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Anomaly Detection in ECG Time signals via Deep Long Short-Term Memory Networks

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Abstract*—Electrocardiography (ECG) signals are widely used to gauge the health of the human heart, and the resulting time series signal is often analyzed manually by a medical professional to detect any arrhythmia that the patient may have suffered. Much work has been done to automate the process of analyzing ECG signals, but most of the research involves extensive preprocessing of the ECG data to derive vectorized features and subsequently designing a classifier to discriminate between healthy ECG signals and those indicative of an Arrhythmia. This approach requires knowledge and data of the different types of Arrhythmia for training. However, the heart is a complex organ and there are many different and new types of Arrhythmia that can occur which were not part of the original training set. Thus, it may be more prudent to adopt an anomaly detection approach towards analyzing ECG signals. In this paper, we utilize a deep recurrent neural network architecture with Long Short Term Memory (LSTM) units to develop a predictive model for healthy ECG signals. We further utilize the probability distribution of the prediction errors from these recurrent models to indicate normal or abnormal behavior. An added advantage of using LSTM networks is that the ECG signal can be directly fed into the network without any elaborate preprocessing as required by other techniques. Also, no prior information about abnormal signals is needed by the networks as they were trained only on normal data. We have used the MIT-BIH Arrhythmia Database to obtain ECG time series data for both normal periods and for periods during four different types of Arrhythmias, namely Premature Ventricular Contraction (PVC), Atrial Premature Contraction (APC), Paced Beats (PB) and Ventricular Couplet (VC). Results are promising and indicate that Deep LSTM models may be viable for detecting anomalies in ECG signals.

I. Introduction

Electrocardiography (ECG) is the process of recording an electrical signals of the heart over a period of time by placing electrodes on a patient's body. The electrodes detect the changes on the skin that happen from the heart muscle heartbeat. An ECG can be used to measure the rate and rhythm of heartbeats, the size and position of the heart chambers, the presence of any damage to the heart's muscle cells or conduction system, the effects of cardiac drugs, and the function of implanted pacemakers [5]. An ECG is still one of the primary diagnostic tests for detecting cardiovascular abnormalities and automated analysis of ECG signals is of immense value to cardiac specialists.

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Anomaly detection refers to the detection of unseen abnormalities in large volumes of non-anomalous data. It is a challenging topic with ECG time series data in particular due to the sheer volume of the data, the subtle periodic patterns that may be too fast or too slow for the human eye to detect, the variation in signals from patient to patient, and the different time scales of arrhythmia that might occur. Many approaches have been used for analyzing ECG signals and various studies have been performed to classify various cardiac arrhythmia. Some of these include Self-organizing maps (SOM) [9], Autoregressive Modeling [7], c-means clustering [10], Multilayer Perceptron (MLP)[11] and RBF Neural Network [8]. These approaches typically derive time-frequency features for classification via wavelet coefficients [6] or autoregressive coefficients[7].

Much work has also been done to detect anomalous ECG signals. Li et al[13] used transfer learning to classify unlabeled signals from target users by transferring knowledge from supervised source signals. The above techniques however require hand coded features and rely on the availability of labeled data for all the different types of abnormalities. However, given the variety of patients and different waveforms generated by the different abnormalities, such data may not be readily available. Polat et al[14] use a least square SVM to classify normal and abnormal signals, Researchers have also used time series novelty detection techniques [13], [15], [11], however these require extensive computation to predict on any new series.

In this paper we present a predictive approach to detect anomalous behavior via Deep LSTM neural networks. The advantage of this approach is that it 1) involves little or no preprocessing of the data, 2) does not require hand coded features but works directly on raw signals, and 3) does not require prior knowledge of abnormalities to work.

LSTMs have an advantage over traditional RNNs on tasks involving long time delays between events. Some tasks require the network to extract information conveyed by the duration of intervals between these events. LSTM can solve such highly non-linear task as well, by learning to precisely measure time intervals, using LSTM cells with peephole connections that allow them to inspect their current internal states [4].

