EAI Endorsed Transactions
on AI and Robotics
Research Article EAI.EU

DeepDiabFusion: An Interaction-Aware Neural Network Architecture for Diabetes Prediction

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Abstract

Accurate prediction of diabetes onset is essential for effective early diagnosis and clinical intervention. This study presents a performance analysis of several machine learning (ML) algorithms applied to the Pima Indians Diabetes Dataset (PIDD), with a primary focus on a novel Artificial Neural Network (ANN) architecture, referred to as DeepDiabFusion. The proposed model integrates feature-wise normalization, parallel dense sublayers, and an interaction-aware fusion mechanism to capture complex feature relationships often overlooked by conventional models. Comparative experiments were conducted against seven traditional ML algorithms, including Logistic Regression, Random Forest, and Gradient Boosting, as well as state-of-the-art ANN-based models from recent literature. Performance was evaluated using accuracy, precision, recall, and area under the curve (AUC) metrics. The proposed model achieved an accuracy of 93.04%, precision of 86.21%, recall of 93.10%, and AUC of 0.951—outperforming all baseline and previously reported models. These results demonstrate the superior classification performance and practical applicability of the proposed ANN framework in clinical decision support systems for early diabetes detection and management.

Keywords: diabetes prediction, Artificial Neural Networks (ANN), Pima Indians Diabetes Dataset (PIDD), machine learning, accuracy

Received on 30 November 2024, accepted on 17 May 2025, published on 04 June 2025

doi: 10.4108/airo.7998

1. Introduction

Diabetes is a chronic disease affecting over 422 million people globally, as reported by the World Health Organization (WHO) [1]. In 2021, Uzbekistan's diabetes prevalence was 6.3%, meaning approximately 1,351,800 people had diabetes, according to the International Diabetes Federation (IDF) [2]. Diabetes is a chronic condition that can cause serious damage to the heart [3], kidneys [4], eyes [5], blood vessels, and nerves. Early prevention and detection are crucial to prevent complications and save lives [6]-[7].

Machine Learning (ML) methods offer powerful tools for identifying individuals at risk through data-driven analysis. Various ML models such as Decision Trees (DT) [8], Random Forest (RF) [9], Support Vector Machines (SVM) [10], Logistic Regression (LR) [11], and ensemble learning [12] strategies have been successfully employed for diabetes prediction tasks due to their ability to uncover hidden patterns in clinical data.

However, despite these advancements, many existing approaches fail to address key limitations such as dataset imbalance, feature interaction modeling, or the need for tailored architectures. Recent research has increasingly

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focused on improving the performance of classification models, particularly for imbalanced medical datasets. For example, the authors [13] proposed a dynamic sampling strategy for deep learning networks that outperforms conventional methods on multiclass imbalanced datasets. Another study [14] achieved 99.6% accuracy on hypothyroid data by optimizing neural network weights using learning automata, underscoring the importance of specialized ANN configurations and feature selection strategies for reliable medical diagnosis.

In this context, our paper shifts the focus toward the design and evaluation of a novel Artificial Neural Network (ANN) architecture specifically tailored to the Pima Indians Diabetes Dataset (PIDD). Rather than comparing standard ML models in isolation, our primary aim is to introduce a custom ANN design capable of enhancing predictive accuracy and generalization through structured interaction modeling. The contributions of this paper are:

- **Development of a customized ANN architecture:** A novel Artificial Neural Network (ANN) architecture is introduced, meticulously designed for structured clinical datasets. The model integrates feature-wise normalization, parallel dense sublayers, and an interaction-aware fusion mechanism, collectively enhancing its capacity to learn complex patterns inherent in medical data.
- **Incorporation of attention-inspired mechanisms:** The proposed framework embeds an attention-like component to model inter-feature dependencies effectively. This mechanism enables the dynamic weighting of feature interactions, thereby addressing limitations associated with traditional feedforward ANN architectures.
- **Rigorous comparative evaluation:** The proposed ANN is comprehensively evaluated against seven conventional machine learning algorithms—namely Logistic Regression, k-Nearest Neighbors, Random Forest, Stochastic Gradient Descent, Gradient Boosting, Decision Tree, and Linear Discriminant Analysis—using standard performance metrics including accuracy, precision, recall, and AUC.
- **Benchmarking against state-of-the-art models:** A detailed performance comparison is conducted with existing studies employing both classical and ANN-based models on the Pima Indians Diabetes Dataset (PIDD). The results consistently demonstrate the superiority of the proposed ANN in terms of classification accuracy and robustness.
- **Enhanced interpretability and clinical applicability:** Through its modular design and structured interaction modeling, the proposed model improves interpretability, making it a promising candidate for deployment in clinical decision support systems aimed at early detection and intervention in diabetes management.

The remainder of this paper is structured as follows: Section 2 presents a comprehensive review of existing literature on machine learning and artificial neural network (ANN) approaches for diabetes prediction, emphasizing their methodologies and inherent limitations. Section 3 describes the methodological framework employed in this study, including data preprocessing steps and the architectural design of the proposed ANN model. Section 4 reports the experimental results and provides a comparative performance analysis between the proposed model, conventional machine learning algorithms, and previously published ANN-based studies. Finally, Section 5 concludes the paper by summarizing the key findings, discussing their practical implications, outlining current limitations, and proposing directions for future research.

2. Related Work

In recent years, the application of machine learning (ML) and deep learning techniques to medical diagnosis has gained substantial attention, particularly for conditions like diabetes where early detection is critical. Numerous studies have explored both traditional ML algorithms and advanced neural network architectures to predict diabetes risk using clinical datasets such as the Pima Indians Diabetes Dataset (PIDD).

This section reviews the state-of-the-art in diabetes prediction, categorizing related work into two major streams: classical ML-based approaches and ANN-based deep learning methods. By analyzing the strengths and limitations of these approaches, we highlight the research gaps that motivate the development of a novel ANN architecture introduced in this study.

2.1. Machine Learning Approaches for Diabetes Prediction

Traditional ML models such as Logistic Regression, Decision Trees, Random Forests, SVM, and Gradient Boosting have been widely used for diabetes prediction due to their simplicity and effectiveness on structured datasets like PIDD. While these models perform well in many cases, they often face limitations in handling imbalanced data and capturing complex feature interactions. This subsection reviews key studies employing ML approaches for diabetes prediction, highlighting their strengths and shortcomings.

