Topological feature characterization of comatose patients

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***Abstract*—Post-cardiac arrest coma, a consequence of post-cardiac arrest anoxic brain injury (PCABI), significantly impacts patient survival, with neurological prognosis guiding withdrawal of life-sustaining therapy (WLST). Continuous electroencephalography (EEG) enables real-time monitoring of brain activity, detecting connectivity patterns associated with recovery or deterioration. In this study, we applied the Mapper algorithm with Isomap filtering $(k = 8, p = 30\%)$ to analyze EEG-derived functional connectivity networks, revealing that patients with poor outcomes exhibited significantly higher network density and efficiency. These findings suggest that maladaptive network reorganization may be linked to worse prognoses, highlighting the potential of topological data analysis (TDA) as a complementary approach for brain network characterization in coma assessment.**

***Index Terms*—Topological Data Analysis, Mapper Algorithm, Brain Connectivity, Coma Prognosis, Graph Theory, EEG, Functional Networks.**

I. Introduction

Post-cardiac arrest coma, a major consequence of post-cardiac arrest anoxic brain injury (PCABI), affects over 80% of ICU-admitted patients after out-of-hospital cardiac arrest (OHCA), with two-thirds dying before discharge, mainly due to withdrawal of life-sustaining therapy (WLST) based on poor neurological prognosis [1]. Predictive models rely on indirect clinical criteria, limiting decision-making reliability. While fMRI assesses brain connectivity, its use in comatose patients is restricted, whereas continuous electroencephalography (EEG) provides real-time brain activity monitoring, detecting patterns linked to recovery or deterioration [2].

Studying functional activation dynamics and resting-state network patterns is ongoing, but comparing the brain connectivity of comatose patients with that of healthy subjects may not be appropriate due to severe structural and functional damage. Topological Data Analysis (TDA) overcomes Graph Theory limitations by capturing higher-order interactions through simplicial complexes [3]. Persistent homology has identified network structures supporting functional integration [4], enabled network comparisons [5, 6], revealed modularity in task-based fMRI [7, 6], detected loops and cycles [8, 9], and segmented brain states [10, 6], though its use in resting-state networks remains underexplored.

Applying TDA to EEG signals offers a promising approach, leveraging EEG's accessibility, cost-effectiveness, and high temporal resolution to identify high-order connectivity patterns, such as synchronization loops, which provide insights into brain functional organization and recovery. In clinical contexts, TDA has distinguished abnormal connectivity in depression [11] and linked network reorganization in coma patients to reduced functional connectivity and altered hub hierarchy, with implications for prognosis [12]. Lower connectivity density (14%) suggests a role in neurological recovery, aligning with the "functional reorientation" concept [13] [14], where recovery depends on alternative structural pathways. A network diffusion model found that while graph metrics showed differences, only propagation time correlated with consciousness levels, highlighting reliance on less efficient functional routes.

This study employs the topological Mapper method, which reduces high-dimensional data while preserving topological and geometric information [15]. Mapper effectively uncovers complex brain network structures, identifying hidden subgroups and global topological changes related hypo- and hyperconnectivity. Its adaptability to various data types and robustness to noise make it a valuable tool for studying brain connectivity [7].

II. Materials and methods

Data

This study uses preprocessed clinical electroencephalography (EEG) data from 100 patients, evenly divided into two groups based on neurological prognosis: 50 with a good outcome (CPC 1–2) and 50 with a poor outcome (CPC 3–5) [2]. Five-minute EEG recordings, obtained 48 hours after cardiac arrest from patients with continuous or discontinuous activity, were processed to remove artifacts using automated algorithms and independent component analysis (ICA). The cleaned data were reconstructed with exact low-resolution electromagnetic tomography (eLORETA) and parcellated using the automated anatomical atlas (AAL), extracting 78 virtual cortical electrodes. The signals were then filtered into delta (1–4 Hz), theta (4–8 Hz), and alpha (8–13 Hz) frequency bands for analysis. The final dataset includes time series and connectivity matrices structured for statistical analysis and visualization. [2].

The raw data are represented as matrices with dimensions $78 \times m$, where 78 corresponds to the number of brain regions defined by the parcellation based on the AAL atlas [16], and m represents the number of temporal samples of the preprocessed signal.

