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Provisioning A Novel Combined Learning Pattern For Diabetes Prediction Using Variable Representation And Evaluation Indexes

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ABSTRACT

Diabetes represents a significant global health challenge, particularly as the prevalence of individuals at risk continues to rise. Diabetes is classified as a chronic disease; diabetes is responsible for a substantial number of fatalities annually. Early prediction of diabetes is essential for halting its progression and mitigating the risk of severe associated complications, including cardiovascular disease and renal damage. This research proposes an innovative Deep Learning (DL) clinical decision support system designed to optimize diabetes prediction accuracy using machine learning. The proposed DL methodology combines a stacking pattern based on learning with various DL architectures, specifically ANN, LSTM networks, and CNN, to form a Combined Learning Network Pattern (CLNet). To enhance diabetes prediction capabilities, the DL framework employs a pattern that integrates meta-level patterns. The novel DL patterns are trained to utilize three distinct diabetes information sets. Pertinent variables are obtained from the information set utilizing the proposed methodology. Key evaluation metrics such as accuracy, precision, recall, specificity, F1-score, MCC, and ROC/AUC are employed to assess the effectiveness of the proposed CLNet patterns. When applied to the information sets, the Combined Learning Network Pattern (CLNet) exhibited improved performance compared to the other proposed CLNet pattern, obtaining accurate results rates of 99.5%, 98.8%, and 98.4%, respectively. The analysis reveals that the proposed CLNet patterns exhibit enhanced performance in diabetes prediction compared to previous studies.

Keywords: *diabetics, prediction, deep learning, hybridization, variables*

1. INTRODUCTION

With more and more diabetic individuals at risk, diabetes is a widespread health concern internationally. It results in a significant death toll [1]. Diabetes, commonly known as DM, is a metabolic disorder characterized by chronically, abnormally high blood glucose levels caused by the body's reduced ability to utilize glucose effectively. Diabetic ketoacidosis, chronic renal failure, nonketotic hyperosmolar coma, foot ulcers, retinal damage, cardiovascular disease, stroke, and chronic renal failure are among the severe consequences linked to DM. Developed during pregnancy, T1D and T2D are the three main forms of DM [2]. T1D is caused by inadequate insulin synthesis and typically affects individuals under 30. Typical symptoms consist of elevated blood sugar levels, frequent urination, and intense thirst. Patients with type 1 diabetes usually require medication for management. In contrast, chronic metabolic disorder is a prevalent condition where the body struggles to produce or effectively respond to insulin properly. It primarily affects middle-aged and older persons and is frequently linked to lifestyle choices, food habits, obesity, smoking, high cholesterol (hyperlipidemia), hypertension (hyperglycemia), and a lack of physical activity. Pregnancy can also be used to diagnose gestational diabetes [3]. This illness poses a significant risk to public health, necessitating ongoing prevention and treatment initiatives.

Over 420 million individuals worldwide have DM, and over 650 million adults are considered obese; since 1975, the number of obese people has tripled, following WHO criteria [4]. Over time, the chronic illness known as DM has increased in prevalence. A primary international health concern is the massive upward trend in the number of people with metabolic disorder. The top 15 countries with the highest DM rates are listed [5]. Many diabetes patients tend to underestimate the severity of their health condition in the early stages of the disease. Since delayed diagnosis causes a high annual mortality rate and several health issues, methods for early detection and prediction of DM must be developed. The prevalence of DM patients is rising, which is a serious health issue [7]. It is critically essential to predict DM in individuals of all ages. Consequently, timely implementation of suitable lifestyle modifications can aid in halting the advancement of DM and its associated health issues [8]. At the moment, the scientific community is focused on using powerful computer techniques to predict DM in an early and accurate manner. Soft computing techniques and artificial intelligence (AI) play key roles. Top 15 countries with the highest incidence of diabetes [8]. In turning abstract ideas into valuable applications. These systems are used in various human health-related fields, including medical diagnostics. AI and machine learning (ML) provide benefits over manual diagnosis by enabling automated early detection and prediction of DM [9]. There is now a sizable corpus of research on DM self-management and automatic detection strategies utilizing ML and AI approaches [10].

Traditional ML algorithms have produced encouraging results for predicting and categorizing DM into DM-positive and DM-negative cases [11] – [12]. However, using a DL framework can significantly improve the accuracy of DM diagnosis [13]. To our knowledge, DL techniques have not been used in any available investigations. This study proposes a novel CLNet prediction framework that employs DL algorithms as base-level patterns, including CNN, ANN, and LSTM. After that, DL is put into practice using patterns that use meta-level patterns like CNN, LSTM, and ANN to enhance DM prediction. The pattern can identify distinct patterns and variables in the information thanks to the mixing of several neural network architectures. The DL combines the predictions from each base pattern to optimize the pattern's capacity to maintain accuracy with new information and minimize over-fitting. The following is a summary of this study's main contributions:

1. To develop a clinical decision support system (DSS) for predicting diabetes that employs DL methods and a pattern.

2. To enhance variable extraction and prediction accuracy by combining several DL techniques, including LSTM, CNN, and ANN known as the Combined Learning Network Pattern (CLNet).

3. Three diabetes information sets known as the short information set (PIMA-IDD-I) with 768 cases, a big information set (DDFH-G) with 2000 instances, and a multi-class information set (IDPD-I) with 1000 instances are used to train the DL pattern.

4. To give medical practitioners a tool for highly accurate early prognosis and individualized patient care in diabetes management.

5. A comparison with the latest methods has been carried out to investigate the effectiveness of the proposed CLNet. This assessment confirms that the proposed CLNet developed pattern exceeds current techniques and shows that it is the best at predicting diabetes.

The work is divided into sections as follows: Section 2 discusses a wider analysis of diverse approaches. The methodology is presented in Section 3, with results outlined in Section 4. The work summary is outlined in Section 5.

2. RELATED WORKS

The importance of identifying diabetes has been explored in many research studies that employ ML and DL methods [14]. For instance, a Gestational DM prediction system based on explainable ML was proposed. The author put forth an ML-based pattern for T2D detection and categorization. BERT was proposed for the identification of DM utilizing unstructured information from electronic health records. For DM detection, the author in [15] used a health survey and Indian demographic information to develop Gaussian Naive Bayes (NB), linear discriminant analysis, LR, SVM, DT, KNN, RF and Extreme Gradient Boosting (XGB) [16] – [18]. Comprehensive diabetes management in a primary care setting was examined. The author presented a DM prediction pattern based on SVM, KNN, DT, RF, adaptive boosting, LR, and DL. The investigator developed XGB, RF with recursive variable elimination, and ANN for diagnosing diabetic retinopathy in the Chinese population. The author in [19] did another relevant work in which they offered a questionnaire-based survey that uses SVM, DT, LR, gradient boost, XGB, and RF to address prevalent risk factors of DM [20]. To identify T2D, the author suggested a soft voting method that combines light gradient boosting XGB and RF. They employed 9822 screening samples with 82 appropriate characteristics to conduct their study.