In [9], a prognosis model for gestational diabetes mellitus (GDM) was proposed using multiple machine learning classifiers including logistic regression, support vector machines (SVM), k-nearest neighbors (KNN), and random forest (RF). The study employed group-based mean (GBM) imputation to handle missing values and applied min-max normalization to improve data quality. Classification performance was evaluated using accuracy, precision, recall, F1-score, and ROC curves. Among all models, RF achieved the highest accuracy of 92.10% after normalization. While this work focused on data preprocessing and classifier comparison, it did not introduce novel model architectures or advanced interaction modeling. In [10], a predictive framework for diabetes detection was developed using supervised learning algorithms applied to the Pima Indians Diabetes Dataset. The study implemented five models: linear

kernel SVM, RBF kernel SVM, k-nearest neighbor (k-NN), artificial neural network (ANN), and multifactor dimensionality reduction (MDR). Preprocessing steps included outlier removal, k-NN imputation, and feature selection using the Boruta algorithm. Performance evaluation based on accuracy, recall, precision, F1-score, and AUC showed that SVM-linear and k-NN achieved the highest AUC values of 0.90 and 0.92, respectively. While ANN was used, it followed a standard architecture with no structural enhancements. In [11], a comparative analysis was conducted using Logistic Regression (LR) and Decision Tree Classifier (DTC) on the Pima Indians Diabetes Dataset. The study applied preprocessing steps including normalization and trained the models using an 80:20 train-test split. Evaluation metrics such as accuracy, precision, recall, F1-score, specificity, and sensitivity were used to assess model performance. The results showed that LR achieved higher accuracy (82.46%) compared to DTC (78.57%). Although both algorithms were assessed thoroughly, the study focused solely on classical ML models and did not explore deep learning approaches or custom neural network architectures.

In [12], a comparative study was conducted using both classical and hybrid machine learning models for diabetes prediction on the Pima Indians Diabetes Dataset and an early-stage diabetes dataset. Classical models such as Multilayer Perceptron (MLP), k-Nearest Neighbors (k-NN), Support Vector Machine (SVM), and Naïve Bayes were evaluated alongside hybrid ensemble methods including Random Forest, AdaBoost, XGBoost, Extra Trees, Gradient Boosted Trees (GBT), and a stacked generalization approach. The study found that the stacked generalization model achieved the highest accuracy of 83.9% on the Pima dataset, outperforming all other models. However, the work focused primarily on combining multiple learners through meta-classification and did not explore architectural customization within a single model. In [15], a rule-based classifier framework was proposed for diabetes prediction using Principal Component Analysis (PCA) to reduce the dimensionality of the Pima Indians Diabetes Dataset. The study evaluated three models—Decision Tree, Naïve Bayes, and Support Vector Machine (SVM)—with and without PCA. The goal was to generate minimal classification rules with high accuracy. Results showed that Naïve Bayes achieved the highest accuracy (77.36%) after PCA was applied, followed by Decision Tree (76.22%) and SVM (68.68%). While the model benefited from dimensionality reduction, it relied solely on traditional classifiers and did not address advanced learning techniques or interaction-aware modeling.

In [16], several classification algorithms including Naive Bayes, Sequential Minimal Optimization (SMO), Reduced Error Pruning Tree (REPTree), and Simple Logistic Regression were evaluated on the Pima Indians Diabetes Dataset. The study applied the SMOTE oversampling technique to handle class imbalance, followed by 10-fold cross-validation for performance evaluation. Results showed that Simple Logistic Regression achieved the highest accuracy (75.7%), followed closely by REPTree and SMO. Naive Bayes performed the least accurately. While the study focused on classical classifiers and basic resampling techniques, it did not explore deep learning architectures or interaction-aware learning. In [17], a cross-country evaluation framework was introduced to assess the performance of machine learning models trained on the Pima Indians Diabetes Dataset and tested on a hospital dataset from Bangladesh. The study applied four classifiers—Decision Tree, k-Nearest Neighbor (KNN), Random Forest, and Naïve Bayes—after conducting preprocessing steps such as normalization and handling unit mismatches across datasets. Three-fold cross-validation and hyperparameter tuning were used to optimize model performance. Random Forest achieved the highest AUC (0.83) on the PIMA test set, while Naïve Bayes yielded the best AUC (0.84) on the Bangladeshi dataset. Despite robust evaluation, the models relied on traditional architectures and lacked mechanisms to model nonlinear feature interactions. In [18], a comparative study was conducted using five machine learning algorithms—K-Nearest Neighbor (KNN), Naïve Bayes (NB), Logistic Regression (LR), Random Forest (RF), and Support Vector Machine (SVM)—to predict diabetes based on the Pima Indians Diabetes Dataset. The authors applied preprocessing steps including mean imputation for missing values, normalization, and Pearson correlation for feature selection. The study evaluated models using both train-test split (70/30) and K-fold cross-validation, reporting that SVM achieved the highest accuracy (83%) using the split method. Although the framework achieved competitive results, it primarily focused on classical classifiers and statistical feature filtering.

In [19], a comparative analysis of five machine learning classifiers—Naïve Bayes, Random Forest, Logistic Regression, Neural Network, and Support Vector Machine—was conducted on the Pima Indians Diabetes Dataset using Weka. Preprocessing involved outlier removal and missing value imputation using mean and median techniques. The models were evaluated using 10-fold cross-validation with metrics such as accuracy, precision, recall, F1-score, and ROC-AUC. Logistic Regression achieved the highest accuracy (77.2%) and ROC-AUC (0.832), followed by SVM and Naïve Bayes. Although neural networks were included in the evaluation, the architecture used was standard feedforward without modification. In [20], a comparative analysis was performed using six machine learning algorithms—Support Vector Machine (SVM), Random Forest (RF), Gradient Boosting (GB), Decision Tree (DT), K-Nearest Neighbor (KNN), and Logistic Regression (LR)—to predict diabetes in female patients using the Pima Indians Diabetes Dataset. The study applied preprocessing steps including mean imputation for missing values and conducted model training using an 80:20 train-test split. SVM achieved the highest accuracy (83.5%), followed closely by RF (82.8%). Although the study evaluated a range of classical models, it did not explore any deep learning approaches or customized architectures. In [21], a comparative study was conducted to evaluate the performance of various machine learning algorithms—Logistic Regression, Decision Tree, Random Forest, k-Nearest Neighbor (KNN), Naive Bayes, AdaBoost, and XGBoost—for predicting diabetes risk among the Pima Indian population. The study employed a

comprehensive preprocessing pipeline, encompassing missing value imputation, feature selection using correlation analysis and Recursive Feature Elimination (RFE), and data standardization. Among the various machine learning models evaluated, the Random Forest classifier demonstrated superior performance across all key metrics. Specifically, it achieved an accuracy of 78.12%, precision of 75.68%, recall of 55.13%, F1 score of 63.87%, and an area under the curve (AUC) of 0.83. Despite the model diversity, the study primarily focused on ensemble-based and classical classifiers without proposing any novel architecture.

In [22], a hyperparameter-tuned diabetes prediction model was developed using four classical classifiers—K-Nearest Neighbor (KNN), Support Vector Machine (SVM), Decision Tree (DT), and Random Forest (RF)—on multiple preprocessed versions of the Pima Indians Diabetes Dataset (PIDD). Each version of the dataset was generated through different preprocessing strategies, including missing value removal, mean imputation, and outlier exclusion. The study implemented exhaustive hyperparameter tuning for each classifier to optimize the F1 score and accuracy. The highest performance was achieved using the Random Forest model on the version of PIDD where rows with missing values were excluded, yielding a precision of 74.47%, recall of 72.73%, and accuracy of 80.52%. Although the study demonstrates rigorous preprocessing and optimization techniques, it does not incorporate any deep learning architectures or model explicit feature interaction mechanisms. In [23], four ensemble-based machine learning classifiers—Decision Tree Classifier (DTC), AdaBoost Classifier (ABC), Gradient Boosting Classifier (GBC), and Extra Trees Classifier (ETC)—were evaluated for type 2 diabetes prediction using the Pima Indians Diabetes Dataset (PIDD). The study addressed class imbalance through up-sampling and applied an 80:20 train-test split. Among all models, the ETC achieved the highest performance, reporting an AUC of 0.96. Other models, such as AdaBoost and GBC, yielded moderate ROC values ranging between 0.75 and 0.90. Although the study incorporated robust preprocessing and evaluation techniques, it focused exclusively on ensemble classifiers and did not explore deep learning or Artificial Neural Network (ANN)-based architectures.

