Time Series Classification Using Recurrence Triangle Analysis

1. Introduction

1. Background – The Real-World Challenge

Time series from biomedical sensors and physical systems often exhibit complex nonlinear behavior. In many practical settings, labels are unavailable, and signals are short and noisy—making reliable classification difficult.

2. Why Existing Methods Fall Short

Common approaches (e.g., feature engineering, transforms, symbolic models, deep learning) often:

- ➢ Miss fine-scale dynamical structure
- ➢ Require labeled datasets
- ➢ Provide limited interpretability

As a result, key dynamical differences remain hidden, and diagnostic potential is limited by label scarcity, even in high-performing supervised recurrence triangle-based studies (Hasan et al., 2025)

3. Our Objective

Develop a framework that:

- ➢ Classifies time series without supervision
- ➢ Captures interpretable local micro-patterns
- ➢ Delivers high accuracy even with limited data

2. Method – Recurrence Triangle-based Framework

We convert each time series into a recurrence plot (RP) (Marwan et al., 2007) and analyze its local triangular motifs (Hirata, 2021). The workflow process can be described as follows:

Step 1– Acquire time series data

Captures nonlinear behavior from physiological systems

Step 2– Convert to recurrence plots

Reveals hidden state-space structure through proximity recurrence.

Step 3– Extract recurrence triangles of size L

Identifies micro-dynamical patterns missed by global measures.

Step 4– Compute type-wise probability distributions

Converts geometry into a statistically discriminative signature.

Step 5– Rank motifs by discriminative information

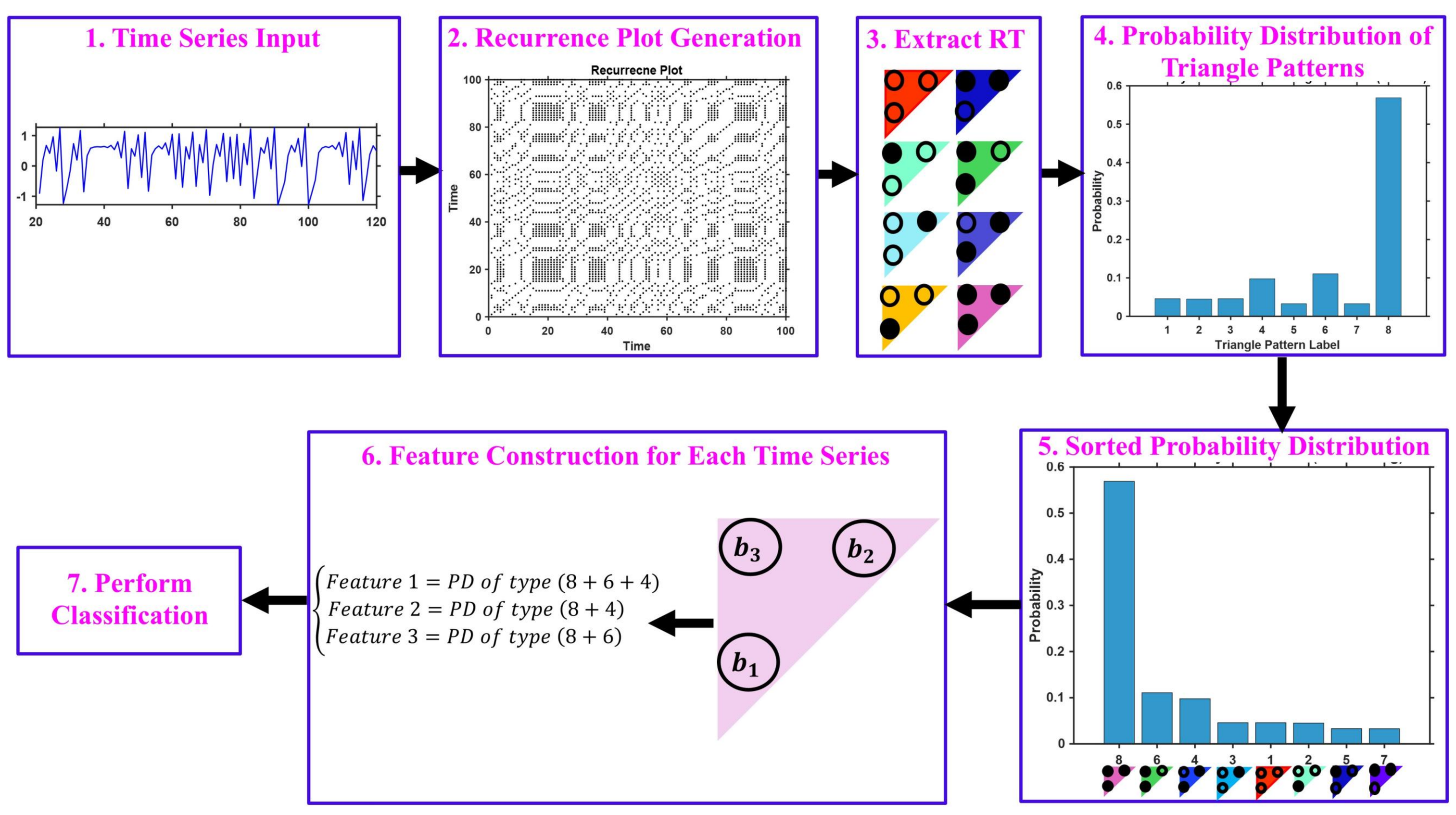
Prioritizes patterns most sensitive to class-specific differences.

