```
Start coding or generate with AI.
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Double-click (or enter) to edit

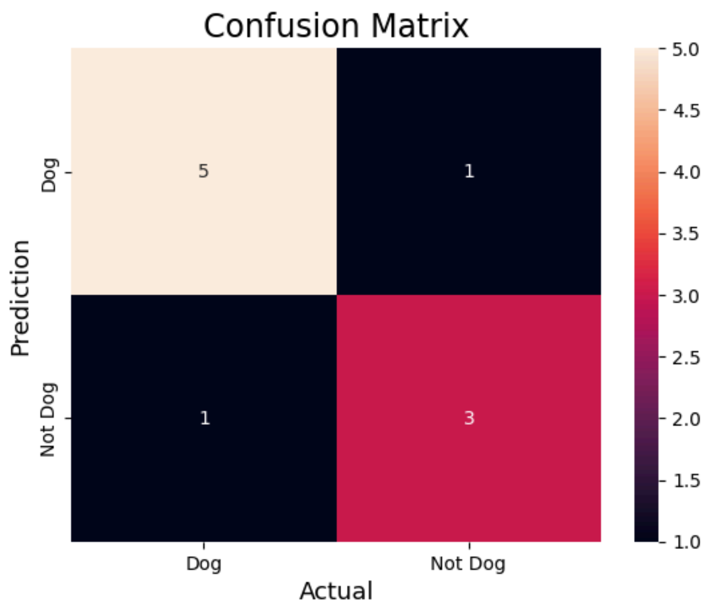
1

```
import numpy as np
from sklearn.metrics import confusion_matrix
import seaborn as sns
import matplotlib.pyplot as plt

#Create the NumPy array for actual and predicted labels.
actual    = np.array(
  ['Dog','Dog','Dog','Not Dog','Dog','Not Dog','Dog','Dog','Not Dog','Not Dog'])
predicted = np.array(
  ['Dog','Not Dog','Dog','Not Dog','Dog','Dog','Dog','Dog','Not Dog','Not Dog'])

#compute the confusion matrix.
cm = confusion_matrix(actual,predicted)

#Plot the confusion matrix.
sns.heatmap(cm,
            annot=True,
            fmt='g',
            xticklabels=['Dog','Not Dog'],
            yticklabels=['Dog','Not Dog'])
plt.ylabel('Prediction',fontsize=13)
plt.xlabel('Actual',fontsize=13)
plt.title('Confusion Matrix',fontsize=17)
plt.show()
```



2

```
from sklearn.datasets import load_breast_cancer
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import confusion_matrix
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score

# Load the breast cancer dataset
X, y= load_breast_cancer(return_X_y=True)
X_train, X_test, y_train, y_test = train_test_split(X, y,test_size=0.25)

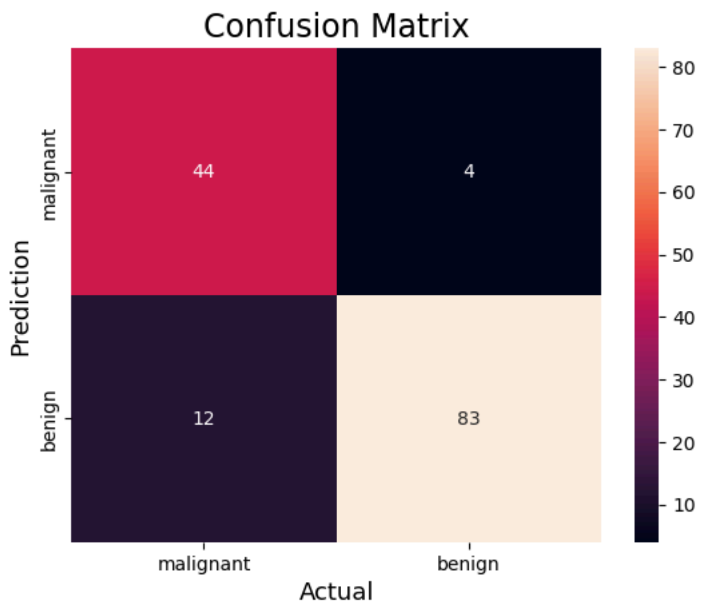
# Train the model
tree = DecisionTreeClassifier(random_state=23)
tree.fit(X_train, y_train)

# preduction
y_pred = tree.predict(X_test)

# compute the confusion matrix
cm = confusion_matrix(y_test,y_pred)

#Plot the confusion matrix.
sns.heatmap(cm,
            annot=True,
            fmt='g',
            xticklabels=['malignant', 'benign'],
            yticklabels=['malignant', 'benign'])
plt.ylabel('Prediction',fontsize=13)
plt.xlabel('Actual',fontsize=13)
plt.title('Confusion Matrix',fontsize=17)
plt.show()


