

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 |
|---------------------|---------------|--------|
| Random Forest | 0.16s | 1.0000 |
| Logistic Regression | 1.39s | 1.0000 |
| XGBoost | 0.17s | 1.0000 |

Best Model: Random Forest

4. Performance Metrics

Training Metrics:

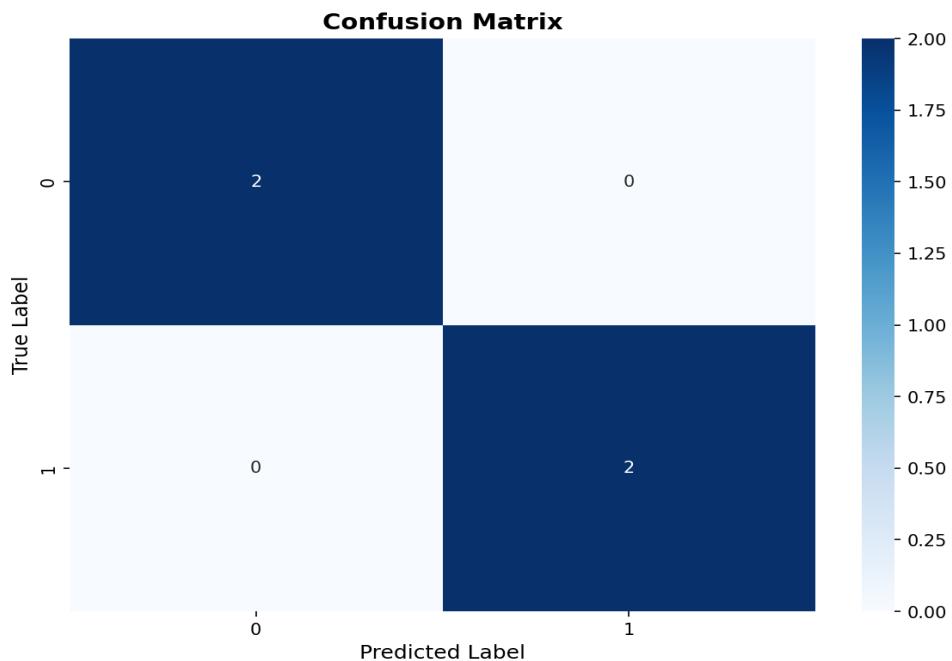
| Metric | Value |
|-----------|--------|
| Accuracy | 1.0000 |
| Precision | 1.0000 |
| Recall | 1.0000 |
| F1 Score | 1.0000 |
| Roc Auc | 1.0000 |

Validation Metrics:

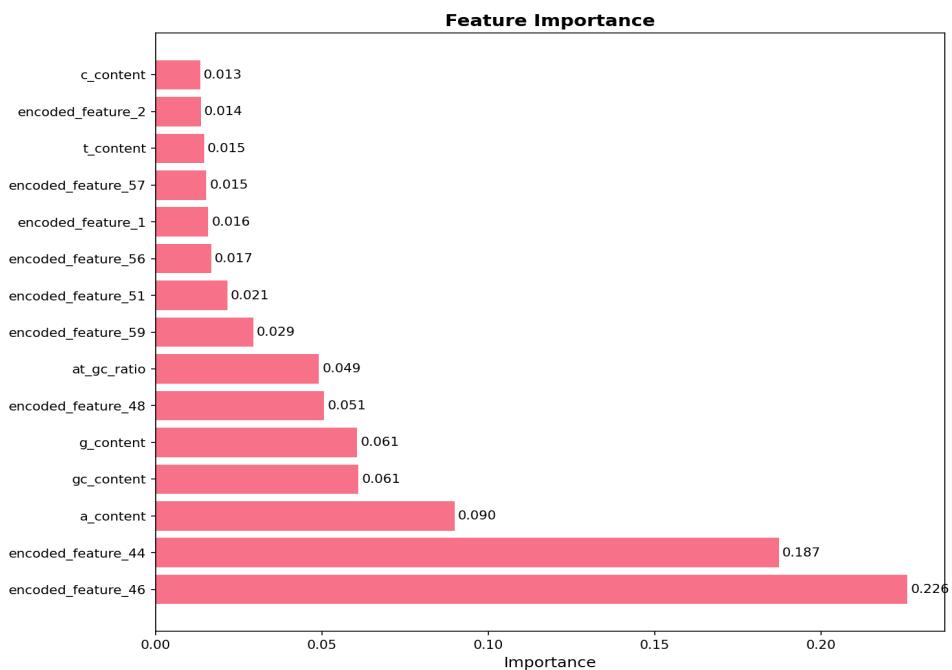
| Metric | Value |
|-----------|--------|
| Accuracy | 1.0000 |
| Precision | 1.0000 |
| Recall | 1.0000 |
| F1 Score | 1.0000 |
| Roc Auc | 1.0000 |

5. Visualizations

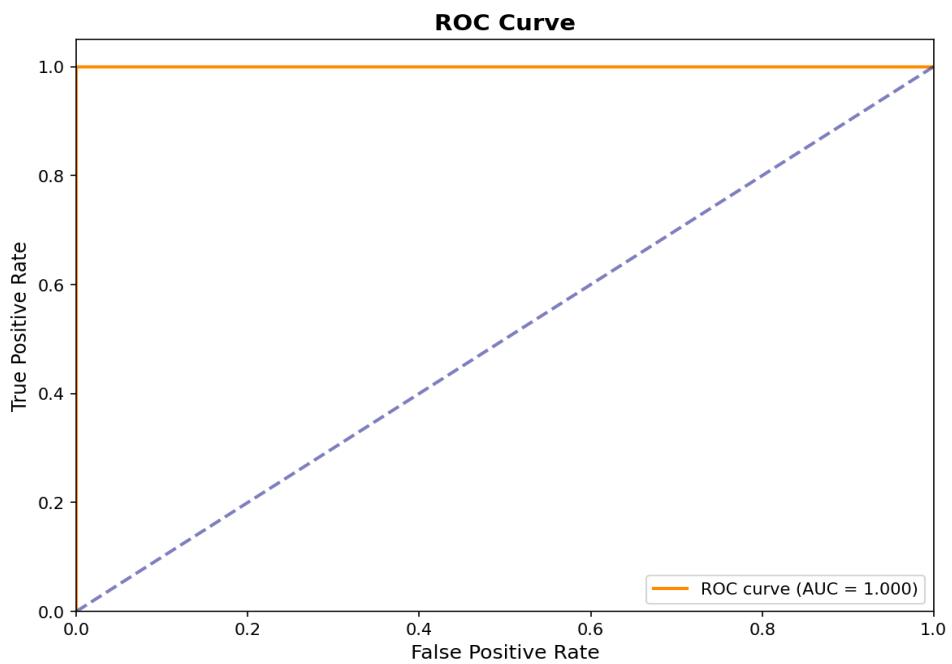
Confusion Matrix



Feature Importance



Roc Curve



6. Training Summary

Total training time: 2.58 seconds

Key Events:

[SUCCESS] Random Forest - Score: 1.0000
[SUCCESS] Logistic Regression - Score: 1.0000
[SUCCESS] XGBoost - Score: 1.0000
[SUCCESS] Best model: Random Forest (Score: 1.0000)

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