```
import pandas as pd
import numpy as np

import math
import warnings
import string

import matplotlib.pyplot as plt
from matplotlib.legend_handler import HandlerLine2D

from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import MinMaxScaler
import statsmodels.api as sm
import statsmodels.formula.api as smf

from sklearn.model_selection import train_test_split
from sklearn.metrics import confusion_matrix, classification_report
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay
from sklearn.tree import DecisionTreeClassifier
from sklearn import metrics
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.model_selection import GridSearchCV
from sklearn.model_selection import cross_validate
from sklearn.model_selection import KFold

from sklearn.model_selection import RepeatedStratifiedKFold
from sklearn.model_selection import cross_val_score

from sklearn.feature_selection import SequentialFeatureSelector

import seaborn as sns

warnings.filterwarnings("ignore")



cvd_data = pd.read_csv("/content/sample_data/cardio_data.csv", sep=";")


cvd_data.head()
```

	id	age	gender	height	weight	ap_hi	ap_lo	cholesterol	gluc	smoke	alco	active	cardio
0	0	18393	2	168	62.0	110	80	1	1	0	0	1	0
1	1	20228	1	156	85.0	140	90	3	1	0	0	1	1
2	2	18857	1	165	64.0	130	70	3	1	0	0	0	1
3	3	17623	2	169	82.0	150	100	1	1	0	0	1	1
4	4	17474	1	156	56.0	100	60	1	1	0	0	0	0

```
print(f"Number of columns: { cvd_data.shape[1] }")
print(f"Number of rows: { cvd_data.shape[0] }")
```

```
Number of columns: 13
Number of rows: 70000
```

```
cvd_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 70000 entries, 0 to 69999
Data columns (total 13 columns):
 #   Column       Non-Null Count  Dtype
---  ------       --------------  -----
 0   id           70000 non-null  int64
 1   age          70000 non-null  int64
 2   gender       70000 non-null  int64
 3   height       70000 non-null  int64
 4   weight       70000 non-null  float64
 5   ap_hi        70000 non-null  int64
 6   ap_lo        70000 non-null  int64
 7   cholesterol  70000 non-null  int64
 8   gluc         70000 non-null  int64
 9   smoke        70000 non-null  int64
 10  alco         70000 non-null  int64
 11  active       70000 non-null  int64
 12  cardio       70000 non-null  int64
dtypes: float64(1), int64(12)
memory usage: 6.9 MB
```

```
cvd_data.describe()
```

	id	age	gender	height	weight	ap_hi	ap_lo	
count	70000.000000	70000.000000	70000.000000	70000.000000	70000.000000	70000.000000	70000.000000	7
mean	49972.419900	19468.865814	1.349571	164.359229	74.205690	128.817286	96.630414	
std	28851.302323	2467.251667	0.476838	8.210126	14.395757	154.011419	188.472530	
min	0.000000	10798.000000	1.000000	55.000000	10.000000	-150.000000	-70.000000	
25%	25006.750000	17664.000000	1.000000	159.000000	65.000000	120.000000	80.000000	
50%	50001.500000	19703.000000	1.000000	165.000000	72.000000	120.000000	80.000000	
75%	74889.250000	21327.000000	2.000000	170.000000	82.000000	140.000000	90.000000	
max	99999.000000	23713.000000	2.000000	250.000000	200.000000	16020.000000	11000.000000	

```
def detect_outliers(df,q1,q3):
  for col in df.columns:
    df_feature = df[col]
    Q1 = df_feature.quantile(q1)
    Q3 = df_feature.quantile(q3)
    IQR = Q3 - Q1
    print(f'Feature_name: {col}-------------')
    print(f'Percentiles: {int(q1*100)}th={Q1}, {int(q3*100)}th={Q3}, IQR={IQR}')
    lower, upper = Q1 - 1.5 * IQR, Q3 + 1.5 * IQR
    outliers = [x for x in df_feature if x < lower or x > upper]
    print('Identified outliers: %d \n' % len(outliers))

detect_outliers(cvd_data[['age',    'gender',   'height',   'weight',   'ap_hi',    'ap_lo',    'cholesterol',  'gluc', 'smoke' ,'alco',    'activ
```

```
Feature_name: age-------------
Percentiles: 5th=15069.0, 95th=23259.0, IQR=8190.0
Identified outliers: 0

Feature_name: gender-------------
Percentiles: 5th=1.0, 95th=2.0, IQR=1.0
Identified outliers: 0

Feature_name: height-------------
Percentiles: 5th=152.0, 95th=178.0, IQR=26.0
Identified outliers: 49

Feature_name: weight-------------
Percentiles: 5th=55.0, 95th=100.0, IQR=45.0
Identified outliers: 22

Feature_name: ap_hi-------------
Percentiles: 5th=100.0, 95th=160.0, IQR=60.0
Identified outliers: 50

Feature_name: ap_lo-------------
Percentiles: 5th=70.0, 95th=100.0, IQR=30.0
Identified outliers: 1036

Feature_name: cholesterol-------------
Percentiles: 5th=1.0, 95th=3.0, IQR=2.0
Identified outliers: 0

Feature_name: gluc-------------
Percentiles: 5th=1.0, 95th=3.0, IQR=2.0
Identified outliers: 0

Feature_name: smoke-------------
Percentiles: 5th=0.0, 95th=1.0, IQR=1.0
Identified outliers: 0

Feature_name: alco-------------
Percentiles: 5th=0.0, 95th=1.0, IQR=1.0
Identified outliers: 0

Feature_name: active-------------
Percentiles: 5th=0.0, 95th=1.0, IQR=1.0
Identified outliers: 0
```

