Course-End Project: Healthcare

Problem statement:

Cardiovascular diseases are the leading cause of death globally. It is therefore necessary to identify the causes and develop a system to predict heart attacks in an effective manner. The data below has the information about the factors that might have an impact on cardiovascular health.

Dataset description:

Variable Description

Age Age in years

Sex 1 = male; 0 = female

cp| Chest pain type

trestbps Resting blood pressure (in mm Hg on admission to the hospital)

chol Serum cholesterol in mg/dl

fbs Fasting blood sugar > 120 mg/dl (1 = true; 0 = false)

restecg Resting electrocardiographic results

thalach Maximum heart rate achieved

exang Exercise induced angina (1 = yes; 0 = no)

oldpeak ST depression induced by exercise relative to rest

slope Slope of the peak exercise ST segment

ca Number of major vessels (0-3) colored by fluoroscopy

thal 3 = normal; 6 = fixed defect; 7 = reversible defect

Target 1 or 0

In [3]:
```
# Importing important libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

In [4]:
```
#Importing the dataset

dataset=pd.read_csv("health_dataset.csv")
```

1. Preliminary analysis:

a). Perform preliminary data inspection and report the findings on the structure of the data, missing values, duplicates, etc.

In [5]:
```
dataset.head()
```

Out[5]:

	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

Here all the columns are numerical so no need of conversion, trestbps,chol,thalach,oldpeak,age having contineous values other colums have categorical values like 0,1,2,3,4

In [6]:
```
type(dataset)
```

Out[6]:
```
pandas.core.frame.DataFrame
```

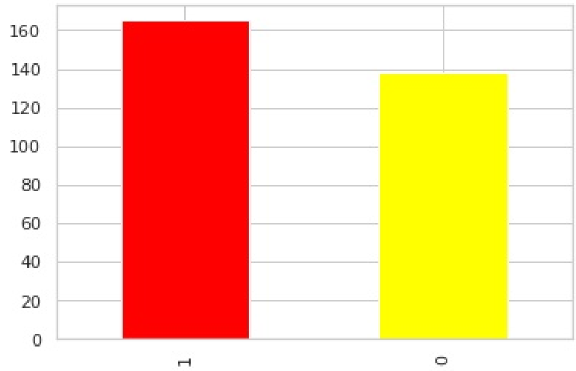
In [7]:
```
#Shape of dataset
dataset.shape
```

Out[7]:
```
(303, 14)
```

In [8]:
```
#how many class of one feature or target.
#in this dataset we have to check how many person have Cardiovascular diseases or not.
#0---- no Cardiovascular diseases
#1---- have chances of Cardiovascular diseases
#so this is clear that this is a classification problem

dataset["target"].value_counts()   #balanced data, it will count total no of entry in each categories
```

Out[8]:
```
1    165
0    138
Name: target, dtype: int64
```

In [28]:
```
# lets show the distribution of data using bar plot

dataset["target"].value_counts().plot(kind='bar', color=["red","yellow"])
plt.show()
```



Plot shows person having Cardiovascular diseases(1) =165 and person does not have Cardiovascular diseases(0)=138

data is quite balanced so we go for futher findings like null values ,missing values or any conversions needed.

In [29]:
```
#info
dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       303 non-null    int64  
 1   sex       303 non-null    int64  
 2   cp        303 non-null    int64  
 3   trestbps  303 non-null    int64  
 4   chol      303 non-null    int64  
 5   fbs       303 non-null    int64  
 6   restecg   303 non-null    int64  
 7   thalach   303 non-null    int64  
 8   exang     303 non-null    int64  
 9   oldpeak   303 non-null    float64
 10  slope     303 non-null    int64  
 11  ca        303 non-null    int64  
 12  thal      303 non-null    int64  
 13  target    303 non-null    int64  
dtypes: float64(1), int64(13)
memory usage: 33.3 KB
```

In [30]:
```
#checking for missing values

