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Multivariate spatiotemporal using INLA: analysis of sexually transmitted infections in West Java, Indonesia

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ABSTRACT

Sexually transmitted infections (STIs), including human immunodeficiency virus (HIV) and hepatitis B/C, pose a significant public health challenge in Indonesia, particularly in West Java, the country's most populous province. This study seeks to analyze the spatiotemporal distribution of STIs to enhance disease management strategies. Spatiotemporal multivariate M-models utilizing integrated nested laplace approximation (INLA) inference were applied to the Indonesian National Health Insurance data covering the period from 2015 to 2022 in West Java. Fifteen models were developed based on three spatial models, each paired with a temporal prior and five interaction types. The analysis identified the proper conditional autoregressive model with temporal interaction (pCAR type 2) as the best-performing model. This model revealed distinct temporal patterns in each region that did not influence neighboring areas. Notably, the posterior mean relative risk for HIV and hepatitis B/C was found to be higher in northern West Java (>1.00); however, the region most at risk for each infection differs, partially due to a lack of correlation between HIV and hepatitis B/C (\rho=-0.15). These findings underscore the need for customized mitigation strategies tailored to specific diseases and regional differences in risk patterns.

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1. INTRODUCTION

Sexually transmitted infections (STIs) are a serious global health problem, with more than one million cases detected daily worldwide [1]. STIs are caused by a variety of pathogens, including viruses, bacteria, fungi, and parasites, which are spread through sexual contact [2]. This issue is also a concern in Indonesia. Globally, the number of STI cases, especially HIV, hepatitis B and C, and other STIs, has continued to rise, with millions of new infections reported each year [3]. In 2020, there were 543,100 people living with human immunodeficiency virus (HIV)/acquired immunodeficiency syndrome (AIDS) in Indonesia, with West Java among the three provinces with the highest number of cases [4]. In addition to HIV, Indonesia ranks second in the WHO South East Asian Region (SEAR) in the number of hepatitis B cases. In the first semester of 2022, West Java reported 2,649 cases of hepatitis B and 1,207 cases of hepatitis C [5]. This condition is even more alarming considering that 7.1%, or around 18 million Indonesians, are infected with hepatitis B, of whom 50%

are at risk of chronic infection, and 900,000 people have the potential to develop liver cancer. Globally, around 2.9 million people living with HIV are also infected with the hepatitis C virus, and 2.6 million are infected with hepatitis B. These statistics highlight the urgent need for more comprehensive epidemiological studies to identify spatial and temporal patterns of STI transmission.

The surge in cases of STIs in West Java province, which has the highest number of cases, requires a comprehensive analysis to understand the distribution pattern and map the relative risk. Understanding the distribution pattern and risk of STIs at the district and city level is the basis for formulating effective prevention strategies in the region. This study aims to provide deeper insight into the distribution and its risk mapping of STIs in West Java. The findings of this study are expected to serve as a reference in formulating more appropriate and efficient prevention policies. In addition, this study supports the achievement of Sustainable Development Goals (SDGs) Target 3.3, which targets the control and elimination of epidemics such as AIDS, tuberculosis, malaria, hepatitis, and other infectious diseases by 2030 [6], [7].

Univariate analysis is often used in epidemiological research to describe patterns and distributions of disease in a region in one variable dimension. For example, research conducted by Niragire *et al.* [8], analyzed HIV disease univariately. Research by Sousa *et al.* [9] analyzed hepatitis univariately. These diseases were only analyzed individually. Although widely used, this approach has limitations because it cannot capture interactions between variables, especially in the context of complex and interrelated diseases. Multivariate analysis allows researchers to consider the relationships between several variables simultaneously [10]. A spatial multivariate approach is certainly needed in analyzing HIV and hepatitis B and C, both of which have an STI background. Studies on these two diseases have been reported in the literature [11]–[16]. However, none of these studies have used a spatial multivariate method in a model analyzing both diseases simultaneously. Studies that consider HIV and hepatitis B and C on a large scale are still rare, even though these diseases often occur together with the same background. Furthermore, a simultaneous analysis of both diseases has not yet been conducted in West Java.

