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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

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dependence information in estimating the relative risk [8]. Bayesian CAR model was used in several studies of diseases mapping [9-11].

The existence of the temporal dependencies can be accommodated using several techniques based on the pattern of the data. [12] proposed a parametric trend for temporal component and [13] introduced dynamic nonparametric formulation for the linear predictor.

The study of multiple diseases becomes an important issue in diseases mapping. The basic idea in developing the multiple disease mapping is that the infectious diseases are common has some diseases sharing risk-factors–lifestyle variables, environmental or genetic factors [13]. The existing sharing risk factors may be seen from the similarity of the pattern of the spatial distribution of the risk of the disease. Proper multivariate conditional autoregressive (MCAR) is used modeling multiple infectious diseases [14]. MCAR has used for modeling of disease risks correlations across diseases and over geographical areas. Bayesian hierarchical shared component models (SCMs) with shared and disease-specific risks prior components for modeling of multivariate diseases that share common risk factor(s) was introduced [15].

Disease dengue is mosquito-transmitted viral diseases that are endemic in Asia and Africa. Indonesia is the country in South East Asia with the highest risk of dengue disease for every year [16]. High rates of dengue disease cases may be followed by high rates of other infectious diseases such as chikungunya. This is because of the dengue disease and chikungunya is transmitted to human by same vector the mosquitoes *Aedes Aegypti*, which are found easily throughout the tropical country [16]. Therefore, it can be said the population of *Aides Aegypty* becomes the shared risk factor of the dengue disease and chikungunya infectious diseases. Bandung is a capital city of Wes Java –Indonesia has a serious problem with both of the diseases [17]. The incidence rates always higher than the expected rate. The EWS is needed to suppress the incidence rate of both of the diseases.

In this paper, we developed a Bayesian spatiotemporal shared component model for estimating multiple infectious diseases –chikungunya and dengue disease in Bandung, Indonesia. The rest of the paper is organized as follows. Section 2 presents the Method of spatiotemporal and shared component model. Section 3 presents the results. Section 4 presents the discussion of the results.

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 $Y(s,t) \equiv \{y(s,t),(s,t) \in \Re^2 \times \Re\}$ with s represent area level spatiotemporal data [18]. The set spatial areas s_{11}, ... , s_{nT} were used to present the spatiotemporal pattern of dengue and chikungunya disease risk in Bandung. Let $\{y_{it} : i = 1,...,n \text{ and } t = 1,...,T\}$ 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 data for $T=3$ year from 2012 until 2014. Number of cases y_{it} follows a Poisson distribution with parameter $\lambda_{it} = E_{it}\theta_{it}$:

$$y_{it} \sim Poisson(E_{it}\theta_{it})$$
$$P(y_{it} \mid E_{it}\theta_{it}) = \frac{e^{-E_{it}\theta_{it}}(E_{it}\theta_{it})^{y_{it}}}{y_{it}!} \quad (1)$$

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

$$E_{it} = N_{it} \times \frac{\sum_{i=1}^{n} y_{it}}{\sum_{i=1}^{n} N_{it}}$$

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

$$\log(\theta_{it}) = \eta_{it} = f_{fixed} + f_{random} \quad (2)$$

and f_{fixed} explains fixed effect for regression covariates $\mathbf{x}$ and f_{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:

$$\eta_{it} = \alpha + \omega_i + \nu_i + \phi_t + \delta_{it} + \mathbf{x}_{it}^{/}\boldsymbol{\beta} \quad (3)$$

where α denotes overall relative risk over space and time ω_i and ν_i are spatially structured, spatially unstructured components and ϕ_t denotes temporally random component respectively and $\boldsymbol{\beta}$ denote regression coefficient of $\mathbf{x}$. The spatially structured component is commonly modeled as Conditional Autoregressive (CAR) prior [1, 8, 20]. The CAR can be written as:

$$\omega_i \mid \omega_{-i}, W, \kappa_\omega \sim N\left(\frac{\sum_{j=1}^{n} w_{ij}\omega_j}{\sum_{j=1}^{n} w_{ij}}, \frac{1}{\kappa_\omega \sum_{j=1}^{n} w_{ij}}\right) \quad (4)$$

where $\sum_{j=1}^{n} w_{ij} = n_i$ is the number of neighbors of area i and w_{it} is the (i,j)th element of the spatial weight's matrix **W**. Here, queen spatial contiguity matrix is used to present the spatial dependence. The κ_ω denotes a precision hyperparameter of ω_i. Based on the limitation of length time periods of our data set, we assume that the temporal structure ϕ_t follows Random Walk of the first order (RW1). Its prior distribution is given by [11]:

$$\phi_t \mid \phi_{t-1} \sim N\left(\phi_{t-1}, 1/\kappa_\phi\right) \quad (5)$$

The specification prior of the interaction component δ_{it} is assumed follows type IV interaction model where the spatially and temporally structured effects ω_i. and ϕ_t 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:

$$\log(\theta_{it1} \mid \vartheta) = \log(E_{it1}) + \alpha_1 + \varphi_{it}\gamma + \omega_{i1} + \nu_{i1} + \phi_{t1} + \delta_{it} + \mathbf{x}_{it}^{/}\boldsymbol{\beta} \quad (6)$$

$$\log(\theta_{it2} \mid \vartheta) = \log(E_{it2}) + \alpha_2 + \frac{\varphi_{it}}{\gamma} + \omega_{i2} + \nu_{i2} + \phi_{t2} + \delta_{it2} + \mathbf{x}_{it}^{/}\boldsymbol{\beta} \quad (7)$$

where $(\theta_{itk}|\boldsymbol{\vartheta})$ is the expectation of y_{itk}; k = 1,2 conditioning on the random effects $\vartheta = (\varphi', \omega', \nu', \phi', \delta')', \varphi = (\varphi_{it}', .., \varphi_{nt}')'$ 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; γ 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 $\pi(\mathbf{y}|\boldsymbol{\vartheta})$, 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 $\boldsymbol{Q}$ and the third stage defines controlling hyperparameter model [18]. For the first stage, we assume that number incidences of diseases follow Poisson distribution $y_{it} \sim Poisson\left(E_{it}e^{\eta_{it}}\right)$ where

$\mathbf{y}_i = (y_{i1}, ..., y_{iT})'; \mathbf{x}_i = (x_{i1}, ..., x_{iT})'$ and $\mathbf{E}_i = (E_{i1}, ..., E_{iT})'$.

The likelihood function:

$$\pi(\mathbf{y} \mid \mathbf{E}e^{\eta}) = \prod_{i=1}^{n}\prod_{t=1}^{T} p\left(y_{it} \mid E_{it}e^{\eta_{it}}\right) \propto \prod_{i=1}^{n}\prod_{t=1}^{T} \frac{e^{-E_{it}e^{\eta_{it}}}(E_{it}e^{\eta_{it}})^{y_{it}}}{y_{it}!} \quad (8)$$

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

$$\pi(\omega \mid \kappa_\omega) \propto \kappa_\omega^{\frac{n-1}{2}} \times \exp\left(-\frac{\kappa_\omega}{2}\sum_{i\sim j}\left(\omega_i - \omega_j\right)^2\right)\forall t \propto \kappa_\omega^{\frac{n-1}{2}} \times \exp\left(-\frac{1}{2}\omega'\mathbf{Q}_\omega\omega\right)\forall t \quad (9)$$

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

$$\Delta\phi_t = \phi_t - \phi_{t-1} \sim N(0, 1/\kappa_\phi) \quad (10)$$

The density for ϕ is derived from its T-1 increments as

$$\pi(\phi \mid \kappa_\phi) \propto \kappa_\phi^{\frac{T-1}{2}} \times \exp\left(-\frac{\kappa_\phi}{2}\sum_{i\sim j}\left(\omega_i - \omega_j\right)^2\right)\forall t \propto \kappa_\phi^{\frac{T-1}{2}} \times \exp\left(-\frac{1}{2}\phi'\mathbf{Q}_\phi\phi\right)\forall i \quad (11)$$

The prior density of the interaction **δ** type IV can be written as:

$$\pi(\mathbf{d}\mid\kappa_\delta)\propto\kappa_\delta^{-\frac{n(T-1)}{2}}\exp\left(-\frac{\kappa_\delta}{2}\sum_{t=1}^{T}\sum_{i\sim j}\left(\Delta\delta_{it}-\Delta\delta_{jt}\right)^2\right)\forall it$$
$$\propto\kappa_\delta^{-\frac{n(T-1)}{2}}\exp\left(-\frac{\kappa_\delta}{2}\mathbf{d}'\mathbf{Q}_\delta\mathbf{d}\right)\forall it \quad (12)$$

We define the prior density of shared component φ equals to the prior density ω and with the precision matrix $\mathbf{Q}_\varphi$. For five models, $\mathbf{Q}(\kappa)=\{\mathbf{Q}_\nu,\mathbf{Q}_\omega,\mathbf{Q}_\phi,\mathbf{Q}_\delta,\mathbf{Q}_\varphi\}$ is a precision matrix with $\mathbf{Q}(\kappa_l)=\kappa_l\mathbf{R}_{\kappa_l}$; l=1,2,…,5 and $\mathbf{R}_{\kappa_l}$ 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]:

$$\mathbf{Q}(\kappa_l)=\left(\mathbf{I}-\frac{\rho}{\lambda_{\max}}\mathbf{C}(\kappa_l)\right) \quad (13)$$

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

The unknown precision $\kappa=\{\kappa_\nu,\kappa_\omega,\kappa_\phi,\kappa_\delta,\kappa_\varphi\}$ constitute the third stage and we assume that for every model $\kappa_l\sim Gamma\ (1,0.00005)$.

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

$$\pi(\vartheta,\kappa\mid\mathbf{y})\propto\pi(\kappa)\left|\mathbf{Q}_\kappa\right|^{1/2}\times\exp\left(-\frac{1}{2}\vartheta'\mathbf{Q}_\kappa\vartheta\right)+\sum_{i=1}^{n}\sum_{t=1}^{T}y_{it}\log(E_{it}e^{\eta_{it}})-E_{it}e^{\eta_{it}} \quad (14)$$

where $\vartheta=(\nu',\omega',\phi',\delta',\varphi')'$. 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

$$\pi(\vartheta_l\mid\mathbf{y})=\int\pi(\vartheta_l\mid\kappa,\mathbf{y})\pi(\kappa\mid\mathbf{y})d\kappa \quad (15)$$

where $\kappa=\{\kappa_\nu,\kappa_\omega,\kappa_\phi,\kappa_\delta,\kappa_\varphi\}$. The marginal posterior $\pi(\kappa\mid\mathbf{y})$ of the hyperparameters κ can be approximated using Laplace Approximation s [18]:

$$\tilde{\pi}(\kappa\mid\mathbf{y})\propto\frac{\pi(\vartheta,\kappa\mid\mathbf{y})}{\pi_G(\vartheta_l\mid\kappa,\mathbf{y})}=\left.\frac{\pi(\mathbf{y}\mid\vartheta,\kappa)\pi(\vartheta\mid\kappa)\pi(\kappa)}{\pi_G(\vartheta_l\mid\kappa,\mathbf{y})}\right|_{\vartheta=\vartheta^*(\kappa)} \quad (15)$$

where $\tilde{\pi}(\kappa\mid\mathbf{y})$ is a Gaussian approximation to the full conditional of ϑ and $\vartheta^*(\kappa)$ is the mode of the full conditional for a given value of κ_l.

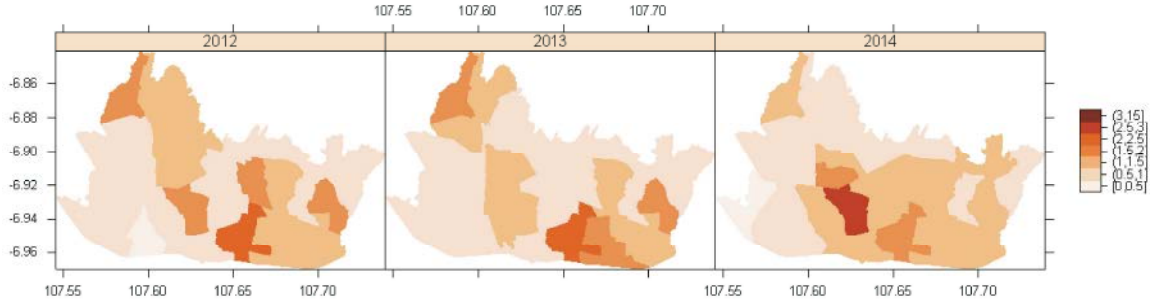
```
MODEL=Y ~ -1+X1+X2+X3+X4+X5+X6 + Intercept +f(i1,model="besag",graph=W)+
f(j1,copy="i1",hyper=list(theta=list(fixed=FALSE, param=c(1,1),
range=c(0,Inf))))+ f(i2,model="besag",graph=W)+ f(j2,copy="i2",
hyper=list(theta=list(fixed=FALSE, param=c(1,1), range=c(0,Inf))))+
f(i3,model="besag",graph=W)+f(j3,copy="i3",hyper=list(theta=list(fixed=FALS
E, param=c(1,1), range=c(0,Inf))))+f(i4,model="besag",graph=W)+
f(j4,copy="i4",hyper=list(theta=list(fixed=FALSE,  param=c(1,1),
range=c(0,Inf))))+ f(ID1,model="bym", graph=W,
hyper=list(theta=list(initial=log(1), param=c(0.5,0.0005))))+
f(IT1,model="rw1")+ f(IT2,model="iid")+ f(ID3,model="besag",
graph=W,group=IT3,control.group=list(model="rw1"))
RMODEL <- inla(MODEL,family="poisson", data=DATA, E=E, control.predictor=
list(compute=TRUE,link=1),control.compute=list(dic=TRUE,cpo=TRUE))
```

RESULTS

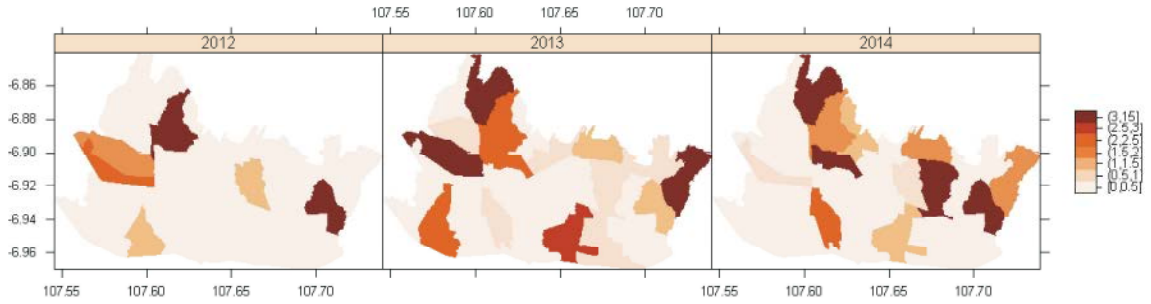
Based on the data from the health department of Bandung city, the total population of Bandung city was 2,455,517 in 2012 and 2,470,802 in 2014. The population increased by 0.62%. The total number incidences of dengue disease and chikungunya were 5,096 and 190 in 2012 respectively. In 2013 the number 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 aegipty is believed as a shared risk factor.

Table 1: Statistics of SIR for dengue disease and chikungunya

	Dengue disease			Chikungunya		
Year	Mean SIR	Minimum SIR	Maximum SIR	Mean SIR	Minimum SIR	Maximum SIR
2012	1.06	0.48	2.09	0.77	0	13.72
2013	1.07	0.52	2.45	0.98	0	5.03
2014	1.06	0.45	2.59	1.3	0	8.67



(a) SIR of Dengue disease



(b) SIR of Chikungunya

Fig. 1: Maps of the SIR for (a) Dengue disease and Chikungunya between 2012 and 2014

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

	2012		2013		2014	
	Dengue disease	Chikungunya	Dengue disease	Chikungunya	Dengue disease	Chikungunya
Dengue disease	1	-	1	-	1	-
Chikungunya	0.060571	1	0.103485	1	-0.06317	1

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 R^2. DIC is defined as $DIC = \bar{D} + p_D$ 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 3: DIC Comparison

	Shared Component	Dengue disease	Chikungunya
DIC	1150.998	773.260	803.980

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 forselecting the best fit model. $MAP_j = \frac{1}{90}\sum_{i=1}^{n}\sum_{t=1}^{T}\left(\left|\hat{y}_{it(j)} - y_{it(j)}\right|\right)$ and pseudo $\tilde{R}_j^2 = 1 - \frac{\sum_{i=1}^{n}\sum_{t=1}^{T}\left(\hat{y}_{it(j)} - y_{it(j)}\right)^2}{\sum_{i=1}^{n}\sum_{t=1}^{T}\left(\hat{y}_{it(j)} - \bar{y}_{it(j)}\right)^2}$ for j = dengue disease and chikungunya

Table 4: MAP Comparison

	Disease	
	MAP Dengue disease	MAP Chikungunya
Shared Component	2.504718	0.9154278
Dengue disease	3.982442	-
Chikungunya	-	0.5133877

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 $\tilde{R}^2$ 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 5: Pseudo R^2

	Disease	
	$\tilde{R}^2$ Dengue disease	$\tilde{R}^2$ Chikungunya
Shared Component	0.9966181	0.9964736
Dengue disease	0.9874726	-
Chikungunya	-	0.9919791

Table 6: The parameters estimate of shared component Bayesian spatiotemporal model

Variable	Mean	Sd	0.025quant	0.5quant	0.975quant
Hygiene Index	-0.0019	0.0035	-0.0088	-0.0019	0.0049
Larvae –Free Home Index	0.0232	0.0231	-0.022	0.0231	0.0688
Rainfall	-0.0358	0.024	-0.0831	-0.0358	0.0111
Temperature	-6.9406	4.7439	-16.2898	-6.9318	2.3528
Humidity	2.0293	1.3942	-0.7038	2.0266	4.7734
Healthy Housing Index	0.0217	0.0184	-0.0142	0.0216	0.0582
Intercept1	11.2413	9.5279	-7.4524	11.2287	29.9819
Intercept2	9.7159	9.5213	-8.9708	9.7054	28.4385

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 *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 *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 *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 *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

Disease	Year	Dengue disease	Chikungunya
Dengue disease	2012	1	
	2013	1	
	2014	1	
Chikungunya	2012	4.73 (3.70-5.76)	1
	2013	6.30 (5.25-7.18)	1
	2014	-4.26 (-5.23-(-3.55))	1

Note: The main body of the table represent 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.

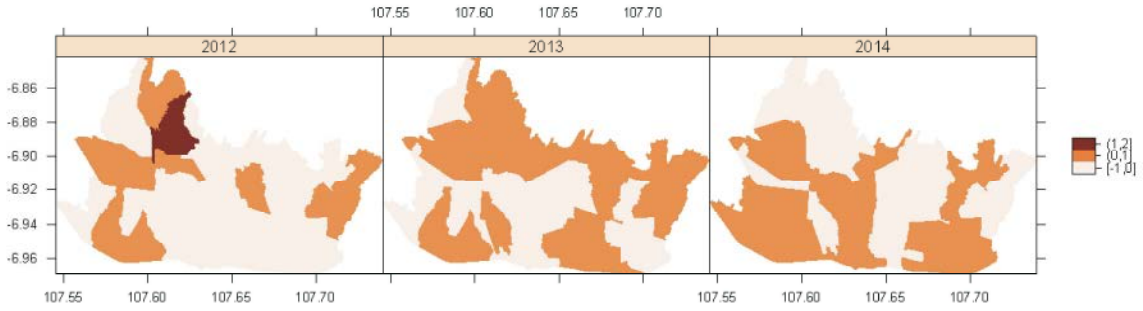
Table 7 presents the relative weight, or level importance, that each shared component has for the different dengue disease and Chikungunya diseases. The effect of a number of female *Aides Aegyti* mosquito was more important for dengue disease disease in every year.

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 *Aides 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.

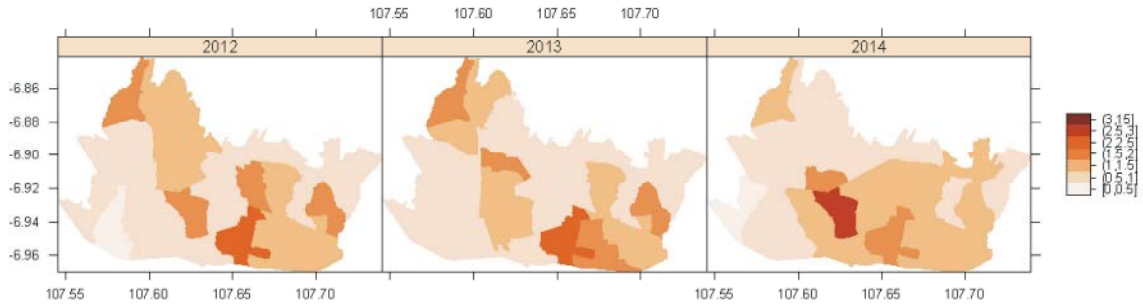
Table 8: Posterior mean (95% CI) relative risk of dengue disease and chikungunya in the shared components analysis

Year	Dengue disease	Chikungunya
2012	1.06 (0.56-1.57)	0.90 (0.40-1.41)
2013	1.07 (0.56-1.58)	0.97 (0.46-1.48)
2014	1.07 (0.56-1.57)	1.33 (0.82-1.83)

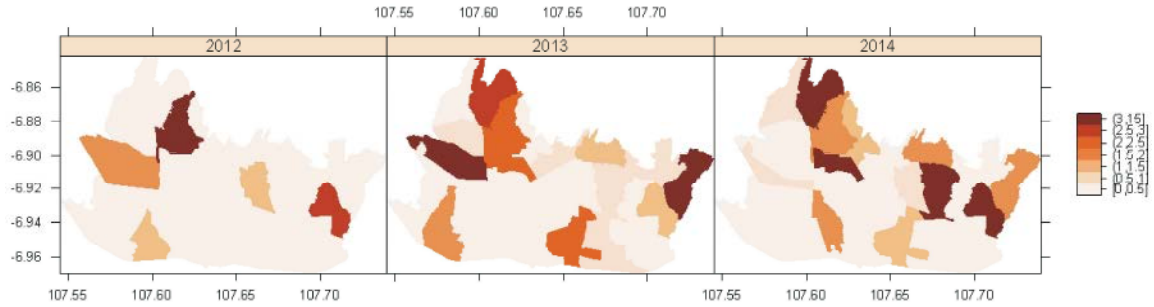
Although the average of the relative risk high, it is not significant. For the chikungunya, only in 2014, the relative risk is high. This is because of some districts in Bandung uninfected.



(a) Shared Components



(a) Relative risk of the dengue disease disease



(b) (Relative Risk of the chikungunya disease

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

	Dengue disease			Chikungunya		
	Mean SIR	Minimum SIR	Maximum SIR	Mean SIR	Minimum SIR	Maximum SIR
2012	1.061	0.499	2.070	0.900	0.080	13.540
2013	1.070	0.513	2.475	0.970	0.025	4.959
2014	1.065	0.469	2.604	1.328	0.006	8.586

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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