Application of Neural Network for ECG-based Biometrics System Using QRS Features

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ARTICLE INFO

Article history's:

Received : 01 Feb 2022
Revised : 01 Mar 2022
Accepted : 16 Mar 2022

Keywords:

Biometrics
ECG
Neural network
QRS Features
Machine learning

ABSTRACT

Applications of Biometrics technology are extremely popular today, ranging from access control to automation. Fingerprint is the oldest and the most widely used biometrics technology. However, its key features are externally exposed which make it tend to be easily forged. This study investigates the possibility of electrocardiogram (ECG) signal as an alternative modality for biometrics systems. Besides that, the study is conducted using the ECG database under arrhythmia conditions to accommodate the real-world application since arrhythmia exists in large-scale world populations. In this study, a total of 8,972 datasets from 47 subjects were modeled using a machine learning technique (i.e., one-dimensional convolution neural network or 1-D CNN). The results showed that the accuracy (F1-score) of 92% and 0.25 of loss was achieved. Furthermore, we prove that the proposed model is a good fitting based on the visualization plot of the train-test. These findings show that the proposed model is reasonable enough for an ECG-based biometrics system though it's not the best in the literature.

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1. INTRODUCTION

Todate, Biometrics has been extensively applied in diverse electronic products (e.g., smartphones or wearable devices) with the purpose ranging from access control to automation. It is also widely applied in various sectors from digital transaction to the entertainment industry. Basically, Biometrics methods are categorized into two groups based on how it is measured: physiological and behavioral [1]. The physiological measurement is based on physical characteristics such as fingerprints, facial pattern, eyes (iris and retina), vein pattern, DNA, blood, etc. Whereas the behavioral measurement including voice, hand signature, gait, and gesture (see **Fig. 1**). The biometrics system using those modalities has shown promising performance to improve the traditional systems using passwords [2]. However, those modalities tend to be easily forged or damaged since the features are physically exposed [3] [4] [5].

On the other hand, the Electrocardiogram (ECG), a graphical representation of the heart's electrical activity, is attracting a huge attention as an alternative modality in human biometrics over the past few decades [6-11]. The reason is because it presents unique characteristics between one person and another depending on the anatomy of the hearts. Besides that, it is hard to forge because its key features are invisible. Finally, it is all-time available if the person is alive. However, just like other biometrics modalities, ECG also faces its challenges. The ECG signal is most likely variant to some conditions, such as: mental stress, physical activity or exercise, and arrhythmia. Furthermore, it is also susceptible to noise. Therefore, it is highly important to design a reliable model to handle signal variability in ECG to achieve an accurate identification.

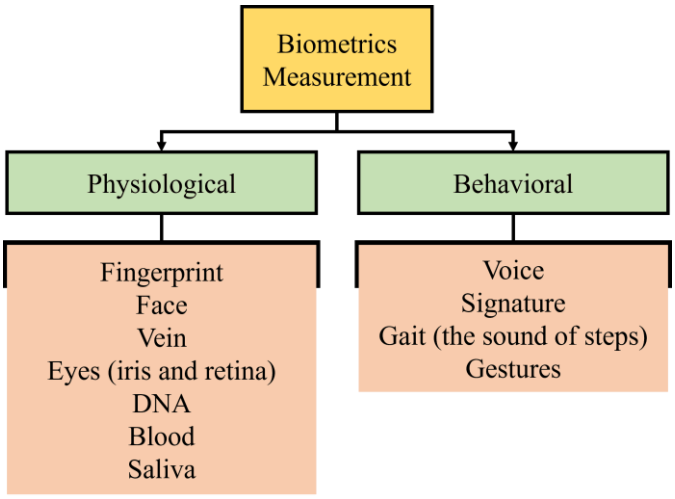

Fig. 1. The classification of biometrics measurement.

Over the past few decades, many studies have been conducted in the area of ECG-based biometrics [6-11]. Some studies conducted their own measurement or recordings to get the ECG datasets while some others used publicly available databases. Table 1 provides the summary of the public ECG databases. Study from Biel et al. [6] using a single channel ECG recording is known as the first attempt in observing ECG for biometrics purposes. They used SIEMENS ECG equipment to extract a set of temporal and amplitude features directly. The ECG database from 20 persons under healthy condition is used for testing purposes and 100% identification rate was achieved. Fatemian et al. [9] demonstrated the usage of public databases (i.e., PTB [12] and NSRDB [13]) to investigate ECG-based biometrics. The system is tested on healthy subjects (294 subjects of PTB; 13 subjects of NSRDB) and achieved the highest accuracy of 99.61%. Most of the study investigates the system under healthy (normal) heart conditions. Instead, few studies consider the effect of arrhythmia on the biometrics system.

