Hierarchical Clustering with Dynamic Time Warping for Automatic Detection and Labeling of Triggering Asynchrony in Patient-Ventilator Interaction during Mechanical Ventilation

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Abstract

The patient-ventilator asynchronies in the ICU can significantly impact the management and prognosis of mechanical ventilation. Currently, machine learning methods have shown promise in effectively identifying patient-ventilator asynchrony (PVA). However, there is still a lack of training datasets for PVA detection. In this study, a hierarchical clustering with dynamic time warping (DTW) method is presented to perform automatic identification and labeling of trigger asynchrony waveforms within our abnormal breathing cycle dataset for automatic identification and labeling of abnormal waveform datasets in mechanical ventilation, thereby reducing the workload of hand labeling. The experimental results show that our method can efficiently identify both ineffective triggering and double triggering from a large amount of abnormal ventilation data. These two types of trigger abnormalities are widely observed in patient-ventilator asynchronies (PVAs) during mechanical ventilation. Automatically identifying and annotating these abnormalities is crucial for reducing the burden of manual labeling, promoting the creation of PVA training datasets.

Keywords: Mechanical Ventilation, Patient-Ventilator Asynchrony, Hierarchical Clustering, Intensive Care Unit

1. Introduction

Acute respiratory failure, caused by infection, trauma, and major surgery, presents a common challenge in the intensive care unit (ICU). Mechanical ventilation is the primary method for providing respiratory support to these patients (JM et al., 2023). However, abnormal patient-ventilator asynchrony (PVA) often results in harm and discomfort for critically ill patients. The common types of PVA are categorized into major asynchrony events, including ineffective triggering, auto-triggering, and double-triggering, and minor events, such as premature cycling and delayed cycling (Lerogeron et al., 2023b). Abnormal PVA events can usually be detected through visual inspection of ventilation waveforms by professional clinicians (Bakkes et al., 2023). But, this PVA detection method is

often limited by time constraints, subjectivity, and the difficulty of continuous monitoring, which may lead to overlooking a significant number of PVA events (Jiang et al., 2022; Sunshine and Fuller, 2021). So, automatic detection of PVA events from ventilation waveforms is important for reducing the potential risk of patient injury induced by mechanical ventilation and improving patient outcomes.

Dynamic Time Warping (DTW) is an algorithm for measuring the similarity between two time series by finding the optimal alignment between them through dynamic programming (Liu et al., 2024). Dynamic Time Warping (DTW) algorithm has emerged as a versatile tool in time series analysis, offering several distinct advantages. It addresses the inherent challenges posed by temporal misalignment and varying velocities within time series data, making it particularly valuable when dealing with sequences of different lengths or speeds. In addition, DTW can enable effective handling of outliers and irregularities due to its robustness against noise and local variations (Raffel and Ellis, 2016). Indeed, these advantages establish DTW as the preferred choice for classifying complex biomedical time series signals, such as ECG, EEG, and ventilation waveforms, across various applications (Choi et al., 2023; Tuzcu and Nas, 2005; Lerogeron et al., 2023a). However, during mechanical ventilation, variations in personalized ventilation parameter settings for different patients often result in significant differences even among the same type of PVA waveforms. This presents a new challenge in identifying and labeling abnormal PVA waveforms using DTW method. Hence, we employ an unsupervised hierarchical clustering method based on DTW comparison. Initially, we rapidly cluster the dataset into various categories based on waveform patterns for each ventilated patient's respiratory cycles. This improves the speed of similarity comparison of ventilation waveforms while also simplifying the complexity of waveform comparisons across different patients.

In our previous work, we developed a respiratory cycle waveform dataset categorized into normal and abnormal data. In this work, herein, we utilized a DTW-based hierarchical clustering to find and label specific types of PVA waveforms within the abnormal dataset. In this study, we implemented a bottom-up hierarchical clustering approach for grouping abnormal breathing-cycle waveforms. Using DTW comparison, we computed the distance matrix between different cycle flow waveforms. This DTW distance matrix is used for hierarchical clustering to determine whether these two cycle waveforms can be merged into the same cluster. Our testing result shows the hierarchical clustering with DTW can significantly enable the automated identification and labeling of both ineffective triggering and double triggering from the large abnormal breathing cycle datasets.

