## Practical 12: Logistic Regression for Classification Using Scikit-Learn

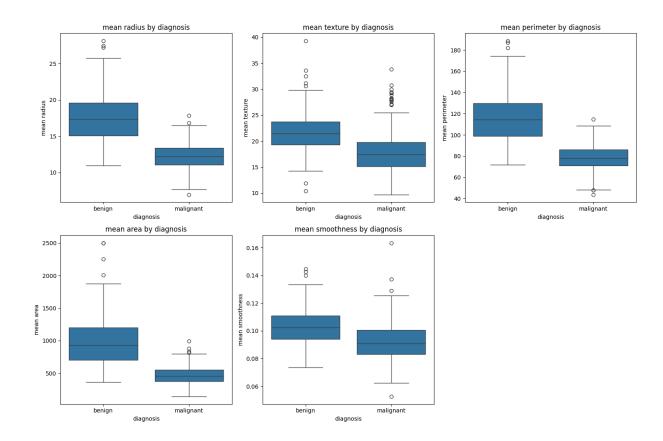
```
In [1]: # Import necessary libraries
        import numpy as np
        import pandas as pd
        import matplotlib.pyplot as plt
        import seaborn as sns
        from sklearn.model selection import train test split
        from sklearn.linear model import LogisticRegression
        from sklearn.preprocessing import StandardScaler
        from sklearn.metrics import accuracy score, confusion matrix, classification
        from sklearn.datasets import load breast cancer
In [2]: # a. Load the breast cancer dataset
        data = load breast cancer()
        # Create a DataFrame with the feature data
        X = pd.DataFrame(data.data, columns=data.feature names)
        y = pd.Series(data.target, name='target')
        # Display information about the dataset
        print(f"Dataset shape: {X.shape}")
        print(f"Number of classes: {len(np.unique(y))}")
        print(f"Class distribution:\n{y.value counts()}")
        print("\nTarget names:")
        for i, name in enumerate(data.target names):
            print(f"Class {i}: {name}")
        # Display the first 5 rows of the feature data
        X.head()
       Dataset shape: (569, 30)
       Number of classes: 2
       Class distribution:
       target
       1
            357
            212
       Name: count, dtype: int64
       Target names:
       Class 0: malignant
       Class 1: benign
```

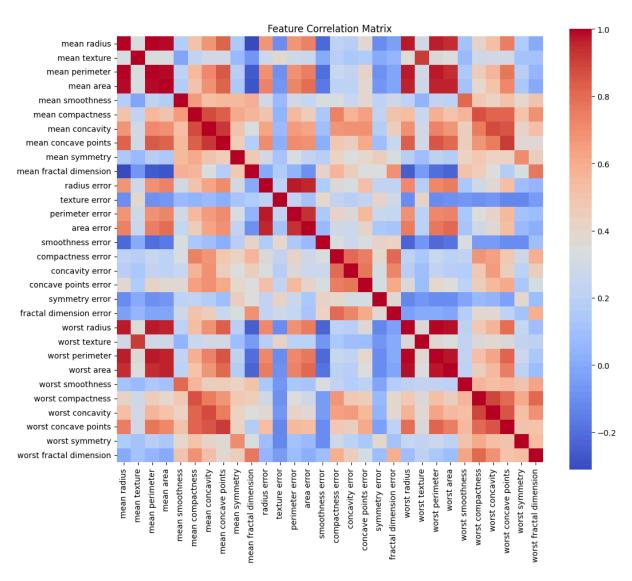
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	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	c
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	

