Relationships between Resting State fMRI and EEG Brain Connectivity Across Frequency Bands

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Background

Whole brain functional connectomes hold promise for understanding human brain activity across a range of cognitive and pathological states. Resting-state (rs) functional MRI studies have contributed to the brain being considered at a macroscopic scale as a set of interacting regions. Interactions are defined as correlation-based signal measurements. The neuronal basis of these interactions have been investigated based on electrophysiological measurements:

- Local fMRI-EEG coupling is well studied with intra-cranial recordings
- Different EEG frequencies have been linked to different cognitive states
- Specific frequency features of the scalp EEG signal have been related to resting-state (rs) fMRI

However, **the coupling/relationship/neurophsiological basis of whole brain rs connectivity is** less well understood[2]

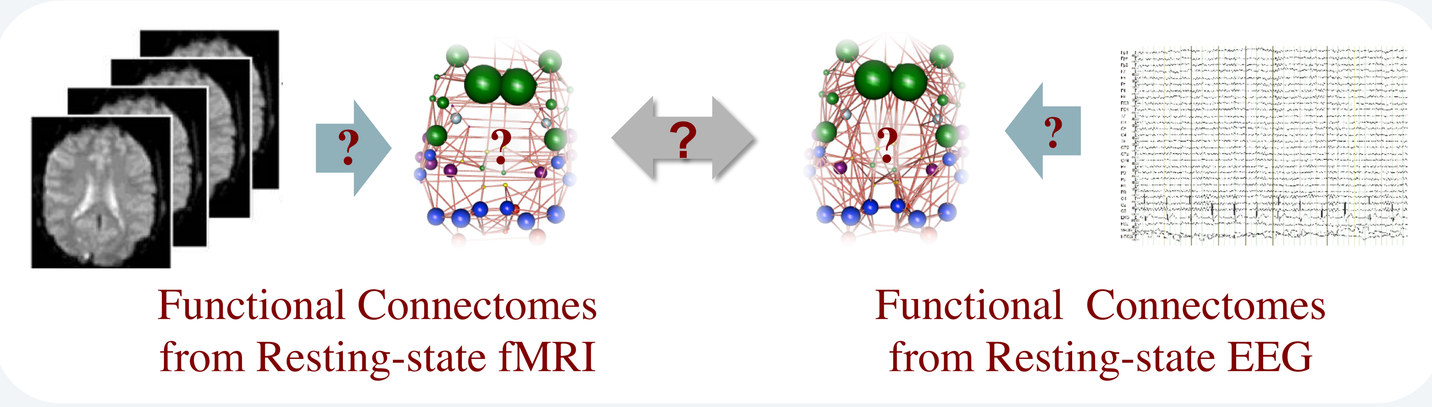


Fig. 1: Exploring the relationship between EEG and fMRI with a prediction framework[1]

Simultaneous EEG-fMRI offers the opportunity:

- To observe brain network dynamics with high spatio-temporal resolution
- To directly compare their covariance structure

We utilize these measurements to compare the connectomes derived from rs-fMRI and EEG band limited power by:

1. Relating connectomes derived from the Hilbert envelope of the source localised EEG signal to connectomes derived from rs-fMRI
2. The development of a statistical framework based on inference[1] that allows:
   - To learn the relationship between fMRI and EEG whole-brain functional connectomes
   - The identification of the most prominent connections that contribute to this relationship

