



Mathematical Biology Seminar

Monday, March 25, 2024

3 pm MDT - 457 CAB (in person)

Join Zoom Meeting

<https://ualberta-ca.zoom.us/j/98497695684?pwd=SG5pcUVR50xucW5xd0xBTm1VVc0tEUT09>

Meeting ID: 984 9769 5684

Passcode: 32123



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Early detection of disease outbreaks and non-outbreaks using incidence data

Early detection of novel disease outbreaks and non-outbreaks is essential for minimizing associated consequences. Existing methods are often context-specific, require a long preparation time, and non-outbreak prediction remains understudied. Here, we propose a novel framework using the feature-based time series classification (TSC) method to forecast the occurrence or absence of outbreaks. We can identify incipient differences between the pre-transition sequence (pre-pandemic) and the null bifurcation sequence (normality). These distinctions are reflected in 22 statistical features (22SF) and 5 early warning signal indicators (5EWSI) from incidence sequences, allowing the framework to effectively discriminate these two scenarios in synthetic data. Following the framework, we train 32 classifiers on noise-induced Susceptible–Infected–Recovered (SIR) model simulations. All classifiers demonstrate effectiveness in cases long before the outbreak timing and retain comparable accuracy in classifying much shorter time series. Additionally, we conduct three real case studies involving national-level COVID-19 data and SARS data from Hong Kong, with two classifiers exhibiting consistently good performance on these empirical testing sets. The emergence and re-emergence of infectious disease are inevitable, however, early detection of impending outbreaks through this framework can aid in implementing optimal interventions and reduce misjudgments of risks.

COLLABORATIVE MATHEMATICAL BIOLOGY GROUP

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