Previous studies have not explicitly explored multivariate spatiotemporal interactions among different STIs, nor have they applied models that integrate multiple spatial priors (intrinsic conditional autoregressive (iCAR), Leroux CAR (LCAR), and proper CAR (pCAR)) with temporal structures such as random walks. Moreover, few studies have leveraged national-scale health insurance data (BPJS) as a primary source, which may provide a more accurate and representative picture of disease prevalence at the sub-provincial level. This gap motivates the need for methodological improvements that can better capture the complex epidemiological landscape of STIs in Indonesia.

To address these limitations, this study introduces several key contributions. First, it applies a multivariate spatiotemporal M-model framework to jointly analyze HIV, hepatitis B, and hepatitis C across 27 districts and cities in West Java during 2015–2022. Second, it employs integrated nested Laplace approximation (INLA), which allows for computationally efficient and accurate Bayesian inference, making it superior to traditional MCMC approaches in high-dimensional spatial models [17]. Third, this study utilizes National Health Insurance Indonesia (BPJS) Health de-identified data, which has not been previously explored in STI modeling, thereby providing a novel and reliable epidemiological database. These contributions position the present research as both methodologically and substantively distinct from prior works.

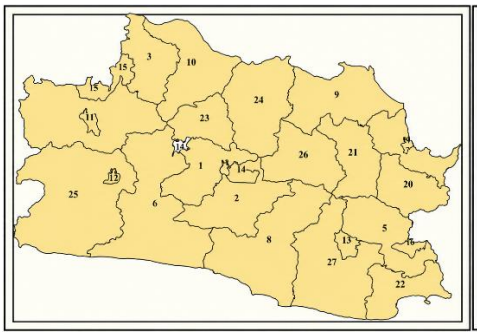
The remainder of this article is organized as follows. Section 2 describes the study area and data and outlines the methodological framework, including multivariate spatiotemporal M-models, spatial prior specifications, and Bayesian inference using INLA. Section 3 presents and discusses the results, comparing candidate models under different spatial priors and spatiotemporal interaction structures, interpreting the estimated disease risk patterns, and examining their implications in relation to existing literature and public health priorities. Finally, section 4 concludes the study by summarizing the main findings and contributions and outlining directions for future research.

2. METHOD

2.1. Study area and data

Data in this research were obtained from BPJS Health data that contain user claims data for 27 districts and cities in West Java from 2015 to 2022. The total number of HIV patients is 689, and the total number of hepatitis B/C patients is 878. These figures are aggregated by district and city. These data were obtained by submitting a request to BPJS at the following link: https://data.bpjs-kesehatan.go.id/bpjs-portal/action/landingPage.cbi. To safeguard individual patient confidentiality, BPJS has implemented a de-identification process for its data samples before granting access to external parties. As such, any attempts to re-identify individuals in the data are highly unlikely without the explicit consent of BPJS. A signed integrity pact has been submitted as one of the procedures to request the data.

The map of West Java (with cities and districts) can be seen in Figure 1. The dataset includes yearly aggregated case counts of HIV, hepatitis B and C, stratified by district/city.



1	Bandung Barat	15	Cimahi City
2	Bandung	16	Cirebon City
3	Bekasi	17	Depok City
4	Bogor	18	Sukabumi City
5	Ciamis	19	Tasikmalaya City
6	Cianjur	20	Kuningan
7	Cirebon	21	Majalengka
8	Garut	22	Pangandaran
9	Indramayu	23	Purwakarta
10	Karawang	24	Subang
11	Bandung City	25	Sukabumi
12	Banjar City	26	Sumedang
13	Bekasi City	27	Tasikmalaya
14	Bogor City		

