Capstone Project: Heart Disease Prediction using Machine Learning

By

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Background: Heart disease is very common among different ages. People with certain blood sugar level, cholesterol level etc., may exhibit symptoms for heart disease. It is important to find a smart way to speculate possibility of heart disease given certain physiological status. UCI ML database has a large, collected data for heart disease will be used to develop a ML model. Historically great effort has been made to detect prime arbitrator of heart disease given various parameters [1]. This work highlights on few analytical metrics without proposing a ML prediction methodology(s). There has been a necessity to do a systematic analysis on "primary" causes of heart disease to trigger alarm for a person. Overall analytics and prediction can be compiled as a streamlined process to work on any probable future datasets. As a part of the work author will be creating a ML pipeline to predict possibility of heart disease using multiple candidate ML methods. This will be done to ensure reliability of overall prediction.

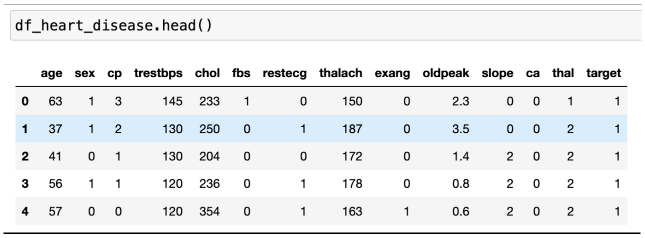
Problem Statement: This data has several parameters that encompasses a relationship between person's general health status and potential heart risk. A ML model can be used to extract important parameter (aka features) while analyzing the data. Eventually ML model can be used to predict heart risk.

Dataset source and Input: In this project UCI ML dataset on heart disease has been used [2]. The dataset has a wide range of input features collected from patients at a Cleveland V.A. hospital. The raw data from UCI website needed rigorous pre-processing. Since the scope of the project is to develop ML scheme with preliminary data analytics, we have collected the dataset from Kaggle website [4] as a csv file (filename: 'heart_disease_dataset_UCI.csv').

Dataset description: The csv file has 14 columns. 13 of them are features and 14th column is the Boolean target variable defining chance of heart risk or not. Detail variable description can be seen as:

- **age**: The person's age in years
- **sex**: The person's sex (1 = male, 0 = female)
- **cp**: 0 = typical angina, 1 = atypical angina, 2 = non-anginal pain, 3 = asymptomatic
- **trestbps**: The person's resting blood pressure (mm Hg on admission to the hospital)
- **chol**: The person's cholesterol measurement in mg/dl
- **fbs**: The person's fasting blood sugar (> 120 mg/dl, 1 = true; 0 = false)
- **restecg**: Resting electrocardiographic measurement (0 = normal, 1 = having ST-T wave abnormality, 2 = showing probable or definite left ventricular hypertrophy by Estes' criteria)
- **thalach**: The person's maximum heart rate achieved
- **exang**: Exercise induced angina (1 = yes; 0 = no)
- **oldpeak**: ST depression induced by exercise relative to rest ('ST' relates to positions on the ECG plot. See more here)
- **slope**: 0 = upsloping, 1 = flat, 2 = downsloping
- **ca**: The number of major vessels colored by flourosopy (0-3)
- **thal**: A blood disorder called thalassemia: 0: NULL (dropped from the dataset previously), 1: fixed defect (no blood flow in some part of the heart), 2: normal blood flow, 3: reversible defect (a blood flow is observed but it is not normal)
- **target**: Heart disease (0 = no, 1 = yes)

