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Investigation Of Diabetes Data with Permutation Feature Importance Based Deep Learning Methods

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Abstract

Diabetes is a metabolic disease that occurs due to high blood sugar levels in the body. If it is not treated, diabetes-related health problems may occur in many vital organs of the body. With the latest techniques in machine learning technologies, some of the applications can be used to diagnose diabetes at an early stage. In this study, the data set from the laboratories of Medical City Hospital Endocrinology and Diabetes Specialization Center Al Kindy Training Hospital was used. The dataset consists of 3 different classes: normal, pre-diabetes and diabetes. The obtained diabetes dataset was classified using Long Short-Term Memory (LSTM), Convolutional Neural Network (CNN) and Gated Recurrent Unit (GRU) deep learning methods. The classification performance of each algorithm was evaluated with accuracy, precision, sensitivity and F score performance parameters. Among the deep learning methods, 96.5% classification accuracy was obtained with the LSTM algorithm, 94% with the CNN algorithm and 93% with the GRU algorithm. In this study, the Permutation Feature Importance (PFI) method was also used to determine the effect of features in the data set on classification performance. With this method, study reveals that the HbA1c feature is an important parameter in the used deep learning methods. Both the results obtained with the LSTM algorithm and the determination of the most important feature affecting the classification success reveal the originality of the study. It shows that the obtained results will provide healthcare professionals with a prognostic tool for effective decision-making that can assist in the early detection of the disease.

Keywords: Diabetes, Classification, Deep learning, Permutation importance feature.

Diyabet Verilerinin Permütasyon Önem Özelliği Temelli Derin Öğrenme Yöntemleriyle İncelenmesi

Öz

Diyabet, vücuttaki yüksek kan şekeri seviyesi nedeniyle meydana gelen metabolik bir hastalıktır. Tedavi edilmediği takdirde, vücudun birçok hayati organında diyabete bağlı sağlık sorunları meydana gelebilir. Makine öğrenme teknolojilerindeki son teknikler ile diyabet hastalığını erken bir aşamada teşhis edebilen uygulamalar kullanılabilir. Bu çalışmada Medical City Hastanesi Endokrinoloji ve Diyabet Uzmanlık Merkezi Al Kindy Eğitim Hastanesi laboratuvarlarından elde edilen veri seti kullanılmıştır. Veri seti, Normal, pre diyabet ve diyabet şeklinde 3 farklı sınıftan oluşmaktadır. Elde edilen diyabet veri seti Uzun-Kısa Vadeli Bellek (LSTM), Evrişimsel Sinir Ağları (CNN) ve Geçitli Tekrarlayan Birim (GRU) derin öğrenme yöntemleri kullanılarak sınıflandırılmıştır. Her algoritmanın sınıflandırma başarımı; doğruluk, kesinlik, duyarlılık ve F skor başarım parametreleri ile değerlendirilmiştir. Derin öğrenme yöntemlerinden, LSTM algoritmasıyla %96.5, CNN algoritmasıyla % 94 ve GRU algoritmasıyla %93 sınıflandırma doğruluğu elde edilmiştir. Bu çalışmada ayrıca veri setindeki özelliklerin sınıflandırma başarımına etkisini belirlemek için Permütasyon önem özelliği yöntemi de kullanılmıştır. Bu yöntem ile HbA1c özelliğinin kullanılan derin öğrenme yöntemlerinde önemli bir parametre olduğu ortaya konulmuştur. Gerek LSTM algoritması ile elde edilen sonuçlar, gerekse sınıflandırma başarısına etki eden en önemli özelliğin tespiti çalışmanın özgünlüğünü ortaya koymaktadır. Elde edilen sonuçların sağlık çalışanlarına hastalığın erken tespitine yardımcı olabilecek etkin karar verme için prognostik araç sağlayacağını göstermektedir.

Anahtar Kelimeler: Diyabet, Sınıflandırma, Derin öğrenme, Permütasyon önem özelliği.

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1. Introduction

Diabetes is a chronic disease, caused by an inability to produce or use insulin effectively, resulting in serious health issues such as heart disease, (Battineni et al. 2019; Rajput and Khedgikar 2022). According to the International Diabetes Federation (IDF), there are approximately 463 million diabetics in the world in 2019. In adults the ages between 20 and 79, 1 in every 11 has diabetes. In addition, according to the IDF, it is estimated that 578 million adults in 2030 and 700 million adults in 2045 will (Makroum et al. 2022). Diabetes can generally be classified into 3 categories: Type 1 diabetes (T1D) occurs due to deficient insulin production. Type 2 diabetes (T2D) results from the body's ineffective use of insulin. Gestational diabetes occurs during pregnancy. This type of diabetes occurs as a result of changes in hormones during (Fazakis et al. 2021).