Data preprocessing

EEG signal matrices were processed to analyze functional connectivity while minimizing spurious effects from passive propagation. Initially, data dimensionality was assessed, and if rank deficiency was detected, a correction was applied using singular value decomposition (SVD) to ensure a complete representation of the 78 regions of interest (ROIs). Symmetric orthogonalization defined in [17] was performed to remove shared components between signals, preserving region-specific variability. The signal envelope was extracted using the Hilbert Transform to capture amplitude modulation. Pearson correlation between the envelopes was computed, providing a functional connectivity measure.

The 78×78 matrices obtained from the envelope correlation computation were processed using a correlation-based pseudometric [18], defined as:

$$d_{ij} = \begin{cases} 1, & \text{if } c_{ij} \leqslant 0 \\ \sqrt{1 - c_{ij}^2}, & \text{if } c_{ij} > 0 \end{cases}$$

Whete c_{ij}, with $i, j = 1, \ldots, 78$ is the correlation of the evelope calculated between regions i and j.

This transformation shifts the analysis space to a pseudometric space quantifying similarity between regional activity patterns, enabling the identification of synchronized activity clusters. The resulting distance matrices serve as input for the Mapper algorithm.

Mapper algorithm

Given a dataset X of N points, specifically 78×78 correlation distance matrices of EEG signals, and a filter function $f : X \to \mathbb{R}^2$, we compute its image I and construct an open cover by partitioning I into k overlapping intervals [15]. This covering step defines a topology where each interval I_j corresponds to a subset $X_j = \{x \mid f(x) \in I_j\}$, forming a cover of X. A partial clustering is then applied to group points within each cover based on their distances in the original space.

To construct a TDA-based network, **DBSCAN** is used for clustering, as it determines clusters based on density without requiring a predefined number [19]. Clusters are represented as graph nodes, with edges connecting nodes that share data points. Formally, if clusters C_i and C_j from overlapping subsets X_i and X_j satisfy $C_i \cap C_j \neq \varnothing$, an edge is drawn. This network reveals patterns, connectivity structures, and hidden subgroups in the data.

Measures

The topology and structure measures of Mapper graphs were computed, including the **number of connected components, clustering coefficients, efficiency, modularity**, and **density**, according to the definitions presented in [20]. These measures have significant neurobiological interpretability and are consistent with previous studies such as [13] and [14].

Selection of parameters and statistical analysis

The parameters were selected based on the reviewed literature. Initially, filter functions and coverings suggested by the theory in [15], [21], [22], and [19] were chosen. An exploratory analysis was conducted using a sample of five elements per outcome group (poor or good). Two filter functions were considered: *Principal Component Analysis* (PCA) and *Isometric Mapping* (Isomap), the latter being a nonlinear dimensionality reduction method. The parameters k and p were adjusted, varying k in $[6, 10]$ and p between 30% and 50%. *Mapper* graphs were constructed for each of the 10 samples, modifying the parameters in each iteration. For each configuration, the metrics defined in II were computed and analyzed statistically. A normality test determined the inferential procedure, either a t-test or a Mann-Whitney-Wilcoxon test. Figure 1 provides a summarized description of the proposed analysis process.

III. Results

Using the selected parameters $(f = Isomap, k = 8, p = 30\%)$, processing was performed on eight previously unprocessed data points per outcome group. The difference test revealed a significant difference in density measures (p-value $= 0.028$) and efficiency coefficient (p-value $= 0.024$). It was observed that both density and efficiency coefficient were higher in poor outcomes compared to good outcomes.

