Analyzing the impact of feature selection on the accuracy of heart disease prediction

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\begin{abstract}
Heart Disease has become one of the most serious diseases that has a significant impact on human life. It has emerged as one of the leading causes of mortality among the people across the globe during the last decade. In order to prevent patients from further damage, an accurate diagnosis of heart disease on time is an essential factor. Recently we have seen the usage of non-invasive medical procedures, such as artificial intelligence-based techniques in the field of medical. Specially machine learning employs several algorithms and techniques that are widely used and are highly useful in accurately diagnosing the heart disease with less amount of time. However, the prediction of heart disease is not an easy task. The increasing size of medical datasets has made it a complicated task for practitioners to understand the complex feature relations and make disease predictions. Accordingly, the aim of this research is to identify the most important risk-factors from a highly dimensional dataset which helps in the accurate classification of heart disease with less complications. For a broader analysis, we have used two heart disease datasets with various medical features. Firstly, we performed the correlation and inter-
\end{abstract}
dependence of different medical features in the context of heart disease. Secondly, we applied a filter-based feature selection technique on both datasets to select most relevant features (an optimal reduced feature subset) for detecting the heart disease. Finally, various machine learning classification models were investigated using complete and reduced features subset as inputs for experimentation analysis. The trained classifiers were evaluated based on Accuracy, Receiver Operating Characteristics (ROC) curve and F1-Score. The classification results of the models proved that there is a high impact of relevant features on the classification accuracy. Even with a reduced number of features, the performance of the classification models improved significantly with a reduced training time as compared with models trained on full feature set.

Keywords: Heart Disease, Machine Learning, Dimensionality Reduction, Feature Correlation, Feature Selection

1. Introduction

Heart disease is rapidly increasing across the globe. As per a research report published by the World Health Organization (WHO), in 2016 approximately 17.90 million people died from heart disease [1]. This much number accounts for approximately 30% of all deaths worldwide. Nearly 55% of the heart patient die during the first 3 years, and the treatment costs for heart disease are around 4% of the annual healthcare expenditure. [2]. Observing the increasing stats, accurate and timely detection and treatment of this serious illness is very essential for disease prevention and effective utilization of medical resources.

Due to the recent technological advancements, the field of medical sciences has seen a remarkable improvement over time [3, 4]. Specially, machine learning (ML) has been widely used in the field of cardiovascular medicine and has established a potential space [5]. The basic framework of ML is built on models that take input data (such as text or images) and through the usage of some statistical analysis and mathematical optimizations provides the desired
prediction results (e.g., disease, no disease, neutral) [6]. ML models can be trained on tons of raw electronic medical data gathered from low-cost wearable devices to allow efficient heart disease diagnosis with less resources and improved accuracy [7].

During the training process, ML models require a large number of data samples to avoid overfitting [8]. However, the inclusion of the large number of data features is not required for reasons related to the curse of dimensionality [9] [10]. Mostly, medical datasets cover related as well as redundant features. Unnecessary features do not contribute any meaningful information to the prediction task, and also creates noise in the description of target (output class) which leads to prediction errors [11]. Furthermore, such features increase the complexity of ML models and make the system runs slowly due to increased training time. To overcome the curse of dimensionality only those features which are closely related with the target should be selected/identified from datasets and provided as inputs to ML models [12]. Relevant feature selection can aid in performance improvement by decreasing the model complexity and increasing prediction accuracy which is very important in medical diagnosis [13].

Because of the benefits outlined previously, feature selection techniques are being actively used in the area of heart diseases and strokes [14] [15] [16]. The contributions of this research are listed as follows:

• The study uses two datasets of heart disease patients from different sources to cover a broader study of medical features.

• To perform the correlation and interdependence study between different features in datasets with respect to heart disease.

• The identification of the most relevant medical features which aids in the prediction of heart disease using a filter-based feature selection technique.

• Different ML classification models such as Logistic Regression (LR), De-
cision Tree (DT), Naive Bayes (NB), Random Forest (RF), Multi Layer Perceptron (MLP) etc., are used on the datasets to identify the suitable models for the problem.

- The classification models were tested on full as well as the reduced feature subset to observe the impact of feature selection on the performance of models.

- With the spirit of reproducible research, the code of this article is shared in GitHub.

2. Related Work

ML has appeared to be an effective technique for assisting in the heart disease diagnosis, however the high dimensionality of datasets is a fundamental issue for ML prediction models. Feature selection is one of the techniques which is used to select only the most relevant features from datasets features that influence the disease outcome most. The identification of the most important features from the high dimensional datasets is an important aspect that can improve the accuracy of prediction models hence reduce the number of medical injuries.

In [17], Zhang et al. developed an efficient feature selection technique called weighting-and ranking-based hybrid feature selection (WRHFS) to determine the risk of heart stroke. For the weighing and ranking of features, WHRFS used a variety of filter-based feature selection techniques such as fisher score, information gain and standard deviation. The proposed technique selected 9 important input features out of 28 based on the knowledge provided for heart stroke prediction. In another research [18], the authors worked on the extraction of relevant risk factors form a large feature space for an efficient heart disease prediction. The features were selected based on their individual ranks.