2. Method

2.1. Data Source

In this study, waveform data from mechanical ventilation were collected from 10 ventilated ICU patients at Zhongda Hospital Affiliated to Southeast University, spanning a total ventilation time of 150 hours from March 1, 2022, to June 30, 2022. The abnormal cycle waveform dataset contains 15,704 abnormal cycle samples. The abnormal breathing-cycle data generated from 80 hours of Synchronized Intermittent Mandatory Ventilation with Pressure Support Ventilation (SIMV+PSV) and 70 hours of PSV.

2.2. DTW Algorithm for Waveform Comparison

Given two breathing-cycle waveform data $V = (v_1, v_2, \ldots, v_n)$ and $V' = (v'_1, v'_2, \ldots, v'_m)$. In order to perform DTW alignment for the two waveform sequences, a binary matrix $\mathcal{A}$ needs to be constructed firstly for the DTW matrix calculations.

Then, the dynamic programming algorithm is employed to determine the optimal matching distance between the two waveforms in the dot product of the binary matrix. The objective function is as follows (Keogh and Pazzani, 2001):

$$DTW(V, V') = min(\frac{\sqrt{\sum_{K=1}^{K} w_k}}{K}) \tag{1}$$

where K in the denominator is mainly used to compensate for warping paths of different lengths. Since there are more "point pairs" in the alignment path of longer time series, more distances are accumulated. To make distances between time series of different lengths comparable, the total distance needs to be divided by the path length.

During the alignment of respiratory flow waveforms, DTW recursively accumulates the minimum distance to determine the optimal alignment path. The dynamic programming in the algorithm relies on the following formula to find the sum of dot product distances of matrices (Tavenard, 2021; Bakkes et al., 2020):

$$D_{i,j} = \min_{\mathcal{A}(V \to i, V' \to j)} \sum_{(k,l)} d(v_k, v'_l)^q \tag{2}$$

If admissible path remains continuous, the solution for DTW path can be simplified as follows:

$$D_{i,j} = d(V_k, V'_l)^q + \min(D_{i-1,j}, D_{i,j-1}, D_{i-1,j-1}) \tag{3}$$

This distance matrix is used as the basic feature set of hierarchical clustering (Nielsen and Nielsen, 2016) to realize the evaluation of waveform similarity. The flowchart the DTW algorithm is illustrated in Figure 1. When aligning two breathing-cycle waveforms, V and V', a similarity matrix is established. Point-to-point warping is then used to align V with V' within the matrix. Finally, the dynamic programming algorithm is used to determine the shortest path between the two waveforms as the DTW path.
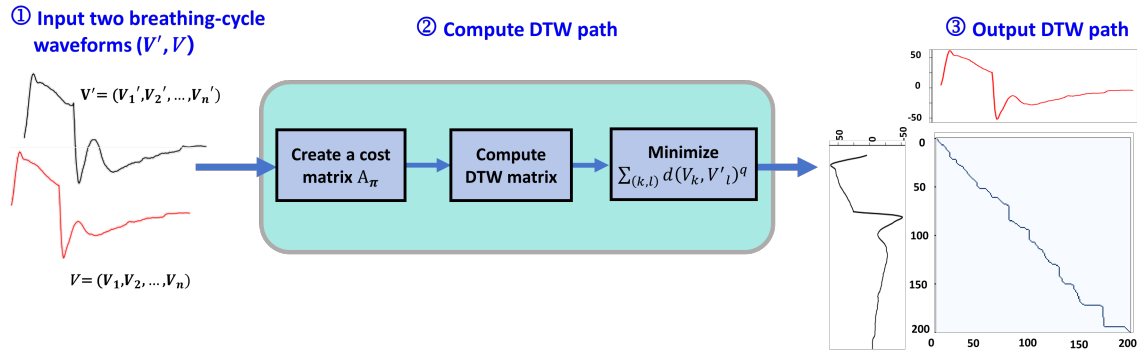

Figure 1: Graphical Illustration for DTW path calculation.

