Real-time detection of HIV outbreaks among people who inject drugs and modelling of subsequent epidemic states

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Introduction

- HIV outbreaks among people who inject drugs (PWID) are not uncommon ⇒ serious impact on public health.
- Various statistical methods have been proposed for prospective outbreak detection.
- In comparison with other diseases, HIV outbreaks among PWID differ in their size, duration, post-epidemic level.
- A few studies have intended to detect epidemic states after outbreak onset and addressed the problem retrospectively.

Objective: To compare through simulations the performance of various methods for detecting in real time: i) the growth, ii) non-increasing (plateau and/ or decline) and iii) post-epidemic state of such outbreaks.

Statistical Methods

Methods for outbreak detection in real time

- A two-state Hidden Markov Model (HMM)

$$\begin{pmatrix} 1-p_{12} & p_{12} \\ 0 & 1 \end{pmatrix} \text{ and } Y_t \sim NB(\mu_t, r_t), \text{ where}$$

$$\mu_{t|Z_t=1} = \mu_{t-1} \text{ and } \mu_{t|Z_t=2} = \mu_{t-1}e^{\beta_1},\ \beta_1 > 0$$

$$r_{t|Z_{t=1}} = r_1 \text{ and } r_{t|Z_{t=2}} = r_2 \text{ such that } r_1 < r_2$$

- A method based on prediction interval (PI) (Figure 2)
- A novel approach HMM-PI that combines the former two:

$$\begin{pmatrix} w_t(1-p_{12}) & 1-w_t(1-p_{12}) \\ 0 & 1 \end{pmatrix},\ w_t = \begin{cases} \frac{Y_t-U}{Y_t} & , Y_t > U \\ 1 & , Y_t \leq U \end{cases}$$

- Regression methods: Farrington algorithm, OutbreakP
- Control charts: Poisson Cumulative Sum (PCUSUM) and Exponentially Weighted Moving Average (PEWMA).

➢ HMM, PI and HMM-PI were properly modified to **detect in real time the subsequent epidemic states**.

Performance evaluation: sensitivity, specificity, timeliness (i.e., difference between the start of each state and the first alarm signal after its onset).

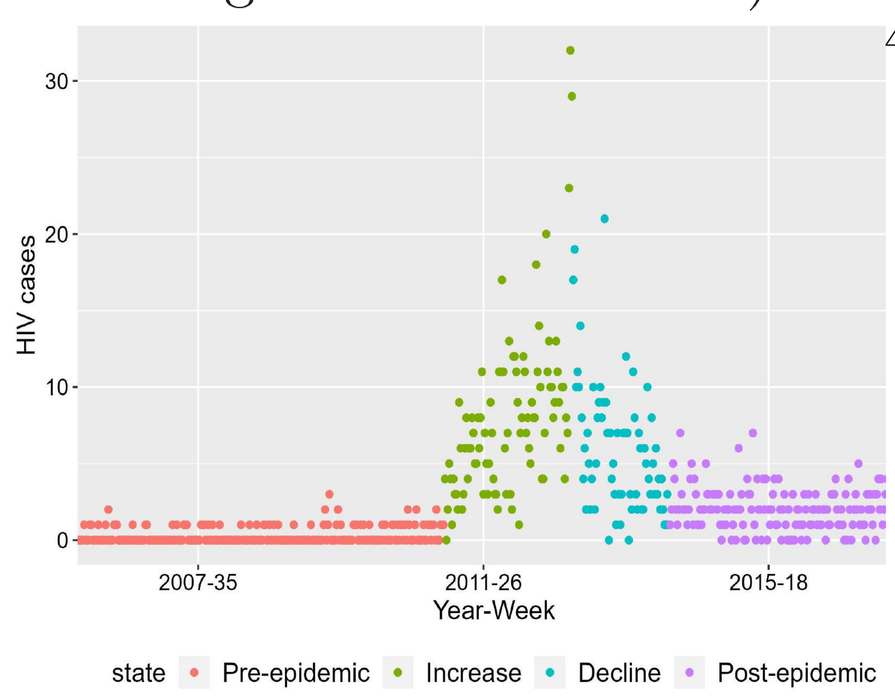

Figure 1: Weekly HIV cases among PWID in Greece. Data from The European Surveillance System (TESSy) of the European Centre for Disease Prevention and Control (ECDC).

