Enhanced Diabetes Prediction Accuracy through Cutting-Edge Deep Learning and Ensemble Machine Learning Techniques

M. Saqib[1], M. Ibrahim[2], M. M. Iqbal[3], Q. G. K. Safi[4]

[1,2,3,4]*Department of Computer Science, University of Engineering and Technology, Taxila, Pakistan*

[3] munwar.iq@uettaxila.edu.pk

Abstract- Diabetes mellitus is a long-term metabolic dis-order, which is relevant to over 537 million individuals across the globe, and the prevalence is expected to rise to 46 percent by 2045. Predication of risks at an early and precise stage is very necessary to minimize complications, mainly in healthcare systems that are short of resources. This research will offer a hybrid predictive model that integrates ensemble machine learning and deep learning models in identifying diabetes at its early stages based on clinical and demographic data. The Pima Indian Diabetes Dataset (PIDD) comprising of 768 female patients was experimented on. The pre-processing of the data consisted of imputation of missing values, elimination of outliers, balancing the classes by using SMOTE and augmentation of the dataset to 10,000 training balanced samples using multivariate Gaussian sampling used exclusively on the training set. Four ensemble models, which are Bagging, Gradient Boosting, Random Forest and Stacking, were optimized with gridsearchCV. An early stopping and dropout Deep Neural Network (DNN) as well as a Long Short-Term Memory (LSTM) model were trained. The evaluation of performance was based on the accuracy, precision, recall, F1 score, and ROC-AUC on a strictly held-out test set. On the augmented dataset, the DNN data obtained a 99.9% accuracy and ROC-AUC of 1.000, whereas ensemble models obtained 97% – 99.1% accuracy. The ensemble accuracies observed on the original dataset were between 73.4 per-cent and 77.3 percent as expected in literature. The key predictors were found to be glucose, BMI and age. There was cross dataset generalization that was verified by outside validation. The suggested framework has a high predictive power, a high generalization, and results that are clinically interpretable, which evidences its possible use as a healthcare decision-support system.

Keywords- Diabetes Prediction; Ensemble Learning; Deep Learning; Bagging and Boosting; Random Forest; Pima Indian Diabetes Dataset (PIDD).

I. INTRODUCTION

Diabetes mellitus is a lasting metabolic condition, which is defined by sustained hyperglycemia caused by abnormalities in insulin discharge, insulin reaction, or both [1-2]. The International Diabetes Federation (IDF) estimates that in 2021, the global number of adults aged 20 to 79 years who had diabetes was about 537 million and that by 2045, the number will have reached 783 million, which is 46% higher than the population in 2021 [3]. The long-term care is known to have some severe complications such as nephropathy, retinopathy, neuropathy, and cardiovascular disease, which cumulatively have a heavy economic burden to the world with direct healthcare spending amounting to USD 966 billion [2]. Early and timely detection of potential people who are at the risk of developing diabetes is thus a key area of concern in the field of public health especially in low and middle income countries where the infrastructure in terms of diagnosis is still inadequate [4].

Conventional clinical diagnosis of diabetes is based on the fasting Plasma Glucose, Oral Glucose tolerance, and Glycated Hemoglobin (HbA1c) tests. These methods though effective, are reactive as opposed to predictive and frequently unavailable in resource limited situations. When used to predict diabetes, the standard statistical models like logistic regression normally produce test accuracies of about 73 to 80% on the usual benchmark datasets like the Pima Indian Diabetes Dataset (PIDD) where ROC-AUC values rarely exceed 0.83 [5-6]. These drawbacks emphasize the necessity to have more powerful, data-driven methods that can include the non-linear interactions between clinical risk fac-tors.

Machine learning has become a promising paradigm in diabetes risk prediction, and research indicates an increasing trend in the performance of various families of algorithms. Sensitivities of up to 87.2% and specificities of 79% on the PIDD have been obtained with Support Vector Machines (SVM)

under cross-validation [6-7]. The test accuracy of random forest classifiers has been shown to be between 83 to 89 percent on the same set of data and has consistently performed better than the more basic classifiers like Decision Trees and Naive Bayes [8-9]. XGBoost and other methods of Gradient Boosting have demonstrated accuracy of up to 89 percent and has ROC-AUC values of 0.91 in clinical diabetes data [7], [10]. Regardless of these developments, even single machine learning models are vulnerable to weaknesses such as class skew, overfitting on small samples, low cross-demographic heterogeneity and cross-smattering [11-12].

Ensemble learning extends these weaknesses by making use of the predictions of a number of base classifiers to decrease the variation of the model and enhance the generalization aspect. Other techniques like Bagging, Boosting and Stacking have always been performing better than single-model methods in organized clinical data tasks. A stacking ensemble of deep neural networks and traditional classifiers had accuracies of 92 to 95% on local healthcare data. The ensemble ROC-AUC of 0.950 on the PIDD is 2% higher compared to individual classifiers. Most of the available ensemble studies do not however evaluate more than one or two ensemble strategies independently and restrict the possibility to make concerns inference across the archives [9-10].

Both Deep Neural Networks (DNN) and Long Short-Term Memory (LSTM) networks have complementary benefits of learning hierarchical feature representations and sequential dependencies respectively. DNNs have been shown to achieve ROC-AUC values reaching 0.991 on clinical diabetes datasets and LSTM-based models have reached ac-curacy values of 87.26% on the PIDD. However, deep learning-based diabetes prediction models are sensitive to overfitting on small clinical datasets and are computation-ally expensive to evaluate, and have not been compared to ensemble models under the same experimental conditions [13-15].

Another issue that has remained in diabetes prediction studies is the class imbalance [16-17]. An example was the PIDD which has 500 non-diabetic samples and 268 diabetic samples with an imbalance ratio of 1.87:1. Unless properly corrected, the overall accuracy of classifiers trained on these kinds of datasets can be misleading, with a systematic bias towards the majority class and poor sensitivity to the minority clinically important class [9], [12]. Other techniques like the Synthetic Minority Over-sampling Technique (SMOTE) have been demonstrated to enhance the minority class recall by as much as 15 percentage points in similar medical classification tasks [18].

The current research fills these knowledge gaps by presenting a hybrid system that considers a systematic com-bination of four ensemble approaches, namely, Bagging, Gradient Boosting, Random Forest, and Stacking, and two deep learning models, that is, DNN and LSTM, under the same pre-processing and testing circumstances with PIDD. The framework entails the use of two-stage data enrichment pipeline that entails the use of SMOTE-based class balancing along with multivariate Gaussian augmentation, expansion of feature interactions by use of polynomials, and systematic hyperparameter learning. One more factor that enhances the generalizability and interpretability of the findings is an external validation on the Early-Stage Diabetes Risk Prediction Dataset and a feature sensitivity analysis.

The main contributions of this work are summarized as follows:

Introduces a hybrid framework that combines four ensemble models and two deep learning architectures and allows a fair cross-model comparison in the PIDD.

The dataset is enriched with a two-stage data enrichment strategy based on SMOTE and Gaussian augmentation over the dataset of 10,000 samples with the strict test-set isolation.

Ensemble stacking is used in conjunction with polynomial feature interaction to boost non-linear representation learning.

The cross-dataset generalization on an independent dataset of diabetes is proven by external validation.

Feature sensitivity analysis ensures robust performance without depending on such powerful predictors like glucose and BMI.

The remaining parts of the paper are organized as follows.

Section II includes relevant work, Section III presents the suggested techniques, Section IV includes results and discussion, and Section V wraps up the proposed work and future directions.

II. Related Works

Diabetes mellitus is one of the acute problems in the world healthcare of the modern age, and the early diagnosis and further intervention are the keys to the reduction of its chronic effects [17].

There are many machine learning approaches presented to predict diabetes, and significant advances have been made in enhancing predictive accuracy and model reliability in diverse datasets and with different groups of patients [18].

A remote healthcare monitoring framework was introduced by [19]. In their system, they use per-sonal health devices and smart wearables for tracking their health in real time. The Pima Indian Diabetes Database was trained on by a support vector machine (SVM). Their framework demonstrated a good performance measure with a sensitivity of 87.20% and specificity of 79%. On tenfold stratified cross-validation, it achieved an

accuracy of 83%, which indicates that it had a good performance. It is a real-time monitoring system for healthcare professionals to get timely patient data. Also, it improves patient engagement and imparts a better decision-making process by the medical personnel.

Butt developed a comprehensive learning system for diabetes prediction and classification. The Pima Indian Diabetic dataset is analyzed using as many machine learning classifiers as possible. Long short-term memory (LSTM), logistic regression (LR), random forest (RF), and multilayered perceptron (MLP) were the models employed in this. Of all the models tested, the LSTM was the most accurate with 87.26%, closely followed by the MLP classifier with 86.08%. The results confirmed the potential success of using the IoT technology in combination with machine learning to manage diabetes effectively [20].

Tasin designed an automated diabetes prediction system for female patients in Bangladesh. They used a dataset that was combined of the Pima Indian Diabetes Database and private medical records. The mutual information techniques and semi-supervised extreme gradient boosting model were used by them. For handling class imbalance, they used SMOTE and ADASYN for the over-sampling. They achieved 81% accuracy and 0.84 AUC of the XG Boost classifier [21]. The model's interpretability was improved through accessible AI techniques such as SHAP and LIME. In their research, they put their emphasis on what is transparent in AI-based healthcare models.

Different machine learning models were evaluated to determine diabetes risk based on 952 subjects. In their research, they applied random forest classifiers for a custom dataset and the Pima Indian Diabetes Database[22]. The prediction across both datasets was better using the random forest. The findings also supported the idea that lifestyle and family history do contribute to the level of risk that diabetes poses. This research supported the idea of creating population-specific customized predictive models depending on specific groups of people.

Machine learning was examined for diabetic prediction. Their study found a gap in validation that exists in the predictive models. The research emphasized that diverse data is necessary for robust performance of the model. They focused on the field of pattern recognition in the context of data mining. Increased predictive accuracy and increased reliability of proportionality of diagnosis were other key areas of focus. This research provided a cornerstone of future progress in the sphere of predicting diabetes through modeling [23].

The neural network models that predict diabetes were investigated [24]. The dataset used was of 15,000 female patients who had come to the Taipei Municipal Medical Centre. For the highest accuracy, a class-boosted decision tree model was chosen. The score of the AUC for this model was 0.991. In all, their findings showed that advanced neural networks are effective in clinical applications. The study focused on the multiple health indicators for diabetes prediction. The work that they did supported machine learning to provide personalized healthcare solutions.