[1] https://github.com/Sammyy092/analyzing-the-impact-of-feature-selection-on-heart-disease-prediction
The authors used Latent Feature Selection (ILFS) method to rank the features which is a probabilistic latent graph-based feature selection technique. The results of the model were competitive using only half of the features from the set of 50. In [19], a feature selection model for detecting the risk of heart disease is proposed. The proposed model combined the glow-worm swarm optimization algorithm based on the standard deviation of the features to extract the quality features from a electronic healthcare record (EHR) of a community hospital in Beijing. 6 features including high blood pressure, Alkaline Phosphatase (ALP), age and Lactate Dehydrogenase (LDH) were indicated as important features to detect stroke excluding the family hereditary factors. The authors of [20] focused on finding the most relevant features from EHR to predict the early-stage risk of death from heart disease. The authors used minimum redundancy maximum (mRmR) relevance and recursive feature elimination (RFE) feature selection approaches based on NB for the selection of features. Two medical features i.e., Serum Creatinine and Ejection Fraction were ranked higher by both feature selection technique as compared to other. When provided to a prediction model as input, the selected features proved out to be most important as an overall accuracy of 80% was achieved. Singh et al. [21], proposed an efficient approach for stroke prediction using the Cardiovascular Health Study (CHS) dataset. They used DT algorithm for feature selection and then principal component analysis (PCA) technique for reducing the dimensionality of feature space. Finally, the MLP network was used to construct the classification model. The model trained on the optimal feature set achieved 97.7% accuracy in detecting the stroke and outperformed other techniques in comparison. A wrapper based Genetic Algorithm (GA) is used in [22] to select the most significant features to detect heart disease. The proposed feature selection algorithm identifies 7 features out of 16 to detect heart disease from Cleveland heart disease dataset. The resultant features were supplied to support vector machine (SVM) for the accuracy evaluation. The classifier acquired 88.34% using the reduced feature set whereas only 83.34% was achieved when using whole dataset features. In terms of ROC
curve, the GA-SVM performed well also when compared with the various existing feature selection algorithms also. This study [23] proposes a new heart disease prediction model by combining ML with deep learning techniques. The least absolute shrinkage and selection operator (LASSO) penalty method based on LinearSVC was applied as the feature selection module to generate a feature subset closely related to target. 12 most relevant features were chosen from dataset obtained from Kaggle and inputted to the MLP network. As per the experimental results, the proposed model obtained an accuracy of 98.56% with 99.35% recall and 97.84% precision. In [5], a ML based heart disease diagnosis system is proposed. Seven popular classifiers LR, k-Nearest Neighbor (K-NN), MLP, SVM, NB, DT, and RF were used for the classification of heart disease patients. Three feature selection algorithms RelieF, mRMR, and LASSO were used to select highly correlated features with target class. It was observed that the classification performance of models increased in terms of accuracy and computation time using the feature selection techniques. The LR model showed best accuracy of 89% when used with RelieF.

The main objective of this research [24] was to predict the heart disease using minimal subset of features and adequate accuracy. To achieve this objective, the authors employed a two-stage feature subset retrieving technique. Three popular feature selection techniques i.e., (embedded, filter, wrapper) were used to extract a feature subset based on a boolean process-based common “True” condition. To select the suitable prediction model, RF, SVM, K-NN, NB, XGBoost and MLP models were trained on the data. The experimental results showed that XGBoost classifier integrated with wrapper technique provided the best prediction results for heart disease. A comparative analysis of different classifiers was performed in [25] for the classification of the heart disease with minimal attributes. ML classifiers such as NB, LR, sequential minimal optimization (SMO), RF etc., were trained for the accurate detection of heart disease. To obtain the optimal feature subset, RelieF, chi-squared and correlation-based feature subset evaluator were utilized. 10 features were selected from the set of 13 to train the classifiers. The SMO classifier achieved
the highest accuracy of 86.468% when inputted with the optimal feature set obtained by chi-squared feature selection technique. Despite their relevance, one major drawback of existing works on heart disease prediction is the lack of systematic guidance when selecting the input features for the development of prediction models which is an important aspect in terms of predictive performance. Previous research proposals chose features mostly in an impromptu manner without incorporating latest medical research findings. Mostly the focus is on the prediction models and their final prediction performance. However, a very less attention is paid on the correlation between different medical features and their individual importance in the prediction of heart disease. A few works present analysis of medical features but for the purpose of heart disease detection only. This research aims at addressing the ineffective feature selection in previous studies on heart disease prediction. Two heart disease patient datasets collected from different sources were utilized in this research to cover a broader study of features related to heart disease and to identify various medical procedures. To further analyze the role of each parameter in the prediction task, we obtain the interdependence and importance of the collected set of medical features. A detailed analysis of ML models trained on both full and selected feature set is provided to analyze the impact of feature selection techniques on the prediction performance as well as the identification of suitable classifiers for the specified problem.

3. Proposed Methodology

This research paper highlights the importance feature selection in the accurate classification of heart disease. Figure 1 demonstrates the workflow of the proposed methodology for heart disease prediction.

3.1. Datasets

In this research, two datasets named as cardiovascular disease (CVD) and Framingham were utilized to study the impact of different features on the occurrence of heart disease and to develop ML-based system for heart disease prediction.
Figure 1: Flowchart of the proposed methodology describing each step for heart disease prediction.

detection. The study uses two datasets to cover a broader study of medical features and various clinical pathways used for the detection of heart stroke. The datasets were collected from different sources. The datasets contained some main medical features like ‘age’, ‘hypertension’, ‘glucose levels’, ‘blood pressure’, ‘cholesterol’ etc. which are closely related to the occurrence of disease and provides a great flexibility for heart disease analysis. The datasets were chosen based on two criteria. The first criterion was the variance in the medical procedures, so to study the different medical procedures and the role of each feature in the context of heart disease. Secondly, the datasets were chosen based on the data availability. Datasets from different sources possess different amount of data and collection of features. So, we have chosen datasets which were offering a good volume of data and having a level of simi-
larity in terms of features.

3.1.1. CVD

The CVD dataset is controlled by McKinsey & Company which was a part of their healthcare hackathon\(^2\). The dataset can be accessible from a free dataset repository\(^3\). The collected dataset included 29072 patient observation with 12 data features. 11 of them are the common clinical symptoms and are considered as input features whereas the 12th feature ‘stroke’ is the target feature indicating whether a patient has had stroke or not. The complete description of data features for CVD dataset is given in Table 1.

3.1.2. Framingham

The Framingham dataset was created during an ongoing cardiovascular study involving the residents of Framingham, Massachusetts, and is available at the Kaggle website\(^4\). The dataset is mostly used in classification tasks to identify whether a patient has a chance to develop coronary heart disease (CHD) in 10 years. The dataset contains 4,240 patient records and 15 features, where each feature indicates a risk factor. 14 input features were used to detect the decisional feature i.e., 10-year risk of CHD. Table 2 shows the description about the data features in Framingham dataset.

