OF A MASSIVELY REPEATED BLOCK DESIGN TASK Benjamin Gutierrez<sup>1</sup>, Daniel A Handwerker<sup>1</sup>, Javier Gonzalez-Castillo<sup>1</sup>,

Vinai Roopchansingh<sup>2</sup>, Laura Buchanan<sup>1</sup>, Peter A Bandettini<sup>1,2</sup>

Subject 1

1. Section on Functional Imaging Methods, LBC, National Institute of Mental Health, Bethesda, MD 2. Functional FMRI Facility, National Institute of Mental Health, Bethesda, MD



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fMRI is limited by our ability to distinguish neuronally interesting signal fluctuations from artifacts and noise. A recently developed technique uses multi-echo fMRI scans to empirically remove artifacts (Kundu 2011 & 2013). In this study we show how multi-echo denoising effects the signal quality and stability of the very common fMRI block design study.

In a typical fMRI study, protons are excited and a slice is acquired after an echo time that is optimized for blood oxygen level dependent (BOLD) signal changes. For multi-echo fMRI, the same slice is rapidly acquired at several echo times after each excitation. Multi-echo denoising is based on the idea that the magnitude of a BOLD weighted signal will scale with echo time, but artifacts that aren't BOLD weighted will be constant (Kruger 2001 & Peltier 2002). ME-ICA denoising splits multi-echo data into ICA components, removes the components that are unlikely to represent BOLD fluctuations, and then reconstructs a denoised time series with the remaining components (Kundu 2011)

Using the same experiment design as (Gonzalez-Castillo 2012), we collected 103 runs of the same task across multiple days, but acquired multi-echo rather than single-echo fMRI. By fitting responses and calculating activation maps for each run separately, using standard single-echo and multi-echo processing methods, we were able to see how using a multi-echo approach to a standard task-based fMRI analysis can improve results.

# METHODS

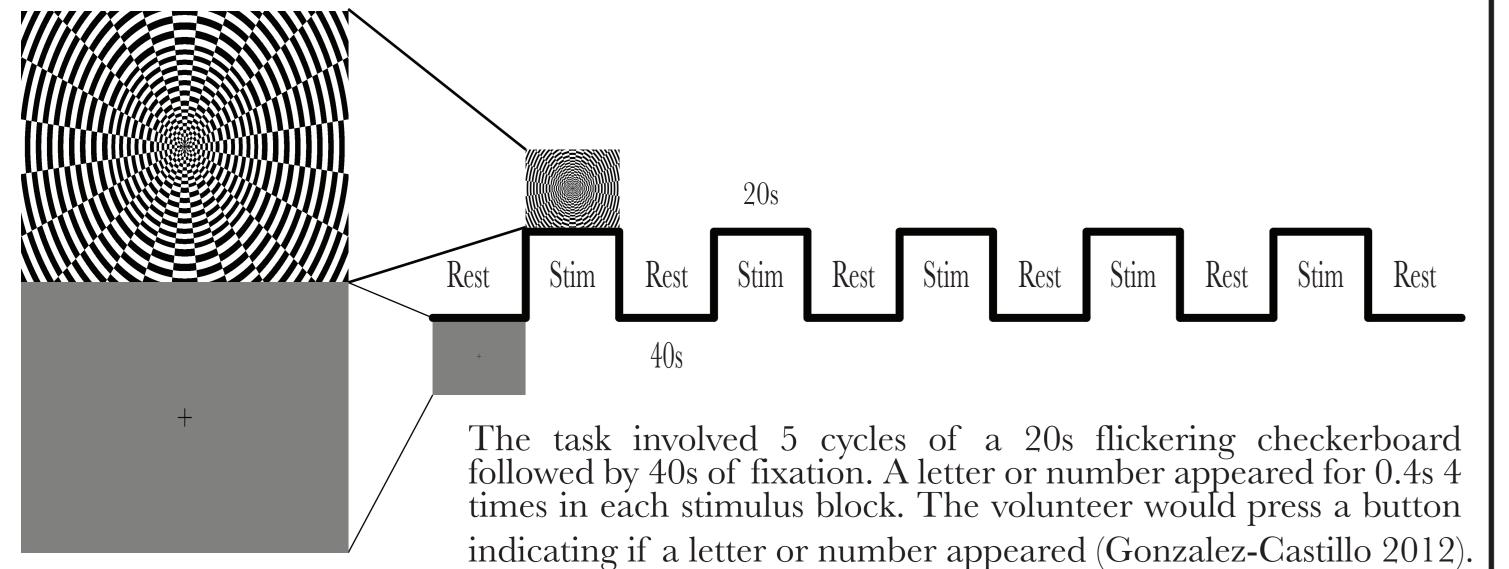
### **Data Collection**

GE 3T MR 750 MRI scanner, GE 32 channel head coil. GRE EPI, TR=2s, TE=15.4, 29.7, & 44.0ms, FA=75°

