Coronary Artery Disease Prediction using Machine Learning Classifiers

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***Abstract*—In this project, we aim to train supervised machine learning models to predict whether a person with some given input characteristic features has 10 years future risk of coronary artery disease. We performed an exploratory data analysis to calculate and describe the basic statistics related to the data. Further, the dimension of the dataset is reduced. At last, we have tried to perform a comparative analysis between two models kNN and Logistic Regression in order to select the best classifier algorithm.**

***Keywords*—** *Coronary Artery Disease, Logistic Regression, kNN, Supervised Learning, EDA.*

I. Introduction

Machine Learning is used in a variety of areas all around the world. The healthcare industry is no different. Coronary Artery Disease (CAD) is the formation of plaque in the arteries that provide your heart with oxygen-rich blood. Plaque produces a blockage, which can lead to a heart attack. CAD is an extremely widespread illness all over the world, it is impacted by several modifiable risk factors. Predictive models built using machine learning (ML) algorithms may assist doctors to diagnose CAD at an early stage and improve results and in turn, also save many lives. As per the World Health Organisation's (WHO), 2020 report cardiovascular diseases are the leading cause of death worldwide, claiming the lives of an estimated 17.9 million people each year. According to the Registrar General of India, CAD was responsible for 23% of all deaths and 32% of adult deaths between 2010 and 2013.

II. Literature Survey

There has been extensive work done to create algorithms that give better results for predicting CAD. In one of the approaches, a supervised ML algorithm was used which incorporated genetic algorithms and weighted kNN was applied to categorize individuals with type 2 diabetes mellitus (T2DM) based on the presence or absence of coronary heart disease (CHD) problems[1]. In a different approach, the k-Nearest Neighbor (k-NN) and Random Forest classifiers are two extensively used supervised learning techniques. Using them the accuracy of Random Projections using the k-NN classifier vs MTD Feature Selection and Random Forest for predicting artery disease is compared[2]. In very recent work, a comparison of different supervised learning models for the prediction of CAD was done. The comparisons revealed that utilizing a whole set and a subset of features as input for the Random Forest and XGBoost algorithms produced the best results[3].

III. Implementation

1. Selection of an appropriate dataset

To train any model in the supervised form of learning, a training dataset consisting of preferably independent and identical distribution (I.I.D) is required. While selecting the dataset, the following criteria were taken into consideration. The data must be uniform, relevant, comprehensive, diverse, as well as representative of the problem at hand. After extensive analysis of multiple datasets available online, we decided to move forward with a dataset from ongoing cardiovascular research in the town of Framingham, Massachusetts which is also openly available on the Kaggle website[4]. The dataset consists of 15 features (and an attribute of original outputs) and 4240 records. The features can be divided into behavioral, demographic, and medical information, with each division having numerical or categorical features.

The goal of the supervised machine learning classifier is, given the features for an unknown individual, to predict if that individual has a 10-year risk of future CAD.

2. Data Cleaning and Preprocessing

The performance of any algorithm relies on the quality of the sample it is trained on. If the training dataset consists of missing or duplicate data, that must be handled as many algorithms do not support such values. Moreover, the presence of outliers in the dataset tends to increase the variance (increasing the spread of distribution) and decrease the statistical power of the distribution. Therefore, if possible, the outliers must be removed or handled carefully.

- Missing Values Handling:

The missing number of values in ‘glucose’ is 388, which is considered as comparatively a significant amount in comparison to the missing values of other features (such as *‘education’, ‘cigsPerDay’, ‘BPMeds’, ‘totChol’, ‘BMI’*) in the dataset with approximately 4000 records. Therefore, the missing values of ‘glucose’ are handled in the following way: All the cells where the values were previously missing were replaced by the mode of all the records of the ‘glucose’ feature. Furthermore, in the rest of the features with missing values, the whole record with the missing value was removed since there were insignificant numbers of missing values present in those records. Finally, the dataset with zero missing values was achieved.

- Duplicate Values Handling:

In the dataset, there were no duplicate values present.

- Removable Outliers Handling:

From the box plot, it is clearly visible that there are plenty of outliers present in the attributes ‘totChol’, ‘sysBP’, ‘diaBP’, ‘cigsPerDay’, ‘glucose’ etc. Out of which only ‘totChol’ and ‘sysBP’ consist of outliers (one each) that are very sparse from the rest of the data and hence can be neglected. The rest of the outliers are kept as they were before since they are very close to the distribution of the features they belong to. The box plot of the dataset before and after the removable outliers handling is as shown in the fig. 3.2.1 and fig. 3.2.2 respectively.