An SVM method was created to predict T2D from electronic medical records. Similarly, the author suggested a regression tree and LR-based prediction pattern for determining whether females with gestational diabetes will require insulin therapy. They looked at samples from 775 women who were diagnosed with gestational DM based on the IADPSG. Using PIMA-IDD-I, the author in [21] offered a KNN-based pattern for DM prediction, whereas the author proposed an ANN pattern with an accuracy of 80.79% for DM prediction. The author in [22] used PIMA-IDD-I to create RF, NB, and J48 DT for DM categorization and prediction. The author used majority voting to apply ANN, RF, XGB, and adaptive boosting for DM prediction. The patterns KNN, DT, RF, and SVM were created. The author also used the PIMAIDD-I and IDPD-I information sets to propose LR, NB, and RF approaches with a soft pattern. Their proposed pattern attained 97% and 81% accuracy utilizing the information set, respectively. The author in [23] used IDPD-I to create a multi-layer perceptron to forecast DM. For T2D prediction, the author in [24] created KNN, SVM, RF, and DL. Using the PIMA-IDD-I and IDPD-I information sets, they trained the patterns. Using the PIMA-IDD-I information set, the author in [26] presented RF and SVM, which produced 83% and 81.4% precision scores, respectively. Similar to this, the RF pattern was proposed in [27] for DM prediction, and it produced accuracy ratings of 85.6%, 82%, and 82.26%, respectively. The following are some current applications of DL techniques in DM detection and prediction. To predict diabetics, the author in [28] created DL approaches utilizing CNN for categorization and trained the pattern using PIMAIDD. The author used ANN and ML methods. They discovered that the RL and the SVM methods perform well for DM prediction. The researchers conducted experiments involving different configurations of hidden layers within their ANN architecture and found that the pattern incorporating two concealed layers attained a precision of 88.6%. The author used a deep ANN with an encoder to classify the PIMA-IDD-I. Using DL techniques, the author developed a technique for differentiating between normal and diabetic HRV signals. To identify complex dynamic changes over time factors from the HRV information, they constructed CNN and LSTM. A deep belief network is one of the DL techniques that was developed to categorize and forecast the course of impaired glucose tolerance. Showing a high degree of accuracy of 81.25%, the deep belief network outperformed other ML algorithms. Using the PIMA-IDD-I and DDFH-G information sets, the author suggested ANN, ANN, DT, and KNN patterns for DM prediction. Similarly, the author used ANN to detect and categorize DM. They obtained an accuracy of 85.09% using the PIMA-IDD-I for evaluation [29].

While normal information-driven methods struggle to find enough labeled information and make the results easily comprehensible, DL approaches typically require large amounts of information. These issues can be successfully addressed using DL as a constraint and guide in the current information-driven patterns. In particular, there are not always enough electronic health records accessible to train DL patterns in constructing healthcare decision support systems. Currently, the introduction of learning methods in a particular electronic medical information set [29] can considerably improve the effectiveness of DL approaches. Using DL techniques to extract knowledge from electronic health records is a useful but complex undertaking for diagnosis and prediction. Undiagnosed diabetes can hurt the kidneys, liver, and other organs in the human body. This medical condition affects people of all ages. Numerous studies have tried to use ML and DL approaches to predict and categorize diabetes in the literature. However, a research need is highlighted by the absence of the DL method for diabetes prediction from the current categorization and prediction approaches. However, when dealing with large and multi-class information sets, state-of-the-art methods face a major obstacle characterized by decreased accuracy. The suggested DL attempts to solve this issue by introducing variable optimization and categorization techniques to make highly accurate predictions about DM. This paper suggests a new clinical decision support system that combines a pattern with DL architectures, including ANN, CNN, and LSMT. As base-level patterns, these DL architectures are employed. To improve the prediction of DM, DL is developed (i.e., meta-level) by adding novel patterns [30]. The fact that none of the current patterns have been trained on the many kinds of diabetes information sets is another limitation of earlier research. The suggested DL patterns in this work are trained using three distinct diabetic information sets. The information sets include a multi-class IDPD-I with 1000 samples, a large DDFH-G with 2000 samples, and a tiny PIMA-IDD-I with 768 samples. Additionally, the suggested study addresses the relevance of the outcomes produced by the DL system and compares it with recent state-of-the-art research [30].

3. METHODOLOGY

Fig 1 shows the suggested DL framework. Information sets, information preprocessing, variable selection, information splitting, base-level patterns, and performance-based assessment are all steps in the DL framework.

3.1. Information set description

The DL is calibrated and experimented with using three diabetes information sets, namely PIMIA-IDD-I, DDFH-G, and IDPD-I. To predict DM across two classes (DM-positive and DM-negative) and three classes (pre-diabetes, diabetic, and non-diabetic), respectively, the information sets are divided into binary and multi-class categorizations. The information sets are divided into three categories: PIMIA-IDD-I, DDFH-G, and IDPD-I, which are small, large, and multi-class information sets, respectively. The ensuing subsections provide a detailed explanation of the suggested information sets. The UCI Repository is the source of the PIMA-IDD-I. There are 768 samples of diabetes patients, with nine different variables in each sample. Equal numbers of participants with diabetes, pre-diabetes, and no diabetes are included in these records. The final column represents a binary target variable, where a null value signifies the absence of diabetic conditions in the patient. In contrast, a value of 1 denotes the existence of pre-diabetic or diabetic conditions or diabetes. Two thousand cases with eight variables each comprise the DDFH-G information set, which comes from the Hospital Frankfurt in Germany, and 768 patients with eight attributes each comprise the PIMA-IDD-I information set. The main distinction between the DDFH-G information set and the information sets used in the research and Dwivedi is the greater quantity of information points in DDFH-G. The characteristics cover a wide range, from skin thickness to the number of pregnancies. It is seen in the information set that several characteristics, including skin thickness, blood pressure, insulin, glucose, and BMI, show zero values, which is not realistic. The mean value of the corresponding variable column containing the missing values is thus used to replace these instances, which are kept as missing information. The IDPD-I information set was collected from the Iraqi population, specifically from facilitated by the Specialized Center for Endocrinology and Diabetes at Al-Kindy Teaching Hospital and the laboratory at Medical City Hospital. There are 1000 samples in the IDPD-I. There are 435 females and 565 males in the IDPD-I, with ages ranging from 20 to 79. It is divided into three classes: 53 samples are classified as Predicted Diabetic (P), 103 samples are classified as Non-Diabetic (N), and 837 samples are classified as Diabetic (Y). Patient Number, Age, Gender, Blood Sugar Level, Cholesterol, Creatinine Ratio (Cr), Urea, Body Mass Index (BMI), HBA1C, Fasting Lipid Profile (VLDL, LDL, Triglycerides, HDL Cholesterol), and Class (signaling the diabetic patient's status as Diabetic, Non-Diabetic, or Pre-Diabetic) are among the eleven physical examination indicators that define these samples.

