Project: Predicting Heart Disease with Classification Machine Learning Algorithms

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1. Introduction

Scenario:

You have just been hired at a Hospital with an alarming number of patients coming in reporting various cardiac symptoms. A cardioligist measures vitals & hands you this data to peform Data Analysis and predict whether certain patients have Heart Disease.

Goal:

-To predict whether a patient should be diagnosed with Heart Disease. This is a binary outcome.

Positive (+) = 1, patient diagnosed with Heart Disease

Negative (-) = 0, patient not diagnosed with Heart Disease

-To experiment with various Classification Models & see which yields greatest accuracy.

- Examine trends & correlations within our data

- determine which features are important in determing Positive/Negative Heart Disease

Features & Predictor:

Our Predictor (Y, Positive or Negative diagnosis of Heart Disease) is determined by 13 features (X):

1. age (#)

2. sex : 1= Male, 0= Female (Binary)

3. (cp)chest pain type (4 values -Ordinal):Value 1: typical angina ,Value 2: atypical angina, Value 3: non-anginal pain , Value 4: asymptomatic (

4. (trestbps) resting blood pressure (#)

5. (chol) serum cholestoral in mg/dl (#)

6. (fbs)fasting blood sugar > 120 mg/dl(Binary)(1 = true; 0 = false)

7. (restecg) resting electrocardiographic results(values 0,1,2)

8. (thalach) maximum heart rate achieved (#)

9. (exang) exercise induced angina (binary) (1 = yes; 0 = no)

10. (oldpeak) = ST depression induced by exercise relative to rest (#)

11. (slope) of the peak exercise ST segment (Ordinal) (Value 1: upsloping , Value 2: flat , Value 3: downsloping)

12. (ca) number of major vessels (0-3, Ordinal) colored by fluoroscopy

13. (thal) maximum heart rate achieved - (Ordinal): 3 = normal; 6 = fixed

defect; 7 = reversable defect

In [1]:

```
import numpy as np
import pandas as pd
import matplotlib as plt
import seaborn as sns
import matplotlib.pyplot as plt
```

In [2]:

```
# # 2. Data Wrangling

# In[191]:


filePath = 'heartDisease.csv'

data = pd.read_csv(filePath)

data.head(5)
```

Out[2]:

	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

In [3]:

```
print("(Rows, columns): " + str(data.shape))
data.columns
```

Out[3]:

```
(Rows, columns): (303, 14)
Index(['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach',
       'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target'],
      dtype='object')
```

In [4]:

```
data.nunique(axis=0)# returns the number of unique values for each variable.
```

Out[4]:

```
age          41
sex           2
cp            4
trestbps     49
chol        152
fbs           2
restecg       3
thalach      91
exang         2
oldpeak      40
slope         3
ca            5
thal          4
target        2
dtype: int64
```

In [5]:

```
#summarizes the count, mean, standard deviation, min, and max for numeric variables.
data.describe()
```

Out[5]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.366337	0.683168	0.966997	131.623762	246.264026	0.148515	0.528053	149.646865	0.326733
std	9.082101	0.466011	1.032052	17.538143	51.830751	0.356198	0.525860	22.905161	0.469794
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.000000
25%	47.500000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	133.500000	0.000000
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	153.000000	0.000000
75%	61.000000	1.000000	2.000000	140.000000	274.500000	0.000000	1.000000	166.000000	1.000000
max	77.000000	1.000000	3.000000	200.000000	564.000000	1.000000	2.000000	202.000000	1.000000

Luckily we have no missing data to handle!

In [6]:

```
# Display the Missing Values

print(data.isna().sum())
```

```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          0
thal        0
target      0
dtype: int64
```

Let's see if theirs a good proportion between our positive and negative results. It appears we have a good balance between the two.

