

Cardiocvascular Disease Prediction

DataSource : Kaggle[sulianova]

Team -

[BL.EN.U4AIE19007] Apoorva Mani

[BL.EN.U4AIE19010] Bhuvanashree Murugadoss

[BL.EN.U4AIE19027] Karna Sai Nikhilesh Reddy

Importing Dependencies

```
In [18]: import sys # Not Required
import warnings
import os
import pickle
import numpy as np
import pandas as pd
import matplotlib as mpl
from matplotlib import pyplot as plt
from pandas.plotting import scatter_matrix
import seaborn as sns

from sklearn.base import BaseEstimator, TransformerMixin
from sklearn.impute import SimpleImputer
from sklearn.model_selection import train_test_split, StratifiedShuffleSplit, cross_val
from sklearn.preprocessing import OneHotEncoder, StandardScaler
from sklearn.pipeline import Pipeline, FeatureUnion
from sklearn.metrics import accuracy_score, classification_report, confusion_matrix, pl

# Machine Learning Algorithms
from sklearn.linear_model import LogisticRegression
from sklearn.naive_bayes import GaussianNB
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import BaggingClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import VotingClassifier
from sklearn.ensemble import RandomForestClassifier

# Ignoring Warnings
warnings.filterwarnings(action='ignore')

# Fixing matplotlib inline and label sizes
%matplotlib inline
mpl.rcParams['axes', labelsizes=14)
mpl.rcParams['xtick', labelsizes=12)
mpl.rcParams['ytick', labelsizes=12)
```

File Locations for Images, Dataset, Pickles and Models

```
In [19]: # Root Directory
PROJECT_ROOT_DIR = os.getcwd()

# Dataset Directory
DATASET_NAME = 'cardiovascular-disease-dataset.csv'
DATASET_DIR = 'datasets'
DATASET_PATH = os.path.join(PROJECT_ROOT_DIR, DATASET_DIR)

def load_dataset(path=DATASET_PATH, filename=DATASET_NAME, sep=';'):
    dataset_location = os.path.join(path, filename)
    return pd.read_csv(dataset_location, sep)

# Pickle and Model Directory
PM_DIR = 'Pickles_And_Models'
PM_PATH = os.path.join(PROJECT_ROOT_DIR, PM_DIR)
os.makedirs(PM_PATH, exist_ok=True)

def save_object(object_ , pickle_name, pm_path = PM_PATH):
    path = os.path.join(pm_path, pickle_name)
    pickle.dump(object_, open(path, 'wb'))
    print('Saving Pickle', path)

def load_object(pickle_name, pm_path = PM_PATH):
    path = os.path.join(pm_path, pickle_name)
    object_ = pickle.load(open(path, 'rb'))
    print('Loaded Pickle', path)
    return object_
```

Load Dataset

```
In [ ]: cardio = load_dataset()
cardio.columns
```

```
Out[ ]: Index(['id', 'age', 'gender', 'height', 'weight', 'ap_hi', 'ap_lo',
             'cholesterol', 'gluc', 'smoke', 'alco', 'active', 'cardio'],
            dtype='object')
```

```
In [ ]: cardio.drop('id', axis=1, inplace=True)
save_object(cardio, 'Initial_cardio.dataframe')
cardio.head()
```

Saving Pickle E:\Github\SEMESTER-3\PML_Project\Pickles_And_Models\Initial_cardio.dataframe

```
Out[ ]:
```

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

Basic Data Information

```
In [ ]: cardio.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 70000 entries, 0 to 69999
Data columns (total 12 columns):
#   Column          Non-Null Count  Dtype
---  -
0   age             70000 non-null   int64
1   gender          70000 non-null   int64
2   height          70000 non-null   int64
3   weight          70000 non-null   float64
4   ap_hi           70000 non-null   int64
5   ap_lo           70000 non-null   int64
6   cholesterol     70000 non-null   int64
7   gluc           70000 non-null   int64
8   smoke          70000 non-null   int64
9   alco           70000 non-null   int64
10  active          70000 non-null   int64
11  cardio          70000 non-null   int64
dtypes: float64(1), int64(11)
memory usage: 6.4 MB
```

```
In [ ]: cardio.describe(include='all')
```

```
Out[ ]:
```

	age	gender	height	weight	ap_hi	ap_lo	cholesterc
count	70000.000000	70000.000000	70000.000000	70000.000000	70000.000000	70000.000000	70000.000000
mean	19468.865814	1.349571	164.359229	74.205690	128.817286	96.630414	1.36687
std	2467.251667	0.476838	8.210126	14.395757	154.011419	188.472530	0.68025
min	10798.000000	1.000000	55.000000	10.000000	-150.000000	-70.000000	1.00000
25%	17664.000000	1.000000	159.000000	65.000000	120.000000	80.000000	1.00000
50%	19703.000000	1.000000	165.000000	72.000000	120.000000	80.000000	1.00000
75%	21327.000000	2.000000	170.000000	82.000000	140.000000	90.000000	2.00000
max	23713.000000	2.000000	250.000000	200.000000	16020.000000	11000.000000	3.00000

Checking for Null Values

```
In [ ]: cardio[cardio.isnull().any(axis=1)]
## We can see that there were no null values in dataset, we will move further with Dupl
```

```
Out[ ]: age gender height weight ap_hi ap_lo cholesterol gluc smoke alco active cardio
```

Checking for Duplicate Values

```
In [ ]: cardio_duplicate_values = cardio[cardio.duplicated(keep=False)]
print('Shape of duplicates:', cardio_duplicate_values.shape)
cardio_duplicate_values.sort_values(by=['age']).head()
```

```
Shape of duplicates : (48, 12)
```

```
Out[ ]: age gender height weight ap_hi ap_lo cholesterol gluc smoke alco active cardio
```

	age	gender	height	weight	ap_hi	ap_lo	cholesterol	gluc	smoke	alco	active	cardio
40365	14552	1	158	64.0	120	80	1	1	0	0	1	0
6325	14552	1	158	64.0	120	80	1	1	0	0	1	0
64169	16160	1	168	65.0	120	80	1	1	0	0	1	1
17101	16160	1	168	65.0	120	80	1	1	0	0	1	1
1204	16793	1	165	68.0	120	80	1	1	0	0	1	0

```
In [ ]: # We can observe that 24 instances were being duplicated, we will try to remove them fr
cardio.drop(index=cardio[cardio.duplicated()].index, axis=0, inplace=True)
print('After removing duplicates :', cardio.shape)
```

After removing duplicates : (69976, 12)

Outliers Detection

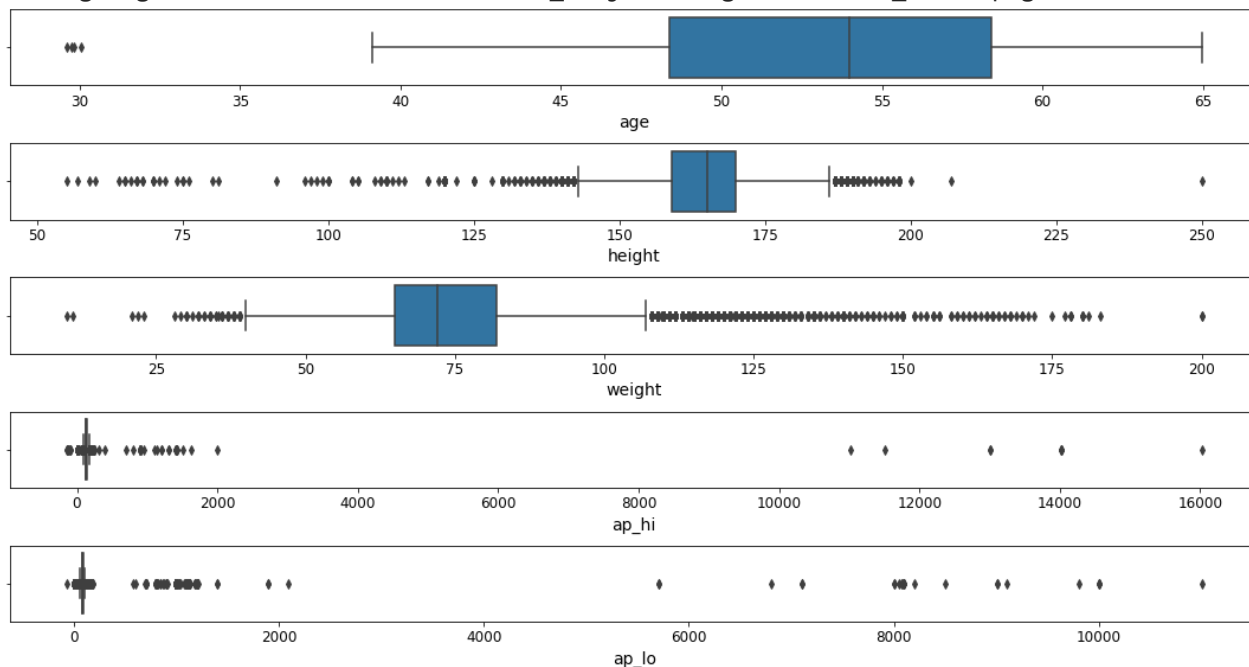
```
In [ ]: # Outliers Detection
continuous_features = ['age', 'height', 'weight', 'ap_hi', 'ap_lo']
fig, axes = plt.subplots(nrows=len(continuous_features), ncols=1, figsize=(15,8));

sns.boxplot(cardio['age']/365, ax=axes[0])

for (index, column) in enumerate(continuous_features[1:], 1):
    sns.boxplot(cardio[column], ax=axes[index])

save_fig('Outliers_Found')
plt.show()
```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\Outliers_Found.png



```
In [ ]: # We will do manual adjustment/deletion instead of zscore method due to it being medica

cardio.drop(cardio[(cardio['height'] < 80) | (cardio['height'] > 220)].index, inplace=T
cardio.drop(cardio[cardio['weight'] < 35].index, inplace=True)
```

```
cardio.drop(cardio[(cardio['ap_hi'] < 50) | (cardio['ap_hi'] > 225)].index, inplace=True)
cardio.drop(cardio[(cardio['ap_lo'] < 50) | (cardio['ap_lo'] > 180)].index, inplace=True)
```

