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Original Article

Predictive Screening for Chronic Kidney Disease: Leveraging LSTM-Based Machine Learning for Early Diagnosis

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Abstract: *Chronic Kidney Disease also recognized as Chronic Renal Disease, is an uncharacteristic functioning of kidney or a failure of renal function expanding over a period of months or years. Habitually, chronic kidney disease is detected during the screening of people who are known to be in threat by kidney problems, such as those with high blood pressure or diabetes and those with a blood relative Chronic Kidney Disease (CKD) patient. So the early prediction is necessary in combating the disease and to provide good treatment. This work proposes the use of machine learning techniques for LSTM classifier. Final output predicts whether the person is having CKD or not by using minimum number of features.*

Keywords: *Chronic Kidney Disease (CKD), Predictive Screening, Early Diagnosis, Long Short-Term Memory (LSTM), Recurrent Neural Networks (RNNs), Machine Learning, Temporal Data, Time Series Analysis.*

I. INTRODUCTION

Medical data covers a wide range of information such as progress notes, laboratory test results, discharge summaries, patient demographics, transfer and discharge dates, pharmacy information, hospital admission, radiology reports, pathology reports and radiology images. Individual patient care is a major challenge faced by healthcare industry since there is no maintenance or collection of data in a structured manner. Further, the evidence, decision making, statistical analysis, diagnosis and drug administration are required for medical data. In clinical activities that are conducted on a daily basis, the computer-based diagnostic processing has become a new norm [1]. Medical imaging is a broader term applied to a wide range of different image modalities. With the help of radiology, the internal structures of human body like spleen, heart, liver and kidney are viewed at high-quality spatial resolution by these modalities.

Today's health care organizations started opting for computer-aided medical systems, thanks to their ability to process huge amount of data and information. Furthermore, robust and reliable computer-aided systems are generally used in medical image processing, symptoms analysis, diagnosis, prediction, treatment recommendation and statistical analysis. Medical data classification is one of the emerging fields of research in data mining which is aimed at error-free diagnosis. Disease classification, diagnosis and prediction are improved with the help of these algorithms. According to some predefined classes, the classification technique segregates the data [2]. For each data point, the class is predicted. There are two kinds of classification such as binary and multilevel classification. In this chapter, the general medical data classification, data mining approaches,

Title: Leveraging Machine Learning Techniques for Early Prediction of Chronic Kidney Disease: An LSTM Classifier Approach

Chronic Kidney Disease (CKD), also referred to as Chronic Renal Disease, is a prevalent health condition characterized by abnormal kidney function or renal failure that progresses over months or years. It poses a significant public health challenge globally, with its incidence and prevalence steadily rising. Early detection and timely intervention are crucial for effectively managing CKD and reducing its associated morbidity and mortality rates.

Traditionally, CKD diagnosis relied heavily on laboratory tests and clinical evaluations, often detecting the disease at advanced stages when treatment options are limited. However, advancements in medical technology, particularly in the field of machine learning, offer promising opportunities for early prediction and intervention. This work proposes the utilization of machine learning techniques, specifically Long Short-Term Memory (LSTM) classifiers, to predict CKD at its incipient stages using a minimal set of features.

Chronic Kidney Disease encompasses a spectrum of renal disorders characterized by progressive loss of kidney function over time. Common risk factors include hypertension, diabetes mellitus, obesity, and a family history of kidney disease. The disease progression is typically asymptomatic in its early stages, making early detection challenging yet imperative for effective management.

Early prediction of CKD holds paramount importance in improving patient outcomes and reducing the burden on healthcare systems. By identifying individuals at high risk of developing CKD before symptoms manifest, healthcare providers can implement preventive measures, lifestyle modifications, and therapeutic interventions to slow disease progression and mitigate complications.

Machine learning techniques have demonstrated remarkable potential in various medical domains, including disease prediction and diagnosis. These algorithms can analyze vast amounts of data, identify complex patterns, and generate predictive models with high accuracy. In the context of CKD, machine learning offers a non-invasive and cost-effective approach to risk stratification and early detection.