2.2. ANN-Based Models and Deep Learning for Medical Data

Artificial Neural Networks (ANNs) and deep learning models have become increasingly popular in diabetes prediction due to their capacity to model complex, nonlinear relationships in medical data. Several studies have demonstrated that ANN-based approaches can outperform traditional ML models when applied to datasets such as PIDD. However, many rely on generic architectures, limiting their adaptability and effectiveness in clinical prediction tasks. This subsection reviews notable ANN-based studies focused on diabetes prediction and highlights their contributions and limitations.

In [24], an artificial neural network (ANN)-based classifier was implemented as part of a unified machine learning framework for diabetes prediction using the Pima Indians Diabetes Dataset (PIDD). The dataset was preprocessed by removing correlated features, and training was conducted using a 70:30 train-test split. The ANN architecture comprised a standard feedforward structure with one hidden layer and sigmoid activation, though the exact number of neurons was not specified. Performance evaluation was carried out using 10-fold cross-validation and included metrics such as accuracy, precision, recall, F1-score, and specificity. Among the six evaluated classifiers, the ANN model yielded the lowest performance, with an accuracy of 68%, precision of 67%, recall of 68%, F1-score of 67%, and specificity of 41%. These results indicate a limited capacity of the ANN to generalize across imbalanced clinical data. In [25], an artificial neural network (ANN) model was developed alongside Random Forest and K-means clustering for early prediction of diabetes using the Pima Indians Diabetes Dataset. The study employed principal component analysis (PCA) for feature reduction and binning techniques for categorical transformation of variables such as glucose, BMI, blood pressure, and age. Association rule mining was used to identify frequent attribute combinations, with findings confirming the strong influence of BMI and glucose on diabetes risk. The ANN model achieved the highest classification accuracy of 75.7% and AUROC of 0.816, outperforming both Random Forest and K-means. While the study demonstrated performance benefits, the ANN used a simple architecture and focused on parameter tuning (e.g., hidden neurons, learning rate) rather than structural innovation. In [26], an artificial neural network (ANN) model was developed for predicting diabetes using the Pima Indians Diabetes Dataset. The study used 688 records for training and 80 for testing and applied mean imputation to handle missing values. Priority-based weighting was manually assigned to features, and the model was built in core Python using a basic feedforward ANN with sigmoid activation and backpropagation for training. The system achieved an ROC value of 0.88 and an error rate of 8%, indicating strong classification performance. However, the architecture relied on manual parameter tuning without introducing structural innovations or interaction-aware modeling.

In [27], an improved artificial neural network (ANN) model was proposed for diabetes prediction using a custom framework called ABP-SCGNN (Artificial Backpropagation–Scaled Conjugate Gradient Neural Network). The model was trained on the Pima Indians Diabetes Dataset with various hidden neuron configurations ranging from 5 to 50. The best validation accuracy of 93% was achieved using 20 hidden neurons, outperforming conventional models like multilayer perceptron (MLP) and Bayesian regularization. The study also reported lower mean squared error (MSE) and higher regression correlation coefficients compared to standard ANN methods. While the architecture included enhanced training procedures and gradient-based optimization, the model retained a single-layer structure without integrating feature interaction modeling or parallel subpaths. In [28], a neural network-based prediction system was proposed to identify diabetes using the Pima Indians Diabetes Dataset. The architecture

consisted of a simple three-layer feedforward ANN with one hidden layer of 12 neurons and sigmoid activation. The system was implemented using TensorFlow and Keras, and trained over 500 epochs. Data preprocessing included normalization and feature filtering, followed by user interaction through a chatbot and GUI interface. The model achieved over 85% accuracy on the test data. While the system incorporated practical elements such as user-friendly prediction tools, it relied on standard neural network configurations without incorporating deeper architectural improvements or feature interaction mechanisms. In [29], three artificial neural network (ANN) models with varying hidden layers were implemented for diabetes prediction using the Pima Indians Diabetes Dataset. The authors applied extensive preprocessing including mean imputation, outlier removal, correlation-based feature selection, and normalization. The ANN with two hidden layers and 400 epochs achieved the highest accuracy of 88.6%, outperforming both one-layer and three-layer configurations. While the study demonstrated the performance impact of network depth and hyperparameter tuning, the ANN architecture remained sequential and lacked structural enhancements for feature interaction modeling.

In [30], an improved artificial neural network (ANN) model was proposed for diabetes prediction, evaluated alongside traditional classifiers such as Multilayer Perceptron (MLP), Support Vector Machine (SVM), k-Nearest Neighbor (KNN), and Decision Tree (DT) using the Pima Indians Diabetes Dataset. The study implemented standard scaling and min-max normalization, followed by iterative tuning of hyperparameters including learning rate, regularization, and hidden layer size. The improved ANN achieved the highest accuracy (89.2%) and outperformed all baseline models across precision, recall, and F1-score. The model used a two-layer feedforward architecture trained via backpropagation and adaptive learning but lacked structural innovations such as parallel subpaths or feature interaction layers. In [31], an artificial neural network (ANN) model was developed and compared with Support Vector Machine (SVM) and k-Nearest Neighbor (KNN) algorithms for predicting diabetes using the Pima Indians Diabetes Dataset. The ANN was implemented with four hidden layers and ReLU activation, and the model was trained with different epoch and batch size settings. Among all models, ANN achieved the highest accuracy (84.64%), outperforming SVM (81.65%) and KNN (76.34%) across precision, recall, and F1-score. The study highlighted the importance of batch size and training iterations in improving ANN performance but did not introduce structural innovations beyond layer scaling.

