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```
[10]: import numpy as np
import pandas as pd
data=pd.read_csv(r'/content/hypothyroid.csv')
data.head()
```

```
[10]:  age sex on thyroxine query on thyroxine on antithyroid medication sick \
0  41  F          f          f          f          f          f
1  23  F          f          f          f          f          f
2  46  M          f          f          f          f          f
3  70  F          t          f          f          f          f
4  70  F          f          f          f          f          f

    pregnant thyroid surgery l131 treatment query hypothyroid ... TT4 measured \
0          f          f          f          f          f ...          t
1          f          f          f          f          f ...          t
2          f          f          f          f          f ...          t
3          f          f          f          f          f ...          t
4          f          f          f          f          f ...          t

    TT4 T4U measured    T4U FTI measured    FTI TBG measured TBG referral source \
0  125          t    1.14          t    109          f    ?          SVHC
1  102          f     ?          f     ?          f    ?          other
2  109          t    0.91          t    120          f    ?          other
3  175          f     ?          f     ?          f    ?          other
4   61          t    0.87          t    70          f    ?          SVI

    binaryClass
0             P
1             P
2             P
3             P
4             P

[5 rows x 30 columns]
```

```
[ ]: data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
```

RangeIndex: 3772 entries, 0 to 3771

Data columns (total 30 columns):

| # | Column | Non-Null Count | Dtype |
|----|---------------------------|----------------|--------|
| 0 | age | 3772 non-null | object |
| 1 | sex | 3772 non-null | object |
| 2 | on thyroxine | 3772 non-null | object |
| 3 | query on thyroxine | 3772 non-null | object |
| 4 | on antithyroid medication | 3772 non-null | object |
| 5 | sick | 3772 non-null | object |
| 6 | pregnant | 3772 non-null | object |
| 7 | thyroid surgery | 3772 non-null | object |
| 8 | I131 treatment | 3772 non-null | object |
| 9 | query hypothyroid | 3772 non-null | object |
| 10 | query hyperthyroid | 3772 non-null | object |
| 11 | lithium | 3772 non-null | object |
| 12 | goitre | 3772 non-null | object |
| 13 | tumor | 3772 non-null | object |
| 14 | hypopituitary | 3772 non-null | object |
| 15 | psych | 3772 non-null | object |
| 16 | TSH measured | 3772 non-null | object |
| 17 | TSH | 3772 non-null | object |
| 18 | T3 measured | 3772 non-null | object |
| 19 | T3 | 3772 non-null | object |
| 20 | TT4 measured | 3772 non-null | object |
| 21 | TT4 | 3772 non-null | object |
| 22 | T4U measured | 3772 non-null | object |
| 23 | T4U | 3772 non-null | object |
| 24 | FTI measured | 3772 non-null | object |
| 25 | FTI | 3772 non-null | object |
| 26 | TBG measured | 3772 non-null | object |
| 27 | TBG | 3772 non-null | object |
| 28 | referral source | 3772 non-null | object |
| 29 | binaryClass | 3772 non-null | object |

dtypes: object(30)

memory usage: 884.2+ KB

```
[ ]: print(data.isnull().sum())
```

| | |
|---------------------------|---|
| age | 0 |
| sex | 0 |
| on thyroxine | 0 |
| query on thyroxine | 0 |
| on antithyroid medication | 0 |
| sick | 0 |
| pregnant | 0 |
| thyroid surgery | 0 |
| I131 treatment | 0 |

```

query hypothyroid          0
query hyperthyroid         0
lithium                    0
goitre                     0
tumor                      0
hypopituitary              0
psych                      0
TSH measured               0
TSH                        0
T3 measured                0
T3                         0
TT4 measured               0
TT4                       0
T4U measured               0
T4U                       0
FTI measured               0
FTI                       0
TBG measured               0
TBG                       0
referral source            0
binaryClass                0
dtype: int64

```

```

[6]: from sklearn.preprocessing import LabelEncoder

# Create a LabelEncoder instance
enc = LabelEncoder()

# Encode only categorical columns
categorical_cols = data.select_dtypes(include=['object']).columns
for col in categorical_cols:
    data[col] = enc.fit_transform(data[col])

data.info() # Check the data types again

```

```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3772 entries, 0 to 3771
Data columns (total 30 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   age                                   3772 non-null   int64
1   sex                                   3772 non-null   int64
2   on thyroxine                         3772 non-null   int64
3   query on thyroxine                   3772 non-null   int64
4   on antithyroid medication            3772 non-null   int64
5   sick                                 3772 non-null   int64
6   pregnant                             3772 non-null   int64
7   thyroid surgery                      3772 non-null   int64

```