Figure 1. Mapping of cities/districts in West Java Province

2.2. Spatiotemporal M-models

The overarching statistical framework for multivariate mapping issues can be outlined as follows. Suppose O_{itj} and E_{itj} denote the observed and expected incidence of cases for the *i*-th geographical area, *t*-th period, and *j*-th disease, respectively, will now be associated with a particular disease. R_{itj} is a relative risk, while μ_{itj} is a mean of the distribution. The number of observed cases in each area, time, and disease follows a Poisson distribution,

$$O_{itj}\,|R_{itj} \sim Poisson\left(\mu_{itj} = E_{itj}\,.\,R_{itj}\right) \quad (1)$$

$$log\ \mu_{itj} = log\ E_{itj} + log\ R_{itj} \quad (2)$$

where,

$$log\left(R_{itj}\right) = \alpha_j + \theta_{ij} + \gamma_{tj} + \delta_{itj} \quad (3)$$

Here α_j is the intercept for the *j*-th disease event, θ_{ij} and γ_{tj} represent the spatial and temporal primary effects, while δ_{itj} signifies the spatial and temporal interaction in the *j*-th disease. Two matrices with spatial and temporal random effects in their columns, represented by $\vartheta = \{\theta_{ij} : i = 1, \dots, I;\ j = 1, \dots, J\}$ and $\tau = \{\gamma_{tj} : t = 1, \dots, T; j = 1, \dots, J\}$ as well as a matrix that captures the spatial and temporal interactions within each disease event, represented by $\Delta_j = \{\delta_{itj} : i = 1, \dots, I : t = 1, \dots, T\}$. The strength of multivariate modeling lies in the ability to incorporate the interdependence between spatial and temporal patterns of various disease events into the model. This integration enables the enhancement of estimation accuracy and the identification of risk factors associated with the phenomenon being studied.

To comprehend how the correlations between spatial risks and global temporal trends across different disease events are integrated into the model, the matrices ϑ and τ are formulated as (4) and (5):

$$\vartheta = \varphi_\theta M_\theta \quad (4)$$

$$\tau = \varphi_\gamma M_\gamma \quad (5)$$

where φ_θ and φ_γ represent random effects matrices of dimensions $I\ x\ K_\theta$ and $T\ x\ K_\gamma$, respectively, with columns arranged sequentially according to spatially and temporally correlated distributions. The matrices M_θ and M_γ, with dimensions $K_\theta\ x\ J$ and $K_\gamma\ x\ J$, play a role in establishing dependencies among different columns of ϑ and τ. Specifically, the correlation between the columns ϑ signifies the spatial pattern correlation among the diseases under research, while the correlation between its rows indicates spatial correlation within the diseases. Similarly, the columns of τ represents for temporal pattern. Various spatial priors have been explored in the literature to address spatial dependencies. For example, in the realm of multivariate, there is the pCAR. Additionally, the LCAR and iCAR were also investigated for the column φ_θ and used in this research. In summary, the columns φ_θ are characterized by a multivariate normal distribution with a covariance matrix Ω and a mean of 0, the expression of which is contingent on the spatial prior, while the temporal component φ_γ uses random walk of order 1 (RW1). For the temporal component, RW1 was selected because it assumes smooth yearly changes, which is epidemiologically reasonable for gradually evolving epidemics like HIV and hepatitis. The differences in the characteristics of the three priors that will be used in the research are described

in Table 1. $W = (w_{il})$ represents the spatial adjacency matrix, with $w_{ii} = 0$, $w_{il} = 1$ indicating neighbor relationships between i-th and l-th areas and 0 otherwise, $D_w = diag(w_{1+}, \ldots, w_{n+})$, where the diagonal element w_{i+} denotes the number of neighbors for the i-th area, λ is a spatial dependence parameter, and I_n is an identity matrix of n-dimension.

