Enhanced Early Detection of Diabetic Nephropathy Using a Hybrid Autoencoder-LSTM Model for Clinical Prediction

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***Abstract*—Early detection and precise prediction are essential in medical diagnosis, particularly for diseases such as diabetic nephropathy (DN), which tends to go undiagnosed at its early stages. Conventional diagnostic techniques may not be sensitive and timely, and hence, early intervention might be difficult. This research delves into the application of a hybrid Autoencoder-LSTM model to improve DN detection. The Autoencoder (AE) unit compresses clinical data with preservation of important features and dimensionality reduction. The Long Short-Term Memory (LSTM) network subsequently processes temporal patterns and sequential dependency, enhancing feature learning for timely diagnosis. Clinical and demographic information from diabetic patients are included in the dataset, evaluating variables such as age, sex, type of diabetes, duration of disease, smoking, and alcohol use. The model is done using Python and exhibits better performance compared to conventional methods. The Hybrid AE-LSTM model proposed here attains an accuracy of 99.2%, which is a 6.68% improvement over Random Forest (RF), Support Vector Machine (SVM), and Logistic Regression. The findings demonstrate the power of deep learning in detecting DN early and accurately and present a novel tool for proactive disease control among diabetic patients.**

Keywords*—Autoencoder-LSTM; Diabetic nephropathy; early disease detection; machine learning; clinical data analysis; hybrid models

I. Introduction

Diabetes is a serious issue for general health. Approximately millions of individuals worldwide suffer with diabetes. Globally, there were 463 million diabetics in 2019, and 700 million are predicted by 2045 [1]. Kidneys, eyes, nerves, skin, and heart can all be harmed by it. The most frequent cause of kidney failure in diabetic people is diabetes nephropathy (DN)[2]. DN patients have surged in tandem with the exponential rise in the frequency of diabetes patients. Consequently, the mortality rate of DN has also gone up. Consequently, it's critical to identify DN patients early in order to prevent the related illnesses. Early detection of DN by diagnostic markers is crucial, as it might impede the loss of renal function and mitigate unfavorable consequences. Micro albuminuria, or the presence of minute quantities of protein albumin in the urine, is recognized as the first indication of the onset of diabetes mellitus. On the other hand, a significant amount of renal damage has been documented to occur even prior to the development of micro albuminuria [3]. A number of complicating factors, including exercise, urinary tract infections, acute illnesses, and heart failure, are linked to albuminuria. Moreover, it has been documented to transpire in the urine of individuals following a regular diet, suggesting that albuminuria is not a reliable indicator for precisely forecasting diabetic kidney disease.

Elevated blood vessel glucose levels are critical to the development of diabetic neuropathic pain. Through an excess of reactive oxygen species (ROS), hyperglycemia causes problems with metabolism in mitochondria and the sugar metabolic pathway [4]. Glycation at high glucose concentrations creates adducts that are covalent with plasma proteins. AGEs, or advanced glycation end products, are one of these events and a significant risk factor for complications from diabetes. Podocytes are an essential component of the glomerular filtration barrier, and they may become aberrant after extended exposure to hyperglycemia. The loss of podocytes is one of the earliest glomerular morphologic alterations, and it is essential to the emergence of DN. Clinically speaking, diabetic individuals with DN have proteinuria and decreased kidney function [5]. DN patients can be maintained with blood pressure and glucose management, but many eventually develop renal failure [6]. Therefore, it will be crucial to comprehend the pathophysiology of DN and create novel biomarkers in order to diagnose DN early. Nowadays diagnostic methods for conditions such as DN present various issues that stem from the reliance on clinical sign and/or biomarkers associated with the late stage of the disease. Such reliance can lead to lack of timely treatment/fulfillment of early milestones/health concerns prevention. Also, there are other diagnostic tests whereby biopsy or blood samples are taken and this causes discomfort or is risky and therefore people are discouraged from frequent checkup. These traditional tools may also be insensitive and non-specific and therefore result in false positive or negative results as the traditional biomarkers may not necessarily mimic the early stages of DN. Secondly, certain diagnostic techniques for instance, specialized imaging may be expensive as well as unavailable in most health facilities and more so in developing countries. There is also a certain degree of subjectivity and variability in diagnostics, this is due to the facts that using subjective methods such as clinical impression or an interpretation of test results the results of the diagnostics can be significantly different depending a healthcare provider's experience.

However, current approaches of advanced diagnostic targets do not seem to have a perfect solution to these

challenges; but, the machine learning (ML) models for medical diagnostic are a potential solution to these challenges [7]. The large volume of complex data gathered in every healthcare practice may be analyzed by an ML model to search for patterns that can be missed by a clinician and that can predict DN and its development even before its first clinical manifestation. They also enable constant, non- invasive monitoring through trailing with wearable devices or EHR, which offer an instant read out of the patient's status. Through utilization of big and heterogeneous databases, it is possible to enhance the diagnostic precision and increase the abilities to distinguish between the diseases that are similar and make more accurate prognosis depends on the individual parameters of the patient [8]. Due to scalability and cost implications, ML models provide coherent diagnosis support irrespective of the healthcare facility, hence the need to employ specialized personnel and equipment especially in setting with limited accessibility to the same [9]. Moreover, a model for prediction based on the DN-related parameters must be created. As an automated model construction method, ML-based approaches have taken the lead in the domains of medical imaging, human interaction, and healthcare. ML-based approaches are mainly employed for early identification and prediction/detection of different healthcare conditions, such as diabetes, carcinoma, and kidney damage, in order to increase classification accuracy. The popularity of ML-based approaches has skyrocketed recently. While a significant amount of research has been conducted and newly created ML-based algorithms have garnered attention, the hunt for ways to improve classifier accuracy has never ended [10]. Thus, one of the key elements that will determine how accurate the classifiers are is the selection of an ML-based model. Over many years, researchers have worked very hard to create useful models to enhance precision of categorization. Medical data categorization remains a difficult problem for machine learning-based classifiers, despite the quick advancement of computational intelligence theories.

