

# Flock Optimization Algorithm-Based Deep Learning Model for Diabetic Disease Detection Improvement

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**Abstract:** Worldwide, 422 million people suffer from diabetic disease, and 1.5 million die yearly. Diabetes is a threat to people who still fail to cure or maintain it, so it is challenging to predict this disease accurately. The existing systems face data over-fitting issues, convergence problems, non-converging optimization complex predictions, and latent and predominant feature extraction. These issues affect the system's performance and reduce diabetic disease detection accuracy. Hence, the research objective is to create an improved diabetic disease detection system using a Flock Optimization Algorithm-Based Deep Learning Model (FOADLM) feature modeling approach that leverages the PIMA Indian dataset to predict and classify diabetic disease cases. The collected data is processed by a Gaussian filtering approach that eliminates irrelevant information, reducing the overfitting issues. Then flock optimization algorithm is applied to detect the sequence; this process is used to reduce the convergence and optimization problems. Finally, the recurrent neural approach is applied to classify the normal and abnormal features. The entire research implementation result is carried out with the help of the MATLAB program and the results are analyzed with accuracy, precision, recall, computational time, reliability scalability, and error rate measures like root mean square error, mean square error, and correlation coefficients. In conclusion, the system evaluation result produced 99.23% accuracy in predicting diabetic disease with the metrics.

**Keywords:** Diabetic Disease Classification System, Flock Optimization Algorithm Deep Learning Model (FOADLM), Gaussian Filtering, Convergence Problem

## Introduction

Diabetic disease (de la Torre *et al.*, 2020) is a chronic and metabolic disease with high blood sugar levels. Diabetic disease causes eye infections, heart disease, blood vessel problems, nerves, and kidney infections. A typical diabetic has type 2 diabetes (Tigga and Garg 2020), commonly occurring in adults; the body does not get enough insulin. In type 1 disease, the pancreas generates a low amount of insulin. For both type 1 and type 2, around 422 million people are affected by the diabetic condition, especially in middle and low-income countries (Nojehdehi *et al.*, 2018). Therefore, diabetic disease should be identified earlier to eliminate the risk factors. Generally, diabetic patients have frequent urination, hunger, thirst, vision changes, weight loss, and fatigue symptoms. These symptoms (Eijaz *et al.*, 2022)

are used to identify diabetic patients in an earlier stage, but people fail to mark the symptoms. As a result, people face several health complications and causes like heart disease, eye problems, etc., (Mirzazada *et al.*, 2021; Huiwen *et al.*, 2021). Several researchers consider these difficulties in creating automatic systems for developing the diabetic disease classification system (Azad *et al.*, 2021).

The DDC system has been developed by applying data mining and machine learning techniques (Abdulqadir *et al.*, 2021; Rghioui *et al.*, 2021) because it can process extensive data. The data mining techniques are used on the clinical data to perform the data cleaning and transformation process, which minimizes computation complexity and time. In addition, machine learning techniques (Khan *et al.*, 2021; Kudari, 2021) such as Artificial Neural Networks (ANN), Support Vector Machine (SVM), Decision Tree (DT), K-Nearest

Neighbouring (KNN), and Hidden Markov Model (HMM) are applied to classify the diabetic features. The traditional classifiers effectively work on the diabetic features; however, the researchers enhance their analyses by using the Deep-learning Neural Network (DNN) (Zak and Krzyżak, 2020) to improve the overall diabetic disease prediction efficiency. The DNN approach improves classification performance using multiple layers, functionalities, and a pre-training model. The deep learning model automatically extracts the features from the raw input data and requires minimum training to classify the high-dimensional data. Deep learning networks do not rely on prior data and knowledge; it has high-level abstraction and feature representation (García-Ordás *et al.*, 2021) than any machine learning model. It can learn important relationships in any data that is both unstructured and unlabeled and records for future reference with similar symptoms or diseases.

The motivation behind this research background is to improve the accuracy of diabetic disease detection effectively. Traditional deep learning models have been processed the high data volume; therefore, existing systems fail to classify the efficient parameters and also because of insufficient system flexibilities. The pooling layers reduce the dimensionality of data, which causes information loss between the features. The existing model failed to meet the convergence problem, non-converging optimization complex predictions, and latent and predominant feature extraction. Especially in the deep learning type Long Short Term Memory (LSTM), the neural network failed to initialize the random weight initialization, which is prone to data overfitting. Hence, to avoid dropout, the input and recurrent connections of LSTM units are probabilistically excluded from activation and weight updates while training the network. The evaluation of the method proposed using accuracy, error rates, precision, recall, and correlation coefficients is demonstrated.

Therefore, the primary purpose of this study is to address the above-discussed challenges and improve overall diabetic disease detection accuracy. The objective is achieved by applying the Flock Optimization Algorithm-based Deep Learning Model (FOADLM). The discussed approach employs a meta-heuristic optimization algorithm to generate the diabetes sequence while considering the feature association; effectively analyzing each feature aids in resolving the discussed challenges and maximizing overall prediction accuracy. The discussed system was implemented using the MATLAB tool and system efficiency was evaluated using performance metrics.

This section discusses the literature survey of various researchers' opinions regarding the diabetic disease detection process, which helps to get the idea and framework for developing the DDC system.

Nadesh and Arivuselvan (2020), the cardiovascular disease risk is predicted using a deep learning model. The deep model utilizes the autoencoder to estimate risk using the reconstruction error data. The whole heart disease dataset is divided into training and testing sets to perform the prediction. The experimental results show that the auto-encoder-based approach attained a maximum of 96.16%.

Wang *et al.* (2020) combined Variational Decomposition Modal (VDM) and Improved Particle Swarm Optimization by optimizing Long Short-Term Memory Networks (IPSO-LSTM). The method uses the CGM data to investigate diabetic disease. The effective utilization of the particle swarm algorithm procedure achieves high prediction accuracy 30, 45 and 60 min in advance. The execution complexity of the proposed method is high due to the assimilation of hard-level optimization and learning techniques. Multi-information consideration of the subject is not accounted which would improve the accuracy of the prediction.

