Predicting the heart disease or not

1.Problem Definition

With the give data we have to predict whether the person is having heart disease or not

2.Data Definition

This is a multivariate type of dataset which means providing or involving a variety of separate mathematical or statistical variables, multivariate numerical data analysis. It is composed of 14 attributes which are age, sex, chest pain type, resting blood pressure, serum cholesterol, fasting blood sugar, resting electrocardiographic results, maximum heart rate achieved, exercise-induced angina, oldpeak — ST depression induced by exercise relative to rest, the slope of the peak exercise ST segment, number of major vessels and Thalassemia. This database includes 76 attributes, but all published studies relate to the use of a subset of 14 of them. The Cleveland database is the only one used by ML researchers to date. One of the major tasks on this dataset is to predict based on the given attributes of a patient that whether that particular person has heart disease or not and other is the experimental task to diagnose and find out various insights from this dataset which could help in understanding the problem more.

DATA LINK:https://archive.ics.uci.edu/dataset/45/heart+disease

3 Evaluation

We need 95%+ accuracy to pursue with this project

4.Features details

We can refer to the data link given above for the features details

Preparing the tools

In [1]:
```
#EDA
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline

#Models
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier

#ModelEvaluation
```

```
from sklearn.model_selection import train_test_split,GridSearchCV,Randomize
from sklearn.metrics import classification_report,confusion_matrix
from sklearn.metrics import precision_score,recall_score,f1_score
from sklearn.metrics import RocCurveDisplay
from sklearn import metrics

#Saving model
import pickle
```

In [2]:
```
#Loading the data
hd=pd.read_csv("heart-disease.csv")
hd
```

Out[2]:

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

303 rows × 14 columns

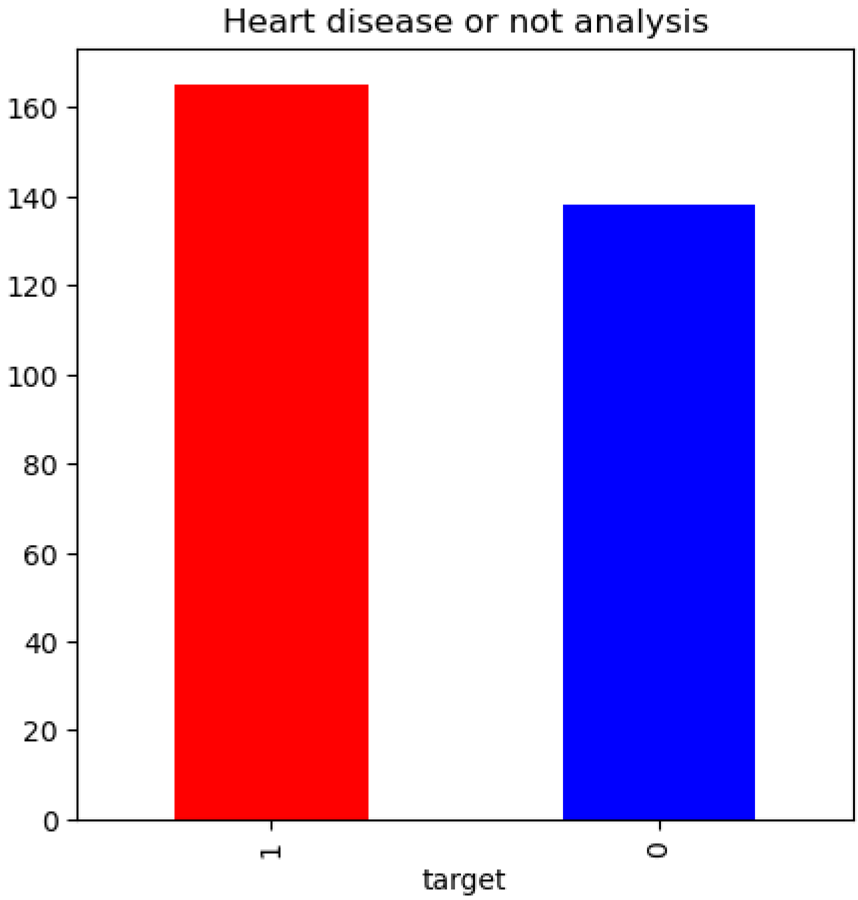
EDA

Basically eda is done to have a basic probability of the heart disease based on individual dimensions/columns. Vizualization are done so that if we have to present somewhere we can easily explain with the graphs to any non technical person instead of showing just the numbers

In [3]:
```
#To check whether the values of heart disease or not are almost same if the
hd["target"].value_counts()
```

Out[3]:
```
target
1    165
0    138
Name: count, dtype: int64
```

In [4]:
```
#vizualizing the above data to have the clear and comparitive vision
hd["target"].value_counts().plot(kind='bar',color=['red','blue'],figsize=(5
plt.title("Heart disease or not analysis");
#Target 0 is not heart disease and 1 for heart disease
```



