Random Forest Algorithm Intuition:

    Random Forest is an ensemble learning method that builds
    multiple decision trees during training and merges their
    predictions to improve accuracy and prevent overfitting.
    Each decision tree is built on a random subset of features
    and data samples , and the final prediction is based on
    the combined predictions of all trees.

Advantages of Random Forest:

    High Accuracy: Random Forests generally provide high
    accuracy due to the combination of multiple decision
    trees.
    Handles Missing Values: Random Forests can handle missing
    data without imputation.
    Reduced Overfitting: The randomness in feature selection
    and data sampling reduces overfitting compared to
    individual decision trees.
    Feature Importance: It can provide insights into feature
    importance, aiding in feature selection.

Disadvantages of Random Forest:

    Complexity: Random Forests can be computationally
    intensive and may require tuning of hyperparameters.
    Less Interpretability: While they offer feature
    importance, interpreting individual tree decisions can be
    challenging.
    Training Time: Training a Random Forest model can take
    longer compared to simpler algorithms like Decision Trees.

Difference between Random Forests and Decision Trees:

    Random Forests are an ensemble of decision trees, while
    Decision Trees are single trees.
    Random Forests introduce randomness in feature selection
    and data sampling to reduce overfitting, whereas Decision
    Trees can easily overfit on training data.

Relationship between Random Forests and Nearest Neighbors:

    Random Forests and k-Nearest Neighbors (KNN) are different
    algorithms.
    Random Forests use decision trees for classification,
    while KNN classifies based on the majority class among its
    k-nearest neighbors.

In [ ]:
```
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
```

```
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay,accu
from sklearn.preprocessing import StandardScaler
```

import and analyse data

In [ ]:
```
dataset = pd.read_csv('heart-disease.csv')
```

In [ ]:
```
dataset.head()
```

Out[ ]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	tha
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	