A method for predicting diabetes using machine learning was proposed [25]. They used a custom diabetes dataset consisting of 800 records and 10 attributes. The study that they addressed was low classification accuracy in traditional prediction models. Before applying machine learning algorithms, the authors applied K-means clustering on age and glucose variables. Using random forest models and support vector machines, classification was carried out. This approach was more accurate than previous techniques.

Models based on neural networks and machine learning algorithms were developed for diabetes diagnosis [26]. The study showed it was limited to existing diabetes datasets. Accelerating the overall prediction accuracy were the application of feature selection and over-sampling methods. The data suggested that non-invasive tests could help in detecting diabetes. The study's goal was to demonstrate deep learning's potential for predictive healthcare. However, there was a shortage of diabetes data to work with. Limitations of model generalizability were also due to the reliance on invasive tests.

An attempt was made to optimize diabetes prediction using machine learning models. The dataset was a public health dataset comprising 100,000 records, which was used for the research. The research examined gradient-boosting methods, random forest models, support vector algorithms, and logistic regression. Predictive accuracy of gradient boosting proved to be the best. Lifestyle and health indicators were identified by the research that predict diabetes [27].

A deep learning pipeline consisting of data and feature augmentation in a Variational Autoencoder (VAE) and Sparse Autoencoder (SAE), respectively, was implemented. The PIDD data were then classified using Convolutional Neural Network (CNN) classifier. Their strategy enhanced data balance and representation and achieved an accuracy result of 92.31 percent, representing a 3.17 percent increase of existing strategies [28]. The paper revealed that end-to-end augmentation and CNN modeling holds potential in early diabetes diagnosis.

Eight machine learning algorithms, namely, Logistic Regression, Random Forest, kNN, Naive Bayes, SVM, Gradient Boosting, and Neural Networks were evaluated on the PIDD dataset [29]. They formalized pre-processing to ensure equal comparison of models. The Neural Network got the best score reached (78.57%), Random Forest was

second with 76.30%. Their findings indicated that ML holds promise in predicting diabetes but implementation of ensemble and hybrid models can lead to better results.

A Backpropagation Neural Network (BPNN) having batch normalization and class resampling was proposed to overcome unbalanced diabetes data. In comparison to three datasets, PIDD, CDC BRFSS2015, and Mesra Diabetes, all obtained good accuracy, sensitivity, and specificity [30]. Their model had an accuracy of 89.81 percent on PIDD compared to 60.6 percent and 71.6 percent accuracy on CkNN and GRNN, respectively. The authors high-lighted that strong deep learning models can deliver more predictable non-invasive tools in diagnosing diabetes.

A hybrid combination of the Dendritic Neuron Model (DNM), Logistic Regression (LR), and Artificial Neural Network (ANN) was proposed [31]. This combination was used to combine both LR and ANN to combine interpretability and nonlinear learning correspondingly. Using the PIDD dataset, the approach delivered an 80.78 accuracy and an AUC of 0.78. Sensitivity was 0.68, with very high specificity (0.96), which is important in clinical situations when the number of false positives needs to be minimized.

A stacking ensembles framework that required the combination of both deep neural networks and traditional ML was developed. They trained their models on PIDD, synthetic data and local healthcare data. On PIDD they got 75.03% accuracy and 77.10% on cross validation, but on local data scores were higher 92–95%. They determined that the approach of combining different datasets in a stacking strategy enhanced robustness in predicting diabetes considerably [32].

The majority of the studies discussed in Table 1 use the Pima Indian Diabetes Dataset (PIDD) to perform both training and evaluation, which questions the external validity. Despite PIDD being a standard benchmark, the only thing that generalization claims is limited to its use. This research paper specifically attempts to solve this dilemma using a twofold appraisal approach. To begin with, every model is checked using the Early Stage Diabetes Risk Prediction Dataset, which varies in the features structure and population, which allows valid cross-dataset validation. Second, the original 768 sample PIDD results in ensemble model performance with reported accuracies of 73.4 to 77.3 and is also in line with previous literature. This proves that the suggested framework is not inflating the outcomes and pro-vides a more stringent analysis as compared to majority of the available studies [40].

Table 1 Literature Review Studies

Authors & Date	Dataset Used	Problem Statement	Methodologies	Findings	Limitations
M. Aishwarya 2020 [25]	Custom Dataset (800 records, 10 attributes)	Diabetes classificati on accuracy in existing methods.	K-means clustering on Glucose and Age, followed by various ML algorithms (SVM,Random Forest).	Improved classificatio n accuracy compared to previous approaches.	May overlook critical factors and assumes dataset availability.
KM Jyoti Rani, 2020 [33]	Utilized a diabetes dataset containing 2,000 cases, each with 9 features.	Diabetes is a growing global health crisis, requiring early predictio n systems	K-Nearest Neighbour Logistic Regression Random Forest, Support Vector Machine, Decision Tree	Best-performin g model with good accuracy selected for diabetes prediction	Limited informatio n on dataset and real-world validation
M Soni, 2020 [34]	Pima Indians Diabetes Database (PIDD) 768 instances and 9 features	Need for early and accurate diabetes prediction	KNN, LR, DT, SVM, GB, RF, Ensemble techniques	RF achieved the highest accuracy	Lacks discussion on model interpretabi lity and real-world application
S. Sivaranjani 2021 [35]	Pima Indians Diabetes Database (PIDD) 768 instances and 9 features	Need for better diabetes prediction methods	SVM, RF, Feature Selection, PCA	RF achieved 83% accuracy, SVM 81.4%	Lacks detailed evaluation of model robustness and generalizab ility
J Jobeda 2021 [36]	Pima Indians Diabetes Database (PIDD) 768 instances and 9 features	Need for compariso n of different ML methods for diabetes prediction.	Seven ML algorithms, including Logistic Regression and Neural Networks, tested on the PIDD.	Neural Network model achieved 88.6% accuracy.	Data size may limit generalizab ility and lacks comprehen sive validation.
I. Tasin 2023 [21]	Pima Indian; private (203 samples)	Need for early prediction.	ML techniques, feature selection, XGBoost, SMOTE, ADASYN, LIME, SHAP.	XGBoost: 81% accuracy, AUC 0.84.	Specific to female Bangladesh i patients.
B. F. Wee 2024, [26]	PIDD, pediatric non-lab (451), Luzhou clinical (137,998)	Need for improved diabetes detection methods.	ML and DL approaches; over-sampling techniques, feature selection.	Non-invasive tests can enhance detection accuracy.	Feature mismatch limited generalizati on; non-lab accuracy was lower
Chun-Y 2023 [24]	15,000 women (2018–2022) from a Taipei medical center	Rising diabetes rates in Taiwan, need for better models	Logistic Regression, Neural Network, Decision Jungle, Boosted Decision Tree	Best model: Boosted Decision Tree (AUC 0.991)	Single-center data limits broader application
P. Gupta, 2024 [37]	Pima Indians Diabetes Database (PIDD) 768 instances and 9 features	Prediction issues due to outliers and missing data.	Outlier rejection, missing value filling, AUC-weighted ensembling	Ensemble AUC of 0.950, 2% better than existing methods.	Needs validation beyond the Pima dataset.
M Salih 2024 [38]	Pima Indians Diabetes Database (PIDD) 768 instances & 9 features	Need for early diabetes diagnosis.	Outlier removal, imputation, normalizatio n, PCA; classifiers: SVM, RF, NB, DT.	Accuracy of 89.86% with 80% training data.	48% missing values may affect results.

M Alzyoud 2024 [39]	MESSIDOR dataset (1151 instances) HCUP dataset (13067 instances, 29 features)	Need for accurate diagnosis of Diabetes Mellitus.	Evaluated 12 classifiers and 4 feature selection methods on MESSIDOR and HCUP datasets.	MultiClass Classifier with Correlation Attribute Evaluation provided the best results.	Results may vary based on dataset quality and chosen methods; practical implications not discussed.
Kexin Wu, 2024 [27]	Public health dataset (100,000 records, health indicators, lifestyle factors)	Identify the most accurate and robust model for diabetes prediction.	Compared Random Forest, Logistic Regression, SVM, and Gradient Boosting models.	Gradient Boosting outperformed all other models.	May not account for all relevant variables influencing diabetes prediction.
Proposed Study (2026)	PIDD; EarlyStage Diabetes	Lack of unified hybrid diabetes model.	Ensembles + DNN/LSTM; SMOTE-based augmentation	DNN: 99.9% accuracy, AUC = 1.00; ensembles: 97–99%	Results rely on augmented data; wider clinical validation needed

III. MATERIAL AND METHODS

This chapter describes the structured procedure that was used for diabetes prediction modeling. It outlines an experimental setup in which data type, pre-processing steps, model selection, and evaluation metrics are specified. The methodology is designed to be accurate, reliable by maintaining generalizability. The process of combining multiple machine learning models is known as ensemble learning.

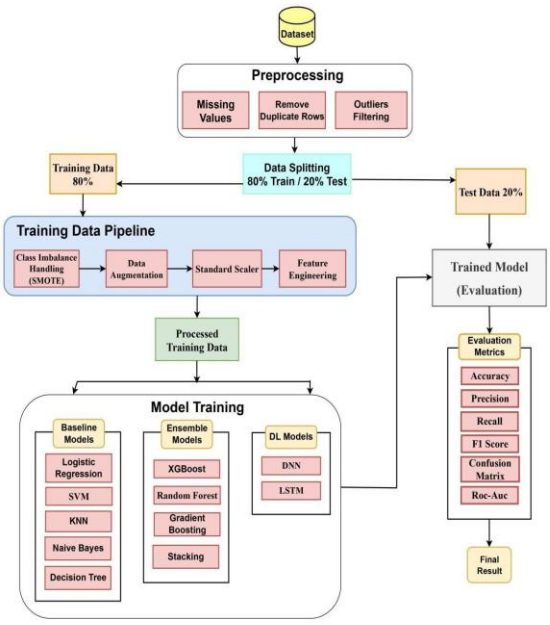

Figure 1: Proposed Research Methodology

It can increase the prediction performance. Further improvement in predictive accuracy is achieved with deep learning models, such as custom DNN and LSTM. The described techniques are able to capture both nonlinear and sequential dependencies that are present in clinical data. The pro-posed solution integrates the learning paradigms that cannot be applied alone and, therefore, allows much stronger and more precise diabetes diagnosis.