LSTM, a type of recurrent neural network (RNN), excels in modeling sequential data and capturing long-range dependencies. Unlike traditional feedforward neural networks, LSTM networks incorporate memory cells and gates to retain information over extended time intervals, making them well-suited for analyzing time-series data such as longitudinal health records.

This study proposes the development of an LSTM classifier for early prediction of CKD using a minimal number of features derived from comprehensive health assessments. By leveraging patient demographics, clinical biomarkers, medical history, and lifestyle factors, the LSTM model aims to identify subtle patterns indicative of CKD onset or progression.

Despite the potential benefits, several challenges exist in implementing machine learning models for CKD prediction. These include data heterogeneity, imbalanced datasets, feature selection, model interpretability, and ethical considerations related to data privacy and algorithmic bias. Addressing these challenges is essential to ensure the reliability and ethical use of predictive models in clinical practice.

It is anticipated that the LSTM classifier, trained on a diverse dataset comprising both CKD and non-CKD cases, will exhibit robust predictive performance, enabling early identification of individuals at risk of CKD development. The implementation of such a predictive tool in clinical settings can facilitate proactive interventions, personalized treatment strategies, and improved patient outcomes.

In conclusion, the integration of machine learning techniques, particularly LSTM classifiers, holds promise for advancing early prediction and risk stratification in chronic kidney disease. By harnessing the power of data-driven approaches, healthcare providers can shift towards proactive and personalized care paradigms, ultimately enhancing the quality of life for individuals at risk of CKD.

In summary, this introduction provides an overview of chronic kidney disease, emphasizes the significance of early prediction, introduces LSTM classifiers as a potential solution, outlines the proposed methodology, discusses challenges and considerations, and highlights expected outcomes and implications. By leveraging machine learning, particularly LSTM, in CKD prediction, this research aims to contribute to proactive healthcare practices and improved patient outcomes.

II. SUREVEY

In 2015, Jerlin Rubini L and Eswaran P compared the analysis of four different data classifier techniques such as Random Tree (RT), Random Forest (RF), Decision Tree (DT) and Simple Cart. It becomes important to have appropriate prediction models for Chronic Kidney Disease (CKD) for healthcare domain experts. Since a huge chunk of medical information remains unstructured, which needs to implement efficient models and can produce insightful results.

In the study conducted by Jerlin Rubini L et.al, the researchers presented a correlation-based feature selection (CFS) technique that classifies and predicts the results. This method extracts crucial features and classifies them into CKD or not. Nominal, numerical and both of its attributes were used in this research work. The results from the proposed method compared with three ranker approaches namely Gain Ratio, Information Gain and Relief F approach for feature selection.

For the prediction of the medical dataset, data mining plays an essential role. Jerlin Rubini Lambert and Eswaran P proposed a technique from hidden knowledge to extract unknown information. Multilayer perceptron, logistic regression and radial basis function networks were proposed using chronic kidney disease dataset. Prediction accuracy, F-score, type I error, type II error, type I error rate and type II error rate were obtained as comparative measures in this research work.

Merlin Rubini Lambert et.al P utilized future prediction model of Chronic Kidney Disease (CKD), a valuable and supportive model for human healthcare. The exact outcomes were acquired through proficient models thanks to big data that contained clinical information. The nearness of CKD utilized information grouping calculations.

Jerlin Rubini L and Eswaran P suggested the Feature selection (FS) approach which minimizes the computational complexity and improves the classification performance in the identification of CKD. Since numerous bio-inspired FS methodologies are developed in recent years, there is a need to examine the performance of feature selection approaches attained by different algorithms on the identification of CKD. It is a new framework for classification and prediction of CKD.

Lassi Autio et al. Analysed the efficacy of multilayer perceptron networks in the classification of eight different medical data sets that possessed usual challenges in terms of non-uniform distributions between output classes and small-sized training datasets. The earlier-discussed possibility to balance a class distribution through the artificial extension of small-sized dataset was tested herewith.

To support clinical dependability, medical imaging fuses medical images and this scenario is highly helpful. Velmurugan Subbiah Parvathy et al. considered this scenario as the first phase in medical diagnostics and investigation. Fused Multimodality Medical Image (FMMI) extracts few features such as XOR pattern and texture in the second phase. Deep Neural Network (DNN) with Optimization, confirms the fused image as to whether begin or malignant with the point of recognition.