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2.3. Hierarchical Clustering with DTW

In order to improve classification efficiency and reduce matching difficulty, a DTW-based bottom-up hierarchical clustering method was used to merge the most similar abnormal waveform data into one cluster. The fundamental steps of the algorithm in our work are as follows (Murtagh and Contreras, 2017; Begum et al., 2014):

(1) Initially, each breathing-cycle waveform in our abnormal waveform dataset is set as an individual cluster.

(2) Determine whether two clusters, C1 and C2, can be merged into a single cluster based on their DTW path.

(3) Iterate the above step 2 until similar abnormal cycles are successfully clustered.

The hierarchical clustering algorithm in this study is shown in Figure 2A. In Figure 2B, the bottom cluster A-F represents different abnormal breathing-cycle waveform (Ran et al., 2023). The similarity between the two clusters is calculated, and the two most similar clusters are merged. The clustering process is repeated until a root cluster node is reached.

In our work, in our study, clustering outcome statistics serve as a criterion for terminating clustering. If the proportion of abnormal waveform samples within a single cluster exceeds 50% of the total samples, a new iteration of clustering will be performed for that cluster. This iterative mechanism can effectively lower the impact of irregular waveforms on the clustering. Here, we utilized the silhouette coefficient, ranging from -1 to 1, to evaluate the clustering results. A coefficient closer to 1 indicates stronger intra-cluster similarity and inter-cluster separation, suggesting a more significant clustering effect (Fahad, 2019). The final cluster types were validated by a professional physician. The use of silhouette coefficient can enhance the robustness of the clustering evaluation.
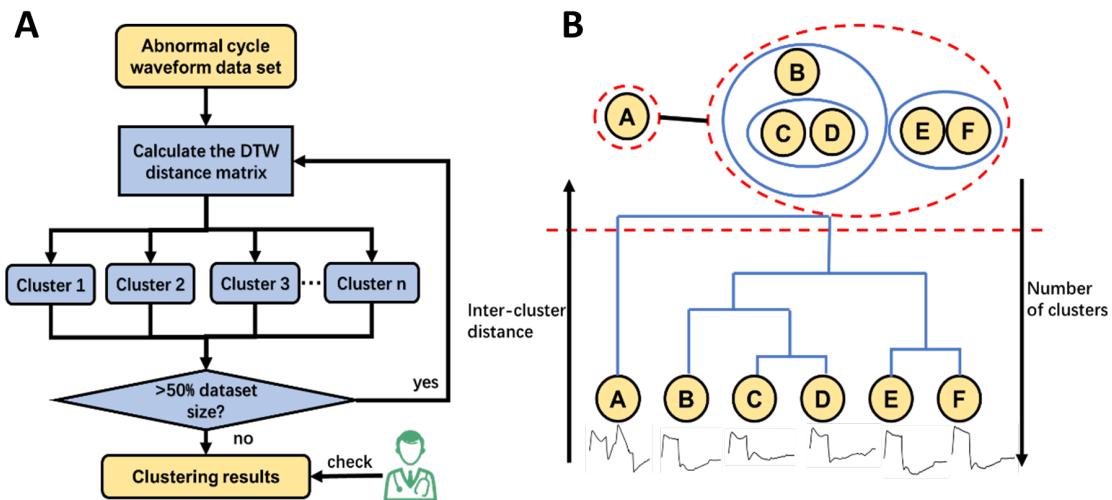

Figure 2: (A) The Flowchart of the DTW-based hierarchical clustering algorithms. (B) The graphical schematic of the bottom-up hierarchical clustering approach employed in this study, where A-F represent various breathing-cycle waveform samples.

