About me: Experienced Data enthusiast here. Currently working for Roche Pharmaceutical firm.

🔗 LinkedIn

In this workbook , you can find the outcomes of certain activities such as

(i) bagging model vs stand alone model

(ii) Implementation of Naive bayes model

(ii) Use case of Z score test to remove outliers

(iii) Use case of Randomsearchcv

In [2]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import joblib
from collections import Counter
from numpy import where, mean
from sklearn import linear_model
from sklearn.preprocessing import OneHotEncoder
from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import train_test_split
from sklearn import tree
from sklearn.datasets import make_classification
from sklearn.svm import SVC
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import RepeatedStratifiedKFold
from sklearn.tree import DecisionTreeClassifier

%matplotlib inline
```

In [67]:
```
df = pd.read_csv(r'heart disease.csv')
df_N = df
df
```

Out[67]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	40	M	ATA	140	289	0	Normal	172	N	0.0	Up	0
1	49	F	NAP	160	180	0	Normal	156	N	1.0	Flat	1
2	37	M	ATA	130	283	0	ST	98	N	0.0	Up	0
3	48	F	ASY	138	214	0	Normal	108	Y	1.5	Flat	1
4	54	M	NAP	150	195	0	Normal	122	N	0.0	Up	0
...	...	...	...	...	...	...	...	...	...	...	...	...
913	45	M	TA	110	264	0	Normal	132	N	1.2	Flat	1
914	68	M	ASY	144	193	1	Normal	141	N	3.4	Flat	1
915	57	M	ASY	130	131	0	Normal	115	Y	1.2	Flat	1
916	57	F	ATA	130	236	0	LVH	174	N	0.0	Flat	1
917	38	M	NAP	138	175	0	Normal	173	N	0.0	Up	0

918 rows × 12 columns

In [68]:

```
df.describe()
```

Out[68]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisease
count	918.000000	918.000000	918.000000	918.000000	918.000000	918.000000	918.000000
mean	53.510893	132.396514	198.799564	0.233115	136.809368	0.887364	0.553377
std	9.432617	18.514154	109.384145	0.423046	25.460334	1.066570	0.497414
min	28.000000	0.000000	0.000000	0.000000	60.000000	-2.600000	0.000000
25%	47.000000	120.000000	173.250000	0.000000	120.000000	0.000000	0.000000
50%	54.000000	130.000000	223.000000	0.000000	138.000000	0.600000	1.000000
75%	60.000000	140.000000	267.000000	0.000000	156.000000	1.500000	1.000000
max	77.000000	200.000000	603.000000	1.000000	202.000000	6.200000	1.000000

In [69]:

```
df.isnull().sum()
```

Out[69]:

```
Age               0
Sex               0
ChestPainType     0
RestingBP         0
Cholesterol       0
FastingBS         0
RestingECG        0
MaxHR             0
ExerciseAngina    0
Oldpeak           0
ST_Slope          0
HeartDisease      0
dtype: int64
```

Removing outliers using z-score Way 1:

In [23]:

```
df_N['Age_zs'] = (df_N.Age - df_N.Age.mean())/(df_N.Age.std())

# setting limit of z score between -3 & 3:
df_N = df_N[(df_N['Age_zs'].between(-3,3))]

df_N
```

Removing outliers using z-score Way 2 (using scipy):

In [70]:
```
from scipy.stats import zscore

# df_obj = df.select_dtypes(exclude=object)
df_obj_exl = ['Age', 'RestingBP', 'Cholesterol', 'MaxHR', 'Oldpeak']

# applying zscore to all columns if you want
# df_zscore = df[df_obj_exl].apply(zscore)

def outlier_rem(data):
    temp_list = []
    for column in df_obj_exl:
        data[column+'zs'] = zscore(data[column])
        temp_list.append(column+'zs')
        data = data[(data[column+'zs'].between(-3,3))]
    data = data.drop(temp_list, axis=1)
    data.reset_index(inplace=True,drop=True)
    return data

# pass your dataframe here
df_New = outlier_rem(df)

print(df_New)
df_New
```

```
     Age Sex ChestPainType  RestingBP  Cholesterol  FastingBS RestingECG  \
0     40   M           ATA        140          289          0     Normal
1     49   F           NAP        160          180          0     Normal
2     37   M           ATA        130          283          0         ST
3     48   F           ASY        138          214          0     Normal
4     54   M           NAP        150          195          0     Normal
..   ...  ..           ...        ...          ...        ...        ...
894   45   M            TA        110          264          0     Normal
895   68   M           ASY        144          193          1     Normal
896   57   M           ASY        130          131          0     Normal
897   57   F           ATA        130          236          0        LVH
898   38   M           NAP        138          175          0     Normal