In [ ]:
```
dataset.isnull().sum()
```

Out[ ]:
```
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 [ ]:
```
dataset.describe()
```

Out[ ]:

	age	sex	cp	trestbps	chol	fbs	r
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.0
mean	54.366337	0.683168	0.966997	131.623762	246.264026	0.148515	0.5
std	9.082101	0.466011	1.032052	17.538143	51.830751	0.356198	0.5
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.0
25%	47.500000	0.000000	0.000000	120.000000	211.000000	0.000000	0.0
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.0
75%	61.000000	1.000000	2.000000	140.000000	274.500000	0.000000	1.0
max	77.000000	1.000000	3.000000	200.000000	564.000000	1.000000	2.0

since dataset is clean and preprocessed correctly already we'll move to next steps

feature engineering

In [ ]:
```
numerical_features = ['age', 'trestbps', 'chol', 'thalach', 'oldpeak']
scaler = StandardScaler()
# scale numerical values to comparable ranges
dataset[numerical_features] = scaler.fit_transform(dataset[numerical_feat
```

In [ ]:
```
dataset.head()
```

Out[ ]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak
0	0.952197	1	3	0.763956	-0.256334	1	0	0.015443	0	1.087338
1	-1.915313	1	2	-0.092738	0.072199	0	1	1.633471	0	2.122573
2	-1.474158	0	1	-0.092738	-0.816773	0	0	0.977514	0	0.310912
3	0.180175	1	1	-0.663867	-0.198357	0	1	1.239897	0	-0.206705
4	0.290464	0	0	-0.663867	2.082050	0	1	0.583939	1	-0.379244

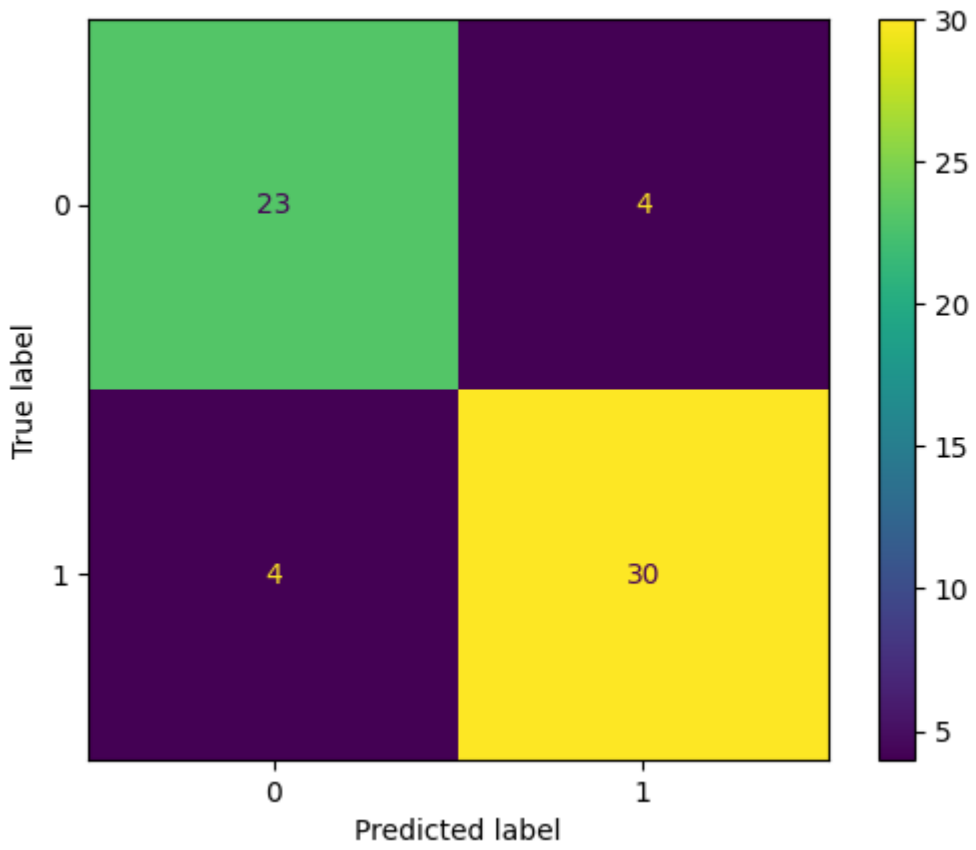
In [ ]:
```
X = dataset.drop(['target'], axis=1)
y = dataset['target']
```

In [ ]:
```
Xtrain, Xtest, ytrain, ytest = train_test_split(X, y, test_size=0.2, rand
```

train using default params

In [ ]:
```
def_model =RandomForestClassifier()
```

In [ ]:
```
def_model.fit(Xtrain,ytrain)
y_pred1 = def_model.predict(Xtest)
cm1 = confusion_matrix(ytest,y_pred1)
disp1 = ConfusionMatrixDisplay.from_predictions(ytest,y_pred1)
```



In [ ]:
```
print(classification_report(ytest, y_pred1))
```

```
              precision    recall  f1-score   support

           0       0.85      0.85      0.85        27
           1       0.88      0.88      0.88        34

    accuracy                           0.87        61
   macro avg       0.87      0.87      0.87        61
weighted avg       0.87      0.87      0.87        61
```

In [ ]:
```
accuracy_score(ytest, y_pred1)
```

Out[ ]: 0.8688524590163934

Precision

```
For class 0 (no heart disease), the precision is 0.78,
meaning that when the model predicts no heart disease, it
is correct 78% of the time.
For class 1 (presence of heart disease), the precision is
0.82, indicating that when the model predicts heart
disease, it is correct 82% of the time.
```

Recall

```
The recall for class 0 is also 0.78, which means that of
all the actual no heart disease cases, the model correctly
identifies 78%.
The recall for class 1 is 0.82, so the model correctly
```

```
identifies 82% of all actual heart disease cases.
```

F1-Score

```
The F1-score for both classes is quite balanced, with 0.78
for class 0 and 0.82 for class 1. This score gives a
combined idea of how precise and robust the model's
predictions are.
```

Accuracy

```
The overall accuracy of the model is 0.80, meaning the
model correctly predicts the presence or absence of heart
disease 80% of the time across all cases.
```

Analysis