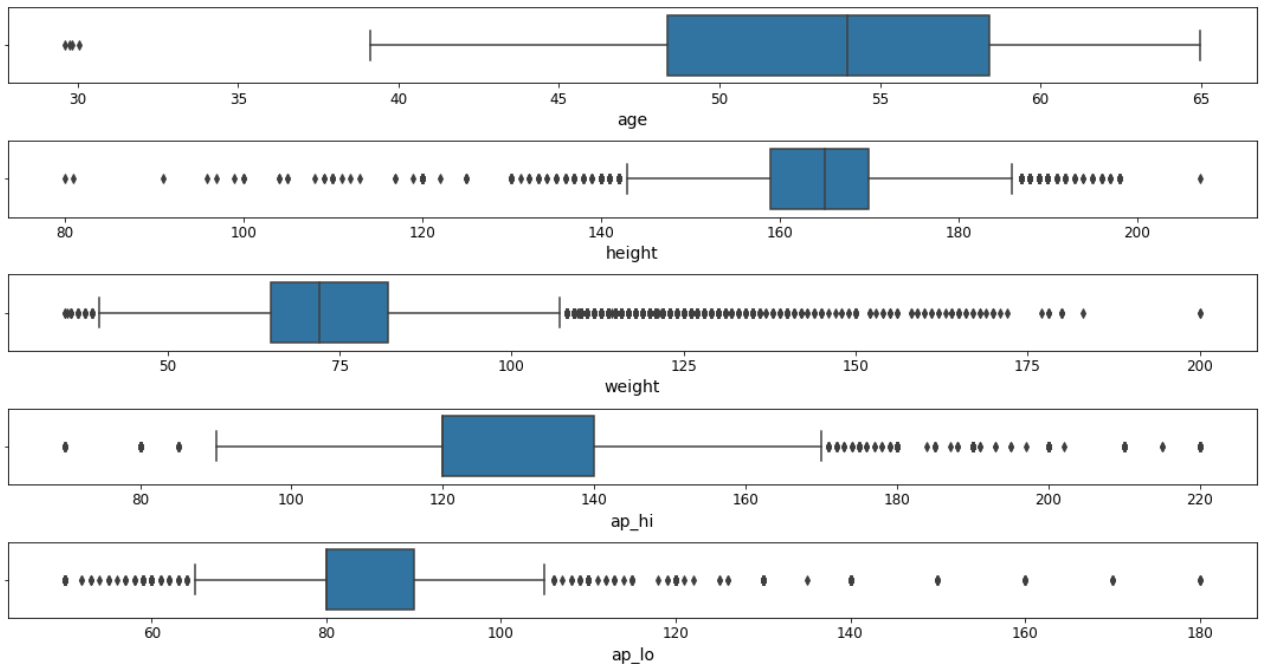
```
In [ ]: # Outliers Detection
continuous_features = ['age', 'height', 'weight', 'ap_hi', 'ap_lo']
fig, axes = plt.subplots(nrows=len(continuous_features), ncols=1, figsize=(15,8));

sns.boxplot(cardio['age']/365, ax=axes[0])

for (index, column) in enumerate(continuous_features[1:], 1):
    sns.boxplot(cardio[column], ax=axes[index])

save_fig('Outliers_Removed')
plt.show()
```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\Outliers_Removed.png

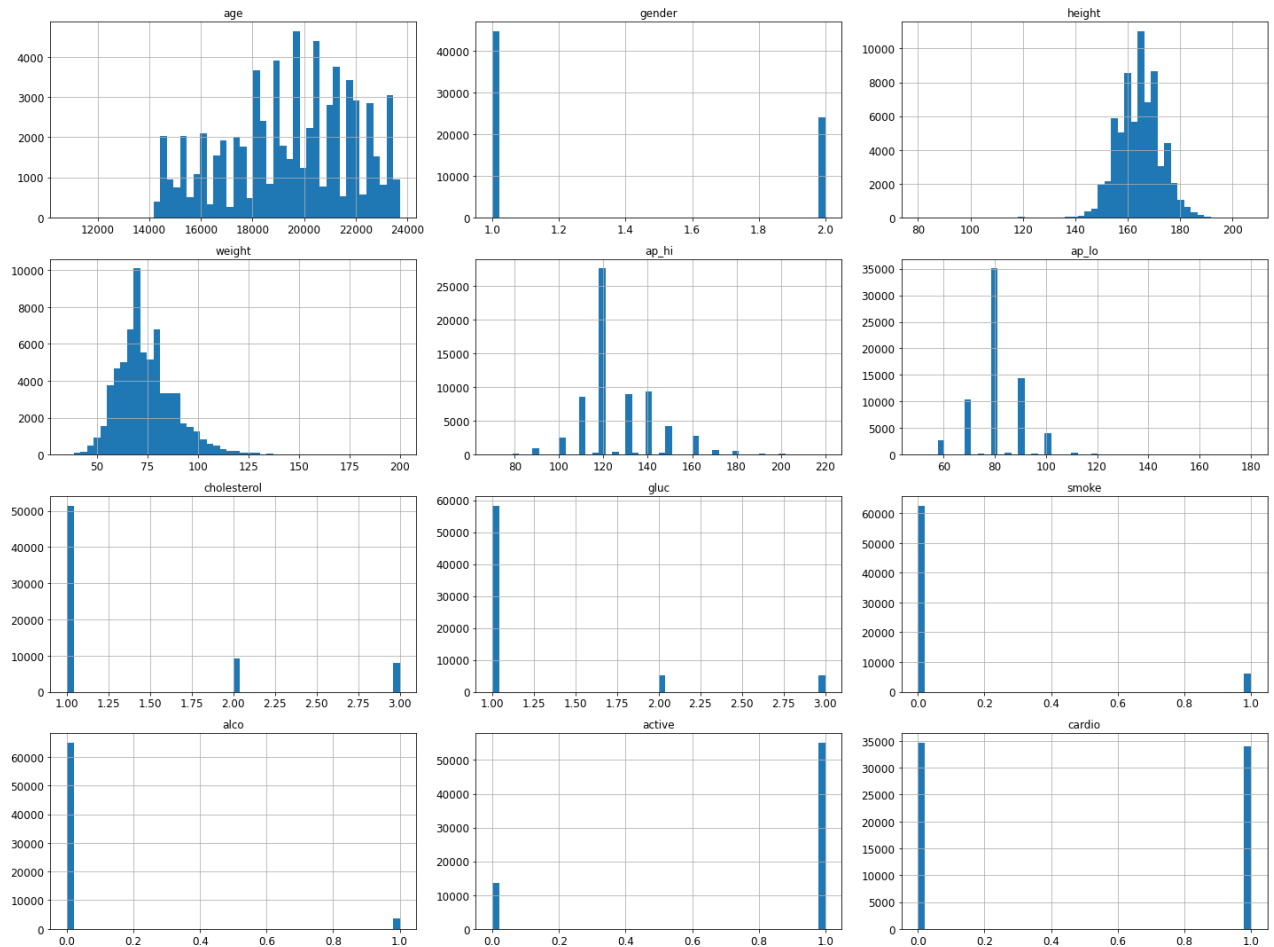


We can observe that after implementing Outlier removal we have got more useful data. Majority of the Outliers presented in **ap_hi**, **ap_lo** and **height** columns.

