Spatial Correlation Communities in Panoramic Optical Mapping

Estela Sánchez-Carballo[1], Francisco M Melgarejo-Meseguer[1], Jimena Siles-Paredes[2], Saleem-Ullah[2], Angélica Quadros[2], João Salinet[2], José Luis Rojo-Álvarez[1]

[1] Department of Signal Theory and Communications, Telematics and Computing Systems, Universidad Rey Juan Carlos, Madrid, Spain
[2] HEartLab, Federal University of ABC, Sao Bernardo do Campo, Brazil

Abstract

Panoramic optical mapping provides rich spatiotemporal information on cardiac electrical activity through video recordings, where each pixel corresponds to a signal evolving over time, yielding thousands of signals per subject. In this study, we propose a novel method for analyzing high-volume data. The approach reduces the temporal dimensionality of the signals using manifold learning and then identifies groups of signals using community detection (Louvain algorithm) and clustering (K-means). The two grouping techniques were compared both qualitatively and quantitatively using the modularity index. For Subject 1 (sinus rhythm), Louvain identified 16 communities with a modularity of 0.8763, while K-means identified 14 clusters with a modularity of 0.8492. For Subject 2 (atrial tachycardia), Louvain found 12 communities (modularity 0.8282) and K-means 15 clusters (modularity 0.8049). In both cases, Louvain achieved slightly higher modularity, suggesting more coherent community structures. This methodology enables visualization of thousands of signals in an interpretable latent space, and it may have the potential to reveal organizational patterns in the heart, highlight preprocessing requirements, and provide insights into the propagation of electrical impulses.

1. Introduction

Cardiac arrhythmias represent a significant health issue in our society, affecting more than 60 million people worldwide. Depending on the type of arrhythmia, patients can develop serious complications such as stroke, heart failure, or even sudden cardiac death if the condition is not promptly recognized and treated [1]. Therefore, it is fundamental to study and develop new approaches that enable a comprehensive understanding of arrhythmias, including their underlying mechanisms and their spatiotemporal organization within the heart.

Panoramic optical mapping (POM) involves acquiring images of the heart from multiple viewpoints using multiple optical cameras. Each camera has its own specific field of view, thus enabling the extraction of information from different regions of the heart. Therefore, this imaging technique provides fluorescent recordings of the electrophysiological activity across the entire epicardial surface, providing detailed information on the spatiotemporal propagation of electrical activity responsible for maintaining cardiac arrhythmias [2].

POM provides spatiotemporally rich information in the form of a video, where each pixel corresponds to a signal that evolves over time. Therefore, a complete dataset for a single subject can consist of thousands of signals. Manifold learning (MnL) techniques can help analyze such large datasets by reducing their temporal dimensions to two or three, enabling the visualization of all the information simultaneously in a latent space that preserves the most relevant features of the original data. Additionally, the embedded space allows further analyses, such as identifying groups of signals with shared characteristics, which may reveal regions of abnormal electrical conduction and other electrophysiological phenomena [3].

In this study, we propose a methodology that enables a comprehensive analysis of the information provided by POM, combining MnL with a comparison of two different group-detection techniques that can regionalize heart areas and allow the study of their behavior. The structure of this work is as follows. The methodology is detailed in Section 2, the experiments performed and results obtained are presented in Section 3, and the conclusions are summarized in Section 4.

2. Methodology

The methodology proposed in this work consists of reducing the temporal dimensionality of the data to three using Uniform Manifold Approximation and Projection (UMAP) [4], identifying communities in the embedded space with the Louvain algorithm [5] or clusters with K-means [6], and reconstructing the original image. The

three methods are summarized in this Section.