Table 1. Differences in the characteristics of the three priors [17]

Prior	Var	Ω
iCAR	$\frac{\sigma^2}{w_{i+}}$	$\sigma^{-2}(D_w - W)$
pCAR	$\frac{\sigma^2}{w_{i+}}$	$\sigma^{-2}(D_w - \lambda W)$
LCAR	$\frac{\sigma^2}{1 - \lambda + \lambda w_{i+}}$	$\sigma^{-2}(\lambda(D_w - W) + (1 - \lambda)I_n)$

There are five interactions used in the study for each prior: four spatiotemporal interactions and a non-spatiotemporal additive interaction. In spatiotemporal interactions, Type 1 defines data that is spatially and temporally differentiated or unstructured, so there is no single spatial and temporal pattern interaction. Type 2 shows spatiotemporal data with temporal pattern interactions. Type 3 is the opposite of Type 2: spatial-temporal data with spatial pattern interactions. Type 4 is the most complex type, with spatial and temporal pattern interactions. Here γ is data temporally differentiated, with no temporal interactions, α is data temporally differentiated, with temporal interactions, δ is data spatially differentiated, with no spatial interaction, and ϕ is data spatially differentiated, with spatial interactions. All these types of models' interactions can be referred to in more detail in [17], [18]. To clarify the modeling process, a conceptual workflow of the M-model framework applied in this study is illustrated in Figure 2.

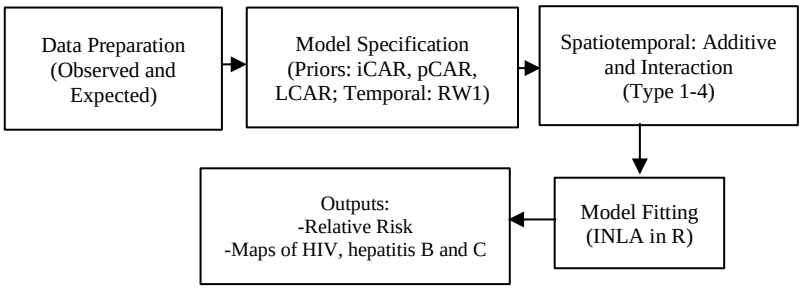


Figure 2. Conceptual workflow of M-models with INLA

2.3. Integrated nested Laplace approximation

INLA is a Bayesian statistical technique employed to calculate parameters in hierarchical statistical models [19]. It enables the application of intricate and adaptable models beyond conventional Bayesian inference techniques, offering quicker computational speed and improved precision in outcomes [20]–[24]. INLA finds utility across diverse domains such as epidemiology, ecology, and social sciences for analyzing intricate data and estimating parameters within hierarchical models [25]–[28]. In this study, INLA was chosen because it can handle high-dimensional latent Gaussian models efficiently and has been proven to provide accurate approximations in spatiotemporal disease mapping compared to traditional MCMC. All computations were conducted in R-INLA (R version 4.2.2), and the modeling codes are made available in supplementary materials to ensure replicability.

3. RESULTS AND DISCUSSION

The results of this study are presented in figures, tables, and maps to facilitate interpretation. Figure 3 presents crude rates (per 100,000 BPJS users) for HIV, hepatitis B, and C in West Java. Figure 3(a) shows a consistent upward trend of HIV incidence over the study period, while hepatitis B and C exhibit fluctuating patterns without a clear trajectory. The number of surviving HIV patients handled by BPJS increased proportionally with incidence, suggesting improved treatment coverage and access over time, as shown in Figure 3(b). For hepatitis B and C, survival outcomes became more closely aligned with incidence

after 2017, which may reflect expanded diagnostic and treatment services in the national health system. Notably, in 2020, all three diseases recorded simultaneous declines, likely a result of healthcare disruptions due to the COVID-19 pandemic, while in 2022, hepatitis B and C incidence dropped steeply but survival remained stable, indicating possible under-detection rather than true epidemiological decline. Figure 3(c) displays an irregular fluctuation of mortality patterns. However, since 2017, HIV and hepatitis B/C deaths have shown parallel increases, suggesting overlapping vulnerabilities in healthcare response or shared comorbidities.