Section II describes the LSTM and Deep LSTM network architectures used in this paper. Section III gives details about the data collection and network training approach. Section IV gives experimental results and conclusion is given in section

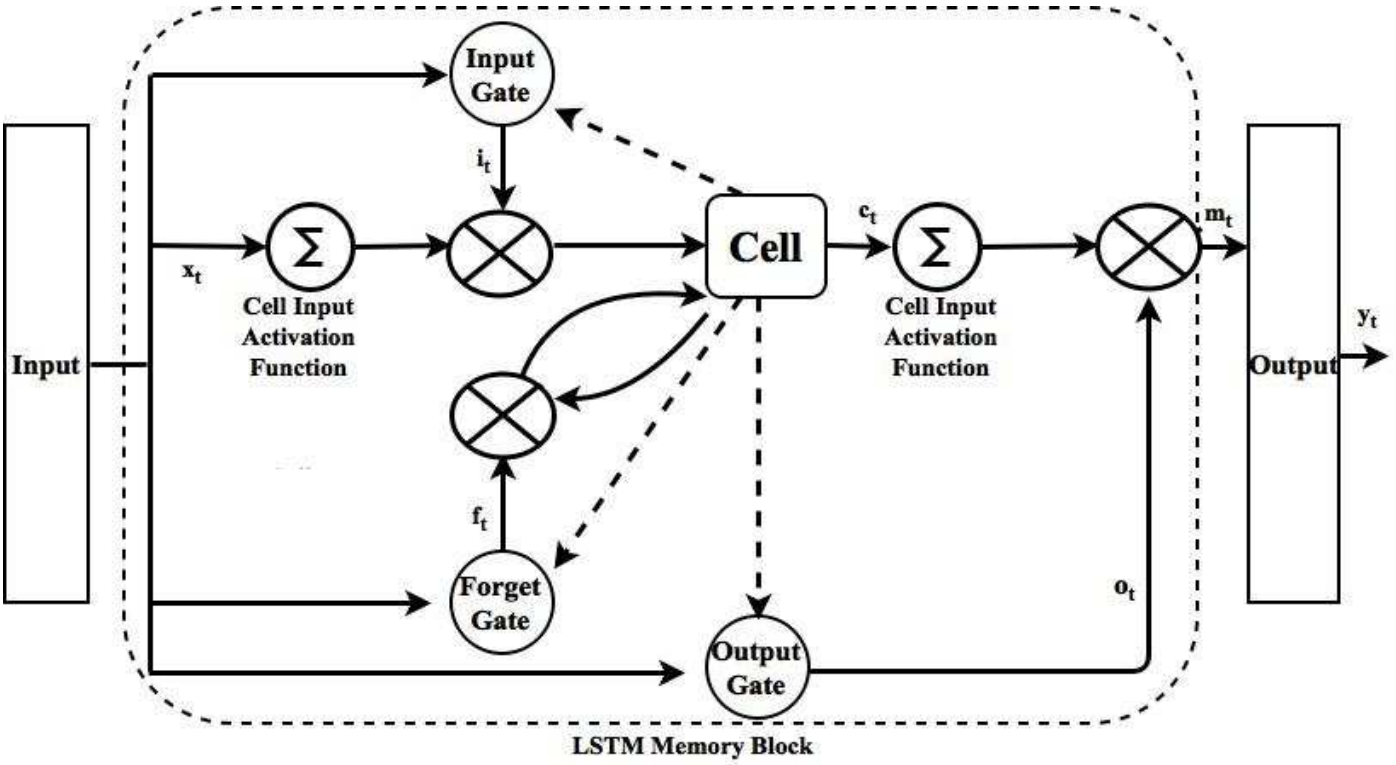


Fig. 1: LSTM Block Diagram with three multiplicative gates :an input gate, forget gate and an output gate.

V.

