The ENIGMA MEG resting state analysis pipeline

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Introduction:
The ENIGMA consortium was initially created to investigate low powered genetic effects on hippocampal volume by combining MRI data across multiple sites. Building on this idea, the ENIGMA MEG working group was recently formed to combine MEG data across sites with over 30 participating labs across the globe. Compared with MRI analysis, additional complexity is present in cross-site MEG analysis because of inherent differences in vendor specific data formats, sensor geometries, noise levels, noise mitigation techniques and anatomical integration. The first project of this working group is to investigate source level spatial-spectral changes associated with age, gender, and patient populations. The ENIGMA MEG resting state pipeline is built on top of standard tools to read MEG BIDS format and process data into csv outputs in an automated fashion. As a proof of concept, the current analysis pipeline has been run on several major open access MEG datasets including: CAMCAN, MEGUK, MOUS, NIH HV, NIH MI, and OMEGA. Following validation of the pipeline on repository data, working group members can perform their analyses locally and provide anonymized csv results for meta-analysis.

Methods:
The ENIGMA MEG resting state pipeline uses MNE, MNE-BIDS, MEGNET, and FOOOF python packages to load, clean, localize activity to the brain and process source level spectral information. The T1w MRI scans were processed through Freesurfer to create a cortical reconstruction. The pipeline includes the following steps: [MRI] source space calculation, automated MEG/MRI coregistration including atlas based fiducial localization and minimum distance fit (if fiducial localizers are not included with the anatomical data), [MEG] 1-45Hz filtering, 300Hz downsampling, deep learning based MEGNET automatic ICA removal, epoching, noise/data covariance estimation, lcmv beamformer calculation, epoch projection, parcel data extraction, multi-taper power spectral density (PSD) estimation, and normalization by total spectral power. The FOOOF algorithm fits the 1/f background spectrum and oscillatory peaks compile results to a csv file. Group analysis is performed by merging the spectral outputs with the BIDS participants.tsv file and fitting a least squares regression.

Results:
The average time for data analysis (excluding cortical reconstruction) was approximately 30 minutes on a modern system with RAM usage between 2.5-5Gb depending on the size of the raw MEG data. As seen in figure 1, the compiled data demonstrated significant overlap with previously reported literature including the dominant anterior/posterior gradient of the alpha rhythm, known beta predominance in the somato-motor region, and anterior frontal and frontal midline theta peaks. This automated routine shows consistent and robust findings with minimal preprocessing effort.
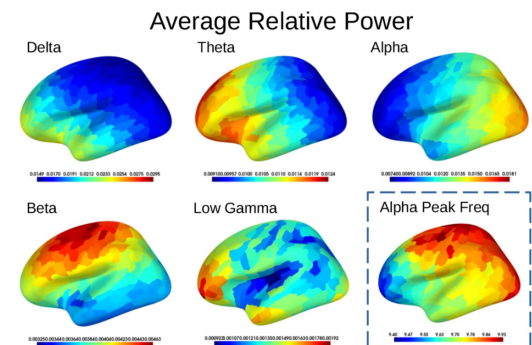

·Figure 1: Localized relative PSD averaged in standard frequency bands: Delta [1-3], Theta [3-6], Alpha [8-12], Beta [13-35], Low Gamma [35-45]. FOOOF fitted alpha peak in Hz plotted at each

Conclusions:
The ENIGMA MEG resting state pipeline is an easy to use open source codebase that has been used here to demonstrate consistent findings with previously published data. The ease of use allows automated data analysis that can be performed by typical MEG users without significant manual intervention. Future plans include incorporating data from the working group members and data harmonization for the following categories: site, hardware vendor, eyes open/closed, seated/supine. In summary the ENIGMA MEG resting state pipeline opens the doors for large scale cross-site analyses that will ultimately lead to more robust and reproducible findings.