In [5]:
```
#To see the dtype of all the columns whether all the columns are in int or 
hd.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 [6]:
```
#To find the null values in the data
hd.isna().sum()
```

Out[6]:
```
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
```

In [7]:
```
#To check the number of males and females in the data to have a basic overvi
hd['sex'].value_counts()
```

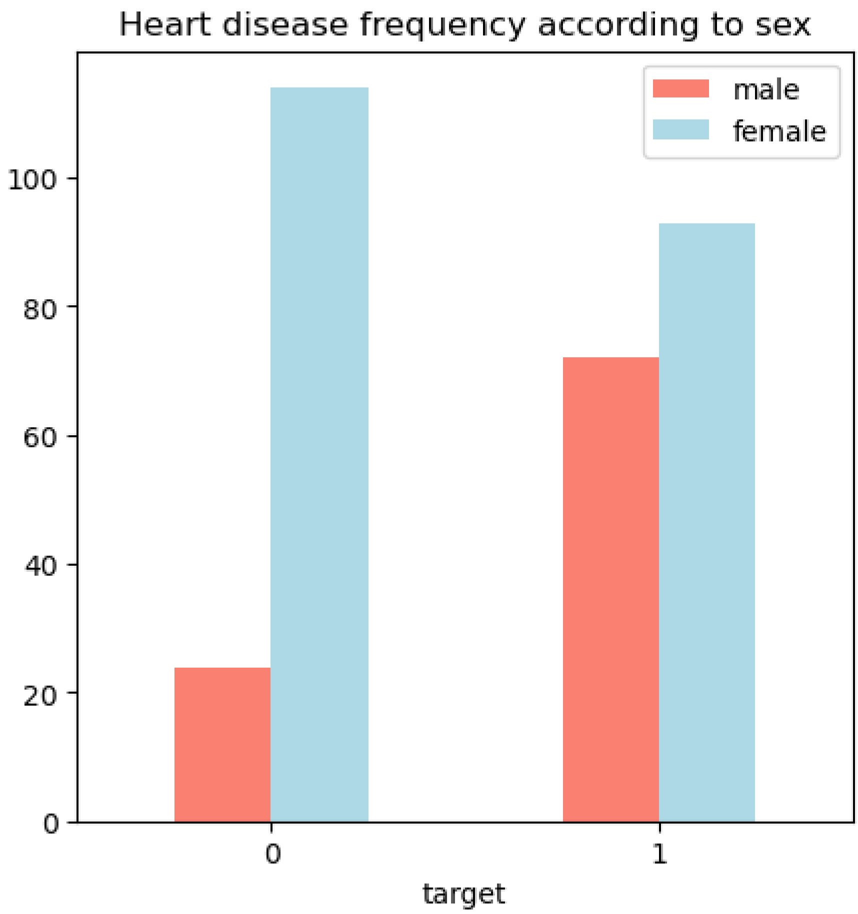
Out[7]:
```
sex
1    207
0     96
Name: count, dtype: int64
```

In [8]:
```
#To check whether the number of male having hd or not and female having hd o
pd.crosstab(hd.target,hd.sex)
```

Out[8]:

sex	0	1
target		
0	24	114
1	72	93

In [9]:
```
#Vizualizing the above matrix for better understanding
#Sex 0 is for female and 1 is for male
#Target 0 is not heart disease and 1 for heart disease
pd.crosstab(hd.target,hd.sex).plot(kind='bar',color=['salmon','lightblue'],f
plt.title("Heart disease frequency according to sex");
plt.legend(['male','female'])
plt.xticks(rotation=0);
```

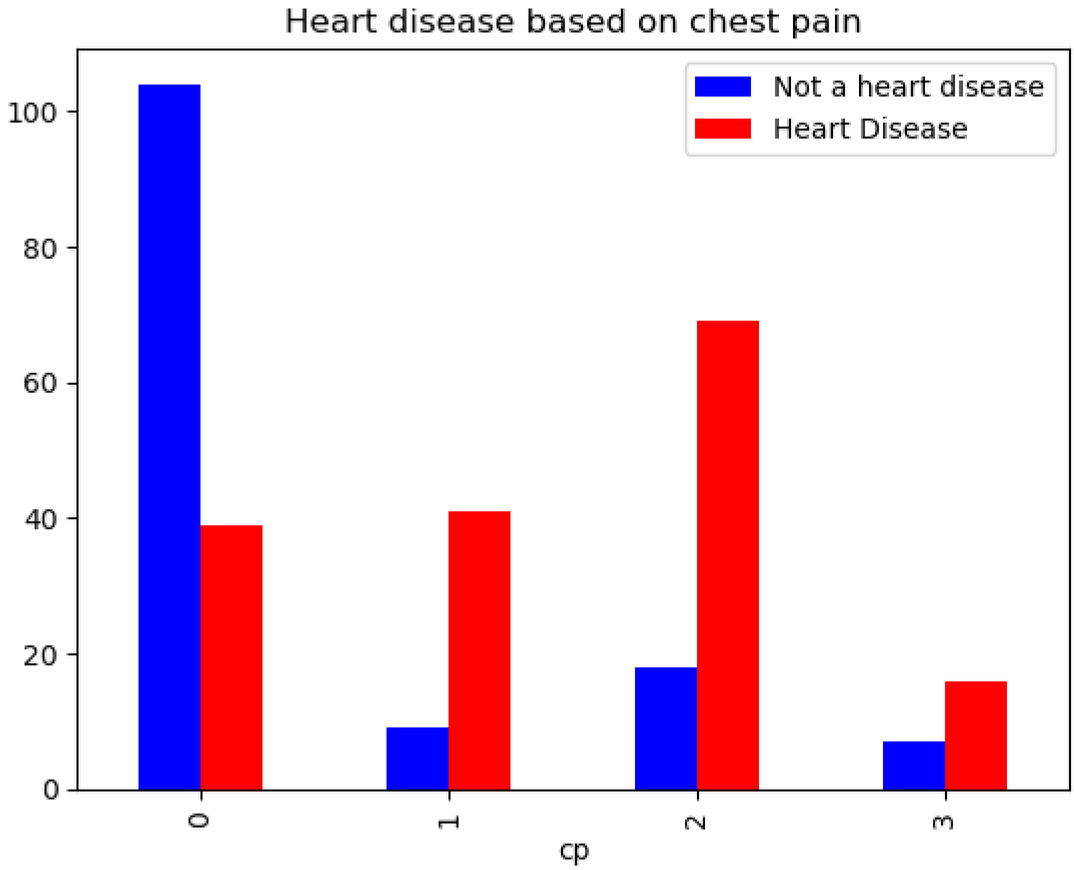


In [10]:
```
#Depending upon the chest pain checking whether the person can have probabi
pd.crosstab(hd.cp,hd.target)
