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Original Article

Develop the Hybrid Weighed Quantum Shark Optimization with a Faster Mask Deep Convolutional Neural Network to Improve the Performance Analysis of Predicting Diabetes at an Early Stage

R. Annamalai Saravanan

Department of Computer Science with Cyber Security, Hindusthan College of Arts & Science, Coimbatore, Tamilnadu, India.

Corresponding Author : malai24003@gmail.com

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***Abstract* -** *Diabetes is an illness in which the pancreas secretes insulin that is not effective, resulting in a long-term disease. Early diagnosis of diabetes gives patients with diabetes a better opportunity to live healthy lifestyles. Deep learning also removes the need to extract features, unlike traditional methods of analysis that were used. The PIMA Indian diabetic information can be used to identify and predict Type 2 diabetes mellitus through a hybrid machine learning approach to continuous monitoring through publicly available datasets. In order to enhance the accuracy of the diabetic diagnosis at the initial stages, the given study suggests a hybrid model integrating the Weighted Quantum Shark Optimization (WQSO) and Faster Mask Deep Convolutional Neural Network (FMDCNN). The WQSO algorithm combines weighted strategies and Quantum Shark Optimization (QSO) in order to optimize the training of the FMDCNN. FMDCNN is a model that is trained to effectively analyze medical imaging information in order to diagnose diabetes in its early forms. Apply the WQSO solution space calculation and automatically adjust the parameters of the FMDCNN in order to obtain better predictive performance. The proposed system has a good record of accurately predicting early-stage diabetes, as manifested by the comparison of the approach with the current methods and in-depth analysis of the performance. As a result, the proposed system allows doctors to access vital statistics in real-time and obtain comprehensive patient profiles through real-time monitoring.*

***Keywords* -** *Diabetes prediction, Early detection, Weighed Quantum Shark Optimization, Faster Mask Deep Convolutional Neural Network, Hybrid optimization, Deep Learning, Medical image analysis, Predictive modeling.*

1. Introduction

Diabetes Mellitus (DM) often affects people during their most productive years, leading to a variety of long-term impairments that significantly impact both the patients and society. DM is a major global health burden, expected to affect 643 million individuals by 2030, which is one out of every nine people, and 784 million by 2045, which is one out of every eight adults [1]. Middle- and low-income nations are home to 81% of the world's diabetic adults, or four out of five people. In 2021, diabetes caused an estimated 6.7 million fatalities, equivalent to one death every five seconds. Approximately 240 million people live in nations with middle to low incomes, or 44% of the total diabetic population, go undiagnosed [2]. With a 316% increase over the last 15 years, the global health expenditure due solely to diabetes is estimated to have reached USD 996 billion in 2021 [3]. Insulin-producing neurons are destroyed in type 1 diabetes. People with diabetes must continuously monitor their levels of blood sugar and make necessary adjustments by injecting glucose at predetermined intervals in accordance with a doctor's approved procedure. This is needed since it is insulin, which helps the cells to uptake glucose [4]. The main problem associated with the management of diabetes is the optimization of insulin doses to avoid the occurrence of hypoglycemia and hyperglycemia. This is also made difficult by the fact that glucose levels are determined by a variety of factors, including the intake of insulin, food, lifestyle, mental health, and stress, as well as physical exercise. Continuous Glucose Monitoring (CGM) and other types of continuous monitoring of diabetes have made tremendous progress, although it is an intrusive technology. It is only able to give data regarding glycaemic status at a certain time, which may be tricky in cases where the insulin levels may be too elevated or too low [5].

Thus, a proactive detection system could significantly increase the daily management of diabetes by patients. In case the insulin production or secretion is limited, there is an increase in blood sugar, which is one of the symptoms of a metabolic disease called diabetes. It is predicted that by the year 2040, one in every ten people will have developed diabetes. The increasing levels of diabetes are being caused by individual behaviors, various lifestyles, and living standards. Consequently, it is advantageous to research how to identify and cure diabetes at a faster and more precise rate. Genomic variations play a major role in the diagnosis of this illness [6].

Such patterns will be analyzed to produce more accurate and closer results that will assist people in adopting healthier lifestyles that will have minimal chances of causing diabetes in the near future. The focused disease diagnosis will help people who are at risk of getting an illness in the future to become healthier and postpone or even avoid the development of the disease. Machine learning can be used in two key aspects in this regard: anomaly diagnosis and future disease screening. It is possible to predict the development of diabetes using forward prediction algorithms that examine previous and current health history [7].

This is because lifestyle behavior, including nutrition, physical activity, and diet, could significantly determine its growth. Type 2 diabetes is a disease marked by a reduction in the quality of life and life expectancy. It is possible to manage the disease by changing one's way of life and using medications [8]. To prevent potentially fatal complications of type 2 diabetes, it is necessary to diagnose and treat them in time. The accuracy of medical diagnosis-based disease prediction and future forecasting has been the subject of extensive research. In most cases, a combination of many gene patterns triggers a disease. Combinatorial gene sequence recognition, using training genes obtained from sick individuals and reference genes from healthy individuals, was rigorously analyzed [9].

Analyzing the chemical makeup of human genes is incredibly useful for predicting diseases passed down through generations. Genomics studies can help individuals reduce their future risk of disease by altering their lifestyle. DNA analysis assists in better predicting diseases caused by genetic mutations. Biomedical engineers have identified a large gene data collection that has the potential to aid in the prediction of various diseases. Applying the hypothesized process to the Neural Network technique makes it possible to detect gene patterns that damage human body cells [10].

Methods using Neural Networks to forecast illnesses would have low computational delay and high accuracy. Diabetes is a chronic illness that occurs when insulin is not working properly or when body cells do not respond to insulin. During metabolic activity, the hormone insulin converts glucose from meals into energy. Diabetes-related persistent hyperglycemia is associated with long-term harm, malfunction, and damage to several tissues, particularly the urinary tract, eyes, cardiovascular system, blood vessels, and neurons. Risk factors for diabetes include lifestyle choices such as being sedentary, smoking, having high cholesterol, and high blood pressure [11].

Diabetes affects people of all ages, from young children to adults, and symptoms vary among individuals. Maintaining normal blood sugar levels requires medical intervention for some people, including medication, insulin injections, and behavioral modifications, while for others, it is as simple as making healthier choices [12].

Every year, some 1.6 million people die from diabetes, and another 2.2 million people die from excessive blood sugar. Diabetes is one of the seven leading causes of mortality globally, as reported by the World Health Organization. India ranks second in the total number of people diagnosed with diabetes. Early detection of diabetes risks using machine learning methodologies and technology can reduce harmful consequences. Machine Learning (ML) can discover patterns in massive datasets [13]. Data analysis is one of the phases involved in Knowledge Discovery in Databases (KDD). Data mining includes finding and classifying data flaws and data relationships. Machine Learning Techniques (MLTs) are utilized to identify diabetes in its early stages [14].

Diabetes-related Diseases (DD) now account for the highest global mortality toll.

Medical researchers attempt to cluster and recognize the symptoms of medical data by using different MLTs at different points in time. The feature selection is an artificial intelligence mechanism to learn that involves the identification of important features and the elimination of those features that are irrelevant. Another MLT is classification, which is applied in the scientific, commercial, and industrial fields to vast databases to find the answer. In order to classify data, one needs to come up with the rules according to which the classification of the data will be done [15].

1.1. Problem Statement

Since diabetes is a complex and multi-dimensional condition, there is a massive epidemiological challenge in diagnosing diabetes at the earliest stage possible. Environmental variables, lifestyle choices, and inherited susceptibility to diabetes interact in a very complex manner. Early diagnosis is needed to begin treatment promptly and prevent the long-term effects, such as cardiovascular diseases, kidney complications, and neurological injuries. The data set that must be combined to make predictions includes such clinical measurements as lipid profiles and blood glucose level, demographics of a patient, lifestyle factors like nutrition and physical activity, as well as medical imaging data like MRI or retinal scan. The contemporary algorithmic methodologies, like optimization algorithms like genetic algorithms or quantum mechanics-inspired ones, therefore, to make efficient and reliable models to predict, the artificial intelligence techniques, such as deep learning structures, are necessary. This could be used as an indicator of performance to determine how effective the system is in picking people who are at risk of contracting this illness. Improved health outcomes and less financial strain on healthcare systems can result from accurate early diabetes prediction, leading to focused treatments, individualized patient care plans, and healthcare resource optimization.

1.2. Motivation

Scientific information, diagnostic information, and doctor instructions are only some instances of the many sources of the massive amounts of unstructured data produced by healthcare associations. A great deal of demand is placed on the healthcare business. The importance of using data analytics and shaping big data in healthcare is highlighted by the fact that the healthcare sector generates data in several formats, including text, images, audio, video, and Electronic Health Records (EHR). Diabetes mellitus is a chronic illness caused by high blood sugar levels. The main objectives of the many compelling factors that drive the creation of efficient methods to forecast diabetes at the earliest stages are to improve medical results and lower the expense of this illness for people and healthcare providers.

