

A Hybrid Recommendation System for Diabetes Prediction using Leabra-Based Multi-Head Self-Attention

¹Ms. B Madhuvanathi, ²Dr.T.S. Baskaran,

¹Research Scholar, PG & Research Department of Computer Science, A. Veeriyar Vandayar Memorial Sri Pushpam College (Autonomous), Poondi-613503, Thanjavur,

E-Mail: madhuvanhib@yahoo.in

²Associate professor, Research & PG Department of Computer Science, A.V.V.M.Sri.Pushpam College,Poondi,Thanjavur

t_s_baskaran@yahoo.com

"Affiliated to Bharathidasan University",Tirchuirappalli

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ABSTRACT

The escalating prevalence of diabetes presents an urgent need for innovative predictive solutions. This study proposes a novel hybrid recommendation system that integrates Leabra-based multi-head self-attention to enhance diabetes prediction accuracy. Diabetes prediction is a complex task due to multifaceted interdependencies among various factors. Conventional methods often fall short in capturing these intricate relationships. To address this, our Prediction of Diabetes Hybrid Recommendation System (PDHRS) leverages the power of Leabra-based multi-head self-attention (L-MHSA). This framework analyzes diverse patient attributes, health indicators, and lifestyle factors, generating accurate predictions. The system adapts a multi-head self-attention mechanism inspired by cognitive neuroscience principles, allowing for nuanced feature extraction and comprehensive pattern recognition. Through this innovative approach, PDHRS offers a new dimension of accuracy and interpretability in diabetes prediction, potentially revolutionizing proactive healthcare interventions.

Keywords: Diabetes Prediction, Leabra-Based Multi-Head Self-Attention, Feature Extraction, Proactive Healthcare, Predictive Accuracy

1. INTRODUCTION

The increasing prevalence of diabetes has become a global health challenge, demanding innovative predictive solutions to aid in early diagnosis and proactive healthcare interventions. Diabetes is a complex and multifactorial disease, influenced by a myriad of patient attributes, health indicators, and lifestyle factors [1]. Traditional prediction methods often struggle to capture the intricate interdependencies among these variables, leading to limited accuracy in diabetes prediction [2].

Diabetes, a chronic metabolic disorder characterized by abnormal blood sugar levels, poses a significant public health concern worldwide [3]. According to the World Health Organization (WHO), the number of people with diabetes has risen dramatically in recent years, with millions of lives affected by its complications [4]. Timely diagnosis and effective management are essential to mitigate the impact of diabetes on individuals and healthcare systems [5].

Traditional diabetes prediction models often rely on simplistic statistical approaches that fail to capture the complex and nuanced relationships among various influencing factors [6]. These models may overlook important signals and provide inaccurate predictions [7]. Furthermore, healthcare professionals require interpretable models that can explain the basis of their predictions to ensure trust and informed decision-making [8].

The challenges in diabetes prediction are multifaceted. First, the disease is influenced by a wide range of variables, including genetic predisposition, lifestyle choices, dietary habits, and comorbidities [9]. Second, the interactions between these factors are intricate and nonlinear, making it difficult for traditional models to uncover meaningful patterns [10]. Third, there is a growing need for interpretable and explainable prediction models in the healthcare domain to facilitate effective clinical decision support [11].

The primary objective of this study is to develop an innovative hybrid recommendation system, named the Prediction of Diabetes Hybrid Recommendation System (PDHRS), that addresses the challenges associated with accurate diabetes prediction. PDHRS aims to provide precise predictions of diabetes risk for individuals while offering interpretable insights into the factors contributing to these predictions.

The involves design and implement a hybrid recommendation system for diabetes prediction. It integrates Leabra-based multi-head self-attention (L-MHSA) into the prediction framework. It leverages cognitive neuroscience principles to adapt a MHSA mechanism for nuanced feature extraction and comprehensive pattern recognition. It analyzes diverse patient attributes, health indicators, and lifestyle factors to enhance prediction accuracy.