Ezzat *et al.* (2021) introduced a gravitational search-optimized deep-learning approach for diagnosing COVID-19 disease. The optimized network processes the chest X-ray images to diagnose COVID-19. Here, DenseNet121 architecture is applied to detect the affected rate of COVID-19 using a social ski driver. This process ensures up to 94% accuracy on the test set.

AlZubi *et al.* (2020) introduced the tubu-optimized sequence modular network for predicting Parkinson's brain disorders from IoT-based collected data. The created system reduces the false classification accuracy and improves the disease prediction rate with maximum speed.

Haque *et al.* (2021) introduced an adaptive neuro-fuzzy inference system for making the diabetic classification process. The analysis system uses the MNSI dataset, which has 10543 samples, to analyze the diabetic details. The collected information is processed according to the fuzzy rules that help to identify the diabetic disease with 91.17% accuracy. However, this method needs improvement to increase the accuracy, and data correlation should be analyzed to enhance the overall performance.

Fitriyani *et al.* (2019) Applied the Ensemble Learning Approach (ELA) for creating the diabetic prediction model. The method uses the T2D dataset information to process the introduced ELA function. The method uses the ensemble layers and deep learning parameters to compute the normal and diabetic features with 96.74% of the dataset. Even though the method works effectively, this process requires optimization to enhance overall efficiency.

Yin *et al.* (2019) introduced the diabdeep approach to detecting diabetic disease using wearable medical sensors. The sensors continuously record the patient's health information processed by an effective neural network. The network uses the multiple layers that use the

sigmoid activation function to obtain the output. During the analysis, ImageNet dataset information is utilized for analyzing the diabetic information. The successive utilization of the learning function improves diabetic recognition accuracy by up to 95.7% of accuracy.

Li *et al.* (2019) utilize the multi-convolution layer that works effectively in parameter reduction, whereas the system fails to classify the efficient parameter due to insufficient system flexibility. The system resolves the other research work issues effectively. However, this method has a few disadvantages. High-quality training data is required for retaining prolonged accuracy results. The validation instances increase the time lag and the modifications are common regardless of the data stream and quantity.

According to the above researcher's opinion, ideas, and thoughts, the DDC system performance should be increased by reducing the discussed challenges. From the guidelines of various researchers' work, the main objective of the work is listed as follows.

To maintain the system flexibility using data sampling techniques incorporated in the first layer as data assimilation incorporated with flock optimization in CNN to investigate the optimal state and relationship between the data, which classifies the data features with flexibility and accuracy.

Investigate the latent and predominant features by applying the sampling and flock optimization techniques. Effectively extracting features minimizes the deviation between real-time and predicted glucose values.

Applying the flock optimization techniques in neural networks involved in the system computation helps to provide the best solution for imbalanced and assimilating data. This process is used to minimize the computation complexity and time complexity issues.

## Materials and Methods

The entire process is carried out using MATLAB R 2021 a tool for analyzing the implemented dataset.

The collected dataset is pre-processed with the Gaussian filtering approach for removing unnecessary data, noise removal, and overfitting issues. The latent feature extraction process involves sex, insulin, glucose level, BMI, and age using sampling and flock optimization techniques based on different characteristics. These extracted features are processed with the LSTM recurrent variant.

### *Diabetic Disease Classification System Using Flock Optimization Algorithm-Based Deep Learning Model (FOADLM)*

This section discusses the working process of the Flock optimization algorithm deep learning model-based

diabetic disease classification system. The main intention of this system is to maximize diabetic disease prediction accuracy by minimizing the deviation between the actual and predicted values. Data imbalance issues must be resolved during the analysis to manage the system's flexibility and complexity. Large datasets with intricate patterns and difficult challenges are frequently well-suited for DL. DL may be a reasonable option because the challenge of detecting diabetes illness is complex and necessitates the analysis of a sizable volume of data. DL models frequently need a lot of data to train. DL can be supported by a large dataset for identifying diabetes disease. In this case, the deep learning network effectively analyses the feature using flock optimization techniques on the network layer. The derived features successfully resolve the concerns with data availability. The most accurate identification of normal and diabetic features is made possible by efficiently using activation functions and network parameters.

The objective of the work is attained by applying the Flock Optimization Algorithm Deep Learning Model (FOADLM) optimized feature modeling approach based created Diabetic Disease Classification system (DDC). Then, the detailed working process of the introduced FOADLM system is illustrated in Fig. 1.

The processing task involves the first step, which is to clean up the input dataset of any noise. Noise is undesired or irrelevant information that may compromise the precision of disease prognosis. After the noise has been eliminated, the data is analyzed to obtain pertinent information crucial for diagnosing and categorizing cases of diabetes illness. The feature extraction procedure is optimized using the flock optimization algorithm. Finding the most pertinent and instructive elements inside these clusters is the aim. Sampling approaches, including simple random and cluster sampling, are used to hone the feature selection further. Based on data similarities, clusters are constructed and subgroups of data are chosen for examination. These methods speed up computation and increase the accuracy of disease prediction. The chosen features are mapped to produce vectors of characteristics that represent the data. For this, convolution and pooling layers are used, which entail mathematical processes to change the characteristics into a format appropriate for additional analysis. The result of these assignments is to improve the precision of diabetes illness identification. To categorize people as normal or to have diabetes disease based on the extracted features, the chosen features and optimized feature vectors are fed into an ML or deep learning model, such as Long Short Term Memory (LSTM).

Figure 1 illustrates that the working architecture of the introduced Flock Optimization Algorithm-based

Deep Learning Model (FOADLM) optimized feature modeling approach created the Diabetic Disease Classification system (DDC) (Abdulqadir *et al.*, 2021; Rghioui *et al.*, 2021). The algorithm uses different stages such as data collection, pre-processing (Sanjeevi *et al.*, 2022), feature extraction (Balasubramanian *et al.*, 2023), selection, and classification to analyze the diabetic data. Each step uses a specific processing function while investigating the diabetic information. Moreover, optimization techniques are incorporated with deep learning (García-Ordás *et al.*, 2021) that optimize the feature vector derivation and prediction process performance. In addition, the optimized learning process in the network reduces the feature map dimensionality, which directly indicates that the method chooses the appropriate features from the feature set. It shows that the introduced optimization technique improves overall prediction performance and accuracy by solving the discussed issues. The detailed working process of the presented FOADLM approach is explained below.

