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Research Paper

Enhancing Diabetes Prediction through Ensemble Machine Learning Models on Survey-Based and Clinical Data

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Abstract

Machine learning (ML) has emerged as a significant asset in bioinformatics, particularly for early disease prediction, by leveraging various data types ranging from genetic markers to survey data. This research concentrates on diabetes prediction through the application of machine learning algorithms to data sourced from the National Health and Nutrition Examination Survey (NHANES). We built a binary classification system by looking at data from more than 5,500 non-pregnant adults. This system used reported diagnoses and plasma glucose levels to assign diabetes labels. Feature selection focused on important factors like age, waist circumference, and cholesterol, which led to a more focused set of 16 features. We trained five separate machine learning models, including Logistic Regression, K-Nearest Neighbors, Random Forests, Gradient Boosting, and Support Vector Machines. Then, to make the predictions more accurate, we combined them into an ensemble model. The ensemble did not perform better than the Gradient Boosting model, which had an AUC of 0.84. However, changing the decision threshold made it easier for diabetic patients to remember things. This study shows how useful survey data can be for predictive modeling for disease detection. It also shows how this information could be used in real life for public health programs that aim to manage and prevent diabetes.

Keywords: Diabetes Prediction; Gradient Boosting; Machine Learning; NHANES; Plasma Glucose Levels; Nutrition; National Health.

1. Introduction

Artificial Intelligence has arisen as a vital device in the consistently growing field of bioinformatics, assuming a critical part in illness forecast, customized medication, and clinical decision-making. The capacity of ML models to dissect huge volumes of organic information and concentrate on significant examples has fundamentally upgraded the early analysis and forecasting of different infections [1]. One of the most encouraging uses of ML in medical care is the expectation of illness beginning in view on different information sources like genetic data, biomarkers, clinical imaging, and patient study information.

An especially significant area of exploration has been the early forecast of sicknesses like cancer, where ML models have exhibited extensive progress in recognizing potential malignancies considering hereditary

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transformations and imaging information [2]. Comparative endeavors have been coordinated toward neurodegenerative infections like Alzheimer's and Parkinson's, with prescient [1].

Past hereditary and imaging information, another option, yet exceptionally significant information hotspot for sickness expectation is overview-based health data. Reviews, for example, the National Health and Nutrition Examination Survey (NHANES), gather self-reported and clinically estimated well-being in- formation from a different population, making them a rich asset for epidemiological examinations [3]. The rising accessibility of huge-scope study datasets gives another road to further developing sickness expectation models, particularly for conditions firmly connected to lifestyle and social elements. For example, the expectation of metabolic issues, for example, diabetes, has been fundamentally upgraded by integrating segment, dietary, and active work information into ML models [4]. Not at all like conventional demonstrative strategies, which frequently depend on costly and tedious research facility tests, overview-based ML models offer a financially savvy and versatile option for infection screening.

Past examinations have investigated the achievability of involving review information for infection expectation, with promising outcomes. One striking review applied Help Vector Machines (SVM) to foresee the beginning of diabetes utilizing NHANES information, accomplishing a region under the beneficiary working trademark (ROC) bend (AUC-ROC) of 0.8 [4-5]. While these outcomes are empowering, there stays extensive opportunity to get better in expectation precision and model interpretability. Besides, this present reality sending of ML-based sickness expectation models requires cautious thought of element choice, model straightforwardness,
and possible predispositions in overview information.

In this work, we expand past efforts by using the NHANES dataset to work on the prescient execution of ML models for diabetes beginning. Our methodology includes testing different characterization strategies, including troupe learning techniques, to improve model power and generalizability [5]. Furthermore, we center around the interpretability of our models, giving insights into the most persuasive variables contributing to diabetes risk. The general objective is to foster a model that further develops expectation exactness as well as offers significant and noteworthy experiences for medical services experts and policymakers [6].