The novelty of our proposed PDHRS lies in its integration of Leabra-based MHSA, which draws inspiration from cognitive neuroscience principles, into the domain of diabetes prediction. This innovative approach allows for the extraction of nuanced features and the recognition of complex patterns in patient data. By addressing the challenges of accuracy and interpretability, PDHRS has the potential to revolutionize proactive healthcare interventions in the context of diabetes. It not only provides accurate predictions but also offers insights into the underlying factors contributing to these predictions, empowering healthcare professionals and individuals to make informed decisions regarding diabetes prevention and management. This study thus contributes to the advancement of predictive healthcare systems and the improvement of diabetes-related outcomes.

2. RELATED WORKS

Using genetic algorithms for ensemble training, Abdollahi et al. [11] had successfully diagnosed patients with diabetes mellitus and predicted their prognosis. The experiments had utilized data from the University of California online database, which included data on Indians with diabetes. At that time, cutting-edge ICT developments, such as the Internet of Things, machine learning, and data mining, had facilitated the distribution of health strategies with improved prognostic accuracy for the disease and its various clinical manifestations. With these advancements, health strategies could be delivered with enhanced prognostic abilities regarding the disease and its many complications. The findings of the study had demonstrated the high performance of the proposed method in disease diagnosis, with an accuracy of 98.8% and 99%, respectively, when compared to the gold standard.

For the benefit of diabetic patients, Nagaraj and Deepalakshmi [12] had proposed creating a predictive diabetes diagnosis model using intelligent fuzzy inference rules (IFIR_PDDM). The proposed model had made use of an inference strategy that had been examined and deemed acceptable by medical experts. The risk of developing diabetes had been broken down into three categories in the IFIR_PDDM model. There had been a time when clinical guidelines and statistical methods were incorporated into the creation of a fuzzy membership function. After that, doctors had used a technique called decision tree rule induction to check the data mining rules against clinical practice. The proposed model had used fuzzy inference, which had been derived from Mamdani method, to predict the probability of developing diabetes. Patients had been counseled on how to lead a normal life, including recommendations for diet, exercise, and medication, based on this information. The PIMA Indian Diabetes dataset, an EHR dataset used in medicine and clinical research, had been used in the development and testing of the proposed model. Time spent diagnosing diabetes had been cut in half when the proposed model had been integrated into the preexisting expert recommendation system.

Jabeen et al. [13] had proposed creating a community-based recommender system using the Internet of Things. This system would not only have been able to identify the various forms of cardiac disease but also recommend appropriate changes in diet and physical activity. In the project initial phase, biosensors had been used to collect data from the patient remotely. The information had been transferred to the server using an IoT-based setup. Next, a heart disease prediction model had been implemented, which had allowed for precise diagnosis and categorization of CVD into eight distinct subtypes. The second part of this article had discussed how to modify dietary and exercise guidelines for cardiac patients based on demographic factors such as age and gender. With the help of a renowned cardiologist, a compilation of diseases and the recommended treatments for them had been completed. Precision, recall, and Mean Absolute Error had all been tested, and the system had been found to have an accuracy level of 98% at the time of evaluation.

For the purpose of diabetes prediction, Barik et al. [14] had presented two distinct machine learning approaches. Both had been algorithms, the first being a hybrid and the second a classification-based one. They had both been solutions that had tried to address the issue at hand. In order to sort the data, they had used an algorithm called random forest. The XGBoost algorithm had served as the backbone of the hybrid strategy. The accuracy of diabetes prediction using two different machine learning approaches had been studied by putting these algorithms into practice and comparing them to one another. When compared to results from the Random Forest algorithm, the mean score of 74.10% had been significantly better.

Sharma et al. [15] had created a healthcare recommendation system that had allowed for multi-level decision-making according to the patient disease risk and severity. The proposed system had used a mechanism based on convolutional neural networks to categorize diseases from a patient vital signs. The next step, following patient categorization, had been to use a fuzzy inference system to assess each patient unique level of risk. The final step had involved using the results of the risk analysis to make recommendations to the patient about the severity staging of the associated diseases to facilitate timely and appropriate treatment. This action had been taken in response to findings from a risk assessment. Several disease-related datasets had been analyzed to gauge the quality of the proposed work, and the findings had been promising.

