Machine Learning Engineer Nanodegree

Capstone Project

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I. Definition

Heart disease is the number one killer according to World Health Organization (WHO) statistics [1]. Millions of people die every year because of heart disease and large population of people suffers from heart disease. Prediction of heart disease early plays a crucial role for the treatment. If heart disease could be predicted before, lots of patient deaths would be prevented and a more accurate and efficient treatment way could be provided. In this work we are trying to early diagnose the heart disease using machine learning methods.

Problem Statement

This is a classification problem. I measure the presence of heart disease in the patient based on the used dataset. Various machine learning approaches are used for addressing heart disease diagnosis issue like found in [2], [3], [4], [5], [6], [7], [8]. And there are more papers in this field.

However, the data has multiple categories for presence of disease but, I will use binary classification to distinguishing absence (value 0) from presence of heart disease (values 1, 2, 3, and 4).

Metrics

The performance of the proposed system was computed by different metrics like accuracy, precision and recall.

Accuracy is computed dividing number of predictions which are correct by number of all predictions. The obtained result is multiplied by 100 to get value as percentage.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

where TP, TN, FP and FN demonstrate in order of the number of True Positives, True Negatives, False Positives and False Negatives. TP demonstrates the number of instances which are sick and diagnosed accurately. FP demonstrates the number of instances which are healthy and diagnosed wrongly as they are sick. FN demonstrates the number of instances which are sick, but the instances are diagnosed wrongly. TN contains several instances which are healthy, and the instances are diagnosed accurately

Precision denotes the ratio of the instances that are predicted as having heart disease and they have heart disease.

$$Precision = \frac{TP}{TP + FP}$$

Recall denotes the proportion of the instances that are have heart disease are predicted as having heart disease.

$$Recall = \frac{TP}{TP + FN}$$

F_1 score is a measure of a test's accuracy.

$$F_1 = \frac{2\,.\,Precision\,.\,Recall}{Precision + Recall}$$

So, instead of using precision and recall in the output we could use F_1 score.

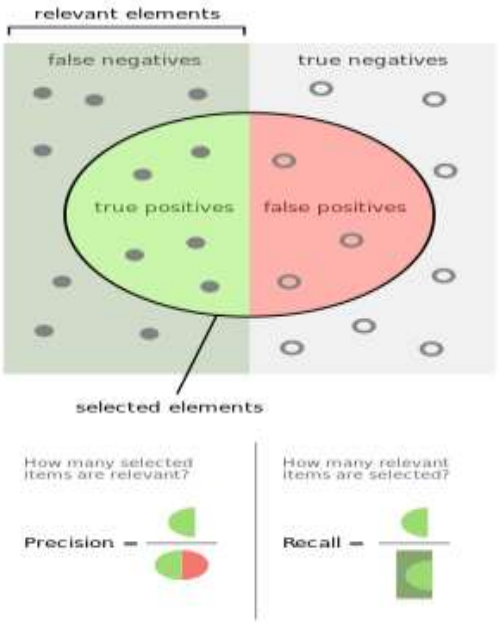


Figure 1 Precision and Recall

II. Analysis

Data Exploration

We are using the heart disease data set available from the [UC Irvine Machine Learning Repository](). This data set dates from 1988 and consists of four databases: Cleveland (303 instances), Hungary (294), Switzerland (123), and Long Beach VA (200). Each database provides 76 attributes, including the predicted attribute. There are many missing attribute values. In addition, the Cleveland data set became corrupted after the loss of a computing node, and the surviving data set contains only 14 attributes per instance. Counting only instances with non-missing values for these 14 attributes, the total for all four databases is 299 instances (297 from Cleveland alone). This is the data set I will be using, and for simplicity I will be referring to it as the Cleveland data set.