A better quality of life for those with diabetes can be achieved by early identification, which allows for proactive measures to avoid or postpone the onset of problems. Healthcare practitioners can successfully control blood sugar levels by identifying persons at high risk before symptoms emerge. It will enable targeted lifestyle modifications, observation interventions, and potentially drug treatments. Some of the indirect costs related to diabetes include hospitalizations, prescriptions, and lost productivity, which are significant. Diabetes affects medical facilities to a great extent financially. However, this can be reduced through early diagnosis and treatment to eliminate the costly treatment. It is in compliance with the broader shift in favor of personalized medicine to enhance patient outcomes by early detection. Predictive analytics enables the doctor to tailor therapies according to the risk profile of patients, which is why the proactive management of health and optimal health outcomes all become achievable through predictive analytics.

1.3. Research Gap

Although there is extensive research on the application of machine learning and deep learning models in the field of diabetes prediction, a number of challenges have not been addressed. Conventional paradigms tend to use manual feature engineering that is not always scalable and general to diverse patient groups. The current methods of deep learning, though efficient, are unable to tune their hyperparameters optimally, and often find themselves in local minima, and their ability to make predictions becomes limited. Genetic Algorithms, PSO, and simple Quantum-inspired models are optimization algorithms that do not have adaptive weighting and do not effectively search high-dimensional spaces. Additionally, existing CNN-based diabetes prediction algorithms do not support finer-grained and faster extraction of features needed to predict diabetes at its initial stages. Research that combines the use of more complex quantum-inspired optimization and more effective deep convolutional models to provide better predictive capability is also scarce. Thus, there is a research gap to create a more accurate, robust, and clinically application-focused self-optimizing hybrid model of weighted quantum optimization and an improved deep network to predict diabetes at its early stages.

2. Related Works

Noninvasive blood glucose monitoring has recently received several approaches and applications that have been based on machine learning. These methods either depend only on the level of glucose or are not yet accurate enough to be regarded as a reliable indicator of the potentially dangerous glycemic conditions. Proposed are noninvasive blood glucose monitoring systems that are tailored to the requirements of the particular user and which can be accessed via smartphones [16]. Such a system would track different variables like insulin, food, and medicine intake, physical activity, and sleep quality to detect cases of abnormal blood glucose levels. It would automatically record the information about the users in relation to their eating, taking medications, insulin, sleep, and exercise every day and approximate their current level of blood glucose [17].

Another way of forecasting the level of sugar in blood might entail the incorporation of medical data into a language-compatible program to model a glucose expression. This phrase would consider the previous glucose levels, intake of carbohydrates, and insulin injection [18]. This approach would investigate a new methodology based on personalized blood glucose prediction models on the basis of using symbolic regression through language evolution based on the previous research. In symbolic regression, mathematical expressions are developed via genetic programming methods to use the data to evolve the expression [19]. The language-based framework would, in this case, develop the expressions that reflect the complicated interdependences among past glucose levels, carbohydrate consumption, and insulin injections, which lead to a predictive model of blood level. It may be compared to a model that involves the use of Latent Variables with External inputs (LVX) to make predictions. Such a comparison would illustrate the efficiency and possible benefits of the language-based method in the accurate and effective prediction of the level of sugar in the blood [20].

With the growth of obesity and the inability to engage in physical exercise, diabetes has become one of the health issues of great concern in modern culture. Lack of appropriate diagnosis on time promotes diabetes to a life-threatening illness. These effects can only be averted if diabetes is recognized and diagnosed on time.

Consequently, the body excretes elevated blood glucose levels through urine [21]. Despite the abundance of glucose in the blood, cells fail to receive sufficient fuel for their development and essential functions, which is essential to address diabetes assessment of data and forecasting diseases as classification problems. Classifying information is a topic of great interest to scientists in artificial intelligence and economics. Various domains, such as ecological, psychological, medical, advertising, computer vision, and artificial intelligence, use data categorization for a variety of uses [22].

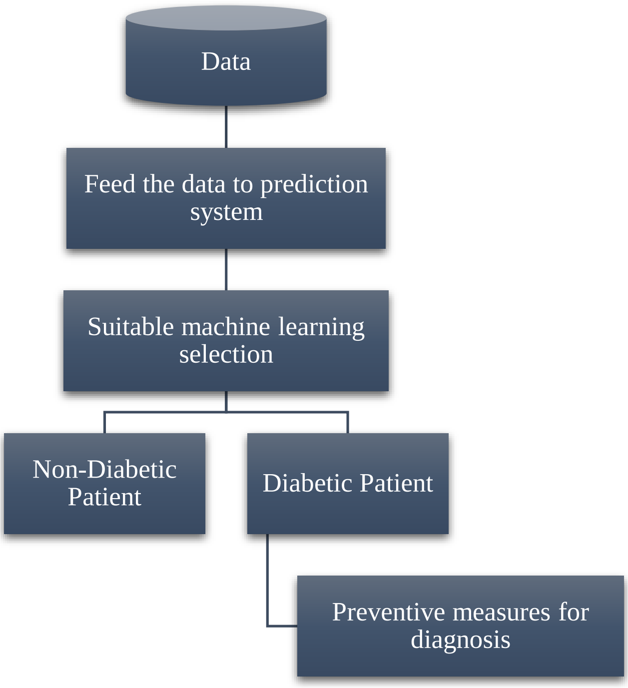


Fig. 1 Flow process of diabetic disease prediction

Classifying objects into several groups is the main goal of information segmentation. Classification involves assigning a value or label to each data object in a given dataset, according to specific characteristics or qualities. Large volumes of information may be arranged and interpreted by practitioners and scholars using this method, producing insightful findings and forecasts [23].

The steps used to forecast the onset of diabetes are shown in Figure 1. Patients should provide their current medical records, after which a suitable machine-learning algorithm is selected. The prediction based on the selected algorithm determines the patient's diagnosis of diabetes. If diabetes is identified, the patient can be diagnosed and given the necessary preventative measures and advice. This approach involves methods for extracting useful insights from data using machine learning and data mining [24]. The data mining techniques, tools, and applications of machine learning relevant to diabetes diagnosis are analyzed. Both supervised and unsupervised learning scenarios utilize association rules. The Support Vector Machine (SVM) remains one of the best classification algorithms for extracting important data and building new hypotheses [25].

When analyzing high-dimensional information, dimensionality reduction and choosing samples techniques are crucial, especially when it comes to diabetic predictions. To improve the accuracy of models and comprehension, these approaches are frequently coupled with conventional machine learning methods.

After identifying suitable dimensionality reduction and sample selection methods, application frameworks are developed to incorporate these techniques effectively. Deep Learning (DL) has made significant advancements in healthcare, leveraging the increased availability of healthcare data and the rapid evolution of DL approaches [26]. These methods are capable of extracting clinically relevant information from vast amounts of healthcare data, which can be used for diagnosis, prognosis, treatment, and prevention. DL enables more efficient patient monitoring and less complicated therapies, contributing to a more adaptable approach to conventional medicine, capable of addressing a wide range of complex diseases [27].

3. Proposed System

Figure 2 depicts the combination WQSO-FMDCNN architecture, which was created to increase the effectiveness and accuracy of initial diabetic diagnosis.

Using concepts from deep learning and optimization influenced by quantum mechanics, this novel approach addresses the complex challenges of medical diagnostics, particularly those related to diabetes prediction. The incorporation of weighted strategies into WQSO enhances its flexibility, allowing for finer-grained control over optimization parameters that are crucial for optimizing deep learning models such as the FMDCNN.

The FMDCNN, a customized form of deep Convolutional Neural Network (CNN) created for medical image processing, can efficiently analyze and interpret complicated medical information such as diabetes-related diagnostic images and medical measurements. This hybrid framework aims for real-time or large-scale deployment in clinical settings, improving model efficiency through quicker training or inference times. Key objectives include optimizing model parameters for greater prediction accuracy, enhancing convergence speed during training, and ensuring scalability and generalizability across varied datasets and patient populations. The creation of the hybrid WQSO-FMDCNN architecture might greatly improve current techniques to perform early diabetic prediction.

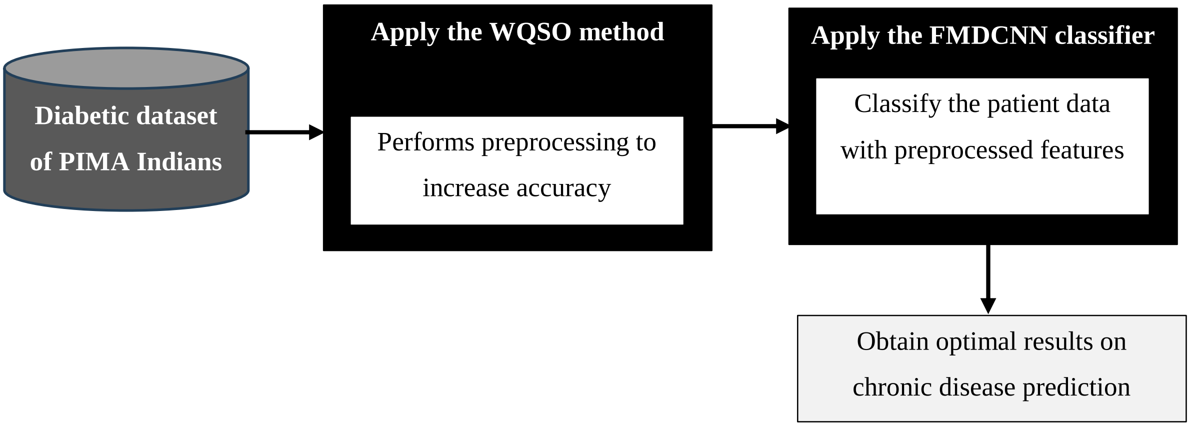


Fig. 2 Proposed architecture

Table 1. Dataset description

Dataset Name	**PIMA Indian Diabetes**
Description	Contains PIMA Indians' medical data, with an emphasis on diabetes diagnosis.
Data Type	Tabular
Feature	Blood pressure, insulin, age, skin thickness, BMI, pregnancy, glucose, diabetes, and outcome (diabetes/non-diabetes).
Instances	769

3.1. Datasets

Table 1 describes the PIMA Indian Diabetes dataset, including its description, data type, attributes, and total number of occurrences.