     MaxHR ExerciseAngina  Oldpeak ST_Slope  HeartDisease
0      172              N      0.0       Up             0
1      156              N      1.0     Flat             1
2       98              N      0.0       Up             0
3      108              Y      1.5     Flat             1
4      122              N      0.0       Up             0
..     ...            ...      ...      ...           ...
894    132              N      1.2     Flat             1
895    141              N      3.4     Flat             1
896    115              Y      1.2     Flat             1
897    174              N      0.0     Flat             1
898    173              N      0.0       Up             0

[899 rows x 12 columns]
```

Out[70]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	40	M	ATA	140	289	0	Normal	172	N	0.0	Up	0
1	49	F	NAP	160	180	0	Normal	156	N	1.0	Flat	1
2	37	M	ATA	130	283	0	ST	98	N	0.0	Up	0
3	48	F	ASY	138	214	0	Normal	108	Y	1.5	Flat	1
4	54	M	NAP	150	195	0	Normal	122	N	0.0	Up	0
...	...	...	...	...	...	...	...	...	...	...	...	...
894	45	M	TA	110	264	0	Normal	132	N	1.2	Flat	1
895	68	M	ASY	144	193	1	Normal	141	N	3.4	Flat	1
896	57	M	ASY	130	131	0	Normal	115	Y	1.2	Flat	1
897	57	F	ATA	130	236	0	LVH	174	N	0.0	Flat	1
898	38	M	NAP	138	175	0	Normal	173	N	0.0	Up	0

899 rows × 12 columns

In [71]:

```
print('No. of patients without Heart disease:',len(df_New[df_New['HeartDisease']==0]))
print('No. of patients with Heart disease:',len(df_New[df_New['HeartDisease']==1]))
```

```
No. of patients without Heart disease: 407
No. of patients with Heart disease: 492
```

-->From the above counts, we can say that the dataset don't need any over or under sampling

In [72]:

```
X = df_New.drop(['HeartDisease'],axis=1)
y = df_New['HeartDisease']

# test-train split:
X_train, X_test, y_train, y_test = train_test_split(X,y,test_size=0.2)
X_train.reset_index(inplace=True,drop=True)
X_test.reset_index(inplace=True,drop=True)
```

In [73]:

```
X_train
```

Out[73]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope
0	41	M	ASY	110	289	0	Normal	170	N	0.0	Flat
1	61	M	ASY	138	166	0	LVH	125	Y	3.6	Flat
2	54	M	ASY	150	365	0	ST	134	N	1.0	Up
3	41	M	ATA	125	269	0	Normal	144	N	0.0	Up
4	57	M	ASY	132	207	0	Normal	168	Y	0.0	Up
...	...	...	...	...	...	...	...	...	...	...	...
714	62	M	ASY	135	297	0	Normal	130	Y	1.0	Flat
715	54	F	NAP	130	294	0	ST	100	Y	0.0	Flat
716	46	M	ATA	140	275	0	Normal	165	Y	0.0	Up
717	62	F	ASY	140	268	0	LVH	160	N	3.6	Down
718	62	F	ASY	150	244	0	Normal	154	Y	1.4	Flat

719 rows × 11 columns

ONE HOT ENCODING

In [74]:

```
# One Hot Encoding function to encode all categorical string columns

def onehotencoding(dataframe_name):
    column_names_obj = dataframe_name.select_dtypes(include=object)
    ohe = OneHotEncoder(drop='first',handle_unknown='ignore')
    df_N=dataframe_name
    for i in column_names_obj:
        feature_cols = ohe.fit_transform(dataframe_name[[i]]).toarray()
        feature_cols_names = np.array(ohe.categories_).ravel()
        feature_cols_names = feature_cols_names[1:]
        feature = pd.DataFrame(feature_cols,columns=feature_cols_names)
        df_N = pd.concat([df_N,feature],axis=1)
    df_N = df_N.drop(column_names_obj, axis=1) #dropping categorical columns
    return df_N
```

In [75]:
```
#Pass your dataset here
df_enc_train = onehotencoding(X_train)
print(df_enc_train)
df_enc_test = onehotencoding(X_test)
```

```
     Age  RestingBP  Cholesterol  FastingBS  MaxHR  Oldpeak    M  ATA  NAP  \
0     41        110          289          0    170      0.0  1.0  0.0  0.0
1     61        138          166          0    125      3.6  1.0  0.0  0.0
2     54        150          365          0    134      1.0  1.0  0.0  0.0
3     41        125          269          0    144      0.0  1.0  1.0  0.0
4     57        132          207          0    168      0.0  1.0  0.0  0.0
..   ...        ...          ...        ...    ...      ...  ...  ...  ...
714   62        135          297          0    130      1.0  1.0  0.0  0.0
715   54        130          294          0    100      0.0  0.0  0.0  1.0
716   46        140          275          0    165      0.0  1.0  1.0  0.0
717   62        140          268          0    160      3.6  0.0  0.0  0.0
718   62        150          244          0    154      1.4  0.0  0.0  0.0