```

8   I131 treatment      3772 non-null   int64
9   query hypothyroid   3772 non-null   int64
10  query hyperthyroid   3772 non-null   int64
11  lithium              3772 non-null   int64
12  goitre               3772 non-null   int64
13  tumor               3772 non-null   int64
14  hypopituitary       3772 non-null   int64
15  psych               3772 non-null   int64
16  TSH measured        3772 non-null   int64
17  TSH                 3772 non-null   int64
18  T3 measured         3772 non-null   int64
19  T3                  3772 non-null   int64
20  TT4 measured        3772 non-null   int64
21  TT4                 3772 non-null   int64
22  T4U measured        3772 non-null   int64
23  T4U                 3772 non-null   int64
24  FTI measured        3772 non-null   int64
25  FTI                 3772 non-null   int64
26  TBG measured        3772 non-null   int64
27  TBG                 3772 non-null   int64
28  referral source     3772 non-null   int64
29  binaryClass         3772 non-null   int64

```

dtypes: int64(30)

memory usage: 884.2 KB

```
[ ]: data.head()
```

```

[ ]:   age  sex  on thyroxine  query on thyroxine  on antithyroid medication  \
0    34    1             0             0             0
1    15    1             0             0             0
2    40    2             0             0             0
3    67    1             1             0             0
4    67    1             0             0             0

      sick  pregnant  thyroid surgery  I131 treatment  query hypothyroid  ...  \
0        0         0             0             0             0  ...
1        0         0             0             0             0  ...
2        0         0             0             0             0  ...
3        0         0             0             0             0  ...
4        0         0             0             0             0  ...

      TT4 measured  TT4  T4U measured  T4U  FTI measured  FTI  TBG measured  TBG  \
0              1   28             1   72             1   10             0   0
1              1    3             0  146             0  234             0   0
2              1   10             1   48             1   22             0   0
3              1   83             0  146             0  234             0   0
4              1  201             1   44             1  199             0   0

```

| | referral source | binaryClass |
|---|-----------------|-------------|
| 0 | 1 | 1 |
| 1 | 4 | 1 |
| 2 | 4 | 1 |
| 3 | 4 | 1 |
| 4 | 3 | 1 |

[5 rows x 30 columns]

```
[ ]: data=data.drop_duplicates()
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
```

```
Int64Index: 3711 entries, 0 to 3771
```

```
Data columns (total 30 columns):
```

| # | Column | Non-Null Count | Dtype |
|----|---------------------------|----------------|-------|
| 0 | age | 3711 non-null | int64 |
| 1 | sex | 3711 non-null | int64 |
| 2 | on thyroxine | 3711 non-null | int64 |
| 3 | query on thyroxine | 3711 non-null | int64 |
| 4 | on antithyroid medication | 3711 non-null | int64 |
| 5 | sick | 3711 non-null | int64 |
| 6 | pregnant | 3711 non-null | int64 |
| 7 | thyroid surgery | 3711 non-null | int64 |
| 8 | I131 treatment | 3711 non-null | int64 |
| 9 | query hypothyroid | 3711 non-null | int64 |
| 10 | query hyperthyroid | 3711 non-null | int64 |
| 11 | lithium | 3711 non-null | int64 |
| 12 | goitre | 3711 non-null | int64 |
| 13 | tumor | 3711 non-null | int64 |
| 14 | hypopituitary | 3711 non-null | int64 |
| 15 | psych | 3711 non-null | int64 |
| 16 | TSH measured | 3711 non-null | int64 |
| 17 | TSH | 3711 non-null | int64 |
| 18 | T3 measured | 3711 non-null | int64 |
| 19 | T3 | 3711 non-null | int64 |
| 20 | TT4 measured | 3711 non-null | int64 |
| 21 | TT4 | 3711 non-null | int64 |
| 22 | T4U measured | 3711 non-null | int64 |
| 23 | T4U | 3711 non-null | int64 |
| 24 | FTI measured | 3711 non-null | int64 |
| 25 | FTI | 3711 non-null | int64 |
| 26 | TBG measured | 3711 non-null | int64 |
| 27 | TBG | 3711 non-null | int64 |
| 28 | referral source | 3711 non-null | int64 |