II. LSTM Network Architectures

A typical recurrent neural network with sigmoidal activation units suffers from what is called the 'vanishing gradient problem'. The problem pertains to the loss of information with time due to decaying gradient values as one traverses backwards through layers during back-propagation. Hochreiter et al[16] solved this problem via the use of multiplicative input,output and forget gates in order to preserve state information. Details of the LSTM architecture are provided below:

A. Conventional LSTM

A conventional LSTM network has three layers. One input layer, one hidden (i.e. LSTM) layer and one output layer. The key unit of LSTM layer is its memory blocks. Each memory blocks has multiple cells which have recurrent connections among them. A conventional LSTM has three multiplicative gates :an input gate (i), forget gate (f) and an output gate (o) which are adaptive in nature. The input gate is used to learn, what information is to be stored in memory. The forget gate is used to learn how long information is stored, and the output gate is used to learn when the stored information can be used. A single memory block is shown in Figure1.

An LSTM network (shown in Figure 1) computes a mapping from an input sequence $x = (x_1, ..., x_T)$ to an output sequence $y = (y_1, ..., yT)$ by calculating the network unit activations using the following equations iteratively from $t = 1$ to T:

$$i_t = \sigma(W_{ix}x_t + W_{im}m_{t-1} + W_{ic}c_{t-1} + b_i) \quad (1)$$

$$f_t = \sigma(W_{fx}x_t + W_{mf}m_{t-1} + W_{cf}c_{t-1} + b_f) \quad (2)$$

$$c_t = f_t \odot c_{t-1} + i_t \odot g(W_{cx}x_t + W_{cm}m_{t-1} + b_c) \quad (3)$$

$$o_t = \sigma(W_{ox}x_t + W_{om}m_{t-1} + W_{oc}c_t + b_o) \quad (4)$$

$$m_t = o_t \odot h(c_t) \quad (5)$$

$$y_t = \phi(W_{ym}m_t + b_y) \quad (6)$$

where W denote weight matrices (e.g. W_{ix} is the matrix of weights from input gate to the input), W_{ic} ,W_{fc} and W_{oc} are diagonal weight matrix of peephole connections. b is the bias vector (e.g. b_i is the input gate bias vector). σ is the logistic sigmoid function and i, f, o and c are respectively the input gate, forget gate, output gate and cell activation vector. $\odot$ is element wise product of the vectors, g and h are the cell input and cell output activation functions. ϕ is the network output activation function and in this paper it is linear[1].

B. Deep LSTM

Deep LSTM networks are built by stacking multiple recurrent LSTM layers as shown in Figure 2. The network is deep in the sense that each LSTM layer's output works as

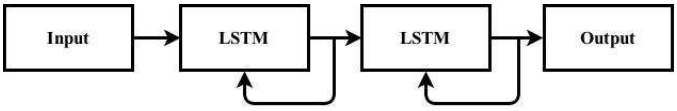


Fig. 2: Stacked LSTM Network Architecture[3].

an input to the next LSTM layer. Each recurrent layer may be unfolded in time to an equivalent feed forward network whose layers share the same parameters. As demonstrated in [12], stacking recurrent layers allows for processing of the sequence at different timescales and yields a richer set of temporal features.

III. Experiments

A. Data Collection

We have used the MIT-BIH Arrhythmia Database, which has over 4000 long-term Holter recordings taken from PhysioBank[2]. PhysioBank contains digital recordings of physiologic signals which are used for the purpose of biomedical research. The database contains 48 records which are slightly over 30 minutes long[2]. We analyzed one minute recordings of ECG signals.These recordings have both non-anomalous and anomalous temporal sequences. In this paper, we focus on five types of beats/rhythms:

1) Normal Sinus Rhythm (NSR):
It is a default rhythm shown in Figure 3(a). A normal heart rhythm is called normal sinus rhythm (NSR for short). An NSR will have a heart rate between 50 and 100 beats per minute and a normal impulse formation from the SA node (P wave)[1].
2) Premature Ventricular Contractions (PVCs):
Premature contraction simply means an "early beat" or "skipped beat", that disturbs the heart's rhythm. PVCs may happen singly or in pairs (known as couplets), every other beat (bigeminy) or in multiform. PVCs are one of the most common heart rhythm abnormalities[1]. They commence in the lower chambers of the heart or in ventricles. One single PVC is shown in figure 3(b). All beats are normal except last beat.
3) Atrial Premature Contractions (APCs):
It is also the most common heart rhythm abnormality. It commence in the upper chambers of the heart or in atria. APCs are also premature or skipped beats which occur earlier than normal beats. Figure-3(c) is an example of a single PAC. The first four beats are normal, but the fifth beat occurs early[1].
4) Paced Beats (PBs):
Beats which occur at a particular rate or speed are known as paced beats. Figure 3(d) is an example of Paced rhythms. First three beats are normal then Paced beats start.
5) Ventricular Couplets (VCs):
Ventricular couplet involve the occurrence of two consecutive PVCs. Figure 3(e) is an example of a ventricular couplet or two consecutive PVCs. The first, second, fourth and fifth beats are PVCs[1].