### Pre-Processing

The first step of this study is pre-processing, which removes unwanted data from the collected dataset. Generally, the dataset consists of data, missing values, irrelevant information, and outlier data. Identifying the features of an implemented dataset with missing values is denoted as NotaNumber (NaN). For each feature with missing values, calculate the mean of the available data points in the future. The process involves summing all the available values and dividing by the number of non-missing values. Replace the missing values in each feature with the calculated value for that feature. It suggests that the identical average value for the relevant column is used to replace each missing value in a specific column. The implemented dataset is now full and suitable for analysis after mean imputation because the imputed columns no longer have any missing values. Pre-processing processes can proceed with Gaussian filtering to improve the collected information quality and minimize noise after the missing values have been correctly attributed.

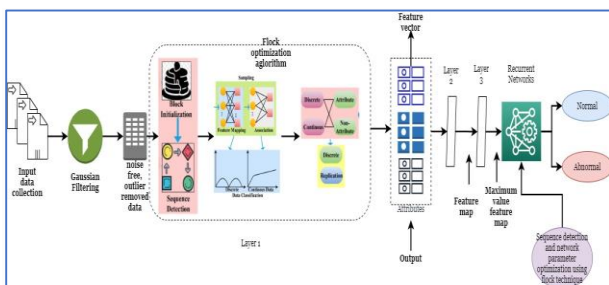


Fig. 1: Architecture of FOADLM-DDC system

The unwanted details affect the diabetic prediction efficiency; the unwanted data creates data overfitting issues. The problem is overcome by applying the Gaussian filtering approach, which utilizes the Gaussian function as an impulse response to remove the unwanted details. The Gaussian function reduces the uncertainty principle issues while analyzing the data with minimum delay. During the noise removal, the filter uses the convolution operations with the Gaussian function. Consider the input data  $I (i_1, i_2, i_3, \dots, i_n)$  which has a few irrelevant or noisy information that must be removed before processing. The input has to be convoluted with the Gaussian function  $G_\sigma(x, y)$  to remove the noise. The  $G_\sigma(x, y)$  value is defined as using Eq. 1 that represents the Gaussian function:

$$G_\sigma(x, y) = \frac{1}{2\pi\sigma^2} e^{-\frac{(x^2+y^2)}{2\sigma^2}} \quad (1)$$

Gaussian filtering is frequently used to remove noise from data because it successfully preserves the fundamental structure of the data while minimizing the consequences of unpredictable or undesirable fluctuations, called noise. Gaussian filters smooth the data and retain the low-frequency aspects (important features) while lowering the high-frequency aspects (noise). The reason for choosing this is because the Gaussian function gives data points closer to the filter kernel's center larger weights and data points farther out lower weights. In essence, gaussian filtering is a form of weighted averaging. A weighted average of each data point's neighbors, with the weights specified by the Gaussian distribution, is used in place of each original data point. Through weighted averaging, outliers, and random noise are less noticeable. The dimension or dispersion of the Gaussian distribution is controlled by a Gaussian filter's bandwidth, which is frequently represented by the symbol  $\sigma$ . A bigger value produces a wider dispersion and smoother filtration, while a shorter distribution and more focused filtering are produced by a lower value. In contrast, a higher value results in a broader Gaussian distribution, resulting in a lower-frequency filtering with a wider bandwidth. In this instance, the filter's smoothing effect is more pronounced, affecting a wider range of data points and it reduces noise more effectively.

The Gaussian function with the convolution process removes the noise from data and the filtered input ( $fI$ ) is obtained. Suppose the dataset has missing information; it must be received by computing the median value for the remaining column values. This process is repeated until it removes the noise information. The noise removal process helps reduce the data overfitting issue used to manage the computation difficulties in the diabetic prediction process.

## Feature Extraction

The second step is extracting the features from the noise-free input data. After removing noise from the dataset, it has been fed into the first layer. The layer uses the flock optimization algorithm-based searching process to extract the features. During the feature searching process, the flock optimization algorithm divides the dataset according to different characteristics (sex, insulin, glucose level, BMI, age, etc.). The dataset is clustered according to many factors (sex, age, BMI, insulin, glucose level, etc.). These clusters are created to extract important traits and connections among the data elements more easily. Storage needs for a tiny dataset with a limited number of features such as one with less than 1000 attributes) and using common numeric data types, for example, 32-bit floating could range from just a thousand Megabytes (MB) to tens of Gigabytes (GB).

The flock optimization algorithm (Balasubramaniyan *et al.*, 2023) works according to the starling bird's movement and behavior. During the flock's motion, it is related to the neighboring birds and independent of the adjacent distance. Therefore, starling birds respond to the other birds according to the topological distance. The feature extraction process works according to the behavior of the starling birds in the swarm intelligence searching space. The search process utilizes different functions to evaluate each feature to obtain the best features in the data list.

The search space has a set of software agents that are moved in the search space according to their characteristics and movements. In the starling process, agents use three region concepts to select the features. For movements and making decisions inside the search space, software agents performing optimization tasks require explicit representations, defined attributes, and behaviors. They engage with the environment, assess fitness, and modify their behavior following optimization objectives. The flock optimization algorithm's roles should be used to categorize agents. This categorization might encompass traits like how agents move and make decisions during the optimization process and how they align with, repel from, or are drawn to particular features or regions.

The selected agent is aligned with its partner, repulsed by its partner, and attracted to its partner. According to these three characteristics, agents are selected in the search space. The chosen agents search the features in the search space and the movement is updated according to the agent's position and velocity. These features are more helpful in identifying the best solution (pbest). The velocity is updated according to Eq. 2, which defines the velocity updating in the search process for each feature:

$$pbest = xp_i - x_i \quad (2)$$

In Eq. 2,  $x_i$  is represented as the agent's present position, and the  $xp_i$  is denoted as the  $i^{\text{th}}$  best measurement location. The identified pbest solution is used to determine the search direction in the search space. For every search process, the agents' positions and velocities have been updated to reduce the difficulties in the sequence detection process. As said, for every search, the agent  $i$  velocity has to be updated and is denoted as  $v_i$  and finally, the average value of velocity increments is computed. After computing the velocity value, the agent position value is updated. During the search process, agents are chosen randomly with replacement agents. For every agent  $i$ , the partner  $j$  must be selected with the condition  $d_{ij} < rA$ . Here  $rA$  is denoted as the repulsion and  $d_{ij}$  is represented as the distance between the agents. This process uses the roulette wheel selection process to select the neighboring agent  $j$ . Equation 3 defines the probability value calculation for identifying the agents in the search process:

$$p_j = \frac{(1/d_{ij})}{\sum_k(1/d_{ik})} \quad (3)$$

According to Eq. 3, the neighboring agents are computed within the  $rA$  for agent  $i$ . This process repeats every data in the search space. The search process should be greater than the population in the search space. Usually, the population time is used to search the features in the search space. The search process computes the pbest solution by using the fitness function. According to the solution, a sequence of features is detected in the data list. The valuable features are identified when the relationship between the data is analyzed.