3.2. Pre-Processing

Data pre-processing is one of the important part of ML life cycle as it makes data analysis easy and increases the accuracy and speed of the ML algorithms \(^26\). We applied some pre-processing steps as the collected dataset were having missing values and class imbalance problems. Referring the CVD dataset, the dataset contained a total of 43400 patient records out of which 14754 values

\(^2\)https://datahack.analyticsvidhya.com/contest/mckinsey-analyticsonline-hackathon/
\(^3\)https://inclass.kaggle.com/asaumya/healthcare-dataset-stroke-data
\(^4\)https://www.kaggle.com/amanaajmera1/framingham-heart-study-dataset
| Attribute         | Description |
|-------------------|-------------|
| i.d               | patient’s i.d |
| gender            | includes ("male": 0, "female": 1, "other": 2) |
| age               | patient’s age (continuous) |
| hypertension      | suffering from hypertension ("yes":1, "no":0) |
| heart_disease     | suffering heart disease ("yes":1, "no":0) |
| ever_married      | marital status of patient ("yes":1, "no":0) |
| work_type         | job status ("children":0, "govt_job":1, "never_worked":2, "private":3, "self_employed":4) |
| residence_type    | ("rural":0, "urban":1) |
| avg_glucose_level | average glucose level of blood (continuous) |
| bmi               | body mass index (decimal value) |
| smoking_status    | ("never smoked":0, "formerly smoked":1, "smokes":2) |
| stroke            | ("yes":1, "no":0) |

Table 1: Description of features CVD dataset
| Attribute       | Description                                                                 |
|-----------------|----------------------------------------------------------------------------|
| age             | patient's age (continuous)                                                 |
| male            | ("male":0, "female":1)                                                   |
| education       | level of education (1 to 4)                                                |
| currentSmoker   | ("smoker":1, "non smoke":0)                                               |
| CigsPerDay      | average number of ciggerates consumed per day (continuous)                 |
| BPMeds          | on blood pressure medication ("yes":1, "no":0)                            |
| prevalentStroke | previous stroke history ("yes": 1, "no":0)                                |
| prevalenHyp     | hypertensive ("yes":1, "no":0)                                            |
| diabetes        | previous diabetes history("yes":1, "no":0)                               |
| totCHol         | cholestrol level (continuous)                                              |
| sysBP           | systolic blood pressure (decimal)                                          |
| diaBP           | diastolic blood pressure (decimal)                                         |
| BMI             | body mass index (decimal)                                                  |
| HeartRate       | heart rate measure (continuous)                                            |
| glucose         | glucose level (continuous)                                                 |
| TenYearCHD      | target ("yes": 1, "no": 0)                                                |

Table 2: Description of features Framingham dataset
were missing or null. Whereas, 4240 patient records were available for Framingham dataset of which 645 values were null. A null value does not necessarily mean that the value does not exist, but it is unknown. In medical datasets, mostly the null or missing value is usually due to a lack of collection or the practitioner may not consider the observation since the medical test is considered to be low yield for the patient. Data imputation methods are useful in handling the missing data, however their usage in medical field is limited and specific efficacy for disease detection is not clear [27]. Most of the times, researchers do not consider the observations with missing values and drop the incomplete cases intentionally, since the traditional data imputation methods are not sufficient to capture the missing data complexities in health care applications [28, 29]. However, only a deep knowledge of specific disease will likely aid in the selection of the suitable data imputation methods. As per the mentioned analysis, we dropped all the observations with null value from both the datasets to avoid any accuracy biases.

Furthermore, looking at the class distribution, both datasets were highly unbalanced in nature. Only 548 patients out of 29,072 in CVD dataset had stroke conditions, whereas 28,524 patients had no occurrence of stroke. In Framingham dataset, only 557 patient records showed the risk of CHD out of 3101. The unbalanced nature of the datasets leads to classification errors during the training of ML models [30]. As a result, we adopted a ’Random Down-Sampling’ technique to mitigate the adverse effects caused by unbalanced data. We made two classes referred as ‘minority’ and ‘majority’ classes. The patients with heart disease were included in minority class, whereas the patients having no symptoms were included in majority class. In the case of CVD dataset, 548 observations were included into the minority class and the remaining 28,524 were considered as majority class. We created a balanced dataset of 1096 observations by selecting all 548 observations from minority class and 548 random observations from a total of 28,524 majority cases. Same process was performed for Framingham dataset where 557 random observations from 3101 majority cases were derived making a total of 1114 obser-
vations in a balanced dataset shape. In this way, two balanced datasets were made to study the features importance and disease classification in an efficient manner.

3.3. Feature Correlation Analysis

Feature correlation is a method which helps in understanding the underlying relationships between various data features present in a dataset. Feature correlation can be useful in many ways such as determining the interdependencies between the data features and how each feature effects the output feature [31]. We obtained the correlation values between the data features by calculating the correlation coefficients of the feature matrix $M$ having dimension $p \times q$, denoted as: $M = [v_1, v_2, \ldots, v_q]$, where $v_1, v_2, \ldots, v_q$ are the vectors having $q$ number of features. $p$ indicates the length of the vector, where each vector is a complete medical procedure at a specific time. The computed correlation values between different medical features and the target disease for each dataset are shown Figure 2.

As we can see from the Figure 2 of the 11 features of CVD dataset 4 features are having a positive correlation with the decision feature i.e., ‘stroke’. Fea-
features 'age', 'hypertension', 'heart_disease' and 'avg_glucose_lvl' are having values 0.57, 0.24, 0.27 and 0.2 when correlated with 'stroke' showing a significant correlation. Similarly, for framingham dataset, features 'age', 'sysBP', 'prevalentHyp', 'diabBP' and 'glucose' showed positive values of 0.23, 0.22, 0.18, 0.15 and reflect the motif of the desired output feature 'TenYearCHD'. For both the datasets, features like 'gender', 'bmi', 'heart rate' and other non-medical features like smoking habits, education, social status and living standards showed very less correlation with the output feature having no or very less effect on the output. Overall, the common medical features like 'age', 'hypertension' and 'glucose' in both datasets are closely related with the outcome and can be considered as the important risk factors.

As per medical research findings, with aging, major changes can be observed in the heart and blood vessels. For example, the heartbeat rate is not as fast during any physical activity as it could when you are younger. The age-related changes may raise a person’s risk of heart disease according to National Heart, Lung, and Blood Institute Trusted Source [32]. Hypertension is an established risk factor for stroke, ischemic heart disease and renal dysfunction [33]. Hypertension causes the blood pressure over the normal range. The higher blood pressure levels make the arteries less elastic and decreases the oxygen and blood flow towards the heart which potentially leads to a heart disease. The diabetic patients are more likely to develop heart disease at an earlier stage. High blood glucose from diabetes causes stronger contraction of blood vessels that control your heart and blood vessels which leads to heart disease [34]. Over time, this process can lead to a heart stroke.

