Myocardial Infarction Prediction Using Deep Learning

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Abstract. Myocardial infarction, known as heart attack, is one of the leading causes of world death. It occurs when blood heart flow is interrupted by part of coronary artery occlusion, causing the ischemic episode to last longer, creating a change in the patient's ECG. In this work, a method was developed for predicting patients with MI through Frank 3-lead ECG extracted from Physionet's PTB ECG Diagnostic Database and using instantaneous frequency and spectral entropy to extract features. Two neural networks were applied: Long Short-Term Memory and Bi-Long Short-Term Memory, obtaining a better result with the first one, with an accuracy of 78%.

Keywords: Electrocardiogram · Myocardial infarction · Deep Learning · Long Short-Term Memory

1 Introduction

Coronary heart disease is one of the leading killer diseases in the world and the deadliest in the US [2]. In this disease type, myocardial infarction (MI) is characterized by a part of the heart not being supplied with blood due to an occlusion of a coronary artery. As a result, the heart muscle is permanently damaged if it is not intervened immediately, leading to the death of its tissue. Thus, early identification and diagnosis become crucial to avoid sequelae of MI, such as heart failure or arrhythmia. This is called silent disease, as patients only know they have a myocardial infarction when they suffer an attack. American Health Association published that 750,000 Americans have a heart attack once per year, and 210,000 have recurrent heart attacks. Reaching a value of 72% for silent heart attacks [1].

Myocardial ischemia is the initial step when patients develop MI, which results from an imbalance between oxygen supply and demand. Before a patient has MI, the ischemia has reversible effects, and the heart cells can recover. However, during myocardial infarction, the ischemia episode lasts longer, causing the heart muscle to die and the heart signal ECG change [3].

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The acute myocardial infarction diagnosis usually uses an electrocardiogram (ECG) as an integral part of the patient's diagnosis with suspected MI. ECG abnormalities due to MI are detected in the PR segment, QRS complex, ST segment, or T wave signals [5]. The diagnosis of heart disease there is two devices used to perform the diagnosis of heart disease: the 12-lead ECG and the three-channel Frank. The standard ECG has some leads almost aligned or derived from the others and, consequently, contain redundant information, not presenting spatial information such as the cardiac vector orientation. Frank Orthogonal Leads uses fewer leads and capture more information compared to 12-lead Holter ECG, even spatial information [2].

In 2018 Mohammad Kachuee et al. [9] proposed a heartbeats classifier using deep convolutional neural networks. They used five different arrhythmia according to the AAMI EC57 standard, using the knowledge acquired for classifying myocardial infarction, obtaining a prediction with an average accuracy of 95 .9%. Two years later, Makimoto et al. [10] also created an AI using a convolutional neural network (CNN) equipped with a 6-layer architecture to accurately recognize ECG images and patterns achieving an accuracy of 81.4%.

Ardan et al. [3], in a different approach to the convulsional neural networks used a fuzzy inference system and obtained the characteristics of the MI through the S and T peaks ending with a sensitivity in the detection system test of 73%.

Recently, Adyasha Rath et al. [13] applied three cycles of LSTM network with 256, 128, and 64 modules in each stage, employing 20% random drop-offs of weights between modules. With two types of training schemes and validation (80 and 20%) and (70 and 30%) dataset was obtained with the best performance of 86.98% in accuracy, 93.82% in precision, 88.02% in sensitivity, 71.60% in specificity, and 91.50% in F1-score, respectively. It should be noted that these results were obtained using the 12 conventional lead ECGs.

This study aims to predict possible MI patients from characteristics extracted from the 3 Frank lead ECGs using two approaches with different neural networks: one with long-term memory (LSTM) and another with Bi-Long Short-Term Memory (BiLSTM).

The remaining work is organized in the following sections: Sect. 2 describes the dataset, data augmentation, resource extraction, network, and methods used to classify the patients. Section 3 shows the results and discussion, and finally, Sect. 4 draws the main conclusions concerning the study.

2 Materials and Methods

2.1 Data

This work analyzes cardiovascular signals extracted from the PTB Diagnostic ECG Database of PhysioNet [6,8]. The dataset consists of ECG recordings from 290 patients, each containing 5 individual recordings. In each record, 15 signals were measured simultaneously: the conventional twelve leads and the three Frank lead ECGs, with each signal, digitized at 1000 samples per second. For this study, only the three Frank lead ECGs were used, as represented in Fig. 1.