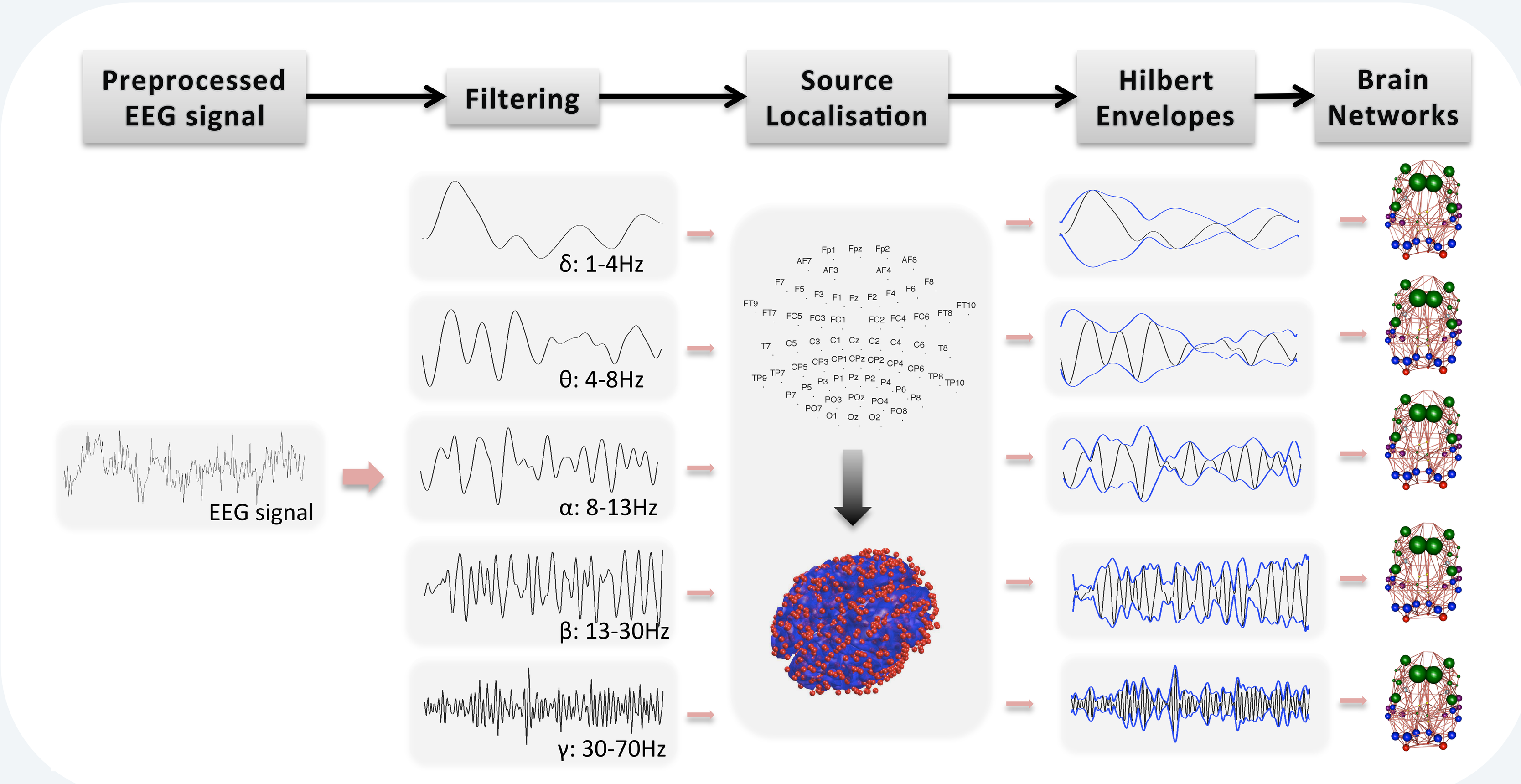
Our results indicate that:

- The performance of predicting fMRI from EEG connectomes is better than vice-versa
- Connectomes derived in low frequency EEG bands resemble best rs-fMRI connectivity

