```
import pandas as pd
df = pd.read_csv('/content/breast_cancer_survival.csv')
print(df.head())
features = df.drop('Patient_Status', axis=1)
target = df['Patient_Status']
print("Features:")
print(features.head())
print("Target:")
print(target.head())
\square
       Age Gender Protein1 Protein2 Protein3 Protein4 Tumour_Stage
        42 FFMALE
                    0.95256 2.15000 0.007972 -0.048340
                                                                   TT
     1
        54
            FEMALE
                    0.00000
                              1.38020 -0.498030 -0.507320
                                                                   II
           FEMALE -0.52303 1.76400 -0.370190 0.010815
        78 FEMALE -0.87618
                              0.12943 -0.370380 0.132190
     3
                                                                    Ι
        42 FEMALE 0.22611 1.74910 -0.543970 -0.390210
                                                                   II
                           Histology ER status PR status HER2 status Surgery_type \
    0 Infiltrating Ductal Carcinoma Positive Positive
                                                          Negative
                                                                          Other
     1 Infiltrating Ductal Carcinoma Positive Positive
                                                           Negative
                                                                          0ther
       Infiltrating Ductal Carcinoma Positive Positive
                                                           Negative
                                                                     Lumpectomy
     3 Infiltrating Ductal Carcinoma Positive Positive
                                                          Negative
                                                                          Other
     4 Infiltrating Ductal Carcinoma Positive Positive
                                                                     Lumpectomy
                                                          Positive
       Date_of_Surgery Date_of_Last_Visit Patient_Status
     a
            20-May-18
                              26-Aug-18
                                                 Alive
     1
            26-Apr-18
                               25-Jan-19
                                                  Dead
             24-Aug-18
                               08-Apr-20
     3
            16-Nov-18
                              28-Jul-20
                                                 Alive
     4
            12-Dec-18
                              05-Jan-19
                                                 Alive
     Features:
       Age Gender Protein1 Protein2 Protein3 Protein4 Tumour Stage \
           FEMALE 0.95256 2.15000 0.007972 -0.048340
     a
        42
                                                                   II
     1
        54 FEMALE 0.00000
                              1.38020 -0.498030 -0.507320
                                                                   II
     2
        63
            FEMALE -0.52303
                              1.76400 -0.370190 0.010815
                                                                   II
        78 FEMALE -0.87618 0.12943 -0.370380 0.132190
     3
                                                                    Т
        42 FEMALE 0.22611 1.74910 -0.543970 -0.390210
                                                                   II
                           Histology ER status PR status HER2 status Surgery_type \
    0 Infiltrating Ductal Carcinoma Positive Positive
                                                          Negative
                                                                          Other
                                                           Negative
       Infiltrating Ductal Carcinoma Positive Positive
                                                                          Other
       Infiltrating Ductal Carcinoma Positive Positive
                                                          Negative
                                                                     Lumpectomy
       Infiltrating Ductal Carcinoma Positive Positive
                                                                          Other
                                                          Negative
     4 Infiltrating Ductal Carcinoma Positive Positive
                                                          Positive
                                                                     Lumpectomy
      Date_of_Surgery Date_of_Last_Visit
     0
            20-May-18
                              26-Aug-18
             26-Apr-18
                               25-Jan-19
             24-Aug-18
                               08-Apr-20
     2
                              28-1111-20
            16-Nov-18
     3
     4
            12-Dec-18
                               05-Jan-19
     Target:
         Alive
     0
     1
          Dead
         Alive
         Alive
     3
         Alive
     Name: Patient_Status, dtype: object
```

```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder, StandardScaler
from sklearn.svm import SVC
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy score
label_encoders = {}
for column in df.select_dtypes(include=['object']).columns:
    le = LabelEncoder()
    df[column] = le.fit_transform(df[column])
    label_encoders[column] = le
X = df.drop('Patient_Status', axis=1)
y = df['Patient_Status']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
svm_model = SVC(kernel='linear')
svm_model.fit(X_train_scaled, y_train)
svm_predictions = svm_model.predict(X_test_scaled)
svm_accuracy = accuracy_score(y_test, svm_predictions)
print(f'SVM Accuracy: {svm_accuracy}')
rf_model = RandomForestClassifier(n_estimators=100, random_state=42)
rf_model.fit(X_train, y_train) # No need to scale data for Random Forest
rf_predictions = rf_model.predict(X_test)
rf_accuracy = accuracy_score(y_test, rf_predictions)
print(f'Random Forest Accuracy: {rf_accuracy}')
     SVM Accuracy: 0.7910447761194029
     Random Forest Accuracy: 0.8059701492537313
label encoders = {}
for column in df.select_dtypes(include=['object']).columns:
    le = LabelEncoder()
    df[column] = le.fit_transform(df[column])
    label_encoders[column] = le
X = df.drop('Patient_Status', axis=1)
y = df['Patient Status']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
svm_model = SVC(kernel='linear')
svm_model.fit(X_train_scaled, y_train)
svm_predictions = svm_model.predict(X_test_scaled)
rf_model = RandomForestClassifier(n_estimators=100, random_state=42)
rf_model.fit(X_train, y_train) # No need to scale data for Random Forest
rf_predictions = rf_model.predict(X_test)
def calculate_metrics(y_true, y_pred, model_name):
    accuracy = accuracy_score(y_true, y_pred)
    precision = precision_score(y_true, y_pred, average='weighted')
    recall = recall_score(y_true, y_pred, average='weighted')
    f1 = f1_score(y_true, y_pred, average='weighted')
    print(f"{model name} Metrics:")
    print(f"Accuracy: {accuracy}")
    print(f"Precision: {precision}")
    print(f"Recall: {recall}")
    print(f"F1-Score: {f1}\n")
calculate_metrics(y_test, svm_predictions, "SVM")
calculate_metrics(y_test, rf_predictions, "Random Forest")
```

SVM Metrics:

Accuracy: 0.7910447761194029 Precision: 0.6432835820895523 Recall: 0.7910447761194029 F1-Score: 0.707794361525705

Random Forest Metrics: Accuracy: 0.8059701492537313 Precision: 0.672002888781897 Recall: 0.8059701492537313 F1-Score: 0.7328021546403322

/usr/local/lib/python3.10/dist-packages/sklearn/metrics/_classification.py:1344: UndefinedMetricWarning: Precision is ill-defined and be _warn_prf(average, modifier, msg_start, len(result))

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