3.4. Feature Selection

The main motivation of this research is to select the medical features that can improve the accuracy of heart disease prediction. Feature selection is the process of selecting a subset of most relevant features from a larger collection of original features, that influence the outcome most. The advantages of feature selection include: data quality improvement, less computational time by pre-
diction model, predictive performance improvement and efficient data collection process.

In this work we have used a filter-based feature selection technique namely, ANOVA-F test to identify most important features from both datasets. Filter-based feature selection techniques employ the use of statistical methods such as similarity, dependence, information, distance to point out the important dependencies or correlation between the input and the target features [35].

Analysis of Variance (ANOVA) is a collection of parametric statistical models and their estimation procedures that determines if the means of two or more samples of data originate from the same distribution. F-test also known as F-statistic, is a set of statistical tests that uses some statistical techniques to calculate the ratio of variance values such variance of two separate samples etc. The ANOVA method is a type of F-statistic referred here as an ANOVA f-test. It is a univariate statistical test where each feature is compared to the target feature, to see whether there is any statistically significant relationship between them [36]. Mostly, ANOVA is used in such classification tasks where the type of input features is numerical the target feature is categorical.

The ANOVA-F test can be implemented in python language using the f_classif() function provided by scikit-learn library. The f_classif() function is used in selecting the most important features (features with largest values) via the SelectKBest class. SelectKBest is a method made available in the scikit-learn which takes a scoring function and ranks the features by these scores. Here The scoring function is f_classif() i.e., ANOVA-F test and we have defined SelectKBest class to identify most important features from datasets. The equation to obtain ANOVA-F values is given below:

\[
\text{variance\_between\_groups} = \frac{\sum_{i=1}^{J} j_i (\bar{K}_i - \bar{K})^2}{(S - 1)}
\]

\[
\text{variance\_within\_groups} = \frac{\sum_{i=1}^{S} \sum_{p=1}^{j_i} (K_{ip} - \bar{K}_i)^2}{(N - S)}
\]
\[ F_{\text{value}} = \frac{\text{variance\_between\_groups}}{\text{variance\_within\_groups}} \]

where \( N \) is the overall sample size, \( S \) is the number of groups, \( j_i \) is the number of observations in the \( jth \) group, \( \bar{K}_i \) is the \( ith \) group sample mean, \( \bar{K} \) is the overall mean of the data, \( K_{ip} \) is the \( pth \) observation in the \( ith \) out of \( S \) groups.

Figure 3: Feature importance scores for each feature in both datasets.

The feature importance scores obtained using the ANOVA-F test are shown in figure 3 (a) and (b) for both datasets. According to the statistics in figure 3 (a), the most important features for predicting ‘stroke’ are ‘age’, ‘hypertension’, ‘heart\_disease’ and ‘avg\_glucose\_lvl’ possessing suitable scores when related with the outcome. However, features ‘gender’, ‘bmi’, ‘residence\_type’ and ‘smoking\_status’ showed less or 0 significance for the feature ‘stroke’. Looking at 3 (b), we can observe that features ‘age’, ‘prevalentHyp’, ‘diabetes’, ‘sysBP’, ‘diaBP’ and ‘glucose’ obtains highest scores as compared to the other features of the dataset when related to ‘TenYearCHD’. Looking at the importance values of the features for each dataset, we can observe a similarity with the correlation results listed in section 3.3 i.e., in most cases the features related with age, hypertension, glucose, blood pressure has a significant influence in the prediction of the heart disease. Similarly, the features identified using ANOVA-F test are also listed as the potential risk factors for heart disease as cited by the American Heart Association.
4. Evaluation Matrices

We have used three popular performance evaluation metrics \( i.e., \) Accuracy, F1-score and ROC to evaluate the performance of ML classification models \([38]\). Confusion matrix is a table that helps ML practitioners to describe the performance of a classification model. Confusion matrix consists of four used to determine the performance matrices of a classifier and can be described as (1) True Positive (\( TP \)) test result that correctly classify the presence of heart disease in patient, (2) True Negative (\( TN \)) test result that correctly classify the absence of heart disease in patient, (3) False Negative (\( FN \)) test result that wrongly classify that a particular patient does not have heart disease and (4) False Positive (\( FP \)) test result which wrongly classify that a particular patient has heart disease. In medical field, \( FN \) are considered as most harmful predictions. For a given dataset of size \( n \), accuracy is measured as

\[
\text{Accuracy} = \frac{(TP + TN)}{(TP + FP + FN + TN)}
\]

F1-Score is the harmonic mean of Precision and Recall.

\[
\text{Precision} = \frac{TP}{(TP + FP)}
\]

\[
\text{Recall} = \frac{TP}{(TP + FN)}
\]

\[
F1 - \text{Score} = \frac{2(Precision \times Recall)}{(Precision \times Recall)}
\]

The Receiver Optimistic Curves (ROC) examine the classification capability of a classification model. It evaluates the “true positive rate” and “false positive rate” in a ML model output.

\[
TPR = \frac{TP}{(TP + FN)}
\]

\[
FPR = \frac{FP}{(FP + TN)}
\]
5. Results and Discussions

In this section, we will discuss the performance of the selected classification models from different perspectives. First, we checked the performance of model individually for both datasets with full features to examine which models work well for each dataset. Secondly, we evaluated the performance of the models on the selected set of feature to analyze the effect of feature selection technique on the accuracy of the classifiers. The classifiers performance was checked using the Accuracy, F1-score and ROC evaluation matrices.

5.1. Classification results using full feature set

In this section, all the ML models were tested on both datasets using full set of features to predict the binary disease outcome. We trained all the prediction models on entire data with 80% training and 20% testing subsets. The overall computational time consumed during the training of prediction models was 10.98 iterations per second (it/s) for CVD dataset and 24.20 iterations per second (it/s) using framingham dataset. Table 3 and 4 shows the binary classification results of the ML model in predicting the heart disease for both datasets.