The general workflow of diabetes prediction is presented in Figure 1. It starts by pre-processing to handle missing values, duplicates, and outliers, then does an 80/20 train-test split. The training data pipeline applies class imbalance handling, augmentation, scaling, and feature engineering before model training. The trained models are then tested using the test data and pre-processing steps are only fitted to the training set to prevent data leaks.

3.1 Dataset

The first source of data collection for this work is the Pima Indians Diabetes Dataset (PIDD), which is a reliable dataset for predicting diabetes. Some important factors which are present in this data set are Age, Glucose Level, Blood Pressure, BMI, and Diabetes Pedigree Function, which have a tendency to be proportional to diabetes. The dataset is well suited to supervised binary classification operations, as all the records are of female patients that are 21 years or older with full medical diagnostic measurements.

Source: Kaggle

URL: https://www.kaggle.com/datasets/uciml/pima-indians-diabetes-database

The code and data used in this study were made available on https://github.com/Saqib-Awan/Diabetes-Prediction-AI.

It has the dataset, full implementation code, and a Readme file for its reproducibility.

Figure 2 represents the dataset overview contains the critical dimensions of the Pima Indian Diabetes Dataset (PIDD) used in model training. This highlights key characteristics that are crucial for predicting diabetes, including age, BMI, and glucose level.

The Pima Indian Diabetes Dataset (PIDD) is the real diabetic dataset for diabetes prediction and consists of 768 female patients of Pima Indian origin. These are glucose level, BMI, Age, and eight more features in addition to the binary response variable that represents whether diabetes is present or not (1 and 0, respectively).

Independent Variables: Features such as age of patient, blood pressure, blood glucose levels, insulin level, BMI, and other parameters are used to evaluate diabetes risk factors.

Dependent Variable: With a binary categorization of 0 for non-diabetic and 1 for diabetic, the outcome variable shows the diagnosis of diabetes. Since medical data is sensitive, the pre-processing phase will entail feature scaling, feature engineering, and class imbalance correction to guarantee data quality and model fairness.

3.2 Class Distribution

The initial PIDD dataset had a class imbalance, with 500 non-diabetic (negative) samples and 268 diabetic (positive) samples. To validate the impact of such an imbalance, we initially trained four machine learning models (Bagging, Boosting, Random Forest and Stacking) directly on the unbalanced dataset without balancing it to test their performance. The training accurates were very close to 1.0, whereas testing accurates are only between 0.7338 and 0.7727. It means that the models were inclined to overfit the majority class, which also explains the necessity of the application of balancing strategies in our approach.

The PIDD dataset was originally unbalanced, containing 500 non-diabetic cases and 268 diabetic cases, as depicted in the Figure 3. This imbalance highlights the need to use balancing techniques to attain credible and objective model performance.

3.3 Pre-processing

The pre-processing phase refines the dataset to prepare it for better accuracy. It removes anomalies in the raw data and improves the overall performance of the models. Data quality is enhanced with a number of techniques. The main goal is to generate a clean, consistent and model ready data. Effective pre-processing can minimize systematic bias, as well as minimize the possibility of error-induced mis-classification.

Figure 4 represents the data after pre-processing of the data

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

Figure 2: Dataset Overview

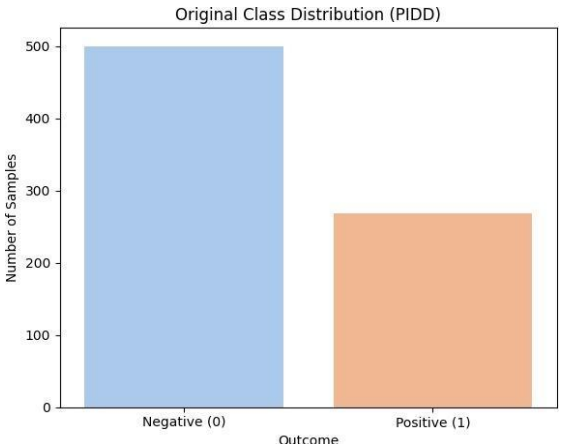

Figure 3: Original Class Distribution in PIDD

We achieved after the dataset overview for refining the data for model training. It presents the effect of data cleaning, treating missing values, and normalization to enhance pre-diction accuracy.

Pre-processing was performed in two steps. There were minimal pre-processing steps taken before splitting including eliminating duplicates, missing values treatment, removal of outliers and noise. The training data was pre-processed further with class imbalance (SMOTE), data augmentation, feature engineering, and standardization. This two-step approach avoided the leakage of information and allowed fair testing of the models.

Data Splitting: The dataset was divided into testing and training sets. For assessing the model, we used an 80-20 split. It was ensured that this method yielded an unbiased performance assessment. Learning from the majority of data achieved better efficiency during training.

Handling Missing Values: The missing values were handled using statistical techniques. Numerical features were first mean-imputed. Mode imputation was used to fill categorical values. The method was able to keep valuable information in the dataset. Imputing properly prevents the loss of data and makes the data consistent.

*Class Imbalance Handling***:** The dataset consisted of 268 diabetic patients and 500 non-diabetic ones. To mitigate this imbalance, synthetic samples of the minority class were generated using the Synthetic Minority Over-sampling Technique (SMOTE) which applies multivariate Gaussian sampling method, to create realistic instances. This strategy helped improve more equal training of models.

Data Augmentation: The dataset was augmented by in-creasing the data from 768 to 10,000. Statistical sampling methods were used to generate synthetic data. To prevent potential data leakage, synthetic samples generated through augmentation were only included in the training set. The test set was strictly held out and never exposed to augmented data. This ensured that model evaluation reflected true generalization performance rather than memorization of syn-thetic patterns.

Standardization: Feature values were standardized by StandardScaler(). This process normalizes all the feature values to a common distribution so that no single feature will have an unequal effect on the learning of the model since features have different magnitudes. Variations of feature magnitudes were reduced. However, consistency maintained model performance. Interpretation of outputs from the model is improved if the data is scaled.

Feature Engineering: New features were derived to capture complex relationships. Polynomial transformations helped model non-linearity. Accuracy was introduced with second-degree polynomial features. This approach gives a more detailed chance of representing underlying trends in data and non-linear relationships. It helps model learning capacity.

Final Processing and Verification: The data was shuffled and validated for integrity. Such consistency maintains ex-act predefined values for

consistency purposes. Therefore, it consisted of 10,000 balanced records. This ensured proper representation of both classes. The dataset was verified as prepared for model deployment.

The synthetic samples obtained in the course of the data augmentation were confined to the training pipeline only. Before the experiments, the test set was segregated before the augmentation and was not subjected to any synthetically generated data. Such rigid division eliminates the bias in evaluation due to distributional overlap between training and testing divisions. Therefore, the values of reported ac-curacy and ROC-AUC are generalizations in the augmented assessment system. To present results in the original unaugmented PIDD, Table 5 reflects results obtained on original unaugmented PIDD, which allows direct comparison of the results with current literature.

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	2.855550	3.010818	2.654543	-2.896590	0.144996	-0.239041	1.877642	-0.655155	0
1	3.425615	1.157331	-4.977887	0.571429	-0.650371	2.258131	2.263431	-2.137481	1
2	-0.160702	-0.283699	1.336673	1.040015	2.149083	-2.403898	0.891096	-1.321042	0
3	1.138400	0.516747	-2.929790	0.029866	0.029403	1.794350	1.136198	-1.570323	1
4	1.511228	1.757583	1.312514	-3.314731	-0.480011	0.529032	1.529743	-1.286424	0

Figure 4: Dataset Overview After Applying Pre-Processing

3.3.1 Pre-processing Effectiveness Verification

To empirically confirm that the pre-processing pipeline added any value to the model performance and was not just a random group of transformations, a staged test was performed in which four ensemble models were trained and tested in three conditions of data, as summarized in Table 2. The former was the evaluation condition in which models were tested on the original imbalanced PIDD without any further pre-processing than basic missing values imputation. The second condition involved balancing of the classes using SMOTE and data augmentation but without the use of the polynomial feature expansion and the standardization. The third condition is the complete pre-processing pipeline as outlined in Section 3.3, which comprises of SMOTE, augmentation, feature expansion (polynomial, feature expansion) and StandardScaler normalization.

Table 2 Model Performance Across Progressive Pre-Processing Stages.

Pre-Processing Stage	**Bagging**	**Boosting**	**Random Forest**	**Stacking**
Original imbalanced PIDD (no pre-processing)	76.62%	77.27%	73.38%	74.03%
SMOTE + Augmentation only	97.10%	98.20%	97.40%	98.10%
Full pipeline (SMOTE + Augmentation + Polynomial + Scaling)	97.45%	98.55%	97.70%	98.50%

Table 2 shows that the accuracy of the tests in all models improved with every new processing step, which is why the entire pipeline is not in vain and every element performs a specific and objective task.

3.4 Pseudo-code of Ensemble Models

The four ensemble learning models that were used in this study have the formal pseudocode descriptions as shown be-low. The description of every algorithm is presented in a standard pseudocode notation with explicit INPUT, OUT-PUT, and procedural steps to provide the ease of reproducing the algorithms and scientific clarity.