The multivariate spatiotemporal M-models produced fifteen competing models across different priors and interaction types in Table 2. The model's performance was evaluated using three statistics: the logarithmic score (LS), the Watanabe-Akaike information criterion (WAIC), and the deviance information criterion (DIC). These statistics are commonly used in Bayesian modeling to assess a balance between model complexity and fit, with lower values indicating better-performing models. Among all models, the pCAR Type 2 demonstrated the lowest values across all criteria, indicating the best overall fit. The superior performance of pCAR Type 2 can be attributed to its flexibility in capturing local dependence while accommodating broader spatial-temporal interactions. In addition, pCAR has advantages in terms of multivariate generalization and adaptive options with flexible spatial dependence (multidimensional) and local influence functions [29]. This suggests that spatial clustering of cases, influenced by mobility patterns along the Pantura route, is better represented by this prior. Table 2 shows that spatiotemporal Type 2 interactions consistently provided optimal results, suggesting that temporal shocks (e.g., policy changes, treatment availability, or behavioral shifts) have stronger explanatory power than purely spatial clustering or complex space-time combinations. Furthermore, the type 2 interaction model also implies that the temporal effects of RW 1 play a significant role in shaping local temporal patterns in each region. However, this model states that the temporal patterns of one region are uncorrelated with those of other regions, which also indicates that temporal patterns of different diseases in one area do not influence the temporal patterns in its surroundings.

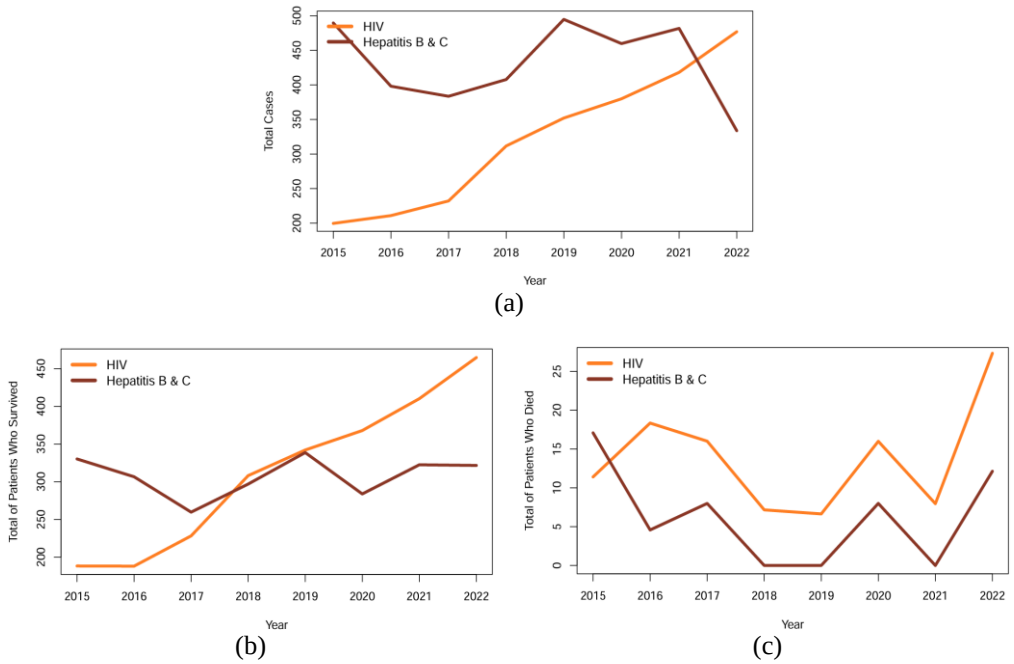


Figure 3. Crude rates (per 100.000) BPJS Data in West Java 2015-2022 for; (a) incidence cases, (b) incidence of surviving patients, and (c) incidence of death patients

The posterior mean of the specific spatial risk and the exceedance probabilities of HIV and hepatitis B and C are provided in Figure 4. In Figure 4(a), the North-Central region shows a high posterior mean of the specific spatial risk $\exp(\theta_{ij})$ for HIV, with the highest risk in Indramayu at a value of 3.181. In contrast, the eastern part of West Java, namely Cirebon and Ciamis, exhibits a high posterior mean of the specific spatial risk for hepatitis B and C, as shown in Figure 4(b). Geographically, almost all districts and cities along the Pantura (North Coast) route have a high risk for STIs, including HIV, hepatitis B, and C. The Pantura route also experiences high mobility, as it is a major transportation link in Java [30], [31]. Cities and districts along this route include Bekasi, Karawang, Subang, Indramayu, and Cirebon.