      TA  Normal   ST    Y  Flat   Up
0    0.0     1.0  0.0  0.0   1.0  0.0
1    0.0     0.0  0.0  1.0   1.0  0.0
2    0.0     0.0  1.0  0.0   0.0  1.0
3    0.0     1.0  0.0  0.0   0.0  1.0
4    0.0     1.0  0.0  1.0   0.0  1.0
..   ...     ...  ...  ...   ...  ...
714  0.0     1.0  0.0  1.0   1.0  0.0
715  0.0     0.0  1.0  1.0   1.0  0.0
716  0.0     1.0  0.0  1.0   0.0  1.0
717  0.0     0.0  0.0  0.0   0.0  0.0
718  0.0     1.0  0.0  1.0   1.0  0.0

[719 rows x 15 columns]
```

SCALING

In [80]:
```
def scaling_process(dataframe):

    df_scaling = dataframe

#    Please pass the list of numerical features for which you want to apply scaling
    scaled_features = scaling.fit_transform(df_scaling[['Age','RestingBP','Cholesterol','FastingBS','MaxHR','Oldpeak
```

```
    scaled_features_names = scaling.feature_names_in_.tolist()
    scaled_features_df = pd.DataFrame(scaled_features,columns=scaled_features_names)
    df_scaled = df_scaling.drop(columns=scaled_features_names)
    df_enc = pd.concat([df_scaled,scaled_features_df], axis=1)

    return df_enc
```

In [81]:
```
from sklearn.preprocessing import StandardScaler
scaling = StandardScaler()
df_enc_train_scl = scaling_process(df_enc_train)
print(df_enc_train_scl)
df_enc_test_scl = scaling_process(df_enc_test)
```

```
       M  ATA  NAP   TA  Normal   ST    Y  Flat   Up       Age  RestingBP  \
0    1.0  0.0  0.0  0.0     1.0  0.0  0.0   1.0  0.0 -1.328136  -1.286021
1    1.0  0.0  0.0  0.0     0.0  0.0  1.0   1.0  0.0  0.800553   0.357069
2    1.0  0.0  0.0  0.0     0.0  1.0  0.0   0.0  1.0  0.055512   1.061251
3    1.0  1.0  0.0  0.0     1.0  0.0  0.0   0.0  1.0 -1.328136  -0.405794
4    1.0  0.0  0.0  0.0     1.0  0.0  1.0   0.0  1.0  0.374815   0.004979
..   ...  ...  ...  ...     ...  ...  ...   ...  ...       ...        ...
714  1.0  0.0  0.0  0.0     1.0  0.0  1.0   1.0  0.0  0.906987   0.181024
715  0.0  0.0  1.0  0.0     0.0  1.0  1.0   1.0  0.0  0.055512  -0.112385
716  1.0  1.0  0.0  0.0     1.0  0.0  1.0   0.0  1.0 -0.795964   0.474433
717  0.0  0.0  0.0  0.0     0.0  0.0  0.0   0.0  0.0  0.906987   0.474433
718  0.0  0.0  0.0  0.0     1.0  0.0  1.0   1.0  0.0  0.906987   1.061251

     Cholesterol  FastingBS     MaxHR   Oldpeak
0       0.861142  -0.524235  1.307888 -0.866406
1      -0.278521  -0.524235 -0.481024  2.770054
2       1.565324  -0.524235 -0.123242  0.143722
3       0.675831  -0.524235  0.274294 -0.866406
4       0.101367  -0.524235  1.228381 -0.866406
..           ...        ...       ...       ...
714     0.935266  -0.524235 -0.282256  0.143722
715     0.907470  -0.524235 -1.474864 -0.866406
716     0.731424  -0.524235  1.109120 -0.866406
717     0.666565  -0.524235  0.910352  2.770054
718     0.444192  -0.524235  0.671830  0.547773

