Histogram-weighted Networks for Feature Extraction, Connectivity and Advanced Analysis in Neuroscience

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Summary

Network-level analysis of various features, especially if it can be individualized for a single-subject, is proving to be a valuable tool in many applications(Raamana and Strother 2017; Evans 2013; Palaniyappan et al. 2015; Tijms et al. 2012; Xu et al. 2017; Raamana et al. 2015; Lerch et al. 2006; He, Chen, and Evans 2007). This package extracts single-subject (individualized, or intrinsic) networks from node-wise data by computing the edge weights based on histogram distance between the distributions of values within each node. Input features could be from any modality (fMRI, MEG, EEG, eye-tracking), so long as they can be turned into numbers. Individual nodes could be an ROI or a patch or a cube, or any other unit of relevance in your application. This is a great way to take advantage of the full distribution of values available within each node, relative to the simpler use of averages (or another summary statistic). A rough scheme of computation is shown in Figure 1.

Note on applicability and target audience

Although this technique was originally developed for cortical thickness analysis in neuroimaging research, this is a generic and powerful technique that could be applied to any features such as gray matter density, PET uptake values, functional activation data, EEG features or any other domain. All that is needed is a set of nodes/parcellation that have one-to-one correspondence across samples/subjects in your dataset.

The target audience is users of almost all neuroimaging modalities who 1. preprocessed dataset already, 2. have some base features (node- or patch-wise, that are native to the given modality) extracted using other packages (metioned above), and 3. who would like to analyze network-level or covariance-type or connectivity relations among the base features.

What does the hiwenet package do?

- This packages takes in vector of features and their membership labels (denoting which features belong to which groups - alternatively referred to as nodes in a graph), and computes their pair-wise histogram distances, using a chosen method.
- This package is designed to be domain-agnostic, and hence a generic input format was chosen.
- This `hiwenet.extract` could be used to extract advanced network-level /connectome features producing feature similar to the following tools from nilearn and MNE, but on a per-subject basis:

Construction of histogram-distance weighted networks (HiWeNet)
Example shown using cortical thickness features, but any other modality would also work.
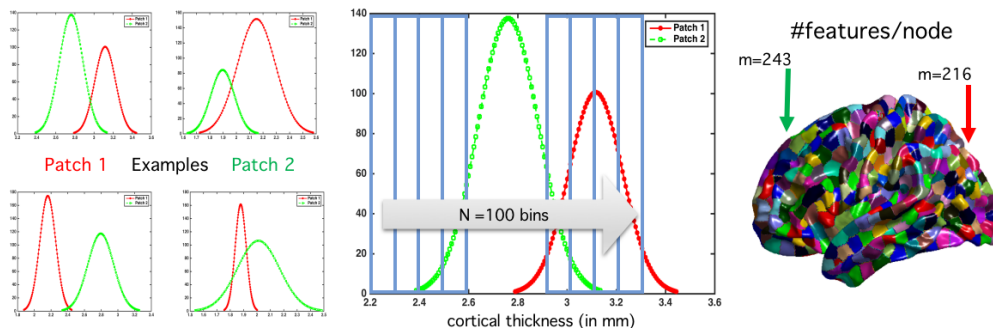
The four smaller subpanels on the left show typical distributions of cortical thickness values for four random pairs of patches (in green and red) in a given subject (shown on cortical visualization on right). They demonstrate the means and shape of these distributions can vary substantially as you traverse across different pairs of cortical patches. The large panel in the middle illustrates the type of binning used to construct the histogram from each patch.

Figure 1: illustration

- – MNE.extract_label_time_course
  - – or nilearn.input_data.NiftiLabelsMasker.transform - see here and here.
- However, we plan to add interfaces to tools e.g. via a scikit-learn compatible API/interface is also in the works. Stay tuned.
- Users also have the ability to input an arbitrary function (outside histogram distance family) to extract networks that is appropriate for their application.
- Refer to examples directory and the docs for more detailed and usage examples.

requirements

`hiwenet` package is built on the following packages: (Oliphant 2007; Walt, Colbert, and Varoquaux 2011; Hagberg, Swart, and S Chult 2008; Maier et al. 2017)

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