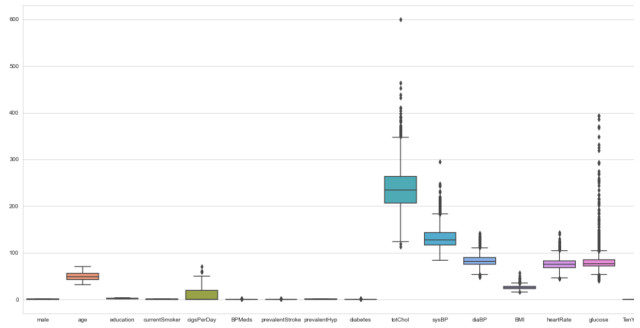

Figure 3.2.1 - Before outliers handling

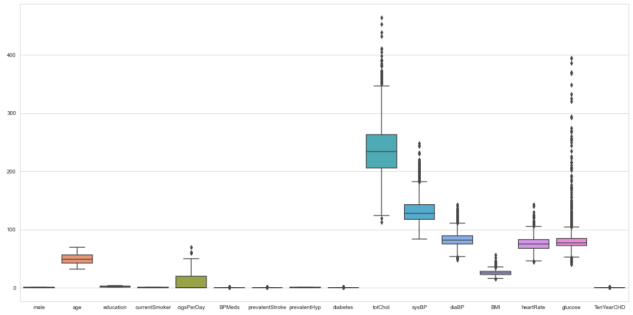

Figure 3.2.2 - After outliers handling

3. *Exploratory Data Analysis:*

Initially, the summary statistics of each and every feature was viewed which showed the count, mean, standard deviation, minimum and maximum values and other statistics of each of the 15 features. Moreover, to understand how linearly each pair of features is dependent on one another, a correlation matrix was formed as a heatmap plot in python. A correlation matrix is used in situations where it is not very easy to visualize the dependence of the output variable on each input variable individually.

Inference from the correlation matrix: we found some pairs of the features that have a very high correlation coefficient. For example, sysBP & diaBP (0.78), cigsPerDay & currentSmoker (0.77), and sysBP & prevalentHyp (0.7). This means these features are highly correlated and quite linearly dependent on each other. Which can unnecessarily increase the time and space complexity.

More features in the dataset do not always support better performance if they are not independent. The dependent features can lead to a redundant dataset with unrequired noise in the model. Therefore, from the above-mentioned pairs, we can select only one feature that has more significance on the output variable.

Further, a univariate analysis was performed on the dataset. In this feature-wise analysis, for two different types of features: 1) numerical features ['cigsPerDay', 'totChol', 'sysBP', 'diaBP', 'BMI', 'heartRate', 'glucose'] and 2) categorical features ['male', 'education', 'currentSmoker', 'BPMeds', 'prevalentStroke', 'prevalentHyp', 'diabetes'] was carried out. In numerical features, from their histograms or violin plots the distribution of some of the features was found to be nearly Gaussian such as BMI, glucose, and totalChol. Whereas through categorical feature analysis some of the highly imbalanced features were found such as BPMeds, prevalentStroke, and diabetes.

In bivariate analysis, the pair plots are difficult when data is higher dimensional and there are a lot of records. Therefore, selective pairwise feature analysis is done for this dataset. The pairs were selected on the basis of the correlation coefficient and general idea of dependence of two features.

At last, in multivariate analysis, more than two features were analyzed altogether. This analysis is needed when there is interdependence between more than two features. For example, high correlation between 'sysBP' and 'diaBP' implies that they are dependent features. Further, there is also a high correlation between 'prevalentHyp' and 'sysBP'. Which means that if we consider only one out of these three features. the dataset would be more independent.

4. *Resampling by oversampling positive cases*

The number of cases in our dataset was categorized as either positively diagnosed or negatively diagnosed and the plot obtained is shown in fig. 3.4.1

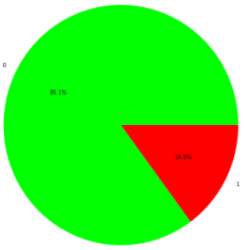

Figure 3.4.1

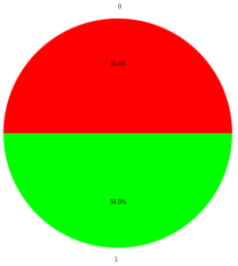

Figure 3.4.2

Fig. 3.4.1 clearly shows that the cases which were negatively diagnosed with CHD are much more than the positive ones. This is a class imbalance problem that affects the prediction since this is a classification problem and it is advised to have equal numbers of both cases. This issue can be resolved using two different approaches. One is the Cost function-based approach and the other is the sampling-based approach. Since the cost function based approach is rarely used in practice, we resample our imbalanced dataset by duplicating the minority data which here are the positively diagnosed cases. After duplicating the data we obtain a similar number of cases in both categories and once again the plot after duplicating is shown in fig. 3.4.2.

