Capstone Project:
Determine and examine factors that play a significant role in increasing the rate of heart attacks.
Also, use the findings to create and predict a model.

In [46]:
```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings('ignore')
```

In [47]:
```
#reading data
data = pd.read_csv("heart.csv")
df = pd.read_csv("o2Saturation.csv")
data.head()
```

Out[47]:

	age	sex	cp	trtbps	chol	fbs	restecg	thalachh	exng	oldpeak	slp	caa	thall	output
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 [48]:
```
df.head()
```

Out[48]:

	98.6
0	98.6
1	98.6
2	98.6
3	98.1
4	97.5

In [49]:
```
#pip install pandas-profiling
```

In [30]:
```
import dtale
d = dtale.show(data)
```

In [31]:
```
d
```

Out[31]:

In [ ]:

In [50]:
```
data.describe()
```

Out[50]:

	age	sex	cp	trtbps	chol	fbs	restecg	thalachh	exng	oldpeak	slp	caa	thall	output
count	303.000000	303.000000	303.000000	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	0.729373	2.313531	0.544554
std	9.082101	0.466011	1.032052	17.538143	51.830751	0.356198	0.525860	22.905161	0.469794	1.161075	0.616226	1.022606	0.612277	0.498835
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.000000	0.000000	0.000000	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	0.000000	2.000000	0.000000
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	153.000000	0.000000	0.800000	1.000000	0.000000	2.000000	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	1.000000	3.000000	1.000000
max	77.000000	1.000000	3.000000	200.000000	564.000000	1.000000	2.000000	202.000000	1.000000	6.200000	2.000000	4.000000	3.000000	1.000000

Exploratory data analysis(EDA)

In [51]:
```
data["output"].unique()
```

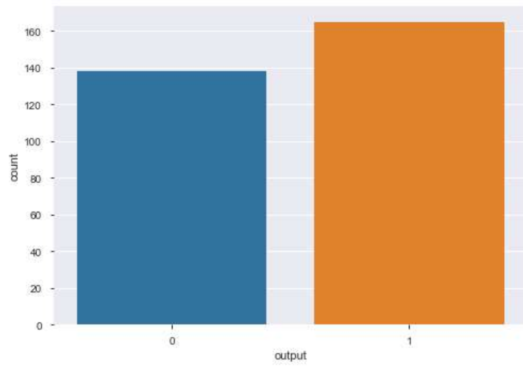
Out[51]:
```
array([1, 0], dtype=int64)
```

In [52]:
```
tar = data["output"]
target_dist = data.output.value_counts()
print(target_dist)
sns.countplot(tar)
```

```
1    165
0    138
Name: output, dtype: int64
```

Out[52]:

```
<AxesSubplot:xlabel='output', ylabel='count'>
```



In [53]:

```
#here we calculate the percentage of people who have had an attack vs those without.
heart_attack = target_dist[1]*100 /303
no_attack = target_dist[0]*100/303

print("percentage of pations who have had an attack:",heart_attack)
print("percentage of pations who have  never had an attack", no_attack)
```

```
percentage of pations who have had an attack: 54.45544554455446
percentage of pations who have  never had an attack 45.54455445544554
```

checking relationship amoung variables

In [54]:

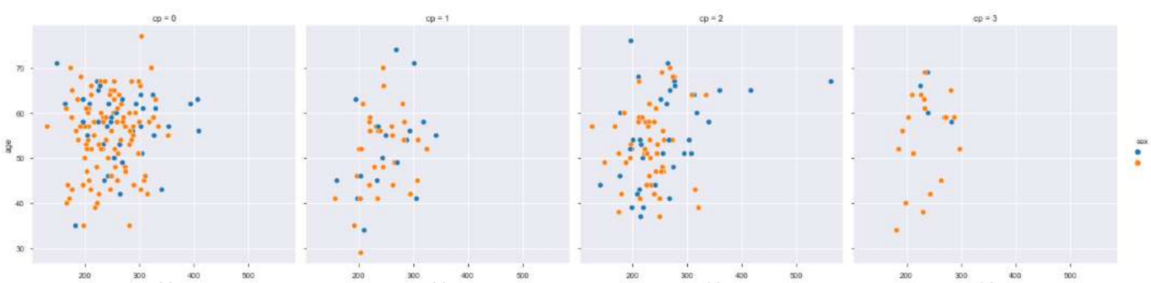
```
data.head()
```

Out[54]:

	age	sex	cp	trtbps	chol	fbs	restecg	thalachh	exng	oldpeak	slp	caa	thall	output
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 [56]:

```
rela = sns.relplot(x = "chol", y = "age" , hue = "sex", data = data , col = "cp")
```



from the analysis above,

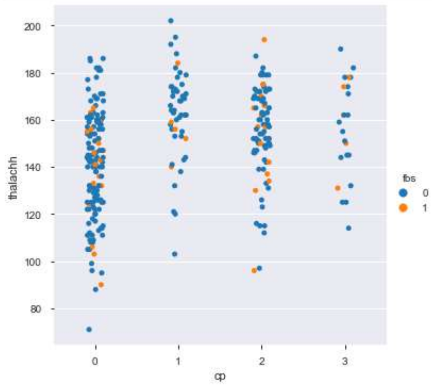
I am checking the relationship between variables using seaborn replot chart and from the result we can deduct that people between the age of 50 years and 65 are experiencing cp = 0 (AGINA)

which is the most common pain among the lists.

Also, we can conclude that these chest pains and cholesterol levels indicate that it is mostly among women that men (as shown on the charts)

categorical plots

In [57]:
```
cat = sns.catplot(x ="cp",y = "thalachh" , hue = "fbs" , data = data)
```



fasting blood sugar (fbs) > 120 if true denoted by 1 else 0 - (1 = True , 0 = false)

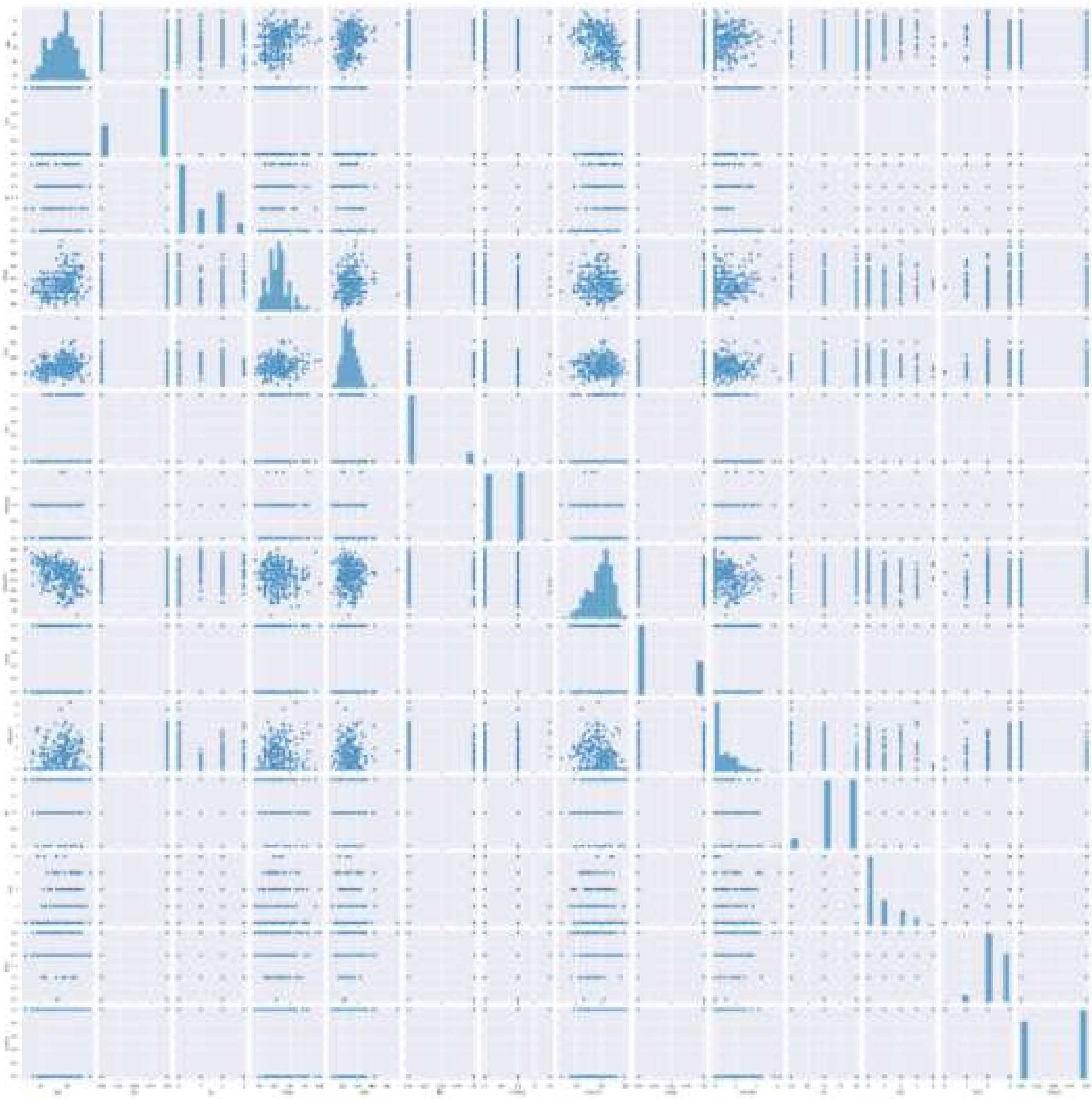
from the categorical plot above we can deduce that cp [0] is the common chest pain(cp) experienced by the patients followed by cp [2], cp [1] and lastly cp [3].

