A Clustering Based Approach for R-Peak Detection in an Electrocardiogram Signal

Juan Marquina Cancino
Facultad de Ingeniería.
Universidad Panamericana Campus Bonaterrra.
Aguascalientes, México.
0226259@up.edu.mx

Ricardo A. Gutiérrez Esparza
Facultad de Ingeniería.
Universidad Panamericana Campus Bonaterrra.
Aguascalientes, México.
0226154@up.edu.mx

***Abstract*—In electrocardiogram analysis, R-peak detection is a common problem that has been approached in multiple ways for more than 35 years. It is a steppingstone in the identification of more complex structures, such as the QRS-complex. This work presents a technique to identify the position of R-peaks in an electrocardiogram signal that uses Fast Fourier Transform to filter and normalize lead II of the electrocardiogram, a custom max pooling algorithm to select candidates for the R-peaks, and hierarchical clustering to locate the actual R-peaks. The PTB Diagnostic ECG Database was used for testing, comparing the described method with the results given by the BioSPpy library for 549 electrocardiograms, obtaining a sensitivity of 93.08% and a positive predictivity of 78.35%.**

Keywords—Electrocardiogram, Fast Fourier Transform, hierarchical clustering, R-peak, QRS-complex.

I. INTRODUCTION

An electrocardiogram (ECG) is a graphical representation of the activity of the human heart measured using electricity. More formally, "it is a measure of how the electrical activity of the heart changes over time as action potentials propagate through the heart during each cardiac cycle" [1]. To measure an ECG, at least two electrodes have to be placed in the surface of the skin so the potential difference between them can be read. Things like the position of the electrodes can change the visual representation that we get. Most modern ECGs are taken using 10 electrodes that give us 12 different leads. Perhaps the most interesting leads are I, II and III, which are called limb leads because they are obtained from the differential of the electrodes in the right arm, left arm and left leg.

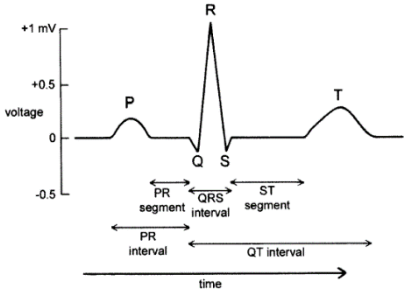

Fig. 1. Typical ECG waveform.

The waveform of a single cycle from a typical ECG looks like figure 1. It is showing data exclusively from lead II, and as we can see, there are several peaks, segments, and intervals to the waveform.

It starts with a P-wave, followed by the QRS-complex, and it ends in the T-wave. Each of the segments and intervals can be used to detect anomalies and conditions that might require treatment. Perhaps the most important part of the ECG is the QRS-complex, which can assist us in the diagnosis of conditions such as ventricular hypertrophy, bundle branch block and tachycardia [2]. In the middle of the QRS-complex we have the R-peak. Being able to detect this peak is a crucial part in the identification of the QRS-complex, and it is also useful by itself: the interval between consecutive R-peaks tells us the heart rate.

Although it might seem trivial, identifying the R-peak through software is a big challenge that researchers have been trying to tackle for more than 35 years. There have been different approaches to solving this problem, the most common ones involve using the first derivative [3], as well as some variation of it [4]. Other techniques include the usage of more advanced techniques, such as artificial neural networks [5].

The approach presented here uses the unsupervised machine learning technique known as hierarchical clustering to identify R-peaks. Data is preprocessed first by using Fourier Fast Transform (FFT) and a pooling technique. This is not the first proposition of a hierarchical clustering-based approach, Chen-Maharatna [6] presented a technique that used the wavelet transform to detect one or two peaks in 1.2 second sliding windows. Although it is not mentioned, it is a complex algorithm that might have a high runtime, however, it is a tradeoff for its high performance. For the approach presented here, instead of using hierarchical clustering to find the R-peaks directly, after filtering and normalizing the signal with FFT, we find some candidates through a max pooling technique. We then flatten the data to a one-dimensional vector space and apply hierarchical clustering to identify R-peaks. That way, we do not have a very strict window size limitation, because we are not limited to one or two R-peaks per execution.