Histogram for all features each with 50 bins

```
In [ ]: cardio.hist(bins=50, figsize=(20,15))
save_fig('Cardio_Histogram_Full')
plt.show()
```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\Cardio_Histogram_Full.png

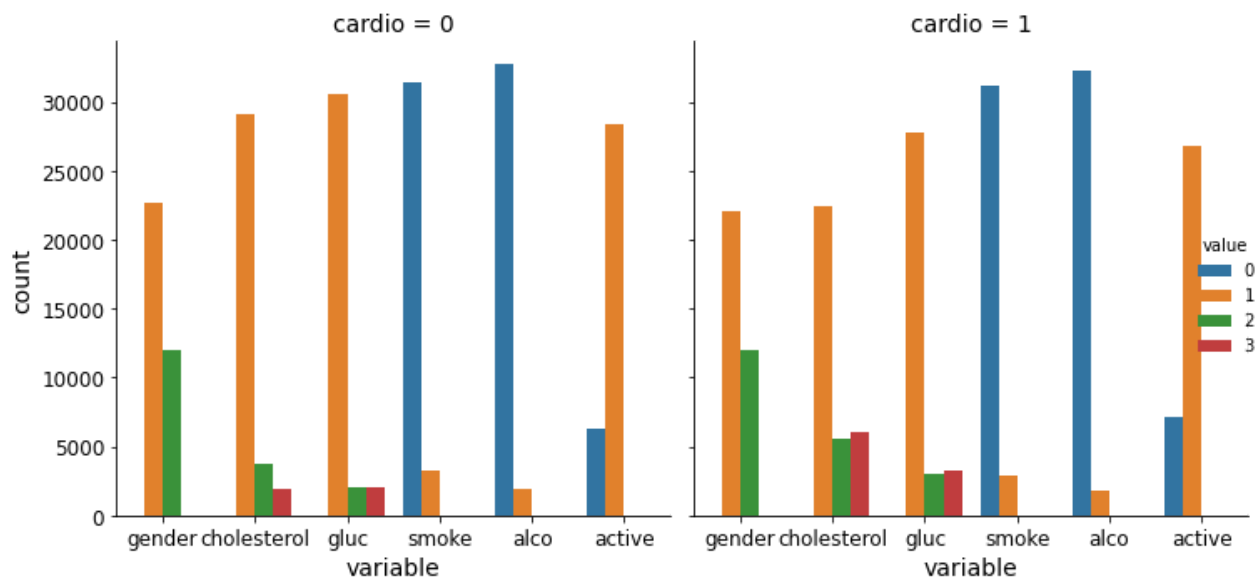


From the above plots, we have observed that **Cholesterol** and **Glucose** have each 3 classes in them. We have to separate them into different columns.

Distributions of Categorical Features

```
In [ ]: cat_features = ['gender', 'cholesterol', 'gluc', 'smoke', 'alco', 'active']
df_long = pd.melt(cardio, id_vars=['cardio'], value_vars=cat_features)
sns.catplot(x="variable", hue="value", col="cardio", data=df_long, kind="count")
save_fig('Categorical_Features_Comparison')
plt.show()
```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\Categorical_Features_Comparison.png



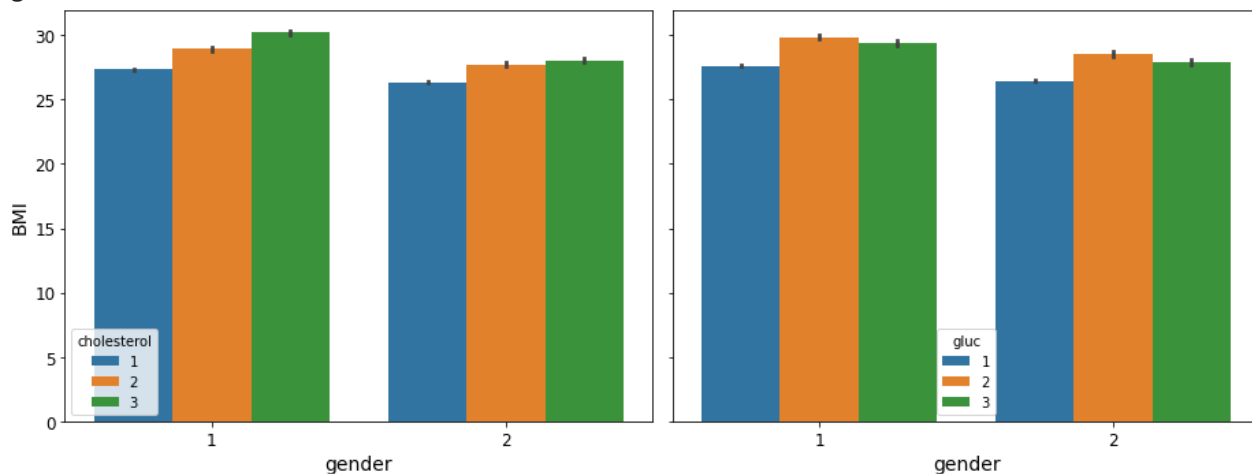
```
In [ ]: cat_column = ['cholesterol','gluc']

fig, axes = plt.subplots(nrows=1, ncols=len(cat_column), figsize=(13,5), sharey=True)
fig.subplots_adjust(hspace=0.4, wspace=0.4)
BMI = cardio['weight']/((cardio['height']/100)**2)

for (index, column) in enumerate(cat_column):
    sns.barplot(x='gender',y=BMI, data=cardio, hue=column, ax=axes[index])

axes[0].set_ylabel('BMI')
save_fig('BMI_vs_Gender_Category_Analysis')
plt.show()
```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\BMI_vs_Gender_Category_Analysis.png



Dataset Splitting

Splitting of Cardio Dataset into training and testing set with Stratified Shuffle Split method

```
In [ ]: save_object(cardio, 'Final_cardio.dataframe')
```

Saving Pickle E:\Github\SEMESTER-3\PML_Project\Pickles_And_Models\Final_cardio.dataframe

```
In [ ]: cardio['age_cat'] = pd.cut(cardio['age'],
                                   bins=[0, 16000, 18000, 20000, 21000, 22000, 23000, np.inf],
                                   labels=[1, 2, 3, 4, 5, 6, 7])
cardio['age_cat'].value_counts()
```

```
Out[ ]: 3    20111
        5    11292
        2     9859
        4     8319
        1     8035
        6     6249
        7     4816
        Name: age_cat, dtype: int64
```

