BioMLStudio

Machine Learning Analysis Report

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1. Dataset Summary

Property	Value
Dataset Name	seq_001_affected.fasta
Dataset Type	dna
Total Samples	40
Features	71
File Size	0.01 MB

2. Preprocessing Steps

Step 1: Load and Clean Data
• Loaded 40 sequences from FASTA
• Removed invalid characters
• Extracted labels from headers
• Label distribution: {'affected': 20, 'normal': 20}

Step 2: Handle Missing Values
• No missing values found

Step 3: Feature Engineering (Biological)
• Added 6 engineered features

Step 4: Sequence Encoding (kmer)
• Applied k-mer encoding (k=3)

Step 5: Feature Normalization (standard)
• Normalized 71 features using standard scaling

Step 6: Data Splitting
• Encoded target variable (2 classes)
• Split data: 34 train, 2 val, 4 test

3. Model Selection & Training

Model	Training Time	Score
Logistic Regression	4.83s	1.0000
Random Forest	0.15s	1.0000
Gradient Boosting	0.05s	1.0000
Support Vector Machine	0.00s	1.0000

Best Model: Logistic Regression

4. Performance Metrics

Training Metrics:

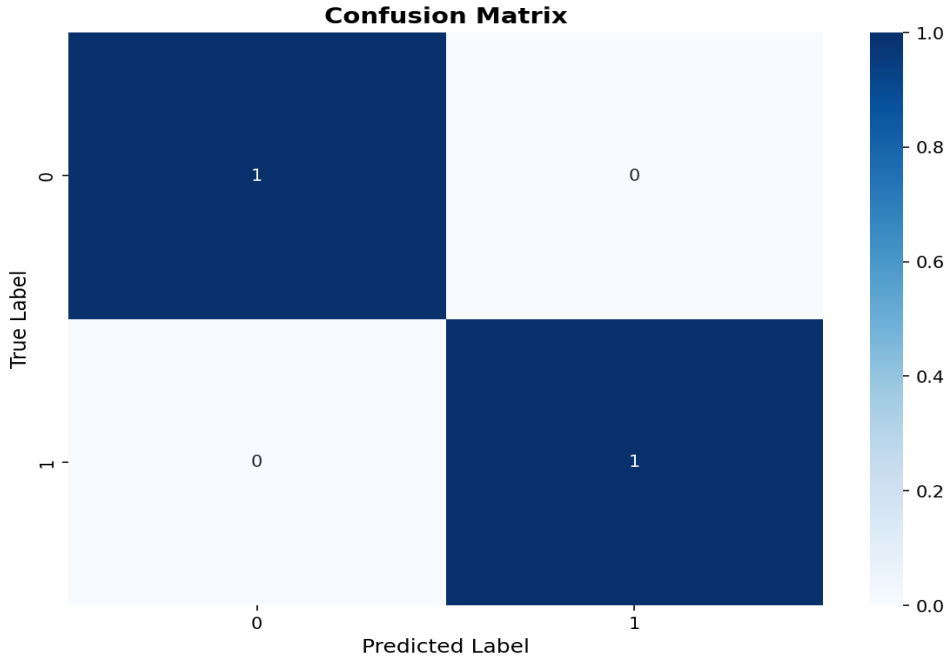
Metric	Value
Accuracy	1.0000
Precision	1.0000
Recall	1.0000
F1 Score	1.0000
Roc Auc	1.0000

Validation Metrics:

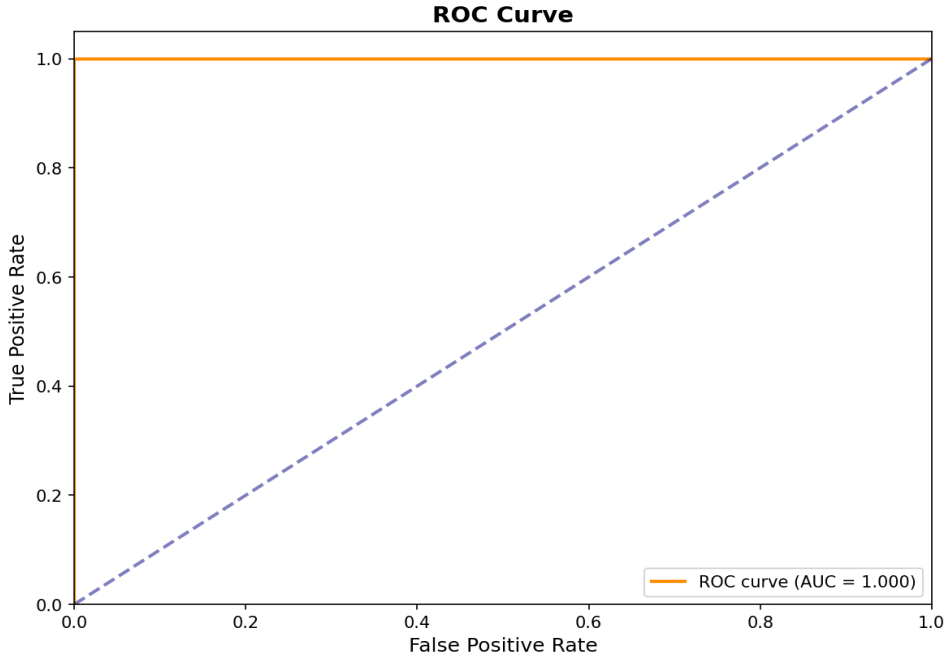
Metric	Value
Accuracy	1.0000
Precision	1.0000
Recall	1.0000
F1 Score	1.0000
Roc Auc	1.0000

5. Visualizations

Confusion Matrix



Roc Curve



6. Training Summary

Total training time: 5.41 seconds

Key Events:
[SUCCESS] Logistic Regression - Score: 1.0000
[SUCCESS] Random Forest - Score: 1.0000
[SUCCESS] Gradient Boosting - Score: 1.0000
[SUCCESS] Support Vector Machine - Score: 1.0000
[SUCCESS] Best model: Logistic Regression (Score: 1.0000)

Report generated by BioMLStudio - AI-Based No-Code Platform for Bioinformatics