[719 rows x 15 columns]
```

In [82]:
```
X_train = df_enc_train_scl
X_test = df_enc_test_scl
```

Support Vector Machine (SVM) model

In [83]:
```
from sklearn.svm import SVC
model = SVC()
model.fit(X_train,y_train)
```

Out[83]:
```
▾ SVC
SVC()
```

In [84]:
```
model.score(X_train,y_train)
```

Out[84]:
```
0.8984700973574409
```

In [85]:
```
model.score(X_test,y_test)
```

Out[85]:
```
0.9111111111111111
```

--> When I performed SVM modeling without scaling, I clearly saw a drop of around 15-20% accuracy.

Naive Bayes model

In [90]:
```
from sklearn.naive_bayes import GaussianNB
model = GaussianNB()
model.fit(X_train, y_train)

print(model.score(X_train,y_train))
print(model.score(X_test,y_test))
```

```
0.8525730180806675
0.9
```

- ***Here we see some overfitting as train set accuracy is higher than test set. Reason might be the fact that Naive bayes strictly consider all features other than target feature as independent features.***

- ***To avoid these kind of problems, we use L1 or L2 regularisation techniques or some bagging methods which we used down below***

In [86]:
```
from sklearn.ensemble import RandomForestClassifier
model_RF = RandomForestClassifier(n_estimators=10)
""" n_estimators --> This's the no. of times the model gonna create different sest of random data and give us
                     mean of all the outcomes. """
model_RF.fit(X_train, y_train)
```

Out[86]:
```
RandomForestClassifier
RandomForestClassifier(n_estimators=10)
```

In [87]:
```
print(model_RF.score(X_train,y_train))
print(model_RF.score(X_test,y_test))
```

```
0.9930458970792768
0.8888888888888888
```

Below, I've used random search cv to find which is best combination of hyperparameter for lasso model

In [92]:
```
from sklearn.model_selection import RandomizedSearchCV
param_dist = { 'n_estimators': list(range(1,100)),
               'random_state':list(range(1,100))}
randomCV = RandomizedSearchCV(BaggingClassifier(), param_distributions=param_dist, n_iter=8,cv=3,random_state=42)

randomCV.fit(X_train,y_train)
print(randomCV.best_params_)
```

```
{'random_state': 71, 'n_estimators': 45}
```

Bagging method (using SVM model):

In [88]:
```
from sklearn.ensemble import BaggingClassifier
bag_model = BaggingClassifier(
                base_estimator=SVC(),
                n_estimators=45,
                max_samples=0.8,
                oob_score=True,
```

```
                random_state=71)
bag_model.fit(X_train, y_train)
bag_model.oob_score_
```

```
/home/ec2-user/anaconda3/envs/python3/lib/python3.10/site-packages/sklearn/ensemble/_base.py:156: FutureWarning: `ba
se_estimator` was renamed to `estimator` in version 1.2 and will be removed in 1.4.
  warnings.warn(
```

Out[88]: 0.8525730180806675

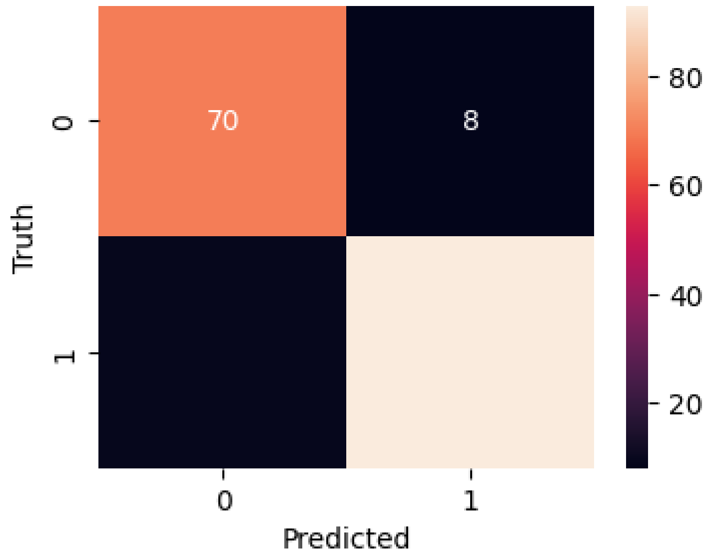
In [ ]:
```
""" OOB (out-of-bag) score is a performance metric for a machine learning model, specifically for ensemble models
    such as random forests. It is calculated using the samples that are not used in the training of the model,
    which is called out-of-bag samples. """
```

In [93]:
```
from sklearn.metrics import confusion_matrix
y_pred = bag_model.predict(X_test)
cm = confusion_matrix(y_test, y_pred)
cm
```

Out[93]:
```
array([[70,  8],
       [ 9, 93]])
```

In [95]:
```
%matplotlib inline
import matplotlib.pyplot as plt
import seaborn as sn
plt.figure(figsize=(4,3))
sn.heatmap(cm, annot=True)
plt.xlabel('Predicted')
plt.ylabel('Truth')
```

Out[95]: Text(20.72222222222222, 0.5, 'Truth')



In [89]:
```
bag_model.score(X_test, y_test)
```

Out[89]: 0.9055555555555556

Conclusion:

--> Here we can clearly see 0.5% to 2% increase in accuracy score for bagging model compared to normal stand alone model.

Happy Learning! 🙂