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MAPPING SUB-DISTRICTS-LEVEL AND PREDICTING SPATIAL SPREAD OF COVID-19 DEATH CASE IN JAKARTA

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Abstract: Currently, the number of deaths caused by COVID-19 continues to increase significantly, especially in areas with high population density and mobility such as Jakarta, Indonesia. Spread of infectious diseases has a spatial closeness which results in cases of COVID-19 deaths also have a spatial dependency which is influenced by cases of deaths in the surrounding area. This study aims to map and predict the number of COVID-19 deaths using the Bayes Linear Mixed Model (LMM) method involving spatial random effects. The response variable is number of deaths and the explanatory variable are number of positive cases of COVID-19 and population density with sub-district area units in Jakarta. Response variable is divided into 6 schemes (PSBB 1, PSBB Transition 1, PSBB 2, PSBB Transition 2, PPKM 1 and PPKM 2) which is adjusted to the policies and social distancing activities from Jakarta provincial government, and assumed to have a normal distribution with INLA (Integrated Nested Laplace Approximation) inference approach. Some important results from this study are: in all 6 social distancing schemes, the number of

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positive cases of Covid-19 has a significant effect on the increase in number of deaths, while population density has a significant effect along with the increasing variance value of response data. The Bayes LMM has successfully mapped the spread of COVID-19 cases with the best RMSE value of 3.31. The mapping results show that several sub-districts with high population density and sub-districts located on Jakarta border have a high risk of death. Furthermore, the PSBB and PSBB Transition social distancing schemes are considered to be quite effective in suppressing the diversity number of deaths. However, it is different from the PPKM scheme where it is predicted that there will be an increase in the number of high-risk districts for COVID-19 up to 51% per day.

Keywords: spatial; INLA; social distancing; COVID-19; auto-regressive.

2010 AMS Subject Classification: 62H11, 62F15.

1. INTRODUCTION

Disease risk maps are very important for describing information, spatial influences and temporal variations of disease. In addition, the map can also identify high risk areas relative to others. Estimates of disease risk are based on information on observed cases of disease, the number of individuals at risk, and may also include covariates / other information such as demographic and environmental factors. The hierarchical Bayes model is usually used for mapping disease risk mapping [1]. Because the model is able to describe the diversity of response variables as a function of the risk of covariates and other random effects that cannot be explained, but have an effect on the diversity of response variables. The use of Bayes model provides a flexible and robust approach to calculating the effect of covariates and accommodating spatial and spatial-temporal correlations in risk estimation [2].

There are two approaches to Bayesian inference. The first approach is a simulation-based Bayes inference which is implemented through the Markov chain Monte Carlo (MCMC) method. The second approach is INLA (Integrated Nested Laplace Approximation) analytical-based inference, namely by using the Laplace nested approximation on the distribution of prior parameter and hyperparameter. INLA is an alternative to the MCMC's convergence problem and designed

for the Gaussian latent model, which can produce estimates of the distribution of prior parameters (and hyperparameters) accurately and efficiently [3].

Bayes modeling with INLA inference which is designed as a Gaussian latent model, has the flexibility to involve random components (mixed model). By using various assumptions of the distribution of responses, INLA can produce Linear Mixed Model (LMM) to Generalized Linear Mixed Model (GLMM). The random components in LMM / GLMM can be spatial influences, temporal trends and smoothing. Influences / spatial dependencies on area data include using autoregressive assumptions of order 1 or 2, conditional autoregressive and kriging interpolation. Several studies regarding risk mapping of COVID-19 based on information / spatial dependencies include [4], to map the risk of COVID-19 spread in India using kriging spatial interpolation. [5] examines the correlation between COVID-19 cases and socio-economic, environmental and demographic problems using autoregressive spatial regression.