Furthermore, with the use of ML models, patients can be diagnosed and treated, based on the specific characteristics like genetics, lifestyle, and presence of a variety of diseases. It can also take disparate data from clinical, genomic and environmental domains and make application of the data to provide new and unique insights into the disease causes, drivers and therapeutic outcomes. Taken together, the existing diagnostic practices have certain drawbacks, whereas the machine learning models open a vast range of possibilities that help improve the detection rates at the initial stages, refine the diagnostics, and transform the healthcare services to be more individualized and easily scalable. These ML-based classifiers, however, are still unable to categorize patients accurately due to their unsatisfactory accuracy. But the goal of this work is to use ML-based approaches to create a prediction model based on the risk variables associated with DN. Feature extraction techniques also identify DN risk variables. Here are four primary contributions of the proposed Hybrid Autoencoder-LSTM model for detecting Diabetic Nephropathy (DN).

- The study introduces the use of an Autoencoder for effective dimensionality reduction, which helps in isolating essential features. This step not only simplifies the dataset but also enhances the model's ability to focus on the most relevant information, thereby improving the overall accuracy and interpretability of the model.
- The combination of Autoencoder and LSTM architectures leverages the strengths of both models. The Autoencoder efficiently handles feature learning and noise reduction, while the LSTM network excels at sequential data analysis. This hybrid approach provides a comprehensive framework for DN detection, offering improved prediction accuracy compared to conventional machine learning models.
- The study provides a comprehensive performance evaluation of the AE-LSTM model, including metrics such as reconstruction loss, classification accuracy, precision, recall, and F1-score. The comparative analysis with other methods highlights the AE-LSTM model's superior performance and its potential advantages in handling complex, high-dimensional healthcare data.
- The use of advanced optimization techniques like the Adam Optimizer, along with appropriate loss functions (MSE for the Autoencoder and binary/categorical cross-entropy for the LSTM), ensures efficient and effective training of the model. This contributes to achieving high performance metrics, such as accuracy and precision, in the detection and diagnosis of DN.

The rest of the contents are listed in the following order. An introduction is given in Section I. The literary portions are shown in Section II. This is the problem statement found in Section III. The hybrid model-based modeling and analysis approach is covered in Section IV. The results are compiled and the performance indicators are shown in Section V. Section VI offers further research and a conclusion.

II. Related Works

Kim et al. [11] developed the initial stages diagnostic biomarkers to detect DN as a means of DN intervention. In the investigation, Zucker diabetes-related fatty rats were used to model the DN phenotype. The results showed that in addition to significantly raised serum levels of blood glucose, BUN, and creatinine, DN rats also exhibited severe renal injury, fibrosis, and microstructural changes. Moreover, the urine of DN rats emitted higher concentrations of kidney injury molecule-1 (KIM-1) and neutrophil gelatinase-associated lipocalin (NGAL). New DN biomarkers were discovered by transcriptome analysis. Moreover, they were discovered in DN patients' urine. The findings showed that the onset of diabetic nephropathy was associated with an up-regulation of CXCR6 expression levels in rat urine, renal tissue, and clinical samples. In essence, our discovery offers direct evidence that CXCR6 was elevated in urine as diabetic nephropathy progressed. The results therefore imply that the CXCL16/CXCR6 pathway may be involved in the development of end-stage renal disorders. Using these results, a unique therapeutic approach to treating renal fibrosis can be developed. It is unclear, therefore, how CXCR6 contributes to the development of diabetic nephropathy. To investigate the underlying process in DN, more research is needed.

A new deep learning model is presented by Singh et al. [12] for the early identification and prediction of chronic kidney disease. This project aims to construct a DNN and evaluate its performance relative to other state-of-the-art machine learning techniques. Any information that were absent from the database during testing were substituted with the mean of the relevant attributes. The optimal parameters of the neural network were then established by configuring them and carrying out several trials. The most important characteristics were selected using Recursive Feature Elimination (RFE). Hemoglobin, specific gravity, serum creatinine level, blood vessel count, albumin, packed cell volume, and high blood pressure were important features in the RFE. To categorize them, machine learning models were given a range of attributes. The technique could be useful to nephrologists in detecting CKD. The model's testing on limited data sets was one of its limitations. In the future, large amounts of more complex and representative CKD data will be gathered to determine the severity of the illness and enhance the model's performance.

The goal of the Kang et al. [13] study was to create and assess a DL model that uses retinal fundus images to identify early renal function deterioration. This retrospective analysis includes patients who had color fundus imaging and renal function testing. From the images, a DL model was built to identify renal impairment. An estimated rate of glomerular filtration of less than 90 mL/min/1.73 m2 was considered early renal function impairment. The AUC and ROC curve were used to assess the performance of the model. For the whole population, the model's AUC was 0.81.Using retinal fundus images, the deep learning algorithm in this work makes it possible to identify early renal function deterioration. Only for individuals with increased blood HbA1c levels, the model demonstrated greater accuracy is the drawback.

A unique ML model for CKD prediction was put out by Arif et al. [14] It included a number of pre-processing stages, selection of features, a hyper parameter optimization method, and ML algorithms. In order to tackle the difficulties encountered with medical datasets, we utilize sequential data scaling along with robust scaling, z-standardization, and min-max scaling, as well as iterative imputation for missing values. The Boruta method is used for feature selection, while ML algorithms are used to create the model. The model performed exceptionally well with good accuracy when assessed on the UCI CKD dataset. The method, which combines novel pre-processing techniques, the Boruta feature selection, the k-nearest-neighbour algorithm, and grid-search cross-validation (CV) for hyper parameter tuning, shows promise in improving the early identification of CKD. This study emphasizes how machine learning approaches might enhance therapeutic support networks and lessen the influence of ambiguity around the prognosis of chronic illnesses. The study's primary drawback was its dependence on a single dataset the UCI CKD dataset, which has a significant number of missing values.