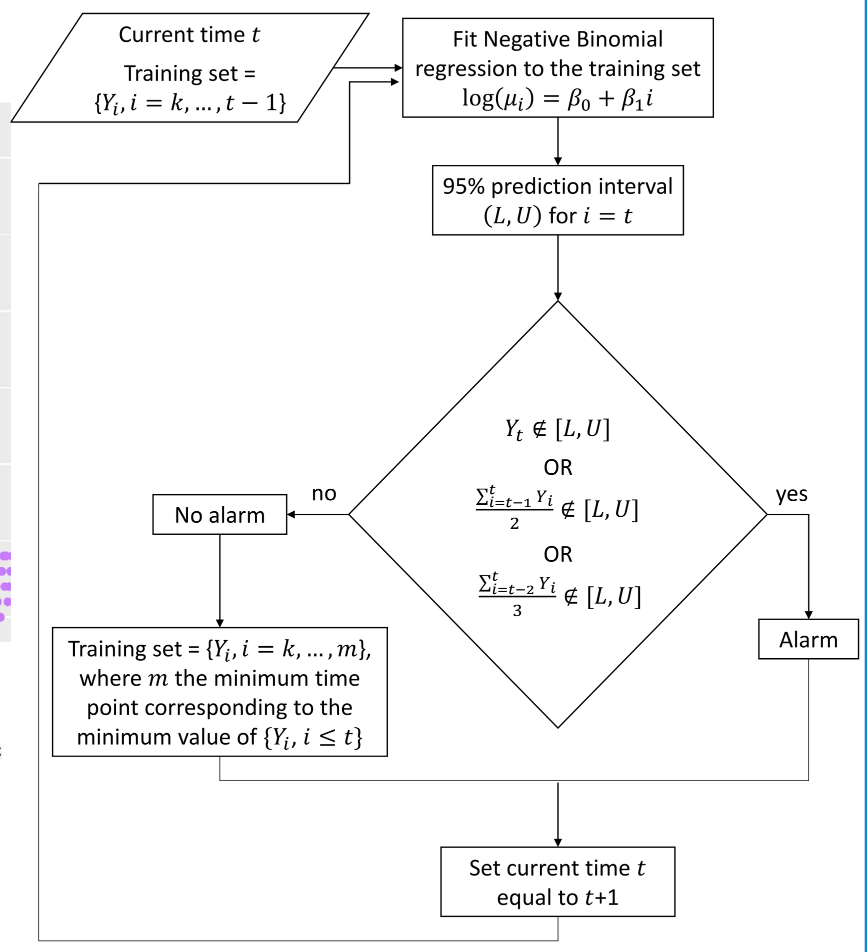

Figure 2: Schematic outline of the PI method for outbreak detection

Simulation study

Motivating example

- HIV outbreak among PWID in Greece (Figure 1).
- An epidemic curve comprises five states: 1. pre-epidemic, 2. increase, 3. plateau, 4. decline, 5. post-epidemic.

Simulation strategy

1. Epidemic state Z_t for week t based on Figure 1 data.
2. Weekly counts Y_t for week t from a Negative Binomial with overdispersion $r_{t|Z_t}$ and mean $\mu_{t|Z_t}$ depending on Z_t:

$$\mu_{t|Z_t \in \{1,3,5\}} = \mu_{t-1} \text{ and}$$

$$\mu_{t|Z_t \in \{2,4\}} = f(\mu_{t-1}),\ f \text{ growth/decline.}$$

Simulation scenarios

Eight scenarios were simulated assuming different:

- epidemic states (with/without plateau),
- epidemic shapes (constant/exponential),
- time progress (abrupt/gradual) and
- pre-outbreak levels (low/high).