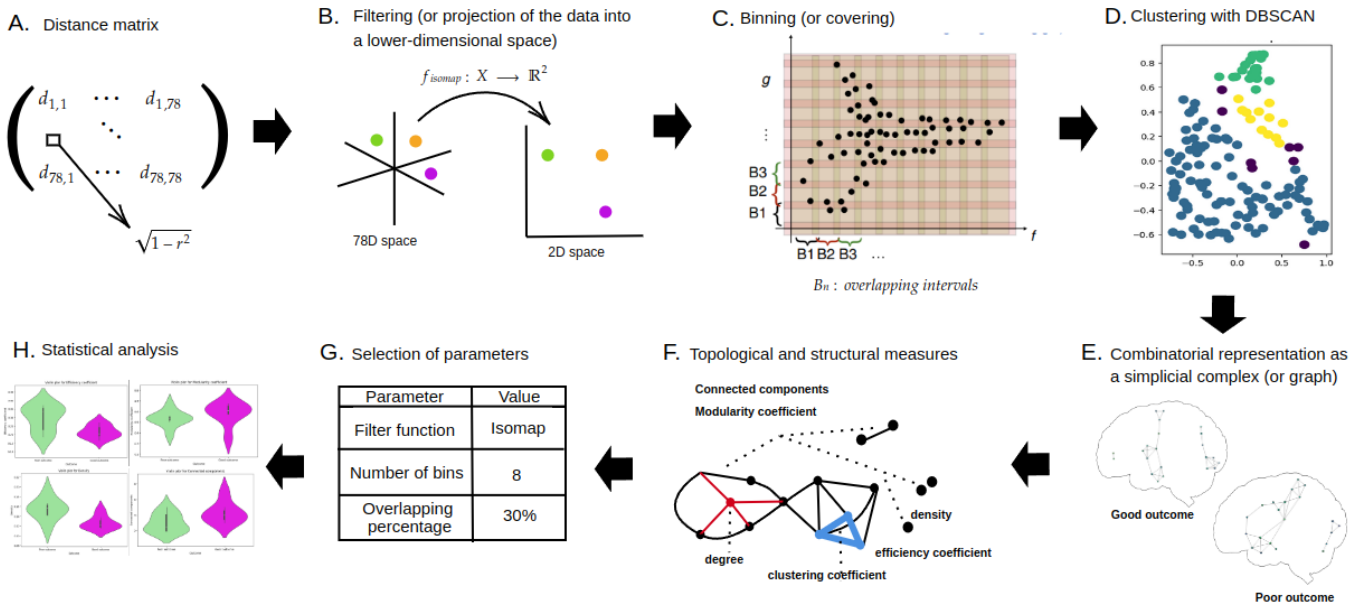

Fig. 1: Mapper algorithm workflow and topological analysis.

Figure 2 presents violin plots illustrating the difference test results, along with a sample Mapper graph for each outcome group.

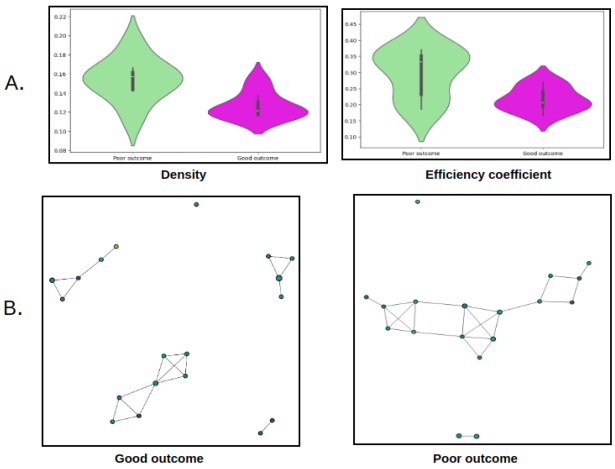

Fig. 2: **A.** Violin plots for density and efficiency coefficient metrics. **B.** Mapper graphs for good and poor outcome.

IV. Conclusions

This study applied the Mapper algorithm with Isomap filtering ($k = 8, p = 30\%$) to analyze the network topology of comatose patients, revealing significant differences in key graph measures between outcome groups. Specifically, patients with poor outcomes exhibited higher network density and efficiency compared to those with good outcomes. These findings highlight the potential of topological data analysis (TDA) to capture meaningful structural differences in brain networks that may be linked to patient prognosis.

The Mapper algorithm proved to be a useful tool for uncovering these differences, providing a low-dimensional representation of high-dimensional neuroimaging data while preserving local and global structures. Its ability to highlight network topology variations suggests that TDA-based methods could complement traditional graph-theoretical analyses in the study of brain connectivity.

For future work, we aim to improve the selection of parameters by implementing an enhanced version of the Mapper algorithm, optimizing its adaptability to complex neuroimaging data. Additionally, we plan to explore topological features derived from this improved Mapper approach, integrating it with extended persistence techniques to gain deeper insights into the structural organization of brain networks in comatose patients.

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