HbA1c is an important blood parameter that indicates the risk of diabetes complications. The HbA1c value < 6.0% is for healthy people, and the HbA1c value between 6.0% and 6.5% is in people for pre-diabetes, which is characterized by blood sugar levels higher than normal but also called borderline diabetes (Karabiber and Savaş 2021; Rajput and Khedgikar 2022) and the HbA1c value is not high enough to be classified as diabetic. However, pre-diabetes cases lead to diabetes in the near future (Rajput and Khedgikar 2022).

Diagnosis or early diagnosis of diabetes depends on a doctor's intuition and experience. However, in some cases, it can lead to errors and excessive medical costs that affect the quality of service. The healthcare industry collects a large amount of healthcare-related data, but this data is not used effectively in undetected cases (Bhardwaj et al. 2022). As a result, it is thought that different advanced mechanisms and various software-based algorithms are required for automatic diagnosis and early detection of diseases with better accuracy. For example, the development of machine learning algorithms helps to process large amounts of data and extract the underlying data model that facilitates decision making (Er and Işık 2021).

In recent years, machine learning algorithms, especially deep neural networks, have been used for important applications in the field of health (Shishvan, Zois, and Soyata 2018). Machine learning algorithms can be modeled with nonlinear methods to identify people at risk. In addition, the importance of algorithm parameters in the model can be determined (Sadeghi et al. 2022).

Many machine learning algorithm techniques have been presented in the literature for diabetes classification. Most commonly used are Support Vector Machines (SVM) (Sisodia and Sisodia 2018; Tafa, Pervetica, and Karahoda 2015), Artificial Neural Networks (ANN) (Sun and Zhang 2019), Logistic Regression (LR) (Kumari, Kumar, and Mittal 2021; Qawqzeh et al. 2020), k-nearest neighbor (kNN) (Kandhasamy and Balamurali 2015), Random Forest (RF) (Kumari et al. 2021), Naive Bayes (NB) (Kumari et al. 2021; Sisodia and Sisodia 2018; Tafa et al. 2015), Decision Trees

(DT) (Sisodia and Sisodia 2018), CNN(Er and Işık 2021; Swapna, Soman, and Vinayakumar 2018), LSTM (Er and Işık 2021; Swapna et al. 2018), and GRU(Alhassan et al. 2018). Qawqzeh et al. (Qawqzeh et al. 2020) applied the LR technique for the classification of diabetes data. With 459 training and 128 test data, he achieved 92.3% classification accuracy in his proposed model. Tafa et al. (Tafa et al. 2015) used SVM and NB classification algorithms with a data set consisting of 402 patients taken from 3 different locations in Kosovo. It was classified with an accuracy of 95.52% with the SVM method and 94.52% with the NB method. Sisodia and Sisodia (Sisodia and Sisodia 2018) applied NB, SVM, and DT algorithms to the Pima Indians Diabetes dataset. The classification accuracy was 76.3% with the NB method, 65.1% with the SVM method and 73.82% with the DT method. Kumari et al. (Kumari et al. 2021) studied the Pima Indians Diabetes Dataset and applied NB, RF and LR methods. The accuracy was 74.12% with the NB method, 77.48% with the RF method, and 74.89% with the LR method. Swapna et al. (Swapna et al. 2018) used the CNN and CNN-LSTM methods to classify diabetes. It achieved 93.6% accuracy with the CNN algorithm and 95.1% with the CNN-LSTM algorithm. Er et al. (Er and Işık 2021) used deep learning-based CNN, LSTM, and CNN+LSTM methods for the classification of diabetes. In the proposed model, different training and testing rates were used and the highest accuracies were obtained with 80% training and 20% testing rates. In the classification results, 83.25% of the CNN method, 85.21% of the LSTM method and 86.45% of the CNN+LSTM methods were obtained. Alhassan et al.(Alhassan et al. 2018) King Abdullah International Research Centre Diabetes (KAIMRCD) dataset and LSTM and GRU methods were used. In the proposed method, it was classified with 97% accuracy.