In the research work conducted by Santhos Kumar et al., Emperor Penguin Optimization (EPO) algorithm‘s multi-objective version was proposed with chaos i.e., multiobjective chaotic EPO (MOCEPO). This methodology had set the objectives as the reduction in the number of selected genes (NSG) and increase the classification accuracy (CA). It remains an important challenge to identify the biomarkers from genomic data.

A new Support Vector Machine (SVM) parameter tuning scheme was proposed in the research. Liming Shen et al. was deployed fruit fly optimization algorithm (FOA) The proposed FOA-SVM technique handled the set of parameters efficiently in SVM. Further, the efficiency of FOA-SVM was performed against four established datasets such as Wisconsin breast cancer dataset, Pima Indians diabetes dataset, Parkinson dataset and thyroid disease dataset.

To segregate microarray medical datasets, Mohapatra et al. Proposed two different variants of kernel ridge regression (KRR) such as wavelet kernel ridge regression (WKRR) and radial basis kernel ridge regression (RKRR). To overcome the dimensionality of microarray datasets, modified cat swarm optimization (MCSO) was deployed from the naturally inspired evolutionary algorithm.

Holoentropy based Correlative Naive Bayes classifier and MapReduce Model (HCNB-MRM) was proposed by Chitrakant Banchhor et al. . The proposed technologies simplified the process and select the optimum features from a big dataset. MapReduce model was used to increase the performance of big data classification using probability index table, and posterior probability of the testing data samples. The proposed HCNB-MRM method was verified for its performance under few measures such as specificity, sensitivity and accuracy while it attained 93.5965% and 94.3369% accuracy for localization dataset and skin dataset compared to other techniques. Shankar et al. in 2019 considered important features such as scale-invariant change, surface, and histogram from attractive reverberation pictures of the mind, extricated with a transitional yield. The authors proposed different techniques such as Decision Tree, Convolutional Neural Network classifiers and K Nearest Neighbor which were customized to encompass Group Grey Wolf Optimization (GGWO) strategy. These techniques were utilized to differentiate the diminished arrangement of helpful highlights. This approach attained 96.23% accuracy.

III. PROPOSED SYSTEM

Chronic kidney disease (CKD) is a global public health problem that affects millions of people worldwide. It is a condition that involves the gradual loss of kidney function over time, leading to a variety of symptoms and complications, including high blood pressure, anemia, bone disease, and an increased risk of cardiovascular disease. CKD is often asymptomatic in its early stages, making it difficult to diagnose and treat before it progresses to more severe forms. Therefore, early detection and prevention are critical to managing CKD and improving patient outcomes.

The traditional method for diagnosing CKD involves monitoring kidney function over time, usually through blood and urine tests. However, this method can be time-consuming and may not detect the disease until it has progressed to a more advanced stage. Additionally, there is a lack of awareness among the general public about the early signs and symptoms of CKD, which can delay diagnosis and treatment.

In recent years, there has been growing interest in using machine learning (ML) algorithms to predict the likelihood of developing CKD. These algorithms can analyze large datasets of patient information to identify patterns and risk factors associated with the disease. By using these algorithms, healthcare providers can potentially identify patients who are at high risk of developing CKD and implement preventative measures to slow or stop the progression of the disease.

The use of ML algorithms for CKD prediction has the potential to revolutionize the way the disease is diagnosed and managed. By identifying high-risk patients earlier, healthcare providers can implement targeted interventions, such as lifestyle modifications, medication therapy, or renal replacement therapy, to slow or stop the progression of the disease. Additionally, ML algorithms can be used to develop personalized treatment plans based on each patient's individual risk factors and medical history, improving patient outcomes and reducing the burden of the disease on healthcare systems worldwide.

However, there are several challenges associated with the implementation of ML algorithms for CKD prediction. One of the major challenges is the lack of high-quality data available for training these algorithms. Electronic health records, medical imaging data, and genomic data can be used to develop ML algorithms for CKD prediction, but these data sources may be incomplete, inaccurate, or inconsistent. Additionally, there are concerns about data privacy and security, which must be addressed to ensure patient confidentiality and trust.

