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Modeling suspected malaria cases in Papua province with second order Besag-York-Mollie 2 spatial regression

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Abstract

The number of malaria cases in Indonesia has increased in recent years. The highest malaria cases in Indonesia are in the eastern region, namely Papua Province, where in 2021 there were 86,022 cases. This study aims to model suspected malaria cases in Papua using the Integrated Nested Laplace Approximation (INLA) approach. Modelling is carried out with two different orders to see the difference in determining the best results. The results showed that second-order spatial modelling provides better results than first order modelling because the RMSE value is smaller than the first-order model. Based on these results, it is concluded that the INLA approach with second-order spatial modelling is effective for analysing and predicting suspected malaria cases in Papua. Therefore, these results can be used as a reference in developing malaria control strategies in the region.

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INTRODUCTION

Malaria is an infectious disease caused by the Plasmodium parasite (Nureye & Assefa, 2020). The disease is not transmitted from human to human. Most cases of malaria are transmitted through infected Anopheles female mosquitoes (Talapko et al., 2019). The Plasmodium species that cause malaria in humans are P. falciparum, P. vivax, P. ovale, P. malariae, and P. knowlesi (Huber et al., 2023). The most common symptom experienced by people with malaria is fever (Bria et al., 2021). However, some individuals with positive malaria test results report symptoms of chills and headache without fever (Kumari et al., 2020; van Eijk et al., 2020).

A serious impact of recurrent malaria infection in children in endemic areas is the risk of anaemia, which can impact their health and survival (Phiri et al., 2024; Teketelew et al., 2023). In addition, malaria also contributes significantly to increased morbidity and mortality, as well as impairment in educational performance at school (Gao et al., 2023; Ssemata et al., 2023). Malaria during pregnancy poses particular risks, associated with maternal anaemia, prematurity, fetal death, and low birth weight (Mangusho et al., 2023; Phyo et al., 2022).

The Annual Parasite Incidence (API) rate of malaria in Indonesia has increased in recent years. In 2017, the API of malaria in Indonesia was 1.0 cases per 1,000 population with 261,617 positive cases. The API decreased to 0.8 cases per 1,000 population in 2018, resulting in a decrease in the number of positive cases to 222,085 cases, and in 2019, the number of APIs increased again to 0.9 cases per 1,000 population and 250,644 positive cases. The API rate remained at 0.9 per 1,000 population in 2020, but the number of positive cases increased to 254,050. In 2021, the API rate was 1.1 cases per 1,000 population and 304,607 positive cases were reported. The 2021 malaria report

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showed the highest number of API cases and positive cases in the last five years, making Indonesia an endemic country (Ministry of Health of the Republic of Indonesia, 2021).

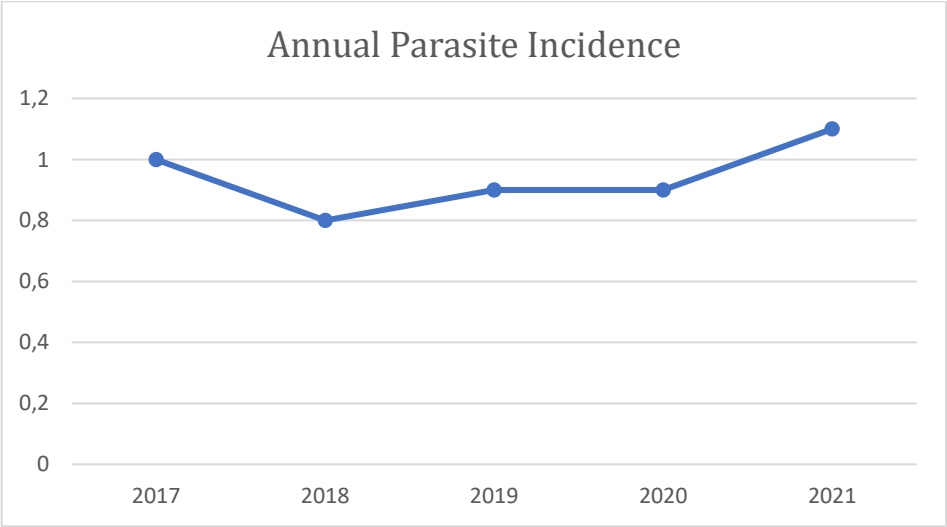

Figure 1. Annual Parasite Incidence malaria in Indonesia

Several prior studies have explored malaria in depth with diverse methodologies and notable outcomes. For instance, in research by Ndiaye et al. (2021) employing genetic analysis techniques, genetic variations in malaria parasites were linked to resistance against specific antimalarial medications. Conversely, Adeola et al. (2019) utilized SARIMA in a mathematical modeling study to forecast malaria transmission patterns based on environmental factors like rainfall and temperature. Moreover, Mosha et al. (2020) conducted research using a logistic regression model, revealing a significant association between malaria vector population density and malaria disease prevalence rates. Furthermore, spatial analysis by (Iddrisu et al., 2024) pinpointed "hotspots" or regions with elevated malaria incidence rates, offering crucial insights for malaria control and mitigation efforts.

Modeling and mapping diseases play a crucial role in early detection of high-risk areas, aiding in disease prevention (Kitawa et al., 2023; Pourghasemi et al., 2020). Research on modelling malaria cases was conducted by Lubinda et al. (2021) using Markov Chain Monte Carlo (MCMC)-based inference. The MCMC method is commonly used for Bayesian inference but faces challenges in high computational burden. As the model complexity increases, the computational time required for Bayesian inference through MCMC becomes longer (Blangiardo & Cameletti, 2015). Therefore, researchers utilized the Integrated Nested Laplace Approximation (INLA) method to enhance the MCMC method in previous studies.