In [32], an IoT-integrated framework was proposed for diabetes prediction, incorporating an Artificial Neural Network (ANN) alongside other machine learning and deep learning models. The ANN employed a standard feedforward architecture and served as a baseline for evaluating performance. Using real-time data collected from wearable IoT devices, the ANN achieved an accuracy of 68% and the highest recall among all models at 56%. While the system effectively combines IoT and predictive analytics, the study did not introduce any architectural enhancements or novel design elements within the ANN model. In [33], an improved artificial neural network (IANN) model was developed for diabetes prediction using the Pima Indians Diabetes Dataset. The proposed model was based on a modified Multilayer Perceptron (MLP) implemented using Keras and TensorFlow. The architecture consisted of four hidden layers using ReLU and sigmoid activation functions, along with dropout for regularization. The model was trained using stratified 10-fold cross-validation and evaluated with metrics including accuracy, precision, recall, and F1-score. The IANN achieved a training accuracy of 79% and a test accuracy of 77%, with a maximum precision of 83% and recall of 81%. While the architecture showed performance improvements over classical models such as Naive Bayes, Random Forest, and J48, it retained a sequential structure and did not explore interaction-aware mechanisms or feature-level modularization. In [34], a comparative study was conducted to evaluate the performance of six machine learning algorithms—Support Vector Machine (SVM), k-Nearest Neighbor (KNN), Artificial Neural Network (ANN), Logistic Regression (LR), Naïve Bayes (NB), and Decision Tree (DT)—alongside an ontology-based classifier using the Pima Indians Diabetes Dataset. The study used Weka and Protégé for implementation and evaluated models using accuracy, precision, recall, F-measure, and ROC area under both 10-fold cross-validation and 66% split test mode. The ontology classifier achieved the highest accuracy (77.5% and 79.7%) and precision (81.2%) across both validation modes. ANN achieved 75.4% accuracy with 10-fold validation and 83.6% in the split mode. Although the study highlighted the potential of combining ontology and ML, the ANN model remained structurally simple without integrating interaction-aware learning or architectural enhancements.

In [35], a prediction model for type 2 diabetes mellitus was developed using seven classifiers—Artificial Neural Network (ANN), K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Naïve Bayes (NB), Decision Tree (DT), Random Forest (RF), and Linear Discriminant Analysis (LDA)—trained and tested on the Pima Indians Diabetes Dataset (PIDD). The ANN architecture consisted of an input layer, two hidden layers with 10 neurons each, and a sigmoid-activated output layer. After applying preprocessing techniques such as normalization and encoding, the ANN achieved an accuracy of 78.1% on PIDD. While this performance was competitive, the architecture remained relatively shallow and lacked feature interaction modeling. In [36], a hybrid machine learning framework incorporating an Artificial Neural Network (ANN) was proposed for diabetes prediction, evaluated specifically on the Pima Indians Diabetes Dataset (PIDD). The ANN model achieved a test accuracy of 70.56%, with a sensitivity of 58.75% and a precision of 57.31% under a 70:30 train-test split. When the split was adjusted to 75:25, the accuracy improved to 71.35%. Although the study conducted detailed metric-based evaluations, the ANN employed a conventional architecture without any architectural customization or explicit modeling of feature interactions. In [37], a hybrid model combining Latent Dirichlet Allocation (LDA) and an Artificial Neural Network (ANN) was proposed for diabetes classification

using the Pima Indians Diabetes Dataset (PIDD). The approach leveraged LDA-generated probability distributions to initialize the weights of a backpropagation-based ANN, aiming to enhance predictive performance. Feature selection was conducted using a bivariate filter and Pearson correlation to retain the most relevant attributes. On the PIDD, the ANN-LDA model achieved a notable accuracy of 93%, outperforming several baseline classifiers, including KNN (76%), Logistic Regression (78%), SVM (87%), and a standalone ANN (82%). Despite the improved performance through hybridization, the ANN architecture remained sequential and did not incorporate advanced design elements such as parallel dense layers or interaction-aware feature fusion. In [38], a basic feedforward artificial neural network (ANN) was implemented as one of the baseline models for diabetes prediction using the Pima Indians Diabetes Dataset (PIDD). The ANN consisted of a single hidden layer and was evaluated using standard classification metrics. It achieved an accuracy of 79.55%, which was lower than that of ensemble methods like MLHA and XGBoost. While the ANN served as a performance benchmark, it lacked structural enhancements such as multi-path processing or interaction-aware layers.

2.3. Research Gap and Our Contribution

Despite extensive research on diabetes prediction using the Pima Indians Diabetes Dataset (PIDD), several key limitations persist across existing studies. Classical machine learning algorithms such as Logistic Regression, Decision Trees, Random Forests, and Support Vector Machines have demonstrated reasonable predictive performance. However, these models often fall short in effectively handling class imbalance, generalizing across diverse patient populations, and capturing complex nonlinear relationships among clinical features.

More recently, artificial neural network (ANN)-based approaches have been introduced to address some of these challenges. While such methods have shown improved accuracy, the majority employ conventional feedforward architectures with minimal structural modification. Prior studies typically rely on sequential dense layers and standard activation functions, with limited emphasis on feature-level interaction modeling or architectural customization. Although a few hybrid models and parameter optimization strategies have been proposed, they often lack architectural transparency and are not benchmarked comprehensively against both traditional and deep learning methods.

To address these gaps, we propose a novel ANN architecture tailored specifically for structured clinical data such as PIDD. The proposed model integrates:

- Feature-wise normalization, allowing for stable and individualized scaling of input variables;
- Parallel dense sublayers, enabling diverse transformation paths and improved feature representation; and
- Interaction-aware fusion, which explicitly captures nonlinear dependencies between features.

This architectural design aims to enhance model generalization, classification accuracy, and interpretability. Additionally, we conduct a systematic performance comparison against classical ML models and recent ANN-based frameworks to validate the effectiveness of our approach.

3. Methodology

This section presents the design of the proposed Artificial Neural Network (ANN) architecture for diabetes risk prediction using structured clinical data. The architecture is specifically developed to address the limitations of conventional ANN models by incorporating feature-wise normalization, an attention-inspired feature interaction mechanism, and a parallel feature enrichment path (see Figure 1). The model is trained and evaluated on the Pima Indian Diabetes dataset.

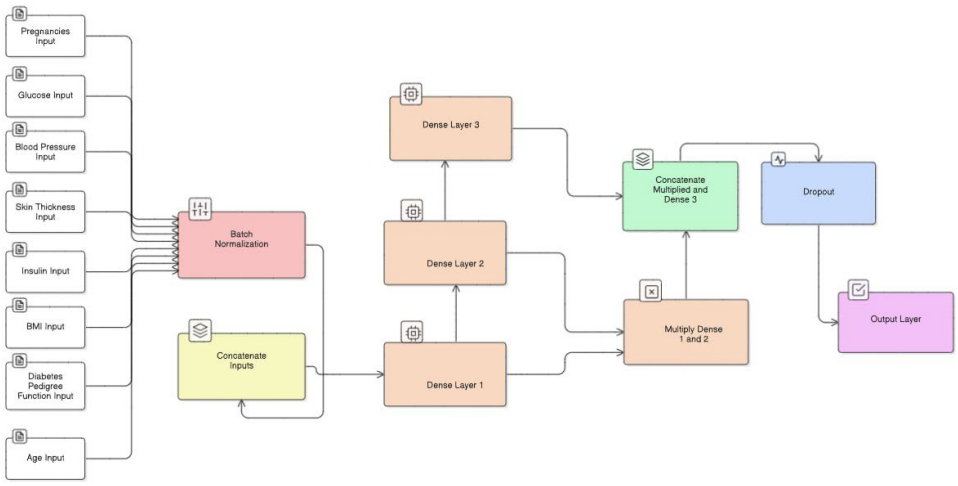

Figure 1. Proposed DeepDiabFusion model for diabetes prediction

3.1. Dataset

The Pima Indians Diabetes Dataset (PIDD) is used in this study. The PIDD is originally from the National Institute of Diabetes and Digestive and Kidney Diseases [39]. The dataset consists of 768 observations, with 268 cases of diabetes and 500 non-diabetic cases. It includes eight numerical medical predictor attributes and one binary target attribute, as detailed in Table 1. In this study, we split the PIDD dataset into training and validation sets, with 653 samples used for training and 115 for testing.