3.2. Pre-processing

Any information items, including missing values, were methodically removed from the information set to prepare it for DL training and guarantee superior outcomes. First, all entries with duplicate and null/missing values were eliminated from the three district information sets. Certain variables, including skin thickness, insulin, blood pressure, glucose, and BMI, show zero values in the information sets, which is unrealistic. The mean value of the corresponding attribute column containing the missing values is thus used to replace these occurrences, which are kept as missing samples. Additionally, the MinMaxScaler was employed to standardize the information values before integrating them into the pattern. There was a notable class imbalance in the original information set, with most of the samples being negative and just 20% of the samples belonging to the positive class. The SMOTE was employed to augment the representation of the minority class within the information set, thereby addressing the issue of class imbalance. Given that the information was categorical and the target variable was binary, categorization patterns were utilized to determine the predictive performance of DM. The goal of this thorough information before the treatment method is to improve the suggested DL's performance and capacity for making accurate predictions.

Diabetic prediction process

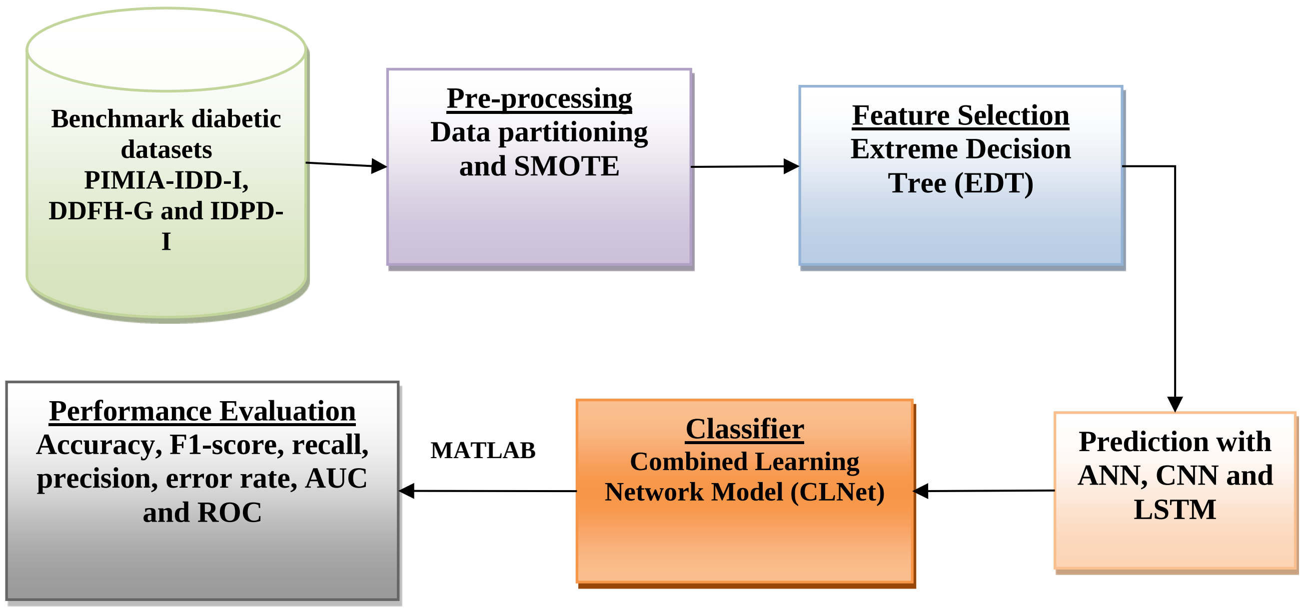


Fig 1. Block of the CLNet

3.3. Information partitioning

Here, the normalized and preprocessed diabetic information sets are divided into two subsets: the training and test sets. Information splitting is a methodological approach that includes partitioning an information set into distinct categories. The proposed division of the information sets follows an 80:20 ratio, wherein 20% of the information is allocated for evaluating the DL pattern (testing). In comparison, the remaining 80% is leveraged for training the DL pattern. The test set comprises information samples designated for assessing the effectiveness of the DL, whereas the training set encompasses information samples employed to learn and adjust the pattern parameters.

3.4. Variable selection

The variable selection method identifies and selects relevant variables from a vast array of available attributes to enhance precision while reducing computational complexity and latency. It is possible to assess each variable's significance in diabetes information sets by using the pattern characteristics attribute. Each function of the results is assigned a variable value score, indicating its significance and influence on the dependent variable. A higher score is associated with greater significance or appropriateness of the variable. In the present study, the Gini relevance technique is employed to utilize the Extreme Decision Tree (EDT) to isolate the most important variables from the information set. This pattern incorporates a predefined class that aids in evaluating variable importance, particularly within Tree-Based patterns, thereby proving to be highly effective for analyzing variable significance. By employing the EDT, we can obtain important insights for our investigation and pinpoint the salient characteristics that greatly influence the system's predicted performance.

3.5. Prediction process

Following variable determination, the patterns were constructed using ANN, CNN, Hybrid CNN-LSTM, and LSTM, and the four DL prediction and categorization techniques. The sections that follow provide descriptions of the suggested patterns.

a) Artificial Neural Networks

As illustrated in Fig 2, an ANN is a computer system composed of numerous basic yet interconnected processing units. These units are processed using different external inputs. The architecture of the ANN proposed in this study is informed by a non-recurrent network that utilizes a supervised back-propagation algorithm, which facilitates the integration of multiple weighted hidden layers. This approach is commonly applied across diverse fields, comprising image processing, speech recognition, robotic control, sentiment analysis, forecasting, artificial intelligence, and the management of control and protection systems in power systems. The human brain can be connected to an ANN. The human brain is composed of many effective neurons. Every information input travels through neural signaling, which interprets, calculates, and processes the information before sending it on to the subsequent neuron unit. Although the aggregate processing speed of each neuron or node is slow, the network's overall speed is compromised incredibly speedily and optimized. The input layer, hidden layers, neurons, and ANNs created for this study are all discussed. By establishing best practices, the quantity count of elements in the initial and intermediate layer is equivalent to that of the feature layer. The output layer, designed for high-dimensional case prediction, comprises two neurons, whereas the second hidden layer contains five neurons. The prediction layer utilizes a Softmax activation function, typically employed for binary categorization, while the hidden layers implement the ReLU activation function.

