DIABETES DISEASE PREDICTION CLASSIFICATION USING ADAPTIVE RECURRENT NEURAL NETWORKS

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Abstract—**Nowadays, diabetes is one of the most common chronic diseases, which causes innumerable deaths each year. Therefore, diabetes early prediction is an important process for a healthy lifestyle. To address this problem, the Adaptive Recurrent Neural Network (ARNN) based Gated Recurrent Unit with Rectified Linear Unit (GRU-ReLU) technique is proposed to predict diabetes disease. Initially, the diabetes dataset fed into the Hot Encoding Preprocessing (HEP) method is to be collected to remove the noise from the diabetes dataset. Then the preprocessed dataset is trained into the Optimal Recursive Feature Selection (ORFS) algorithm to select the best features of diabetes. Finally, the proposed ARNN based on the GRU-ReLU technique is used to model diabetes weight patterns to predict the disease. RLU is a form of an activation function trained to achieve better performance in diabetes prediction. Predicting diabetes in its early stages can lead to better treatments. In this proposed ARNN based on the GRU-ReLU method, classification accuracy, precision, sensitivity, specificity, and execution time are analyzed to evaluate system performance. The experimental results show the high performance of state-of- the-art methods compared to existing methods.**

Keywords —*Gated Recurrent Unit, Rectified Linear Unit, Hot Encoding Pre-Processing, Adaptive Recurrent Neural Network, Optimal Recursive Feature Selection*

I. INTRODUCTION

Diabetes is a chronic disease that poses a major threat to human health. Diabetes is caused by insufficient insulin secretion or biological effects of the disorder, or both. Defects are characterized by a higher blood glucose level than normal. With the development of living standards and sedentary lifestyles, it is becoming increasingly common. In medicine, the diagnosis of diabetes is carried out based on fasting glucose, glucose tolerance, and random blood glucose levels. Diabetes can be divided into two categories by entering Type 1 Diabetes (T1D) and Type 2 Diabetes (T2D). Most people with T1D are under the age of 30 and are usually young. Typical clinical symptoms are thirst, high blood sugar levels, and frequent urination.

This type of diabetes cannot be cured effectively with oral medications by itself. It is more common for middle-aged and older people with T2D to be associated with obesity, hypertension, dyslipidemia, atherosclerosis, and other disorders.

These are two types of diabetes disease that can cause life-threatening complications: stroke, heart attack, chronic renal failure, diabetic foot syndrome, disgusting neurological disorder, encephalopathy, adrenal tumor, liver glucagon cirrhosis, and many other complications. By getting an early diagnosis, we can control the disease. Deep learning allows people to make preliminary decisions about diabetes based on routine physical examination data, which doctors can use.

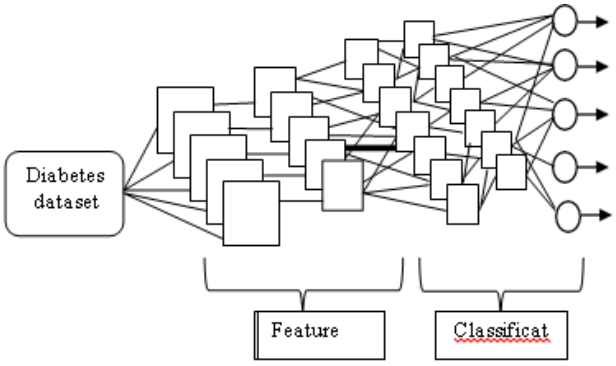


Fig.1. Deep learning-based diabetes prediction process

Fig. 1 depicts the deep learning-based diabetes prediction process. To predict diabetes disease, the proposed method consists of three steps: preprocessing, feature analysis, and classification. Despite the opinion that they appear to be biased towards this type of problem, the theoretical basis and empirical research are limited by the lack of qualification deviations and boundaries. The rest of this paper is arranged as follows. Section 2 introduces the related work on diabetes and deep learning. Section 3 describes our proposed Hot Encoding Preprocessing model in detail. Section 4 conducts the experimental evaluation as well as an investigation into the experimental results. . Sections 5 describe the results and discussion. Finally, Section 6 presents conclusions and future work.

