

4-25-2018

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Recommended Citation

Widyaningsih, Yekti and Pin, Tjiong Giok (2018) "A SPACE-TIME SCAN STATISTIC TO DETECT CLUSTER ALARMS OF DENGUE MORTALITY IN INDONESIA, 2005," *Makara Journal of Science*: Vol. 12: Iss. 1, Article 8.

Available at: <https://scholarhub.ui.ac.id/science/vol12/iss1/8>

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A SPACE-TIME SCAN STATISTIC TO DETECT CLUSTER ALARMS OF DENGUE MORTALITY IN INDONESIA, 2005

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Abstract

This article presents a space-time scan statistic, useful for evaluating space-time cluster alarms, and illustrates the method to investigate a recent dengue mortality alarm in Indonesia. Space-time scan statistics account for multiple testing inherent in a cluster alarm. The baseline process may be any inhomogeneous Poisson process with intensity proportional to some known function. Confounders in a particular time can be adjusted for. Three cluster alarms of dengue mortality in Indonesia in 2005 were statistically significant. Space-time scan statistics are useful as screening tools for evaluating which cluster alarms merit further investigation and which clusters are probably chance occurrences.

Keywords: clusters, dengue mortality, space-time scan statistics, poisson process

1. Introduction

The total number of dengue fever cases in Indonesia is the highest in the world after Thailand [1]. The disease was detected for the first time in Indonesia in the year 1968, precisely, in Surabaya, East Java. Since that time until 1998, the average number of the cases was about 18,000 cases each year, and 700 to 750 of the cases were fatal. In 1998 the number of cases was 15,452 in Jakarta, causing death in 134 cases [2]. The number of cases of dengue fever, which is a 5-years cyclic disease, was 5,800 cases, reported in May 2003, with a mortality number of 32. The number of cases in 2003 was 2.5 times the number of cases in 2002. For activities in the prevention of the disease the government, through the Department of Health, allocated 2 billion rupiah for fogging, guidance, and counseling [3].

According to reports on disease outbreaks in Indonesia, health officials are often asked to evaluate local disease cluster alarms. After the case definition is established, it is important to know, if the cluster has occurred by chance or the outbreak was so great that it is probably due to some common elevated risk factor of limited geographical and/or temporal extension. Because of these needs, the space-time scan statistic is now frequently used in surveillance for the detection of disease clusters. The standard approach is to look at a single disease, such as leukemia incidence, breast

cancer mortality and dengue mortality [4]. In 2005, the number of people who suffered of dengue increased rapidly in Indonesia therefore we are interested in investigating whether there are any geographical clusters of dengue mortality in Indonesian areas.

2. Geographical Data and Dengue Fever

In the year 2005 the population of Indonesia was about 240 millions. As an archipelago Indonesia consists of thousands small islands and five big islands i.e. Sumatra, Kalimantan, Java, Sulawesi, and Papua. There are 33 provinces, 440 districts, and 5900 sub-districts spread on the islands [5]. Two seasons in Indonesia are the dry season and wet season with a transition period in September. The dengue fever is a disease transmitted through *Aedes Aegypti* female mosquito bites. The *Aedes Aegypti* population increase during the transition period causing the increase of dengue fever cases. During the transition period cistern and puddles of water are found everywhere and are favorable for the maintenance of the mosquito life cycle. These conditions often appear in flat land, densely populated, with an unhealthy environment.

3. A Space-Time Scan Statistic

The 1-dimensional scan statistic has been used to study disease clusters in time, and a 2-dimensional scan

statistic has been proposed for studying purely spatial disease clusters. The Space-time scan statistic is defined by a cylindrical window with a circular geographic base and with height corresponding to time [6].

Mortality dengue cases are assumed to have a Poisson distribution with constant risk over spaces and time under null hypothesis, and with different risk inside and outside at least one cylinder under the alternative hypothesis. For each cylinder the numbers of mortality dengue cases inside and outside the cylinder are noted, together with the expected number of mortality dengue cases reflecting the population cases at risk. On the basis of these numbers, the likelihood is calculated for each cylinder. The cylinder with the maximum likelihood, and with more than the expected number of cases, is denoted the most likely cluster.

Likelihood Ratio Test

Let us assume that we have a set of data collected at a set of discrete time steps $k = 1..k_{base}$, and at a set of discrete spatial locations s_i . For each s_i at each time step k , we are given a count c_i^k and a baseline b_i^k . In this paper, the counts are the number of fatal dengue disease cases in a given spatial region over a given time interval, whereas the baselines are the number of dengue cases. In all cases, we assume that counts c_i^k are generated by some distribution with mean proportional to $b_i^k q_i^k$, where q_i^k is the rate (or expected ratio of count to baseline). Our goal, then, is to find whether there is any region (set of locations s_i) and time interval ($k = k_{min} ... k_{max}$) for which the rates are significantly higher than expected.