```

29 binaryClass          3711 non-null   int64
dtypes: int64(30)
memory usage: 898.8 KB

```

```
[ ]: data.describe()
```

```

[ ]:
      count  age      sex  on thyroxine  query on thyroxine  \
count  3711.000000  3711.000000  3711.000000  3711.000000
mean    46.493937    1.266505    0.125034    0.013473
std     20.863642    0.525220    0.330802    0.115306
min      0.000000    0.000000    0.000000    0.000000
25%     28.000000    1.000000    0.000000    0.000000
50%     50.000000    1.000000    0.000000    0.000000
75%     63.000000    2.000000    0.000000    0.000000
max     93.000000    2.000000    1.000000    1.000000

      count  on antithyroid medication  sick  pregnant  thyroid surgery  \
count    3711.000000  3711.000000  3711.000000  3711.000000  3711.000000
mean          0.011318    0.039612    0.014282    0.014282
std          0.105795    0.195072    0.118666    0.118666
min           0.000000    0.000000    0.000000    0.000000
25%           0.000000    0.000000    0.000000    0.000000
50%           0.000000    0.000000    0.000000    0.000000
75%           0.000000    0.000000    0.000000    0.000000
max           1.000000    1.000000    1.000000    1.000000

      count  I131 treatment  query hypothyroid  ...  TT4 measured  TT4  \
count    3711.000000    3711.000000  ...  3711.000000  3711.000000
mean         0.015899         0.063056  ...    0.953921  119.133118
std         0.125100         0.243096  ...    0.209685   98.238113
min          0.000000         0.000000  ...    0.000000   0.000000
25%          0.000000         0.000000  ...    1.000000  21.000000
50%          0.000000         0.000000  ...    1.000000  79.000000
75%          0.000000         0.000000  ...    1.000000 226.000000
max          1.000000         1.000000  ...    1.000000 241.000000

      count  T4U measured  T4U  FTI measured  FTI  TBG measured  \
count    3711.000000  3711.000000  3711.000000  3711.000000  3711.0
mean         0.911884   64.854756    0.912423   108.715980    0.0
std         0.283502   31.330172    0.282718    97.032357    0.0
min          0.000000   0.000000    0.000000   0.000000    0.0
25%          1.000000   46.000000    1.000000   17.000000    0.0
50%          1.000000   57.000000    1.000000   56.000000    0.0
75%          1.000000   71.000000    1.000000  221.000000    0.0
max          1.000000  146.000000    1.000000  234.000000    0.0

```

```
TBG referral source binaryClass
```

| | | | |
|-------|--------|-------------|-------------|
| count | 3711.0 | 3711.000000 | 3711.000000 |
| mean | 0.0 | 3.267583 | 0.921584 |
| std | 0.0 | 1.097079 | 0.268861 |
| min | 0.0 | 0.000000 | 0.000000 |
| 25% | 0.0 | 3.000000 | 1.000000 |
| 50% | 0.0 | 4.000000 | 1.000000 |
| 75% | 0.0 | 4.000000 | 1.000000 |
| max | 0.0 | 4.000000 | 1.000000 |

[8 rows x 30 columns]

```
[ ]: # Convert relevant columns to numeric, forcing errors to NaN
data['age'] = pd.to_numeric(data['age'], errors='coerce')
data['TT4'] = pd.to_numeric(data['TT4'], errors='coerce')
data['T4U'] = pd.to_numeric(data['T4U'], errors='coerce')
data['FTI'] = pd.to_numeric(data['FTI'], errors='coerce')

# Check for missing values after conversion
print(data.isnull().sum())

# Handle missing values if necessary (e.g., drop or fill)
data = data.dropna() # Example: drop rows with missing values

# Normalize the columns
data['age'] = (data['age'] - data['age'].min()) / (data['age'].max() -
↳data['age'].min())
data['TT4'] = (data['TT4'] - data['TT4'].min()) / (data['TT4'].max() -
↳data['TT4'].min())
data['T4U'] = (data['T4U'] - data['T4U'].min()) / (data['T4U'].max() -
↳data['T4U'].min())
data['FTI'] = (data['FTI'] - data['FTI'].min()) / (data['FTI'].max() -
↳data['FTI'].min())
```

| | |
|---------------------------|---|
| age | 0 |
| sex | 0 |
| on thyroxine | 0 |
| query on thyroxine | 0 |
| on antithyroid medication | 0 |
| sick | 0 |
| pregnant | 0 |
| thyroid surgery | 0 |
| I131 treatment | 0 |
| query hypothyroid | 0 |
| query hyperthyroid | 0 |
| lithium | 0 |
| goitre | 0 |
| tumor | 0 |