In this study, the condition was effectively identified using the PIMA Indians diabetes database. There are 768 instances in the PIMA Indians' diabetic collection for learning. A label for each training instance is provided by the eight features and class variables that are part of it. In the dataset, each incident is categorized as either diabetes (positive) or non-diabetic (negative).

3.2. Pre-Processing

The main goal of choosing characteristics is to increase prediction accuracy. In this research, important characteristics from the PIMA Indians diabetes dataset were selected using FMDCNN. To simplify the process of predicting and classifying diabetic chronic illness, standard discriminative analysis is employed to eliminate superfluous features. Simplifying the procedure with CNNs is the main goal of the proposed WQSO-FMDCNN design. Within the input dataset P, consider the number of features, or characteristics $\{s_1, E_2, E_3, \ldots,\}$. For a more accurate prediction of diabetic chronic illness, more relevant features are selected from the dataset P. The initial step in utilizing the FMDCNN separation function is to sort the dataset's characteristics into two groups: relevant and irrelevant. The following is the mathematical expression of it:

$$S = \frac{Var_b}{Var_w} = \frac{Ls_w P}{Ls_b P} \tag{1}$$

Several factors are involved, according to Equation (1): The division function is denoted by S, and Var_b is the dispersion between the two groups, L is a vector utilized for dividing characteristics into two groups, and Var_w is the linear classifier vector's best projecting orientation. A scatter matrix (dimension decrease) is indicated both inside and between the groups s_w and s_b.

The next step is to build the scatter matrix. The following is an estimate of the scatter matrix inside and between the subsets:

$$S_w(m) = \sum_{m=1}^{n} \sum_{a \in m} (S)(S)^T \tag{2}$$

Equation (2) uses m as the scatter matrix inside the subset, a as the characteristic for the splitting functional "$\boldsymbol{S}$," and T as the matrix's transposition. The following describes the distribution of the matrix among the subgroups.

$$S_b(m) = \sum_{m=1}^{n} (Var_w)(Var_w)^T \tag{3}$$

$S_b(m)$, the distribution matrix between the subsets and FMDCNN splits the characteristics of the collection into two groups according to the variability within and the transpose in Equations (3). The pertinent subgroup is then utilized to forecast chronic diabetes illness. It takes longer for the deep neural network (ANN) architecture to analyze the pertinent data subset explicitly. FMDCNN is used to normalize the characteristic subset. Equation (4) uses the standardized value j'.

$$j' = \frac{(a_x - a_{min})}{(a_{max} - a_{min})} \tag{4}$$

$$Q_1 = a.quantile(0.25) \tag{5}$$

$$Q_3 = a.quantile(0.75) \tag{6}$$

$$IQR = Q_3 - Q_1 \tag{7}$$

Table 2. PIMA dataset: missing values

Sl.No.	Attributes Type	Missing Values
1	Age	0
2	Pregnancies	0
3	Blood pressure	36
4	Glucose	6
5	Skin thickness	228
6	BMI	12
7	Insulin	375
8	Diabetes pedigree	0

One popular database for identifying binary problems is the PIMA Indians Diabetes Database, especially in the context of predicting the onset of diabetes. A common pre-processing challenge with this dataset is handling missing values shown in Table 2 and Interquartile Range (IQR) values in Table 3. These missing values are typically indicated by zeroes in certain columns where zero is not a plausible value. For instance, columns such as Glucose, Blood Pressure, Skin Thickness, Insulin, and BMI often contain zeroes that need to be treated as missing values.

To handle this, the first step involves loading the dataset using a data-handling library such as Pandas. Once the sets of data are loaded, the next step is to identify the columns with inappropriate zeroes. This can be done by iterating over the columns and checking for zeroes. After identifying these missing values, different strategies can be employed for imputation. Conventional restoration strategies include utilizing more sophisticated algorithms like models of regression or k-nearest neighbor algorithms, or substituting the values that are unavailable for the column's mean or median. For any prediction models constructed utilizing the Pima database to be accurate and reliable, the values that are missing must be properly corrected.

Table 3. PIMA dataset IQR values

Sl.No.	Attribute values	Missing Values
1	Age	18.0
2	Pregnancies	6
3	Blood pressure	19
4	Glucose	42.26
5	Skin thickness	33
6	BMI	9.5
7	Insulin	28.26
8	Diabetes pedigree	0.39
9	Result	1

3.3. Feature Selection

Wrapper methods are a common approach to feature selection that consists of the training and testing of a model repeatedly, testing different sets of features. Recursive Feature Elimination (RFE) is one commonly employed wrapper method. RFE gradually removes the most insignificant attributes until the desired number of characteristics is obtained. This process involves the arrangement of components based on their rating of significance, and the component with the lowest ranking is removed. It is then retrained on the smaller set of features, and its performance is measured based on some pre-defined metric. This iterative process removes features one by one until a halting condition is achieved. A predetermined number of characteristics or the point at which the vehicle's efficiency does not significantly increase might serve as the halting conditions.

After the process is finished, the selected subset of significant characteristics is used to train the completed model on the entire dataset. By doing this, the model is guaranteed to keep just the most important elements, which may enhance its comprehension and efficiency.

Finding the characteristic with the lowest Mutual Information (MI) values among all of the characteristics is the aim of redundancy.

Assuming that reducing MI among features aids activity categorization, we find that reducing the value of information redundancy across features is beneficial.

$$M_r = \frac{1}{(f)^2} \sum_{\alpha,\beta \epsilon C} MI(\alpha,\beta) \tag{8}$$

MI is a discrete variable; α and β are variables.

$$R = \frac{1}{(f)} \sum_{\alpha \epsilon C} MI(\alpha,\gamma) \tag{9}$$

The class label for discrete variables is represented by the variable γ in Equation (9). When trying to find the genes that are most relevant to each class and their labels, the F-statistics for calculating the mean of the two groups are very different.

$$R = \frac{1}{(f)} \sum_{\alpha \epsilon C} F_s(\alpha,\gamma) \tag{10}$$

$$M_r = \frac{1}{(f)^2} \sum_{\alpha,\beta \epsilon C} i(\alpha,\beta) \tag{11}$$

Utilizing an ensemble mechanism enhances the mRMR method's ability to analyze the feature map and build a more robust collection of features. The feature selection technique for optimizing gene-data analysis is depicted in Figure 3.

3.4. Hybrid Approach

In FMDCNN, various layers play distinct roles in processing complex data patterns. While fully connected, flattening, convolutional, and softmax layers are fundamental, numerous intermediate layers contribute significantly to the model's functionality. The inner convolutional layers handle complex patterns by decomposing data, such as gene sequences, into meaningful features shown in Figure 4. Every convolutional neural network captures key patterns in the input by applying filters. By reducing the spatial dimensions of the information, pooling layers—which usually come after convolution layers—seek to minimize excess fitting and lower the total number of variables.

For example, the max-pooling layer efficiently summarizes the most important characteristics and increases the computational speed of the model by filtering the input by choosing the highest possible value for every zone.