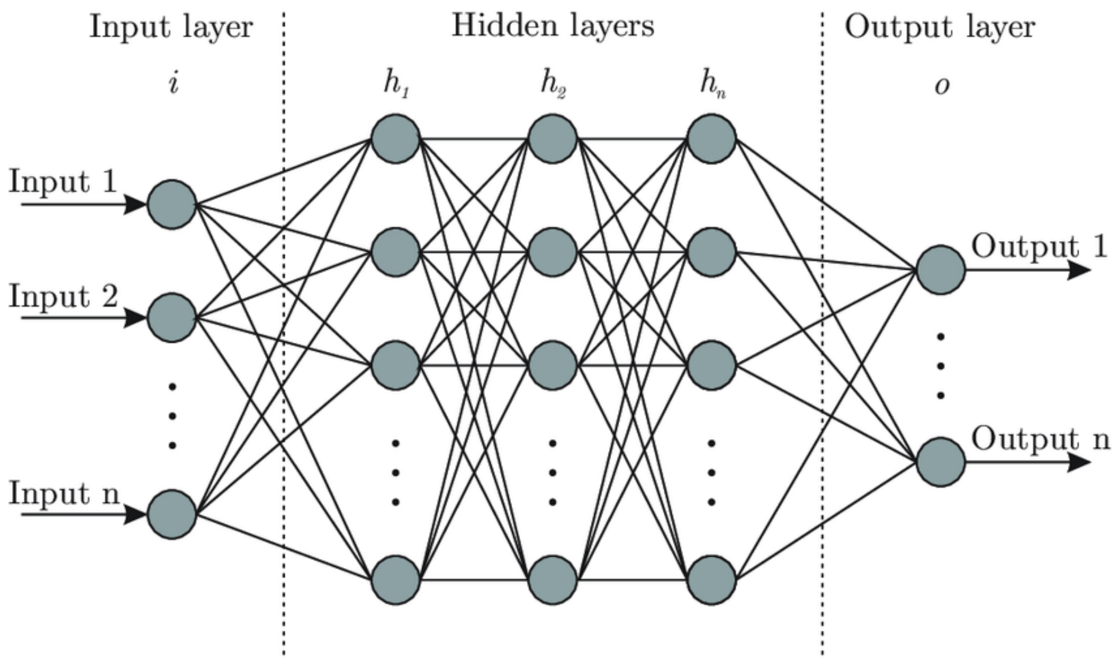


Fig 2. Conventional ANN pattern

b) Convolutional network

One DL technique that can be learned straight from information is a CNN. These are very useful for distinguishing different items by identifying patterns in samples. Moreover, neural networks demonstrate significant utility in classifying image and non-image information. The fundamental concept underlying CNNs is identifying increasingly complex variables by extracting local characteristics from abstract representations of input pipelines transmitted to subordinate systems. As illustrated in Fig. 3, a conventional CNN architecture typically consists of convolutional, pooling, and dense layers. The feature extraction layer generates variable maps as tensors by employing a set of kernels. These kernels perform convolution on the information utilizing specified "strides," generating output volumes with integer precision dimensions. However, the application of spatial stride leads to a reduction in the input volume sizes within the convolutional layer. The input feature map comprises fundamental variables as it is necessary to employ zero padding to populate the input space with missing values. Applying the ReLU function induces non-linearity in the variable maps. By establishing a limiting input of null, the triggering is subsequently determined. A chosen input dimension is down-sampled using the pooling layer to lower the number of variables. Max pooling is a popular technique that keeps the highest value within a designated input space. The Fully Connected layer is responsible for classification and prediction, facilitating information categorization by utilizing the data acquired from the max pooling and convolution components.

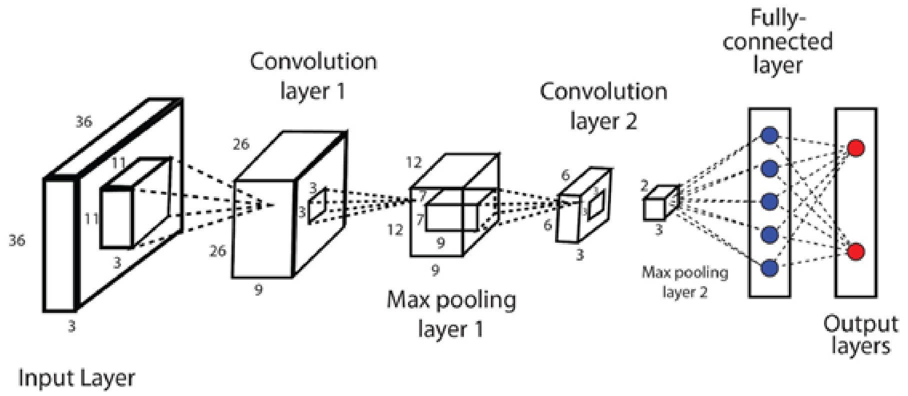


Fig 3. Convolutional Neural Network architecture

c) Long Short-Term Memory

LSTM networks are a component of the DL field. They are widely recognized for their proficiency in capturing persistent connections, notably in tasks requiring temporal understanding related to sequence prediction. It belongs to the class of recurrent neural networks. It receives input and relays it to others as it develops. The cells of the LSTM carry out several functions. Long-term dependencies can be learned, and information can be retained for extended periods in the memory state of an LSTM. Consequently, LSTMs have demonstrated their effectiveness in diverse areas, such as natural language processing, sequential data prediction, and speech recognition. Using a cell state in LSTMs allows them to maintain long-term information, giving them a significant edge over RNNs. This capability enables LSTM networks to retain and connect information from previous time steps to the current one. To accomplish this, LSTMs utilize three controllers: the input, the forget, and the output. Ct and Ct−1 represent the contemporary and earlier memory cells, while it denotes the current input. H_t *and* H_{t-1} allude to the contemporary and earlier outputs, respectively. Fig 4 diagrams the internal architecture structure of an LSTM, highlighting how gates and cell state work together to support information flow and persistent memory throughout the network. Feedback from the dropout layer is directed to the LSTM layer. The mathematical operation consists of four elements: a new memory cell (c_t), an output gate (o_t), a forget gate (f_t), and an input gate (i_t). The computations combine the forward and backward performance using Eq. (1) to Eq. (4). As illustrated below, an LSTM takes in the current observation (X_t) and the past state (h_{t-1}), performs specific calculations, and organizes the results into a hidden state (h):