#	Attribute	Description	Type
1	age	Age in years	int
2	sex	Female or male	bin
3	cp	Chest pain type (typical angina, atypical angina, non-angina, or asymptomatic angina)	cat
4	trestbps	Resting blood pressure (mm Hg)	con
5	chol	Serum cholesterol (mg/dl)	con
6	fbs	Fasting blood sugar (< 120 mg/dl or > 120 mg/dl)	bin
7	restecg	Resting electrocardiography results (normal, ST-T wave abnormality, or left ventricular hypertrophy)	cat
8	thalach	Max. heart rate achieved during thalium stress test	con
9	exang	Exercise induced angina (yes or no)	bin
10	oldpeak	ST depression induced by exercise relative to rest	con
11	slope	Slope of peak exercise ST segment (upsloping, flat, or downsloping)	cat

12	ca	Number of major vessels colored by fluoroscopy	int
13	thal	Thalium stress test result (normal, fixed defect, or reversible defect)	cat
14	num	Heart disease status: number of major vessels with >50% narrowing (0,1,2,3, or 4)	int

The 14th column will be used as classification result to distinguishing absence (value 0) from presence of heart disease (values 1, 2, 3, and 4). We need to transform the column values to only two values "absence (value 0)" and "disease (values 1)".

Here we could find sample of data

	age	sex	cp	restbp	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	num
0	63.0	1.0	1.0	145.0	233.0	1.0	2.0	150.0	0.0	2.3	3.0	0.0	6.0	0.0
1	67.0	1.0	4.0	160.0	286.0	0.0	2.0	108.0	1.0	1.5	2.0	3.0	3.0	2.0
2	67.0	1.0	4.0	120.0	229.0	0.0	2.0	129.0	1.0	2.6	2.0	2.0	7.0	1.0
3	37.0	1.0	3.0	130.0	250.0	0.0	0.0	187.0	0.0	3.5	3.0	0.0	3.0	0.0
4	41.0	0.0	2.0	130.0	204.0	0.0	2.0	172.0	0.0	1.4	1.0	0.0	3.0	0.0

Dataset statistics are as follows:

```
Total number of records: 299
Number of infected patients: 139
Number of healthy patients: 160
Percentage of infected patients: 46.49%
```

	age	sex	cp	restbp	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
count	299.000000	299.00000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000
mean	54.521739	0.67893	3.163880	131.715719	246.785953	0.143813	0.989967	149.327759	0.331104	1.058528	1.605351	0.672241	4.745819
std	9.030264	0.46767	0.964069	17.747751	52.532582	0.351488	0.994903	23.121062	0.471399	1.162769	0.616962	0.937438	1.940977
min	29.000000	0.00000	1.000000	94.000000	100.000000	0.000000	0.000000	71.000000	0.000000	0.000000	1.000000	0.000000	3.000000
25%	48.000000	0.00000	3.000000	120.000000	211.000000	0.000000	0.000000	132.500000	0.000000	0.000000	1.000000	0.000000	3.000000
50%	56.000000	1.00000	3.000000	130.000000	242.000000	0.000000	1.000000	152.000000	0.000000	0.800000	2.000000	0.000000	3.000000
75%	61.000000	1.00000	4.000000	140.000000	275.500000	0.000000	2.000000	165.500000	1.000000	1.600000	2.000000	1.000000	7.000000
max	77.000000	1.00000	4.000000	200.000000	564.000000	1.000000	2.000000	202.000000	1.000000	6.200000	3.000000	3.000000	7.000000

Exploratory Visualization

To understand the nature of data, a visualization below shows each feature plot with a comparison between having heart disease and have no disease. We could observe easily that the percentage on ill and healthy are approximately equal in the dataset which match the percentage we found before (46.49% infected). It looks like it's hard to find a pattern for diagnosis from the chart only.