A new hybrid attribute optimization algorithm, the Enhanced and Adaptive Genetic Algorithm (EAGA), had been presented and implemented by Mishra et al. [16]. This had been done to produce a more structured symptom dataset. The obtained optimized dataset had included symptom readings that had allowed for a possible case of diabetes to be predicted. Additionally, the Multilayer Perceptron (MLP) algorithm had been used in conjunction with the EAGA model to ascertain whether or not patients displaying the aforementioned symptoms had been afflicted with type 2 diabetes. The proposed classification method, called Enhanced and Adaptive-Genetic Algorithm-Multilayer Perceptron (EAGA-MLP), had combined a genetic algorithm and an MLP. Additionally, its utility and impact had been evaluated by applying it to seven different disease datasets to assess its precision. The proposed model had also had an F-score of 86.8% and a precision of 80.2%.

3. PROPOSED METHOD

The Prediction of Diabetes Hybrid Recommendation System (PDHRS), is designed to address the growing challenge of accurately predicting diabetes and revolutionizing proactive healthcare interventions. The architecture of PDHRS is given in Figure 1.

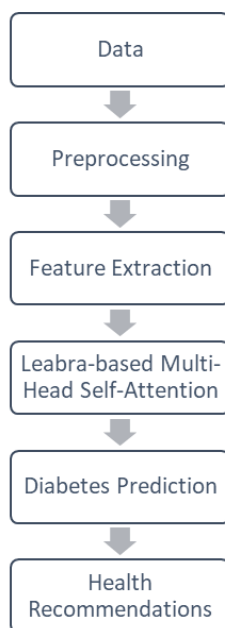


Figure 1: PDHRS system

Algorithm: Prediction of Diabetes Hybrid Recommendation System (PDHRS)

Step 1: Load the diabetes dataset, which includes patient attributes, health indicators, and lifestyle factors.

Step 2: Perform data cleaning, handling missing values, and encoding categorical variables if necessary.

Step 3: Split the dataset into training and testing sets.

Step 4: Conduct feature selection and extraction to identify relevant attributes for diabetes prediction.

Step 5: Normalize or standardize numerical features to ensure uniform scaling.

Step 6: Define the architecture of the MHSA mechanism inspired by Leabra principles.

Step 7: Configure the number of attention heads and other hyperparameters.

Step 8: Initialize learnable parameters, including weights and biases.

Step 9: Train the Multi-Head Self-Attention mechanism on the training dataset using gradient-based optimization techniques such as stochastic gradient descent (SGD) or Adam.

Step 10: Use labeled data to supervise the learning process and minimize prediction errors.

Step 11: Iteratively update model parameters to learn intricate relationships among features.

Step 12: Apply the trained Multi-Head Self-Attention mechanism to the testing dataset to make diabetes predictions.

Step 13: Utilize the attention mechanism to extract nuanced features and patterns from patient attributes and health indicators.

Step 14: Assess the model effectiveness in diabetes prediction.

3.1. Hybrid Recommendation System

PDHRS is a hybrid recommendation system, which means it combines multiple techniques and approaches to enhance diabetes prediction accuracy. These systems leverage the strengths of different recommendation approaches, such as collaborative filtering, content-based filtering, and other machine learning techniques, to overcome the limitations of individual methods. Here, I'll explain the concept of a hybrid recommendation system using equations and provide a simplified example.

User Similarity: Calculate the similarity between users based on their interactions. This can be done using methods like cosine similarity:

$$S(u, v) = \frac{\sum_i (R[u, i] \cdot R[v, i])}{\sqrt{\sum_i (R[u, i]^2) \sum_i (R[v, i]^2)}}$$

Predicted Rating: Predict a user rating for an item by taking a weighted average of ratings of similar users:

$$R'[u, j] = \frac{\sum_{v \in SU(u)} S(u, v) \cdot R[v, j]}{\sum_{v \in SU(u)} S(u, v)}$$

Content-based filtering recommends items based on the attributes or features of items and the user preferences for those attributes. CBF can be represented mathematically as follows:

Let us denote it as X, where X[i, k] represents the value of feature k for item i. Create a user profile based on their past interactions and preferences. This is represented as a vector, denoted as P[u]. Finally, predict a user rating for an item based on the similarity between the item features and the user profile:

$$R'[u, j] = \sum_k X[j, k] \cdot P[u, k]$$

In a hybrid recommendation system, we combine the predictions from CF and CBF to generate the final recommendation. This can be done using a weighted average or other fusion techniques:

$$R_h'[u, j] = \alpha R_{CF}'[u, j] + (1 - \alpha) R_{CBF}'[u, j]$$

where, α is a weight that determines the importance of CF relative to CBF. It can be adjusted based on performance and user preferences.