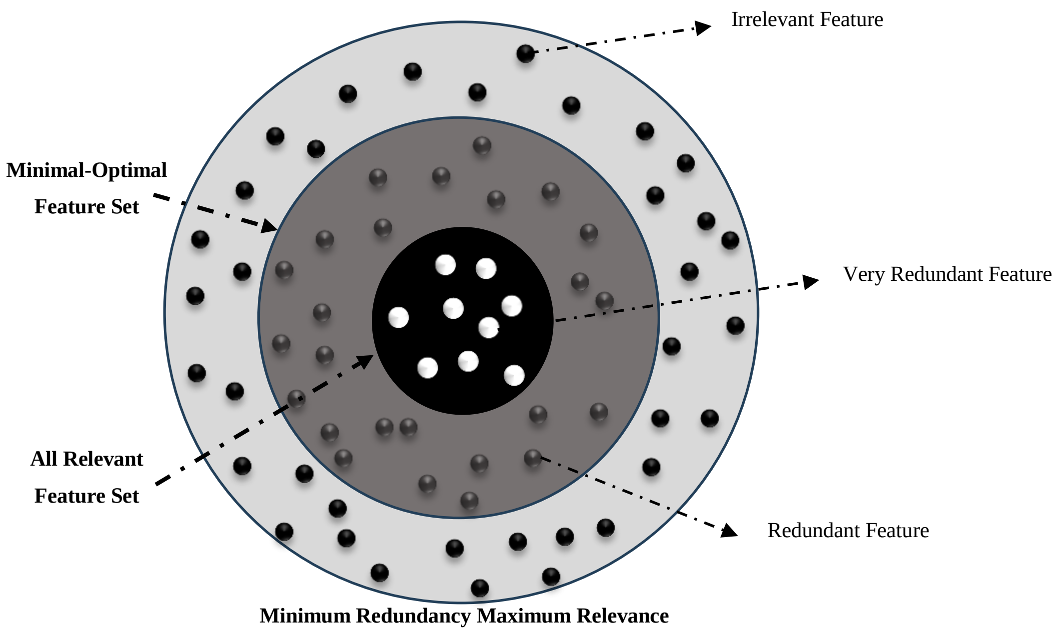


Fig. 3 mRMR features selection method

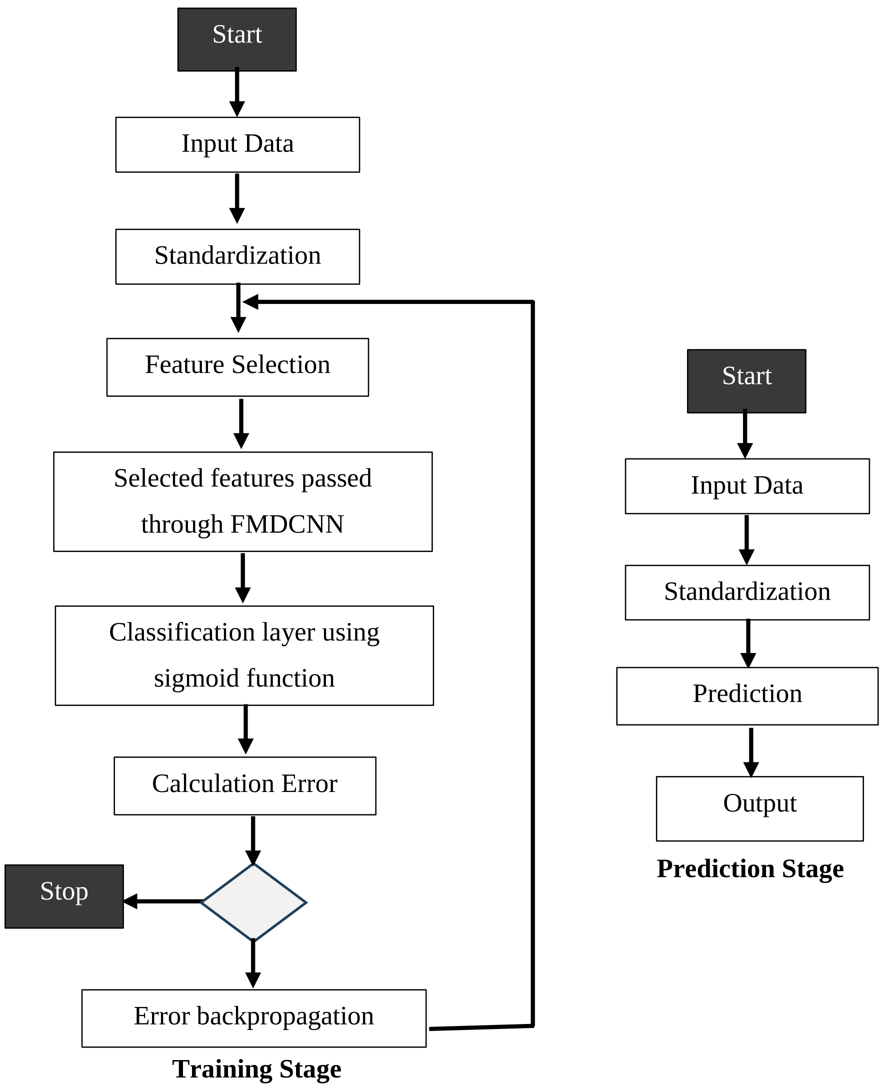


Fig. 4 Process of FMDCNN architecture

The output of the pooled and convolutional layers process is transformed into a single lengthy vector of characteristics by flattened layers, which then use that vector as the input for other layers. This change is necessary for shifting from spatial information to an arrangement suited for fully linked layers. The last phases of the representation are made up of fully linked layers, sometimes referred to as substantial ones.

These layers make it possible to understand intricate, non-linear relationships by connecting each node to each other in the layer before it. After receiving the flattened features vector, the first layer that is fully linked makes accurate forecasts according to the input sequence of genes using weights.

The output probability for tasks associated with classification, like figuring out how likely a gene is to cause an abnormality, is produced by the final layer that is completely connected and a softmax layer.

FMDCNNs are valuable tools for applications like image identification and genetic analysis of sequencing because of their ability to analyze and categorize complex input patterns through the interaction of convolutional neural networks, grouping, reducing, and fully interconnected levels.

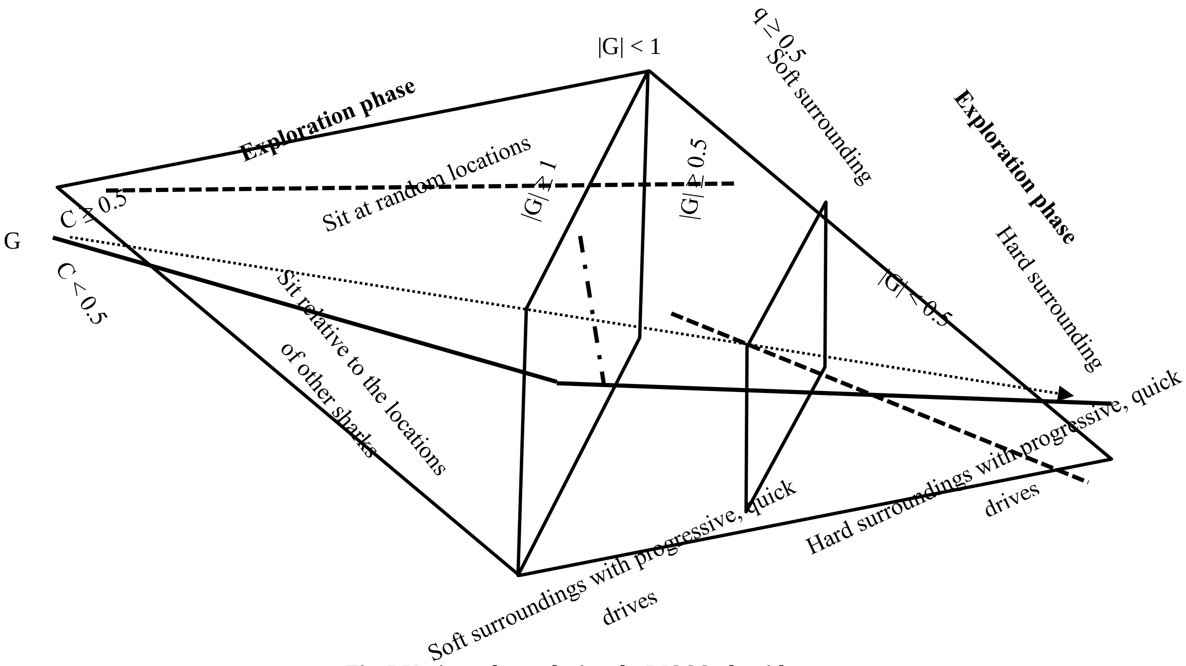


Fig. 5 Various phases during the WQSO algorithm

By iteratively evaluating sequences across the state vector O_x, FMDCNNs can handle sequences of arbitrary length. Each cell's activation function is represented by the tanh. As far as RNN is concerned, the vanishing gradient problem is the biggest obstacle. For every RNN module, the mathematical notations are given in Equations (12-16).

$$N_x = \sigma_N(i_x) \tag{12}$$

$$\sigma_N(i_x) = \sigma_N(\alpha_N z_x + \beta_N R_{x-1} + b_N) \tag{13}$$

$$g_x = \sigma_g(i_t) \tag{14}$$

$$\sigma_g(i_t) = \sigma_g\left(w_g N_x + b_N\right) \tag{15}$$

$$O_x = tanh\left(w_g O_{x-1} + w_{g-1} z_x\right) \tag{16}$$

The input vector z_x, with dimensions 1 × x, is represented by the variable R_x in Equations (12-16). The input vector of dimensions (1 × x) is used to represent the input to the FMDCNN cell. Key aspects are represented by the parameter matrix, which is represented by variables α and β. The value of b_N represents the bias. The mathematical model of the proposed approach and how to use it to get the best possible outcomes. The most recent algorithm in this category, the WQSO method, draws inspiration from nature and is shark-based, metaheuristic, and gradient-free. The sophisticated conduct of the WQSO is on display in its hunting patterns, which are characterized by complex and dynamic environments and victims' attempts to escape. The potential for obtaining a globally optimum solution, rapid convergence, excellent precision, and improved quality are the key benefits of the WQSO method.

Figure 5 shows the WQSO algorithm's working mechanism in steps. Two main phases make up the algorithm: exploration and exploitation. To find prey, the exploration phase mimics the search activity of the Harris Shark. The intelligent search is modeled in the exploitation step.

