Brain network connectivity Analysis

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Abstract

Functional brain connectivity, as revealed through distant correlations in the signals measured by functional Magnetic Resonance Imaging (fMRI), is a promising source of biomarkers of brain pathologies. Spatial Independent Component Analysis (ICA) is an increasingly used data-driven method to analyze functional Magnetic Resonance Imaging (fMRI) data. In this project, we use CanICA (Canonical ICA) to extract sets of mutually correlated brain regions without prior information on the time course of these regions. Furthermore, we use a matrix-variate probabilistic model to extracts the signal on regions defined via a probabilistic atlas, to construct a functional connectome. And finally, we can obtain the connectivity matrix of the brain network based on ADHD resting-state dataset.

I. Introduction

Functional magnetic resonance imaging or functional MRI (fMRI) measures brain activity by detecting changes associated with blood flow. This technique relies on the fact that cerebral blood flow and neuronal activation are coupled. When an area of the brain is in use, blood flow to that region also increases. The primary form of fMRI uses the blood-oxygen-level dependent (BOLD) contrast, discovered by Seiji Ogawa. This is a type of specialized brain and body scan used to map neural activity in the brain or spinal cord of humans or other animals by imaging the change in blood flow (hemodynamic response) related to energy use by brain cells. Since the early 1990s, fMRI has come to dominate brain mapping research because it does not require people to undergo shots nor surgery, to ingest substances, nor to be exposed to ionising radiation. This measure is frequently corrupted by noise from various sources; hence, statistical procedures are used to extract the underlying signal. The resulting brain activation can be graphically represented by color-coding the strength of activation across the brain or the specific region studied. The correlation structure of brain activity, measured via fMRI, reveals stable inter-subject networks of distant brain regions that can be the expression of cognitive function. In particular, some connectivity networks are present in the absence of stimuli. They can reveal intrinsic brain activity and are studied in the resting-state paradigm. These structures are of particular interest to study and diagnose brain diseases and disorders as they can be used for deep probes of brain function on diminished subjects. Not only can they extract medically or cognitively relevant markers on subjects unconscious, or with limited cooperation, but they also give information on higher-level cognitive systems that are challenging to probe via medical imaging or behavioral clinical tests .

Spatial Independent Component Analysis (ICA) is an increasingly used data-driven method to analyze functional Magnetic Resonance Imaging (fMRI) data. To date, it has been used to extract sets of mutually correlated brain regions without prior information on the time course of these regions. Some of these sets of regions, interpreted as functional networks, have recently been used to provide markers of brain diseases and open the road to paradigm-free population comparisons. A hierarchical model for patterns in multi-subject fMRI datasets, akin to mixed-effect group mod-

els used in linear-model-based analysis was proposed in 2010. Here we use the 'CanICA' approach which implements a multivariate random effects model across subjects to extract brain networks in an data-driven way. And we use a matrix-variate probabilistic model to extracts the signal on regions defined via a probabilistic atlas, to construct a functional connectome.

II. Methods

Main modules come first:

- ICA
- Functional Connectivity

i. ICA

i.1 Image Binarization

The ICA method is included in a Nilearn library. In this project we use the library to Extracting resting-state networks. The procedure is as follows:

- We will use sample data from the ADHD 200 resting-state dataset has been preprocessed using CPAC. We use nilearn functions to fetch data from Internet and get the filenames (more on data loading):
- CanICA is a ready-to-use object that can be applied to multi-subject Nifti data, for instance presented as filenames, and will perform a multi-subject ICA decomposition following the CanICA model. As with every object in nilearn, we give its parameters at construction, and then fit it on the data.
- We can visualize the components.At first, we show a map generated from all the components. Then we plot an axial cut for each component separately.

ii. Functional Connectivity

Mask: We know that the most primitive fMRI data is 4-dimensional, contains measurements of space and one-dimensional time.

So our first step is to transform the four-dimensional data to a two-dimensional matrix. It is called Mask. And it is as follows.
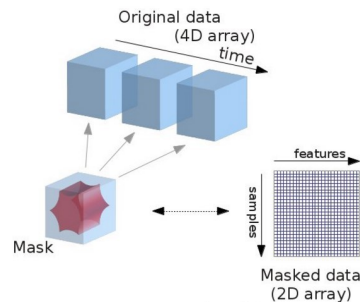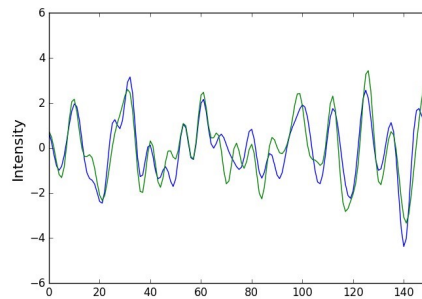

Figure 1: *Mask*

Figure 2: *Mask result of two features*

Timeseries: After masking, the features are still too much. Next we need to do is extract the time series. Due to too many features, we will use resampling to map these features to our existing validated maps. Here we use the Altas map.