```

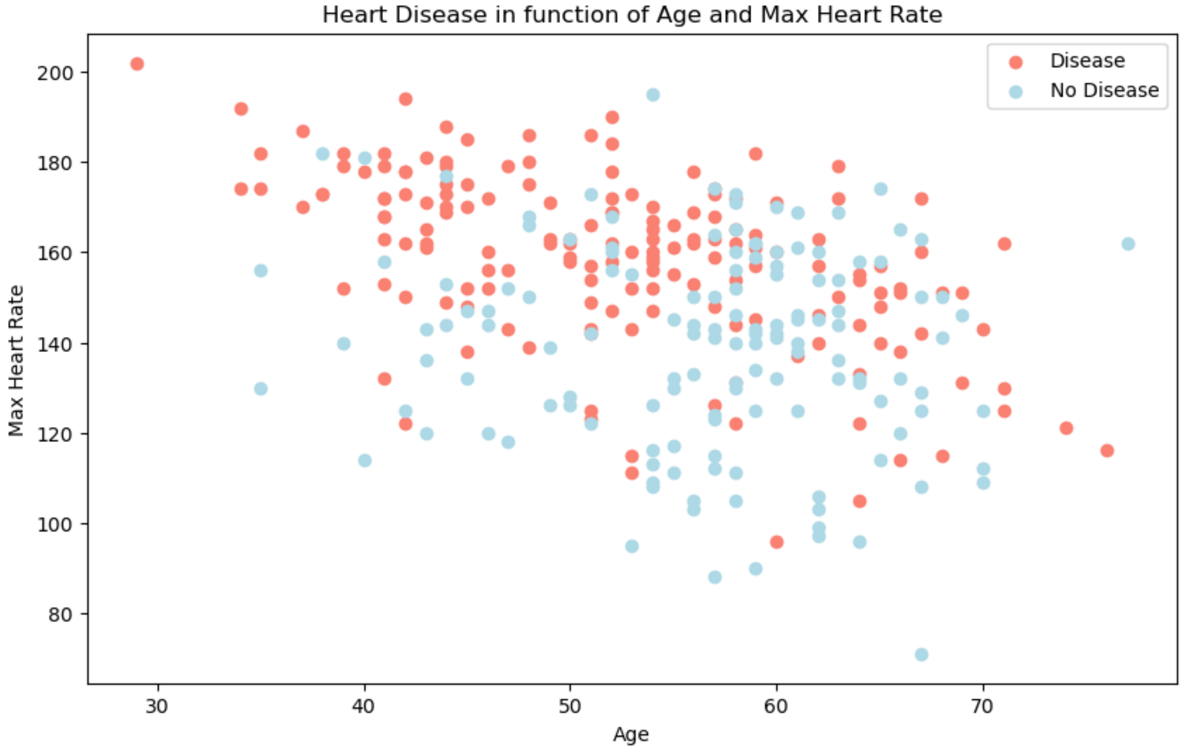
Out[10]:

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

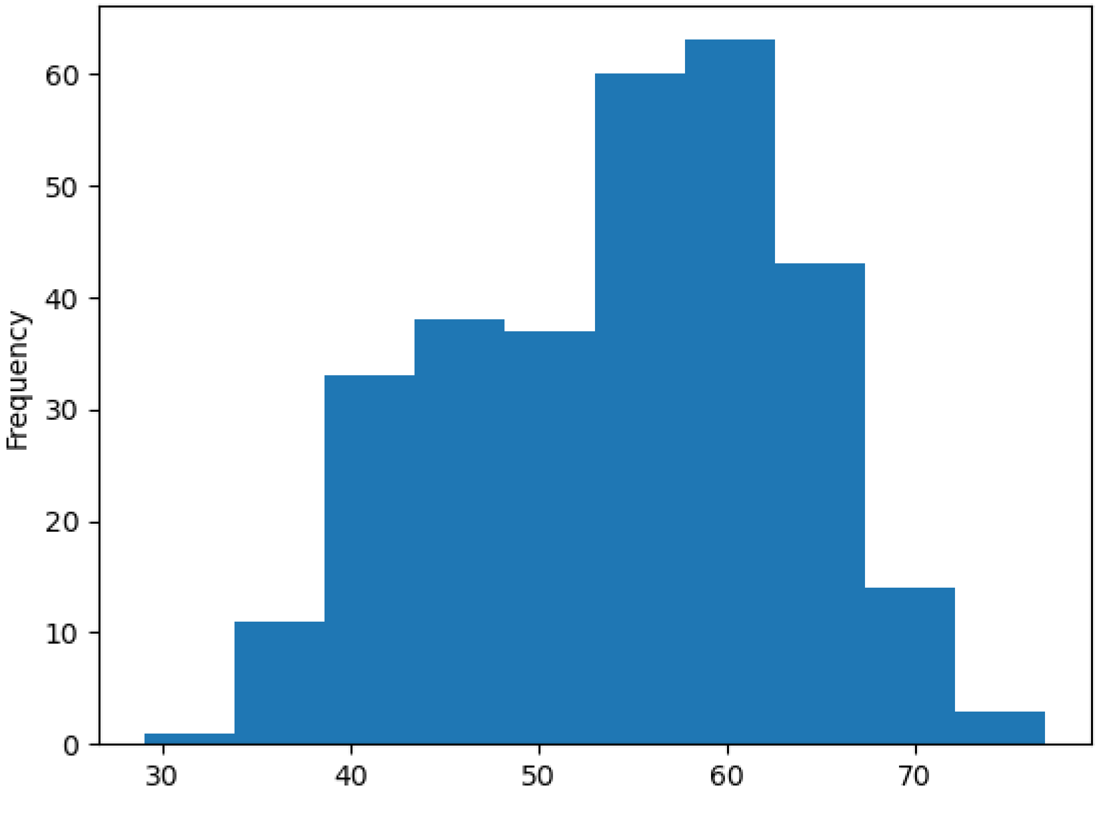
In [11]:
```
#Vizualizing the above matrix
pd.crosstab(hd.cp,hd.target).plot(kind='bar',color=['blue','red'])
plt.title("Heart disease based on chest pain")
plt.legend(['Not a heart disease','Heart Disease']);
```



In [12]:
```
#Checking the heart rate and checking whether the person can have heart dise
plt.figure(figsize=(10, 6))
plt.scatter(hd.age[hd.target==1],
            hd.thalach[hd.target==1],
            c="salmon")
plt.scatter(hd.age[hd.target==0],
            hd.thalach[hd.target==0],
            c="lightblue")
plt.title("Heart Disease in function of Age and Max Heart Rate")
plt.xlabel("Age")
plt.ylabel("Max Heart Rate")
plt.legend(["Disease", "No Disease"]);
```



In [13]:
```
#Checking whether we have data diversity
hd.age.plot(kind='hist');
```



In [14]:
```
hd.head()
```

Out[14]:

	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

In [15]:

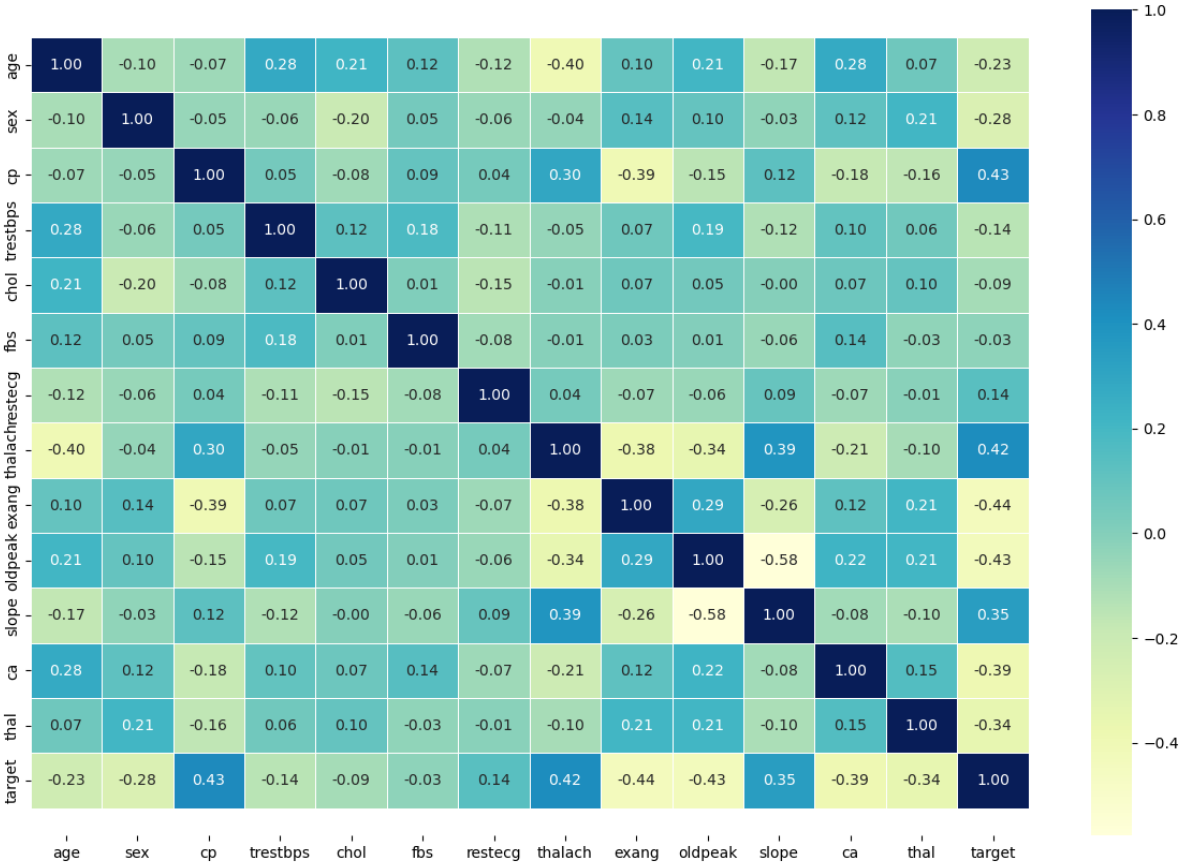
```
#This is done to check the correlation betweeen two dimensions/columns so t
hd.corr()
```

