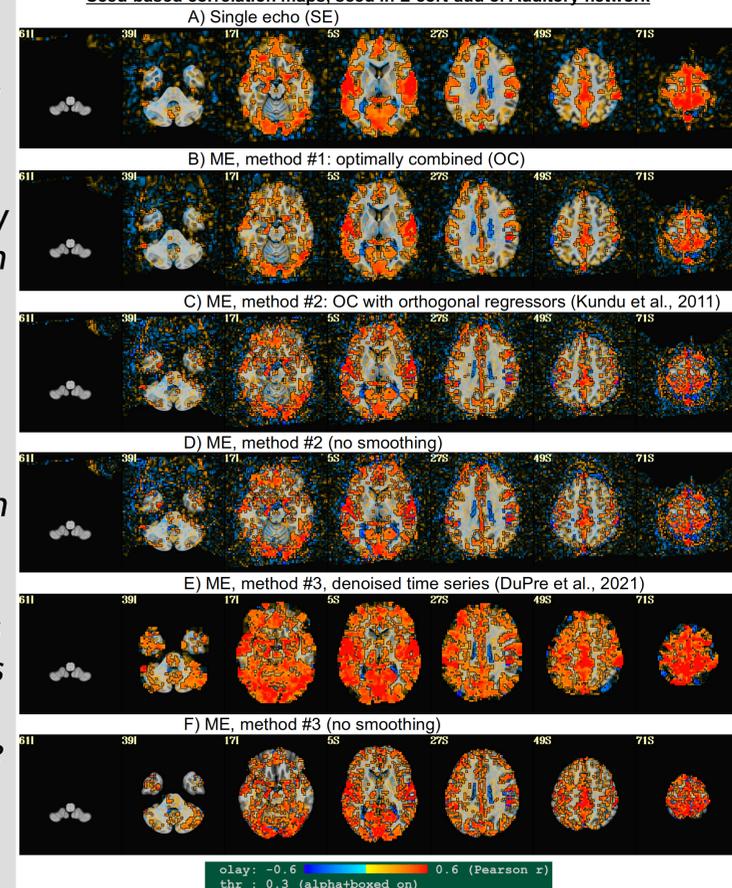
## Results

Seedbased correlation maps, seed in L-PCC of DMN



Seed-based correlation maps from the afni\_proc.py QC HTML, showing (left) the default mode network (DMN) with a seed in the left-posterior cingulate cortex (L-PCC) and (right) the auditory network with a seed in the left-auditory cortex (L-cort\_aud). Pearson correlation values translucently thresholded at a magnitude of  $|r| = 0.3$ . Each image is an axial slice (left=left), with slice coordinate provided (I=inferior, S=superior). By default, afni\_proc.py outputs are not masked, and correlation values are shown throughout the FOV, for QC purposes; the TEDANA software in method #3, however, currently masks the data during processing. These maps also show that spatial blurring is often not necessary during ME processing, due increased SNR from the echoes.

Seed-based correlation maps, seed in L-cort-aud of Auditory network



## Conclusion

ME-fMRI acquisitions can yield higher SNR than standard SE ones. Because ME processing strategies are still under development, it is useful to be to include various ones in a consistent processing framework, which afni\_proc.py does. This allows for easily comparable outputs, which are themselves flexible (e.g., one could use voxelwise or ROI-based comparisons), and integrated QC checks (now, TEDANA's QC is included with afni\_proc.py's QC HTML). Checkout AFNI's APMULTI demo to get started with several possible ME-fMRI processing options.

## Download the Demo

To download AFNI's APMULTI demo (containing full data and scripts), please run:

@Install\_APMULTI\_Demo1\_rest

## Acknowledgment & References

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