The speed of an infectious disease such as COVID-19 spreads greatly depends on human mobility between regions. From the data obtained, death cases in an area have a spatial relationship with the surrounding area. In other words, there is a spatial dependence of death cases of an area with adjacent areas that are close to each other, as is the case in areas at the sub-district unit level in Jakarta. One of the government policies that was born from the global COVID-19 pandemic is social distancing that has greatly affected social life which has a major impact on decreasing economic performance and limiting religious, social and cultural activities. The effect of social distancing implementation of the number of COVID-19 cases can be seen in several research such as [6] study the impact of social distancing and epicenter lockdown in mainland China, [7] which examines at the effectiveness of lockdowns to reduce COVID-19 cases in Spain and [8] use a cross sectional study to examine the effects of distance learning on children's mental health during social distancing implementation.

To date, there have been more than 1 million positive cases in Indonesia with Jakarta as the province with the highest number of cases, which is 25.2% positive cases on a national scale [9]. Therefore, the main objectives of this research are map and predict number of COVID-19 deaths

using Bayes LMM which involve spatial random effects which divided into two categories, spatial structured random components and spatial unstructured random components. The response variable is the cumulative number of daily COVID-19 deaths which are assumed to have normal distribution and are divided into 6 schemes based on the social distancing scheme from Jakarta provincial government. Meanwhile, the explanatory variables are the cumulative number of positive cases and population density in each sub-district unit. In this study, we enhance mapping and prediction results so that mapping and predictions of death cases for each sub-district exceed a certain threshold value can be obtained. In the remaining part of this paper, we present the materials and method consisting dataset description and brief explanation of Bayes Linear Mixed Model in section 2. Mapping, prediction results and discussions are reported in Section 3. Some concluding remarks and possible future developments are summarized in Section 4.

2. MATERIALS AND METHODS

2.1 Dataset Description. The response dataset consists of cumulative number of death cases in 43 sub-districts in Jakarta. Responses are recorded in 6 types of social distancing schemes issued by the government with the criteria as in Table 1. The social restriction regulation with the highest level of tightness is PSSB with the majority of activities being at home. Response data are taken at the end of each scheme, so that there are 6 data pairs in 43 sub-districts. The use of response data on different social distancing schemes is expected to represent the risk of death at each sub-district level from time to time based on the level of compliance with social restrictions from the government. The explanatory variables are cumulative number of confirmed positive cases and population density in each restriction scheme as in the response variable.

The movement of positive cases in each social distancing scheme is represented in Figure 1. From Figure 1, the number of deaths for each sub-district is marked with a curve with a different color. It can be seen that cumulatively positive cases continue to increase from time to time with greater variance value for sub-district level. Until PSBB 2, the variance was still quite small, but different from PSBB Transition to PPKM which had very large variations. Figure 2 represents a

bar chart of the population density for each sub-district. Based on population data for 2019, Jakarta is the capital city of Indonesia which has a population density of 16,704 people / km². In more detail, the sub-district with the highest density is in Tambora which has 596.12 people / km², which also includes Kali Anyar as the urban-village with the highest population density in Southeast Asia [10].

Table 1. Social distancing schemes and its criteria

Social distancing scheme	Criteria	Selected date for response
PSBB 1 (large-scale social restrictions)	a. 100% work from home b. Online education c. Closing 100% places of worship d. Certain trade sectors may be opened very limited	14 June 2020
PSBB Transition 1	a. 50% work from home b. Online education c. Places of worship opened with a capacity of 50% d. All trading sectors may be opened with a capacity of 50%	6 September 2020
PSBB 2	The same as PSBB 1	18 October 2020
PSBB Transition 2	The same as PSBB Transition 1	10 January 2021
PPKM 1 (enforcement of restrictions on community activities)	a. 75% work from home b. Online education c. Places of worship opened with a capacity of 50% d. All trading sectors may be opened with time service restrictions	21 February 2021
PPKM 2	The same as PPKM 1	16 May 2021