In [7]:
```
data['target'].value_counts()
```

Out[7]:
```
1    165
0    138
Name: target, dtype: int64
```

3. Exploratory Data Analysis

Correlations

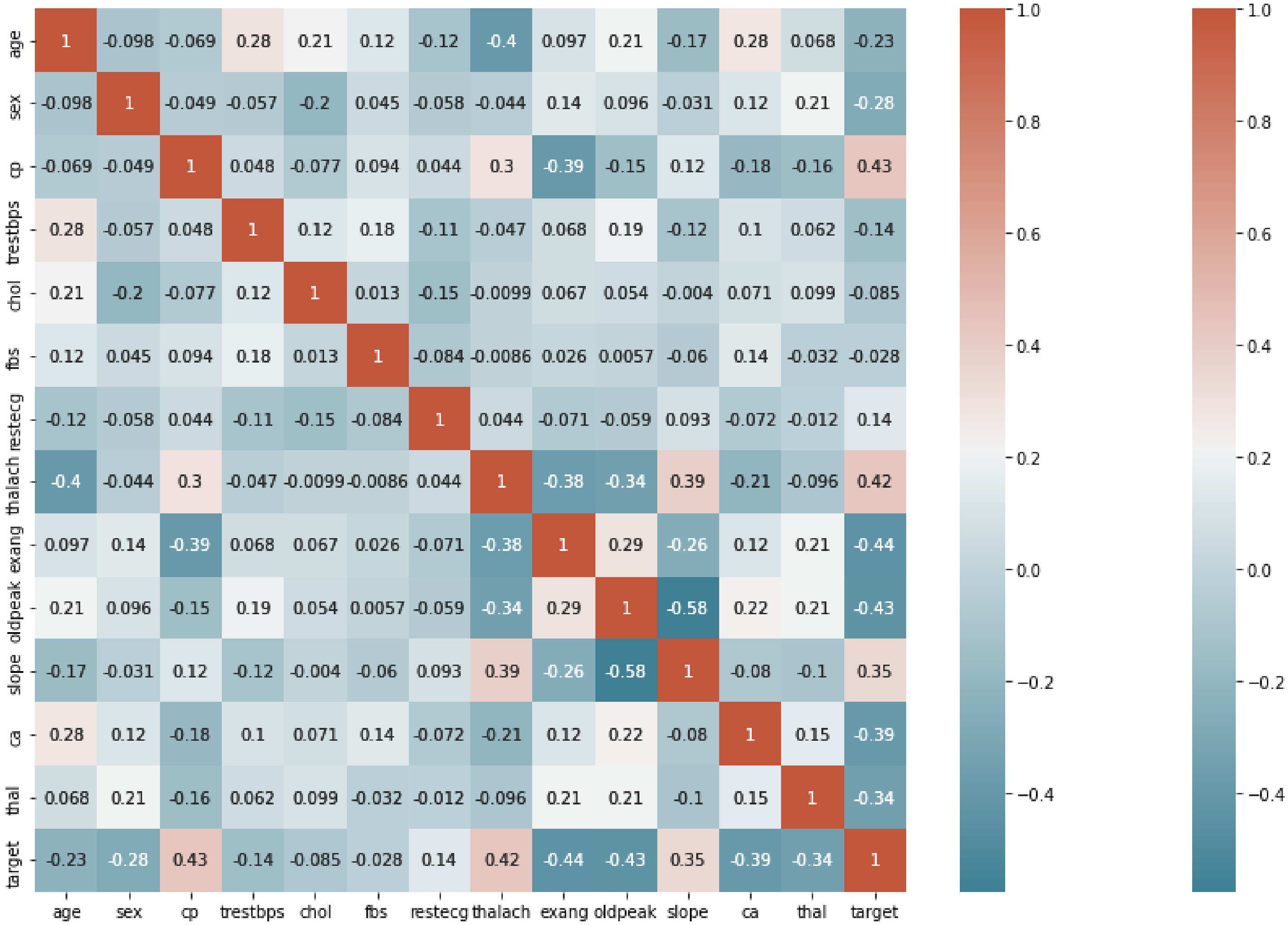
Correlation Matrix-

let's you see correlations between all variables. Within seconds, you can see whether something is positivly or negativly correlated with our predictor (target)

In [8]:
```
# calculate correlation matrix

corr = data.corr()
plt.subplots(figsize=(15,10))
sns.heatmap(corr, xticklabels=corr.columns, yticklabels=corr.columns, annot=True, cmap=sns
sns.heatmap(corr, xticklabels=corr.columns,
            yticklabels=corr.columns,
            annot=True,
            cmap=sns.diverging_palette(220, 20, as_cmap=True))
```

Out[8]:
```
<AxesSubplot:>
```



We can see there is a positive correlation between chest pain (cp) & target (our predictor). This makes sense since, The greater amount of chest pain results in a greater chance of having heart disease. Cp (chest pain), is a ordinal feature with 4 values: Value 1: typical angina ,Value 2: atypical angina, Value 3: non-anginal pain , Value 4: asymptomatic.

In addition, we see a negative correlation between exercise induced angina (exang) & our predictor. This makes sense because when you excercise, your heart requires more blood, but narrowed arteries slow down blood flow.

Pairplots are also a great way to immediatly see the correlations between all variables.

But you will see me make it with only continous columns from our data, because with so many features, it can be difficult to see each one.