Once the primary clustering type is confirmed by professional clinicians, the abnormal breathing-cycle waveform samples can be automatically labeled by our developed software, eliminating the need for manual intervention.

3. Result

In this paper, we use DTW-based hierarchical clustering algorithm to implement further detection and labeling of PVA abnormal waveforms. Due to variations in ventilation parameters, PVA waveforms can differ between patients, while maintaining consistency within the same patient. Consequently, clustering abnormal waveforms from the same patient can yield enhanced results. Since hierarchical clustering does not predefine the number of cluster classes, assessing the clustering effect with silhouette coefficients is crucial to identify the optimal number of clusters. Consequently, in this experiment, the abnormal cycle waveforms were clustered into five categories following the hierarchical clustering process.
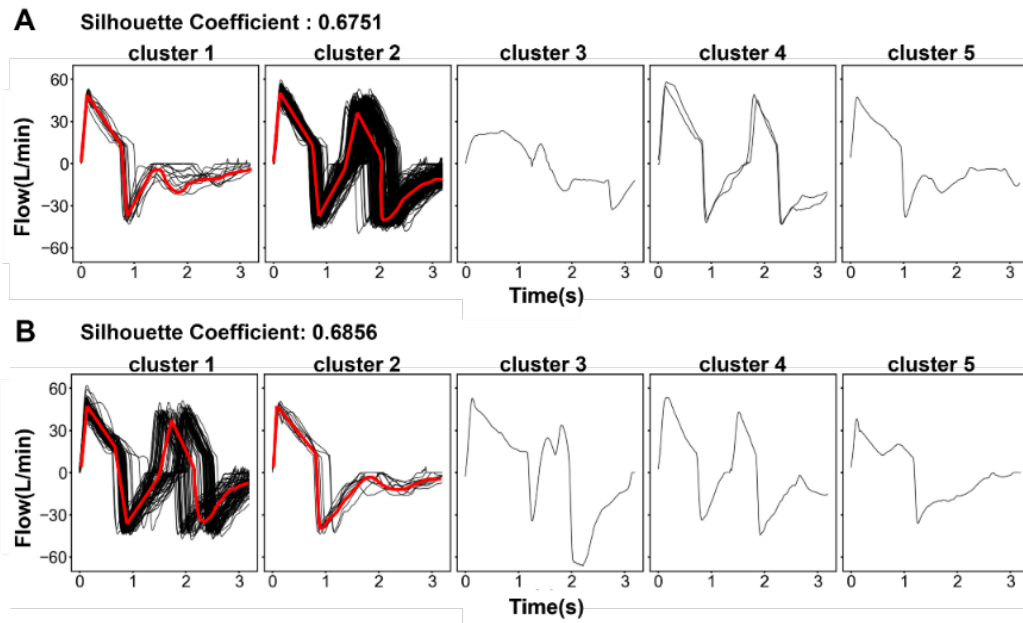

Figure 3: Two clustering results (A) and (B) of the abnormal breathing cycle data from two mechanically ventilated patients by using the DTW-hierarchical clustering algorithm, respectively. Cluster 2 (A) and cluster 1 (B) represent PVA waveforms with double triggering. The red waveforms represent the centroids of their respective clusters.

In this study, a DTW-based hierarchical clustering method successfully identified two types of typical PVA cycle waveforms: ineffective triggering and double triggering. Two group of representative clustering results from two ventilated patients are demonstrated in Figure 3A and B, respectively. Clearly, typical ineffective triggering asynchrony can be observed in cluster 1 in Figure 3A and cluster 2 in Figure 3B, while double triggering asynchrony is evident in cluster 2 in Figure 3A and cluster 1 in Figure 3B. Figure 4 illustrates the double triggering PVA waveforms, character-