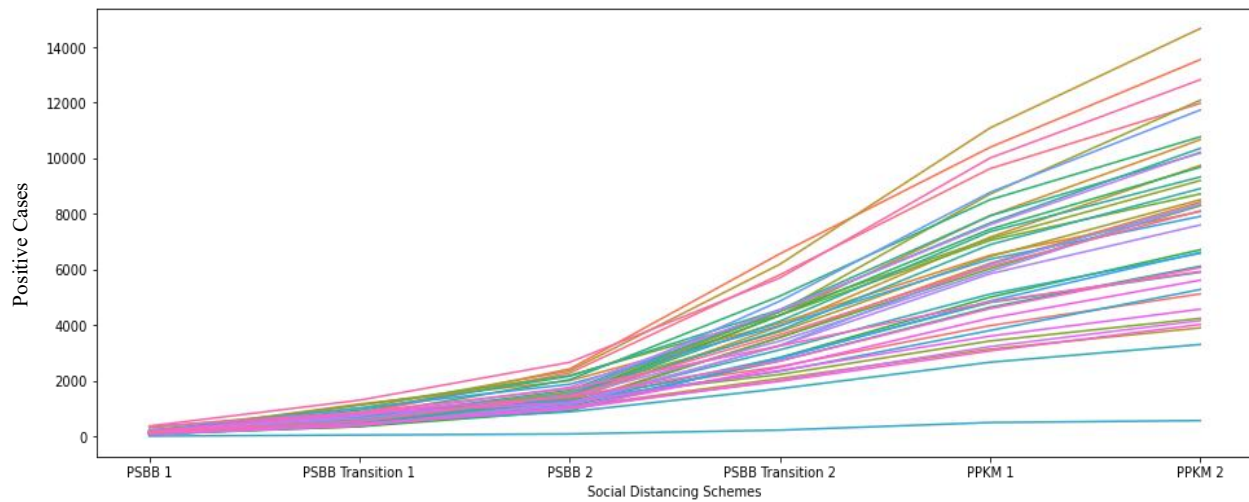


Figure 1. Cumulative positive cases for each sub-district in each social distancing scheme

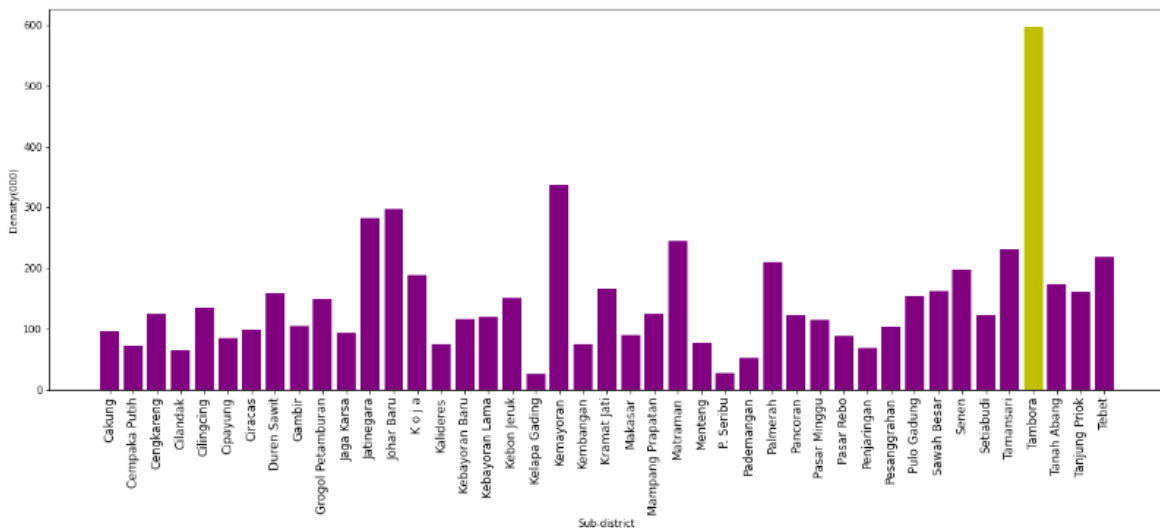


Figure 2. Population density for each sub-district in Jakarta

Figure 3 represents a population density map in Jakarta. The strategic location of Jakarta as the center of government, offices and industry, is surrounded by the capital buffer areas, where mobility occurs from these buffer areas to Jakarta on a daily basis. Tambora as the highest population density is marked with a yellow area. As seen in Figure 3, population density at sub-district level is mostly found in the central and northern parts of Jakarta.