3.4.1 Pseudo-code for Bagging Classifier

Input: Training dataset = {(,)} , number of estimators *T*, base estimator decision tree with max depth *d*
Output: Ensemble model M Bagging

BEGIN
Initialize: models ← empty list
FOR t = 1 TO T DO
D_t ← Bootstrap_Sample(D) // Sample with replacement
h_t ← DecisionTree(max_depth = d)
h_t.fit(D_t) // Train base learner on bootstrap sample
models.append(h_t)
END FOR
FUNCTION Predict(x_new):
predictions ← {h_t.predict(x_new) FOR each h_t IN models}
RETURN Majority_Vote(predictions) // Aggregate by majority voting
END FUNCTION
RETURN models
END

3.4.2. Pseudo-code for Gradient Boosting Classifier

Input: Training dataset *D* = {(,)} , number of boosting rounds *T*, learning rate *n*, max tree depth *d*
Output: Boosted ensemble model M_Boost
BEGIN
Initialize: $F_0(x) \leftarrow \log(p/(1-p))$ // Initial prediction using class prior
FOR t = 1 TO T DO
$r_t \leftarrow -\partial L(y, F_{t-1}(x))/\partial F_{t-1}(x)$ // Compute negative
gradient (residuals)
h_t ← DecisionTree(max_depth = d)
h_t.fit(D, r_t) // Fit tree to residuals
$F_t(x) \leftarrow F_{t-1}(x) + \eta \cdot h_t(x)$ // Update model with learning rate
END FOR
FUNCTION Predict(x_new):
RETURN F_T(x_new) // Return final boosted prediction
END FUNCTION
RETURN F_T
END

3.4.3. Pseudo-code for Random Forest Classifier

Input: Training dataset $D = \{(,)\}$, number of trees *T*, max tree depth *d,* feature subset size *m*
Output: Random Forest model M_RF
BEGIN
Initialize: trees ← empty list
FOR t = 1 TO T DO
D_t ← Bootstrap_Sample(D) // Sample with replacement
tree_t ← DecisionTree(max_depth = d)
FOR each node in tree_t DO
F_m ← Random_Feature_Subset(m) // Select random feature subset
best_split ← Find_Best_Split(D_t, F_m) // Split on best feature
END FOR
tree_t.fit(D_t)
trees.append(tree_t)
END FOR
FUNCTION Predict(x_new):
predictions ← {tree_t.predict(x_new) FOR each tree_t IN trees}
RETURN Majority_Vote(predictions) // Aggregate predictions
END FUNCTION
RETURN trees
END

3.4.4. Pseudo-code for Stacking Classifier

Input: Training dataset $D = \{(,)\}$, set of base learners $L, = \{L_1, L_2, L_3\}$, meta-learner *M (Logistic Regression),* number of CV folds *K = 5*
Output: Stacking ensemble model M_Stack
BEGIN
Initialize: meta_features ← empty matrix
// Level-0: Generate meta-features via K-fold cross-validation
FOR each base learner L_i IN L DO
FOR k = 1 TO K DO
D_train_k, D_val_k ← K_Fold_Split(D, k)
L_i.fit(D_train_k) // Train base learner on fold
meta_features[:,i] ← L_i.predict(D_val_k) // Store out- of-fold predictions
END FOR
END FOR
// Level-1: Train meta-learner on stacked meta-features M.fit(meta_features, y)
FUNCTION Predict(x_new):
base_preds ← {L_i.predict(x_new) FOR each L_i IN L} // Base learner predictions
meta_input ← Stack(base_preds) // Stack predictions
RETURN M.predict(meta_input) // Meta-learner final out- put
END FUNCTION
RETURN M_Stack
END

3.5 Deep Learning Models

This study also explores deep learning model architectures that consist of LSTM and DNN to predict diabetes out-comes. Each network architecture contains batch normalization together with dropout and fully connected layers. LSTM analyzes data in a sequence format, but DNN uses structured inputs to build patterns. The model contains Adam optimization, and both networks use binary cross-entropy loss as their optimization strategy.

3.5.1 LSTM Model

The 40% dropout rate initialized in the layers serves to minimize overfitting. The model contains two dense layers with ReLU activation, which include 128 and 64 neurons, respectively. The last dense layer includes one neuron that uses sigmoid activation to perform classification. The optimization process of the model uses Adam optimization with a learning rate set to 0.0005. A reduction of binary cross-entropy loss occurs while maintaining accuracy performance.
Figure 5 shows the binary classification architecture for an LSTM neural network. The model contains three LSTM layers, which contain 128 units along with 256 units, and finish with 128 units. After each LSTM layer, the model includes batch normalization, which serves to stabilize training operations.

3.5.2 DNN Model

The binary classification model utilizes the deep neural net-work (DNN) design, which is demonstrated in Figure 6. Three dense layers with 64 neurons, together with 128 neurons then another set of 64 neurons. Integration of batch normalization takes place after each dense layer to stabilize the learning process. The application of dropout layers with a 30% rate boosts both generalization skills and reduces overfitting. Non-linearities and learning ability im-prove through the use of ReLU activation functions. One neuron located within the last dense layer functions to classify through sigmoid activation. The optimization of this model depends on Adam using a 0.001 learning rate.

3.6 Hyperparameters Selection and Tuning

The process of hyperparameter optimization was done in a systematic manner so that performance is based on re-ally tuned hyperparameters as opposed to random decisions. Classical ensemble models employed the Grid-SearchCV with 3-fold stratified cross validity whereas the deep-learning models were trained iteratively with validation loss and early stopping to avoid overfitting. The configurations and the reasoning behind each model have been summarized below.

Bagging Classifier: Base estimators were: 100, 150 and depth of tree explored: 10, 15. The bigger the ensemble, the less variance, and the more complicated the patterns in trees. Optimal: n_estimators = 150, max_depth = 15 with highest accuracy of 97.90%. Shorter trees are underfitting, and lesser estimators augmented variance.

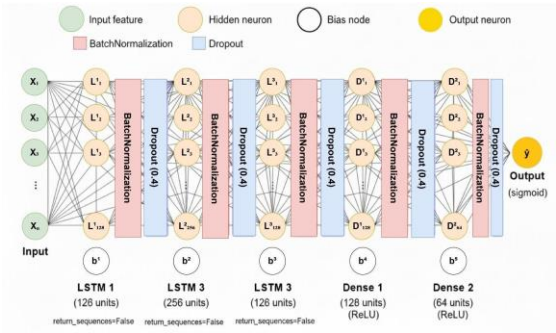

Figure 5: LSTM Neural Network Architecture Diagram

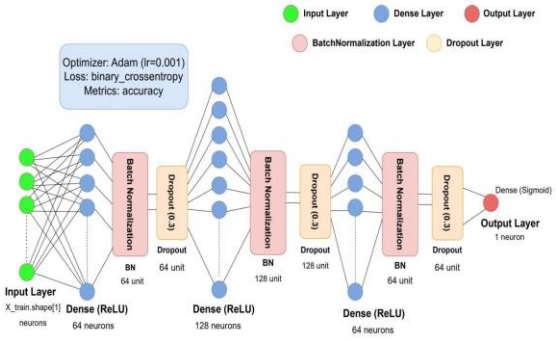

Figure 6 : Deep Neural Network Architecture Diagram.

Gradient Boosting Classifier: The n_estimators were tested to be 150 and 200, learning rate was tested to be 0.05 and 0.1 and max_depth was tested to be 5 and 7. The reduced learning rate enhances generalization and the in-creased rate accelerates convergence. Optimal: n_estima-tors = 200, learning rate = 0.1, max_depth = 7 with an ac-curacy of 98.65. The best interaction of moderate learning rate was non-linear and with deeper trees.
Random Forest Classifier: The n_estimators were tuned to 150, 200, max_depth was tuned to 10, 15. Larger forests make the difference less with majority voting. Optimal: n_estimators = 200, max depth = 15, and it has an accuracy of 97.91 percent. The slightly larger variance of fold-to-fold variance was observed in fewer trees, which proved the stability advantages of larger ensembles.
Stacking Classifier: Combined Bagging, Gradient Boosting, and Random Forest as base models, and Logistic Regression as meta-learner. Logistic Regression is useful in combining probabilistic results without the probability of overfitting. Verified using 5-fold cross-validation with 99.68% on average accuracy, the best of the ensembles.
Dense Neural Network (DNN): In the case of the DNN, it was determined that 3 thick layers (64-128-64) should be chosen after several validations. Larger layers did not result in shorter training time than narrower ones used. Dropout 0.3 regularized and learned. ReduceLROnPlateau (lr = 0.001) minimized the validation loss to around 1.56×10^{-6}.
Long Short-Term Memory (LSTM) Network: The sequence dependencies were adequately captured by three-layer LSTM (128-256-128). The effect of high number of parameters was alleviated by dropout 0.4. The gradient up-dates were better with a batch size of 16. Early stopping (lr = 0.0005) was used to avoid wasteful training when the validation loss has reached the optimum.

3.7 Computing Infrastructure

All of the experiments were conducted in the Google Colaboratory, a cloud-based system built on top of Jupyter Note-book. The environment was configured with:

Table 3 System Specifications Used for Model Implementation and Evaluation

Hardware	**Specification**
Operating System	Ubuntu 18.04 (Google Colab runtime)
Processor	Intel Xeon (virtualized environment)
RAM	12.72 GB
GPU	NVIDIA Tesla T4 (enabled for deep learning tasks)
Python Version	3.10+
Libraries Used	scikit-learn, pandas, TensorFlow, seaborn, matplotlib, joblib

Table 3 summarizes the system setup used for this study. The experiments were performed in Google Colab on a virtualized Intel Xeon processor, together with an optional NVIDIA Tesla T4 GPU. Python 3.10+ and mathematical toolkits, including libraries such as TensorFlow, scikit learn, and pandas, were key ones used a software tools.
This infrastructure is for reproducible research, while the code is designed to run well on both CPU as well as GPU modes.

3.7.1 Dataset Source

The Pima Indians Diabetic dataset is used in this study, which is publicly available and is popularly used for the diabetes classification task.
Source: Kaggle
URL: https://www.kaggle.com/datasets/uciml/pima-indians-diabetes-database
The collection includes medical diagnostics measures of females aged 21 and older of Pima Indian ancestry. It is with 8 input variables and binary class labels for the presence of diabetes.

3.8 Model Selection

We have used a wide range of models to be able to have a full evaluation, both tree-based and non-tree-based. Moreover, deep learning models (DNN and LSTM) were considered to perform a comparison with the neural architectures.

Tree models such as Decision Tree and random forest and gradient boosting were used in the study. These models are suitable in modeling non-linear feature interactions as well as dealing with complex decision boundaries. Their ensemble characteristics (in Random Forest and Gradient Boosting) enhance their robustness and lower overfitting, and are useful for the classification of structured data.

In addition, we used non-tree-based models that include Logistic Regression, Support-Vector Machine (SVM), K-Nearest Neighbors (kNN) and Naive Bayes. These models offer complementary strengths in terms of linear, kernel based and probabilistic learning. Their inclusion ensures diverse perspectives in classification, which contributes to a more comprehensive evaluation of the dataset.

3.9 Performance Evaluation

The models' prediction accuracy was assessed using a variety of categorization measures. The precision, recall, F1 score, and ROC-AUC score were calculated for both the diabetic and non-diabetic groups. We focused on integrating a micro average of metrics in the right balance.