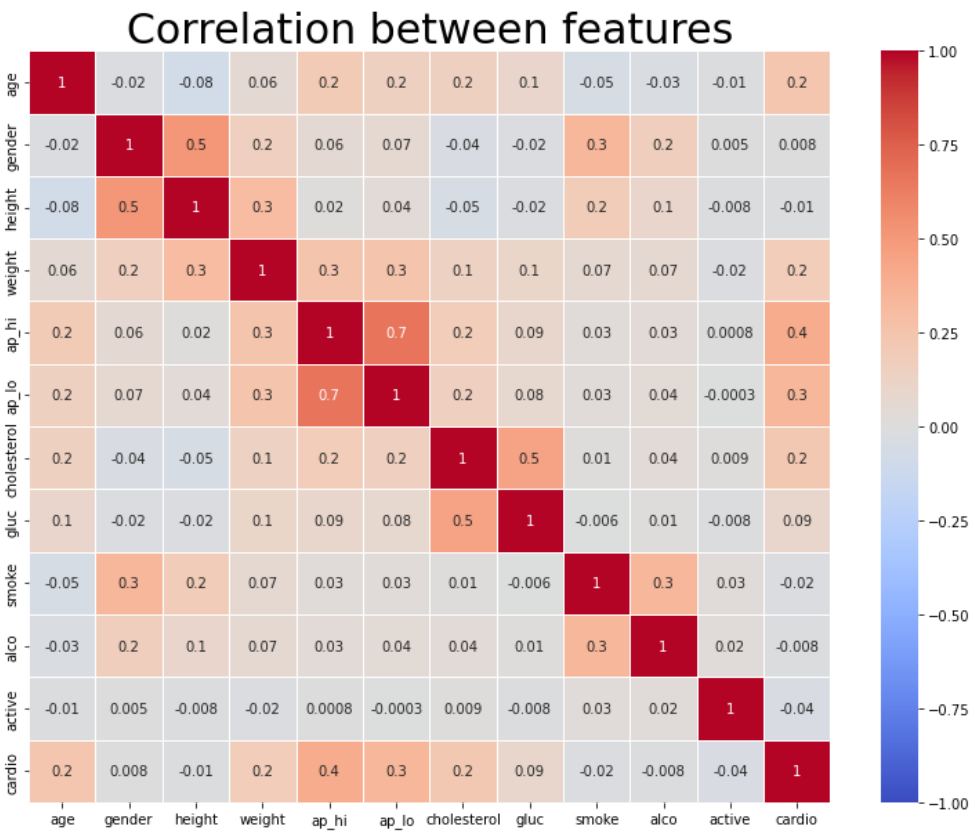
```
cvd_data_cleaned = cvd_data
for col in ['age',  'gender',   'height',   'weight',   'ap_hi',    'ap_lo',    'cholesterol',  'gluc', 'smoke' ,'alco',    'active']:
  Q1 = cvd_data[col].quantile(0.05)
  Q3 = cvd_data[col].quantile(0.95)
  IQR = Q3 - Q1
  lower, upper = Q1 - 1.5 * IQR, Q3 + 1.5 * IQR
  cvd_data_cleaned = cvd_data_cleaned[(cvd_data_cleaned[col] >= lower) & (cvd_data_cleaned[col] <= upper)]


cvd_data_cleaned.head()
```