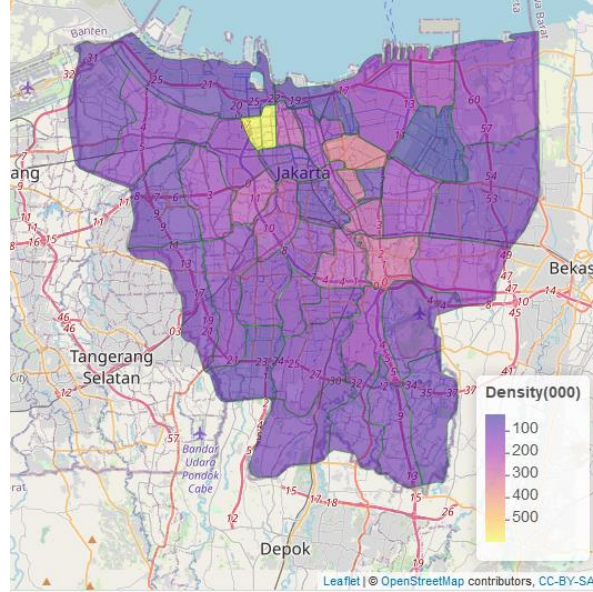


Figure 3. Map of population density for each sub-district in Jakarta

2.2 INLA and Bayes LMM. The code was built using R programming by utilizing several library packages in R, namely "R-INLA" for INLA inference process and "leaflet" for risk map visualization. INLA is a Gaussian latent model with observations $\mathbf{y}' = (y_1, \dots, y_n)$ and parameter ϕ_i which has a linear structure for the predictor η_i by using the link function $g(\cdot)$, so that $g(\phi_i) = \eta_i$. The linear predictors are additively arranged as follows:

$$\eta_i = \beta_0 + \sum_{m=1}^M \beta_m x_{mi} + \sum_{l=1}^L f_l(z_{li}). \quad (1)$$

In equation (1) β_0 is the intercept, set of coefficients $\boldsymbol{\beta} = \{\beta_1, \dots, \beta_M\}$ is the linear effect for covariates $\mathbf{X} = [x_1 \ x_2 \ \dots \ x_M]$ and $\mathbf{f}' = (f_1(\cdot), \dots, f_L(\cdot))$ is a collection of functions that define covariates $\mathbf{z}' = (z_1, \dots, z_L)$. Function $f_l(\cdot)$ can be a smoothing function, non-linear effects, seasonal trends and effects, as well as random components such as spatial and temporal random effects. The Laplace approximation is applied nestedly, to determining the posterior distribution of the hyperparameter and the posterior distribution of parameters. For more details on INLA estimation procedure, statistical properties and recent applications on spatial studies can be seen

in [11, 12, 13].

In predicting spatial spread, Bayes LMM is designed in a hierarchical fashion, by setting prior for parameter and hyperparameter regression with the following equation:

$$\eta_i = \hat{y}_i = b_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \vartheta_i + v_i. \quad (2)$$

In equation (2) y_i is number of deaths in the i -th sub-district which is assumed to be normally distributed $y_i \sim \text{Normal}(\mu_i, \sigma^2)$, with η_i denotes a linear link function $\eta_i = \mu_i$ and $\log\left(\frac{1}{\sigma^2}\right) \sim \log \text{Gamma}(1, 10^{-5})$. The fixed effects of positive cases and population density are represented β_1 and β_2 respectively and assumed to have normal priors $\beta_i \sim \text{Normal}(0, 10^6)$, $i = 1, 2$. The fixed effect of intercept is expressed by b_0 which is assumed to have normal prior $b_0 \sim \text{Normal}(0, 10^6)$. The random component consists of 2 parts. The first part is ϑ_i which states a spatially structured random component that is assumed to follow autoregressive order 1 as in equation (3):

$$\vartheta_i | \vartheta_{-i} \sim \text{Normal}\left(\frac{1}{\#\mathcal{N}(i)} \sum_{j=1}^n c_{ij} \vartheta_j, s_i^2\right), \quad (3)$$