II. RELATED WORK

Diabetes, also known as a chronic disease, is a group of metabolic disorders caused by long-term high sugar levels in the blood. The author analyzes the diabetes risk factor and detection using an ensemble of machine learning (ML) like Support Vector Machine (SVM), Random Forest (RF), Decision Tree (DT), Naive Bayes (NB), and so on, based on the PIMA diabetes dataset [1]. Recently, the study of DL, Reinforcement Learning (RL), and combinations thereof (deep RL) promises a revolutionary future for artificial intelligence. Increasing computing power is faster than applying these technologies and increasing data storage and their size and complexity, reducing the cost of research in various fields [2] and decreasing older data sets.

Many of the previous transfer learning techniques [3] have the power of proof and transfer knowledge that deep learning learns from a huge network domain to train labeled data. The design parameters used to find the classification method are meant for multi-level application [4] system programs of primary antibodies. The motivation is a new unsupervised feature extraction [5] for current representative histopathology and classification of tissue images. Their grades are recognized as having difficult problems for health monitoring and automatic diagnosis by radiologists. The technique is based on a detailed review of previously published surveys and recent in-depth learning at BTC [6]. The purpose of this task is to evaluate a linear black-box method, including a new nonparametric method for learning individual models of glucose response to insulin and diet, which is suitable for model-based prediction and control [7]. When building these models, the challenge is to address large diabetes patients and intra-patient fluctuations in glucose and insulin dynamics. The author proposes a profound learning method that improves editing problems by learning events in biological sequences by marking the patterns of subjects [8]. The training sequence model supported by bidirectional recurrent neural networks can handle the length of a variable array [9].

Machine Learning is an increasingly complex physical and biological phenomenon in fields such as biology, medicine, engineering, and traditional fields such as synthetic biology, new chemical synthesis, and automated biological production. In [10], to understand the increasingly complex data, it must be converted to a new paradigm of medical products and services for patients. Therefore, advanced ensemble classifications have been successfully developed based on the DL algorithm [11] to assess breast cancer's clinical outcome. Therefore, the real challenge is determining the right function for a particular task [12]. The author explores the Deep Neural Network (DNN) algorithm that is used to detect type 1 diabetes. The model focuses on extracting behavioral patterns from sequences of self- monitoring blood glucose measurements on different time scales [13]. However, these methods limit accuracy when applied to incomplete data with insufficient measurement time.

The hyper-heuristic multipurpose evolutionary exploration method is used to find the optimal network hyper [14]. For automatic quantification of food volume in day-to-day clinical practice, you may need a reliable tool for risk assessment and time savings of cardiovascular disease [15]. A multi-level transfer learning method uses a first fine adjustment to fine-tune the knowledge learned from IMAGEnet, mammography data, and DBT data [16]. The improvement of valuable information resources has become an intelligent agricultural learning system and is becoming smarter. DL is a type of machine learning (ML) method [17] that uses artificial neural networks' principles. Classification using ML techniques like SVM, DT, LR, and NB to analyze the best results in diabetes [18].

The Deep Learning Assisted Efficient Adaboost Algorithm (DLA-EABA) [19], which helps in detecting breast cancer, the author proposes using advanced computing technology to detect breast cancer. MRI, ultrasound, and different diagnostics such as digital breast tomo synthesis and mammography, characterize the mass of the breast for prediction task or prognosis, and several imaging modalities[20] start by judging based on learning CNN transfer. The high probability of pixel degradation is restricted to being located near the spatial nucleus's center [21]. Perceptual behavior is a two-way process in the real brain, and it depends on the expectations carried by the feed-forward sensory and feedback pathways. Other neural network learning methods have only been applied to either feed-forward networks or hypotheses, making them less common and adopted by the real brain [22].

The author describes the type 2 diabetes prediction using the Average Weighted Objective Distance (AWOD) approach. AWOD is designed for binary classification problems on relatively small datasets [23]. To identify molecular tumors, pathologists use a manual microscope to label nuclear activity biomarkers

and assign a histochemical score (H-score) to the core of each TMA (Tissue Microarray) for semi-quantitative evaluation. Manual labeling of positively stained nuclei is a time-consuming, inaccurate, and subjective process that differentiates observers [24]. Emotional abnormalities can be elicited by physical fatigue. Emotional fatigue of the concepts and classifications has been introduced one after another. Next, an emotional fatigue detection system is to be designed based on multimodal data [25].