Table 1. The summary of public databases for ECG recordings.

Database/owner name	# of subjects	Heart condition	Sensor placement
PTBDB	290	Healthy Unhealthy	Limbs and Chest
QTDB	105	Healthy (exercising) Unhealthy	Chest
LTSTDB	80	-	Chest
EDB	79	Unhealthy (myocardial ischemia)	Chest
MITDB	47	Arrhythmia	Chest
NSRDB	18	Healthy	-

PTBDB: Physikalisch-Technische Bundersanstalt database; QTDB: QT database; LSTSDB: Long-term ST database; EDB: European ST-T database; MITDB: MIT-BIH Arrhythmia database; NSRDB: MIT-BIH Normal Sinus Rhythm database.

We believe that an ECG-based biometrics system should also consider the arrhythmia condition because a large population of the world is expected to have arrhythmia [14]. Therefore, this study aims to investigate the potential of ECG-based biometrics under arrhythmia conditions using machine learning techniques, i.e., one-dimensional convolution neural network (1-D CNN). CNN has promising performance so far in a pattern

recognition system with 2-D data (images) [15]. We hypothesize that CNN will give a good result as well for 1-D data like ECG.

2. MATERIALS AND METHODS

The block diagram of our proposed method is shown by **Fig. 2**. The raw ECG is preprocessed, segmented and the feature is extracted before being fed into the machine learning model. The model's output is further justified by the decision rules to obtain the identification result.

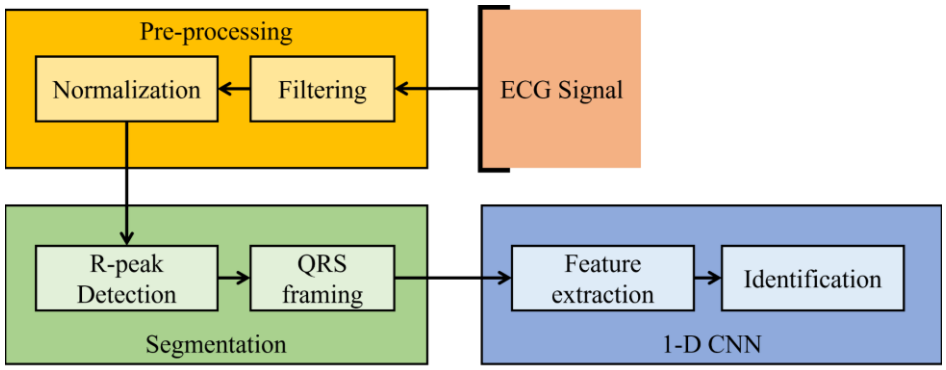

Fig. 2. The block diagram of the proposed model

2.1 ECG Signal

ECG signal is a graphical illustration of the heart's electrical activity. **Fig. 3** shows one-cycle of ECG signal in response to the human's heart electrical activity under normal condition and how it changes when arrhythmia occurs. From the figure, we can see that a typical ECG signal comprises a P-QRS-T wave segment. The P wave annotated the Atrial depolarization. Its normal length is 60-120 ms under normal conditions [16]. The QRS-complex wave is associated with the activation of the ventricles and its duration ranges from 60-90 ms [16]. The T wave indicates the ventricular repolarization or recovery state before starting the next cycle. Its duration is 100-250 ms [16]. When arrhythmia (or an abnormal condition) occurs, the ECG pattern is altered. The duration can be fastened or slowered; the amplitude can be increased or decreased.