B. Learning Task

Consider a univariate time series $X = \{x^{(1)}, x^{(2)}, ..., x^{(n)}\}$, where each point $x^{(t)} \in R$ in the time series represents the ECG recordings at time t, whose elements correspond to the input variable. The prediction model learns to predict the next l values for the input variables.

C. Training

The dataset is divided into four sets: non-anomalous training set (s_N), non-anomalous validation set (v_N), mixture of both anomalous and non-anomalous validation (v_{N+A}) and test (t_{N+A}) sets . A stacked LSTM based Recurrent Network is trained to predict on the non-anomalous training set (s_N) using (v_N) as the validation set for early stopping. The prediction error vectors on v_N are then fit to a Multivariate Gaussian using maximum likelihood estimation. The trained LSTM network is then used to predict on v_{N+A} and the pdf values of the resulting error vectors are recorded. The threshold for discriminating between anomalous and normal values is then determined via by maximizing the F-Score with respect to the pdf threshold. The chosen threshold is then used for discriminating regular and anomalous vectors in the test set t_{N+A} as in Malhotra et al[3].

D. stacked LSTM based RNN Architecture

The network has one node at the input layer for signal at time t and since predictions are made for the next l time steps there are l units at the output layer. We have used LSTM units at hidden layer which are recurrent and fully connected to the subsequent hidden layer. The final hidden layer is fully connected to the output layer. The validation set v_N is used for early-stopping while learning the network weights. Multiple architectures with upto three recurrent hidden layers and varying number of units in each layer were trained and the models with the best validation set performance were selected.

E. LSTM based Anomaly Detection

For the input $x^{(t)}$, the predictions are predicted for every $l < t < n - l$ value l times. Then we calculate an error vector $e^{(t)}$ for point $x^{(t)}$ as $e^{(t)} = [e_1^{(t)}, ..., e_l^{(t)}]$, where $e_i^{(t)}$ is the error difference $x^{(t)}$ and its value predicted at time $t - i$.

A Multivariate Gaussian Distribution is fitted to the error vectors on the validation set. $y^{(t)}$ is the probability of an error vector $e^{(t)}$ after applying Multivariate Gaussian Distribution $\mathcal{N} = \mathcal{N}(\mu, \pm)$. Maximum Likelihood Estimation is used to select the parameters μ and Σ for the points from v_N. In this prediction model v_{N+A} is used to learn the threshold τ by maximizing $F_\beta - score$. $F_\beta - score$ is the trade-off between precision and recall. We have chosen $\beta = 0.1$ to favor Precision over recall because there is no label noise in the normal heart data, whereas, the anomalous data contains segments of normal behavior and suffers from label noise.

$$F_\beta = (1 + \beta^2)\frac{Precision * Recall}{(\beta^2 * Precision) + Recall}$$