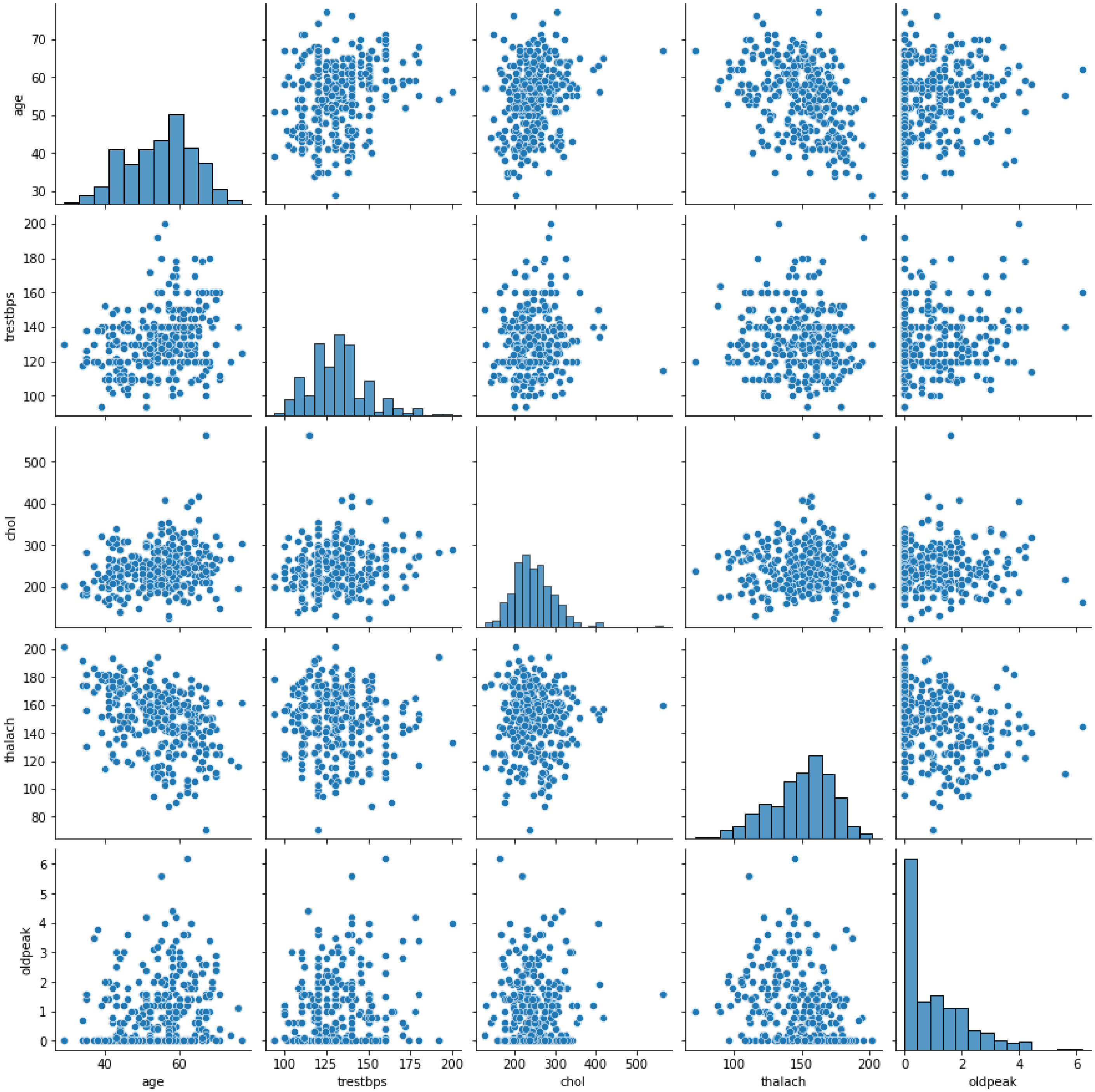
So instead I will make a pairplot with only our continous features.

In [9]:

```
subData = data[['age','trestbps','chol','thalach','oldpeak']]
sns.pairplot(subData)
```

Out[9]:

```
<seaborn.axisgrid.PairGrid at 0x228512df6a0>
```



Chose to make a smaller pairplot with only the continus variables, to dive deeper into the relationships. Also a great way to see if theirs a positve or negative correlation!

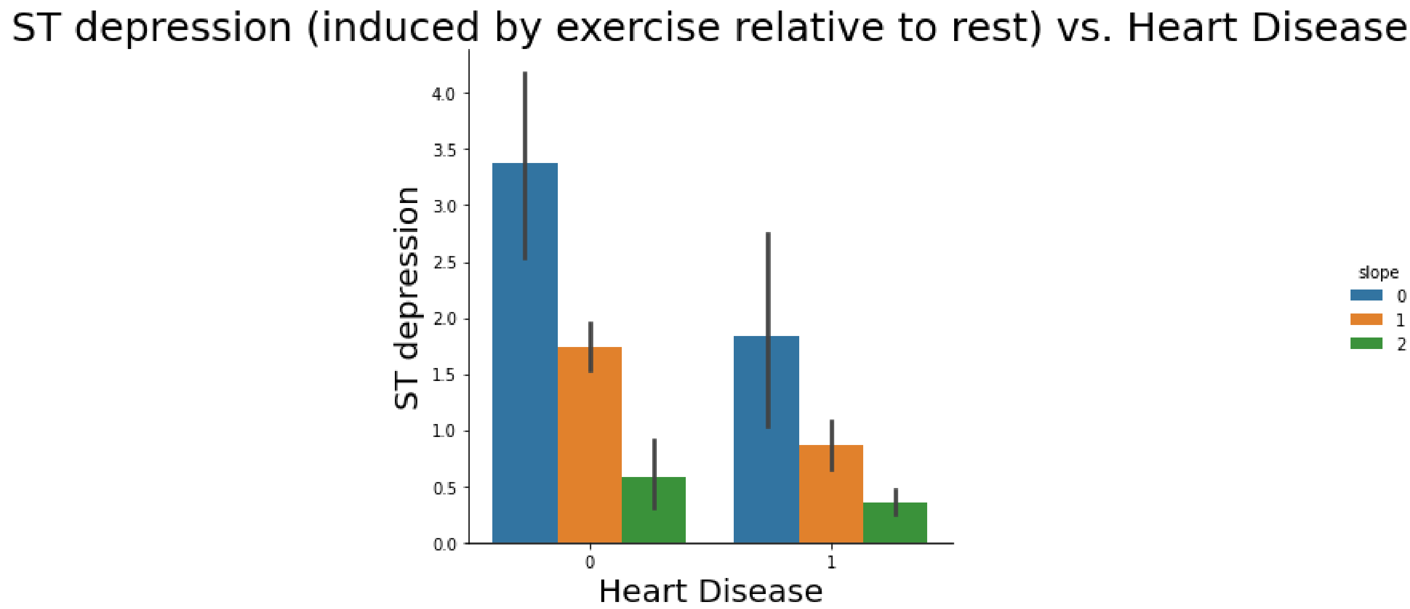
In [10]:

```
sns.catplot(x="target", y="oldpeak", hue="slope", kind="bar", data=data);

plt.title('ST depression (induced by exercise relative to rest) vs. Heart Disease',size=25
plt.xlabel('Heart Disease',size=20)
plt.ylabel('ST depression',size=20)
```