## Sampling Techniques

Sampling techniques are incorporated during the analysis to improve the overall relationship identification process. The sampling process investigates each attribute in the dataset and the clusters are formed according to the data similarities. The main reason for cluster sampling is to improve disease prediction accuracy, make implementation easier, provide convenient access, and have the minimum computation time. In addition, the sampling technique minimizes the variability and ensures feasibility. The cluster samples are first selected in cluster sampling and elements are chosen to form the clusters.

Let's assume the dataset has  $N$  populations in which the  $n$  clusters are selected during sampling. After choosing the cluster, a Simple Random Sampling (SRS) procedure is applied to identify the cluster elements. The SRS process selects the members from the collection of samples, which is done randomly. During the selection, each subset has the same probability value due to this

reason, which is called unbiased sampling. The SRS process gives the same selection chance for everyone in the population, named Equal Probability Sampling (EPSEM). The sampling process analyses the data list; the same probability value-related samples are removed and grouped. This sampling process was repeated for  $k$  size in the data list. Selecting  $N$  number of clusters and  $n$  number of members repeated in multi-stage sampling reduces the computation cost and data searching time. The computed probability value and uniform distributions effectively predict the relationship between the data. Then, each sample is examined and sequence attributes are detected according to the flock optimization process. Detecting the attributes and relationships helps resolve the computation complexity because the interrelationship data only identifies the most relevant patterns related to attributes. The clustered inputs are fed into the multi-layer convolutions to identify the feature vector ( $F$ ). Equation 4 defines the convolution process in the sequence detection to obtain the feature map:

$$z[m] = \sum_{i=-l}^l x[i]. \delta[m - i] \quad (4)$$

Equation 4,  $x[i]$  Input, kernel  $-\delta$  (size 8), convolution result is  $z$  with index  $m$ , in the first layer. Then, the computed convolution  $z[m]$  is transferred into the next convolution layer with a pooling function to obtain the feature map ( $y^*$ ) which is obtained after performing down-sampling in that convolution layer. The maximum feature map ( $Y$ ) is obtained by examining ( $y^*$ ) and the computed features ( $Y$ ) are fed into the recurrent layer to identify the diabetic disease.

### Diabetic Disease Prediction

The recurrent Long-Short Term Memory Network (LSTM) processes the extracted features. The LSTM network has 64 cells with recurrent layers and three gates: Input, forget, and output. Every gate in LSTM has specific functions that help identify the output for a particular input. In addition, the cells have memory units that store every processing information. The memory cells are more valuable to simply the process while computing the outputs. The memory cell updates the processing inputs in every computation in a specified time interval. During the computation, the network has one recurrent layer, 64 cells, and the dropout layer to eliminate irrelevant information. The dropout layer eliminates the overfitting problems that cause to maximize the generalization and prediction accuracy. According to the discussion, every gate output computation is illustrated in Eqs. 5-11 defines the overall LSTM calculations for processing gates to identify the accuracy of diabetic disease among individuals:

$$f_t = \sigma_g(W_f x_t + U_f h_{t-1} + b_f) \quad (5)$$

$$i_t = \sigma_g(W_i x_t + U_i h_{t-1} + b_i) \quad (6)$$

$$O_t = \sigma_g(W_o x_t + U_o h_{t-1} + b_o) \quad (7)$$

$$g_t = \sigma_t(W_g x_t + U_g h_{t-1} + b_g) \quad (8)$$

$$c_t = f_t \circ c_{t-1} + i_t \circ \sigma_t(g_t) \quad (9)$$

$$h_t = O_t \circ \sigma_t(c_t) \quad (10)$$

$$y_t = O_t \circ \sigma_t(c_t) + x_t \quad (11)$$

In the above computations from Eqs. 5-11, input sequences are denoted as the  $x_t = \{x_1, x_2, \dots, x_T\}$ , output sequence is represented as  $y_t = \{y_1, y_2, \dots, y_T\}$ ,  $W$ ,  $U$ , and  $b$  are denoted as the network parameters such as weight and bias. Here,  $c_t$  is represented as the memory cell vector, the forget gate is  $f_t$ . The input gate is denoted as  $i_t$  and the output gate is represented as  $O_t$ . During the computations, the sigmoid activation function  $\sigma_g$ , hyperbolic tangent  $\sigma_t$ , and dot product  $\circ$  are applied to get the output value. Equation 12 defines the computed values are fed into the last recurrent layer, which uses the weights and bias values to estimate the net output:

$$Z_i = \text{sigm}(\sum_{i=1}^N Y_i w_i + b_i) \quad (12)$$

Equation 12, the net output  $Z$  is computed by using the fully connected network parameter weights  $w_i$  and bias value  $b_i$ . The sigmoid activation function is utilized to get the final output, which is computed as  $\text{sigm} = \frac{1}{(1+e^{-a})}$ . The computed output value is compared with the training dataset to estimate the error value. The network parameters are updated to minimize the misclassification error rate if the computed values deviate from the actual value. Here, flock optimization working behavior is used to select the optimized parameters in the search space. The optimization algorithm-based selected process minimizes the classification error rate and improves overall diabetic disease prediction accuracy. Then the DDC system algorithm's overall working process is illustrated in Table 1.