 $5 \text{ rows} \times 30 \text{ columns}$ 

```
In [3]: # b. Exploratory data analysis
        # Let's examine the feature distributions by class
        # Create a DataFrame with both features and target
        df = X.copy()
        df['diagnosis'] = y.map({0: 'benign', 1: 'malignant'})
        # Select a few important features to visualize
        features to plot = ['mean radius', 'mean texture', 'mean perimeter', 'mean a
        # Create box plots to compare feature distributions by class
        plt.figure(figsize=(15, 10))
        for i, feature in enumerate(features to plot):
            plt.subplot(2, 3, i+1)
            sns.boxplot(x='diagnosis', y=feature, data=df)
            plt.title(f'{feature} by diagnosis')
        plt.tight_layout()
        plt.show()
        # Create a correlation heatmap for the features
        plt.figure(figsize=(12, 10))
        corr matrix = X.corr()
        sns.heatmap(corr_matrix, cmap='coolwarm', annot=False, square=True)
        plt.title('Feature Correlation Matrix')
        plt.show()
```





```
# c. Prepare the data for modeling

# Split the data into training and testing sets (70% train, 30% test)
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, rar
print(f"Training set size: {X_train.shape[0]} samples")
print(f"Test set size: {X_test.shape[0]} samples")

# Scale the features using StandardScaler
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

# Convert back to DataFrame for better visualization
X_train_scaled_df = pd.DataFrame(X_train_scaled, columns=X.columns)
X_test_scaled_df = pd.DataFrame(X_test_scaled, columns=X.columns)

# Show the first few rows of scaled data
print("\nScaled features (first 5 rows):")
X_train_scaled_df.head()
```

Training set size: 398 samples Test set size: 171 samples

Scaled features (first 5 rows):

## Out[4]:

		mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	conc
	0	-0.123490	-0.296801	-0.170507	-0.208616	-1.201680	-0.773170	-0.76
	1	-0.228268	-0.657951	-0.253775	-0.296503	-1.804637	-0.587616	-0.09
	2	0.145534	-1.230564	0.245833	-0.010242	0.519184	1.570006	0.73
	3	-0.358532	-0.672207	-0.400937	-0.400014	-1.203862	-0.970650	-0.63
	4	-0.157472	0.967224	-0.208843	-0.241538	-0.254695	-0.700630	-0.75

 $5 \text{ rows} \times 30 \text{ columns}$ 

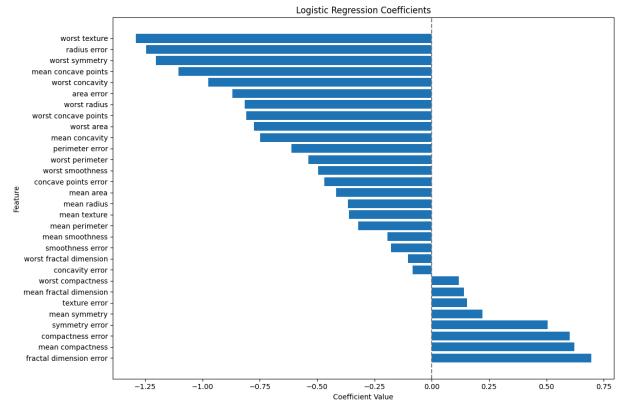
```
In [5]: # d. Create and train the logistic regression model
        model = LogisticRegression(max iter=1000, random state=42)
        model.fit(X train scaled, y train)
        # Get the feature coefficients
        coefficients = pd.DataFrame({
            'Feature': X.columns,
            'Coefficient': model.coef [0]
        }).sort values('Coefficient', ascending=False)
        print("Model Coefficients (Top 10 positive and negative):")
        print("\nTop 10 positive coefficients (features most associated with maligna
        print(coefficients.head(10))
        print("\nTop 10 negative coefficients (features most associated with benign)
        print(coefficients.tail(10))
        # Plot the coefficients
        plt.figure(figsize=(12, 8))
        plt.barh(coefficients['Feature'], coefficients['Coefficient'])
        plt.title('Logistic Regression Coefficients')
        plt.xlabel('Coefficient Value')
        plt.ylabel('Feature')
        plt.axvline(x=0, color='gray', linestyle='--')
        plt.tight layout()
        plt.show()
```

Model Coefficients (Top 10 positive and negative):