dataset.isna().sum()
```

Out[30]:
```
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
```

2. Prepare a report about the data explaining the distribution of the disease and the related factors using the steps listed below:

a. Get a preliminary statistical summary of the data and explore the measures of central tendencies and spread of the data

In [31]:
```
# lets check for statistical report of all numeical calumns as now we have only numeric columns
dataset.describe()
```

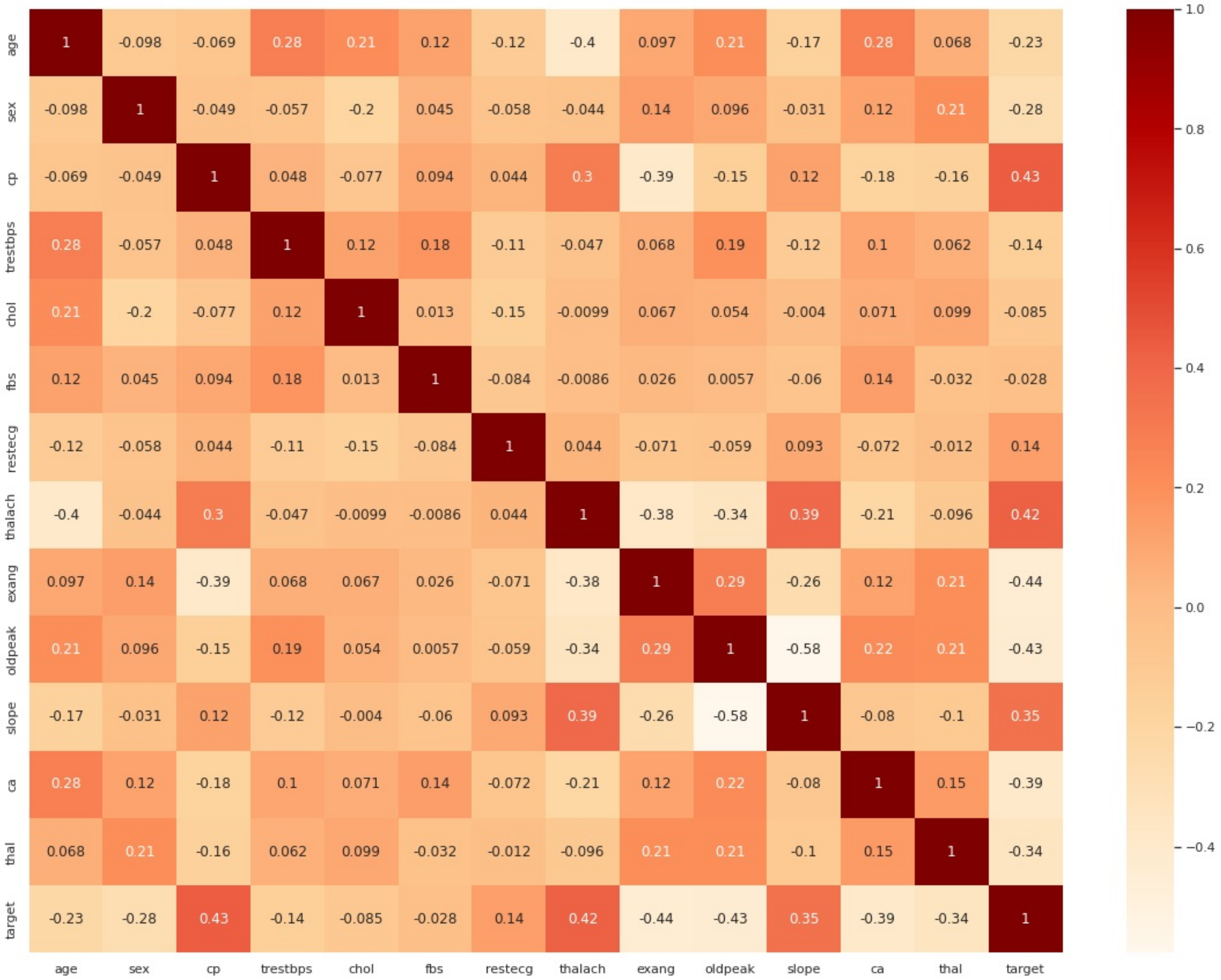
Out[31]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope
count	303.000000	303.000000	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	1.039604	1.399340
std	9.082101	0.466011	1.032052	17.538143	51.830751	0.356198	0.525860	22.905161	0.469794	1.161075	0.616226
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.000000	0.000000	0.000000
25%	47.500000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	133.500000	0.000000	0.000000	1.000000
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	153.000000	0.000000	0.800000	1.000000
75%	61.000000	1.000000	2.000000	140.000000	274.500000	0.000000	1.000000	166.000000	1.000000	1.600000	2.000000
max	77.000000	1.000000	3.000000	200.000000	564.000000	1.000000	2.000000	202.000000	1.000000	6.200000	2.000000

b. Identify the data variables which are categorical and describe and explore these variables using the appropriate tools, such as count plot

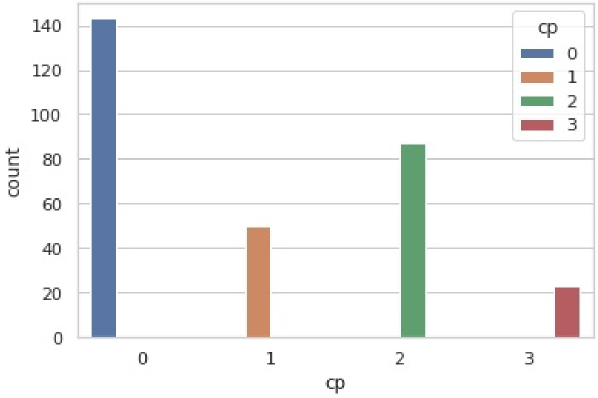
In [32]:
```
plt.figure(figsize=(20,15))
sns.heatmap(dataset.corr(),annot=True,cmap="OrRd")
```

Out[32]: <AxesSubplot:>



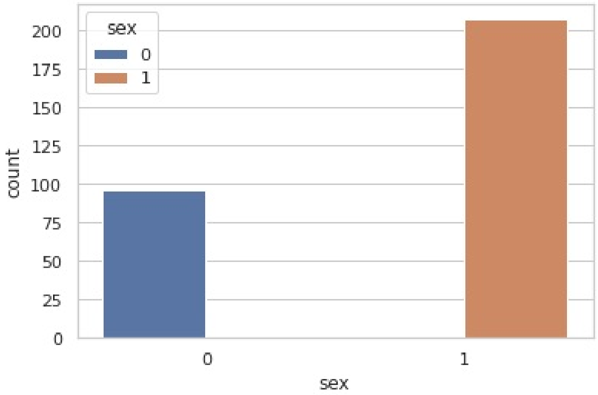
In [33]:
```
import seaborn as sns
sns.set_theme(style="whitegrid")
#sns.countplot(x=dataset["cp"])
sns.countplot(data=dataset, x="cp", hue="cp")
```

Out[33]:
```
<AxesSubplot:xlabel='cp', ylabel='count'>
```



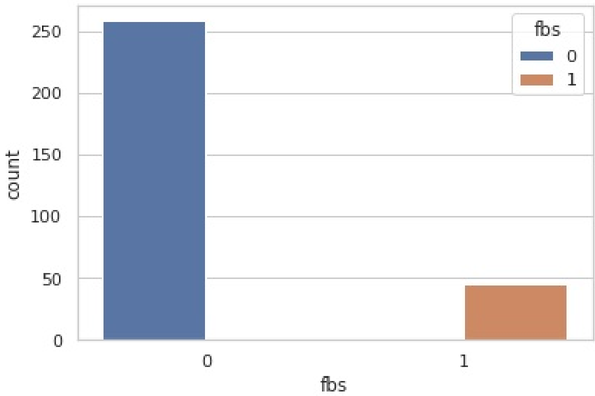
In [42]:
```
sns.countplot(data=dataset, x="sex", hue="sex")
```

Out[42]: <AxesSubplot:xlabel='sex', ylabel='count'>



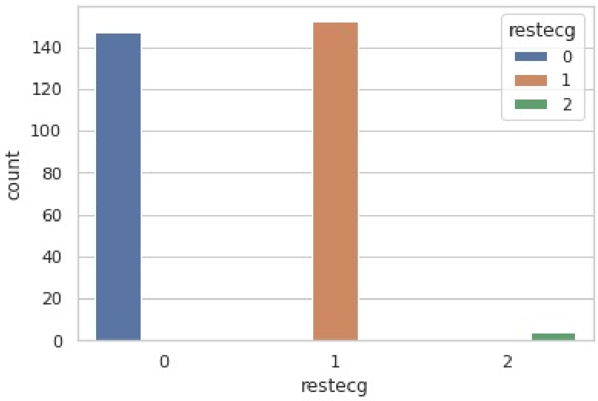
In [43]:
```
sns.countplot(data=dataset, x="fbs", hue="fbs")
```

Out[43]: <AxesSubplot:xlabel='fbs', ylabel='count'>



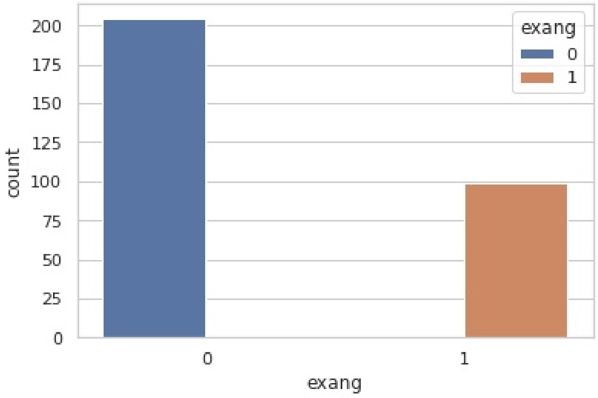
In [44]:
```
sns.countplot(data=dataset, x="restecg", hue="restecg")
```

Out[44]: <AxesSubplot:xlabel='restecg', ylabel='count'>