Out[10]:

```
Text(26.426458333333343, 0.5, 'ST depression')
```



ST segment depression occurs because when the ventricle is at rest and therefore repolarized. If the trace in the ST segment is abnormally low below the baseline, this can lead to this Heart Disease. This is supports the plot above because low ST Depression yields people at greater risk for heart disease. While a high ST depression is considered normal & healthy. The "slope" hue, refers to the peak exercise ST segment, with values: 0: upsloping , 1: flat , 2: downsloping). Both positive & negative heart disease patients exhibit equal distributions of the 3 slope categories.

Violin & Box Plots

The advantages of showing the Box & Violin plots is that it showsthe basic statistics of the data, as well as its distribution. These plots are often used to compare the distribution of a given variable across some categories.

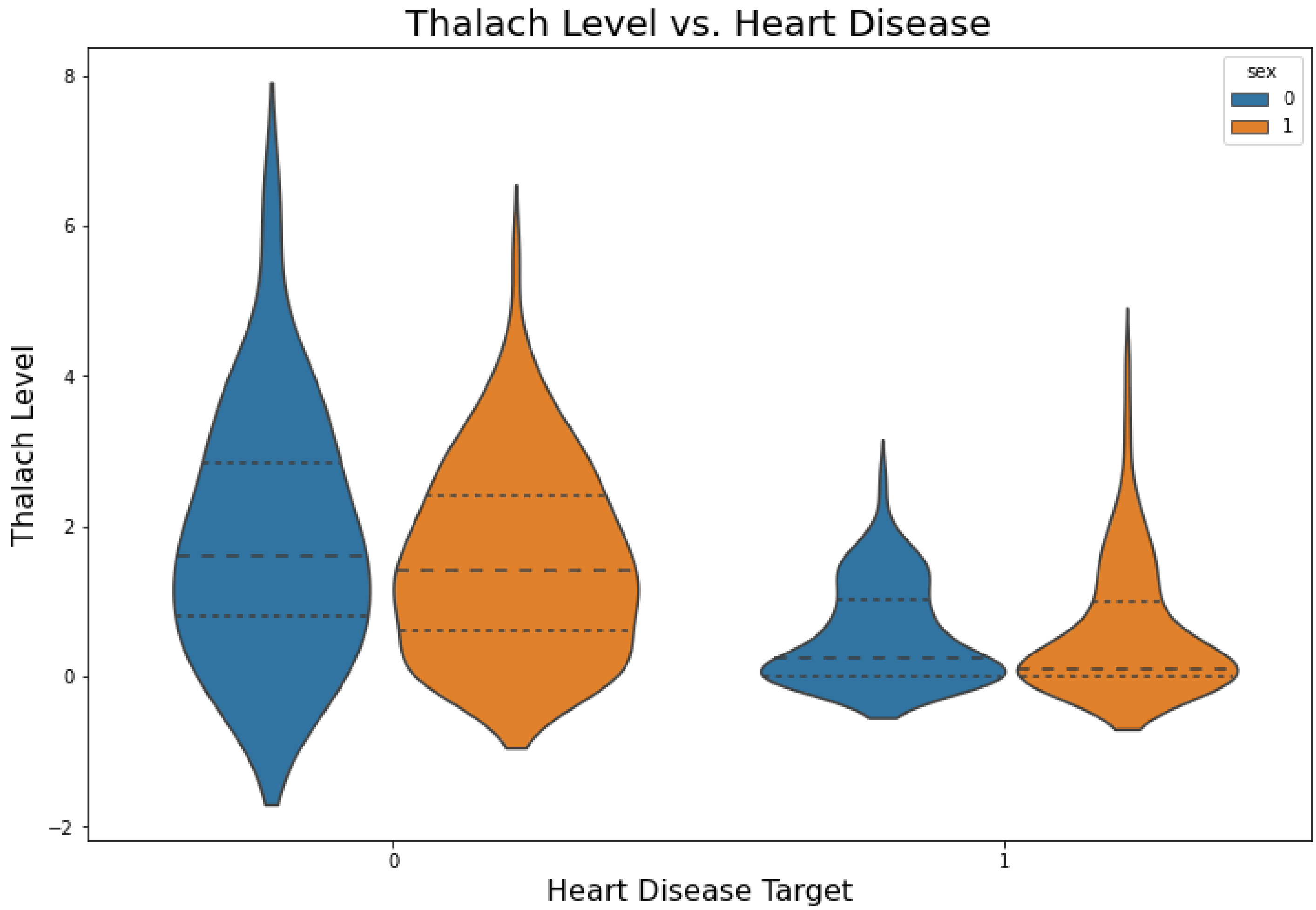
It shows the median, IQR, & Tukey's fence. (minimum, first quartile (Q1), median, third quartile (Q3), and maximum). In addition it can provide us with outliers in our data.

