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Diagnosis Of Diabetes May Be Achieved Via The Use Of Deep Learning And Convolutional Long Short-Term Memory Networks.

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Abstract:

With the rising prevalence of diabetes worldwide, there is a growing need for accurate and timely detection methods to enable early intervention and management. In this study, we propose a novel approach for diabetes detection leveraging the power of deep learning techniques, specifically employing Convolutional Long Short-Term Memory (ConvLSTM) networks.

Our methodology involves the integration of ConvLSTM networks, which combine the spatial understanding of convolutional layers with the temporal memory capabilities of LSTM layers. This unique architecture enables the model to capture both spatial and temporal dependencies within sequential medical data, such as time-series information from glucose monitoring.

To validate the efficacy of our approach, we conducted experiments on a comprehensive dataset comprising diverse patient profiles. The dataset includes information such as glucose levels, insulin sensitivity, and other relevant health indicators. Our proposed ConvLSTM-based model demonstrates superior performance in diabetes detection compared to traditional machine learning methods and other deep learning architectures.

Furthermore, we explore the interpretability of the model predictions, providing insights into the key features and temporal patterns influencing diabetes detection. This not only enhances the model's transparency but also contributes to a better understanding of the complex relationships within the data.

The results of our study indicate that the proposed ConvLSTM-based approach holds promise as an effective and accurate tool for diabetes detection. The integration of deep learning techniques in healthcare, particularly in diabetes diagnosis, can pave the way for more personalized and timely interventions, ultimately improving patient outcomes.

Keywords—Convolutional long short-term memory; diabetes prediction; machine learning; pre-processing

Introduction:

There has been a considerable increase in the incidence of diabetes all over the world over the course of the last few years, which offers a huge challenge for those who are working in the area of public health. It is essential that diabetes be diagnosed as soon as possible and well controlled in order to lessen the likelihood of complications and enhance the patient's prognosis from the disease. It is of the utmost importance to detect diabetes as soon as possible and to take appropriate measures to manage it immediately after diagnosis. Over the course of the last several years, it has been apparent that deep learning methods, namely Convolutional Long Short-Term Memory (ConvLSTM) networks, have developed into an efficient tool for the study of complicated datasets that are in a state of constant change. It has come to light that this information is available. Within the confines of this study project, the characteristics of ConvLSTM networks are used in order to facilitate the development of a solution that is very efficient in determining whether or not diabetes is present. First and foremost, the most important objective that has to be completed is to improve the diagnostic procedures in terms of both their accuracy and their efficiency, respectively.

When it comes to diagnosing diabetes, the techniques that are presently in use often depend on fixed data, such as blood glucose levels, which may not sufficiently capture the nuanced and ever-changing patterns that are crucial to the condition. This causes the approaches to be inadequate. A good illustration of this kind of data item is the quantity of glucose that is present in the blood. It has been shown that deep learning models, in particular those that combine convolutional and recurrent neural network architectures, are particularly effective in a broad range of medical applications. This is the case in particular. It has been observed that this attempt has been successful in a number of different contexts. It is highly recommended to make use of convolutional long-short-term memory (ConvLSTM) networks when it comes to the investigation of time-series data that is relevant to physiological indicators that are related with diabetes. These networks are able to extract both geographical and temporal information from sequential input, which is the reason why this is the case. This is the reason why things are the way they are.

This project's objective is to conduct an analysis of a wide range of datasets, which will consist of imaging data, physiological measures, and medical records, among other types of collected information. ConvLSTM networks will be used in order to successfully attain this goal. The purpose of this research is to improve the accuracy and efficiency of diabetes diagnosis, and it is being carried out with that objective in mind. A approach that has been presented as a means of detecting tiny patterns that may be overlooked by the techniques that are currently being utilized is to take into account the temporal dynamics of pertinent data. This strategy has been proposed as a way to discover these patterns. The approach that has been suggested is the one that is described above. Therefore, this has the potential to result in a more resilient and quick identification of people who are at risk or in the early stages of diabetes, which would allow for proactive intervention and tailored healthcare solutions. This would be a significant step forward in the fight against diabetes. This might be helpful in reducing problems associated with diabetes as well as diabetes itself. In the event that this were to take place, there would be a significant amount of progress regarding the fight against diabetes.