III. THE PROPOSED MODEL OF HEP

The proposed Hot Encoding Preprocessing (HEP) method collects diabetes data to remove the noise from the diabetes dataset. The proposed ARNN based on the GRU technique is used to model diabetes weight patterns to predict the disease. ReLU is a form of an activation function trained to achieve better performance in diabetes prediction. The main objective of this paper is the proposed algorithm to classify diabetes predictions with high classification accuracy and minimizes the time complexity compared with existing algorithms. The Adaptive Recurrent Neural Network (ARNN) method was developed for processing sequential data. The proposed GRU network is to calculate sequential relationships between activity samples. It maps the entire history of network input to predict each output of tariffs and transient relationships between data at each point in time. First, the data is preprocessed using Hot Encoding Preprocessing (HEP) to remove the noise.

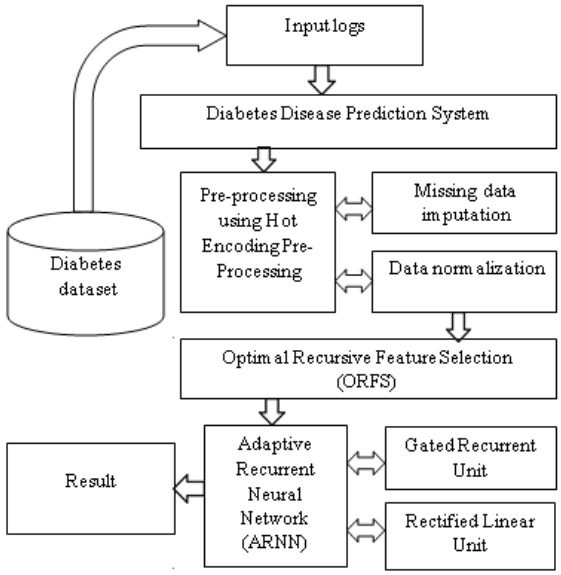


Fig.2. The proposed method architecture for diabetes prediction

The proposed method architecture is presented in fig. 2. Data preprocessing is essential to prepare for diabetes using diabetes datasets that can accept diabetic type data using deep learning. Optimal Recursive Feature Selection (ORFS) is done to identify the best features of diabetes. The proposed ARNN algorithm-based GRU and ReLU technique is used to classify diabetes patients. Early detection of diabetes can lead to better treatment.

3.1 HOT ENCODING PRE-PROCESSING

At this stage, preprocessing is necessary to prepare the data because the real-world medical dataset is full of irrelevant and missing values. These incorrect values cause the most inaccurate classification results. Classification Accuracy (CA) depends upon the correctness of data, so data should be non-ambiguous, precise, and complete. The proposed HEP algorithm minimizes the impact of irrelevant values and finds the missing values to normalize the corresponding attribute ranges. Normalization is a scaling technique in which values are moved and resized.

$$M_f = \sum_c^t \left[(a_{ic} - a_{jc})^2\right]^{1/2} \quad j = 1,2,\dots,l \qquad (1)$$

From the above equation (1) is used to find the missing values and irrelevant data. Let's assume Mf is the Obtained filtering data from the original dataset. ai Is the instance missing values, aj is the instance without missing values, t is the total number of features in the diabetes dataset, and l is the number of instances without missing values.

$$P_n = \frac{M_f - m}{sd} \qquad (2)$$

The data set is sequenced and resized using the above equation (2), Pn is the new normalized preprocessed dataset, Mf observed without missing value data, m refers to the average mean value, and sd defines the average standard deviation. Such medical diabetes data discrepancies may lead to erroneous classification prediction results. Therefore, they should be pre-processed before applying the proposed algorithm to improve results for prediction.

3.2 OPTIMAL RECURSIVE FEATURE SELECTION

After preprocessing, the diabetes dataset is fed into the Optimal Recursive Feature Selection (ORFS) algorithm, which selects the important features for reducing the classification time. ORFS selects the features of the diabetes dataset through a recursive execution process and chooses important features of diabetes depending on the coefficient value or the importance of

the features. This way, it removes the fewest features from the dataset.