Out[15]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach
age	1.000000	-0.098447	-0.068653	0.279351	0.213678	0.121308	-0.116211	-0.398522
sex	-0.098447	1.000000	-0.049353	-0.056769	-0.197912	0.045032	-0.058196	-0.044020
cp	-0.068653	-0.049353	1.000000	0.047608	-0.076904	0.094444	0.044421	0.295762
trestbps	0.279351	-0.056769	0.047608	1.000000	0.123174	0.177531	-0.114103	-0.046698
chol	0.213678	-0.197912	-0.076904	0.123174	1.000000	0.013294	-0.151040	-0.009940
fbs	0.121308	0.045032	0.094444	0.177531	0.013294	1.000000	-0.084189	-0.008567
restecg	-0.116211	-0.058196	0.044421	-0.114103	-0.151040	-0.084189	1.000000	0.044123
thalach	-0.398522	-0.044020	0.295762	-0.046698	-0.009940	-0.008567	0.044123	1.000000
exang	0.096801	0.141664	-0.394280	0.067616	0.067023	0.025665	-0.070733	-0.378812
oldpeak	0.210013	0.096093	-0.149230	0.193216	0.053952	0.005747	-0.058770	-0.344187
slope	-0.168814	-0.030711	0.119717	-0.121475	-0.004038	-0.059894	0.093045	0.386784
ca	0.276326	0.118261	-0.181053	0.101389	0.070511	0.137979	-0.072042	-0.213177
thal	0.068001	0.210041	-0.161736	0.062210	0.098803	-0.032019	-0.011981	-0.096439
target	-0.225439	-0.280937	0.433798	-0.144931	-0.085239	-0.028046	0.137230	0.421741

In [16]:

```
#Vizualizing the correlation matrix to have better view
corr_matrix=hd.corr()
fig,ax=plt.subplots(figsize=(15,10))
ax = sns.heatmap(corr_matrix,
                 annot=True,
                 linewidths=0.5,
                 fmt=".2f",
                 cmap="YlGnBu");
bottom, top = ax.get_ylim()
ax.set_ylim(bottom + 0.5, top - 0.5);
```



Modeling

In [1]:
```
#Here we are dividing the data into two variables X includes the values whic
X=hd.drop('target',axis=1)
Y=hd.target
np.random.seed(42)
X_train,X_test,Y_train,Y_test=train_test_split(X,Y,test_size=0.2)
```

```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
Cell In[1], line 2
      1 #Here we are dividing the data into two variables X includes the va
lues which are used to predict the heart disease and Y includes whether the
person is having heart disease or not
----> 2 X=hd.drop('target',axis=1)
      3 Y=hd.target
      4 np.random.seed(42)

NameError: name 'hd' is not defined
```

In [18]:
```
#Checking the count of training dataset
len(X_train)
```

Out[18]: 242

In [19]:
```
#Checking the count of testing dataset
len(Y_test)
```

Out[19]: 61

In [20]:
```
#Checking the models that we think are suitable for the data
models={"Logistic":LogisticRegression(),
        "Neighbours":KNeighborsClassifier(),
```

```
        "RandomForest":RandomForestClassifier()}
def fit_and_score(models,X_train,X_test,Y_train,Y_test):
    model_scores={}
    for names,model in models.items():
        model.fit(X_train,Y_train)
        model_scores[names]=model.score(X_test,Y_test)
    return model_scores
```

In [21]:

```
#Here we are fitting the data fitting includes training the data using the t
#The trained model based on the previous training dataset predict the Y_test
#score=correctly predicted/total number of testing data(61)
scores=fit_and_score(models=models,
                     X_train=X_train,
                     X_test=X_test,
                     Y_train=Y_train,
                     Y_test=Y_test)
```

```
/home/vedant/anaconda3/lib/python3.11/site-packages/sklearn/linear_model/_l
ogistic.py:460: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regr
ession
  n_iter_i = _check_optimize_result(
```

In [22]:

```
#Scores of all the models
scores
```

Out[22]:

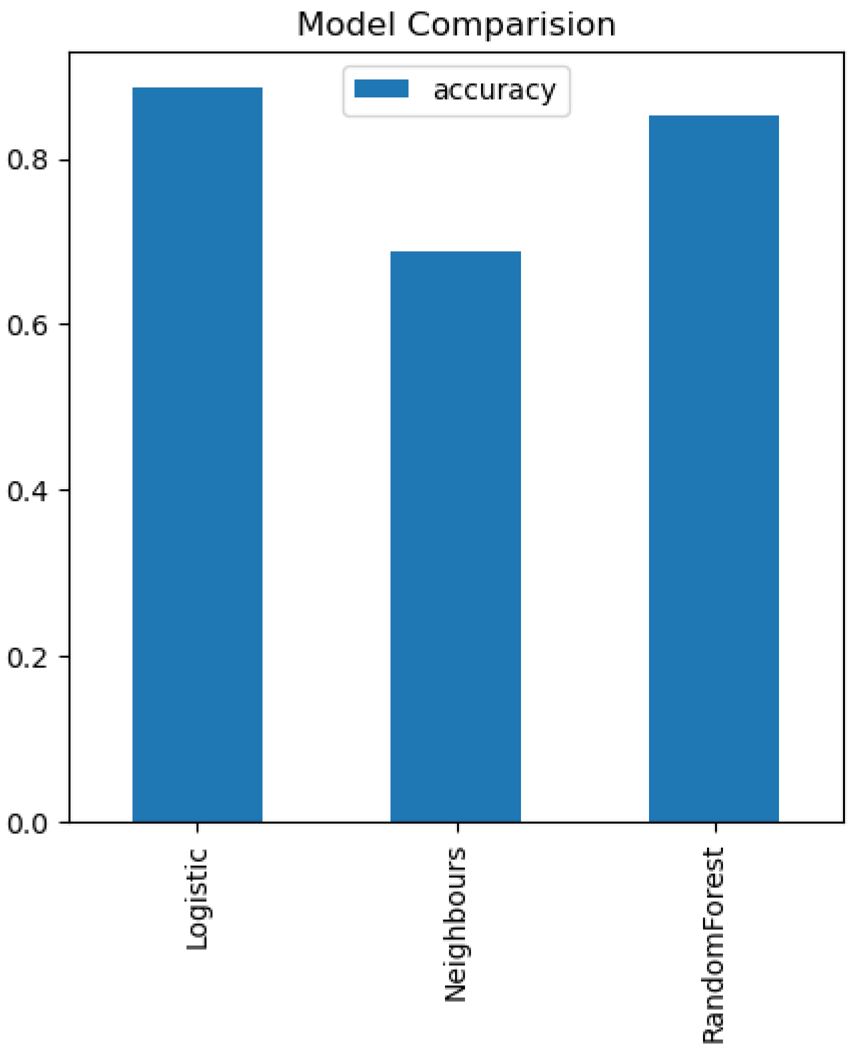
```
{'Logistic': 0.8852459016393442,
 'Neighbours': 0.6885245901639344,
 'RandomForest': 0.8524590163934426}
```

In [23]:

```
#We are having a dataframe for the above scores
result=pd.DataFrame(scores,index=["accuracy"])
```

In [24]:

```
#Vizualizing the dataframe
result.T.plot(kind='bar',figsize=(5,5))
plt.title("Model Comparision");
```



Conclusion:We should move on with the logisticregression model and RandomForest model as it is having more accuracy

Tuning Hyperparameters

In [25]:

```
# Creating a hyperparameter grid for LogisticRegression
log_reg_grid = {"C": np.logspace(-4, 4, 20),
                "solver": ["liblinear"]}