In the following parts, we will undertake an examination of the methodology, the dataset, and the outcomes of the tests that were carried out. Since the proposed strategic approach has the potential to transform the diagnostic process, we will put a special emphasis on the possibility that it has the power to revolutionize the diagnosis of diabetes. This is because the strategy has the capacity to change the diagnostic process. The findings of this study provide an important contribution to the expanding body of literature that studies non-traditional approaches to fighting the diabetes pandemic that is now sweeping the world. The implementation of deep learning strategies in healthcare settings has the potential to enhance diagnostic capabilities, and the work that is being presented here is a contribution to the body of material that has previously been created via the utilization of this approach.

There has been a considerable increase in the incidence of diabetes all over the world over the course of the last few years, which offers a huge challenge for those who are working in the area of public health. Furthermore, it is vital to exercise adequate control over diabetes in order to improve the patient's prognosis and avoid problems from occurring. This is in addition to the fact that it is essential to recognize diabetes as soon as feasible. Deep learning methods, namely Convolutional Long Short-Term Memory (ConvLSTM) networks, have led to the development of a powerful instrument that is capable of being employed for the examination of complicated datasets that are continuously developing. This instrument has been created as a consequence of the utilization of deep learning techniques. Because of the progress that has been made in deep learning techniques, this instrument has been created as a consequence of those improvements. The focus of this research is on a method that is used for the aim of providing an accurate diagnosis of diabetes. For the purpose of investigating this strategy, the characteristics of ConvLSTM networks are capitalized upon. For the purpose of enhancing the diagnostic procedures in terms of both their precision and their effectiveness, this study is being carried out. The goal of this research is to enhance the diagnostic techniques.

Currently, the approaches that are used to diagnose diabetes often depend on the use of unchanging data, such as blood glucose levels. This may not be sufficient to accurately reflect the complex and ever-changing patterns that are characteristic of the condition. It is true that this is the case given that blood glucose levels are a measurement of the amount of glucose that is present in the blood. It has been shown that deep learning models, in particular those that combine convolutional and recurrent neural network architectures, are particularly effective in a broad range of medical applications. This is the case in particular. It has been observed that this attempt has been successful in a number of different contexts. It is highly recommended to make use of convolutional long-short-term memory (ConvLSTM) networks when it comes to the investigation of time-series data that is relevant to physiological indicators that are related with diabetes. These networks are able to extract both geographical and temporal information from sequential input, which is the reason why this is the case. This is the reason why things are the way they are.

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Literature Review

A. DPUMLA (Diabetes Prediction Using Machine Learning Algorithms)

Using methods linked to machine learning, researchers can reliably forecast diabetes outcomes. Among the most famous algorithms are Support Vector Machines (SVM), J48, K-Nearest Neighbours (KNN), with Random Forest also ranking high. [8] Another algorithm that is said to be quite strong is Random Forest. Machine learning (ML) and data mining (DM) were the two methods utilized by Ioannis et al. [7] to calculate the risk of developing diabetes. Data mining is common to both of these methods. To achieve this goal, our study primarily focused on analyzing the many methodologies now accessible in the fields of data mining and machine learning [7]. A lot of time and energy was put in by the writers so that they could conduct comprehensive research on several databases that include diabetes-related data.

Zhu et al. [9] used a logistic regression-based model to forecast the occurrence of diabetes. The authors used principal component analysis and k-means techniques to successfully classify the data provided by the given model. A prediction model was effectively constructed by the authors [10] employing classifiers grounded on the decision tree, naïve Bayes, and random forest methodologies. We used the algorithm on data pertaining to diabetes and correctly understood the results. Furthermore, the authors [11] used several machine learning methods to classify the diabetes data. This work [11] primarily focused on classifying PIMA diabetic data using decision trees and support vector machines (SVM). A commonly used method for partitioning the dataset throughout the procedure is tenfold cross-validation. The data collected by the writers has not undergone any kind of arrangement or preparation by the authors.