Algorithm 1. Diabetes-related features to improve classification performance.

Input: Pre-processed dataset (Pn)

Output: Important Feature selected dataset (If)

Begin

1 : Import the Pre-processed dataset Pn

2 : Calculate the rank the important feature Rm

3 : For each set of features Ai i=1, 2….n do

4 :Rank method $Rm(Pn, Ai)$

5 : $Rm(I+1) \leftarrow If*$

6 : $AI \leftarrow Ai - If*$ (Remove the least feature)

7 : End for

8 : Calculate the importance features (If)

$$I_f = \frac{\cdots_{I-H_L}}{H_1}$$

9 : Obtain the best features selected dataset If

End

Algorithm 1. is a step towards obtaining diabetes-related features to improve classification performance. Let's assume A_i is the n attributes of a dataset, R_m is the rank method, A_I is the filter attributesfrom the least features of l_f^* respectively, H_i is theexpected features, and finally, obtain the important features of diabetes I_f<1are glucose level, Insulin, etc. The ORFS algorithm selects the important features and removes the least features from the preprocessed datasetP_n

3.3 PROCESSING OF DATASET

The diabetes dataset used in this paper is taken from (online and publicly available at Kaggle). The vital objective of using this dataset is to predict diabetes patients. The diabetes dataset contains attributes that are glucose, blood pressure, insulin, BMI, age, and so on. The total number of dataset records is 5000. The training dataset has 70% and the testing dataset has 30%.

3.4 MODELING

This phase is used to identify the early detection of diabetes using ARNN- based GRU-ReLU techniques,

3.4.1 Adaptive Recurrent Neural Network

At this stage, the proposed ARNN algorithm is an artificial neural network that uses an array of any length for a weight-sharing model between each position in the sequence. By representing an ARNN, the encoding can be strongly hidden, and the network output can be in a state that depends on any number of previous inputs. The proposed ARNN contains three layers, specifically an input layer, a hidden layer, and an output layer. The input layer is the first layer through which the characteristics of the dataset are transferred. No calculations occur at this level, and it will be used to pass the function to the hidden layer. The hidden layer is between the input layer and the output layer. This layer performs the calculation of the weights of diabetes and finally passes the information to the output layer. The output layer represents our neural network layer. After culturing the newly created model, it gives results. It is responsible for generating an output variable using the ReLU activation function. Information is stored and accessed through the gates by assigning a counter such as 0 or 1.

3.4.2 Gated Recurrent Units (GRU)

The GRU technique is done to calculate the weightage of diabetes in the hidden layer to predict the disease. It is expected that the time-dependent representation will improve the performance of diabetes prediction. The typical time dependence is expected to improve diabetes recognition performance in this GRU structure presented in fig. 3. The Gated Recurrent Unit (GRU) has a recurrent hidden state, and its activation depends on the processing variable-length array at every moment and the previous moment. More formally, given a sequence = $(x_1, x_2, \cdots, x_t)$, the GRU updates its recurrent hidden state $_t$

$$h_t = \{0\ t = 0\ \varphi(h_{t-1}, x_t)\ otherwise \quad ($$

Assume $\varphi$is a non-linear function, such as a combination of logical sigmoid and affine transformations. Optionally, the GRU may have an output $y = (y1, y2, \cdots, yt)$, which may again be of variable length.

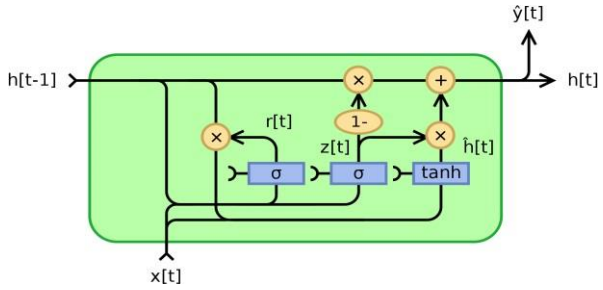


Fig.3. GRU Gate architecture

Input gate: From the input, find the value that needs to use to change the memory. The sigmoid function determines which values can be passed 0 and 1. The tanh function returns -1 to 1 from the weightage values.

$$I_g = \sigma(W_i[P_{t-1}, C_i] + b_i) \quad (4)$$

$$\tilde{S}_c = tanh(W_s[P_{t-1}, C_i] + b_s) \quad (5)$$

Let's assume I_g refers to the input gate, σ is a sigmoid function, P_{t-1} is a previous state, C_i current input state and b_i is a bias vector each size n neurons, Wi is the weight at the current state, W_s weight at cell state.