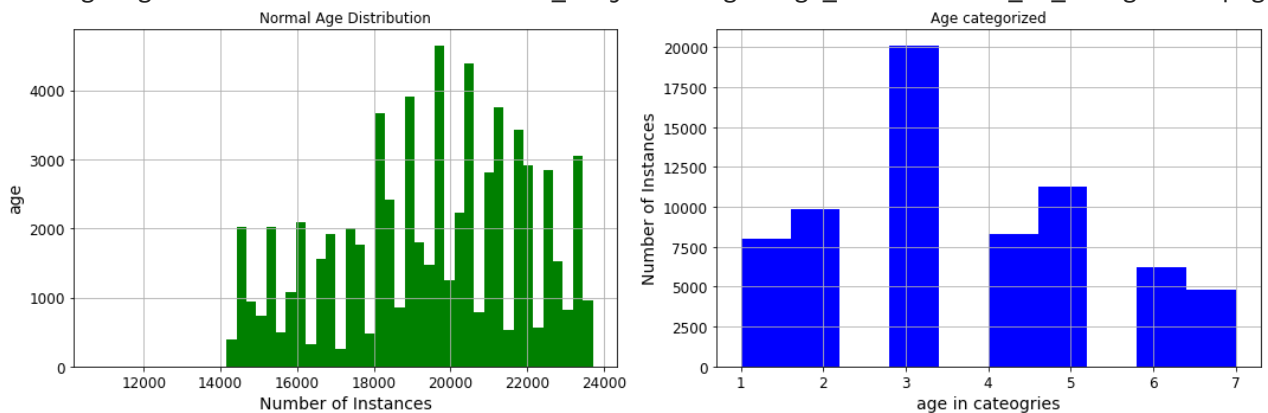
```
In [ ]: fig, axes = plt.subplots(nrows=1, ncols=2, figsize=(15,5))

cardio['age'].hist(bins=50, ax=axes[0], color='g')
axes[0].set(title= 'Normal Age Distribution', xlabel='Number of Instances', ylabel='age')

cardio['age_cat'].hist(ax=axes[1], color='b')
axes[1].set(title= 'Age categorized', xlabel='age in categories', ylabel='Number of Ins')

save_fig('Age_Distribution_vs_Categories')
plt.show()
```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\Age_Distribution_vs_Categories.png



```
cardio_train, cardio_test = train_test_split(cardio, test_size=0.2)
```

```
fig, split = plt.subplots(nrows=1, ncols=2, figsize=(15,5))
```

```
cardio_train['age_cat'].hist(ax=split[0], color='g') split[0].set(title= 'Default Train Set', xlabel='age in bins', ylabel='Number of Instances')
```

```
cardio_test['age_cat'].hist(ax=split[1], color='b') split[1].set(title= 'Default Test Set', xlabel='age in bins', ylabel='Number of Instances')
```

```
plt.tight_layout() plt.show()
```

```
save_object(cardio, 'quicksave.data')
```

```
In [ ]: strat_split = StratifiedShuffleSplit(n_splits=1, test_size=0.2, random_state=42)
for train_index, test_index in strat_split.split(cardio, cardio['age_cat']):
    strat_train_set = cardio.iloc[train_index]
    strat_test_set = cardio.iloc[test_index]
```

```
In [ ]: fig, strat = plt.subplots(nrows=1, ncols=2, figsize=(15,5))
```



```

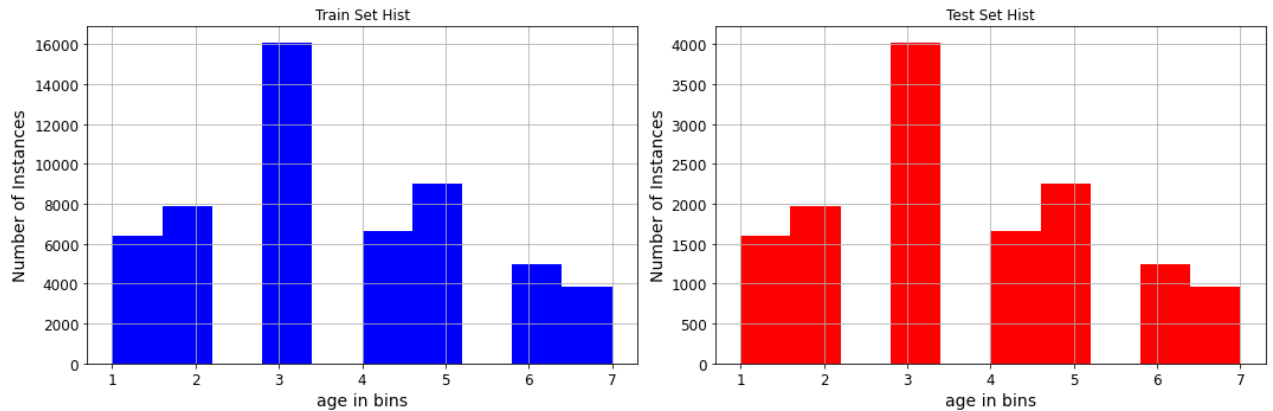
strat_train_set['age_cat'].hist(ax=strat[0], color='b')
strat[0].set(title= 'Train Set Hist', xlabel='age in bins', ylabel='Number of Instances')

strat_test_set['age_cat'].hist(ax=strat[1], color='r')
strat[1].set(title= 'Test Set Hist', xlabel='age in bins', ylabel='Number of Instances')

save_fig('Stratified_Train_Test_Set')
plt.show()

```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\Stratified_Train_Test_Set.png



```

In [ ]: for set_in (strat_train_set, strat_test_set):
        set_.drop('age_cat', axis=1, inplace=True)

```

```

In [ ]: cardio = strat_train_set.copy()

```

```

In [ ]: corr_matrix = cardio.corr()

```

```

In [ ]: corr_matrix['cardio'].sort_values(ascending=False)

```

```

Out[ ]: cardio      1.000000
        ap_hi       0.427615
        ap_lo       0.339710
        age         0.239476
        cholesterol 0.219276
        weight      0.176428
        gluc        0.091428
        gender      0.006667
        alco       -0.008415
        height      -0.013512
        smoke       -0.014269
        active      -0.038482
        Name: cardio, dtype: float64

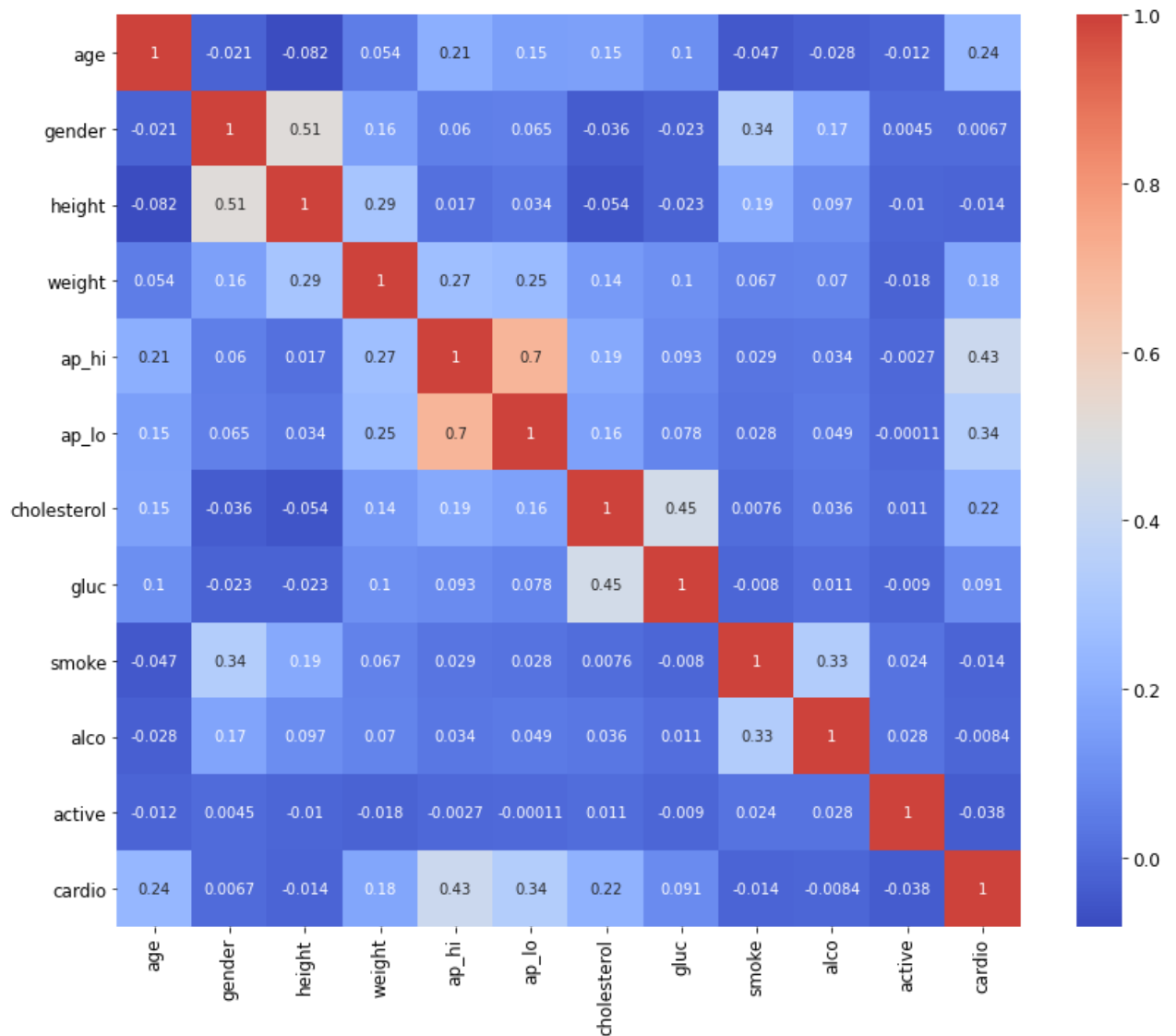
```

```

In [ ]: # Correlation HeatMap
        fig, axes = plt.subplots(1,1,figsize=(12,10))
        sns.heatmap(corr_matrix, annot=True, cmap='coolwarm', ax=axes, center=0.5)
        save_fig('Heat_Map_General')
        plt.show()

```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\Heat_Map_General.png



As we can see that the data is not very much correlated, so we proceed further with Data Transformation Pipelines

```
In [ ]: # save_object(strat_train_set.drop(columns='cardio',axis=1), 'strat_train_cardio.dataframe')
# save_object(strat_train_set['cardio'], 'strat_train_cardio_labels.dataframe')
# save_object(strat_test_set.drop(columns='cardio',axis=1), 'strat_test_cardio.dataframe')
# save_object(strat_test_set['cardio'], 'strat_test_cardio_labels.dataframe')

# cardio = strat_train_set.drop(columns='cardio',axis=1).copy()
# cardio_labels = strat_train_set['cardio'].copy()
```

