Cross-recurrence analysis for pattern matching of multidimensional physiological signals

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ABSTRACT
Cross-recurrence quantification analysis (CRQA), based on the cross-recurrence plot (CRP), is an effective method to characterize and quantify the nonlinear interrelationships between a pair of nonlinear time series. It allows the flexibility of reconstructing signals in the phase space and to identify different types of patterns at arbitrary positions between trajectories. These advantages make CRQA attractive for time series data mining tasks, which have been of recent interest in the literature. However, little has been done to exploit CRQA for pattern matching of multidimensional, especially spatiotemporal, physiological signals. In this paper, we present a novel methodology in which CRQA statistics serve as measures of dissimilarity between pairs of signals and are subsequently used to uncover clusters within the data. This methodology is evaluated on a real dataset consisting of 3D spatiotemporal vectorcardiogram (VCG) signals from healthy and diseased patients. Experimental results show that $L_{\text{max}}$, the length of the longest diagonal line in the CRP, yields the best-performing clustering that almost exactly matches the ground truth diagnoses of patients. Results also show that our proposed measure, $R_{\text{max}}^\tau$, which characterizes the maximum similarity between signals over all pairwise time-delayed alignments, outperforms all other tested CRQA measures (in terms of matching the ground truth) when the VCG signals are rescaled to reduce the effects of signal amplitude.

I. INTRODUCTION
A cross-recurrence plot (CRP) is a method of bivariate time series analysis capable of assessing the nonlinear interrelationships between time series and a cross-recurrence quantification analysis (CRQA) of the CRP quantifies such interrelationships. In recent years, these techniques and recurrence analysis in general have been extended beyond their traditional roles to tasks such as data mining of time series. In this area, CRQA statistics can serve as measures of dissimilarity (or distance) between time series. Such measures can be used for unsupervised or supervised learning (e.g., clustering or classification) of time series signals; this paper focuses on the former. In particular, this paper explores the use of CRQA for pattern matching of vectorcardiogram (VCG) signals, which contain spatiotemporal information on cardiac electrical activity. In addition, a new CRQA measure is proposed that finds the maximum number of co-occurrences among different time delay alignments of signals. The proposed methodology is evaluated on real VCG data for which diagnoses (healthy, left bundle branch block, or myocardial infarction) of patients are known. Experimental results indicate that the longest diagonal line in the CRP, $L_{\text{max}}$, produces superior clustering performance that closely matches the ground truth clustering. Results also indicate that our proposed measure, $R_{\text{max}}^\tau$, yields the closest-matching clustering when the VCG signals are rescaled to reduce the effects of their differing amplitudes.
analyzing the dynamics of social interactions, and automatically identifying cover songs. In this paper, we focus on CRQA to characterize and quantify the pattern similarity between vectorcardiogram (VCG) signals, which are multidimensional, nonlinear, and spatiotemporal (Fig. 1). While CRQA is well-suited for handling signals with the first two properties, it has seen little application to signals with a spatial component. Figure 2 shows the pairwise comparison of representative VCG signals from three groups of patients: a healthy control group (HC), patients with left bundle branch block (LBBB), and patients who experienced anteroseptal myocardial infarction (MI). The top row shows comparisons of signals within the same groups (i.e., intragroup comparisons) and the bottom row between different groups (i.e., intergroup comparisons). The signals in the top row reveal a similar global shape, amplitude, and direction of trajectories, while signals in the bottom row show differences in all three of these respects.

Figure 3 shows the CRPs of the same pairwise comparisons as in Fig. 2. All three CRPs belonging to the intragroup comparisons (top row of Fig. 2) exhibit long diagonal lines (as indicated by the dark and light blue coloring) near the main diagonals of the CRPs.
This suggests that for minimal time-delayed alignments (i.e., shifting one signal relative to the other in time by a small or null amount), the signals share long common trajectories. In addition, the intragroup CRPs as a whole show a higher frequency of diagonal line structures, indicating a higher frequency of co-occurrence of trajectories belonging to the same patient group. Both intragroup and intergroup (bottom row of Fig. 2) CRPs show a high number of horizontal and vertical line structures, which indicates the tendency for any two trajectories to stay in the same region of the phase space. The diagonal line structures, therefore, appear to have more power in discriminating between patient groups.

The objective of this paper is to investigate the ability of CRQA to identify patterns between multidimensional physiological signals and to exploit this information to differentiate between healthy and pathological groups. As such, we propose the following approach (Fig. 4) and perform a real-world case study on a dataset of 93 VCG signals. First, after initial data preprocessing, each pair of VCG signals is compared via a CRP and several CRQA measures are computed, including a novel measure, denoted $R_{\max}$. It gives the maximum number of co-occurrences along a diagonal line parallel to the CRP’s main diagonal (including the main diagonal itself), which characterizes the maximum similarity between two signals over all pairwise time-delayed alignments. Each CRQA measure serves as the basis of a dissimilarity matrix, which in turn is used to produce a self-organized, force-directed network of patients. This network helps one to visualize the closeness of patients in, e.g., a three-dimensional space. A clustering algorithm is then applied on the positions of network nodes to uncover any group structure among the patients. The final clusterings are evaluated both internally and externally to assess the cohesion and separation of clusters and how well they match the ground truth clusters (i.e., the HC, LBBB, and MI groups).

Our contributions are summarized as follows:

1. We propose a novel process for pattern matching of multidimensional, (possibly) spatiotemporal, physiological signals based on CRQA.
2. We propose a new CRQA measure that characterizes the maximum similarity between two signals over all pairwise time-delayed alignments.
3. We leverage CRQA to quantify nonlinear interrelationships between VCG trajectories to differentiate among cardiac conditions, which has not been fully explored in the literature.

This paper is outlined as follows. Section II describes the previous work on pattern matching of time series signals and related work on VCG signals. Section III presents the methodology for pattern matching of multidimensional signals based on CRQA. Section IV shows a case study applying this methodology to real VCG data.
Section V discusses the clinical application of the proposed methodology. Finally, Sec. VI summarizes this work.

II. RESEARCH BACKGROUND

A. Pattern matching of time series signals

As mentioned, an objective of this paper is to use CRQA to find and quantify the degree of similar patterning between multidimensional physiological signals. Other methods have been proposed in the literature, with one of the most popular being Dynamic Time Warping (DTW). This method stretches and compresses signals, subject to certain constraints, in a way that minimizes the sum of weighted distances of aligned points (see Ref. 9 for details). This way, different patterns of time series may be aligned together. However, each signal must be completely aligned with the other signal; consequently, DTW may fail to find obvious alignments and may match a single point to large subsequences. For example, a large difference in the temporal length of signals could lead to the above problems. CRQA, on the other hand, does not align whole signals but rather finds similar patterns at arbitrary positions between the signals’ trajectories. Consequently, only similar patterns are discovered, and no misalignments may occur. In addition, CRQA allows for two signals to have different temporal lengths.