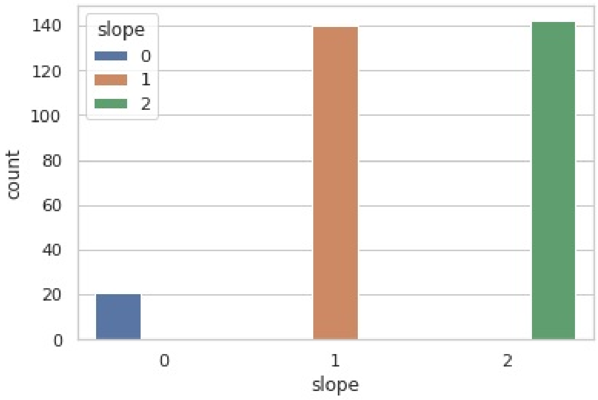
In [45]:
```
sns.countplot(data=dataset, x="exang", hue="exang")
```

Out[45]:
```
<AxesSubplot:xlabel='exang', ylabel='count'>
```



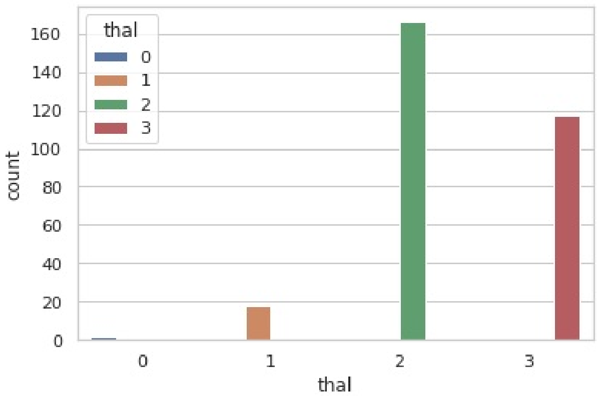
In [46]:
```python
sns.countplot(data=dataset, x="slope", hue="slope")
```

Out[46]:
```
<AxesSubplot:xlabel='slope', ylabel='count'>
```



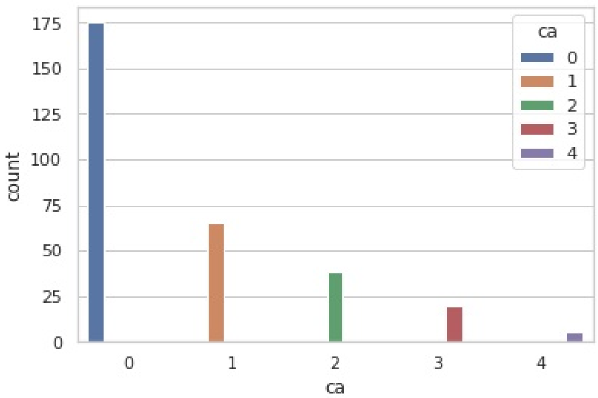
In [47]:
```python
sns.countplot(data=dataset, x="thal", hue="thal")
```

Out[47]:
```
<AxesSubplot:xlabel='thal', ylabel='count'>
```



In [48]:
```python
sns.countplot(data=dataset, x="ca", hue="ca")
```

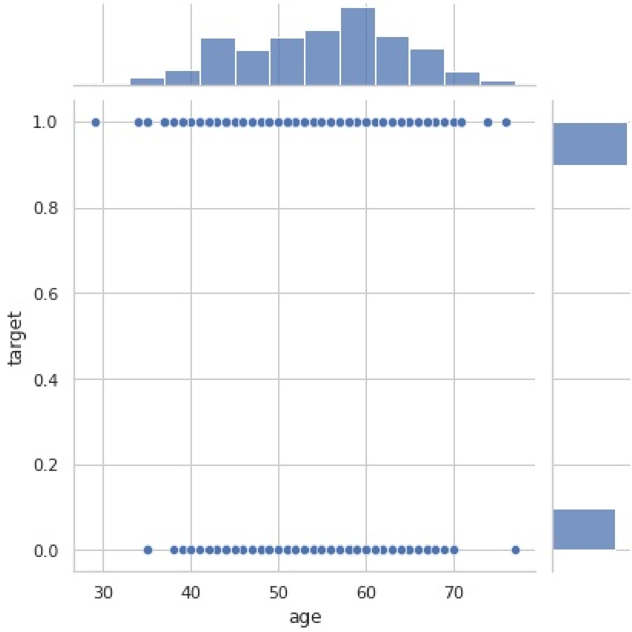
Out[48]:
```
<AxesSubplot:xlabel='ca', ylabel='count'>
```



c. Study the occurrence of CVD across the Age category

In [49]:
```python
sns.jointplot(data=dataset, x="age", y="target")
```

Out[49]:
```
<seaborn.axisgrid.JointGrid at 0x7f8b74b0cf10>
```



d. Study the composition of all patients with respect to the Sex category

In [50]:
```
#Heart Disease Frequency according to Sex, here 1=male ,0=female
dataset.sex.value_counts()
```

Out[50]:
```
1    207
0     96
Name: sex, dtype: int64
```

In [53]:
```
#Creating contingency table to compare sex with target
pd.crosstab(dataset.target, dataset.sex)
```

Out[53]:

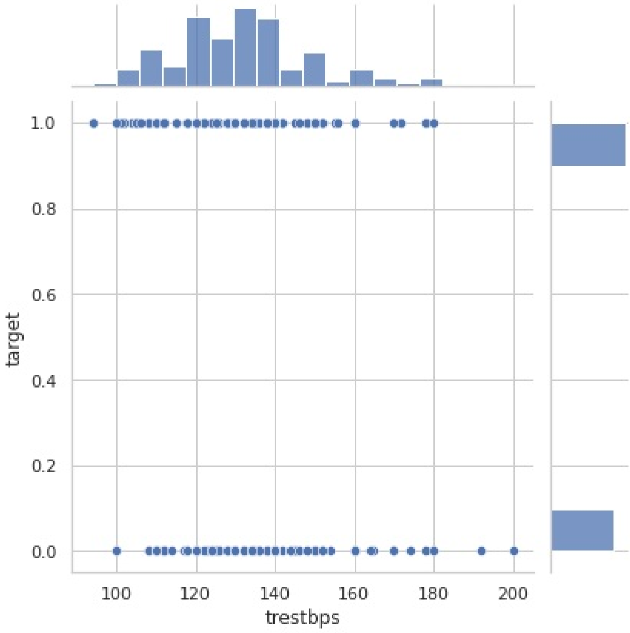
sex	0	1
target		
0	24	114
1	72	93

Here contingency table shows 72 /207 male have chance to Cardiovascular diseases.93/96 female have chance to Cardiovascular diseases. 24 female and 114 male are save from diseases

e. Study if one can detect heart attacks based on anomalies in the resting blood pressure (trestbps) of a patient

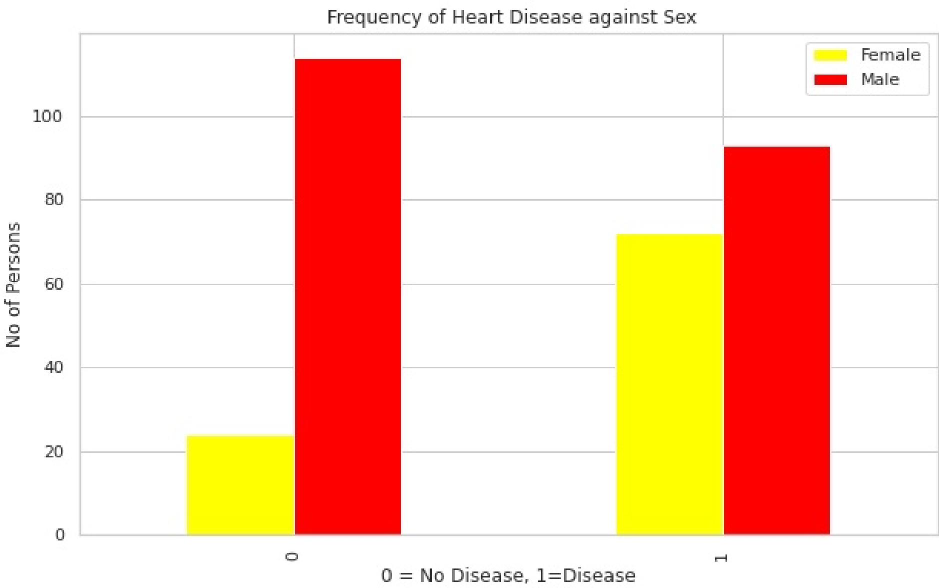
In [65]:
```
#sns.boxplot(x=dataset["trestbps"])
#pd.crosstab(dataset.target, dataset.trestbps)
sns.jointplot(data=dataset, x="trestbps", y="target")
```

Out[65]:
```
<seaborn.axisgrid.JointGrid at 0x7f8b741588d0>
```



if a person having resting blood pressure between 120-150mm hg having more risk of heart attack

In [66]:
```
#Create plot of heart disease against sex
pd.crosstab(dataset.target, dataset.sex).plot(kind="bar",figsize=(10,6),color=["yellow","red"])
plt.title(" Frequency of Heart Disease against Sex")
plt.xlabel("0 = No Disease, 1=Disease")
plt.ylabel("No of Persons")
plt.legend(["Female","Male"]);
```



In [67]:
```
#Heart Disease Frequency vs Chest Pain
```

