

BioMLStudio

Machine Learning Analysis Report

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1. Dataset Summary

Property	Value
Dataset Name	seq_001_unaffected
Dataset Type	dna
Total Samples	120
Features	7
File Size	0.01 MB

2. Preprocessing Steps

Step 1: Load and Clean Data

- Loaded 120 sequences from FASTA
- Removed invalid characters
- Extracted labels from headers
- Label distribution: {'affected': 120}

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 (1 classes)
- Split data: 84 train, 12 val, 24 test

3. Model Selection & Training

Model	Training Time	Score
Random Forest	1.82s	1.0000

Best Model: Random Forest

4. Performance Metrics

Training Metrics:

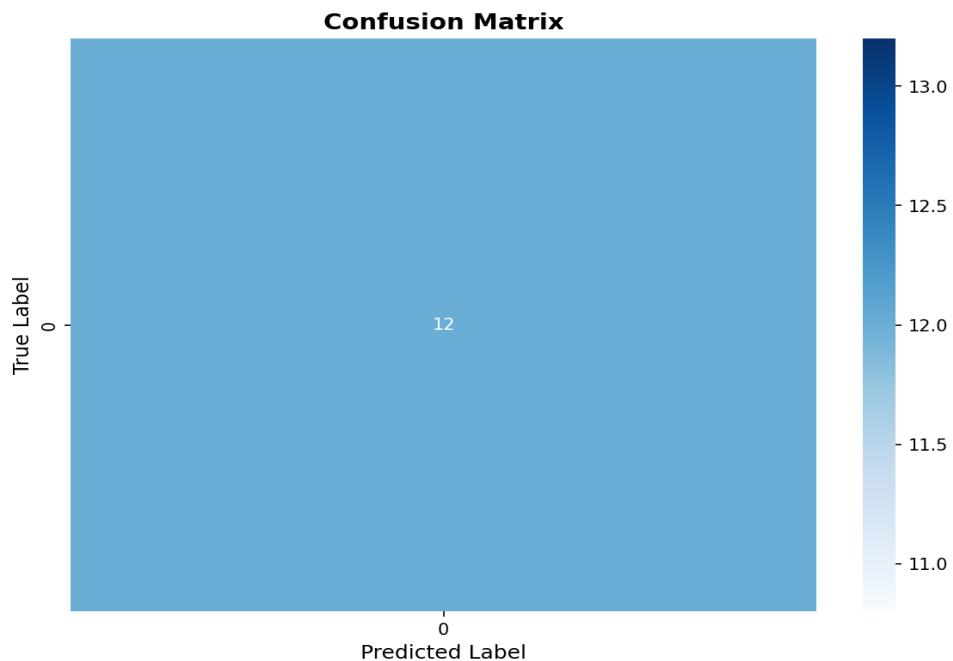
Metric	Value
Accuracy	1.0000
Precision	1.0000
Recall	1.0000
F1 Score	1.0000

Validation Metrics:

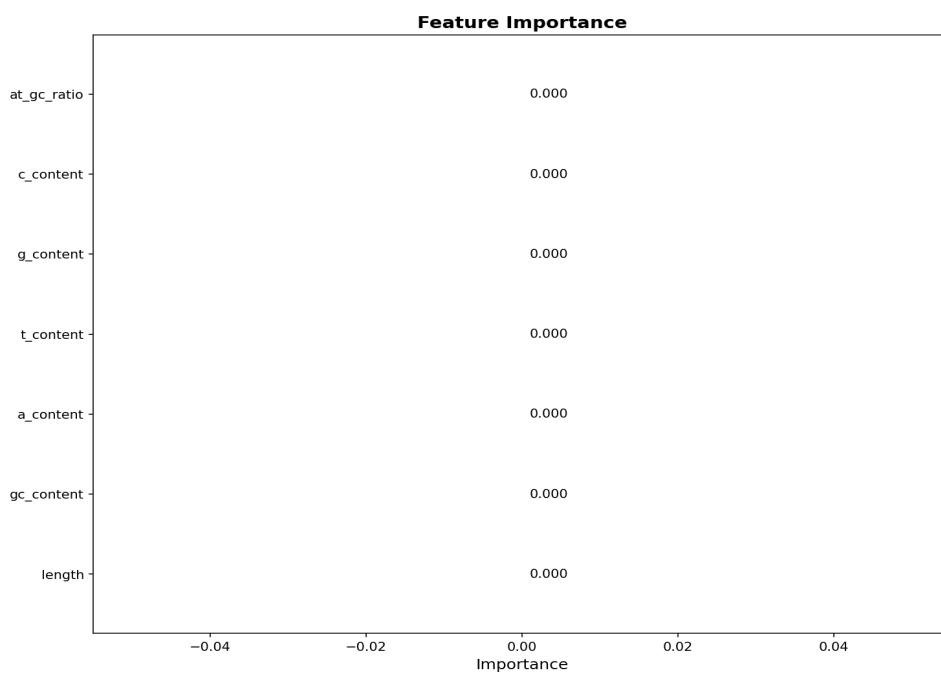
Metric	Value
Accuracy	1.0000
Precision	1.0000
Recall	1.0000
F1 Score	1.0000

5. Visualizations

Confusion Matrix



Feature Importance



6. Training Summary

Total training time: 5.03 seconds

Key Events:

[ERROR] Error training Logistic Regression: This solver needs samples of at least 2 classes in the data, but the data contains only one class: 0

[SUCCESS] Random Forest - Score: 1.0000

[ERROR] Error training Gradient Boosting: y contains 1 class after sample_weight trimmed classes with zero weights, while a minimum of 2 classes are required.

[SUCCESS] Best model: Random Forest (Score: 1.0000)

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