Similar to CRQA, the method of the Longest Common Subsequence (LCSS) finds the longest matching subsequence between two signals. 10 A common subsequence is subject to a distance threshold, where points must be close enough spatially to qualify as “common” (similar to \( \varepsilon \) thresholding in the CRP; see Eq. (1)), and to a temporal threshold, where one point must not be too far ahead (or behind) of a point in the opposite signal to which it is matched. LCSS may not suffer the problems encountered by DTW because not all points are required to be matched. For this reason, LCSS is less sensitive to noise than DTW, a property it shares in common with the CRP. Moreover, LCSS is similar to some CRQA measures, such as \( L_{max} \), the length of the longest diagonal line in a CRP, and to the measure, \( R_{max} \), that we propose later in this study. The CRQA measures do, though, offer the flexibility of embedding the time series signals in a time-delayed phase space. This procedure can help reduce the effect of noise and produce more informative CRPs and consequently more informative CRQA measures.

There is some work on using CRQA for quantifying the similarity between time series signals. Serra et al. 7 used three CRQA measures to quantify the similarity between cover songs. The measures were the longest diagonal line (\( L_{max} \)), the longest curved trace (\( S_{max} \)), and the longest curved trace that allows for disruptions (\( Q_{max} \)), with the latter two being especially useful for capturing changes in tempo (or speed at which the music is played). Spiegel and Albayrak 11 proposed the inverse of the average diagonal line length of a CRP as a distance measure. Later, Spiegel et al. 12,13 proposed the inverse of determinism (\( DET \)) of a joint cross-recurrence plot (JCRP), which is a combination of a CRP and a joint recurrence plot (JRP). A JCRP is useful when comparing multivariate time series where each component represents a distinct quantity; this technique is probably not appropriate for our study because the three dimensions of a VCG represent spatial locations, which should be considered in unison via the CRP. Note that our study is also not restricted to one or a few CRQA measures but rather considers many measures to test CRQA as a technique for pattern matching of multidimensional, spatiotemporal, physiological signals.

Besides direct comparison of temporal signals by methods such as DTW and LCSS, the signals may be represented in a different domain and then compared. One such method is to treat a recurrence plot (RP) from a single time series as an image and apply image processing techniques. For instance, Bello 14 used normalized compression distance (NCD) between RPs to assess the structural similarity between music recordings. Later, Silva et al. 15 calculated a video compression distance measure, namely, the Campana–Keogh distance, between RPs for the purpose of classifying time series (in conjunction with the 1-nearest neighbor classifier). Pertinent to our study, it was found that the RP-based compression distance technique performed better than DTW and the Euclidean distance in classifying time series representing figure shapes. Shape-based time series tend to exhibit repeating patterns and satisfy stationarity, two properties amenable to RPs. Instead of comparing RPs of single time series, our approach compares two spatiotemporal signals directly using a CRP to reveal common patterns between the signals’ trajectories and forms similarity measures based on the recurrence quantification. Additional work is by Michael et al. 16 who utilized information from both RPs and CRPs to form a new compression distance measure between signals.

Most previous studies computed distance (or dissimilarity) measures between RP images. Other studies have used RP images, 17 modified RP images, 18 directly in deep neural networks for time series classification. In addition, Souza et al. 19 first extracted features from RP images to later serve as inputs for a support vector machine classifier. It is now relevant to emphasize the other objective of this paper—to exploit the pattern matching information that CRQA produces for uncovering potential clusters within the data. In other words, this paper focuses on the unsupervised learning of signal similarity through CRQA-based pattern matching. That is, while the ground truth labels of VCG signals (HC, LBBB, and MI) are available, this information is not used in the execution of our method but rather saved to evaluate the final results. The aforementioned work by Spiegel et al. 12 and Spiegel 11 did perform clustering of multivariate time series. In addition, Vlahogianni et al. 17 utilized CRPs to assess the coupling of traffic volume and occupancy, extracted two CRQA measures (\( DET \) and \( L_{max} \)), and clustered traffic patterns. Their focus was on the temporal evolution of traffic, whereas the focus of our study is on identifying cross-recurrence patterns in spatiotemporal trajectories.

B. Pattern matching of vectorcardiogram signals

As shown in Fig. 1, the data in this study consist of 3-lead vectorcardiogram (VCG) signals, which depict the magnitude and direction of electrical forces in the heart in three dimensions. The VCG has been shown to possess many advantages over the popular 12-lead electrocardiogram (ECG). 20 Most fundamentally, VCG portrays the spatial orientation of electrical activity of the heart chambers in addition to its temporal evolution. In addition, studies have shown that the VCG has a higher sensitivity in the detection of myocardial infarction both by itself 21 and in combination with ECG.
criteria. Riera et al. give a comprehensive list of the advantages of the VCG over the ECG.

More specifically, each VCG signal in this study consists of a 3D QRS loop, which corresponds with the QRS complex in the time-domain ECG tracing and represents ventricular depolarization of the heart during a cardiac cycle (i.e., a heartbeat). Changes in the trajectory of the QRS loop have been shown to effectively reflect abnormalities in the electrical activity of the heart due to underlying disease. For instance, phasic changes in the QRS electrical forces, due to myocardial necrosis, are more easily identifiable in the VCG than in the ECG and lead to better detection of myocardial infarction. Moreover, the conduction defect known as the left bundle branch block leads to particular changes in the QRS loop, such as displacement and rotation of forces. In addition, the QRS loop of healthy individuals has been shown to lie in a plane. This planarity is both sensitive and characteristic of normal cardiac functioning, and the absence of such planarity may be indicative of acute myocardial infarction. The specific trajectories of QRS loops, therefore, appear to embody changes related to cardiac disease, specifically MI and LBBB. With these changes being spatiotemporal in nature, our goal is to investigate the ability of CRQA to capture these changes and distinguish between cardiac normalcy and various cardiac diseases.