# Creating a hyperparameter grid for RandomForestClassifier
rf_grid = {"n_estimators": np.arange(10, 1000, 50),
           "max_depth": [None, 3, 5, 10],
           "min_samples_split": np.arange(2, 20, 2),
           "min_samples_leaf": np.arange(1, 20, 2)}
```

In [26]:

```
gs_log_reg_grid=GridSearchCV(LogisticRegression(),param_grid=log_reg_grid,cv
gs_log_reg_grid.fit(X_train,Y_train)
```

```
Fitting 5 folds for each of 20 candidates, totalling 100 fits
```

Out[26]:

```
▸ GridSearchCV
▸ estimator: LogisticRegression
  ▸ LogisticRegression
```

In [27]:
```
gs_log_reg_grid.best_params_
```
Out[27]:
```
{'C': 0.23357214690901212, 'solver': 'liblinear'}
```

In [28]:
```
G_log=LogisticRegression(C=0.23357214690901212,solver='liblinear')
```

In [29]:
```
G_log.fit(X_train,Y_train)
G_log.score(X_test,Y_test)
```
Out[29]:
```
0.8852459016393442
```

In [30]:
```
np.random.seed(42)
rs_rf_grid=RandomizedSearchCV(RandomForestClassifier(),param_distributions=r
rs_rf_grid.fit(X_train,Y_train)
```
```
Fitting 5 folds for each of 10 candidates, totalling 50 fits
```
Out[30]:

▸ **RandomizedSearchCV**

▸ **estimator: RandomForestClassifier**

▸ RandomForestClassifier

In [31]:
```
rs_rf_grid.best_params_