This paper is organized as follows: In Segment 2, we give a point-by-point depiction of the NHANES dataset [7], featuring the critical highlights and preprocessing steps included. In Segment 3, we present experimental results of the proposed models. Segment 4 showcases the experimental results. Segment 5 concludes the article.

2. NHANES Review Information, Element Choice, and Name Determination

The Public Wellbeing and Sustenance Assessment Overview (NHANES) is a huge scope, progressing cross-sectional review intended to survey the wellbeing and wholesome status of people in the US. Directed by the Habitats for Infectious prevention and Counteraction (CDC), NHANES gathers a blend of self-revealed review reactions, research facility test results, and actual assessment information [7]. The overview utilizes a mind boggling, multistage likelihood inspecting plan to guarantee that the information is illustrative of the more extensive U.S. populace for Disease and Control. Information assortment in NHANES happens in two primary stages. In the first place, members complete organized interviews in their homes, giving segmented data, clinical history, and self-revealed way of life decisions. Second, members are welcome to versatile assessment places (MECs) where they go through clinical assessments, including research facility tests, biomarker assortment, and physiological estimations.

2.1 Patient Prohibition and Mark Assignment

Following recent standardized protocols for NHANES-based diabetes research [8], we applied the following exclusion criteria:

- Pregnant members were rejected because of changed glucose digestion.
- Members younger than 20 were avoided.

We relegated names utilizing:

- Self-Revealed Diabetes Diagnosis: Patients replying *yes* to: Has a specialist at any point let you know that you have diabetes? were named 1.

- Plasma Glucose Level Measurement: Fasting Plasma Glucose (FPG) > 126 mg/dL → Mark 1 (diabetic). This dual-criteria approach ensures a more comprehensive capture of both diagnosed and undiagnosed cases [9].

2.2 Feature Selection

We chose 18 clinical and lifestyle features, leaving out those with more than 60% missing data. Based on recent studies on feature engineering [10], we added certain anthropometric markers, such as leg length, and biochemical markers, such as total cholesterol, because they are strongly linked to metabolic syndrome.

Table 1. Features Description

Feature Name	Description	NHANES Code	Feature Importances
AGE	Age at time of screening	RIDAGEYR	0.169
WAIST	Waist circumference(cm)	BMXWAIST	0.107
REL	Blood relatives have diabetes?	MCQ250A	0.087
HEIGHT	Height (cm)	BMXHT	0.086
CHOL	Total cholesterol (mg/dL)	LBXTC	0.085
LEG	Upper Leg Length (cm)	BMXLEG	0.080
WEIGHT	Weight (kg)	BMXWT	0.071
BMI	Body mass index (kg/m^2)	BMXBMI	0.067
RACE	Race/ethnicity	RIDRETH1	0.050
HBP	High blood pressure?	BPQ020	0.046
INCOME	Annual household income (dollars)	INDHHINC	0.039
ALC	Amount of alcohol in past year?	ALQ120Q	0.038
SMOKE	Age started smoking cigarettes regularly	SMD030	0.036
EDU	Education level	DMDEDUC2	0.017
EXER	Daily physical activity level	PAQ180	0.012
GEND	Gender	RIAGENDR	0.011

2.3 Cross-Approval and Test Set

The dataset contained 5515 examples. We performed:

- **Train-Test Split**: 80% (train: 4412 examples), 20% (test: 1103 examples).
- **10-Overlay Cross-Validation**: Utilized for hyperparameter tuning with lattice search to prevent overfitting [11].
- **Bootstrapping**: Applied for strong exactness assessment.

3. Methods

The objective of this study was to foster a strong AI system for foreseeing diabetes in view of NHANES review and clinical information [11]. To accomplish this, we executed individual arrangement models and a gathering model to work on prescient execution. The demonstrating system was directed utilizing scikit-learn [12], a broadly utilized Python-based tool compartment for effective AI, information mining, and measurable investigation.

3.1 Individual Models

We selected five classification algorithms for the proposed experiments which are recognized for high predictive performance in healthcare applications [13]:

- Logistic Regression (LR): A linear model estimating probabilities using the sigmoid function.
- K-Nearest Neighbors (KNN): A non-parametric model classifying samples based on nearest neighbors.