```
#chest pain type
#0: Typical angina: chest pain related decrease blood supply to the heart
#1: Atypical angina: chest pain not related to heart
#2: Non-anginal pain: typically esophageal spasms (non heart related)
#3: Asymptomatic: chest pain not showing signs of disease
```

In [68]:

```
#creating crosstab
pd.crosstab(dataset.cp,dataset.target)
```

Out[68]:

target	0	1
cp		
0	104	39
1	9	41
2	18	69
3	7	16

Bivariate analysis of important features

like cp-chest pain ,trestbps,fbs,restecg,thalach,exang,slope

In [69]:

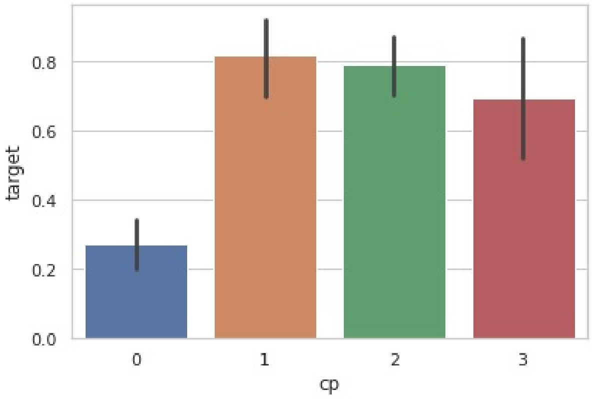
```
#Analysing the 'Chest Pain Type' feature
dataset["cp"].unique()
```

Out[69]:

```
array([3, 2, 1, 0])
```

In [70]:

```
sns.barplot(dataset["cp"],dataset['target'])
plt.show()
```

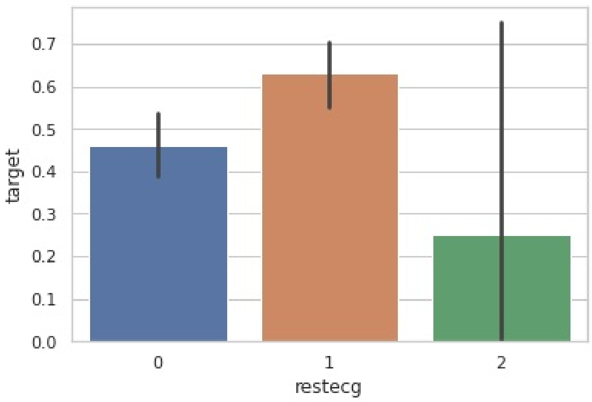


graph shows 1: Atypical angina: chest pain not related to heart have the more no of cases than 2: Non-anginal pain: typically esophageal spasms (non heart related) followed by 3: Asymptomatic: chest pain not showing signs of disease 0: Typical angina: chest pain related decrease blood supply to the heart

so the person with typical anging problem have less chance of Heard disease

In [71]:

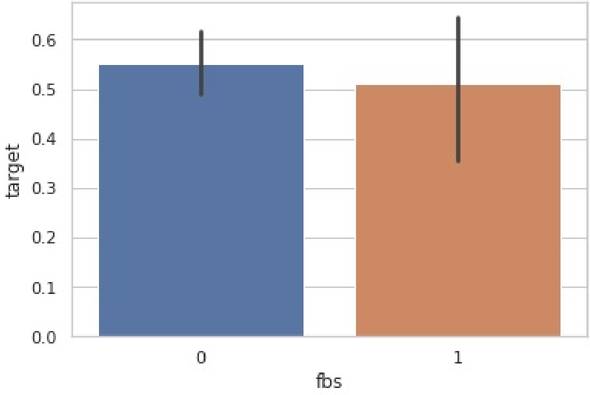
```
#Analysing the restecg feature (Resting electrocardiographic results )
dataset["restecg"].unique()

sns.barplot(dataset["restecg"],dataset["target"])
plt.show()
```



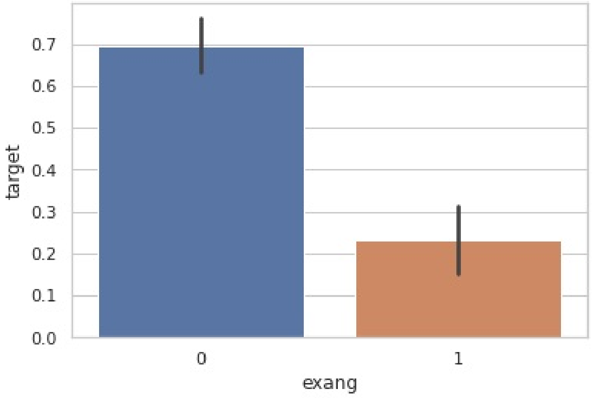
In [72]:

```
#Analysing the fbs feature(Fasting blood sugar > 120 mg/dl (1 = true; 0 = false))
```

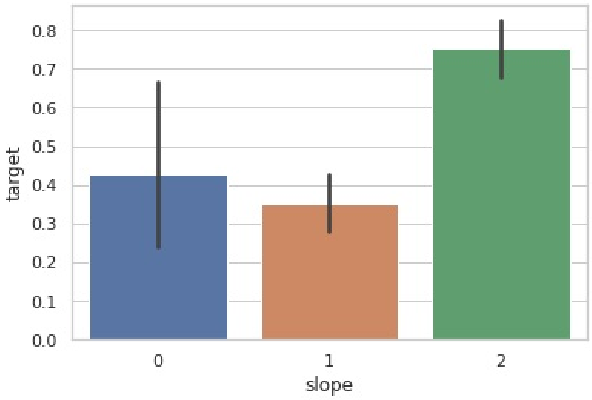
In [72]:
```python
#Analysing the fbs feature(Fasting blood sugar > 120 mg/dl (1 = true; 0 = false))
dataset["fbs"].unique()

sns.barplot(dataset["fbs"],dataset["target"])
plt.show()
```



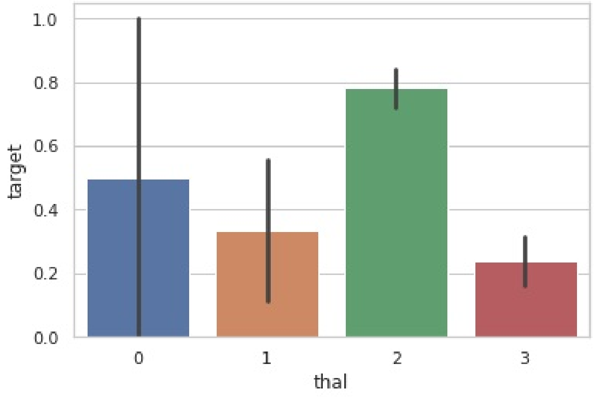
In [73]:
```python
#Analysing the exang feature(Exercise induced angina (1 = yes; 0 = no))
dataset["exang"].unique()