Numerical data is stored in df_heart_disease dataframe:



```
df_heart_disease.head()
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1

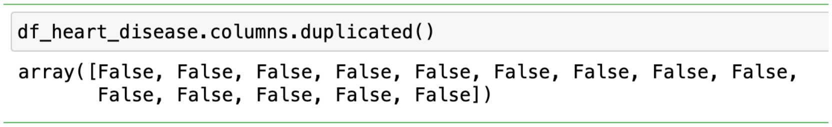
Table: 1

Project Design: For this project ML package Scikit-learn will be used for both supervised and unsupervised ML methods. Sklearn is a rich python library highly applied python package. As ML methodologies we will use classification models like: XGBoost, Random Forest, Logistic regression, Light GBM and Linear Discriminant Anslysis. Idea is to use classification method's capability of capturing both linear and non-linear relationships in the data. To avoid overfitting we will be using k-fold cross validation method on training set. Feature importance will be used to extract comparatively important features. This will help us reduce model order. Model will be deployed on GitHub repo.

1. Data pre-processing: As part of pre-processing following steps will be done to cleanup the data:

i. Find out missing values by looking for NULL values: At this step our goal is to see if there is any missing value i.e. NaN existing in the dataset. If any missing value found that can be replaced or removed by whole row pertaining to that. Key steps:
   a. Execute df_heart_disease.isna().sum()
   b. Visualize the table using package "missingno"

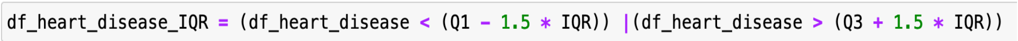
ii. Find out duplicate attributes: Checked for any duplicate columns:



```
df_heart_disease.columns.duplicated()
```

```
array([False, False, False, False, False, False, False, False, False,
       False, False, False, False, False])
```

iii. Look for outliers in the data: In this step we look for any outliers in the data. If the outlier resides outside a prescribed range, those are discarded. Any data outside 5%-95% quantile region will be removed.
   a. Use Pandas IQR function:



```
df_heart_disease_IQR = (df_heart_disease < (Q1 - 1.5 * IQR)) |(df_heart_disease > (Q3 + 1.5 * IQR))
```

   b. Visualize distribution of accepted outliers as usable data (Figure: 1):

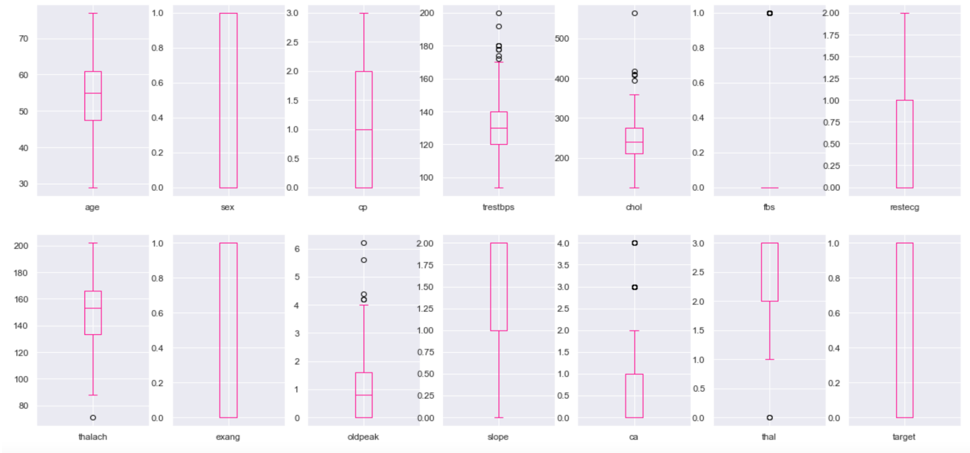
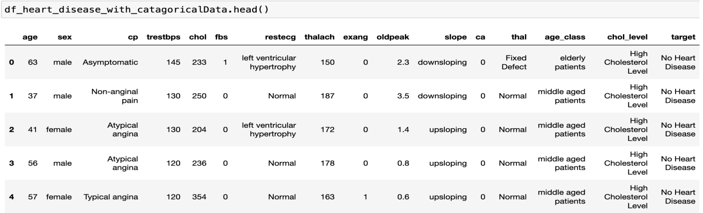


Figure: 1

iv. Rename features if necessary: For the purpose of analysis and understanding numerical features with categorical nature (e.g. thal, chol, sex, etc) were converted to categorical form. This was used in exploratory data analysis:



```
df_heart_disease_with_catagoricalData.head()
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	age_class	chol_level	target
0	63	male	Asymptomatic	145	233	1	left ventricular hypertrophy	150	0	2.3	downsloping	0	Fixed Defect	elderly patients	High Cholesterol Level	No Heart Disease
1	37	male	Non-anginal pain	130	250	0	Normal	187	0	3.5	downsloping	0	Normal	middle aged patients	High Cholesterol Level	No Heart Disease
2	41	female	Atypical angina	130	204	0	left ventricular hypertrophy	172	0	1.4	upsloping	0	Normal	middle aged patients	High Cholesterol Level	No Heart Disease
3	56	male	Atypical angina	120	236	0	Normal	178	0	0.8	upsloping	0	Normal	middle aged patients	High Cholesterol Level	No Heart Disease
4	57	female	Typical angina	120	354	0	Normal	163	1	0.6	upsloping	0	Normal	middle aged patients	High Cholesterol Level	No Heart Disease

Table: 2

2. Data Analytics and Visualization: In this section exploratory data analysis (EDA) has been performed using several visualization approaches. Goal is to develop a clear understanding on the relation between heart risk and different features, how different features are distributed, quality of correlation between features etc.

Feature data spatial distribution: In this case we can visualize how features are distributed. Any feature with unbalanced spatial distribution may trigger quality of data and eventually affect ML results (Figure: 2). Few outliers are observed in the data distribution.

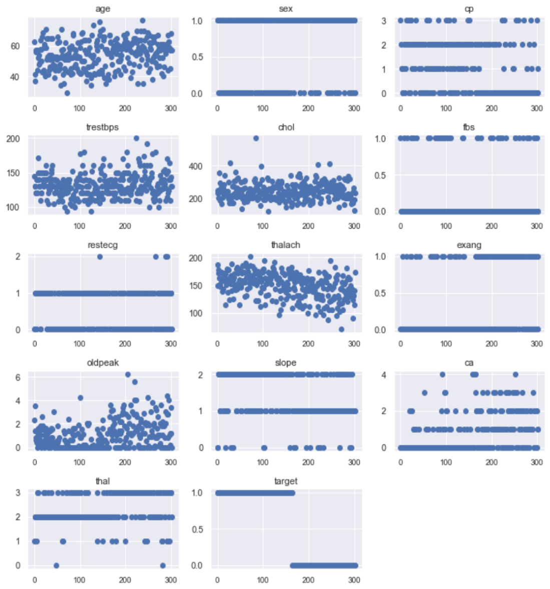


Figure: 2

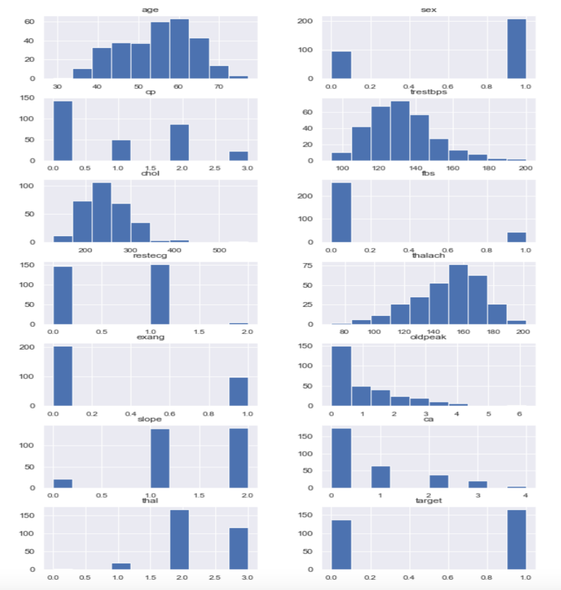
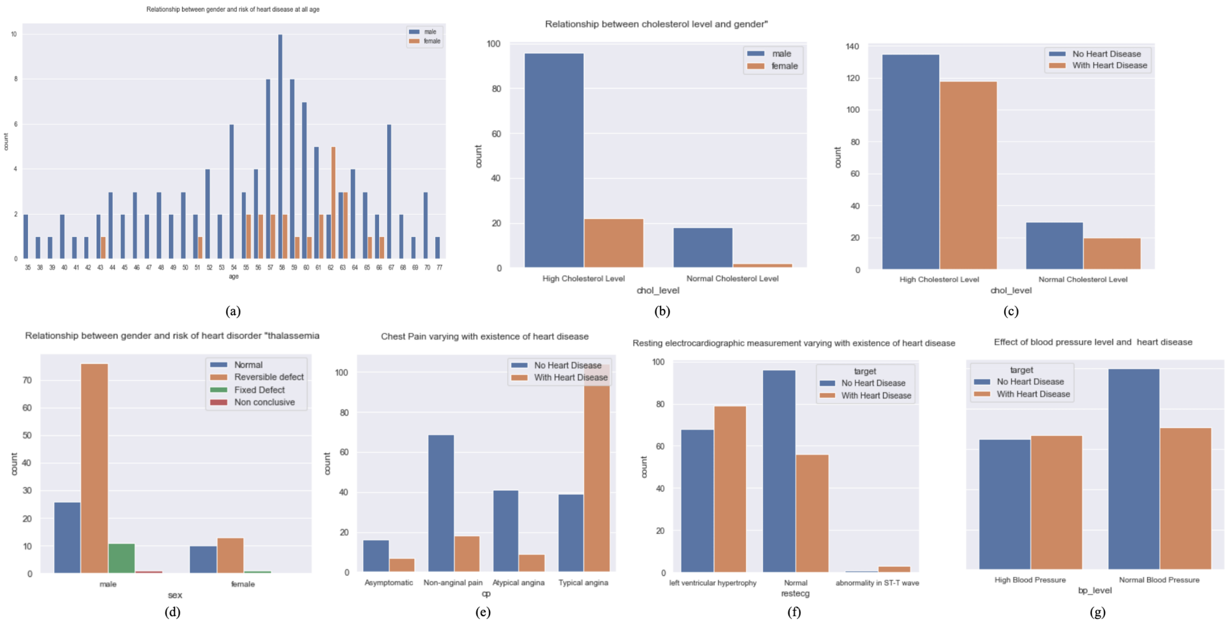