```
Out[31]:
```
{'n_estimators': 310,
 'min_samples_split': 2,
 'min_samples_leaf': 19,
 'max_depth': 5}
```

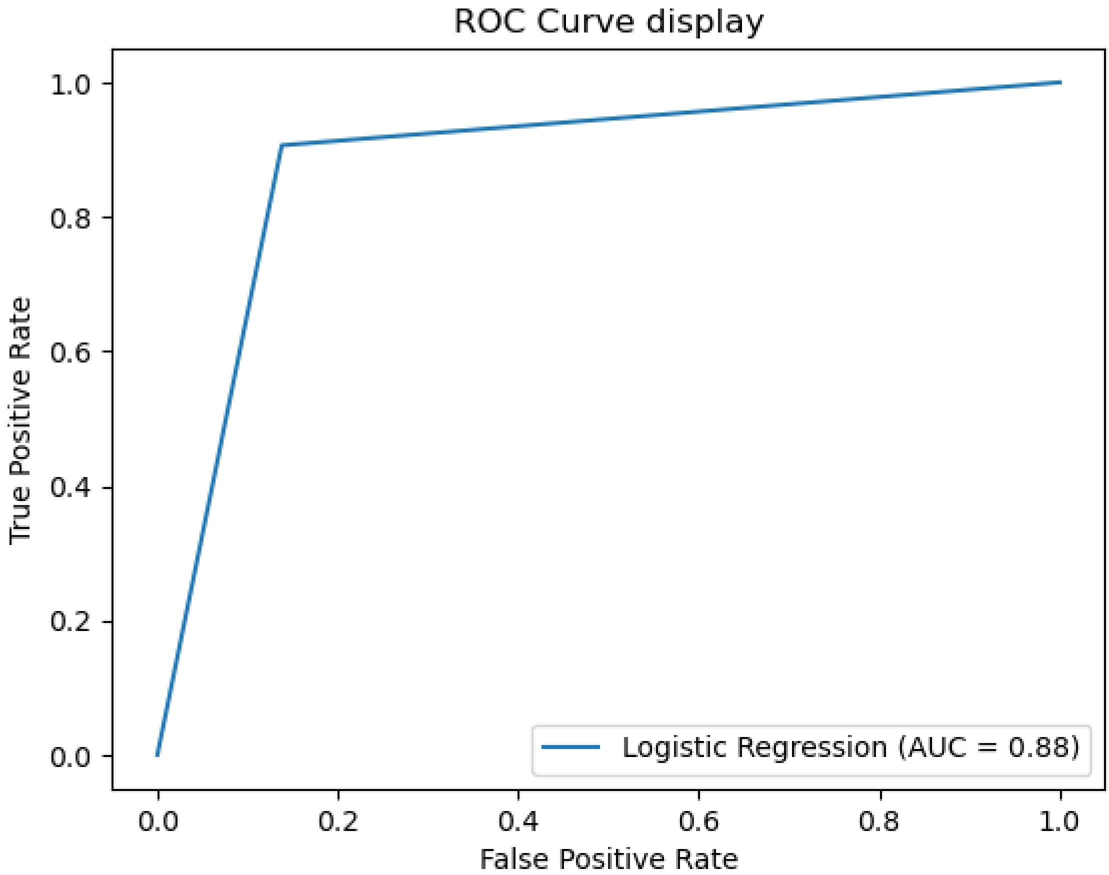
In [32]:
```
R_ran=RandomForestClassifier(n_estimators=310,min_samples_split=2,min_sample
R_ran.fit(X_train,Y_train)
R_ran.score(X_test,Y_test)
```
Out[32]:
```
0.8688524590163934
```

Evaluating the model

In [33]:
```
Y_preds=G_log.predict(X_test)
```

In [34]:
```
Y_preds
```
Out[34]:
```
array([0, 1, 1, 0, 1, 1, 1, 0, 0, 1, 1, 0, 1, 0, 1, 1, 1, 0, 0, 0, 1, 0,
       0, 1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0])
```

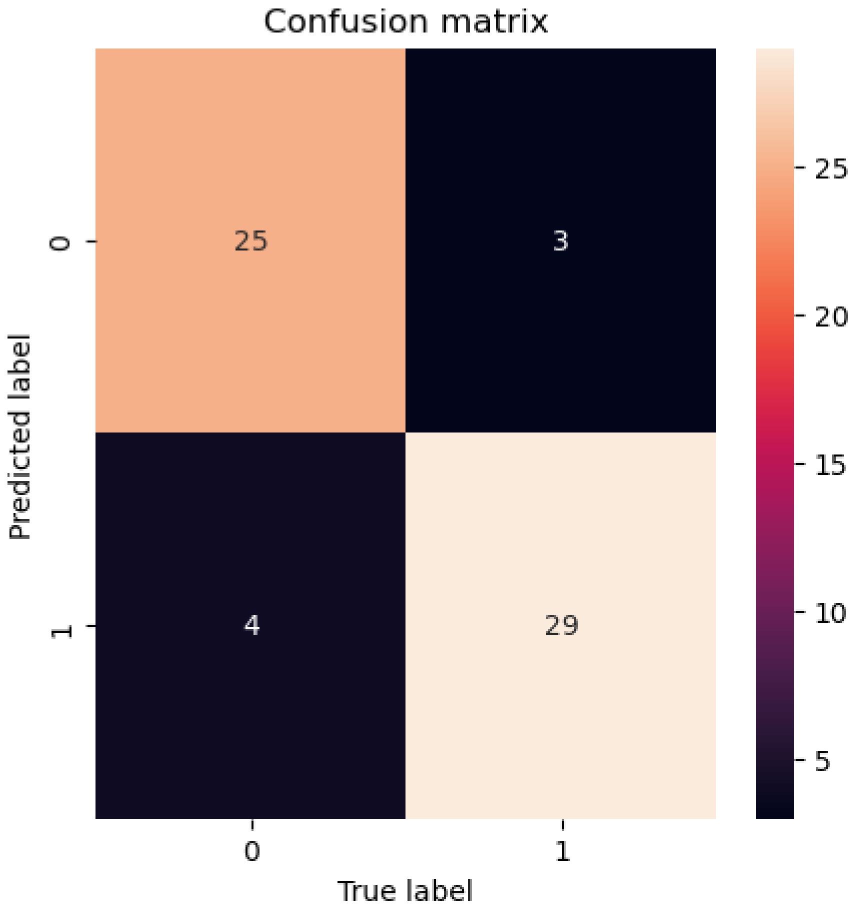
In [35]:
```
fpr, tpr, thresholds = metrics.roc_curve(Y_test,Y_preds)
roc_auc = metrics.auc(fpr, tpr)
display = metrics.RocCurveDisplay(fpr=fpr, tpr=tpr, roc_auc=roc_auc,estimat
display.plot()
plt.title("ROC Curve display")
plt.show()
```



In [36]:
```
cm=confusion_matrix(Y_preds,Y_test)
```

In [37]:
```
plt.subplots(figsize=(5,5))
sns.heatmap(cm,annot=True)
plt.xlabel("True label")
plt.ylabel("Predicted label")
plt.title("Confusion matrix")
```

Out[37]:
```
Text(0.5, 1.0, 'Confusion matrix')
```



In [38]:
```
print(classification_report(Y_test,Y_preds))
```