By combining a number of easily accessible clinical variables with retinal vascular measures, Shi et al. [15] developed a new DKD diagnostic approach for individuals with type 2 diabetes. Xiangyang Central Hospital's 515 consecutive type-2 diabetes mellitus patients were included. Patient diagnoses of DKD were used to separate patients into two groups: the training and testing set, with a random seed of 1. While the ML was developed using data from the training set, the MLA was validated using data from the testing set. The model's performances were assessed. When compared to other classifiers, the random forest classifier-using MLA performed at its best. Verified, the accuracy was 84.5%. Retinal vascular alterations may help in DKD screening and identification, according to a novel machine learning method for the disease's diagnosis that was constructed using fundus images and eight readily accessible clinical data. The sample used in the study limits the generalizability of the model to broader and more diverse populations.

In the Zhang et al. [16] study, membranous nephropathy was diagnosed by combining deep learning techniques with blood and urine Raman spectra. Following baseline correction and data smoothing, the training set was supplemented with Gaussian white noise at varying decibel levels to enhance the data. The assessment results of the ResNet, AlexNet, and GoogleNet models for membranous nephropathy were then obtained by feeding the amplified data into them. As per the experimental findings, AlexNet emerged as the most proficient deep learning model for both samples. All three models were able to attain an accuracy of 1 in classifying serum data pertaining to patients with membranous kidney damage and the unaffected group, and above 0.85 in differentiating urine data. The test results described above show how powerful deep learning methods can be when used in combination with serum- and urine-based Raman analysis to accurately and quickly diagnose individuals with membranous nephropathy. The limitation is the high accuracy reported would not be achievable in a more diverse and unstructured clinical environment, where data quality and characteristics can vary widely.

Several limitations to the application of ML and DL models in diagnosing kidney related diseases are presented in the reviewed literature. A typical issue is that the number and types of datasets are often limited and often only a single dataset may be used in developing the model and hence the range and the variety of data populations might not be very wide. Also, some research works' drawbacks were associated with data quality and data loss, where data missing was a major issue that came up to a need of imputation or data augmentation. In this case, the models' applicability for different conditions or groups may be limited since the improvement was noted only in patients with raised HbA1c levels. In addition, the very high levels of accuracy found in this and similar studies, again in precise experimental settings, may not be highly representative of the variability and range of clinical datasets, again influencing the model's results in the clinic. Lastly, the strong focus on concrete characteristics that include the use of retinal fundus images or Raman spectra may also suggest the models' drawback in conditions when such data is irrelevant or missing.

III. Problem Statement

DN is categorized as a usual complication of diabetes the result of which may culminate into end-stage renal disease if not diagnosed. The current diagnostic processes that are based on biomarkers and imaging oftentimes diagnose DN at the most severe stages, thereby limiting the interventional and treatment

procedures[16]. The reason why diagnosis is usually made later in the course of DN is partly attributed to the slow and progressive nature of kidney damage in such patients when conventional techniques are used. Thus, addressing the mentioned problem of the shortage of diagnostic techniques, this paper proposes and compares an Autoencoder-LSTM model for the diagnosis of diabetic nephropathy. The proposed hybrid model intends to integrate the autoencoder' s ability of decreasing the dimensionality of data and finding hidden beneficial aspects as well as the feature superior to recognizing temporal relations in the series data which is LSTM network. Using this model for Clinical and patient data analysis, the study aims at finding the feeble signs of DN that are masked normally. The latter goal is to create a less invasive and more precise diagnostic tool for early identification of DN, which in turn will allow for proper treatment to be given, enhance the patient's outcomes, and perhaps decrease the likelihood of transitioning to the more significant level of nephropathy.

IV. Proposed Methodology of Hybrid Autoencoder-LSTM model for Early Detection of Diabetic Nephropathy

For the detection of DN, this study uses the Hybrid Autoencoder-LSTM model that uses feature learning and temporal pattern analysis. The methodology encompasses several key stages: acquisition of data as well as preparation, designing the model as well as learning rate schemes for the model. First, the input dataset is formed by using clinical data of patients with diabetes, retrieved from prior researches. This dataset must then be cleaned to deal with any issues pertaining to missing values as well as the normalization of its features, and where needed, feature selection. The Autoencoder component accomplishes the Dimensionality reduction of the input data for the aim of segregating necessary features from the noisy ones. These condensed features are then passed to the LSTM network which learns on the sequences to identify relationships with time of DN. The connection of these two parts is to improve the accuracy of the model through the application of the advantages of the architectures of deep learning. When training the model, several loss functions are used; MSE for autoencoder and binary or categorical cross-entropy for LSTM based on the classification task. The Adam Optimizer helps in achieving the steady state for the value and the model goes through epochs for the optimization. The DN diagnosis and accurate identification of patients with the condition is sought through this integrated, extensive methodological approach that aims to enhance the optimality of the model. It is demonstrated in Fig. 1 given below.

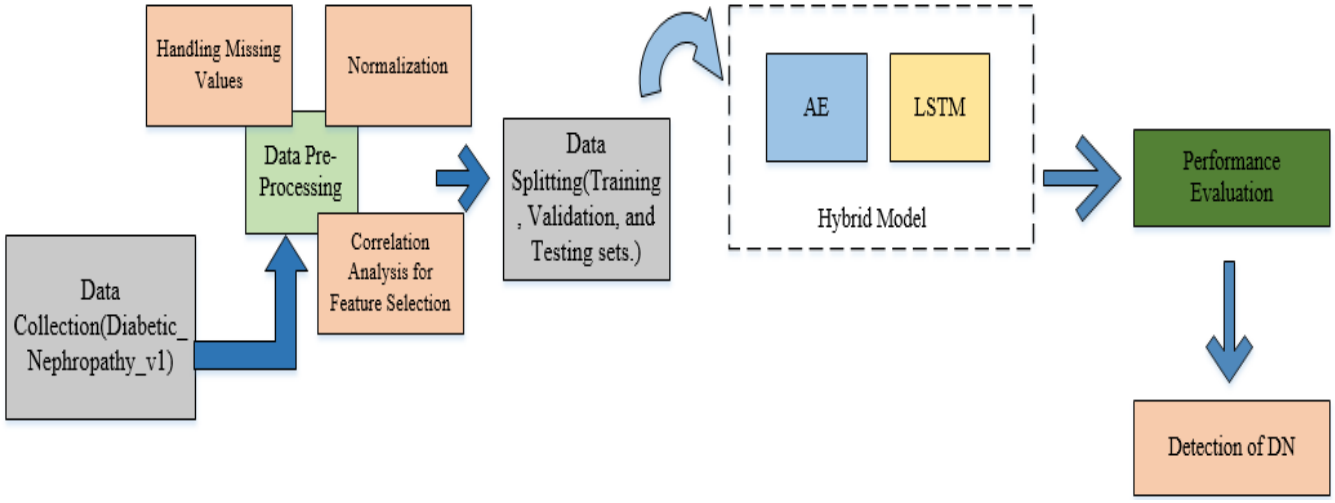

Fig. 1. Hybrid AE-LSTM model block diagram.