Figure: 3

In a similar manner histogram analysis is done to understand data distribution over certain range. Most of the features seem to have skewness over certain range (Figure: 3).

Feature analysis: In this section we can internal variations in each feature and it's relationship with targe i.e. chance of heart risk. First thing comes to mind is relationship between patient age, gender and chance of heart risk. As shown in Figure: 4(a) age has an interesting relationship with hear risk. People in their late 50's-60's have more risk of heart disease. Out of men and women, men have higher heart risk. To supplement that observation we can see male have higher cholesterol than women and also mode defective heart than women (Figure: 4(b, d)). This is probably dietary habit and lifestyle of men in the timeframe of 1980-1990. As we move away from age and gender, we can see from Figures: 4(c, e, f, g) higher cholesterol level and angina has stronger effect on heat disease.



(a)

(b)

(c)

(d)

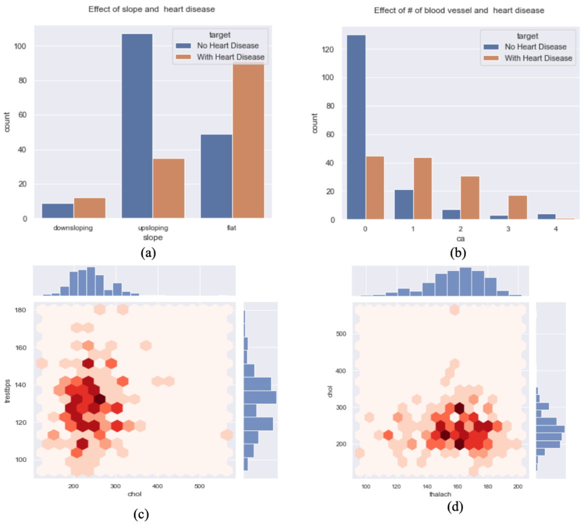
(e)

(f)

(g)

Figure: 4

Further digging into the data gives us some understanding between heart functionality and heart disease. Figures: 5(a, b) tells us that flat slope in peak exercise has relationship with heart risk. This is not really a trait, more of a behavioral patten of heart. On a same note, detected vessels de to fluoroscopy has some relationship with heart risk. Patients without heart risk has no vessel detected as a very frequent case. Figures: 5(c, d) confirms us that max heart rate, high cholesterol and blood pressure so have internal dependency in triggering heart risk. These figures are created for patients with heart risk only.