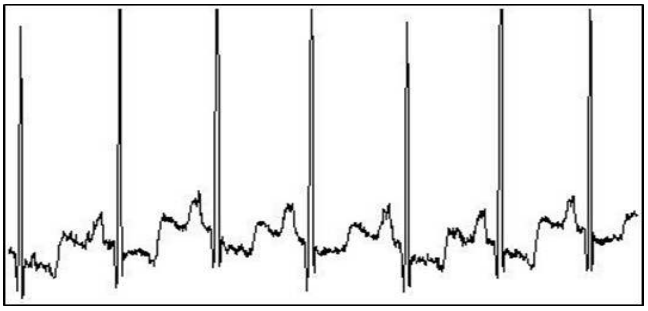
where,

$$Precision = \frac{TruePositive}{TruePositive + FalsePositive}$$

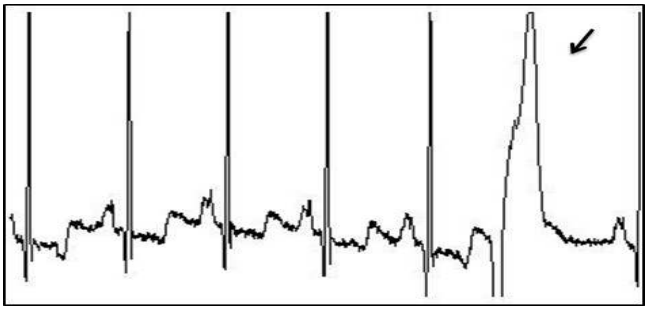
$$Recall = \frac{TruePositive}{TruePositive + FalseNegative}$$

[2]MIT-BIH Arrhythmia Database Directory is available on: http://physionet.org/physiobank/database/mitdb/

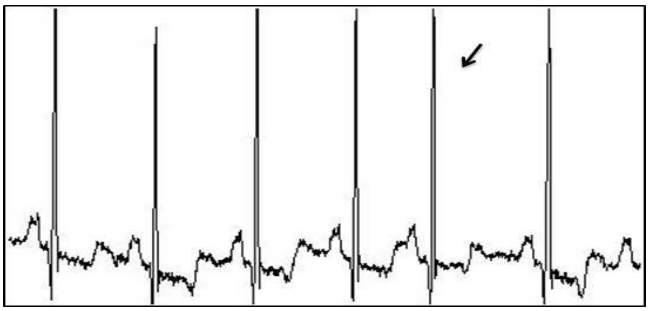
[1]https://www.equimedcorp.com/rhythms/topic/



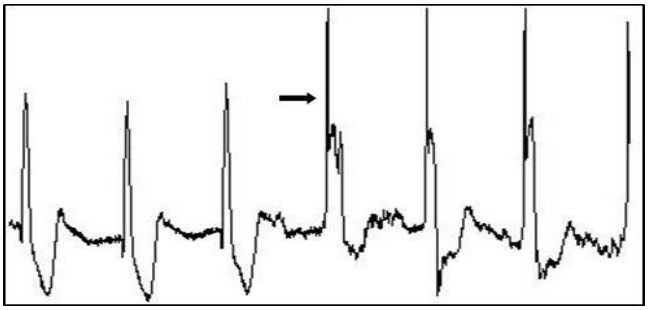
(a) Normal Sinus Rhythms



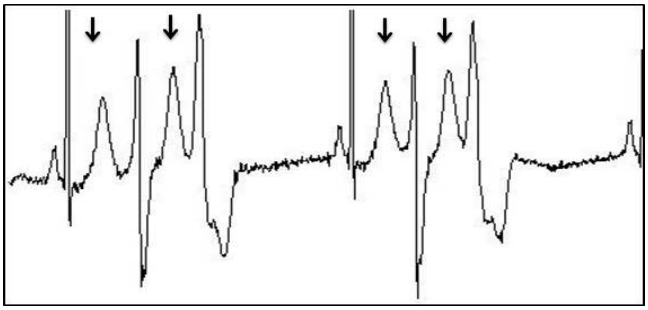
(b) Premature Ventricular Contractions



(c) Atrial Premature Contractions



(d) Paced Beats



(e) Ventricular Couplets

Fig. 3: Five different beats in ECG signals.

and

$$FalsePositiveRate = \frac{FalsePositive}{FalsePositive + TrueNegative}$$

IV. Results and Analysis

A threshold τ is determined via F-score maximization to discriminate anomalous data from normal data on v_{N+A}. This threshold is then used to detect anomalies on the test set t_{N+A} (as shown in table I). A likelihood $p^{(t)}$ of error vector $e^{(t)}$ for validation set (v_{N+A}) and the corresponding threshold τ is shown in Figure 4 (a sample just for two sequences), where the red represents anomalous and green represents non-anomalous ECG signals. Anomalous points belong to positive class and non-anomalous points belong to negative class. Since discrimination implies that the fraction of anomalies detected in the positive class (TPR) be higher than the fraction of anomalous points detected in the negative class (FPR), so we are focusing on ratio between True Positive Rate (TPR) and False Positive Rate (FPR) i.e. a higher ratio indicates better discrimination.