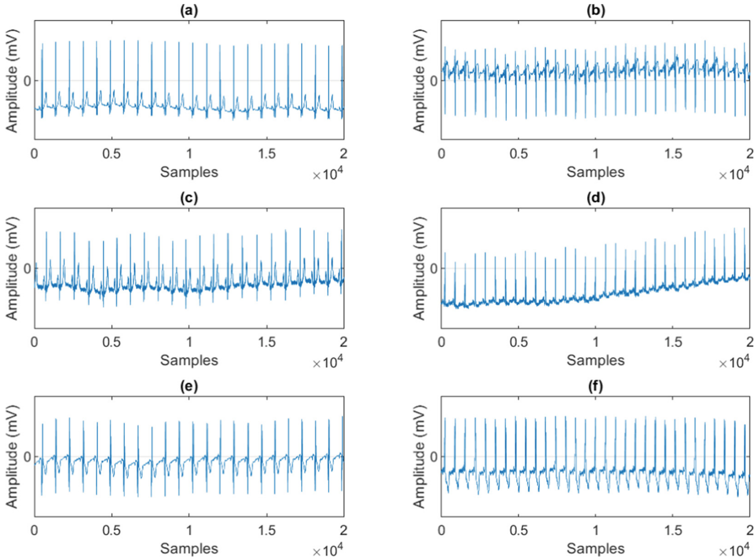

Fig. 1. ECG recordings. (a) Healthy Control with Frank Lead x, (b) MI with Frank Lead x, (c) Healthy Control with Frank Lead y, (d) MI with Frank Lead y, (e) Healthy Control with Frank Lead z, and (f) MI with Frank Lead z.

All 52 available control patients were used, and of the 148 patients with myocardial infarction, 52 were randomly selected to equate with the number of control, leaving the database with a total of 104 patients (52 with MI, 52 as healthy controls).

Each ECG record had an initial length of 115,200. As it was a long record and to increase the number of data, each ECG was divided into four identical parts, each record having a length of 28,800. Each part of the record was treated and added to the database as a new example patient, totaling 416 example patients, where 208 are healthy patients and 208 are patient with MI examples.

2.2 Feature Extraction

Extracting features from the data is critical to improving the classifier's performance. The characterization of ECG signals is achieved by time-frequency methods, such as spectrograms. Figure 2 illustrates this methodology for a healthy subject and a patient with MI.

Two-time parameters are used to extract sequences of features from the spectrograms: the instantaneous frequency and the spectral entropy.

The instantaneous frequency of a signal is a time sequence of features and is associated with the mean of the frequencies available in the signal as it

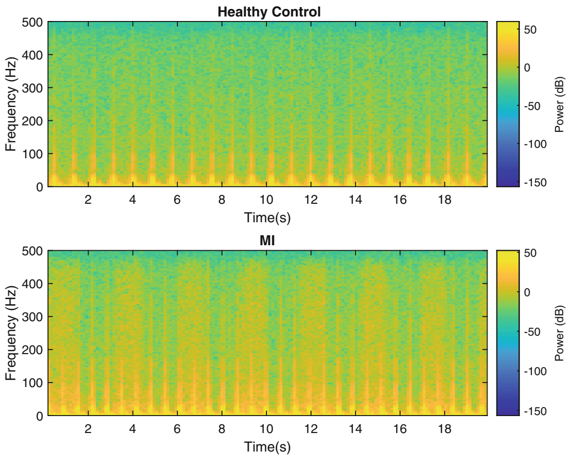

Fig. 2. Spectrum of a Healthy Control and a MI

changes over time. This approach estimates spectrogram using short-time Fourier transforms over time windows, where the time sequence of feature correspond to the centers of the time windows.

The spectral entropy of a signal is a parameter of its spectral power distribution. This parameter considers the normalized power distribution of the signal in the frequency domain as a probability distribution and calculates its entropy. As with instantaneous frequency, the function uses short time windows, and the time sequence of the feature corresponds to the center of the time windows [12]. These two-time sequences of features are represented in Fig. 3 and are then used as input for the LSTM and BiLSTM networks.