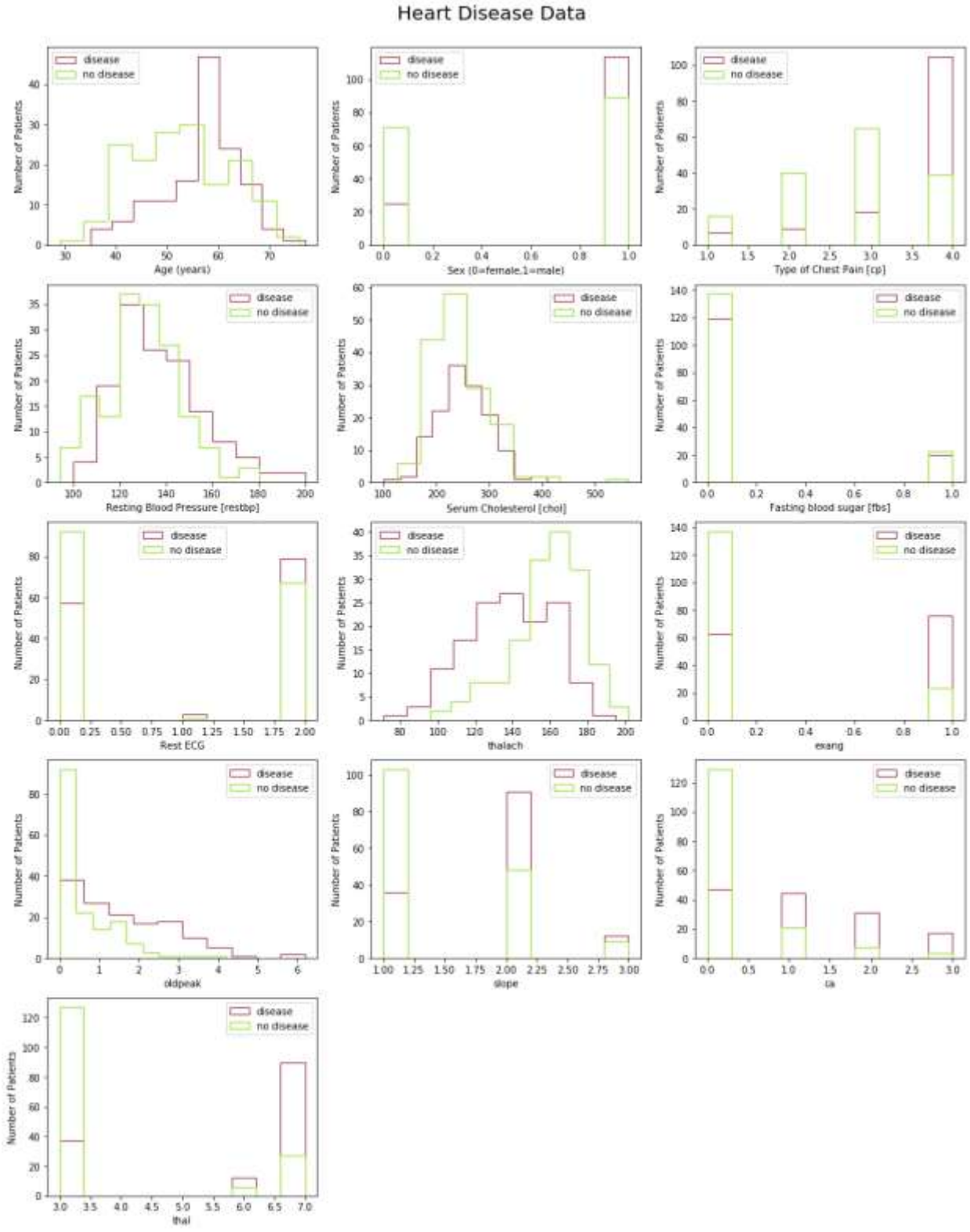


Figure 2 Individual features visualization

Algorithms and Techniques

Our approach is to try many algorithms and compare them to find the best model.

Algorithms used in the project are K-Nearest Neighbor, Random Forest, Gaussian Naïve Bias (GaussianNB), Gradient Boosting, Support Vector Machine(SVM), AdaBoost, stacking ensemble (i.e. Will stack all the previous methods and use logistic regression as meta classifier), and Multilayer Perceptron(MLP).

Then we will use Grid Search method to optimize algorithm's parameters other than MLP.

