

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.datasets import load_breast_cancer
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, confusion_matrix,
accuracy_score, roc_auc_score, roc_curve
```

```
data = load_breast_cancer()
df = pd.DataFrame(data.data, columns=data.feature_names)
df['target'] = data.target
df.head()
```

	mean radius	mean texture	mean perimeter	mean area	mean smoothness \
0	17.99	10.38	122.80	1001.0	0.11840
1	20.57	17.77	132.90	1326.0	0.08474
2	19.69	21.25	130.00	1203.0	0.10960
3	11.42	20.38	77.58	386.1	0.14250
4	20.29	14.34	135.10	1297.0	0.10030

	mean compactness	mean concavity	mean concave points	mean symmetry \
0	0.27760	0.3001	0.14710	0.2419
1	0.07864	0.0869	0.07017	0.1812
2	0.15990	0.1974	0.12790	0.2069
3	0.28390	0.2414	0.10520	0.2597
4	0.13280	0.1980	0.10430	0.1809

	mean fractal dimension	...	worst texture	worst perimeter	worst area \
0	0.07871	...	17.33	184.60	2019.0
1	0.05667	...	23.41	158.80	1956.0

2	0.05999	...	25.53	152.50
1709.0				
3	0.09744	...	26.50	98.87
567.7				
4	0.05883	...	16.67	152.20
1575.0				

	worst smoothness	worst compactness	worst concavity	worst concave
points \				
0	0.1622	0.6656	0.7119	
0.2654				
1	0.1238	0.1866	0.2416	
0.1860				
2	0.1444	0.4245	0.4504	
0.2430				
3	0.2098	0.8663	0.6869	
0.2575				
4	0.1374	0.2050	0.4000	
0.1625				

	worst symmetry	worst fractal dimension	target
0	0.4601	0.11890	0
1	0.2750	0.08902	0
2	0.3613	0.08758	0
3	0.6638	0.17300	0
4	0.2364	0.07678	0

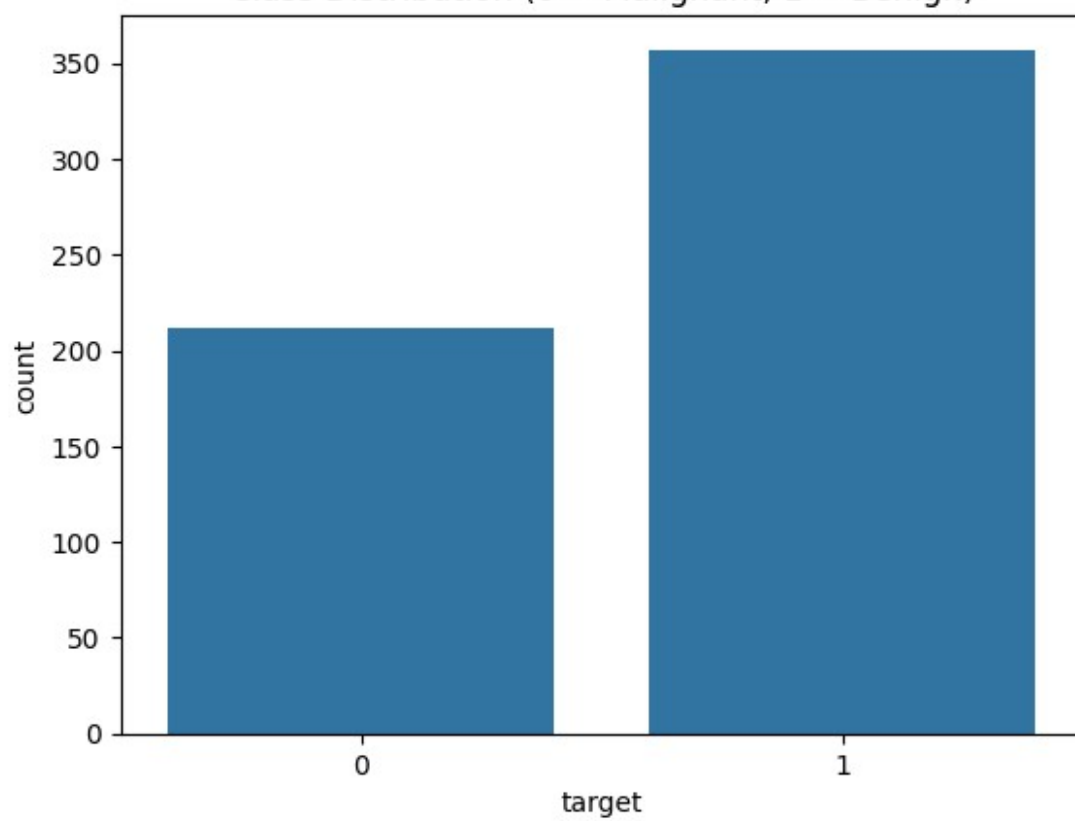
[5 rows x 31 columns]

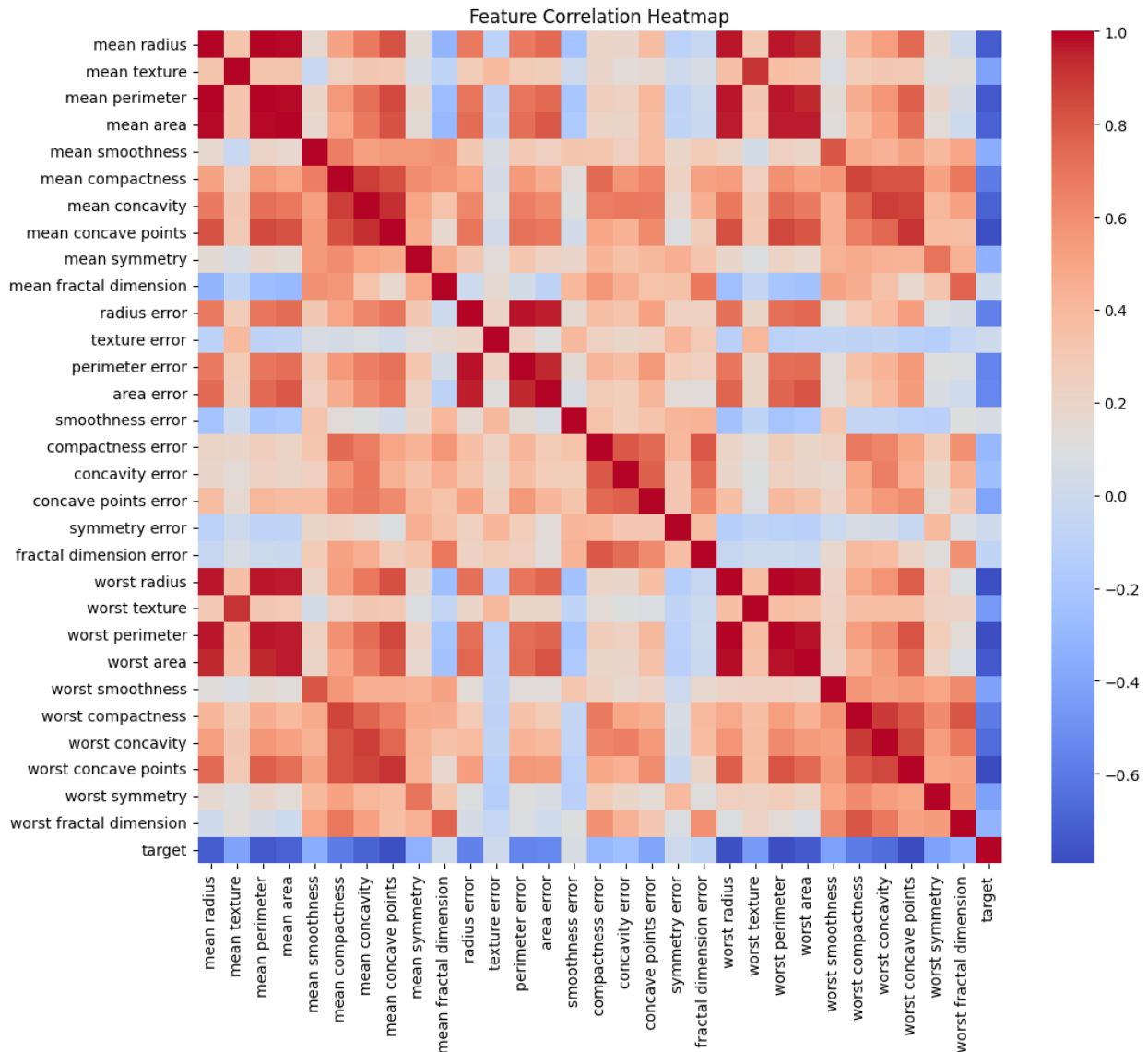
```
# Check class distribution
print(df['target'].value_counts())
sns.countplot(x='target', data=df)
plt.title('Class Distribution (0 = Malignant, 1 = Benign)')
plt.show()
```