To realize the potential of the added information contained in VCGs, several methods have been proposed for utilizing the VCG trajectories for purposes such as cardiac disorder detection. Methods include wavelet decomposition of VCG signals, feature analysis of VCG signals partitioned into octants, parametric basis function modeling of VCG trajectories, dynamic time warping for quantifying the similarity between VCG signals, and the application of machine learning techniques for the detection of cardiac disorders. However, with the exception of Yang and Leonelli, very few studies listed above have looked at the unsupervised learning of VCG signals, with most focusing on classification (i.e., supervised learning) of patients. In addition, little has been done to leverage recurrence plot analysis techniques for studying VCG signals; Yang did extract RQA features from multiscale VCG signals. In addition, few works have attempted to use CRP and CRQA for similarity quantification between VCG signals.

III. RESEARCH METHODOLOGY

The methodology of this paper is shown in Fig. 4. Suppose the dataset consists of N signals. First, each pair of signals is compared via a CRP (there are \( \binom{N}{2} \) such pairwise comparisons). Second, 11 CRQA measures are extracted from the CRP, which provide quantitative measures of the dissimilarity (or similarity) between signals. In the \( N \times N \) symmetric dissimilarity matrix, denoted as \( D \), \( D_{ij} \) is the value of a specific CRQA measure resulting from the CRP between the \( i \)th and \( j \)th signals; thus, 11 CRQA measures yield 11 \( N \times N \) dissimilarity matrices. Third, a self-organizing algorithm is employed to configure nodes in a three-dimensional space. Each node represents a 3D VCG from a patient, and an edge represents the interrelation (i.e., dissimilarity) between two patients. The nodes exert attractive and repulsive forces on each other based on a CRQA dissimilarity measure until convergence to a stable layout. Last, with the positions of network nodes determined, a regularized \( k \)-means algorithm is used to cluster the nodes (i.e., signals). The clusters are then evaluated, both internally for their cohesion and separation and externally for their alignment with the ground truth diagnoses. Subsections III A–III E provide the formal details of each part of the methodology.

A. Cross-recurrence plot

Let \( x^i = \{x^i\}_{t=1}^T \) be the trajectory of the \( i \)th physiological signal in the phase space. In this paper, we assume that all trajectories have the same length \( T \) (note that this is not required by CRPs). We refer to the “main diagonal” of a recurrence plot as the diagonal extending from the lower left to the upper right of the plot, which has length \( T \) by assumption.

The pairwise comparison of the \( i \)th and \( j \)th signals produces a cross recurrence plot using the definition

\[
CR_{i,j}^{ij} = \Theta(\varepsilon - ||x^i_t - x^j_t||), \quad t_1, t_2 = 1, 2, \ldots, T, \tag{1}
\]

where \( \Theta \) is the Heaviside function, \( || \cdot || \) is the Euclidean distance, and \( \varepsilon \) is the threshold distance. When performing \( \binom{N}{2} \) pairwise comparisons, an \( \varepsilon \) must be set for each comparison. Choosing to fix the same \( \varepsilon \) for all pairs may not allow for the effect of amplitude differences and the resulting CRPs may not adequately capture the similarities between certain pairs of signals. Instead, we fix the recurrence rate (RR) across all pairs of signals, allowing \( \varepsilon \) to adjust for each pair to bring about the predetermined RR. The recurrence rate is defined as

\[
RR^{ij} = \frac{1}{T^2} \sum_{t_1=1}^{T} \sum_{t_2=1}^{T} CR_{i,j}^{ij}, \tag{2}
\]

For each pair of signals, we can compute the pairwise distances \( ||x^i_t - x^j_t|| \) and determine the value of \( \varepsilon \) that produces the predetermined RR. This allows all signals to be on an equal footing for a pairwise comparison.

Another recurrence plot method for bivariate analysis of time series signals is the joint recurrence plot. Instead of defining a recurrence when \( x^i_t \approx x^j_t \) as in a CRP, the JRP defines a recurrence when both \( x^i_t \approx x^i_s \) and \( x^j_t \approx x^j_s \). That is, when each signal recurs simultaneously in their respective phase spaces, then a joint recurrence has occurred. As such, it is an appropriate means of analysis for two systems that interact and influence each other. Because the VCG signal of one patient likely does not affect or interact with the VCG signal of another patient, the JRP may not be an appropriate means of bivariate analysis in this study.

B. Cross-recurrence quantification analysis

We considered 11 CRQA measures in the case study. Seven are traditional CRQA measures, which include the diagonal line measures of DET (determinism), \( L_{max} \) (longest diagonal line length), \( L \) (average diagonal line length), and \( ENTR \) (entropy) and the vertical line measures of \( VAM \) (laminarity), \( V_{max} \) (longest vertical line length), and \( TT \) (trapping time). The reader is referred to Ref. 38 for the mathematical definitions. Note that the subscript \( V \) has been added to \( LAM \) and \( TT \) to distinguish them from the horizontal line measures.
Traditional recurrence plots only require vertical, and not horizontal, line measures because RPs are symmetric. However, CRPs are in general not symmetric as they compare two distinct signals. Moreover, the indexing of signals matters. For instance, if the ith signal is compared to the jth signal to produce a CRP and the jth signal is indexed first, then a vertical line of length five refers to a sequence of co-occurrences for a single time point of the jth signal and five time points of the ith signal. A horizontal line of length five means the reverse. Because this paper seeks to explore the potential of CRQA measures in general to characterize the similarity of two signals, we include both vertical and horizontal line measures. The three horizontal line measures are described as

- \( \text{LAM}_V \): The proportion of recurrence points belonging to a horizontal line of length at least \( h_{\text{min}}, h_{\text{min}} \geq 2 \).
- \( H_{\text{max}} \): The length of the longest horizontal line.
- \( TT_V \): The average horizontal line length.

Their mathematical definitions are analogous to the definitions for \( \text{LAM}_T, V_{\text{max}}, \) and \( TT_T \), respectively.

Used in the definitions of several CRQA measures are the quantities \( V_{\text{min}}, V_{\text{min}}, \) and \( h_{\text{min}} \), which denote the minimum length of diagonal, vertical, and horizontal lines, respectively. (The reader is again referred to Ref. 38.) Note that these quantities are all set to be two in this study as is usually recommended in the literature.

To define our novel measure, first, let \( \tau = -T, \ldots, T \), denote the time delay between two time series. For instance, \( \tau = 0 \) refers to no delay, \( \tau = 2 \) means the second (indexed) time series is shifted ahead two time steps, and \( \tau = -3 \) means the second time series is shifted behind three time steps. In the CRP, \( \tau = 0 \) refers to the main diagonal, \( \tau > 0 \) the diagonals above the main diagonal, and \( \tau < 0 \) the diagonals below the main diagonal. Such delays are of interest when comparing two time series because shifting one time series relative to another can reveal similar behavior between them.