In the literature, many machine learning algorithms have been proposed for diagnosing diabetes. In this study, classification with high accuracy rates with the proposed deep learning algorithms explains the importance of the study. In addition, it is thought that determining how much the input parameters will affect the result in the classification algorithms with the PFI method, will guide healthcare professionals in the right way about treatment.

In this study, it was aimed to classify diabetes patients using their medical characteristics as individuals. Three different class characteristics were used: diabetes, pre-diabetes, and no-diabetes. An accuracy rate of 96.5% was obtained with the LSTM method, one of the proposed deep learning algorithms. In addition, the importance of input features in deep learning algorithms was determined by using the PFI method. PFI method in LSTM, CNN and GRU methods and HbA1c feature were determined to be the most important feature in diabetes patient classification.

2. Materials and Methods

2.1. Materials

The dataset used in this study was taken from the Mendeley dataset diabetes dataset. The dataset, published in July 2020, was obtained at the laboratories of Medical City Hospital and the Endocrinology and Diabetes Specialization Centre Al Kindy Training Hospital. The data were obtained from 535 female and 435 male individuals aged between 20-79 living in the city of Baghdad. The data were collected in the database by obtaining from the medical information and laboratory analyzes of the patients. (Ahlam 2020).

Table 1. Details of Diabetes dataset

Parameters	Min	Max	Mean	Std	Unit
Age	20	79	53,528	8,799241	
Urea	0,5	38,9	5,124743	2,935165	mg/dL
Creatinine Ratio	6	800	68,943	59,98475	µmol/L
HbA1c	0,9	16	8,28116	2,534003	mmol/L
Cholesterol	0	10,3	4,86282	1,301738	mmol/L
Triglycerides	0,3	13,8	2,34961	1,401176	mmol/L
HDL	0,2	9,9	1,20475	0,660414	mmol/L
LDL	0,3	9,9	2,60979	1,115102	mmol/L
VLDL	0,1	35	1,8547	3,663599	mmol/L
Body Mass Index	19	47,75	29,57802	4,962388	--

The database contains 1000 people data sets, 103 of whom are no-diabetes, 53 are pre-diabetes and 844 are diabetic. Table 1 shows the characteristics of different diabetes patients such as Age, Urea, Creatine Ratio, HbA1c, Cholesterol, Triglycerides, HDL, LDL, VLDL and Body Mass Index.

2.2. Methods

In this study, diabetes dataset from Mendeley dataset database is classified using deep learning algorithms LSTM, CNN and GRU methods. The effect of each feature in the data set on the classification result was determined by the PFI method.

2.2.1. LSTM (Long Short Term Memory)

LSTM is a special type of Recurrent Neural Network (RNN) approach for modelling sequential data (Hochreiter and Schmindhuber 1997) developed by Hochreiter & Schmidhuber in the late 1990s.

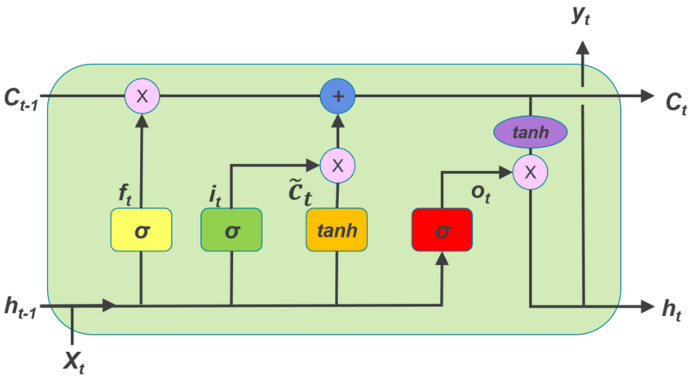


Figure 1. LSTM model (Xiao and Yin 2019)

The LSTM architecture consists of sequential blocks that repeat each other, and as is shown in Figure 1. The LSTM structure typically has three layers: forget, input, and output. In the LSTM architecture, first of all, X_t and h_{t-1} information are used as inputs, and it is decided which information to delete. These operations are performed in the forget layer using f_t Equation (1) and sigmoid is used as the activation function.

$$f_t = sigmoid(W_{f,x} * X_t + W_{f,h} * h_{t-1} + b_f) \tag{1}$$

In the second step, the input layer, where new information will be determined, comes into play and firstly (i_t) the information is updated with the sigmoid function using Equation (2). The tanh function is then used to identify the candidate information that will be used to create the new information with Equation (3).