(a)

(b)

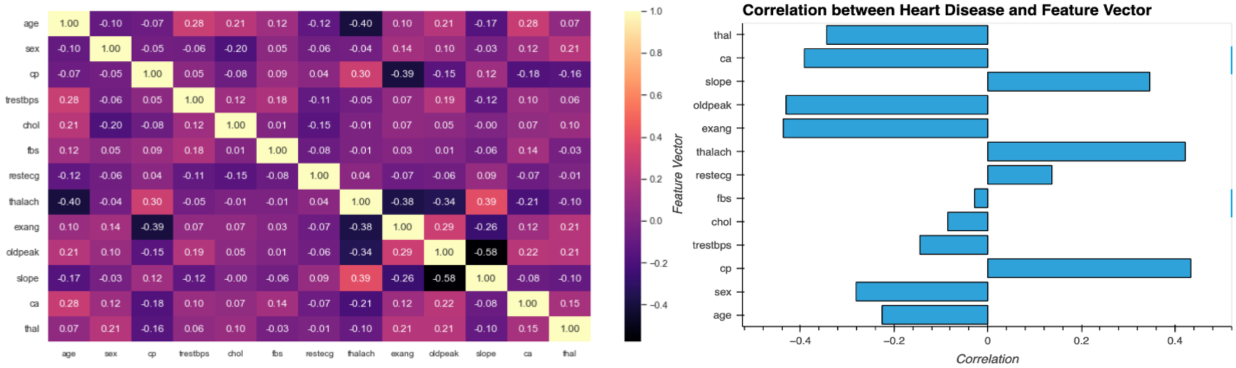
(c)

(d)

Figure: 5

Feature correlation: It is important to understand how different features are correlated. If they are highly correlated, further feature extraction or reduction would be necessary. As shown in

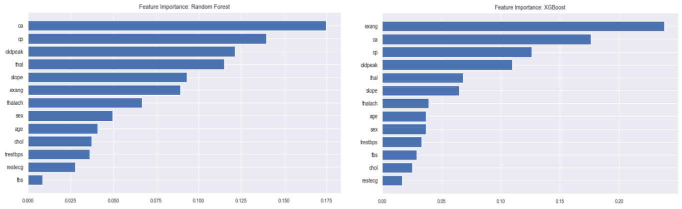
Figures: 6(a, b), features don’t have great correlation in general. Maximum positive value for correlation is with the range of 0.4. Hence it is sufficient to move ahead with these feature vectors for further analysis.



(a) (b)

Figure: 6

Feature importance: As a next part of EDA we are getting into extracting important features from the feature vector. Initially SKlearn’s univariate feature selection function “SelectKBest” was used to sort important features based on their scores. To supplement this result both random forest and XGBoost ML techniques were used to extract important features (Figure: 7). Finally first 80% important features were considered which are common in these three cases.



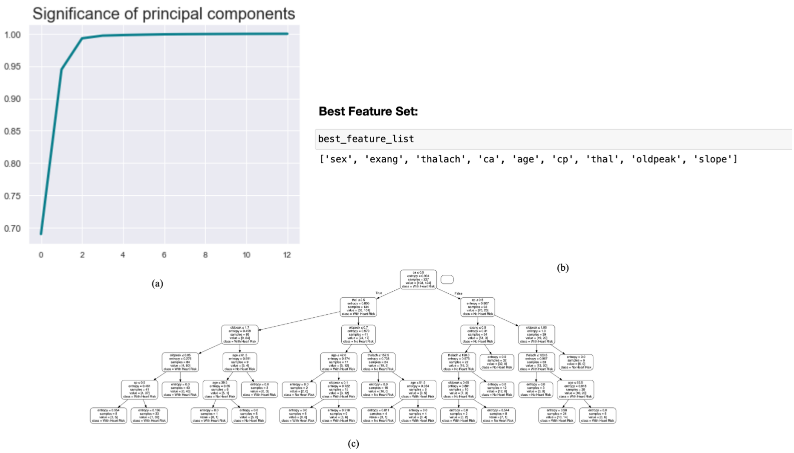
(a) (b)

Figure: 7

From Figure: 7 looks like 6-7 features are important enough to drive the classification model performance. However, there are not same in both these cases. Further principle component analysis was done to get an idea on how many features are actually significant. Figure: 8(a) tells us maximum 4 features are very important. So considering 80% of the features should suffice. Extracted features to be considered are shown in Figure: 8(b). Given this subset of feature we can visualize a simple decision tree to see how they help detecting heart risk.