Another challenge is the ethical considerations associated with using ML algorithms in clinical practice. There are concerns about the potential for bias in these algorithms, which may result in healthcare disparities and unequal access to care. Additionally, there are concerns about the potential for overreliance on these algorithms, which may lead to the devaluation of clinical judgment and decision-making.

Despite these challenges, the use of ML algorithms for CKD prediction has the potential to revolutionize the way the disease is diagnosed and managed. By identifying high-risk patient's earlier and developing personalized treatment plans, healthcare providers can improve patient outcomes and reduce the burden of the disease on healthcare systems worldwide. Therefore, it is critical to continue to explore the benefits and limitations of these tools and develop strategies to address the challenges associated with their implementation in clinical practice.

Using these structured data and deep learning models to predict KCD which is an important issue in worldwide. In order to solve the problem of low accuracy of Long-Short Term Memory (LSTM) model in KCD, this chapter presented a proposed model of LSTM model based on attention mechanism.

IV. CONSTRUCTION OF ATTENTION-LSTM MODEL

A.LSTM MODEL

We will briefly introduce the principle of LSTM model. LSTM is a kind of recurrent neural network, as shown in Fig. 1.

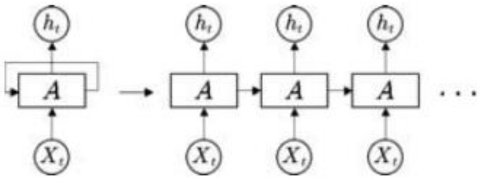


Figure 1: Recurrent neural network (RNN)

However, compared with the conventional RNN, the structure of this repeated module A of LSTM is more complicated, as shown in Fig. 2.

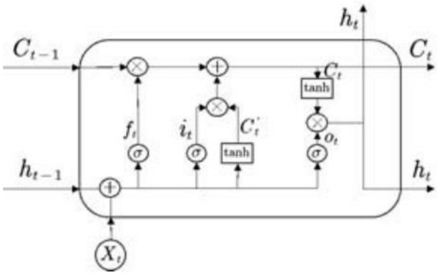


Figure 2: The Structure of LSTM Cell

This module consists of three parts, the forgotten gate, the input gate and the output gate. σ is the Sigmoid function, output a value between 0 and 1, describing how much of each part can pass.

$$f_t = \sigma\left(W_f \cdot [h_{t-1}, x_t] + b_f\right)$$

$$i_t = \sigma\left(W_i \cdot [h_{t-1}, x_t] + b_i\right)$$

$$\tilde{C}_t = \tanh\left(W_c \cdot [h_{t-1}, x_t] + b_c\right)$$

$$C_t = f_t \cdot C_{t-1} + i_t \cdot \tilde{C}_{t'}$$

$$o_t = \sigma\left(W_o\,[h_{t-1}, x_t] + b_o\right)$$

$$h_t = o_t \cdot \tan\mathrm{h}\left(C_t\right)$$

Among them, ft determines how much information we want to discard. It determines how much new information we should add. ot determines how much information we want to output. xt is the input at time t. ht−1 is the output of the previous gate, Wf , Wi, Wc and Wo is the weight, bf , bi , bc and bo is the bias, Ct−1 is the cell state at the previous moment, Ct is the cell state at the current moment.

B. Attention-LSTM Model:

Since the model is difficult to learn information at a time far from the current time, and it may be important for the current value. To overcome the weakness, we tried to add an attention layer to the LSTM network. Referring to the attention implementation steps of [9], we can apply it to the LSTM model. As shown in Fig. 3, the attention layer is added to the LSTM model.

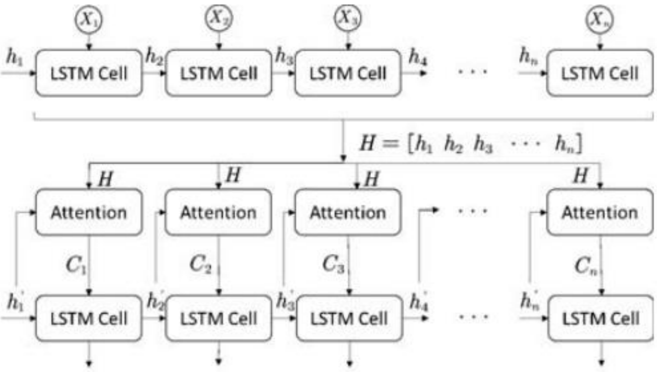


Figure 3: The process of adding an attention mechanism to the LSTM model.