According to the algorithm steps, diabetic diseases are predicted and the effectiveness of the created DDC system is evaluated using experimental results and discussions. According to the research problem, the dropout layer usage eliminates the overfitting issues that make it difficult to maximize prediction and generalization accuracy. If the estimated values differ from the real value, the network parameters are modified to reduce the misclassification error rate, thus automatically solving the convergence issues during training.

**Table 1:** FOADLM algorithm steps

Initialize	
input $I (i_1, i_2, i_3, \dots, i_n)$ ; features $F(f_1, f_2, \dots, f_n)$ , weight $w$ , bias $b$ , search space $S$ with dimension $D$ , fitness function $f(x)$ (initial = 0), total number of elements in the Flock $n_b$ number of birds in the Flock $n_{cb}$ , inertial coefficient $\omega$ , cognitive coefficient $\lambda$ , social coefficient $\gamma$ and topological coefficient $h$ , velocity $\mu_k$ and position of the bird $x_k$ (pre-processing)	
Step 1:	Convoluting $I$ with $G_\sigma(x, y)$ // Gaussian function $G_\sigma(x, y) = \frac{1}{2\pi\sigma^2} e^{-\frac{(x^2+y^2)}{2\sigma^2}}$ The output of step 1: filtered input ( $fI$ ) (Feature extraction)
Step 2:	Analyze $S$ and divide the data according to different characteristics (sex, insulin, glucose level, BMI, age, etc.) For every data, analyze ( $x_k, \mu_k$ ) Evaluate fitness, $f(x) = f(x_k^{(1)}, x_k^{(2)}, x_k^{(3)}, \dots, x_k^{(D)})$ Compare fitness with the particle's best fitness value, then assign the current position as the best Update the best fitness Compare fitness with the best global fitness Update global fitness End loop Transfer $fI$ into multi-layer convolutions to get the feature vector $F$ . // defined convolution as $z[m] = \sum_{i=-l}^l x[i] \cdot \delta[m-i]$ , $x[i]$ input, kernel- $\delta$ (size 8), convolution result is $z$ with index $m$ , in the first layer. //(prediction)
Step 3:	Transfer the $z[m]$ into the next convolution layer with the pooling function to obtain the feature map ( $y^*$ ) which is obtained after performing down-sampling in that convolution layer.
Step 4:	The maximum feature map ( $Y$ ) is obtained by examining ( $y^*$ )
Step 5:	The final $Y$ -predicted convolution layer fed into the recurrent layer //Here LSTM network is trained by using respective inputs and outputs, which helps to predict the incoming input pattern// //The network uses the input vector, output vector, and memory cells to analyze input data//
Step 6:	Fed $Y$ into the input gate, forget gate, and output gate
Step 7:	Get $Y_{out}$ value from the output gate
Step 8:	Update ( $w$ and $b$ ) according to the flock optimization process defined in step 2
Step 9:	Compute the overall out using the sigmoid function ( $Z_i$ )
Step 10:	Predict the patterns as abnormal or normal

## Results and Discussion

This section discusses the Flock Optimization Algorithm-based Deep Learning Model (FOADLM) optimized feature modeling approach based on the Diabetic Disease Classification System (DDC) effectiveness. The DDC system uses the PIMA Indian dataset, OhioT1DM dataset, and Azure diabetic dataset information to evaluate the system's effectiveness. The collected data set information is divided into 80% training set and 20% testing set. The collected data set information is divided into 80% training set and 20% testing set. The training utilizes the same FOADLM procedure, creating patterns that participated during the testing. The created DDC system's effectiveness was analyzed using metrics such as Mean Square Error rate (MSE), Root Mean Square Error rate (RMSE), precision, accuracy, Matthew correlation coefficient, computation time, reliability, and scalability.

### PIMA Indian Dataset

This research uses the PIMA Indian diabetic datasets (UCLML, 2016; Marling and Bunescu, 2020; Microsoft Ignite, 2022), consisting of 9 attributes; the complete information is gathered from the female participants. Diabetic disease has been divided into three types: Type 1, type 2, and gestational; predictive models can be created using ML algorithms that analyze past patient data,

including the dataset mentioned in the research study. These models can discover patterns and connections between several patient characteristics, such as whether or not a patient is pregnant, their blood sugar levels or blood pressure, and the existence or lack of diabetes. Once trained, the algorithm can determine, based on a patient's characteristics, if they are likely to get diabetes. The most useful patient characteristics for diagnosing diabetes can be determined automatically using ML techniques. The feature aids in prioritizing the most essential data, such as blood glucose levels and BMI, while eliminating the less crucial ones, improving the diagnosis model's accuracy. ML models can categorize patients into several groups, including normal or abnormal, as stated by the classification variable in the dataset. Based on patient data, classification algorithms, including deep neural networks and LSTM, can be taught to generate these binary predictions. ML can assist in customizing treatment regimens for particular patients. ML algorithms can suggest individualized treatment approaches, including medication schedules or nutrition programs, by considering a patient's traits and medical background. The advantage of using machine learning to handle and analyze massive and complicated healthcare data is that it does so quickly. It can help medical professionals diagnose patients more quickly and accurately, personalize treatment approaches, and improve patient outcomes in conditions like diabetes.

**Table 2:** Samples of the PIMA Indian dataset

Pregnancies	Glucose	Blood pressure	Skin thickness	Insulin	BMI	Diabetes pedigree function	Age	Outcome
0	119	64	18	92	34.9	0.725	23	0
1	0	74	20	23	27.7	0.299	21	0
5	73	60	0	0	26.8	0.268	27	0
4	141	74	0	0	27.6	0.244	40	0
7	194	68	28	0	35.9	0.745	41	1
8	181	68	36	495	30.1	0.615	60	1
1	128	98	41	58	32.0	1.321	33	1
8	109	76	39	114	27.9	0.640	31	1
5	139	80	35	160	31.6	0.361	25	1

Therefore, female participants are used to collecting the data. So, initially, a pregnancy test should be recorded; if the patient is pregnant, it is easy to identify the type of diabetes. Then the Plasma glucose level should be recorded every 2 h, which is done by performing the oral glucose tolerance test. Next, diastolic blood pressure should be analyzed and then triceps skinfold thickness (mm) should be checked. Afterwards, body mass index ( $(weight(kg)/Height(m)^2)$ ) should be calculated because being overweight may be the reason for the person with diabetes. Additionally, for every 2 h, the serum insulin ( $\mu U/mL$ ) test should be checked and diabetic pedigree function should be examined. The last age of the patients should be noted to understand the diabetic disease prediction process. In addition to this information dataset already has class variables such as 0 (ordinary people) and 1 (presence of diabetic people). This information is collected from 768 patients and the sample Pima Indian Diabetic dataset details are depicted in Table 2.