$$i_t = sigmoid(W_{i,x} * X_t + W_{i,h} * h_{t-1} + b_i) \tag{2}$$

$$\tilde{C}_t = tanh(W_{c,x} * X_t + W_{c,h} * h_{t-1} + b_c) \tag{3}$$

New information is created by Equation (4).

$$C_t = C_{t-1} * f_t + i_t * \tilde{C}_t \tag{4}$$

Equations (5) and (6) are then used in the output layer to obtain the output data.

$$o_t = sigmoid(W_{o,x} * X_t + W_{o,h} * h_{t-1} + b_o) \tag{5}$$

$$h_t = o_t * tanh(C_t) \tag{6}$$

The above-described procedure is iterative. The model learns weight parameters (W) and bias parameters (b) in a manner that reduces the difference between actual training data and LSTM output data (Ayata, Saraclar, and Ozgur 2017; Fischer and Krauss 2018; Sagheer and Kotb 2019).

In this study, a LSTM layer, consisting of 200 blocks was first created for the classification architecture. Four Dense layers were created to provide node transitions between layers and to connect neurons from the previous layer as input to the next layer. There are 100 neurons in the 1st Dense layer, 50 neurons in the 2nd Dense layer, 20 neurons in the 3rd Dense layer, and 3 neurons in the 4th Dense layer as the output classification layer. The probability of each class was obtained by using the SoftMax function, used in multiple classification problems, as an activation function in the 4th Dense layer.

2.2.2. Gated Recurrent Unit (GRU)

The GRU was first suggested by K. Cho et al.(Cho et al. 2014). GRU, is one of the types of LSTM model, was proposed to use less computational resources to achieve LSTM performance. The GRU has a simpler structure with only the update gate and reset gate (Figure 2) (Chen et al. 2022), compared to the LSTM model with three gates. The update gate is a combination of the enter and forget gates in the LSTM model. The reset gate is the gate responsible for forgetting previous information (Bişkin and Çifçi 2021).

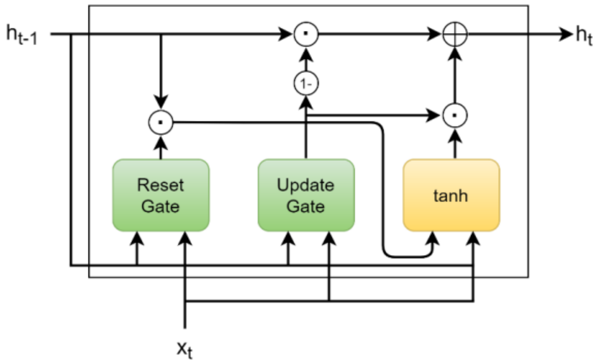


Figure 2. GRU model

In the GRU model, the update gate (u_t) and reset gate (r_t) can be calculated with Equations (7) and (8).

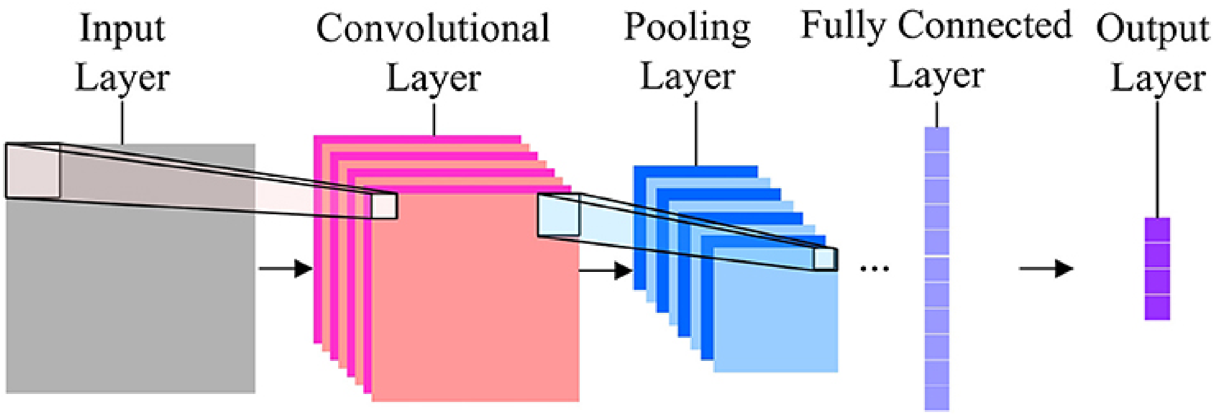
$$u_t = sigmoid\ (W_u[h_{t-1}, x_t] + \ b_u \tag{7}$$

$$r_t = sigmoid\ (W_r[h_{t-1}, x_t] + b_r \tag{8}$$

W_u and W_r update and reset weight parameters. b_u and b_r parameters are bias values.