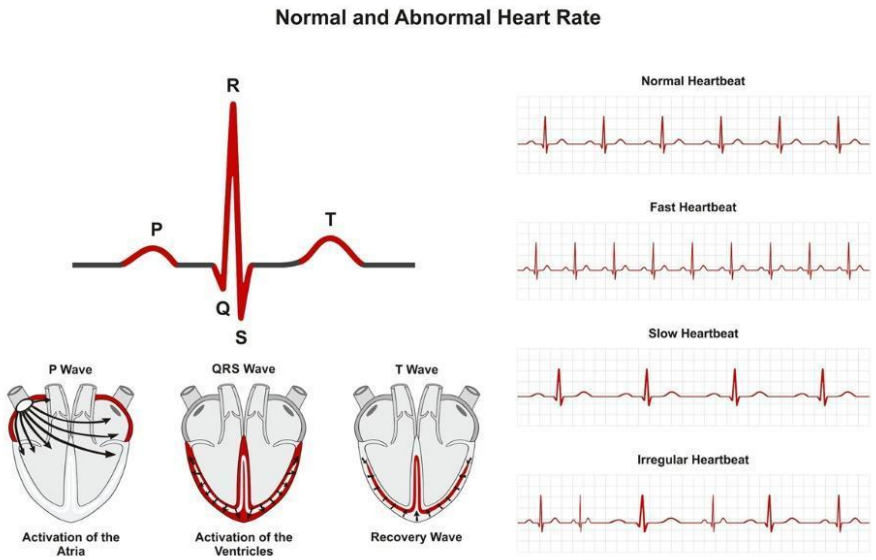

Fig. 3. The illustration of one-cycle ECG signal under normal and arrhythmia condition. The image is copyrighted by Carolina Heart and Leg Center PA [16].

The input of the system in this work is ECG signals from the MITDB database which can be accessed freely at Physionet.org. This database was created by the Beth Israel Hospital (BIH) Laboratory between 1975 and 1979. The database contains 48 half-hour of two-channel ambulatory ECG recordings from 47 subjects. Each recording from this database is sampled at 360 Hz for 30 minutes with 11-bit resolution over a 10 mV range. Each recording consists of two ECG leads: a conventional 12-lead and modified-lead II (MLII). In this study, only MLII is used. Thus, the recordings which are not resulted from MLII are discarded (i.e., record 102 and 104). So totally 46 recordings are used. The duration of each recording varies for each subject.

2.2 Preprocessing

The raw ECG signal from MITD contains some noises due to the electrode materials, electrode placement, baseline-drift, and motion artifacts during measurement. To enhance signal quality, we applied a 1-order Butterworth bandpass filter with sample frequency of 25o Hz and cutoff frequency of 2 Hz to 64 Hz. We also applied the normalization procedure to get the same scale of the voltage. **Fig. 4** shows the example of the raw ECG signal (a) and the pre-processed signal (b).

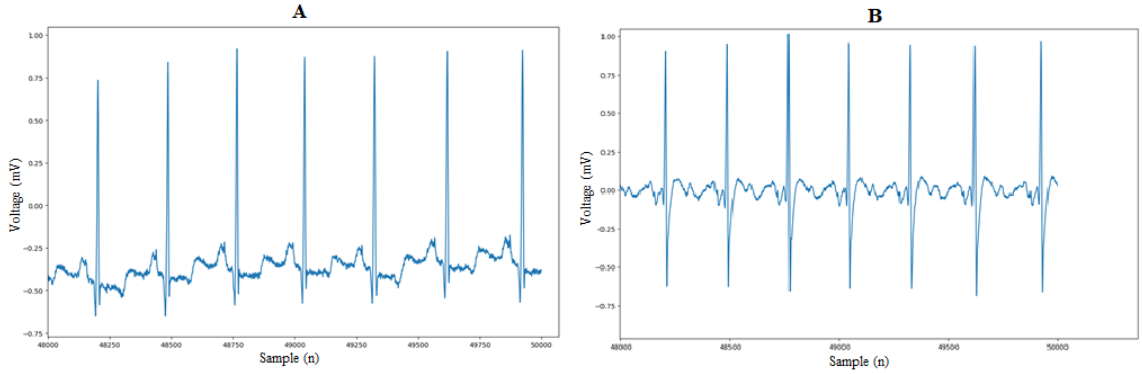

Fig. 4. The ECG signal as the input system. **A.** The raw ECG signal from record 200 in the MITDB. **B.** The ECG signal resulted from the preprocessing procedure.