- Random Forest (RF): An ensemble of decision trees providing robustness to overfitting.
- Gradient Boosting Classifier (GBC): An iterative boosting method minimizing residual errors.
- Support Vector Machine (SVM): A kernel-based method maximizing class separation [14].

Other classifiers such as Naïve Bayes were evaluated but did not perform as well due to feature correlation. Figure 1 shows the schematic of ensemble method.

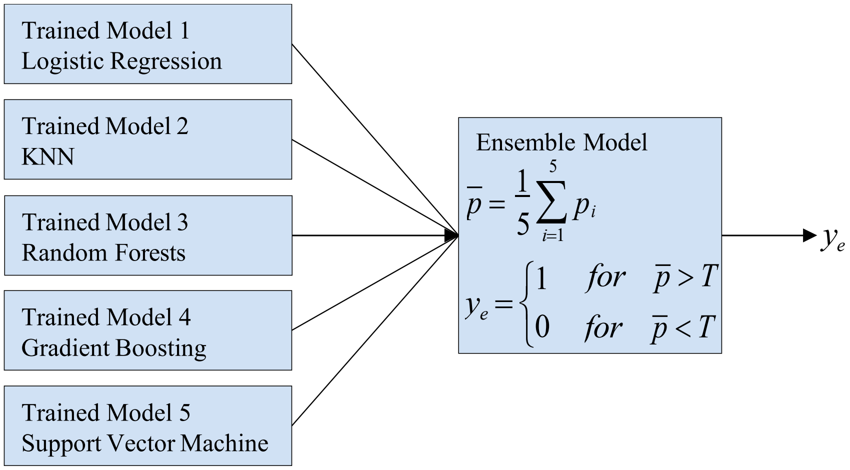

Figure 1. Schematic of Ensemble Method. Each trained model outputs a probability, and the average probability is taken with equal weight given to each model. Finally, a to be determined probability decision boundary T is selected based on tuning from recall results. Typically, T=0.5, but by adjusting T, higher diabetes prediction rates can be obtained at the expense of labeling more healthy patients as diabetics.

3.2 Hyperparameter Tuning

Every model had a number of hyperparameters that needed to be optimized. A complete grid search with 10 values for each parameter would require 10^{10} evaluations, which is not possible with computers. This cuts down on a lot of extra work for the computer, making it possible to fine-tune the model on a personal computer [15]. We chose a two-step approach instead:

Step 1: Coarse Grid Search: A broad sweep across a wide range of hyperparameters to identify promising regions.
Step 2: Fine Grid Search: A focused search within top-performing regions to fine- tune parameters [16].

3.3 Ensemble Model

We put the five individual models together to make a soft-voting ensemble, which made the performance even better. This method uses the fact that different learners are different to lower variance and make the model more generalizable [17]. Each model produced probability estimates p_i, and the final probability $\overline{p}$ was computed as:

$$\overline{p} = \frac{1}{5}\sum_{i=1}^{5} p_i \qquad (1)$$

where $\overline{p}$ represents the averaged probability across all models. The final prediction was determined based on a threshold T, initially set to 0.5. This ensemble strategy is particularly effective in bioinformatics because it mitigates the specific biases inherent in any single algorithm [18].

4. Results

This segment presents the presentation of individual models, the gathering model, and the effect of edge change on review. Furthermore, bootstrapping was utilized to assess changeability in model execution, giving certainty spans to key execution measurements.

4.1 Experimental Results for Individual Models

The generally discriminative force of each model was surveyed utilizing Receiver Operating Characteristic (ROC) curves, displayed in Figure 2. The Area Under the Curve (AUC) was utilized to look at models. Figure 2 shows the Gradient Boosting Classifier (GBC) accomplished the most elevated AUC of 0.83. The Random Woodland (RF) classifier followed intimately with an AUC of 0.81. The K-Nearest Neighbors (KNN) played out the most exceedingly terrible, with an AUC of just 0.68. The AUC values and extra execution measures are summed up in Table 2.

