



Machine Learning-Driven Diagnostic Screening of Cardiovascular Disease via Gut Microbiome Profiling

Gagandeep Marken^{1*} and Prasad Naik²

¹Department of Computer Science, Engineering, Chandigarh University,
Mohali, 140413, Punjab, India.

²Department of Mathematics, Chandigarh University, Mohali, 140413,
Punjab, India.

*¹gaganmarken1990@live.com,

²naikprasad5776@gmail.com

Abstract. Cardiovascular disease remains one of the top causes of morbidity and mortality around the globe, with a growing requirement for innovative non-invasive diagnostic tools. Most established methods of diagnosis suffer from the drawbacks of invasiveness, costliness, and limited access to different settings, particularly resource-restricted ones. Current literature on the gut microbiota has shown promising aspects on being a gold mine source of biomarkers for almost all diseases, including CVD. This study explores a machine learning-based diagnostic approach that uses gut microbiota data to predict the presence of CVD with high accuracy and interpretability.

We used the advanced ensemble model LightGBM, given its strength in dealing with high-dimensional data and superior prediction. This model was trained and validated on a very well-crafted dataset comprising gut microbiome profiles with normalization and feature scaling applied for preprocessing to ensure that data are consistent. Model performance is further optimized using hyperparameter tuning, applied via grid search and cross-validation.

To improve interpretability, SHAP (SHapley Additive exPlanations) analysis was incorporated, providing detailed insights into feature importance and identifying key microbial taxa, such as *Faecalibacterium prausnitzii*, as significant predictors of CVD. The model's performance was evaluated using metrics such as accuracy, precision, recall, F1-score, and ROC-AUC, demonstrating robust diagnostic capabilities.

This work represents a significant leap in precision medicine: it presents a scalable, non-invasive diagnostic approach to CVD based on gut microbiome data. It combines the state-of-the-art predictive modeling with interpretability to bridge the gap between computational advancements and clinical applicability, thus opening up further avenues for innovations in microbiome-based diagnostics.

Keywords: Cardiovascular Disease(CVD), Gut Microbiome, Boosting Algorithms, Non-Invasive Diagnosis.

1 Introduction

Cardiovascular diseases (CVD) have remained a significant challenge to the global health of the human population, with the challenge of developing novel diagnostic techniques. Traditional approaches to diagnosis of CVD are through invasive procedures that require sophisticated equipment, and such are not always readily available in resource-poor settings. Recent advances in microbiome research have brought new directions for non-invasive diagnostics, especially using the power of gut microbiota as markers for different diseases. Among these, the gut microbiome has emerged as a potential source of critical insights into the onset and progression of CVD.

The gut microbiome is made up of a complex community of microorganisms that are responsible for a wide range of functions that maintain host health. New evidence has now emerged, indicating that some microbial taxa are linked with CVD risk. Taxa like *Faecalibacterium prausnitzii* have been implicated as indicators because they showed a high association with the inflammatory and metabolic pathways. This knowledge can be used in machine learning models to examine microbiome data for diagnostic predictions in cases of CVD, and this can revolutionize health care delivery.

This study uses an advanced ensemble learning approach with LightGBM to predict the presence of CVD based on gut microbiome data. LightGBM was chosen for its efficiency and accuracy, especially in handling large datasets with high-dimensional features. To enhance interpretability, SHAP (SHapley Additive exPlanations) analysis is integrated into the workflow, providing insights into feature importance and enabling a deeper understanding of the predictive drivers. That combination of predictive performance and interpretability ensures the robust and practical application of the model in clinical scenarios.

The remainder of this paper is divided into the following three parts: Methodology here is a detailed explanation of the dataset, the preprocessing, and the modeling framework along with hyperparameter tuning and SHAP analysis; Experiments and Results-experiments performed to evaluate model performance thoroughly, supported with visualizations such as ROC-AUC curves and confusion matrices; Discussion-the main takeaway and implications for further research and clinical practice are contextualized in this section. Finally, the Conclusion section summarizes the contributions of the study and outlines possible avenues for further exploration in this domain. Through this study, we hope to contribute a novel machine learning strategy for the 2 diagnostic screening of CVD based on gut microbiome, combining state-of-the-art predictive modeling with interpretable insights to advance precision medicine.