Table 1. Brief description of diabetes dataset

№	Attribute	Description
1	Pregnancies	Number of times a woman gets pregnant
2	Glucose	Plasma glucose concentration
3	Blood pressure	Diastolic blood pressure
4	Skin thickness	Triceps skin fold thickness
5	Insulin	2 h serum insulin
6	BMI	Body Mass Index
7	Diabetes pedigree function	A function that scores the likelihood of diabetes based on family history
8	Age	Age of patient
9	Target variable	Diabetic/Non-diabetic

3.2. Input Features and Preprocessing

Each of the eight clinical variables is treated as an independent input feature. These inputs are passed individually through separate Input Layer components, each of shape (None, 1), followed by dedicated Batch Normalization layers. This feature-wise normalization approach standardizes each attribute based on its specific statistical distribution, thereby enhancing convergence stability and allowing the model to more effectively learn feature-specific patterns without interference from inter-feature scale discrepancies.

3.3. Feature Aggregation

The normalized outputs from all eight input branches are concatenated using a Concatenate layer to produce a unified feature vector of dimension (None, 8). This operation enables the simultaneous processing of all input attributes while preserving the normalized scale of each feature, thus facilitating coherent downstream learning.

3.4. Interaction-Aware Modeling

To capture latent interdependencies among features, the concatenated vector is simultaneously processed through two parallel dense layers, each producing an 8-dimensional output. These outputs are then merged using an element-wise Multiply operation, which functions as an attention-inspired mechanism. This mechanism enables the model to assign dynamic relevance to feature combinations, enhancing its capacity to model complex, nonlinear relationships that may underlie the onset of diabetes.

3.5. Parallel Feature Enrichment

In parallel with the interaction block, the same concatenated input vector is passed through a third dense layer comprising 64 units. This layer functions as a high-capacity pathway for feature abstraction, learning enriched representations through nonlinear transformations. The parallel structure facilitates the simultaneous modeling of both local feature interactions and global abstraction.

3.6. Feature Fusion and Output Layer

The outputs from the interaction-aware module and the enrichment pathway are concatenated to form a comprehensive 72-dimensional feature vector. To mitigate the risk of overfitting, a Dropout layer is applied. The final classification is performed using a dense output layer with a sigmoid activation function, producing a probabilistic output in the range [0,1], indicative of the likelihood of diabetes onset.

This architectural design integrates normalization, parallel processing, and interaction modeling in a unified ANN framework. It demonstrates enhanced generalization and interpretability compared to conventional ANN configurations, making it well-suited for application in clinical decision support systems.

3.7. Formal Equations of the Model

To enhance clarity and ensure reproducibility, the DeepDiabFusion architecture is formally defined through a sequence of mathematical expressions that represent its key components. The model processes structured clinical data consisting of eight features, denoted as $X = [x_1, x_2, \dots, x_8] \in R^8$. The following equations describe the flow of data through the network:

Input normalization

Each input feature undergoes independent batch normalization to standardize its scale:

$$x_i^{norm} = \frac{x_i - \mu_i}{\sqrt{\sigma_i^2 + \epsilon}}, \qquad \forall \in \{1, \dots, 8\} \quad (1)$$

The normalized features are then concatenated to form the normalized input vector:

$$x_{norm} = Concatenate(x_1^{norm}, x_2^{norm}, \dots, x_8^{norm}) \in R^8 \quad (2)$$

Interaction-aware dense paths

The normalized vector is passed through two parallel dense layers, each with 8 units and ReLU activation:

$$h_1 = \phi(x_{norm} \cdot W_1 + b_1), \; h_2 = \phi(x_{norm} \cdot W_2 + b_2) \quad (3)$$

where W_1, $W_2 \in R^{8\times8}$, $h_1, h_2 \in R^8$, and ϕ denotes the ReLU activation function.

Element-wise interaction fusion

The outputs of the parallel paths are combined through element-wise multiplication to model interactions between learned representations:

$$z_{interact} = h_1 \odot h_2 \in R^8 \quad (4)$$

Feature enrichment path

Simultaneously, the normalized input is processed by an additional dense layer with 64 units:

$$z_{enrich} = \phi(x_{norm} \cdot W_1 + b_1),$$
$$W_3 \in R^{8\times64}, z_{enrich} = R^{64} \quad (5)$$

Feature fusion, dropout, and output

The outputs of the interaction and enrichment paths are concatenated:

$$z_{fused} = Concatenate(z_{interact}, z_{enrich}) \in R^{72} \quad (6)$$

To improve generalization and mitigate overfitting, dropout is applied:

$$z_{drop} = Dropout(z_{fused}, p = 0.3) \quad (7)$$

Finally, a dense output layer with sigmoid activation produces the predicted probability of diabetes onset:

$$\hat{y} = \sigma(z_{drop} \cdot W_4 + b_4), \ \hat{y} \in 0,1) \quad (8)$$

where σ denotes the sigmoid function.

4. Experimental Results and Discussion

This section evaluates the performance of the proposed DeepDiabFusion model on the Pima Indians Diabetes Dataset (PIDD). Results are reported using key classification metrics and compared against traditional machine learning algorithms and existing ANN-based models. An ablation study is also included to assess the contribution of individual architectural components.

4.1. Evaluation metrics

We conducted the experiments using four performance evaluation metrics to evaluate the results of the diabetes prediction. Equations 9-11 describe and formulate these metrics.

AUC (Area Under the Curve) is a metric used to evaluate the performance of classification models. It represents the probability that a randomly chosen positive instance will be ranked higher than a randomly chosen negative instance. A higher AUC indicates better model performance.

Accuracy measures a model's ability to predict outcomes correctly. It is calculated as the ratio of accurate predictions to total predictions.

$$Accuracy = \frac{(TP+TN)}{(TP+TN+FP+FN)} \quad (9)$$

Where,

TP = True Positives, TN = True Negatives, FP = False Positives, FN = False Negatives.

Precision measures the accuracy of positive predictions made by a machine learning model. It is calculated by dividing the number of true positive predictions by the total number of positive predictions. A higher precision indicates that the model is better at avoiding false positives.

$$Precision = \frac{TP}{TP+FP} \quad (10)$$

Recall measures the completeness of positive predictions made by a machine learning model. It is calculated by dividing the number of true positive predictions by the total number of actual positive instances. A higher recall indicates that the model is better at avoiding false negatives.

$$Recall = \frac{TP}{TP+FN} \quad (11)$$

4.2. Performance Comparison with Seven Traditional ML Models Used in This Study

In Table 2, the classification algorithms, such as LR, KNN, RF, SGD, GB, DT, LDA, and the proposed ANN, have prediction accuracy of 78.44%, 79.31%, 84.48%, 68.97%, 90.52%, 85.35%, 79.31%, and 93.04%, respectively. In contrast, the proposed ANN based model predicts the diabetes cases more accurately than the other algorithms. In comparison, in terms of prediction precision: the algorithms obtained 62.5%, 75%, 80%, 30%, 80%, 80%, 65%, and 86.21% for LR, KNN, RF, SGD, GB, DT, LDA, and the proposed ANN, respectively.