Furthermore, exceedance probabilities, P(exp(θ_{ij})>1|O), describe the probability that the posterior mean of the specific spatial risk surpasses expectations. Areas with high exceedance probabilities are particularly concerning because they indicate a spike beyond what is statistically expected, and the area may be unprepared for such an increase in cases. For HIV, as shown in Figure 4(c), areas with high exceedance probabilities closely align with the posterior mean of the specific spatial risk mapping and are found around the Pantura route, excluding Cirebon and Bekasi. Additionally, other areas outside the Pantura route, such as Bogor City, Sukabumi City, Bandung City, and Garut, also have high exceedance probabilities. For hepatitis B and C, the patterns differ from those of HIV as presented in Figure 4(d). High exceedance probabilities for hepatitis B and C are found in Depok City, Purwakarta, Cimahi City, Bandung City, Ciamis, Cirebon, and Cirebon City.

Table 2. Values of LS, WAIC, and DIC in 15 models

Interaction	LS	WAIC	DIC
iCAR additive	821.1324	1638.918	1630.92
iCAR type 1	816.6546	1614.403	1616.766
iCAR type 2	**788.6679**	**1557.211**	**1583.755**
iCAR type 3	814.3649	1609.547	1614.589
iCAR type 4	792.2141	1567.372	1585.355
LCAR additive	820.5816	1637.844	1630.348
LCAR type 1	815.7176	1612.828	1615.417
LCAR type 2	**787.2949**	**1556.402**	**1583.408**
LCAR type 3	813.0006	1608.181	1613.205
LCAR type 4	790.1969	1565.868	1584.493
pCAR additive	820.0557	1636.872	1629.377
pCAR type 1	815.4283	1612.146	1614.944
pCAR type 2*	**786.7482**	**1555.445**	**1582.309**
pCAR type 3	812.9863	1608.088	1612.861
pCAR type 4	789.8684	1564.986	1583.27

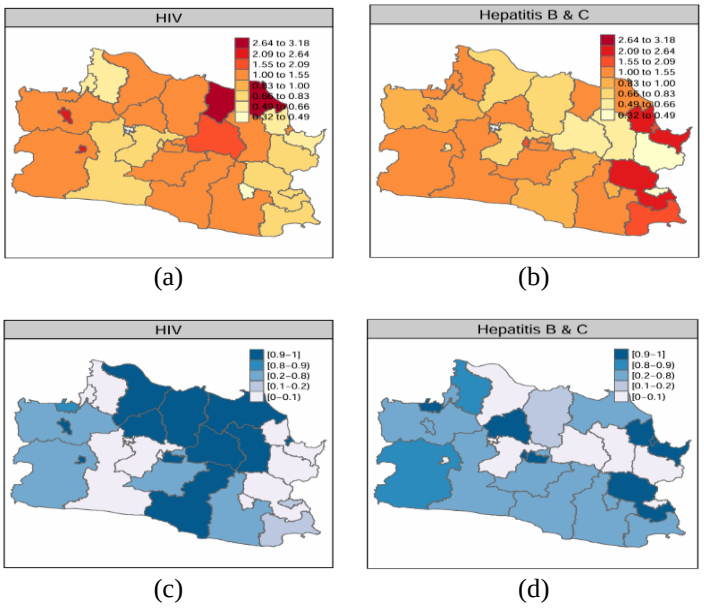


Figure 4. Posterior mean of the specific spatial risk; (a) HIV, (b) hepatitis B and C, and the exceedance probabilities, (c) HIV, and (d) hepatitis B and C