we can also see that the level of fasting blood sugar (fbs) is below 120 meaning that most of the patients fbs is not above 120.

In [ ]:
```

```

In [58]:
```
g =  sns.pairplot(data)
```



In [59]:
```
g
```

Out[59]: <seaborn.axisgrid.PairGrid at 0x2988c27bcd0>

In [ ]:

In [60]:
```
# checking for missing values
data.isnull().sum()
```

Out[60]:
```
age         0
sex         0
cp          0
trtbps      0
chol        0
fbs         0
restecg     0
thalachh    0
exng        0
oldpeak     0
slp         0
caa         0
thall       0
output      0
dtype: int64
```

In [61]:

```python
#checking for duplicate entries
data.duplicated().sum
```

Out[61]:

```
<bound method Series.sum of 0      False
1      False
2      False
3      False
4      False
       ...
298    False
299    False
300    False
301    False
302    False
Length: 303, dtype: bool>
```

In [62]:

```python
data.shape
```

Out[62]:

```
(303, 14)
```

In [63]:

```python
#checking the data types in the dataset
data.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   trtbps    303 non-null    int64  
 4   chol      303 non-null    int64  
 5   fbs       303 non-null    int64  
 6   restecg   303 non-null    int64  
 7   thalachh  303 non-null    int64  
 8   exng      303 non-null    int64  
 9   oldpeak   303 non-null    float64
 10  slp       303 non-null    int64  
 11  caa       303 non-null    int64  
 12  thall     303 non-null    int64  
 13  output    303 non-null    int64  
dtypes: float64(1), int64(13)
memory usage: 33.3 KB
```

In [64]:

```python
#checking for duplicate entries
dup_rows = data[data.duplicated()]
print("Number of duplicated entries are:", dup_rows.shape)
```

```
Number of duplicated entries are: (1, 14)
```

In [65]:

```python
dup_rows.head()
```

Out[65]:

	age	sex	cp	trtbps	chol	fbs	restecg	thalachh	exng	oldpeak	slp	caa	thall	output
164	38	1	2	138	175	0	1	173	0	0.0	2	4	2	1

In [67]:

```python
#droppping the dup row
data.drop([164])
```

Out[67]:

	age	sex	cp	trtbps	chol	fbs	restecg	thalachh	exng	oldpeak	slp	caa	thall	output
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
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
298	57	0	0	140	241	0	1	123	1	0.2	1	0	3	0
299	45	1	3	110	264	0	1	132	0	1.2	1	0	3	0
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3	0
301	57	1	0	130	131	0	1	115	1	1.2	1	1	3	0
302	57	0	1	130	236	0	0	174	0	0.0	1	1	2	0

302 rows × 14 columns

In [68]:

```
#checking for unique values and making them categorical variables
print("cp")
print(*list(data.cp.unique()))
print("restecg")
print(*list(data.restecg.unique()))
```

```
cp
3 2 1 0
restecg
0 1 2
```

In [69]:

```
# now we have to change the features from int to categorical feature using pandas categorical( function)
data.cp = pd.Categorical(data.cp)
data.restecg = pd.Categorical(data.restecg)
```