Define

\[
R_\tau = \sum_{l=1}^{T-\tau} |P_l|, \quad \tau = -T, \ldots, T, \tag{3}
\]

where \( P_l \) is the frequency of diagonal lines of length \( l \) along the diagonal associated with delay \( \tau \). \( R_\tau \) gives the number of recurrence points along diagonal \( \tau \). Note that \( R_\tau \) is simply the recurrence rate along diagonal \( \tau \) with its proportionality removed. That is, if the recurrence rate along diagonal \( \tau \) is defined as

\[
RR_\tau = \frac{1}{T-\tau} \sum_{l=1}^{T-\tau} |P_l|, \tag{4}
\]

then \( R_\tau = (T-\tau) \cdot RR_\tau \).

Our proposed measure is given by

\[
R_\tau^{\text{max}} = \max\{R_\tau : \tau = -T, \ldots, T\}. \tag{5}
\]

That is, \( R_\tau^{\text{max}} \) is the maximum number of recurrence points occurring along a diagonal parallel to the main diagonal. It, therefore, characterizes the maximum similarity between two signals over all pairwise time-delayed alignments.

The reason for choosing to inspect \( \max\{R_\tau\} \) instead of \( \max\{RR_\tau\} \) is that \( RR_\tau \) can be artificially inflated if \( \tau \) is near \( \pm T \). For instance, if a single recurrence point occurs along the diagonal of delay \( \tau = T \), then \( \max\{RR_\tau\} \) is trivially one. Such a measure yields little power in discerning common patterns and trajectories between time series. Instead, a high value of \( R_\tau^{\text{max}} \) shows that there is a delay such that the two time series follow largely similar trajectories in their phase space. Note that \( R_\tau^{\text{max}} \) is similar to \( L_{\text{max}} \) but takes into account all recurrence points along a diagonal regardless of whether they are consecutive or not.

Each of the CRQA measures for the ith and jth signals makes up the \( (i,j) \)th entries of a dissimilarity matrix. This yields 11 dissimilarity matrices, one based on each CRQA measure. Note that we considered the diagonal line measures (i.e., \( \text{DET}, L_{\text{max}}, \text{ENTR}, \) and \( R_\tau^{\text{max}} \)) to be measures of similarity and the vertical and horizontal line measures (i.e., \( \text{LAM}_V, V_{\text{max}}, TT_V, \text{LAM}_H, H_{\text{max}}, \) and \( TT_H \)) as measures of dissimilarity for this study.

### C. Self-organizing visualization

A self-organizing method is used to visualize each patient as a node in a network whose distances from one another correspond to their pairwise dissimilarity. It is a means of reducing the dimensionality of the dissimilarity matrix to allow the nodes to be visualized in a reduced-dimension space and to make the patients amenable to clustering algorithms. In this case study, we produce a 3D visualization of the 93 patients (i.e., signals), and the dissimilarity matrix is reduced from \( 93 \times 93 \) to \( 93 \times 3 \).

The self-organization algorithm is based on finding a minimal energy configuration of a spring-electrical system that assigns attractive and repulsive forces between nodes. Two adjacent nodes in the network (i.e., that share an edge with each other) are assigned both an attractive and repulsive force, while non-adjacent nodes are only assigned a repulsive force. These forces, based on the current distances between nodes, push and pull the nodes into a network configuration of minimal total energy. The algorithm was later modified to include the nonlinear interdependence, and more generally the dissimilarity, between nodes. That is, nodes with a high dissimilarity tend to repel each other, while those with a low dissimilarity (i.e., high similarity) tend to attract each other. Note that in this case study, all patient nodes are considered to be adjacent to each other (i.e., the network is a complete graph), thus, all pairs of nodes are assigned an attractive and repulsive force.

Let \( D(i,j) \) be the dissimilarity between the ith and jth signals, and let \( y(i) \) and \( y(j) \) be their spatial locations. Then, the repulsive force between them is defined as

\[
f_r(i,j) = \frac{-CK^2}{||y(i) - y(j)||}, \tag{6}
\]

and the attractive force between them is defined as

\[
f_a(i,j) = \frac{||y(i) - y(j)||^2}{K}, \tag{7}
\]

where \( C \) regulates the strength of the repulsive force relative to the attractive force, \( K \) is the “natural” distance between nodes for which the nodes encounter no attractive or repulsive forces (called the “natural spring length” in Ref. 41), and \( \alpha \) and \( \gamma \) are tuning parameters. In this study, we use the following values in all of the simulation experiments: \( C = 0.2, K = 1, \alpha = 5, \) and \( \gamma = 5 \).
The combined force on node $i$ is

$$f(i, y, \alpha, \gamma) = \sum_{j \neq i} \frac{-CK^2}{|y(i) - y(j)|^2} e^{-\beta |y(i) - y(j)|} (y(i) - y(j)) + \sum_{j=1}^{N} \frac{|y(i) - y(j)|}{K} e^{-\gamma |y(i) - y(j)|} (y(i) - y(j)),$$

(8)

where $j \neq i$ signifies all nodes $j$ adjacent to node $i$. Note that each repulsive and attractive force has been multiplied through by $(y(i) - y(j))/|y(i) - y(j)|$. Notice that $f(i, y, \alpha, \gamma)$ is, therefore, a vector denoting the total force exerted on node $i$. To obtain the total energy of the network, the force vectors on each node are squared and summed,

$$\text{Network Energy} = \sum_{i=1}^{N} f^2(i, y, \alpha, \gamma), \quad (9)$$

where $f^2$ denotes the dot product of $f$ with itself. The self-organizing algorithm utilized in this paper thus finds the spatial locations, $y(i)$, $i = 1, 2, \ldots, N$, of the nodes that minimizes Eq. (9).

**D. Clustering**

To cluster the nodes based on their spatial locations $y(i)$, a regularized form of $k$-means is used. This method offers the simplicity and widespread applicability of $k$-means without requiring that the number of clusters, $k$, be fixed a priori.