2.2.3. Convolution Neural Network (CNN)

CNN pattern classification, which is an effective tool for feature extraction in CNN data, is widely used in many areas such as image processing, sound processing and pattern recognition (Wang et al. 2017). CNN is similar to traditional ANN in that it consists of neurons that self-optimize through learning. As in the ANN model, each neuron performs operations by taking an input value. One of the biggest differences between CNN and other models is that the layers in it consist of neurons organized in three dimensions (height, width and depth) (O’Shea and Nash 2015). A CNN model generally consists of three main layers: the convolution layer, the pooling layer and the fully connected layer (Figure 3).



The Convolutional Layer: It is the core building block of the CNN model. It constitutes the main part of the computational load of the network. The primary purpose of the convolutional layer is to extract features from the input data. There is no connection between neurons in this layer. In addition, neurons in different layers are locally connected to each other with the weight sharing technique (Wang et al. 2017). During the convolution operation, the filter matrix slides across the height and width of the input dataset, performing the convolved multiplication, thus obtaining a two-dimensional representation. It is then passed through a user-defined activation function to generate a feature map with Equation (9).

$$y_j = f\ (\textstyle\sum_{i \in M_j} x_i^{l-1} \otimes w_{i,j}^l + b_j^l) \tag{9}$$

Here $\otimes$ denotes the convolution operation.

The pooling layer: The pooling layer is typically used between the convolutional layers to reduce the number of parameters and computational load in the CNN architecture. The purpose of the pooling process is to reduce the size of the dataset and to prevent over-learning with network training.

Fully Connected Layer: It is stated that every neuron in the previous layer is connected to every neuron in the next layer. Similar to ordinary neural networks, in a fully connected layer, all neurons of one layer are connected to all neurons of the previous layer. The output from the convolutional and pooling layers represents the high-level attributes of the input dataset. The purpose of the fully connected layer is to use these attributes to classify the input dataset into various classes (Kesici 2019).

2.2.4. Permutation Feature Importance (PFI)

This approach works by assigning a random value to a property based on the relationship between the property and the model output. PFI is an advantageous application in terms of determining the features that affect the result of a model and interpreting the performance of the model.

PFI is an approach used to calculate the importance of features regardless of the model (Otchere et al. 2022). With this approach, it determines the importance of each feature based on the effect of the machine learning model on classification (Altmann et al. 2010). The purpose of the PFI is to calculate how much the performance measure of the model has decreased by randomly extracting the features from the data set. The amount of increase in the RMSE(Ibrahim and Jafari 2019) or MAE (Rengasamy, Rothwell, and Figueredo 2021) values can be determined by the effects of the used features in the model on the classification. The bigger the change, the more important that feature is. Or, when the information about the feature is removed, the increase in the model error determines the importance of the feature (Molnar 2022).

2.2.5. Model Performance Evaluation

In classification problems, the success of the created model is determined by comparing the number of samples assigned to the correct class with the number of samples assigned to the wrong class. Using the confusion matrix (Table 2), the Accuracy, Precision, Sensitivity and F-score values of the model can be calculated.

Table 2. Confusion Matrix

	Positive	Negative
Positive	True Positive (TP)	False Positive (FP)
Negative	False Negative (FN)	True Negative (TN)

Accuracy: It can be calculated as the ratio of the number of correctly classified samples to the total number of samples (Equation 10).

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \tag{10}$$

Precision: The ratio of true positive values to classified positive values (Equation 11).

$$Precision = \frac{TP}{TP+FP} \tag{11}$$

Sensitivity: It is the ratio of the number of correctly classified samples obtained as a result of the created model to the number of positive samples (Equation 12).

$$Sensitivity = \frac{TP}{TP+FN} \tag{12}$$

F – score: It is the harmonic mean of the Sensitivity and Precision values (Equation 13). It is frequently used in literature. Sometimes, when evaluating the performance of models, the evaluation of Precision or Sensitivity alone may be incomplete.

$$F - score = 2\,x\,\frac{Precision\;x\;Sensitivity}{Precision+Sensitivity} \tag{13}$$

3. Experimental Results and Discussion

3.1. Classification

The model developed in this study was implemented using the Python programming language in the Spyder editor. TensorFlow and KERAS libraries were used as deep learning tools. In addition, data analysis was performed using Sci-kit learn and other basic Python libraries. For the calculation a computer with the Windows 10 operating system, an IntelCore i7 2.2 GHz processor and 32 GB RAM was used.