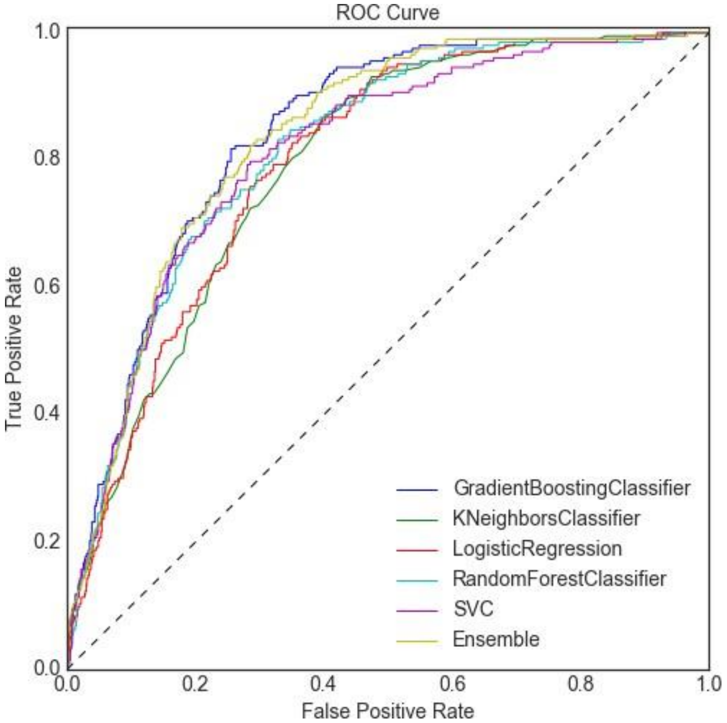

Figure 2. ROC curves are plotted for each individual model and the ensemble model.

Table 2. Comparison of the experimental results based on the selected models.

Model	AUC	F1 Score	Recall	Precision
K-Nearest Neighbors	0.793	0.73	0.82	0.67
Logistic Regression	0.797	0.79	0.81	0.78
Support Vector	0.812	0.79	0.82	0.78
Random Forests	0.817	0.79	0.82	0.79
Gradient Boosting	0.84	0.81	0.82	0.8
Ensemble	0.834	0.78	0.82	0.78

4.2 Experimental Results for Ensemble Model

An ensemble model was made by averaging the likelihood results, everything being equal. Be that as it may, it did not altogether outperform the Slope Supporting Classifier. Its AUC stayed near 0.82 (Table 2), recommending that assembling gave minimal extra advantage.

4.3 Effect of Choice Limit on Recall

The review rate for diabetics was at first low at T = 0.5, yielding a review of just 0.35. By changing the edge to T = 0.78, the review improved to 0.75 for diabetics, at the expense of expanded misleading upsides. Figure 3 represents how review differs with T, while Figure 4 shows review scores across models.