# Finding precision and recall
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy   :", accuracy)
precision = precision_score(y_test, y_pred)
print("Precision :", precision)
recall = recall_score(y_test, y_pred)
print("Recall    :", recall)
F1_score = f1_score(y_test, y_pred)
print("F1-score  :", F1_score)
```



```
Accuracy   : 0.8881118881118881
Precision : 0.9540229885057471
Recall    : 0.8736842105263158
F1-score  : 0.9120879120879121
```

3

```
#Import the necessary libraries
from sklearn.datasets import load_digits
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import confusion_matrix
```

```
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score

# Load the breast cancer dataset
X, y= load_digits(return_X_y=True)
X_train, X_test, y_train, y_test = train_test_split(X, y,test_size=0.25)

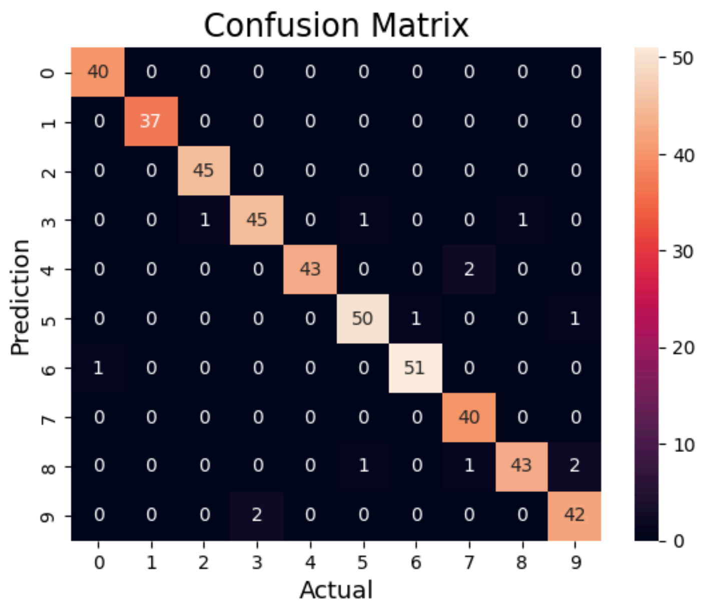
# Train the model
clf = RandomForestClassifier(random_state=23)
clf.fit(X_train, y_train)

# preduction
y_pred = clf.predict(X_test)

# compute the confusion matrix
cm = confusion_matrix(y_test,y_pred)

#Plot the confusion matrix.
sns.heatmap(cm,
            annot=True,
            fmt='g')
plt.ylabel('Prediction',fontsize=13)
plt.xlabel('Actual',fontsize=13)
plt.title('Confusion Matrix',fontsize=17)
plt.show()


# Finding precision and recall
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy   :", accuracy)
```



	0	1	2	3	4	5	6	7	8	9
0	40	0	0	0	0	0	0	0	0	0
1	0	37	0	0	0	0	0	0	0	0
2	0	0	45	0	0	0	0	0	0	0
3	0	0	1	45	0	1	0	0	1	0
4	0	0	0	0	43	0	0	2	0	0
5	0	0	0	0	0	50	1	0	0	1
6	1	0	0	0	0	0	51	0	0	0
7	0	0	0	0	0	0	0	40	0	0
8	0	0	0	0	0	1	0	1	43	2
9	0	0	0	2	0	0	0	0	0	42

```
Accuracy   : 0.9688888888888889
```

4

```
import numpy as np
import matplotlib.pyplot as plt
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import PolynomialFeatures
from sklearn.linear_model import LinearRegression
from sklearn.model_selection import cross_val_score

def true_fun(X):
    return np.cos(1.5 * np.pi * X)

np.random.seed(0)

n_samples = 30
degrees = [1, 4, 15]