c_{ij} represents the neighbor effect where $i \neq j$, $c_{ij} = 1$ if area i and j are neighbors, and 0 otherwise. Let $s_i^2 = \sigma_\vartheta^2 / \#\mathcal{N}(i)$ denotes the variance of area i which depends on the number of neighbors, $\#\mathcal{N}(i)$. Order 1 autoregressive spatial dependence is a derivative of equation (3), which measured based on direct neighbor (order 1) [14]. While the second part is v_i which is a spatially unstructured random component which is assumed to have a normal prior $v_i \sim \text{Normal}(0, \sigma_v^2)$. Prediction and spatial mapping were carried out on each selected date in Table 1 for each social distancing scheme, so that there were 6 data pairs whose prediction accuracy was measured using RMSE (root mean square error).

3. RESULTS AND DISCUSSIONS

The result of estimating fixed effects i.e. intercept b_0 and the coefficient of explanatory variables β_i , $i = 1,2$ in equation (2) are presented in Table 2. Estimated values that have a significant effect are indicated by numbers written in bold. The significance of fixed effect can be seen at the 95% credibility interval that does not contain 0. From Table 2, it can be seen that in general the intercept b_0 does not have a significant effect on death cases, except for the PSBB 2 scheme. The intercept estimator value also has a fairly high standard deviation which is indicated by a fairly wide 95% credibility interval. However, this is different in positive case which has a significant positive effect for the entire scheme. In each sub-district, the greater the positive cases, the greater the increase in death cases. An interesting thing happened to population density variable. In the earlier PSBB implementation in 2020, population density do not yet have a significant effect. However, at the end of PSBB 2 i.e. at the end of 2020 and along with the increase in positive cases, population density have a significant effect on the increase in death cases.

Table 2. Estimator of fixed effects in equation (2)

Social distancing scheme	Estimator of fixed effects (95% Credibility interval)			RMSE
	b_0	β_1	β_2	
PSBB 1	1.458 (-1.032, 3.945)	0.064 (0.049, 0.079)	0.003 (-0.007, 0.014)	3.31
PSBB Transition 1	1.579 (-2.869, 6.021)	0.028 (0.022, 0.035)	0.005 (-0.012, 0.023)	5.10
PSBB 2	-7.279 (-14.063, -0.505)	0.023 (0.019, 0.028)	0.049 (0.027, 0.071)	6.66
PSBB Transition 2	-9.454 (-20.103, 1.180)	0.018 (0.016, 0.021)	0.061 (0.028, 0.094)	10.43
PPKM 1	-11.939 (-25.961, 2.064)	0.017 (0.015, 0.018)	0.082 (0.022, 0.126)	13.91
PPKM 2	-15.098 (-32.713, 2.493)	0.018 (0.016, 0.020)	0.091 (0.035, 0.146)	17.34

The predictive value of \hat{y} from equation (2), which is the posterior mean value of sum of fixed and random effects is represented in Figure 4. The spread prediction of death cases at the beginning of PSBB 1 was seen in the northern part of Jakarta, then increased and spread to a

number of sub-districts in northeast Jakarta, then to the southern, western until to the northwest part of Jakarta. The difference in number of cumulative death cases in each sub-district at earlier start of PSBB 1 policy is very easy to see. This can be seen by a very clear color gradation, which indicates that death case is still concentrated in the yellow sub-district. However, at implementation of PSBB 2 to PPKM 2 the color gradations in each sub-district looked very smooth and evenly distributed, this indicates that number of death cases was no longer concentrated in certain areas, but had spread and with almost the same mortality risk. The modeling accuracy from the results of Bayes LMM in equation (2) can be seen in the latest column in Table 2. Table 2 shows that the modeling in PSBB 1 scheme has the best RMSE value, which is 3.31. However, the increasing number of death cases resulted in a higher variance of responses, resulting in a greater RMSE value. The largest RMSE is in PPKM 2 scheme with 17.34.