Forget Gate: It discovers the details to be discarded from the block. Its expression at the previous state (Pt-1) and the current input (Ci) outputs a number either 0(omit this) or 1(keep this) for each number in the cell state $S\tilde{}c - 1$.

$$f_g = \sigma\,(W_f.[P_{t-1}, C_i] + b_f) \quad (6)$$

Let's assume fg is a forget gate, and Wf weight at forget gate. The above equation is done to calculate the forget gate fg process.

Output Gate: The block inputs and memory are used to determine the output.

$$O_g = \sigma(W_o[P_{t-1}, C_i] + b_o) \quad (7)$$

$$T_h = O_t * tanh(C_i) \quad (8)$$

From the above equations (7) and (8) are used to calculate the output gate process in the Hidden layer (GRU). Where Og is the output gate, Wo denotes weight at recurrent neurons, and T□ = Block Output at instance time.

3.4.3 Rectified Linear Unit

The activation function used in this study is a non-linear rectified linear unit (ReLU) function with an output. The benefits of the ReLU activation function are that its ability to use is similar to that of the human nervous system, and it is easy and quick to train large networks. The ReLU activation function is used in the output layer for predicting diabetes mellitus accurately

$$f(x) = \max(0, x) \quad (9)$$

From the above function (9), the composition of linear units is the most commonly used activation function in deep learning models. A fully connected layer of neurons is connected to all the neurons in the previous layer. This layer calculates the categories predicted by identifying the data. Recognition is done by combining all the features learned from the previous layer. The number of output categories depends on the number of categories that exist in your target dataset. The hierarchical structure uses the ReLU activation function to classify the features generated based on the various types of training data received from the previous layer.

Algorithm 2. The diabetes prediction performance using ARNN-based GRU and RLU techniques

Input: Important Feature selected dataset (If)

Output: Diabetes prediction result

Begin

1 : Initialize the Important Feature selected dataset (If)

2 : Calculate the hidden layer GRU performance □*t*

$$\square_t = \begin{cases} 0 & t = 0 \\ \varphi(Pt-1, Ci) & otherwise \end{cases}$$

3 : Compute the weightages of threshold values

4 : Compute the output layer ReLU activation function performance

$$f(x) = max(0, x)$$

5 : Return diabetes prediction

End

Algorithm 2, described above, predicts diabetes using ARNN-based GRU and RLU techniques. The proposed ARNN algorithm-based GRU-ReLU technique is used to predict early diabetes efficiently.

The proposed modeling system we get the implementation of the result is that the recall result has 84%, precision has 85%, F1- score has 86%, and classification accuracy has 86%. These parameters are calculated by a confusion matrix**.**

IV. EXPERIMENTAL SETUP AND RESULTS

The simulation results analysis is carried out by the Python language anaconda tool environment running on Windows 10. The proposed ARNN is compared to previous systems such as Spatially Constrained Convolutional Neural Network (SC-CNN) [17], Deep Learning Assisted Efficient Adaboost Algorithm (DLA- EABA) [15], and Deep Time Growth Neural Network (DTGNN) [3].

$$\text{Classification Accuracy } (CA) = \frac{TPV+TNV}{TPV+TNV+FNV} * 100 \qquad (10)$$

The above equation(10) is used to calculate classification accuracy (CA) performance, where TPV represents the true positive values, TNV refers to true negative values, and FNV represents the false negative values

4.1 ANALYSIS OF PROPOSED ALGORITHM RESULT PERFORMANCE

Table 1 defines the analysis of classification accuracy (CA) performance for diabetes prediction. The proposed algorithm gives high performance when compared to previous algorithms.