In [70]:

```
# again we check  data.info()
data.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    category
 3   trtbps    303 non-null    int64
 4   chol      303 non-null    int64
 5   fbs       303 non-null    int64
 6   restecg   303 non-null    category
 7   thalachh  303 non-null    int64
 8   exng      303 non-null    int64
 9   oldpeak   303 non-null    float64
 10  slp       303 non-null    int64
 11  caa       303 non-null    int64
 12  thall     303 non-null    int64
 13  output    303 non-null    int64
dtypes: category(2), float64(1), int64(11)
memory usage: 29.4 KB
```

In [71]:

```
# Lets get a discription of our data
data.describe()
```

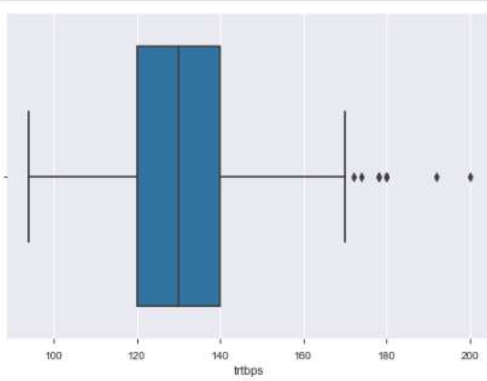
Out[71]:

	age	sex	trtbps	chol	fbs	thalachh	exng	oldpeak	slp	caa	thall	output
count	303.000000	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	131.623762	246.264026	0.148515	149.646865	0.326733	1.039604	1.399340	0.729373	2.313531	0.544554
std	9.082101	0.466011	17.538143	51.830751	0.356198	22.905161	0.469794	1.161075	0.616226	1.022606	0.612277	0.498835
min	29.000000	0.000000	94.000000	126.000000	0.000000	71.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	47.500000	0.000000	120.000000	211.000000	0.000000	133.500000	0.000000	0.000000	1.000000	0.000000	2.000000	0.000000
50%	55.000000	1.000000	130.000000	240.000000	0.000000	153.000000	0.000000	0.800000	1.000000	0.000000	2.000000	1.000000
75%	61.000000	1.000000	140.000000	274.500000	0.000000	166.000000	1.000000	1.600000	2.000000	1.000000	3.000000	1.000000
max	77.000000	1.000000	200.000000	564.000000	1.000000	202.000000	1.000000	6.200000	2.000000	4.000000	3.000000	1.000000

outlier mining

In [72]:

```
#lets viusalize our outliers
sns.boxplot(data["trtbps"])
xlable ="trtbps"
```



In the above analysis,

we can see that all values above 170 are acting as outliers.

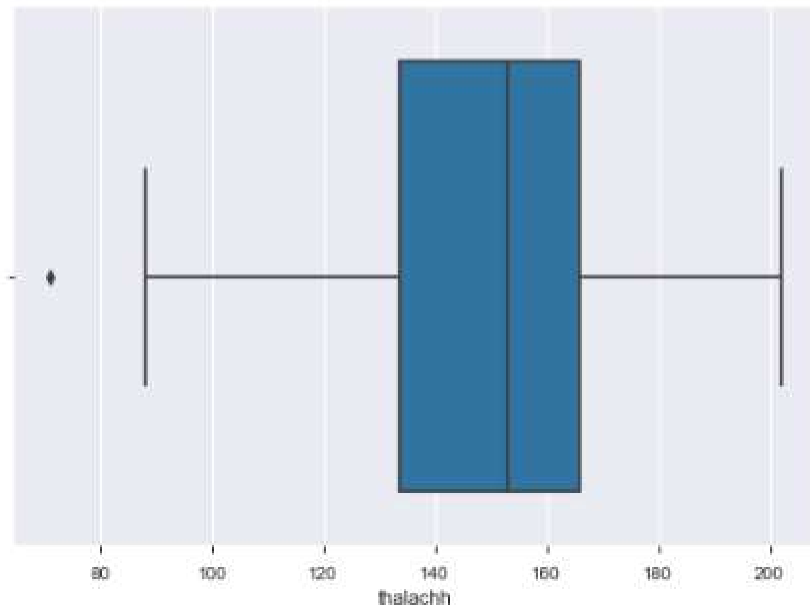
In [73]:

```
#position of the outliers
print(np.where(data['trtbps']>170))
```

```
(array([  8, 101, 110, 203, 223, 241, 248, 260, 266], dtype=int64),)
```