#### OhioT1DM Dataset

The second dataset utilized in this study is the OhioT1DM dataset is available to researchers interested in improving the health and well-being of people with type 1 diabetes. It contains eight weeks' worth of data for 12 people with type 1 diabetes. These people were on insulin pump therapy with Continuous Glucose Monitoring (CGM). They provided blood glucose data, insulin data, self-reported life event data, and data from physiological fitness bands. The dataset includes a CGM blood glucose level every 5 min; blood glucose levels from periodic self-monitoring of blood glucose (finger sticks); insulin doses, both bolus and basal; self-reported mealtimes with carbohydrate estimates; self-reported times of exercise, sleep, work, stress, and illness; and physiological data from fitness bands.

#### Azure Diabetic Dataset

The Diabetes dataset has 442 samples with 10 features, making it ideal to start with machine learning algorithms. These dataset samples are analyzed using the above-discussed methods to get the exact diabetic output. Here, gaussian filtering is applied to remove noise and missing

information from the dataset. Then sampling process is performed to cluster similar information and the sequences are detected according to the flock optimization algorithm. Then, features are extracted using the convolution layer, which the LSTM network processes to predict the exact output. According to the description, outputs are estimated continuously and the system performance is evaluated using the below metrics:

$$Mean\ Square\ Error\ (MSE) = \frac{1}{n} \sum_{i=1}^n (Y_i - \hat{Y}_i)^2 \quad (13)$$

$$Root\ Mean\ Square\ Error\ (RMSE) = \sqrt{\frac{1}{n} \sum_{i=1}^n (Y_i - \hat{Y}_i)^2} \quad (14)$$

Equations 13-14, define the error metrics called *MSE* and *RMSE* calculations where *i* is denoted as the variable, *N* is the number of data actual output is defined as  $Y_i$ , and predicted output is defined as  $\hat{Y}_i$ . Equation 15 defines the precision calculation for accurately identifying the disease among individuals. Equation 16 defines the improved accuracy obtained using the proposed FOADLM method. Equation 17 defines Matthew's correlation coefficient to correlate the features extracted and applied for classifying the disease as normal and abnormal sequences:

$$Precision = \frac{True\ Positive}{True\ positive + false\ positive} \quad (15)$$

$$Accuracy = \frac{True\ Positive + True\ Negative}{True\ Positive + True\ Negative + False\ positive + false\ negative} \quad (16)$$

$$MCC = \frac{TP * TN - FP * FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}} \quad (17)$$

Equations 15-17, *TP* is referred to as the *true positive* means correctly classified diabetic data, *TN* is defined as *true negative* and is correctly identified healthy people. *FP* is defined as false positive means, incorrectly identified diabetic people. *FN* is false negative means incorrectly identifying the correct feature. These metrics are utilized to compare the effectiveness of the FOADLM-DDC system. The system efficiency is compared with different methods such as Deep Neural Network (DNN) (Nadesh and Arivuselvan, 2020),

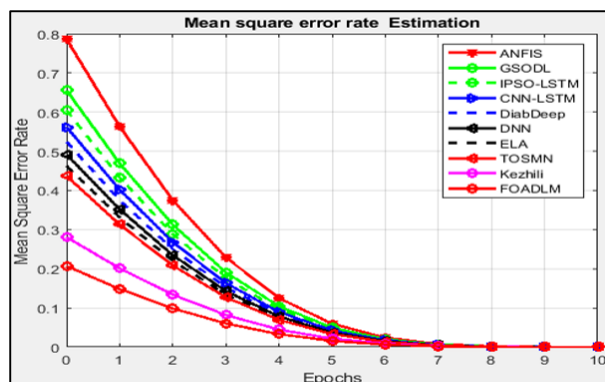


Improved Particle Swarm Optimization optimizing Long Short-Term Memory network (IPSO-LSTM) (Wang *et al.*, 2020), Gravitational Search Optimized Deep Learning (GSODL) (Ezzat *et al.*, 2021), Tubu Optimized Sequence Modular Network (TOSMN) (AlZubi *et al.*, 2020), Adaptive Neuro-Fuzzy Inference System (ANFIS) (Haque *et al.*, 2021), Ensemble Learning Approach (ELA) (Fitriyani *et al.*, 2019), DiabDeep (Yin *et al.*, 2019) and kezhili systems (Li *et al.*, 2019). The obtained results are illustrated in Fig. 2 based on the above discussions.

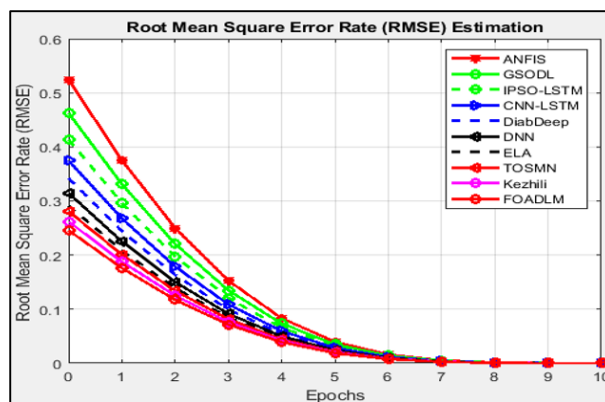
The introduced FOADLM approach attains minimum error value compared to existing methods. The FOADLM method selects the network parameter in an optimized manner that regularizes and optimizes the network parameter. The effective backpropagation of values reduces the deviation between the actual and computed values compared to existing techniques. Here, the sampling process uses the probability values to estimate the similar features in the feature list that are used to simplify the sequence detection process. In addition, the flock optimization algorithm uses the bird's position defined in Eqs. 2-3 helps to improve the search process. For every search, agent characteristics are updated that minimize the computation difficulties. The bird searching procedure applied in the neural network parameter updating process reduces the deviations between the actual and predicted values. The FOADLM attains the minimum RMSE value that indicates the computed output values are effectively matched with the predicted line point. Here, the computed data points are compared with the trained patterns that help to identify the deviation between the actual and predicted values. The method uses the flock's behavior while selecting the network parameters that reduce the error value and increase the data fitting rate. The minimum error rate directly indicates that the system ensures the high recognition accuracy Fig. 2c-d. The FOADLM approach has a high precision value. The high precision value directly indicates that the system accurately predicts the diabetic data. Here, a deep learning network uses the flock optimization techniques in the network layer that analyze the feature effectively. The extracted features effectively resolve the data availability issues. The recurrent neural networks use the different gates that use the network weight and bias ( $w$  and  $b$ ) values with an activation function. The network uses memory cells that continuously store and update the previously processed information. The memory cell, input, output and forget gates  $c_t = f_t \circ c_{t-1} + i_t \circ \sigma_t(g_t)$  (are more useful for predicting the output  $y_t = o_t \circ \sigma_t(c_t) + x_t$ ). The effective utilization of activation function and network parameters identifies the normal and diabetic features with maximum accuracy. The act of