3. Prediction using ML

: In this section we have developed multiple ML models for binary classification problem. Initial efforts were given to make a short list of candidates as ML models. This was followed by hyper-parameter tuning relevant to specific ML models. Our workstream can be summarized as:



```
best_feature_list
['sex', 'exang', 'thalach', 'ca', 'age', 'cp', 'thal', 'oldpeak', 'slope']
```

Figure: 8

ML Model development and tuning strategy:

i. Data split: Data has been split by 75% training data and 25% testing data.

ii. Only best features detected from previous step were considered.

iii. Develop ML models: In this case we develop ML binary classification models with important hyper parameters. Base models always need tuning to achieve better result. In this case *Random Search based hyper-parameter tuning was performed with 5-fold cross validation*. This was done to ensure an computationally efficient yet effective model was obtained. Model parameter summary is:

a. XGBoost model with hyper-parameter range

```
params = {
        'objective':['binary:logistic'],
        'learning_rate': [0.001, 0.005, 0.01, 0.1,0.3,0.5,0.7,1],
        'max_depth': [1, 2, 3, 4, 5, 6, 7],
        'min_child_weight': [1e-5, 1e-3, 1e-2],
        'subsample': [0.01, 0.1, 0.3,0.5,0.7,1],
        'colsample_bytree': [0.7,1],
        'n_estimators': [100, 200, 300, 400, 500, 1000]}
```

b. Random Forest model with hyper-parameter range

```
params = {  'bootstrap': [True, False],
            'max_depth': range(1,10, 1),
            'max_features': ['auto', 'sqrt'],
             'min_samples_leaf': [1, 2, 4],
             'min_samples_split': [2, 5, 10],
            'n_estimators': [100, 200, 300, 400, 500]}
```

c. Logistic regression (LGR) model with hyper-parameter range

```
params = {"max_iter": range(100,500,2),
              "solver" : ['newton-cg', 'lbfgs', 'liblinear'], "C": [0.5, 0.1, 1.0]}
```

d. Light GBM model with hyper-parameter range

```
params = {'num_leaves':range(10,100, 10), 'min_child_samples':range(5,25,5),'max_depth': range(5, 15, 1),
          'learning_rate':[0.05,0.1,0.2],'reg_alpha': [0,0.01,0.03]}
```

e. Linear Discriminant Analysis (LDA) model with hyper-parameter range (ideally don't have any since closed form model)

```
params = {"solver" : ["svd"],
    "tol" : [0.0001,0.0002,0.0003]}
```

iv. After "best_estimator" was obtained it was used to predict on test dataset. Multiple metrics were developed to quantify model's performance.

v. Given all the trained model an ensemble ML model was developed based on Sklearn’s voting classifier.

vi. Model performance metrics are:

   a. Confusion metrics
   b. F1 score
   c. ROC_AUC score
   d. Precision score
   e. Recall score
   f. Accuracy score
   g. Cross validation score

In this project we treated the problem as: Classification Problem (instead of Regression Problem) since many of our feature vectors and target variable are discrete in nature. It is unlikely to have 0.5 assigned to heart risk/no-risk condition. Decision trees are very good at classification problems. We also included well know approaches like LGR and LDA since we are dealing with “Binary Classification” problem.

ML Model performance:

Training performance: It is important to evaluate model training performance with cross-validation samples. This will ensure us to conclude that models are not under trained. As shown in Figure: 9, as expected training scores tend to become steady with increasing CV samples. This is an indication of models are being stable and well trained on the data. LDA and LGR models seem to be behaving batter while training.