In Table I, we optimized the threshold on validation set v_{N+A} by determining the value at which it yields maximum $F_{0.1} - score$. The optimal τ value is then used on test set to classify between anomalous and non-anomalous regions. The result was a 96.45% $F_{0.1} - score$ on the test set. The ratio between true positive rate to false positive rate was also found to be consistently high on the test set t_{N+A}.

data set	F-score	Precision	Recall or TPR	FPR	TPR / FPR
val_{N+A}	0.7911	0.889	0.065	0.008	8.125
$test_{N+A}$	0.9645	0.9750	0.4647	0.0119	39.05

TABLE I: Scores at calculated threshold $\tau = -9.4054$ where $\beta = 0.1$on $val_{(N+A)}$ and predicted for $test_{(N+A)}$. Also F-score, Precision, Recall, FPR and ratio(TPR / FPR) for the chosen architecture {20 and 20 units in first and second LSTM hidden layers}

In Figure 4 we can easily identify that the pdf values are more often lower in the anomalous regions than the normal regions. It should be noted here that it may be possible that

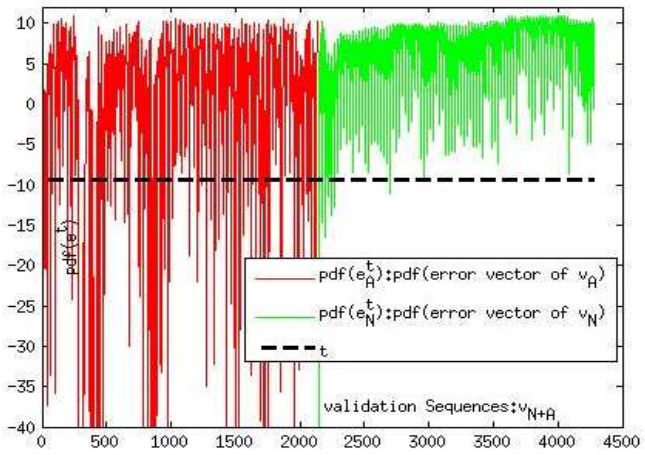


Fig. 4: A threshold $\tau = -9.4054$ is estimated on likelihood $p^{(t)}$ of error vector $e^t_{(N+A)}$ for validation set (v_{N+A})

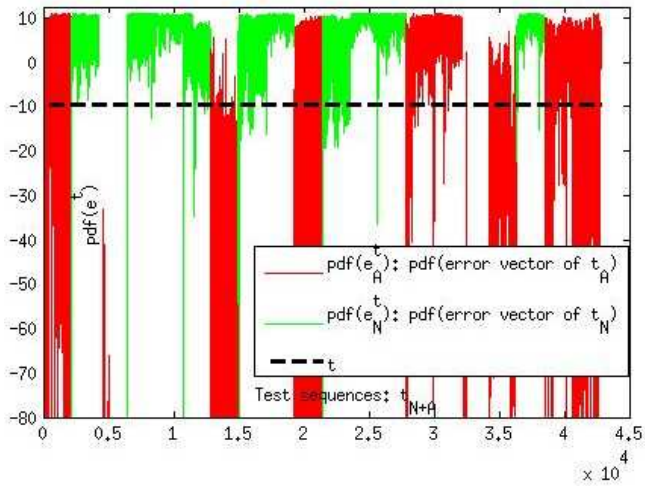


Fig. 6: Anomaly Detection on complete test set $t_{(N+A)}$

the abnormal region may have regions of normality too. This is why we have focused on precision rather than recall.

