From: **Megan Thompson** <mmcthompson97@gmail.com>
Date: Thu, Jan 9, 2020 at 12:54 PM
Subject: Trial Outlier Rejection Code
To: Alfonso Nieto Castañón <alfnie@gmail.com>, Nan Jia <pacificmyth@gmail.com>, Byron Galbraith <byron.galbraith@gmail.com>, Scott Kuzdeba <skuzdeba@gmail.com>

….. I wanted to give everyone a primer on how to use my trial-rejection code. The function can be found at /projectnb/busplab/Experiments/ECoG_fMRI_RS/RepSup_megan/filter_ECoG_trials_across.m Feel free to copy it and modify it as necessary to fit your datasets.

The function filter_ECoG_trials_across takes as an input an "EEGALL" file. This should be pretty standard for a lot of the ECoG analysis pipelines. I use a (very modified version) of Ayoub's preprocessing code. EEGALL is a structure with one cell for each trial block. This outlier rejection will run through and ultimately combine each of the trial blocks.

The current version of my outlier rejection code needs a field called "epoched data" (as in EEGALL{1,blocknumber}.epoched_data(channelnumber,trialnumber)). This is the (hilbert filtered) data broken into the trials length that you are interested in. It doesn't matter how you break it down (mine are the first 2.5 seconds after stimulus presentation), as long as it's broken down into the trial length that you're interested in performing outlier rejection on, each in its own cells. Mine is a cell array for each block of 256 rows (number of channels) by 72 columns (number of trials) each holding a 1x5001 double array of data.

You will also need a variable with the bad channels that you want to remove, EEGALL{1,blocknumber}.badChan. This is just an array of doubles that are the channels that should be ultimately removed from analysis and by extent outlier rejection (because they're already getting rejected and therefore shouldn't count towards median values used to create the rejection threshold).

These are the only two requirements for channel removal. If you are concerned with which trials are being removed, there's code for output plots that is commented out, just uncomment it and you should be able to see the trials removed for each channel.

The only output of the function is an array of the trials removed, across all channels and all blocks. The numbering of trials goes from block 1 channel 1 to block 1 channel 256 to block 2 channel 1 ... block 4 channel 256. So for four blocks of 72 trials, the outlier trials should be between 1 and 73,728. In my datasets, somewhere between 3% and 6.5% of trials is removed, so if you're getting much more than that you might be concerned.

If you want to try it before you adapt it to your own datasets, one of the inputs I used was /projectnb/busplab/Experiments/ECoG_fMRI_RS/RepSup_megan/S357_SpecialEvents_Epoched_nans.mat

On Wed, Dec 11, 2019 at 5:06 PM Scott Kuzdeba <skuzdeba@gmail.com> wrote:

> Hi Nan,
>
> I don't recall filtering bad trials out of the single trial data set (likely the source of the data above), but removed them from the average for the analysis. I removed trials through a few ways. 1) I believe a small number were marked as being invalid by the research group that did the collection. That should be captured in some of the raw data that they sent (or maybe they had already removed it and just made a note of it). 2) The stimulus presentation and voicing onset tables removed some trials where there were voicing errors or artifacts. 3) I ran a kurtosis analysis using one of Ayoub's scripts to look for any outliers. I believe those were the only ways I ended up removing bad trials, I'll need to dig through my code to fully recall but off the top of my head that is what comes to mind. It is easy to rerun the clustering if you have an alternative set of trials with some different ones removed as well. Also, if some errant trials made it through I was normalizing the power in each trial so it shouldn't have had as bad off an effect as relative power (although still would be slightly incorrect).
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> Scott
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> On Mon, Dec 9, 2019 at 3:29 PM Nan Jia <pacificmyth@gmail.com> wrote:
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>> Hi Scott,
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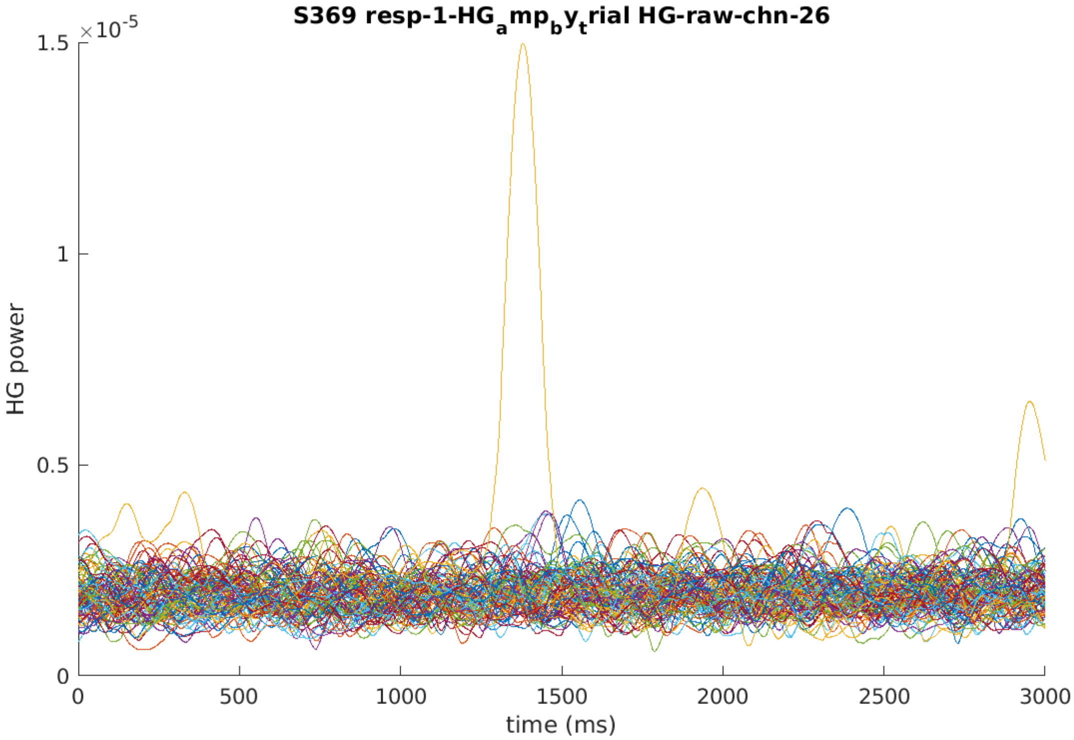
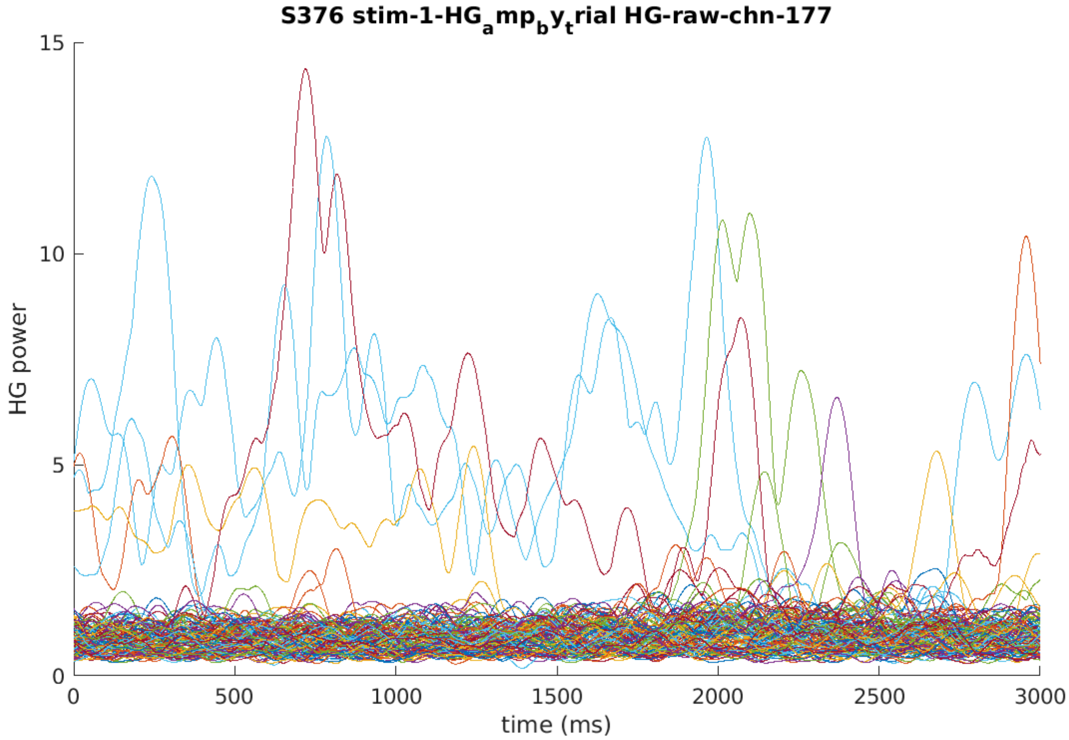
>> One issue we are all swarming on in the last few weeks is noisy trials that seems to be polluting the analysis we are doing. I've attached 2 sample plots for raw HG power for all trials on sample channels - it seems after the create_ECoG_epoch stage of the processing, we would still like to do some additional bad trial filtering. I want to get an idea for how you handled the bad trials in your pipeline - are there mechanisms for bad trial removals?
>> Cheers,
>>
>> Nan





On Tue, Dec 3, 2019 at 4:55 PM Megan Thompson <mmcthompson97@gmail.com> wrote:

The path to my outlier rejection code is
/projectnb/busplab/Experiments/ECoG_fMRI_RS/RepSup_megan/filter_EGOC_trials.m

Currently it prints the data with and without the rejected trials, so you might want to comment that out if it's part of a larger pipeline.

Cheers,
Megan