INTRODUCTION

Background

There is a long history of geographical surveillance of disease by publishing disease atlases. If there are areas with exceptionally high rates, they may give the clues to the etiology of the disease, indicating areas where health care needs to be improved, or to be targeted for preventive measures. Implementing scan statistic, we can do the surveillance of particular disease on particular area. This study applied retrospective space-time permutation scan statistic to construct measles disease surveillance in West Java.

According to the World Health Organization (WHO), vaccination rate has been high enough to make measles relatively uncommon in developed countries, but in developing countries it is still common. Globally, measles deaths went down 60 percent, from an estimated 873,000 deaths in 1999 to 345,000 in 2005. Africa has been the most success area, with annual measles deaths falling by 75 percent in just 5 years, from an estimated 506,000 to 126,000 (UNICEF World Press Release in Wikipedia, 2007).

The ability in detecting measles outbreaks early is important in order to minimize morbidity and mortality through timely implementation of measles prevention and control measures. A scan statistic can be used widely in any field to recognize any significant hotspot in terms to find any spatial areas that have elevated risk than their surroundings.

In space-time, the scan statistic can provide early warning of disease outbreaks and can monitor their spatial spread. This study using a retrospective space-time permutation scan statistic for detecting measles disease hotspot in West Java that utilized only case numbers, with no need for population-at-risk data, where these data are very difficult or irrelevant to be obtained.

This method was applied on annual data of measles disease cases in West Java in 2003 and 2006 periods.

Objective

The objective of this study is to detect measles disease hotspots in West Java in order to reveal its outbreaks using historical data of Podes 2003 and 2006, where the detected hotspots indicated to be taken care due to the condition of health care and preventive measures action must be conducted.

DEFINITIONS

Measles

Measles, also called rubeola, is a highly contagious - but rare - respiratory infection that is caused by a virus. It causes a total-body skin rash and flu-like symptoms, including a fever, cough, and runny nose.

Measles is spread through respiration (contact with fluids from an infected person's nose and mouth, either directly or through aerosol transmission). About 90% of people without immunity sharing a house with an infected person will catch it. Airborne precautions should be taken for all suspected cases of measles. The incubation period usually lasts for 4–12 days (during which there are no symptoms). Infected people remain contagious from the appearance of the first symptoms until 3–5 days after the rash appears (Wikipedia, 2007).

Hotspot

Hotspot is defined as something unusual, anomaly, aberration, outbreak, elevated cluster, critical area, etc (Patil and Taillie, 2004). Hotspot clusters were generated by setting the relative risk in some counties to be larger than one (Song and Kulldorff, 2003). Hotspots are locations or regions that have consistently high levels of disease and may have characteristics unlike those of surrounding areas (Haran, Molineros, & Patil, 2006 in Septiani, 2006).

Scan Statistic

First studied by Naus in 1965, the scan statistic is an elegant way to solve problems of multiple testing when there are closely overlapping spatial areas and/or time intervals being evaluated. Temporal, spatial, and space–time scan statistic are now commonly used for disease cluster detection and evaluation, for a wide variety of diseases.

The basic idea is that there is a scanning window that moves across space and/or time. For each location and size of the window, the number of observed and expected cases is counted. Among these, the most “unusual” excess of observed cases is noted. The statistical significance of this cluster is then evaluated taking into account the multiple testing stemming from the many potential cluster locations and sizes evaluated (Kulldorff et al, 2005).