The parameter used to optimize for each algorithm are as follows:

Algorithm	Parameters
K-Nearest Neighbor	algorithm, n_neighbors, weight
Random Forest	criterion, n_estimators
GaussianNB	N/A
Gradient Boosting	n_estimators, max_depth
SVM	kernerl, C, gamma, probability
AdaBoost	algorithm, learning_rate
Logistic Regression	C
Stacking ensemble	classifiers, use_probas, average_probas, meta_classifier
MLP	activation functions, hidden layer sizes, and epochs

Finally, we compare three ways for dimension reduction and feature selection which are PCA, NMF, and KBest(chi2) to choose one for feature selection to compare full data results to reduced dimension one.

Benchmark

For benchmark, we used two approaches first by using linear model second, by comparing the result to papers that work on the same dataset and try to solve the same problem.

Here we can find the results previously found in other papers using the same dataset.

Title	Year	Accuracy
Optimal feature selection using a modified differential evolution algorithm and its effectiveness for prediction of heart disease	2017	0.85
Efficient Heart Disease Prediction System	2016	0.867
Computational intelligence for heart disease diagnosis: A medical knowledge driven approach	2013	.81 ~ .96
Feature selection for medical diagnosis: Evaluation for cardiovascular diseases	2013	0.85
A highly accurate firefly based algorithm for heart disease prediction	2015	0.88

An integrated decision support system based on ANN and Fuzzy_AHP for heart failure risk prediction	2016	0.91
Classifier ensemble reduction using a modified firefly algorithm: An empirical evaluation	2017	0.89
Heart disease Classification using Neural Network and Feature Selection	2011	0.8
Improving the heart disease Diagnosis by evolutionary algorithm of PSO and Feed Forward Neural Network	2016	0.91
Prediction of Heart Disease Using Neural Network	2017	0.95
Prediction of Heart Disease Using Hybrid Technique for Selecting Features	2017	0.84
Efficient Heart Disease Prediction system using Optimization Technique	2017	0.53
Feature selection for medical diagnosis: Evaluation for cardiovascular diseases	2013	0.89

III. Methodology

Data Pre-processing

We have done the following data preprocessing methods

- Feature scaling for the numerical features 'age', 'restbp', 'chol', 'thalach', 'oldpeak', and 'ca' to be between 0 and 1 this could improve training of many of selected algorithms.
- To detect outliers, we have used interquartile range (IQR) then we detect outliers as the data records detected as outlier in two or more features. After testing we found that when removing outliers, the accuracy decreases so; we rollback this step.
- Transform the 'num' column in which we want to predict to only two values "absence (value 0)" and "disease (values 1)" because the data is not big enough to detect accurately the level of disease.
- Using one-hot encoder to convert discrete categorical values that has more than two values which are 'cp', 'restecg', 'slope', and 'thal'.
- Split and shuffling data into training and testing sets

Implementation

First, we implement the linear model using SGD classifier with default parameters to be our base model. Cross validation is used during the training process.

Second, we implement the MLP model using Keras and training the model for 100 epochs. A validation split of 1% is used during the training with shuffling and checkpoints.

Third, we train each classifier of the following list using the default parameters with cross validation. All classifiers in this step also used in stacked ensemble classifier with logistic regression as meta classifier.

- K-Nearest Neighbor

- Random Forest
- GaussianNB
- Gradient Boosting
- SVM
- AdaBoost
- Stacking ensemble

Accuracy and F1 score calculated for each used classifier.

We choose PCA from the three tested algorithms for dimension reduction as shown in Figure 3

Refinement

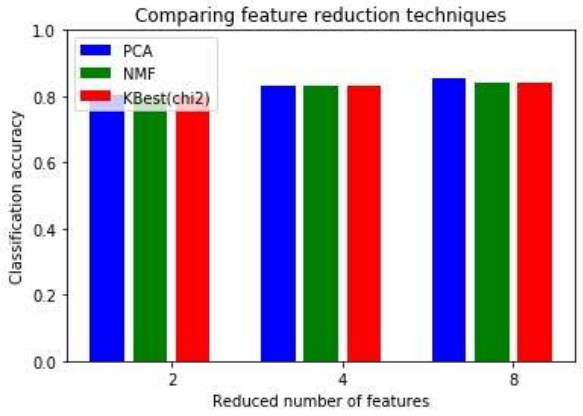
Figure 3 Comparing feature reduction techniques

Using grid search on the hyperparameters mentioned in Algorithms and Techniques section we found the best parameters to be as following.