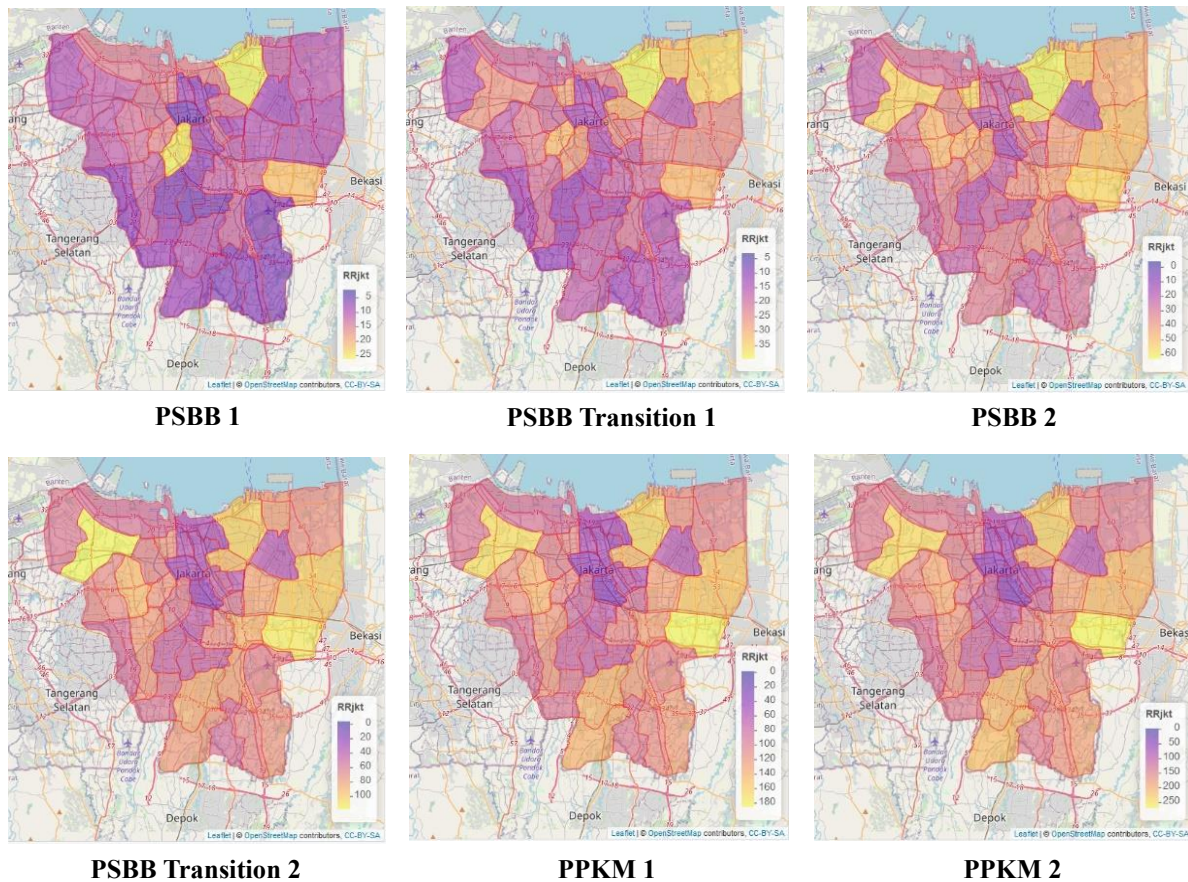


Figure 4. Map of spatial prediction from equation (2) in sub-district units

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We enhance the spatial spread prediction by calculating the probabilities of \hat{y} estimates being greater than a given threshold value. These probabilities are called exceedance probabilities and are useful to assess unusual elevation of disease risk [15]. The map of exceedance probabilities is presented in Figure 5. It can be seen that during PSBB 1 implementation to PSBB 2 there were no districts with a death probability exceeding 100 cases. It can be seen in Figure 5 with a uniform map color which indicates that $P(\text{death cases} > 100)$ is 0. However, in PSBB Transition 2 there was an increase in number of deaths to PPKM 2. In PPKM 2 cases with $P(\text{death cases} > 100)$ were almost evenly distributed throughout Jakarta area, although there were still a few sub-districts with a very small exceedance probability, especially in northern Jakarta. The number of sub-districts with $P(\text{death cases} > 100)$ is summarized in Table 3.