discriminating between data points or instances that reflect non-diabetic situations as opposed to those that indicate diabetic conditions based on attributes is classified as normal and abnormal features. The qualities or traits that describe each data point of individual persons related to people with diabetes are known as features and they play an important role in ML-based classifying tasks. Machine learning models that include the previously outlined FOADLM use the following features as input to determine whether a person is normal (non-diabetic) or abnormal (diabetic). The analyzed features for diabetic disease detection include pregnancies, glucose level, blood pressure, body mass index, insulin level, skin thickness, age factor, and diabetes pedigree function. The goal is to determine which feature combination or pattern in feature values best differentiates between non-diabetic and diabetic situations. The ML model learns from past information in which people's true diabetic status has been identified and then applies this knowledge to produce predictions for fresh, unexplored information based on the value of features.

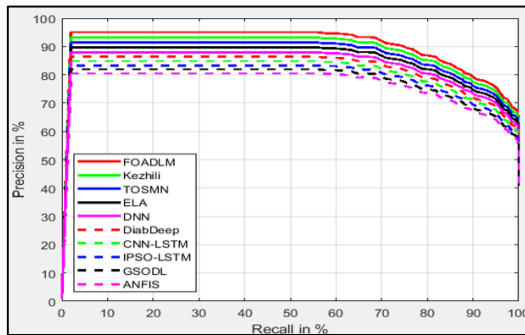
However, the method ensures the minimum computation time and maximum reliability and scalability while analyzing the diabetic features. Then, the obtained results are illustrated in Fig. 3.



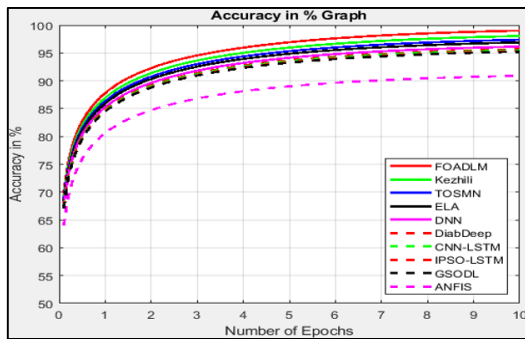
(a)



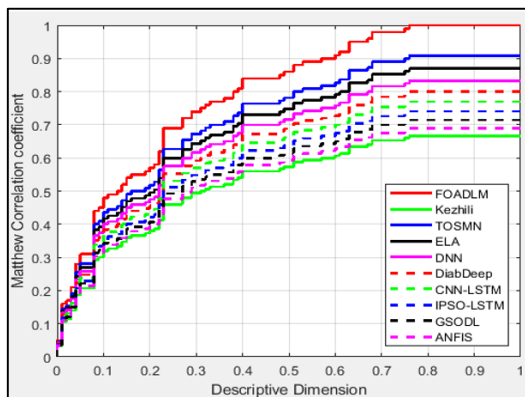
(b)



(c)

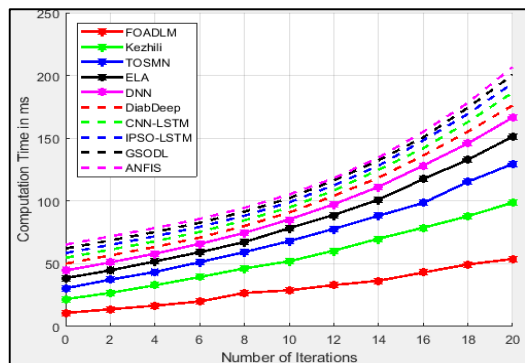


(d)

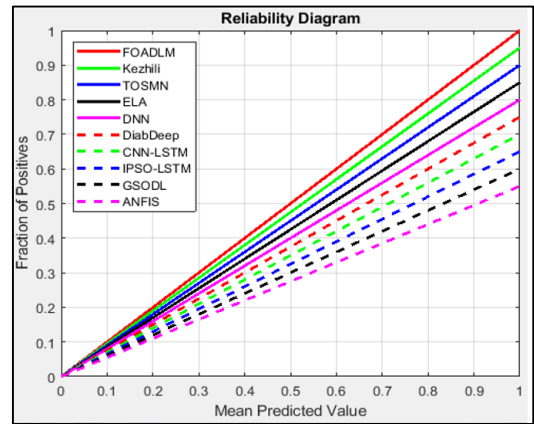


(e)

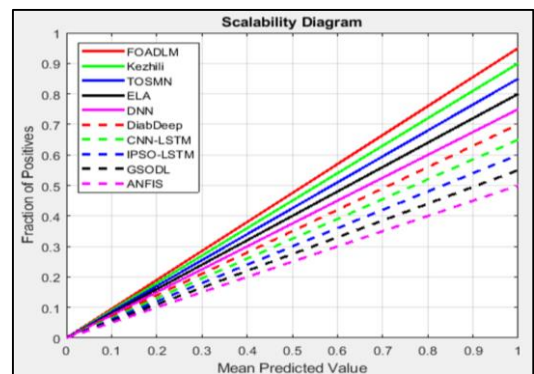
**Fig. 2:** FOADLM system efficiency; (a) Mean square error rate; (b) Root mean square error rate; (c) Precision; (d) Recall; (e) Matthew correlation coefficient



(a)



(b)



(c)

**Fig. 3:** FOADLM Effectiveness Analysis; (a) Computational time; (b) Reliability; (c) Scalability analysis

Figure 2(a) Mean square error rate depicts the source of the input dataset (Marling and Bunescu, 2020; Microsoft Ignite, 2022) with epochs of size 10 for comparison with various algorithms. Similarly, Fig. 2(b) Root mean square rate depicts the source from the input diabetic dataset with the epoch count of 10 iterations for comparison purposes.