```

hypopituitary      0
psych              0
TSH measured       0
TSH                0
T3 measured        0
T3                0
TT4 measured       0
TT4               0
T4U measured       0
T4U               0
FTI measured       0
FTI               0
TBG measured       0
TBG               0
referral source    0
binaryClass        0
dtype: int64

```

```
[ ]: data.head()
```

```

[ ]:      age  sex  on thyroxine  query on thyroxine  on antithyroid medication \
0  0.365591    1            0            0            0
1  0.161290    1            0            0            0
2  0.430108    2            0            0            0
3  0.720430    1            1            0            0
4  0.720430    1            0            0            0

```

```

      sick  pregnant  thyroid surgery  I131 treatment  query hypothyroid ... \
0      0          0              0              0          0 ...
1      0          0              0              0          0 ...
2      0          0              0              0          0 ...
3      0          0              0              0          0 ...
4      0          0              0              0          0 ...

```

```

      TT4 measured      TT4  T4U measured      T4U  FTI measured      FTI \
0              1  0.116183          1  0.493151          1  0.042735
1              1  0.012448          0  1.000000          0  1.000000
2              1  0.041494          1  0.328767          1  0.094017
3              1  0.344398          0  1.000000          0  1.000000
4              1  0.834025          1  0.301370          1  0.850427

```

```

      TBG measured  TBG  referral source  binaryClass
0              0    0              1              1
1              0    0              4              1
2              0    0              4              1
3              0    0              4              1
4              0    0              3              1

```


[5 rows x 30 columns]

```
[ ]: y=data['binaryClass']  
x=data.drop(['binaryClass'],axis=1)
```

```
[ ]: from sklearn.model_selection import train_test_split  
xtrain,xtest,ytrain,ytest= train_test_split(x,y,test_size=0.1,stratify=y)  
print(xtrain.shape)  
print(xtest.shape)  
print(ytrain.shape)  
print(ytest.shape)
```

(3339, 29)

(372, 29)

(3339,)

(372,)

```
[ ]: # Ensure the cell that loads the training data is executed  
from sklearn.model_selection import train_test_split  
xtrain, xtest, ytrain, ytest = train_test_split(x, y, test_size=0.1, stratify=y)  
  
# Check for errors in data loading  
if 'xtrain' in globals():  
    # Fit the XGBClassifier model  
    from xgboost import XGBClassifier  
    svm_model = XGBClassifier()  
    svm_model.fit(xtrain, ytrain)  
else:  
    print("Model not found in the notebook. Please ensure a model is trained to  
    ↪view feature importance.")
```

```
[ ]: from sklearn.metrics import accuracy_score, confusion_matrix,  
    ↪classification_report  
  
# Make predictions on the test set  
predictions = svm_model.predict(xtest)  
  
# Calculate accuracy  
percentage = svm_model.score(xtest, ytest)  
  
# Generate confusion matrix  
res = confusion_matrix(ytest, predictions)  
  
# Print validation confusion matrix  
print("Validation Confusion Matrix:")  
print(res)
```

```

# Print classification report
print("Classification Report:")
print(classification_report(ytest, predictions))

# Check the accuracy on the training set
training_accuracy = svm_model.score(xtrain, ytrain) * 100
testing_accuracy = percentage * 100

print('Training Accuracy = {:.2f}%'.format(training_accuracy))
print('Testing Accuracy = {:.2f}%'.format(testing_accuracy))

```

Validation Confusion Matrix:

```
[[ 25   4]
 [   2 347]]
```

Classification Report:

| | precision | recall | f1-score | support |
|--------------|-----------|--------|----------|---------|
| 0 | 0.93 | 0.86 | 0.89 | 29 |
| 1 | 0.99 | 0.99 | 0.99 | 349 |
| accuracy | | | 0.98 | 378 |
| macro avg | 0.96 | 0.93 | 0.94 | 378 |
| weighted avg | 0.98 | 0.98 | 0.98 | 378 |

Training Accuracy = 100.00%

Testing Accuracy = 98.41%

Since the model has performed well on the test set, it doesn't require any hyperparameter tuning.