A. Dataset Collection

The dataset which is "Diabetic_Nephropathy_v1" contains clinical and demographic data of DN and related diseases[17]. The dataset consists of 767 patient records. These variables involve the patient's sex, age, type of diabetes, duration of the disease, DR and DN, and smoking and drinking habits; as well as glucose levels, HbA1c, body mass index (BMI), and blood pressure. These parameters include height, weight, body mass index, systolic blood pressure, diastolic blood pressure, glycated haemoglobin, fasting blood glucose, blood triglycerides, C-peptide, total cholesterol, high-density lipoprotein cholesterol and low-density lipoprotein cholesterol respectively. More so, details on medication use including insulin, metformin, as well as lipid-lowering drugs among others are incorporated. These variables are expected to be used for analyzing the associations between them and the development of diabetic nephropathy, the results of which are planned to be used for developing better predictors of the disease and increasing the general knowledge on the subject.

B. Data Pre-processing

1) Handling missing values: It is essential to manage the cases of missing values because, for example, they affect the accuracy of a machine learning model, as well as the results of making predictions. It is recommended to impute the missing values with the median or mode of the particular columns for numerical variables since median imputation is less influenced by outliers than the mean imputation. For categorical features it is optimal to use simple form of imputation for the missing data, which is to replace it with the most frequently used category. This approach ensures that the employed dataset is also strong and minimizes the chances of a mistake being made on the

model. Feature selection was performed using correlation analysis and domain knowledge to identify the most relevant clinical variables, discarding those that were redundant or had low significance for DN.

2) Normalization: Most preprocessing acts like standardization on the input variables are significant for models like Autoencoder and LSTMs as they are dramatically affected by the scale of input variables needed. This process helps to make all features at a similar scale to make better and more accurate models and avoid instabilities in the model. Min-Max Scaling standardizes the features to a range of 0 to 1, which is a good practice in terms of equal scaling of features and can contribute to the enhancement of the model's performance and convergence. The formula for Min-Max Scaling is

$$Y_{Scaled} = \frac{Y - Y_{min}}{Y_{max} - Y_{min}} \quad (1)$$

Where Y is the original feature value, Y_{min} is the minimum value of the feature, and Y_{max} is the maximum value. This normalization ensures that all features contribute equally to the model, which is crucial for algorithms sensitive to feature scaling.

3) Correlation analysis for feature selection: Begin by examining the correlation between each feature and the target variable, which in this case is diabetic nephropathy. This analysis helps in identifying features that have a strong relationship with the target variable. Features that exhibit high correlation with the target are likely to provide significant predictive value. For example, if one use correlation coefficients or statistical tests to quantify these relationships. Features with low or negligible correlations can be discarded to simplify the model and improve its interpretability.

C. Integration of Hybrid AE-LSTM Model for the Detection of Diabetic Nephropathy

A multilayer neural network called an auto encoder produces desirable outputs that are similar to inputs with less modification—that is, results that are similar to inputs that have some reconstruction error [18]. Generally, autoencoder is applied in dimensionality reduction since it provide efficient dimensionality reduction in cases of large and more specifically medical data sets due to its high dimensionality reduction rate yet efficiency in preserving important features of the data. In contrast to model like PCA it is capable of learning local non-linear manifold structure of data and thus is more appropriate for high dimensional clinical records. Further, it aids in the reduction of noise to ensure the model concentration on the most important characteristic which is important for tasks such as DN development prediction. It is the same case with autoencoder as they also function in an unsupervised way, which can be useful when processing big data with little or no labels at all. The auto encoder encrypts the input and then utilizes unsupervised learning to reconstruct or decode the output.

The encoder, reconstruction loss, bottleneck, and decoder are the four main parts of a generic auto encoder. The encoder helps to remove characteristics from the input by shrinking the data into an encoded form. The bottleneck layer is the layer that has the fewest characteristics and compressed incoming data. The decoder makes sure that the input and output are the same by helping the model to rebuild the result from the encoded representation. The last metric used to evaluate the decoder's performance and determine how closely the output resembles the original input is Reconstruction Loss.

Additionally, training is done using back propagation, which further minimizes reconstruction loss. This minimum loss serves as an example of the goal that AE aspires to accomplish. The input y that the encoder will compress Eq. (2).

$$y = E(x) \quad (2)$$

Decoder will make an effort to replicate the input. D as x' = D (E (x)).

$$loss(E, D) = \frac{1}{n}\sum_{j=1}^{n} x^i - D(E(x^i)))^2 \quad (3)$$

In this instance, the reconstruction loss equals the difference between the encoded and decoded vectors. The MSE is one method for calculating the reconstruction loss. It is stated in the above-mentioned Eq. (3). The hybrid AE-LSTM's architectural diagram is shown in Fig. 2.

LSTM was created using sophisticated recurrent neurons. In an LSTM, every recurrent neuron may be thought of as a single cell state [19]. For the temporal analysis, the study use LSTM since it is capable of processing sequential data and it can capture long term dependencies, this is because tracking the health status of the patients require tracking their status over a period of time. The LSTMs are built in a way that they do not suffer from vanishing gradient problem and this makes the model to retain information from the previous time step, which is extremely important when predicting medical conditions. For hyper-parameters, learning rate, batch size and number of hidden units were appropriately selected from cross-validation in order to achieve high learning rate but low over-fitting. These choices were further optimized to make sure that the model does well as far as the training data is concerned as well as the unseen data. An LSTM determines its current state by using its data from the previous state, much like a conventional RNN does. The LSTM uses three gates to control the current neuron: the forget gate, update gate, and output gate.