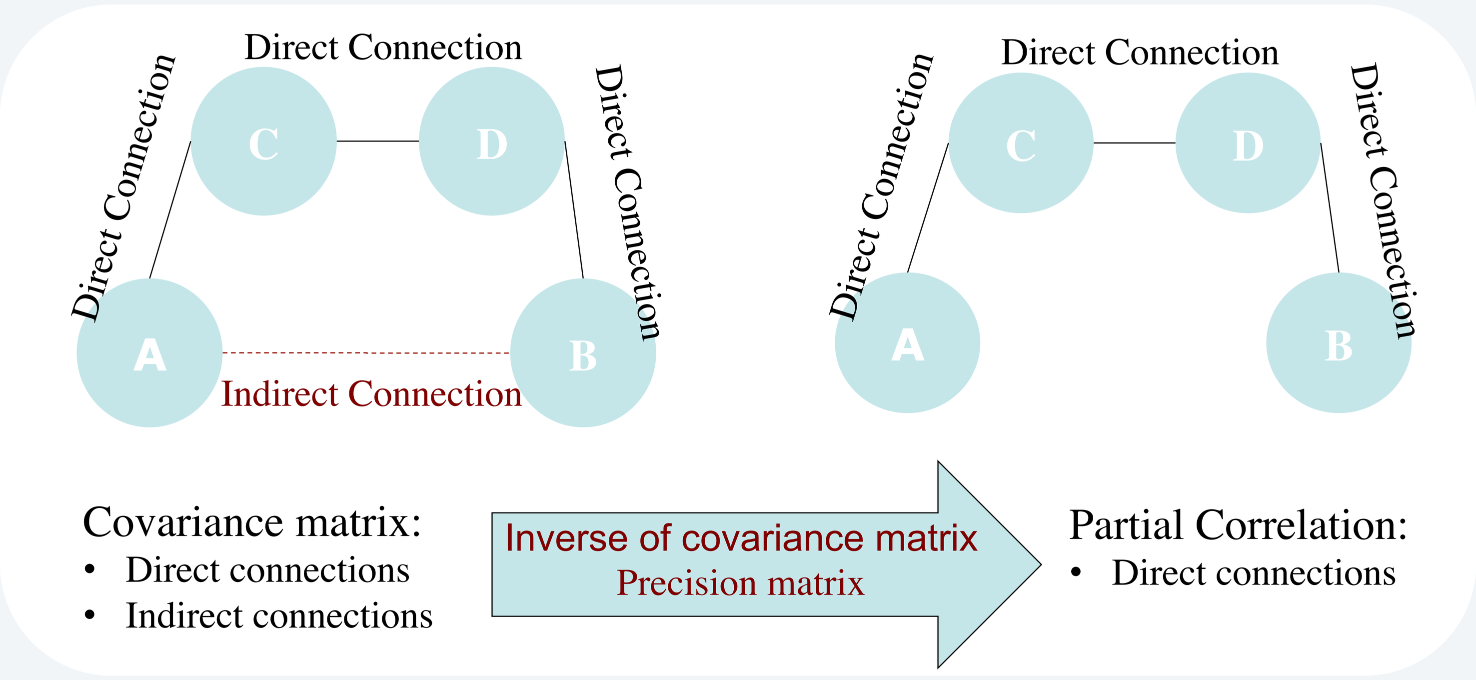
Methods

- **Pre-processing of T1 Weighted images:**
  - Obtain gray-white-csf matter parcellation (Freesurfer)
  - Define 68 cortical regions (Freesurfer)
  - Affine registration to native fMRI space (NiftyReg)
  - Non-rigid registration to MNI space (NiftyReg)
- **Pre-processing of fMRI:**
  - Motion correction (FSL)
  - Spatial smoothing (FSL)
  - Average signal within each region
  - Remove confounds: CSF, white matter and motion parameters
- **Preprocessing of EEG:**
  - Remove scanner artefacts (Brain Vision Analyzer)
  - Remove cardiac pulse artefacts (Brain Vision Analyzer)
  - Down-sample to 250Hz (Brain Vision Analyzer)

