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graynet: single-subject morphometric networks for neuroscience connectivity applications

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Software

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Summary

Connectivity, and network-level features in general, have proven to be valuable tools in several aspects of neuroscience research. Although network analysis is rooted in analysis of functional MRI data, it has recently gained traction in the analyses of morphometric features such as cortical thickness (Evans 2013). Such networks of anatomical covariance (derived based on distributions of features across a group of subjects) provided insight into changes caused by various brain disorders. When we individualize this approach to enable extraction of single-subject network features, they further enriched insights into abnormalities due to disease (Tijms et al. 2012,Raamana et al. (2015),Palaniyappan et al. (2015),Xu et al. (2017)). Moreover, these network-level features demonstrated potential for prognostic applications (Raamana et al. 2015,Raamana et al. (2014)), in addition to being robust to changes in scale and edge weight metrics (Raamana and Strother 2017b).

However, deriving these network-level features from input T1w-MRI data is non-trivial. With this fully-open-source and pure-python library `graynet`, we attempt to make this task easier and extend it to support all currently available morphometric features. Currently, it interfaces directly with the outputs produced by Freesurfer (Fischl 2012) and supports vertex-wise data. We plan to extend this to support volumetric atlases and voxel-wise features such as gray matter density. Together with many convenience scripts (e.g. to launch jobs on the high-performance cluster and assemble the outputs produced), we believe `graynet` makes an useful addition to the neuroimaging in python open source ecosystem.

`graynet` is dependent on the following libraries: `nibabel` (Brett et al. 2016), `networkx` (Hagberg, Schult, and Swart 2005), `numpy` (Oliphant 2007,Walt, Colbert, and Varoquaux (2011)) and `hiwenet` (Raamana and Strother 2017a).

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