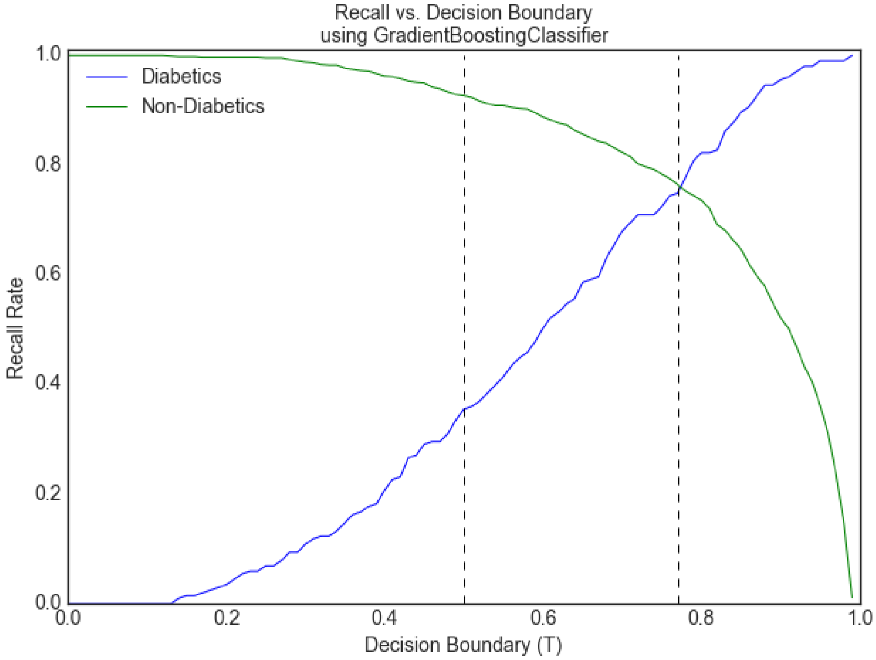

Figure 3. Recall vs. Decision Boundary curves for diabetes and no diabetes for the Gradient Boosting Classifier. At the default classification of T=0.5 (dotted line), the recall rate is 0.93 for non-diabetics and 0.35 for diabetics. For T=0.78 (dotted line) the recall rate for non-diabetics is 0.75 and the recall rate for diabetics is 0.75, representing a large improvement in identifying the diabetics patients.

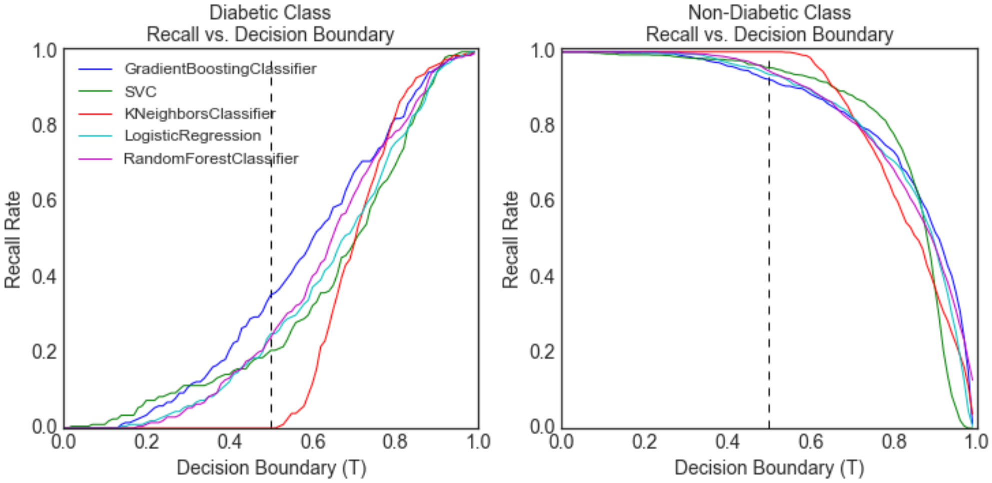

Figure 4. Recall vs. Decision Boundary curves for diabetic and non-diabetics by model.

4.4 Bootstrapped Testing Mistake and Model Stability

To assess model strength, bootstrapping was performed on the best model (Slope Supporting Classifier) with Nboot = 1000. The mean AUC was 0.83 with a 95% certainty timespan, 0.84]. Figure 5 presents the bootstrap ROC curves, showing negligible change in model execution.