In this case, we compare the null hypothesis H_0 : the rate equals q_0 over all locations and times, to the alternative hypothesis $H_1(S)$: the rate is higher than q_0 at the present time k in region S , and equals q_0 over all other locations and times. The likelihood ratio is:

$$\lambda = \frac{\max_{q_{in} \geq q_0} \prod_{s_i \in S} \Pr(c_i^k \sim P_0(b_i^k q_{in}))}{\prod_{s_i \in S} \Pr(c_i^k \sim P_0(b_i^k q_0))}$$

$$= \frac{\max_{q_{in} \geq q_0} \prod_{s_i \in S} e^{-b_i^k q_{in}} q_{in}^{c_i^k}}{\prod_{s_i \in S} e^{-b_i^k q_0} q_0^{c_i^k}} = \frac{\max_{q_{in} \geq q_0} e^{-B_{in} q_{in}} q_{in}^{C_{in}}}{e^{-B_{in} q_0} q_0^{C_{in}}}$$

In this way "in" are sums over region S at time k . This quantity is maximized at $q_{in} = \frac{C_{in}}{B_{in}}$, assuming this quantity is greater than q_0 ; otherwise we have $\lambda = 1$.

Significance is evaluated with Monte Carlo simulation, where the null hypothesis of no cluster is rejected at α level of 0.05 exactly if the simulated p-value is less than or equal to 0.05 for the most likely cluster. In this sense, simulated p-values function in the same way as mathematically calculated p-values. The reported p-values for secondary clusters are conservative [7].

Monte Carlo Simulation

The Monte Carlo method is defined as representing the solution of a problem as a parameter of a hypothetical population, and using a random sequence of numbers to construct a sample of the population, from which statistical estimates of the parameter can be obtained.

Kulldorff [6], created SaTScan software as a tool to run the data needed for the detection. The properties of the data are the scan area geometric, probability distribution of the response under the null hypothesis, and the significance of the statistic test, evaluated with the Monte Carlo simulation [8].

4. Application to Indonesia

The number of dengue cases and mortality data for every province during each month is reported by the Department of Health of Indonesia. In 2005, there were 81,399 cases of dengue with 1107 fatal cases. Mortality dengue cases in Indonesia became a rife rumor in 2005. People need to know in which area and when it reached the highest number. Space-time scan statistic is an appropriate method to detect the outbreak according space and time. Calculations were performed with SaTScan v.7.0 with 999 Monte Carlo replications. The program took 4 seconds to run on 1.6 GHz Pentium Notebook.

Adjustment for most likely clusters were in East Nusa Tenggara, South Sulawesi, West Sulawesi, South East Sulawesi, West Nusa Tenggara, Bali, Gorontalo, South Kalimantan, East Java, Maluku, North Maluku, Central Kalimantan, North Sulawesi, Yogyakarta, East Kalimantan, Central Sulawesi, Central Java, and West Kalimantan areas during August to December 2005 (Table 1 and Figure 1). This area had 22.3% fatal cases of the whole mortality number in all provinces and a P value of 0.001. Therefore this cluster was statistically significant. Calculations also yielded three secondary clusters. The first cluster consisted of Nangro Aceh Darrusalam, North Sumatera and Riau Island areas on January to June 2005 with a p-value of 0.001. The second cluster was West Java area on January 2005 with a p-value of 0.003 and the third cluster consisted of Bangka Belitung and Banten areas on September to October 2005 with a p-value of 0.996. The third secondary cluster was not significant as a hotspot.

Table 1. Cluster Areas of Dengue Mortality the Application of a Space-Time Statistic: Indonesia, 2005

Hotspot Cluster	Months	Number of Mortality Cases	Number of Expected	Relative Risk	Log Likelihood Ratio	p-value
Most Likely Cluster: NTT, SULSEL, SULBAR, SULTRA, NTB, BALI, GRTALO, KALSEL, JATIM, MALUKU, MALUT, KALTENG, SULUT, DIY, KALTIM, SULTENG, JATENG, KALBAR	2005/8/1 - 2005/12/31	247	137.90	2.041	16.940153	0.001
Secondary cluster: NAD, SUMUT, KEPRI	2005/1/1 - 2005/6/30	44	15.98	2.832	16.940153	0.001
Secondary cluster: JABAR	2005/1/1 - 2005/1/31	39	15.88	2.513	12.181097	0.003
Secondary cluster: BABEL, BANTEN	2005/9/1 - 2005/10/31	5	1.27	3.941	3.119414	0.996

