ConvNet based QRS Multilead Delineator in Electrocardiogram signals

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Abstract. The surface electrocardiogram (ECG) is the most widely adopted test to diagnose cardiac diseases. Extracting critical biomarkers from these signals, such as the QRS width, requires delineating the fundamental waves in them. However, even though ECG signals significantly change depending on the recording methodology and cardiac condition, the available QRS delineators are hard to adapt to non-considered cases. We present a machine learning-based multilead ECG delineation method which can successfully delineate QRS complexes. Our approach reached root-mean-square errors (RMSE) of 12.1±0.5 and 18.5±1.1 ms for QRS onset and offset, respectively, when evaluated on the QT database; thus, demonstrating to be comparable to the state-of-the-art. Moreover, these results are similar to the RMSE calculated from differences between the two cardiologists that annotated this database, namely, 14.7 ms for the QRS onset and 17.2 ms for the offset.

1   Introduction

The surface electrocardiogram (ECG) is the most popular non-invasive test employed in clinical practice to diagnose and monitor cardiac diseases. The ECG provides signal-data of the heart's electrical activity. Analysing these signals requires segmenting the beats and delineating the P, QRS and T waves to calculate representative biomarkers. More precisely, segmenting the signal involves identifying and isolating the beats in it, while the delineation process retrieves the exact location of critical points, such as the onsets and offsets of the QRS complexes.

Manually delineating ECG waves is repetitive and time-consuming. Therefore, some automatic delineation methods have been proposed in the literature [5, 1, 2]. However, these systems lack of adaptability to significant differences in the target scenario since the rules composing them have been carefully designed by human experts to match a specific domain, for example, a database comprising ECG signals recorded from athletes while exercising. Indeed, adapting these solutions to non-planned scenarios requires expert knowledge about the task and the system's design, which has limited the acceptance of the existing QRS delineation approaches. On the other hand, machine learning models have the potential to adapt to any domain automatically.

We present a novel two-stepped machine learning-based multilead QRS delineation system. This system first segments the QRS waves from the ECG recording and then delineates them. More precisely, our approach is formed by successive segmentation and delineation modules, each of which is composed of a one-dimensional (1D) convolutional neural network (ConvNet) and a fully-connected neural network (NN). Previous studies have addressed ECG segmentation and detection [6]. Nevertheless, to our knowledge, this is the first work to propose a ConvNet-based QRS delineator.

2   Methods

We propose a delineator system formed by two modules, each of which is composed of two machine learning models (see Figure 1). Figure 1 illustrates these two modules and how the system works. Firstly, the segmentation module, formed by the segmenter and segmentation merger, locates the QRS waves in the ECG signal. Then, the data are windowed again using only areas containing a QRS complex. Finally, the delineation module, which is formed by the delineator and delineation merger, defines the QRS onset and offset marks.
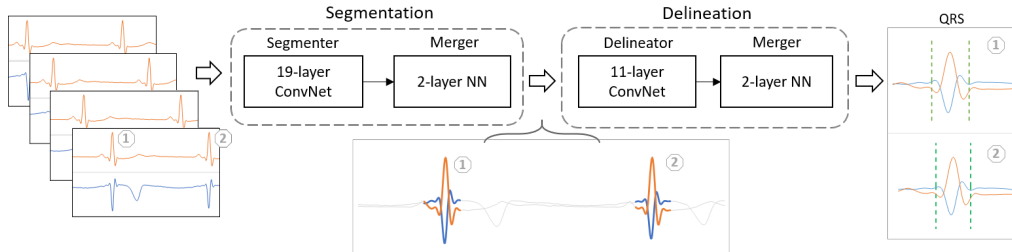

Fig. 1: Delineation system diagram formed by a segmentation and a delineation modules, each composed of a ConvNet and a NN. The first and second modules identify the QRSs and locate its the onsets and offsets, respectively.

2.1   Architecture

The segmenter is a 19-layered 1D ConvNet composed of 16 convolutional and three fully-connected layers. Each convolutional layer is formed by 16 kernels of length 3. These layers implement batch normalisation and use rectified linear unit (ReLU) activation functions. Next, the two hidden fully-connected layers have 128 and 256 neurons, respectively. Furthermore, both layers implement batch normalisation, dropout at a rate of 0.5 and ReLU as the activation functions. Finally, the output layer was another fully-connected layer with as many sigmoid units as the size of the input window to enable the model to perform classification from one-hot encoded labels.

The second model of the segmentation module is the segmentation merger. This model is a 2-layered NN composed of two fully-connected layers, with 512 and one neurons in the first and second layer, respectively. The first layer implements batch normalisation, dropout at rate 0.5 and ReLU as the activation functions. There is a sigmoid output layer.

