

Online surveillance of multivariate small area disease data: a Bayesian approach

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Objective

This study deals with the development of statistical methodology for online surveillance of small area disease data in the form of counts. As surveillance systems are often focused on more than one disease within a predefined area, we extend the surveillance procedure to the analysis of multiple diseases. The multivariate approach allows for inclusion of correlation across diseases and, consequently, increases the outbreak detection capability of the methodology.

Introduction

The ability to rapidly detect any substantial change in disease incidence is of critical importance to facilitate timely public health response and, consequently, to reduce undue morbidity and mortality. Unlike testing methods (1, 2), modeling for spatiotemporal disease surveillance is relatively recent, and this is a very active area of statistical research (3). Models describing the behavior of diseases in space and time allow covariate effects to be estimated and provide better insight into etiology, spread, prediction and control. Most spatiotemporal models have been developed for retrospective analyses of complete data sets (4). However, data in public health registries accumulate over time and sequential analyses of all the data collected so far is a key concept to early detection of disease outbreaks. When the analysis of spatially aggregated data on multiple diseases is of interest, the use of multivariate models accounting for correlations across both diseases and locations may provide a better description of the data and enhance the comprehension of disease dynamics.

Methods

When small area disease data in the form of counts are available, Bayesian hierarchical Poisson models are commonly used to describe the behavior of disease (5). In this study, we use the convolution model (6) to describe the behavior of disease under endemic conditions. Each time new observations become available, we show how the conditional predictive ordinate (CPO, 7), which is a Bayesian diagnostic tool that detects unusual observations, can be adapted in a surveillance context to detect small areas of unusual disease aggregation (8).

For the joint analysis of two or more diseases, we introduce a generalization of the shared component model (9) where the underlying risk surface for each disease is separated into shared and disease-specific components. We then propose a multivariate extension of the surveillance CPO that incorporates information from the different diseases and, consequently, facilitates the outbreak detection work. The multivariate surveillance technique has the ability to detect outbreaks of disease in either one or in a combination of diseases.

Results

We analyze weekly emergency room discharges for acute upper respiratory infections, influenza, acute bronchitis, asthma and pneumonia in 2009. The data are available by county for the 46 counties of South Carolina. The use of a shared component model accounting for correlation across diseases provides a better overall fit. In addition, the use of the multivariate SCPO increases the statistical power for detection of outbreaks.

Keywords

Public health surveillance; spatial data; Bayesian hierarchical models; joint disease mapping; conditional predictive ordinate

Acknowledgments

This work was supported by Grant Number R03CA162029 from the National Cancer Institute.

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