```

[15]: from sklearn import svm
from sklearn.model_selection import train_test_split
from sklearn.datasets import load_iris
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import make_pipeline

# Load a sample dataset (e.g., Iris)
data = load_iris()
X = data.data
y = (data.target == 2).astype(int) # Convert to binary classification (e.g.,
    ↳ class 2 vs rest)

# Split the dataset into training and test sets
Xtrain, xtest, ytrain, ytest = train_test_split(X, y, test_size=0.3,
    ↳ random_state=42)

# Create and train an SVM model with probability estimates enabled
svm_model = make_pipeline(StandardScaler(), svm.SVC(probability=True))

```

```

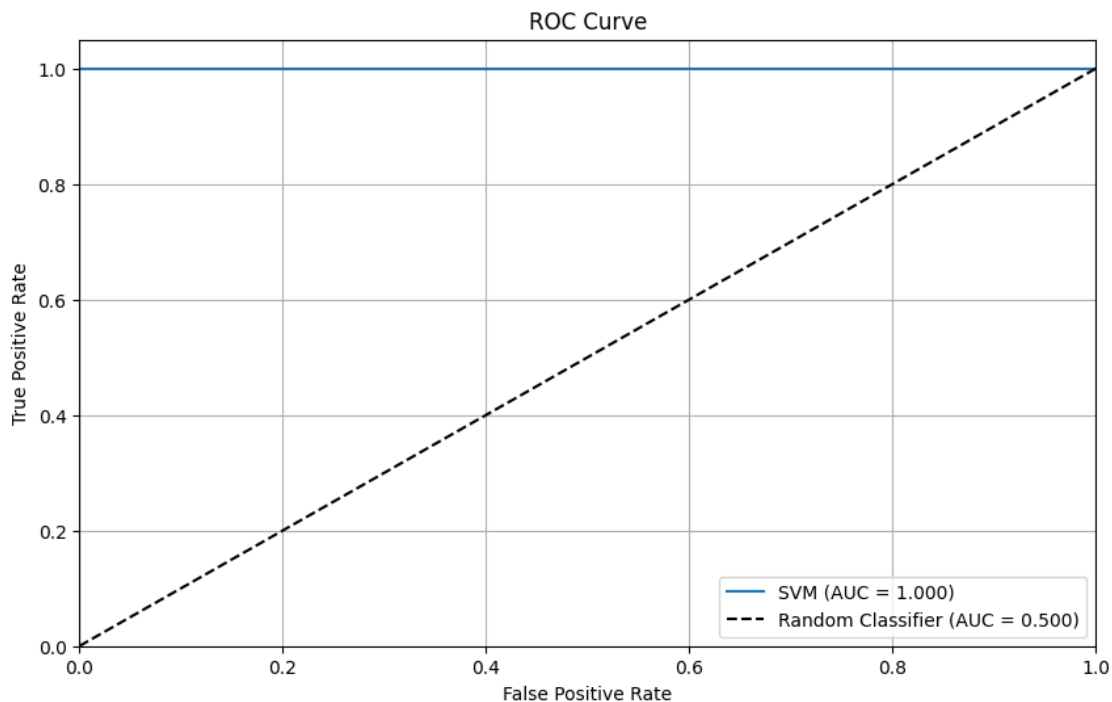
svm_model.fit(Xtrain, ytrain)

# Now you can use the predict_proba method as in your original code
y_pred_proba = svm_model.predict_proba(xtest)[: , 1]

# Calculate FPR, TPR and threshold values
fpr, tpr, thresholds = roc_curve(ytest, y_pred_proba)

# Plot ROC curve
plt.figure(figsize=(10, 6))
plt.plot(fpr, tpr, label='SVM (AUC = {:.3f})'.format(roc_auc_score(ytest,
↪y_pred_proba)))
plt.plot([0, 1], [0, 1], 'k--', label='Random Classifier (AUC = 0.500)')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve')
plt.legend(loc='lower right')
plt.grid(True)
plt.show()

```



```

[ ]: import pandas as pd
import matplotlib.pyplot as plt

```

```

# Convert y to a Pandas Series
y_series = pd.Series(y)

# Get the class distribution
class_counts = y_series.value_counts()

# Plot a pie chart of the target class distribution
plt.figure(figsize=(8, 8))
plt.pie(class_counts, labels=class_counts.index, autopct='%1.1f%%',
        ↪startangle=140, colors=['#ff9999', '#66b3ff'])
plt.title('Distribution of Target Classes')
plt.show()

```