2.3 Segmentation

The aim of the segmentation procedure is to get the QRS-complex segment as it is the most notable segment in ECG signal. The study from Xiang et al. [17] stated that inspecting only the QRS-complex is enough for ECG analysis instead of using the whole PQRST segment. The segmentation process is started with the R-peak detection as the point of interest. R-peak is a spike, the highest amplitude in the PQRST segment, which is a notable point to count the number of heartbeats in common ECG analysis. To conduct R-peak detection in this study, we used an available Python library, i.e., “engzee_detector" from the "ecgdetectors" package. **Fig. 5** shows the detected R-peak on the consecutive ECG signal.

After R-peak was detected, we clipped the ECG signal into 16 samples to the left of R-peak and 15 samples to the right. So, we have a total of 32 samples or equal to 128 ms for one frame which includes the QRS-complex area. This interval is longer than the standard duration of QRS-complex [16] to accommodate the arrhythmia characteristic that might be prolonged. So, the QRS features for each recording are nor discarded. **Fig. 6** shows the 6-cycle of the QRS-complex segment generated by the segmentation procedure for four different subjects: record-100, record-115, record-200, and record-205.

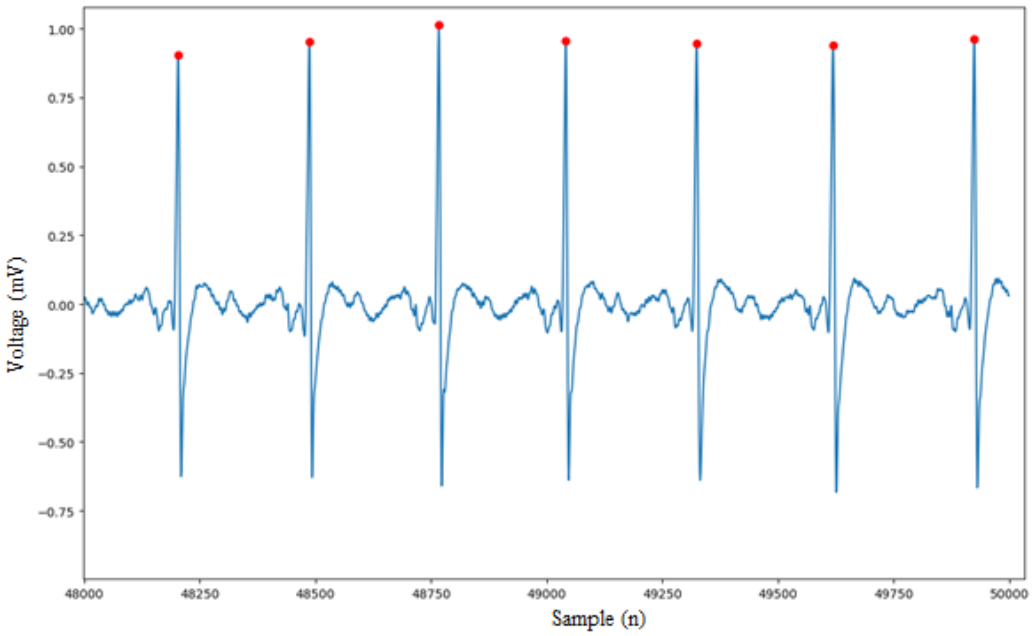

Fig. 5. The output from the R-peak detection procedure.