In [11]:

```
plt.figure(figsize=(12,8))
sns.violinplot(x= 'target', y= 'oldpeak',hue="sex", inner='quartile',data= data )
plt.title("Thalach Level vs. Heart Disease",fontsize=20)
plt.xlabel("Heart Disease Target", fontsize=16)
plt.ylabel("Thalach Level", fontsize=16)
```

Out[11]:

```
Text(0, 0.5, 'Thalach Level')
```

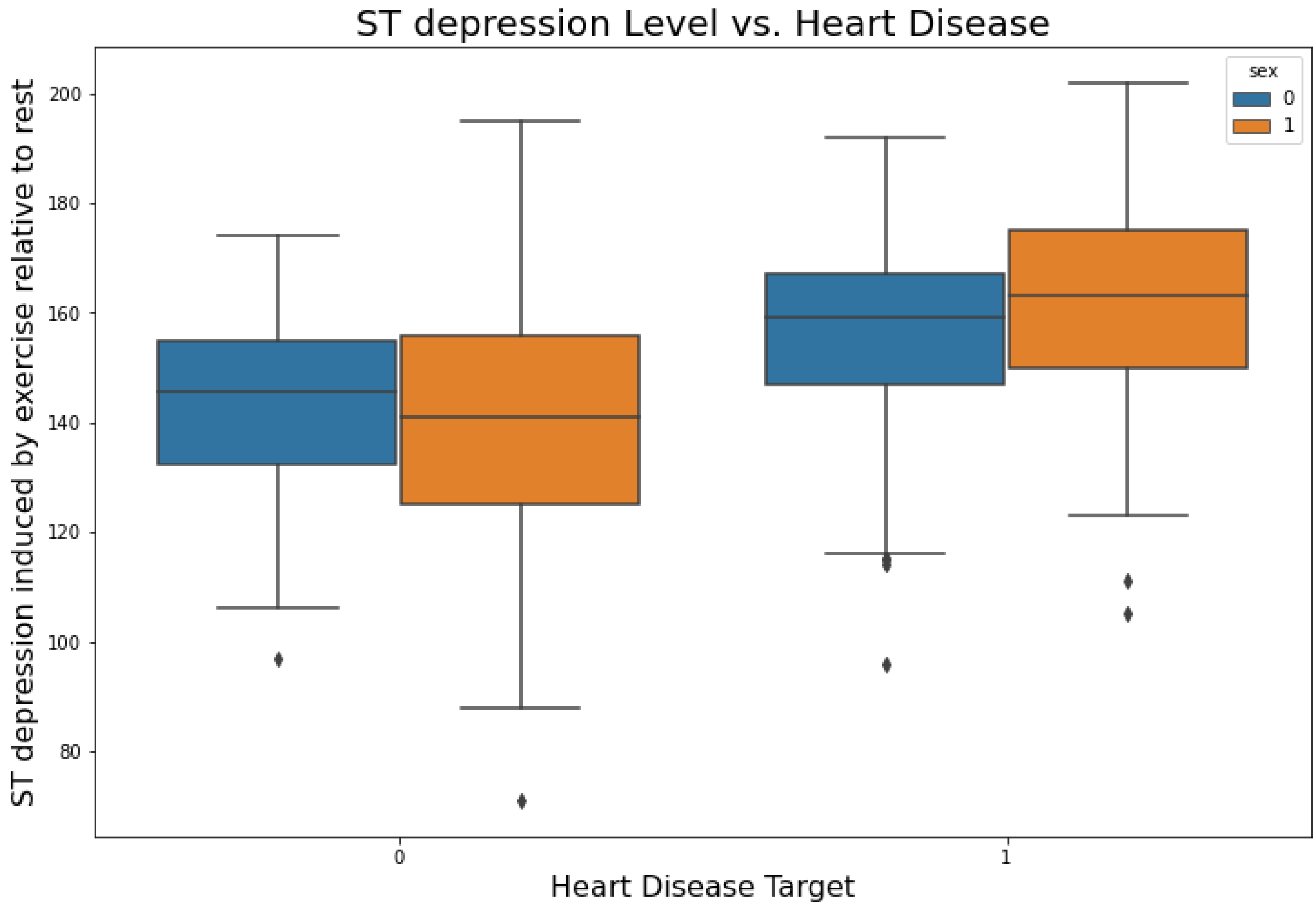


We can see that the overall shape & distribution for negative & positive patients differ vastly. Positive patients exhibit a lower median for ST depression level & thus a great distribution of their data is between 0 & 2, while negative patients are between 1 & 3. In addition, we dont see many differences between male & female target outcomes.