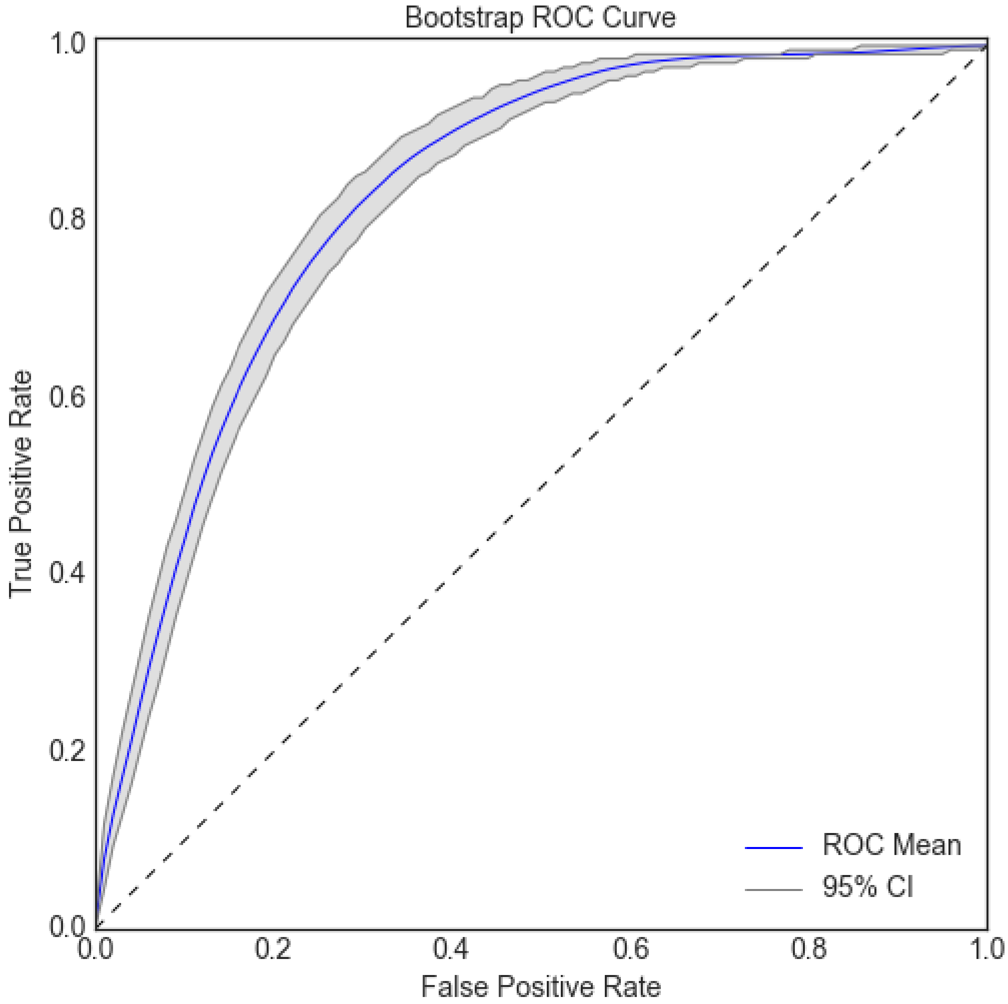

Figure 5. ROC curve for the Gradient Boosting Classifier. Also plotted are the 1-standard deviation spread representing the testing performance for models trained on Nboot bootstrapped samples. The very small difference between the average (middle curve) and the top and bottom curves show that the model performance is not sensitive to the training data.

5. Discussion and Applications

5.1 Model Execution and Insights

The current review investigated the utilization of five AI models; Angle Helping Classifier, Arbitrary Woods, Backing Vector Machine, Calculated Relapse, and K-Closest Neighbors, for the order of diabetic and non-diabetic patients in view of overview information gathered from NHANES. To improve characterization strength, a group model was likewise built, consolidating equivalent probabilistic weighting of the singular models. From the ROC bends of all models (Figure 2), the Angle Helping Classifier arose as the best-performing model, accomplishing the most elevated AUC (as definite in Table 2). Shockingly, the outfit model didn't outperform the exhibition of the Slope Supporting Classifier, in opposition to assumptions considering gathering learning hypotheses like the shrewdness of groups.

