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ABSTRACT

A spatio-temporal absorbing state model for disease and syndromic surveillance

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Objective
Syndromic surveillance for new disease outbreaks is an important problem in public health. Many statistical techniques have been devised to address the problem, but none are able to simultaneously achieve important practical goals (good sensitivity and specificity, proper use of domain information, and transparent support to decision-makers). The objective, here, is to improve model-based surveillance methods by (i) detailing the structure of a hierarchical hidden Markov model (HMM) for the surveillance of disease across space and time and (ii) proposing a new, non-separable spatio-temporal auto-regressive model.

Introduction
The goal of disease and syndromic surveillance is to monitor and detect aberrations in disease prevalence across space and time. Disease surveillance typically refers to the monitoring of confirmed cases of disease, whereas syndromic surveillance uses syndromes associated with disease to detect aberrations. In either situation, any proper surveillance system should be able to (i) detect, as early as possible, potentially harmful deviations from baseline levels of disease while maintaining low false positive detection rates, (ii) incorporate the spatial and temporal dynamics of a disease system, (iii) be widely applicable to multiple diseases or syndromes, (iv) incorporate covariate information and (v) produce results that are readily interpretable by policy decision makers.

Early approaches to surveillance were primarily computational algorithms. For example, the CUSUM[1] technique and its variants (see, for example, Fricker *et al.*[2]) monitor the cumulative deviation (over time) of disease counts from some baseline rate. A second line of work uses spatial scan statistics, originally proposed by Kulldorff[3] with later extensions given in Walther[4] and Neill *et al.*[5]

Methods
As the data layer for the HMM, let,

$$Y_s(t) \sim P(\mu_s(t) + \delta_s(t)\lambda_s(t))$$

where $Y_s(t)$ represents a count of a disease at location s at time t, $\mu_s(t)$ represents a baseline rate of disease, $\delta_s(t) \in \{0,1\}$ is an indicator as to whether or not the disease is in an epidemic state and $\lambda_s(t)$ represents an added rate of disease because of an epidemic state.

As models for the rates of disease (that is, $\mu_s(t)$ and $\lambda_s(t)$), a novel non-separable spatio-temporal structure is assumed. Furthermore, the indicators, $\delta_s(t)$ are assumed to follow an absorbing state Markov chain, where the state transitions are governed by the number of neighbors in an epidemic state.

Conclusions
The model performs well by correctly classifying states as either epidemic or non-epidemic in both a large simulation study and in an application to influenza/pneumonia fatality data.

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