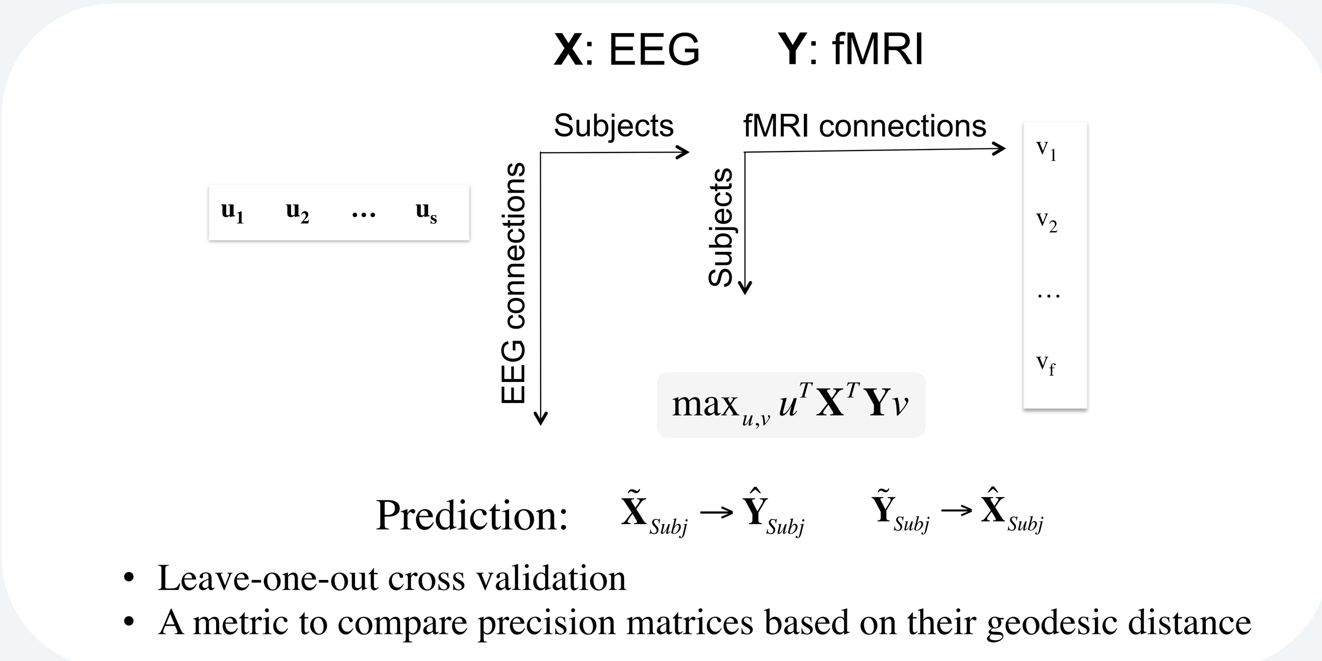
Step 1: Processing of EEG signal[2]



Step 2: Estimating Brain Connectomes from Time-Series[3]



Step 3: Inference based on Space Canonical Correlation Analysis (sCCA)[1,4]



- Leave-one-out cross validation
- A metric to compare precision matrices based on their geodesic distance

Results

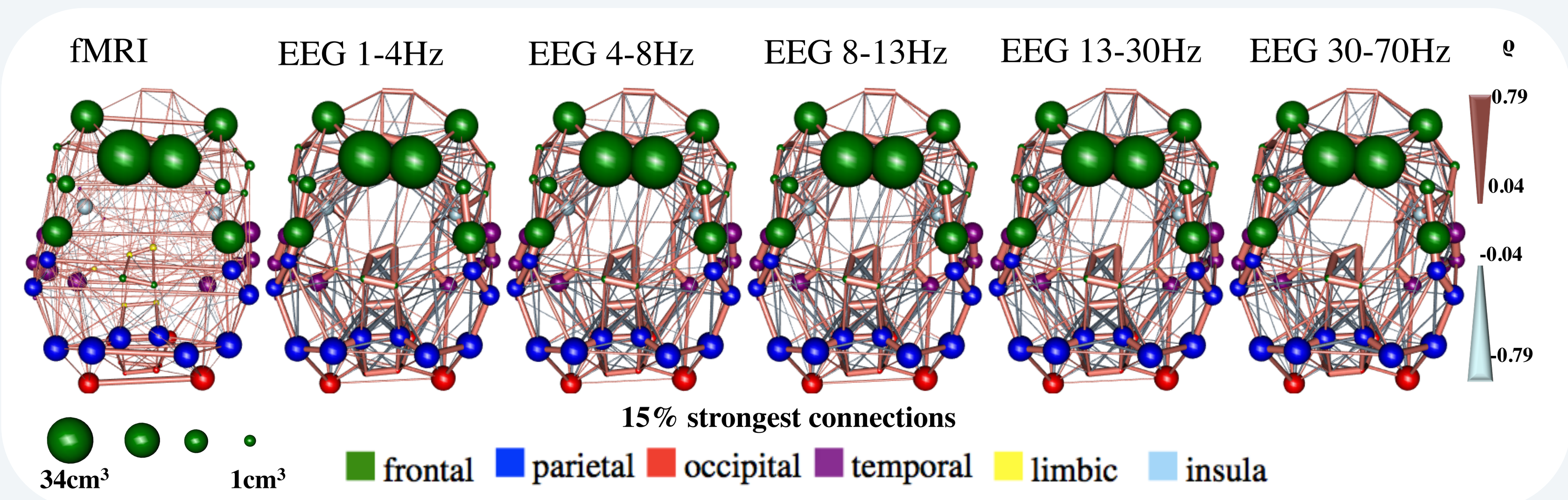


Fig. 2: Average brain connectomes across subjects for fMRI and each EEG band, respectively.