In this research, the posterior means correlation of HIV, hepatitis B, and C indicates a weak relationship (ρ=-0.15). This is in line with the type 2 interaction interpretation model, namely that the temporal pattern of each region and each disease is different (not correlated) and does not affect the surrounding regions. This fact is shown in Figure 4, the mapping of the posterior mean specific spatial risk of HIV, hepatitis B, and C is not similar. High-risk areas of both HIV and hepatitis B and C are in the north (Pantura). For example, in Indramayu, areas with high HIV risk have normal hepatitis B and C risk, while in Cirebon, areas with high hepatitis B and C risk have low HIV risk. Similarly, other areas, particularly those in Pantura, show no overlap in high risk for both diseases; if a region is high risk, it is typically for only one of the diseases. Additionally,

in this research, the posterior mean correlation between the two diseases is negative, which means that the relationship between the two diseases is opposite. This suggests distinct epidemiological mechanisms, likely related to differences in transmission pathways, health-seeking behaviors, or socioeconomic contexts [32]. Such findings emphasize that spatial overlap of risk is limited, and integrated interventions must remain disease-specific despite occurring in similar mobility zones. Posterior mean of the specific spatial risk value for HIV in Indramayu is 3.181, and for hepatitis B and C in Cirebon is 2.268. This means that Indramayu is 3.181 times more at risk of HIV compared to unexposed areas. Likewise, Cirebon is 2.268 times more at risk of hepatitis B and C compared to unexposed areas. Both are areas that lie along the Pantura route and have a very high risk of STIs in West Java.

Figure 5 displays the geographical relative risk pattern and the posterior probability of risk exceedance $P(R_{itj} > 1|O)$ (bottom) for both diseases during 2015-2022. From Figure 5(a), the increased risk for HIV cases is visible on the map, with previously bright areas becoming darker over the observed period. HIV relative risk expanded substantially after 2016. In contrast, the mapping for hepatitis B and C reveals different patterns across regions, with some areas experiencing increases and others decreases in risk, which is displayed in Figure 5(b). Areas with a drastic increase in the risk of hepatitis B and C during the observed period include Cirebon, Cirebon City, and Ciamis, where the color on the map changed from bright to increasingly dark from 2015 to 2022. Meanwhile, for posterior probabilities that the relative risk is greater than 1, $P(R_{itj} > 1|O)$ or the probability that the relative risk of a region exceeds statistical expectations, HIV throughout the year experienced an increase and extreme distribution, as shown in Figure 5(c). It can be seen on the map that in 2015, there was only one area that had a high $P(R_{itj} > 1|O)$, namely Indramayu, which is also included in the Pantura area. As the year progressed, the areas that had a high $P(R_{itj} > 1|O)$ were increasingly booming, and the blue-black areas on the map were getting more and more dark, especially at the end of the observed period. For hepatitis B and C, as in the map of projected incidence risks, there is no discernible pattern in the probabilities of a region having a risk that exceeds expectations, as presented in Figure 5(d). There are decreases and increases in each of the different regions. For example, in two neighboring cities, Bekasi and Karawang experienced a decrease in risk from 2015 to 2017. Cirebon and its surrounding areas had a high probability of risk from 2015 to 2021, which decreased in 2022. While Ciamis experienced an increase $P(R_{itj} > 1|O)$ during the observed period.