The regularized $k$-means objective function is given by

$$\min_{\{U_i\}_{i=1}^{k}} \sum_{i=1}^{k} \sum_{y(i) \in U_i} |y(i) - \mu_i|^2 + \lambda \sum_{i=1}^{k} \sum_{y(i) \in U_i} |y(i) - \mu_i|,$$

(10)

where $\mu_i = (1/|U_i|) \sum_{y(i) \in U_i} y(i)$ is the mean of cluster $U_i$. The objective function is minimized over all clusterings, $\{U_i\}_{i=1}^{k}$, of the nodes and over the number of clusters, $k$. The parameter $\lambda$ is a regularization parameter that controls the trade-off between minimizing the sum of squares of distances to the cluster means (i.e., the $k$-means objective function) and minimizing the number of clusters. As $\lambda$ increases, more incentive is placed on minimizing the number of clusters.

Kulis and Jordan developed an algorithm that was shown to monotonically decrease Eq. (10) with each iteration, which is adopted in this paper. Initially, the algorithm forms one cluster containing all nodes, and this cluster’s mean is taken to be the mean of all nodes. During each iteration, if the minimum distance of $y(i)$ to all current cluster means is above the threshold $\lambda$, then a new cluster is formed with $y(i)$ as its mean. Otherwise, $y(i)$ is assigned to the cluster containing the closest mean to $y(i)$. Note that cluster means are not updated until all nodes have been considered in the current iteration, with the exception that a new mean is formed when a new cluster is formed (where the mean is taken to be the single node that forms the new cluster). A loop through all nodes to update cluster assignments and means is one complete iteration. This process is repeated until convergence. Please see Algorithm 1 in Ref. 42 for specific details.

There are two practical considerations concerning this algorithm. First, the final clustering results of an implementation of this algorithm may depend on the order in which the nodes are considered. Thus, because only local convergence is guaranteed, the algorithm should be implemented multiple times, with each time considering a different ordering (or permutation of 1, $\ldots$, $N$) in which the nodes are considered.

Second, $\lambda$ is a tuning parameter that must be chosen a priori. We used a procedure involving the $k$-means++ initialization algorithm. In standard $k$-means, $k$ centers are chosen uniformly at random from the nodes (i.e., data points). $k$-means++ improves on this by first selecting a single node uniformly at random to serve as a center. It then iteratively selects the remaining $k - 1$ centers according to a probability distribution based on the distances of each node to its current closest center. In other words, nodes farther away from the current centers have a higher probability of being selected as one of the remaining centers. To choose $\lambda$, $k_0$ centers are selected using the $k$-means++ algorithm, the shortest distance from each node to the closest center is computed, and $\lambda$ is taken to be the maximum of such distances. Thus, the selected value of $\lambda$ will encourage the regularized $k$-means algorithm to form $k_0$ clusters, but the algorithm is not forced to choose $k_0$ clusters.

To implement these algorithms, we used the MATLAB function, “Dirichlet Process K-Means,” available in the MATLAB File Exchange.

**E. Performance evaluation**

The final clustering is evaluated both internally and externally. The internal evaluation metric is the silhouette statistic. This metric assesses both cluster cohesion (i.e., the closeness of nodes within a cluster) and separation (i.e., the separation of clusters from one another).

Let $\{U_i\}_{i=1}^{k}$ be a partition of the dataset and suppose that node $i$ belongs to cluster $U_i$. The silhouette statistic of node $i$, denoted $s(i)$, is given by

$$s(i) = \begin{cases} \frac{b(i) - a(i)}{\max\{a(i), b(i)\}} & \text{if } |U_i| > 1, \\ 0 & \text{if } |U_i| = 1, \end{cases}$$

(11)

where

$$a(i) = \frac{1}{|U_i| - 1} \sum_{j \in U_i, j \neq i} |y(i) - y(j)|,$$

(12)

$$b(i) = \min_{c \in \{1, \ldots, k\}, c \neq i} \frac{1}{|U_c|} \sum_{j \in U_c} |y(i) - y(j)|.$$
The external evaluation measure used in this paper is normalized mutual information (NMI). NMI uses an information-theoretic perspective to compare clusterings to a ground truth. It is based on the concept of “entropy,” which quantifies the amount of uncertainty in the distribution of cluster assignments in a given clustering. Let \( U := \{U_1, \ldots, U_k\} \) be a partition. The entropy of \( U \), denoted \( H(U) \), is given by

\[
H(U) = - \sum_{c=1}^{k} p(U_c) \log (p(U_c)),
\]

where \( p(U_c) \) is the proportion of nodes belonging to cluster \( U_c \).

The mutual information between two clusterings quantifies how much knowledge of one clustering reduces the uncertainty in the other clustering. Let \( V := \{V_1, \ldots, V_m\} \) be a second partition of the nodes. Then, the mutual information between \( U \) and \( V \), denoted \( MI(U, V) \), is given by

\[
MI(U, V) = \sum_{c=1}^{k} \sum_{l=1}^{m} p(c, l) \log \left( \frac{p(c, l)}{p(c)p(l)} \right),
\]

where \( p(c, l) \) is the proportion of nodes belonging to both clusters \( U_c \) and \( V_l \).

The mutual information can be normalized so that its values lie in \([0, 1]\). The normalized mutual information (NMI) between \( U \) and \( V \), denoted \( NMI(U, V) \), is given by

\[
NMI(U, V) = \frac{2 \cdot MI(U, V)}{H(U) + H(V)}.
\]

Normalization provides at least two advantages over mutual information. First, mutual information reaches a maximum in the case when two clusterings completely match but also trivially in the case when one clustering consists of \( N \) clusters (i.e., each node is its own distinct cluster). Because entropy tends to increase when the number of clusters increases, NMI penalizes the creation of more clusters by dividing by the individual entropies. Second, because the values are normalized, NMI allows comparisons between clusterings that have different numbers of clusters. Thus, if \( U \) has a higher NMI score when compared to the ground truth than \( V \) does, then \( U \) more closely matches the ground truth, regardless of the number of clusters in each of \( U \) and \( V \).

### IV. CASE STUDY

#### A. Dataset

The data in this case study consist of 12-lead electrocardiograms (ECGs) from 93 patients. The patients are de-identified and equally divided among three groups (i.e., 31 patients each)—healthy control (HC), (anteroseptal) myocardial infarction (MI), and left bundle branch block (LBBB). The data were acquired from GE Healthcare’s MUSE Cardiology Information System at the James A. Haley Veterans’ Hospital. The patients’ 12-lead ECG printouts were obtained from this system and then preprocessed into digitized 12-lead ECG data. A generalized Dower transform was used to transform the ECG data into 3-lead VCG data. The diagnoses of the patients (i.e., normal, LBBB, or MI) were verified by an experienced cardiologist at the hospital.