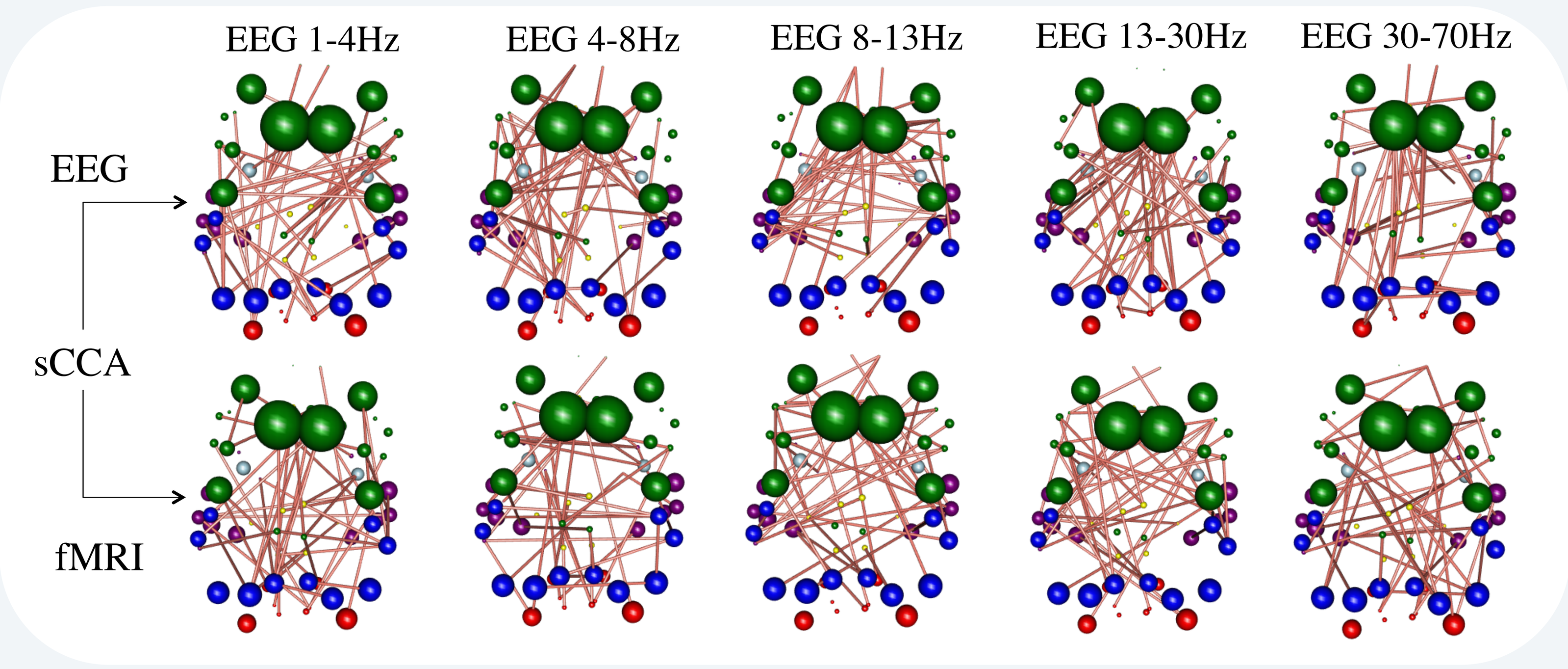


Fig. 4 shows the 2% connections with the highest probability to be selected in 10000 sCCA iterations with sampling with replacement.