33 oblique slices, 3.5mm<sup>3</sup> voxels, 0mm gap, 64x64 grid, ASSET=2.

1mm<sup>3</sup> MPRAGE T1 weighted and proton density weighted scans were collected during each session to use for tissue segmentation and registration.

Data are from two healthy adults (1M, 1F) collected over 9 days. Each day included 10-13 340 sec runs of the same task. Each volunteer had 103 total runs of the task.



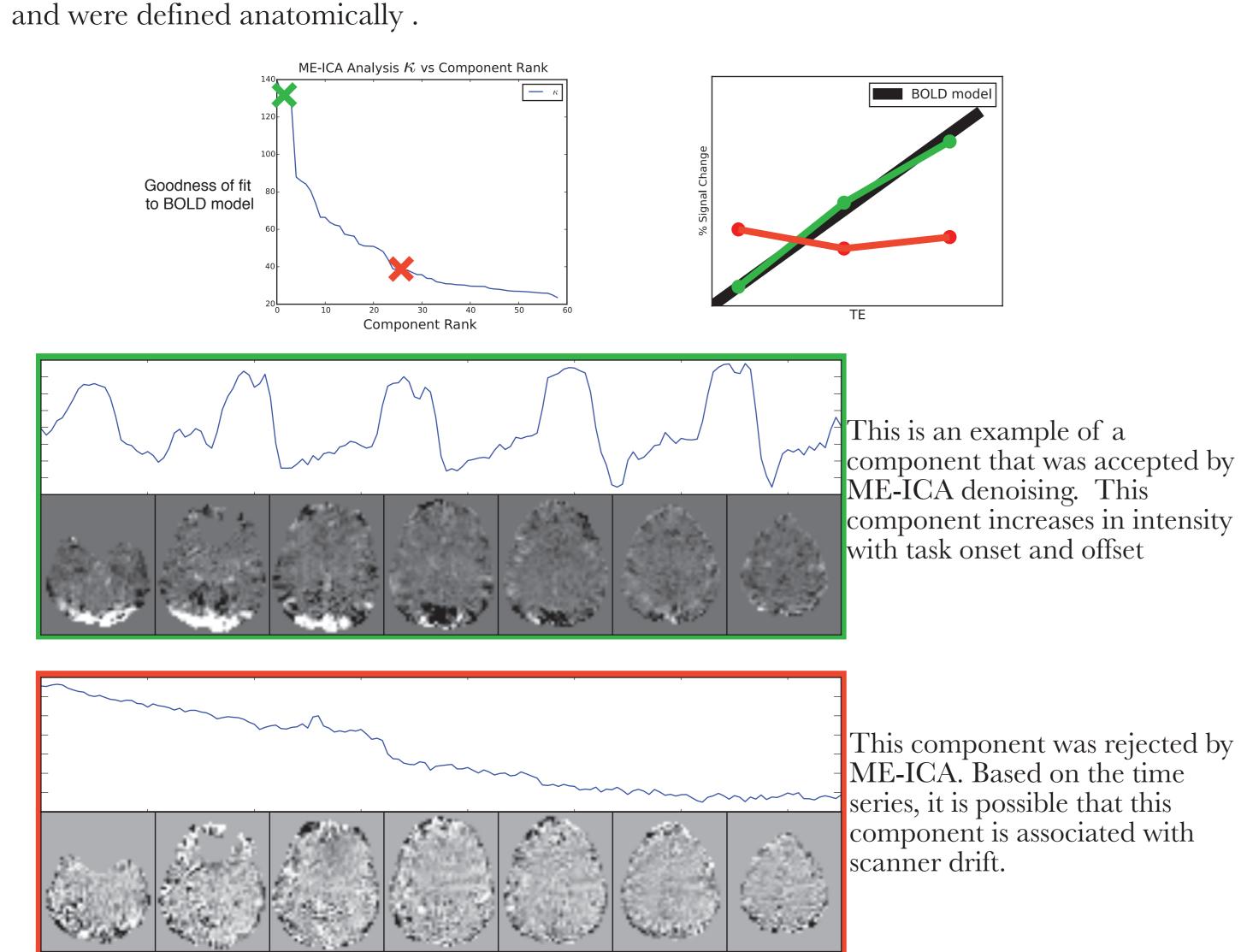
### **Preprocessing**

Data were processed using AFNI and Python (for the ME-ICA denoising code) in each volunteer's native space. The anatomical scans from the 9 sessions were registered to the scan from the first session. The data were despiked, slice time corrected and motion corrected. The first scan of every session was aligned with the anatomical scan from the same day and then the first day's anatomical scan. Alignment and motion correction parameters were calculated on the middle echo time series and applied to all 3 echoes as a single transform matrix.

ME-ICA denoising was then performed using code from https://bitbucket.org/prantikk/me-ica The Optimally Combined time series are a weighted average of the three echoes. The denoising process involved running a spatial