Table 2. Comparison of the proposed model with employed ML models in this study

№	Algorithm	Accuracy %	Precision %	Recall %	AUC
1.	LogisticRegression(random_state=16)	78.44	62.5	71.43	0.7467
2.	KNeighborsClassifier(n_neighbors=7)	79.31	75	68.18	0.7829
3.	RandomForestClassifier()	84.48	80	76.19	0.8342
4.	SGDClassifier(max_iter=5)	68.97	30	60	0.5974
5.	GradientBoostingClassifier()	90.52	80	91.43	0.8803
6.	DecisionTreeClassifier()	85.35	80	78.05	0.8408
7.	LinearDiscriminantAnalysis (n_components=1)	79.31	65	72.22	0.7592
8.	**Proposed**	**93.04**	**86.21**	**93.10**	**0.951**

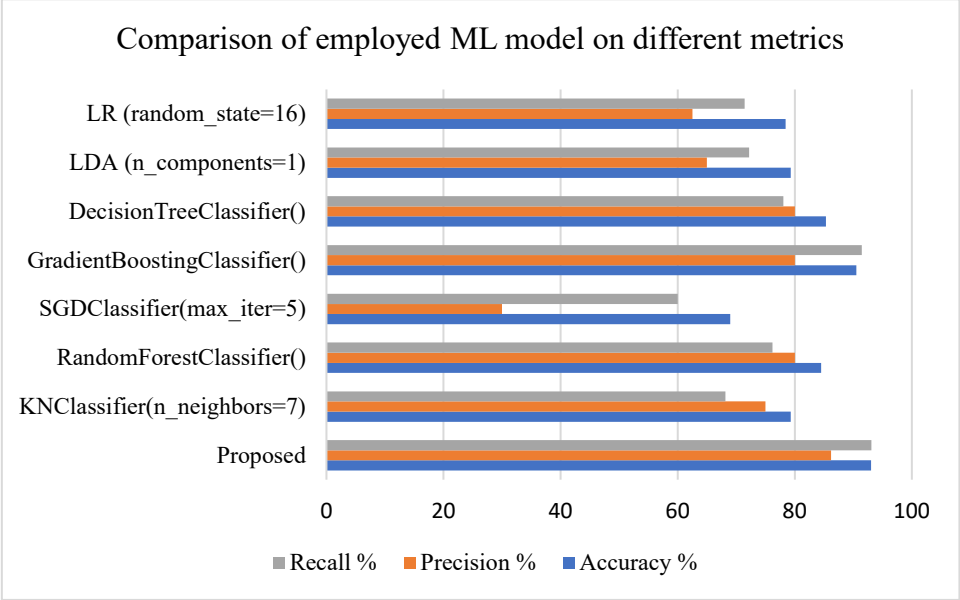

Figure 2. Graphical representation of experimental results

As per Fig. 2, the ANN-based model outperforms the other algorithms in terms of diabetes case prediction precision. In terms of recall, the algorithms demonstrated the following performance: LR (71.43%), KNN (68.18%), RF (76.19%), SGD (60%), GB (91.43%), DT (78.05%), LDA (72.22%), and proposed ANN (93.10%). Comparing recall scores, the proposed ANN based model outperformed the other algorithms (see Figure 2), achieving a recall of 93.10%, while SGD achieved the lowest recall at 60%. When comparing AUC scores, the algorithms achieved the following results: LR (0.7467), KNN (0.7829), RF (0.8342), SGD (0.5974), GB (0.8803), DT (0.8408), LDA (0.7592), and proposed ANN (0.951). In terms of AUC, the proposed ANN based model demonstrated the best performance with a score of 0.951, while SGD achieved the lowest AUC at 0.5974.

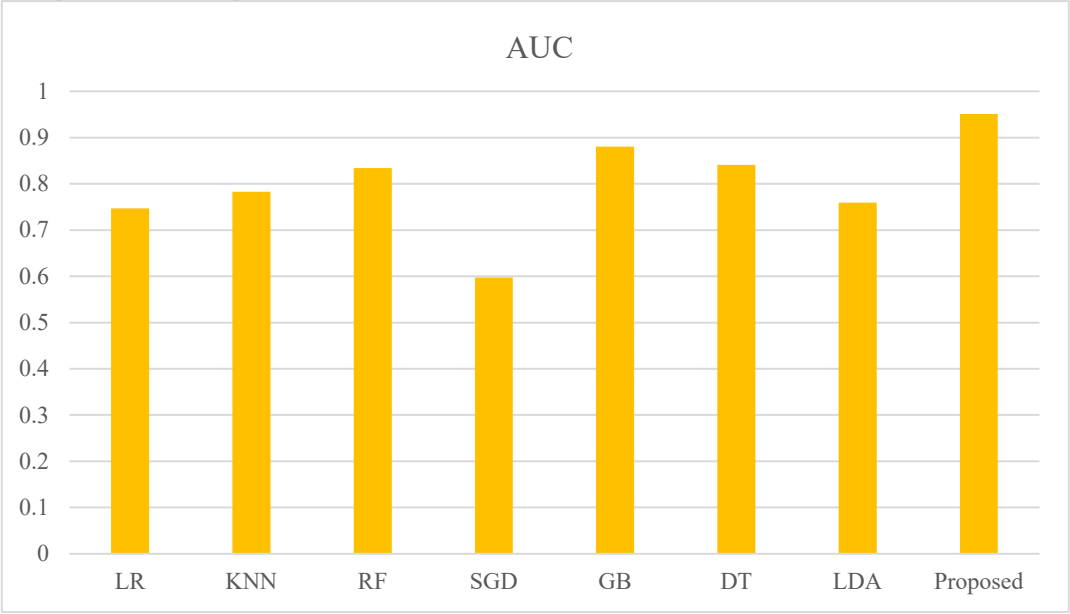

Figure 3. Comparison of experimental results on AUC

4.3. Performance Comparison with Existing ML Models

A detailed comparison of Table 3 and Figure 4 across accuracy, precision, and recall metrics reveals that the proposed ANN model consistently outperforms previous methods. The proposed ANN model achieved the highest accuracy (93.04%), outperforming all previous models on the Pima Indians Diabetes Dataset (PIDD). It was followed by the Random Forest model in [9] with 92.10% and the Linear-Kernel-SVM in [10] with 90.00%. In contrast, the lowest accuracy was reported by Simple Logistic Regression [16] (75.70%), Logistic Regression [19] (77.20%), and Naive Bayes [15] (77.36%), highlighting the limitations of traditional linear and probabilistic classifiers for this dataset.

The Random Forest in [9] achieved the highest precision (90.00%), indicating a low false positive rate. It was followed by Linear-Kernel-SVM in [10] (88.00%) and the proposed ANN model (86.21%). Conversely, Naive Bayes [15] had the lowest precision (67.00%), suggesting a higher rate of incorrect positive predictions, followed by RF [22] and Simple-LR [21].

