# Detecting life-threatening patterns in Point-of-care ECG using efficient memory and processor power\*

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**Abstract.** Currently, Point-of-Care (POC) ECG monitoring works either as plot devices or alarms for abnormal cardiac rhythms using predefined normal trigger ranges. Great effort has been made to improve the accuracy of such monitoring, but in the ICU setting. Thinking outside the ICU setting, where high-end devices are available, we aim to identify, on streaming data, life-threatening heart electric patterns using low CPU and memory, enabling ward monitors, home devices, and even wearable devices to be able to identify such events.

**Keywords:** anomaly detection  $\cdot$  ECG  $\cdot$  matrix profile  $\cdot$  time series  $\cdot$  point-of-care

# 1 Introduction

Currently, Point-of-Care (POC) ECG monitoring works either as plot devices or alarms for abnormal cardiac rhythms using predefined normal trigger ranges. Modern devices also incorporate algorithms to analyze arrhythmias improving their specificity. On the other hand, full 12-derivation ECG machines are complex, are not suited to use as simple monitors and are used with strict techniques for formal diagnostics of hearth electric conduction pathologies. The automatic diagnostics are derived from a complete analysis of the 12-dimension data after it is fully and well collected.

In February 2015, the CinC/Physionet Challenge 2015 was about "Reducing False Arrhythmia Alarms in the ICU" [4]. The introduction article stated that it had been reported that up to 86% of the alarms are false, which can lead to decreased staff attention and an increase in patients' delirium [3, 12, 15].

This subject highlights the importance of correctly identifying abnormal hearth electric patterns. Meanwhile, this opens the opportunity of thinking outside the ICU setting, where we still monitor patients (and ourselves) using devices with low processing power, such as ward monitors, home devices, and wearable devices.

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# 2 Objectives and research question

While this research was inspired by the Physionet's challenge, its purpose is not to beat the state-of-the-art on that challenge but to identify, on streaming data, abnormal heart electric patterns, specifically those which are life-threatening, using low CPU and low memory requirements.

The main question is: can we accomplish this objective using a minimalist approach (low CPU, low memory) while maintaining robustness?

# 3 Related Works

The Physionet's challenge yielded several papers on the subject [5, 7, 10, 11, 16]. However, independently of their approach to this problem, none of the authors reported benchmarks, memory usage, robustness test, or context invariance that could assure its implementation in smaller devices.

# 4 Planned approach

#### 4.1 Dataset

The dataset used is the CinC/Physionet Challenge 2015 public dataset [4], composed of 750 patients with at least five minutes records. The *events* we seek to identify are the life-threatening arrhythmias as defined by Physionet's challenge [4].

## 4.2 Matrix Profile

This work will use the state-of-the-art [6, 8] time series analysis technique called Matrix Profile (MP) that, once computed, allows us to derive frameworks for all sorts of tasks, such as motif discovery, anomaly detection, regime change detection, and others [18]. The MP is known to be an incredible fast algorithm [9, 13], thus viewing on the other side (not to process billions of data points using a desktop), it has a great potential to be used on small devices.

The streaming data coming from a patient is processed to create its MP in real-time. Then, the FLOSS algorithm [9] is computed to detect a regime change. When a new regime is detected, a sample of this new regime is analyzed by a model, and a decision is made. If the new regime is life-threatening, the alarm will be fired.

#### 4.3 Detecting regime changes

The regime change detection will use the FLOSS algorithm [9], an online algorithm built on top of the computed MP. The algorithm is based on the assumption that between two regimes, the most similar shape (its nearest neighbor, 1-NN) is located on "the same side". The details of the algorithm are described

in the original paper [9]. In short, the algorithm keeps track of the number of 1-NN references (called  $Arc\ Counts$ ) that crosses a point in time. As shown in the original article, figures 2 and 3 [9], a drop in the Arc Counts indicates a regime change.

## 4.4 Classification of the new regime

The next step is verifying if the new regime detected is a life-threatening pattern. The aim is not to identify the exact type of the new regime but if it is life-threatening or not. The method of choice is a classification model using shapelets as signatures of such patterns. In this case, we will need to use a set of shapelet candidates, which maximize the classification performance.

Leveraging on the MP concept, we can use the Contrast Profile (CP) [14] to derive a set of shapelets candidates. The CP looks for patterns simultaneously very similar to its neighbors in class A while being very different from the nearest neighbor in class B.

For a complete understanding of the process, in the original article, figure 6 shows a practical example [14].

#### 4.5 Validation

Both processes of detecting regime change and classification of the new regime has its own type of scoring. The extended details is available online [1]. The best parameters will be selected using *nested resampling* [2]. While the regime change will try to minimize the false negatives (keeping the false positives as low as possible), the classification model will try to eliminate the false positives.

#### 4.6 Implementation

Later, this workflow will be experimented on a low-power device, such as an ESP32 microcontroller [17], to validate the concept and measure the performance and benchmarks.

## 5 Expected results and outcomes

Ultimately, this thesis will provide a framework for identifying life-threatening conditions using biological streaming data on devices with low CPU and memory specifications. We expect to achieve a high-quality model for identifying these pathological conditions while maintaining their robustness in the presence of noise and artifacts seen in real-world applications.

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