ICA on the optimally combined time series, removing components that were deemed unlikely to be BOLD weighted, and recombined the remaining components into a denoised data set. The decision criteria were slightly adjusted from the released code to more conservatively keep components. The changes include removing one rejection criterion which occasionally would reject high kappa components because they had high variance, making the rho elbow 95% of it's original value, and adjusting one line of code to better assume high kappa components are BOLD related. The middle echo time series (echo2) with TE=29.7ms was considered a standard single-echo fMRI run for comparison analyses.

A finite impulse General Linear Model (GLM) for reach run was performed on the data. Using the results from the GLM, significance maps (FDR < 0.05), and contrast to noise (CNR: magnitude of the hemodynamic response function divided by the standard deviation of the residuals) were created.

The Calcarine Sulcus and the Lateral Genticulate Nucleus were selected as regions of interest



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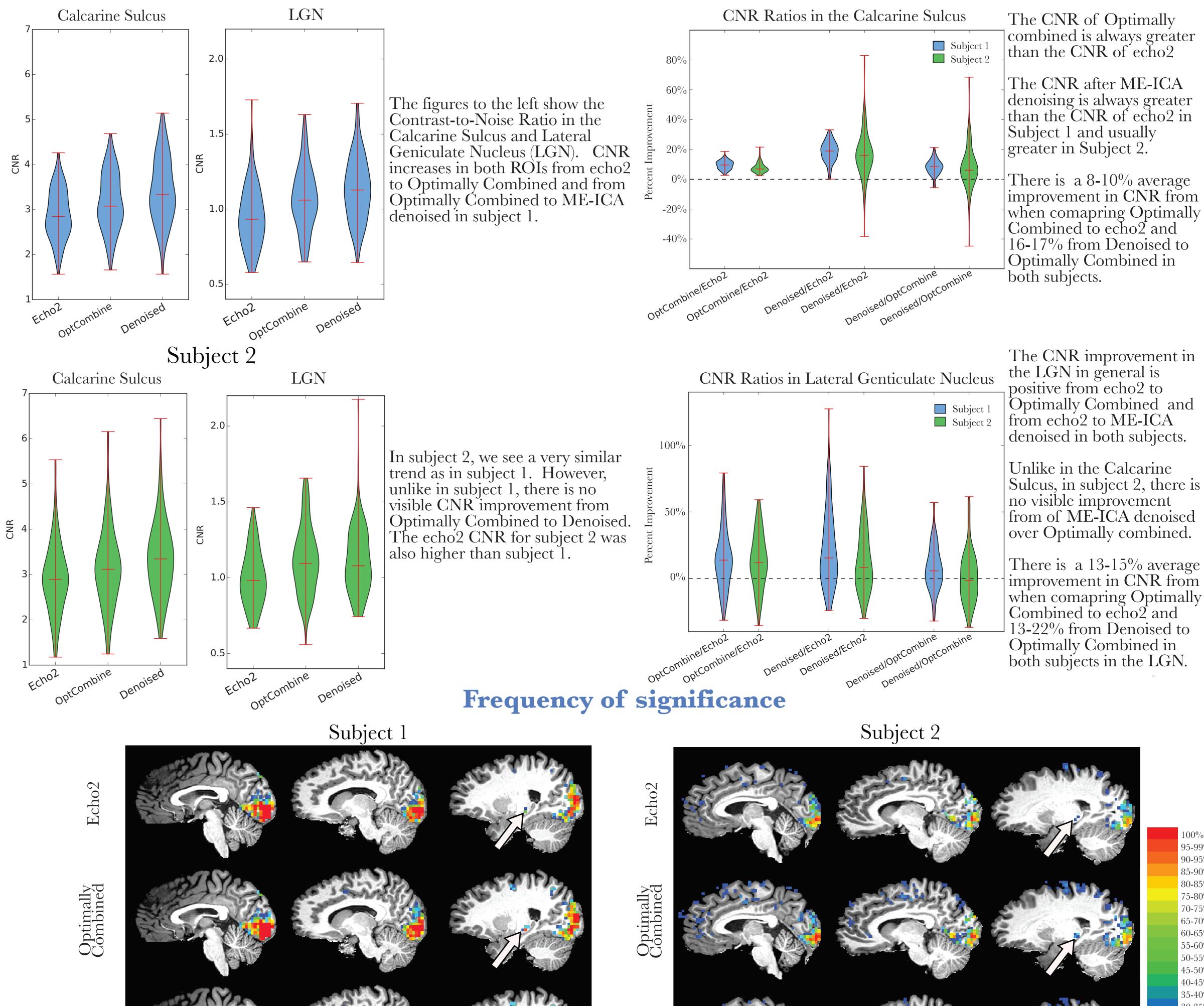
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# RESULTS