Top 10 positive coefficients (features most associated with malignant): Feature Coefficient fractal dimension error 0.694861 19 5 mean compactness 0.622023 15 compactness error 0.600753 18 symmetry error 0.505452 8 mean symmetry 0.221625 11 texture error 0.154407 9 mean fractal dimension 0.139476 25 worst compactness 0.118408 16 concavity error -0.083213 29 worst fractal dimension -0.103243

Top 10 negative coefficients (features most associated with benign):

```
Feature Coefficient
6
         mean concavity
                          -0.747674
23
             worst area
                          -0.774047
27
   worst concave points
                          -0.808050
20
           worst radius -0.814530
13
             area error -0.868623
26
        worst concavity
                          -0.974874
7
    mean concave points -1.103646
28
         worst symmetry
                           -1.202497
10
           radius error
                          -1.244185
21
          worst texture
                           -1.291134
```



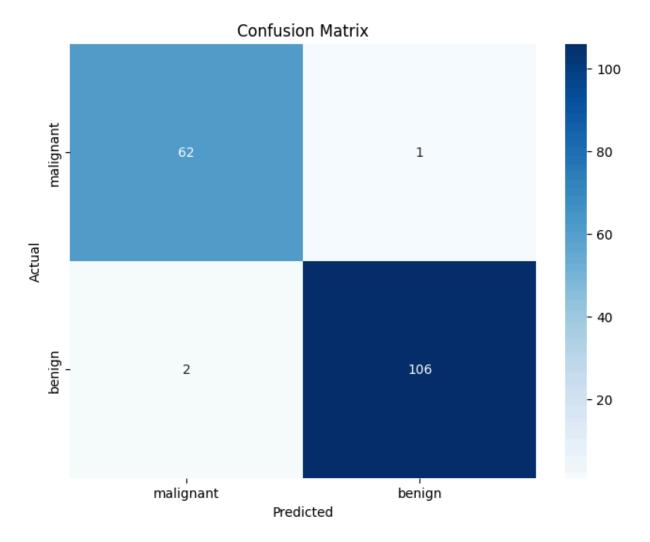
```
In [6]: # e. Make predictions on the test set
y_pred = model.predict(X_test_scaled)
y_pred_prob = model.predict_proba(X_test_scaled)[:, 1] # Probability of the
```

```
# Calculate accuracy
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.4f}")
# Generate classification report
print("\nClassification Report:")
print(classification_report(y_test, y_pred, target_names=data.target_names))
# Create a confusion matrix
cm = confusion matrix(y test, y pred)
plt.figure(figsize=(8, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
            xticklabels=data.target names,
           yticklabels=data.target_names)
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix')
plt.show()
```

Accuracy: 0.9825

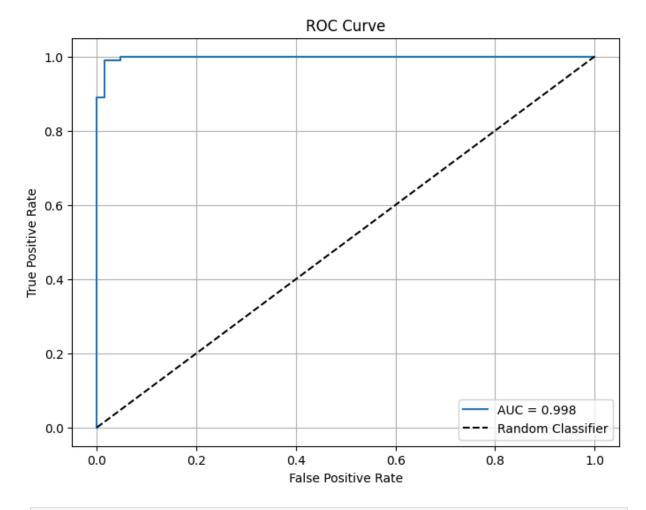
## Classification Report:

	precision	recall	f1-score	support
malignant	0.97	0.98	0.98	63
benign	0.99	0.98	0.99	108
accuracy			0.98	171
macro avg	0.98	0.98	0.98	171
weighted avg	0.98	0.98	0.98	171