2.3 Neural Network

Long Short-Term Memory (LSTM) is a recurrent neural network that models how the human brain operates and discovers the underlying relationships in the sequential data provided with unknown duration time. It operates with a various RNNs that are capable of learning long-term dependencies, particularly in problems using sequence prediction. LSTM has feedback connections used to process the entire signal.

The primary role of the LSTM model is maintained by the memory cell known as the "cell state" which maintains its state over time.

Information can be added to or removed from the cell state. These gates could allow information to enter and leave the cell and contain a multiplication operation point and a sigmoid neural network layer that assists the mechanism (see Fig. 4).

On the other hand, Bi-Long Short-Term Memory (BiLSTM) is an LSTM model with two LSTMs layers [4], Fig. 5. The network is fed with two-time directions: a start-to-finish signal and an end-to-start signal, making the network flow

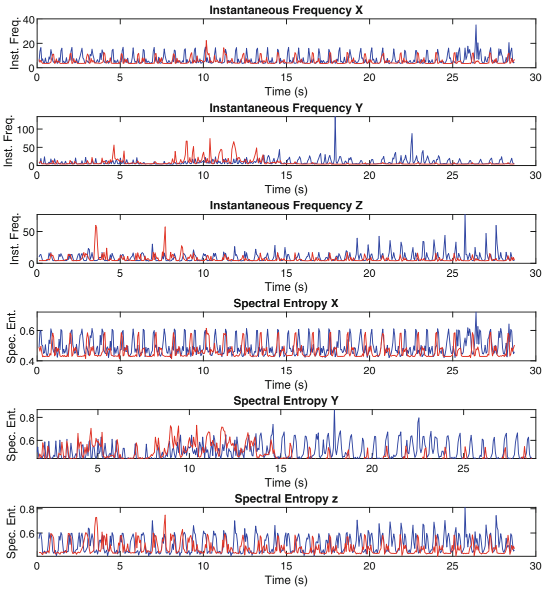

Fig. 3. Feature extracted from each Frank Lead: Healthy (blue) and Sick (red).

in both directions, contributing to the improvement of long-term dependency learning.

2.4 Classifier Performance

Five indicators are used to evaluate and analyze the effectiveness of the classifier's performance: accuracy (ACC) corresponds to the proportion of correct predictions to total predictions; sensitivity (SEN) is the proportion of true positives to the total positives present in the dataset; precision (PRE) is the ratio between true and total predicted positives; specificity (SPE) is the ratio between the true negatives and the total negatives; F1-Score (F1) combines the precision and sensitivity metric using their harmonic mean. The higher value, the more significant the balance between precision and sensitivity.

The following equations describe the performance classifiers used:

$$ACC = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

$$SEN = \frac{TP}{TP + FN} \tag{2}$$

$$PRE = \frac{TP}{TP + FP} \tag{3}$$

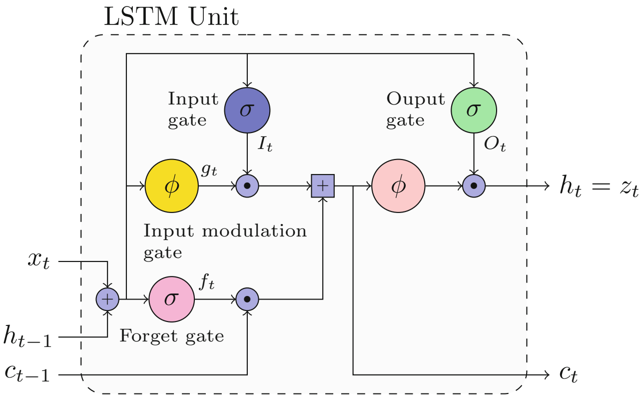

Fig. 4. LSTM unit [11].

$$SPE = \frac{TN}{TN + FP} \tag{4}$$

$$F1 = \frac{2.PRE.SEN}{PRE + SEN} \tag{5}$$

where TP is the true positives value, FP is the false positives value, TN is the value of the true negative, and FN is the value of the false negative.