The goal of establishing a diabetes prediction was judged to be most effectively accomplished via the use of Support Vector Machines (SVM), which was considered to be the most successful way. The PIMA dataset and the Diabetes 130-US dataset, both of which were accessible to Negi and Jaiswal [12], were used in order to accomplish this goal. Both of these datasets were utilized. It was carried out with the purpose of offering a prediction, which was one of the reasons why it was taken into account. In the first place, it was carried out. This was one of the numerous reasons why it was carried out in the first place, and it may be considered one of those causes.

In order to assess whether or not the current machine learning algorithms were capable of reliably predicting diabetes, the researchers put them through their paces by applying them to a variety of datasets. It is necessary to do preprocessing on the data since it is incomplete and contains values that are missing. The processing of this information is required. Using data preprocessing approaches, improvements are being made to the categorization of diabetes. These improvements are being considered. The next portion of this section is going to focus its attention to addressing a variety of deep neural network models that are used for the purpose of diabetes prediction.

B. DNN (Deep Neural Networks)

There has been a rising awareness among academics regarding the possible application of deep learning approaches in the context of the examination of massive datasets [6]. This knowledge has been developing in recent years. The use of DL approaches has also resulted in the achievement of accurate diabetes prediction as a consequence of this.

Through the use of a Deep Neural Network (DNN) in their study, the authors [13] were able to develop a prediction about diabetes. A comprehensive evaluation of this approach was carried out, and the PIMA dataset was used as the foundation for the evaluation. The authors did not pre-process the dataset on purpose since distributed neural networks have the capacity to filter the input and develop biases. This prevents the writers from obtaining accurate results. Distributed neural networks were taken into consideration while making this selection because of their capabilities. It is vital to take the dataset and divide it into 192 different samples in order to accomplish the goal of carrying out the study gathering as well as the investigation that is still in progress.

In the statement that they released, the authors said that the accuracy rate was 88.41 percent. The writers have allowed us to have access to this material.

It is [14] An alternative approach that is based on CNN and CNN-LSTM has been developed in order to do an analysis on the dataset consisting of electrocardiograms. This technique was developed in order to do an analysis of the dataset. One of the goals that led to the development of this strategy was to successfully complete the process of analyzing the dataset.

While the authors were responsible for the construction of both the multilayer neural network and the CNN [15], it is important to note that both the CNN and the multilayer neural network were constructed with the logistic regression model serving as their basis. Both of these structures were developed with the help of this model of logistic regression, which served as the basis for their development. Each and every one of the nine occurrences that are being taken into account is included in the dataset that the authors (16) utilized, and there are a total of nine examples that are being taken into consideration. In order to get a more comprehensive understanding of each and every one of the patients who are participating in the test, nine characteristics are gathered. To add insult to injury, every single patient had data for a total of 10,800 days, which resulted in a total of 97,200 days that were really repeated. In order to guarantee the reliability of the statistics, this was carried out. We were able to get a more profound understanding of the facts as a result of this opportunity. The significance of these two pieces of information cannot be overstated under any circumstances since they are both very significant. The fact that this research was carried out does not change the fact that it did not contain an explanation that was suitable for the features that were used in the investigation.

(16) The Deep Patient model, an unsupervised deep neural network, was developed by Miotto in conjunction with his collaborators. This model was named in recognition of the patient's achievements. This methodology is considered the most appropriate method for categorizing electronic health records, which is the objective of the strategy. This site conducts the assessment and testing of the model using a database containing information on 704,857 patients.

Using a variety of deep learning approaches, the researchers [17] constructed a dataset by conducting experiments on health records obtained from hospitals in Australia.

