Characterizing trial-to-trial variability in MEG data

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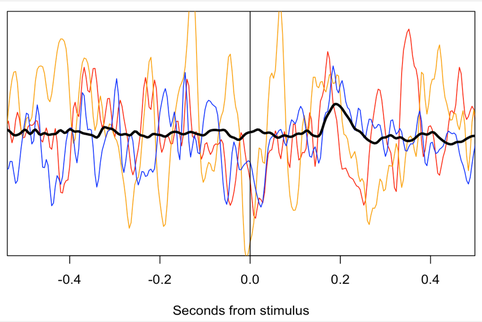
Goal: Identify sources and magnitude of trial-to-trial variability

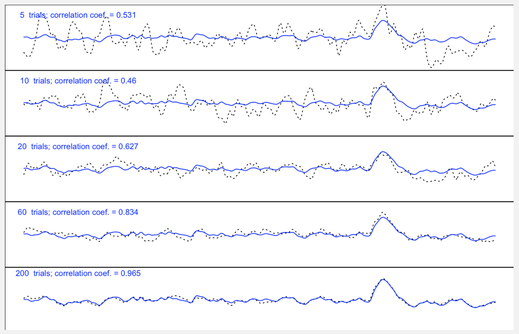
- The brain is likely to react slightly differently on each trial even to the same stimulus, but MEG data contains so much noise it is difficult to analyze how trial-to-trial variations occur and how they may relate to behavior
- To model single-trial evoked responses, which could vary in timing or amplitude, we need a way to characterize how large these variations are
- Single-trial analysis is a fairly new idea in MEG with no dominant method, so the nature of this project is exploratory
- Data is taken from a left-occipital sensor, centered around presentation of a visual stimulus (0 seconds), and measured in picoTeslas (Tesla • 10^{-12})

Averaging across trials removes individual trial features

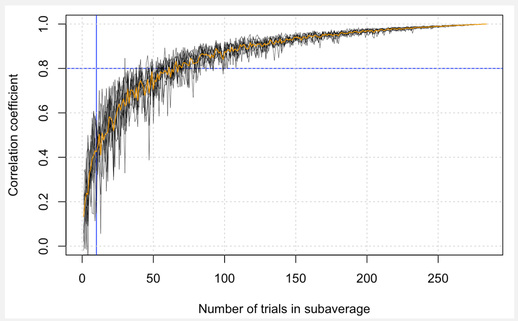


- 3 (of 284) trials with mean across trials (average evoked response)
- Large variation in height and time of peaks

~10 trials necessary to obtain an evoked response



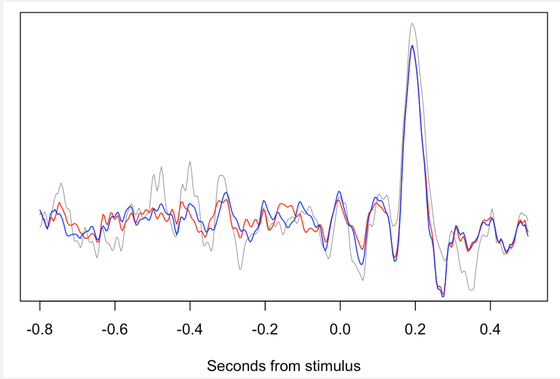
- Subaverages of trials with the average across all- evoked response is discernable at ~10 trials



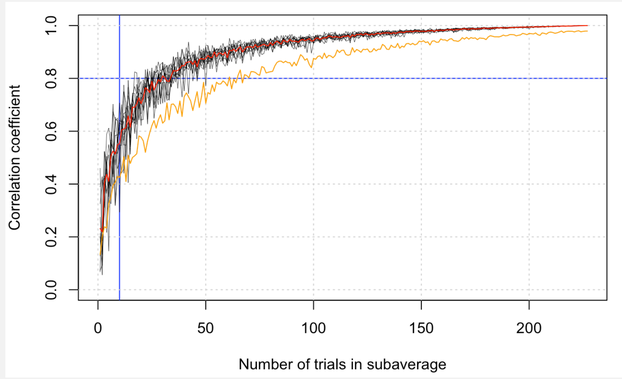
- While individual trials do not correlate well to the averaged evoked response, increasing the size of subaverages gets a continually closer result

Results

Removing oscillatory trials and correcting latency variation strengthens evoked response in subaverages



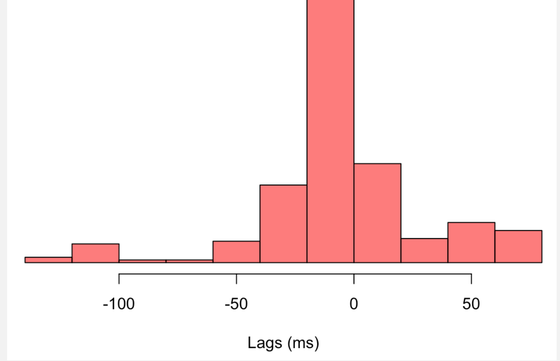
- Small change when shifting is performed without oscillatory trials and without cropping time (gray) compared to a time-crop version (red) indicates that we were able to successfully filter out enough oscillatory peaks that were previously skewing the results