The victim is surprised as many sharks work together and approach it from different angles. Here is a mathematical model of the sharks' position shift at each exploration iteration:

$$C(i+1) = \begin{cases} C_{random}(i) - n_1|C_{random}(i) - 2n_2C(i)| \\ c \geq 0.5 \\ [C_{victim}(i) - C_{avg}(i)] - n_3(L + n_4(U_L)) \\ c < 0.5 \end{cases} \quad (17)$$

The vector representing the sharks' present locations is denoted as C(i). The sharks' position vector for iteration i+1 is denoted as C(i+1). The victim's location is represented by $C_{victim}(i)$. The present shark population's average location is C_{avg}. At each iteration, the values of the random variables c, n_1, n_2, n_3, and n_4 are to be changed from 0 to 1. U represents the maximum value, and L represents the minimum value of these variables. According to $C_{random}(i)$, the shark was selected at random from the present population. To get the sharks' average position using Equation (18):

$$C_{avg}(i) = \frac{1}{M}\sum_{k=1}^{M} C_k(i) \quad (18)$$

Sharks win this game of hunting by getting closer and closer to their prey before coordinating a swift lunge to kill it. Concurrently, the victim's energy depletes as it employs escape options. After a while, the victim's vitality will be depleted, making them easy prey for sharks. Here, victim energy modeling is defined as follows:

$$G = 2G_0(1 - \frac{i}{I}) \quad (19)$$

The sharks adapt their assault strategy in real-time to the target's evasive moves, performing a series of rapid dives around the victim as they go. When it comes to nondestructive seeking, the research established that LF-based actions are the best techniques for hunters. Victims such as rabbits, monkeys, and sharks often exhibit LF-based movement patterns. The WQSO algorithm makes use of LF-based motions. Figure 6 shows one shark using the aforementioned modeling method. A or B is the next best place to be picked up at each level. All sharks use the same principle when seeking.

$$A = C_{victim}(i) - G|SC_{victim}(i) - C(i)| \quad (20)$$

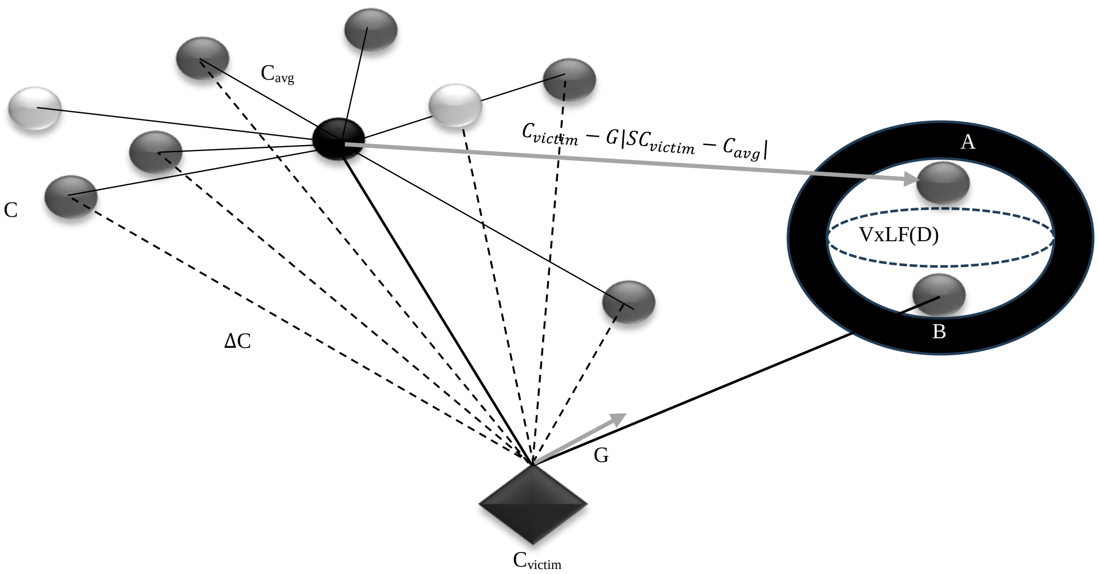


Fig. 6 Overall strategy of vectors of hard surroundings

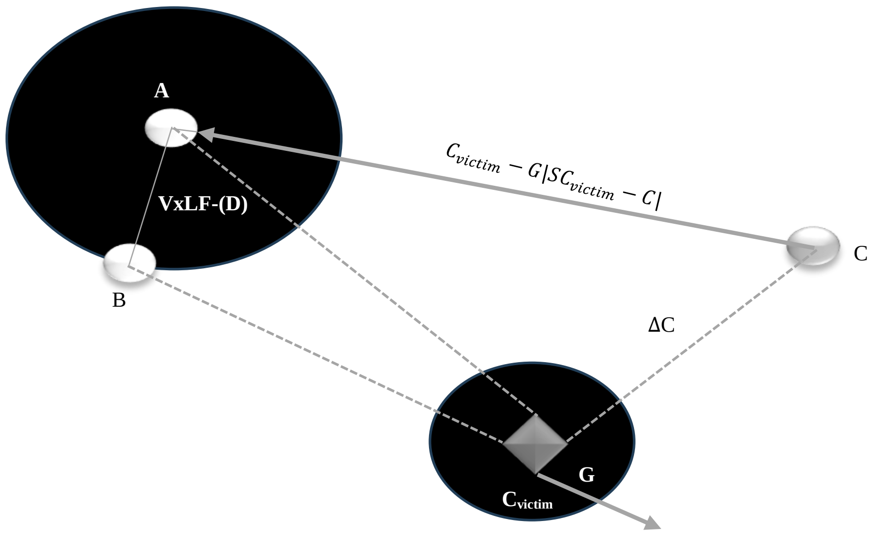


Fig. 7 Overall strategy of vectors of soft surroundings

$$C(i+1) = \begin{cases} A \text{ if } F(A) < F(C(i)) \\ B \text{ if } F(B) < F(C(i)) \end{cases} \quad (21)$$

$$A = C_{victim}(i) - G|SC_{victim}(i) - C_{avg}(i)| \quad (22)$$

$$B = A + V \times LF(D) \quad (23)$$

Figure 7 shows an example of the aforementioned modeling idea with one shark's overall vectors. The LF-based leapfrog motions are complete with several repetitions. Colored dots represent the LF-based patterns, and A or B indicates the next optimal place for iteration.

Algorithm
Step 1: Initialization
Initialize the population of shark solutions S = {S_1, S_2,..., S_n}, where each shark S_i represents a potential set of hyperparameters and feature subsets.
Initialize quantum states for each shark based on quantum superposition principles.

Step 2: Quantum-Inspired Search
Apply quantum principles (e.g., superposition, entanglement) to explore the search space efficiently.

$$\theta_i^{t+1} = \theta_i^t + \Delta\theta \quad (24)$$

Where is the quantum state at iteration t, and A is the quantum rotation angle.

Step 3: Weighted Strategy
Assign weights to sharks based on their fitness values to emphasize promising solutions:

$$w_i = \frac{1}{f(S_i)+\varepsilon} \quad (25)$$

Where e is a tiny variable to prevent multiplication by zero, and f (S) is the fitness score of shark S.

Step 4: Fitness Evaluation
Decode the quantum states to obtain the corresponding hyperparameters and feature subsets.
Train the Faster Mask DCNN using the decoded hyperparameters and selected feature subsets.
Evaluate the performance of the Faster Mask DCNN using a performance metric (e.g., accuracy, AUC):

$$f(S_i) = P(\hat{y}, y) \quad (26)$$

Where $\hat{y}$ the predicted output and y is the actual output.

Step 5: Update Population
Update the population of sharks based on their fitness values and quantum principles.
To create fresh approaches, use genetic algorithms like mutations and crossovers.

Step 6: Convergence Check
Verify convergence using a condition that stops convergence (e.g., the maximum number of iterations with no gain in efficiency).

Step 7: Final Model Training
Use the best set of hyperparameters and feature subsets found by the WQSO to train the final FMDCNN model on the entire dataset.

By utilizing quantum-inspired optimization approaches, this method combines the WQSO-FMDCNN to improve the precision and efficacy of initial diabetic models for forecasting.

To enhance the effectiveness and accuracy of initial diabetes forecasting algorithms,

This approach combines the WQSO- FMDCNN, inspired by quantum mechanics.

4. Results and Explanation

Compared to both existing supervised machine learning algorithms and proposed algorithms. Table 4 displays the results of computational time acquired utilizing the proposed approach. From 2500 to 25000 patients' records are taken into account for the experiments.

Table 4. Computational time of the proposed and existing methods

No. of patients	Computational Time (ms)		
	Hadoop-based clusters	Supervised machine learning algorithms	Proposed method
2500	2.354	1.978	0.883
5000	2.458	2.121	1.101
7500	2.438	2.190	1.344
10000	2.522	2.238	1.422
12500	2.743	2.342	1.613
15000	2.919	2.532	1.823
17500	3.143	2.702	1.989
20000	3.240	2.830	2.222
22500	3.349	2.989	2.428
25000	3.460	3.336	2.559

Table 4 shows that both the current and proposed approaches to computing time performance change as a function of patient count. The proposed approach detects normal and diabetic patients with little computing time, in comparison to current supervised machine learning algorithms and machine learning algorithms on Hadoop-based clusters. Figure 8 shows the result of plotting the computational time against the number of patients using the data from Table 4.