UMAP is a MnL method that projects high-dimensional data into a latent space while preserving both local and global structures. It achieves this by constructing a high-dimensional graph representation of the data and then optimizing a corresponding low-dimensional graph to be as structurally similar as possible to its high-dimensional counterpart. In this framework, UMAP characterizes the similarity between two points $\mathbf{x_i}$ and $\mathbf{x_j}$, in the original space as probabilities (p_{ij}), and likewise between their corresponding embeddings $\mathbf{y_i}$ and $\mathbf{y_j}$ in the lower-dimensional space (q_{ij}). Then, the binary cross entropy (BCE) between p_{ij} and q_{ij}, i.e.,

$$C = \sum_i \sum_j p_{ij} \log\left(\frac{p_{ij}}{q_{ij}}\right) + (1 - p_{ij}) \log\left(\frac{1 - p_{ij}}{1 - q_{ij}}\right), \quad (1)$$

is minimized using the stochastic gradient descent algorithm. The first term of the BCE function encourages the embeddings of neighboring points to move closer together, and is activated when $\mathbf{x_i}$ is a neighbor of $\mathbf{x_j}$, or vice versa, or when both points are neighbors. In contrast, the second term repels the embeddings of non-neighboring points, pushing them farther apart.

The Louvain algorithm uses the UMAP-optimized graph to detect non-overlapping communities by maximizing the graph modularity (GM), defined as follows,

$$GM = \frac{1}{2 \cdot m} \cdot \sum_{ij} \left(\left[A_{ij} - \frac{k_i \cdot k_j}{2 \cdot m} \right] \cdot \delta(c_i, c_j) \right) \quad (2)$$

where m is the number of edges, A_{ij} indicates whether nodes i and j are connected, k_i is the degree of node i, and $\delta(c_i, c_j)$ equals 1 if nodes i and j belong to the same community and 0 otherwise. The Louvain algorithm consists of two phases. During the local optimization phase, nodes are reassigned to neighboring communities if this increases GM, and during the aggregation phase, nodes in the same community are merged into a single node to form a reduced graph. These phases repeat iteratively until GM can no longer be improved.

K-means is a clustering algorithm that divides a dataset into K non-overlapping groups by minimizing the within-cluster variance. It organizes data points $\{\mathbf{y_1}, \mathbf{y_2}, \ldots, \mathbf{y_n}\}$ into K clusters with centroids $\{\boldsymbol{\mu}_1, \boldsymbol{\mu}_2, \ldots, \boldsymbol{\mu}_K\}$. The objective function to minimize is defined as follows,

$$J = \sum_{k=1}^{K} \sum_{\mathbf{x_i} \in \mathbf{C_k}} \|\mathbf{x_i} - \boldsymbol{\mu_k}\|^2, \quad (3)$$

where C_k is the set of points assigned to cluster k, and $\boldsymbol{\mu}_k$ is the centroid of that cluster. The algorithm consists of two steps, i.e., the assignment step, where each point $\mathbf{x_i}$ is assigned to its nearest centroid, and the update step, where
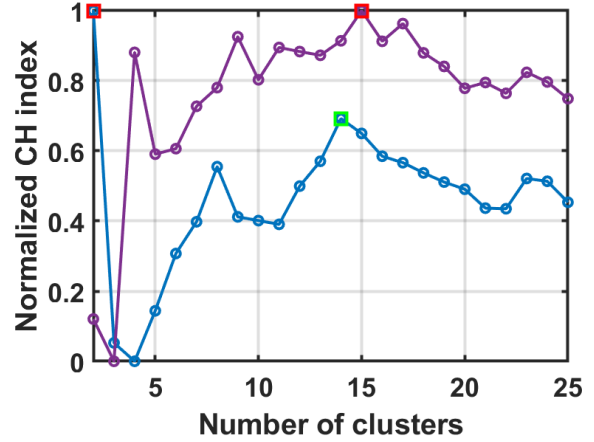

Figure 1: Normalized CH index as a function of the number of clusters for Subjects 1 (blue) and 2 (purple). The global maximum of each curve is marked with a red square, and the second-highest peak for Subject 1 is marked with a green square.

each centroid is recomputed as the mean of the points assigned to it. These steps are repeated until the assignments no longer change or the decrease in J becomes negligible.

