A Bayesian Spatiotemporal Shared Component Model for Detecting Space-Time Variation of the Relative Risk of Dengue and Chikungunya Diseases in Bandung, Indonesia

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Abstract: Incidences of infectious diseases (e.g.: dengue disease, chikungunya, tuberculosis, and diarrhea) have been soaring. According to the World Health Organization, climate change, extreme weather, and environmental factors, such as lack of access to clean water and poor sanitation facilities, have contributed to the outbreaks. Socioeconomic conditions, including income, employment, education, and health behavior, are also important factors that influence the transmission of infectious diseases. Improper handling of infectious diseases leads to a higher negative impact e.g.: increasing the case fatality rate, disrupt the family economy and further disrupt national stability. The government should take preventive action to manage and control the disease transmission. Early identification of an endemic is an important first step in preventing the transmission of infection diseases. Implementation of such early warning systems (EWSs), including roadmaps to prevent or restrict the spread of an infectious disease, is still in its infancy in most (developing) countries. For this purpose, we need to provide the information of the geographical and temporal distribution of the infectious diseases inside a map. The map has to present the accurate information about the high-risk over space and time. For this purpose, models for multiple diseases are required. In this paper, we developed a Bayesian spatiotemporal (BST) model for estimating multiple infectious diseases in Bandung, Indonesia. We use shared component BST approach to accommodate multiple diseases.

Key word: Bayesian • Early Warning System • Multiple Infectious Diseases • Spatiotemporal

INTRODUCTION

The number incidences of many kind infectious diseases (e.g.: dengue disease, chikungunya, diarrhea, tuberculosis, HIV etc.) have been increasing dramatically. The high level of population density, migration, extreme weather changes, environmental factors and the socioeconomic condition causing the rapid transmission of the infectious diseases. Infectious diseases have a serious effect on the public health. Improper handling of infectious diseases lead to the higher negative impact e.g.: increasing the case fatality rate, disrupt the family economy and further disrupt national stability [1-2]. Implementation of such early warning systems (EWSs), including roadmaps to prevent or restrict the spread of an infectious disease, is still in its infancy in most (developing) countries [3]. For this purpose, we need to provide the information of the geographical and temporal distribution of the infectious diseases inside a map in order to investigation and intervention.

The classical approach commonly used in identifying the high-risk area is calculating the standardized incidence ratio for each area (SIR) [4]. However, SIR has been proved not reliable enough, especially for the small area. In case of the small area, the expected rate tends to be small and SIRs tend to be large [5]. A Bayesian smoothing techniques commonly used to overcome the drawbacks of the SIR [6]. The basic idea of this approach is to borrow the information from the relevance neighborhood areas to improve the reliability of the relative risk estimator [7]. Conditional Autoregressive (CAR) model was introduced as a prior distribution to accommodate the spatial
MATERIALS AND METHODS

Spatiotemporal Modeling: Spatiotemporal is used to model dengue and chikungunya disease incidence using Poisson log-linear model approach. Spatiotemporal data can be presented as $Y(s,t) = \{y(s,t), (s,t) \in \Re^2 \times \Re\}$ with s represent area level spatiotemporal data [18]. The set spatial areas $s_{1t}, \ldots, s_{nt}$ were used to present the spatiotemporal pattern of dengue and chikungunya disease risk in Bandung. Let $\{y_{it}: i=1,\ldots,n \text{ and } t=1,\ldots,T\}$ be the dengue or chikungunya count data collected for sub district $i$ at time point $t$. Bandung has $n=30$ and data was collected annually for $T=3$ year from 2012 until 2014. Number of cases $y_{it}$ follows a Poisson distribution with parameter $\lambda_{it} = E_i \theta_{it}$:

$$y_{it} \sim \text{Poisson}(E_i \theta_{it})$$

$$P(Y_{it} | E_i \theta_{it}) = \frac{e^{-E_i \theta_{it}} (E_i \theta_{it})^{y_{it}}}{y_{it}!}$$ (1)

where $E_i$ denotes the expected rate in area $i$ and time $t$, $\theta_{it}$ is the relative risk. The expected rate is calculated as [1]:

$$E_i = N_i \times \frac{\sum_{t=1}^{T} y_{it}}{\sum_{i=1}^{n} N_i}$$

with $N_i$ denotes the number of populations in district $i$ at time $t$. The relative risk can be modeled as $\theta_{it} = e^{\beta_{\text{fixed}} + \beta_{\text{random}}}$ and the log linear form:

$$\log(\theta_{it}) = \eta_{it} = \beta_{\text{fixed}} + \beta_{\text{random}}$$ (2)

and $\beta_{\text{fixed}}$ explains fixed effect for regression covariates $x$ and $\beta_{\text{random}}$ explains the random effect components including spatially and temporally unstructured and structured components. The spatiotemporal model can be written as Generalized Additive Model [19] follows:

$$\eta_{it} = c + \omega_k \times y_{it} + \phi_i + \delta_{it} + x_i \beta$$ (3)

where $\alpha$ denotes overall relative risk over space and time $\omega$, and $\nu$ are spatially structured, spatially unstructured components and $\phi_i$ denotes temporally random component respectively and $\beta$ denote regression coefficient of $x$. The spatially structured component is commonly modeled as Conditional Autoregressive (CAR) prior [1, 8, 20]. The CAR can be written as:
are, where $y$ denotes the number of incidences. The latent $\omega$ is assumed, and $\kappa_\omega$ denotes a precision hyperparameter of $\omega$. Based on the limitation of length time periods of our data set, we assume that the temporal dependence. The $\kappa_\omega$ is the expectation of $\omega$, where $\omega$ is an unknown scale parameter (i.e.: $\omega \sim N(0, \kappa_\omega)$). RW1 for the temporal dependence component $\phi$, is assumed follows type IV interaction model where the spatially and temporally structured effects $\omega$, and $\phi$, are interact [13].

**Shared Component Analysis:** Dengue disease and chikungunya have been assumed have a same risk factor-population of the *Aedes Aegypti* mosquito [21]. The following model formulation presents a typically shared component spatiotemporal for joint diseases:

$$
\log(\theta_{it1} | \phi) = \log(E_{it1}) + \alpha_1 + \theta_{it1} + \\
\omega_{it1} + \nu_{it1} + \phi_1 + \delta_{it} + x_{it} B
$$

$$
\log(\theta_{it2} | \phi) = \log(E_{it2}) + \alpha_2 + \phi_2 + \omega_{it2} + \\
\nu_{it2} + \delta_{it2} + x_{it} B
$$

where $(\theta_{it})$ is the expectation of $y_{it}$; $k = 1,2$ conditioning on the random effects $\phi = (\phi_1, \phi_2, \phi_3, \phi_4, \delta)$ is a random effects representing shared risk effect common to both diseases, and the components $(\omega, \nu, \phi, \delta)$ are equal with the previous. The elements $(\omega, \nu, \phi, \delta)$ are assumed independent; $\gamma$ is an unknown scale parameter (i.e.: relative weight or level importance) allowing for different shared 'risk gradients' with respect to each of the diseases outcomes [13].

**Integrated Nested Laplace Approximation (INLA):** INLA is a new approach of Bayesian analysis. It was developed to overcome the time computation problem of MCMC. Because of the spatiotemporal model is a complex model, here we use INLA to estimate Bayesian Spatiotemporal for dengue and chikungunya disease. The Bayesian spatiotemporal models can be applied into three stages. The first stage defines the observational model $\pi(\mathbf{y} | \mathbf{D})$, where $y$ denotes the number of incidences of the disease in a vector column. Defines the latent Gaussian field (GMRF) in the second stages with precision matrix $Q$ and the third stage defines controlling hyperparameter model [18]. For the first stage, we assume that number incidences of diseases follow Poisson distribution $y_{it} \sim \text{Poisson}(E_{it} e^{D_{it}})$ where

$$
y_j = (y_{i1}, ..., y_{iT})', x_j = (x_{i1}, ..., x_{iT})' \text{ and } E_i = (E_{it1}, ..., E_{iT})' .
$$

The likelihood function:

$$
\pi(y | E^T) = \prod_{i=1}^{n} \prod_{t=1}^{T} p(y_{it} | E_{it} e^{D_{it}}) \propto \prod_{i=1}^{n} \prod_{t=1}^{T} e^{-E_{it} e^{D_{it}}} (E_{it} e^{D_{it}})^{y_{it}}
$$

At the second stage, the latent model for uncorrelated random effects $\nu$ are modeled as $v_{it} \sim N(0, 1/\kappa_\nu)$, where $\kappa_\nu$ the precision hyperparameter for effects $\nu$. The latent model for spatial dependence component $\omega$ is assumed follows Besag, York and Mollié (BYM) model which proportional to the Gaussian distribution. The density function of spatially structure component $\omega$ can be written as:

$$
\pi(\omega | \kappa_\omega) \propto \kappa_\omega^{-2} \times \exp \left( - \frac{\kappa_\omega}{2} \sum_{i-j} (\omega_i - \omega_j)^2 \right) \forall \omega
$$

$$
\propto \kappa_\omega^{-2} \times \exp \left( - \frac{1}{2} \omega Q_{\omega} \omega \right) \forall \omega
$$

Temporal dependence component $\phi$ is assumed follows a first order random walk (RW1). RW1 for the Gaussian vector $\phi = (\phi_1, ..., \phi_t)'$ is constructed assuming independent increments:

$$
\Delta \phi = \phi_t - \phi_{t-1} \sim N(0, 1/\kappa_\phi)
$$

The density for $\phi$ is derived from its $T-1$ increments as

$$
\pi(\phi | \kappa_\phi) \propto \kappa_\phi^{-2} \times \exp \left( - \frac{\kappa_\phi}{2} \sum_{i-j} (\phi_i - \phi_j)^2 \right) \forall \phi
$$

$$
\propto \kappa_\phi^{-2} \times \exp \left( - \frac{1}{2} \phi Q_{\phi} \phi \right) \forall \phi
$$

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The prior density of the interaction $\delta$ type IV can be written as:

$$
\pi(\delta|\kappa_\delta) \propto \kappa_\delta^{\frac{n(T-1)}{2}} \exp\left(-\frac{\kappa_\delta}{2} \sum_{i=1}^{T} \sum_{j=1}^{T} (\Delta \delta_{ij} - \Delta \delta_{ij}^*)^2 \right) \forall \delta
$$

(12)

We define the prior density of shared component $\varphi$ equals to the prior density $\omega$ and with the precision matrix $Q_\omega$. For five models, $Q_\omega = \{Q_1, Q_2, Q_3, Q_4, Q_5\}$ is a precision matrix with $Q(\kappa_l) = \kappa_\omega R_{\kappa_l}$; $l = 1, 2, \ldots, 5$ and $R_{\kappa_l}$ is the structure matrix reflecting the spatial or temporal structure of the $l$th model.

A more general approach to defining the precision matrix is obtained with the following precision matrix [22]:

$$
Q(\kappa_l) = \left( I - \frac{\rho}{\lambda_{\max}} C(\kappa_l) \right)
$$

(13)

Here $I$ is the identity matrix, $\rho$ a spatial or temporal autocorrelation parameter, $C(\kappa_l)$ an adjacency matrix and $\lambda_{\max}$ the maximum eigenvalue of $C(\kappa_l)$. R-INLA assigns a Gaussian prior on $\log\left( \frac{\rho}{\lambda_{\max}} \right)$. This specification ensures that $\rho$ takes values between 0 and 1.

The unknown precision $\kappa = \{\kappa_1, \kappa_2, \kappa_3, \kappa_4, \kappa_5\}$ constitute the third stage and we assume that for every model $\kappa_l \sim \text{Gamma}(1,0.00005)$.

The joint posterior of Bayesian spatiotemporal shared component model can be written by:

$$
\pi(\theta, \kappa | y) \propto \pi(\kappa) | y^{\theta} \pi(\varphi | y) \propto \left( \frac{1}{2} \right)^{\frac{n(T-1)}{2}} \prod_{l=1}^{T} \exp\left(-\frac{1}{2} \theta^T Q_{\kappa_l} \theta \right) \sum_{l=1}^{L} \sum_{i=1}^{n} v_i \log(E_{il}^{\theta_l}) - E_{il}^{\theta_l}
$$

(14)

where $\theta = (\varphi', \varphi', \varphi', \varphi', \varphi')$. In INLA we do not interest with the joint posterior distribution. The main goal is to estimate the marginal posterior distribution of all component of the GMRF

$$
\pi(\theta_l | y) = \int \pi(\theta_l | y, \kappa) \pi(\kappa | y) d\kappa
$$

(15)

where $\kappa = \{\kappa_1, \kappa_2, \kappa_3, \kappa_4, \kappa_5\}$. The marginal posterior $p(\kappa | y)$ of the hyperparameters $\kappa$ can be approximated using Laplace Approximation $s[18]$:

$$
\pi(\kappa | y) \propto \pi(\theta_l, \kappa | y) \pi(\theta_l | \kappa, y) = \pi(y | \theta_l, \kappa, y) \pi(\theta_l | \kappa, y) = \pi(y | \theta_l, \kappa, y) \pi(\theta_l | \kappa, y)
$$

(15)

where $\pi(\kappa | y)$ is a Gaussian approximation to the full conditional of $\varphi$ and $\varphi^*(\kappa)$ is the mode of the full conditional for a given value of $\kappa_l$.

### RESULTS

Based on the data from the health department of Bandung city, the total population of Bandung city was $2,455,517$ in 2012 and $2,470,802$ in 2014. The population increased by 0.62%. The total number incidences of dengue disease and chikungunya were $5,096$ and $190$ in 2012 respectively.

In 2013 the number incidences increased significantly. We found the number incidences were $5,735$ and $459$. The number incidences decreased in 2014 - dengue disease and chikungunya were $3,135$ and $245$ respectively. The variability of the number incidence was influenced by the same factors. The population of mosquitoes of aedes aegypti is believed as a shared risk factor.
Table 1: Statistics of SIR for dengue disease and chikungunya

<table>
<thead>
<tr>
<th>Year</th>
<th>Dengue disease</th>
<th>Chikungunya</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean SIR</td>
<td>Minimum SIR</td>
</tr>
<tr>
<td>2012</td>
<td>1.06</td>
<td>0.48</td>
</tr>
<tr>
<td>2013</td>
<td>1.07</td>
<td>0.52</td>
</tr>
<tr>
<td>2014</td>
<td>1.06</td>
<td>0.45</td>
</tr>
</tbody>
</table>

(a) SIR of Dengue disease

(b) SIR of Chikungunya

Table 2 presents the correlation of incidence rate of dengue disease and chikungunya for 2012 – 2014. Although the correlations are small, the shared component analysis still useful to provide more precisely relative risk estimates and to identify which diseases are more impacted by the number of mosquitoes risk factor.

Our analysis is conducted to obtain more reliable estimates of the relative risk of dengue disease and chikungunya in 2012-2014. The shared component analysis is used based on several criteria of model comparison include Deviance Information Criterion (DIC), Mean Absolute Prediction (MAP) and Pseudo R²; DIC is defined as $\text{DIC} = \bar{D} + p_D$ where $\bar{D}$ is the posterior of the deviance and measure model fit; and $p_D$ is the effective number of model parameters and measures model complexity.

Table 2: Correlation between the standardized incidence ratios for dengue disease and chikungunya between 2012 and 2014

<table>
<thead>
<tr>
<th></th>
<th>Dengue disease</th>
<th>Chikungunya</th>
</tr>
</thead>
<tbody>
<tr>
<td>2012</td>
<td>1</td>
<td>-</td>
</tr>
<tr>
<td>2013</td>
<td>1</td>
<td>0.103485</td>
</tr>
<tr>
<td>2014</td>
<td>1</td>
<td>-0.06317</td>
</tr>
</tbody>
</table>

Table 3: DIC Comparison

<table>
<thead>
<tr>
<th></th>
<th>Shared Component</th>
<th>Dengue disease</th>
<th>Chikungunya</th>
</tr>
</thead>
<tbody>
<tr>
<td>DIC</td>
<td>1150.998</td>
<td>773.260</td>
<td>803.980</td>
</tr>
</tbody>
</table>
The DIC values from Shared Component analysis smaller than the sum of the individual BYM models. The shared component model presents a high improvement of DIC. MAP and Pseudo Determination coefficient are two other criteria for selecting the best fit model. MAP
\begin{equation}
MAP_j = \frac{1}{90} \sum_{i=1}^{n} \sum_{t=1}^{T} \left[ \hat{y}_{it} - \hat{y}_{it}(j) \right]^2
\end{equation}
and pseudo
\begin{equation}
\hat{R}_j^2 = 1 - \frac{\sum_{i=1}^{n} \sum_{t=1}^{T} \left[ \hat{y}_{it} - \hat{y}_{it}(j) \right]^2}{\sum_{i=1}^{n} \sum_{t=1}^{T} \left[ \hat{y}_{it} - \bar{y}_t \right]^2}
\end{equation}
for j = dengue disease and chikungunya

The sum of the MAP for shared component model is smaller than the sum of the individual BYM model, and the average of the pseudo \( \hat{R}_j^2 \) greater than the individual BYM model. The both of criteria present the shared component model has a better fit than individual BYM to predict the relative risk.

<table>
<thead>
<tr>
<th>Disease</th>
<th>MAP Dengue disease</th>
<th>MAP Chikungunya</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shared Component</td>
<td>2.504718</td>
<td>0.9154278</td>
</tr>
<tr>
<td>Dengue disease</td>
<td>3.982442</td>
<td>-</td>
</tr>
<tr>
<td>Chikungunya</td>
<td>-</td>
<td>0.5133877</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Disease</th>
<th>( \hat{R}_j^2 ) Dengue disease</th>
<th>( \hat{R}_j^2 ) Chikungunya</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shared Component</td>
<td>0.9966181</td>
<td>0.9964736</td>
</tr>
<tr>
<td>Dengue disease</td>
<td>0.9874726</td>
<td>-</td>
</tr>
<tr>
<td>Chikungunya</td>
<td>-</td>
<td>0.9919791</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Variable</th>
<th>Mean</th>
<th>Sd</th>
<th>0.025quant</th>
<th>0.5quant</th>
<th>0.975quant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hygiene Index</td>
<td>-0.0019</td>
<td>0.0035</td>
<td>-0.0088</td>
<td>-0.0019</td>
<td>0.0049</td>
</tr>
<tr>
<td>Larvae -Free Home Index</td>
<td>0.0232</td>
<td>0.0231</td>
<td>-0.022</td>
<td>0.0231</td>
<td>0.0688</td>
</tr>
<tr>
<td>Rainfall</td>
<td>-0.0358</td>
<td>0.024</td>
<td>-0.0831</td>
<td>-0.0358</td>
<td>0.0111</td>
</tr>
<tr>
<td>Temperature</td>
<td>-6.9406</td>
<td>4.7439</td>
<td>-16.2898</td>
<td>-6.9318</td>
<td>2.3528</td>
</tr>
<tr>
<td>Humidity</td>
<td>2.0293</td>
<td>1.3942</td>
<td>-0.7038</td>
<td>2.0266</td>
<td>4.7734</td>
</tr>
<tr>
<td>Healthy Housing Index</td>
<td>0.0217</td>
<td>0.0184</td>
<td>-0.0142</td>
<td>0.0216</td>
<td>0.0582</td>
</tr>
<tr>
<td>Intercept1</td>
<td>11.2413</td>
<td>9.5279</td>
<td>-7.4524</td>
<td>11.2287</td>
<td>29.9819</td>
</tr>
</tbody>
</table>

There are six explanatory variables we use to predict the number incidences of dengue disease and chikungunya. Although all the variables do not have significant effect to the number incidences, we obtain the important information from the analysis. This result indicates there are other factors that affect the variation of the number incidence. The most important factors but difficult to obtain is the number of female \textit{Aedes Aegypti} (Yellow Disease Mosquito) which carry and spread the dengue and chikungunya viruses in every district of Bandung. The number this kind mosquito is a risk factor that has significant effect to explain the variability of number incidences of both of diseases. The Bandung city government has done several ways to control the \textit{Aedes Aegypti} breeding. Fogging is one of the most commonly used. However, this way is not effective because the Government does not have accurate information which area has high risk or lower risk. Fogging is only done if dengue disease cases found. While the \textit{Aedes Aegypti} mosquito not only spread dengue virus but also chikungunya. The joint diseases modeling is needed to inform the high-risk clustering area accurately with considering the number of female \textit{Aedes Aegypti} mosquito as an unobserved variable.
Table 7: Posterior median (95% CI) relative weights of dengue disease and chikungunya in the shared components analysis

<table>
<thead>
<tr>
<th>Disease</th>
<th>Year</th>
<th>Dengue disease</th>
<th>Chikungunya</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dengue disease</td>
<td>2012</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2013</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2014</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Chikungunya</td>
<td>2012</td>
<td>4.73 (3.70-5.76)</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>2013</td>
<td>6.30 (5.25-7.18)</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>2014</td>
<td>-4.26 (-5.23-(-3.55))</td>
<td>1</td>
</tr>
</tbody>
</table>

Note: The main body of the table represents the weight of the disease listed along the top row relative to the disease along the left-hand side (with 95% confidence intervals). If the RR is > 1.00 the disease along the top row has more weight if the RR is < 1.00 the disease along the left-hand side has more weight.

Table 7 presents the relative weight, or level importance, that each shared component has for the different dengue disease and Chikungunya diseases. The effect of a number of female *Aedes Aegyti* mosquito was more important for dengue disease in every year.

The relative weight in 2014 has a negative sign. It means dengue disease and chikungunya have a different pattern in spreading. The high-risk district in dengue disease means low-risk of chikungunya. The Figure 2(a) shows in periods 2012 to 2013, the number of female *Aedes Aegyti* mosquito was more important in north districts of Bandung and in 2014 was a more important in south districts. The average of relative risk for dengue disease greater than one which means the number incidences greater than the expected.

Table 8: Posterior mean (95% CI) relative risk of dengue disease and chikungunya in the shared components analysis

<table>
<thead>
<tr>
<th>Year</th>
<th>Dengue disease</th>
<th>Chikungunya</th>
</tr>
</thead>
<tbody>
<tr>
<td>2012</td>
<td>1.06 (0.56-1.57)</td>
<td>0.90 (0.40-1.41)</td>
</tr>
<tr>
<td>2013</td>
<td>1.07 (0.56-1.58)</td>
<td>0.97 (0.46-1.48)</td>
</tr>
<tr>
<td>2014</td>
<td>1.07 (0.56-1.57)</td>
<td>1.33 (0.82-1.83)</td>
</tr>
</tbody>
</table>

Although the average of the relative risk high, it is not significant. For the chikungunya, only in 2014, the relative risk is high. This is because of some districts in Bandung uninfected.
Fig. 2: Maps of the posterior mean estimated relative risk for (a) dengue disease and (b) chikungunya in Bandung city, 2012-2014, using shared component model

Table 9: Statistics of estimated relative risk for dengue disease and chikungunya

<table>
<thead>
<tr>
<th>Year</th>
<th>Dengue disease</th>
<th>Chikungunya</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean SIR</td>
<td>Minimum SIR</td>
</tr>
<tr>
<td>2012</td>
<td>1.061</td>
<td>0.499</td>
</tr>
<tr>
<td>2013</td>
<td>1.070</td>
<td>0.513</td>
</tr>
<tr>
<td>2014</td>
<td>1.065</td>
<td>0.469</td>
</tr>
</tbody>
</table>

DISCUSSION

This research presents the application of share component analysis in spatiotemporal joint disease modeling which applied for dengue disease and chikungunya infectious diseases. The spatiotemporal maps clearly show the space-time different in the relative risk of the both diseases. The Conditional Autoregressive (CAR) model is used to accommodate the spatial autocorrelation and Random walk order 1 (RW1) is used to accommodate the temporal autocorrelation. The resulting maps are clearly smooth and more precise with smaller the confidence interval compares than SIRs result, especially for chikungunya's Maps. Smoothing is important in disease mapping to remove the “noise” and provide the clear map in a pattern of spread of diseases. We can see clearly highest and lowest cluster of relative risk for every year and also clearly the temporal dependency. We can found that the high and the low relative risk both of diseases almost similar in several areas. Both of diseases have a similarity cluster in North of Bandung but different in South of Bandung especially for 2012 and 2013. Sub-Districts in North Bandung have a high risk for both of diseases.

The shared component results inform that the number of female *Aedes Aegypti* mosquitoes as a component have a more significant effect on the dengue disease cases. The number of dengue has almost five times greater effect on dengue disease than chikungunya. This is because more *Aedes Aegypti* mosquitoes are infected with dengue virus than chikungunya virus. The limitation of this research is in the time period. The incubation of both the diseases is 5-7 days. It means the number incidences should be reported every week. However, we only have annual data. The public health office publishes health data only once a year in the annual report. The weekly or monthly data should present more precise results.

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