II. METHODOLOGY

A. Dataset description

Data has been obtained from the PTB Diagnostic ECG Database (PTBDB) [7]. This is a very well-known database that has been used as a test set in most of the papers presented in this work. It features 16 channels of data, 14 for the ECG, 1 for

respiration and 1 for line voltage. Contains 549 records from 290 subjects, 209 men and 81 women, aged 17 to 87. Each patient has been diagnosed. A summary of the diagnostic classes is shown in the table below.

TABLE I. DIAGNOSTIC CLASSES FOR PTBDB

Diagnostic class	Number of subjects[a]
Myocardial infarction	148
Cardiomyopathy / Heart failure	18
Bundle branch block	15
Dysrhythmia	14
Myocardial hypertrophy	7
Valvular heart disease	6
Myocarditis	4
Miscellaneous	4
Healthy controls	52

[a] Clinical summary of 22 patients is not available, this only shows the remaining 268.

Amongst the 14 signals of ECG in this dataset, it features the 12 conventional leads. We are focusing exclusively on the lead II because it is the one that shows the best-defined Q-wave, so it makes it easier for our technique to find R-Peaks. Using lead II for this purpose is not unique to this approach, as previous work also considers it for distinct reasons [4]. ECG signals are described by a collection of µV values sampled at 1 kHz.

B. *Noise reduction using the Fast Fourier Transform*

Without getting too technical, in the context of signal analysis, the FFT is a mathematical operation that changes the domain of a signal from time to frequency. The latter is particularly useful for decomposing a signal consisting of multiple pure frequencies [8]. The FFT was applied to the EGC signals for noise reduction purposes. Once we have the transformed signal, a filter is applied to suppress low frequencies that mostly behave as constants, as well as the higher frequencies that are unusual. Then, the Inverse Fourier Fast Transform (IFFT) is used to return to the time domain.

This technique has been previously used to clean ECG signals [9], and other common approaches include using low-pass and high-pass filters (such as the fourth order Butterworth filters) [6]. Below is a comparison of a raw and a filtered signal with FFT.

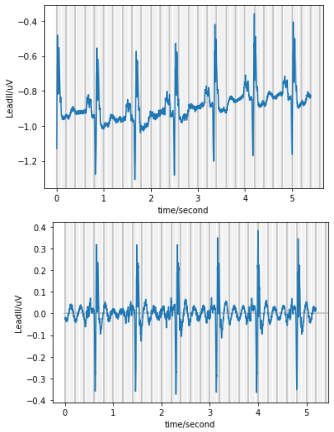

Fig. 2. Raw and filtered ECG signal.

Besides smoothing the signal, it also normalizes it. The resulting signal is also shifted 200ms to the left to trim the start of the signal, which behaves unpredictably as the result of the subsequent transformations.

C. *Pooling technique*

Once noise has been reduced, the first step for identifying R-peaks is looking for the higher signal points. The problem is that each ECG provides different values for those high points, even now that the signal is normalized, and there is not a fixed baseline for every beat, meaning that one beat might start from -0.4V and the next one from a higher or lower voltaje value (taking the Q-Peak as the starting point).

The first step to solve this problem is a pooling technique that selects candidates to be the R-Peaks of the signal. It is an algorithm that orders the signal samples from highest to lowest voltaje, iterates over the higher ones and removes other samples in their vicinity, 50 to each side (which is equivalent to 50ms of signal). Figure 3 shows an example of the execution of the pooling technique.

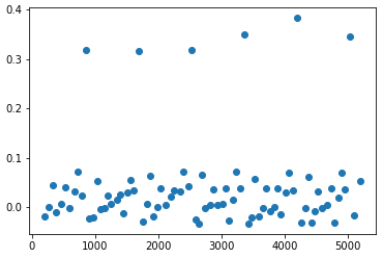

Fig. 3. Signal samples selected by the max pooling algorithm.