3.   Experiments and Results

In this study, data obtained from POM using three cameras were analyzed from two subjects: one with a sinus rhythm (Subject 1) and one with atrial tachycardia (Subject 2). The acquisition protocol is detailed in [2]. The data were preprocessed in two steps. First, a three-dimensional (3D) median filter with a spatial window of 3 × 3 pixels and a temporal depth of 5 samples was applied to eliminate high-frequency noise while preserving physiological information. Second, a 4th-order high-pass Butterworth filter with a cutoff frequency of 1 Hz was applied in a zero-phase manner to eliminate baseline wander without distorting the signal. After filtering, the data were normalized to the [0,1] range. After preprocessing, UMAP was applied to project each signal into a 3D space. After that, both Louvain and K-means were applied to the embedded space, and the modularity index was computed to facilitate a quantitative comparison of the grouping results.

One disadvantage of K-means compared to Louvain is that the number of clusters must be specified beforehand. To determine this value, the Calinski–Harabasz (CH) index was employed. Figure 1 shows the normalized CH index for 2 to 15 clusters for Subject 1 (blue) and Subject 2 (purple). The optimal number of clusters for each subject is highlighted in red, corresponding to 2 clusters for Subject 1 and 15 clusters for Subject 2. However, since 2 clus-
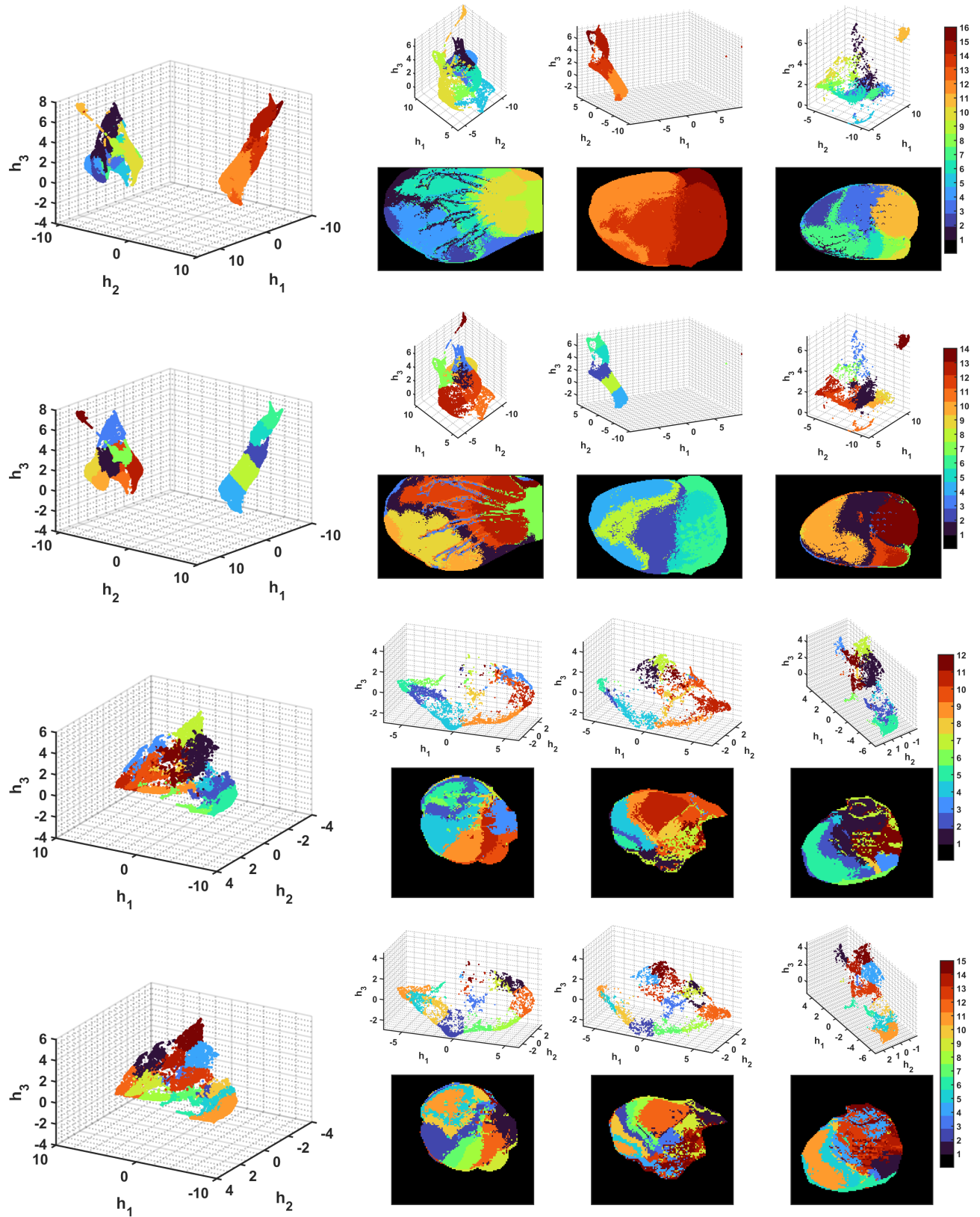
Figure 2: Latent spaces obtained with UMAP (first column), where colors represent communities detected by Louvain (odd rows) or clusters identified by K-means (even rows). Columns two to four show the latent spaces together with their corresponding original image reconstructions for cameras 1, 2, and 3, respectively. The colorbar indicates the number of groups identified in each case and their associated colors.

