A topology-guided early-warning framework for epidemic peaks in tropical settings

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Abstract

Background: Early warning signals (EWS) can anticipate critical transitions in infectious-disease time series, yet their performance in tropical settings with multi-annual forcing and reporting noise remains mixed. Methods: We integrate topological data analysis (TDA) with classical indicators to detect pre-peak regimes. Sliding windows are transformed into delay-embedded point clouds; we compute persistence diagrams and summarize them via persistence landscapes. Features are combined with variance, autocorrelation at lag-1, skewness, and spectral ratio, then classified by gradient boosting. We evaluate dengue, measles, and COVID-19 surveillance data from 2012–2024 across multiple regions. Results: TDA-enriched models improved F1 by 0.11–0.19 over classical EWS, with median lead times of 3–6 weeks before observed peaks. Ablations indicate homological features (H1) contribute most to precision at low prevalence. Conclusions: Topology-guided EWS can augment operational surveillance by providing earlier, more stable alarms in noisy tropical datasets.

Keywords: early warning signals; persistent homology; persistence landscapes; dengue; measles; COVID-19; tropical epidemiology

Introduction

Public-health programs rely on timely detection of epidemic upswings. Classical EWS—variance and autocorrelation—stem from critical-slowing-down theory, but real surveillance data exhibit nonstationarity, under-reporting, and calendar effects. Topological data analysis (TDA) offers complementary descriptors that capture shape changes in reconstructed dynamics. We hypothesize that persistent homology features, combined with standard indicators, yield earlier and more reliable pre-peak alarms.

Methods

Data: Weekly case counts for dengue, measles, and COVID-19 were collected from national bulletins (2012–2024). Pre-processing: series were de-seasonalized via STL and log(1+x) transformed. Windows: length 16 weeks, step 1. Delay embedding: (m=3, τ=1) to form point clouds in ■³ per window. Persistent homology: Vietoris–Rips filtration up to H1; summarized by persistence landscapes (L¹ norms over K fixed λ-breakpoints). Classical indicators: variance, lag-1 AC, skewness, spectral ratio. Classification: gradient-boosted trees with time-aware cross-validation (grouped by outbreak). Outcome: pre-peak window within 3–8 weeks prior to the observed local maximum. Metrics: F1, AUPRC, lead-time in weeks. Ablations: (i) classical-only; (ii) TDA-only; (iii) fusion; (iv) H0 vs H1 contributions.

Results

Performance: Fusion model achieved mean F1=0.72 (± 0.06) vs classical-only 0.56 (± 0.07), $\Delta = +0.16$. Median lead time improved from 2 to 5 weeks. Gains were largest for dengue during low baseline

seasons. Feature importance: H1 landscape coefficients ranked among the top-10 features in 8/9 regions. Calibration improved (ECE \downarrow from 0.14 to 0.08). Error analysis showed fewer false alarms during reporting gaps. Case studies: In Davao Region 2019 dengue, the model raised an alert 5 weeks before the peak; in NCR measles 2018, 4 weeks prior.

Discussion

TDA captures mesoscale changes in reconstructed attractors that precede macroscopic incidence peaks, complementing variance- and autocorrelation-based EWS. While robustness improved, performance depends on window length and seasonal adjustment. Future work includes prospective evaluation within routine dashboards and integration with mobility and climate covariates.

Data & Code Availability

Data & Code Availability: Aggregated weekly series and code to reproduce analyses are available at https://example.org/fmrd-2025-00001 (to be replaced with OSF/Zenodo links).

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Conflicts of Interest

Conflicts of interest: The authors declare no competing interests.

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