

# BioMLStudio

## Machine Learning Analysis Report

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# 1. Dataset Summary

Property	Value
Dataset Name	seq_001_affected
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: 28 train, 4 val, 8 test

### 3. Model Selection & Training

Model	Training Time	Score
Logistic Regression	0.30s	0.7500
Random Forest	4.07s	0.7500
Gradient Boosting	0.20s	0.7500

**Best Model:** Logistic Regression

## 4. Performance Metrics

### Training Metrics:

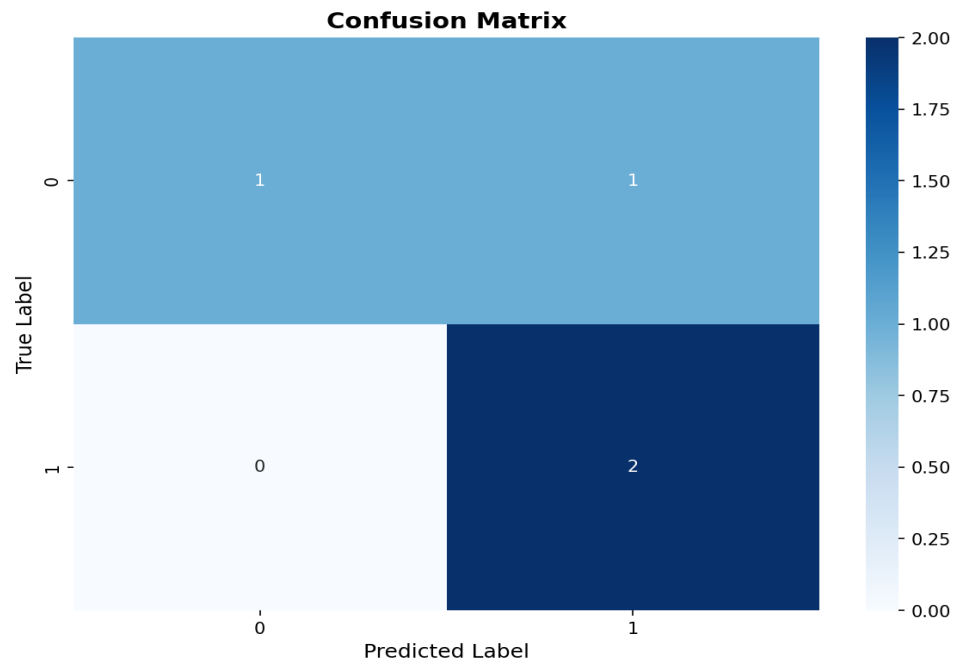
Metric	Value
Accuracy	0.8214
Precision	0.8231
Recall	0.8214
F1 Score	0.8212
Roc Auc	0.8929

### Validation Metrics:

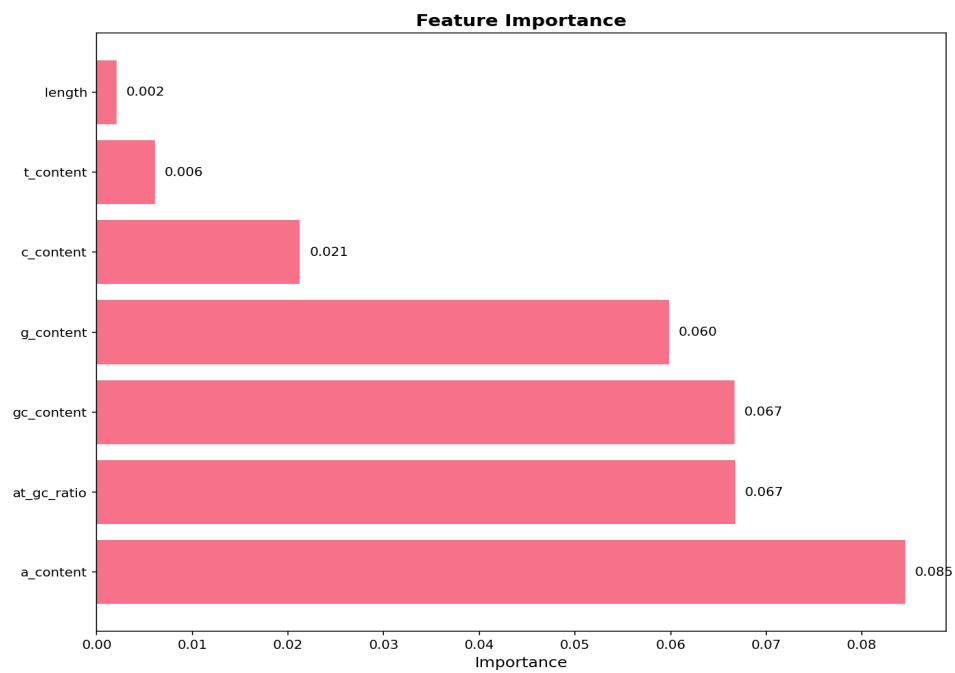
Metric	Value
Accuracy	0.7500
Precision	0.8333
Recall	0.7500
F1 Score	0.7333
Roc Auc	0.7500

## 5. Visualizations

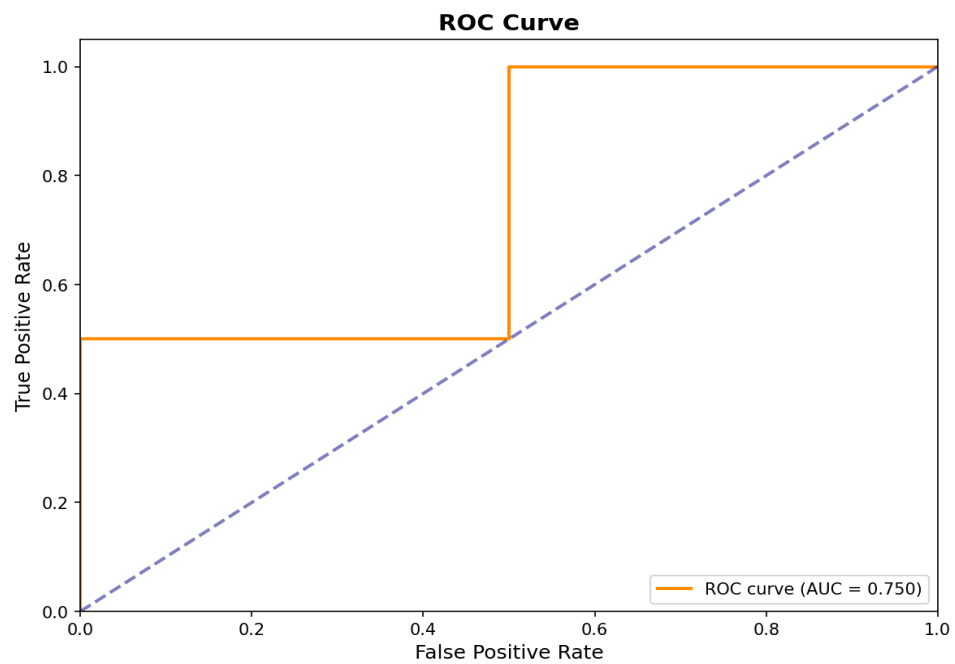
### Confusion Matrix



### Feature Importance



### Roc Curve



## 6. Training Summary

**Total training time:** 6.32 seconds

**Key Events:**

[SUCCESS] Logistic Regression - Score: 0.7500

[SUCCESS] Random Forest - Score: 0.7500

[SUCCESS] Gradient Boosting - Score: 0.7500

[SUCCESS] Best model: Logistic Regression (Score: 0.7500)



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

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