The time duration of the QRS loops varies from patient to patient, and differences between the three patient groups can be seen in the following data: the mean and standard deviations of QRS time durations are 131.6 ± 11.3, 165.2 ± 17.8, and 90.2 ± 26.9 ms for HC, LBBB, and MI, respectively. To evaluate recurrence plot methods, such as JRP and CRP, for similarity assessment between VCG signals, the signals were resampled (using linear interpolation) to be of the same length (129 ms).

#### B. Experimental design

Figure 5 shows the flow chart of the experiments to test the proposed methodology on the VCG dataset. For a given pair of signals \((i, j)\), the CRP is computed, via Eq. (1), by using a value of \( \varepsilon \) that brings about a fixed RR (1%, ..., 99%). A single CRQA measure, chosen from 11 measures (Sec. III B), is computed from the CRP. This process is repeated for all \( \binom{n}{2} \) pairs of signals, using the same RR and obtaining the same CRQA measure for all pairs. This produces a 93 × 93 dissimilarity matrix that serves as the argument for the self-organization method (Sec. III C). Here, the signals are represented by nodes that self-organize to produce a stable network layout whose distances from one another preserve their pairwise dissimilarity. Because the initial layout of the nodes in this algorithm is random, 100 repetitions are performed to produce 100 layouts. With the 3D spatial locations of the nodes known, the regularized k-means algorithm (Sec. IV C 3) is performed. Initially, \( k_0 \) clusters (ranging from 2, ..., 10) are set in the \( k \)-means++ initialization algorithm and the cluster penalty parameter, \( \lambda \), is chosen. Recall that \( \lambda \) encourages \( k_0 \) clusters to be chosen but does not fix the number of

![FIG. 5. Flow diagram of experiments to test the proposed methodology on a VCG dataset.](image-url)
clusters as such. Note that the k-means++ procedure involves selecting randomized centers in choosing $\lambda$ and also note that the order in which the nodes are considered in the clustering algorithm matters. Therefore, 100 repetitions at each value of $k_s$ are performed, with each repetition selecting a different permutation of nodes (1, …, 93) uniformly at random to be considered in the clustering algorithm. Finally, each resulting clustering is evaluated in terms of both NMI and $I$.

To allow comparison between two different systems $x'$ and $x''$ in a CRP, it is common to first normalize the components. Here, “normalize” typically refers to subtracting the mean and dividing by the standard deviation. Applying normalization to the VCG signals, however, particularly scaling by the standard deviation, distorts the shapes of the VCG signals. Maintaining their shapes is important in this application because a given cardiac condition tends to distort the shapes of the VCG signals. Therefore, the methodology was applied separately to the “unscaled” VCG signals and to the “rescaled” signals.

C. Results
1. CRQA dissimilarity matrix

Figure 6 shows patient-to-patient dissimilarity matrices generated from cross-recurrence quantification analysis on the unscaled and rescaled VCG signals. Figure 6(a) describes the structure of the matrices as symmetrical and subdivided into nine $31 \times 31$ squares. For example, “HC-HC” represents patient-to-patient dissimilarity scores when both patients are from the HC group, “HC-LBBB” when one patient is from the HC group and the other is from the LBBB group, and so on.

Figures 6(b) and 6(c) show $L_{\text{max}}$ and $R_{\text{max}}$ dissimilarity matrices, respectively, generated from cross-recurrence analysis on the unscaled VCG signals. The CRQA measures are computed from CRPs using fixed recurrence rates across all pairwise comparisons of patient VCG signals; Figs. 6(b) and 6(c) show the $L_{\text{max}}$ dissimilarity matrix for a 63% RR and the $R_{\text{max}}$ dissimilarity matrix for a 38% RR. Figures 6(d) and 6(e) similarly show the $L_{\text{max}}$ and $R_{\text{max}}$ dissimilarity matrices, respectively, using the rescaled VCG signals; they were generated using recurrence rates of 63% for $L_{\text{max}}$ and 50% for $R_{\text{max}}$. These particular CRQA measures were chosen because $L_{\text{max}}$ produced the clustering that most closely matched the ground truth in terms of NMI when using the unscaled VCG signals, while $R_{\text{max}}$ produced the closest-matching clustering when using the rescaled VCG signals (see Tables I and II).

The dissimilarity measures are mapped onto a color scale, with blue denoting low dissimilarity (i.e., high similarity) and red denoting high dissimilarity (i.e., low similarity). Note that the dissimilarity values are scaled to be between zero and one. Observe that all main-diagonal squares (i.e., intragroup comparisons) in Figs. 6(b)-6(e) exhibit more blue pixels, while the off-diagonal squares (i.e., intergroup comparisons) exhibit more green, yellow, orange, and red pixels. This shows that patients within the same group tend to have lower pairwise dissimilarity scores than patients from different groups. In particular, this observation shows that CRQA measures, functioning as dissimilarity measures, are able to generally distinguish between patient groups. This contrast is most pronounced in Fig. 6(b) (i.e., $L_{\text{max}}$-unscaled) where main-diagonal squares contain many blue-green pixels and off-diagonal squares contain mostly yellow and orange pixels. Figure 6(d) (i.e., $L_{\text{max}}$-rescaled) also displays this quality; however, its HC-MI and LBBB-MI squares contain many more blue pixels. These observations, coupled with the clustering results in Sec. IV C 3, show that a CRP’s longest diagonal line is particularly valuable in distinguishing among cardiac conditions in this dataset, with its value diminishing when VCG signals are rescaled.

On the other hand, Figs. 6(c) and 6(e) show mostly similar color distributions, with the exception that the main diagonal squares in Fig. 6(e) have more blue pixels. Thus, we might expect that $R_{\text{max}}$ slightly improved or held constant its ability to distinguish among patient groups under rescaling, and this is indeed consistent with the results of Sec. IV C 3 as the NMI score increased from 0.75 to 0.82 under rescaling.

2. Self-organizing network

Figure 7 depicts the self-organizing process using the $L_{\text{max}}$ dissimilarity matrix obtained at a RR of 63%. The nodes are initially placed at random in the 3D space [Fig. 7(a)]. In subsequent iterations [Figs. 7(b)-7(d)], the nodes are pulled together, reflecting that attractive forces outweigh repellent forces at these stages of the process. Figure 7(d) shows that nodes with the same diagnoses (HC, LBBB, or MI) begin to cluster together. Nodes then settle into these clusters more distinctively in Figs. 7(e) and 7(f), with the final layout showing that nodes have clustered more or less according to patient diagnoses.