Analogously to the segmentation module, the delineator and the segmentation merger are also a 1D ConvNet and an NN, respectively. Except for having 8 convolutional layers with kernels of size 5, the delineator is composed of the same elements than the segmenter. On the other hand, the delineation merger is identical to the segmentation one.

The number of layers and kernel sizes were chosen to enable our models to learn patterns with length up to 33 instances (i.e. 132 ms), which accounts for most QRS morphologies.

2.2   Data

The proposed method was validated using the QT database (QTDB) [4], which includes 105 two-lead ECG recordings at 250 Hz sampling rate from 7 databases. Moreover, these

recordings are manually annotated by two different experts.These signals were windowed at 2.048 s (i.e. 512 instances); thus, according to RR-interval known ranges, there should be at least one QRS complex in each sample. Then each window was normalised by subtracting the mean of its values and dividing by their standard deviation.

The augmentation strategies implemented to train our models implied using 99%-overlapping when windowing the samples, and adding constants and scaling the values of the ECG signals.

2.3   Methodology

Firstly, the segmenter trains using the augmented and windowed data. Secondly, it predicts segmentation labels on each recording using a sliding window with jumps of 1% instances. Due to the sliding strategy, this process generates a matrix of predictions. Next, the segmentation merger takes this matrix and trains on how to combine these predictions. Once trained, this merger computes a single segmentation prediction for every instance in the recording. Then, the system windows the segments of the signal with a QRS to 256 ms to give some margin to the identified zones. Later, the delineator trains on the task of finding the onset and offset marks using these shorter windows generated by the segmentation module, each of which contains only one QRS complex. Moreover, these samples are augmented again to train the delineator. Once trained, analogous to the segmentation module, the delineator will produce a matrix of predictions using a sliding window strategy. Then, the delineator merger uses this matrix to compute the QRS onset and offset positions.

2.4   Training and evaluation

Some hyperparameters, namely the number of convolutional layers, the kernel sizes and the window lengths, were chosen according to domain knowledge about the of ECG signals and its waves. Furthermore, we used Adam [3] and binary cross-entropy since this task is a one-hot-encoding binary classification problem due to its resemblance to segmentation.

We chose the remaining hyperparameters and validated the system using nested cross-validation with leave-one-database-out and grid search. More precisely, each fold included the recordings from one of the databases included in the QTDB. Then testing performances were computed each time for one fold using leave-one-database-out cross-validation with the others to choose the hyperparameters and learn the models' weights. Consequently, the performances reported are an approximation of how our approach would generalise to other databases. Moreover, the training and assessment were repeated 10 times to assess the reproducibility.

The performance measurements employed in this study were the root-mean-square error (RMSE), the mean error (ME) and the error's sample standard deviation (ESTD) from the differences between the manual annotations and our predictions.

3   Results

Table 1 reports the evaluation measures from from our delineator, [5], [2] and the difference between both annotators in the QTDB.

The methods presented in [5] and [2] are single-lead delineators. The performances of these methods were calculated by, first, producing two predictions per time instance, namely, one per lead. Then, for each time instance, they chose the prediction with less

Table 1: QRS delineation mean error in ms.

Method	RMSE Onset	RMSE Offset	ME Onset	ME Offset	STD Onset	STD Offset
This study	12.1 ± 0.5	18.5 ± 1.1	-2.6	4.4	10.8	15.2
[5]	-	-	4.6	0.8	7.7	8.7
[2]	-	-	7.0	-5.0	4.3	9.9
Difference between annotators	14.7	17.2	5.3	-0.1	11.1	12.2

error according to the true labels. On the other hand, our approach uses both leads to give a single prediction per time instance; thus, avoiding to use the true labels. Moreover, the magnitude of the errors from the differences between the marks given by the two annotators in the QTDB suggests that choosing the better of two predictions each time can significantly boost the performance of the algorithm. Consequently, since our performances are similar to the difference between the annotators and close to the ones reported by [5] and [2], our approach is at least comparable to the state-of-the-art.

4   Conclusions

We propose a ConvNet-based multilead delineation system for QRS complexes in ECG signals. The implemented data augmentation strategies enabled our system to successfully learn from a scarce and highly diverse set of multilead ECG recordings how to delineate QRS complexes. Moreover, the method achieved comparable performances than the state-of-the-art.

Exciting extensions of our work are assessing the proposed delineation system on 12-lead ECG datasets and exploring time-series specific machine learning strategies, such as recurrent neural networks and long-short-term-memory units.

5   Acknowledgements

References

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