

# ConnectomeViewer - Multi-Modal Multi-Level Network Visualization and Analysis in Python

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## Summary

The emerging field of connectomics is concerned with the mapping of brain networks at different spatial and temporal scales. Originally coined to describe structural brain networks only [1, 2], recently the notion of a *connectome* is also used to refer to functional brain networks [3]. To grow in an understanding of complex brain processes, it is indispensable to integrate structural and functional data from various spatial and temporal scales.

Consequently, large datasets of multi-modal data must be acquired, processed, analysed and visualized [4]. The Connectome Viewer provides a Python based framework for the enhanced analysis and visualization of such data in network or surface representation. It employs the Connectome File Format as described on the right-hand side. Flexible organization and sharing of single-subject and large group-based datasets becomes possible.

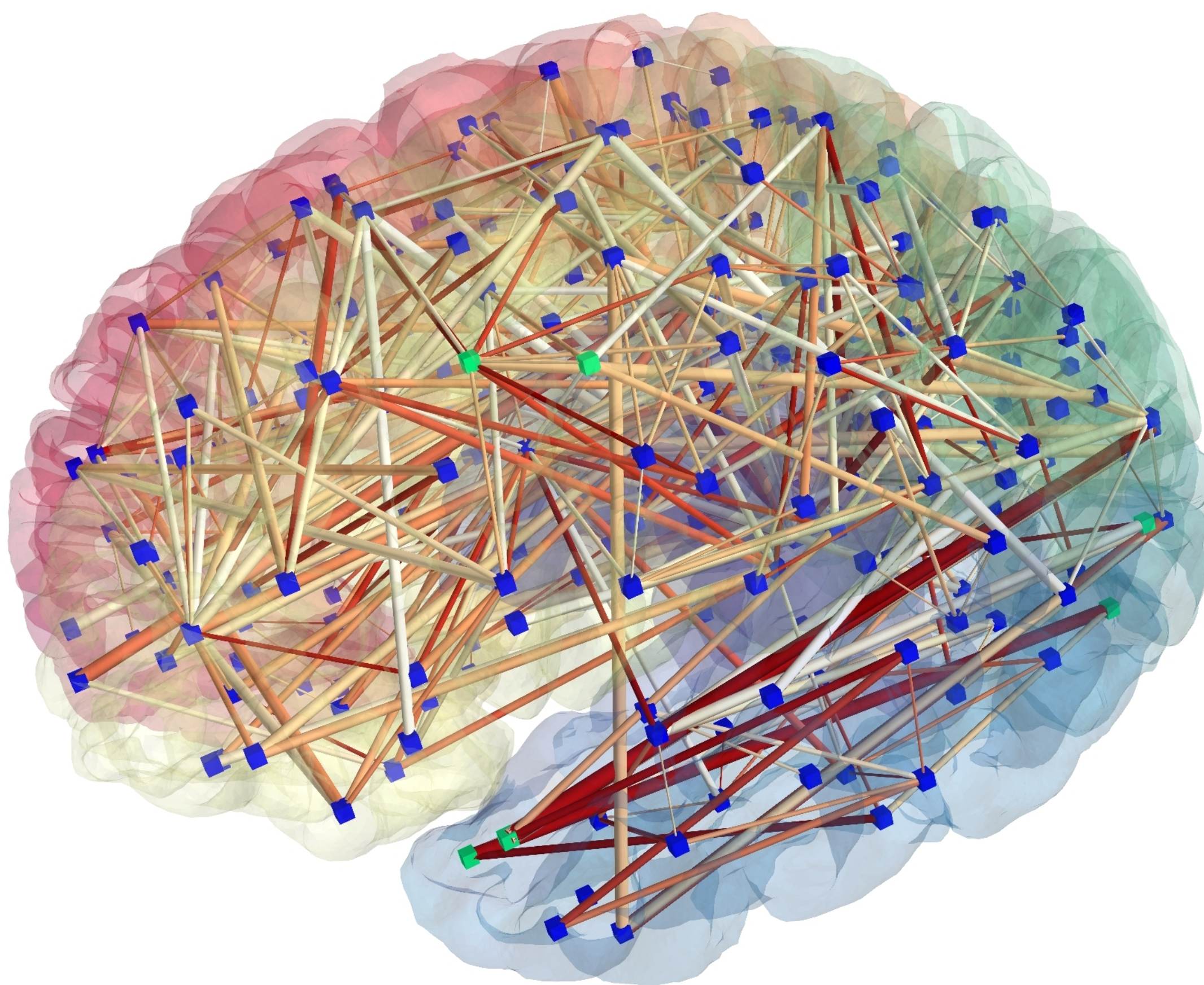


Fig. 1: Diffusion Spectrum Imaging data has been processed by the Connectome Mapping Pipeline, bundling white matter tracts and producing networks in multiple resolutions (number of nodes) and with different edge attributes. The image was rendered using the ConnectomeViewer application. This network has 258 nodes corresponding to cortical and subcortical ROIs (shown as blue cubes and as transparent surfaces), the edges depict threshold and color-coded densities between connecting ROIs.