$$f_t = \sigma(U_f h_{t-1}, \quad W_f X_t + b_f) \tag{1}$$

$$i_t = \sigma(U_i h_{t-1}, W_i X_t + b_i) \tag{2}$$

$$a_t = \tanh(U_c h_{t-1}, W_c X_t + b_c) = \tan(\hat{a}_t) \tag{3}$$

$$o_t = \sigma(U_o h_{t-1}, W_o X_t, b_o) \tag{4}$$

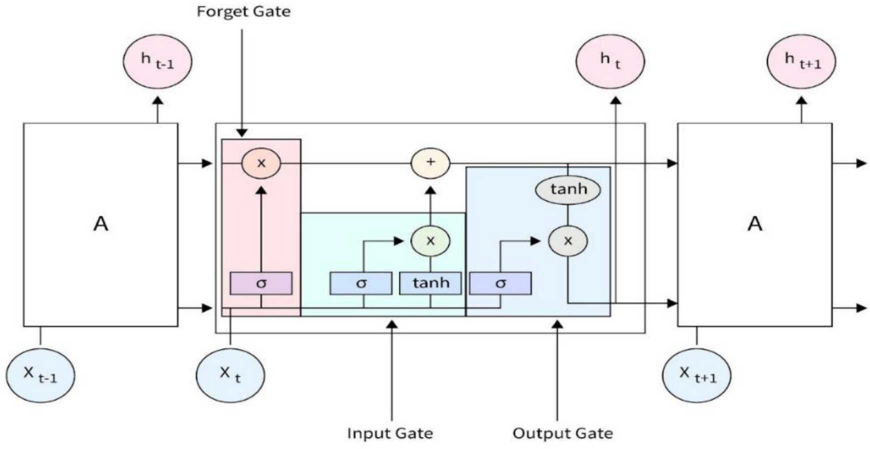


Fig 4. LSTM pattern

d) Hybridization

This research proposed a new CLNet method for predicting diabetic cases using multivariate diabetes information sets. The pattern integrated CNN-LSTM architectures, where the CNN extracted encoding detailed acoustic features information, whereas the LSTM functioned as the anticipation mechanism component. Variables related to diabetes symptoms were gathered from the raw information sets and employed for learning to develop the CNN-LSTM framework using these multivariate diabetes information sets. Fig 5 depicts the 30 layers constituting the proposed CLNet pattern for predicting diabetes: The network consists of 18 convolutional layers, 12 pooling layers, a fully connected layer, an LSTM layer, and a final output layer employing the softmax method. Each convolutional neural block contained a pooling layer, two to three 2D CNNs, and one convolutional block. Additionally, a dropout layer where 20% of neurons are randomly deactivated was incorporated. A convolutional layer with a 3 × 3 kernel size was employed to extract variables initially obtained using the ReLU method. To reduce the dimensionality of the input multidimensional diabetes variables, a max-pooling layer employing 2x2 convolutional kernels was applied. To retrieve patient information, the final phase's LSTM layer received the generated variable map. The output form (none, 8, 8 512) was molded to understand the convolution part. A reshaping technique was used to reduce the input size of the LSTM layer (16, 512). The framework initially studied the sequential pattern elements before transmitting the multidimensional diabetes information through a dense layer to categorize each case into two subsets, like diabetes favorable or diabetes unfavorable (no diabetes).

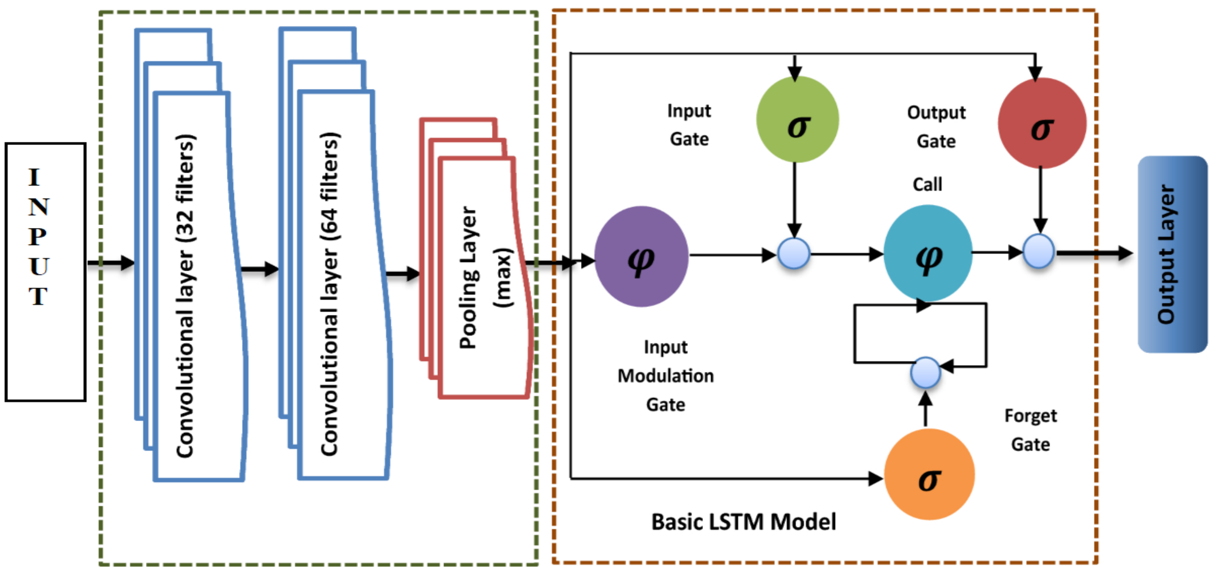


Fig 5. CLNet architecture

4. NUMERICAL RESULTS

Major assessment criteria, including accuracy, f-score, sensitivity, precision, specificity, ROC/AUC, and MCC, are used to assess the suggested DL system. These indicators assess DL performance in a DM prediction task. Each evaluation index is explained in detail in the ensuing subsections. The percentage of correctly predicted instances (including True Negatives (TN) and True Positives (TP)) about all occurrences (including True Negatives (TN), True Positives (TP), False Negatives (FN) and False Positives (FP)) is known as accuracy is calculated using Eq. (5). It is a widely used statistic to assess categorization patterns.

$$Accuracy = \frac{TP + TN}{FN + FP + TP + TN} \tag{5}$$

According to Eq. (6), precision is the proportion of TP predictions among the pattern's FP and TP predictions. It evaluates the DL's capacity to minimize FP while producing accurate positive forecasts. Higher precision numbers indicate fewer FP.

$$Precision = \frac{TP}{FP + TP} \tag{6}$$

Specificity, a TN rate representing the proportion of TN classes that the DL correctly anticipated, is computed using Eq. (7).