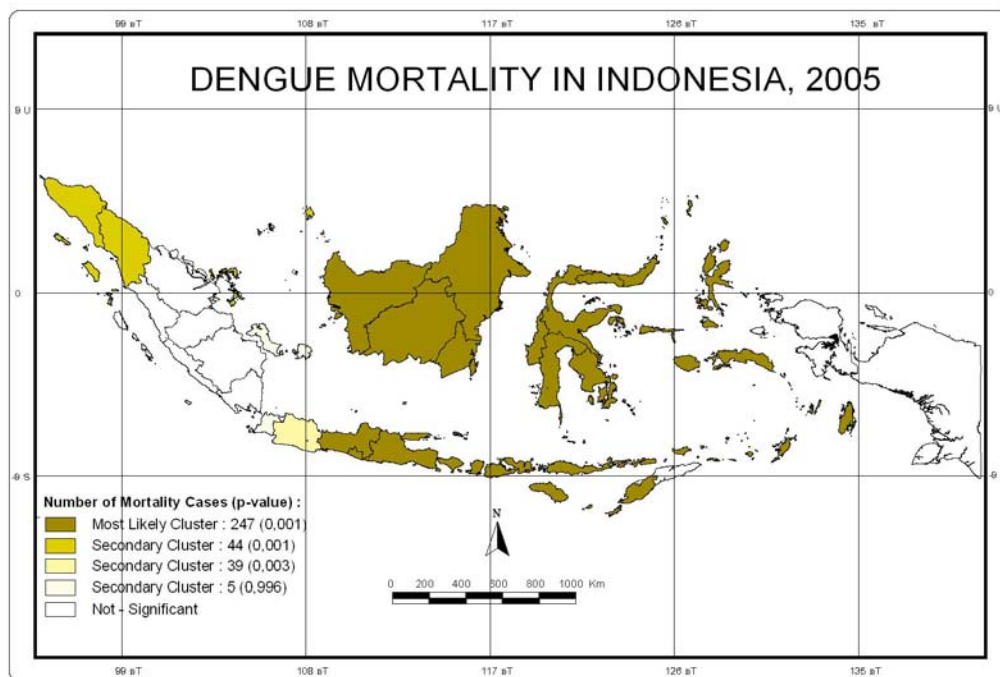


Figure 1. Statistically Significance Space-time Hotspot of Dengue Mortality Clusters in Indonesia, 2005

5. Discussion and Conclusion

The highest response areas and times of dengue mortality in 2005 in Indonesia areas were identified and found to be statistically significant. Mortality dengue cases can be thought of as a Poisson process that generates a number of changes (deaths) in a total of cases with the probability of death based on the total

number of cases is 0.01. So, the number of mortality dengue cases in Indonesia appropriate to a Poisson distribution.

A high number of cases was reported by the newspaper Suara Pembaruan (2005), mentioning that since January to October 2005 there were 50,196 dengue cases in Indonesia, including 701 fatal cases. Table 1 showed

that during the period from January to June 2005, some regions of the west part of Indonesia i.e. some areas of Sumatera and West Java areas were parts of a significant cluster of dengue mortality. After this period, high mortality areas moved to the center part of Indonesia, among others Kalimantan, Sulawesi and East Java, during the period of August to December 2005. Section 2 described favorable environmental conditions for mosquitoes, conditions which can be found in Kalimantan. On this island most areas are flat therefore cistern and puddles of water are easily shaped. In this situation, mosquitoes multiply quickly. As a consequence, the dengue cases increased in this area. Considering favorable conditions for mosquitoes it was concluded that these conditions were found in the west part of Indonesia during the first part of the year, with the highest dengue mortality as a result. This situation moved during the second part of the year to the center part of Indonesia.

Even though Space-time scan statistic method doesn't have a capability to predict the mortality event in a certain space and time, this method will give advantages when using persistently, that the hotspot information can be captured as soon as it happened. As a statistical tool, the space-time scan statistic proved to be useful for identifying cluster alarms. Information of hotspots of the dengue mortality in Indonesia according to space and time is important, needed by the government in order to take a decision and an action policy. The scan statistic is a useful tool to reveal very important information. It could be said that with the scan statistic we can find the needle in the haystack. Not just the information could be revealed, but the level of

statistically significance could be identified with the SaTScan software.

Acknowledgements

Valuable discussions with dr. Joedo Prihartono, MPH, Department of Community Medicine, Faculty of Medicine, University of Indonesia and Prof. dr. Sri S. Margono, SpParK, Department of Parasitology, Faculty of Medicine, University of Indonesia are gratefully acknowledged.

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