Algorithm	Parameters
K-Nearest Neighbor	algorithm='ball_tree', n_neighbors=5, weights='distance'
Random Forest	criterion='entropy', n_estimators=5
GaussianNB	N/A
Gradient Boosting	n_estimators=50, max_depth=3
SVM	kernel='linear', C = 10, gamma = 0.001, probability=True
AdaBoost	algorithm='SAMME.R', learning_rate=0.1
Logistic Regression	C=10.0
Stacking ensemble	use_probas=True, average_probas=True, meta_classifier=logistic regression, classifiers= [KNN, Random Forest, GaussianNB, Gradient Boosting, SVM, AdaBoost]
MLP	Activation functions = relu for input layer and sigmoid for the output layer, hidden layer size = 8, dropout = 0.3 and epochs = 100, optimizer=rmsprop, loss function = binary cross entropy, metric = accuracy

The MLP layers are as following:

```
_________________________________________________________________
Layer (type)                 Output Shape              Param #
=================================================================
dense_1 (Dense)              (None, 22)                506
_________________________________________________________________
dropout_1 (Dropout)          (None, 22)                0
_________________________________________________________________
dense_2 (Dense)              (None, 8)                 184
```



```
_________________________________________________________________
dense_3 (Dense)              (None, 1)                 9
=================================================================
Total params: 699.0
Trainable params: 699.0
Non-trainable params: 0.0
```

IV. Results

Model Evaluation and Validation

The results for the given models are as follows:

Algorithm	Validation Accuracy	Validation F_1	Test Accuracy	Test F_1
Base linear model	0.77	0.77	0.73	0.50
K-Nearest Neighbor	0.83	0.82	0.90	0.88
Random Forest	0.78	0.77	0.83	0.78
GaussianNB	0.84	0.82	0.90	0.88
Gradient Boosting	0.79	0.78	0.90	0.87
SVM	0.81	0.78	0.90	0.87
AdaBoost	0.82	0.80	0.87	0.83
Stacking ensemble	0.83	0.81	0.90	0.88
MLP	0.92	0.91	0.90	0.88

After dimension reduction the results changed to be as following:

Algorithm	Validation Accuracy	Validation F_1	Test Accuracy	Test F_1
K-Nearest Neighbor	0.82	0.81	0.80	0.77
Random Forest	0.81	0.79	0.87	0.85
GaussianNB	0.81	0.80	0.83	0.81
Gradient Boosting	0.81	0.80	0.83	0.81
SVM	0.83	0.81	0.87	0.83
AdaBoost	0.82	0.79	0.87	0.83
Stacking ensemble	0.85	0.84	0.87	0.85
MLP	0.89	0.88	0.83	0.80

From the above tables we can observe that the MLP is the best model in term of high validation accuracy and testing accuracy. It's also affected by the dimension reduction.

On the other hand, stacking ensemble gives high test accuracy and lower training accuracy than MLP. Its test accuracy less affected after dimension reduction. It could be the result of the improvement of random forest results after dimension reduction.

As a result, MLP model is chosen as the best model with high confidence.

Justification

Compared to the base linear model the MLP reach a high improvement in term of validation and testing accuracy.

The result found is better than 9 out of 13 papers mentioned before working on the same dataset. The best of all is that our approach is very simple and straight forward as alternative to other complex and hybrid methods. It's even better than stacked classifier which sum up many other classifiers.

V. Conclusion

In this work we have compared many machine learning techniques for heart diseases classification. We ended up with simple optimized model based on neural network. We also discussed the effect of feature selection and dimension reduction on the classification accuracy.

One of the next steps we could make to improve our results is by working on more complex model by combining neural network with stacked ensemble learning method in multi-stage classifier but, this model could need a bigger dataset or multiple datasets to examine for better results.