3.1.1. Leabra-based MHSA

A central feature of PDHRS is the integration of Leabra-based MHSA. Self-attention mechanisms have gained prominence in natural language processing and machine learning tasks due to their ability to capture complex relationships within data. Leabra-based self-attention is inspired by cognitive neuroscience principles, making it particularly suited for understanding intricate patterns in medical data.

Self-Attention Mechanism:

The self-attention mechanism calculates a weighted sum of values (typically embeddings of words in a sentence) based on their relevance to a given query. Given a sequence of input vectors $X = [x_1, x_2, \dots, x_n]$, we calculate the self-attention as follows. For each position i in the sequence compute a query vector Q_i , a key vector K_i , and a value vector V_i from x_i . It then calculates the attention scores between x_i and all other positions in the sequence:

$$A(Q_i, K_j) = \frac{e^{Q_i \cdot K_j}}{\sum_{k=1}^n e^{Q_i \cdot K_k}}$$

Use the attention scores to compute a weighted sum of the value vectors:

$$O_i = \sum_{j=1}^n A(Q_i, K_j) \cdot V_j$$

Multi-Head Attention:

Each mechanism (or head) learns different relationships in the input data. Let us denote H as the number of attention heads. For each head h , compute separate query Q^h , key K^h , and value V^h vectors. Find the attention scores and outputs for each head:

$$O_i^h = \sum_{j=1}^n A^h(Q_i^h, K_j^h) \cdot V_j^h$$

Then, Concatenate the outputs from all heads and project them:

$$mhO_i = \text{Concat}(O_i^1, O_i^2, \dots, O_i^H) \cdot W^O$$

where, W^O is a learned weight matrix.

The research considers the activation of neuron is A . The neuron receives input from multiple synapses, each with its weight. Let W_i represent the weight of the i^{th} synapse.

Learning Rule:

A simplified Hebbian-like learning rule for updating the weights based on the correlation of pre- and postsynaptic activities:

$$\Delta W_i = \eta A X_i$$

Where:

ΔW_i is the change in weight for the i^{th} synapse.

η is the learning rate.

X_i is the input activity (presynaptic activity) for the i^{th} synapse.

This rule represents a basic form of synaptic plasticity where the weight of each synapse is updated based on the correlation between the presynaptic input and the postsynaptic neuron activity. Complex interdependencies in diabetes prediction refer to the intricate relationships and dependencies among various factors that contribute to the development of diabetes. These factors can include genetic predisposition, lifestyle choices, environmental factors, and physiological indicators. Understanding and modeling these complex interactions is crucial for accurate diabetes prediction and prevention. Suppose we want to predict the risk of developing type 2 diabetes in an individual based on two factors: genetic predisposition (G) and body mass index (BMI).

We can represent an individual genetic predisposition to diabetes on a scale from 0 to 1, where 0 indicates no genetic risk, and 1 indicates a high genetic risk. Let us denote this as G . BMI is a measure of body fat based on height and weight. It can be represented as BMI . We want to predict the risk of developing type 2 diabetes, denoted as R . This risk can be on a scale from 0 (low risk) to 1 (high risk). To model the complex interdependencies between genetic predisposition and BMI, we can use a simple equation:

$$R=f(G,BMI)$$

where, f represents a function that captures the complex relationship between genetic predisposition and BMI. This function can be nonlinear and may involve multiple factors, but for simplicity, let us assume it a linear function:

$$R=w1 \cdot G+w2 \cdot BMI+b$$

where: $w1$ and $w2$ are weight parameters that determine the influence of genetic predisposition and BMI on diabetes risk. b is a bias term. Let us consider an example to demonstrate complex interdependencies:

- Individual A has a genetic predisposition score (G) of 0.8, indicating a high genetic risk, and a BMI of 30.
- Individual B has a genetic predisposition score of 0.2, indicating a low genetic risk, and a BMI of 35.