Looking at the classification results listed in Table 3, the highest accuracy reported was 0.73 achieved by MLP for CVD dataset with ROC of 0.74 and F1-Score of 0.73. Along with MLP other classifiers like LR, SVC and RF worked well and provided reasonable prediction accuracy with full feature set. The reason behind the improved accuracy achieved by MLP is that it is good at discovering patterns from complex medical datasets. Furthermore, this network model is good at generalizing data without having the prior domain knowledge. The worst results were obtained by the dummy classifier i.e., only a 0.46 accuracy when predicting heart stroke. Possible reasons behind poor classification result is that the dummy classifier makes predictions using simple rules which is not useful when dealing with real world problems. The classification results with the same techniques for the framingham dataset
| Model                             | Accuracy | Balanced Accuracy | ROC AUC | F1-Score |
|----------------------------------|----------|-------------------|---------|----------|
| Perceptron                       | 0.73     | 0.74              | 0.74    | 0.73     |
| SGD Classifier                   | 0.72     | 0.73              | 0.73    | 0.71     |
| Logistic Regression              | 0.73     | 0.73              | 0.73    | 0.73     |
| Quadratic Discriminant Analysis  | 0.72     | 0.73              | 0.73    | 0.72     |
| Linear SVC                       | 0.72     | 0.72              | 0.72    | 0.72     |
| SVC                              | 0.71     | 0.72              | 0.72    | 0.71     |
| Nu SVC                           | 0.71     | 0.72              | 0.72    | 0.71     |
| Nearest Centroid                 | 0.71     | 0.72              | 0.72    | 0.71     |
| Calibrated Classifier CV         | 0.71     | 0.72              | 0.72    | 0.71     |
| Bernoulli NB                     | 0.71     | 0.72              | 0.72    | 0.71     |
| Gaussian NB                      | 0.71     | 0.71              | 0.71    | 0.71     |
| Passive Aggressive Classifier    | 0.71     | 0.71              | 0.71    | 0.71     |
| Ridge Classifier CV              | 0.70     | 0.71              | 0.71    | 0.70     |
| Ridge Classifier                 | 0.70     | 0.71              | 0.71    | 0.70     |
| Linear Discriminant Analysis     | 0.70     | 0.71              | 0.71    | 0.70     |
| Random Forest Classifier         | 0.70     | 0.70              | 0.70    | 0.70     |
| AdaBoost Classifier              | 0.70     | 0.70              | 0.70    | 0.70     |
| KNeighbors Classifier            | 0.69     | 0.69              | 0.69    | 0.69     |
| Bagging Classifier               | 0.68     | 0.68              | 0.68    | 0.68     |
| Extra Tree Classifier            | 0.66     | 0.66              | 0.66    | 0.66     |
| LGBM Classifier                  | 0.65     | 0.66              | 0.66    | 0.65     |
| XGB Classifier                   | 0.65     | 0.65              | 0.65    | 0.65     |
| Decision Tree Classifier         | 0.61     | 0.61              | 0.61    | 0.61     |
| Label Spreading                  | 0.60     | 0.60              | 0.60    | 0.60     |
| Label Propagation                | 0.60     | 0.59              | 0.59    | 0.60     |
| Dummy Classifier                 | 0.46     | 0.46              | 0.46    | 0.46     |

Table 3: Classification results of various ML models for CVD dataset using full feature set
| Model                      | Accuracy | Balanced Accuracy | ROC AUC | F1-Score |
|----------------------------|----------|-------------------|---------|----------|
| Linear SVC                 | 0.66     | 0.67              | 0.67    | 0.66     |
| Linear Discriminant Analysis | 0.66     | 0.67              | 0.67    | 0.66     |
| Calibrated Classifier CV   | 0.66     | 0.67              | 0.67    | 0.66     |
| Ridge Classifier CV        | 0.66     | 0.67              | 0.67    | 0.66     |
| Ridge Classifier           | 0.66     | 0.67              | 0.67    | 0.66     |
| Logistic Regression        | 0.65     | 0.66              | 0.66    | 0.65     |
| Nearest Centroid           | 0.64     | 0.66              | 0.66    | 0.64     |
| KNeighbors Classifier      | 0.64     | 0.65              | 0.65    | 0.64     |
| Random Forest Classifier   | 0.64     | 0.65              | 0.65    | 0.64     |
| Bernoulli NB               | 0.63     | 0.64              | 0.64    | 0.63     |
| LGBM Classifier            | 0.63     | 0.64              | 0.64    | 0.63     |
| AdaBoost Classifier        | 0.63     | 0.64              | 0.64    | 0.63     |
| Extra Tree Classifier      | 0.62     | 0.63              | 0.63    | 0.62     |
| XGB Classifier             | 0.62     | 0.63              | 0.63    | 0.61     |
| Decision Tree Classifier   | 0.61     | 0.62              | 0.62    | 0.61     |
| Bagging Classifier         | 0.60     | 0.61              | 0.61    | 0.59     |
| SGD Classifier             | 0.60     | 0.60              | 0.60    | 0.60     |
| Gaussian NB                | 0.57     | 0.60              | 0.60    | 0.53     |
| Passive Aggressive Classifier | 0.58   | 0.59              | 0.59    | 0.57     |
| Nu SVC                     | 0.59     | 0.59              | 0.59    | 0.59     |
| Extra Tree Classifier      | 0.59     | 0.59              | 0.59    | 0.59     |
| SVC                        | 0.58     | 0.58              | 0.58    | 0.58     |
| Quadratic Discriminant Analysis | 0.55   | 0.58              | 0.58    | 0.51     |
| Perceptron                 | 0.57     | 0.55              | 0.55    | 0.55     |
| Label Propagation          | 0.54     | 0.54              | 0.54    | 0.53     |
| Label Spreading            | 0.53     | 0.53              | 0.53    | 0.53     |
| Dummy Classifier           | 0.52     | 0.52              | 0.52    | 0.52     |

Table 4: Classification results of various ML models for Framingham dataset using full feature set.
are shown in Table 4. The accuracy results were not very good as the highest accuracy achieved was 0.66 with 0.67 ROC and 0.66 F1-score. Other algorithms like Linear Discriminant Analysis (LDA), LR and ridge classifier performed the similar. The reason behind weak results might be the range of values between the data features. Feature scaling helps in normalizing the data within a particular range, which can improve the results of the models in general [39, 40]. However, any data manipulation strategy in medical studies may introduce significant biases, that is why we have kept all the feature values unchanged.