Functional connectomes: We then extract times series to build a functional connectome.We use the covariance estimator to determine the connectivity between nodes. Here I use LedoitWolf estimato. This implies that correlations are slightly shrunk towards zero compared to a maximum-likelihood estimate.

III. Results

i. ICA result

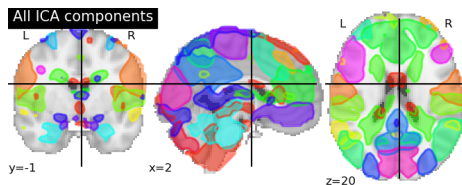We can visualize the components of ICA. Here it shows a map generated from all the components.

Figure 3: *all components*

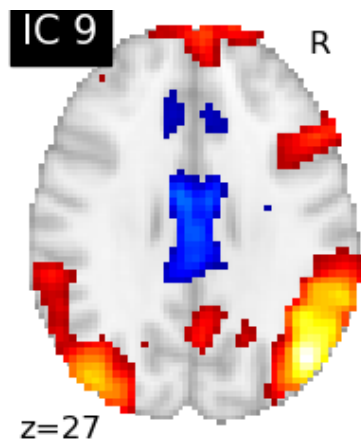Then we show two examples of maps for different ICA components:

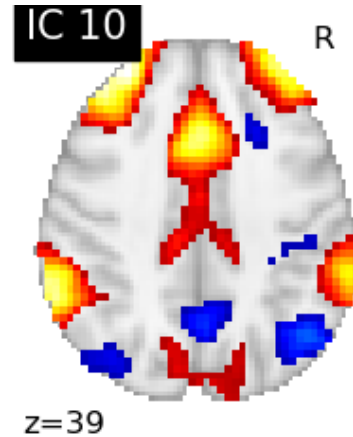

Figure 4: *Map for ICA component 9*

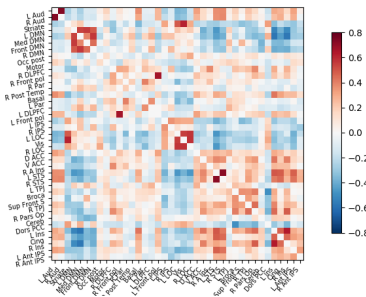**Figure 5:** *Map for ICA component 10*

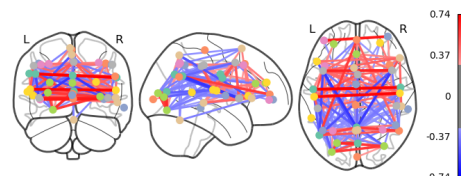**Figure 6:** *correlation matrix*

Figure 7: *graph of the brain network*

ii. Functional connectome

Here is a correlation matrix based on our datasets adhd.Then we show the corresponding graph of the brain network.

IV. Conclusion and future work

In this project, I use the ICA to extract sets of mutually correlated brain region and construct a functional connectome using a matrix-variate probabilistic model. By this, I can get the primary comphrehension of the resting state of the brain network. But recent work suggests that the brain is dynamically multistable. That is, the brain may occupy any of a number of connectivity states over time, each with a distinct network architecture33. Such a multistable model has been applied to discover novel biomarkers for pathology and to track changing cognitive demands.As a result, we need to consider some more complex architecture to analyze the brain network connectivity. Moreover, the github link of this project is .

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References

[1] Varoquaux G, Craddock R C. Learning and comparing functional connectomes across subjects[J]. NeuroImage, 2013, 80: 405-415.

[2] Varoquaux G, Sadaghiani S, Pinel P, et al. A group model for stable multi-subject ICA on fMRI datasets[J]. Neuroimage, 2010, 51(1): 288-299.

[3] Ciric R, Nomi J S, Uddin L Q, et al. Contextual connectivity: A framework for understanding the intrinsic dynamic architecture of large-scale functional brain networks[J]. Scientific reports, 2017, 7(1): 6537.

[4] Varoquaux G, Craddock R C. Learning and comparing functional connectomes across subjects[J]. NeuroImage, 2013, 80: 405-415.

[5] http://nilearn.github.io/

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