ized by triggering twice within a single cycle of mechanical ventilation, resulting in two inspiratory peaks in a single breathing cycle. Both types of triggering asynchrony waveforms were confirmed by professional clinicians and utilized for model training for subsequent PVA identification.
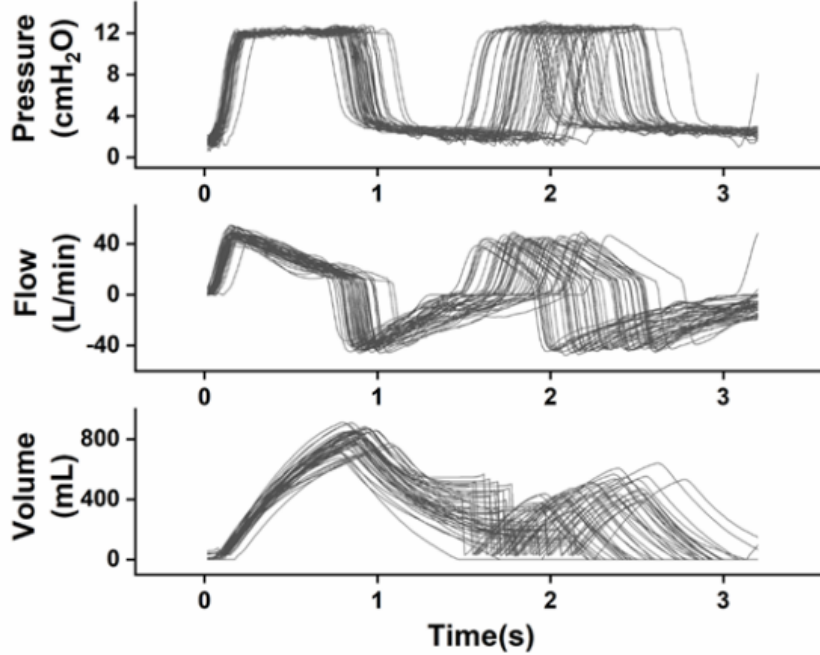

Figure 4: Representative PVA cycle waveforms with double triggering extracted from the clustering results.

Table 1: Detected Abnormal Waveforms: Ineffective vs. Double Triggering.

PVA Type	Cycles
Ineffective triggering	2,471
double triggering	3,427
Total PVA	15,704

Table 1 shows the results after DTW hierarchical clustering. Through hierarchical clustering, 2,471 samples with ineffective triggering and 3,427 samples with double triggering were identified out of the total 15,704 abnormal data points, representing a coverage exceeding 38% of the dataset. This suggests that the adoption of the unsupervised clustering approach can markedly reduce the manual labeling workload, thus advancing the creation of a training dataset for machine learning-based PVA identification.

4. Disscusion

The automatic labeling algorithm proposed in this paper uses DTW algorithm to calculate the distance matrix between the flow waveforms of different mechanical ventilation cycles. In this study,

the hierarchical clustering process may be influenced by two primary factors: an imbalanced sample distribution within the original abnormal dataset, and the presence of highly irregular waveforms that significantly differ from others, resulting in their independent clustering. Thus, setting the cluster number before clustering iteration may compress some samples originally belonging to different types into the same cluster. Therefore, employing a hierarchical clustering mechanism can effectively eliminate the influence of these minority irregular waveforms on clustering results. In addition, during mechanical ventilation, variations in ventilation settings among different patients can lead to significant differences between PVA waveforms of the same type. Therefore, our unsupervised hierarchical clustering method is executed for each ventilated patient, enhancing the effectiveness of DTW-based waveform matching.

5. Conclusion

In this study, we developed a DTW-based hierarchical clustering method for detecting and categorizing specific types of abnormal PVA waveforms. Using a bottom-up clustering approach, the abnormal breathing-cycle waveforms can be divided into five clusters based on DTW path calculation between ventilation waveforms. Our experiments demonstrated that hierarchical clustering with DTW facilitates automated identification and labeling of ineffective and double triggering asynchronies in extensive abnormal breathing cycle datasets, with the assistance of professional clinicians. This highlights the potential of unsupervised clustering to substantially reduce manual labeling efforts, thereby advancing the development of training datasets for machine learning-based PVA identification.

Acknowledgments

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