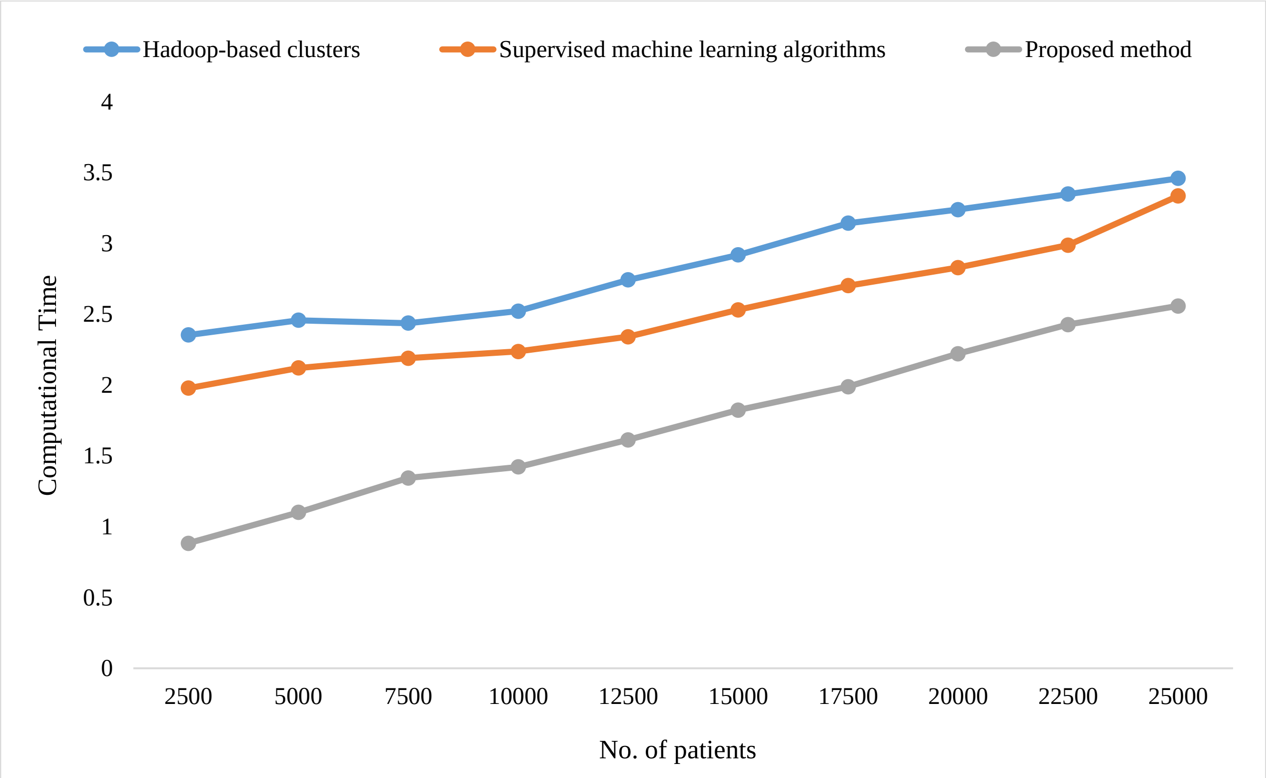


Fig. 8 Computational time using the proposed and existing methods

The proposed approach and existing supervised and machine learning methods in Hadoop-based clusters were observed to measure computational time (Figure 8). For this experiment, 25000 unique patient records from the PIMA dataset were used. The number of patients is represented in the 'x' direction, and their computational time is shown in the 'y direction, as can be seen from the visual depiction. Improved illness prediction capability is directly proportional to higher accuracy. Table 5 displays a comparison of the accuracy performance of three methodologies, including the proposed approach and existing systems. The level of precision achieved from the PIMA Indians diabetic database for individual counts between 2500 and 25000 is shown in Table 5 and Figure 9.

Table 5. Accuracy of proposed and existing methods

No. of patients	Accuracy (%)		
	Hadoop-based clusters	Supervised machine learning algorithms	Proposed method
2500	81.16	85.15	93.46
5000	79.26	83.25	92.06
7500	78.31	83.35	90.96
10000	79.66	81.66	90
12500	78.56	80.56	89.03
15000	77.26	78.25	87
17500	75.36	78.15	83.99
20000	74.56	77.6	85
22500	71.76	77.16	83.93
25000	71	76.66	81.03

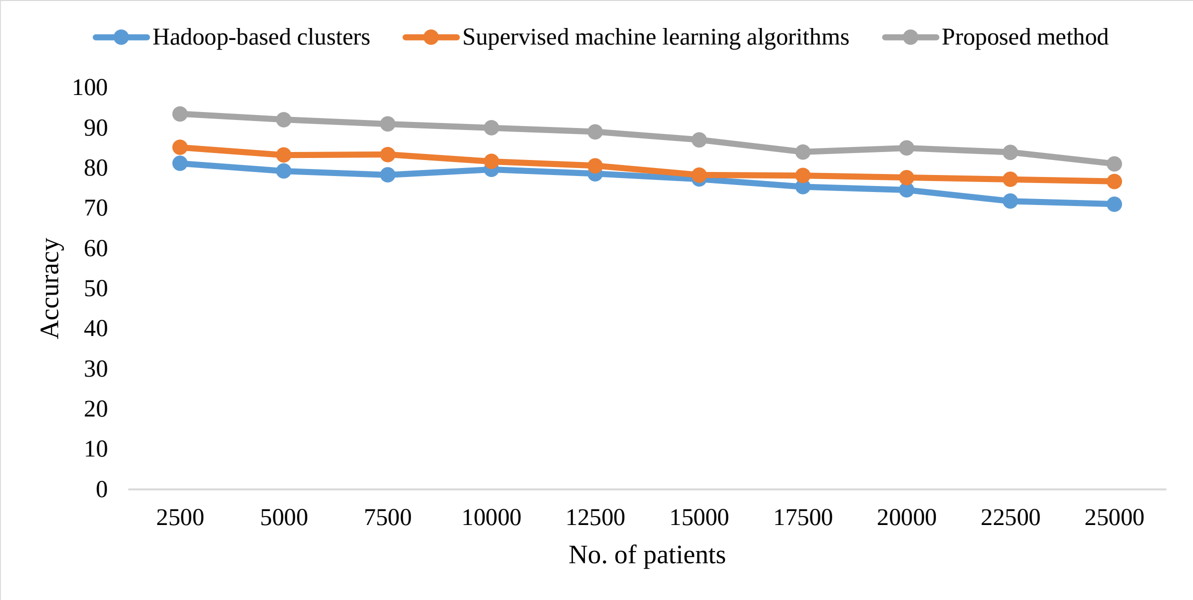


Fig. 9 Accuracy of the proposed and existing methods

When evaluating speedup, the computing time of both the machine and the cluster is considered. The efficacy and scalability of the technique may be shown in Table 6, and Figure 10 compares the results of speedup utilizing the existing methods with the proposed method.

Table 6. Speedup of the proposed and existing methods

No. of patients	Speedup (ms)		
	Hadoop-based clusters	Supervised machine learning algorithms	Proposed method
2500	1.8	0.9	0.5
5000	1.3	1.4	0.9
7500	1.2	1.3	1
10000	1.8	1.2	0.8
12500	1.4	1	0.6
15000	1.3	0.8	0.8
17500	1.2	1.5	0.9
20000	1.8	1.4	0.6
22500	1.8	1.3	0.9
25000	1.8	1.2	1

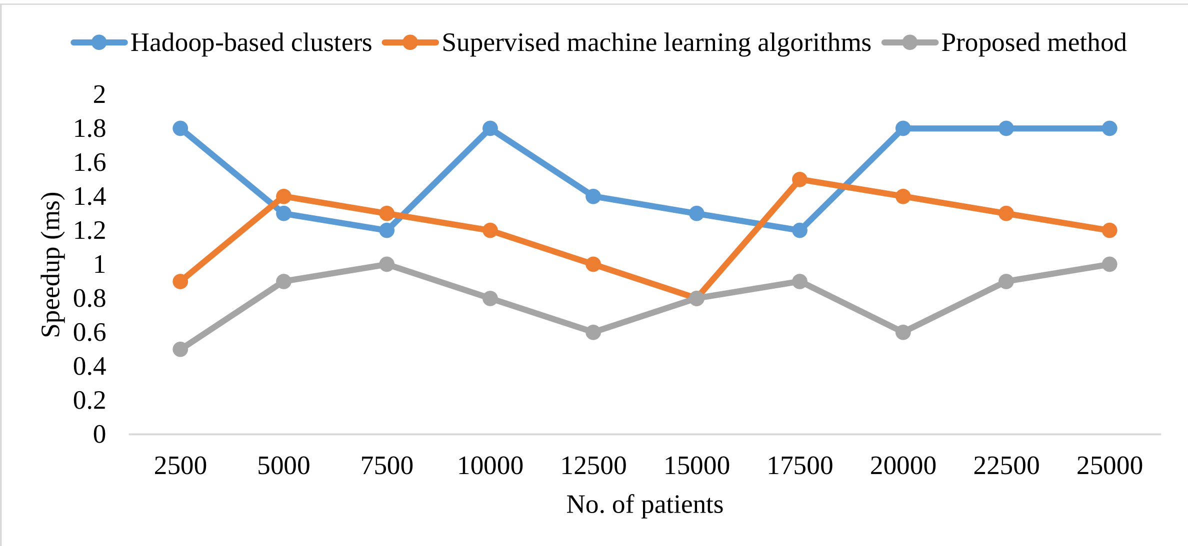


Fig. 10 Speedup of the proposed and existing methods

Table 7. F-score of proposed and existing methods

No. of patients	F-Score (%)		
	Hadoop-Based Clusters	**Supervised machine learning algorithms**	**Proposed method**
2500	84.46	85.56	93
5000	83.16	84.56	88.16
7500	83.36	85	88.36
10000	82.26	84.46	86.56
12500	82.16	83	86.26
15000	81.06	82.26	84.86
17500	80.56	81.46	81.86
20000	81.06	81.26	82.56
22500	80.56	80.96	81
25000	77.36	78.26	78.36

