📖 Homework: KNN and SVM Implementation

Course: Artificial Intelligence
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A. Wine data classification using SVM

Collab and Github Links

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1. Import the libraries

In [1]:
```
## Load dependencies
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.datasets import load_wine
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.svm import SVC
from sklearn.preprocessing import label_binarize, StandardScaler
from sklearn.metrics import accuracy_score, confusion_matrix, classificatior
from itertools import cycle
import seaborn as sns
```

2. Load the dataset

In [2]:
```
# Load dataset
data = load_wine()
```

```
X, y = data.data, data.target
feature_names = data.feature_names
```

3. Show the unique targets and features:

The dataset has 13 features and 3 targets.

In [3]:
```
## show the target names and the number of unique features and target
print(data.target_names)
print(len(np.unique(y)))
print(len(feature_names))
print(feature_names)
```

```
['class_0' 'class_1' 'class_2']
3
13
['alcohol', 'malic_acid', 'ash', 'alcalinity_of_ash', 'magnesium', 'total_ph
enols', 'flavanoids', 'nonflavanoid_phenols', 'proanthocyanins', 'color_inte
nsity', 'hue', 'od280/od315_of_diluted_wines', 'proline']
```

4. Display the features and labels in tabular format:

In [4]:
```
# Create a DataFrame with features and target
df = pd.DataFrame(X, columns=feature_names)
df['target'] = y

# Display the first 5 rows
print(df.head(5))
```

```
   alcohol  malic_acid   ash  alcalinity_of_ash  magnesium  total_phenols  \
0    14.23        1.71  2.43               15.6      127.0           2.80   
1    13.20        1.78  2.14               11.2      100.0           2.65   
2    13.16        2.36  2.67               18.6      101.0           2.80   
3    14.37        1.95  2.50               16.8      113.0           3.85   
4    13.24        2.59  2.87               21.0      118.0           2.80   

   flavanoids  nonflavanoid_phenols  proanthocyanins  color_intensity   hue  
\
0        3.06                  0.28             2.29             5.64  1.04   
1        2.76                  0.26             1.28             4.38  1.05   
2        3.24                  0.30             2.81             5.68  1.03   
3        3.49                  0.24             2.18             7.80  0.86   
4        2.69                  0.39             1.82             4.32  1.04   

   od280/od315_of_diluted_wines  proline  target  
0                          3.92   1065.0       0  
1                          3.40   1050.0       0  
2                          3.17   1185.0       0  
3                          3.45   1480.0       0  
4                          2.93    735.0       0  
```

5. Split the dataset (70 % for training and 30% for testing):

In [5]:
```
# Split into train (70%) and test (30%)
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, rar
```