The k-fold cross-validation method compares a large number of fitted models and avoids overfitting, evaluating the performance of neural networks. This method randomly splits the data into k portions. $k - 1$ portions are used for training and one for validation. This process is repeated k times. The general estimation error is the average test error of the iterations [7]. For this study, a k-fold with $k = 5$ was applied.

3 Results and Discussion

Each neural network was trained and tested two times with different training and test specification options. Two classes (healthy and sick) and six characteristics extracted from each patient were inserted into the neural networks, these being the instantaneous frequency and spectral entropy for each Frank lead ECG (v_x, v_y, v_z). The features for the two groups in the dataset are illustrated in Fig. 6. These features can characterize relatively well healthy and MI patients.

A 5-fold cross-validation was used, obtaining 80% of each group for training and 20% for testing. For all tests, a learning rate of $\alpha = 0.001$ was used, with two fully connected layers of size 20 and one of size 2 (two groups), followed by softmax and classification layers. The described model is illustrated in Fig. 7.

Initially, the LSTM neural network was used, with 100 Hidden Units and 80 MaxEpochs but varying the Mini Batch Size between 100 and 80. Table 1 and

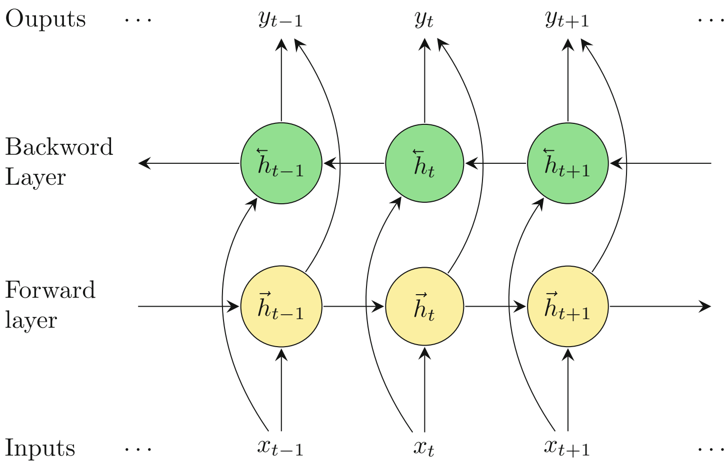

Fig. 5. Bi-LSTM layers [11].

Table 2 summarize the training and testing results, respectively. The best result was obtained when the Mini Batch Size was 80, obtaining test values of 78.13% for accuracy, 75.02% for sensitivity, 80.10% for precision, 81.27% for specificity, and 77.32% for F1-Score.

However, in BiLSTM, with the exact specifications used for the LSTM tests, there was a slight improvement in the training results, but the test results were lower when compared to the LSTM results. As with the LSTM, the best test results were achieved when the Mini Batch Size was 80, achieving 74.51% accuracy, 77.96% sensitivity, 74.96% accuracy, 71.24% specificity, and 75.37% of F1-Score. These results can be consulted in Tables 3 and 4 for training and testing, respectively.

Table 1. LSTM Train

NumHiddenUnits = 100, MaxEpochs = 80, MiniBatchSize = 100									
K=	TN	FN	TP	FP	ACC (%)	SEN (%)	PRE (%)	SPE (%)	F1 (%)
1	152	23	143	15	88.59	86.14	90.51	91.02	88.27
2	143	19	147	23	87.35	88.55	86.47	86.14	87.50
3	139	13	154	27	87.99	92.22	85.08	83.73	88.51
4	153	22	145	13	89.49	86.83	91.77	92.17	89.23
5	151	27	139	16	87.09	83.73	89.68	90.42	86.60
Mean ± std					88.10 ± 0.97	87.50 ± 3.15	88.70 ± 2.82	88.70 ± 3.59	88.02 ± 1.00
NumHiddenUnits = 100, MaxEpochs = 80, MiniBatchSize = 80									
K=	TN	FN	TP	FP	ACC(%)	SEN(%)	PRE(%)	SPE(%)	F1(%)
1	153	21	145	14	89.49	87.35	91.19	91.62	89.23
2	154	18	148	12	90.96	89.16	92.50	92.77	90.80
3	142	14	153	24	88.59	91.62	86.44	85.54	88.95
4	156	24	143	10	89.79	85.63	93.46	93.98	89.38
5	147	34	132	20	83.78	79.52	86.84	88.02	83.02
Mean ± std					88.52 ± 2.78	86.65 ± 4.56	90.09 ± 3.25	90.39 ± 3.50	88.28 ± 3.02

