**Details About Functional Connectivity Notebook:**  
  
A **functional connectome** refers to the network of functional connections between different regions of the brain, typically inferred from neuroimaging data. Unlike the structural connectome, which maps the physical or anatomical connections (like white matter tracts), the functional connectome focuses on how different brain regions interact dynamically over time, especially during specific tasks or at rest.

Functional connectivity is often measured using functional magnetic resonance imaging (fMRI), which tracks fluctuations in blood oxygenation (BOLD signals) as a proxy for neuronal activity. These fluctuations are analyzed to identify regions of the brain that exhibit synchronized activity, suggesting they are functionally connected. This is particularly common in studies of resting-state fMRI, where spontaneous low-frequency BOLD signal fluctuations reveal coherent networks of brain regions that are functionally linked even when no explicit task is being performed.

Functional connectomes can also be constructed using other techniques like electroencephalography (EEG) or magnetoencephalography (MEG), which offer higher temporal resolution but lower spatial resolution compared to fMRI. These methods capture the fast dynamics of brain activity and can be combined with fMRI to provide a more comprehensive view of brain connectivity.

In essence, the functional connectome represents the brain’s dynamic communication pathways and helps researchers understand how different regions work together to support cognitive functions and behaviors. It is also used to study how these connections change in various neurological conditions or disorders.

**Brain parcellation** refers to the process of dividing the brain into distinct regions or parcels that are believed to have specific functional, structural, or connectivity properties. In the context of brain imaging analysis, particularly for constructing a functional connectome, brain parcellation plays a crucial role by defining the nodes or regions between which functional connectivity is measured.

Key Aspects of Brain Parcellation:

1. Functional vs. Structural Parcellation:

• Functional parcellation groups together areas of the brain that show similar patterns of activity, often based on fMRI data. The assumption is that regions with correlated activity are likely to serve similar functional roles.

• Structural parcellation, on the other hand, is based on anatomical features such as cytoarchitecture (the cellular composition of brain regions) or white matter tracts derived from diffusion MRI.

2. Granularity:

Brain parcellations can vary in their level of detail, from coarse divisions into a few large regions to fine-grained divisions into hundreds of smaller parcels. The choice of granularity depends on the specific research question and the type of analysis being conducted.

3. Methods for Parcellation:

Several methods are used to create brain parcellations, including:

• Clustering algorithms (e.g., k-means, spectral clustering) that group voxels based on similarity in functional connectivity patterns.

• Data-driven approaches, such as independent component analysis (ICA) or hierarchical clustering, which can identify functionally homogeneous regions without prior anatomical constraints.

• Multimodal approaches, which combine different types of imaging data (e.g., structural and functional MRI) to create more comprehensive parcellations.

4. Applications in Functional Connectome Construction:

Brain parcellations are essential for constructing functional connectomes because they define the regions between which connectivity is measured. Instead of analyzing connectivity at the voxel level (which can be noisy and computationally intensive), researchers calculate connectivity between predefined parcels, improving signal-to-noise ratio and interpretability. For example, in resting-state fMRI studies, functional connectivity is often measured as the correlation between the average time series of BOLD signals within each parcel.

5. Challenges and Variability:

Different parcellation schemes can lead to different interpretations of brain connectivity because they may vary in how they divide the brain and how many parcels they include. This variability highlights the importance of choosing an appropriate parcellation scheme for specific research goals.

In summary, brain parcellation is a fundamental step in analyzing brain imaging data and constructing functional connectomes. It allows researchers to simplify complex neuroimaging data by dividing the brain into meaningful regions that can be studied for their connectivity patterns, functions, and roles in various cognitive processes or diseases.

Here we are doing **Brain parcellation using atlas files.**

**Why atlas bcoz it creates anatomical map.**

**Extracting signals on a parcellation**

To extract signal on the parcellation, the easiest option is to use NiftiLabelsMasker. As any "maskers" in nilearn, it is a processing object that is created by specifying all the important parameters, but not the data:

The Nifti data can then be turned to time-series by calling the NiftiLabelsMasker fit\_transform method, that takes either filenames or NiftiImage objects.