This approach is known as 'Oversampling'. Which can lead to overfitting. Therefore, we will resolve this problem using a different technique in future as mentioned in the presentation.

5. *Dimensionality Reduction using feature selection (χ^2 test)*

We can see our dataset consists of 15 independent variables. But for any model, it is preferred to have an optimum number of independent variables. This is where the feature selection process comes into play. We here use χ^2 test to extract variables that contribute to ten year CHD the most. This is a trade-off where we trade a tiny amount of

our accuracy with a lower number of dimensions and hence low computational expense.

A χ^2 value determines the dependence of response(here, ten-year CHD) on initially added features. The higher the χ^2 value, the higher is the dependence of feature on the response and hence we are here looking for features that will have a high χ^2 value with a ten-year CHD response. Performing χ^2 analysis we see that not all the attributes contribute significantly towards the ten-year CHD and hence we can remove some of these attributes. We pick up top 10 features having highest χ^2 value namely: sysBP, glucose, age, cigsPerDay, totChol, diaBP, prevalentHyp, male, BPMeds and diabetes. These features seem to be contributing more towards the occurrence of CHD 10 years in future. From this point onwards we will be using these 10 features in our model and get accuracy on these features.

6. Model Prediction

As we know there is no way to priorly tell which model predicts accurate results for a given dataset; the only way to get a good ML model is to apply several models and test their accuracy on a test set. Here we are looking into a classification problem, this classification is whether an individual will be diagnosed with CHD 10 years down the line. This is clearly a binary classification and we denote 1 for a positive case while 0 for a negative case. We will here use an example of a parametric (logistic regression) and an example of non-parametric (kNN).

A. Logistic regression

Logistic regression is a multi-class classifier that uses a parametric approach for classification. This is a conditional probability method denoted as $P(Y|X;\theta)$, where Y is the event of whether the individual will be diagnosed by CHD and X are the independent variables and θ are the parameters to be optimized. A logistic function that gives probability is given as

$$P(Y|X;\theta) = \frac{1}{1+e^{-a}}\ , where\ a = W^T X + b$$

Here, a is known as the logit function and is a function of parameters and independent variables. Here, we would be using the 10 independent variables obtained based on χ^2 test.

B. kNN

k- Nearest neighbors or more popularly known as kNN is a non-parametric model which predicts the output based on nearest neighbors for the unknown target value. This assumes the fact that similar target values reside in a similar vicinity.

Here we use kNN in a hyperdimensional space with independent variables being the features one discussed earlier and ten year CHD being the target predicted value to be predicted. As in parametric models, we could discard the input data once the parameters are optimized, opposed to that in non-parametric models it is important to keep the input data while predicting the target value for the dataset.

For this particular problem, we have decided the value of K based on the performance measures Accuracy, F1 score as well as Area under the ROC curve. All the three measures had their best possible values when the value of K was 3.

IV. Results

After getting the confusion matrix for both the models, the performance measures considered are 1) Accuracy, 2) F1-score and 3) Area under the receiver operating characteristic (ROC) curve which is in short known as AUC. Accuracy is a good performance measure when the dataset is symmetric i.e. false negative values and false positives values are very close. And also, if false negative values and false positives have similar costs. However, in the case of disease prediction, the cost of false negative values is way more than the cost of false positives. In such cases F1-score should be used as a performance measure.

In addition to the above two, AUC is very useful in the evaluation of the performance of binary classification models. This measure provides a graphical representation of the performance as shown in the figures mentioned in the presentation. Area Under Curve is the likelihood that the model ranks a random positive example higher than a random negative example. It is important because it is scale invariant as well as class threshold invariant.

	Accuracy	AUC	F1 score
Logistic regression	0.674153	0.733124	0.682909
K-nearest neighbours	0.899853	0.899493	0.907734

V. Conclusion

It can be inferred from the results of the performance measure that kNN is a better model for CAD prediction than Logistic Regression. To verify this, further the SNR of the data can be calculated and verified as a part of future work. For the dataset with high value of SNR, kNN always performs better than Logistic Regression. In addition to this, further we wish to use some advanced techniques (eg. PCA) for dimensionality reduction and compare the new results with the previous results. And we also plan to apply other classifiers (such as random forest, gradient boost) and evaluate the performance.

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APPENDIX