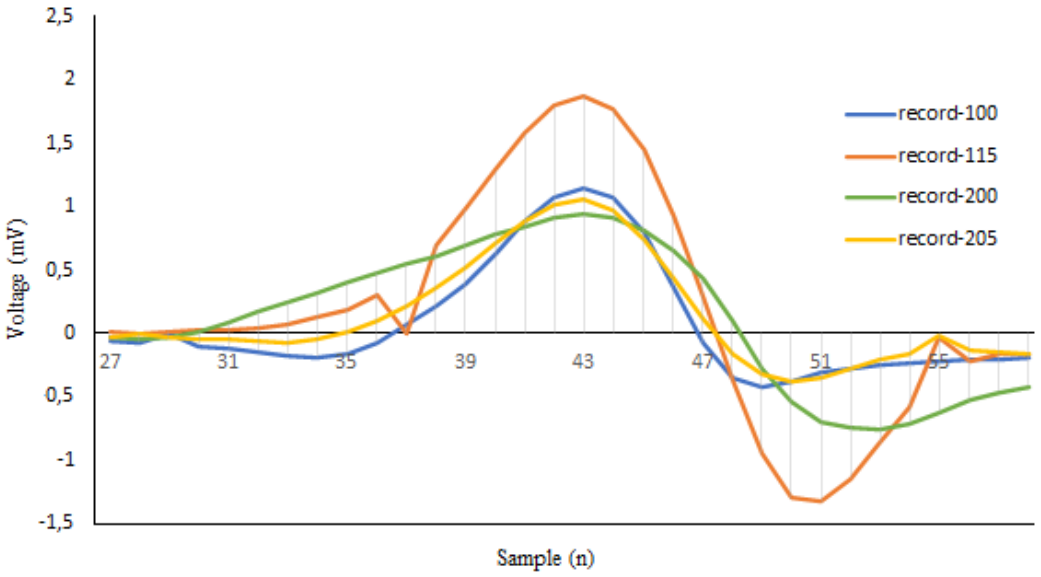

Fig. 6. The example of the QRS wave segmentation results from four subjects.

The QRS-complex data from all recordings (i.e., 47 subjects) were then collected into one csv file. The configuration of this csv file can be seen in Table 2. The first column is QRS indexing from 1 to 8,972. The 2nd to 25th column is the QRS cycles from all recordings. The last column is the label to give notation which QRS cycle belongs to which record for each row.

Table 2. The configuration of the csv file containing QRS data from all recordings

1st col.	2nd to 25th col.	26th col.
QRS data index-1	QRS data-1	Recording label-1
.	.	.
.	.	.
.	.	.
QRS data index-8,792	QRS data-8,792	Recording label-8,792

2.4 1-D CNN

CNN is a promising deep learning neural network algorithm for classification. In this work, CNN is used to do feature extraction and identification tasks. The feature extraction task is handled by the convolution layers and pooling layers, with kernel size 3x1 and 2x1, respectively. The identification task is handled by the classification function, Softmax. The CNN takes input as 2-D arrays. In contrast, ECG is 1-D arrays with amplitude values. Thus, the original CNN structure needs to be adjusted. **Fig. 7** displays the proposed 1-D CNN architecture in this work. The CNN model comprises 9 layers: one input layer, two Convolution layers, two Max Pooling layers, one Dropout layer which is added after the second convolution layer, two ReLU activation layers which are added after each convolution layer, and two dense layers. In the first dense layer, one ReLU activation layer was also added. Before the first dense layer, the data is flattened into a 1-D array. Finally, in the second dense layer, the Softmax function was applied as the classification function to do the identification task.

2.5 Evaluation Method

To evaluate the performance of our proposed model, we calculated the accuracy in the form of F1-score. The loss graph of the train-test set is also visualized to examine whether the model is a good fitting or not. The F1-score can be calculated once the confusion matrix is generated. The confusion matrix is basically a table consisting of the relationship between the predicted and actual classes in the form of four metrics: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN), as shown in **Fig. 8.** TP indicates the correctly predicted positive class. It means that when the actual class is Subject-1, then the predicted class is also Subject-1. TN indicates the correctly predicted negative class. For example, given the actual class is not subject-1, then the system also predicts it as not subject-1. FP means when the actual class is not subject-1 (no) then the system wrongly predicts it as subject-1 (yes). FN means when the actual class is subject-1 (yes) then the system predicts it as not-subject-1 (no). In the biometrics system, the goal is to get the TP and FP rate as high as possible. However, in real application, FP and FN conditions also can not be ignored.

The accuracy is commonly used for evaluation in many identification systems. High accuracy is usually assumed as a high correct identification rate. The accuracy is simply calculated as the ratio of correctly predicted observation over the total observation. Mathematically, it is written as follows:

$$Accuracy = \frac{TP+TN}{(TP+TN+FP+FN)} \quad (1)$$

However, when facing the uneven class distribution in the dataset, high accuracy value usually is not enough to represent that the model will work well when given a new input further. On the other hand, F1-score, a weighted average of the precision and recall is better to consider for evaluation.

