Install Packages

```
from sklearn import datasets
from sklearn.model_selection import train_test_split
from sklearn import svm
from sklearn import metrics

# Load dataset
cancer = datasets.load_breast_cancer()

# Display basic info
print("Features:", cancer.feature_names)
print("Labels:", cancer.target_names)
print("Data shape:", cancer.data.shape)
print("Target:", cancer.target)

# Split data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(
    cancer.data, cancer.target, test_size=0.3, random_state=42
)

# Create and train the model
clf = svm.SVC(kernel='linear')
clf.fit(X_train, y_train)

# Make predictions
y_pred = clf.predict(X_test)

# Evaluate the model
print("Accuracy:", metrics.accuracy_score(y_test, y_pred))
print("Precision:", metrics.precision_score(y_test, y_pred))
print("Recall:", metrics.recall_score(y_test, y_pred))
```

```
Features: ['mean radius' 'mean texture' 'mean perimeter' 'mean area'
 'mean smoothness' 'mean compactness' 'mean concavity'
 'mean concave points' 'mean symmetry' 'mean fractal dimension'
 'radius error' 'texture error' 'perimeter error' 'area error'
 'smoothness error' 'compactness error' 'concavity error'
 'concave points error' 'symmetry error' 'fractal dimension error'
 'worst radius' 'worst texture' 'worst perimeter' 'worst area'
 'worst smoothness' 'worst compactness' 'worst concavity'
 'worst concave points' 'worst symmetry' 'worst fractal dimension']
Labels: ['malignant' 'benign']
Data shape: (569, 30)
Target: [0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0
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Accuracy: 0.9649122807017544
Precision: 0.9636363636363636
Recall: 0.9814814814814815
```