Among them, Xi, i ∈ (1, n) is the input, hi is the intermediate output result of each cell, hi are input into each attention model as H, and the elements of the next layer h i are used as H to calculate the similarity and weight coefficient, and finally get the attention coefficient. The specific attention model is shown in below figure.

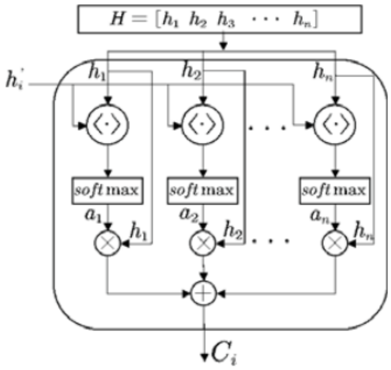


Figure 4: The internal structure of attention model

Finally, a weighted summation operation is performed to obtain the Attention value Ci. The formula used in the attention layer is as follows:

$$H = [h_1\ h_2\ \cdots\ h_n]$$

$$H_i^{'} = \left[h_i^{'}\ h_i^{'}\ \cdots\ h_i^{'}\right]$$

$$sim_i = H_i^{'} \cdot H^T$$

$$a_i = \frac{e^{sim_i}}{\sum_{j=1}^{L_h} e^{sim_j}}$$

$$C_i = \sum_{j=1}^{L_h} a_i \cdot h_j$$

In the above equations, uses vector H and H to calculate similarity to obtain weights, uses the softmax function to normalize the weight, uses the normalized weight ai and hi weighted sum. The result of weighted summation is the attention weight value Ci.The implementation of the Attention layer is to retain the intermediate output results of the input sequence by the LSTM encoder, and then calculate the similarity between the intermediate output results of the previous layer and the current output to obtain the weight factor, and finally obtain the attention coefficient.

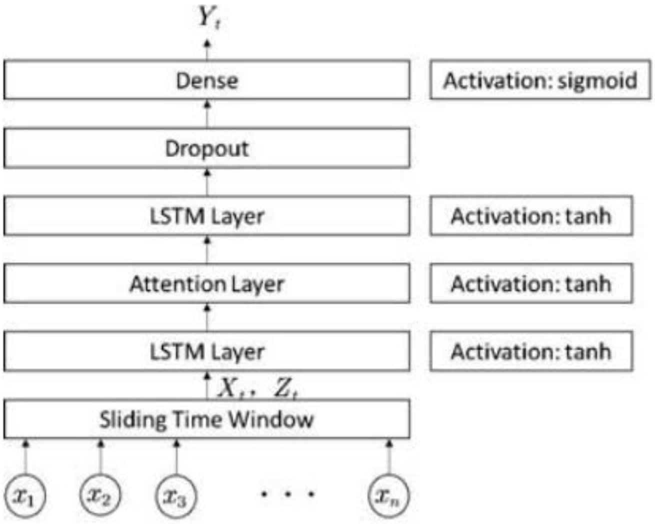


Figure 5: Attention-LSTM network architecture.

As shown in above Fig, we use the original traffic flow data to construct a feature matrix and label vector through a sliding time window method, and obtain the attenton weights based on the correlation between the values in matrix X and the values in vector Z through the attention layer and generate the final prediction Y .

C. Proposed algorithm 1:

Input: Data

Output: A trained Attention-LSTM model.

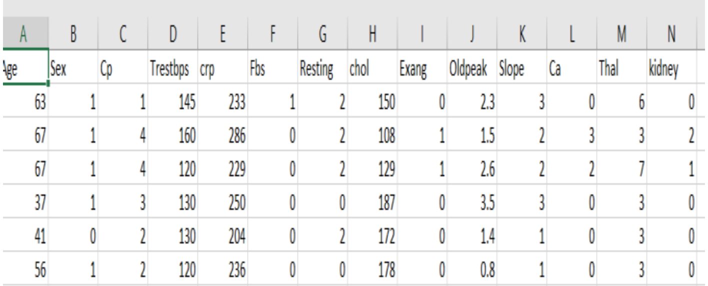
- Construct a dataset with a sliding time window, including Xt and Zt.
- Normalization Xt and Zt.
- Input features matrix Xt and current disease vector Zt to A-LSTM network.
- while training epoch does not reach the set value do
- Put (Xt, Zt) into the Attention-LSTM network for forward propagation.
- Calculate the attention weight corresponding to each element
- Generate Yt
- Caculate mean square error.
- Use RMSProp update weights for A-LSTM network.
- end while
- return A trained Attention-LSTM model.

The performance of the LSTM model based on the attention mechanism is verified for long time series and large prediction lag time. All prediction models use the same data set and are built in the same way. In the LSTM model, we set 2 hidden layers, the number of hidden layer neurons is 64 and 64, and the learning rate is 0.05. The network optimizer is also RMSprop. The process of Attention-LSTM model training is shown in Algorithm 1.

V. SIMULATION RESULT

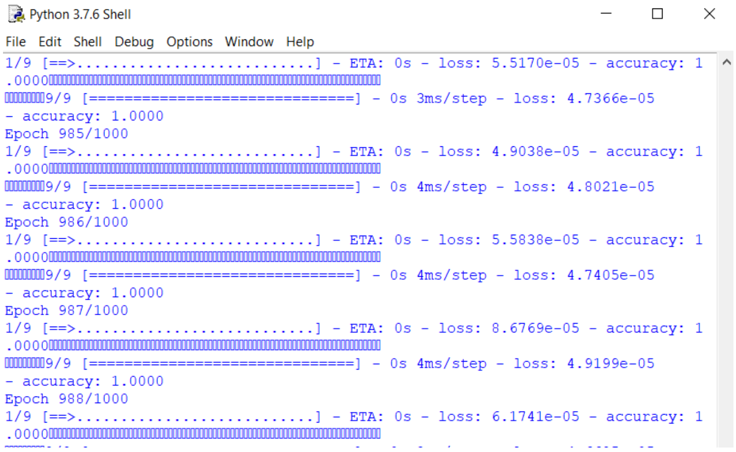
A. Dataset and per processing:

We implement all the approaches based on the data extracted Kagglw website. We split the dataset randomly into the training, validation and testing subset with a ratio of 0.7:0.1:0.2, namely the size of the training, validation and testing subset. For each predictive model, we train it in a mini-batch way with 1,024 sequences per epoch and conduct 100 iterations. In order to enhance the models' generalization performance, the data was divided independently and each model was trained and tested 10 times in our work. Finally we report the mean evaluation metrics on the 10 testing results.



A	B	C	D	E	F	G	H	I	J	K	L	M	N
Age	Sex	Cp	Trestbps	crp	Fbs	Resting	chol	Exang	Oldpeak	Slope	Ca	Thal	kidney
63	1	1	145	233	1	2	150	0	2.3	3	0	6	0
67	1	4	160	286	0	2	108	1	1.5	2	3	3	2
67	1	4	120	229	0	2	129	1	2.6	2	2	7	1
37	1	3	130	250	0	0	187	0	3.5	3	0	3	0
41	0	2	130	204	0	2	172	0	1.4	1	0	3	0
56	1	2	120	236	0	0	178	0	0.8	1	0	3	0

Figure 6: Data set information



```
1/9 [==>...........................] - ETA: 0s - loss: 5.5170e-05 - accuracy: 1
.0000▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯
▯▯▯▯▯▯▯▯▯9/9 [==============================] - 0s 3ms/step - loss: 4.7366e-05
- accuracy: 1.0000
Epoch 985/1000
1/9 [==>...........................] - ETA: 0s - loss: 4.9038e-05 - accuracy: 1
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▯▯▯▯▯▯▯▯▯9/9 [==============================] - 0s 4ms/step - loss: 4.8021e-05
- accuracy: 1.0000
Epoch 986/1000
1/9 [==>...........................] - ETA: 0s - loss: 5.5838e-05 - accuracy: 1
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▯▯▯▯▯▯▯▯▯9/9 [==============================] - 0s 4ms/step - loss: 4.7405e-05
- accuracy: 1.0000
Epoch 987/1000
1/9 [==>...........................] - ETA: 0s - loss: 8.6769e-05 - accuracy: 1
.0000▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯
▯▯▯▯▯▯▯▯▯9/9 [==============================] - 0s 4ms/step - loss: 4.9199e-05
- accuracy: 1.0000
Epoch 988/1000
1/9 [==>...........................] - ETA: 0s - loss: 6.1741e-05 - accuracy: 1
.0000▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯▯
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Figure 7: Classification result

B. Classification Accuracy:

Classification Accuracy is what we usually mean, when we use the term accuracy. It is the ratio of number of correct predictions to the total number of input samples.

$$Accuracy = \frac{Number\ of\ Correct\ predictions}{Total\ number\ of\ predictions\ made}$$

It works well only if there are equal number of samples belonging to each class.For example, consider that there are 98% samples of class A and 2% samples of class B in our training set. Then our model can easily get **98% training accuracy** by simply predicting every training sample belonging to class A.

When the same model is tested on a test set with 60% samples of class A and 40% samples of class B, then the **test accuracy would drop down to 60%.** Classification Accuracy is great, but gives us the false sense of achieving high accuracy.

The real problem arises, when the cost of misclassification of the minor class samples are very high. If we deal with a rare but fatal disease, the cost of failing to diagnose the disease of a sick person is much higher than the cost of sending a healthy person to more tests.

VI. CONFUSION MATRIX

Confusion Matrix as the name suggests gives us a matrix as output and describes the complete performance of the model. Let's assume we have a binary classification problem. We have some samples belonging to two classes : YES or NO. Also, we have our own classifier which predicts a class for a given input sample. On testing our model on 165 samples, we get the following result.

Table No 1: Matrix

N=165	Predicted :NO	Predicted :YES
Actual: NO	50	10
Actual: YES	5	100

A. There are 4 important terms:

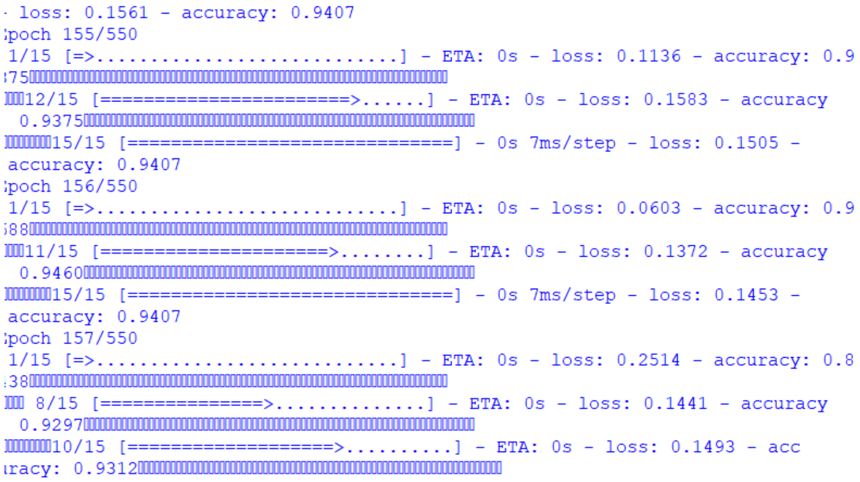
- True Positives: The cases in which we predicted YES and the actual output was also YES.
- True Negatives: The cases in which we predicted NO and the actual output was NO.
- False Positives: The cases in which we predicted YES and the actual output was NO.
- False Negatives: The cases in which we predicted NO and the actual output was YES.

Accuracy for the matrix can be calculated by taking average of the values lying across the **"main diagonal"** i.e

$$Accuracy = \frac{TruePositive + TrueNegative}{TotalSample}$$

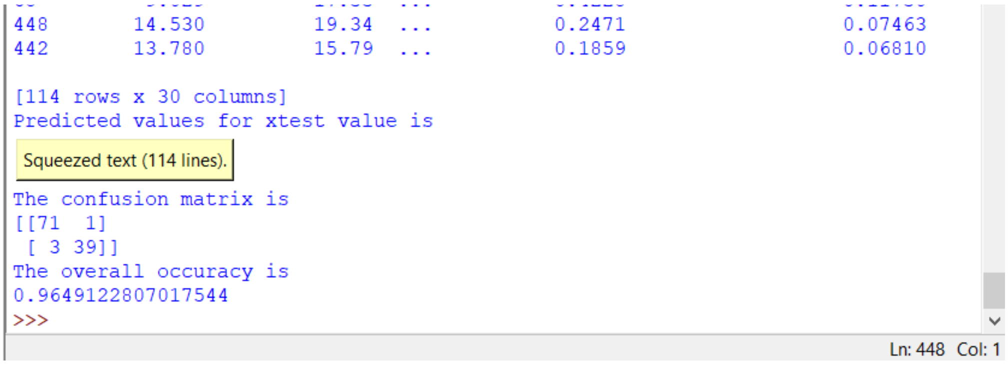
$$\therefore Accuracy = \frac{100 + 50}{165} = 0.91$$

Confusion Matrix forms the basis for the other types of metrics.



```
 loss: 0.1561 - accuracy: 0.9407
poch 155/550
1/15 [=>............................] - ETA: 0s - loss: 0.1136 - accuracy: 0.9
75
12/15 [=======================>......] - ETA: 0s - loss: 0.1583 - accuracy
 0.9375
15/15 [==============================] - 0s 7ms/step - loss: 0.1505 -
accuracy: 0.9407
poch 156/550
1/15 [=>............................] - ETA: 0s - loss: 0.0603 - accuracy: 0.9
88
11/15 [=====================>........] - ETA: 0s - loss: 0.1372 - accuracy
 0.9460
15/15 [==============================] - 0s 7ms/step - loss: 0.1453 -
accuracy: 0.9407
poch 157/550
1/15 [=>............................] - ETA: 0s - loss: 0.2514 - accuracy: 0.8
38
 8/15 [===============>..............] - ETA: 0s - loss: 0.1441 - accuracy
 0.9297
10/15 [===================>..........] - ETA: 0s - loss: 0.1493 - acc
racy: 0.9312
```

Figure 8: Model Training



```
448      14.530      19.34  ...       0.2471          0.07463
442      13.780      15.79  ...       0.1859          0.06810

[114 rows x 30 columns]
Predicted values for xtest value is
Squeezed text (114 lines).
The confusion matrix is
[[71  1]
 [ 3 39]]
The overall occuracy is
0.9649122807017544
>>>
```

Figure 9: Performance Analysis

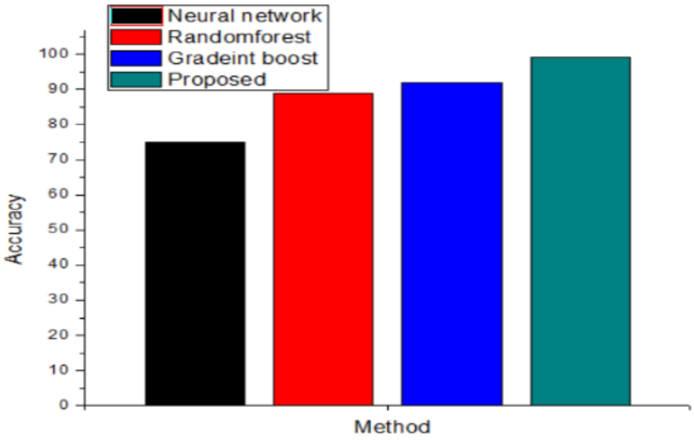


Figure 10: Performance Analysis

When compare to other learning models like neural network, random forest and gradient approach, the proposed model achieved a higher accuracy.

VII. CONCLUSION

This work deals with the prediction of CKD in people. Prediction is done using the machine learning technique, LSTM . In this classification problem SVM classifies the output into two classes with CKD and without CKD. The main objective of this study was to predict patients with CKD using less number attributes while maintaining a higher accuracy. Here we obtain an accuracy of about 96 percentages.

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