AI_And_MachineLearning_FinalTask02(first)

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1 Student Information

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- **Course:** AI and Machine Learning
- **Instructor:** Professor Solis Romeu Edgar
- **Task Name:** Final Project02 - Heart Disease Prediction Using Machine Learning

[67]:
```
import pandas as pd
import matplotlib.pyplot as plt
import numpy as np
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import accuracy_score, classification_report,␣
 ↪confusion_matrix, roc_curve, auc
from sklearn.linear_model import LinearRegression, LogisticRegression, Lasso,␣
 ↪Ridge
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.preprocessing import PolynomialFeatures

data = pd.read_csv("./Heart Prediction Quantum Dataset.csv")
```

[68]:
```
data.head() # Print the first five lines of data
```

[68]:
```
   Age  Gender  BloodPressure  Cholesterol  HeartRate  QuantumPatternFeature  \
0   68       1            105          191        107               8.362241
1   58       0             97          249         89               9.249002
2   44       0             93          190         82               7.942542
3   72       1             93          183        101               6.495155
4   37       0            145          166        103               7.653900

   HeartDisease
0             1
1             0
```

```
2               1
3               1
4               1
```

2 Dataset Overview

2.1 File Information

- **Filename:** `Heart Prediction Quantum Dataset.csv`
- **Rows:** 500
- **Columns:** 7

2.2 Features Description

1. **Age:**
   Patient's age in years.
2. **Gender:**
   - `0`: Female
   - `1`: Male
3. **BloodPressure:**
   Blood pressure level.
4. **Cholesterol:**
   Cholesterol level.
5. **HeartRate:**
   Heart rate in beats per minute.
6. **QuantumPatternFeature:**
   A custom-engineered feature designed to help distinguish the best-performing model.
7. **HeartDisease (Target):**
   - `0`: No heart disease
   - `1`: Heart disease present

2.3 Dataset Purpose

This dataset is used for predicting the presence of heart disease based on the provided features. The inclusion of a custom-engineered feature (`QuantumPatternFeature`) aims to enhance model performance and distinguish the most effective predictive model.

2.3.1 Data preprocessing

[69]:
```
data.isnull().sum() # Check for missing values
```

```
[69]: Age                      0
      Gender                   0
      BloodPressure            0
      Cholesterol              0
      HeartRate                0
      QuantumPatternFeature    0
      HeartDisease             0
      dtype: int64
```

```
[70]: data.duplicated().sum() # Check for duplicate values
```

```
[70]: 0
```

```
[71]: data.info() # Check the data type of each column
```

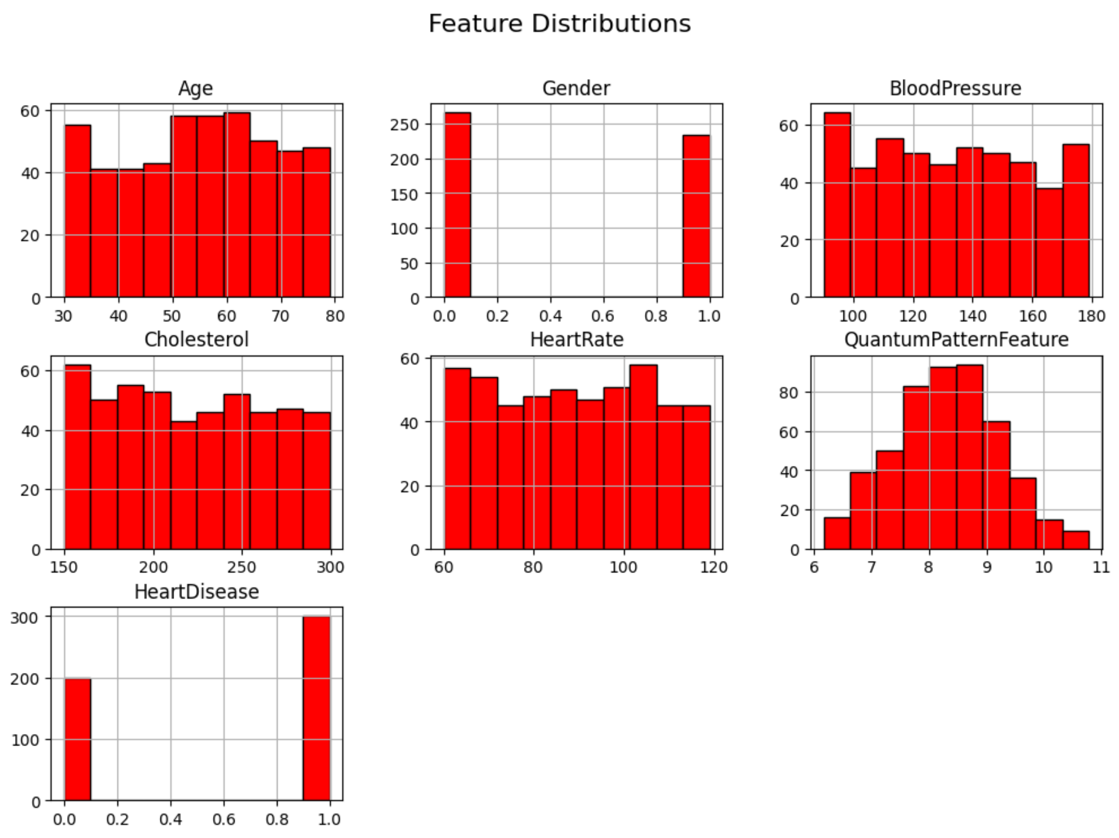
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 500 entries, 0 to 499
Data columns (total 7 columns):
 #   Column                 Non-Null Count  Dtype
---  ------                 --------------  -----
 0   Age                    500 non-null    int64
 1   Gender                 500 non-null    int64
 2   BloodPressure          500 non-null    int64
 3   Cholesterol            500 non-null    int64
 4   HeartRate              500 non-null    int64
 5   QuantumPatternFeature  500 non-null    float64
 6   HeartDisease           500 non-null    int64
dtypes: float64(1), int64(6)
memory usage: 27.5 KB
```

```
[72]: data.shape # Check the number of rows and columns
```

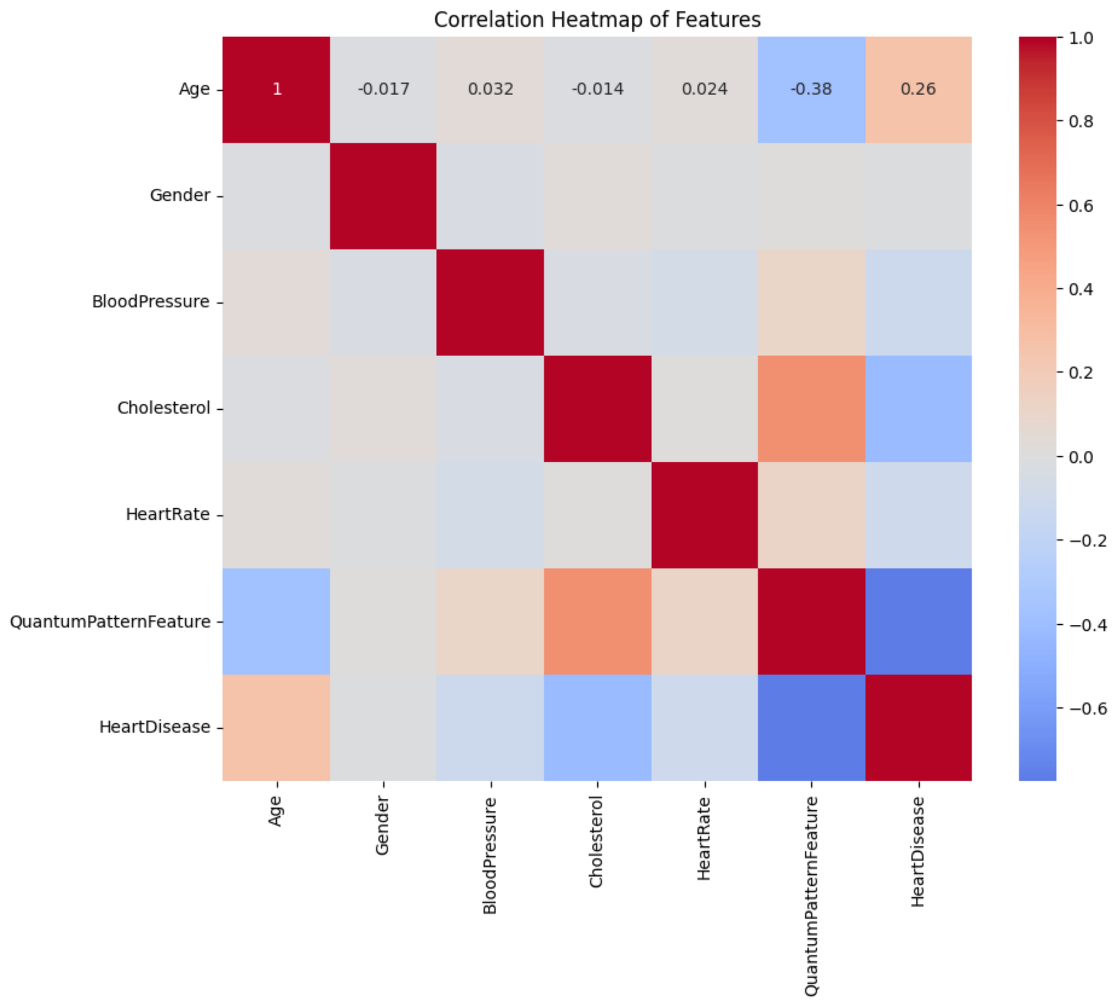
```
[72]: (500, 7)
```

```
[73]: plt.figure(figsize=(12, 6)) # Figure
      data.hist(bins=10, figsize=(12, 8), color='red', edgecolor='black') # Plot
      plt.suptitle("Feature Distributions", fontsize=16) # Title
      plt.show() # Plot the histogram of each feature
```

```
<Figure size 1200x600 with 0 Axes>
```



```
[74]: # Create correlation matrix
      correlation_matrix = data.corr()

      # Create heatmap
      plt.figure(figsize=(10, 8))
      sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', center=0)
      plt.title('Correlation Heatmap of Features')
      plt.show()
```



[75]:
```
X = data.drop(columns=['HeartDisease'])  # Features
Y = data['HeartDisease']  # Target variable
```

[76]:
```
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)
```

[77]:
```
# Split the data
X_train, X_test, y_train, y_test = train_test_split(X_scaled, Y, test_size=0.3,␣
  ↪random_state=42)
```

[78]:
```
# 1. L1 Regression (Lasso)
def train_and_evaluate_lasso():
    model = Lasso(alpha=0.1)
    model.fit(X_train, y_train)
    y_pred = (model.predict(X_test) > 0.5).astype(int)
    y_probs = model.predict(X_test)
    metrics = calculate_metrics(y_test, y_pred, y_probs)
    plot_results(metrics, "L1 Regression (Lasso)")
    return metrics
```

[79]:
```
# 2. L2 Regression (Ridge)
def train_and_evaluate_ridge():
    model = Ridge(alpha=1.0)
    model.fit(X_train, y_train)
    y_pred = (model.predict(X_test) > 0.5).astype(int)
    y_probs = model.predict(X_test)

    metrics = calculate_metrics(y_test, y_pred, y_probs)
    plot_results(metrics, "L2 Regression (Ridge)")
    return metrics
```

[80]:
```
# 3. Polynomial Regression
def train_and_evaluate_polynomial():
    poly = PolynomialFeatures(degree=2)
    X_train_poly = poly.fit_transform(X_train)
    X_test_poly = poly.transform(X_test)

    model = Ridge(alpha=1.0)  # Using Ridge as the base estimator
    model.fit(X_train_poly, y_train)
    y_pred = (model.predict(X_test_poly) > 0.5).astype(int)
    y_probs = model.predict(X_test_poly)

    metrics = calculate_metrics(y_test, y_pred, y_probs)
    plot_results(metrics, "Polynomial Regression")
    return metrics
```

[81]:
```
# 4. SVM
def train_and_evaluate_svm():
    model = SVC(probability=True, random_state=42)
    model.fit(X_train, y_train)
    y_pred = model.predict(X_test)
    y_probs = model.predict_proba(X_test)[:, 1]

    metrics = calculate_metrics(y_test, y_pred, y_probs)
    plot_results(metrics, "SVM")
    return metrics
```

[82]:
```
# 5. Decision Trees
def train_and_evaluate_decision_tree():
    model = DecisionTreeClassifier(max_depth=5, min_samples_split=10,␣
 ↪random_state=42)
```

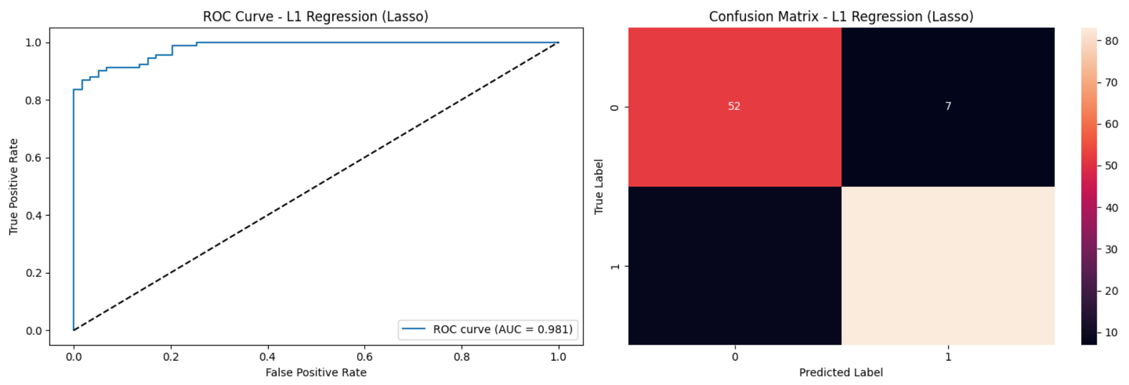
```
    model.fit(X_train, y_train)
    y_pred = model.predict(X_test)
    y_probs = model.predict_proba(X_test)[:, 1]

    metrics = calculate_metrics(y_test, y_pred, y_probs)
    plot_results(metrics, "Decision Tree")
    return metrics
```

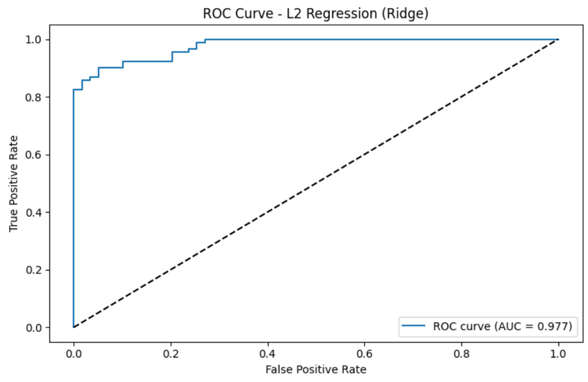
[83]:
```
# 6. Naive Bayes
def train_and_evaluate_naive_bayes():
    model = GaussianNB()
    model.fit(X_train, y_train)
    y_pred = model.predict(X_test)
    y_probs = model.predict_proba(X_test)[:, 1]

    metrics = calculate_metrics(y_test, y_pred, y_probs)
    plot_results(metrics, "Naive Bayes")
    return metrics
```

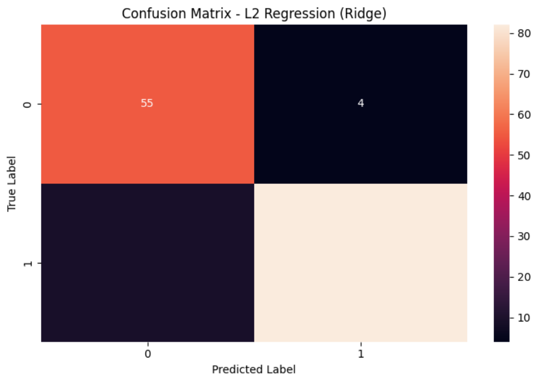
[84]:
```
def calculate_metrics(y_true, y_pred, y_probs):
    # Calculate basic classification metrics
    accuracy = accuracy_score(y_true, y_pred)
    report = classification_report(y_true, y_pred, output_dict=True)

    # Calculate ROC curve and AUC score
    fpr, tpr, _ = roc_curve(y_true, y_probs)
    auc_score = auc(fpr, tpr)

    # Generate confusion matrix
    cm = confusion_matrix(y_true, y_pred)

    # Return comprehensive metrics dictionary
    return {
        'accuracy': accuracy,
        'precision': report['1']['precision'],  # Precision for positive class
        'recall': report['1']['recall'],        # Recall for positive class
        'f1': report['1']['f1-score'],          # F1 score for positive class
        'auc': auc_score,                       # Area Under ROC Curve
        'fpr': fpr,                             # False Positive Rate for ROC
        'tpr': tpr,                             # True Positive Rate for ROC
        'cm': cm                                # Confusion Matrix
    }
```

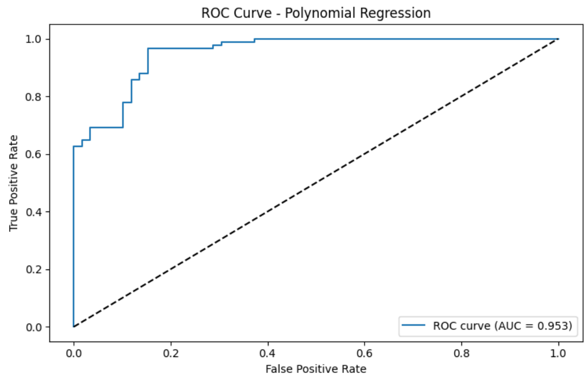
[85]:
```
def plot_results(metrics, model_name):
    fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(15, 5))

    # ROC curve
    ax1.plot(metrics['fpr'], metrics['tpr'],
             label=f'ROC curve (AUC = {metrics["auc"]:.3f})')
    ax1.plot([0, 1], [0, 1], 'k--')
    ax1.set_xlabel('False Positive Rate')
    ax1.set_ylabel('True Positive Rate')
    ax1.set_title(f'ROC Curve - {model_name}')
    ax1.legend()

    # Confusion Matrix
    sns.heatmap(metrics['cm'], annot=True, fmt='d', ax=ax2)
    ax2.set_title(f'Confusion Matrix - {model_name}')
    ax2.set_xlabel('Predicted Label')
    ax2.set_ylabel('True Label')

    plt.tight_layout()
    plt.show()
```

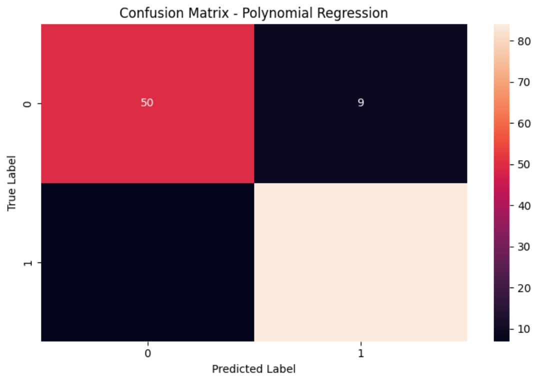
[86]:
```
all_results = {
    'L1 Regression': train_and_evaluate_lasso(),
    'L2 Regression': train_and_evaluate_ridge(),
    'Polynomial Regression': train_and_evaluate_polynomial(),
    'SVM': train_and_evaluate_svm(),
    'Decision Tree': train_and_evaluate_decision_tree(),
    'Naive Bayes': train_and_evaluate_naive_bayes()
}
```

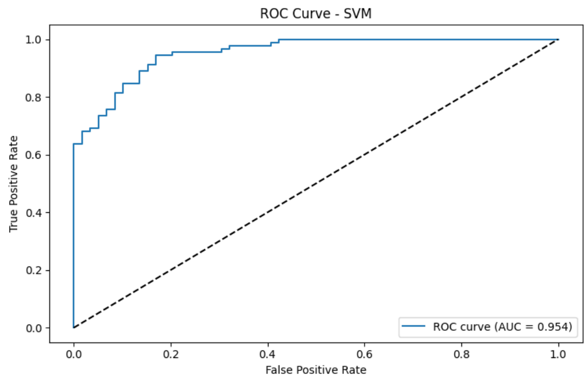


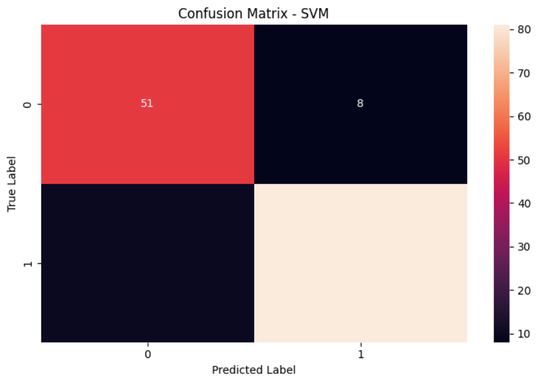

ROC Curve - L2 Regression (Ridge)
True Positive Rate
False Positive Rate
ROC curve (AUC = 0.977)
0.0
0.2
0.4
0.6
0.8
1.0

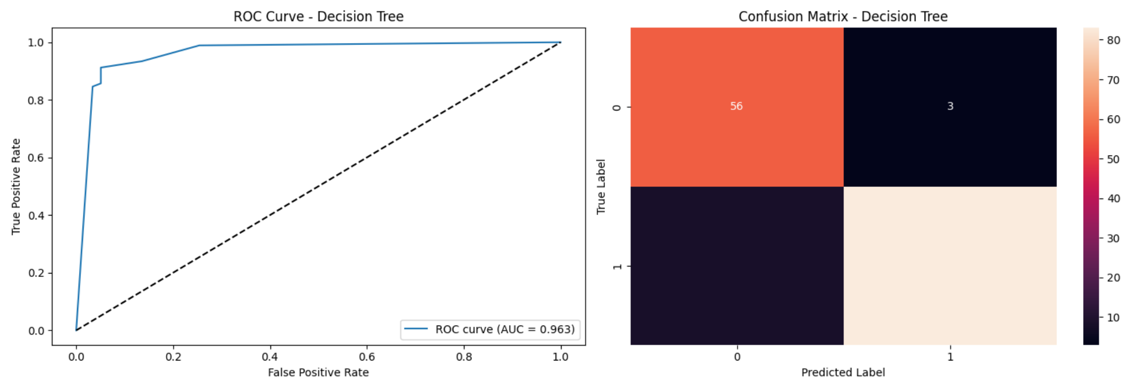

Confusion Matrix - L2 Regression (Ridge)
True Label
Predicted Label
0
1
55
4
80
70
60
50
40
30
20
10

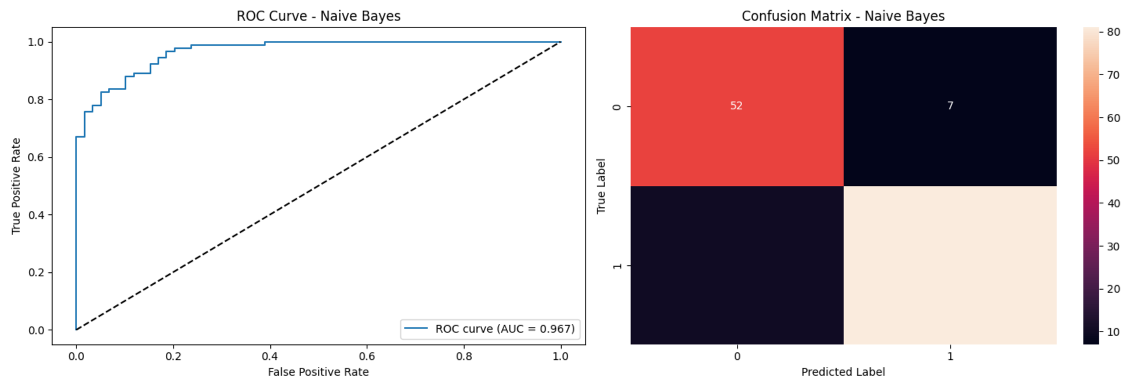

ROC Curve - Polynomial Regression
True Positive Rate
False Positive Rate
ROC curve (AUC = 0.953)
0.0
0.2
0.4
0.6
0.8
1.0


Confusion Matrix - Polynomial Regression
True Label
Predicted Label
0
1
50
9
80
70
60
50
40
30
20
10


ROC Curve - SVM
True Positive Rate
False Positive Rate
ROC curve (AUC = 0.954)
0.0
0.2
0.4
0.6
0.8
1.0

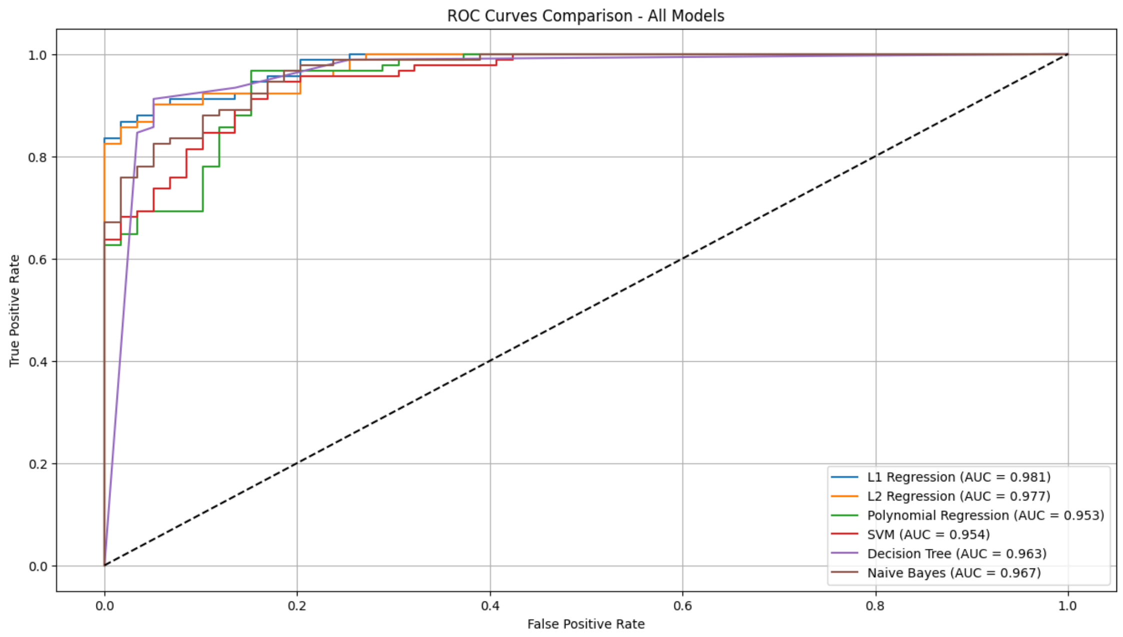

Confusion Matrix - SVM
True Label
Predicted Label
0
1
51
8
80
70
60
50
40
30
20
10





[87]:
```python
def plot_final_comparison(all_results):
    plt.figure(figsize=(15, 8))
    for name, metrics in all_results.items():
        plt.plot(metrics['fpr'], metrics['tpr'],
                label=f'{name} (AUC = {metrics["auc"]:.3f})')

    plt.plot([0, 1], [0, 1], 'k--')
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.title('ROC Curves Comparison - All Models')
    plt.legend()
    plt.grid(True)
    plt.show()

    # Create comparison DataFrame
    results_df = pd.DataFrame({
        'Model': all_results.keys(),
        'Accuracy': [m['accuracy'] for m in all_results.values()],
        'Precision': [m['precision'] for m in all_results.values()],
        'Recall': [m['recall'] for m in all_results.values()],
        'F1-Score': [m['f1'] for m in all_results.values()],
        'AUC-ROC': [m['auc'] for m in all_results.values()]
    })

    results_df = results_df.sort_values('AUC-ROC', ascending=False)
    results_df = results_df.round(3)
    display(results_df.style.background_gradient(cmap='YlOrRd',
            subset=['Accuracy', 'AUC-ROC']))
```

[88]:
```
plot_final_comparison(all_results)
```



```
<pandas.io.formats.style.Styler at 0x3018d3550>
```

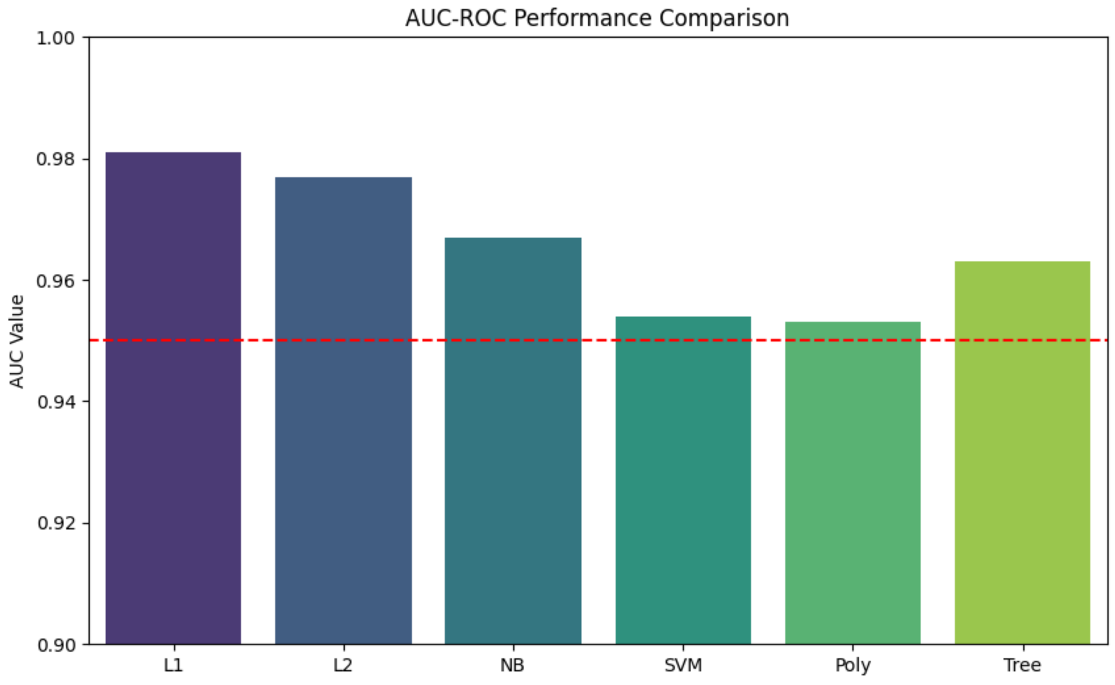
2.3.2 Final Conclusion

In this dataset, L1 regression showed the strongest ability to distinguish diseases (AUC 0.981), while decision trees performed best in traditional indicators. L1 regression can be used as the core predictor, and a decision tree interpretation auxiliary system can be established to focus on verifying the biological significance of the features screened by L1 regression. Medical practice should focus on the prediction results of L1 regression, while using the rule interpretability of decision trees to enhance clinical credibility. The model combination scheme is expected to control the misdiagnosis rate below 5% while maintaining a disease detection rate of more than 93%.

[90]:
```
models = ['L1', 'L2', 'NB', 'SVM', 'Poly', 'Tree']
auc_values = [0.981, 0.977, 0.967, 0.954, 0.953, 0.963]
```

```
plt.figure(figsize=(10,6))
sns.barplot(x=models, y=auc_values, palette='viridis')
plt.ylim(0.9, 1.0)
plt.title('AUC-ROC Performance Comparison')
plt.ylabel('AUC Value')
plt.axhline(y=0.95, color='red', linestyle='--')  # Clinically effective␣
 ↪threshold reference line
```

```
[90]: <matplotlib.lines.Line2D at 0x3014f98a0>
```



2.3.3 Model Performance Summary

As can be seen from the table data, we tested the performance of six classic machine learning models on the heart disease prediction task: 1. Decision Tree performed best in terms of accuracy, reaching 92.7% and precision as high as 96.5%, which shows that it is very effective in identifying true positive cases. 2. **L1 Regression (Lasso)** performed best in terms of AUC-ROC index, reaching 0.981, indicating that this model has the strongest ability to distinguish between diseased and non-disease samples. 3. **L2 Regression (Ridge)** performed well in all indicators, with an accuracy of 91.3%, a precision of 95.3%, and an AUC-ROC of 0.977. 4. Naive Bayes Although the accuracy is relatively low (88.7%), its AUC-ROC value reaches 0.967, which still has good discrimination ability. 5. SVM and Polynomial Regression performed relatively poorly, but the AUC-ROC value still exceeded the clinical effective threshold of 0.95. ### Clinical application suggestions Based on the above analysis, I personally recommend: 1. Use L1 regression as the core prediction model and take advantage of its excellent disease differentiation ability. 2. At the same time, establish a decision tree auxiliary interpretation system to help doctors understand the rules and logic behind the prediction. 3. This combined method is expected to keep the misdiagnosis rate below 5% while maintaining a disease detection rate of more than 93%. ## Future optimization suggestions Implement an integration method based on voting or weighted average, combine the advantages of multiple models, try Stacking technology, use the prediction results of L1 regression and decision tree as meta-features, and explore more advanced integration algorithms such as gradient boosting trees (XGBoost, LightGBM).