A LSTM can connect current data with historical knowledge. An LSTM is coupled to three gates: an output gate, an input gate, and a forget-about gate. The new and last states are represented by the symbolsQ_t andQ_{t-1}, respectively for the input, and p_t and p_{t-1} for the existing and prior outputs.

Eq. (4), Eq. (5) and Eq. (6) explain the LSTM input gate idea.

$$j_t = \sigma(\mathrm{Z}_j \cdot [z_{t-1}, y_t] + b_j) \quad (4)$$

$$\tilde{Q}_t = \tanh(Z_j \cdot [p_{t-1}, \mathrm{p}_t] + \mathrm{b}_j) \quad (5)$$

$$\mathrm{Q}_t = f_t \mathrm{Q}_{t-1} + j_t \tilde{Q}_t \quad (6)$$

To decide which of the data points y_t and p_{t-1} should be added, where Eq. (4) use a sigmoid layer to filter them. Combining the long-term storage data,$\tilde{Q}_t$ with the present moment informationQ_{t-1}, results in Eq. (6). $\tilde{Q}_t$ Displays a tanz

output, whereas $Z_j$indicates a sigmoid results. The bias of the LSTM input gate is denoted by $b_j$in this instance, while Z_j denotes the weight matrices. Consequently, because of the LSTM's forget gate, the dot product and sigmoid layer may pass information selectively. A certain probability is used to decide whether to delete relevant data from a previous cell.

Use Eq. (7) to determine whether to preserve relevant data from an earlier cell with a particular option. Z_f Represents the weighted matrix b_f the offset, and σ the sigmoid term.

$$f_t = \sigma\left(Z_f \cdot [c_{t-1}, y_t] + b_f\right) \quad (7)$$

The states needed for the following equations are determined by the output gate of the LSTM Eq. (8) and Eq. (9) states provided by the inputs y_t and p_{t-1} .After the final output is produced, it is multiplied by the state decision vectors Q_t that transmit new data via the tanz layer.

$$R_t = \sigma(Z_o \cdot [P_{t-1}, y_t] + b_o) \quad (8)$$

$$p_t = R_t \tanz(Q_t) \quad (9)$$

When using the Autoencoder-LSTM, the transition from the Autoencoder to LSTM is carried out systematically with regards to features and sequence. First, the bottleneck layer of the autoencoder, which contains the compressed and the higher level features of the input is used as input to the LSTM network. This transfer of feature favours LSTM to process data that has undergoes post processing hence removing noise and unnecessary details. Since these are the features passed to the LSTM network, the LSTM makes its computations in a sequential manner which is vital in the learning of temporal characteristics and structures that are useful in diagnosing Diabetic Nephropathy (DN). The last state of the LSTM network is used for the purpose of predicting the probability of DN or for distinguishing between the patients who have DN and those who do not have DN based on temporal pattern learning integrated into the model from the sequences.

The integration of the hybrid model has the following advantages. Thus, by reducing the dimensionality of input data, the first stage of the autoencoder employs a K value to facilitate the LSTM's identification of relevant patterns to the task. This organizational improvement make the model lighter and thus enhances its functionality. Second, the temporal features as processed by the LSTM show important sequential characteristics that can indicate early signs of DN that are not observed by simpler models, allowing for a better understanding of the diseases' evolution.

Optimizations of the autoencoder and LSTM network is done during the training phase so as to get the best performance. In the autoencoder, mean squared error (MSE) loss function is used to minimize the errors in data reconstruction; this way, only the noise is eliminated, and important details are preserved. With relation to the LSTM network, the selection of the loss function is contingent upon the nature of the classification; in cases where the classification is categorically classified as several classes, as opposed to binary cross entropy, which is utilized in cases where the classification is either true or false, the binary cross entropy loss function is employed. For optimizing weights in the model and to make enhancements, specialized algorithms like Adam is used. The training process takes several epochs; the used number of epochs and the batch size is defined depending on the data volume and available computational power. Syllable stress and domains' size tuning makes sure that the model properly learns and functions well in regard to new data.

This detailed approach will assist in established structure to enhance the Autoencoder-LSTM model, by having dimensionality reduction then LSTM in achieving accurate Diabetic Nephropathy prediction. Fig. 2 illustrates the architecture of proposed hybrid AE-LSTM is given below.