The proposed ANN model again led in recall (93.10%), showing its effectiveness in correctly identifying diabetic cases. Random Forest [9] and Extra Trees Classifier [23] also performed strongly, with recall scores of 93.00% and 92.00%, respectively. In contrast, the lowest recall was observed in RF [21] (55.13%), followed by RF [11] and NB [15], indicating that these models missed a significant number of actual positive cases.

These comparisons demonstrate the superiority of the proposed ANN architecture across all three metrics, underscoring the effectiveness of its architectural enhancements such as parallel dense paths and interaction-aware fusion. They also highlight the limitations of conventional models, particularly in generalizing well across all evaluation criteria.

Table 3. Comparison of our experimental results with previous studies on traditional ML models

Ref.	Year	Dataset	Algorithm/Model	Accuracy %	Precision %	Recall %
[16]	2020	PIDD	Simple LR	75.7	75.8	75.8
[19]	2021	PIDD	LR	77.2	76.7	77.2
[15]	2019	PIDD	NB	77.36	67	62
[17]	2020	PIDD	RF	77.9	81	89
[21]	2023	PIDD	RF	78.12	75.68	55.13
[22]	2023	PIDD	RF	80.52	74.47	72.73
[11]	2021	PIDD	LR	82.46	76	61
[18]	2021	PIDD	SVM	83	79	63
[12]	2023	PIDD	SG	83.9	83.7	76.7
[23]	2023	PIDD	ET	89	86	92
[10]	2022	PIDD	Linear Kernel SVM	90	88	87
[9]	2021	PIDD	RF	92.10	**90**	93
Proposed		PIDD	ANN	**93.04**	86.21	**93.10**

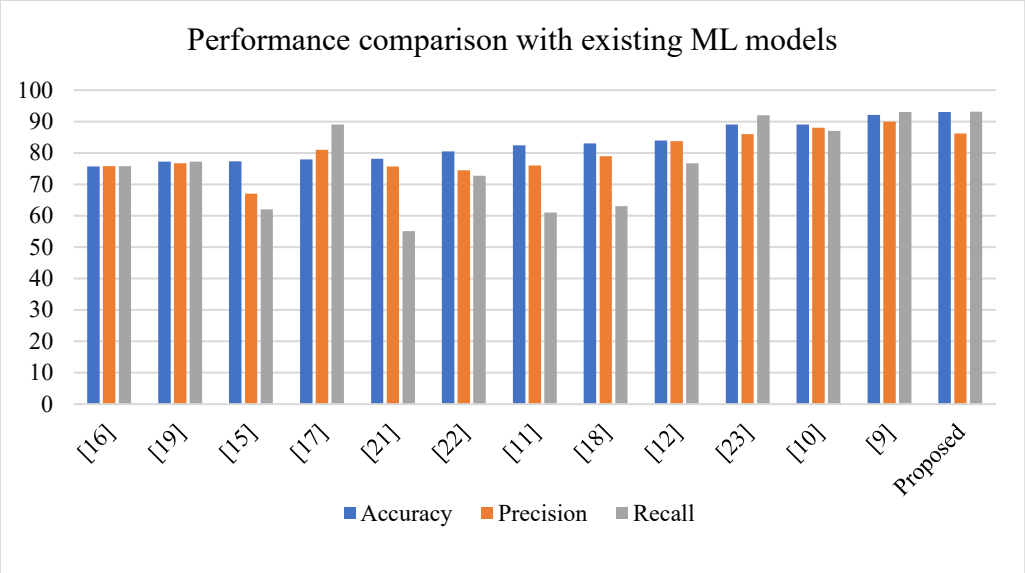

Figure 4. Comparison of the proposed model with existing ML studies in terms of accuracy, precision, and recall

4.4. Performance Comparison with Existing ANN-Based Studies

An evaluation of accuracy across ANN-based models in Table 4 and Figure 5 show that the proposed model achieved the highest performance with an accuracy of 93.04%, marginally surpassing prior works in [27] and [37], both of which reported 93.00%. Other notable high-performing models include [26] and [30], which reported 92.00% and 89.20%, respectively. In contrast, the weakest results were observed in [24] and [32], both reporting 68.00%, followed by [36] at 71.35%. These findings highlight the superior classification capability of the proposed architecture, which outperforms traditional ANN implementations by integrating architectural innovations such as feature-wise normalization and parallel sublayer design.

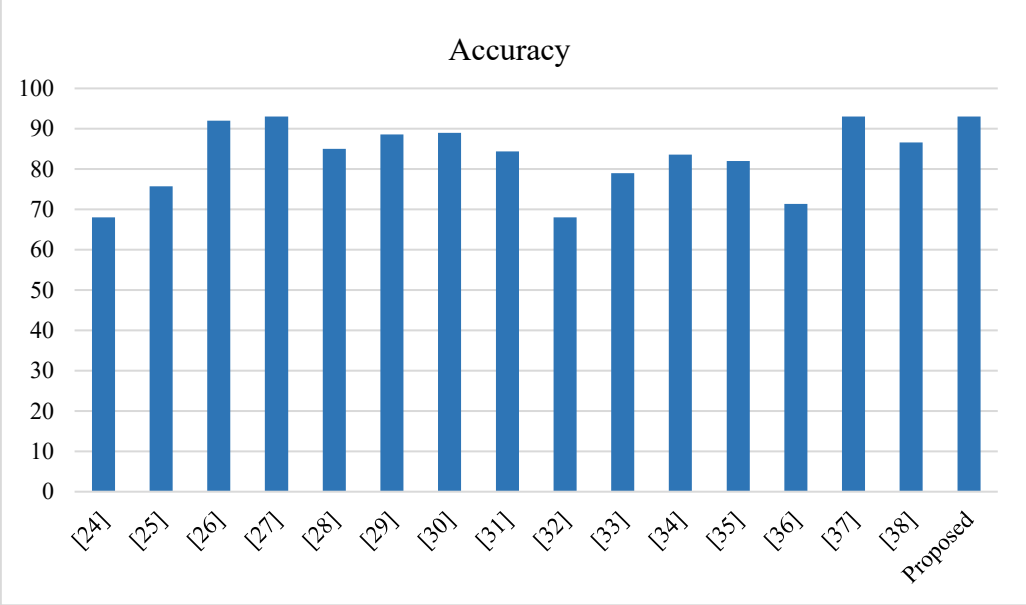

Figure 5. Comparison of the proposed model with existing ANN-based studies in terms of accuracy

In terms of precision, the proposed ANN model achieved a high score of 86.21%, outperforming most previous studies. While [30] reported a slightly higher precision of 88.00%, the proposed model still exceeded the results of [34], which achieved 83.60%. Meanwhile, the lowest precision values were recorded in [36] (59.21%), [32] (66.00%), and [24] (67.00%). These results emphasize the effectiveness of the proposed model not only in classifying positive cases accurately but also in reducing false positives—a critical factor in clinical diagnostic applications.

Regarding recall, the proposed model achieved the best result with a value of 93.10%, indicating its high sensitivity in correctly identifying diabetic cases. This score slightly exceeded the results of [30] (89.00%), and those of [29] and [37], which each reported 88.00%. In contrast, [32] had the lowest recall at 56.00%, followed by [36] at 65.21%, and [24] at 68.00%. The substantial improvement in recall demonstrates the proposed model's ability to reduce false negatives, thereby increasing its clinical utility for early diabetes detection.