In [12]:
```
plt.figure(figsize=(12,8))
sns.boxplot(x= 'target', y= 'thalach',hue="sex", data=data )
plt.title("ST depression Level vs. Heart Disease", fontsize=20)
plt.xlabel("Heart Disease Target",fontsize=16)

plt.ylabel("ST depression induced by exercise relative to rest", fontsize=16)
```

Out[12]:
```
Text(0, 0.5, 'ST depression induced by exercise relative to rest')
```



Positive patients exhibit a hightened median for ST depression level, while negative patients have lower levels. In addition, we dont see many differences between male & female target outcomes, expect for the fact that males have slightly larger ranges of ST Depression.

Filtering data by positive & negative Heart Disease patient

In [13]:

```
# Filtering data by positive Heart Disease patient
pos_data = data[data['target']==1]
pos_data.describe()
```

Out[13]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang
count	165.000000	165.000000	165.000000	165.000000	165.000000	165.000000	165.000000	165.000000	165.000000
mean	52.496970	0.563636	1.375758	129.303030	242.230303	0.139394	0.593939	158.466667	0.139394
std	9.550651	0.497444	0.952222	16.169613	53.552872	0.347412	0.504818	19.174276	0.347412
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	96.000000	0.000000
25%	44.000000	0.000000	1.000000	120.000000	208.000000	0.000000	0.000000	149.000000	0.000000
50%	52.000000	1.000000	2.000000	130.000000	234.000000	0.000000	1.000000	161.000000	0.000000
75%	59.000000	1.000000	2.000000	140.000000	267.000000	0.000000	1.000000	172.000000	0.000000
max	76.000000	1.000000	3.000000	180.000000	564.000000	1.000000	2.000000	202.000000	1.000000

Filtering data by negative Heart Disease patient

In [14]:

```
# Filtering data by negative Heart Disease patient
neg_data = data[data['target']==0]
neg_data.describe()
```

Out[14]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang
count	138.000000	138.000000	138.000000	138.000000	138.000000	138.000000	138.000000	138.000000	138.000000
mean	56.601449	0.826087	0.478261	134.398551	251.086957	0.159420	0.449275	139.101449	0.550725
std	7.962082	0.380416	0.905920	18.729944	49.454614	0.367401	0.541321	22.598782	0.499232
min	35.000000	0.000000	0.000000	100.000000	131.000000	0.000000	0.000000	71.000000	0.000000
25%	52.000000	1.000000	0.000000	120.000000	217.250000	0.000000	0.000000	125.000000	0.000000
50%	58.000000	1.000000	0.000000	130.000000	249.000000	0.000000	0.000000	142.000000	1.000000
75%	62.000000	1.000000	0.000000	144.750000	283.000000	0.000000	1.000000	156.000000	1.000000
max	77.000000	1.000000	3.000000	200.000000	409.000000	1.000000	2.000000	195.000000	1.000000

In [15]:

```
print("(Positive Patients ST depression): " + str(pos_data['oldpeak'].mean()))
print("(Negative Patients ST depression): " + str(neg_data['oldpeak'].mean()))
```

```
(Positive Patients ST depression): 0.5830303030303029
(Negative Patients ST depression): 1.5855072463768118
```

In [16]:

```
print("(Positive Patients thalach): " + str(pos_data['thalach'].mean()))
print("(Negative Patients thalach): " + str(neg_data['thalach'].mean()))
```

```
(Positive Patients thalach): 158.46666666666667
(Negative Patients thalach): 139.1014492753623
```

From comparing positive and negative patients we can see there are vast differenes in means for many of our Features. From examing the details, we can observe that positive patients experience heightened maximum heart rate achieved (thalach) average. In addition, positive patients exhibit about 1/3rd the amount of ST depression induced by exercise relative to rest (oldpeak).

4. Machine Learning + Predictive Analytics

Prepare Data for Modeling

Assign the 13 features to X, & the last column to our classification predictor, y

In [17]:

```
X = data.iloc[:, :-1].values
y = data.iloc[:, -1].values
```

Split: the dataset into the Training set and Test set

In [18]:
```
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test = train_test_split(X,y,test_size = 0.2, random_state = 1)
```

Normalize: Standardizing the data will transform the data so that its distribution will have a mean of 0 and a standard deviation of 1.

In [19]:
```
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
x_train = sc.fit_transform(x_train)
x_test = sc.transform(x_test)
```

Modeling /Training

We will now Train various Classification Models on the Training set & see which yields the highest accuracy.

We will compare the accuracy of Logistic Regression, K-NN, SVM, Naives Bayes Classifier, Decision Trees, Random Forest, and XGBoost. Note: these are all supervised learning models.