Precision is correctly identified positive classes from all the predicted positive classes. Whereas recall (or sensitivity) is the correctly identified positive class from all the actual positive classes. In general, F1-score is calculated as follow:

$$F1 - score = 2 * \frac{(Precision * Recall)}{(Precision + Recall)} \quad (2)$$

where Precision and Recall are calculated using following equations:

$$Precision = \frac{TP}{TP+FP} \quad (3)$$

$$Recall = \frac{TP}{Total\ Actual\ Positive} = \frac{TP}{TP+FN} \quad (4)$$

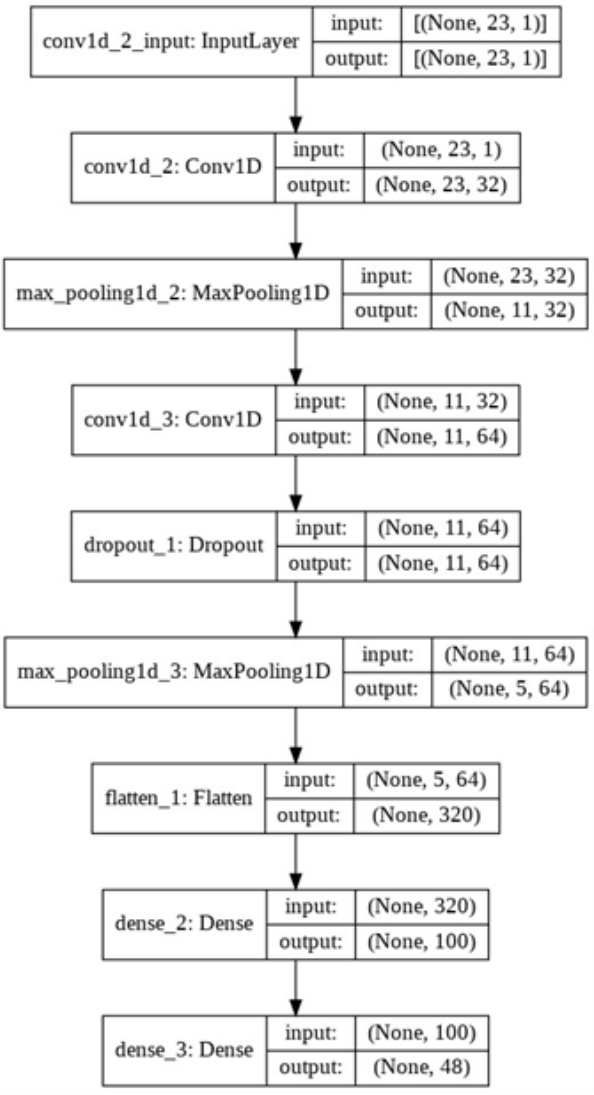

Fig. 7. The architecture of the proposed 1-D CNN model

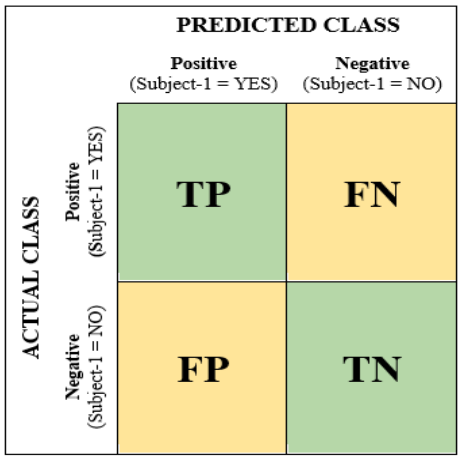

Fig. 8. The layout of the confusion matrix

3. RESULT AND DISCUSSION

This work proposed a novel ECG-based biometric system using 1-D CNN to analyze the QRS-complex features from a large dataset. A total of 8,792 ECG datasets from 47 subjects under arrhythmia condition was observed. The number of ECG samples in this study varies from one subject to another. For example, record-124 has only 113 samples, while record-215 has 261 samples. This is due to the duration of each ECG recording varies for each subject. In other words, we have imbalanced datasets in this study.

Therefore, we used the F1-score as the evaluation metric. As we can see in **Fig. 9**, the F1-score of 92% achieved at 10th epochs for both train and test set. This score is good enough to correctly identify actual data. However, it is lower than the state-of-the-art in the literature [6, 9, 11]. The reason is due to the use of CNN which typically works for 2-D data like images might not really be suitable for 1-D data like ECG. Another possibility is the number of layers applied in the 1-D architecture are too small. The reasons need to be investigated further in the future work, such as comparing the kernel size, implementing different segmentation procedures like DWT application, or observing the PQRST segment instead of only QRS complex, or applying different pre-processing technique to enhance the signal quality due to high variance under arrhythmia condition.