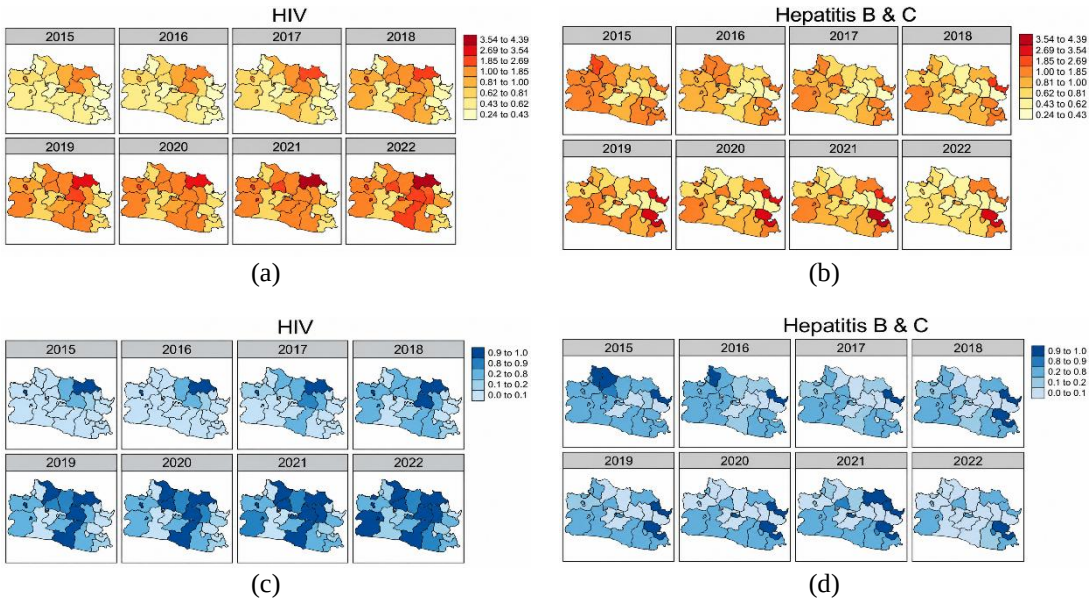


Figure 5. Map of estimated relative risk; (a) HIV, (b) hepatitis B and C, and posterior probabilities that the relative risk is greater than 1, (c) HIV, and (d) hepatitis B and C

Overall, these findings confirm that HIV incidence and spatial risk are rising in Pantura districts, driven by mobility and economic activity, while hepatitis B and C risks are regionally distinct, concentrated in eastern districts with different drivers [33], [34]. The best-performing model, pCAR Type 2, highlights the importance of flexible priors that accommodate both localized clustering and temporal unique patterns in each area and disease. From a policy perspective, this means that West Java health authorities should prioritize HIV

prevention and treatment expansion in Pantura, while simultaneously targeting hepatitis B/C vaccination and screening in Cirebon and Ciamis. The observed negative correlation also implies that integrated health strategies must account for disease-specific dynamics rather than assuming shared hotspots. Finally, while the study provides robust spatiotemporal evidence, limitations remain due to reliance on BPJS administrative data, which may underrepresent uninsured populations, and the absence of explicit socioeconomic or behavioral covariates. Future studies should integrate mobility and demographic data to strengthen causal interpretations and refine intervention strategies.

4. CONCLUSION

This research shows the application of multivariate spatiotemporal M-models in mapping HIV, hepatitis B, and C in West Java, with pCAR Type 2 identified as the best-performing model. The model's superior fit highlights its ability to capture both local clustering and unique temporal patterns, offering a more flexible and realistic representation of disease dynamics in each region. Our results reveal that HIV risk is strongly concentrated and expanding along the Pantura mobility corridor, while hepatitis B and C risks are distributed differently, with hotspots in eastern districts such as Cirebon and Ciamis. Importantly, the negative correlation between HIV and hepatitis B/C risks indicates distinct epidemiological mechanisms, suggesting that integrated interventions must remain disease-specific despite geographic overlap. For the health authorities of West Java, these findings imply that HIV prevention and treatment programs should be intensified in Pantura districts, whereas hepatitis B and C interventions should prioritize vaccination, screening, and follow-up care in eastern regions. Spatiotemporal mapping of exceedance probabilities further suggests that some areas may face unexpected spikes in cases, underscoring the need for early warning systems and resource allocation strategies tailored to high-mobility zones.

The novelty of this research lies in its multivariate spatiotemporal approach, which captures heterogeneity between diseases and provides evidence that risk dynamics are shaped more by temporal shocks and mobility than by static spatial clustering. Beyond methodological contributions, our study emphasizes the practical value of advanced modeling for targeted disease control in high-risk regions. Future research should integrate socioeconomic, behavioral, and mobility-related covariates to better explain the observed spatial heterogeneity. Methodologically, the use of alternative priors such as BYM and BYM2 could further refine inference and improve model performance. Ultimately, this work demonstrates how spatiotemporal disease modeling can inform precision public health strategies in rapidly changing epidemiological landscapes.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are available by applying to BPJS at following link: https://data.bpjs-kesehatan.go.id/bpjs-portal/action/landingPage.cbi.

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