$$Specificity = \frac{TN}{FN + TN} \tag{7}$$

The percentage of TP cases that the DL accurately predicts using Eq. (8) is known as sensitivity. It evaluates the DL to record positive examples.

$$Sensitivity = \frac{TP}{FN + TP} \tag{8}$$

Eq. (9) calculates the F-Score, the harmonic mean of precision and sensitivity. Taking into account both FP and FN offers a fair assessment of a DL's performance.

$$F1 - score = 2 * \frac{Precision * Recall}{Precision + Recall} \tag{9}$$

MCC is used to assess the validity of binary categorizations. Because it considers both TP and FP in addition to TN and FN, it is particularly useful when working with unbalanced information sets. Eq. (10) can be used to calculate it mathematically.

$$MCC = \frac{TN * TP - FN * FP}{\sqrt{(TP + FN) * (TN + FP) * (TP + FP) * (TN + FN))}} \tag{10}$$

4.1. Result analysis

The performance of the suggested DL in terms of accuracy, f-score, sensitivity, precision, specificity, ROC/AUC, and MCC utilizing PIMAIDD-I, DDFH-G, and IDPD-I for DM prediction is shown experimentally in this section. Based on various kinds of assessment measures, Tables 1 to 3 present a performance comparison of the DL-based meta-level patterns and the DL-based base-level patterns. Precision, accuracy, specificity, sensitivity, MCC, and f-score are among the evaluation measures. A thorough analysis of several patterns on the PIMA-IDD-I information set is provided in Table 1. While the LSTM and CNN also produce competitive results, the ANN has the highest accuracy (92%), precision (93%), and sensitivity (93%) among the base-level patterns. Overall assessment metrics for each base pattern are regularly outperformed by the meta-level patterns, which are the base patterns. In particular, the ANN performs better overall, achieving notable accuracy (98%), precision (97%), and specificity (98%). According to accuracy, precision, specificity, sensitivity, f-score, and MCC of 97.23%, 97.34%, 96.54%, 96.44%, 97.06%, and 93.07% utilizing PIMA-IDD-I. Accuracy, precision, specificity, sensitivity, f-score, and MCC scores of 94.81%, 93.93%, 93.88%, 94.2%, 93.78%, and 92.28% were all higher for CNN when using PIMA-IDD-I. This illustrates how effectively base patterns can be combined to improve prediction power. The MCC values demonstrate the suggested DL's proficiency with binary categorization problems. As demonstrated in Fig 6, the results highlight how DL enhances the accuracy and resilience of the suggested DL patterns for the PIMA-IDD-I information set.

Table 1. Comparison with dataset 1

Evaluation Index	DL patterns			
	Conventional ANN	Conventional CNN	Conventional LSTM	Proposed CLNet
Accuracy (%)	92.7	97.2	94.8	98.8
Precision (%)	92.6	97.3	93.9	97.9
Specificity	92.8	96.5	93.8	98.4
Sensitivity	92.7	96.4	94.02	98
F1-score	91.1	97	93.78	97.8
MCC	90.4	93.07	92.2	94.5

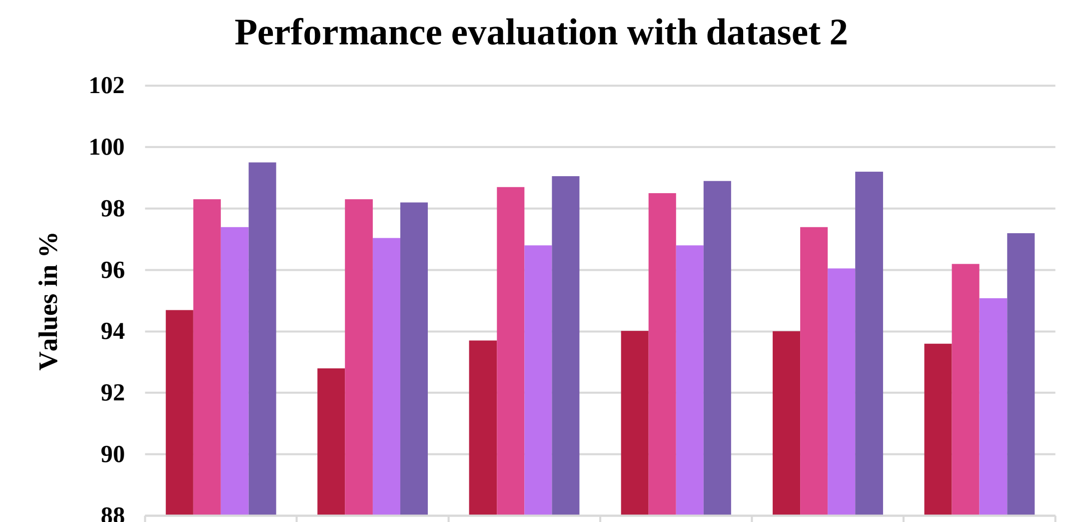
Table 2. Comparison with dataset 2

Evaluation Index	DL patterns			
	Conventional ANN	Conventional CNN	Conventional LSTM	Proposed CLNet
Accuracy (%)	94.7	98.3	97.4	99.5
Precision (%)	92.8	98.3	97.04	98.2
Specificity	93.7	98.7	96.8	99.05
Sensitivity	94.02	98.5	96.8	98.9
F1-score	94.01	97.4	96.05	99.2
MCC	93.6	96.2	95.08	97.2

Table 3. Comparison with dataset 3

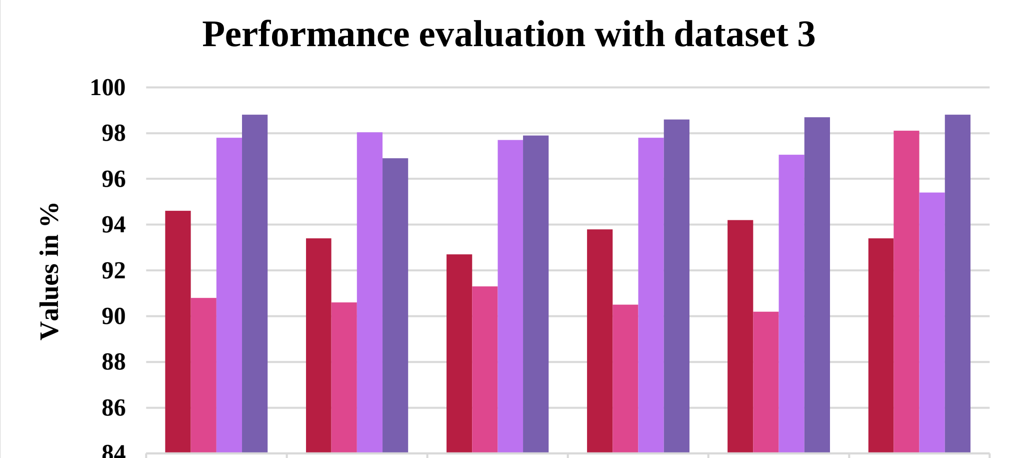
Evaluation Index	DL patterns			
	Conventional ANN	Conventional CNN	Conventional LSTM	Proposed CLNet
Accuracy (%)	94.6	90.8	97.8	98.8
Precision (%)	93.4	90.6	98.03	96.9
Specificity	92.7	91.3	97.7	97.9
Sensitivity	93.8	90.5	97.8	98.6
F1-score	94.2	90.2	97.05	98.7
MCC	93.4	98.1	95.4	98.8