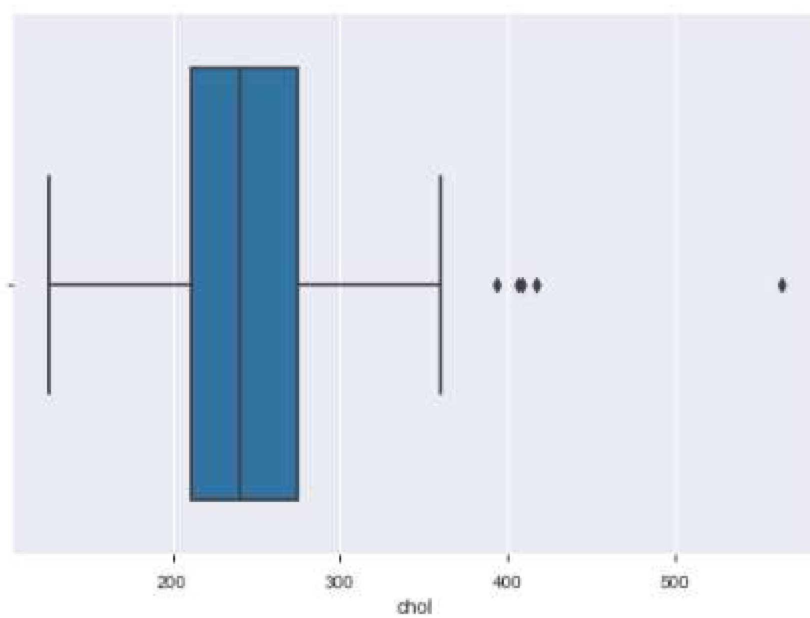
In [74]:

```
# outliers for thalach
sns.boxplot(data["thalachh"])
xlable ="thalachh"
```



In [75]:

```
sns.boxplot(data["chol"])
xlable ="chol"
```



detecting and removing outliers using the z-score

The Z-score is the signed number of standard deviations by which the value of an observation or data point is above the mean value of what is being observed or measured.

In [76]:
```
from scipy import stats

z = np.abs(stats.zscore(data))
print(z)
```

```
[[0.9521966  0.68100522 1.97312292 ... 0.71442887 2.14887271 0.91452919]
 [1.91531289 0.68100522 1.00257707 ... 0.71442887 0.51292188 0.91452919]
 [1.47415758 1.46841752 0.03203122 ... 0.71442887 0.51292188 0.91452919]
 ...
 [1.50364073 0.68100522 0.93851463 ... 1.24459328 1.12302895 1.09345881]
 [0.29046364 0.68100522 0.93851463 ... 0.26508221 1.12302895 1.09345881]
 [0.29046364 1.46841752 0.03203122 ... 0.26508221 0.51292188 1.09345881]]
```

Looking the code and the output above, it is difficult to say which data point is an outlier. Let's try and define a threshold to identify an outlier.

In [77]:
```
threshold = 3
print(np.where(z > threshold))
```

```
(array([ 28,  48,  85,  92, 158, 163, 164, 204, 220, 221, 223, 246, 248,
       251, 272, 281], dtype=int64), array([ 4, 12,  4, 11, 11, 11, 11,  9,  4,  9,  3,  4,  3, 11,  7, 12],
      dtype=int64))
```

Don't be confused by the results.

The first array contains the list of row numbers and second array respective column numbers, which mean z [28][1] have a Z-score higher than 3.

In [78]:
```
print(z[28][1])
```

```
1.4684175155588415
```

In [79]:
```
clean_data = data[(z < 3).all(axis=1)]
```

In [80]:
```
#before outliers
data.shape
```

Out[80]:
```
(303, 14)
```

In [81]:
```
clean_data.shape
```

Out[81]:
```
(287, 14)
```

Here, as we can see we have dropped 16 entries that were outliers.

checking correlation between our variables

In [82]:
```
corr= clean_data.corr()
corr.style.background_gradient(cmap='PuOr')
```