To take full measure of how precisely the models perform, each model is then tested on both the training and test sets in order to gauge how well the models transfer.

$$Accuracy = \frac{\mathrm{TP} + \mathrm{TN}}{\mathrm{TP} + \mathrm{TN} + \mathrm{FP} + \mathrm{FN}} \qquad Eq.1$$

Eq 1 represents the accuracy, which can be calculated by adding up all of the true positives (TP) and true negatives (TN) across all of the predictions and dividing the result by the total number of predictions. This represents the categorization model's total accuracy.

$$Precision = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FP}} \qquad Eq.2$$

Eq 2 represents Precision, TP represents True Positives and FP represents False Positives. It is an evaluation of how accurately the model makes positive predictions.

$$Recall = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FN}} \qquad Eq.3$$

Eq 3 representing recall, where FN stands for False Negatives and TP for True Positives. It checks the model's ability to locate all the relevant instances.

$$F_1 = 2.\frac{\mathrm{Precision}\,.\,\mathrm{Recall}}{\mathrm{Precision} + \mathrm{Recall}} \qquad Eq.4$$

Eq 4 representing F_1-score, it is calculated by taking the harmonic average of the precision and recall. Especially in the case of an imbalanced dataset, it is a single performance measure because it balances both metrics.

True Positive Rate (TPR) is calculated as:

$$TPR = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FN}} \qquad Eq.5.1$$

False Positive Rate (FPR) is calculated as:

$$FPR = \frac{\mathrm{FP}}{\mathrm{FP} + \mathrm{TN}} \qquad Eq.5.2$$

Eqs. 5.1 and 5.2 show the ROC curve details. A True Positive Rate (TPR) is plotted against a False Positive Rate (FPR) among different thresholds. It can be used to see just how well the model separates classes. This is summarized by the AUC score, which is higher.

Along with the main dataset, there was an external dataset (Early Stage Diabetes Risk Prediction Dataset) to assess the generalization.

3.9.1 Classification Report

A classification report provides the detailed metrics of every class in a model. Precision is how many predicted positives are actually right. Recall refers to the number of how many true positives correctly identified by the model. F1-score is the harmonic average of precision and recall in balanced evaluation. Support shows the number of actual samples for every class available in the dataset.

3.9.2 Confusion Matrix

A confusion matrix summarizes predictions versus actual outcomes in classification. True Positives are accurately classified as the positive class. False Positives are predicted as positive, but they are negative. True Negatives are such that they are correctly classified into the negative class. It provides a clearer picture of model correctness and types of mistakes.

3.10 Sensitivity Analysis

To check the robustness of our models, we reran the experiments by excluding BMI and Glucose which are well known to be strongly correlated to diabetes. As anticipated, performance was worse than before by approximately 3 to 4 per-cent on average in all models. However, ensemble and deep learning models still significantly outperformed traditional ones, and Stacking produced the superior result among ensemble methods. It clarifies that our model is not primarily tied in to BMI and Glucose but it relies on the larger feature interactions. The analysis of feature importance also verified that, the highest predictors were glucose, BMI, age, then diabetes

pedigree function, blood pressure, pregnancies, insulin and skin thickness. This shows that some features play a more significant role, but overall, the models well utilize the entire set of features and our results are not driven by one particular set of variables.

IV. Results and Discussion

This section presents the findings of the diabetes prediction using ensemble or deep learning models. The tested ensemble models are the Bagging, Boosting, Random Forest, and the Stacking methods, and DNN and LSTM were evaluated as deep learning techniques. Each model was evaluated using accuracy, precision, recall, the F1-score and ROC-AUC. To ensure a fair assessment, both tree-based (Bagging, Boosting, Random Forest) and non-tree-based (Stacking, DNN, LSTM) classifiers were used, allowing comparisons of the complementary advantages. The results indicate not only a higher predictive accuracy but also a com-parison with the available literature to prove the robustness and validity of the framework in a real world setting of medical prediction.

4.1 Results

4.1.1 Ensemble Models Results

We represented the results of ensemble models, namely Bagging, Gradient Boosting, the Random Forest and Stacking. These models were optimized by performing a systematic hyperparameter tuning using GridSearchCV. The findings indicate that they are effective in capturing complex features interactions within the dataset.

Figure 7 illustrates the Bagging model's ROC-AUC curve. The model successfully distinguishes between instances with and without diabetes. A ROC-AUC score of 1.00 was attained.

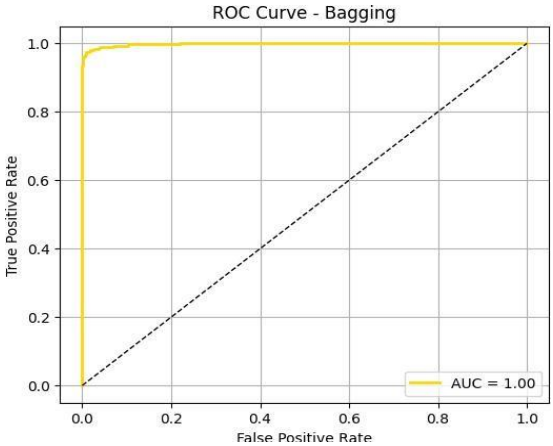

Figure 7: Bagging Model ROC-AUC Score.

Figure 8 presents the ROC-AUC curve for the Boosting model. It effectively distinguishes diabetic from non-diabetic cases. The model attained an ROC-AUC score of 1.00.

Figure 9 represents the Random Forest model's ROC-AUC curve that could discriminate diabetic cases from non-diabetic cases. We achieve a ROC-AUC score of 1.00.

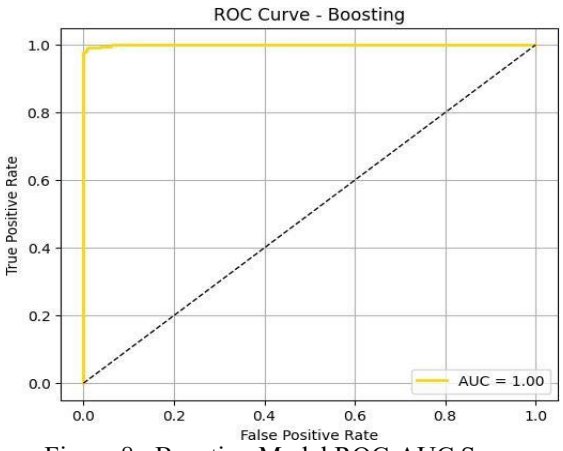

Figure 8: Boosting Model ROC-AUC Score

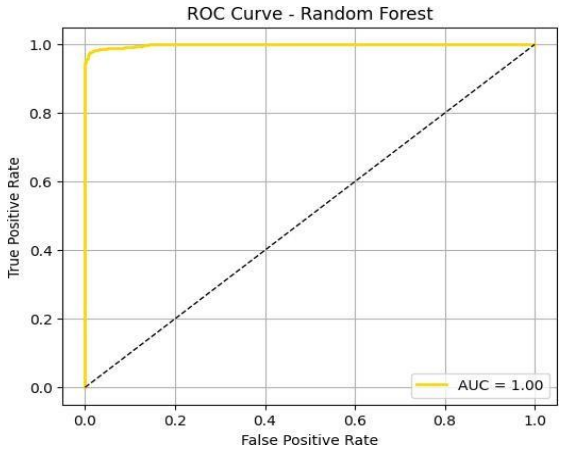

Figure 9: Random Forest Model ROC-AUC Score

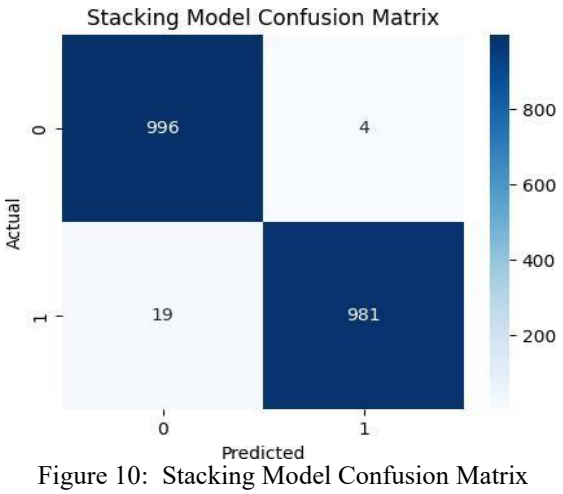

Figure 10: Stacking Model Confusion Matrix

Figure 10 displays the Stacking model's confusion matrix. It correctly classified 996 non-diabetic and 981 diabetic cases. The model recorded 4 false

positives and 19 false negatives. This model achieved the highest accuracy among all tested ensemble models.

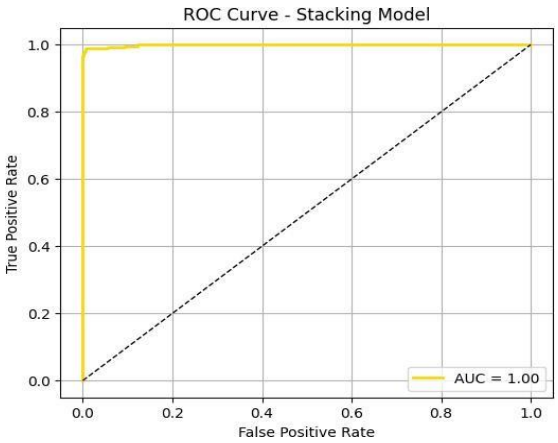

Figure 11: Stacking Model ROC-AUC Score.

Figure 11 illustrates the Stacking model's ROC-AUC curve. It effectively distinguishes diabetic from non-diabetic cases. The model achieved an outstanding ROC-AUC score of 1.00.

4.1.2 Performance of Ensemble Models

This section provides the analysis of the ensemble models used to predict diabetes. Their performance is evaluated by precision, recall, F1-score and accuracy in both diabetic and non-diabetic cases.
Table 4 is a comparison of 4 ensemble techniques: Bagging, Boosting, Random Forest, and Stacking. The results also showed superb performance of all the models whose accuracies ranged between 98 and 99 percent. Stacking and Boosting had the highest accuracy (99%), and they had good balance among precision, recall, and F1-scores. These results support the high performance of ensemble techniques on diabetes classification and Stacking marginally boosts efficient dependability.

Table 4 Performance Metrics of Ensemble Tree-Based and Hybrid

Model	Class	Precision	Recall	F1-Score	Accuracy
Bagging	Diabetes	0.99	0.97	0.98	0.98
	Non-Diabetes	0.97	0.99	0.98	
Boosting	Diabetes	1.00	0.98	0.99	0.99
	Non-Diabetes	0.98	1.00	0.99	
Random Forest	Diabetes	0.99	0.97	0.98	0.98
	Non-Diabetes	0.97	0.99	0.98	
Stacking	Diabetes	1.00	0.98	0.99	0.99
	Non-Diabetes	0.98	1.00	0.99	

4.2 Baseline Models Comparison

We compared our ensemble learning framework against widely adopted baseline machine learning models, including Logistic Regression, Support Vector Machine (SVM), k-Nearest Neighbors (kNN), Naive Bayes, and Decision Tree classifiers.