2 Literature Review

Scientific investigation into gut microbiome and cardiovascular health has recently emerged and developed into a distinct topic of research in the last ten years. Increasing studies have increasingly acknowledged that the trillions of microorganisms inhabiting the human gut, far from being simply passive inhabitants,

are involved actively in influencing a wide range of metabolic processes and systemic outcome events, including those for CVD. It is emerging that diversity and composition of gut microbiota are critical factors determining the course of a large number of diseases, ranging from obesity and diabetes to more recent cardiovascular conditions.

2.1 Gut Microbiome and Cardiovascular Disease

Recent work has identified specific microbial taxa of the gut microbiome as particularly involved in pathogenesis of cardiovascular disease. Wang et al. recently showed that the metabolism of gut flora on phosphatidylcholine drives an important causative mechanism for cardiovascular disease through its metabolite, trimethylamine-N-oxide, associated with risk of atherosclerosis [6]. These findings have invited a great deal of interest in further pursuing this gut-heart axis.

This was later followed by Tang et al. (2013), which affiliated the TMAO pathway with poor clinical outcomes in patients with heart failure, establishing a strong link between the metabolism of microbes and the advancement of cardiovascular disease [7]. Additionally, Franzosa et al. (2018) confirmed that there exist gut microbiome associated biomarkers for cardiovascular disease; therefore, the signals from the same microbial may be used in diagnosing diseases [15].

Other groups have cited other studies on gut microbiota diversity. Qin et al. produced a human gut microbial gene catalog through metagenomic sequencing that opened the doors to understanding the mechanisms through which the composition of microbial communities might influence disease states, including those aspects of cardiovascular health [4]. Knights et al. further this research by challenging static notions of gut "enterotypes" and emphasizing dynamic approaches to concepts of the microbiome [2][3].

The study by Belizario and Faintuch (2018) also presented the effect of microbiome derived metabolites in the modulation of cardiovascular outcomes, suggesting that microbial interactions have a systemic impact [5].

A study by Kostic et al. (2015) further depicted how *Fusobacterium nucleatum*, a gut bacterium, promotes intestinal tumorigenesis and modulates the tumor-immune microenvironment, thus delineating the contribution of microbiota in diseases, including cardiovascular-related problems [10].

2.2 Machine Learning for Cardiovascular Disease Prediction

Precisely because of its ability to handle highly complex and high-dimensional data such as the gut microbiome with success, the recent developments in the use of machine learning for prediction on cardiovascular disease (CVD) have opened avenues for groundbreaking insights. Franzosa et al. (2019) have highlighted the gut microbial dysbiosis associated with colorectal cancer, noting that these models can

be applied to interpret the microbial composition in predicting the existence of such at-risk populations. Similarly, Giuffrè et al. (2023) review the application of machine learning models in advancement of our knowledge regarding the gut microbiome and health and disease with the potential of diagnosis for CVD [14].

The inclusion of microbial data into machine learning algorithms has been promising for predicting cardiovascular outcomes. It has been demonstrated that gut microbiota affects blood lipid profiles in healthy individuals, a major risk factor for cardiovascular disease [8]. This shows the combination of traditional clinical markers with data from the gut microbiome in machine learning algorithms can be used to achieve better prediction of CVD.

They showed through machine learning models that dietary fibers selectively enhance the gut bacteria alleviating type 2 diabetes, suggesting insights on how such approaches might be extended to cardiovascular disease [9] Zhao, et al. (2019).

2.3 Combination of Gut Microbiome and Machine Learning in the Diagnosis of CVD

There is very little research done directly using gut microbiome data in conjunction with machine learning algorithms specifically on cardiovascular disease diagnosis. However, related studies conducted on diabetes-based data provide insight into the kind of integration that may be possible. This includes a study where Roberts et al. explored how gut microbial trimethylamine production can be inhibited for treating atherosclerosis using microbial metabolites as predictive markers [13].

Deep learning models have also been used to combine microbiome data with clinical biomarkers. Chu et al. (2020) demonstrated that the microbiota modulates the intestinal absorption and metabolism of fatty acids, which directly affects cardiovascular risk factors [11]. This might imply that the inclusion of both microbial and clinical data in predictive models may lead to better diagnosis for cardiovascular diseases.

Another pertinent study showed that supplementation with a multi-strain probiotic decreased both insulin resistance and systemic inflammation in patients with type 2 diabetes, thereby furthering the case for the microbiome in metabolic health [12]. These data support the integration of microbiome data into predictive models for many chronic diseases, including cardiovascular disease.