```
# Correlation heatmap
plt.figure(figsize=(12, 10))
sns.heatmap(df.corr(), cmap='coolwarm')
plt.title('Feature Correlation Heatmap')
plt.show()
```

```
target
1      357
0      212
Name: count, dtype: int64
```

Class Distribution (0 = Malignant, 1 = Benign)





```
X = df.drop('target', axis=1)
y = df['target']

# Normalize features
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

# Train-test split
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y,
test_size=0.2, random_state=42)

model = RandomForestClassifier(n_estimators=100, random_state=42)
model.fit(X_train, y_train)

y_pred = model.predict(X_test)
```

```

# Accuracy & confusion matrix
print("Accuracy:", accuracy_score(y_test, y_pred))
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred))
print("Classification Report:\n", classification_report(y_test,
y_pred))

# ROC-AUC Curve
y_prob = model.predict_proba(X_test)[: , 1]
fpr, tpr, _ = roc_curve(y_test, y_prob)
roc_auc = roc_auc_score(y_test, y_prob)

plt.plot(fpr, tpr, label=f'ROC Curve (AUC = {roc_auc:.2f})')
plt.plot([0,1], [0,1], 'k--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve')
plt.legend()
plt.show()

```

Accuracy: 0.9649122807017544

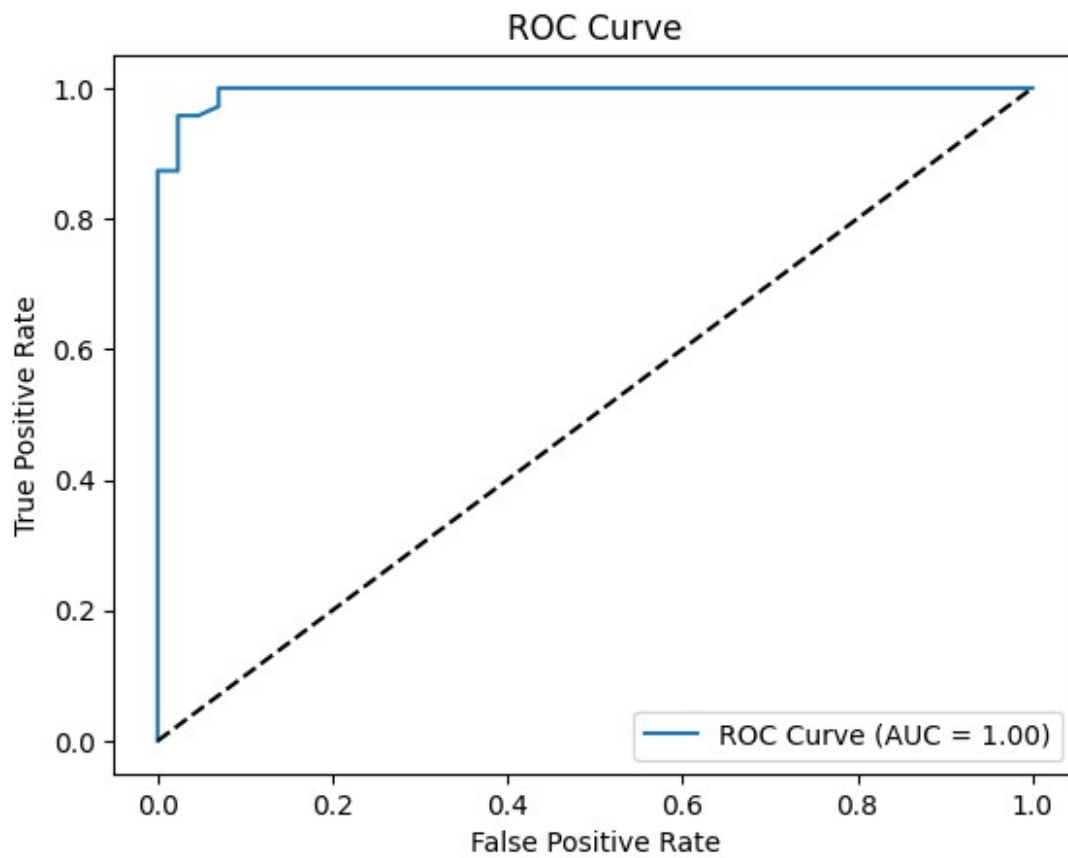
Confusion Matrix:

```
[[40  3]
```

```
[ 1 70]]
```

Classification Report:

	precision	recall	f1-score	support
0	0.98	0.93	0.95	43
1	0.96	0.99	0.97	71
accuracy			0.96	114
macro avg	0.97	0.96	0.96	114
weighted avg	0.97	0.96	0.96	114



```
importances = model.feature_importances_  
indices = np.argsort(importances)[::-1]  
  
plt.figure(figsize=(10, 6))  
sns.barplot(x=importances[indices], y=X.columns[indices])  
plt.title('Feature Importances')  
plt.show()
```