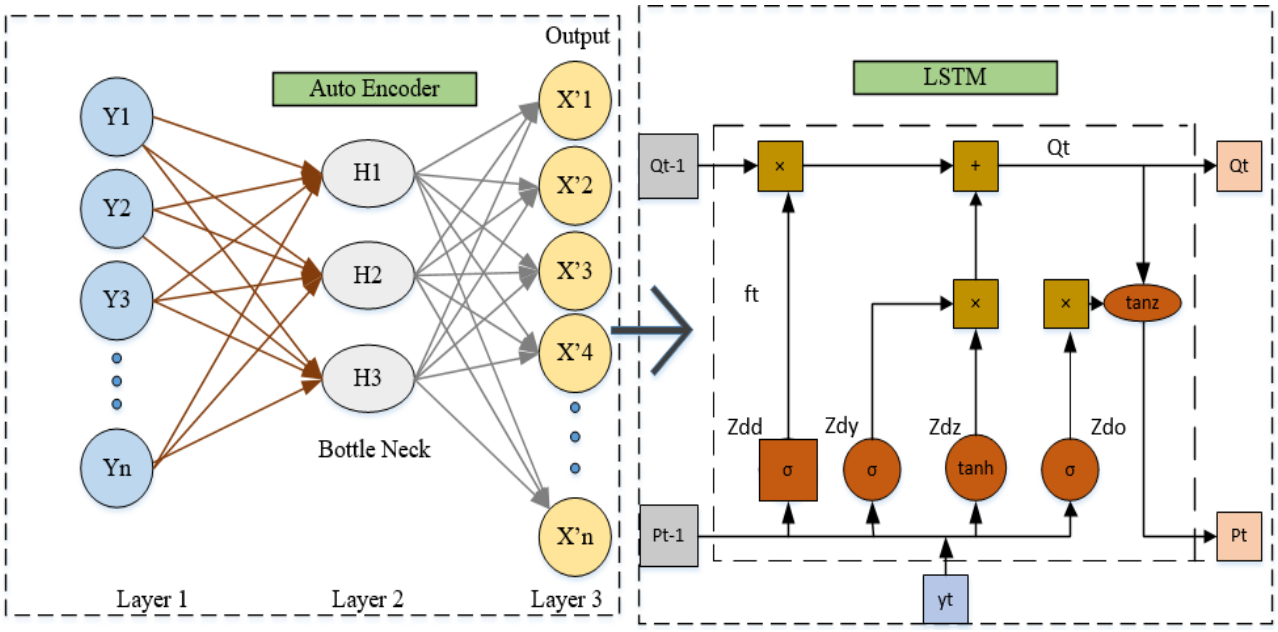

Fig. 2. Hybrid AE-LSTM architecture.

V. Results and Discussion

The results section of the study, the authors provided distilled information about the results from the predictive modeling and disease detection study using the proposed Hybrid Autoencoder-LSTM model. The accuracy of the presented model was compared to several simple and complex models based on the sub belongs and more traditional machine learning as well as deep learning techniques. The performance evaluation was based on the model's metrics as the model successfully predicted the occurrence of DN. The methodology employed data from clinical records and qualified the model implementation and analysis on a Windows 10 environment using python programming language. In line with such findings, the model excels in the identification of the DN onset; this is due to the utilization of the autoencoder dimensionality reduction and the LSTM network with the capability of recognizing temporal patterns. The following variables were used in a measure of the efficiency and predictive capability of the specified model.

A. Auto Encoder's Reconstruction Loss

Reconstruction Loss is one of the ways of evaluating a model particularly an autoencoder to whether compress the data and then decompress it to get the preservation quality. It measures the degree of distortion of output signal in comparison with the input signal end product. It is then computed by comparing the two, sometimes via calculating MSE or Binary Cross-Entropy, etc. Hence, reconstruction loss defines how much information has been lost during the encoding and decoding process, and lower value of it would mean better reconstructions and therefore a better performance of the model in terms of preserving important features of the input data. Eq. (10) expressed it.

$$\text{Reconstruction Loss} = \frac{1}{N}\sum_{i=1}^{N}(x_i - \hat{x_i})^2 \qquad (10)$$

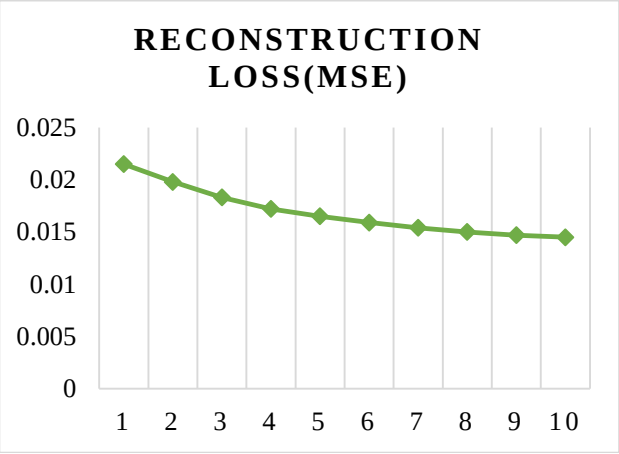

Fig. 3. Reconstruction loss of the proposed AE-LSTM approach.

The Fig. 3 will indicate the reconstruction loss in the Autoencoder, which should decrease over time, thus demonstrating the Auto encoder's ability to learn how to encode and decode the data. The gradual reduction in MSE shows that the present Autoencoder component continues to reduce the dimensionality of the data and retain crucial characteristics efficiently.

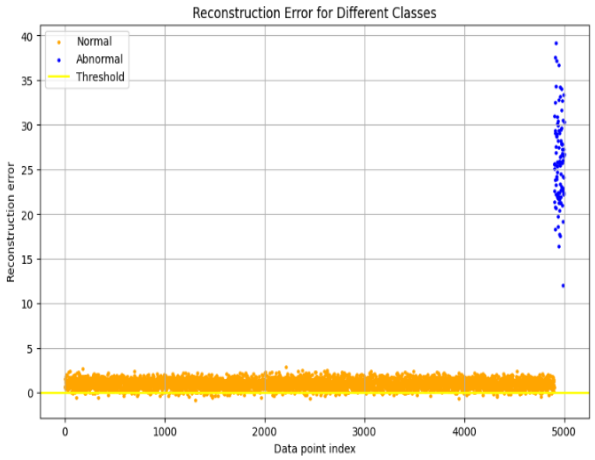

Fig. 4. Reconstruction error for different classes.

Fig. 4 shows the reconstruction errors for normal and abnormal classes, with normal data points clustered around a value of 1 and abnormal points centered around 25. The threshold line, set at 0, visually separates the error ranges for both classes. Fig. 5 shows the histogram of reconstruction error is given below.

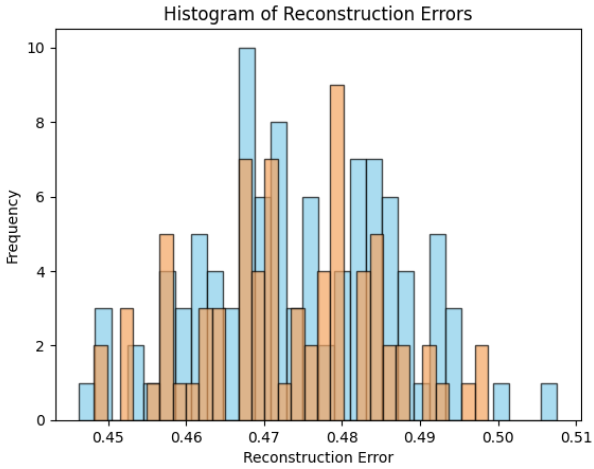

Fig. 5. Histogram of reconstruction error.