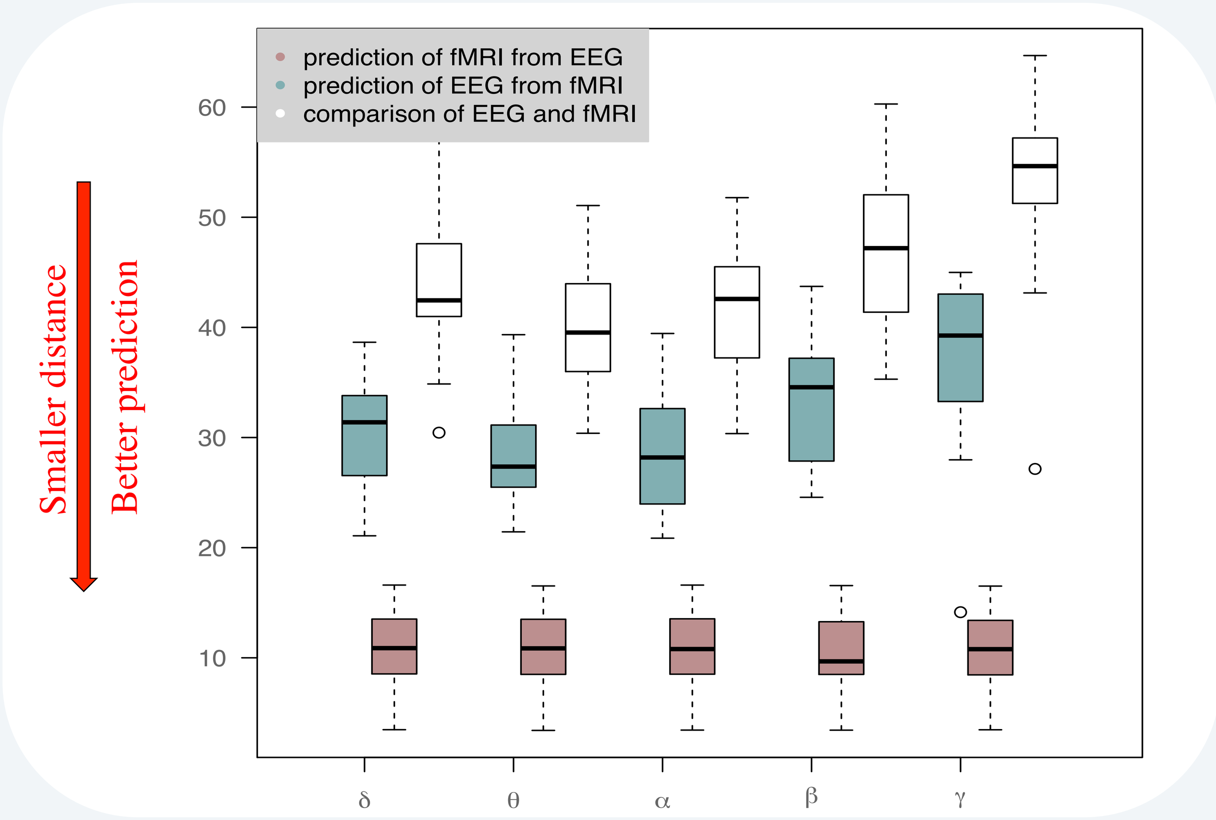


Fig. 3: The white boxplots indicate the intra-subject comparison between EEG and fMRI connectomes, the green boxplots indicate the prediction performance of EEG from fMRI and vice-versa is shown with the brown boxplots.

Conclusions

This finding has several important implications. It shows that there are signatures of rs-fMRI dynamics across EEG frequencies, consistent with the concept of nested oscillations found within EEG[5] and it likely reflects the greater dynamic information content captured by EEG. This implies that scalp EEG can be used to provide similar information to rs-fMRI based cortical connectomes at substantially reduced cost while providing much greater dynamic information content. This might be because of the coarse brain parcellation, which limits spatial resolution to the size of the underlying cortical regions. However, most current fMRI studies tend to examine connectivity at this scale.

References: [1] Deligianni et al. IEEE Trans Med Imag 2013 [2] Brookes et al. NeuroImage 2011 [3] Schafer, J. et al. Statist Appl Genet Mol Biol 2005 [4] Witten et al. Stat Appl Genet Mol Biol 2009 [5] Penny et al. J Neurosci Meth 2008