5.2. Classification results using reduced feature set

Given the goal of identifying the potential bio-markers and to analyze the impact of feature selection technique on the classification accuracy, we selected the most prominent features from the full feature space based on individual feature scores. The features impacting the outcome most for each dataset were identified by ANOVA-F test as shown in Figure 3 (a) and (b). As per the feature scores, 4 features i.e., \{age, hypertension, heart_disease, avg_glucose_lvl\} were selected for CVD dataset out of 11. Only 5 features out of 15 from framingham dataset i.e., \{age, prevalentHyp, sysBp, diaBp, glucose\} were chosen considering the feature weights obtained using ANOVA-F test. We evaluated the performance of each classification model using only the selected features as inputs. Table 5 shows the classification performance of each model using the reduced feature subset from CVD dataset. The analysis showed that even after limiting the number of features, ML models showed better performance as compared to the models using full feature set. The highest accuracy achieved was 0.74 by SVC model with 0.74 F1-Score and 0.74 ROC with only 4 input features. Considering Table 6 results, the highest accuracy achieved is 0.71, which is higher than all the accuracy results using full feature set for framingham dataset. Furthermore, the models trained on reduced feature set also consumed less computational time i.e. only 3.86 iterations per second(it/s) using CVD and 15.52 iterations per second(it/s) using
framingham dataset. We have also validated our findings by comparing our work with other published proposals [41, 42] where same datasets were used with full feature set and the obtained accuracy results were less or equal to the results that we obtained using reduced feature set. Overall, the experimental results proved that the performance of the ML models increased significantly by using only the relevant features. Furthermore, during the training of classification models using the reduced feature set, a less computational iterations per second (it/s) were observed. These experimental results clear the concepts about the impact of feature selection techniques, that it not only reduces the size feature space, but it also improves performance of ML models also in various aspects.

6. Conclusion and Future Works

Heart disease is the most fatal disease which is rapidly increasing and became one of the causes of death around the world. The damage caused by this disease can be reduced significantly, if adequate treatment procedures are applied at the early stages. This paper studies the prediction of heart disease and the selection of the important features. The main goal of this research study is to observe the impact of feature selection techniques on the performance of ML models. This analysis was performed for CVD and Framingham heart disease datasets which are available online. In this research, first, we performed a data pre-processing step in which data transformation, cleansing and balancing were involved. Secondly, we used a filter-based feature selection technique namely the ANOVA-F test to identify the most important features from the datasets for an effective heart disease prediction. Using the ANOVA-F test most relevant features with outcomes from both datasets were identified using the individual feature scores. We observed that features like age, hypertension, glucose, previous heart disease, and blood pressure were found to reflect the most important risk factors for heart disease except the traditional factors using both datasets. Furthermore, the classification experiments were
| Model                        | Accuracy | Balanced Accuracy | ROC AUC | F1-Score |
|------------------------------|----------|-------------------|---------|----------|
| SVC                          | 0.74     | 0.75              | 0.74    | 0.74     |
| Nearest Centroid             | 0.74     | 0.75              | 0.74    | 0.74     |
| Logistic Regression          | 0.73     | 0.74              | 0.73    | 0.73     |
| SGD Classifier               | 0.73     | 0.73              | 0.73    | 0.73     |
| Linear SVC                   | 0.72     | 0.73              | 0.72    | 0.73     |
| Linear Discriminant Analysis | 0.72     | 0.73              | 0.72    | 0.73     |
| Ridge Classifier CV          | 0.72     | 0.73              | 0.72    | 0.73     |
| Ridge Classifier             | 0.72     | 0.73              | 0.72    | 0.73     |
| Quadratic Discriminant Analysis | 0.72     | 0.73              | 0.72    | 0.72     |
| Calibrated Classifier CV     | 0.72     | 0.73              | 0.72    | 0.72     |
| Label Spreading              | 0.71     | 0.71              | 0.71    | 0.71     |
| Bagging Classifier           | 0.70     | 0.70              | 0.70    | 0.70     |
| AdaBoost Classifier          | 0.70     | 0.71              | 0.70    | 0.71     |
| Label Propagation            | 0.70     | 0.70              | 0.70    | 0.70     |
| Bernoulli NB                 | 0.70     | 0.70              | 0.70    | 0.70     |
| Nu SVC                       | 0.70     | 0.70              | 0.70    | 0.70     |
| LGBM Classifier              | 0.70     | 0.70              | 0.70    | 0.70     |
| Extra Trees Classifier       | 0.69     | 0.70              | 0.69    | 0.69     |
| XGB Classifier               | 0.69     | 0.70              | 0.69    | 0.69     |
| Random Forest Classifier     | 0.69     | 0.70              | 0.69    | 0.69     |
| Guassian NB                  | 0.69     | 0.69              | 0.69    | 0.69     |
| Decision Tree Classifier     | 0.68     | 0.69              | 0.68    | 0.69     |
| Etra Tree Classifier         | 0.68     | 0.69              | 0.68    | 0.69     |
| KNeighbors Classifier        | 0.67     | 0.68              | 0.67    | 0.68     |
| Perceptron                   | 0.64     | 0.64              | 0.64    | 0.64     |
| Passive Aggressive Classifier| 0.63     | 0.63              | 0.63    | 0.63     |
| Dummy Classifier             | 0.50     | 0.50              | 0.50    | 0.50     |