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In brain imaging analysis, **confounds** are extraneous variables that can distort or bias the relationship between the brain imaging data (input) and the outcome of interest (e.g., a clinical diagnosis or cognitive measure). These variables are not the primary focus of the study but can influence the results, leading to incorrect conclusions about the brain-behavior relationships being examined.  
  
  
This code provides a comprehensive guide to analyzing functional connectivity and resting-state fMRI data using the Nilearn library. Below are the key points and steps covered in the code:

Overview

The code demonstrates how to:

1. Extract time series to build a functional connectome.

2. Generate single-subject maps of seed-to-voxel and seed-to-seed correlations.

3. Perform group analysis of resting-state fMRI using Independent Component Analysis (ICA) with CanICA.

4. Compare ICA with Dictionary Learning for extracting brain networks.

Setup

• Libraries and Modules: The code imports essential libraries such as `nilearn`, `matplotlib`, `pandas`, and `numpy` for fMRI data processing, visualization, and analysis.

• Data: Resting-state fMRI data from ADHD subjects is used. The data is stored in `.nii.gz` format, and confound files (e.g., motion parameters) are provided in `.csv` format.

Key Sections

1. Extracting Time Series to Build a Functional Connectome

• Brain Parcellation: Uses the Harvard-Oxford atlas to define brain regions of interest (ROIs). The parcellation is visualized using Nilearn’s plotting tools.

• Signal Extraction: The `NiftiLabelsMasker` is used to extract time series from the parcellation atlas for each subject’s resting-state data. Confounds such as motion parameters are included to clean the signal.

• Functional Connectome: A correlation matrix representing functional connectivity between brain regions is computed using `ConnectivityMeasure`. The matrix is visualized as a heatmap.

• Without Confounds: The same process is repeated without including confounds to show the importance of regressing out confounding variables.

2. Seed-to-Voxel Correlation Maps

• Seed Region Definition: A spherical seed region is defined in the Posterior Cingulate Cortex (part of the Default Mode Network).

• Time Series Extraction: The `NiftiSpheresMasker` extracts the mean time series from the seed region, while confounds are regressed out.

• Seed-Based Correlation: Correlation between the seed region and each voxel in the brain is computed, generating a seed-to-voxel correlation map. This map is visualized using Nilearn’s plotting functions.

3. Seed-to-Seed Correlation Maps

• Multiple Seed Regions: Several spherical seed regions are defined, and their time series are extracted using `NiftiSpheresMasker`.

• Partial Correlation Matrix: A partial correlation matrix between the seed regions is computed using `ConnectivityMeasure`. This matrix represents direct connections between regions, excluding indirect effects.

• Connectome Visualization: The connectome (correlation matrix) is visualized on a glass brain using `plot\_connectome`.

4. Group Analysis Using ICA (CanICA)

• CanICA Setup: The CanICA object performs multi-subject ICA decomposition on resting-state fMRI data. It extracts 20 independent components representing brain networks.

• Visualization of Components: The components are visualized as spatial maps using Nilearn’s plotting functions.

5. Dictionary Learning

• Comparison with ICA: Dictionary learning, an alternative to ICA, is applied to the same dataset. It seeks to extract sparse spatial maps that better represent brain networks.

• Visualization: Similar to ICA, dictionary learning components are visualized, allowing comparison between the two methods.

Important Concepts

• Confounds: Including confounds (e.g., motion parameters) during signal extraction helps reduce noise and improve the accuracy of connectivity measures.

• Functional Connectome: A graph-like representation where nodes correspond to brain regions and edges represent functional interactions based on correlation measures.

• Seed-Based Correlation: A way to explore how activity in one region correlates with activity across the entire brain.

Conclusion

This code provides a detailed workflow for analyzing resting-state fMRI data using Nilearn, covering both individual subject analyses (seed-based correlations) and group-level analyses (ICA). It also emphasizes the importance of handling confounds and compares different techniques (ICA vs Dictionary Learning) for extracting brain networks.