Data Transformation Pipelines

```
In [4]: cardio = load_object('Final_cardio.dataframe')

X_train = load_object('strat_train_cardio.dataframe')
y_train = load_object('strat_train_cardio_labels.dataframe')

X_test = load_object('strat_test_cardio.dataframe')
y_test = load_object('strat_test_cardio_labels.dataframe')
```

Loaded Pickle /content/Pickles_And_Models/Final_cardio.dataframe

Loaded Pickle /content/Pickles_And_Models/strat_train_cardio.dataframe
 Loaded Pickle /content/Pickles_And_Models/strat_train_cardio_labels.dataframe
 Loaded Pickle /content/Pickles_And_Models/strat_test_cardio.dataframe
 Loaded Pickle /content/Pickles_And_Models/strat_test_cardio_labels.dataframe

```
In [5]: class DataFrameSelector(BaseEstimator, TransformerMixin):

    def __init__(self, attribute_names):
        self.attribute_names = attribute_names

    def fit(self, X, y=None):
        return self

    def transform(self, X):
        return X[self.attribute_names].values

target_feature = ['cardio']
cat_attributes = ['cholesterol', 'gluc']
num_attributes = ['age', 'gender', 'height', 'weight', 'ap_hi', 'ap_lo', 'smoke', 'alco']
new_cat_attributes = ['cholesterol_1', 'cholesterol_2', 'cholesterol_3', 'gluc_1', 'gluc_2', 'gluc_3']

num_pipeline = Pipeline([
    ('selector', DataFrameSelector(num_attributes)),
    ('imputer', SimpleImputer(strategy='median')),
    ('std_scaler', StandardScaler())
])

cat_pipeline = Pipeline([
    ('selector', DataFrameSelector(cat_attributes)),
    ('cat_encoder', OneHotEncoder(sparse=False))
])

full_pipeline = FeatureUnion(transformer_list=[
    ('Numerical_Pipeline', num_pipeline),
    ('Categorical_Pipeline', cat_pipeline)
])
```

```
In [6]: X_train.head(2)
```

```
Out[6]:
```

	age	gender	height	weight	ap_hi	ap_lo	cholesterol	gluc	smoke	alco	active
3280	22640	2	167	78.0	160	100	1	1	0	0	1
40230	20613	1	156	88.0	150	80	1	1	0	0	1

```
In [7]: full_pipeline.fit(X_train)
```

```
Out[7]: FeatureUnion(n_jobs=None,
                    transformer_list=[('Numerical_Pipeline',
                                     Pipeline(memory=None,
                                             steps=[('selector',
                                                     DataFrameSelector(attribute_names=['age',
                                                                 'gender',
                                                                 'height',
                                                                 'weight',
                                                                 'ap_hi',
                                                                 'ap_lo',
                                                                 'smoke',
                                                                 'alco'],
                                                                 target_feature=['cardio'],
                                                                 new_cat_attributes=['cholesterol_1',
                                                                 'cholesterol_2',
                                                                 'cholesterol_3',
                                                                 'gluc_1',
                                                                 'gluc_2',
                                                                 'gluc_3'],
                                                                 num_attributes=['age',
                                                                 'gender',
                                                                 'height',
                                                                 'weight',
                                                                 'ap_hi',
                                                                 'ap_lo',
                                                                 'smoke',
                                                                 'alco'],
                                                                 cat_attributes=['cholesterol',
                                                                 'gluc'],
                                                                 num_pipeline=num_pipeline,
                                                                 cat_pipeline=cat_pipeline),
                                                     'Numerical_Pipeline')],
                                             memory=None),
                                     ('Categorical_Pipeline',
                                     Pipeline(memory=None,
                                             steps=[('selector',
                                                     DataFrameSelector(attribute_names=['cholesterol',
                                                                 'gluc'],
                                                                 target_feature=['cardio'],
                                                                 new_cat_attributes=['cholesterol_1',
                                                                 'cholesterol_2',
                                                                 'cholesterol_3',
                                                                 'gluc_1',
                                                                 'gluc_2',
                                                                 'gluc_3'],
                                                                 num_attributes=['age',
                                                                 'gender',
                                                                 'height',
                                                                 'weight',
                                                                 'ap_hi',
                                                                 'ap_lo',
                                                                 'smoke',
                                                                 'alco'],
                                                                 cat_attributes=['cholesterol',
                                                                 'gluc'],
                                                                 num_pipeline=num_pipeline,
                                                                 cat_pipeline=cat_pipeline),
                                                     'Categorical_Pipeline')],
                                             memory=None),
                                     ('std_scaler', StandardScaler())],
                    n_jobs=None)
```

```

lo',
ke',
o',
ive'])),

('imputer',
 SimpleImputer(add_indicator=False,
               copy=True,
               fill_value=None,
               missing_values=nan,
               strategy='median',
               verbose=0)),

('std_scaler',...
 with_mean=True,
 with_std=True))),

(verbose=False)),
('Categorical_Pipeline',
 Pipeline(memory=None,
          steps=[('selector',
                  DataFrameSelector(attribute_names=['cho
lesterol',
c'])),

('cat_encoder',
 OneHotEncoder(categories='auto',
               drop=None,
               dtype=<class 'numpy.float
64'>,

               handle_unknown='error',
               sparse=False))),

(verbose=False))],
transformer_weights=None, verbose=False)

```

In [8]: `save_object(full_pipeline, 'full_pipeline.transformer')`

Saving Pickle /content/Pickles_And_Models/full_pipeline.transformer

In [9]: `X_train = pd.DataFrame(data=full_pipeline.transform(X_train), columns=num_attributes+new_`
`X_test = pd.DataFrame(data=full_pipeline.transform(X_test), columns=num_attributes+new_`

In [10]: `X_train.head(2)`

Out[10]:

	age	gender	height	weight	ap_hi	ap_lo	smoke	alco	active	cholesterol
0	1.286661	1.371339	0.325114	0.266796	1.997143	1.941350	-0.310522	-0.237641	0.494967	
1	0.465335	-0.729214	-1.048238	0.965196	1.398966	-0.143682	-0.310522	-0.237641	0.494967	

Machine Learning Algorithms Implementation

Logistic Regression

In []: `grid_values={`
`"C" : [0.001,0.01,1,5,10,25,50],`
`"penalty" : ["l1","l2"]`

```

}

grid_search=GridSearchCV(LogisticRegression(),grid_values,cv=10)
grid_search.fit(X_train,y_train)

print("tuned hpyerparameters :(best parameters) ",grid_search.best_params_)
print("accuracy :",grid_search.best_score_)

```

tuned hpyerparameters :(best parameters) {'C': 25, 'penalty': 'l2'}

accuracy : 0.7276502482814405

```

In [ ]: #Training the model with the optimised parameters
log_reg = LogisticRegression(C = 25, penalty = 'l2')
log_reg.fit(X_train, y_train)

#KFold cross-validation for evaluating the model
cv = KFold(n_splits=10, random_state=1, shuffle=True)
scores = cross_val_score(log_reg, X_train, y_train, scoring='recall', cv=cv, n_jobs=-1)

# Reporting the performance
print('Accuracy: %.3f | Scores: (%.3f)' % (np.mean(scores), np.std(scores)))

```

Accuracy: 0.669 | Scores: (0.009)

```

In [ ]: # Testing Set
log_reg = LogisticRegression(C = 25, penalty = 'l2')
log_reg.fit(X_train, y_train)
log_pred_test = log_reg.predict(X_test)
print('Testing dataset')
print(confusion_matrix(y_test,log_pred_test))
print(classification_report(y_test,log_pred_test))
print(accuracy_score(y_test,log_pred_test))

```

Testing dataset

```
[[5505 1550]
 [2142 4540]]
```

	precision	recall	f1-score	support
0	0.72	0.78	0.75	7055
1	0.75	0.68	0.71	6682
accuracy			0.73	13737
macro avg	0.73	0.73	0.73	13737
weighted avg	0.73	0.73	0.73	13737