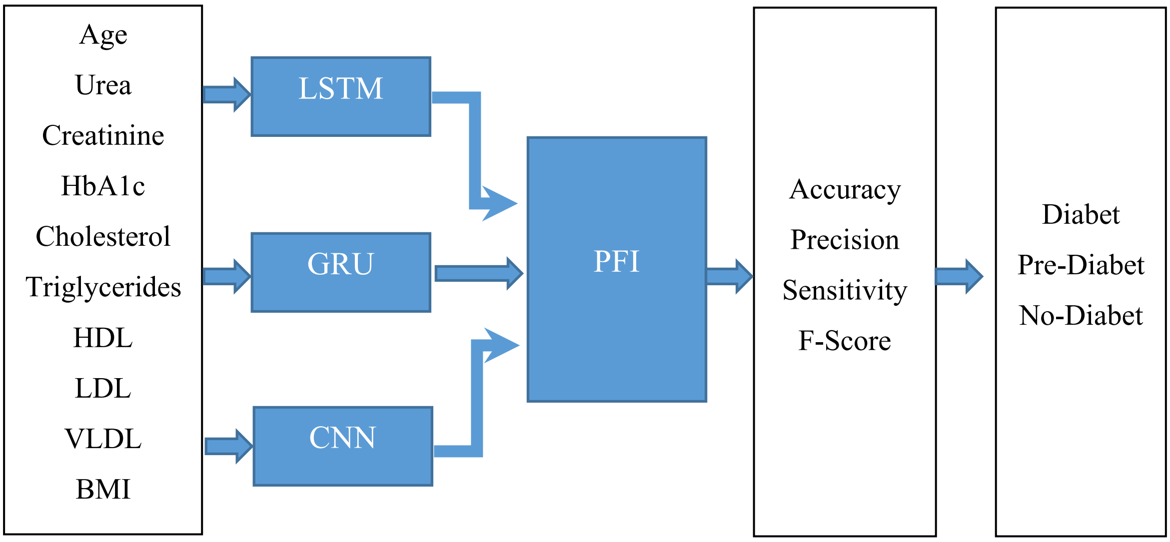


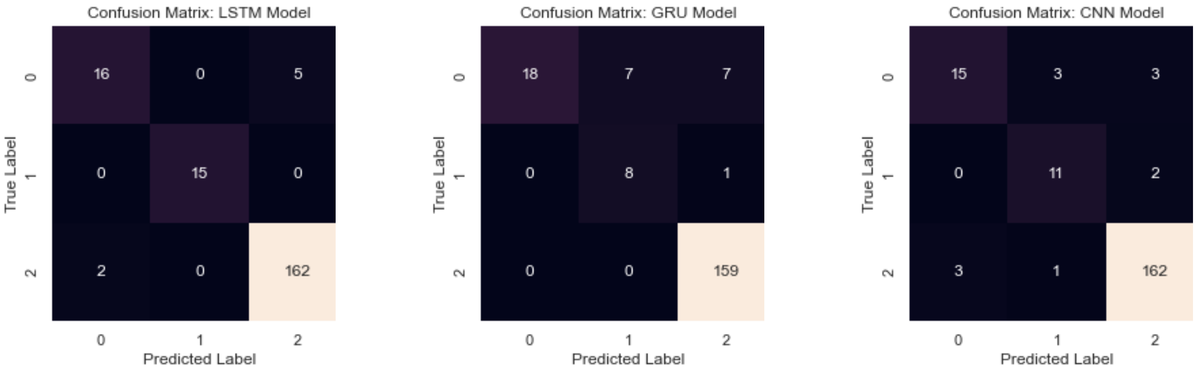
Figure 4. Block diagram of classification

A classification model (Figure 4) was developed with LSTM, GRU and CNN deep learning methods by using the data set obtained from Medical City Hospital Endocrinology and Diabetes Specialization Centre Al Kindy Training Hospital laboratories. The data set was organized using 10 different features belonging to 1000 people. Input parameters are Age, Urea, Creatine ratio, HbA1c, Cholesterol, Triglyceride, HDL, LDL, VLDL and Body Mass Index values of the developed model were used. Diabetes, pre-diabetes and no-diabetes labels and model performance criteria accuracy, precision, sensitivity and F-score values obtained as a result of the analysis of data belonging to 3 different classes are shown in Table 3.