	id	age	gender	height	weight	ap_hi	ap_lo	cholesterol	gluc	smoke	alco	active	cardio
0	0	18393	2	168	62.0	110	80	1	1	0	0	1	0
1	1	20228	1	156	85.0	140	90	3	1	0	0	1	1
2	2	18857	1	165	64.0	130	70	3	1	0	0	0	1
3	3	17623	2	169	82.0	150	100	1	1	0	0	1	1
4	4	17474	1	156	56.0	100	60	1	1	0	0	0	0

```
cvd_data_cleaned = cvd_data_cleaned.drop(columns=["id"])
```

```
plt.rcParams.update({'font.size': 10})
fig, ax = plt.subplots(figsize=(13, 10))
sns.heatmap(cvd_data_cleaned.corr(), annot = True,  center= 0, cmap= 'coolwarm',vmin=-1, vmax=1, ax=ax, fmt='.1g', linewidths=.5);
plt.title('Correlation between features', fontsize = 30)
plt.show()
```




```
cvd_data_cleaned = cvd_data_cleaned.drop(columns=["ap_lo"])
```

```
cvd_data_scaled=cvd_data_cleaned.copy()

columns_to_scale = ['age', 'weight', 'ap_hi','height']

stdscaler = StandardScaler()
cvd_data_scaled[columns_to_scale] = stdscaler.fit_transform(cvd_data_cleaned[columns_to_scale])

cvd_data_scaled.head()
```

	age	gender	height	weight	ap_hi	cholesterol	gluc	smoke	alco	active	cardio
0	-0.434132	2	0.453195	-0.850710	-0.926193	1	1	0	0	1	0
1	0.309378	1	-1.061678	0.768277	0.774598	3	1	0	0	1	1
2	-0.246127	1	0.074477	-0.709928	0.207667	3	1	0	0	0	1
3	-0.746123	2	0.579435	0.557105	1.341528	1	1	0	0	1	1
4	-0.806495	1	-1.061678	-1.273054	-1.493123	1	1	0	0	0	0

```
cardio_scaled_mm=cardio_cleaned.copy()
columns_to_scale_mm = ['age', 'weight', 'ap_hi','height']
mmscaler = MinMaxScaler()
cardio_scaled_mm[columns_to_scale_mm] = mmscaler.fit_transform(cardio_cleaned[columns_to_scale_mm])

cardio_scaled_mm.head()
```

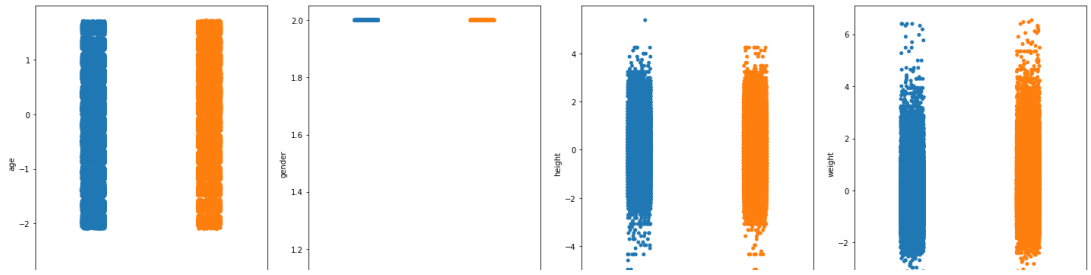
	age	gender	height	weight	ap_hi	ap_lo	cholesterol	gluc	smoke	alco	active	cardio
0	0.588076	2	0.585106	0.326923	0.434783	80	1	1	0	0	1	0
1	0.730159	1	0.457447	0.474359	0.565217	90	3	1	0	0	1	1
2	0.624003	1	0.553191	0.339744	0.521739	70	3	1	0	0	0	1
3	0.528455	2	0.595745	0.455128	0.608696	100	1	1	0	0	1	1
4	0.516918	1	0.457447	0.288462	0.391304	60	1	1	0	0	0	0

```
X_cardio = cvd_data_scaled.drop(columns = ['cardio'])
y_cardio = cvd_data_scaled['cardio']


plt.figure(figsize=(20,25), facecolor='white')
plotnumber = 1

for column in X_cardio:
    if plotnumber<=16 :
        ax = plt.subplot(4,4,plotnumber)
        sns.stripplot(y_cardio,X_cardio[column])
    plotnumber+=1

plt.tight_layout()
```