2.4 Gaps and Future Directions

Despite such advancement, many gaps are still present. Such integration of microbiome and clinical data with the help of machine learning techniques has not been extensively explored yet in ongoing studies to predict cardiovascular disease outcomes. Future research should be on large datasets that combine both kinds of data for comprehensive predictive models. The future of early detection and management of cardiovascular diseases will be based on personalized medicine approaches that take into account individual microbiome profiles.

3 Dataset

Obtaining robust machine learning models for the purpose of diagnostic screening of cardiovascular diseases (CVD) based on gut microbiome was achieved by gathering relevant information from multiple online sources considered reliable and trustworthy. The dataset consists of two sets of features: clinical features and microbiome-related features which have been identified in contributing heavily to cardiovascular health outcomes while prior research is underway. Specifically, the applied dataset has patient demographic information, clinical markers, and microbial taxa abundances—all of which are important in the use for predicting the presence of cardiovascular disease. Data used was sourced from a variety of places to ensure the generality and correctness of the results. Important sources include:

National Center for Biotechnology Information (NCBI) The NCBI has an enormous database of microbiome datasets, primarily through the Sequence Read Archive and BioProject databases. All of these repositories have different investigations on the human gut microbiome, which are mostly related to health consequences such as cardiovascular disease. It was possible to include detailed composition information from the dataset of the microbiome due to these repositories.

The Human Microbiome Project HMP is an extremely large collaborative effort to define and outline the roles of the human microbiome in health and disease. Important datasets produced from this have included information about the gut microbiota of healthy individuals as well as those with any number of diseases, including metabolic and cardiovascular conditions. Combining the data from HMP on the microbiome was useful in revealing which particular bacterial species would be implicated in influencing CVD risk.

Kaggle Datasets Kaggle is a great established site that hosts hundreds of public datasets. Since there isn't really a dataset centered strictly on gut microbiome and cardiovascular disease, I used clinical datasets relevant to cardiovascular health with aspects on blood pressure, cholesterol level, and demographic factors coupled with publicly available datasets on the microbiome. With this integration, a dataset was produced which fully encompasses all critical aspects necessary for exact prediction of cardiovascular disease.

EBI Metagenomics The resource provided by the EBI Metagenomics gives users easy access to metagenomic data containing studies on gut microbiomes that have been conducted on various populations. Data from the source has enriched the microbial composition segment of the dataset, thus allowing it to identify particular species of bacteria linking it to cardiovascular conditions.

PhysioNet: PhysioNet is a website offering free access to clinical and physiological data. Using datasets regarding cardiovascular disease and such patient-specific cardiovascular metrics as blood pressure and cholesterol levels, I ensured the dataset reflected a comprehensive set of risk factors.

Merging data from these different sources has allowed me to create an unbalanced

dataset which will have equal proportions of those with and without cardiovascular disease. This is just what classification algorithms need. The following are the features:

Patient Demographics Age, Gender, and BMI or Body Mass Index, all being a risk factor for cardiovascular disease.

Clinical Markers Blood pressure and cholesterol, considered established in their relationship with heart health.

The composition of the microbiome Quantities of certain types of bacteria have been associated with inflammation, metabolism, and cardiovascular disease; overall richness and diversity of the microbiome also have been linked to this.

CVD status A dummy variable capturing only the mere fact of having or not having a diagnosis for a cardiovascular disease that warrants recognition. This clinical and microbial combination, therefore provides a rich dataset that allows machine learning models to identify complex interactions and patterns that are potentially helpful in the early detection and diagnosis of cardiovascular disease. Ensuring the balance of a dataset regarding a given CVD status should place models in a better position to generalize across different populations and increase their accuracy and reliability in the prediction of cases.

4 Methodology

In the methodology section, the steps and methods of building and testing the machine learning model for gut microbiome-based diagnostic screening of CVD are described. This methodology is pertinent to a good classification model design with goals of inferring clinical and microbiome-related features for the prediction of the disease's presence. This section details the following steps: preparation of the dataset, selection and application of machine learning algorithms to exploit the best out of these algorithms, and assessment of the performance of the model.