Figure 2(c) Precision compares two performance metrics, precision, and recall, with the various algorithms taken from existing studies. Likewise, Fig. 2(d) Accuracy vs Recall shows the prediction accuracy based on various epochs for input diabetic source taken from the previously mentioned dataset (Marling and Bunescu, 2020; Microsoft Ignite, 2022) with the comparison of various algorithms.

Figure 2(e) Matthew correlation coefficient depicts Matthew correlation coefficient with the source taken from (Marling and Bunescu, 2020; Microsoft Ignite, 2022) considering evaluation metrics  $TP$ ,  $FP$ ,  $TN$  and  $FN$ . These values illustrate the quality of diabetic classification models' prediction accuracy levels measured previously in the accuracy calculation.

**Table 3:** Overall accuracy analysis

No.	Methods	Accuracy %
1	Deep Neural Network (DNN) (Nadesh and Arivuselvan, 2020)	96.16
2	Improved Particle Swarm Optimization Optimizing Long Short-Term Memory network (IPSO-LSTM) (Wang <i>et al.</i> , 2020)	95.00
3	Gravitational Search Optimized Deep Learning (GSODL) (Ezzat <i>et al.</i> , 2021)	95.00
4	Tubu Optimized Sequence Modular Network (TOSMN) (AlZubi <i>et al.</i> , 2020)	98.52
5	Adaptive Neuro-Fuzzy Inference System (ANFIS) (Haque <i>et al.</i> , 2021)	91.17
6	Ensemble Learning Approach (ELA) (Fitriyani <i>et al.</i> , 2019)	96.74
7	DiabDeep (Yin <i>et al.</i> , 2021)	95.30
8	Kezhili systems (Li <i>et al.</i> , 2019)	98.63
9	FOADLM	99.23

The successful utilization of each function in the network improves the overall recognition rate. In addition to this, the method has a flock optimization procedure that reduces the misclassification error rate. In addition, the method uses the learning parameter and objective functions that minimize the data availability issues in various iterations. The continuous training improves the overall prediction rate and classifies the features with minimum computation time. During the implementation, sampling techniques that investigate the data characteristics and relationships help minimize the deviations in computed output. In addition to this, it improves the system's flexibility, reliability, and scalability.

This effectiveness is determined in MSE and RMSE metrics. Our work uses the LSTM approach to train the data feature, which helps to reduce the computation time of diabetic prediction. In addition, it correlates the data from the previous stage of analysis. This training process improves the overall relationship between the evaluated data using the Matthew correlation coefficient and precision metrics. The results discussed comparing obtained results with prior research or relevant benchmarks to provide highlights for improvement and suggestions for future research where further investigation is needed based on the findings. Ensuring that the information has backed any conclusions from the findings and is not being unfairly interpreted to justify unfounded assertions related to diabetic disease detection using FOADLM. Then, the overall obtained efficiency is illustrated in Table 3.

Table 3 clearly states that the introduced method FOADLM approach attains 99.23% accuracy while classifying the diabetic data. The effective utilization of the sampling techniques and filtering approaches overcomes the data overfitting issues. The minimum overfitting data leads to a reduction in the error rate and also improves the diabetic disease recognition accuracy compared to the other methods.

The high-level description of the methodology, algorithm steps, and process involved in the research of diabetic disease detection gives enough detail to replicate the study, particularly focusing on the use of FOADLM for

feature extraction and optimization in diabetic disease detection. A step-by-step explanation of FOADLM, including the specific equations, parameters, and how agents interact with the algorithm. This is followed by specific details on data pre-processing, including the Gaussian filter with missing value imputation and noise removal processes. Precise information on how features are extracted, selected, and transformed from the data, including the feature selection criteria. The details of dataset division, storage, and source with a configuration of neural network and parameters used in evaluating performance metrics. The results include tables or graphs with performance metrics and statistical analysis performed.

## Conclusion

The effectiveness of investigating diabetic disease detection is improved by using the FOADLM approach. Three distinct datasets have been utilized to assess the performance of FOADLM in diabetic disease prediction. For pre-processing the diabetic source information is performed by Gaussian filtering to eliminate noise, followed by clustering using a sampling process to simplify the detection sequence. The identified sequence is been processed using a fully convolutional layer to predict feature vectors. A neural network was employed to recognize diabetic features, with FOA optimizing network parameters to reduce classification error with metrics called mean square error rate and root mean square error rate. The research study concentrated on the use of FOADLM to predict diabetic disease, highlighting crucial components such as data pre-processing, extraction of features, optimization, and overfitting reduction. The noteworthy accuracy of 99.23% illustrates the FOADLM technique's possibility of success in predicting people with diabetic disease. The proposed technique provides a potential approach for accurate diabetic detection by efficiently resolving various processes and outperforming existing methods in terms of detection accuracy. The study results demonstrate FOADLM's potential as a reliable method for diabetic prediction. The future research direction involves the application of optimization techniques in the feature selection process thereby reducing the computational burden and enabling a faster approach to predicting diabetic disease.

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## Author's Contributions

**Divager Balasubramaniyan:** Designed the study, developed the methodology, and implemented the software.

**Nor Azura Husin:** Curated the data and drafted the original manuscript.

**Norwati Mustapha:** Performed the visualization and investigation.

**Nurfadhlin Mohd Sharef:** Provided the software and validation.

**Teh Noranis Mohd Aris:** Reviewed and edited the manuscript.

## Ethics

This article is original and contains unpublished material. The corresponding author confirms that all of the other authors have read and approved the manuscript and no ethical issues involved.

## Conflict of Interest

The authors declare that they have no conflict of interest.

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