

Development of a Framework for Annotated Connectomes to Support Presurgical Localization in Epilepsy

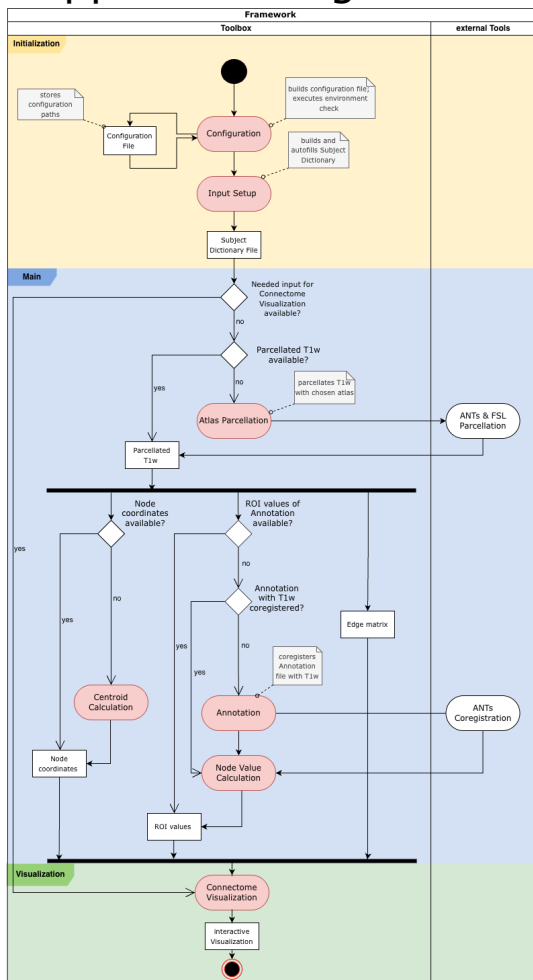


Fig. 1: Framework UML Activity Diagram.

Problem Description

Around 30% of epilepsy patients are drug-resistant. In these cases, surgical resection remains an effective option for reducing seizures. A successful resective surgery depends on an individualized understanding of brain networks.

The rising field of connectomics aims to model the brain's structural and functional connections ('nodes' and 'edges') to reveal dysfunctional network patterns. Enriching these so-called connectomes with multimodal metadata, such as structural metrics, functional imaging measures, and clinical biomarkers results in a powerful concept for improving presurgical planning. However, current clinical workflows use fragmented, modality-specific approaches that fail to effectively integrate multimodal neuroimaging data in individualized connectomes.

In this thesis, a modular proof-of-concept Python framework was developed that constructs simplified biologically annotated connectomes from multimodal neuroimaging data to improve presurgical planning for epilepsy patients.

Methods

The framework was developed using an iterative approach with four core requirements: modularity and extensibility, modality independence, spatial consistency and the usage of established tools. Implemented as a Jupyter Notebook with three integrated packages (Initialization, Main, Visualization), the framework used a JSON-based data structure and registered annotation data to a common anatomical reference space. Node placement was based on atlas parcellation; node values were aggregated with summary measures and multimodal data input was simplified with data abstraction principles. The framework was validated on three clinical test cases with different atlas parcellations and preprocessing input formats.

Results

The framework successfully generated biologically annotated connectomes for all three test cases. Multimodal data (nodes attached with t-statistics and ALFF values) was integrated with connectivity matrices and visualized in two interactive 3D visualization approaches.



(a) 100 nodes with t-statistics annotations.

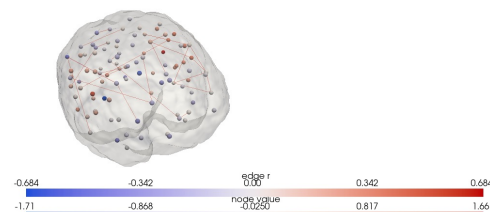


(b) 400 nodes with t-statistics annotations.

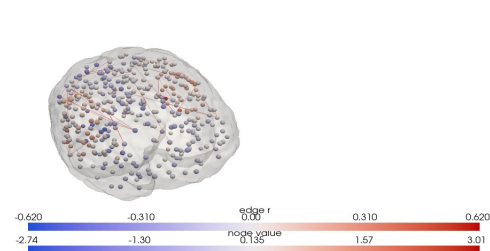


(c) 100 nodes with ALFF annotations.

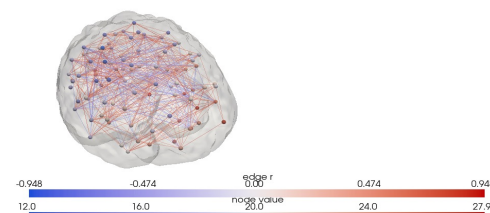
Fig. 2: 'Hyve' visualization results for different node sizes and annotations with edge threshold $|r| = 0.5$.



(a) 100 nodes with t-statistics annotations.



(b) 400 nodes with t-statistics annotations.



(c) 100 nodes with ALFF annotations.

Fig. 3: 'NetworkX' visualization results for different node sizes and annotations with edge threshold $|r| = 0.5$.

The modular architecture enabled flexible execution of pipeline components, with the ability to integrate external precomputed data without code modifications.

In conclusion, this framework establishes a foundation for constructing biologically annotated connectomes, ready for further development to improve personalized, network-based presurgical planning in epilepsy.

Franziska Baum

Advisor (HSLU): Prof. Dr. Philipp Schütz

Supervisor (FHTW): Dipl.-Ing. Andrea Balz

External Examiner: PD Dr. sc. Philipp Stämpfli

Cooperation Partner: Mag. Dr. Florian Ph.S. Fischmeister – DINLAB / MUW