Table.1. Analysis of Classification Accuracy (CA) performance

No of data	SC-CNN[17] in %	DLA-EABA[15] in %	DTGNN [3] in %	GRU-ReLU in %
1000	54	58	62	**68**
2000	57	61	65	**72**
3000	61	64	68	**79**
4000	65	68	70	**84**
5000	67	70	71	**86**

Fig. 4 defines the analysis of Classification Accuracy (CA) performance for diabetes prediction. The proposed ARNN-based GRU-ReLU algorithm Classification Accuracy (CA) performance result is 86% for 5000 data points.

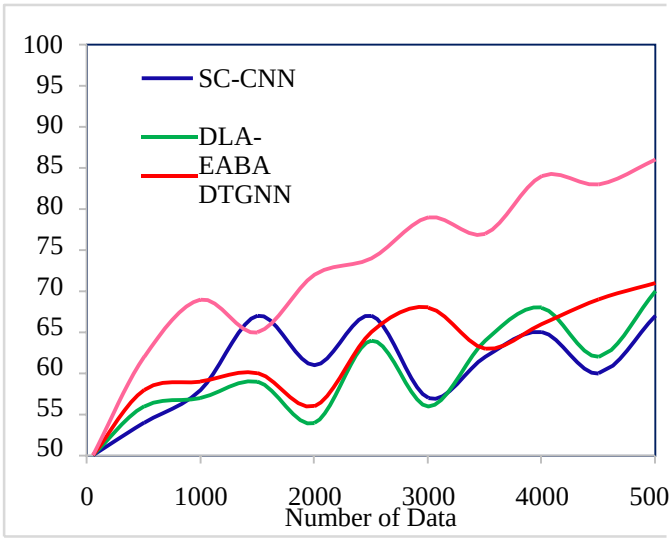


Fig.4. Analysis of Classification accuracy performance

$$Precision = \frac{TPV}{TPV+FPV} \quad *100 \qquad (11)$$

From the above equation, (11) is used to calculate the precision performance. Precision is the correctly identified diabetes case, a positive value where FPV refers to false-positive values.

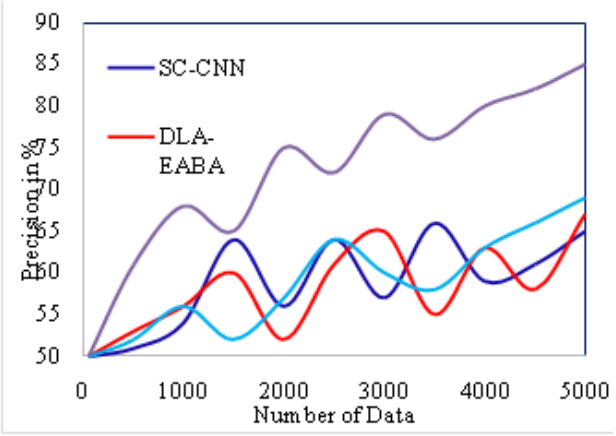


Fig.5. Analysis of precision performance

Fig. 5 describes the analysis of precision performance for diabetes prediction. The proposed ARNN-based GRU-ReLU precision performance result is 85%.

$$Recall = \frac{TPV}{TPV+FPV} *100 \qquad (12)$$

From the above equation, (12) explains the precision performance, and the recall is the ability to

predict positive diabetes classes correctly detected.

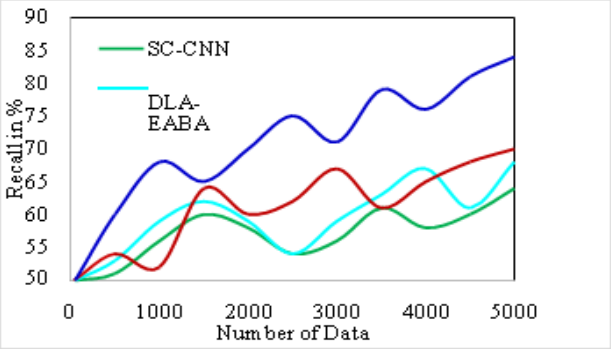


Fig.6. Analysis of recall performance

Fig.6 shows the analysis of recall performance for diabetes prediction. The proposed ARNN-based GRU-ReLU recall performance result is 84% for 5000 data.

$$F1\ score = \frac{precision * Recall}{precision + Recall} * 100 \qquad (13)$$

From the above equation, (13) is used to calculate the diabetes F1 score result performance. The F1 score computes the weighted average score of diabetes recall and precision performance.