Table 5: Classification results of various ML models for CVD dataset using reduced feature set
| Model                     | Accuracy | Balanced Accuracy | ROC AUC | F1-Score |
|--------------------------|----------|------------------|---------|----------|
| Perceptron               | 0.71     | 0.72             | 0.72    | 0.71     |
| AdaBoost Classifier      | 0.71     | 0.71             | 0.71    | 0.71     |
| SGD Classifier           | 0.69     | 0.69             | 0.69    | 0.69     |
| Logistic Regression      | 0.69     | 0.69             | 0.69    | 0.69     |
| Bernoulli NB             | 0.68     | 0.69             | 0.69    | 0.68     |
| Linear Discriminant Analysis | 0.68 | 0.68             | 0.68    | 0.68     |
| Ridge Classifier CV      | 0.68     | 0.68             | 0.68    | 0.68     |
| Ridge Classifier         | 0.68     | 0.68             | 0.68    | 0.68     |
| Linear SVC               | 0.68     | 0.68             | 0.68    | 0.68     |
| Calibrated Classifier CV | 0.68     | 0.68             | 0.68    | 0.68     |
| Gaussian NB              | 0.66     | 0.68             | 0.68    | 0.65     |
| SVC                      | 0.67     | 0.67             | 0.67    | 0.67     |
| Nearest Centroid         | 0.66     | 0.67             | 0.67    | 0.66     |
| KNeighbors Classifier    | 0.65     | 0.66             | 0.66    | 0.65     |
| Bagging Classifier       | 0.63     | 0.64             | 0.64    | 0.63     |
| Quadrant Discriminant Analysis | 0.62 | 0.64             | 0.64    | 0.58     |
| Decision Tree Classifier | 0.62     | 0.62             | 0.62    | 0.61     |
| Extra Tree Classifier    | 0.62     | 0.62             | 0.62    | 0.62     |
| Random Forest Classifier | 0.62     | 0.62             | 0.62    | 0.62     |
| Label Spreading          | 0.59     | 0.59             | 0.59    | 0.59     |
| Label Propagation        | 0.58     | 0.58             | 0.58    | 0.58     |
| LGBM Classifier          | 0.57     | 0.58             | 0.58    | 0.57     |
| Nu SVC                   | 0.57     | 0.58             | 0.58    | 0.57     |
| XGB Classifier           | 0.57     | 0.57             | 0.57    | 0.57     |
| Passive Agressive Classifier | 0.57 | 0.56             | 0.56    | 0.57     |
| Dummy Classifier         | 0.55     | 0.56             | 0.56    | 0.55     |
| Extra Tree Classifier    | 0.51     | 0.51             | 0.51    | 0.51     |

Table 6: Classification results of various ML models for framingham dataset using reduced feature set
performed with full as well as the reduced feature sets to analyze the effect of selected features on the prediction accuracy of various ML prediction models. Using the full feature set the highest accuracy achieved was 0.73 for CVD and 0.66 for the Framingham heart disease dataset. After using the reduced feature set the accuracy increased to 0.75 and 0.71 for both datasets. The analysis showed that even after limiting the number of features, ML models showed better performance as compared to the models using a full feature set. The experimental results reveal that by employing a feature selection technique, we may accurately classify the heart disease even with a small number of features and less time. We can conclude that using the feature selection only the most important features related to heart disease are selected which reduces the computational complexities and improve the accuracy of prediction models. In the intended future work, we will try to work on enhancing the prediction accuracy by using a vast combination of ML and deep learning models [43] to obtain the best feasible model for the heart disease diagnosis. We will benchmark our analysis on additional datasets as a part of our future work. We will also try to use more than one feature selection technique to obtain more feasible feature subsets which are more direct with medical studies.

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References

[1] S. Nalluri, R. V. Saraswathi, S. Ramasubbarreddy, K. Govinda, E. Swetha, Chronic heart disease prediction using data mining tech-
niques, in: Data engineering and communication technology, Springer, 2020, pp. 903–912.

[2] R. A. Manji, J. Witt, P. S. Tappia, Y. Jung, A. H. Menkis, B. Ramji-awan, Cost–effectiveness analysis of rheumatic heart disease prevention strategies, Expert review of pharmacoeconomics & outcomes research 13 (6) (2013) 715–724.

[3] P. Saranya, P. Asha, Survey on big data analytics in health care, in: 2019 International Conference on Smart Systems and Inventive Technology (ICSSIT), IEEE, 2019, pp. 46–51.

[4] G. Sivapalan, K. K. Nundy, S. Dev, B. Cardiff, D. John, ANNet: a lightweight neural network for ecg anomaly detection in IoT edge sensors, IEEE Transactions on Biomedical Circuits and Systems 16 (1) (2022) 24–35.

[5] A. U. Haq, J. P. Li, M. H. Memon, S. Nazir, R. Sun, A hybrid intelligent system framework for the prediction of heart disease using machine learning algorithms, Mobile Information Systems 2018 (2018).

[6] A. Gavhane, G. Kokkula, I. Pandya, K. Devadkar, Prediction of heart disease using machine learning, in: 2018 second international conference on electronics, communication and aerospace technology (ICECA), IEEE, 2018, pp. 1275–1278.

[7] N. K. Kumar, G. S. Sindhu, D. K. Prashanthi, A. S. Sulthana, Analysis and prediction of cardio vascular disease using machine learning classifiers, in: 2020 6th International Conference on Advanced Computing and Communication Systems (ICACCS), IEEE, 2020, pp. 15–21.

[8] S. Yeom, I. Giacomelli, M. Fredrikson, S. Jha, Privacy risk in machine learning: Analyzing the connection to overfitting, in: 2018 IEEE 31st Computer Security Foundations Symposium (CSF), IEEE, 2018, pp. 268–282.
[9] O. O. Aremu, D. Hyland-Wood, P. R. McAree, A machine learning approach to circumventing the curse of dimensionality in discontinuous time series machine data, Reliability Engineering & System Safety 195 (2020) 106706.

[10] S. Manandhar, S. Dev, Y. H. Lee, S. Winkler, Y. S. Meng, Systematic study of weather variables for rainfall detection, in: Proc. International Geoscience and Remote Sensing Symposium (IGARSS), 2018.

[11] V. Pavithra, V. Jayalakshmi, Review of feature selection techniques for predicting diseases, in: 2020 5th International Conference on Communication and Electronics Systems (ICCES), IEEE, 2020, pp. 1213–1217.

[12] J. Cai, J. Luo, S. Wang, S. Yang, Feature selection in machine learning: A new perspective, Neurocomputing 300 (2018) 70–79.

[13] G. Wang, F. Lauri, A. H. El Hassani, A study of dimensionality reduction’s influence on heart disease prediction, in: 2021 12th International Conference on Information, Intelligence, Systems & Applications (IISA), IEEE, 2021, pp. 1–6.

[14] B. Remeseiro, V. Bolon-Canedo, A review of feature selection methods in medical applications, Computers in biology and medicine 112 (2019) 103375.

[15] M. S. Pathan, Z. Jianbiao, D. John, A. Nag, S. Dev, Identifying stroke indicators using rough sets, IEEE Access 8 (2020) 210318–210327.

[16] C. S. Nwosu, S. Dev, P. Bhardwaj, B. Veeravalli, D. John, Predicting stroke from electronic health records, in: 2019 41st Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC), IEEE, 2019, pp. 5704–5707.