Table 2. LSTM Test

NumHiddenUnits = 100, MaxEpochs = 80, MiniBatchSize = 100									
K=	TN	FN	TP	FP	ACC (%)	SEN (%)	PRE (%)	SPE (%)	F1 (%)
1	32	13	29	9	73.49	69.05	76.32	78.05	72.50
2	32	6	36	10	80.95	85.71	78.26	76.19	81.82
3	30	9	32	12	74.70	78.05	72.73	71.43	75.29
4	29	7	34	13	75.90	82.93	72.34	69.05	77.27
5	35	16	26	6	73.49	61.90	81.25	85.37	70.27
Mean ± std					75.71 ± 3.10	75.53 ± 9.91	76.18 ± 3.77	76.02 ± 6.35	75.43 ± 4.46
NumHiddenUnits = 100, MaxEpochs = 80, MiniBatchSize = 80									
K=	TN	FN	TP	FP	ACC (%)	SEN (%)	PRE (%)	SPE (%)	F1 (%)
1	35	14	28	6	75.90	66.67	82.35	85.37	73.68
2	33	10	32	9	77.38	76.19	78.05	78.57	77.11
3	33	7	34	9	80.72	82.93	79.07	78.57	80.95
4	35	12	29	7	77.11	70.73	80.56	83.33	75.32
5	33	9	33	8	79.52	78.57	80.49	80.49	79.52
Mean ± std					78.13 ± 1.95	75.02 ± 6.42	80.10 ± 1.64	81.27 ± 3.01	77.32 ± 2.97

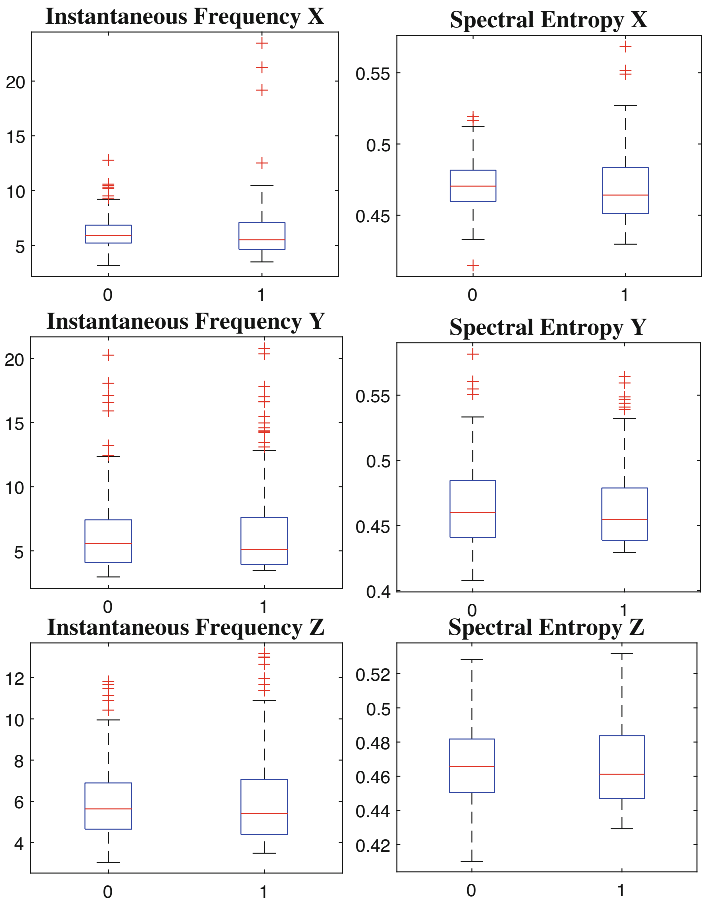

Fig. 6. Boxplot of the extracted features for two groups of patients: healthy (0) and sick (1).