As we can see, we now have two clear groups of high voltage samples, and we are interested in grouping the top ones, which are the R-peaks.

D. *Hierarchical clustering*

Before applying hierarchical clustering, we first reduce the dimensionality of the data, effectively disregarding the domain of the signal. Time is not relevant for clustering because, to identify R-peaks, we only need the higher voltage samples.

Once the selected samples are on the new one-dimensional vector space, we apply hierarchical clustering. Agglomerative Clustering with Ward linkage was the selected model, because it allows to specify the number of clusters (we are interested in only two clusters), and the Ward linkage minimizes the variance of the clusters that are being merged, which makes sense for the shape of our one-dimensional data.

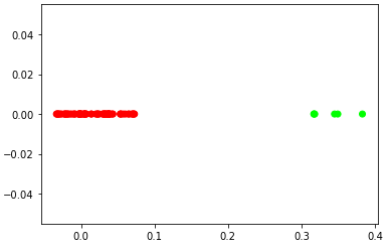

Fig. 4. Selected samples classified in the one-dimensional vector space.

The hierarchical clustering is now able to identify the R-Peaks of the ECG, and now we can return to the original vector space to determine the location of the R-peaks.

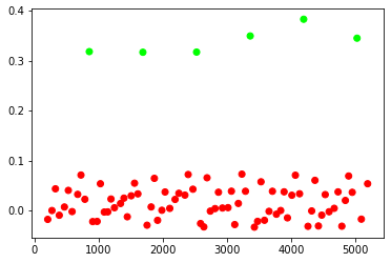

Fig. 5. Selected samples classified in the usual vector space.

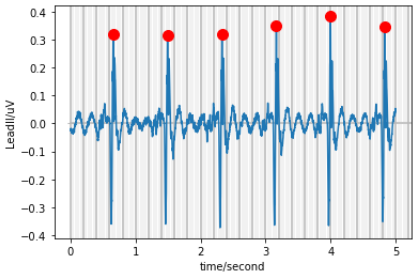

Fig. 6. ECG with the R-peaks found by this approach.

III. Results

A. Obtaining real R-peaks of the used dataset

A challenge faced during the testing phase is that PTBDB does not provide any data of the R-peaks or any other metric that could help us to identify if the technique described in this work is being accurate. The only label provided is clinical information of some of the subjects. Other authors that have used this dataset in investigations such as [4] have pointed out that manual labeling is required. To avoid the complexity of manually getting the correct position of the peaks, and for us to get an idea of the functionality of our approach, we turned to BioSPpy, a toolbox for bio signal processing written in Python. This toolbox contains a module for ECG analysis that implements the approach described by Hamilton [10] for QRS detection, which has a reliable performance. This module allows us to extract the positions of the R-peaks, which will be used to assess the functionality. A tolerance of ±5ms will be applied in the location of the R-peaks, because in practice it would still be considered an accurate location, as printed ECGs usually have a resolution of 20ms.

B. Description of the metrics used

As pointed out in [4], the most commonly used metrics to analyze the performance of R-peak detection algorithms are sensitivity (S_e) and positive predictivity ($+P$). These are defined as follows:

$$S_e = \frac{TP}{TP + FN}$$

$$+P = \frac{TP}{TP + FP}$$

Where TP (true positives) are the peaks correctly detected, FN (false negatives) are the peaks that were not detected, and FP (false positives) are peaks detected in incorrect positions.

C. Results and insights

The metrics obtained for the presented approach are shown in table II.

TABLE II. Results

Metric	Value (%)
Sensitivity (S_e)	93.08
Positive predictivity ($+P$)	78.35

Positive predictivity is particularly low for this technique because in some of the records, particularly the ones from subjects with health conditions, the signal has a higher amplitude, so the difference between R-peaks and other parts of the signal thins out, making it difficult for hierarchical clustering.