sns.barplot(dataset["exang"],dataset["target"])
plt.show()
```



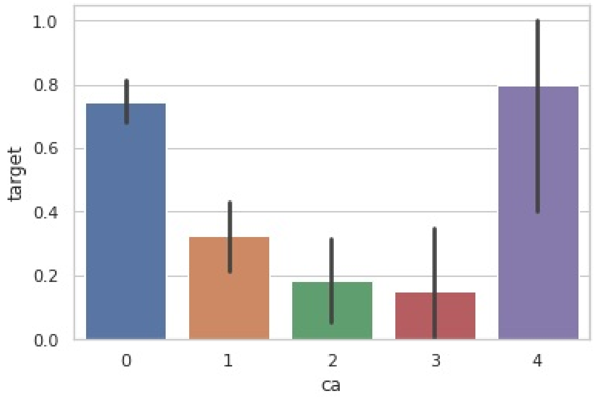
In [74]:
```python
#Analysing the slope feature(Slope of the peak exercise ST segment)
dataset["slope"].unique()

sns.barplot(dataset["slope"],dataset["target"])
plt.show()
```



In [75]:
```python
#Analysing the thal feature (thal having three values ,3 = normal; 6 = fixed defect; 7 = reversible defect)
dataset["thal"].unique()

sns.barplot(dataset["thal"],dataset["target"])
plt.show()
```

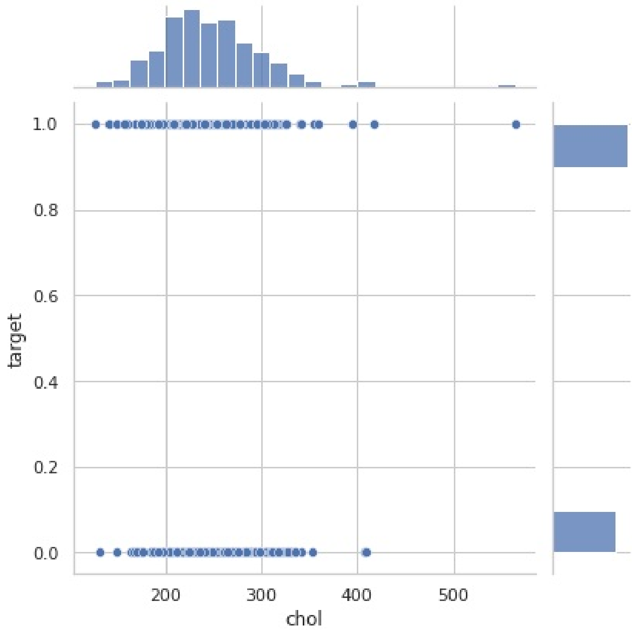


In [76]:
```
#Analysing the ca feature (Ca=Number of major vessels (0-3) colored by fluoroscopy)
dataset["ca"].unique()

sns.barplot(dataset["ca"],dataset["target"])
plt.show()
```



f. Describe the relationship between cholesterol levels and a target variable

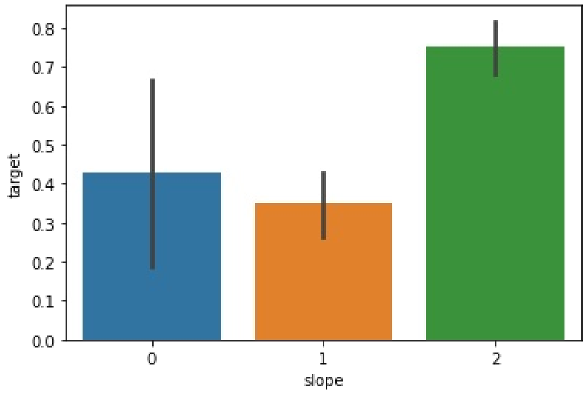
In [77]:
```
#Analysing the chol feature (Serum cholesterol in mg/dl)
dataset["chol"].unique()

#sns.barplot(dataset["chol"],dataset["target"])
sns.jointplot(data=dataset, x="chol", y="target")

plt.show()
```



g. State what relationship exists between peak exercising and the occurrence of a heart attack

In [28]:
```
#Analysing the slope feature(Slope of the peak exercise ST segment)
dataset["slope"].unique()

sns.barplot(dataset["slope"],dataset["target"])
#sns.jointplot(data=dataset, x="slope", y="target")
```

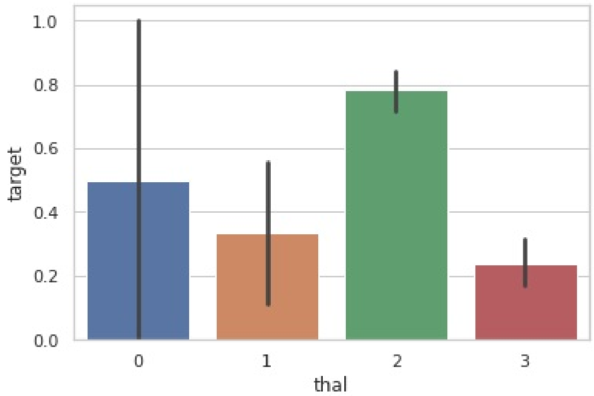
```
plt.show()
```



h. Check if thalassemia is a major cause of CVD

In [79]:
```
#sns.jointplot(data=dataset, x="thal", y="target")
sns.barplot(dataset["thal"],dataset["target"])
```

Out[79]: <AxesSubplot:xlabel='thal', ylabel='target'>



thalassemia is one of the cause of heart attack , in graph we see that thal type 2 having more chance of heart attack

j. Use a pair plot to understand the relationship between all the given variables

Pairplot():-

The pairplot() function offers a similar blend of joint and marginal distributions. Rather than focusing on a single relationship, however, pairplot() uses a “small-multiple” approach to visualize the univariate distribution of all variables in a dataset along with all of their pairwise relationships:

In [85]:
```
sns.pairplot(dataset)
```

Out[85]: <seaborn.axisgrid.PairGrid at 0x7f8b609bad10>

Data Processing

b. Based on these findings, remove duplicates (if any) and treat missing values using an appropriate strategy we now use get_dummies method to create dummys for categorical variables.before fitting data to model data should be scaled,or not have any string variables

In [86]:
```
#segregarting the categorical variables and continuous ones
categorical_val = []
continous_val = []
for column in dataset.columns:
    if len(dataset[column].unique()) <= 10:
        categorical_val.append(column)
    else:
        continous_val.append(column)

print("The list selected categorical columns for which we create dummies:-",categorical_val)
```