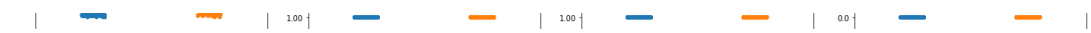



```
X_train, X_test, y_train, y_test = train_test_split(X_cardio, y_cardio, test_size = 0.30, random_state = 0)
```



```
print("Gradient Boost Classifier")
grad_params = {'n_estimators' : list(range(50,100,10)),'max_depth' : list(range(3,11,1))}
grad = GridSearchCV(GradientBoostingClassifier(), grad_params,n_jobs=-1,cv=10,scoring='recall')
grad.fit(X_train, y_train)
grad_boost = grad.best_estimator_
print("Best Estimator")
print(grad_boost)
```

```
Gradient Boost Classifier
Best Estimator
GradientBoostingClassifier(max_depth=5, n_estimators=90)
```



```
booster_def = GradientBoostingClassifier(max_depth=5,n_estimators=90, min_samples_split=1200, min_samples_leaf=80, max_features=10, subsample=0.75
boost_model = booster_def.fit(X_train, y_train)

y_pred = boost_model.predict(X_test)

boosting_acc = accuracy_score(y_test, y_pred)
cm_bossting = confusion_matrix(y_test, y_pred)
tpr_boost = cm_bossting[1][1] /(cm_bossting[1][0] + cm_bossting[1][1])

print('Accuracy:', boosting_acc)
print('Sensitivity (TPR) =', tpr_boost)

print('\n Confusion matrix \n \n')
print(classification_report(y_test, y_pred ))

from sklearn.metrics import ConfusionMatrixDisplay
ConfusionMatrixDisplay.from_estimator(boost_model, X_test, y_test)
plt.show()
```

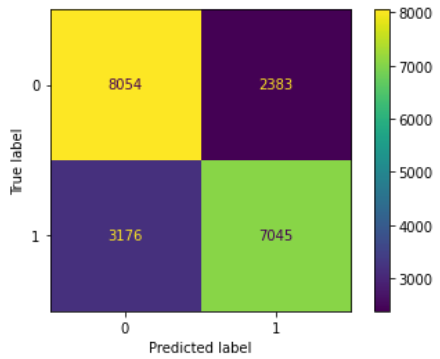
```
Accuracy: 0.7309032820214929
Sensitivity (TPR) = 0.6892671949907054

 Confusion matrix


              precision    recall  f1-score   support

           0       0.72      0.77      0.74     10437
           1       0.75      0.69      0.72     10221

    accuracy                           0.73     20658
   macro avg       0.73      0.73      0.73     20658
weighted avg       0.73      0.73      0.73     20658
```




```
y_pred_train = boost_model.predict(X_train)
boosting_acc_train = accuracy_score(y_train, y_pred_train)
print('Train Accuracy:', boosting_acc_train)
```

```
Train Accuracy: 0.7407676348547718
```

age in days

gender - 1: woman, 2: man

```
height in cm
weight in kg
ap_hi - Systolic blood pressure (first number)
cholestrol - 1: normal, 2: above normal, 3: well above normal
gluc - 1: normal, 2: above normal, 3: well above normal
alco - whether patient takes alcohol or not (0 or 1)
smoke - whether patient smokes or not (0 or 1)
active - physical activity (0 or 1)
```

```
new_data = [[9496,  1,  153,    53.0,   110,    1,  1,  0,  0,  1]]
X_new = pd.DataFrame(new_data,columns = ['age', 'gender',   'height',   'weight',   'ap_hi','cholesterol',  'gluc', 'smoke' ,'alco',    'active'])

columns_to_scale = ['age', 'weight', 'ap_hi','height']

X_new[columns_to_scale] = stdscaler.transform(X_new[columns_to_scale])

X_new.head()
```

	age	gender	height	weight	ap_hi	cholesterol	gluc	smoke	alco	active
0	-4.039042	1	-1.440396	-1.484227	-0.926193	1	1	0	0	1

```
from numpy.ma.core import concatenate
y_new_pred = boost_model.predict(X_new)
y_new_pred_df =  pd.DataFrame(y_new_pred, columns=['prediction'])
new_prediction = pd.concat([X_new, y_new_pred_df], axis=1)
new_prediction
```

	age	gender	height	weight	ap_hi	cholesterol	gluc	smoke	alco	active	prediction
0	-4.039042	1	-1.440396	-1.484227	-0.926193	1	1	0	0	1	0

```
feature_imp = boost_model.feature_importances_
features = ['age',  'gender', 'height', 'weight', 'ap_hi','cholesterol',  'gluc', 'smoke' ,'alco',  'active']
plt.barh(features, feature_imp, align="center")
```

```
<BarContainer object of 10 artists>
```