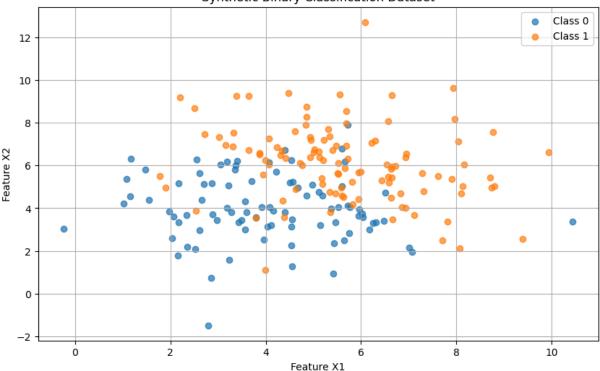
```
In [7]: # f. Calculate and plot ROC curve
fpr, tpr, thresholds = roc_curve(y_test, y_pred_prob)
auc = roc_auc_score(y_test, y_pred_prob)

plt.figure(figsize=(8, 6))
plt.plot(fpr, tpr, label=f'AUC = {auc:.3f}')
plt.plot([0, 1], [0, 1], 'k--', label='Random Classifier')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve')
plt.legend(loc='lower right')
plt.grid(True)
plt.show()
```



```
In [8]: # a. Create a synthetic dataset
        np.random.seed(42)
        # Generate two features
        n \text{ samples} = 200
        X1 = np.random.normal(loc=5, scale=2, size=n_samples)
        X2 = np.random.normal(loc=5, scale=2, size=n samples)
        # Create a decision rule for binary classification
        y true = (X1 + X2 > 10).astype(int)
        # Add some noise to make it more realistic
        noise indices = np.random.choice(n samples, size=int(n samples * 0.1), repla
        y_true[noise_indices] = 1 - y_true[noise_indices]
        # Create a DataFrame for better handling
        synthetic df = pd.DataFrame({
            'X1': X1,
             'X2': X2,
            'target': y true
        })
        # Visualize the dataset
        plt.figure(figsize=(10, 6))
        plt.scatter(synthetic_df[synthetic_df['target'] == 0]['X1'],
                    synthetic df[synthetic df['target'] == 0]['X2'],
```

## Synthetic Binary Classification Dataset



Class distribution: target 1 110 0 90

Name: count, dtype: int64

Training set size: 140 samples Test set size: 60 samples

```
In [10]: # c. Train a logistic regression model on the synthetic data
         model syn = LogisticRegression(random state=42)
         model syn.fit(X train syn, y train syn)
         # Print the model coefficients
         print(f"Intercept: {model syn.intercept [0]:.4f}")
         print(f"Coefficient for X1: {model syn.coef [0][0]:.4f}")
         print(f"Coefficient for X2: {model syn.coef [0][1]:.4f}")
         print(f"\nLogistic Regression Equation:")
         print(f"log(p/(1-p))) = \{model syn.intercept [0]:.4f\} + \{model syn.coef [0][6]\}
        Intercept: -7.3562
        Coefficient for X1: 0.6232
        Coefficient for X2: 0.8821
        Logistic Regression Equation:
        log(p/(1-p)) = -7.3562 + 0.6232 * X1 + 0.8821 * X2
In [11]: # d. Evaluate the model on the synthetic test set
         y pred syn = model syn.predict(X test syn)
         accuracy syn = accuracy score(y test syn, y pred syn)
         print(f"Accuracy on test set: {accuracy syn:.4f}")
         # Display classification report
         print("\nClassification Report:")
         print(classification_report(y_test_syn, y_pred_syn))
         # Create a confusion matrix
         cm syn = confusion matrix(y test syn, y pred syn)
         plt.figure(figsize=(8, 6))
         sns.heatmap(cm syn, annot=True, fmt='d', cmap='Blues',
                     xticklabels=['Class 0', 'Class 1'],
                     yticklabels=['Class 0', 'Class 1'])
         plt.xlabel('Predicted')
         plt.ylabel('Actual')
         plt.title('Confusion Matrix - Synthetic Data')
         plt.show()
        Accuracy on test set: 0.9000
        Classification Report:
                      precision recall f1-score
                                                      support
                   0
                           0.86
                                     0.92
                                               0.89
                                                            26
                   1
                           0.94
                                     0.88
                                               0.91
                                                            34
                                               0.90
                                                           60
            accuracy
                           0.90
                                     0.90
                                               0.90
                                                            60
           macro avg
```