```
this model shows a good balance between precision and
recall, indicating it is equally skilled at identifying
positive cases among the actual positives and minimizing
false positives.
The balanced macro and weighted averages indicate that the
model performs consistently across both classes
```

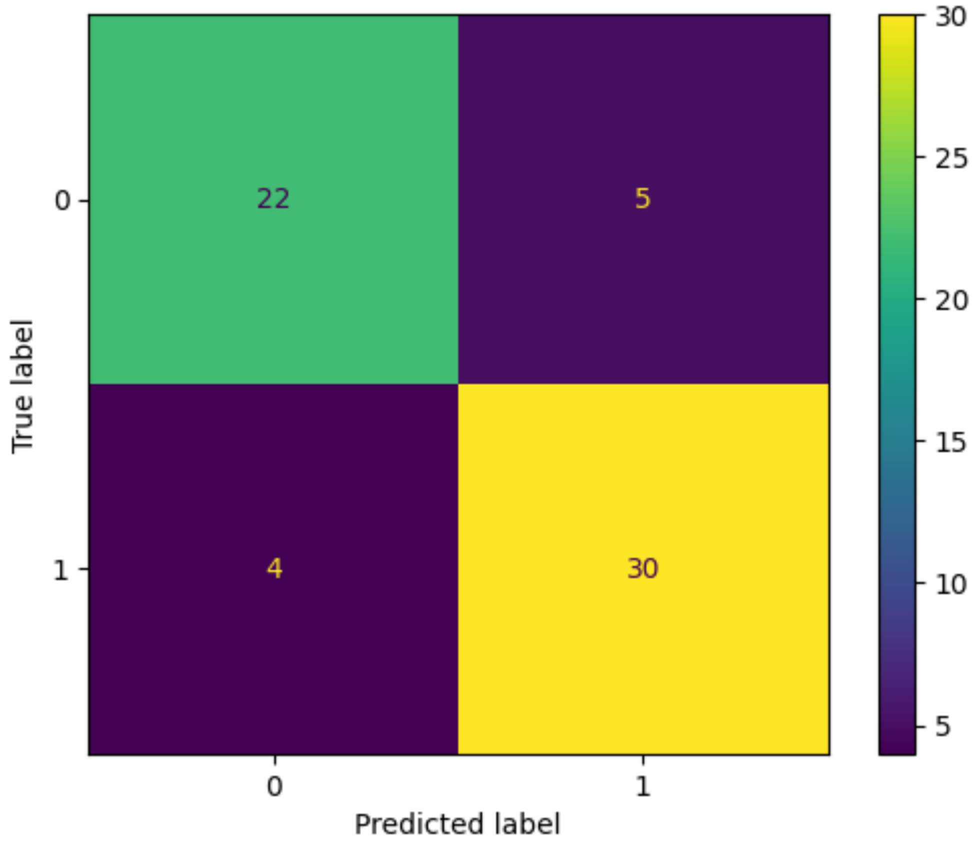
now using different params

In [ ]:

```
model = RandomForestClassifier(n_estimators=500,n_jobs=-1, random_state=0
model.fit(Xtrain, ytrain)
y_pred2 = model.predict(Xtest)
cm = confusion_matrix(ytest, y_pred2)
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=np.uniq
```

In [ ]:

```
disp.plot()
plt.show()
```



In [ ]:
```
print(classification_report(ytest, y_pred2))
```

```
              precision    recall  f1-score   support

           0       0.85      0.81      0.83        27
           1       0.86      0.88      0.87        34

    accuracy                           0.85        61
   macro avg       0.85      0.85      0.85        61
weighted avg       0.85      0.85      0.85        61
```

Precision

```
Class 0 (No Heart Disease): Precision has improved to
0.85, meaning the model is more accurate in predicting
negative cases
Class 1 (Presence of Heart Disease): Precision is slightly
higher at 0.86, indicating a slight improvement in
correctly predicting positive cases.
```

Recall

```
Class 0: Recall has improved to 0.81, suggesting that the
model is now better at identifying all actual negative
cases as negative.
Class 1: Recall has increased to 0.88, meaning the model
has become more effective at catching true positive cases.
```

F1-Score

    The F1-scores have increased to 0.83 for class 0 and 0.87
    for class 1, reflecting a balanced improvement in
    precision and recall for both classes

Accuracy

    The overall accuracy has risen to 0.85. This improvement
    suggests that the adjustments to the number of trees and
    maximum depth have made the model better at classifying
    both conditions correctly across all predictions.

In [ ]:

```

```