To keep away from an unfeasible computational weight, individual model hyperparameters were tuned independently as opposed to enhancing them with regards to the outfit. This could have forestalled the outfit model from utilizing the most correlative parts of various classifiers. The outfit model treated every one of the five classifiers similarly, even though a few models (for example, K-Closest Neighbors) had essentially lower execution. Weighting models in view of their AUC, as opposed to treating them, similarly, might have further developed in general group execution. A more modern group strategy, like a stacked model (where the expectations of individual classifiers are utilized as highlights for a meta-classifier), could have caught multifaceted element collaborations better.

Preprocessing steps assumed a huge part in model execution, especially given the presence of missing information. Missing information was taken care of through mean attribution for mathematical elements (like BMI and level) and mode ascription for straight out factors, (for example, liquor utilization and level of pay). While this approach guaran- teed no missing qualities, more complex attribution methods, like prescient displaying for missing qualities or network factorization, could additionally refine model exactness.

An especially significant thought is the effect of ascription procedures on model predisposition. Mean ascription expects a typical dispersion of mathematical elements, which may not be fitting for slanted information circulations. Additionally, mode ascription for downright factors could present inclinations on the off chance that the missing information isn't missing totally aimlessly (MCAR). Future work could investigate the effect of utilizing AI based attribution techniques, for example, K-closest neighbor ascription or Bayesian attribution, to work on prescient execution.

5.2 Applications and Reasonable Considerations

Diagnostic Utility in Clinical Choice Making A critical thought in sick- ness order models is their relevance in certifiable clinical direction. The model introduced here is intended for early diabetes recognition utilizing basic, effectively realistic overview and biometric information. The chose highlights, reactions to survey things and fundamental assessment estimations (Table 1), were decided to permit harmless, practical screening. A significant compromise in characterization models for sickness identification is the harmony among review and accuracy. Of course, a choice limit of T = 0.5 created a review pace of just 35% for diabetics, implying that 65% of diabetic cases were not recognized. Given the objective of augmenting early recognition, this review rate was considered lacking.

To address this, the choice limit was acclimated to T = 0.78, yielding a review pace of 75% for diabetics. Notwithstanding, this came at the expense of expanding the misleading positive rate, implying that more non-diabetics were erroneously delegated diabetics. Impact on Medical services Asset Allocation While expanding review works on early recognition, it additionally has huge ramifications for medical services asset portion. If 75% of genuine diabetics are distinguished, among the all-out populace of 5,500 patients, around 5, 515 × 0.81 × 0.75 = 3, 350.

Non-diabetic people would be hailed as possibly diabetic. Accordingly, an expected 2,165 patients (40% of the populace) would require further screening or symptomatic testing. This addresses a compromise among responsiveness and particularity that medical care suppliers should consider while executing such models practically speaking.

The monetary attainability of carrying out AI put together screening devices depends with respect to various elements. Extra testing (e.g., HbA1c or fasting blood glucose tests) for erroneously hailed non-diabetics brings about direct medical care costs. Cost of Misleading Negatives: Undetected diabetics could foster complexities requiring costly mediations later. Population-Level Scalability: Sending such models in enormous scope screening programs (e.g., public wellbeing check-ups) requires computational productivity and foundation contemplations. From a general well-being point of view, the model's capacity to dispose of 60% of superfluous screenings while keeping a 75% review rate makes it a promising device for beginning phase diabetes location in low-asset settings.

6. Conclusion

In rundown, this review assessed five AI classifiers for diabetes expectation utilizing NHANES information. While the Angle Helping Classifier outflanked different models, the troupe strategy didn't yield upgrades because of equivalent weighting of models and restricted hyperparameter tuning. By changing the choice limit, review was fundamentally improved at the expense of particularity, showing a compromise vital for clinical execution. Future investigations ought to zero in on advancing hyperparameter tuning, upgrading highlight designing, and coordinating profound learning strategies to additionally work on prescient exactness.

Data Availability Statement

Not applicable.

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Conflicts of Interest

The author declares no conflicts of interest.

Ethical Approval and Consent to Participate

Not applicable.

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