Step 6– Keep only top informative motifs

Remove noise and maximizes separability between subject groups.

Step 7– Cluster with k-means (unsupervised)

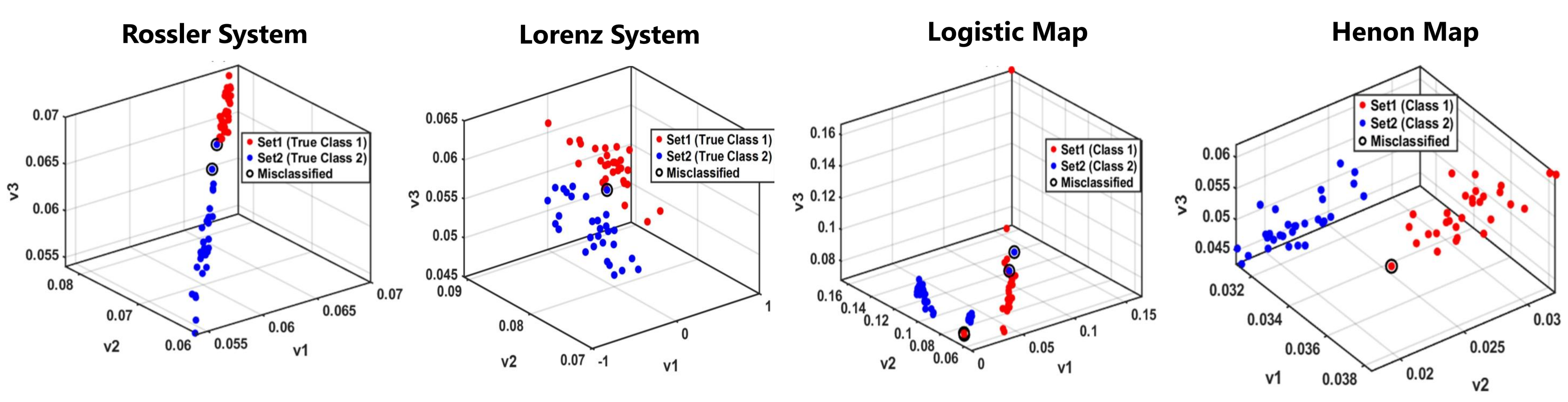
Classifies subjects without labels or model training.



3. Results

We evaluated the RT-based unsupervised classifier on both continuous chaotic systems (Rossler, Lorenz) and discrete maps (Logistic, Henon). Gaussian noise was added to test robustness under realistic conditions. Our recurrence triangle-based method generates compact, interpretable features that cleanly separate nonlinear dynamics without any labels.