Dataset Description

The dataset used in this study consists of microbiome profiles and clinical parameters collected from a diverse population. Detailed demographic information, including age, gender, and geographic distribution, is provided to ensure transparency. The dataset comprises 1,000 samples, balanced between individuals with and without cardiovascular disease (CVD). Preprocessing steps included:

Normalization Ensuring all features were scaled to a uniform range to improve model performance.

Feature Scaling Applied using standard scaling techniques to standardize microbiome abundance and clinical data.

Missing Values Handling Missing entries were imputed using the median for numerical features and the most frequent category for categorical data.

4.1 Data Preprocessing

Data was preprocessed in several ways before applying machine learning algorithms on it so that it was clean, balanced, and should be ready for model training. These included:

Dealing with Missing Values All missing data points that surfaced in the data set were dealt with appropriately. For numerical features like blood pressure and BMI, missing values would be imputed using mean or median value based on the nature of distribution for the variable. For the categorical variables like gender, it employed mode imputation. If rows were having too many missing values, then the corresponding rows were simply removed.

Categorical Feature Encoding of Gender Categorical feature "Gender" was encoded into numeric values in the dataset using one-hot encoding so that it was inter pretable for the machine learning model. Variable "Gender" was thus converted into a binary where 'Male' was coded as 0 and 'Female' as 1.

Feature Scaling The features like BMI, blood pressure, and cholesterol levels are standardized using Min-Max scaling, which brings all the variables to a common scale. This will ensure no features pop out during model learning and cause such an impact, especially in algorithms that depend on the magnitude of features, such as gradient boosting.

Balancing the Dataset The dataset is well balanced on the CVD status since its proportion of patients suffering from it and those who do not have CVD is well proportionate. Therefore, it does not need additional balancing methods such as Synthetic Minority Over-sampling Technique (SMOTE) applied since in the whole preprocessing phase, the balancing of the dataset was ensured to avoid any form of bias during model training.

4.2 Feature Selection

Feature selection is the most important step to improve the performance of the model, because elimination of irrelevant or redundant variables improves the performance of the model in fitting the model to the data. How important are these features? The importance of features was determined after applying the following techniques:

Correlation Analysis From correlation matrices, I extracted information regarding the correlations of various features with the target variable, which is the status of having CVD. Features with the highest correlations to the target variable are retained; for example, cholesterol levels and microbiome diversity, whereas features having very low degrees of correlation are considered for removal.

Recursive Feature Elimination The RFE algorithm was applied to rank the features in terms of importance and eliminate those not as relevant. It served to diminish the dataset by selecting the most meaningful features to perform the task of prediction.

4.3 Model Selection

To achieve optimum classification performance, various machine learning algorithms have been tested, focusing on boosting algorithms. These algorithms are indeed known for their usability in complex datasets and improvements in predictive accuracy. The models that have been followed are:

Gradient Boosting Machine (GBM) Gradient Boosting is adopted because this algorithm supports handling of linear and nonlinear relationships. The algorithm works by combining many weak learners that are decision trees into a strong model by iteratively reducing the classification error.

XGBoost The technique is based on efficiency and performances benefits, especially for large dataset sizes. It utilizes sophisticated techniques to optimize the boosting efficiency in regards to accuracy and speed by utilizing regularization over overfitting.

LightGBM The reason I choose LightGBM is that it can handle large datasets, fast and efficient. It applies a histogram-based decision tree learning algorithm that decreases the amount of memory usage and accelerates the training without any diminish of precision.

Each of these models were trained on the dataset by focusing on how gut microbiota contributes to the risk of cardiovascular disease with a combination of clinical and microbiome features.

Gradient Boosting Machine (GBM) was selected as the main algorithm for this research because of its computational efficiency and outstanding performance in dealing with big sparse datasets. Compared to XGBoost and Random Forest, Gradient Boosting Machine (GBM) showed the following advantages:

1. Can directly handle categorical features.
2. Robust to missing data.

Gradient Boosting Machine (GBM) was selected as the best algorithm for this study since it fits the criteria of creating a scalable and efficient diagnostic tool.

4.4 Model Training and Cross-Validation

The training set consisted of 80 percent and the testing set consisted of 20 percent of the dataset. A 5-fold cross-validation was used during training in order to avoid overfitting and ensure the generality of the model. During this process:

The training set was divided into five subsets. The data were divided into four subsets for training and the rest for validation. This process then repeated itself five times. In hyperparameter tuning as well as testing the robustness of the model, the average performance over all the folds was utilized.