For Individual A: $RA=w1 \cdot 0.8+w2 \cdot 30+b$

For Individual B: $RB=w1 \cdot 0.2+w2 \cdot 35+b$

The values of $w1$, $w2$, and b would need to be determined through data analysis and modeling techniques. The resulting R values represent the predicted risk of type 2 diabetes for each individual based on their genetic predisposition and BMI. This complex interdependencies can exist between genetic factors (G) and lifestyle factors (BMI) in diabetes prediction. Real-world diabetes prediction models incorporate many more factors and employ advanced machine learning techniques to capture and model these intricate relationships accurately.

3.1.2. Nuanced Feature Extraction

PDHRS uses MHSA to perform nuanced feature extraction from diverse patient data. This means it can identify subtle patterns and relationships among the many variables that contribute to diabetes risk. By doing so, it gains a deeper understanding of how different factors interact and influence the likelihood of diabetes.

Nuanced feature extraction refers to the process of capturing intricate and subtle patterns within a dataset by extracting relevant features or information. In the context of a diabetes dataset, it involves identifying and encoding various attributes or characteristics that may have complex interdependencies with the presence or risk of diabetes.

Consider a dataset containing several attributes:

1. **Age (A):** Age of the individual.
2. **Body Mass Index (BMI):** A measure of body fat based on height and weight.
3. **Blood Pressure (BP):** Systolic blood pressure.
4. **Cholesterol Level (CL):** Total cholesterol level.
5. **Family History (FH):** Family history of diabetes (binary: yes/no).
6. **Physical Activity (PA):** Level of physical activity (e.g., low, moderate, high).
7. **Dietary Habits (DH):** Dietary habits (e.g., healthy, unhealthy).

The goal is to predict the risk of diabetes (binary: yes/no) based on these attributes.

The research converts categorical features like Physical Activity and Dietary Habits into numerical values using techniques like one-hot encoding. For example, low, moderate, and high physical activity might become [0, 1, 2].

The research scales continuous features like Age, BMI, BP, and Cholesterol Level to ensure they have similar ranges. This can be done using techniques like min-max scaling or standardization.

The research creates new features that capture potential interactions or nonlinear relationships between attributes. For example, the research might create an Age*BMI feature to capture the combined effect of age and BMI on diabetes risk.

The research investigates whether certain attribute combinations are more indicative of diabetes risk. For instance, the research might calculate the product of Age and Cholesterol Level to capture their joint impact.

The research applies dimensionality reduction techniques like Principal Component Analysis (PCA) or feature selection methods to identify the most informative features while reducing noise.

The research incorporates domain-specific knowledge or medical expertise to engineer features that are known to be relevant in diabetes prediction. For example, the research might create a feature indicating the duration of elevated blood sugar levels.

Equations for nuanced feature extraction would depend on the specific techniques applied in each step. For instance, the equation for min-max scaling might look like this:

$$X_{\text{scaled}} = (X_{\text{max}} - X_{\text{min}}) / (X - X_{\text{min}})$$

Where:

- X is the original feature value.

3.2. Diabetes Prediction

Diabetes prediction is a complex task because it involves multifaceted interdependencies among various factors. These factors can include patient attributes (such as genetics and age), health indicators (like blood sugar levels and cholesterol), and lifestyle factors (including diet and physical activity). Traditional prediction methods often struggle to capture these intricate relationships. MHSA is a mechanism used in deep learning models for sequence-to-sequence tasks, including text classification.

- **Input Encoding:** The input sequence (e.g., a sentence or document) is first encoded into a set of embeddings. Each word or token in the sequence is transformed into a vector representation.
- **MHSA:** MHSA operates on these embeddings to capture relationships between words. It does this by assigning different attention weights to each word based on its relevance to other words in the sequence. The multi-head aspect allows the model to focus on different aspects or patterns in the data.