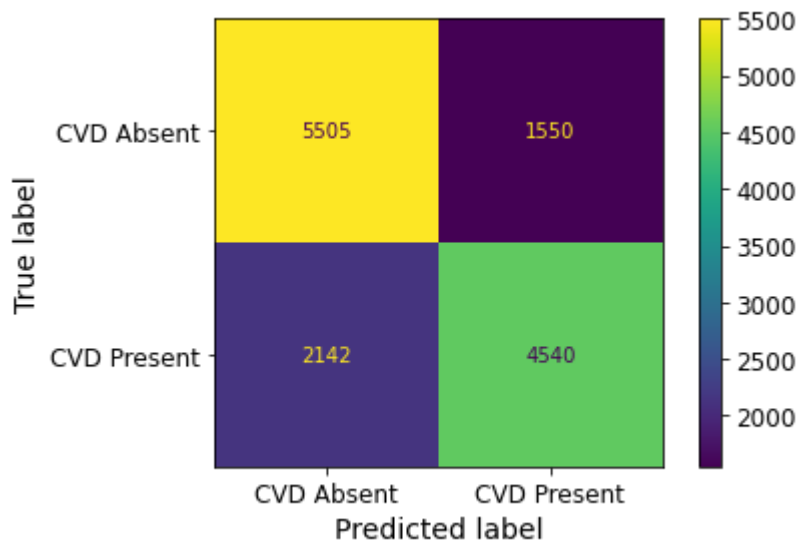
0.731236805707214

```

In [ ]: plot_confusion_matrix(log_reg, X_test, y_test, display_labels = ['CVD Absent', 'CVD Pre
save_fig('Confusion_matrix_Logisitic')
plt.show()

```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\Confusion_matrix_Logisitic.png



```
In [ ]: save_object(log_reg, 'Logistic_Regression.model')
```

Saving Pickle E:\Github\SEMESTER-3\PML_Project\Pickles_And_Models\Logistic_Regression.mo
del

Naive Bayes

```
In [ ]: gauss_nb = GaussianNB()
gauss_nb.fit(X_train, y_train)
gnb_pred_test = gauss_nb.predict(X_test)

print('Testing dataset')
print(confusion_matrix(y_test, gnb_pred_test))
print(classification_report(y_test, gnb_pred_test))
print(accuracy_score(y_test, gnb_pred_test))
```

Testing dataset

[[5488 1567]

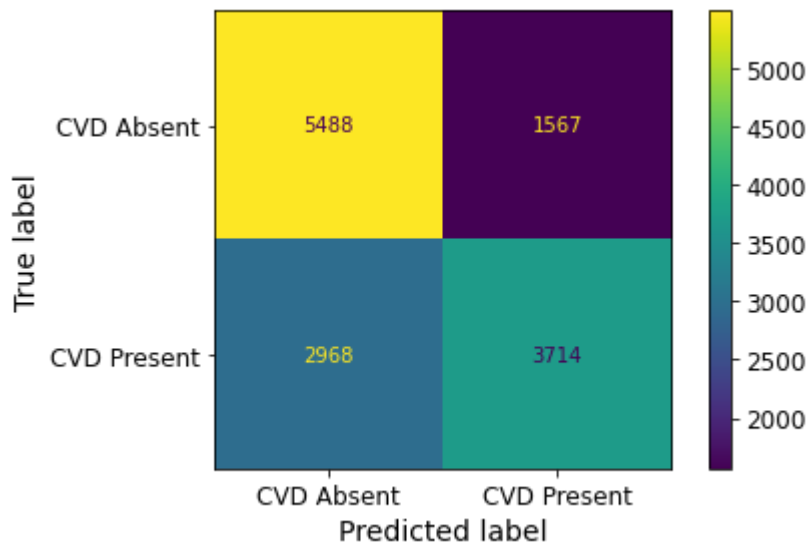
[2968 3714]]

	precision	recall	f1-score	support
0	0.65	0.78	0.71	7055
1	0.70	0.56	0.62	6682
accuracy			0.67	13737
macro avg	0.68	0.67	0.66	13737
weighted avg	0.68	0.67	0.67	13737

0.6698696949843488

```
In [ ]: plot_confusion_matrix(gauss_nb, X_test, y_test, display_labels = ['CVD Absent', 'CVD Pr
save_fig('Confusion_matrix_Naive_Bayes')
plt.show()
```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\Confusion_matrix_Naive_Bayes.png



```
In [ ]: save_object(gauss_nb, 'Naive_Bayes.model')
```

Saving Pickle E:\Github\SEMESTER-3\PML_Project\Pickles_And_Models\Naive_Bayes.model

K Nearest Neighbors

```
In [ ]: hyperparameters={
    "n_neighbors" : [1, 5, 10, 25, 50, 75],
    "p" : [1, 2] # manhattan_distance (L1), and euclidean_distance (L2)
}

grid_search=GridSearchCV(KNeighborsClassifier(),hyperparameters,cv=10, verbose=1, n_job
grid_search.fit(X_train,y_train)

print("tuned hpyerparameters :(best parameters) ",grid_search.best_params_)
print("accuracy :",grid_search.best_score_)
```

Fitting 10 folds for each of 12 candidates, totalling 120 fits

[Parallel(n_jobs=-1)]: Using backend LokyBackend with 8 concurrent workers.

[Parallel(n_jobs=-1)]: Done 34 tasks | elapsed: 1.1min

[Parallel(n_jobs=-1)]: Done 120 out of 120 | elapsed: 4.6min finished

tuned hpyerparameters :(best parameters) {'n_neighbors': 75, 'p': 1}

accuracy : 0.7289059087703583

```
In [ ]: #Training the model with the optimised parameters
knn = KNeighborsClassifier(n_neighbors = 75, p = 1)
knn.fit(X_train, y_train)

#KFold cross-validation for evaluating the model
cv = KFold(n_splits=10, random_state=1, shuffle=True)
scores = cross_val_score(knn, X_train, y_train, scoring='accuracy', cv=cv, n_jobs=-1)

# Reporting the performance
print('Scores -> Mean: %.3f | STD: (%.3f)' % (np.mean(scores), np.std(scores)))
```

Scores -> Mean: 0.728 | STD: (0.005)

```
In [ ]: # Testing Set
knn = KNeighborsClassifier(n_neighbors = 25, p = 1)
knn.fit(X_train, y_train)
knn_pred_test = knn.predict(X_test)
```

```
print('Testing dataset')
print(confusion_matrix(y_test,knn_pred_test))
print(classification_report(y_test,knn_pred_test))
print(accuracy_score(y_test,knn_pred_test))
```

Testing dataset

[[5346 1709]

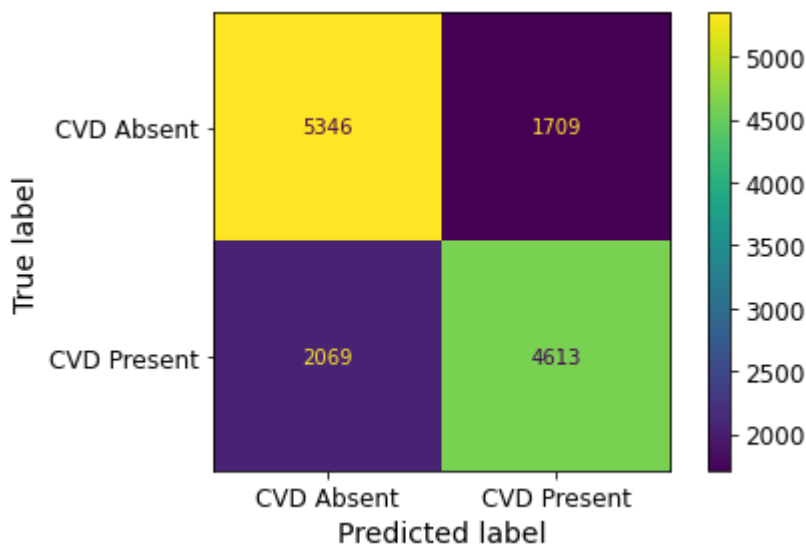
[2069 4613]]

	precision	recall	f1-score	support
0	0.72	0.76	0.74	7055
1	0.73	0.69	0.71	6682
accuracy			0.72	13737
macro avg	0.73	0.72	0.72	13737
weighted avg	0.73	0.72	0.72	13737

0.7249763412681081

```
In [ ]: plot_confusion_matrix(knn, X_test, y_test, display_labels = ['CVD Absent', 'CVD Present']
save_fig('Confusion_Matrix_KNN')
plt.show()
```

Saving figure E:\Github\SEMESTER-3\PML_Project\images\Confusion_Matrix_KNN.png



```
In [ ]: save_object(knn, 'KNN.model')
```