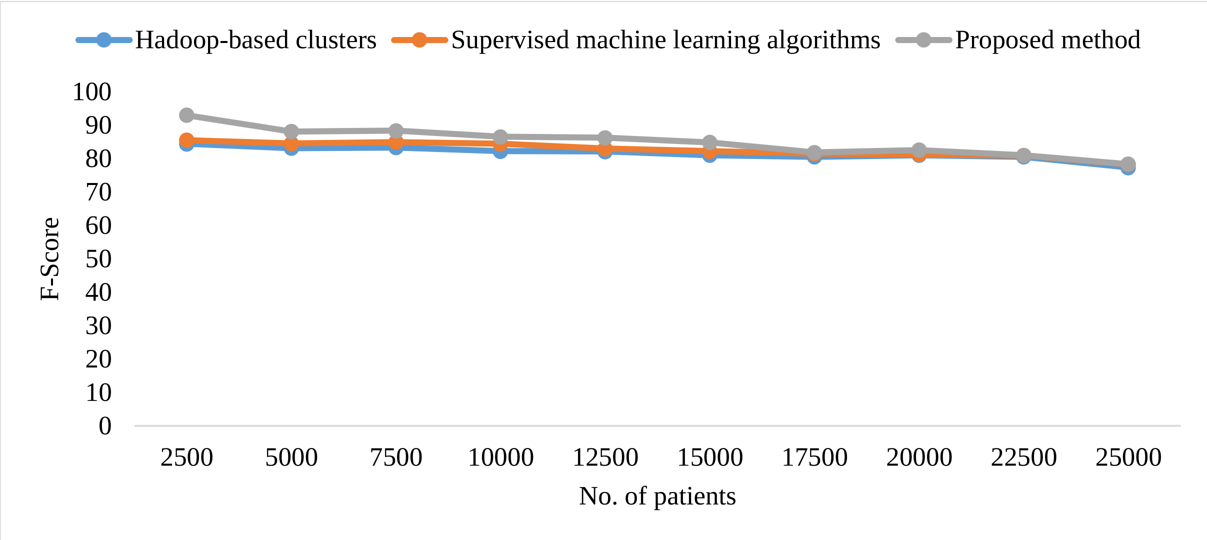


Fig. 11 F-Score of the proposed and existing methods

The F-scores of the proposed and current approaches are displayed in Figure 11 and Table 7. The link between the two components (F-Score on the vertical axis and client count on the horizontal) shows that the F-Score falls as the total number of individuals receiving treatment rises.

Table 8. Performance metrics of the proposed and existing methods

System	Sensitivity	Precision	Specificity	AUC
Proposed Method	0.93	0.91	0.95	0.97
Hadoop-based clusters	0.89	0.86	0.92	0.94
Supervised machine learning algorithms	0.86	0.84	0.90	0.92

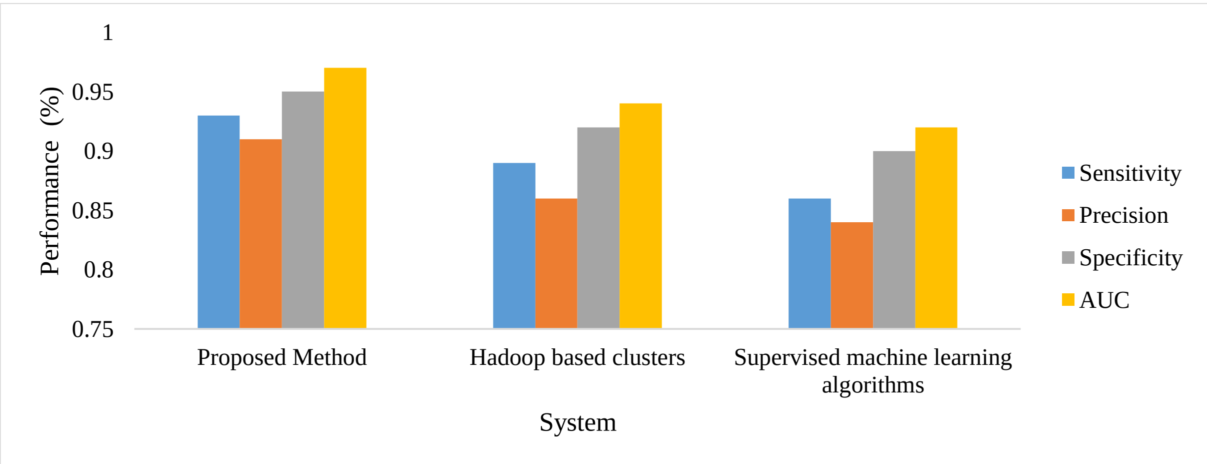


Fig. 12 Performance metrics of the proposed and existing methods

The performance measures of the proposed hybrid and existing systems are shown in Table 8 and Figure 12.

Table 9. MSE and RMSE of the proposed and existing methods

System	MSE	RMSE
Proposed Method	0.023	0.149
Hadoop-based clusters	0.036	0.188
Supervised machine learning algorithms	0.041	0.200

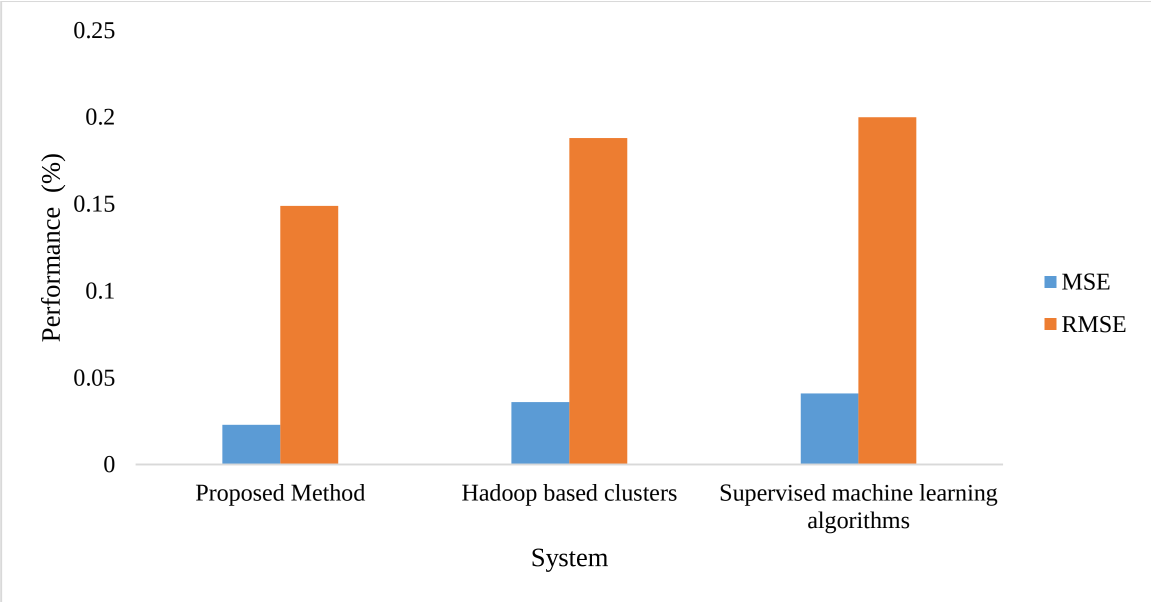


Fig. 13 MSE and RMSE of the proposed and existing methods

When compared to the existing and the proposed system in terms of MSE and RMSE, shown in Table 9 and Figure 13. This proves that the proposed method is superior at predicting the onset of diabetes in its early stages.

Table 10. Confusion matrix

System	Predicted Positive	Predicted Negative
Actual Positive	182	12
Actual Negative	22	192

Table 10 displays the matrix of confusion that was used to evaluate the effectiveness of the proposed WQSO-FMDCNN.