Table 4. Comparison of our experimental results with previous studies on ANN models

Ref.	Year	Dataset	Algorithm/Model	Accuracy %	Precision %	Recall %	AUC
[24]	2018	PIDD	ANN	68	67	68	-
[25]	2019	PIDD	ANN	75.7	-	-	0.816
[26]	2019	PIDD	ANN	92	-	-	-
[27]	2021	PIDD	ANN	93	-	-	-
[28]	2021	PIDD	ANN	85	-	-	-
[29]	2021	PIDD	ANN	88.6	-	88	-
[30]	2021	PIDD	ANN	89.2	**88**	89	-
[31]	2022	PIDD	ANN	84.64	78	79	-
[32]	2022	PIDD	ANN	68	66	56	-
[33]	2022	PIDD	ANN	79	83	81	-
[34]	2022	PIDD	ANN	83.6	83.6	77.5	0.772

[35]	2023	PIDD	ANN	78.1	-	-	-
[36]	2023	PIDD	ANN	71.35	59.21	65.21	-
[37]	2024	PIDD	ANN-LDA	93	81	88	-
[38]	2024	PIDD	ANN	86.58	-	-	-
Proposed		PIDD	ANN	**93.04**	86.21	**93.10**	**0.951**

4.5. Ablation Study: Assessing the Impact of Architectural Components

To evaluate the individual contributions of key architectural components in the proposed DeepDiabFusion model, an ablation study was conducted. This analysis systematically deconstructs the architecture by removing or modifying specific modules, allowing us to assess their relative impact on overall model performance. The study focuses on three critical components: (i) the interaction-aware fusion block, (ii) the parallel enrichment path, and (iii) the feature-wise normalization mechanism.

Five experimental variants were created for comparison:

- **Full Model (DeepDiabFusion):** Includes all components—feature-wise normalization, interaction block, enrichment path, and dropout.
- **No Interaction Block:** Excludes the two parallel dense layers and the element-wise multiplication, retaining only the enrichment path.
- **No Enrichment Path:** Removes the enrichment path, relying solely on the interaction-aware block.
- **No Feature Normalization:** Disables all batch normalization layers applied to individual inputs.
- **Baseline ANN:** A standard two-layer feedforward ANN without any architectural enhancements.

The comparative results are summarized in Table 5.

Table 5. Performance comparison from ablation study of DeepDiabFusion architecture

Variant	Accuracy %	Precision %	Recall %	AUC
DeepDiabFusion (Full)	**93.04**	**86.21**	**93.10**	**0.951**
No Interaction Block	89.35	80.45	88.30	0.9156
No Enrichment Path	87.83	79.18	86.80	0.9012
No Feature Normalization	85.50	75.21	84.00	0.8751
Baseline ANN	82.17	72.46	80.33	0.8468

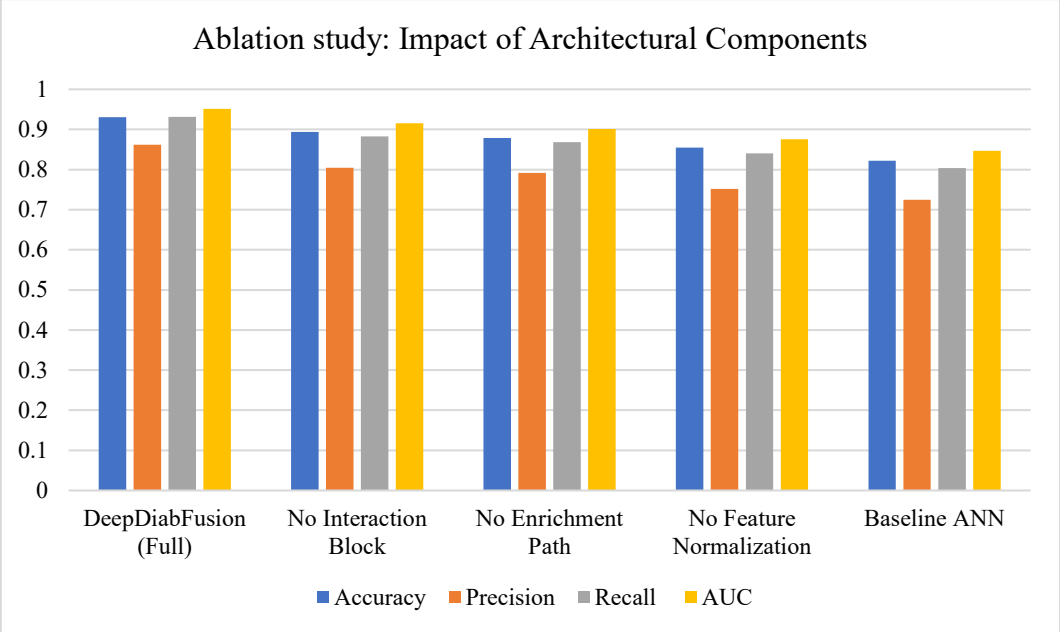

Figure 5. Performance comparison from ablation study of DeepDiabFusion architecture

Figure 5 illustrates the impact of removing individual components—interaction block, enrichment path, and feature-wise normalization—from the proposed DeepDiabFusion model. The full model achieves the highest performance across all evaluation metrics (Accuracy, Precision, Recall, and AUC), validating the contribution of each architectural component.

The ablation results clearly demonstrate the additive value of each architectural module. Removing the interaction block resulted in a substantial decline in recall and AUC, confirming its importance in modeling feature dependencies. The enrichment path also proved essential for capturing abstract feature representations, as reflected in the drop in precision and overall accuracy. Additionally, the exclusion of feature-wise normalization adversely affected all metrics, indicating its role in stabilizing training and improving generalization. The baseline ANN performed worst across all measures, reinforcing the effectiveness of the proposed architectural enhancements.

These findings validate the design of DeepDiabFusion and underscore the significance of each component in improving the predictive accuracy and robustness of diabetes classification models.

5. Conclusion

This study introduced DeepDiabFusion, a novel artificial neural network (ANN) architecture designed to enhance the accuracy and robustness of diabetes prediction using structured clinical data. The proposed model integrates feature-wise normalization, parallel dense sublayers, and an interaction-aware fusion mechanism to better capture complex, nonlinear relationships among input features.

Experimental evaluations on the Pima Indians Diabetes Dataset (PIDD) demonstrate that DeepDiabFusion outperforms both conventional machine learning algorithms and existing ANN-based models across multiple performance metrics. The model achieved an accuracy of 93.04%, precision of 86.21%, recall of 93.10%, and an area under the curve (AUC) of 0.951, confirming its effectiveness in reliable risk classification.

In addition to its predictive strength, the model's modular architecture contributes to improved scalability and interpretability. Its ability to model structured feature interactions makes it a promising tool for broader applications in medical data analysis.

Future work will focus on extending the architecture by incorporating explicit attention mechanisms, validating performance across diverse datasets, and investigating hybrid ensemble approaches. These developments aim to further enhance the model's generalizability and utility in real-world medical contexts.

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