Table 3. Classification performance metrics

Model	Train Accuracy	Accuracy	Precision	Sensitivity	F- Score
LSTM	%100	%96,50	%96,84	%96,50	%96,62
GRU	%96,63	%93,00	%95,95	%92,50	%93,49
CNN	%100	%94,00	%94,26	%94,00	%94,06

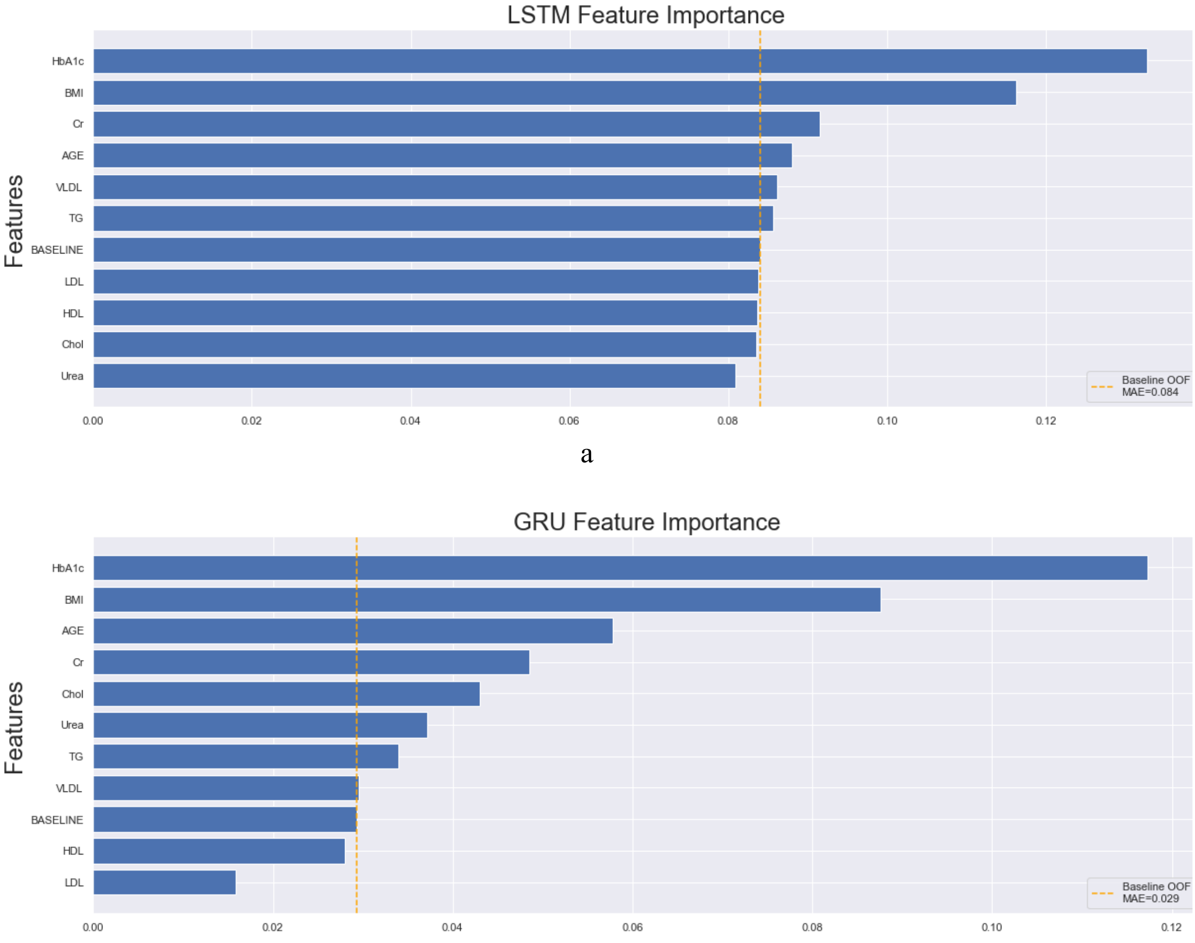
In the model, performed with the LSTM method, the training set was classified with an accuracy of 100.00%. 200 LSTM blocks and ReLu activation function are used in the model. Dense layer is used together with the ReLu activation function to connect the nodes of the layers together. SoftMax activation function is used in the output layer. The developed model was tested, and it achieved an accuracy rate of 96.50%. In the confusion matrix, shown in Figure 5, 0, shows data for no-diabetes, 1 for pre-diabetes, and 2 for diabetes.