Model 1: Logistic Regression

In [20]:
```
    from sklearn.metrics import classification_report
from sklearn.linear_model import LogisticRegression

model1 = LogisticRegression(random_state=1) # get instance of model
model1.fit(x_train, y_train) # Train/Fit model

y_pred1 = model1.predict(x_test) # get y predictions
print(classification_report(y_test, y_pred1)) # output accuracy
```

```
              precision    recall  f1-score   support

           0       0.77      0.67      0.71        30
           1       0.71      0.81      0.76        31

    accuracy                           0.74        61
   macro avg       0.74      0.74      0.74        61
weighted avg       0.74      0.74      0.74        61
```

Model 2: K-NN (K-Nearest Neighbors)

In [21]:
```
from sklearn.metrics import classification_report
from sklearn.neighbors import KNeighborsClassifier

model2 = KNeighborsClassifier() # get instance of model
model2.fit(x_train, y_train) # Train/Fit model

y_pred2 = model2.predict(x_test) # get y predictions
print(classification_report(y_test, y_pred2)) # output accuracy
```

```
              precision    recall  f1-score   support

           0       0.78      0.70      0.74        30
           1       0.74      0.81      0.77        31

    accuracy                           0.75        61
   macro avg       0.76      0.75      0.75        61
weighted avg       0.76      0.75      0.75        61
```

Model 3: SVM (Support Vector Machine)

In [22]:
```
from sklearn.metrics import classification_report
from sklearn.svm import SVC

model3 = SVC(random_state=1) # get instance of model
model3.fit(x_train, y_train) # Train/Fit model

y_pred3 = model3.predict(x_test) # get y predictions
print(classification_report(y_test, y_pred3)) # output accuracy
```

```
              precision    recall  f1-score   support

           0       0.80      0.67      0.73        30
           1       0.72      0.84      0.78        31

    accuracy                           0.75        61
   macro avg       0.76      0.75      0.75        61
weighted avg       0.76      0.75      0.75        61
```

Model 4: Naives Bayes Classifier

In [23]:
```
from sklearn.metrics import classification_report
from sklearn.naive_bayes import GaussianNB

model4 = GaussianNB() # get instance of model
model4.fit(x_train, y_train) # Train/Fit model

y_pred4 = model4.predict(x_test) # get y predictions
print(classification_report(y_test, y_pred4)) # output accuracy
```

```
              precision    recall  f1-score   support

           0       0.79      0.73      0.76        30
           1       0.76      0.81      0.78        31

    accuracy                           0.77        61
   macro avg       0.77      0.77      0.77        61
weighted avg       0.77      0.77      0.77        61
```

Model 5: Decision Trees

In [24]:
```
from sklearn.metrics import classification_report
from sklearn.tree import DecisionTreeClassifier
```

```
model5 = DecisionTreeClassifier(random_state=1)  # get instance of model
model5.fit(x_train, y_train) # Train/Fit model

y_pred5 = model5.predict(x_test) # get y predictions
print(classification_report(y_test, y_pred5)) # output accuracy
```

```
              precision    recall  f1-score   support

           0       0.68      0.70      0.69        30
           1       0.70      0.68      0.69        31

    accuracy                           0.69        61
   macro avg       0.69      0.69      0.69        61
weighted avg       0.69      0.69      0.69        61
```

Model 6: Random Forest

In [25]:

```
from sklearn.metrics import classification_report
from sklearn.ensemble import RandomForestClassifier

model6 = RandomForestClassifier(random_state=1)# get instance of model
model6.fit(x_train, y_train) # Train/Fit model

y_pred6 = model6.predict(x_test) # get y predictions
print(classification_report(y_test, y_pred6)) # output accuracy
```

```
              precision    recall  f1-score   support

           0       0.88      0.70      0.78        30
           1       0.76      0.90      0.82        31

    accuracy                           0.80        61
   macro avg       0.82      0.80      0.80        61
weighted avg       0.81      0.80      0.80        61
```

Model 7: XGBoost

In [26]:

```
from xgboost import XGBClassifier

model7 = XGBClassifier(random_state=1)
model7.fit(x_train, y_train)
y_pred7 = model7.predict(x_test)
print(classification_report(y_test, y_pred7))
```

```
              precision    recall  f1-score   support

           0       0.84      0.70      0.76        30
           1       0.75      0.87      0.81        31

    accuracy                           0.79        61
   macro avg       0.79      0.79      0.78        61
weighted avg       0.79      0.79      0.79        61
```

From comparing the 7 models, we can conclude that Model 6: Random Forest yields the highest accuracy. With an accuracy of

80%.

We have precision, recall, f1-score and support:

Precision : be "how many are correctly classified among that class"

Recall : "how many of this class you find over the whole number of element of this class"

F1-score : harmonic mean of precision and recall values.

F1 score reaches its best value at 1 and worst value at 0.

F1 Score = 2 x ((precision x recall) / (precision + recall))

Support: # of samples of the true response that lie in that class.

Making the Confusion Matrix

In [27]:

```
from sklearn.metrics import confusion_matrix, accuracy_score
cm = confusion_matrix(y_test, y_pred6)
print(cm)
accuracy_score(y_test, y_pred6)
```

```
[[21  9]
 [ 3 28]]
```

Out[27]:

```
0.8032786885245902
```

21 is the amount of True Positives in our data, while 28 is the amount of True Negatives.

9 & 3 are the number of errors.

There are 9 type 1 error (False Positives)- You predicted positive and it’s false.

There are 3 type 2 error (False Negatives)- You predicted negative and it’s false.

Hence if we calculate the accuracy its # Correct Predicted/ # Total.

In other words, where TP, FN, FP and TN represent the number of true positives, false negatives, false positives and true negatives.

(TP + TN)/(TP + TN + FP + FN).

(21+28)/(21+28+9+3) = 0.80 = 80% accuracy

Note: A good rule of thumb is that any accuracy above 70% is considered good, but be careful because if your accuracy is extremly high, it may be too good to be true (an example of Overfitting). Thus, 80% is the ideal accuracy!