6. Standardize the features:

In [6]:
```
# Standardize features
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

7. Train the data using an SVM linear Kernel:

In [7]:
```
# Train Linear SVM Model
svm_model = SVC(kernel='linear', probability=True, random_state=42)
svm_model.fit(X_train, y_train)
```

Out[7]:
```
▾ SVC
SVC(kernel='linear', probability=True, random_state=42)
```

8. Run Predictions on Test data and get the accuracy score:

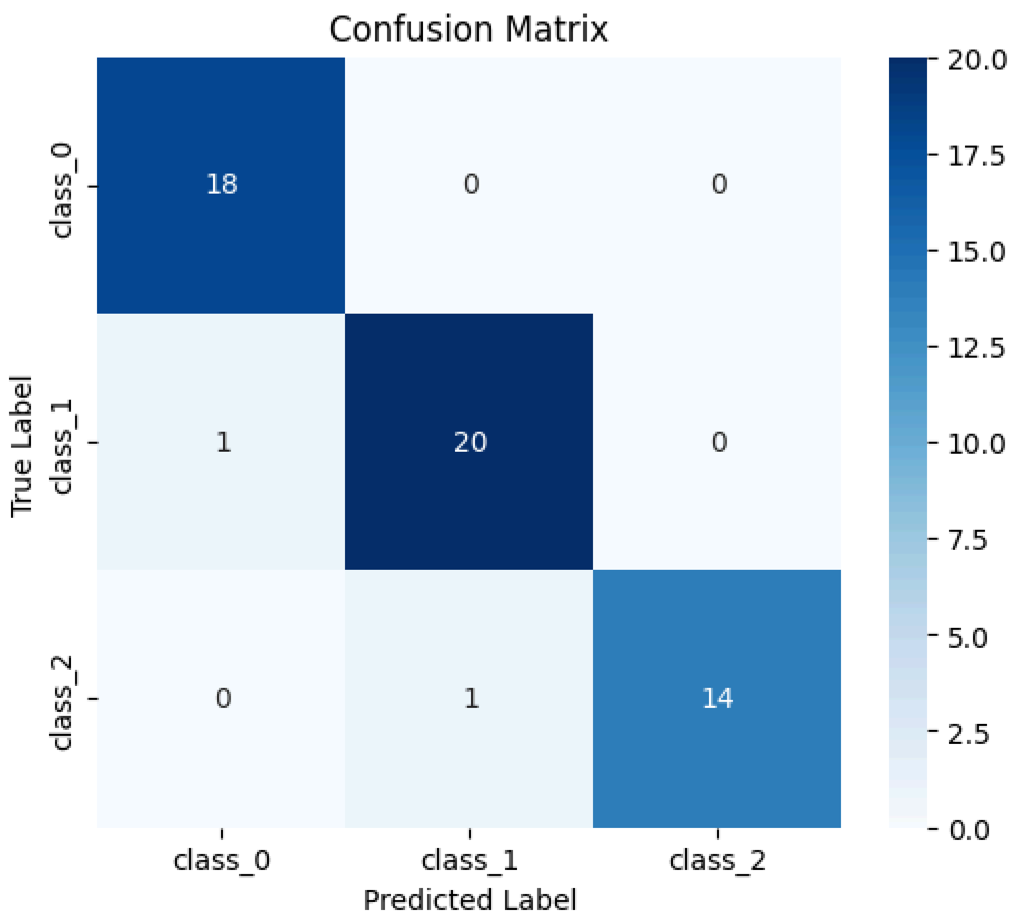
In [8]:
```
# Predict on test data
y_pred = svm_model.predict(X_test)

# Compute accuracy
accuracy = accuracy_score(y_test, y_pred)
print(f"Model Accuracy: {accuracy:.2f}")
```

```
Model Accuracy: 0.96
```

9. Plot a confusion matrix for the dataset:

In [9]:
```
conf_matrix = confusion_matrix(y_test, y_pred)
print("Confusion Matrix:")
print(conf_matrix)
# Plot Confusion Matrix
plt.figure(figsize=(6, 5))
sns.heatmap(conf_matrix, annot=True, fmt='d', cmap='Blues', xticklabels=data
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix')
plt.show()
```

```
Confusion Matrix:
[[18  0  0]
 [ 1 20  0]
 [ 0  1 14]]
```



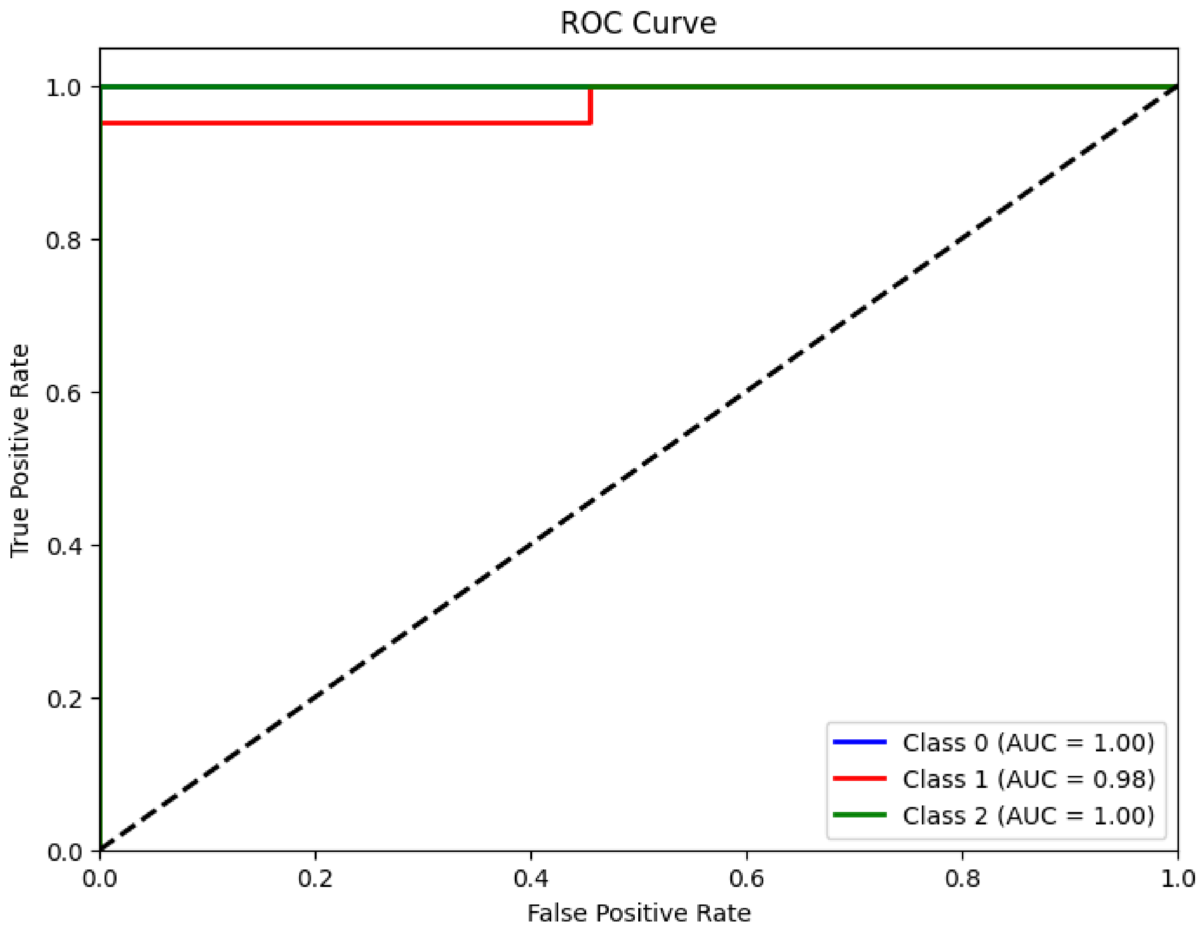
10. Print a classification report:

In [10]:
```
# Classification Report
print("Classification Report:")
print(classification_report(y_test, y_pred))

# Compute ROC curve and AUC
y_test_binarized = label_binarize(y_test, classes=[0, 1, 2])
y_score = svm_model.decision_function(X_test)
```

```
Classification Report:
              precision    recall  f1-score   support

           0       0.95      1.00      0.97        18
           1       0.95      0.95      0.95        21
           2       1.00      0.93      0.97        15

    accuracy                           0.96        54
   macro avg       0.97      0.96      0.96        54
weighted avg       0.96      0.96      0.96        54
```

11. Plot a ROC Curve for each class:

In [11]:
```
n_classes = len(np.unique(y))

plt.figure(figsize=(8, 6))
colors = cycle(['blue', 'red', 'green'])
for i, color in zip(range(n_classes), colors):
    fpr, tpr, _ = roc_curve(y_test_binarized[:, i], y_score[:, i])
    roc_auc = auc(fpr, tpr)
    plt.plot(fpr, tpr, color=color, lw=2, label=f'Class {i} (AUC = {roc_auc:

plt.plot([0, 1], [0, 1], 'k--', lw=2)
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve')
plt.legend(loc='lower right')
plt.show()
```



12. Test model generalization using 5-Fold Cross-Validation

In [12]:
```
# Perform 5-Fold Cross-Validation
cv_scores = cross_val_score(svm_model, X_train, y_train, cv=5)
print(f"Cross-Validation Scores: {cv_scores}")
print(f"Mean Cross-Validation Accuracy: {cv_scores.mean():.2f}")
```

```
Cross-Validation Scores: [0.96       0.96       1.         1.         0.9583
3333]
Mean Cross-Validation Accuracy: 0.98
```

B. Predict Diabetes progression using KNN regression

Collab and Github Links

Open in Colab

[🔗 View on GitHub]

1. Import the libraries

```
In [13]: ## Load dependencies
import numpy as np
import matplotlib.pyplot as plt
from sklearn.datasets import load_diabetes
from sklearn.model_selection import train_test_split, cross_val_score
# from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsRegressor
from sklearn.preprocessing import label_binarize, StandardScaler
from sklearn.metrics import accuracy_score, confusion_matrix, classificatior
from itertools import cycle
import seaborn as sns
```

2. Load the dataset

```
In [19]: # Load dataset
# Load dataset
data = load_diabetes()
X, y = data.data, data.target
feature_names = data.feature_names
```

3. Show the unique targets and features:

```
In [20]: ## show the target names and the number of unique features and target
print("Unique target values (rounded):", len(np.unique(np.round(y))))
print("Number of features:", len(feature_names))
print("Feature names:", feature_names)
```

```
Unique target values (rounded): 214
Number of features: 10
Feature names: ['age', 'sex', 'bmi', 'bp', 's1', 's2', 's3', 's4', 's5', 's
6']
```

4. Display the features and labels in tabular format:

```
In [21]: # Create DataFrame with features
df = pd.DataFrame(X, columns=feature_names)
# Add target column
```

```
df['target'] = y
# Display the first 10 rows
print(df.head(10))
```

```
        age       sex       bmi        bp        s1        s2        s3  \
0  0.038076  0.050680  0.061696  0.021872 -0.044223 -0.034821 -0.043401
1 -0.001882 -0.044642 -0.051474 -0.026328 -0.008449 -0.019163  0.074412
2  0.085299  0.050680  0.044451 -0.005670 -0.045599 -0.034194 -0.032356
3 -0.089063 -0.044642 -0.011595 -0.036656  0.012191  0.024991 -0.036038
4  0.005383 -0.044642 -0.036385  0.021872  0.003935  0.015596  0.008142
5 -0.092695 -0.044642 -0.040696 -0.019442 -0.068991 -0.079288  0.041277
6 -0.045472  0.050680 -0.047163 -0.015999 -0.040096 -0.024800  0.000779
7  0.063504  0.050680 -0.001895  0.066629  0.090620  0.108914  0.022869
8  0.041708  0.050680  0.061696 -0.040099 -0.013953  0.006202 -0.028674
9 -0.070900 -0.044642  0.039062 -0.033213 -0.012577 -0.034508 -0.024993

         s4        s5        s6  target
0 -0.002592  0.019907 -0.017646   151.0
1 -0.039493 -0.068332 -0.092204    75.0
2 -0.002592  0.002861 -0.025930   141.0
3  0.034309  0.022688 -0.009362   206.0
4 -0.002592 -0.031988 -0.046641   135.0
5 -0.076395 -0.041176 -0.096346    97.0
6 -0.039493 -0.062917 -0.038357   138.0
7  0.017703 -0.035816  0.003064    63.0
8 -0.002592 -0.014960  0.011349   110.0
9 -0.002592  0.067737 -0.013504   310.0
```

5. Split the dataset (70 % for training and 30% for testing):

In [22]:
```
# Split into train (70%) and test (30%)
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, rar
print("Training set size:", X_train.shape[0])
print("Test set size:", X_test.shape[0])
```

```
Training set size: 309
Test set size: 133
```

6. Standardize the features

In [23]:
```
# Standardize features
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

7. Create a KNN Regression model and fit with train data

In [24]:
```
# Train KNN Regression Model (K=5)
knn_model = KNeighborsRegressor(n_neighbors=5)
knn_model.fit(X_train, y_train)
```

Out[24]:

```
▾ KNeighborsRegressor
KNeighborsRegressor()
```

8. Run prediction on test data

In [25]:

```
# Predict on test data
y_pred = knn_model.predict(X_test)
```

9. Compute the Mean Squared Error

In [26]:

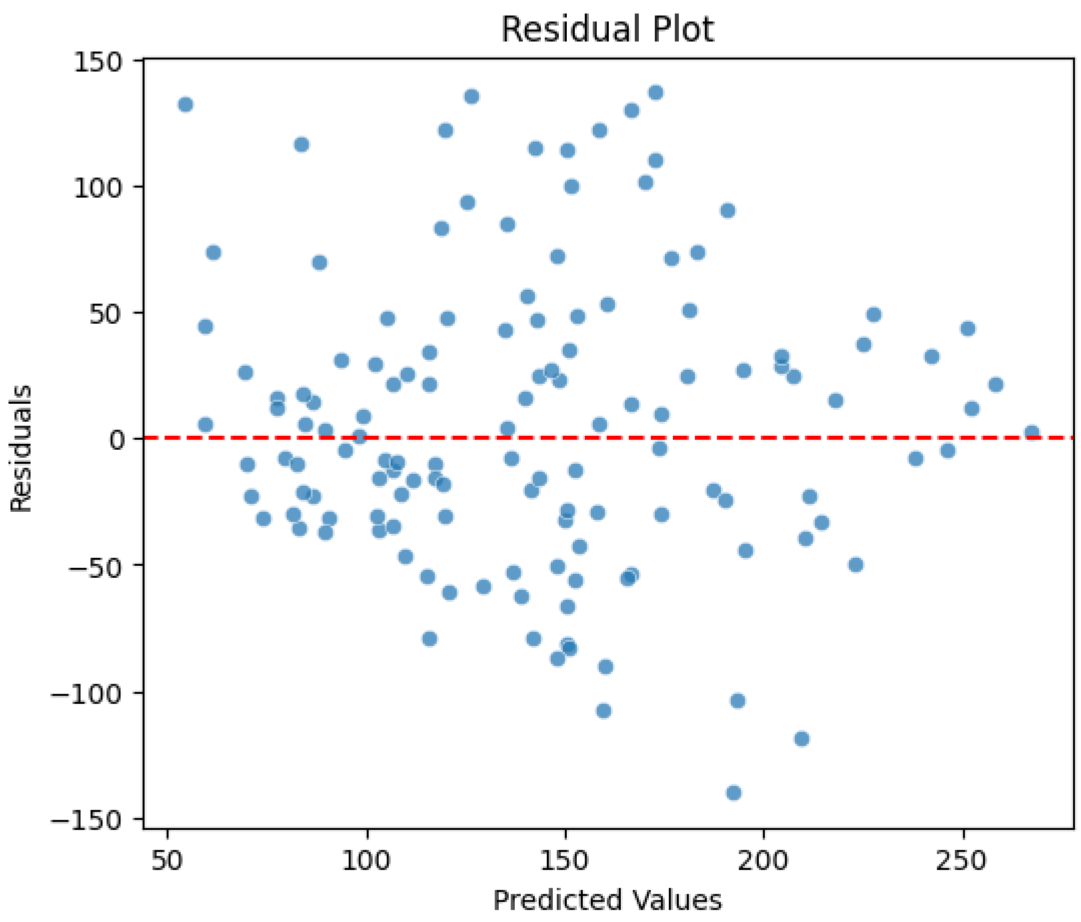
```
# Compute Mean Squared Error
mse = mean_squared_error(y_test, y_pred)
print(f"Mean Squared Error: {mse:.2f}")
```

```
Mean Squared Error: 3277.74
```

10. Plot a Residual Scatter Plot

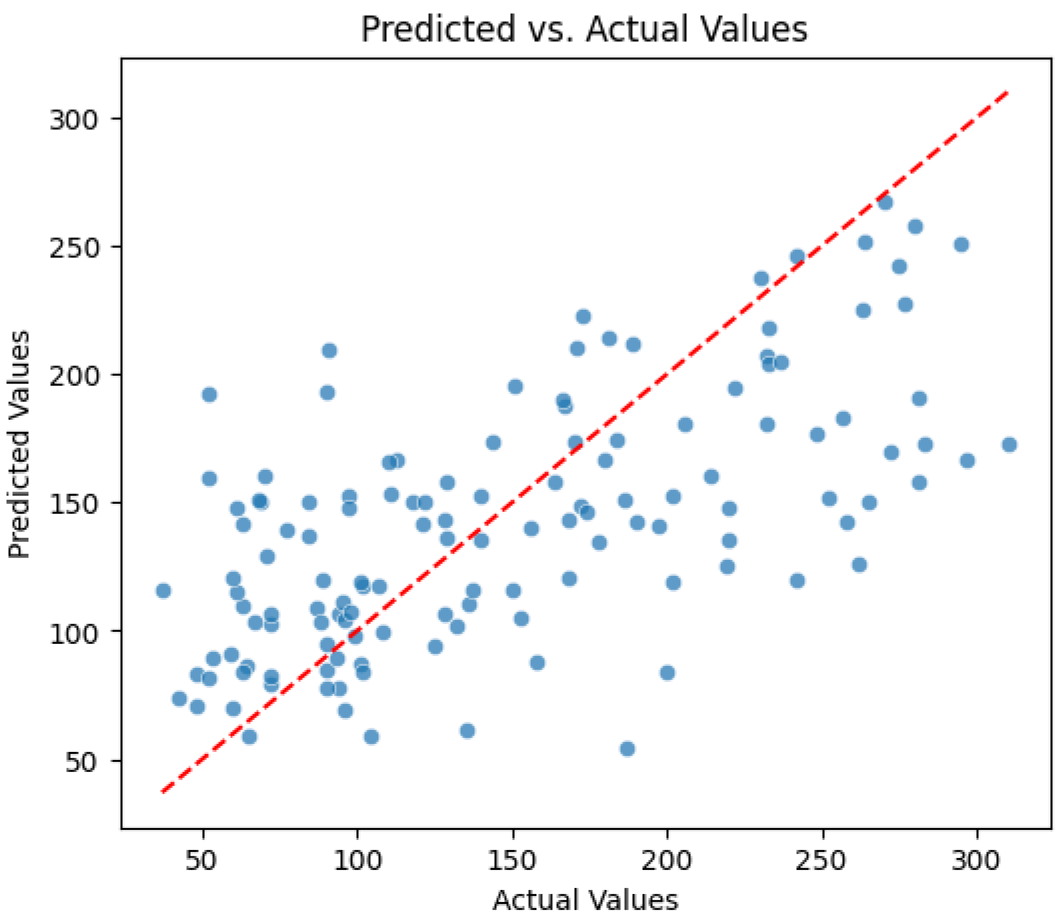
In [27]:

```
# Residual Plot
residuals = y_test - y_pred
plt.figure(figsize=(6, 5))
sns.scatterplot(x=y_pred, y=residuals, alpha=0.7)
plt.axhline(y=0, color='r', linestyle='--')
plt.xlabel('Predicted Values')
plt.ylabel('Residuals')
plt.title('Residual Plot')
plt.show()
```



11. Diplay Predicted vs Actual Values on test set

In [28]:
```
# Predicted vs. Actual Plot
plt.figure(figsize=(6, 5))
sns.scatterplot(x=y_test, y=y_pred, alpha=0.7)
plt.plot([y_test.min(), y_test.max()], [y_test.min(), y_test.max()], 'r--')
plt.xlabel('Actual Values')
plt.ylabel('Predicted Values')
plt.title('Predicted vs. Actual Values')
plt.show()
```



12. Calculate the Root Mean Squared Error

In [29]:
```
# Root Mean Squared Error
rmse = np.sqrt(mse)
print(f"Root Mean Squared Error: {rmse:.2f}")
```

```
Root Mean Squared Error: 57.25
```

13. Perform 5-Fold Cross-Validation

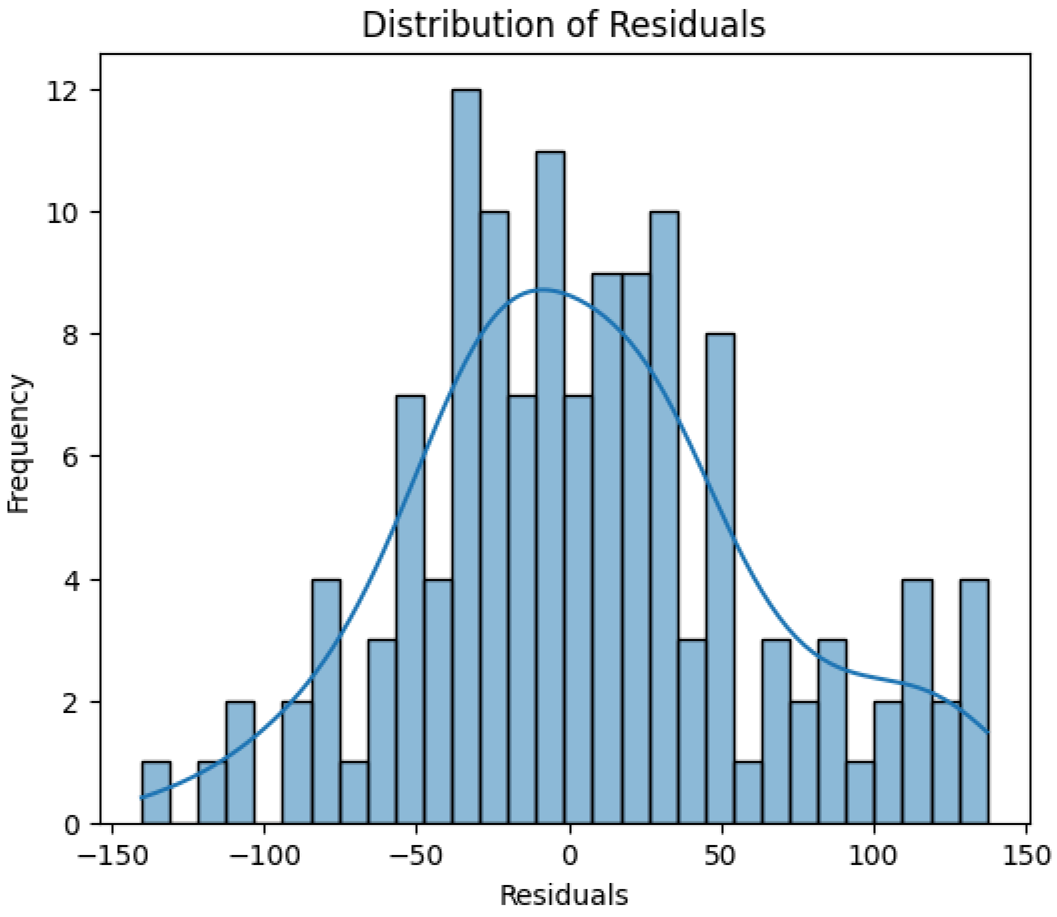
In [30]:
```
# Perform 5-Fold Cross-Validation
cv_scores = cross_val_score(knn_model, X, y, cv=5, scoring='neg_mean_squarec
cv_mse = -np.mean(cv_scores)
print(f"Cross-Validation MSE Scores: {-cv_scores}")
print(f"Mean Cross-Validation MSE: {cv_mse:.2f}")
```

```
Cross-Validation MSE Scores: [3167.19191011 4022.18067416 3556.56681818 355
1.07136364 3807.57      ]
Mean Cross-Validation MSE: 3620.92
```

14. Plot a Histogram of Residuals

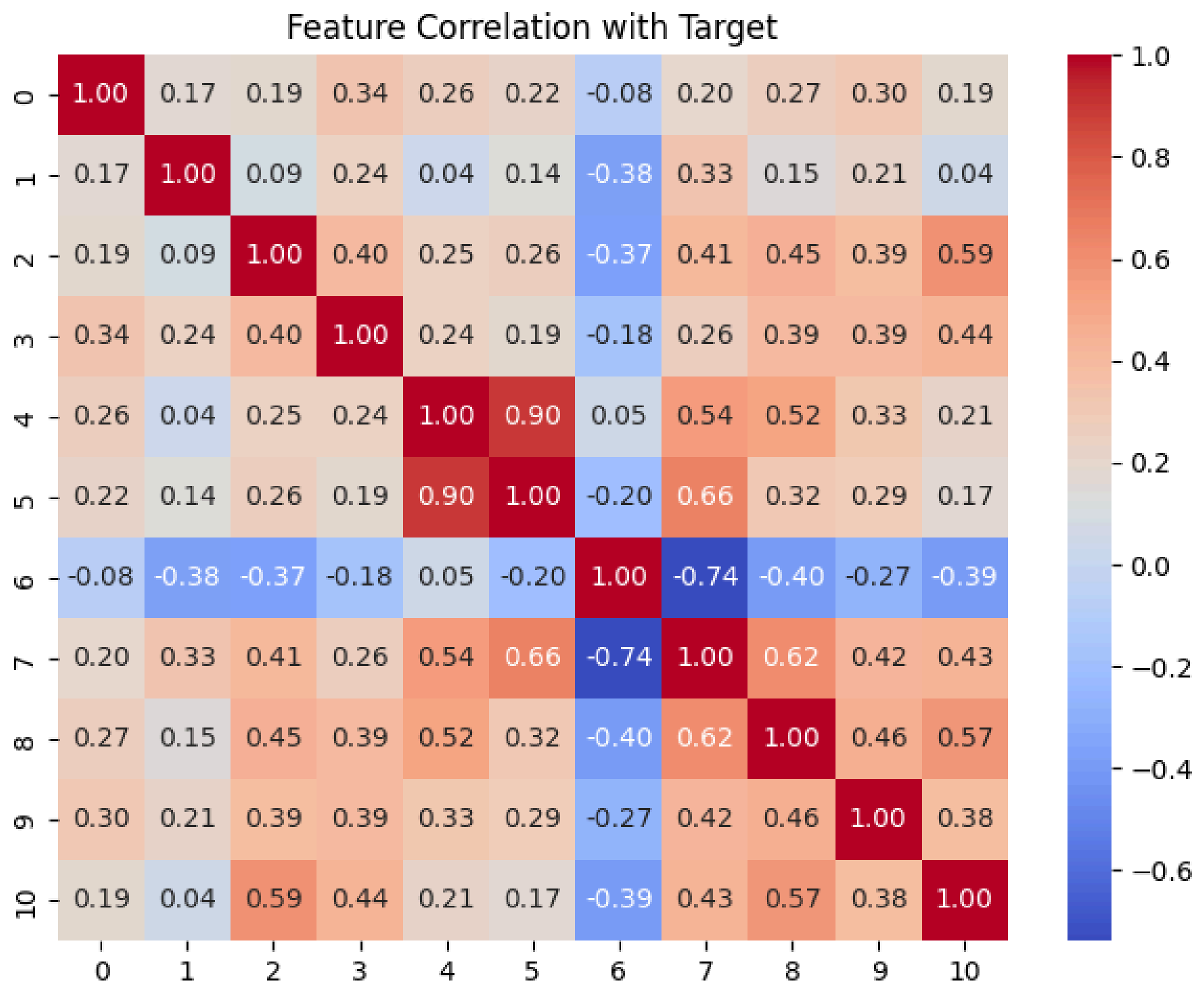
In [31]:
```
#Histogram of Residuals
plt.figure(figsize=(6, 5))
sns.histplot(residuals, bins=30, kde=True)
```

```
plt.xlabel('Residuals')
plt.ylabel('Frequency')
plt.title('Distribution of Residuals')
plt.show()
```



15. Show colleration between features and the target

```
In [32]: plt.figure(figsize=(8, 6))
         sns.heatmap(np.corrcoef(X.T, y), annot=True, fmt=".2f", cmap="coolwarm")
         plt.title("Feature Correlation with Target")
         plt.show()
```



	0	1	2	3	4	5	6	7	8	9	10
0	1.00	0.17	0.19	0.34	0.26	0.22	-0.08	0.20	0.27	0.30	0.19
1	0.17	1.00	0.09	0.24	0.04	0.14	-0.38	0.33	0.15	0.21	0.04
2	0.19	0.09	1.00	0.40	0.25	0.26	-0.37	0.41	0.45	0.39	0.59
3	0.34	0.24	0.40	1.00	0.24	0.19	-0.18	0.26	0.39	0.39	0.44
4	0.26	0.04	0.25	0.24	1.00	0.90	0.05	0.54	0.52	0.33	0.21
5	0.22	0.14	0.26	0.19	0.90	1.00	-0.20	0.66	0.32	0.29	0.17
6	-0.08	-0.38	-0.37	-0.18	0.05	-0.20	1.00	-0.74	-0.40	-0.27	-0.39
7	0.20	0.33	0.41	0.26	0.54	0.66	-0.74	1.00	0.62	0.42	0.43
8	0.27	0.15	0.45	0.39	0.52	0.32	-0.40	0.62	1.00	0.46	0.57
9	0.30	0.21	0.39	0.39	0.33	0.29	-0.27	0.42	0.46	1.00	0.38
10	0.19	0.04	0.59	0.44	0.21	0.17	-0.39	0.43	0.57	0.38	1.00

```
In [ ]:
```