```
The list selected categorical columns for which we create dummies:- ['sex', 'cp', 'fbs', 'restecg', 'exang', 's
lope', 'ca', 'thal', 'target']
```

In [87]:
```
categorical_val.remove('target')
dataset = pd.get_dummies(dataset, columns = categorical_val)
```

In [92]:
```
dataset.head(2)
```

Out[92]:

	age	trestbps	chol	thalach	oldpeak	target	sex_0	sex_1	cp_0	cp_1	...	slope_2	ca_0	ca_1	ca_2	ca_3	ca_4	thal_0
0	0.952197	0.763956	-0.256334	0.015443	1.087338	1	0	1	0	0	...	0	1	0	0	0	0	0
1	-1.915313	-0.092738	0.072199	1.633471	2.122573	1	0	1	0	0	...	0	1	0	0	0	0	0

2 rows × 31 columns

In [93]:
```
#standardizing the data
from sklearn.preprocessing import StandardScaler

scale = StandardScaler()
scaled_columns = ['age', 'trestbps', 'chol', 'thalach', 'oldpeak']
dataset[scaled_columns] = scale.fit_transform(dataset[scaled_columns])
```

In [94]:
```
dataset.head()
```

Out[94]:

	age	trestbps	chol	thalach	oldpeak	target	sex_0	sex_1	cp_0	cp_1	...	slope_2	ca_0	ca_1	ca_2	ca_3	ca_4	thal_0
0	0.952197	0.763956	-0.256334	0.015443	1.087338	1	0	1	0	0	...	0	1	0	0	0	0	0
1	-1.915313	-0.092738	0.072199	1.633471	2.122573	1	0	1	0	0	...	0	1	0	0	0	0	0
2	-1.474158	-0.092738	-0.816773	0.977514	0.310912	1	1	0	0	1	...	1	1	0	0	0	0	0
3	0.180175	-0.663867	-0.198357	1.239897	-0.206705	1	0	1	0	1	...	1	1	0	0	0	0	0
4	0.290464	-0.663867	2.082050	0.583939	-0.379244	1	1	0	1	0	...	1	1	0	0	0	0	0

5 rows × 31 columns

In [95]:
```
#Train Test split
from sklearn.model_selection import train_test_split

predictors = dataset.drop("target",axis=1)
target = dataset["target"]

X_train,X_test,Y_train,Y_test = train_test_split(predictors,target,test_size=0.20,random_state=0)
print("Size of traing dataset{x_train, y_train}:-",X_train.shape,Y_train.shape)
print("Size of testing dataset{x_test, y_test}:-",X_test.shape,Y_test.shape)

#the train and testing data should be same size
```

```
Size of traing dataset{x_train, y_train}:- (242, 30) (242,)
Size of testing dataset{x_test, y_test}:- (61, 30) (61,)
```

we do the accuracy score comparision of diferent classifications models like Logistic Regression SVM XGboost KNN Randomforest

3. Build a baseline model to predict the risk of a heart attack using a logistic regression and random forest and explore the results while using correlation analysis and logistic regression (leveraging standard error and p-values from statsmodels) for feature selection

In [96]:
```
from sklearn.metrics import accuracy_score
#Logistic Regression
from sklearn.linear_model import LogisticRegression

lr = LogisticRegression()

lr.fit(X_train,Y_train)
```

```
Y_pred_lr = lr.predict(X_test)
score_lr = round(accuracy_score(Y_pred_lr,Y_test)*100,2)

print("The accuracy score achieved using Logistic Regression is: "+str(score_lr)+" %")
```

```
The accuracy score achieved using Logistic Regression is: 88.52 %
```

In [97]:

```
from sklearn.ensemble import RandomForestClassifier
clf = RandomForestClassifier(criterion = 'gini',
                             max_depth = 8,
                             n_estimators=200,
                             min_samples_split=10,
                             random_state=5)
#fitting the training data
clf.fit(X_train,Y_train)

y_pred = clf.predict(X_test)

from sklearn.metrics import confusion_matrix
confusion_matrix(Y_test,y_pred)
#as we see in confusion matrix we have good classification(22,31) and  very less miss classification(5,3) so ou
```

Out[97]:

```
array([[22,  5],
       [ 3, 31]])
```

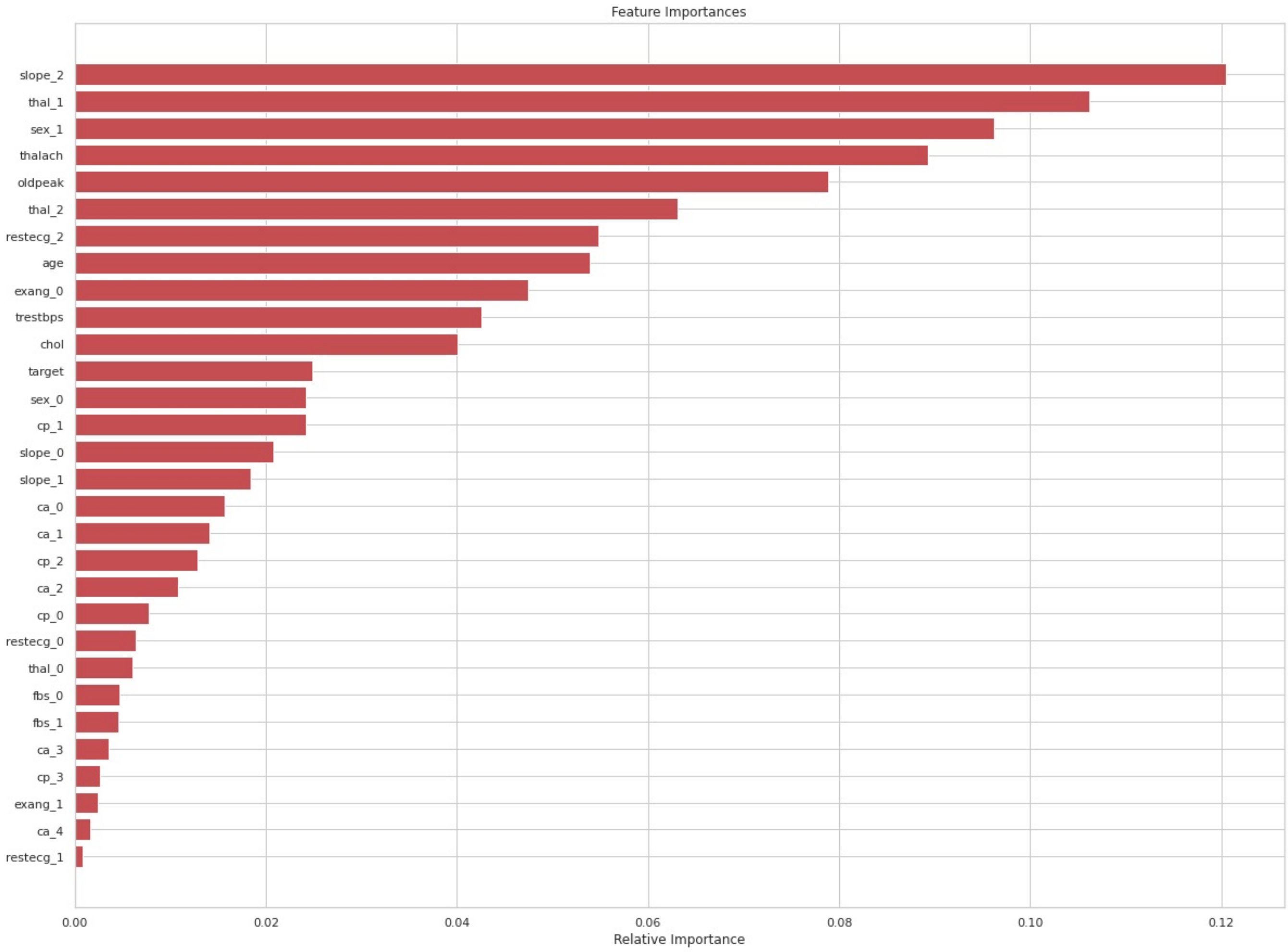
In [98]:

```
from sklearn.metrics import accuracy_score

score_rf=round(accuracy_score(Y_test,y_pred)*100,2)
print("The accuracy score achieved using Random forest Classifier is: "+str(score_rf)+" %")
```

```
The accuracy score achieved using Random forest Classifier is: 86.89 %
```

In [99]:

```
features = dataset.columns
importances = clf.feature_importances_
indices = np.argsort(importances) #the sorting is done in asc order

plt.figure(figsize=(20,15))
plt.title("Feature Importances")
plt.barh(range(len(indices)),importances[indices],color='r',align='center')
plt.yticks(range(len(indices)),[features[i] for i in indices])
plt.xlabel('Relative Importance')
plt.show()
```



In [100…

```
#SVM
from sklearn import svm

sv = svm.SVC(kernel='linear')
```

```python
sv.fit(X_train, Y_train)

Y_pred_svm = sv.predict(X_test)
score_svm = round(accuracy_score(Y_pred_svm,Y_test)*100,2)

print("The accuracy score achieved using Linear SVM is: "+str(score_svm)+" %")
```

```
The accuracy score achieved using Linear SVM is: 81.97 %
```

In [101…

```python
#Xgboost
import xgboost as xgb

xgb_model = xgb.XGBClassifier(objective="binary:logistic", random_state=42)
xgb_model.fit(X_train, Y_train)

Y_pred_xgb = xgb_model.predict(X_test)
score_xgb = round(accuracy_score(Y_pred_xgb,Y_test)*100,2)

print("The accuracy score achieved using XGBoost is: "+str(score_xgb)+" %")
```

```
The accuracy score achieved using XGBoost is: 83.61 %
```

In [102…

```python
#KNN
from sklearn.neighbors import KNeighborsClassifier

knn_clf = KNeighborsClassifier()
knn_clf.fit(X_train, Y_train)

Y_pred_clf = knn_clf.predict(X_test)

score_knn = round(accuracy_score(Y_pred_clf,Y_test)*100,2)
print("The accuracy score achieved using KNN Classifier is: "+str(score_knn)+" %")
```

```
The accuracy score achieved using KNN Classifier is: 78.69 %
```

Conclusion

Our model is predicting very well the give dataset with the use of diferent classificarion models

In [106…

```python
print("*****************************Models and their accuracy****************************************")
print("The accuracy score achieved using Logistic Regression is:- "+str(score_lr)+" %")
print("The accuracy score achieved using Random forest Classifier is:- "+str(score_rf)+" %")
print("The accuracy score achieved using XGBoost is:- "+str(score_xgb)+" %")
print("The accuracy score achieved using Linear SVM is:- "+str(score_svm)+" %")
print("The accuracy score achieved using KNN Classifier is:- "+str(score_knn)+" %")
```

```
*****************************Models and their accuracy****************************************
The accuracy score achieved using Logistic Regression is: 88.52 %
The accuracy score achieved using Random forest Classifier is: 86.89 %
The accuracy score achieved using XGBoost is: 83.61 %
The accuracy score achieved using Linear SVM is: 81.97 %
The accuracy score achieved using KNN Classifier is: 78.69 %
```

After implementing five classification models and comparing their accuracy, we can conclude that for this dataset Logistic Regression Classifier is the appropriate model to be used.

In [ ]:

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