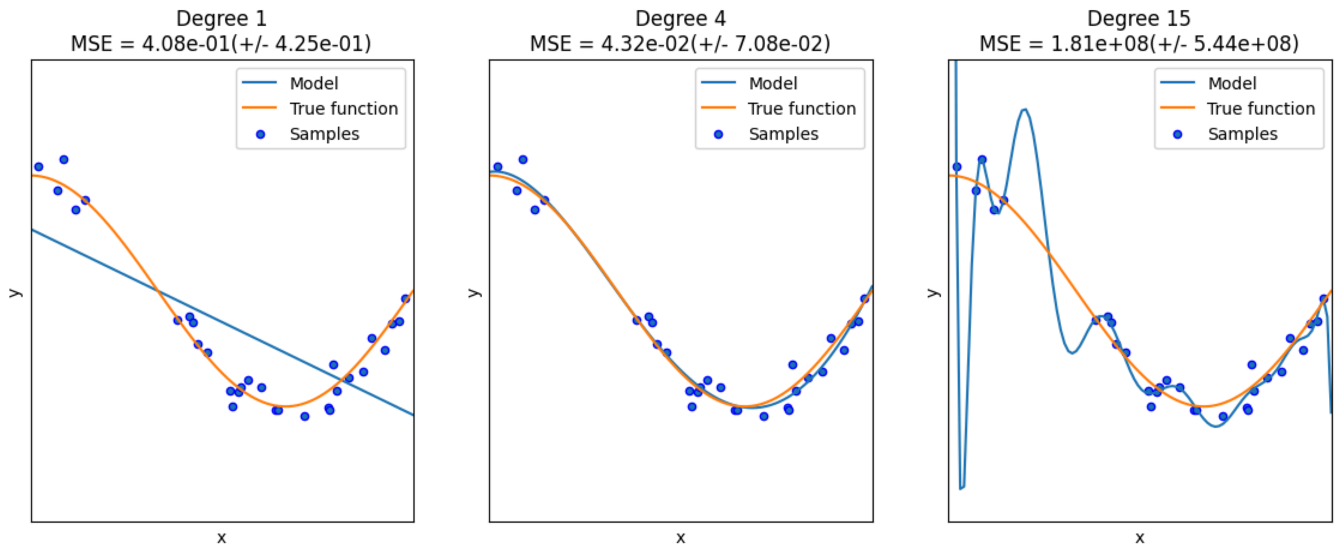
X = np.sort(np.random.rand(n_samples))
y = true_fun(X) + np.random.randn(n_samples) * 0.1

plt.figure(figsize=(14, 5))
for i in range(len(degrees)):
    ax = plt.subplot(1, len(degrees), i + 1)
    plt.setp(ax, xticks=(), yticks=())

    polynomial_features = PolynomialFeatures(degree=degrees[i], include_bias=False)
    linear_regression = LinearRegression()
    pipeline = Pipeline(
        [
            ("polynomial_features", polynomial_features),
            ("linear_regression", linear_regression),
        ]
    )
    pipeline.fit(X[:, np.newaxis], y)

    # Evaluate the models using crossvalidation
    scores = cross_val_score(
        pipeline, X[:, np.newaxis], y, scoring="neg_mean_squared_error", cv=10
    )

    X_test = np.linspace(0, 1, 100)
    plt.plot(X_test, pipeline.predict(X_test[:, np.newaxis]), label="Model")
    plt.plot(X_test, true_fun(X_test), label="True function")
    plt.scatter(X, y, edgecolor="b", s=20, label="Samples")
    plt.xlabel("x")
    plt.ylabel("y")
    plt.xlim((0, 1))
    plt.ylim((-2, 2))
    plt.legend(loc="best")
    plt.title(
        "Degree {}\nMSE = {:.2e}(+/- {:.2e})".format(
            degrees[i], -scores.mean(), scores.std()
        )
    )
plt.show()
```



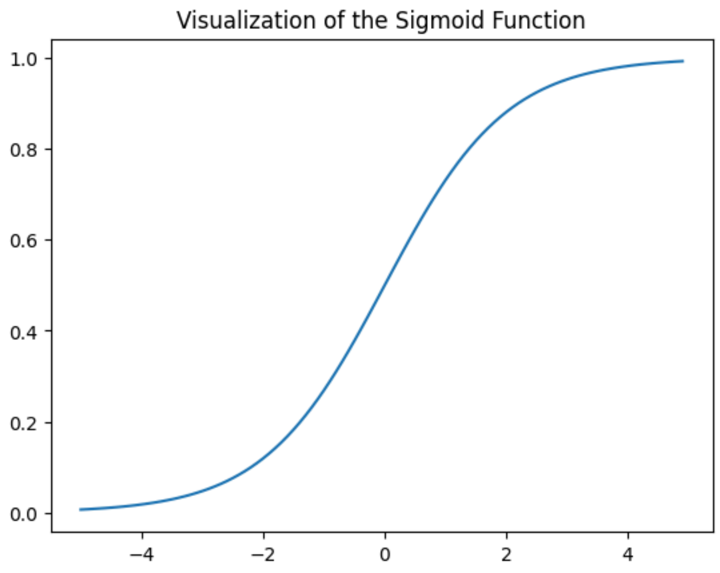
5

```
import numpy as np
import matplotlib.pyplot as plt

def sigmoid(z):
    return 1 / (1 + np.exp( - z))

plt.plot(np.arange(-5, 5, 0.1), sigmoid(np.arange(-5, 5, 0.1)))
plt.title('Visualization of the Sigmoid Function')

plt.show()
```


Visualization of the Sigmoid Function