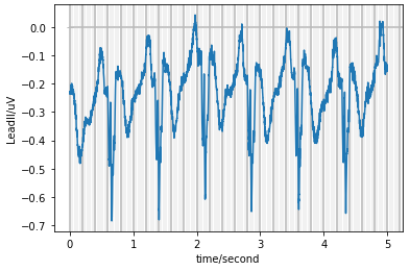

Fig. 7. ECG with high amplitude signal.

Here is a comparison with other approaches cited in this work. Bear in mind that, although the same metrics where used, some of them, such as [4], only considered the number of R-peaks detected in the signal to determine TP, FP and FN. It might not be the best approach, because position is more important that the sole amount of heart beats detected by the ECG.

TABLE III. Comparison with prior work on R-peak detection

Prior work	Sensitivity (%)	Positive predictivity (%)
Pan-Tompkins [3]	99.75	99.54
Hamilton [10]	99.74	99.81
Banerjee [4]	99.89	99.93
Proposed	**93.08**	**78.35**

IV. Conclusion

While the performance metrics of the presented approach are not as high as prior work on R-peak detection, it is a good starting point for making improvements. As mentioned earlier, the main problem are those signals with higher amplitudes, so a good starting point could be to try out other filtering techniques, such as Butterworth high-pass filter and low-pass filter, or the discrete wavelet transform, to see if they can help with these signals.

Using FFT to filter high and low frequencies was useful. Normalizing the signal helped to approximate 0V as baseline for the ECG, removing the need of performing a linear regression to find said baseline, which we originally planned.

Being able to identify R-peaks is useful by itself, to detect the heart rate, for example. However, this project also serves as a starting point for identifying and measuring more complex ECG intervals, such as the QRS-complex, which can help us to diagnose several conditions such as ventricular hypertrophy, bundle branch block and tachycardia [2]. Further work needs to be done to achieve this, but we are on a good track.

REFERENCES

[1] A. Dupre, S. Vincent, and P. A. Iaizzo, "Handbook of Cardiac Anatomy, Physiology, and Devices". New Jersey: Humana Totowa, 2006, pp. 191 - 201. J. Clerk Maxwell, A Treatise on Electricity and Magnetism, 3rd ed., vol. 2. Oxford: Clarendon, 1892, pp.68–73.

[2] J. M. Carmona, M. Jiménez, and L. Carmona, "Electrocardiograma". Málaga: Servicio de Cardiología del Hospital Virgen de la Victoria. pp. 8 – 13.

[3] J. Pan and W.J. Tompkins, "A real time QRS detection algorithm", IEEE Transactions on Biomedical Engineering, Vol. BME - 32, 1985.

[4] S. Banerjee, "A First Derivative Based R-peak Detection and DWT Based Beat Delineation Approach of Single Lead Electrocardiogram Signal", IEEE Region 10 Symposium (TENSYMP), 2019.

[5] J. Memić, "ECG Signal Classification Using Artificial Neural Networks: Comparison of Different Feature Types", IFMBE proceedings, 2017.

[6] H. Chen, and H. Maharatna, "An Automatic R-peak Detection Method Based on Hierarchical Clustering", IEEE Biomedical Circuits and Systems Conference (BioCAS), 2019.

[7] A. Goldberger, L. Amaral, L. Glass, J. Hausdorff, P.C. Ivanov, R. Mark, J.E. Mietus, G.B. Moody, C.K. Peng, and H.E. Stanley, "Components of a new research resource for complex physiologic signals", PhysioBank, PhysioToolkit, and PhysioNet, 101 (23), pp. e215–e220, 2000.

[8] C. Maklin, "Fast Fourier Transform: How to implement the Fast Fourier Transform algorithm in Python from scratch", Towards Data Science, 2019.

[9] S. Berrahal, and N. Boudriga, "ECG features extraction using fast Fourier transform", Wearable and Implantable Medical Devices, pp. 179 - 214, 2020.

[10] P. Hamilton, "Open Source ECG Analysis", Somerville: E.P. Limited, 2002.