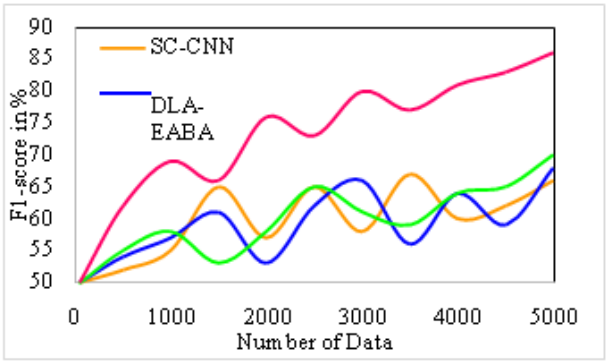


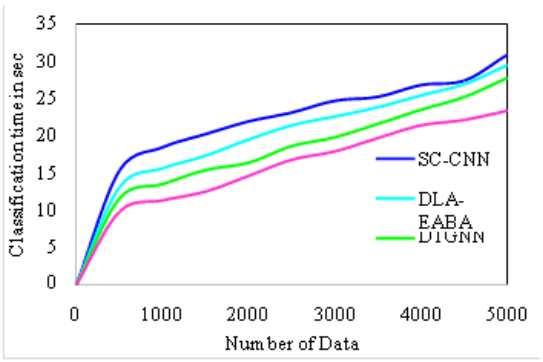
Fig.7. Analysis of F1 score performance

Fig.7 defines the F1 score performance for diabetes prediction. The proposed ARNN-based GRU- ReLU technique F1 score performance result is 86% for 5000 data.

$$Time\ complexity = \frac{T * (T-1)}{Total\ processing\ time} \qquad (14)$$

Where T=number of the iteration

Analysis of time complexity for diabetic prediction result is shown in the fig. 8. In this result of time complexity, the proposed ARNN-based GRU-ReLU result is 23.4 sec of classification time for 5000 diabetic data.



Similarly, the existing methods SC-CNN, DLA- EABA, and DTGNN provide 30.9 sec, 29.5 sec, and 27.8 sec of classification time for 5000 data.

V. Discussion

The previous algorithms are SC-CNN, DLA-EABA, and DTGNN. The diabetes prediction systems give low accuracy performance and high time complexity. During classification, it provides wrong results. To resolve the problem, the proposed ARNN-based GRU-ReLU techniques are used to provide high accuracy performance with low time complexity. The proposed algorithm parameter results are: classification performance is 86%, recall performance is 84%, precision performance is 85%, F1-score performance is 86%, and time complexity performance is 23.4sec for 5000 data points. The proposed algorithm gives higher performance than the existing SC-CNN, DLA-EABA, and DTGNN algorithms.

VI. Conclusion

This paper aims to explore an ARNN-based GRU-ReLU technique for diabetes prediction using a diabetes dataset. The proposed deep learning technique improves the prediction of diabetes. In addition, the proposed method also uses an efficient preprocessing mechanism called Hot Encoding Multicollinearity. The Hot Encoding Processing method removes the noise and missing data effectively compared to other preprocessing methods. The proposed ARNN-based GRU-ReLU approach is implemented for the prediction of the disease in the early stage.It provides a complex input format to verify and predict the best results using the proposed Rectified Linear Unit activation function. The proposed method provides better performance compared to other existing methods. The proposed algorithm provides classification accuracy (CA)

performance result of 86%, precision performance result of 85%, recall performance result of 84%, F1-score performance result of 86%, and 23.4sec classification time for 5000 diabetic data. The proposed method provides better performance compared to other existing methods. Future work will also focus on improving the model for determining all possible complications, including an ordered sequence of proportions of possible complications. An improved classification performance while maintaining a low level of time complexity. By including other deep learning algorithms and techniques, the work of automatic diabetes analysis can be expanded and improved.

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