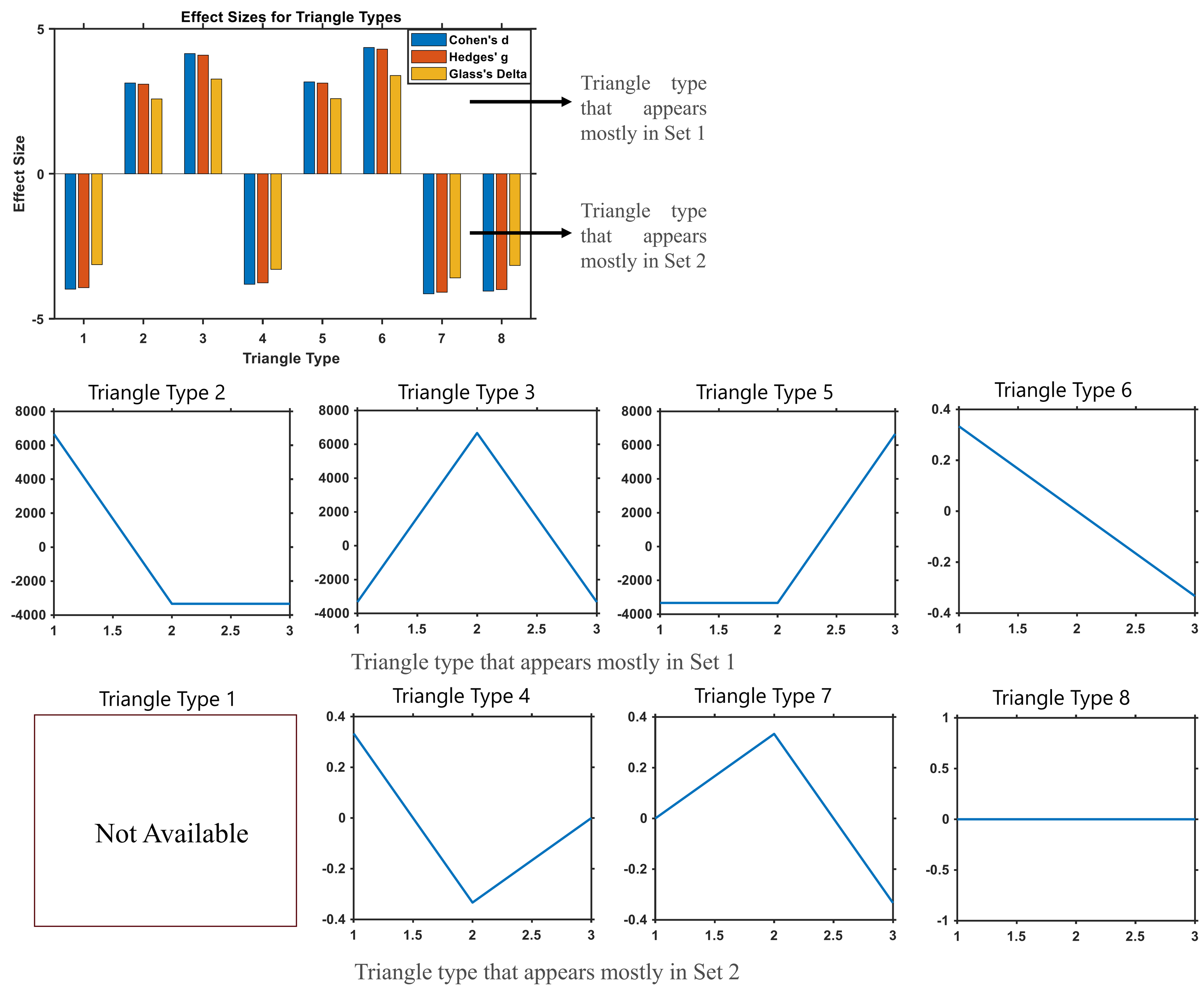
Dynamical System	Type	Accuracy
Rossler System	Continuous	96.7%
Lorenz System	Continuous	98.3%
Logistic Map	Discrete	93.3%
Henon Map	Discrete	96.7%



4. Discussion

To demonstrate interpretability, we quantified motif-level class differences in the Rossler dataset using effect-size analysis (Turner & Bernard, 2006). Several triangle types show large separations, indicating they capture the microstructures driving dynamical differences between classes.

To verify that these motifs reflect real system behavior, we reconstructed signals from RPs following Hirata et al. (2008).



The key insights are:

- ➢ The highly informative motifs are explicitly identifiable.
- ➢ Motif-class relationships are interpretable through effect sizes.
- ➢ Top motifs remain discriminative even under noise, which supports real-world use.
- ➢ Although visualized here for the Rossler system, the same procedure generalizes to all tested continuous and discrete systems.

5. Conclusion

Our recurrence triangle-based framework produces compact, interpretable features that:

- ➢ Separate nonlinear systems accurately without labels.
- ➢ Remain robust to noise and short signals.
- ➢ Enable scalable deployment to real biosignal analysis.

References

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