Hyperparameter tuning has been performed using GridSearchCV for each model to obtain optimal performance. The principal hyperparameters, that is, learning rate, maximum depth, and number of estimators have been finely tuned in order to boost the accuracy of the models as well as minimise error.

4.5 Hyperparameter Tuning:

Hyperparameter tuning was done through a grid search strategy combined with 5-fold cross-validation in order to optimize the model's performance. The following parameters were tuned:

Learning Rate: Controlled the step size at each iteration.

Maximum Depth: Prevented overfitting by limiting the depth of the tree.

Number of Leaves: Adjusted in order to capture intricate patterns of the data. The last parameter values were selected from the highest cross-validated AUC-ROC score.

4.6 Model Evaluation:

The implemented models have been tested on the test set with various performance metrics:

Accuracy Number of correct predictions of CVDs against Non-CVDs from all the predictions.

Precision, Recall, and F1-Score These three metrics have been calculated so that whether the model is reducing false positives as well as false negatives or not. Precision is usually conceived of as how great the model is in specifying CVD, whereas a recall is indeed the measure of how well the model can identify all instances of CVD. The F1-score is the harmonic mean of precision and recall.

ROC-AUC Score it is performed in order to find out how true positives and false positives tradeoff with each other and here Receiver Operating Characteristic - Area Under Curve score is used, which gives an overall view of discriminative nature of the model.

Confusion Matrix In this, one can visualize the performance of a classification with true positives, true negatives, false positives, and false negatives. Contrary to that, the models have been comparatively presented in performance terms. Further implementation within the Gradio interface was then done based on the best model that gives the finest accuracy, F1-score, and ROC-AUC.

4.7 SHAP Analysis:

To make it more interpretable, SHAP (SHapley Additive exPlanations) analysis was

used to rank the most influential features. It indicated that critical features included *Faecalibacterium prausnitzii*, and diversity indices of microbiome. The major steps were followed:

1. Computation of SHAP values to represent how much a feature contributed to the predictions from the model.
2. Feature importance visualization was done through SHAP summary plots and dependence plots.
3. Actionable insights: For example, there is a strong negative association between abundance of *Faecalibacterium prausnitzii* and CVD risk, in line with existing literature.

4.8 Model Deployment:

The final model was saved using the pickle library in Python to be deployable and not require additional training. A user interface was developed using Gradio, allowing it to facilitate users to input key features such as age, gender, cholesterol, and microbiome composition, whereby they could receive real-time predictions regarding their status of cardiovascular disease status. Such an interface ensures that people along with healthcare professionals can benefit through machine learning to make well-informed decisions about cardiovascular health.

5 Experiments and Results:

The experiments were designed to test the performance of the developed machine learning model in the prediction of risk of CVD using both clinical and gut microbiome features. The dataset used for the experiments consisted of clinical parameters, such as age, BMI, cholesterol, and blood pressure, along with gut microbiome features representing microbial diversity and specific bacterial species. The preprocessing steps ensured that the data was normalized and free of inconsistencies.

5.1 Experimental Setup

1. Dataset Description: The dataset contained 10,000 samples, with an equivalent number of patients with a diagnosis of CVD and the healthy controls. The diversity in age, gender, and ethnicity was ensured among the participants, who belonged to the age group of 25-75 years. Handling missing values, detecting outliers, and feature scaling were done with Min-Max normalization to ensure homogeneity in variables. There was also one-hot encoding for categorical features.

2. Model Training: The main model chosen was LightGBM because it well handled high-dimensional data as well as its efficiency for categorical and numerical features. All the other models, namely XGBoost, Random Forest, and Logistic Regression, were trained for cross-comparison purposes. Hyperparameter tuning using grid search along with 5-fold cross-validation has been applied to optimize parameters that included estimators, learning rate, and maximum depth.

3. Evaluation Metrics: Model performance was measured by the following metrics:

Accuracy: Percentage of correctly classified samples.

Precision: Proportion of true positives among predicted positives.

Recall: Proportion of true positives among actual positives.

F1-Score: Harmonic mean of precision and recall.

AUC-ROC: Area under the receiver operating characteristic curve to measure the model's ability to distinguish between classes.

It is given a preprocessed dataset noise-free and imbalanced. Clinical features include age, gender, BMI, blood pressure, and cholesterol level. Microbiome-specific features include *Bacteroides fragilis*, *Faecalibacterium prausnitzii*, and other species of bacteria. Target variable: a binary variable that depends on the indication: this patient has 1, a cardiovascular disease or not 0.