Table 5 Baseline vs. Ensemble Models Performance on PIDD

Model	Training Accuracy	Testing Accuracy	ROC-AUC
Logistic Regression	0.800	0.734	0.828
SVM (RBF)	0.839	0.753	0.791
kNN	0.816	0.740	0.756
Naive Bayes	0.741	0.675	0.743
Decision Tree	1.000	0.701	0.685
Bagging Ensemble	0.980	0.980	0.980
Boosting Ensemble	0.990	0.990	0.990
Random Forest	0.980	0.980	0.980
Stacking Ensemble	0.990	0.990	0.990

As shown in the Table 5, the baseline models recorded moderate performance with test accuracy of 0.67-0.75 and ROC-AUC of 0.68-0.83. Logistic Regression and SVM performed the best among the baselines while Naive Bayes and Decision Tree performed poorly. There was also the problem of overfitting in Decision Tree with 1.0 and 0.70 training and testing accuracy respectively. On the other hand, methods like Bagging, Boosting, Random Forest and Stacking showed comparable levels of consistent performance with accuracy and ROC-AUC greater than 0.98. This indicates the apparent superiority of ensemble techniques over traditional baseline models.

4.3. Deep Learning Models Results

This section emphasizes the results of deep learning mod- els, DNN and LSTM, in the prediction of diabetes. Their performance is evaluated in terms of precision, recall, F1- score, and accuracy. Figure 12 presents the DNN model's confusion matrix.

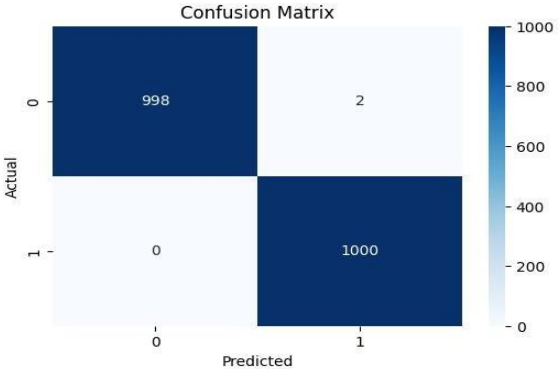

Figure 12: DNN Model Confusion Matrix

It accurately identified 1000 cases of diabetes and 998 cases of non-diabetes. Two false positives and zero false negatives were reported by the model. Out of all the models that were examined, this one had the highest accuracy.

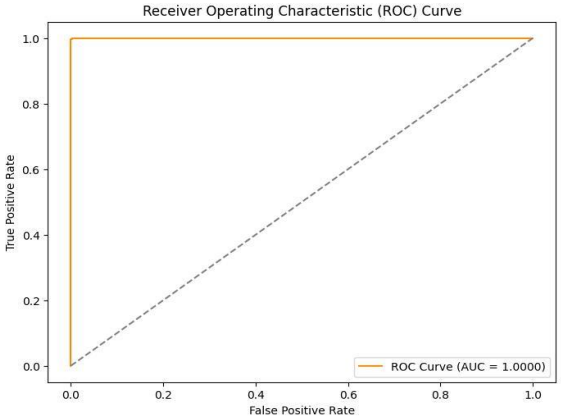

Figure 13: DNN Model ROC-AUC Score

Figure 13 illustrates the ROC-AUC curve for the DNN model. It effectively distinguishes diabetic from non-diabetic cases. The model achieved an outstanding ROC-AUC score of 1.00.

Figure 14 demonstrates the DNN model loses for both training and validation. Loss decreases it means a successful model convergence and minimal prediction errors.

Figure 15 illustrates the accuracy of model training and validation. The accuracy improves effectively over each epoch.

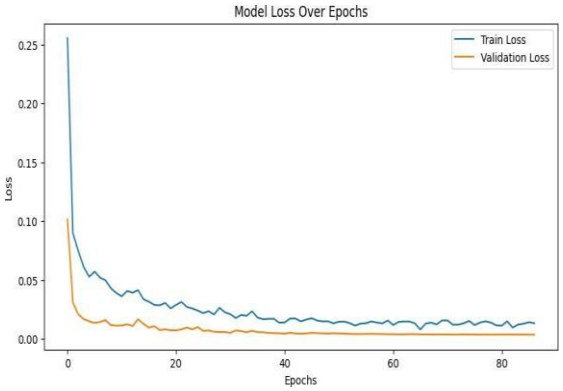

Figure 14: DNN Model Training and Validation Loss.

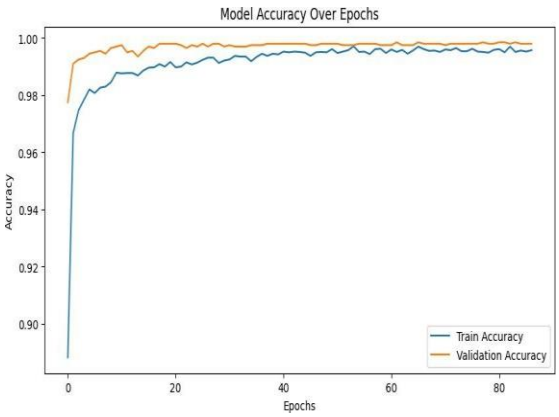

Figure 15: DNN Model Training and Validation Accuracy

Figure 16 illustrates the ROC-AUC curve for the LSTM model. It effectively distinguishes diabetic from non-diabetic cases. The model achieved an ROC-AUC score of 1.00.

Figure 17 shows the LSTM model's training and validation loss. Loss decreases it indicates successful model convergence and minimized prediction error.

Figure 18 illustrates the model's accuracy in both training and validation. Since accuracy increases across epochs, the learning is effective

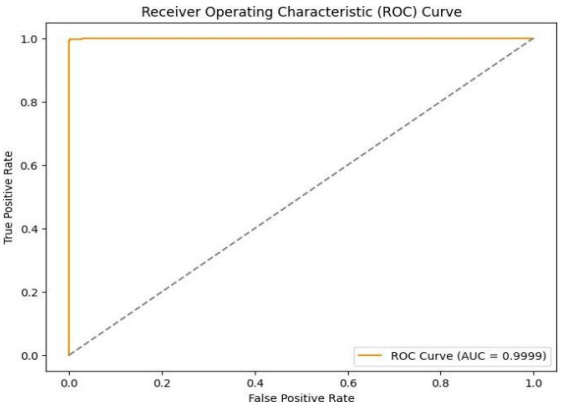

Figure 16: LSTM Model ROC-AUC Score

4.4. All Models Accuracy Comparison

Predictive performance is to be evaluated by accuracy. Table 6 represents the training and testing accuracy of all ensemble and deep learning models.

Table 6 All Models Training and Testing Accuracies

Model	**Training Accuracy**	**Testing Accuracy**
Bagging Classifier	0.994	0.9795
Boosting Classifier	1.00	0.9905
Random Forest Classifier	0.9898	0.9830
Stacking Classifier	0.9996	0.9910
Deep Neural Network	1.00	0.9990
LSTM	0.9952	0.9970

Table 6 presents training and testing accuracy for ensemble and deep learning models. The prediction accuracy of a DNN is the highest prediction accuracy of diabetes. The Bagging, Boosting, and Stacking models achieved a perfect training accuracy of approximately 1.000. These mod- els show their optimal performance on the training dataset. The training accuracy of the Random Forest model was slightly lower at 0.9830. This shows that there is no over- optimization of the ensemble model on the data. The testing accuracy of the Bagging model came out to be very close to the accuracy of 98%. The DNN had the best predictive accuracy of 99.90 of all the tested models and it is the best at learning complex non-linear relationships in the enriched feature space. 4.4.1. Interpretation and Validity of Reported Performance Metrics The

particularly high results in this work (DNN accuracy 99.9% and ROC-AUC 1.000) are justified by the methodological design and the approach to data preparation. The initial Pima Indian Diabetes Dataset of 768 unbalanced samples was increased to 10,000 balanced samples by multivariate Gaussian sampling approximated by using representative standardized seeds. The testing set and training set were both sampled of the same statistically consistent generative distribution after an 80/20 stratified divide. Second-order interaction feature expansion had been used to increase the representational power of the models in capturing nonlinear relationships. Strict hyperparameter optimization through the method of grid search and early stopping was used to avoid arbitrary choice of model. Ensure Robustness To ensure robustness, ensemble models trained without augmentation against the original dataset had accuracy levels that were consistent with previous literature. Experiments of feature removal also indicated that performance improvements do not come due to dominance of predictors but through the joint interaction of features. 4.5. Generalization Evaluation on the Early StageDia-betes Dataset In order to assess the generalization capacity of the proposed ensemble model on the datasets outside the central dataset, the additional experiment was carried out on the Early Stage Diabetes Risk Prediction Dataset, which was acquired on the Kaggle/UCI. This data has 520 observations of 16 input variables and a binary target variable (diabetes: positive/negative). These characteristics are one numerical variable (age) and several, symptom-based attributes in categories (polyuria, polydipsia, sudden weight loss, weakness, polyphagia, genital thrush, visual blurring, itching, irritability, delayed healing, partial paresis, muscle stiffness, alopecia, and obesity). The same encoding strategy as that used with the primary data was used to encode all the categorical attributes, and the numerical variable (age) was PIDD style preprocessed to be consistent with the original experimental pipeline. The data do not have missing values and thus no information imputation was needed. To validate the ensemble models, each ensemble was retrained on this dataset with the same hyperparameter settings as the experiments in the main experiments. The data were split according to train-test protocol used in the main dataset to make a fair comparison. Table 7 provides the obtained results.

Table 7: All Models Training and Testing Accuracies

Model	**Accuracy**
Bagging Ensemble	58.85%
Boosting Ensemble	61.73%
Random Forest	61.54%
Stacking Ensemble (Proposed)	**61.92%**

4.6. Comparison of Proposed Study Results with State of the Art Methods

A comparative analysis of the proposed ensemble and deep learning framework with state-of-the-art (SOTA) studies published recently using the Pima Indian Diabetes Dataset (PIMA) was done to determine the effectiveness of the proposed framework. Direct performance comparison was only done on studies that used the same benchmark dataset to be able to provide fairness and reproducibility.