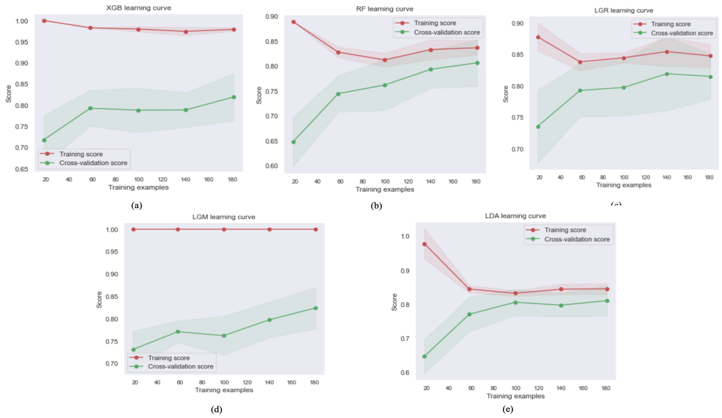
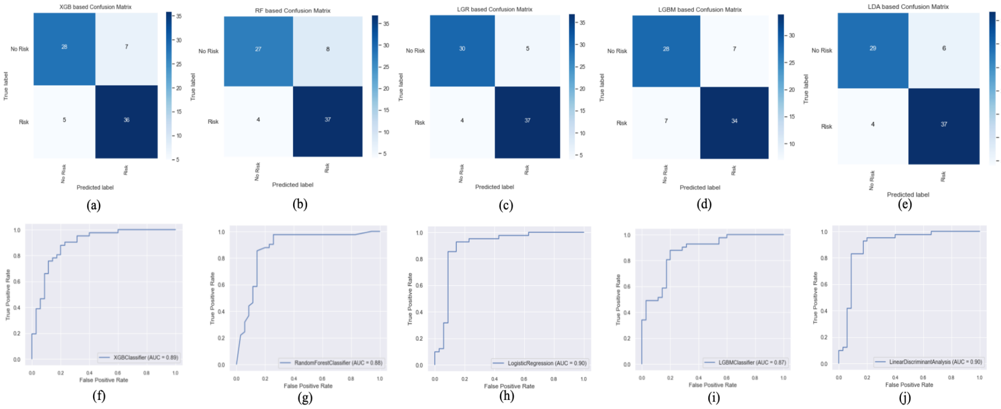


Figure: 9

Model accuracy metrics: Based on Figures: 10 ans 11 we can have a clear understanding on the model accuracy calculated on whole and test dataset. Figures: 10 (1-e) shows LGR and LDA models have slightly better accuracy compared to XGBoost, Random Forest and Light GBM models. LDA and LGR has higher True positive and almost same true negative (In this case: No Risk is considered positive and risk is negative). In this case False Positive is more crucial since we don’t want to label a patient with heart risk as no risk condition. Given that we can see LGR and LDA are slightly better by having lower false positives. ROC_AUC scores also depict how the models are with True vs. False positive rates. As expected, in Figure: 10 LGR and

LDA have steepest increase in True Positive rates given lower range of False Positive Rate (for test dataset). Based on these matrices we can see LGR and LDA models have better prospect in this dataset. However, Figure: 11 shows LGM model has much higher True positive and negative rates as well as low false positive rate. Given training score from Figure: 9, we can conclude that there might be a possibility for overfitting in the LGM model. This can be supplemented by poor confusion metrics in Figure: 10, done on test dataset. Similar observation was made for Random Forest model since it did well on full dataset compared to test dataset. It appears that LGR and LDA are consistent compared to XGBoost model.

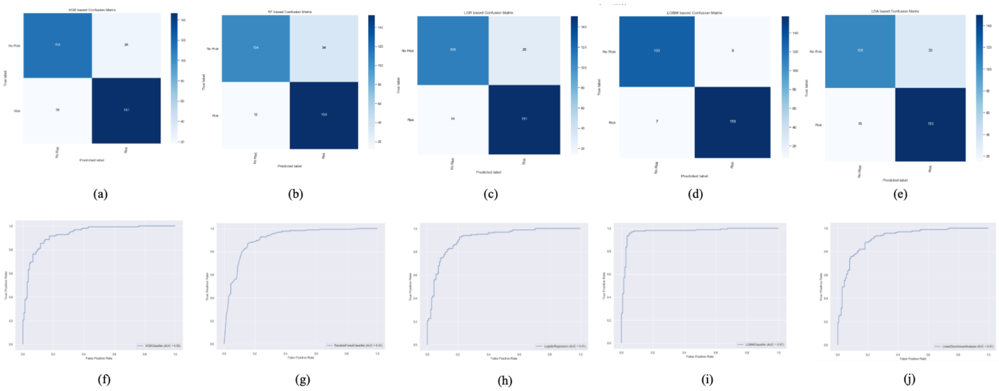
Model performance evaluation: In order to build a deeper understanding on the model accuracy we calculated some of the key metrices. Goal is to conclude which model can be better