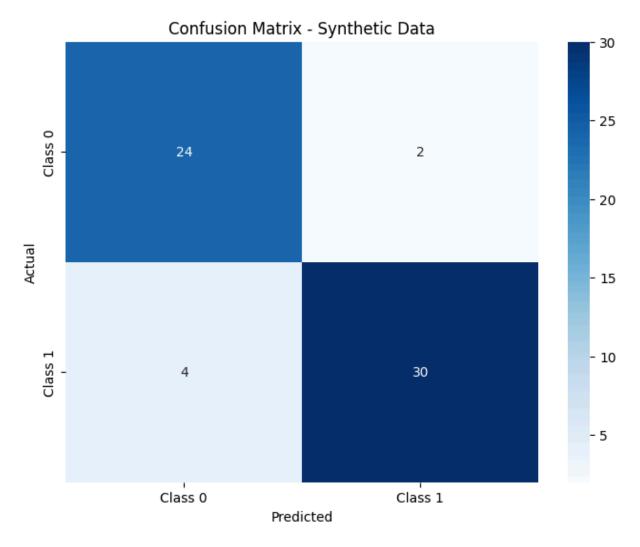
0.90

weighted avg

0.90

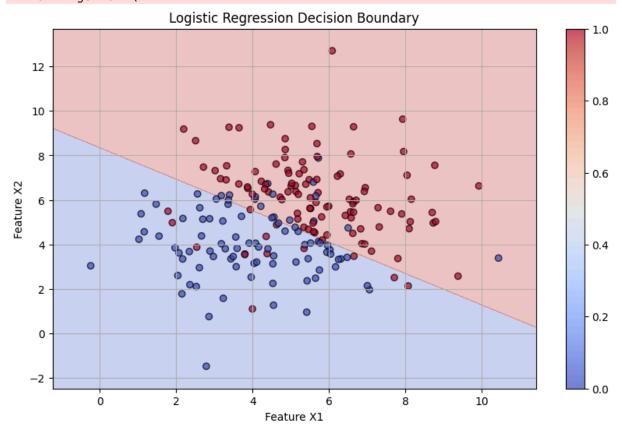
0.90

60



```
In [12]: # e. Visualize the decision boundary
         def plot decision boundary(X, y, model, title='Decision Boundary'):
             # Set up grid for visualization
             h = 0.02 # step size in the mesh
             x_{min}, x_{max} = X.iloc[:, 0].min() - 1, <math>X.iloc[:, 0].max() + 1
             y \min, y \max = X.iloc[:, 1].min() - 1, X.iloc[:, 1].max() + 1
             xx, yy = np.meshgrid(np.arange(x min, x max, h), np.arange(y min, y max,
             # Make predictions on the meshgrid
             Z = model.predict(np.c [xx.ravel(), yy.ravel()])
             Z = Z.reshape(xx.shape)
             # Plot the decision boundary and points
             plt.figure(figsize=(10, 6))
             plt.contourf(xx, yy, Z, alpha=0.3, cmap='coolwarm')
             plt.scatter(X.iloc[:, 0], X.iloc[:, 1], c=y, cmap='coolwarm', edgecolors
             plt.xlabel('Feature X1')
             plt.ylabel('Feature X2')
             plt.title(title)
             plt.colorbar()
             plt.grid(True)
             plt.show()
```

c:\Users\admi\AppData\Local\Programs\Python\Python311\Lib\site-packages\skle
arn\utils\validation.py:2739: UserWarning: X does not have valid feature nam
es, but LogisticRegression was fitted with feature names
 warnings.warn(



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