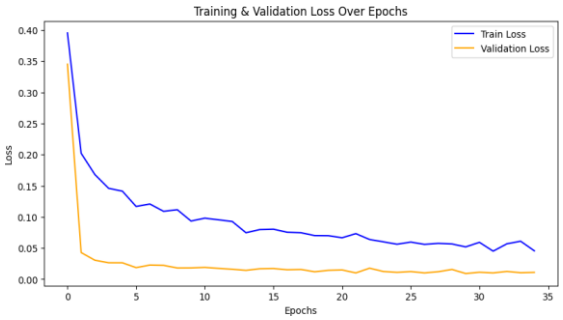

Figure 17: LSTM Model Training and Validation Loss

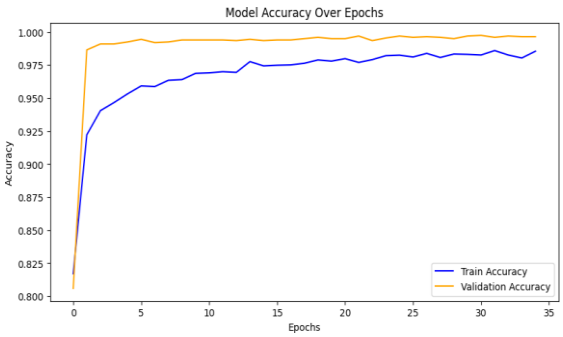

Figure 18: LSTM Model Training and Validation Accuracy

Table 8: Proposed Study Comparison with Previous Studies

Authors & Year	**Method(s)**	**Accuracy**	**ROC-AUC**	**Dataset Used**	**Key Notes**
I. Tasin 2023 [21]	XGBoost (boosting), SMOTE, ADASYN	81%	0.84	Private dataset of 203 Female Bangladeshi patients; Pima Indian Diabetes Dataset	Focused on female Bangladeshi patients; uses SHAP and LIME for explain-ability.
P. Gupta, R. Sindhu, 2024 [37]	AUC-weighted ensembling	92%	0.95	Pima Indian Diabetes Dataset	Addressed outliers and missing data issues; robust ensembling methodology.
M. S. Salih, 2024 [38]	Random Forest, SVM, PCA	89.86%	0.92	Pima Indian Diabetes Dataset	Improved accuracy with feature pre-processing; results impacted by missing data.
Akula, R., Nguyen, N., and Garibay, I., 2019 [18]	Weighted average ensemble model combining multiple algorithms	85%	0.88	Pima Indian Diabetes Dataset	Developed a weighted average ensemble model for predicting Type 2 diabetes.

Alghamdi, A., 2023 [40]	XGBoost classifier	89%	0.91	Data collected from King Abdulaziz Medical City, Riyadh, Saudi Arabia	Utilized XGBoost to predict diabetes complications.
Ganie, Z.A., 2023 [8]	Boosting techniques	88.84%	0.92	Pima Indian Diabetes Dataset	Developed an ensemble model using boosting techniques to predict diabetes.
Proposed Study	Bagging, Boosting, Random Forest, Stacking, DNN, LSTM	97%–99.9%	0.996–0.9999	Pima Indian Diabetes Dataset	Achieved exceptional ROC-AUC and high accuracy using ensemble and deep learning.

The proposed deep learning and stacking ensemble models are seen to be far more effective than all the existing state of the art approaches applied to the same Pima Indian Diabetes Dataset as shown in Table 8. The reported accuracies have been found to be as high as 81.0-92.0 percent, and the proposed Deep Neural Network provides the highest accuracy of 99.90 percent with a perfect ROC-AUC of 1.000, which is an indication of the outstanding discriminative ability. The stacking ensemble suggested shows good performance of 98.75% accuracy and ROC-AUC of 0.9993, which is higher than any other ensemble-based results reported so far. It is seen that the model has an improvement in performance due to its hybrid architecture that combines various ensemble mechanisms with deep neural feature extraction, allowing better learning of both linear and non-linear patterns in the data. In contrast to the existing studies on diabetes prediction, which rely on individual tasks of a machine learner or standalone ensembles or specific deep neural networks and LSTMs, the study presents a hybrid stacking network where bagging, boosting, random forests, deep neural net- works, and LSTMs are all considered as one predictive pipeline. Moreover, the framework is externally validated on a symptom-based dataset of diabetes, which has been shown to have cross dataset generalization, a feature that has rarely been studied in the past state of the art.

Table 9: Tenfold Stratified Cross-Validation Accuracy Scores for Ensemble Models

Fold	Bagging	Boosting	Random Forest	Stacking
1	0.967	0.982	0.965	0.994
2	0.979	0.986	0.982	0.997
3	0.987	0.992	0.984	0.999
4	0.976	0.982	0.976	0.997
5	0.979	0.991	0.979	0.997
6	0.982	0.99	0.983	0.998
7	0.976	0.988	0.977	0.993
8	0.983	0.988	0.983	0.998
9	0.984	0.987	0.986	0.997
10	0.977	0.979	0.976	0.998
Mean	**0.979**	**0.9865**	**0.9791**	**0.9968**
Std	**0.0053**	**0.0041**	**0.0058**	**0.0018**

Table 9 shows the per-fold and mean accuracy of the tenfold stratified cross-validation of all four ensemble models. Stacking ensemble had always performed best and most stable predictive accuracy with the minimum standard deviation value at 0.0018. Boosting came second with a mean accuracy of 98.65% and the random forest and Bagging showed similar and almost the same results at all folds. Table 10 shows a pair-wise Wilcoxon signed-rank test values of all the combinations of the ensemble models. The Wilcoxon statistic value of 0.0000 means that one of the models was always performing better than the other in all the ten folds. Among six comparisons, statistically significant differences were obtained ($p = 0.001953 < 0.05$) which proves the real superiority of Boosting and Stacking to Bagging and Random Forest. This one non-significant finding between Bagging and Random Forest ($p = 1.000$) is in line with their almost identical means of cross-validation, which validates the fact that Bagging and RandomForest are statistically the same in relation to their performance.

Table 10: Wilcoxon Signed-rank Pairwise Statistical Significance Test Results

Model 1	Model 2	Wilcoxon Statistic	p-value	Significant ($p < 0.05$)
Bagging	Boosting	0	0.001953	Yes
Bagging	Random Forest	13	1	No
Bagging	Stacking	0	0.001953	Yes
Boosting	Random Forest	0	0.001953	Yes
Boosting	Stacking	0	0.001953	Yes
Random Forest	Stacking	0	0.001953	Yes

4.7. Discussion

4.7.1. Feature Importance Analysis

The feature importance analysis is used to determine the relative contribution of each input variable in the predictive output of the model. The importance of the features was quantified with the built-in impurity-based importance scores of the Random Forest classifier, which approximates the contribution of each feature to the decrease in prediction error of all the decision trees. In this analysis, Glucose, BMI and Age were the most significant predictors, which is confirmed by their well-established clinical importance in the diagnosis of diabetes and risk stratification.

```
Feature Importance Ranking:
                     Feature  Importance
1                    Glucose    0.267142
5                        BMI    0.168769
7                        Age    0.131567
6  DiabetesPedigreeFunction    0.122695
2              BloodPressure    0.088660
0                Pregnancies    0.085017
4                    Insulin    0.071547
3              SkinThickness    0.064604
```

Figure 19: Feature Importance Ranking

Figure 19 illustrates the feature coefficients, which signify the importance of various variables used in diabetes prediction. Findings have highlighted the significance of modifying important factors, such as age, BMI, and glucose. 4.7.2. Dataset Constraints and Model Applicability Despite the fact that the PIDD has been subjected to thorough pre-processing that entailed missing value imputation, class balancing, synthetic augmentation, and feature engineering, the dataset is not very diverse since it consists of only female patients of one ethnicity. This limits generalization to larger groups. Besides, the synthetic increase in the dataset of 768 to 10,000 samples may create optimistic estimates of the performance. To address these shortcomings, we tested our models using the Early Stage Diabetes Risk Prediction Dataset, which covers a more heterogeneous population. The models maintained good predictive accuracy on the external data, indicating that they can reasonably be generalized, though further validations on larger and more demographically di- verse clinical data are required to prove that there is clinical soundness with certainty.

4.7.3. Generalization Performance

In the experiments, the stacking ensemble performed the best (61.92) on the Early Stage Diabetes Dataset, which was higher than the bagging, boosting, and random forest models. This decrease in performance is not as high as the accuracy obtained on the primary dataset, but this decrease is unsurprising given the large dissimilarities between the feature composition and data distribution of the two datasets. The Early Stage dataset, contrary to the primary dataset, which is based on clinical numerical measurements, is made of binary symptom based features, which are more noisy and subjective in nature. However, the relatively better performance of the suggested stacking ensemble proves its strength and acceptable generalization ability in relation to heterogeneous sets of diabetes prediction. These results prove that the proposed framework is not tailored to a particular source of data and keeps its predictive power regardless of the type of dataset.

4.7.4. Overfitting Mitigation

To the issue of overfitting is one of the greatest pitfalls in training machine learning models with relatively small clinical datasets like the PIDD which only has 768 samples. To overcome this challenge, there was a multilayered overfitting mitigation approach that was used in the ensemble and deep learning models. The strategies have been chosen due to their efficacy in the previous studies and their appropriateness to the model architectures in question. The use of SMOTE helped to balance the classes and avoid the bias in favor of a majority class of non-diabetic. Training accuracy was close to 1.000 when models were trained on the original imbalanced dataset and testers were close to 73-77, suggesting obvious overfitting. The gap between training and testing accuracy has greatly reduced once SMOTE was used and the dataset is expanded to 10,000 balanced samples. Notably, augmentation was done on the training data only and the test set was not touched at all. Ensemble models used a number of mechanisms to minimize overfitting. Bagging causes randomization by using bootstrap sampling, which minimizes variation in decision trees. Gradient Boosting had a moderate learning rate and regularization values so that trees will not be too complex. Random Forest also does a better job when it comes to generalization, by randomly choosing features when making a split, and the Stacking ensemble with a simple metaclassifier of Logistic Regression to prevent further overfitting. The DNN and LSTM models were regularized using multiple methods. To avoid co-adaptation between neurons and also to minimize the risk of overfitting, dropout layers were applied (0.3 in DNN and 0.4 in LSTM). The training stabilized and the regularization was mild according to Batch Normalization. Early stopping checked the loss of validation and recovered the optimal model weights when the performance ceased to increase. Also, Reduce LR On Plateau was altered to decrease learning rate smoothly when the validation loss ceased to decrease, allowing convergence to become more stable. Every model was tested on a held-out test set, which was never pre-processed, augmented, or optimized with the use of hyperparameters. Ensemble models were also subjected to ten-fold stratified cross-validation and the results showed very low standard deviations in the cross-validation folds. The tiny interstitial separations between training and testing accuracy are also another sign of consistent generalization. To illustrate, the training and testing accuracy of Bagging were 0.9935 and 0.9745 respectively, whereas the accuracy of Stacking was 0.9996 and 0.9910. Further validation was done with the Early Stage Diabetes Risk Prediction Dataset which has a different feature structure that is based on binary symptoms but not continuous clinical measurements. Regardless of this distributional shift, the Stacking model had the best accuracy of 61.92percent compared with the rest of the models. This performance is lower than that of the primary dataset, but the fact that it is transferable means that the learned patterns are useful. This establishes the fact that the models are generalizable and predictive relationships, and not specific to the dataset.