Out[82]:

	age	sex	trtbps	chol	fbs	thalachh	exng	oldpeak	slp	caa	thall	output
age	1.000000	-0.072391	0.304702	0.177192	0.133044	-0.400067	0.112509	0.193431	-0.155421	0.368764	0.055830	-0.226750
sex	-0.072391	1.000000	-0.039006	-0.141218	0.058432	-0.053999	0.146867	0.166430	-0.054768	0.135552	0.244047	-0.302926
trtbps	0.304702	-0.039006	1.000000	0.143586	0.167890	-0.075059	0.065089	0.156988	-0.103302	0.057947	0.027382	-0.119281
chol	0.177192	-0.141218	0.143586	1.000000	-0.005337	-0.030874	0.085002	0.032452	0.011007	0.113238	0.049204	-0.099821
fbs	0.133044	0.058432	0.167890	-0.005337	1.000000	-0.007962	-0.009093	0.003692	-0.046927	0.151021	-0.014622	-0.011438
thalachh	-0.400067	-0.053999	-0.075059	-0.030874	-0.007962	1.000000	-0.392686	-0.353441	0.379395	-0.297154	-0.123956	0.431519
exng	0.112509	0.146867	0.065089	0.085002	-0.009093	-0.392686	1.000000	0.298277	-0.240616	0.153605	0.222884	-0.429082
oldpeak	0.193431	0.166430	0.156988	0.032452	0.003692	-0.353441	0.298277	1.000000	-0.546473	0.260600	0.175196	-0.424443
slp	-0.155421	-0.054768	-0.103302	0.011007	-0.046927	0.379395	-0.240616	-0.546473	1.000000	-0.085347	-0.068961	0.323948
caa	0.368764	0.135552	0.057947	0.113238	0.151021	-0.297154	0.153605	0.260600	-0.085347	1.000000	0.127607	-0.463258
thall	0.055830	0.244047	0.027382	0.049204	-0.014622	-0.123956	0.222884	0.175196	-0.068961	0.127607	1.000000	-0.354579
output	-0.226750	-0.302926	-0.119281	-0.099821	-0.011438	0.431519	-0.429082	-0.424443	0.323948	-0.463258	-0.354579	1.000000

As we can see the relationship between variables is quite low but there is relationship between the variables.

separating independend colums from target columns

In [83]:
```
x = clean_data.iloc[:,0:12]
y = clean_data.iloc[:, -1]
```

In [84]:
```
x
```

Out[84]:

	age	sex	cp	trtbps	chol	fbs	restecg	thalachh	exng	oldpeak	slp	caa
0	63	1	3	145	233	1	0	150	0	2.3	0	0
1	37	1	2	130	250	0	1	187	0	3.5	0	0
2	41	0	1	130	204	0	0	172	0	1.4	2	0
3	56	1	1	120	236	0	1	178	0	0.8	2	0
4	57	0	0	120	354	0	1	163	1	0.6	2	0
...	...	...	...	...	...	...	...	...	...	...	...	...
298	57	0	0	140	241	0	1	123	1	0.2	1	0
299	45	1	3	110	264	0	1	132	0	1.2	1	0
300	68	1	0	144	193	1	1	141	0	3.4	1	2
301	57	1	0	130	131	0	1	115	1	1.2	1	1
302	57	0	1	130	236	0	0	174	0	0.0	1	1

287 rows × 12 columns

In [85]:
```
y
```

Out[85]:
```
0      1
1      1
2      1
3      1
4      1
      ..
298    0
299    0
300    0
301    0
302    0
Name: output, Length: 287, dtype: int64
```

scalling our data

In [86]:
```
# Scaling all the variables to a range of 0 to 1
from sklearn.preprocessing import MinMaxScaler
features = x.columns.values
scaler = MinMaxScaler(feature_range = (0,1))
scaler.fit(x)
x = pd.DataFrame(scaler.transform(x))
x.columns = features
```

In [93]:
```
x
```

Out[93]:

	age	sex	cp	trtbps	chol	fbs	restecg	thalachh	exng	oldpeak	slp	caa
0	0.708333	1.0	1.000000	0.593023	0.399254	1.0	0.0	0.543860	0.0	0.522727	0.0	0.000000
1	0.166667	1.0	0.666667	0.418605	0.462687	0.0	0.5	0.868421	0.0	0.795455	0.0	0.000000
2	0.250000	0.0	0.333333	0.418605	0.291045	0.0	0.0	0.736842	0.0	0.318182	1.0	0.000000
3	0.562500	1.0	0.333333	0.302326	0.410448	0.0	0.5	0.789474	0.0	0.181818	1.0	0.000000
4	0.583333	0.0	0.000000	0.302326	0.850746	0.0	0.5	0.657895	1.0	0.136364	1.0	0.000000
...	...	...	...	...	...	...	...	...	...	...	...	...
282	0.583333	0.0	0.000000	0.534884	0.429104	0.0	0.5	0.307018	1.0	0.045455	0.5	0.000000
283	0.333333	1.0	1.000000	0.186047	0.514925	0.0	0.5	0.385965	0.0	0.272727	0.5	0.000000
284	0.812500	1.0	0.000000	0.581395	0.250000	1.0	0.5	0.464912	0.0	0.772727	0.5	0.666667
285	0.583333	1.0	0.000000	0.418605	0.018657	0.0	0.5	0.236842	1.0	0.272727	0.5	0.333333
286	0.583333	0.0	0.333333	0.418605	0.410448	0.0	0.0	0.754386	0.0	0.000000	0.5	0.333333