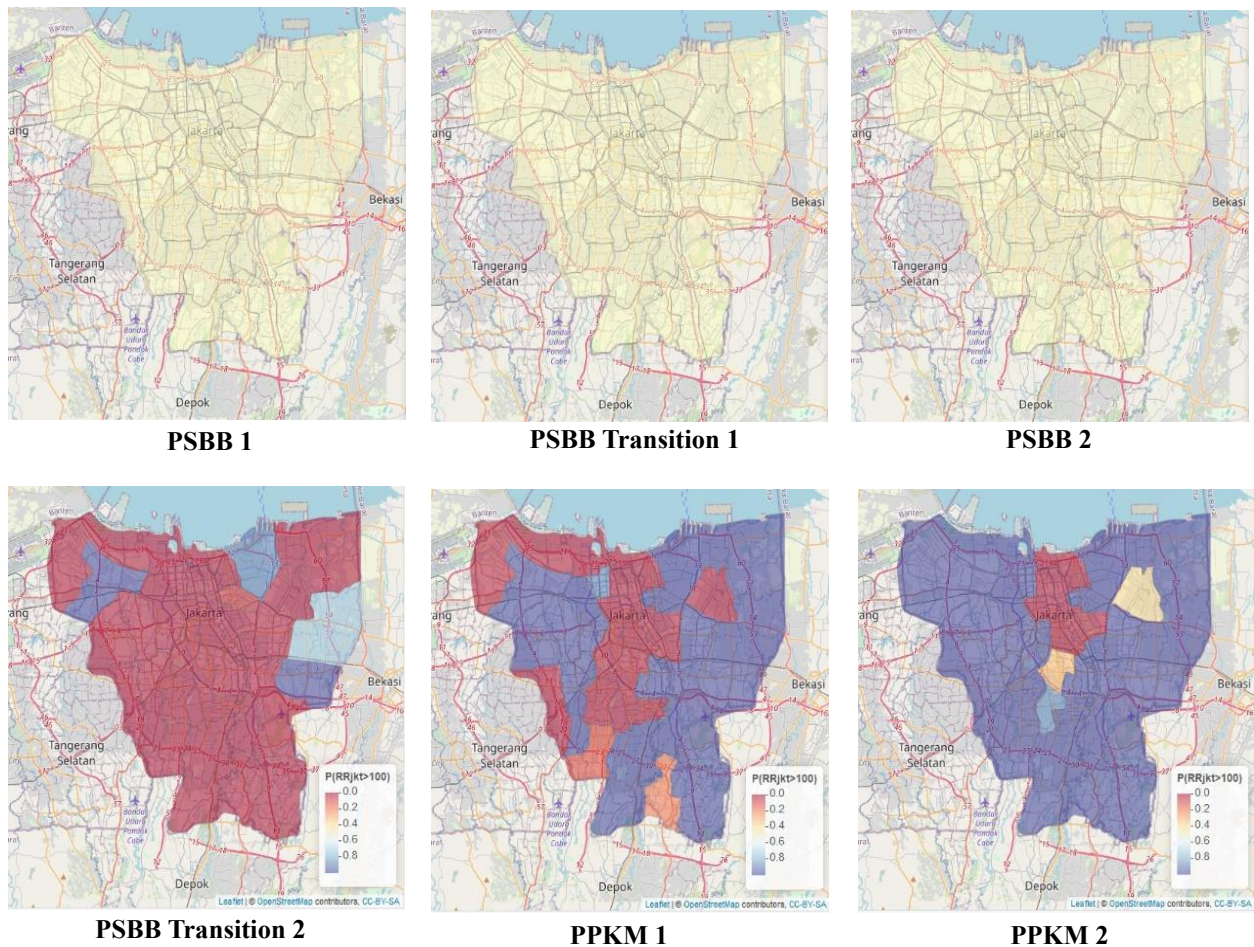


Figure 5. Map for exceedance probability with $P(\text{death cases} > 100)$

Table 3 is obtained from the results of mapping the number of districts with the criteria $P(\text{death cases} > 100)$ more than or equal to 0.5, 0.75 and equal to 1. In table 3, in the first 3 social distancing schemes, there are no sub-districts with more than 100 deaths. This can be seen from value of $P(\text{death cases} > 100)$ is 0. However, in PSBB Transition 2 there were 4 sub-districts with $P(\text{death cases} > 100) \geq 0.5$. Then it increased to 22 sub-districts in PPKM 1 and continued to increase by 32 sub-districts in PPKM 2. From this value we can calculate the daily increase in the number of high-risk sub-districts of COVID-19 with $P(\text{death cases} > 100)$ more than or equal to 0.5, 0.75 and equal to 1. During PSBB Transition 2 implementation period, number of high-risk sub-districts increased by 5% per day. This value continued to experience a sharp increase to 51% per day at PPKM 1 and then decreased to 38% at PPKM 2.

Table 3. Exceedance probability and sub-district elevation of COVID-19 risk

$P(\text{death cases} > 100)$	N = Number of sub-district with $P(\text{death cases} > 100)$					
	PSBB 1	PSBB Transition 1	PSBB 2	PSBB Transition 2	PPKM 1	PPKM 2
≥ 0.5	0	0	0	4	22	32
≥ 0.75	0	0	0	3	22	32
$=1$	0	0	0	0	14	28
Sub-district elevation of COVID-19 risk = (N/days) %						
≥ 0.5	-	0	0	5%	51%	38%
≥ 0.75	-	0	0	4%	51%	38%
$=1$	-	0	0	0%	33%	33%

Table 3 implies that the type of social distancing scheme will determine the speed at which number of high-risk sub-districts of COVID-19 will increase. During 2020, PSBB and PSBB Transition schemes were quite effective. The daily increase in number of high-risk sub-district is very slow, around 5%. However, in early 2021 the social distancing scheme was changed to PPKM 1, where in this scheme the increase of high-risk sub-districts jumped very significantly to 51% per day, although in PPKM 2 there was a decrease of up to 38% per day. Until the final PPKM 2 observation, 28 sub-districts had more than 100 deaths. It is hoped that the social restriction scheme can continue to be studied so that high-risk sub-districts do not continue to increase. However,

from the existing predictions, there is a downward trend in addition rate of high-risk sub-districts to PPKM 2 by 33%. Although not directly involved as a variable in the modeling in equation (2), the PSBB and PSBB Transition social distancing schemes are considered to be quite effective in suppressing the diversity of cumulative number of deaths.