Figure 8 shows the network energy [Eq. (9)] at each iteration of the self-organizing process depicted in Fig. 7. The network energy of the initial random layout is $\approx 29 \times 10^9$. It decreases rapidly and then stabilizes around an approximate value of 168, the network energy of the final layout. The network energy at each iteration shown in Fig. 7 is approximately $29 \times 10^9$, $1.5 \times 10^{10}$, $287 \times 10^9$, $4.6 \times 10^{10}$, $135,000$, and $168$. It thus decreases by several orders of magnitude before a stable network layout is reached.

3. Clustering

Table I shows the clustering results from experiments (Sec. IV B) on the unscaled VCG signals. The first row gives the highest NMI score achieved among all clusterings generated using each respective CRQA dissimilarity measure. The next three rows give the number of clusters, recurrence rate, and silhouette scores for each of these clusterings. Notice that $L_{\text{max}}$ produced the clustering closest to the ground truth with $\text{NMI} = 0.88$. Other CRQA measures that produced clusterings with relatively good NMI scores are $\text{ENTR, } R_{\text{max}}, \text{TT}_1, \text{V}_{\text{max}}, \text{TT}_1\text{f, and } H_{\text{max}}$.

The clustering associated with $L_{\text{max}}$ that produced an NMI score of 0.88 (Table I) is depicted in Fig. 9. The proposed methodology accurately identifies three clusters, and the clusters almost exactly match the ground truth, with the exception that four LBBB patients (or nodes), are incorrectly clustered with MI patients. The
FIG. 6. (a) Structure of the CRQA dissimilarity matrix. (b) and (c) Color mapping plots of (b) $L_{\text{max}}$ and (c) $R_{\text{max}}$ dissimilarity matrices associated with unscaled VCG signals. (d) and (e) Color mapping plots of (d) $L_{\text{max}}$ and (e) $R_{\text{max}}$ dissimilarity matrices associated with rescaled VCG signals.
TABLE I. Clustering results from experiments (Sec. IV B) on the unscaled VCGs. The highest NMI score is emboldened.

| NMI (best) | DET | \( I_{\text{max}} \) | \( L \) | ENTR | \( \text{LAM}_V \) | \( \text{TT}_V \) | \( V_{\text{max}} \) | \( \text{LAM}_H \) | \( \text{TT}_H \) | \( H_{\text{max}} \) |
|------------|-----|----------------|-------|------|----------------|-------------|-------------|----------------|-------------|-------------|-------------|
| 0.75       | 0.30 | 0.88           | 0.41  | 0.80 | 0.37          | 0.74        | 0.73        | 0.47          | 0.68        | 0.65        |
| No. of clusters | 4   | 3              | 3     | 2    | 3             | 10          | 4           | 2             | 2           | 2           |
| RR         | 38  | 2              | 63    | 61   | 75            | 3           | 53          | 43            | 2           | 2           |
| \( \bar{s} \) | 0.40 | 0.26           | 0.40  | 0.23 | 0.26          | 0.26        | 0.25        | 0.46          | 0.24        | 0.34        |

TABLE II. Clustering results from experiments (Sec. IV B) on the rescaled VCGs. The highest NMI score is emboldened.

| NMI (best) | DET | \( I_{\text{max}} \) | \( L \) | ENTR | \( \text{LAM}_V \) | \( \text{TT}_V \) | \( V_{\text{max}} \) | \( \text{LAM}_H \) | \( \text{TT}_H \) | \( H_{\text{max}} \) |
|------------|-----|----------------|-------|------|----------------|-------------|-------------|----------------|-------------|-------------|-------------|
| 0.82       | 0.27 | 0.65           | 0.43  | 0.51 | 0.22          | 0.55        | 0.48        | 0.36          | 0.65        | 0.65        |
| No. of clusters | 4   | 9              | 7     | 7    | 11            | 4           | 4           | 11            | 5           | 2           |
| RR         | 50  | 1              | 63    | 15   | 9             | 2           | 99          | 69            | 2           | 60          |
| \( \bar{s} \) | 0.38 | 0.23           | 0.30  | 0.21 | 0.22          | 0.20        | 0.27        | 0.28          | 0.28        | 0.19        |

FIG. 7. Self-organizing process using the \( L_{\text{max}} \) dissimilarity matrix obtained at a 63% RR. The process is shown at the following iterations: (a) 1: initial, (b) 130, (c) 185, (d) 280, (e) 320, and (f) 400: final. Note that all edges are omitted from the presentation (each pair of nodes has an edge between them in the self-organizing network).
three clusters exhibit separation; e.g., separating lines can be placed between the clusters in the 2D representation of Fig. 9. However, some patients lie on the border of their clusters and could easily be identified with other clusters, and the clusters exhibit some cohesion. These observations are reflected in this clustering’s average silhouette score of 0.40.

To further examine the four incorrectly clustered patients, we plot their VCG signals (cyan) against representative VCG signals from LBBB (blue) and MI (red) groups, seen in Figure 10. Because the VCG signals are 3D, two different angles are shown to convey their similarities and differences. Figure 10(a) shows the misclustered LBBB signals evolving in a more similar direction and maintaining a more similar spatial orientation as the MI signal than the representative LBBB signal. Figure 10(b), rather, shows that the misclustered LBBB signals maintain a similar global shape to the representative LBBB signal and do not resemble the shape of the MI signal. The maximal vector amplitude, i.e., the norm of the longest vector within a VCG signal, is calculated as 1.96 for the representative LBBB signal, 0.72 for the MI signal, and 0.86, 1.09, 1.10, and 1.65 for the misclustered LBBB signals. It is, therefore, conceivable that the misclustered LBBB signals are being mistaken as...
MI signals because the amplitudes of the misclustered LBBB signals are shorter than typical of LBBB signals and because the CRP is distance-based. To reduce the effect of differences in amplitude and to place more emphasis on the global signal shape, we opted to rescale each VCG signal and rerun the methodology. Table II shows the clustering results of the rescaled VCG signals. Our proposed measure, $R_{\text{max}}$, produced the clustering with the highest NMI score (NMI = 0.82), although it was lower than the NMI score produced from $L_{\text{max}}$ under the unscaled VCGs. It performed significantly better than the other CRQA measures, with the next closest NMI score being 0.65 (a difference in NMI of 0.17) associated with $L_{\text{max}}, TT_h,$ and $H_{\text{max}}$. However, the clustering algorithm identifies four groups, one more than the ground truth. In addition, the silhouette score decreased slightly from 0.40 (the value of $s$ produced by $L_{\text{max}}$ under the unscaled VCGs) to 0.38.

