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: 28 train, 4 val, 8 test

3. Model Selection & Training

Model	Training Time	Score
Logistic Regression	1.66s	1.0000
Random Forest	0.14s	1.0000
Gradient Boosting	0.05s	1.0000

Best Model: Logistic Regression

4. Performance Metrics

Training Metrics:

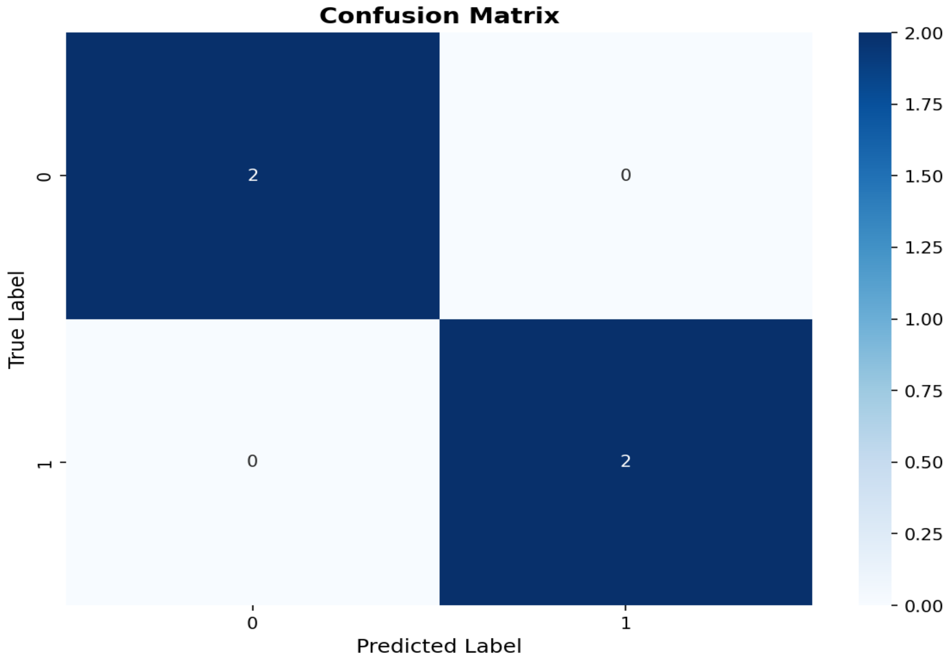
Metric	Value
Accuracy	1.0000
Precision	1.0000
Recall	1.0000
F1 Score	1.0000
Roc Auc	1.0000

Validation Metrics:

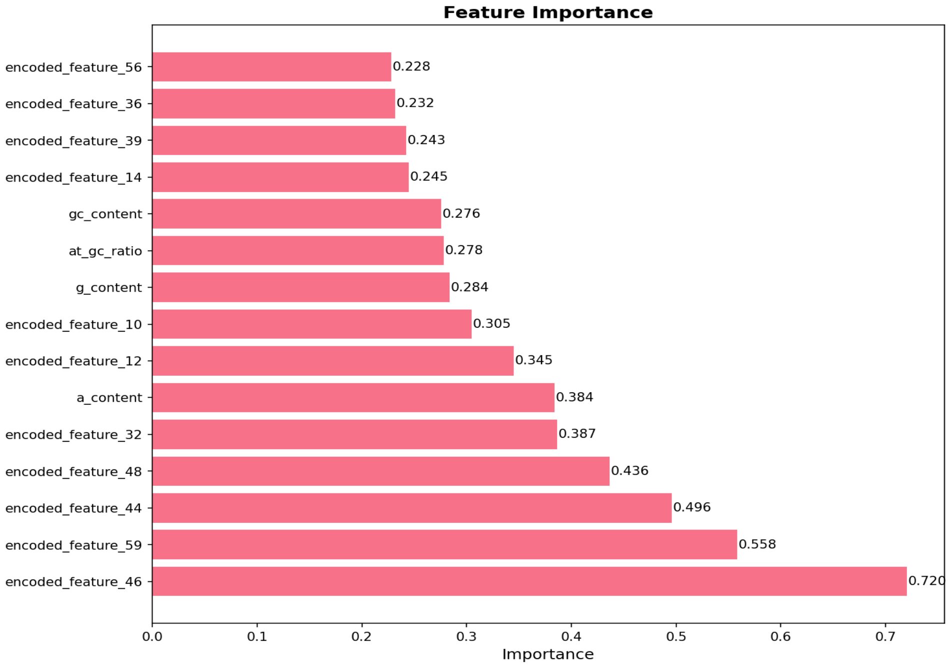
Metric	Value
Accuracy	1.0000
Precision	1.0000
Recall	1.0000
F1 Score	1.0000
Roc Auc	1.0000

5. Visualizations

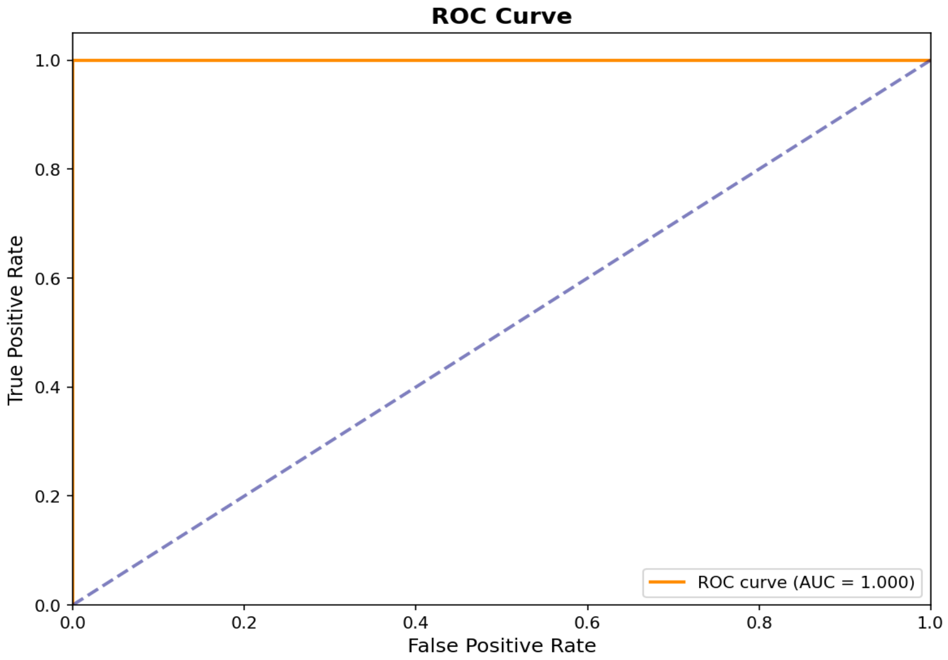
Confusion Matrix



Feature Importance



Roc Curve


ROC Curve
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0
ROC curve (AUC = 1.000)

6. Training Summary

Total training time: 2.49 seconds

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

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