ters were insufficient to analyze structural or mechanistic features of the signals, we selected $K = 14$ for Subject 1, corresponding to the second-highest CH index, marked with a green square in the plot.

Figure 2 shows the complete latent spaces (left) and the latent spaces only with the points of each camera, along with the original image reconstruction with the colors of the groups encountered. Communities obtained by Louvain are shown in the first and third rows for Subjects 1 and 2, respectively, and clusters obtained by K-means are shown in the second and fourth rows for Subjects 1 and 2, respectively. In Subject 1, there are two well-differentiated clouds of points, one of them corresponding to the information in cameras 1 and 3, and the other one corresponding to the information in camera 2. Both Louvain and K-means offer grouping strategies that are similar in this case, with Louvain detecting 16 communities compared to 14 clusters for K-means. The modularity values were 0.8763 for Louvain and 0.8492 for K-means, indicating that both approaches achieved high-quality partitions, although Louvain provided a slightly better community structure. In Subject 2, the ROI was smaller, which may suggest a shared field of view among the different cameras. This overlap may explain why both Louvain and K-means identified signals in the upper part of camera 1, the lower-left part of camera 2, and the left part of camera 3 as belonging to the same community. In this case, Louvain detected 12 communities and K-means 15 clusters, with modularity values of 0.8282 and 0.8049, respectively. These results show that both methods generated meaningful groups, with Louvain achieving a slightly higher modularity, suggesting improved consistency in the detected community structure.

By focusing on the reconstructed images in Fig. 2, it can be observed that some groups lie close to each other while others are farther apart, suggesting a progression of communities that may reflect the propagation of the electrical impulse across the epicardium. Each group represents a region of the epicardial surface whose signals exhibit similar behavior, which may be associated with underlying organizational patterns of electrical activity. In addition, some communities appear to contain noisier signals, likely due to a higher noise level in the original recordings. This, in turn, influences the grouping strategy and can be used to identify which sets of signals require additional preprocessing, as well as the type of preprocessing, to improve subsequent analyses.

4.   Conclusions

This work proposes a methodology for analyzing large datasets of high-dimensional POM signals using MnL and grouping algorithms, i.e., Louvain and K-means. Our approach enables the simultaneous analysis of thousands of recordings from a single patient, providing a spatiotemporal view of epicardial POM signals that may yield insights into organizational patterns in the heart, additional preprocessing requirements, and even the propagation of electrical impulses. When comparing Louvain community detection and K-means clustering, Louvain achieved higher modularity, although K-means produced comparable values for the K selected in both subjects. Future studies will aim to further characterize the embeddings, examine how points are distributed in the original space, and interpret the physiological meaning of the communities observed in the image reconstructions.

Acknowledgments

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Address for correspondence:

Estela Sánchez–Carballo
Dep. of Signal Theory and Communications
University Rey Juan Carlos, Fuenlabrada (Madrid), Spain
Mail to: estela.sanchezc@urjc.es