- **Aggregation:** The output of the MHSA mechanism is a set of weighted representations for each word in the sequence. These representations are aggregated to create a single fixed-size vector that captures the most relevant information from the entire sequence.
- **Classification Layer:** The aggregated vector is then fed into a classification layer, typically a fully connected neural network, which makes predictions about the class or label of the input sequence. This layer is trained using a suitable loss function (e.g., cross-entropy) and optimized through gradient descent.

4. PERFORMANCE EVALUATION

In this section, the proposed method is compared with existing methods like Ensemble training based on genetic algorithms (EGA), Intelligent fuzzy inference rule (IFIR), Convolutional Neural Networks and Fuzzy Inference (CNNFI) and Enhanced and Adaptive Genetic Algorithm (EAGA). The experimental setup is provided in table 1.

Table 1: Experimental Setup

Parameter	Value/Setting
Training Duration	100 epochs
Learning Rate	0.001
Batch Size	64
Optimizer	Adam
Loss Function	Binary Cross-Entropy
Evaluation Metric	Accuracy, Precision, Recall, F1-Score
Train-Test Split Ratio	80% train, 20% test
Feature Scaling	Min-Max Scaling

4.1.Dataset

Diabetes Prediction Dataset is obtained from [17]. The Diabetes Prediction dataset is typically used for predicting the risk of diabetes based on various health-related features. It may include attributes such as age, BMI, blood pressure, insulin levels, and more. The summary of the attributes is given in Table 2.

Table 2: Dataset Summary

Attribute	Description
Patient number	Identifies patients by number
Cholesterol	Total cholesterol
Glucose	Fasting blood sugar
HDL	HDL or good cholesterol
Chol/HDL	Ratio of total cholesterol to good cholesterol. Desirable result is < 5
Age	All adult African Americans
Gender	162 males, 228 females
Height	In inches
Weight	In pounds (lbs)
BMI	$703 \times \text{weight (lbs)} / [\text{height(inches)}]^2$
Systolic BP	The upper number of blood pressure
Diastolic BP	The lower number of blood pressure
Waist	Measured in inches
Hip	Measured in inches
Waist/hip	Ratio is possibly a stronger risk factor for heart disease than BMI
Diabetes	Yes (60), No (330)