Feature Importance

Feature Importance provides a score that indicates how helpful each feature was in our model.

The higher the Feature Score, the more that feature is used to make key decisions & thus the more important it is.

In [28]:

```
# get importance
importance = model6.feature_importances_

# summarize feature importance
for i,v in enumerate(importance):
    print('Feature: %0d, Score: %.5f' % (i,v))
```

```
Feature: 0, Score: 0.07814
Feature: 1, Score: 0.04206
Feature: 2, Score: 0.16580
Feature: 3, Score: 0.07477
Feature: 4, Score: 0.07587
Feature: 5, Score: 0.00828
Feature: 6, Score: 0.02014
```

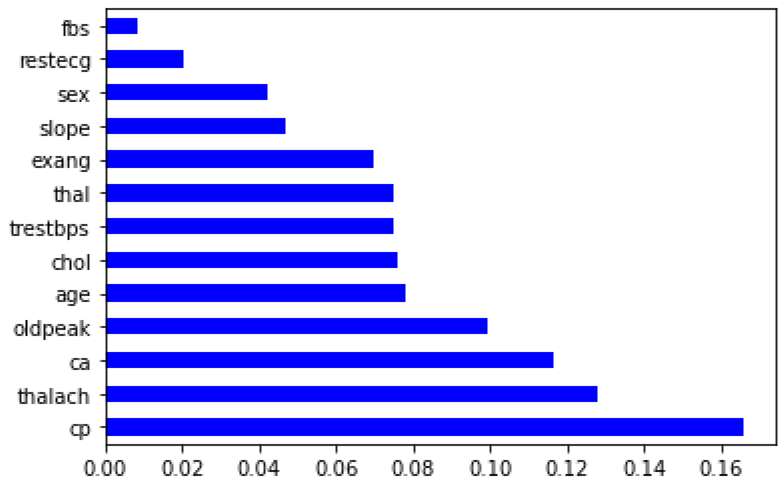
```
Feature: 7, Score: 0.12772
Feature: 8, Score: 0.06950
Feature: 9, Score: 0.09957
Feature: 10, Score: 0.04677
Feature: 11, Score: 0.11667
Feature: 12, Score: 0.07473
```

In [29]:

```python
index= data.columns[:-1]
importance = pd.Series(model6.feature_importances_, index=index)
importance.nlargest(13).plot(kind='barh', colormap='winter')
```

Out[29]:

```
<AxesSubplot:>
```



From the Feature Importance graph above, we can conclude that the top 4 significant features were chest pain type (cp), maximum heart rate achieved (thalach), number of major vessels (ca), and ST depression induced by exercise relative to rest (oldpeak).

Predictions

Scenario: A patient develops cardiac symptoms & you input his vitals into the Machine Learning Algorithm.

He is a 20 year old male, with a chest pain value of 2 (atypical angina), with resting blood pressure of 110.

In addition he has a serum cholestoral of 230 mg/dl.

He is fasting blood sugar > 120 mg/dl.

He has a resting electrocardiographic result of 1.

The patients maximum heart rate achieved is 140.

Also, he was exercise induced angina.

His ST depression induced by exercise relative to rest value was 2.2.

The slope of the peak exercise ST segment is flat.

He has no major vessels colored by fluoroscopy,

and in addition his maximum heart rate achieved is a reversable defect.

Based on this information, can you classify this patient with Heart Disease?

In [30]:
```
print(model6.predict(sc.transform([[20,1,2,110,230,1,1,140,1,2.2,2,0,2]])))
```

```
[1]
```

Yes! Our machine learning algorithm has classified this patient with Heart Disease. Now we can properly diagnose him, & get him the help he needs to recover. By diagnosing him early, we may prevent worse symtoms from arising later.

Predicting the Test set results:

First value represents our predicted value,

Second value represents our actual value.

If the values match, then we predicted correctly.

We can see that our results are very accurate!

In [31]:
```
y_pred = model6.predict(x_test)
print(np.concatenate((y_pred.reshape(len(y_pred),1), y_test.reshape(len(y_test),1)),1))
```

```
[[0 0]
 [1 1]
 [0 0]
 [0 0]
 [0 0]
 [0 0]
 [0 0]
 [1 1]
 [0 0]
 [1 1]
 [1 1]
 [0 0]
 [1 0]
 [0 0]
 [0 0]
 [1 0]
 [1 1]
```

```
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Conclusions

1. Our Random Forest algorithm yields the highest accuracy, 80%. Any accuracy above 70% is considered good, but be careful because if your accuracy is extremly high, it may be too good to be true (an example of Overfitting). Thus, 80% is the ideal accuracy!

2. Out of the 13 features we examined, the top 4 significant features that helped us classify between a positive & negative Diagnosis were chest pain type (cp), maximum heart rate achieved (thalach), number of major vessels (ca), and ST depression induced by exercise relative to rest (oldpeak).

3. Our machine learning algorithm can now classify patients with Heart Disease. Now we can properly diagnose patients, & get them the help they needs to recover. By diagnosing detecting these features early, we may prevent worse symtoms from arising later.

Thank you

Saad alsharif