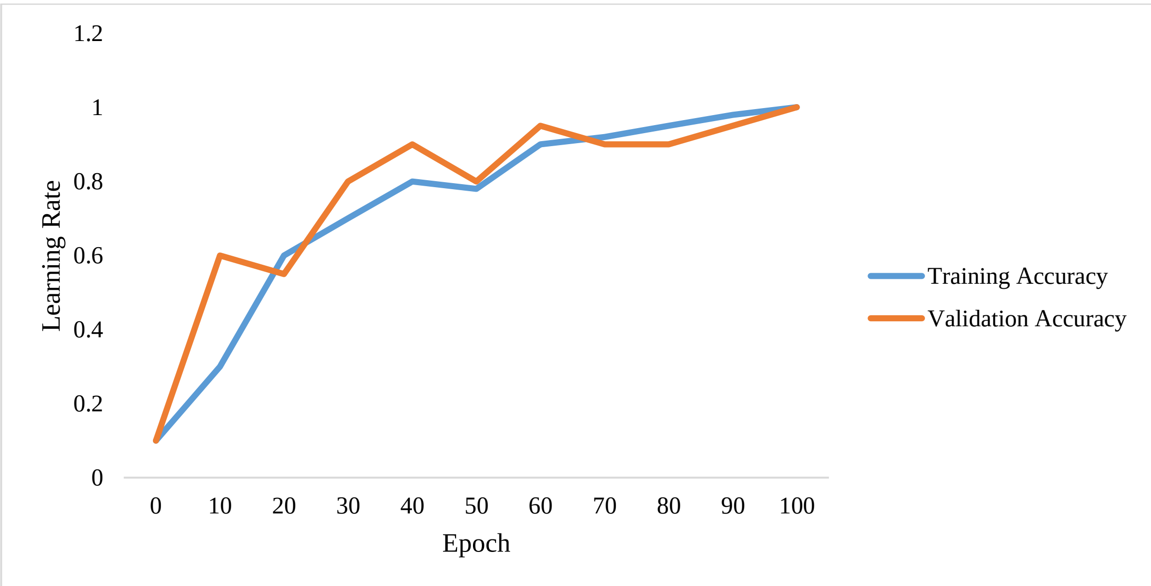
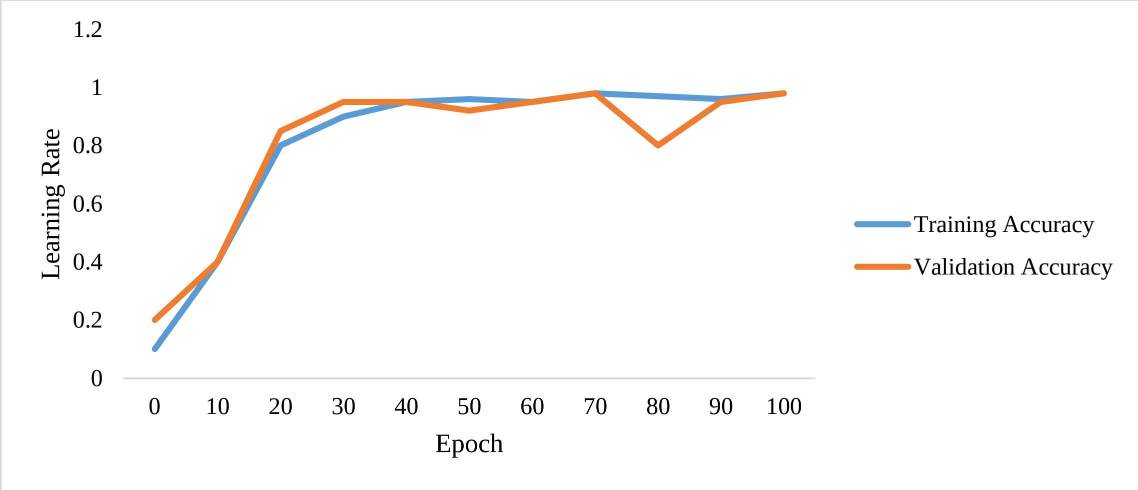
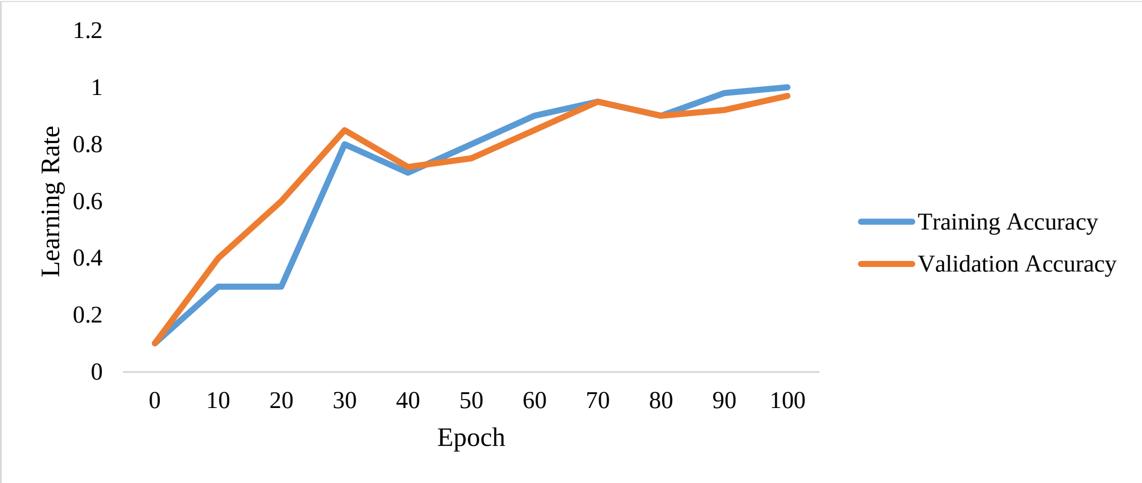


Fig. 14 Learning rate = 0.1 and validation and training accuracy with epoch = 100



(a) Batch size is 16



(b) Batch size is 256

Fig. 15 Proposed system performance.

Optimal settings for the experiment, including epoch, learning rate, and batch size, are shown in Figures 14 and 15.

Table 11. Training and validation loss

System	Training Loss	Validation Loss
Proposed Method	0.016	0.021
Hadoop-based clusters	0.026	0.031
Supervised machine learning algorithms	0.036	0.041

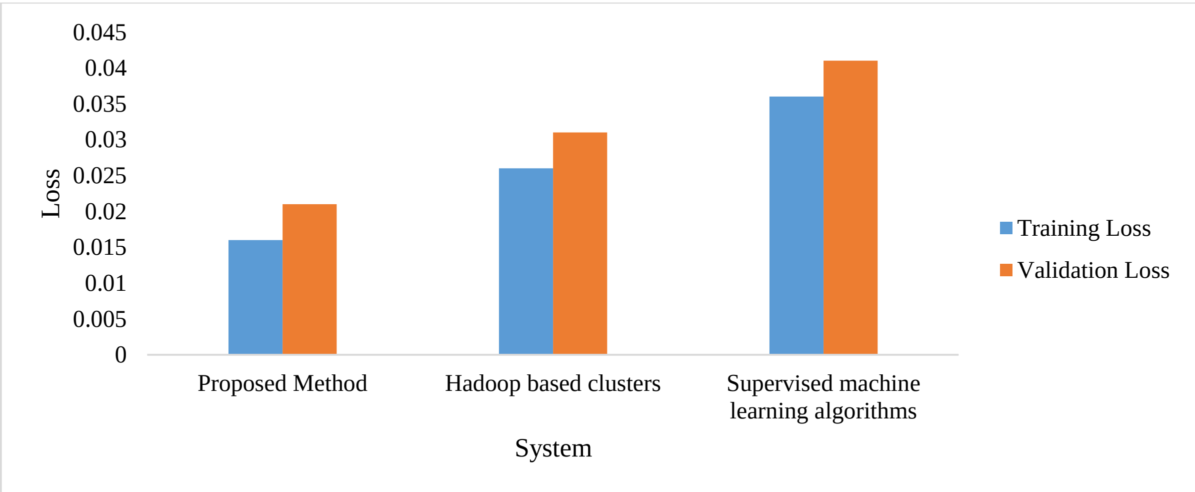


Fig. 16 Losses in instruction and assessment

When comparing the existing and the proposed systems, the proposed systems outperform them in terms of training and validation loss. The proposed approach is a more solid and trustworthy model for early-stage diabetes prediction as it reduces training and validation losses.

5. Conclusion and Future Enhancement

The goal of this study is to use an algorithm combination involving a WQSO-FMDCNN to enhance the assessment of the performance of preliminary diabetic predictions.

Using ideas inspired by quantum mechanics to strike a balance between exploration and exploitation, the WQSO algorithm efficiently traverses the search space of feature subsets and hyperparameters. The model's overall performance was much improved by this hybrid technique, which identified the most relevant characteristics and appropriate hyperparameter combinations. In comparison to other models, our experimental findings show that the proposed WQSO-Faster Mask Precision, sensitivity, reliability, and Area Under the Curve (AUC) are all improved by the DCNN technique. The proposed system fits the initial information more accurately and may apply to fresh information more effectively since it exhibits lower training and verification loss.

These findings demonstrate that the proposed system is reliable and robust for predicting diabetes in its early stages, and they highlight the system's potential as a tool for healthcare providers to make accurate and timely diagnoses. The WQSO-FMDCNN system has the potential to be much improved in the future, expanding its usefulness in predicting diabetes in its early stages.

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