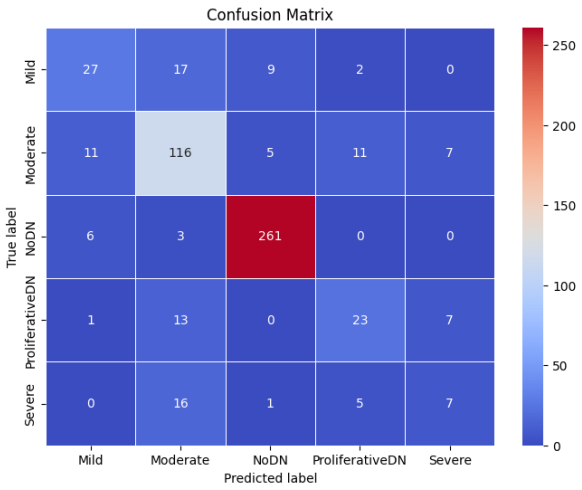

Fig. 6. Confusion matrix.

Fig. 6 shows a heat map of the confusion matrix, displaying the performance of a classification model across five categories: It includes Mild, Moderate, No DN, Proliferative DN and Severe. The diagonal values are the correctly predicted patterns giving high accuracy for some of the top categories such as "No DN" (261 instances correctly classified). Other discrepancies such as the 17 Mild examples classified as Moderate as well as the 16 Severe specimens also classified as Moderate can also be observed from off- diagonal values. Different colors define importance of the data and stress on the distribution of errors and correct predictions.

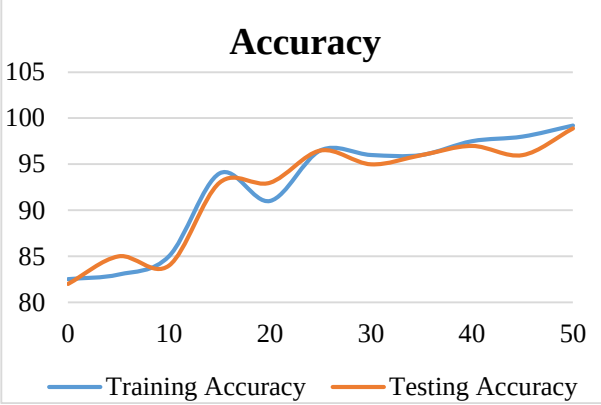

Fig. 7. Training and testing accuracy of the proposed AE-LSTM approach.

Fig. 7 shows that the performance metrics indicating the increase in model's ability to identify relevant patterns for DN detection have escalated exponentially. Thus, it is not surprising that the accuracy recorded during this study was a phenomenal 99.2%% shows that the model is very well trained and is in condition to be able to make sound predictions with the help of encoded features and temporal data. The training accuracy graph shows them gradually rising up to a certain point proving that the model gains better and better understanding of the training data set during the training process. The testing accuracy curve is also smooth and similar to the training accuracy which might depict a good generalization of the model with unseen data. Hence the little difference between the training and testing accuracy shows that the model performed very well by reducing the risk of over fitting as well as improving the robustness of the model.

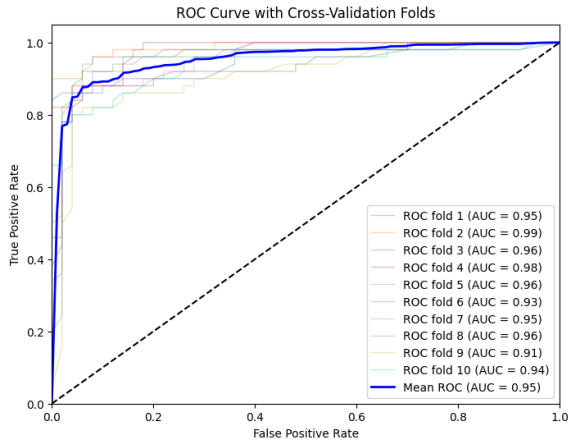

Fig. 8. ROC of the proposed approach.

Fig. 8 shows the ROC curve for the proposed AE-LSTM approach, illustrating how well the model distinguishes between positive and negative cases. The high AUC suggests that the AE-LSTM approach is effective in correctly classifying the data, making it a reliable method for early detection and diagnosis. The results demonstrate that using autoencoder for feature extraction combined with LSTM for classification is a successful strategy in this study.

B. Performance Metrics

1) Accuracy: A method's accuracy is measured by the proportion of test cases it can identify correctly on a certain test set. It is computed as follows in Eq. (11)

$$Accuracy = \frac{RN+RP}{RP+AP+RN+AN} \quad (11)$$

2) Precision: Precision is the ratio of all positively recognized cases to the total number of properly identified positive occurrences by the model. It is quantified in Eqn. (12) is as follows.

$$Precision = \frac{True\ Positives}{(True\ Positives+False\ Positives)} \quad (12)$$

3) Recall: Recall is the idea of the positive cases that the framework correctly detects. It is calculated as follows in Eq. (13).

$$Recall(sensitivity) = \frac{True\ Positives}{True\ Positives+False\ Negatives} \quad (13)$$

4) F1-Score: When there is a large difference in the number of students in one class compared to the other, the F1 score might be helpful. To access the F1 score is apply the Eq. (14) as follows.

$$F1\ Score = 2 \times \frac{(Precision*Recall)}{(Precision+Recall)} \quad (14)$$

When assessing someone, one should consider their F1 score as it provides a useful and unbiased means of gauging recall and accuracy.

C. Consideration with Other ML Approaches

Table I concern the relative comparison of the overall effectiveness of the considered classification algorithms. It can also be seen that, the proposed AE+LSTM method has the maximum accuracy of 99%. 2%, and the EWs are 98. 75%, 98. 92%, with an excellent SW of 98. 79%. These results indicate that the AE+LSTM is not only able to pinpoint the true positive instances but it also keeps a good harmony between Precision and Recall. On the other hand, the Accuracy index of the SVM is fairly impressive recording a 98. Achieves a 96% level of accuracy, solid values for the precision and recall rates, however has a slightly lower F1-score. The same can be said about the Multivariate Logistic Regression method, which also yields the 0.95 of accuracy, but does not rank as high as the AE+LSTM. RF method also behaves well, but has the lowest performance indicators with accuracy equal to 85%, and less TS, PR, and F1-MACV. Thus, it is established that the AE+LSTM approach performs better as compared to the other methods studied for the classification of the data, especially with reference to precision and recall, which are quite

significant signs of how effectively the model is useful for a wide range of data patterns. It is illustrated in Fig. 9. The proposed Hybrid Autoencoder-LSTM model significantly improves early DN detection by enhancing feature extraction and temporal pattern learning. Its ability to reduce dimensionality while maintaining critical diagnostic information ensures higher accuracy than traditional methods. This advancement enables timely medical intervention, improving patient outcomes. The study highlights AI's potential in transforming predictive healthcare with scalable and reliable diagnostic models.

