

Accounting for acceleration of disease rates with age in biosurveillance systems: The SIMPLE Method

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OBJECTIVE

To better estimate disease burden in the elderly population we illustrate an approach—the Slope Intercept Modeling for Population Linear Estimation (SIMPLE) method—that summarizes age-specific disease rates in the 65+ population using the observed exponential increase in disease rates with age in this dynamic and rapidly growing population subgroup.

BACKGROUND

Accurate and precise estimation of disease rates for a given population during a specified time frame is a major concern for public health practitioners and researchers in biosurveillance [1]. Many diseases follow distinct patterns [2]; incidence and prevalence of many diseases increase approximately exponentially with age, including many cancers, respiratory infections, and gastroenteritis [3]. With increasing demographic information available in biosurveillance systems leading to more complex and comprehensive disease databases, seeking concise and informative summary measures of disease burden over space and time is becoming more critical for public health surveillance [4]. In this paper we present two summary measures of disease burden in the elderly that simultaneously reflect disease dynamics and population characteristics.

METHODS

Using a database of approximately 17 million Medicare hospitalization claims for 15 influenza seasons (1991-2006) and US Census Bureau counts, we estimated age-specific, influenza alone and influenza-related hospitalization incidence in the elderly by influenza season on the national and state levels for the population age 65 to 99. Influenza season was defined as the twelve-month period from July through the following June to capture the seasonal peak that generally occurs between January and March [5]. The Slope Intercept Modeling for Population Linear Estimation (SIMPLE) method uses simple linear regression of log-transformed age-specific disease rates on age. Disease patterns are represented by two resultant regression parameters, an intercept, representing expected influenza and influenza-related incidence at age 65, and a slope, representing the degree of exponential increase of influenza-related incidence by age for the elderly. We then performed a sensitivity analysis using R-squared values to determine how precisely the measures represent the actual age-specific

disease rates and compared those on the national and state levels.

RESULTS

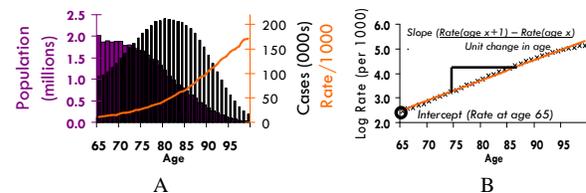


Fig. 1: Age-specific population (Census 2000, purple), average annual number of pneumonia and influenza cases (black) and incidence (orange) population [Panel A], and illustration of SIMPLE methodology [Panel B]

For influenza and influenza related disease, results of the sensitivity analysis showed that for the national elderly population, this SIMPLE regression method had R-squared values between 0.95 and 0.99, depending upon the influenza season. On the state level, the regression models showed that age predicted between 59 and 99 percent of the variability in the log of the disease rate. Hawaii and Alaska consistently had the lowest R-squared values, but also had the overall lowest rates of disease. However, states that had the highest overall rates of disease tended to have the highest R-squared values. R-squared values for influenza alone were lower, but still ranged between 0.84 and 0.97 for influenza on the national level.

CONCLUSIONS

The SIMPLE method produces two summary measures of disease burden that can be used to estimate and predict disease severity in biosurveillance systems. These measures reflect both disease and population processes and can be used for a variety of diseases. This approach works best for diseases with high incidence and can be adapted for use on multiple spatial and temporal scales.

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