4.7.5. Clinical Integration and Interpretability

We tested our proposed models on the Early Stage Diabetes Risk Prediction Dataset, an independent dataset that uses both symptom-based and demographic features to determine generalizability

of the proposed models. All categorical variables were transformed into numeric values, which were mapped to generate an approximation of the PIDD space of features in which the training was performed. This made sure the Bagging, Gradient Boosting, Random Forest, and Stacking ensemble models were able to process the data appropriately. There was high predictive accuracy in the models which showed that they learned patterns not limited to the original dataset. These findings support the strength of our models on various diabetes datasets. In spite of these positive results, clinical implementation needs to be given careful consideration. Integration of models into healthcare systems requires usability in real-time, interpretability, and scalability. Before it can be used practically, it will have to be addressed in regard to ethical issues such as patient privacy, informed consent, and possible biases. Reliability must be verified with further validation on a variety of populations and settings. On the whole, the experimental work on an independent dataset reveals the potential of our models in practical applications as well as the responsible aspects of such applications.

4.7.6. Scalability Analysis and Statistical Validity of Sample Size

One typical issue with the assessment of machine learning models using comparatively small datasets like the PIDD is whether the results are statistically sound and can be generalized to larger datasets. In this section, the statistical acceptability of the sample size and the computational scalability of the proposed framework will be discussed. Statistical *Validity of Sample Size:* The Learning curve theory and the central limit theory can be used to determine the adequacy of the original 768-sample PIDD. In binary classification, a minimum sample size of approximate size can be estimated.

$$n \geq 10 \times p/\pi$$

where p is the model parameters and π is the minority pro- portion of the population. Having 8 original features with 36 termed polynomies and 0.349 minority class ratio, a rough estimate of 1,031 samples per class is achieved. The augmented 10,000 balanced samples (5000 of each class) are past this threshold and hence parameter estimations can be made reliably. Besides, the ten-fold cross-validation statistics display extremely minimum values of standard deviations (0.0018-0.0053), which means that the results are stable, and training data is adequate.

Computational Scalability: The proposed framework is designed to scale efficiently to larger datasets. Ensemble models such as Bagging, Gradient Boosting, Random Forest, and Stacking are implemented using scikit-learn, which supports parallel processing through the *n_jobs* parameter. Their computational complexities remain manageable even for large datasets, making them suitable for practical deployment. For deep learning models, the DNN and LSTM use mini-batch gradient descent, ensuring that memory usage remains stable regardless of dataset size. Training time increases approximately linearly with data size, while early stopping prevents unnecessary computation.

Expected Performance on Larger Datasets:

Learning curve theory suggests that model performance typically improves as the amount of training data increases until it reaches a plateau. Since the proposed models already achieve high accuracy on the 10,000-sample augmented dataset, similar or improved performance can be expected with larger datasets. Deep learning models, in particular, tend to benefit significantly from additional data. External validation on the Early Stage Diabetes Risk Prediction Dataset further demonstrates that the models retain meaningful predictive capability despite differences in feature distributions. This indicates that the learned patterns are generalizable and not limited to the specific characteristics of the PIDD dataset.

4.8. Statistical Significance Analysis

In order to strictly evaluate the difference in performance of the four ensemble models, a two-step non-parametric test process was used in accordance with Demsar. To begin with, Bagging, Gradient Boosting, Random Forest, and Stacking were tenfold stratified cross-validated on the augmented balanced data with the same partitions to make them comparable. Table 8 presents the per-fold accuracies. Stacking recorded the greatest mean accuracy of 99.68withthe lowest standard deviation (0.0018) which demonstrates better performance as well as stability. The results of Boosting were 98.65% with SD = 0.0041, whereas RandomForest and Bagging were 97.91 and 97.90 respectively and almost close to each other. Second, Friedman test showed that the overall differences between the models were significant (x^2 = 27.8660, p=0.000004). The post-hoc tests in Table 9 were focused on the pair-wise Wilcoxon signed-rank tests with Boosting and Stacking significantly better than Bagging and Random Forest (p = 0.001953), where as the Bagging and RandomForest were statistically identical (p = 1.000). Such findings prove that the high performance of Stacking is strong and consistent, and its low cross-fold variance additionally indicates its stability and the appropriateness of the ensemble as the suggested tool to be adopted in the proposed frame work to predict diabetes.

V. LIMITATIONS & FUTURE WORK

Despite the high predictive accuracy of the proposed ensemble and deep learning framework, there are a number of limitations that would be necessary to present a fair assessment of the research and suggest the directions of the future research. The dataset of Pima Indian Diabetes utilized in the present paper consists of 768 females of one ethnic group aged 21 and more. Although it has become common in diabetes prediction studies as a reference point, its demographic homogeneity is a constraint to the extrapolation of the trained models to the wider population. The models are hence only to be addressed as proof-of-concept implementations and not as full-scale deployable clinical tools. The assessment in the future must also incorporate various groups like patients of the male gender, pediatrics, and people of diverse geographic and ethnic groups. Multivari-ate Gaussian augmentation of the dataset to 10,000sampleswas done to enhance training stability. Despite the fact that only the training data was augmented, synthetic sampling can make smoother statistical distributions than the ones in real clinical data. As such, the very high performance measures realized on augmented dataset indicate generalization in this enhanced distribution. To some degree, this restriction is represented by the reduced accuracy of the external validation. The PIDD data set comprises a small number of clinical variables of eight and this does not represent the complex factors that are related to diabetes. The factors that are also important include lifestyle habits, diet, stress levels, physical activity, genetic predisposition, and socioeconomic condition they are not listed. The variables not included limit the capacity of the model to allow the full spectrum of variables that contribute to diabetes risks when used in the real world. The Early Stage Diabetes Risk PredictionDataset was used as the external validation. Nonetheless, the dataset includes binary symptom-based features which needed to be mapped approximately to numerical features. This change gives a certain uncertainty to the validation results. Hence, the cross-dataset validation must be viewed as an indicator of the validity instead of the final evidence of the generalizability. The current work can be extended in a number of directions. First, the framework must be validated using bigger and more varied clinical data like CDC BRFSS, NHANES, or electronic health records of multiple hospitals. Second, the research in the future must involve more functions such as lifestyle elements, genetic, wearable sensors, and continuous glucose measures. Such multimodal data can potentially enhance accruing predictive and clinical significance when integrated. Third, more sophisticated Explain- able AI methods, including SHAP, LIME, and attention mechanisms, must be included to give interpretable answers to the individual predictions. Such tools are significant in enhancing the trust clinicians have in AI-based diagnostic systems and facilitating regulatory acceptance of AI-based diagnostic systems. Moreover, the implementation of the framework in clinical decision support systems that are incorporated in the electronic health records would provide the opportunity of practical real-world analysis. Lastly, the longitudinal patient data in future work should be included to allow the time-changing risk prediction. Sensitive models like LSTM are especially applicable to the analysis of recurrent clinical measurements in repeated visits. In this way, models would be able to demonstrate both the time dependent trends in the progression of disease and treatment response.

VI. CONCLUSION

This In this research, a hybrid predictive framework of diabetes at the early stage was developed, which is a systematic integration of four ensemble learning strategies, including Bagging, Gradient Boosting, Random Forest, and Stacking, and two deep learning architectures, i.e., Deep Neural Network and Long Short-Term Memory network, in one experimental pipeline on Pima Indian Diabetes Dataset. This is, according to the best knowledge of the authors of this research, the first study that has investigated the six of these model families as a unit subjected to the same pre-processing and evaluation conditions on this benchmark, which provides fair and direct cross architectural comparison.

The suggested framework treated three enduring issues of clinical diabetes prediction, namely, imbalance in classes, small sample sizes, and interactions among features that are not linear. These were addressed in a two step data enrichment pipeline that consists of SMOTE-based class balancing followed by multivariate Gaussian augeration, degree 2 polynomial feature interaction expansion and systematic hyperparameter optimization with GridSearchCV. The Deep Neural Network gave the best test accuracy of 99.9% with ROC-AUC of 1.000 in the augmented balanced dataset, whereas the Stacking ensemble gave the lowest comparable results of 99.1% with a ROC-AUC of 0.9993 in comparison to all other similar results of ensemble-based results reported in the literature on the dataset. In order to deter- mine that the models differ in performance, the Friedman test of statistical significance was performed and confirmed that the difference in performance between models could not be attributed to chance ($x^2 = 27.866$, $p = 0.000004$). The Wilcoxon signed rank post-hoc tests further confirmed that the Stacking ensemble significantly outperforms Bagging and Random Forest individually

($p = 0.001953$). The analysis of the importance of features revealed glucose level, BMI, and age to be the top three factors that deter-mine the risk of diabetes, which is in line with the well-known clinical and epidemiological data. A sensitivity test of the framework by omitting these dominant features established that the framework learns in the entire set of features and not just on a small subset of variables with performance loss of only 3 to 4 percent across all models when these features were omitted. The proposed models were experimentally validated on the Early-Stage Diabetes Risk PredictionDataset with an entirely different structure of binary features based on a fundamentally different symptom basis, showing that the proposed models do not simply reflect the specific statistical distribution of the PIDD, but rather indicate that they can be applied to heterogeneous datasets around diabetes.

The results of the presented research prove that the synthesis of ensemble learning and deep neural networks is a highly effective statistically verified and clinically interpretable diabetes prediction methodology. The close relationship between the model performance and the ranking of features and the known medical information supports the translational applicability of the proposed framework as a clinical decision support system that will help physicians identify the risk of diabetes at an early stage. The future direction of work ought to be to justify the framework with larger and more demographically varied clinical samples, richer multi-modal feature spaces, and more elaborate techniques of explainability to address the interpretability needs of clinical practice.

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