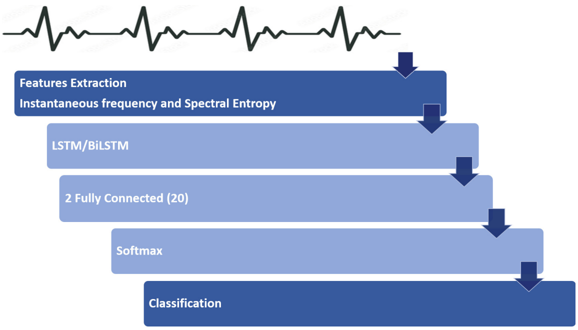

Fig. 7. Network structure

Table 3. BiLSTM Train

NumHiddenUnits = 100, MaxEpochs = 80, MiniBatchSize = 100									
K=	TN	FN	TP	FP	ACC (%)	SEN (%)	PRE (%)	SPE (%)	F1 (%)
1	146	5	161	21	92.19	96.99	88.46	87.43	92.53
2	164	20	146	2	93.37	87.95	98.65	98.80	92.99
3	155	4	163	11	95.50	97.60	93.68	93.37	95.60
4	155	21	146	11	90.39	87.43	92.99	93.37	90.12
5	165	21	145	2	93.09	87.35	98.64	98.80	92.65
Mean ± std					92.91 ± 1.86	91.46 ± 5.33	94.48 ± 4.29	94.35 ± 4.73	92.78 ± 1.95
NumHiddenUnits = 100, MaxEpochs = 80, MiniBatchSize = 80									
K=	TN	FN	TP	FP	ACC (%)	SEN (%)	PRE (%)	SPE (%)	F1 (%)
1	139	31	135	28	82.28	81.33	82.82	83.23	82.07
2	150	17	149	16	90.06	89.76	90.30	90.36	90.03
3	132	3	164	34	88.89	98.20	82.83	79.52	89.86
4	129	9	158	37	86.19	94.61	81.03	77.71	87.29
5	155	17	149	12	91.29	89.76	92.55	92.81	91.13
Mean ± std					87.74 ± 3.59	90.73 ± 6.35	85.91 ± 5.15	84.73 ± 6.63	88.08 ± 3.64

Table 4. BiLSTM Test

NumHiddenUnits = 100, MaxEpochs = 80, MiniBatchSize = 100									
K=	TN	FN	TP	FP	ACC (%)	SEN (%)	PRE (%)	SPE (%)	F1 (%)
1	33	11	31	8	77.11	73.81	79.49	80.49	76.54
2	36	17	25	6	72.62	59.52	80.65	85.71	68.49
3	32	21	20	10	62.65	48.78	66.67	76.19	56.34
4	30	10	31	12	73.49	75.61	72.09	71.43	73.81
5	32	15	27	9	71.08	64.29	75.00	78.05	69.23
Mean ± std					71.39 ± 5.36	64.40 ± 10.98	74.78 ± 5.69	78.37 ± 5.28	68.88 ± 7.76
NumHiddenUnits = 100, MaxEpochs = 80, MiniBatchSize = 80									
K=	TN	FN	TP	FP	ACC (%)	SEN (%)	PRE (%)	SPE (%)	F1 (%)
1	33	11	31	8	77.11	73.81	79.49	80.49	76.54
2	35	10	32	7	79.76	76.19	82.05	83.33	79.01
3	24	9	32	18	67.47	78.05	64.00	57.14	70.33
4	23	3	38	19	73.49	92.68	66.67	54.76	77.55
5	33	13	29	8	74.70	69.05	78.38	80.49	73.42
Mean ± std					74.51 ± 4.61	77.96 ± 8.90	74.12 ± 8.18	71.24 ± 14.03	75.37 ± 3.49

4 Conclusion and Future Work

In this work, a method was created for identifying myocardial infarction patients through the 3 Frank lead ECGsextracted from The PTB Diagnostic ECG Database from Physionet and applying two neural networks: LSTM and BiLSTM. The results obtained for the two networks were similar, with the LSTM obtaining a superior result in accuracy for the testing values of 78% for a testing value of 74% of the BiLSTM.

To improve the obtained results, future work may involve increasing or improving the characteristics that differentiate healthy patients from sick patients to optimize the classifier. Another approach for future work would be the separation of the different types of MI, with the criterion of separation being the location of the myocardial attack.

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