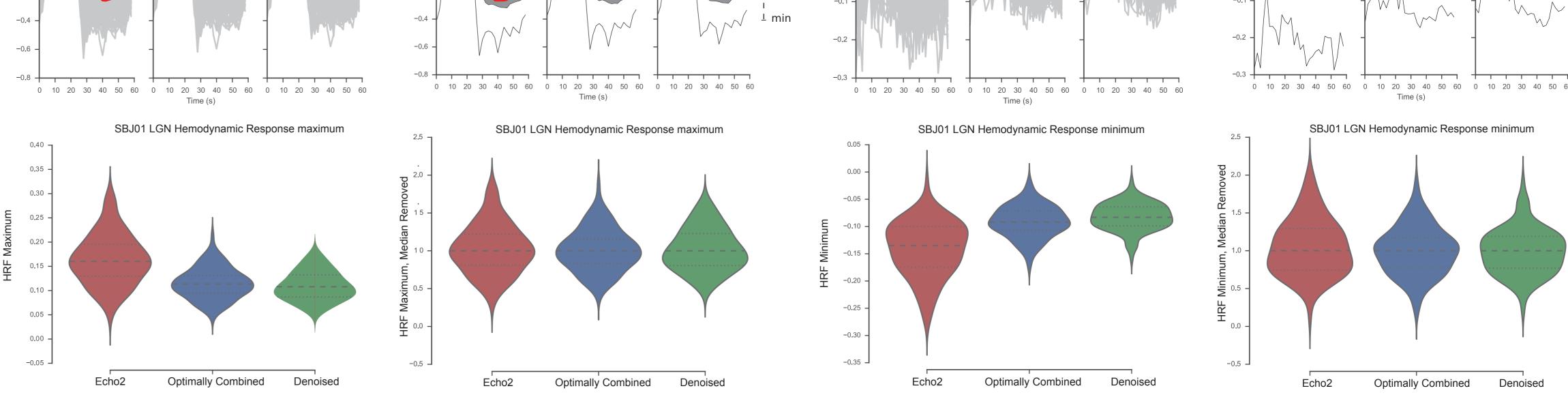
### Contrast to noise

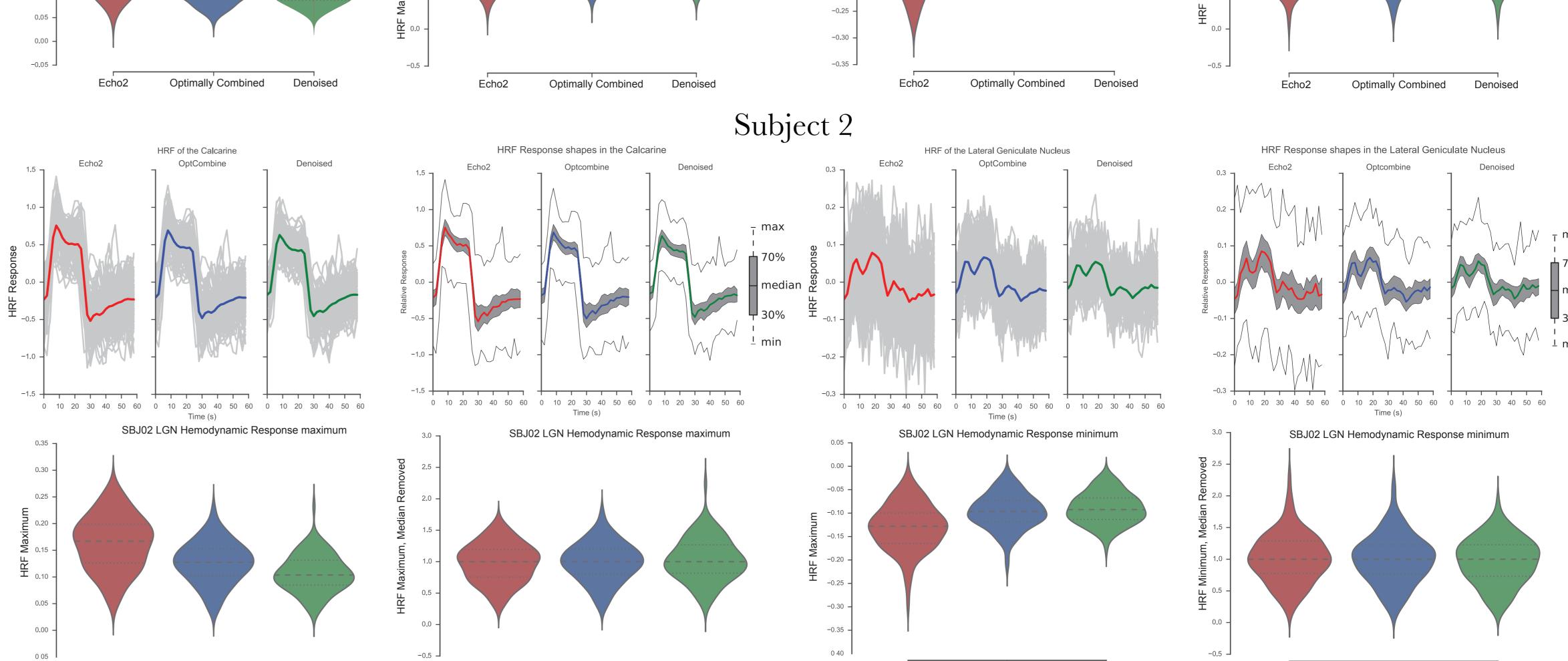


The figures on the left shows voxels that were active in at least 25% of the GLMs. The blue to red color scale represents a voxel being significant in more individual GLMs. Looking down a column, it can be seen that more voxels reach threshold and more voxels achieve activation in a higher number of runs. The LGN is visible in all three processing methods, however it is most well defined in the Denoised row of the table.

Hemodynamic Responses

# Subject 1





Here we examine the HRF and time series of both subjects in the LGN and Calcarine Sulcus. There is a noticeable reduction in variability from echo2 to Optimally Combined and then to Denoised in the LGN for both the time series and HRF. The max and min plots of the HRF show that there is a reduction in the magnitude of the maximum and minimum of the HRF. However, when the median is removed, we see that this change is proportional to the relative sizes of the HRFs. This indicates that our reduction in CNR comes from reduction in noise.

# CONCLUSIONS

Multi-echo imaging provides two methods of reliable CNR improvement and HRF variance reduction. In regions of robust activation, ME-ICA denoising provides an even larger boost in these two metrics. In areas of less robust activation, like the LGN, ME-ICA did not reliably improve CNR in a single run. The HRF shows improvement in variability from a reduction in noise when using multi-echo data processing methods.

These results suggest a promising future for ME-ICA denoising, but the higher variance in CNR after denoising shows the method can be improved. Future work will focus on finding better ways to use the multi-echo information to empirically identify and keep relevant signal and remove noise.

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