In Figure 6, the pdf values corresponding to the complete test set is shown along with the optimized threshold. The region below the threshold line indicates anomalies and that above the threshold indicates normal rhythm.

A related objective of this paper is to show that the deep LSTM generalize to multiple anomaly types (Arrhythmias). To evaluate this we need to know the accuracy of detection for each anomaly type. In order to compare the performance of the models on the different anomaly types, the $F_{0.1} - score$ are computed independently for the four different anomalies, with Paced Beats yielding higher $F_{0.1} - score$ i.e. 99.31% (as shown in Table II). The APC signal is the least distinguishable from normal, but even here the TPR/FPR is greater than 12 and hence is detected. The Receiver operating characteristic (ROC) curve is drawn in Figure 7 for complete test set $t_{(N+A)}$ and four abnormalities. Due to the issue of label noise in the abnormal class the Recall is quite low, but it bears mentioning again that what is pertinent for a detector is the ratio of the True Positive Rate which remains consistently high.

Abnormality	F-score	Precision	Recall or TPR	FPR	TPR / FPR
VC	0.9306	0.9559	0.2555	0.0118	21.65
PVC	0.9818	0.9909	0.5109	0.0047	108.70
APC	0.85	0.9231	0.0953	0.0079	12.06
PB	0.9931	0.9930	0.9986	0.007	142.65

TABLE II: Abnormality Score at $\tau = -9.4054$ and $\beta = 0.1$

In Figure 5, the sample signals of four different abnormalities is shown. Figure 5(a), 5(b), 5(c), 5(d), detects VC, PVC, APC and PB respectively, in ECG time signals.

Training of recurrent networks using gradient descent is generally quite slow. However, since we are interested in modeling normal behavior, training only has to be done once offline. The testing time for a 20 minute ECG signal with 42800 points is about 0.5 seconds on a 16 core CPU machine.

