

# BioMLStudio

## Machine Learning Analysis Report

Generated: December 04, 2025 at 11:53

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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	1.48s	1.0000
Random Forest	0.13s	1.0000
Gradient Boosting	0.04s	1.0000

**Best Model:** Logistic Regression

## 4. Performance Metrics

### Training Metrics:

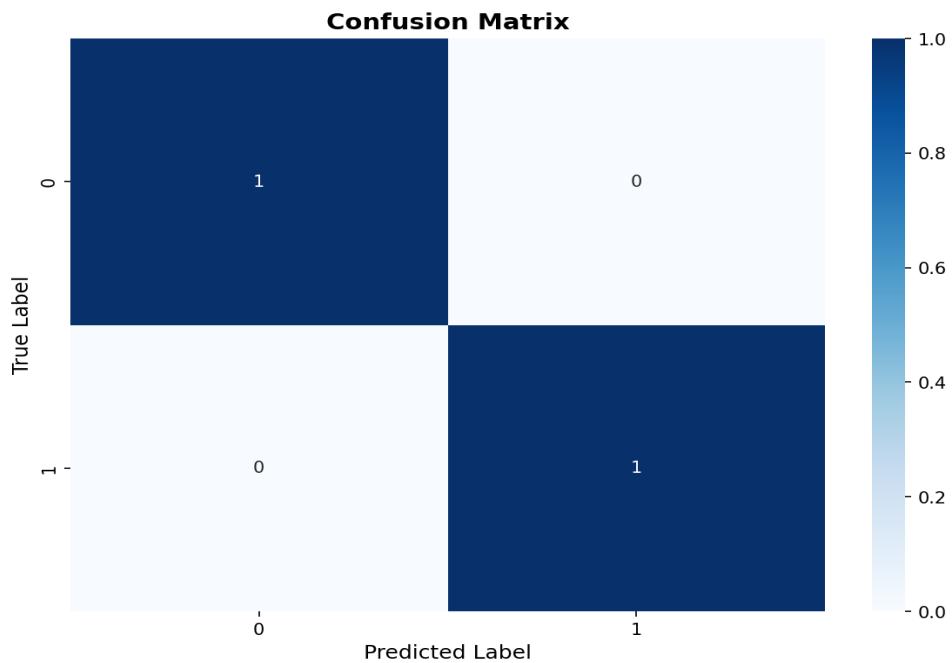
Metric	Value
Accuracy	1.0000
Precision	1.0000
Recall	1.0000
F1 Score	1.0000
Roc Auc	1.0000

### Validation Metrics:

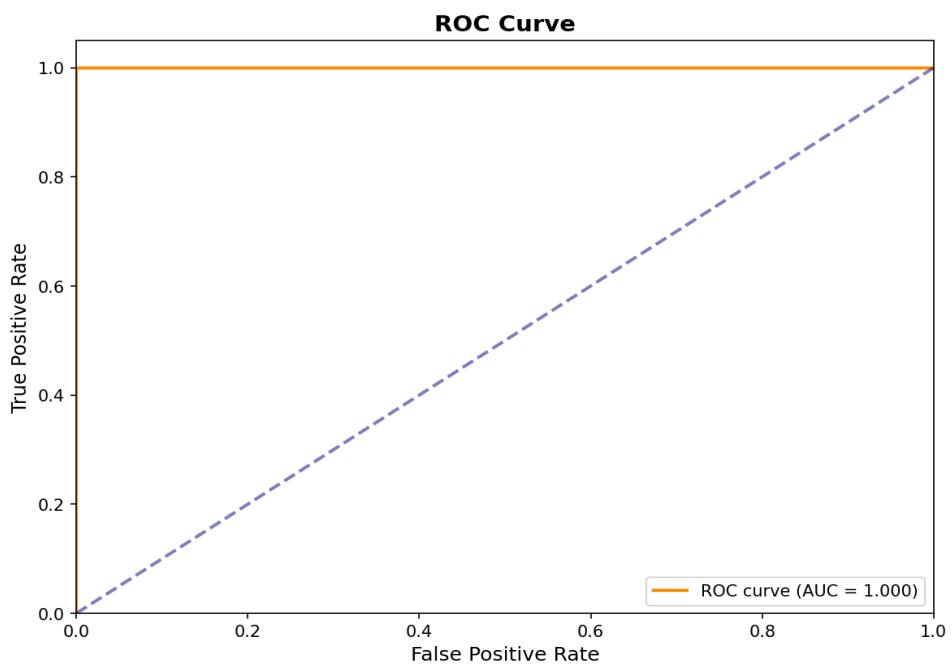
Metric	Value
Accuracy	1.0000
Precision	1.0000
Recall	1.0000
F1 Score	1.0000
Roc Auc	1.0000

## 5. Visualizations

### *Confusion Matrix*



### *Roc Curve*



## 6. Training Summary

**Total training time:** 2.03 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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