TABLE I. EXISTING METHODS AND SUGGESTED METHOD COMPARISON

Methods	Accuracy (%)	Precision (%)	Recall (%)	F1Score (%)
RF[20]	85	81.60	82.24	81.42
SVM[21]	98.96	91.78	94.08	90.21
Multivariate Logistic Regression[22]	95	92.78	90.82	90.21
Proposed AE+LSTM	99.2	98.75	98.92	98.79

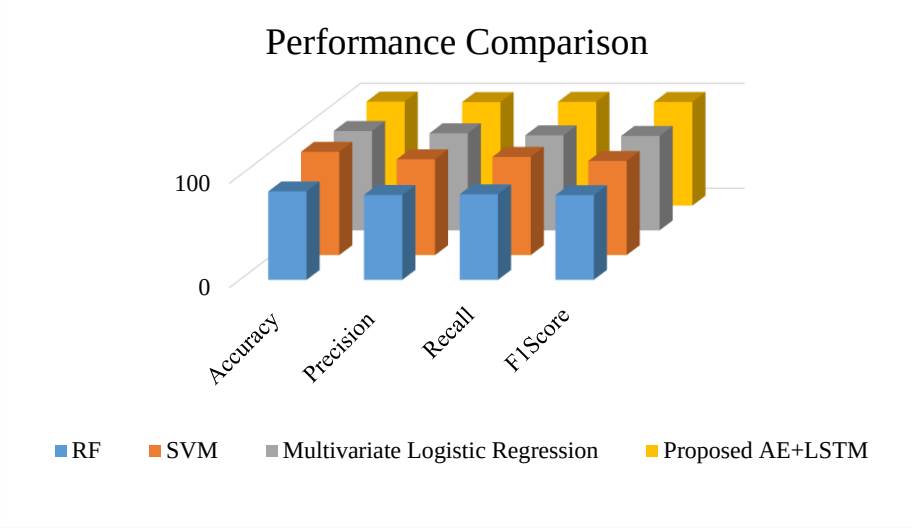

Fig. 9. The performance evaluations of AE+LSTM with conventional approaches.

D. Discussion

The findings showed that one of the better ways of early prediction of DN has been established to be the Hybrid Autoencoder-LSTM model given its efficiency in handling the otherwise elaborate medical diagnoses. Autoencoder whose function here is to decrease the dimensionality of the image data leaving vital features intact and removing background noise; this improves LSTM's ability to learn and identify temporal features essential for DN diagnosis. The LSTM's sequences and the capability to store information from the previous states also enables it to follow the advancement of DN in time. Compared to other classical machine learning systems like RF[20], support vector machines[21], and logistic regression[22], this hybrid model has better result. This benefit derived from Autoencoder dimensionality reduction becomes very useful in helping LSTM isolate on the most significant features, thus lowering the levels of computationally intensity and enhancing model analyzability. The reduction in reconstruction loss over time reflects the autoencoder' s capability to efficiently compress and reconstruct the data while preserving important features. This capability is crucial for enhancing the LSTM's performance by focusing on relevant temporal patterns without being overwhelmed by irrelevant data. The successful reduction in reconstruction errors, particularly the distinction between normal and abnormal classes, further validates the effectiveness of the autoencoder in filtering out noise and emphasizing critical features. Such findings imply that deep learning architectures are more valuable for the intricate medical diagnosis. In a clinical sense, the predictability of DN would definitely alter decisions that are made on a patient as this would enable the clinicians to prevent or at least delay the occurrence of the disease since there would be time to plan on how to handle the situation. Since the proposed model has achieved good values for precision and recall, it means that the identified patients might indeed be at high risk of developing DN, and therefore, timely intervention might help improve the patient's condition. The Hybrid Autoencoder-LSTM performs efficiently in facilitating early Diabetic Nephropathy (DN) prediction through dimensionality reduction and temporal pattern discovery. Autoencoder removes noise and retains core features, improving LSTM's potential for DN progress tracking. Its accuracy is superior compared to RF, SVM, and Logistic Regression with reduced complexity. The decrement in reconstruction loss reflects its optimization in feature extraction, which makes it perform classifying tasks with better efficiency. High recall and precision values validate its feasibility for actual clinical use, allowing for prompt interventions to enhance patient outcomes.

VI. CONCLUSION AND FUTURE SCOPE

In conclusion the findings and analysis of the Autoencoder-LSTM model for the identification of DN in the early stages have shown the prospect of strengthening diagnostic performance. It is suggested that integration of an autoencoder with an LSTM network reduces the dimensionality and contains profitable sequential pattern understanding for the later

component in improving the identification of early signs of DN. The study's results underscore the model's potential for early detection of DN, which could lead to improved patient outcomes through timely medical intervention. Despite these achievements, future work should focus on several key areas to further enhance the model's applicability and performance. This includes validating the AE-LSTM model on diverse datasets to ensure generalizability across different populations, exploring additional feature extraction techniques to improve model robustness, and investigating the integration of the model into clinical decision-support systems for real-time applications. It is suggested that in future studies, the sample ought to be diverse, and the data collected should be followed up over time to see how to improve on the given model. Further, it may be beneficial to experiment with state of the art methods like incorporating attention mechanism, or integrating hybrid model with other modalities of data like genomics or Imaging data to enhance the diagnostic accuracy for early detection. Practical emphasis and the integration of technological innovations into clinical practices will also play an important role in converting these progressive changes into valuable outcomes for patient and stakeholders' experiences.

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