Fig 6. Performance evaluation with information set 1



	Accuracy	precision	specificity	sensitivity	MCC	
ANN	94.7	92.8	93.7	94.02	94.01	93.6
CNN	98.3	98.3	98.7	98.5	97.4	96.2
LSTM	97.4	97.04	96.8	96.8	96.05	95.08
CLNet	99.5	98.2	99.05	98.9	99.2	97.2

Fig 7. Performance evaluation with information set 2



	Accuracy	precision	specificity	sensitivity	MCC	
ANN	94.6	93.4	92.7	93.8	94.2	93.4
CNN	90.8	90.6	91.3	90.5	90.2	98.1
LSTM	97.8	98.03	97.7	97.8	97.05	95.4
CLNet	98.8	96.9	97.9	98.6	98.7	98.8

Fig 8. Performance evaluation with information set 3

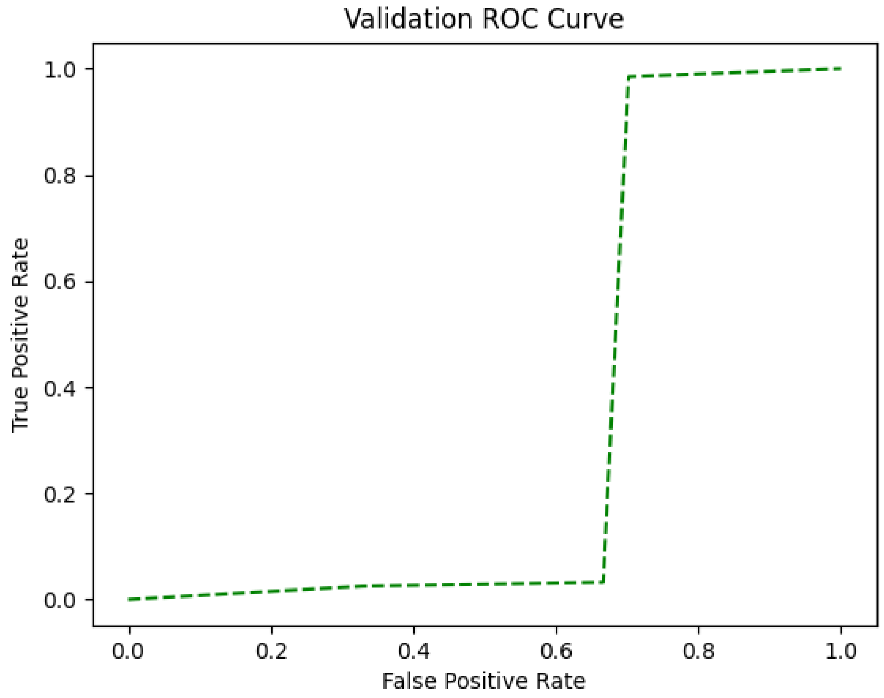


Fig 9. ROC comparison of proposed CLNet

A thorough evaluation of DL performance on the DDFH-G information set is given in Table 2. Fig 7 also provides a graphic representation of the comparison. While the LSTM and CNN patterns also show comparable results, the ANN stands out in the field of base patterns with the highest accuracy (94.77%), precision (93.65%), sensitivity (94.02%), and F-Score (94.01%). Interestingly, base patterns are routinely outperformed by DL patterns on all evaluation metrics. The ANN exhibits remarkable performance with a noteworthy accuracy of 99.51% and high values for specificity, precision, F-Score, and sensitivity. With precision, accuracy, sensitivity, specificity, MCC, and F-score of 98.34%, 98.36%, 98.54%, 98.77%, 96.20%, and 97.43% respectively, the LSTM demonstrated strong performance using DDFH-G. With accuracy, precision, specificity, sensitivity, F-score, and MCC scores of 97.44%, 97.04%, 96.88%, 96.85%, 96.06%, and 95.07%, respectively, the CNN demonstrated strong performance while employing DDFH-G. Merging the predictions from base patterns demonstrates the potential of the suggested DL. A thorough assessment of DL performance on the IDPD-I information set is given in Table 3. With its excellent accuracy (94.62%), precision (93.43%), and sensitivity (93.88%), the ANN outperforms the other base patterns. The CNN and LSTM patterns also provide competitive performance, demonstrating the variety of base-level architectures. Interestingly, the meta-level patterns perform better than the basic patterns on several evaluation metrics. With remarkable accuracy (98.5%), precision (98.3%), and sensitivity (98.02%), the ANN stands out and exemplifies the value of mixing various base patterns. With accuracy, precision, specificity, sensitivity, F-score, and MCC scores of 97.8%, 98.03%, 97.75%, 97.5%, 97.06%, and 95.4%, respectively, the LSTM also outperformed when using IDPD-I. The CNN also produced strong results with accuracy, precision, specificity, sensitivity, F-score, and MCC scores of 96.89%, 96.90%, 97.22%, 96.62%, 96.70%, and 94.87%, respectively. These results demonstrate how well the suggested DL patterns perform when improving predictive accuracy using IDPD-I. The obtained outcomes demonstrate how effective DL patterns are at multi-class categorization tasks. This demonstrates how DL might help healthcare DSSs by enhancing pattern performance and robustness in disease prediction.