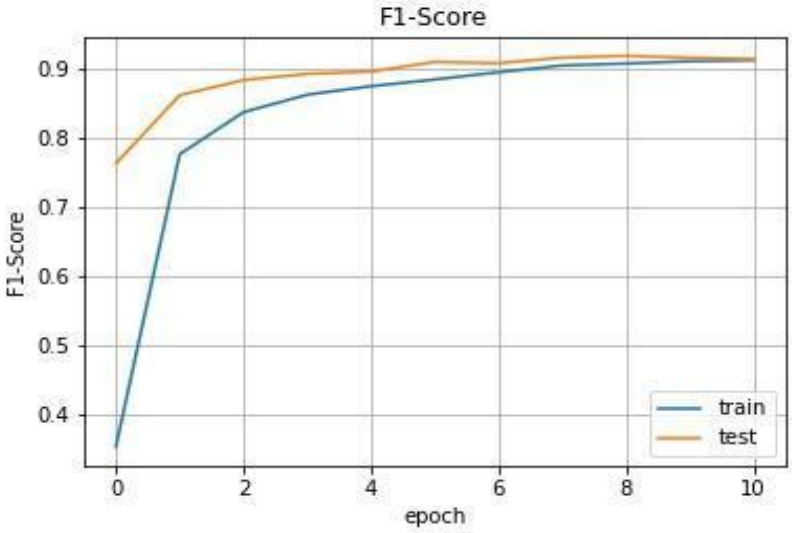

Fig 9. The F1 score graph of train versus test set

Meanwhile, based on the visualization of the loss graph between the train and test set (**Fig. 10**), we can see that the proposed model is not overfitting. It is indicated by the train and test graph which coincide with each other. We also can see that the obtained loss is about 0.25 at 10th epoch. Although in the simulation parameter we set the epoch value as 200, the simulation stopped at about 10 epochs. This is because we also applied the early stopping and model checkpoint in the simulation parameter. Both are used as a regularization procedure to prevent the model from being overfit.

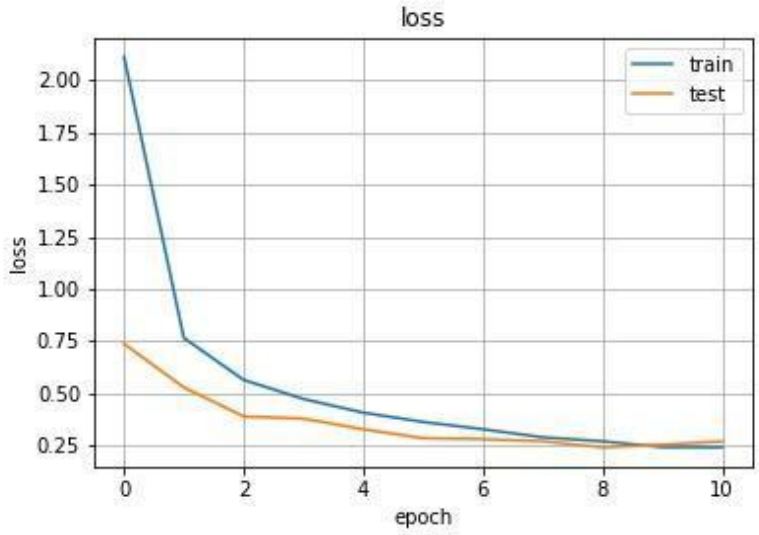

Fig 10. The loss graph of train versus test set.

4. CONCLUSION

In this work, a 1-D CNN is applied to identify 47 subjects under arrhythmia condition based on their QRS-complex features and yields a comparative identification rate though it's not the best in the literature. To get the QRS-complex segment, R-peak needs to be detected first from a consecutive ECG signal of each record. Then, from the detected R-peak, the ECG signal is clipped to 16 samples to the left and 15 samples to the right to make a QRS frame of 128 ms which is equivalent to one heart cycle or one heartbeat.

To evaluate the proposed model, we used the MIT-BIH Arrhythmia database which is freely accessed at Physionet.org. The results show that the proposed model yielded 92% of accuracy in the form of F1-score and loss of 0.25 which are reasonable enough for a biometric system. However, this work needs further investigation to improve the feasibility of our proposed model, such as: applying different pre-processing technique to enhance the signal quality, applying different scheme to conduct ECG segmentation like using DWT or autocorrelation, or considering the use of whole PQRST segment instead of only QRS-complex.

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