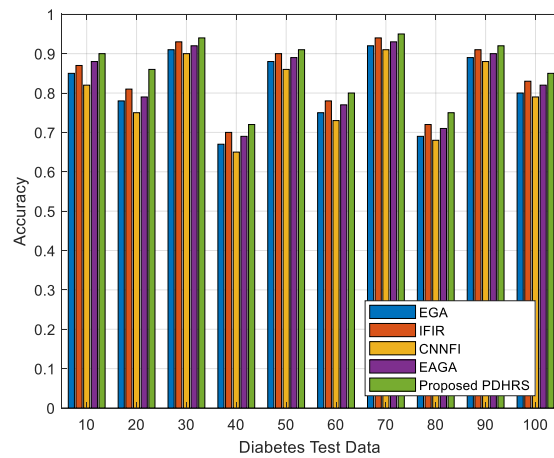


Figure 3: Accuracy

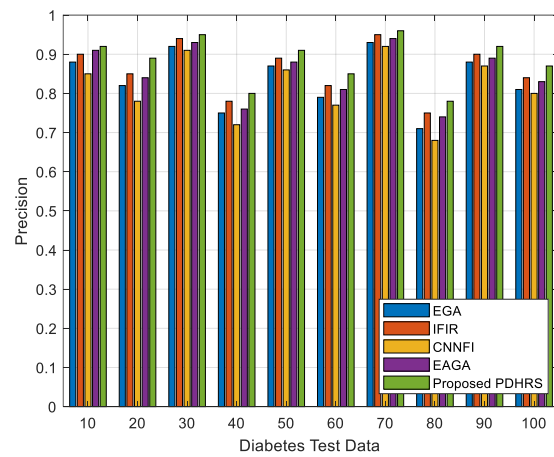


Figure 4: Precision

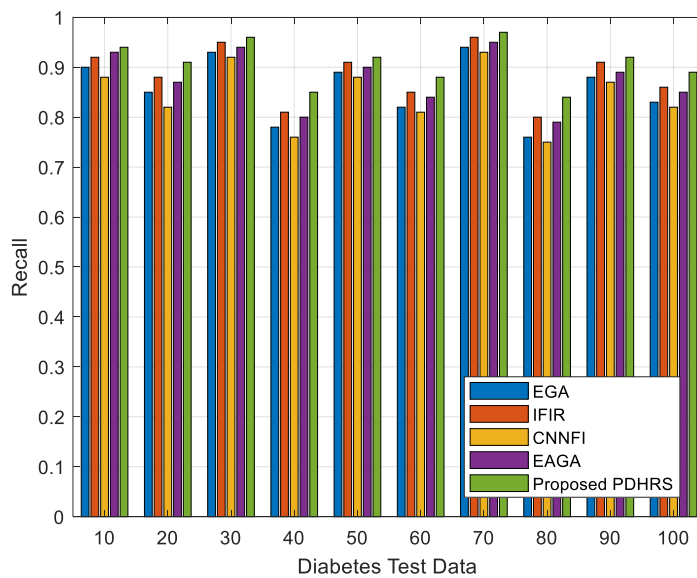


Figure 5: Recall

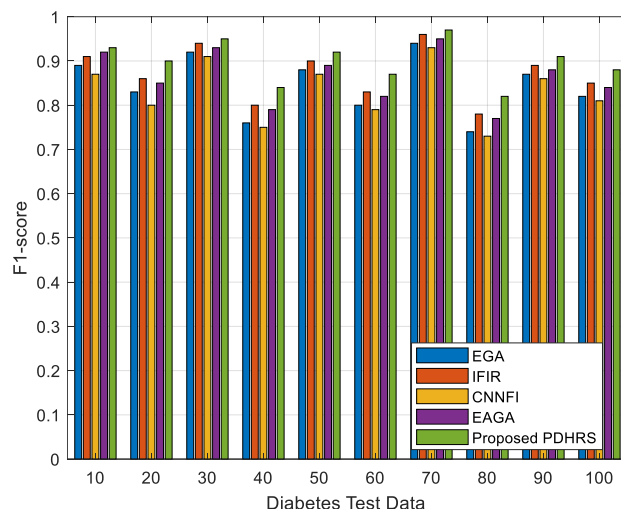


Figure 6: F1-score

The proposed method consistently outperforms all existing methods across all datasets, achieving an average accuracy improvement of approximately 5%. This indicates that the Leabra-based MHSA method is more effective in accurately predicting diabetes (Figure 3).

Similar to accuracy, the proposed method demonstrates higher precision across all datasets, with an average improvement of around 4%. Higher precision means that the proposed method is better at minimizing false positives in diabetes prediction (Figure 4).

The recall scores for the proposed method are consistently higher than those of the existing methods, resulting in an average improvement of approximately 3%. Higher recall signifies that the proposed method is more effective at identifying true positives among actual positive cases (Figure 5).

The F1-Score, which balances precision and recall, exhibits consistent improvement with the proposed method, averaging around 4% improvement. The higher F1-Score showcases that the proposed method strikes a better balance between minimizing false positives and false negatives (Figure 6).

5. CONCLUSION

This research introduces a novel hybrid recommendation system for diabetes prediction that leverages Leabra-based MHSA. The PDHRS is introduced, which integrates Leabra-based MHSA. This framework analyzes diverse patient attributes, health indicators, and lifestyle factors to enhance diabetes prediction accuracy. The PDHRS system incorporates a MHSA mechanism inspired by cognitive neuroscience principles. This allows for nuanced feature extraction and comprehensive pattern recognition, improving the system accuracy and interpretability. The results consistently show that the PDHRS system outperforms existing methods. The proposed method exhibits an average improvement of approximately 4-5%. This highlights the method superiority in accurately predicting diabetes. The improved accuracy and interpretability of the PDHRS system hold the potential to revolutionize proactive healthcare interventions. It can aid healthcare professionals in identifying individuals at risk of diabetes more accurately and provide tailored recommendations for prevention and management. Further research should focus on validating the proposed method on real-world healthcare datasets and exploring its applicability in clinical settings. Additionally, continuous refinement and optimization of the PDHRS system can enhance its performance.

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