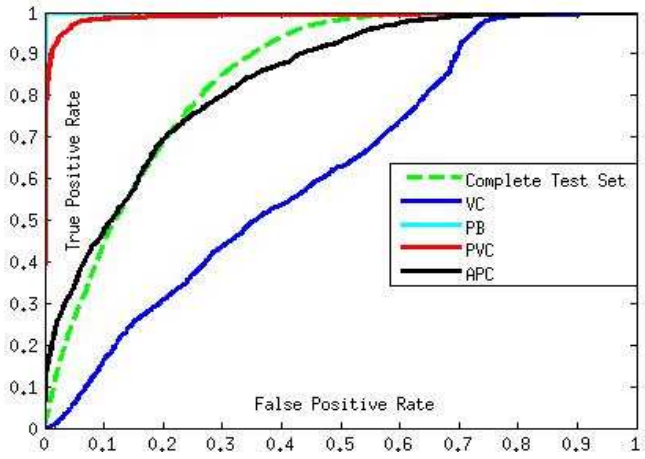
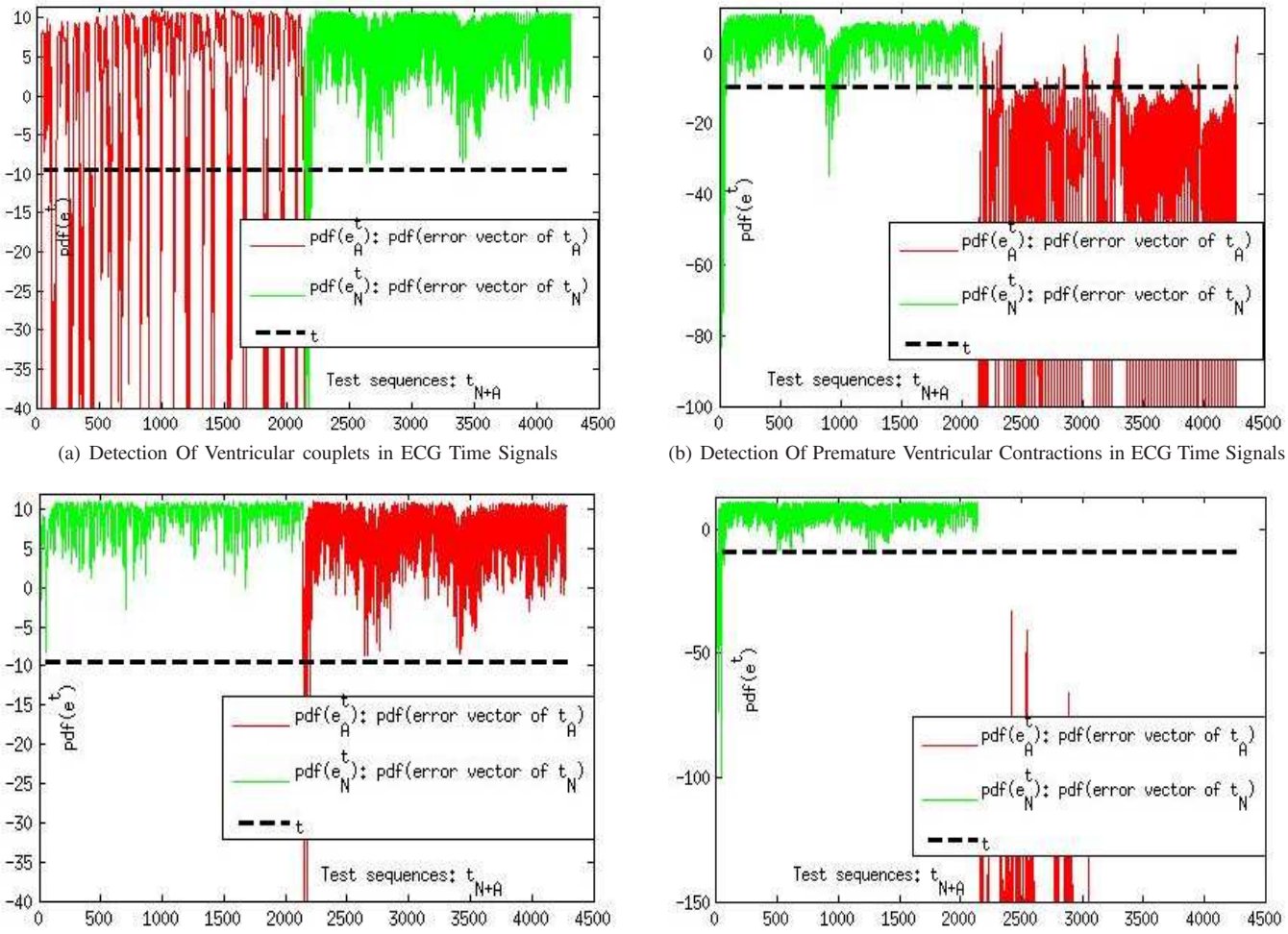


Fig. 7: ROC curve for complete test set and four abnormalities

V. Conclusion

We propose Deep LSTMs for anomaly detection in ECG time signals. LSTMs have additional retentive power over other recurrent architectures because of their ability to overcome the vanishing gradient problem. Stacking recurrent hidden layers allows for the processing of the data at different time scales and generation of a richer set of temporal features. In this work we have investigated the applicability of Deep LSTM networks for detecting cardiac arrhythmias in ECG signals. The technique offers several advantages in that these networks are quite fast once they are trained, and do not require knowledge of the abnormalities, hand crafted features or pre-processing of the data. Experiments show that the technique is able to detect multiple types of abnormalities among ECG signals. It may be beneficial to compute a different threshold for each window of time which may improve detection of point anomalies. Additionally, if this method is to be used by a medical practitioner, recall may be given higher priority, although the number of false positives tend to increase substantially. Overall it appears that stacked LSTMs may be a viable candidate for anomaly detection in ECG signals.



(a) Detection Of Ventricular couplets in ECG Time Signals

(b) Detection Of Premature Ventricular Contractions in ECG Time Signals

(c) Detection Of Atrial premature Contractions in ECG Time Signals

(d) Detection Of Paced Beats in ECG Time Signals

Fig. 5: Abnormality Detection in ECG time signals.

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