Saving Pickle E:\Github\SEMESTER-3\PML_Project\Pickles_And_Models\KNN.model

Support Vector Machines (SVM)

```
In [11]: '''
hyperparameters={
    "C" : [0.1, 10],
    "gamma" : [0.1, 1],
    "kernel" : ['linear']
}

grid_search=GridSearchCV(SVC(), hyperparameters,cv=2, verbose=1, n_jobs=-1)
grid_search.fit(X_train,y_train)

print("tuned hyperparameters :(best parameters) ",grid_search.best_params_)
print("accuracy :",grid_search.best_score_)
```



```
...
```

```
Out[11]: '\nhyperparameters={\n      "C" : [0.1, 10],\n      "gamma" : [0.1, 1],\n      "kernel" : [\n1\ninear\']\n}\n\ngrid_search=GridSearchCV(SVC(), hyperparameters,cv=2, verbose=1, n_jobs=-1)\ngrid_search.fit(X_train,y_train)\n\nprint("tuned hyperparameters :(best parameters) ",grid_search.best_params_)\nprint("accuracy :",grid_search.best_score_)\n\n'
```

```
In [ ]: #Training the model with the optimised parameters
svm = SVC(C=0.1, gamma=1, kernel='linear')
svm.fit(X_train, y_train)

#KFold cross-validation for evaluating the model
cv = KFold(n_splits=5, random_state=1, shuffle=True)
scores = cross_val_score(svm, X_train, y_train, scoring='accuracy', cv=cv, n_jobs=-1)

# Reporting the performance
print('Scores -> Mean: %.3f | STD: (%.3f)' % (np.mean(scores), np.std(scores)))
```

```
In [27]: svm = SVC(C=0.1, gamma=1, kernel='linear')
svm.fit(X_train, y_train)
```

```
In [24]: svm_pred_test = svm.predict(X_test)
print('Testing dataset')
print(confusion_matrix(y_test,svm_pred_test))
print(classification_report(y_test,svm_pred_test))
print(accuracy_score(y_test,svm_pred_test))
```

Testing dataset

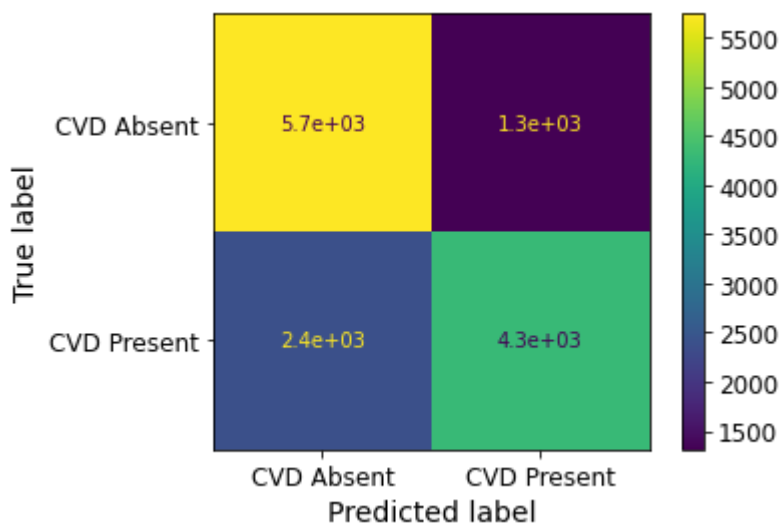
[[5744 1311]

[2387 4295]]

	precision	recall	f1-score	support
0	0.71	0.81	0.76	7055
1	0.77	0.64	0.70	6682
accuracy			0.73	13737
macro avg	0.74	0.73	0.73	13737
weighted avg	0.74	0.73	0.73	13737

0.7308000291184392

```
In [26]: plot_confusion_matrix(svm, X_test, y_test, display_labels = ['CVD Absent', 'CVD Present']
plt.show())
```



```
In [25]: save_object(svm, 'SVM.model')
```

Saving Pickle /content/Pickles_And_Models/SVM.model

Decision Trees

```
In [22]: #Training the model with the default parameters
tree_clf = DecisionTreeClassifier()
tree_clf.fit(X_train,y_train)

#KFold cross-validation for evaluating the model
cv = KFold(n_splits=10, random_state=1, shuffle=True)
scores = cross_val_score(tree_clf, X_train,y_train, scoring='accuracy', cv=cv, n_jobs=-1)

# Reporting the performance
print('Accuracy: %.3f (%.3f)' % (np.mean(scores), np.std(scores)))
```

Accuracy: 0.633 (0.005)

```
In [ ]: pipeline = Pipeline([('clf',tree_clf)])
parameters = {
    'clf__max_depth': np.linspace(1,10,10),
    'clf__min_samples_split': (1,2,3,4,5),
    'clf__min_samples_leaf': (1,2,3,4,5)
}
grid_search = GridSearchCV(pipeline, parameters, n_jobs=-1)
grid_search.fit(X_train,y_train)

grid_search.best_score_
```

```
In [ ]: best_parameters = grid_search.best_estimator_.get_params()
for param_name in sorted(parameters.keys()):
    print(f'{param_name} : {best_parameters[param_name]}')
```

```
In [ ]: #Training the model with the optimised parameters
tree_clf = DecisionTreeClassifier(max_depth=5,min_samples_leaf=1,min_samples_split=2)
tree_clf.fit(X_train,y_train)

#KFold cross-validation for evaluating the model
cv = KFold(n_splits=10, random_state=1, shuffle=True)
scores = cross_val_score(tree_clf, X_train,y_train, scoring='accuracy', cv=cv, n_jobs=-1)

# Reporting the performance
print('Accuracy: %.3f (%.3f)' % (np.mean(scores), np.std(scores)))
```

```
In [23]: save_object(tree_clf, 'Decision_Tree.model')
```

Saving Pickle /content/Pickles_And_Models/Decision_Tree.model

Ensemble Methods

```
In [16]: def plot_crossval_boxplot(models):
    outcome = []
    model_names = []

    for model_name, model in models:
```

```

k_fold_validation = KFold(n_splits=10)
results = cross_val_score(model, X_train, y_train, cv=k_fold_validation, scoring='accuracy')
outcome.append(results)
model_names.append(model_name)

fig = plt.figure()
fig.suptitle('Comparison of the Cross Validation Accuracy Scores')
ax = fig.add_subplot(111)
plt.boxplot(outcome)
ax.set_xticklabels(model_names)
plt.show()

```

Bagging and Pasting Ensemble Methods

```

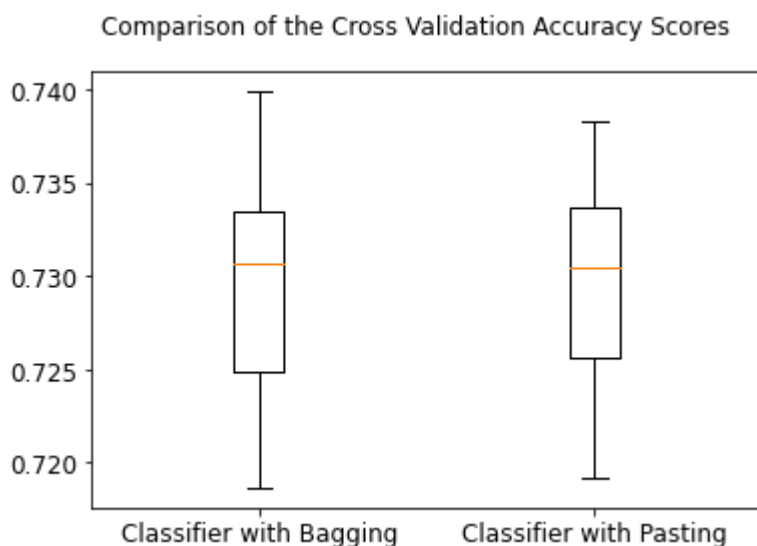
In [17]: #Bagging
bag_clf = BaggingClassifier(DecisionTreeClassifier(),
                           n_estimators=500,
                           max_samples=100,
                           bootstrap=True,
                           n_jobs=-1)

#Pasting
pas_clf = BaggingClassifier(DecisionTreeClassifier(),
                           n_estimators=500,
                           max_samples=100,
                           bootstrap=False,
                           n_jobs=-1)

bag_clf.fit(X_train, y_train)
pas_clf.fit(X_train, y_train)

plot_crossval_boxplot(['Classifier with Bagging', bag_clf), ('Classifier with Pasting',

```



Hard and Soft Voting in the Ensemble Method

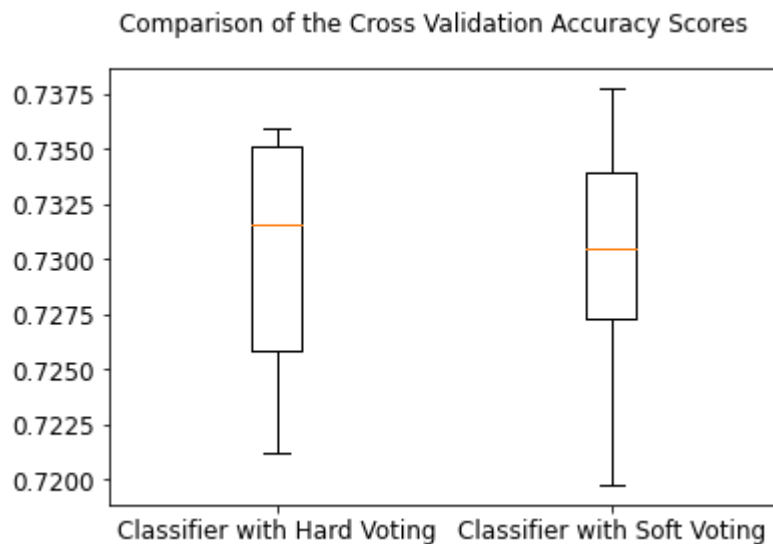
```

In [18]: #Warning - takes 3 mins to compile
hard_voting_clf = VotingClassifier(estimators=[('bagging', bag_clf), ('pasting', pas_clf)])
soft_voting_clf = VotingClassifier(estimators=[('bagging', bag_clf), ('pasting', pas_clf)])