Results

Simulation results

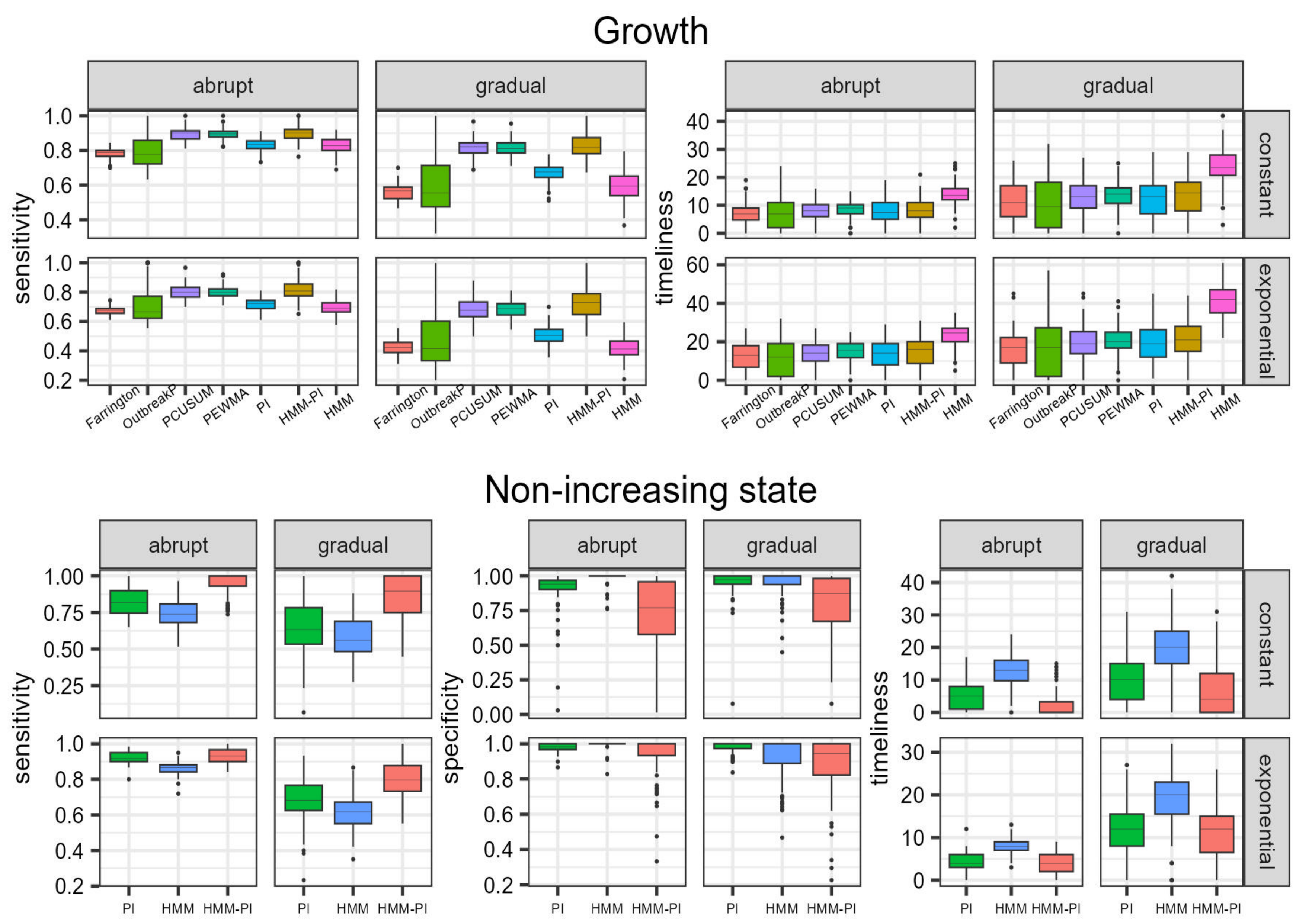

Figure 3: Scenarios without plateau assuming high pre-epidemic level

➢ Growth: All methods gave excellent specificity.

➢ Post-epidemic state

- No method gave a satisfying balance between all metrics.
- PI best-performing (high specificity,moderate timeliness).

➢ Neither the inclusion of plateau nor the assumption of low pre-epidemic cases significantly affected performance.

Real data application

➢ Growth: all methods had excellent performance; HMM-PI ranked first (≈ 100% sensitivity and specificity, 0 timeliness).

➢ Non-increasing state: HMM-PI best-performing.

➢ Post-epidemic state: PI best-performing.

Conclusions

- No method is a panacea for identifying all epidemic states.
- HMM-PI seems promising for detecting epidemic growth.
- PI should be used for the subsequent epidemic states.
- Although HMM performed poorly in real time, it can provide useful insights if applied retrospectively.

Extensions: Model HIV positivity rate instead of HIV cases.

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