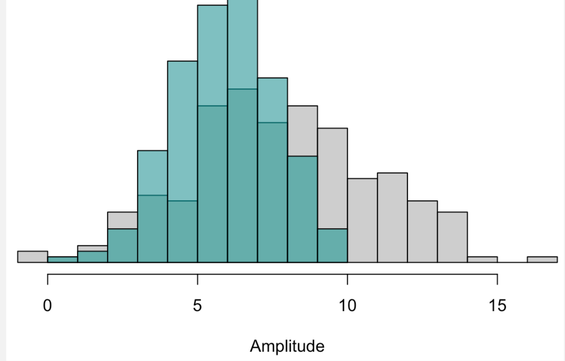
- Averaging more quickly recovers the evoked response as we increase number of trials after removing oscillatory trials and performing shifts (red)
- By removing shift variation and outlier trials, we have removed some of the trial-to-trial variability

Shifted and filtered data provides better estimates of variability

- These would provide starting values for a hierarchical model describing single-trial variability



- Removing problematic oscillatory trials and estimating single trial shifts obtained the distribution above- roughly symmetrical and centered at 0, with standard deviation 8.8 ms



- Amplitudes estimated using subaverages of 5 (teal) or each individual trial's amplitude (gray)
- A subaverage of 5 was chosen to cancel out enough noise to obtain reliable evoked responses, as individual trial amplitudes were not a reliable estimate

Conclusions

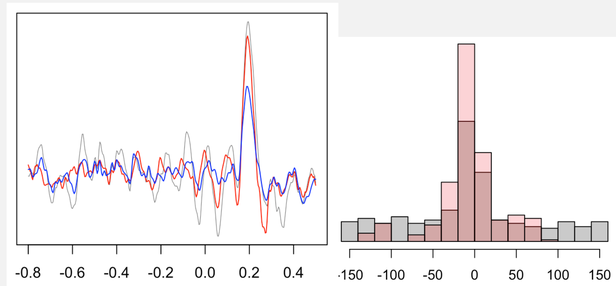
- Types of trial-to-trial variability include latency and amplitude variation of evoked responses, in addition to ongoing activity before and after stimulus presentation and response.
- An outlier-corrected version of Woody's original method was successful in aligning trials to remove much of the shift variation. It was also shown that the basic Woody filter can fail in this kind of data due to high-powered oscillations dominating some trials. Identifying and removing these trials may also be important for further of study of the oscillations themselves.
- By removing latency variation, we are better able to assess amplitude variation; however, taking a peak from each individual trial is still too noisy due to effects of ongoing activity- subaverages of 5 share information across trials to shrink estimates toward the mean to minimize influence of noise.
- Overall, this helps characterize the types of trial-to-trial variation present in MEG including estimates of shift and amplitude variance, which is helpful for further modeling of single trials.

Goal: Isolate and remove sources of variation

- Previous work suggests evoked responses can occur at different latencies across trials, which may be one source of trial-to-trial variation
- Responses are not perfectly aligned, so averaging activity spread across time results in an average that does not resemble the underlying shape

Shifting trials based on correlation improves evoked response in averages

- Aligning trials by their individual evoked responses helps removes variability
- We use variants of a cross-correlation method [Woody 1967] to determine the most likely time shift for each trial

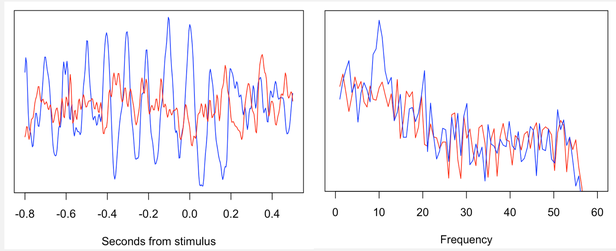


- Trials shifted to the position of max correlation- resulting in a noticeably stronger evoked response (original mean in blue)
- Cross-correlation was cropped to a smaller window (red) to account for large lag values, which indicate shifts to oscillations resembling an evoked response (original in gray)

Removing oscillating trials better represents activity

- Filtering out oscillatory trials is preferable as time windows can be harder to pick

Periodograms revealed oscillations at 10Hz for problematic trials



- Oscillatory and non-oscillatory trials with their periodograms (corresponding colors)
- A peak at a small range around 10Hz on the periodogram identified and removed oscillating trials

References

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Acknowledgments

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