4. CONCLUSIONS

This study examines the mapping and spatial prediction of COVID-19 death cases in Jakarta using Bayes LMM methods. Death cases as response data recorded based on social distancing scheme from time to time with positive cases and population density from 43 sub-districts as the explanatory variables. Positive cases have a significant effect on death cases in each social distancing scheme. However, the significance of population density only occurs in PSBB 2 to PPKM 2 schemes where there is a greater variation of positive cases in each sub-district. Mapping with Bayes LMM produces accurate predictions with the best RMSE of 3.31 at the start of PSBB 1 implementation scheme. The RMSE value is getting bigger up to PPKM 2, this is due to several possibilities including the variation of data which is also getting bigger so that the assumption of normal distribution for the response is no longer appropriate.

Several aspects in this research can be developed including: 1) non-normal response distribution. The greater variation of response data results in the consideration of using non-normal distributions, such as Poisson distribution as in the following researches [16, 17, 18]. 2) non-intercept modeling. In general, the intercept value of Bayes LMM for each social distancing scheme does not have a significant effect. Modeling can be developed without using intercept and replace it with some random effect such as a temporal trend as in [19, 20]. 3) Longitudinal data modeling. Observation of response data over time is a longitudinal data that can also be developed as further research. The increasing variation of data makes it possible to develop longitudinal data modeling using LMM and GLMM concepts [21]. Random effects can be combined into modeling which includes random effects unique to each sub-district and also temporal random effects as in [22, 23].

Health data can provide information to identify public health problems and are needed for disease management. This information is important as an effort to prevent and control various health conditions, especially infectious diseases such as COVID-19. Disease risks presented in this research in the form of a map provide a quick visual summary and make it possible to identify spatial patterns / dependencies, which may be difficult or overlooked if presented only in tabular form.

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CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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