## Features

A large number of features allow user-friendly interaction with the data.

- node selection, edge attribute selection, thresholding, camera synchronized viewing, network-surface representation toggling
- IPython shell integration: full-blown scripting, manipulate visualization parameters, generate image sequences, Connectome data sources are exposed and custom quantitative analysis can be performed
- characterize brain connectivity, network analysis methods are provided, ready to be applied [5], including plotting capabilities
- Plugin architecture for extension to custom needs and sharing of functionality in the community. Already provided are database access, diffusion MRI and sLORETA [6] EEG functional connectivity import and analysis, interface to the TrackVis [7] to visualize tracks with automatic ROI generation

## Python Packages

Standing on the shoulder of giants, the Connectome Viewer builds upon many scientific computing and application building libraries:

- Enthought Envisage App Framework / Traits** (*Required*) Building extensible plugin applications
- Mayavi2** (*Required*) 3D Scientific Data Visualization. Building of Visualization Pipelines, wrapping Visualization Toolkit [8]
- NetworkX** (*Required*) Creation, manipulation, and study of the structure, dynamics, and functions of complex networks [9]
- Scipy/NumPy** (*Required*) Scientific computing basic package, includes linear algebra, Fourier transform, random number capabilities
- Brain Connectivity Toolbox** (*Optional*) Provides a set of established network analysis measures [5]
- Matplotlib** (*Optional*) 2D Plotting library for publication quality figures, fully scriptable
- Neuroimaging in Python** (*Optional*) An environment for the analysis of structural and functional neuroimaging data. *NiPy* creation of processing pipelines, *DiPy* Diffusion MRI analysis [10]

**Acknowledgment** Financial support from Department of Radiology, University Hospital Center and University of Lausanne (CHUV-UNIL), and Signal Processing Lab 5, EPFL, Switzerland and Swiss National Science Foundation.

## Connectome File Format

Open container format for archiving and compression of raw and processed multi-modal data, including metadata. To maximize interoperability, open community-driven formats for network-based, surface-based, and volume-based data have been employed.

```
<?xml version="1.0" encoding="UTF-8"?>
<viewer xmlns="http://www.connectome.ch/"
  xmlns:xsi="http://www.w3.org/2001/XMLSchema"
  xsi:schemaLocation="http://www.connectome.ch/
    connectome.xsd">
```

### Metadata

*Format: XML*

Authors, References, any more data as key-value pair

### Networks

*Format: GraphML*

Any properties on nodes and edges: Label, Color, URL, ...

### Volumes

*Format: Nifti*

Segmentation, fMRI, Probability Map, T1-/T2-weighted, ...

### Surfaces

*Format: Gifti*

Labels, Surface Sets

### Tracks

*Format: TrackVis*

Fiber tracks with properties: FA, ADC, Segmentation, ...

### Time Series

*Format: HDF5*

Any time series data: EEG, MEG, ECoG, fMRI

Network nodes, surface patches and voxel ROIs may be interlinked accordingly.

Furthermore, a Python Input-Output library generating, validating and saving Connectome Files is shipped with the ConnectomeViewer and can also be used stand-alone.

## Download

The ConnectomeViewer is distributed under the open-source GNU Public License and is available from <http://www.connectomeviewer.org/>. Tutorials and example datasets are provided.

## References

- [1] Hagmann et al. (2008) Mapping the Structural Core of Human Cerebral Cortex. PLoS Biol
- [2] Sporns et al. (2005) The Human Connectome. PLoS Comput Biol
- [3] Biswal et al. (2010) Toward discovery science of human brain function. Proc Natl Acad Sci USA.
- [4] <http://humanconnectomeproject.org/>
- [5] Rubinov et al. (2010) Complex network measures of brain connectivity: uses and interpretations. NeuroIm-age
- [6] R.D. Pascual-Marqui (2002). Standardized low resolution brain electromagnetic tomography (sLORETA). Meth Find Exp Clin Pharmacol
- [7] Wang et al. (2007) - [www.trackvis.org](http://www.trackvis.org)
- [8] Mayavi2 - [code.enthought.com/projects/mayavi/](http://code.enthought.com/projects/mayavi/)
- [9] NetworkX - [networkx.lanl.gov](http://networkx.lanl.gov)
- [10] Neuroimaging in Python - [nipy.sourceforge.net](http://nipy.sourceforge.net)