```

```
hard_voting_clf.fit(X_train, y_train)
soft_voting_clf.fit(X_train, y_train)

plot_crossval_boxplot(['Classifier with Hard Voting', hard_voting_clf), ('Classifier wi
```



Random Forest Classifier (Similar to Bagging with Decision Tree Algorithm)

```
In [31]: # Training the model with the default parameters
rf_clf = RandomForestClassifier()
rf_clf.fit(X_train, y_train)

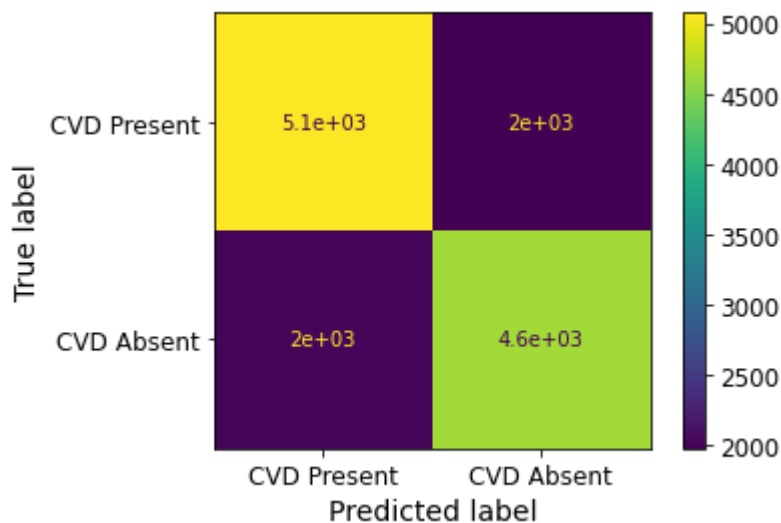
# KFold cross-validation for evaluating the model
cv = KFold(n_splits=10, random_state=1, shuffle=True)
scores = cross_val_score(rf_clf, X_test, y_test, scoring='accuracy', cv=cv, n_jobs=-1)

# Reporting the performance
print('Accuracy: %.3f (%.3f)' % (np.mean(scores), np.std(scores)))
```

Accuracy: 0.717 (0.012)

```
In [32]: #How well can the default paramters predict?
y_pred = rf_clf.predict(X_test)
plot_confusion_matrix(rf_clf, X_test, y_test, display_labels = ['CVD Present', 'CVD Abse
```

```
Out[32]: <sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x7f0eec0bb588>
```



```
In [33]: # Warning takes 5 mins to compile
...
pipeline = Pipeline([('clf', rf_clf)])
parameters = {
    'clf__max_depth': (1,2,3,4,5),
    'clf__min_samples_split': (1,2,3),
    'clf__min_samples_leaf': (1,2,3)
}
grid_search = GridSearchCV(pipeline, parameters, n_jobs=-1)
grid_search.fit(X_train, y_train)

grid_search.best_score_
Best score obtained = 0.7297333333333335
...
```

```
Out[33]: "\npipeline = Pipeline([('clf', rf_clf)])\nparameters = {\n    'clf__max_depth': (1,2,3,4,5),\n    'clf__min_samples_split': (1,2,3),\n    'clf__min_samples_leaf': (1,2,3)\n}\ngrid_search = GridSearchCV(pipeline, parameters, n_jobs=-1)\ngrid_search.fit(X_train, y_train)\ngrid_search.best_score_\nBest score obtained = 0.7297333333333335\n"
```

```
In [34]: best_parameters = grid_search.best_estimator_.get_params()
for param_name in sorted(parameters.keys()):
    print(f'{param_name} : {best_parameters[param_name]}')

...
Best Estimators obtained:
clf__max_depth : 5
clf__min_samples_leaf : 1
clf__min_samples_split : 2
...
```

```
In [35]: #Training the model with the optimised parameters
rf_clf1 = RandomForestClassifier(max_depth=5, min_samples_leaf=1, min_samples_split=2)
rf_clf1.fit(X_train, y_train)

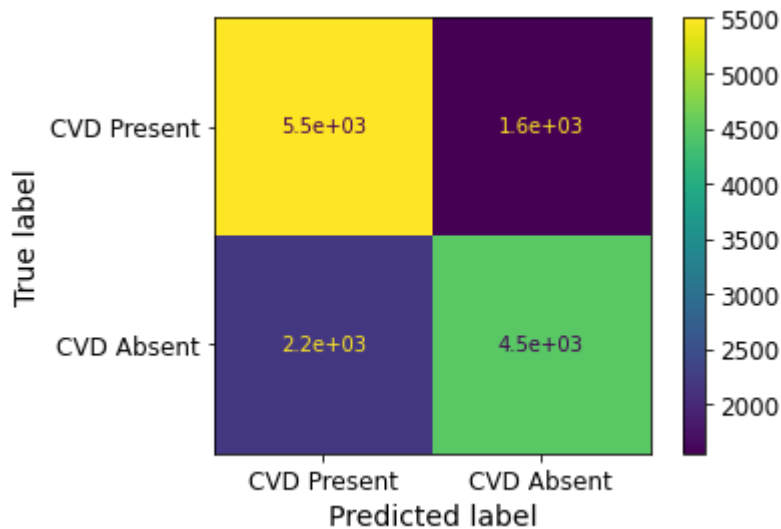
#KFold cross-validation for evaluating the model
cv = KFold(n_splits=10, random_state=1, shuffle=True)
scores = cross_val_score(rf_clf1, X_test, y_test, scoring='accuracy', cv=cv, n_jobs=-1)

# Reporting the performance
print('Accuracy: %.3f (%.3f)' % (np.mean(scores), np.std(scores)))
```

Accuracy: 0.728 (0.015)

```
In [36]: #How well can the default paramters predict?
y_pred = rf_clf1.predict(X_test)
plot_confusion_matrix(rf_clf1, X_test, y_test, display_labels = ['CVD Present', 'CVD Abs
```

```
Out[36]: <sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x7f0eebf3cc0>
```



```
In [37]: save_object(rf_clf1, 'Random_Forest.model')
```

Saving Pickle /content/Pickles_And_Models/Random_Forest.model

Model Analysis

```
In [42]: log_reg = load_object('Logistic_Regression.model')
gnb = load_object('Naive_Bayes.model')
knn = load_object('KNN.model')
svm = load_object('SVM.model')
decision_tree = load_object('Decision_Tree.model')
random_forest = load_object('Random_Forest.model')
```

Loaded Pickle /content/Pickles_And_Models/Logistic_Regression.model
 Loaded Pickle /content/Pickles_And_Models/Naive_Bayes.model
 Loaded Pickle /content/Pickles_And_Models/KNN.model
 Loaded Pickle /content/Pickles_And_Models/SVM.model
 Loaded Pickle /content/Pickles_And_Models/Decision_Tree.model
 Loaded Pickle /content/Pickles_And_Models/Random_Forest.model

```
In [65]: models = [log_reg, gnb, knn, svm, decision_tree, random_forest]
models_cols = ['Logistic_Regression', 'Naive_Bayes', 'KNN', 'Support_Vector_Machines',
```

```
In [66]: predictions = [model.predict(X_test) for model in models]
conf_mat =[confusion_matrix(y_test, model_pred).reshape(1,-1).tolist()[0] for model_pre
accuracy_score_table = [accuracy_score(y_test, model_pred) for model_pred in prediction
```

```
In [70]: final_comparison = pd.DataFrame( data=conf_mat, index=models_cols , columns= ['True CVD
```

```
In [72]: final_comparison['accuracy_score'] = accuracy_score_table
```

```
In [74]: final_comparison.sort_values('accuracy_score', ascending=False)
```

```
Out[74]:
```

	True CVD Absent	False CVD Absent	False CVD Present	True CVD Present	accuracy_score
Logistic_Regression	5505	1550	2142	4540	0.731237
Support_Vector_Machines	5744	1311	2387	4295	0.730800
Random_Forest	5502	1553	2186	4496	0.727815
KNN	5346	1709	2069	4613	0.724976
Naive_Bayes	5488	1567	2968	3714	0.669870
Decision_Tree	4455	2600	2496	4186	0.629031

In []: