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Multiple endemic disease risk modeling using a Bayesian spatiotemporal shared components model

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A B S T R A C T

Traditionally, endemic diseases such as dengue, diarrhea, and tuberculosis are modeled separately, which leads to a limited understanding of current disease dynamics and an inaccurate evaluation of the parameters of the different models. In this study, we propose a joint spatiotemporal model to predict the risks of multiple endemic diseases and identify hotspots. The model includes spatial shared component random effects and a covariate for healthy behavior. The model was applied to the joint modeling of dengue, diarrhea, and tuberculosis in thirty districts in Bandung, Indonesia over a five-year period. Our findings show that the joint model was effective in understanding the characteristics of the diseases. One potential advantage of using shared component models is that they can identify diseases with spatial or temporal distribution patterns and consider shared risk factors that may be spatially correlated, such as climate. It is recommended to conduct exploratory analyses to determine the correlation between the risks of the diseases being studied and the reference disease before using this type of model.

1. Introduction

Tropical countries often have a wealth of natural resources, but they may also face various public health challenges due to the presence of endemic diseases such as dengue, malaria, diarrhea, tuberculosis, and many others (Chowdhury et al., 2018). These diseases can be transmitted through various mechanisms, including direct or indirect contact, droplet transmission, vector-borne transmission, sexual transmission, and mother-to-child transmission (Seventer & Hochberg, 2017). It is important to take measures to prevent the spread of these diseases, such as practicing good hygiene, using insect repellent, and getting vaccinated when available. It is also important to seek medical treatment if you are experiencing symptoms of these diseases (CDC, 2022). Identifying the spatiotemporal hotspots for infectious diseases is an important strategy for controlling disease transmission and implementing early warning systems (Jaya & Folmer, 2020, 2022). *Hotspots* refer to areas or times where the incidence of a particular disease is significantly higher than the average for a particular region or population (Aguayo et al., 2020). By identifying and monitoring hotspots, public health authorities can target interventions and resources to the areas where they are most needed, helping to reduce the overall burden of the disease (Taal et al., 2022). This can include implementing measures such as vaccination campaigns, improving access to clean water and sanitation, and providing education about disease prevention. In addition to identifying hotspots, it is also important to implement surveillance systems to track the spread of infectious diseases and monitor trends in disease incidence. This can help public health authorities respond quickly to outbreaks and implement appropriate control measures to prevent further transmission. Overall, the identification of spatiotemporal hotspots and the implementation of effective surveillance systems are crucial for the early warning and control of infectious diseases (Castillo-Chavez, 2010).

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Modeling multiple infectious diseases simultaneously is important because it allows researchers and public health officials to better understand the interactions and potential impacts of different diseases on a population. By understanding these interactions, it becomes possible to develop more effective strategies for controlling and mitigating the spread of multiple diseases (Lawsona & Rotejanaprasert, 2018). There are several approaches that can be used to model multiple infectious diseases simultaneously, including compartmental models, network models, and agent-based models (Yao et al., 2022). Each of these approaches has its own strengths and limitations, and it is important to choose the most appropriate method based on the specific needs of the situation. One important consideration when modeling multiple infectious diseases is to accurately capture the interactions between the diseases. For example, if one disease makes an individual more susceptible to another disease, this must be considered in the model. Similarly, if one disease can protect against another disease (such as how some vaccines provide immunity to multiple diseases), this should also be included in the model. Overall, the ability to model multiple infectious diseases simultaneously is an important tool for understanding and mitigating the spread of these diseases in a population (Lawson & Rotejanaprasert, 2018). Bayesian shared component models can be useful for modeling multiple infectious diseases simultaneously because they allow for the incorporation of information from multiple sources and the integration of multiple data types (Norwood et al., 2020). The Bayesian method is a powerful statistical technique that allows for the estimation and inference of regression models using additional information provided in the form of prior probabilities. This approach has gained significant popularity in recent decades, and is expected to become the dominant method in statistical analysis in the coming years. One key advantage of the Bayesian method is that it provides more reliable estimates due to the incorporation of prior information. This can lead to more accurate predictions and a better understanding of the underlying relationships within the data. Overall, the Bayesian method offers a valuable alternative to traditional statistical techniques and is well-suited for a wide range of applications in data analysis and modeling (Jaya et al., 2019a).

In a Bayesian shared component model, each disease is modeled as a separate component, and there is a shared component that represents the underlying risk factors or processes that influence the spread of all the diseases Knorr-Held and Best (2001). This allows the model to capture the common factors that may be driving the transmission of multiple diseases, as well as the specific factors that are unique to each disease. One advantage of using a Bayesian shared component model is that it allows for the incorporation of prior knowledge or beliefs about the diseases as well as the incorporation of new data as it becomes available. This makes it possible to update the model as new information becomes available and to make more accurate predictions about the spread of the diseases. Overall, Bayesian shared component models can be a useful tool for understanding and modeling the spread of multiple infectious diseases simultaneously and for developing effective strategies for controlling and mitigating the spread of these diseases (Jaya et al., 2022).

Several studies, such as Knorr-Held and Best (2001) and Jaya & Folmer (2022), have utilized the shared component model. However, this study focuses specifically on the number of cases without considering covariates. The authors of this study developed a shared component model that accounts for three different types of disease and includes covariates. In addition, this study also performed hotspot calculations based on exceedance probability. Exceedance probability is a statistical concept that is often used in the analysis of environmental data for the purpose of identifying spatiotemporal cluster hotspots, or areas where a certain threshold has been exceeded (Lawson & Rotejanaprasert, 2014; Jaya et al., 2019b). For example, exceedance probability may be used to identify areas where the concentration of a particular pollutant exceeds a certain level or where the likelihood of a natural disaster occurring is higher than average. To calculate exceedance probability, data is collected and analyzed to determine the probability that a certain threshold will be exceeded at a particular location. This probability is then used to identify areas where the risk of a particular event or phenomenon is higher than average. Hotspot analysis using exceedance probability can be an effective way to identify areas where preventive measures or remediation efforts may be needed. Parameter estimation in this study was conducted using the Integrated Nested Laplace Approximation (INLA) method (Blangiardo et al., 2013). The mentioned methodology will be applied to major endemic diseases in Bandung, Indonesia, including dengue, diarrhea, and tuberculosis (TB). Dengue, diarrhea, and tuberculosis are all common infectious diseases in tropical countries, including Indonesia (Sihaloho et al., 2021). Dengue fever is transmitted by the bite of an infected Aedes mosquito and can cause high fever, severe headache, muscle and joint pain, and other symptoms (Schaefer et al., 2022). Diarrhea is often caused by infections or food poisoning and can lead to dehydration if not properly treated (Nemeth & Pfleghaar, 2022). TB is caused by the bacterium Mycobacterium tuberculosis and is transmitted through the air when a person with TB disease of the lungs or throat exhales, talks, sings, or coughs (Patterson & Wood, 2019). Bandung, as one of the metropolitan cities and one of the largest cities in West Java (Marhamah & Jaya, 2020).

The following Sections of this study are structured as follows: Section 2 discusses the spatiotemporal shared component model; section 3 presents the application of this model; section 4 presents the discussions; section 5 provides the conclusions drawn from the study.

2. Bayesian Spatiotemporal Shared Components Model

Spatiotemporal disease mapping is a way of visualizing and analyzing the distribution of disease cases over both space and time. This can be useful for identifying trends and patterns in the distribution of disease cases, as well as identifying risk

factors that may contribute to the occurrence of the disease (Banerjee et al., 2015; Lawson 2018; Jaya & Folmer 2020; Yin et al., 2014). To perform spatiotemporal disease mapping, researchers typically collect data on the number of cases of a particular disease in different geographical locations over a certain time (Yin et al., 2014). This data can then be analyzed to understand the distribution of disease cases across space and time, and to identify trends and patterns in the data. There are a variety of statistical techniques and tools that can be used to perform spatiotemporal disease mapping, including geostatistical methods, spatial regression models, and spatial temporal models. These techniques can be used to estimate the risk of disease in different locations, identify risk factors for the disease, and predict the future distribution of the disease. Spatiotemporal disease mapping can be used to inform public health policies and interventions, such as targeted vaccination campaigns or health education programs, to reduce the incidence of disease and improve population health. In the context of disease mapping, the Poisson distribution can be used to model the number of cases of a particular disease in each area over a certain time period. The Poisson distribution is a probability distribution that represents the number of times an event occurs within a given time or space. It is often used in the analysis of public health data because it is a discrete probability distribution, meaning it can only take on integer values, and it is often used to model the number of occurrences of an event.

Let y_{itd} denote the numbers of confirmed cases for region $i = 1, \dots, n$, period $t = 1, \dots, T$ and disease $d = 1,2,3$ corresponds to dengue (1), diarrhea (2), and TB (3), follow Poisson distribution with means and variances equal to $\lambda_{itd} = E_{itd}\theta_{itd}$. Therefore (Jaya & Folmer, 2020):

$$y_{itd}|E_{itd}, \theta_{itd} \sim Poisson(E_{itd}\theta_{itd}), \tag{1}$$

where E_{itd} and θ_{itd} are the expected count and the relative risk of disease d for region $i = 1, \dots, n$, period $t = 1, \dots, T$. The expected count E_{itd} can be formulated as (Jaya et al., 2022):

$$E_{itd} = N_{itd}p_d \tag{2}$$

with N_{itd} is the number of population at risk of disease d and p_d denotes the constant probablity of disease d across all regions and times (Last, 2001). The crude risk is measured by standardized incidence ratio (SIR) which is formulated as (Clayton & Kaldor, 1987):

$$SIR_{itd} = \frac{y_{itd}}{E_{itd}} \tag{3}$$

The SIR is a common estimator for estimating disease risk, but according to Clayton and Kaldor (1987), it can be unreliable due to sampling variation. In order to obtain a more accurate and reliable estimate of disease risk, it is necessary to take into account spatial and temporal autocorrelation. Spatial autocorrelation refers to the statistical dependence between observations that are geographically close to each other, while temporal autocorrelation refers to the dependence between observations that are collected at different points in time. Accounting for these factors can help to improve the accuracy and reliability of disease risk estimates, and can provide a more complete understanding of the dynamics of infectious diseases. In addition, to generate more accurate and reliable estimates of disease risk, it is also necessary to model multiple disease risks simultaneously (Jaya & Folmer, 2022). The the relative risk θ_{itd} should be modeled as log liniear model to account for spatial and temporal random effects components. The general model can be written as:

$$\log \theta_{itd} = \alpha_d + \sum_{k=1}^{K} \beta_{k,d}x_{itk} + \omega_{i,d} + \upsilon_{i,d} + \phi_{t,d} + \varsigma_{t,d} + \delta_{it,d} + \varphi_d\widetilde{\omega}_{i,d} + \varrho_d\tilde{\phi}_{t,d} \tag{4}$$

In this model, α_d is the intercept which represents global risk for the d-th disease. The covariates denote by x_{itk} with the slope regression parameters $\beta_{k,d}$. The $\omega_{i,d}$ and $\upsilon_{i,d}$ terms represent the spatially structured and unstructured random effects, respectively. These terms capture the spatial dependence and heterogeneity for the d-th disease respectively. The $\phi_{t,d}$ and $\varsigma_{t,d}$ terms represent the temporally structured and unstructured random effects, respectively. They capture for temporal autocorrelation and heteroscedasticity. The $\delta_{it,d}$ term represents the interaction effect, which consists of a pair of spatially and temporally structured or unstructured random effects. This term captures the combined effects of spatial and temporal differences on the outcome variable. Finally, $\widetilde{\omega}_{i,d}$ and $\tilde{\phi}_{t,d}$ denote the spatial and temporal shared component with φ_d and ϱ_d represent the scale spatial and temporal parameters. Overall, these mixed effects model aims to understand the variation in the outcome variable due to both spatial and temporal differences, as well as the interaction between these two factors.

For the spatially structured effect the intrinsic conditional autoregressive model (iCAR) prior (Besag et al., 1991) is usually used. The iCAR prior for $\omega_{i,d}$ is (Besag et al., 1991):

$$\omega_{i,d}|\boldsymbol{\omega}_{-i,d}, \sigma^2_{\omega_d}, \mathbf{W} \sim \mathcal{N}\left(\frac{\sum_{j=1}^{n} w_{ij}\omega_{j,d}}{\sum_{i=1}^{n} w_{ij}}, \frac{\sigma^2_{\omega_d}}{\sum_{i=1}^{n} w_{ij}}\right) \tag{5}$$

The spatial weigh matrix consists of $n \times n$ element w_{ij} which is defined as:

$$w_{ij} = \begin{cases} 1 \text{ if } i \text{ and } j \text{ are adjacent neighbors} \\ 0 \text{ otherwise} \end{cases}$$

and $\sigma^2_{\omega_d}$ is the variance parameter of $\omega_{i,d}$. The spatially shared components $\widetilde{\omega}_{i,d}$ is also assigned an iCAR prior. The spatially unstructured random effects $\upsilon_{i,d}$ are modelled by an exchangeable Normal prior (Osei & Stein, 2017):

$$\upsilon_{i,d}|\sigma^2_{\upsilon_d} \sim \mathcal{N}\left(0, \sigma^2_{\upsilon_d}\right) \tag{6}$$

where $\sigma^2_{\upsilon_d}$ denote the variance parameter of $\upsilon_{i,d}$. Random walk of order one (RW1) is a common prior for the temporal trend $\phi_{t,d}$ is a (Schrodle & Held, 2011).

$$\phi_{t+1,d} - \phi_{t,d}|\sigma^2_{\phi_d} \sim \mathcal{N}\left(0, \sigma^2_{\phi_d}\right), \tag{7}$$

with $\sigma^2_{\phi_d}$ the variance parameter of $\phi_{t,d}$. The temporally shared components $\tilde{\phi}_{t,d}$ is also assigned a RW1 prior. For the temporally unstructured component ς^h_t we assume an exchangeable Normal distribution as prior (Schrodle & Held, 2011):

$$\varsigma_{t,d}|\sigma^2_{\varsigma_d} \sim \mathcal{N}\left(0, \sigma^2_{\varsigma_d}\right), \tag{8}$$

where $\sigma^2_{\varsigma_d}$ is the variance parameter of $\varsigma_{t,d}$. For the interactions terms $\delta_{it,d}$ four types of priors have been proposed (see Jaya & Folmer, 2020 and Knorr-Held, 2000). The space-time interaction term captures the deviation from global spatial or temporal trends, which can be important for understanding the evolution of the disease. The most interesting type of interaction is Type IV, which captures deviations from global spatial or temporal trends and can provide a more nuanced understanding of the disease process. Overall, the use of priors for spatiotemporal interaction can help to improve our understanding of the distribution of disease cases over space and time and can inform the development of public health interventions to reduce the incidence of the disease (Knorr-Held, 2000). We employ exceedance probability to identify spatiotemporal hotspots, which are high-risk areas in both time and space that policymakers and health authorities must pay special attention to (Jaya & Folmer, 2020, 2022). It is formulated as the probaility of the of the relative risk of disease d of region i and time t is greater than specific threshold c, that is,

$$\Pr\left(\hat{\theta}^d_{it} > c|\mathbf{g}\right) = 1 - \int_{\hat{\theta}^d_{it} \leq c} p\left(\hat{\theta}^d_{it}|\mathbf{g}\right) d\theta^d_{it} \tag{9}$$

To identify spatiotemporal hotspots, we additionally require the probability threshold, denoted by γ. A spatiotemporal unit is categorized as a spatiotemporal hotspot if $\Pr\left(\hat{\theta}^d_{it} > c|\mathbf{g}\right) > \gamma$. We assume to $c = 1$ and $\gamma = 0.90$ (Lawson & Rotejanaprasert, 2014). Jaya & Folmer (2021) offer further information. The parameters and hyperparameters of (4) and (9) are estimated by the integrated nested Laplace approximation (INLA) (Blangiardo et al., 2013). The INLA approach is implemented in the R-INLA package and can be used to estimate posterior densities in a computationally efficient way. The INLA method has been widely used in various statistical modeling applications and has been shown to be a reliable and accurate method for posterior density estimation (Rue et al., 2009; Jaya & Folmer, 2020, 2022).

3. Application

3.1 Data exploration

Dengue, diarrhea, and TB data with population at risk were obtained from the http://data.bandung.go.id/. Table 1 shows a brief description of the incidence of the three infectiousness-endemic diseases considered in Bandung each year. Among the three infectiousness endemic diseases addressed in this study, diarrhea and tuberculosis were the most and least prevalent, respectively.

Table 1
Registered number of the cases of dengue, diarrhea, TB

Diseases	2016	2017	2018	2019	2020	Total
Dengue	3.880	1.786	2.826	4.424	2.790	15.706
Diarrhea	51.099	57.525	59.511	51.267	28.208	247.610
Tuberculosis	1.107	1.003	1.100	7.491	2.440	13.141

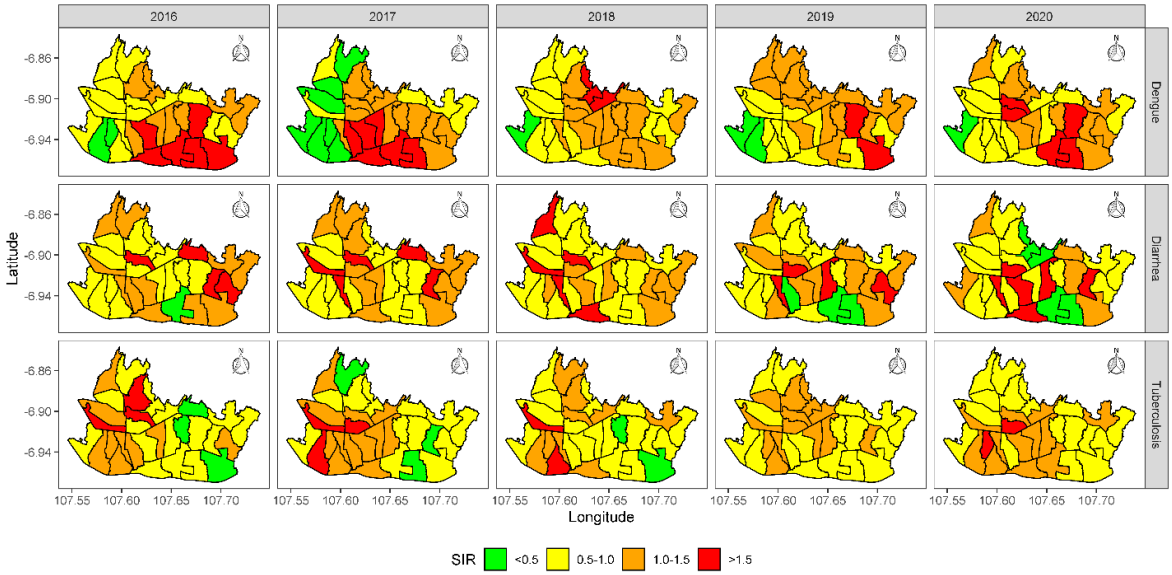

Fig. 1. Spatiotemporal distribution of dengue, diarrhea, and TB diseases between 2016-2020

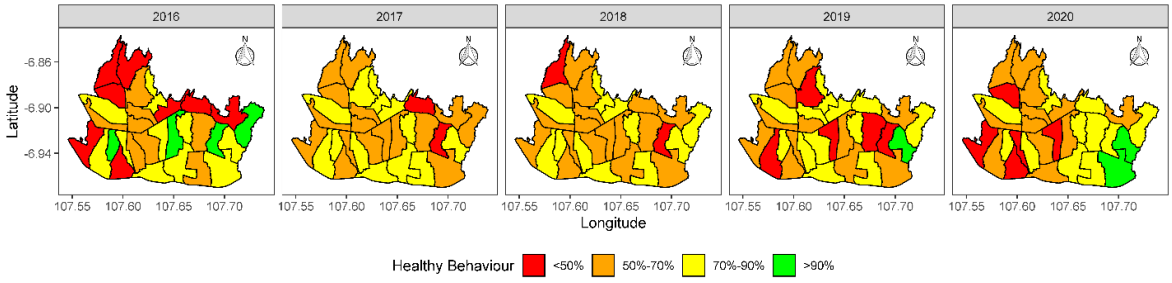

Fig. 2. Spatiotemporal distribution of healthy behavior index between 2016-2020

Fig. 1 and Fig. 2 show the spatiotemporal distribution of the standardized incidence risk for three infectious diseases as the multivariate response variable and the healthy behavior index as the predictor. It seems there are spatial clusters, but there is no time trend, neither response variable nor predictor, as shown by the random temporal pattern. Our analysis revealed moderate to strong correlations in the spatial distribution of disease incidences among three endemic diseases. This suggests that these diseases may have shared risk factors or similar transmission dynamics, and highlights the importance of considering the potential interplay between multiple diseases when designing interventions or public health policies

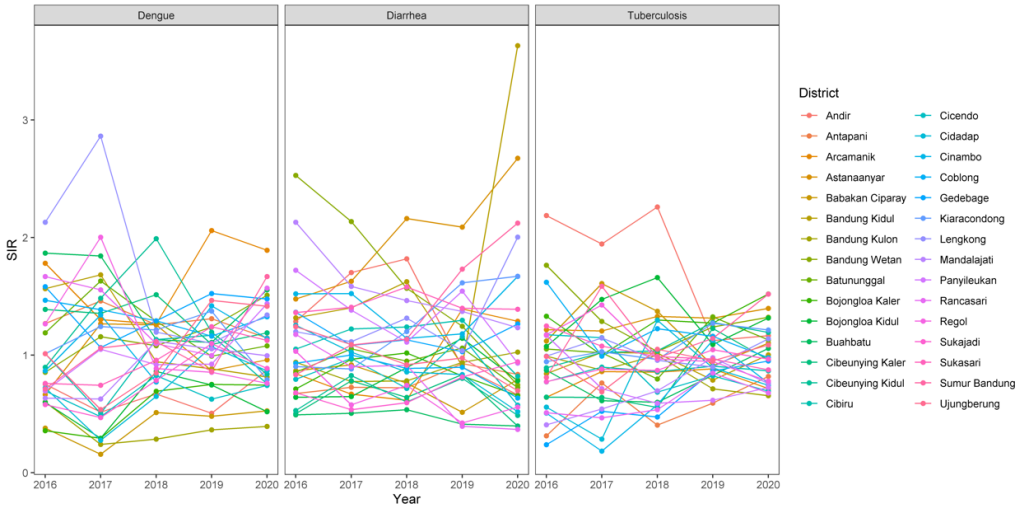

Fig. 3. Temporal trend of the standardized incidence ratio (SIR) for three infectious diseases between 2016-2020

Fig. 3 shows that the value of SIR for each district in Bandung city tends to range between 0.5-1.5 annually. For fever and diarrhea, the tendency is relatively similar, but this is not the case for tuberculosis. For tuberculosis, the value of SIR in 2020 is skewed towards the value of one.

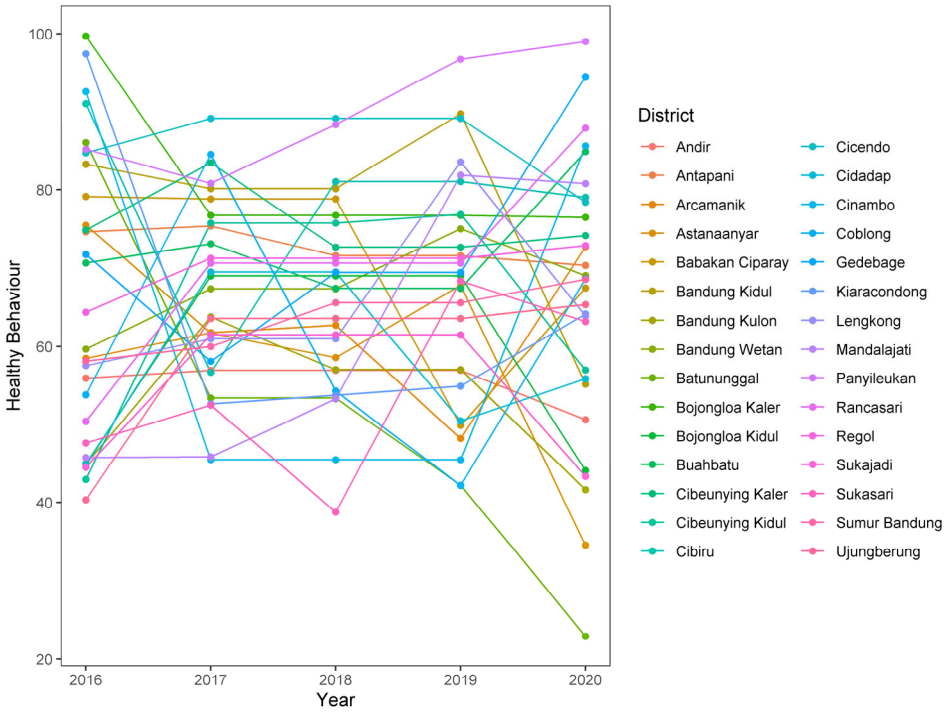

Fig. 4. Temporal trend of the healthy behavior index between 2016-2020

Fig. 4 shows that the value of healthy behavior index tends to range between 40% and 90%. However, in 2020, the Batununggal district recorded a very low value of healthy behavior index at 20%. After conducting a thorough data exploration, we decided to model the spatial shared component effects and the behavior index in our analysis. This decision was based on the fact that the temporal variation in our data did not vary significantly over time, and therefore modeling these factors would likely provide a more accurate and reliable representation of the data. By considering both the spatial and behavioral aspects of the data, we can gain a deeper understanding of the underlying patterns and relationships within the data.

$$\log \theta_{itd} = \alpha_d + \sum_{k=1}^{K} \beta_{k,d} x_{itk} + \varphi_d \widetilde{\omega}_{i,d} \tag{10}$$

3.2 Model Estimation

To estimate model (9), we use Bayesian INLA. The posterior mean of the fixed effects for this model is presented in Table 2, while the random effects are presented in Table 3.

Table 2
Posterior mean of fixed effect component

		Mean	SD	q(0.025)	q(0. 50)	q(0. 975)
Intercept						
Intercept	Dengue	-0.053855	0.035171	-0.123014	-0.053819	0.015040
	Diarrhea	0.315259	0.012149	0.291407	0.315259	0.339090
	Tuberculosis	0.228948	0.039100	0.152046	0.228994	0.305521
Slop*	Dengue	0.000948	0.000518	-0.000070	0.000948	0.001964
	Diarrhea	-0.004555	0.000181	-0.004911	-0.004555	-0.004200
	Tuberculosis	-0.003392	0.000587	-0.004544	-0.003392	-0.002240

*) Healthy behavior index

Healthy behavior had a negative influence on tuberculosis and TB, but a positive effect on dengue, indicating that the spread of the dengue virus also happened in places with a generally clean environment, as Aedes aegypti mosquitoes may nest anywhere, especially in clean puddles.

Table 3
Posterior mean of random effect components

	Mean	SD	$q(0.025)$	$q(0.50)$	$q(0.975)$
SD for spatial shared components	0.1170	0.0109	0.0950	0.1174	0.1374
$\phi_{Diarrhea}$	6.9074	0.4449	6.1355	6.8677	7.8630
$\phi_{Tubercolusis}$	0.9193	0.1541	0.6516	0.9056	1.2501

The study revealed that the pattern of any dengue virus was substantially similar to that of diarrhea, as indicated by the diarrhea phi more than one, but tuberculosis had a weaker similarity, as indicated by a phi effect value less than one. This is evident from Fig. 5 and Fig. 6 as well.

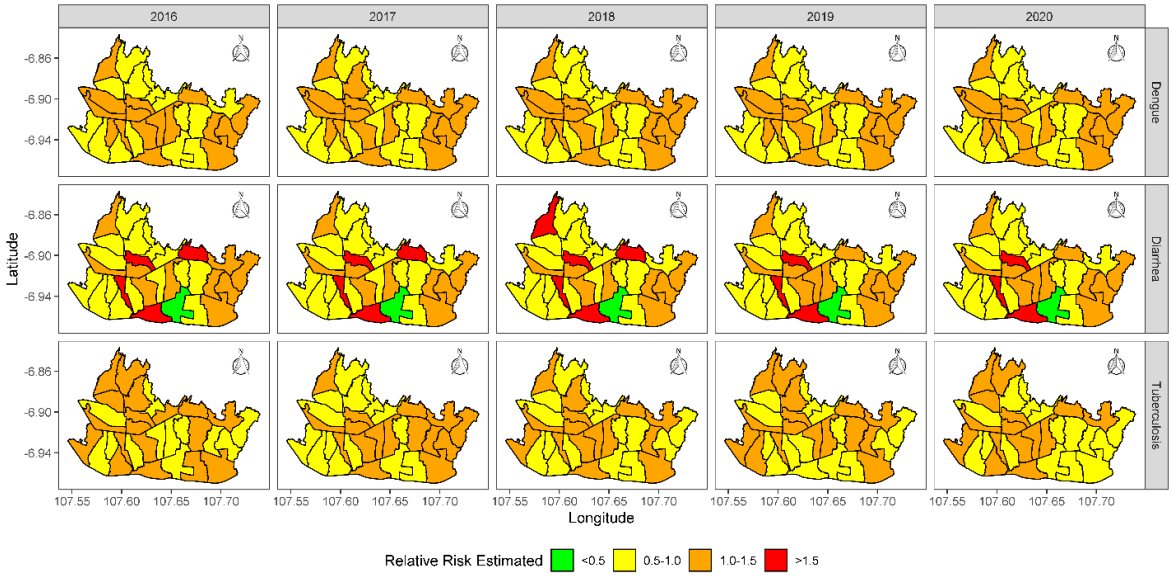

Fig. 5. Smoothed related risk distribution in space and time

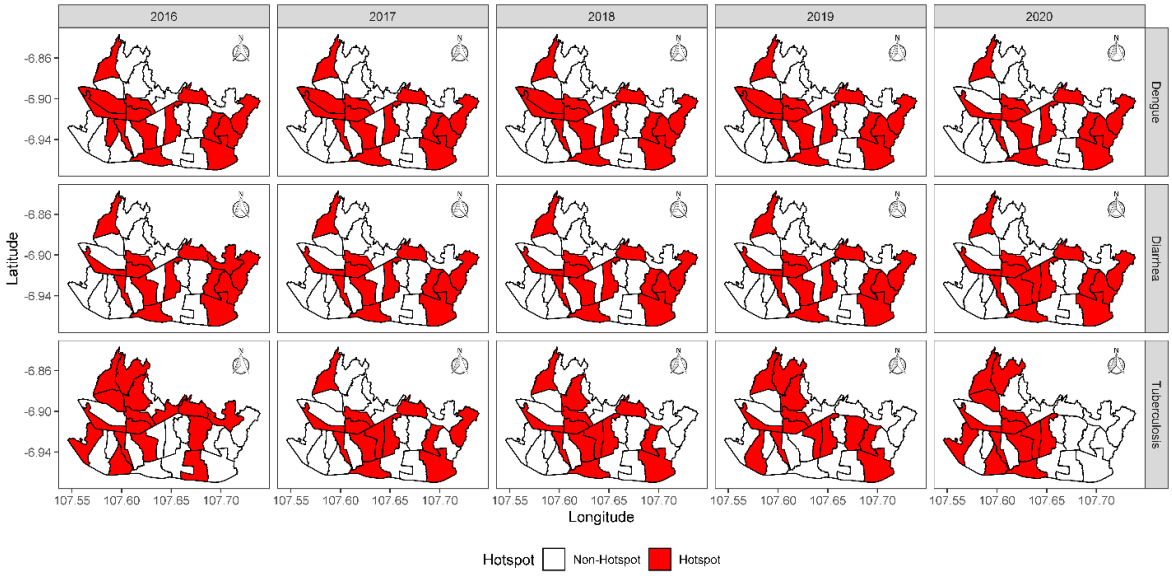

Fig. 6. Spatiotemporal distribution of hotspot for three infectious diseases

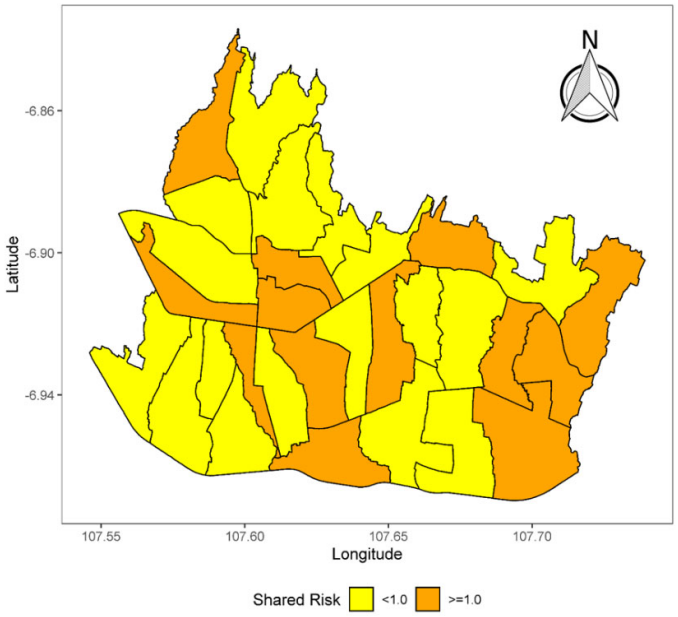

Fig. 7. Spatial endemic diseases clustering

The study demonstrates that the combination of the three diseases in the analysis creates a risk cluster shared by all three diseases. It is probable that the relative danger will be relatively high in the eastern and northern regions. The government must intervene significantly in these regions to manage infectious diseases. According to the results of the shared component model analysis, we found that 12 out of 30 locations, or approximately 40% of districts, have a high risk of dengue and diarrhea transmission The districts are Sukasari, Andir, Astana Anyar, Bandung Wetan, Sumur bandung, Lengkong, Kiara condong, Mandalajati, Cibiru, Penyileukan, Cinambo and Gedebage.

4. Discussion

This research introduces a Bayesian spatiotemporal hierarchical model for jointly analyzing dengue, diarrhea, and TB. By combining these diseases in a single model, we can gain a more complete understanding of their transmission dynamics and reduce bias in the estimation of their individual parameters, leading to improved prediction and mapping (Ibáñez-Beroiz et al., 2011; Jaya et al., 2022; MacNab, 2010). In addition, there are several advantages to using a Bayesian shared component model for analyzing the transmission of multiple diseases. Comprehensive understanding of disease dynamics: By combining multiple diseases in a single model, it is possible to gain a more comprehensive understanding of the transmission dynamics of each disease and how they may be related to each other. Improved prediction and mapping: The shared component model allow for the incorporation of shared risk factors, which can lead to more accurate prediction and mapping of disease transmission. Reduction of bias: By considering the effect of shared risk factors, the shared component model can reduce bias in the estimation of the parameters of the individual disease equations, leading to more reliable results. Flexibility: The Bayesian shared component model is flexible and can be adapted to different types of data and situations. Robustness: The Bayesian approach is known for its robustness, which means that it can produce reliable results even when the data is incomplete or has some level of uncertainty. The model considers the common and temporal patterns of the diseases, reflecting similarities and differences in the spatial and temporal distribution of the relative risks associated with each disease. We developed a shared component model by incorporating a covariate for healthy behavior. We believe that this variable has a significant impact on the spatiotemporal variation of dengue, diarrhea, and TB. Our research findings showed meaningful results. Healthy behavior harmed diarrhea and tuberculosis but not dengue. Diarrhea and TB are commonly found in slum areas (Pemberton et al., 2007). Dengue is generally found in relatively clean environments because mosquito vectors breed in clean swimming pools (Dom et al., 2016). In the model that we developed, we assumed that there was no temporal dependence, only spatial dependence, represented by the shared component. We observed that the spread patterns of the three diseases did not have a specific temporal trend or pattern, so their spread patterns were relatively the same each year. The choice of a simple model that only includes shared component information is intended to help better understand the spatial clusters of the three different types of diseases and to show whether the three diseases have the same spatial pattern. A spatiotemporal model might include complete information such as spatial and temporal dependence and their interaction, but this could obscure the spatial component, which might be overshadowed by other random components. This is because each random component can have strong collinearity. For spatially shared component modeling, we used the iCAR model. Through Bayesian iCAR modeling, we obtained more reliable disease mapping associated with disease risk (Jaya et al., 2022; Jaya & Folmer, 2020; Moraga & Lawson, 2012). It is interesting to see that healthy behaviors can have different effects on different diseases. It's important to note that the transmission patterns of different diseases can be quite different, so it's not surprising that healthy behaviors might have different effects on them. It is also interesting to see

that the spatial distribution patterns for dengue and diarrhea are similar but different from TB. This suggests that there are different factors at play in the transmission of these diseases. Dengue and diarrhea probably share some unknown weather-related risk factors, while TB has its own unknown environmental health-related risk factors. It is important to keep studying and learning about how different diseases spread so that public health policies and interventions can be made to help reduce the number of people who get sick.

5. Conclusion

One potential benefit of using shared component models is that they can help identify diseases that have spatial or temporal distribution patterns. This is especially true when there is a reasonably strong spatial correlation between the diseases being studied and the reference diseases. In our study, we found this to be the case for dengue and diarrhea. Shared component modeling is useful because it considers shared risk factors that may be spatially correlated, such as climate. Before using this type of model, it is recommended to conduct exploratory analyses to determine the correlation between the risks of the diseases being studied and the reference disease.

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