(a) (b) (c) (d) (e)

(f) (g) (h) (i) (j)

Figure: 10

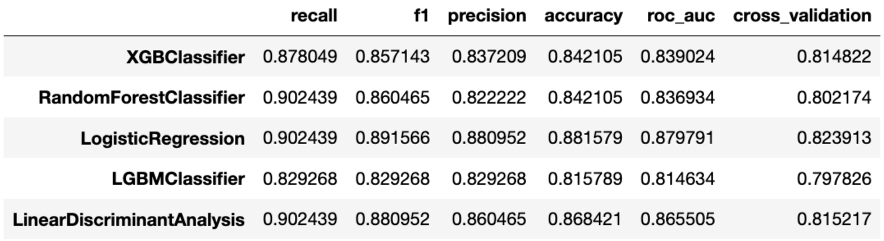


(a) (b) (c) (d) (e)

(f) (g) (h) (i) (j)

Figure: 11

performing for predicting heart risk. As measuring scales we used f1, precision, recall, accuracy, roc_auc, and cross-validation scores. In this dataset we are more interested in precision, f1 and accuracy scores to start with. Since the data has almost balanced distribution of “No Risk” and “Risk” conditions, we can use accuracy as a good metric to get overall picture.



	recall	f1	precision	accuracy	roc_auc	cross_validation
XGBClassifier	0.878049	0.857143	0.837209	0.842105	0.839024	0.814822
RandomForestClassifier	0.902439	0.860465	0.822222	0.842105	0.836934	0.802174
LogisticRegression	0.902439	0.891566	0.880952	0.881579	0.879791	0.823913
LGBMClassifier	0.829268	0.829268	0.829268	0.815789	0.814634	0.797826
LinearDiscriminantAnalysis	0.902439	0.880952	0.860465	0.868421	0.865505	0.815217

Table: 3

As shown in Table: 3, LGR and LDA models have higher accuracy. In addition, f1 and precision scores are higher compared to other models. Recall score seems to be higher for LGR and LDA but RF classifier exhibits similar accuracy. Cross-validation tells us that models are reasonably well fitted since all of them are with in similar range of values.

4. Benchmark model: Accuracy of the model was compared with [1] and [3]. In the current work LGR has highest accuracy of 88.16%. In the literature we have seen accuracy was within the range of 87%-90%. Model accuracy was also compared with Kaggle competition models. Current model seemed to be within similar range of accuracy since Kaggle models have accuracy withing the range of 85%-90% [5]. An ensemble ML model was also developed using Sk-learn’s Voting Classifier. Idea was to make sure we get a better superset of all these individual models. Accuracy from this model seemed to be within similar accuracy range (Please see the Jupyter Notebook).

5. Conclusion: In this project we have performed a rigorous data analysis to understand factors affecting heart risk. Eventually we developed multiple ML classification models and tuned our parameters. Model behaves with 87%-88% accuracy on unknown test data.

Reference:

1. Jindal, Harshit, et al. "Heart disease prediction using machine learning algorithms." IOP Conference Series: Materials Science and Engineering. Vol. 1022. No. 1. IOP Publishing, 2021.
2. https://archive.ics.uci.edu/ml/datasets/Heart+Disease
3. Albahr, Abdulaziz, et al. "Computational Learning Model for Prediction of Heart Disease Using Machine Learning Based on a New Regularizer." Computational Intelligence and Neuroscience 2021 (2021).
4. https://www.kaggle.com/datasets/cherngs/heart-disease-cleveland-uci
5. https://www.kaggle.com/datasets/cherngs/heart-disease-cleveland-uci/code?datasetId=576697&sortBy=voteCount