The performance of three DL on three distinct information sets is evaluated in Fig 7. The ROC curve in Fig 9 show how discriminatively each pattern can categorize DM as positive or negative. With an AUC of 92%, which indicates strong accuracy for prediction, the ANN stands out as the best performer. The CNN comes in second with an AUC of 96%, while the LSTM is in the middle with an AUC of 92%. Likewise, Fig 8 shows how these patterns are assessed with the IDPD-I. AUC values for the ANN, CNN, and LSTM are 94%, 91%, and 90%, respectively. With an AUC of 97%. The LSTM comes in second with 96% and the CNN with 94% utilizing DDFH-G. Together, these results demonstrate how different base-level patterns perform, demonstrating how effective base-level patterns are at predicting DM. The ROC curve and AUC values for the suggested DL patterns used for the PIMA-IDD-I information set are shown graphically. Each DL pattern's performance is shown according to its AUC value: CNN, LSTM, and ANN. With the greatest AUC value of 98%, the ANN performs well in both positive and negative DM case categorization and prediction. With a bit lower AUC value (94%), the CNN pattern comes in second, while the LSTM pattern is in the middle with an AUC of 97%. The performance of these patterns is shown using IDPD-I, where the ANN, LSTM, and CNN obtained AUC scores of 98%, 98%, and 97%, respectively. AUC scores for the ANN, LSTM, and CNN are similarly displayed in Fig 8 with DDFH-G as 99%, 98%, and 97%, respectively. These findings demonstrate how well the suggested DL patterns categorize and forecast DM-related events. Higher AUC values indicate better effectiveness in differentiating between DM-positive and DM-negative cases. The AUC values are a quantitative indicator. The performance evaluation of the suggested DL patterns is shown in Fig 6 to Fig 8. The experimental findings show how well three distinct DM information sets perform when assessed using the three DL configurations of ANN, LSTM, and CNN. The accuracy numbers demonstrate the suggested DL patterns' capacity for prediction. Using PIMA-IDD, ANN produced the best accuracy of 98.81%, while LSTM and CNN also produced encouraging accuracy ratings of 97.3% and 94.1%, respectively. Similarly, DDFH-G performs well, attaining an accuracy of 99.1% with ANN, 98.6% with LSTM, and 97.4% with CNN. Lastly, accuracy values of 98.5%, 97.8%, and 96.9% were demonstrated by the IDPD-I, ANN, LSTM, and CNN, respectively. These results comprehensively evaluate the suggested DL patterns' ability to predict DM with Accuracy.

4.2. Discussion

When comparing the DL patterns to the latest ML and DL techniques, the experimental results show a significant enhancement in the Accuracy of DM predictions. The suggested DL framework's early prediction and intervention capabilities can greatly benefit medical professionals. A comparison of ML and DL approaches for DM prediction using various diabetic information sets is presented. Furthermore, CNN and BILSTM, Deep Belief Network, and ANN are examples of DL approaches. The accuracy findings show how well these methods work on diabetes information sets. However, using an DL framework has significantly improved the accuracy of DM prediction. Additionally, utilizing DDFH-G, the suggested DL patterns obtained encouraging accuracy of 99%, 98%, and 97%, respectively. The suggested DL patterns, which comprise LSTM (97%), CNN (94%), and ANN (98%) using PIMAIDD are shown to have the most promising accuracy out of all the patterns. Lastly, utilizing the IDPD-I, DL obtained 98.4%, 97.8%, and 96.9% accuracy for ANN, LSTM, and CNN, respectively. This implies that it has been shown that the suggested DL system is very effective for DM prediction tasks. Furthermore, with accuracies ranging from 76% to 88%, conventional ML patterns including RF, NB, RF, SVM and LR have done rather well. It is evident that while traditional patterns for ML, such as RF, LR, and SVM, attained a respectable degree of accuracy, they could not match the DL patterns' greatest accuracy levels. Furthermore, compared to current methods, DL techniques produced categorization results with dependable accuracy. Early DM prediction is crucial, and achieving a greater accuracy rate in DM prediction is unquestionable. For DM prediction, the researchers have therefore put forth several ML and DL techniques, including BiLSTM, ANN, Deep ANN and DBN, all of which have shown competitive performance. Specifically, CNN and BILSTM exhibited high accuracy is 92.31% and 94.0%. These findings demonstrate how well DL patterns can identify complex structures in electronic medical information.

4.3. Implications

Developing a new DL framework for DM prediction exceeds the capabilities of current leading methods, marking the study's key theoretical contribution. These patterns perform better than most other patterns because of their distinct architecture and particular combination of learning techniques. This reduces the possibility of over-fitting and improves DL's generalization skills, allowing it to gather useful information from electronic medical records and produce more precise clinical forecasts and DSSs. The DL seeks to find novel patterns and characteristics associated with DM in electronic medical information to help doctors and specialists make an initial diagnosis of diabetic patients. Because it enables early prediction and action, this can greatly benefit the medical community. By improving early prediction and individualized treatment plans, the enhanced DL can be included in clinical decision support systems, improving patient outcomes and lessening the pressure on healthcare institutions.

4.4. Limitations and future research

Notwithstanding the advantages of the suggested DL, we also recognize that there are information quality issues and the complexity, validation, and generalization of other illnesses. The quality of the input information has a significant impact on prediction accuracy. Incomplete or inaccurate medical records can impact the prediction's performance and result in predictions that are not reliable. Future studies will concentrate on developing a revolutionary automatic clinical decision-making system for DM prediction and prevention that uses reinforcement learning approaches to overcome these limitations. We intend to create a smart system based on reinforcement learning to provide T1D and T2D patients with individualized dietary and treatment recommendations. Other chronic diseases can be predicted by extending the suggested DL. We also intend to validate the suggested DL using other diabetic information sets. To further improve the DM prediction system that helps health organizations, hybrid approaches that combine the advantages of DL and conventional techniques can also be investigated in the future [47]. For example, more computationally efficient design of DL algorithms can be achieved by applying additional optimization techniques.

5. CONCLUSION

In this work, we investigated the potential of DL to predict diabetes using a clinical decision support system. CNN, LSTM, and ANN were among the DL patterns combined in the suggested DL. The technique with meta-patterns was implemented by combining the predictions of DL approaches. To predict diabetes across two classes (DM-positive and DM-negative) and three classes (diabetic, non-diabetic, and pre-diabetes), respectively, this study presented a novel DL technique for binary categorization and multi-class categorization. Small, big, and multi-class diabetic information sets was used to train the suggested DL. The key variables from these information sets were extracted using the EDT approach for variable selection. This makes it possible for the pattern to pinpoint crucial elements for improving prediction accuracy and managing over-fitting when the DL is being trained. Major assessment methodologies, including F-score, MCC, ROC/AUC, sensitivity, specificity, Accuracy, and precision, were used to assess the DL. The ANN achieved superior performance compared to the other proposed patterns, with accuracy rates of 99.51%, 98.81%, and 98.45% on the three information sets respectively. DL's potential for clinical use is highlighted by its results in ANN. The results indicated that diabetes can be effectively predicted using the predictive DL method. The LSTM and CNN patterns exhibited impressive performance, achieving high Accuracy, precision, MCC, ROC/AUC scores, and sensitivity. This research enhances DL's ability to generalize and minimizes the risk of over-fitting, leading to more accurate clinical predictions for diabetes and other chronic diseases. Future healthcare organizations can benefit from the DL's ability to anticipate a variety of chronic diseases.

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