a b c

Figure 5. Confusion Matrix

As a result of the LSTM classification method, the importance of the features that affect the output classification result of the features defined as input to the model was calculated by the PFI method (Figure 5.a). The commonly used metric, mean absolute error (MAE), was used to assess the classification quality. As a result of the PFI, it was found that the most effective parameter in diabetes was HbA1c, followed by the Body Mass Index parameter and the age parameter (Figure 6.a).



b

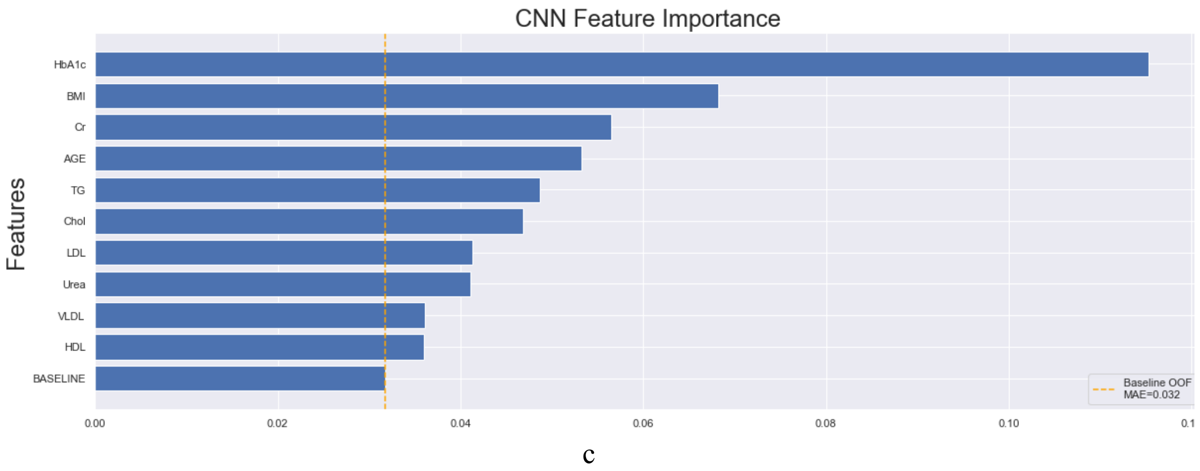


Figure.6 Permutation Feature Importance (PFI)

As a result of the GRU method, an accuracy rate of 93.00% was obtained with the test data (Table 3). In the GRU method, the ReLu activation function and a model consisting of 100 blocks are proposed. A SoftMax activation function is used at the output of the model. The confusion matrix of the GRU model is shown in Figure 5.b. In the developed model with the GRU algorithm, it is seen that the HbA1c value, one of the input parameters, has the highest effect on the classification process as a result of the permutation importance feature method (Figure 6.b).

As a result of the proposed method with the CNN algorithm, 94.00% of the test data was classified correctly. The CNN model consists of a ReLu activation function and 16 filter layers. The SoftMax function is used in the output layer of the model. The obtained results with the CNN algorithm are shown in Figure 5.c. As a result of the permutation importance feature method, as in the LSTM and GRU methods, the input parameter HbA1c was obtained as the parameter with the highest effect in the classification process (Figure 6.c).

4. Conclusion

The diagnosis of diabetes, which is a medical problem today, is important in its early stages. In this study, it was aimed to detect diabetes by parameters such as blood parameters and body mass index.

In this study, the classification of diabetes patients is proposed by using deep learning methods LSTM, GRU and CNN algorithms. The permutation importance features method was used to analyses the classification performance of the features in the data set.

The LSTM algorithm has achieved a success rate of 96.50% in the problem of diabetes patient classification. The effect of the features given as input to the model on the classification result was determined by using the permutation importance feature method. The HbA1c parameter was determined as the most effective parameter in the classification with LSTM, GRU and CNN algorithms.

The deep learning-based diabetes diagnosis system will make a great contribution to early diagnosis by specialist physicians and to starting treatment in a shorter time. In addition, it is thought that HbA1c and body mass index parameters will make a great contribution to physicians' pre-diagnosis of diabetes.

Authors' Contributions

All authors contributed equally to the study.

Statement of Conflicts of Interest

There is no conflict of interest between the authors.

Statement of Research and Publication Ethics

The author declares that this study complies with Research and Publication Ethics.

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