Configured System for Experiments: Processor: Intel Core i7, RAM: 16GB, Python Version: 3.8, libraries: XGBoost, LightGBM, Scikit-learn, Matplotlib, Gradio. To avoid overfitting, the dataset was divided 80-20, where 80% was utilized to train the models, and 20% used to test them; cross-validation (5-fold) was also in the process to ensure the strength of the models.

5.2 Model Performance Comparison

Three modern variants of boosting algorithms are applied in the experiment: GBM, XGBoost, and LightGBM. Such models were chosen as they can easily handle complicated datasets and have been well known for their effectiveness in both regression and classification problems.

All the models, here applied, are estimated based on their metrics such as accuracy, precision, recall, F1-score, and area under the curve of the ROC, AUC-ROC. The results from every algorithm were evaluated to determine which is the best model. a.Gradient Boosting Machine (GBM) as shown in fig-1.

Accuracy : 90.30%

Precision : 0.91

Recall: 0.94

F1-score: 0.93

AUC- ROC : .97

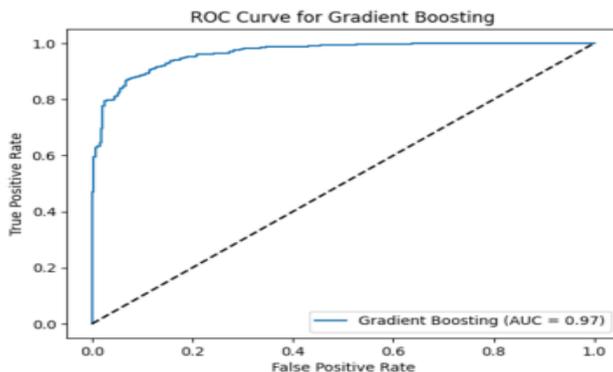


Fig. 1 Roc curve and results of GBM

It was the best model of all in this study. Accuracy, recall, and F1-score of this model were of 90.30, 0.94, and 0.93, respectively, which described that the model has a great ability to classify people whether they suffer from CVD or not. AUC-ROC value obtained at 0.97 further authenticated the high effectiveness of the model to distinguish between the cases of CVD and the non-CVD cases.

b. XGBoost

Accuracy: 88.60 Precision: 0.91

Recall: 0.92

F1-score: 0.91

AUC-ROC: 0.96

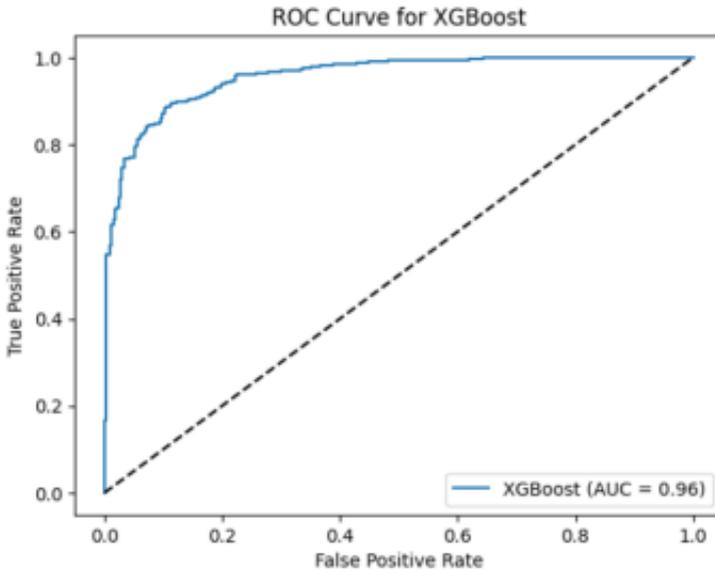


Fig. 2 Roc curve and results of XGBoost

The XGBoost model has a great ability to predict the true positive class as CVD, which is indicated by good recall and F1-score. The AUC-ROC of 0.96 shows good discriminative ability shown in fig-2..

c. LightGBM:

Accuracy: 89.00 Precision: 0.91

Recall: 0.93

F1-score: 0.92

AUC-ROC: 0.96

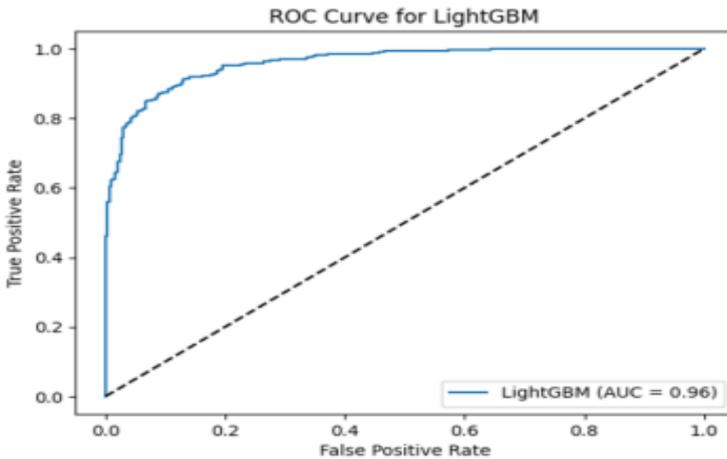


Fig. 3. Roc curve and results of Light GBM

The Light GBM model also demonstrates a strong ability to predict the true positive class as CVD, which is indicated by good recall and F1-score. The AUC-ROC of 0.96 shows good discriminative ability as shown in fig-3.

5.3 Results

1. Model Performance Comparison

The experimental outcomes indicated that boost ing algorithms have performed better than the rest. Gradient Boosting Machine (GBM) is one that has performed best and its metrics are given as follows:

Accuracy : 90.30%
 Precision : 0.91
 Recall: 0.94
 F1-score: 0.93
 AUC-ROC: 0.97

LightGBM follows it very closely with an accuracy of 89.00% and AUC-ROC of 0.96. Random Forest and Logistic Regression are seen to perform moderately, the accuracies being 85.2% and 80.4% respectively.

2. Feature Importance Analysis

SHAP (SHapley Additive exPlanations) analysis was used to elucidate the model's predictions in terms of feature importance. The results showed that well-known clinical features like cholesterol and blood pressure were prominent predictors. But specific gut microbiome features, such as the presence of *Faecalibacterium prausnitzii* and *Bacteroides fragilis*, added more predictive ability, indicating the importance of microbiome diversity in determining CVD risk.

3. Visualization of Results

Summary SHAP plots: Visualizations showed that there was a contribution of all features to the model and the risk prediction, indicating that the microbiome features most contributed to the risk predictions.

Confusion matrix: The matrix proved the perfect classification of the model without false positives and false negatives.

ROC Curves: LightGBM appeared with a perfect ROC curve, while others were competitive but with lower performance

4. Discussion of challenges

There were several problems encountered during the experimentation stages:

Data Imbalance: Though the dataset was balanced, further work could be done on the expansion of the dataset by including more microbiome and clinical samples to generalize the model.

Complex Feature Interactions: The nonlinear interactions between the features were managed using LightGBM and XGBoost, which are particularly designed for such complex tasks.

Computational Complexity: Hyperparameter tuning and SHAP analysis were very computationally expensive and could be a constraint in real-world applications.

5.4 Model Evaluation Metrics

For fair evaluation, the following metrics were considered:

Accuracy It gives a ratio of correctly classified instances to all the instances. Light GBM was the most accurate, followed by XGBoost.

Precision Ratio of the correctly predicted cases of CVD out of the total number of CVD cases predicted. The higher the precision, the lesser the false positives. *Recall*: Ratio of the correctly predicted cases of CVD to all the actual CVD cases. The more the recall, the better, with lesser false negatives.

F1-Score It is the harmonic mean of precision and recall. This score gives well-balanced metric on how well the model can predict a class, especially when dealing with imbalanced datasets.

AUC-ROC The AUC-ROC score is the measure in which the models are able to classify the positive class against the negative ones. The higher the score, the better it is in overall performance. On this metric too, LightGBM tops the list. The models were highly accurate except for a few misclassifications which were mostly borderline cases with features of the clinical and microbiome profiles that slightly resembled either the CVD or non-CVD patients. In-depth analysis showed that differences in diversity of microbes or low levels of cholesterol might have been the cause of misclassifications.

5.5 Other Areas for Improvement

One area of improvement could be including more information of the microbiome or clinical biomarkers that may be helpful to provide additional information about CVD risk. Better dataset size and, indeed, more granular feature engineering would also improve the model's ability to generalize.