```
              precision    recall  f1-score   support

           0       0.89      0.86      0.88        29
           1       0.88      0.91      0.89        32

    accuracy                           0.89        61
   macro avg       0.89      0.88      0.88        61
weighted avg       0.89      0.89      0.89        61
```

In [39]:
```
cv_acc=cross_val_score(G_log,X,Y,cv=5,scoring="accuracy")
```

In [40]:
```
cv_acc=np.mean(cv_acc)
```

In [41]:
```
cv_acc
```

Out[41]:
```
0.8479781420765027
```

In [42]:
```
cv_pre=cross_val_score(G_log,X,Y,cv=5,scoring="precision")
```

In [43]:
```
cv_pre=np.mean(cv_pre)
```

In [44]:
```
cv_pre
```

Out[44]:
```
0.8215873015873015
```

In [45]:
```
cv_re=cross_val_score(G_log,X,Y,cv=5,scoring="recall")
```

In [46]:
```
cv_re=np.mean(cv_re)
```

In [47]:
```
cv_re
```

Out[47]:
```
0.9272727272727274
```

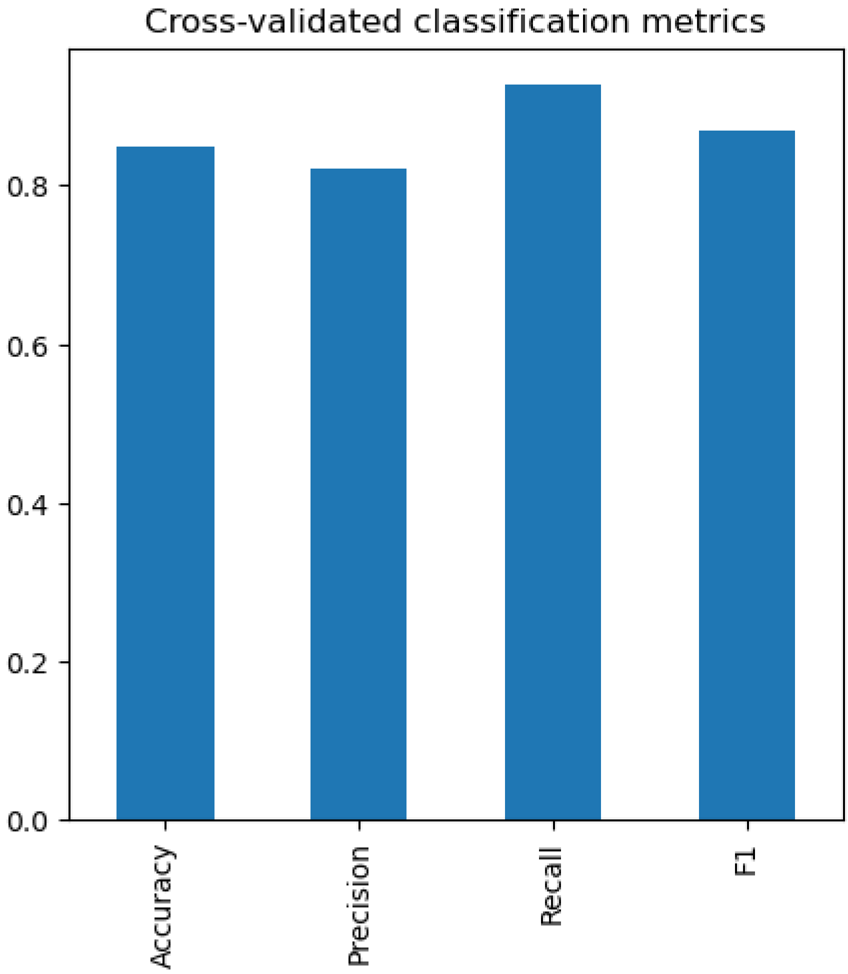
In [48]:
```
cv_f1=cross_val_score(G_log,X,Y,cv=5,scoring="f1")
```

In [49]:
```
cv_f1=np.mean(cv_f1)
```

In [50]:
```
cv_f1
```

Out[50]:
```
0.8705403543192143
```

In [51]:
```
cv_metrics = pd.DataFrame({"Accuracy": cv_acc,"Precision": cv_pre,"Recall":
cv_metrics.T.plot.bar(title="Cross-validated classification metrics",legend=
```



Feature Importance

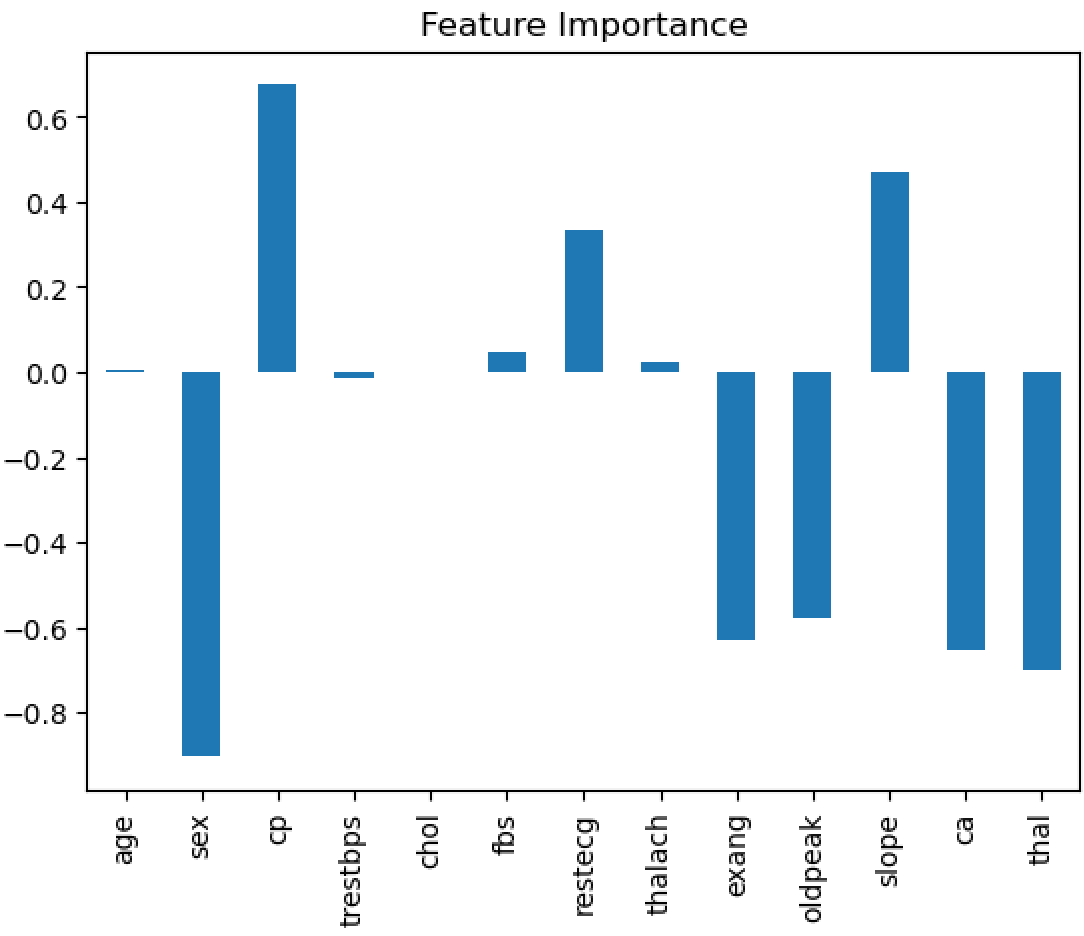
In [52]:
```
fmatrix=G_log.coef_
```

In [53]:
```
feature_dict = dict(zip(hd.columns, fmatrix[0]))
feature_dict
```

Out[53]:
```
{'age': 0.003699223396114675,
 'sex': -0.9042409779785583,
 'cp': 0.6747282348693419,
 'trestbps': -0.011613398123390507,
 'chol': -0.0017036431858934173,
 'fbs': 0.0478768694057663,
 'restecg': 0.33490207838133623,
 'thalach': 0.024729380915946855,
 'exang': -0.6312041363430085,
 'oldpeak': -0.5759099636629296,
 'slope': 0.47095166489539353,
 'ca': -0.6516534354909507,
 'thal': -0.6998421698316164}
```

In [54]:
```
features_imp=pd.DataFrame(feature_dict,index=[0])
```

In [55]:
```
features_imp.T.plot.bar(legend=False)
plt.title("Feature Importance");
```



Saving a model

In [56]:
```
pickle.dump(G_log,open("heart-disease-model.pkl","wb"))
```

In [57]:
```
model=pickle.load(open("heart-disease-model.pkl","rb"))
```

In [58]:
```
model.score(X_test,Y_test)
```

Out[58]:
```
0.8852459016393442
```