They used an RNN model to forecast the occurrence of both type 1 and type 2 diabetes, as stated by the authors [18]. In their forecast, the scientists drew on the PIMA dataset, which showed that "Glucose" is the most important attribute, followed by age, births, blood pressure, skin thickness, testosterone, and a family history of diabetes. While the analysis was being validated, the training dataset and 20% of the testing dataset were split into 80%.

A convolutional neural network using enhanced feature selection and data pre-processing methods is proposed for use in diabetes prediction in this study. The next section contains the proposed method.

The characteristics cannot be adequately extracted by the current models. Preprocessing methods for data were improperly integrated into the current models. Current models are unable to fill in the blanks. Furthermore, current models do not include neural networks or error propagation. In addition to improving the Diabetes prediction job, the suggested model eliminates all of the issues listed above. What follows is the rest of the paper. Section 2 lays out the suggested approach. The datasets and some outcomes from the current and planned methods are described in the fourth section.

Methods & Materials

Ninety percent of all cases of diabetes are classified as type II. This sickness may lead to insulin resistance or insulin loss, both of which are very serious conditions. In most cases, the onset of type II diabetes occurs around the age of 40. Dietary and lifestyle choices that are now being made by those younger than 30 years old put them at risk for developing this condition. Through the use of frequent examinations and questionnaires that detect the problem at an early stage, individuals are able to recognize it and take appropriate action.

There has been a significant amount of research conducted on the interpretability of clinical decision support systems (CDSS) in an attempt to enhance the accuracy and practicability of these systems. Nevertheless, optimizing this aspect of the issue is still very important. The use of fluid rules is appropriate in the field of medicine since interpretability is such an important concern.

A great number of healthcare systems produce a substantial volume of clinical data while simultaneously acquiring valuable insights. Through the use of machine learning techniques, the practitioner is able to do a speedy analysis of this data [9]. By making these decisions, a person may reduce their risk of acquiring diabetes, which can have fatal implications, as well as the risk of harming other organs. In order to extract information from medical data and generate predictions regarding illnesses, a variety of different machine learning approaches have been developed.

On the other hand, the long short-term memory (LSTM) [21] is a kind of RNN that makes advantage of feedback links. The ability of LSTM models to handle extended sequences of input data is accomplished with great efficiency.

An input gate, an output gate, a forgotten gate, and a cell are the four gates that are often found in a long-term short-term memory (LSTM) system. The three gates are responsible for controlling the data that is coming in and going out of the cell, and the cell remembers values at random intervals.

LSTM networks are particularly advantageous when it comes to processing, estimating, and categorizing time series data. This is due to the fact that unexpected events in time series may be delayed. The vanishing gradient is a problem that is associated with typical RNN training, and LSTMs are designed to solve this problem. One of the advantages of LSTM in comparison to RNNs, hidden Markov models, and other sequence learning algorithms is that it pays relatively little attention to the length of gaps, which is beneficial in a variety of applications.

In comparison to a common recurrent unit, the cell memory unit of an LSTM cell provides it with a distinct benefit. It's possible that the cell vector will assimilate some of the new information while simultaneously encapsulating the concept of losing some of the memory that it had previously retained. It is only possible to demonstrate this by carefully examining the sequence sorting and cell equations that lie under the surface.

A. TLSTM (Traditional-LSTM)

In an LSTM network, the components that make up the network are memory cells and four gates specifically. According to the information provided in reference [19], an LSTM network is comprised of four gates: a forget gate (f), an input gate (i), a control gate (c), and an output gate (o).

It is feasible to extract and remember the underlying data pattern, which eliminates the problem of typical RNN algorithms being dependent on data for an extended period of time [19]. The TLSTM architecture is shown in Figure 1, which may be found here [20]. In the architecture, the inputs that are present are denoted by the letters $ht-1$, xt , and b . The phrase $ht-1$ represents the previous cell state, the word xt represents the current input vector, and the word b represents bias. It is essential to keep these three terms in mind. The ct output, which is one of the outputs of the architecture that will be utilized, is a representation of the contents of memory that are now being used. The design also includes another output, which is the ht output, which provides information about the present condition of the cell. The information that is stored in the memory cell is influenced by the four gates that were discussed earlier in this paragraph. The forget gate will return a value that falls anywhere between 0 and 1, inclusive. It is this value that determines the quantity of information from the memory cell that came before it that ought to be ignored. In the event that the forget gate produces a value that is close to zero, this signifies that a significant chunk of the memory that was linked with the previous timestamp will be disregarded when the new time stamp is formed. When it comes to the value that is quite near to one, the converse is true. In accordance with the equations that are shown below, the gates of the TLSTM are stated as follows:

Equation 1 represents the forget gate of TLSTM [20] as,

$$f_t = \alpha g(w_f x_t + u_f h_{t-1} + b_f)$$

Equation 2 represents the input gate of TLSTM as,

$$i_t = \sigma g(w_i x_t + u_i h_{t-1} + b_i) \quad (2)$$

Equation 3 represents the control gate of TLSTM as,

$$c_t = f_t \times c_{t-1} + i_t \times \sigma h(w_c x_t + u_c h_{t-1} + b_c) \quad (3)$$

Equations 4 and 5 represent the output of TLSTM,

$$o_t = \sigma g(w_o x_t + u_o h_{t-1} + b_o) \quad (4)$$

$$h_t = o_t \times \sigma h c_t \quad (5)$$

Within the confines of this particular setting, the sigmoid function is represented by the symbol σg , whereas the hyperbolic tangent function is indicated by the sign σh . The letter w and the letter u are synonymous with the concept of weights. These weights, in many instances, are responsible for preventing the issue of gradients from becoming a vanishing problem.

We have employed fifty T-LSTM units in each layer. These units are located in each layer. It is the responsibility of each layer to determine an attention value for each and every input into the system. The attention value, which is also helpful in creating the final prediction, may be used to judge whether or not the information included in the statement is relevant. The thick layer makes it feasible to reach a definitive conclusion about whether or not a patient has diabetes. This is made possible with the aid of an attention vector.

Figure 1 makes it abundantly obvious that there is no relationship between the contents of the memory that was utilized in the past and any of the gates that are present in the network. This is evident from the fact that there is no connection between the two. It is possible that this will result in an unanticipated condition in the case that the output gate is locked. The efficiency of tasks that involve prediction and classification is thus diminished as a consequence of this. Because of this, the primary purpose of this research is to apply CLSTM to the classification of patients who have diabetes and to illustrate how CLSTM is able to overcome the limitations that TLSTM must contend with when doing so.

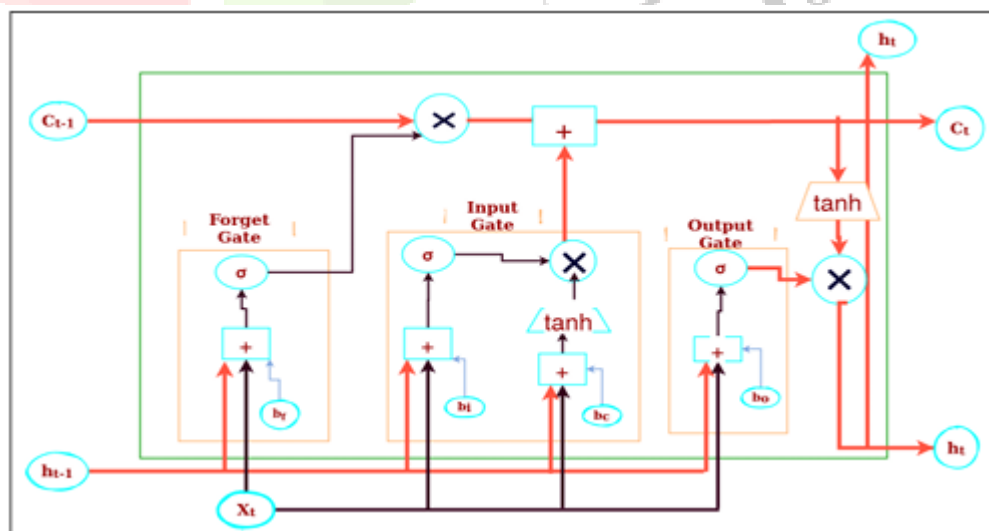


Fig. 1. Architecture of Traditional LSTM.

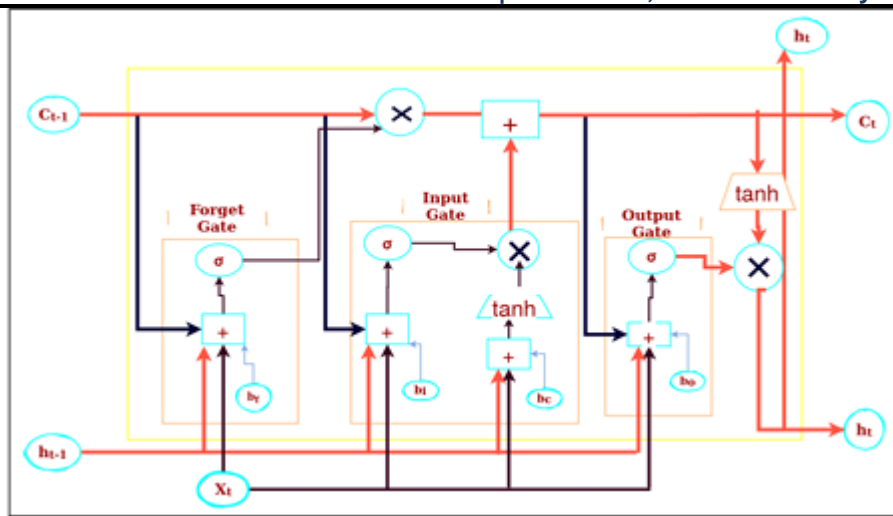


Fig. 2. Architecture of Convolutional LSTM.

B. CLSTM (Convolutional-LSTM)

Traditional LSTM do not access previous memory cell contents [19] even when the output gate of the model is closed. CLSTM negates this by adding an extra link to all the other gates from the previous memory. Fig. 2 [20] shows CLSTM diagram and its operation.

An additional parameter (former c_{t-1} memory content) is in CLSTM compared to TLSTM to provide previous memory cells' impact even when the output gate is closed.

The CLSTM four gates function with the help of the following equations:

Equation 6 represents the forget gate of CLSTM as,

$$f_t = \sigma(w_f x_t + u_f h_{t-1} + v_f c_{t-1} + b_f) \quad (6)$$

Equation 7 represents the input gate of CLSTM as,

$$i_t = \sigma(w_i x_t + u_i h_{t-1} + v_i c_{t-1} + b_i) \quad (7)$$

Equation 8 represents the control gate of CLSTM as,

$$c_t = f_t c_{t-1} + i_t \tanh(w_c x_t + u_c h_{t-1} + v_c c_{t-1} + b_c) \quad (8)$$

Equations 9 and 10 represents the output of CLSTM as

$$o_t = \sigma(w_o x_t + u_o h_{t-1} + v_o c_{t-1} + b_o) \quad (9)$$

$$h_t = o_t \times \sigma_h(c_t) \quad (10)$$

This article developed a CLSTM-based model of diabetes prediction and is tested on the Pima Indian Diabetes dataset.

C. Proposed Model

An example of the model that has been provided for the purpose of diabetes prediction may be seen in Figure 3. The PIMA dataset is pre-processed at the beginning of the procedure, and then features that are essential to the analysis are selected at a later stage. The dataset is split into two sets, the train set and the test set, so that it may be used for training and evaluation purposes.

Alterations are made to the hyperparameters of the TLSTM and CLSTM models throughout the subsequent stage of the design process. After finishing the training phase on the dataset, we started the process of computing various parameters for the purpose of performance evaluation. This was done in order to evaluate how well the

dataset performed. Measurements of the accuracy for a number of different test sizes are included in the research so that an estimate of the performance of the proposed model may be provided.

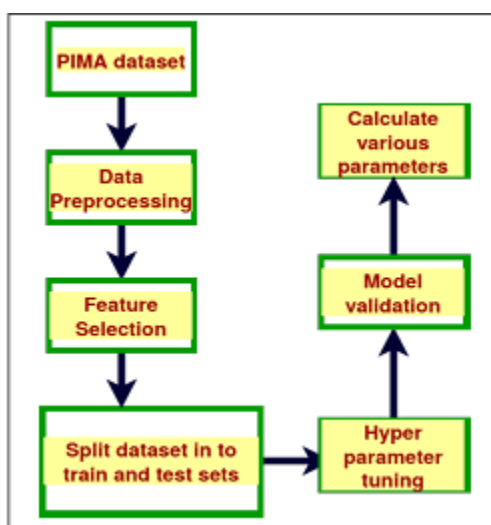


Fig. 3. Proposed Model for Diabetes Prediction.

D. Dataset Description

In the beginning, we will execute the methods for dataset preparation by using the PIMA dataset. This is going to be the first part of our approach that we will implement. There are 768 individuals whose information is stored in the database, and nine distinct characteristics have been accumulated for each individual patient. There are ladies ranging in age from 21 to 81 years old, and the dataset includes information from all of them.

Every row is comprised of six characteristics; these characteristics are exclusive to the chemical examination, whilst the remaining parts provide an overview of the physical examination. Last but not least, the diabetes status of the patient is the last entry in the row of properties.

If the patient has diabetes, a number of 1 indicates that they have the condition, whereas a value of 0 denotes that they do not have diabetes. According on the patient's condition, the last column of each row may include either a 1 or a 0, depending on the situation.

The total number of pregnancies that a particular woman has had is shown in the first column of the dataset, while the plasma glucose concentration is shown in the second column. The diastolic blood pressure is shown in the third column of the dataset, while the triceps skin fold thickness is displayed in the fourth column. Both of these columns are included in the dataset. Additionally, the person's blood insulin levels for the last two hours are shown in the fifth column, while the body mass index (BMI) of the individual is displayed in the sixth column. This dataset presents the pedigree feature in the seventh column, the age in the eighth column, and the incidence of diabetes as a fraction of one in the final column. All of these columns are shown in the dataset. A representation of the data that pertains to the different components of the PIMA dataset can be seen in Figure 4. A significant number of the PIMA dataset's attributes are connected, as seen in Figure 5.

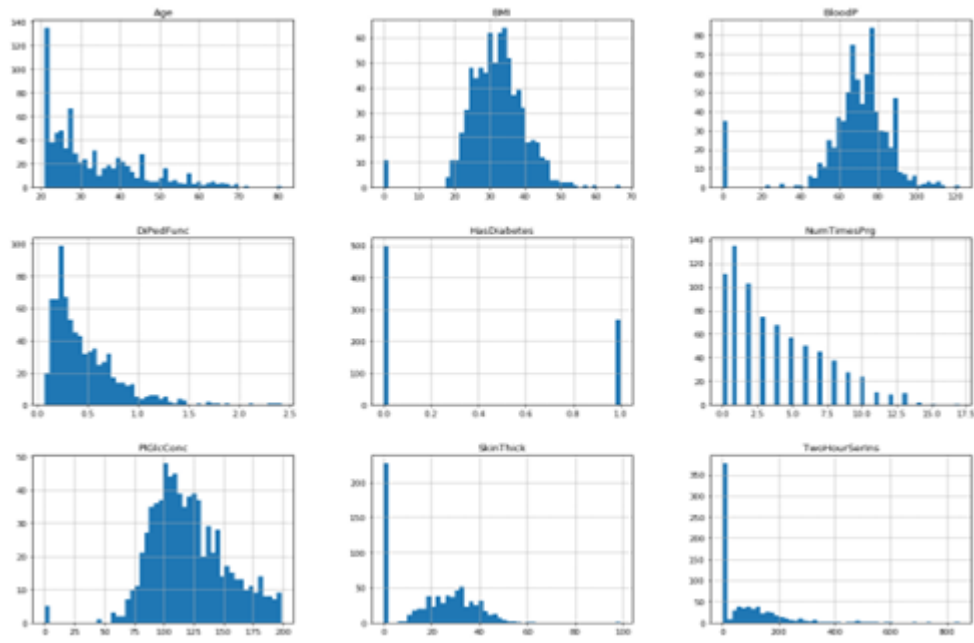


Fig. 5. Attributes in the PIMA Dataset.

Results & Discussion

The comparison of various models like neural networks, machine learning and deep learning systems are presented in this section.

A. Experimental Setup

This study use the TLSTM and CLSTM models to forecast feature selection. We started by pre-processing the dataset using the techniques covered in the previous section. Feature selection is accomplished using the Random Forest method. Our research indicates that insulin, age, glucose, BMI, and blood pressure are the five most important variables.

Table 1 displays the information that was used to create the hyper parameters of the TLSTM and CLSTM models. Table 1 shows the hyper parameter optimization settings that we found to be the most accurate. Using the built-in libraries in Python, we have created our model. The dataset is pre-processed and its characteristics are selected using Python as well.

Table 2 displays the results of several models that were run on the PIMA dataset. The accuracy values achieved by Naïve Bayes, SVM, DT, and K-means are similar. The TLSTM and CLSTM models outperformed the prior methods in terms of accuracy. This section states that the mentioned machine learning algorithms are classic ones. In Table 2 you can see all of the experimental data that we collected. The results showed that out of all the machine learning models that were previously accessible, TLSTM and CLSTM had the best performance.

Table I. Hyperparameters of TLSTM And CLSTM

Parameter	TLSTM	CLSTM
Learning Rate	0.02	0.01
Batch size	32	32
Hidden layers	50	50
Epoch	50	50

TABLE II. Comparison Of Various Models on PIMA DATASET

Model	Accuracy (test set 10%)	Accuracy (test set 20%)
Naive Bayes	79.6%	78.6%
SVM	79.2%	78%
Decision Trees	78.4%	77.2%
MLP	80%	82%
K means	77%	72%
TLSTM	92.5%	93.7%
CLSTM	96.8%	95.6%

It is clear from the findings that are reported in this section that the suggested model is superior to all of the models that are currently in use. The TLSTM and CLSTM models have achieved results that are more accurate than those produced by any of the other machine learning models currently in use. Due to the fact that the machine learning models do not accurately capture the characteristics, the outcomes are lower when compared to the model that was presented. Furthermore, the suggested model takes care of the data pre-processing and feature selection in an appropriate manner, which is the reason why our model has achieved results that are high.

Conclusion

The purpose of this research is to create a diabetes prediction model, and the CLSTM and TLSTM algorithms will be used in order to achieve this goal. In light of the fact that the severity of diabetes is continuing to rapidly worsen, it is very essential for researchers to work quickly in order to create models that are capable of accurately forecasting issues. Utilizing deep learning algorithms in the technique that has been offered allows for improved accuracy in diabetes prediction. This is accomplished via the use of the approach. Additionally, in order to do multivariate imputation, the method that has been provided takes use of chained equations, which are a strong pre-processing tool. This is done in order to accomplish the task. Through the use of the PIMA dataset, the objective of this study is to examine and investigate a wide range of different categorization methods. In order to conduct an analysis of the many different machine learning and deep learning strategies that are presently accessible, this research takes use of the PIMA dataset. As is evident from the data shown in Table 2, the results obtained by the CLSTM model are much superior than those obtained by its predecessors. Starting from this point forward, the CLSTM algorithm will be the basis upon which we will construct the whole framework that we want to construct at some time in the future. It will be possible to access this framework over the internet or through a mobile application, and it will be of service to medical professionals in predicting the beginning of diseases such as diabetes and other disorders at an earlier level from the beginning.

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