These results illustrate two key observations. First, the raw (i.e., unscaled) amplitudes of the VCG signals clearly hold some power in distinguishing between patient groups. It is, therefore, advisable to preserve the natural amplitudes of the signals. Second, $R_{\text{max}}$ adequately characterizes and quantifies the pattern similarity between VCG signals in this study, especially when the amplitude is not to be stressed as a distinguishing feature.

Last, Fig. 11 shows how NMI varies across recurrence rates. For each RR, a point is plotted that gives the highest NMI score obtained for that RR. The black line is associated with $L_{\text{max}}$ and the unscaled VCG signals, and the blue line is associated with $R_{\text{max}}$ and the rescaled VCG signals. The peaks of each are shown by red dashed lines. The peaks occur at relatively high RRs, which implies the need for a high number of recurrence points for CRQA measures to be able to adequately and accurately distinguish between groups. In addition, Fig. 11 shows that clustering performance can be sensitive to RR, indicating that some caution should be taken in choosing the threshold $\varepsilon$ [Eq. (1)].

![Figure 11](image-url)  
**FIG. 11.** The variation of NMI scores with respect to recurrence rates. The black curve corresponds to the $L_{\text{max}}$ measure and unscaled VCG signals, and the blue curve corresponds to the $R_{\text{max}}$ measure and the rescaled VCG signals.

V. DISCUSSION

This paper proposes a methodology for pattern matching and clustering of multidimensional physiological signals. In particular, the proposed methodology is applied to a case study of 93 patient VCG signals. The ECG, however, is still the most commonly used method for measuring cardiac electrical activity. 3 The VCG dataset in this paper, in fact, was obtained from 12-lead ECG data using an inverse Dower transform. 4 As discussed in Sec. II B, VCG possesses several advantages over the ECG; the VCG includes both spatial and temporal information on electrical activity, and VCG QRS loops, in particular, can identify ailments associated with ventricular depolarization, such as LBBB and MI. From a computational standpoint, the VCG is advantageous because the data are only three-dimensional, helping to circumvent the “curse of dimensionality.” While there is a loss of information during the transformation of 12-lead ECG into 3-lead VCG, it has been shown that over 90% of ECG energy can be represented in the three-dimensional VCG subspace. 5,6 Thus, transforming higher-dimensional ECG data into 3D VCG data has advantages in the clinical setting. However, the proposed methodology is still applicable to higher-dimensional ECG data if such data are preferred.

Our methodology can be used to perform real-time pattern matching and clustering of physiological data, as shown in Fig. 12. A new patient’s VCG signal may be collected via the sensing systems in telemedicine settings (e.g., using a body sensor network) or during the patient’s physical visit to a clinic. Their signal is added to the preexisting database of $N$ patients. The $(N + 1)$th patient’s VCG signal is compared to all others via the CRP, and various CRQA measures are extracted. As such, a new row and column is added to the $N \times N$ CRQA dissimilarity matrices. Self-organization and clustering are then performed, allowing clinicians to visualize and assess the relationship of the $(N + 1)$th patient’s cardiac electrical activity with all other patients. This information in turn can be used to predict cardiac conditions based on clustering results, and it even allows for classification models to be developed based on the coordinates of patients in the reduced space.

Nowadays, medical databases contain data on a great number of patients; thus, there is a need for efficient implementation of the CRQA-based pattern matching methodology. There has been recent work on developing scalable algorithms for fast computation of RQA measures. 7–13 In addition, to reduce computational complexity in the self-organizing algorithm, fast force approximations have been proposed. 14 These approximations can be used in conjunction with a multilevel approach, which helps convergence toward a global minimum (instead of a local minimum) for scaling up to networks of millions of nodes (i.e., patients) and billions of edges. 15

Moreover, such databases may also contain data on patient covariates that are especially relevant to cardiac functioning, such as patient age, body mass index, blood pressure, cardiovascular history, and family history. Recall that the self-organization algorithm reduces the dimensionality of the CRQA dissimilarity matrices and provides coordinates for each patient (in our case study, each patient has three coordinates). The coordinates may be correlated with other patient covariates, allowing for additional inferences to be made regarding patient cardiac healthcare. In any case, synthesizing
CRQA pattern dissimilarity information with other heterogeneous patient data will allow for better-informed clinical decision making. In this study, we identified one CRQA measure, namely, $L_{\text{max}}$, that produced a well-separated clustering that almost exactly reflects patient diagnoses. It is unlikely, however, that $L_{\text{max}}$ alone can account for all of the variations between patient VCG signals. A composition of CRQA dissimilarity matrices, such as the weighted average of selected CRQA dissimilarity matrices, may provide more accurate clustering results. It is important to note that some CRQA dissimilarity matrices may be highly correlated with each other. For instance, $L_{\text{max}}$ and $R_{\text{max}}$ could be correlated because they both seek maximum diagonal line structures in the CRP. Future studies can focus on developing a methodology to account for unwanted correlation between CRQA dissimilarity matrices.\textsuperscript{35,44}

VI. CONCLUSIONS

We propose a novel methodology to leverage CRP, CRQA, and network modeling for pattern matching and unsupervised learning of multidimensional physiological signals. This paper focuses on a case study of the VCG signals of 93 patients who were diagnosed into three groups—healthy control, left bundle branch block, and myocardial infarction. The results indicate that CRQA has strong capacity to discover patterns in spatiotemporal signals and uncover groups in the data that reflect the ground truth diagnoses of an experienced cardiologist. It also shows that diagonal structures are particularly important in the similarity assessment of VCG signals using CRPs. In particular, $L_{\text{max}}$ and our proposed measure, $R_{\text{max}}$, produced the clusterings closest to the ground truth in the unscaled and rescaled VCG signals, respectively. The groups in general exhibit good separation and cohesion; a few patients, however, lie on the border of their respective clusters or are intermingled with patients with different diagnoses. In summary, this study provides evidence that CRQA has a high capacity for distinguishing between multidimensional, especially spatiotemporal, signals and paves the way for future work to further exploit recurrence analysis for pattern matching of multidimensional physiological time series.
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DATA AVAILABILITY

The data that support the findings of this study are available from James A. Haley Veterans’ Hospital. Restrictions apply to the availability of these data, which were used under license for this study. Data are available from the authors upon reasonable request and with the permission of James A. Haley Veterans’ Hospital.

REFERENCES

8. The constraints depend on the particular DTW method that is used.