287 rows × 12 columns

In [109…

```
# Create Train & Test Data
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.3, random_state=101)
```

Preprocessing data(part ii)

In [99]:

```
from sklearn.preprocessing import MinMaxScaler
#instantiate Minmax scaler and use it to rescale x_train and x_test
scaler = MinMaxScaler()
rescaled_xtrain = scaler.fit_transform(x_train)
rescaled_xtest = scaler.transform(x_test)
```

In [ ]:

1 linear model (Logistic)

In [100…

```
from sklearn.linear_model import LogisticRegression
model = LogisticRegression()

result = model.fit(rescaled_xtrain,y_train)
```

In [101…

```
# Import confusion_matrix
from sklearn.metrics import confusion_matrix

# use model to predict intances from the set and store it

y_pred = model.predict(rescaled_xtest)

# get the accuracy score and print it
print("Accuracy score of logistic regression classifier :",
     model.score(rescaled_xtest , y_test))


#print confusion matrix
confusion_matrix(y_test , y_pred)
```

```
Accuracy score of logistic regression classifier : 0.7241379310344828
```

Out[101…

```
array([[31, 15],
       [ 9, 32]], dtype=int64)
```

In [ ]:

2 Random Forest

In [110…
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.datasets import make_classification
# create a model with 100 trees
model_fr = RandomForestClassifier(n_estimators=100,
                                  bootstrap = True,
                                  max_features = 'sqrt')
#fit on training data
model_fr.fit(x_train , y_train)
```
Out[110…
```
RandomForestClassifier(max_features='sqrt')
```
In [111…
```
#make predictions
rf_preds = model_fr.predict(x_test)
# Probabilities for each class
rf_probs = model.predict_proba(x_test)[:, 1]
```

We make class predictions (predict) as well as predicted probabilities (predict_proba) to calculate the ROC AUC. Once we have the testing predictions, we can calculate the ROC AUC.

In [114…
```
from sklearn.metrics import roc_auc_score

# Calculate roc auc
roc_value = roc_auc_score(y_test, rf_probs)
print("ROC SCORE :", roc_value)
```
```
ROC SCORE : 0.8504772004241782
```
In [119…
```
#print confusion matrix
confusion_matrix(y_test , rf_preds)
```
Out[119…
```
array([[36, 10],
       [ 7, 34]], dtype=int64)
```

3 XgBoost

In [117…
```
pip install xgboost
```
```
Requirement already satisfied: xgboost in c:\users\26377\anaconda3\lib\site-packages (1.5.2)
Requirement already satisfied: scipy in c:\users\26377\anaconda3\lib\site-packages (from xgboost) (1.5.2)
Requirement already satisfied: numpy in c:\users\26377\anaconda3\lib\site-packages (from xgboost) (1.19.2)
Note: you may need to restart the kernel to use updated packages.
```
In [122…
```
# https://anaconda.org/anaconda/py-xgboost
from xgboost import XGBClassifier
model_xg = XGBClassifier()
model_xg.fit(x_train, y_train)
preds = model.predict(x_test)
```
```
[07:56:18] WARNING: C:/Users/Administrator/workspace/xgboost-win64_release_1.5.1/src/learner.cc:1115: Starting in XGBoost 1.3.0, the default evaluat
ion metric used with the objective 'binary:logistic' was changed from 'error' to 'logloss'. Explicitly set eval_metric if you'd like to restore the
old behavior.
```
In [ ]:
```
#evaluation
```

saving model for production

In [89]:
```
import joblib

# save the model to disk
filename = 'finalized_Churn_Model.sav'
joblib.dump(model_xg, filename)
```
Out[89]:
```
['finalized_Churn_Model.sav']
```
In [91]:
```
# Load the model from disk
loaded_model = joblib.load(filename)
result = loaded_model.score(x_test, y_test)
print(result)
```
```
0.7931034482758621
```
In [ ]: