

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	7
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 (auto)

- Unknown encoding method: auto

Step 5: Feature Normalization (standard)

- Normalized 7 features using standard scaling

Step 6: Data Splitting

- Encoded target variable (2 classes)
- Split data: 33 train, 3 val, 4 test

3. Model Selection & Training

Model	Training Time	Score
Logistic Regression	6.33s	0.6667
Random Forest	3.82s	0.6667
Gradient Boosting	0.20s	0.6667
Support Vector Machine	0.21s	0.6667
XGBoost	2.90s	0.6667

Best Model: Logistic Regression

4. Performance Metrics

Training Metrics:

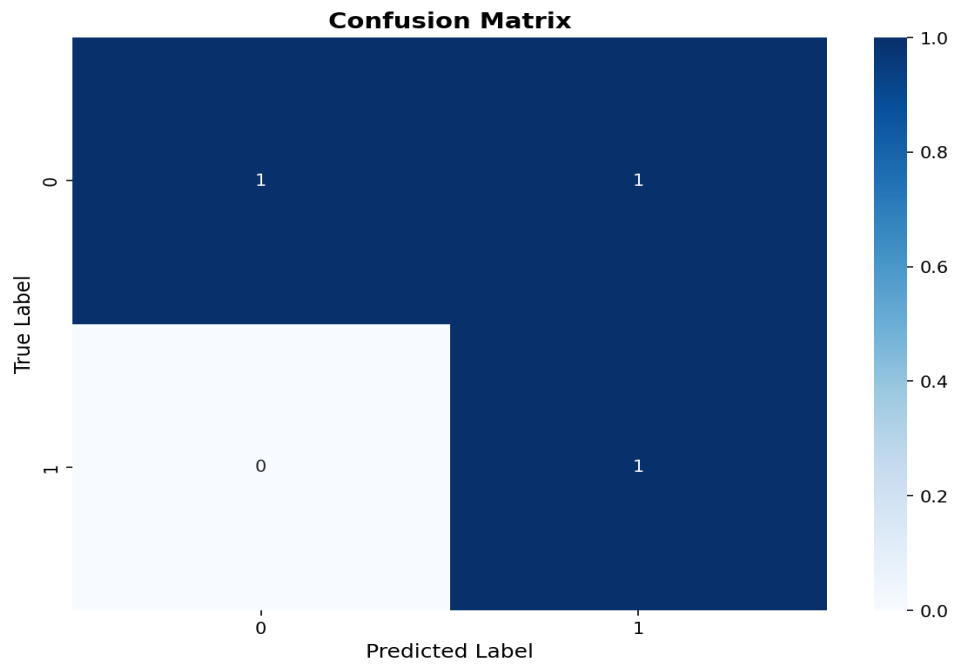
Metric	Value
Accuracy	0.8182
Precision	0.8182
Recall	0.8182
F1 Score	0.8182
Roc Auc	0.9210

Validation Metrics:

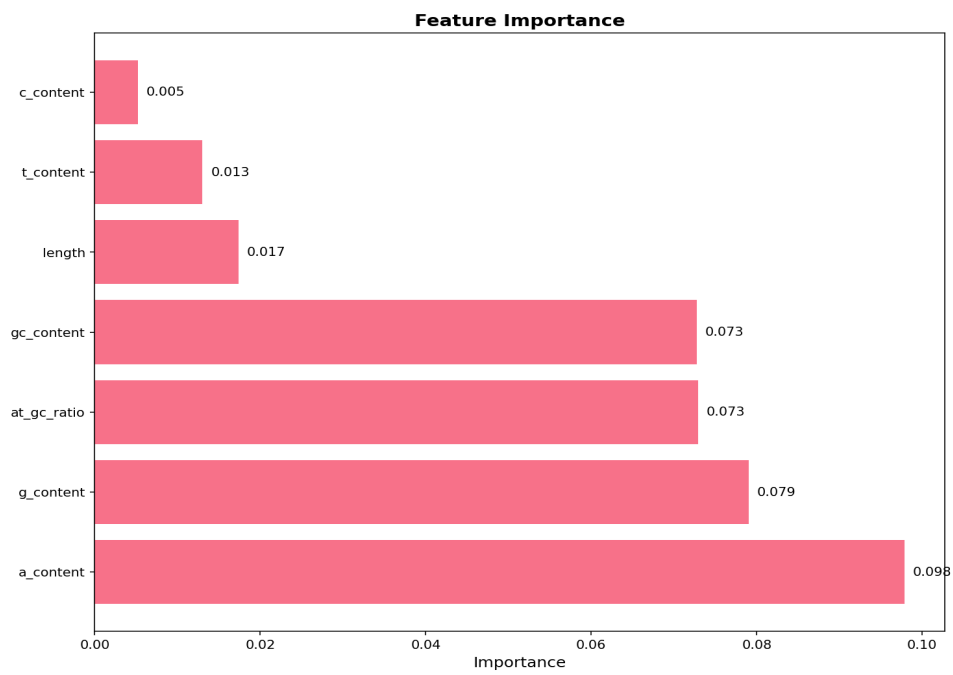
Metric	Value
Accuracy	0.6667
Precision	0.8333
Recall	0.6667
F1 Score	0.6667
Roc Auc	0.7500

5. Visualizations

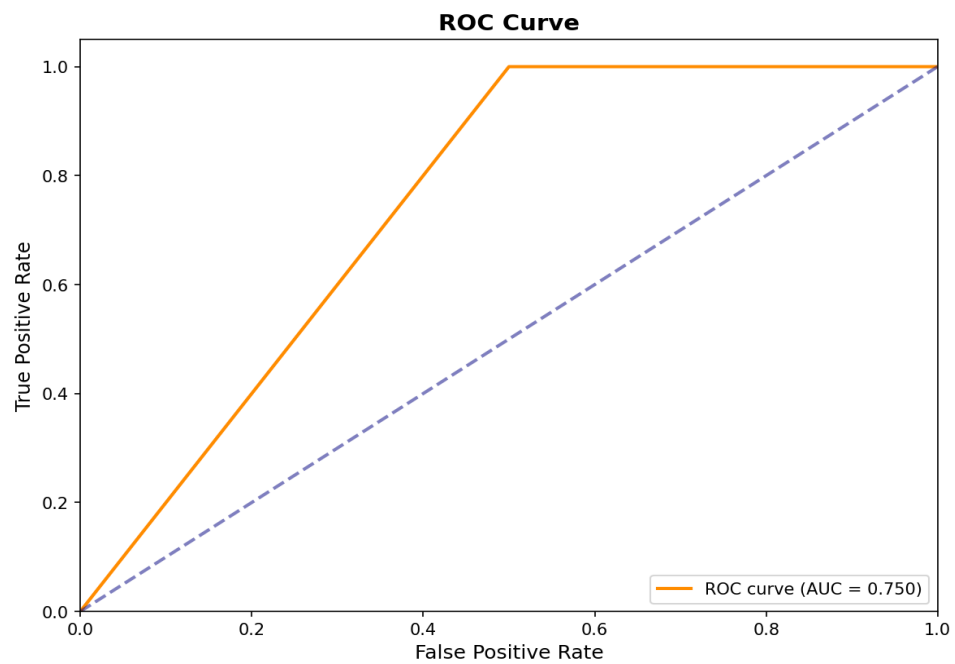
Confusion Matrix



Feature Importance



Roc Curve



6. Training Summary

Total training time: 14.85 seconds

Key Events:

[SUCCESS] Logistic Regression - Score: 0.6667

[SUCCESS] Random Forest - Score: 0.6667

[SUCCESS] Gradient Boosting - Score: 0.6667

[SUCCESS] Support Vector Machine - Score: 0.6667

[SUCCESS] XGBoost - Score: 0.6667

[SUCCESS] Best model: Logistic Regression (Score: 0.6667)

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

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