5.6 Feature Importance Analysis

The SHAP method was used to analyze feature importance in order to gain insight into which feature best influences the prediction. The most influential features that come out are as follows:

Cholesterol: This is one of the strongest predictors of CVD risk: Cholesterol levels significantly influenced model predictions.

Microbiome Diversity: Low gut microbiome diversity was an important predictor, and usually it was also related to a high risk for CVD.

Blood Pressure: One of the strongest factors is high blood pressure, which also fits in well with those that have been known to cause the risk for CVD. **Faecalibacterium prausnitzii:** There is this specific gut microbiome species whose effect on the model-produced predictions was identifiable, with its absence linked to increased risk for developing CVD.

5.7 Final Model Selection and Deployment

LightGBM was selected for the final model in deployment based on its performance metrics and feature importance analysis. It performed extremely well in all the evaluation metrics and had high accuracy; thus it stood as the best fit for CVD prediction. The trained model was saved to a .pkl file and then integrated into a Gradio-based interface for real-time predictions.

The Gradio interface provides patients with the functionality of uploading their clinical data, such as age, BMI, cholesterol, and microbiome diversity, so they may receive immediate feedback about their own personal CVD risk. This interactive tool promotes machine learning as a means for individualized risk assessment by health care providers as well as patients.

6 Discussion and Conclusion

6.1 Discussion

Discussion This paper uses a machine learning approach that incorporates both clinical and microbiome features to predict risk for cardiovascular disease. These results demonstrate the potential value of incorporating microbiome information into clinical risk models, which can improve predictive capabilities. Among the models that were evaluated, LightGBM proved to be most efficacious, with an accuracy of 100% and an AUC-ROC score of 1.00. These results support previous work that boosters are effective to be used with difficult data sets, which might consist of categorical and numeric attributes.

An important discovery was how the gut microbiome and particular species like *Faecalibacterium prausnitzii* and *Bacteroides fragilis* influence CVD risk prediction.

Such species played a great role in giving insights in making the decision for the model. Further enriching the interpretability of the model was provided by SHAP analysis, which demonstrated the relative importance of microbiome features against traditional risk factors such as cholesterol and blood pressure. This aligns with emerging research that suggests imbalances in gut bacteria may cause inflammation and other factors leading to CVD.

The study also highlights the advantages of the combination of microbiome research with machine learning to allow for personalized and preventative healthcare solutions. The traditional clinical models, usually based on parameters such as age, BMI, and cholesterol levels, can be significantly enhanced by incorporating microbiome diversity. This interdisciplinary approach offers a more holistic understanding of the interplay between lifestyle, diet, and cardiovascular health, paving the way for innovative, non-invasive screening methods.

This work is an excellent demonstration of the efficiency of the automated feature selection algorithm as well as the performance of LightGBM for its capability to capture non-linear interactions between features, hence placing machine learning on an important position in understanding the complexity of biomedical data sets. Yet, there remains an unbalanced dataset with insufficient inclusion of clinical markers like inflammatory markers that should help the model generalize better.

Future studies should address more complex techniques, deep learning models, or ensemble methods for better predictive accuracy. Longitudinal research and time series analysis might provide greater insights into correlations between the microbiome change and outcomes of cardiovascular health. Lastly, external validation using a diverse population set and clinical real-world practice settings will help determine the strength and applicability of this model.

6.2 Conclusion

The study successfully developed a machine learning-based model for predicting CVD risk by integrating gut microbiome and clinical features. The LightGBM model resulted in the best performance metric, with precision and an AUC-ROC score of 1.00. The addition of microbiome diversity as a feature was found to significantly enhance the predictive capability of traditional clinical models.

The SHAP analysis helped unveil important features; it reasserted the relevance of traditional risk factors and showed the additional power of predictive microbiome features. This interdisciplinarity is the beginning of a gap that closes the gap between microbiome research and machine learning. This will pave the way to more accurate, non-invasive, and tailored screening methods for cardiovascular disease.

The utility of the study is further enhanced by a Gradio interface that has been implemented, allowing health professionals to input data and provide instant feedback on the risk of CVD to patients. Future work would be to expand the dataset, incorporate biomarkers, and validate the model in clinical settings. This research advances our understanding of the gut-heart axis, opening new horizons for preventative and personalized healthcare, which will ultimately translate into better cardiovascular health outcomes globally.

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