[17] Y. Zhang, Y. Zhou, D. Zhang, W. Song, A stroke risk detection: improving hybrid feature selection method, Journal of medical Internet research 21 (4) (2019) e12437.
[18] H. M. Le, T. D. Tran, L. Van Tran, Automatic heart disease prediction using feature selection and data mining technique, Journal of Computer Science and Cybernetics 34 (1) (2018) 33–48.

[19] Y. Zhang, W. Song, S. Li, L. Fu, S. Li, Risk detection of stroke using a feature selection and classification method, IEEE Access 6 (2018) 31899–31907.

[20] M. Al Mehedi Hasan, J. Shin, U. Das, A. Yakin Srizon, Identifying prognostic features for predicting heart failure by using machine learning algorithm, in: 2021 11th International Conference on Biomedical Engineering and Technology, 2021, pp. 40–46.

[21] M. S. Singh, P. Choudhary, Stroke prediction using artificial intelligence, in: 2017 8th Annual Industrial Automation and Electromechanical Engineering Conference (IEMECON), IEEE, 2017, pp. 158–161.

[22] C. B. Gokulnath, S. Shantharajah, An optimized feature selection based on genetic approach and support vector machine for heart disease, Cluster Computing 22 (6) (2019) 14777–14787.

[23] D. Zhang, Y. Chen, Y. Chen, S. Ye, W. Cai, J. Jiang, Y. Xu, G. Zheng, M. Chen, Heart disease prediction based on the embedded feature selection method and deep neural network, Journal of Healthcare Engineering 2021 (2021).

[24] N. Hasan, Y. Bao, Comparing different feature selection algorithms for cardiovascular disease prediction, Health and Technology 11 (1) (2021) 49–62.

[25] K. V. V. Reddy, I. Elamvazuthi, A. A. Aziz, S. Paramasivam, H. N. Chua, S. Pranavanand, Heart disease risk prediction using machine learning classifiers with attribute evaluators, Applied Sciences 11 (18) (2021) 8352.
[26] J. Huang, Y.-F. Li, M. Xie, An empirical analysis of data preprocessing for machine learning-based software cost estimation, Information and software Technology 67 (2015) 108–127.

[27] S. Sachan, F. Almaghrabi, J.-B. Yang, D.-L. Xu, Evidential reasoning for preprocessing uncertain categorical data for trustworthy decisions: An application on healthcare and finance, Expert Systems with Applications 185 (2021) 115597.

[28] H. Wang, J. Tang, M. Wu, X. Wang, T. Zhang, Application of machine learning missing data imputation techniques in clinical decision making: taking the discharge assessment of patients with spontaneous supratentorial intracerebral hemorrhage as an example, BMC Medical Informatics and Decision Making 22 (1) (2022) 1–14.

[29] M. R. Stavseth, T. Clausen, J. Røislien, How handling missing data may impact conclusions: A comparison of six different imputation methods for categorical questionnaire data, SAGE open medicine 7 (2019) 2050312118822912.

[30] M. Buda, A. Maki, M. A. Mazurowski, A systematic study of the class imbalance problem in convolutional neural networks, Neural Networks 106 (2018) 249–259.

[31] N. Gopika, A. M. K. ME, Correlation based feature selection algorithm for machine learning, in: 2018 3rd International Conference on Communication and Electronics Systems (ICCES), IEEE, 2018, pp. 692–695.

[32] R. G. Williams, G. D. Pearson, R. J. Barst, J. S. Child, P. Del Nido, W. M. Gersony, K. S. Kuehl, M. J. Landzberg, M. Myerson, S. R. Neish, et al., Report of the national heart, lung, and blood institute working group on research in adult congenital heart disease, Journal of the American College of Cardiology 47 (4) (2006) 701–707.
[33] E. Escobar, Hypertension and coronary heart disease, Journal of human hypertension 16 (1) (2002) S61–S63.

[34] R. Huxley, F. Barzi, M. Woodward, Excess risk of fatal coronary heart disease associated with diabetes in men and women: meta-analysis of 37 prospective cohort studies, Bmj 332 (7533) (2006) 73–78.

[35] A. Bonmert, X. Sun, B. Bischl, J. Rahnenführer, M. Lang, Benchmark for filter methods for feature selection in high-dimensional classification data, Computational Statistics & Data Analysis 143 (2020) 106839.

[36] P. Mishra, U. Singh, C. M. Pandey, P. Mishra, G. Pandey, Application of student’s t-test, analysis of variance, and covariance, Annals of cardiac anaesthesia 22 (4) (2019) 407.

[37] E. J. Benjamin, P. Muntner, A. Alonso, M. S. Bittencourt, C. W. Callaway, A. P. Carson, A. M. Chamberlain, A. R. Chang, S. Cheng, S. R. Das, et al., Heart disease and stroke statistics—2019 update: a report from the american heart association, Circulation 139 (10) (2019) e56–e528.

[38] S. Dev, F. M. Savoy, Y. H. Lee, S. Winkler, Nighttime sky/cloud image segmentation, in: Proc. International Conference on Image Processing (ICIP), 2017.

[39] D. Thara, B. PremaSudha, F. Xiong, Auto-detection of epileptic seizure events using deep neural network with different feature scaling techniques, Pattern Recognition Letters 128 (2019) 544–550.

[40] M. Jain, T. AlSkaif, S. Dev, Validating clustering frameworks for electric load demand profiles, IEEE Transactions on Industrial Informatics 17 (12) (2021) 8057–8065.

[41] S. Dev, H. Wang, C. S. Nwosu, N. Jain, B. Veeravalli, D. John, A predictive analytics approach for stroke prediction using machine learning and neural networks, Healthcare Analytics 2 (2022) 100032.
[42] J.-J. Beunza, E. Puertas, E. García-Ovejero, G. Villalba, E. Condes, G. Koleva, C. Hurtado, M. F. Landecho, Comparison of machine learning algorithms for clinical event prediction (risk of coronary heart disease), Journal of biomedical informatics 97 (2019) 103257.

[43] B. P. Das, M. S. Pathan, Y. H. Lee, S. Dev, Estimating ground-level nitrogen dioxide concentration from satellite data, in: Proc. Photonics & Electromagnetics Research Symposium (PIERS), IEEE, 2021, pp. 1176–1182.