Most disease risk mapping models are typically developed using a Bayesian approach. Artiono (2019) conducted research on leptospirosis disease mapping in Bantul, Indonesia, revealing that agricultural land exerted a greater influence compared to agricultural livelihoods. Certain areas exhibited a high risk of new leptospirosis cases. Djuraidah et al. (2022) investigated TB cases on Java Island utilizing Bayesian Conditional Autoregressive (CAR) with INLA, indicating that the percentage of non-smokers played a significant role in decreasing the number of TB patients in Java. Another study by Rachmawati et al. (2021) focused on mapping and predicting COVID-19 deaths using the Bayes Linear Mixed Model (LMM) method with spatial random effects. The findings highlighted the substantial impact of the number of positive COVID-19 cases on the rise in deaths. While the modeling applied first-order neighboring elements, modeling endemic infectious diseases would benefit from employing second-order neighborhoods to capture a more accurate representation of spatial patterns and complex spatial interactions.

The high morbidity rate of malaria illustrates the lack of public awareness about the importance of health. This needs more attention so that the morbidity rate can be reduced. One of the efforts that can be made is to explore information about the causes of high malaria cases. Malaria cases can be reduced if it is known what variables affect it. The magnitude of the influence of a variable can provide advice or input for the provincial government in making policies to reduce

malaria rates. In this case, suspected malaria cases can be modelled in mathematical equations with several explanatory variables that affect morbidity and mortality rates in Papua Province.

The data to be used in this research is suspected malaria case data. A malaria suspect is someone who is suspected of being infected with malaria based on clinical symptoms that appear (Kigozi et al., 2021). Suspect data is used because it allows early detection of infections that may occur before clear clinical symptoms appear. Early detection and appropriate treatment of suspected malaria is key in the management of this disease to prevent more serious complications (Akafity et al., 2024; Mace et al., 2022).

Based on the explanation and literature study that has been carried out, this research aims to carry out spatial mapping of malaria using the Besag York Mollie 2 approach. The spatial modelling will be conducted with spatial neighbourhood elements of order 1 and order 2. This is conducted to compare both models and select the model that best fits the data and provides the most accurate results. The model selection is based on the smallest Root Mean Square Error (RMSE) value.

This article will discuss the model of suspected malaria cases in Papua with INLA. The section on this article consists of 4 sections. The second section discusses the exploration and illustration of the data that will be used in this study. The next section discusses the results and discussion of this study including the model and its interpretation. The last section discusses the conclusions of this study.

METHOD

This research uses malaria suspect data in Papua obtained from BPS in Papua, downloaded at https://papua.bps.go.id. The data is in the form of annual data on suspected malaria in 2021 consisting of 29 regencies/city. The variables to be used in the research can be seen in Table 1.

Table 1. Dependent variable and independent variables

Dependent Variable	Independent Variable
Suspected malaria cases (y)	Elevation (x_1)
	Human development index (x_2)
	Sanitation (x_3)
	Health facilities (x_4)

Figure 2 is a representation of the relative condition of each regency with red indicating areas with a high number of cases and yellow indicating areas with low cases. The number of suspected malaria cases in Papua Province in 2021 was recorded at 246,705 cases. The highest number of cases in Papua Province occurred in Mimika Regency with 102,024 cases, while the lowest case came from Central Mamberamo Regency with 11 cases.

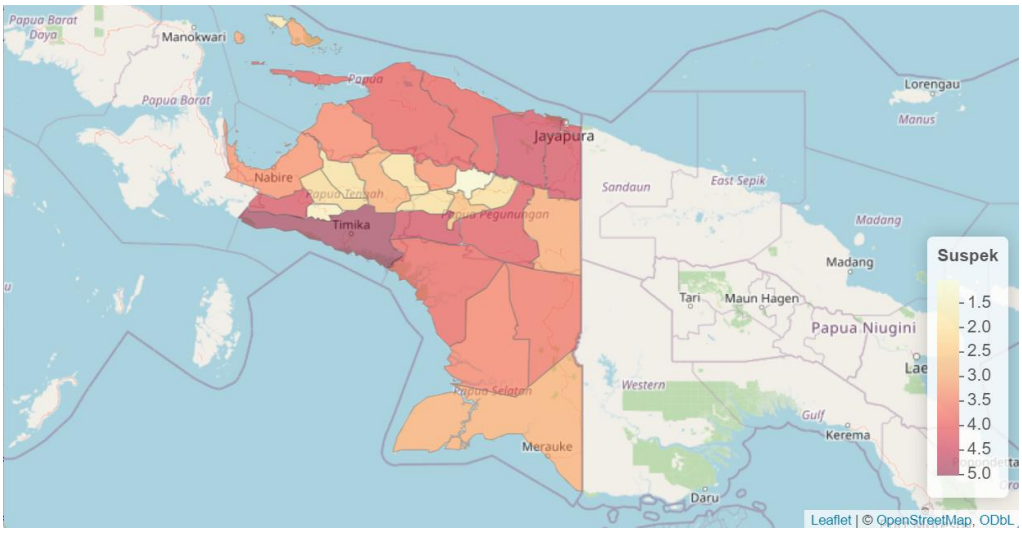

Figure 2. Malaria suspect data in Papua

Figure 3 shows data on elevation, human development index (HDI), sanitation, and health facilities per district in Papua Province. The highest area elevation is in Puncak Regency and the lowest area elevation is in Asmat Regency. Then, the highest HDI is in Jayapura City while the lowest HDI is in Nduga Regency. The highest sanitation is in Mimika Regency while the lowest sanitation is in Paniai Regency and Intan Jaya Regency. The regency with the highest number of health facilities is Merauke Regency while the lowest number of health facilities is Intan Jaya Regency.

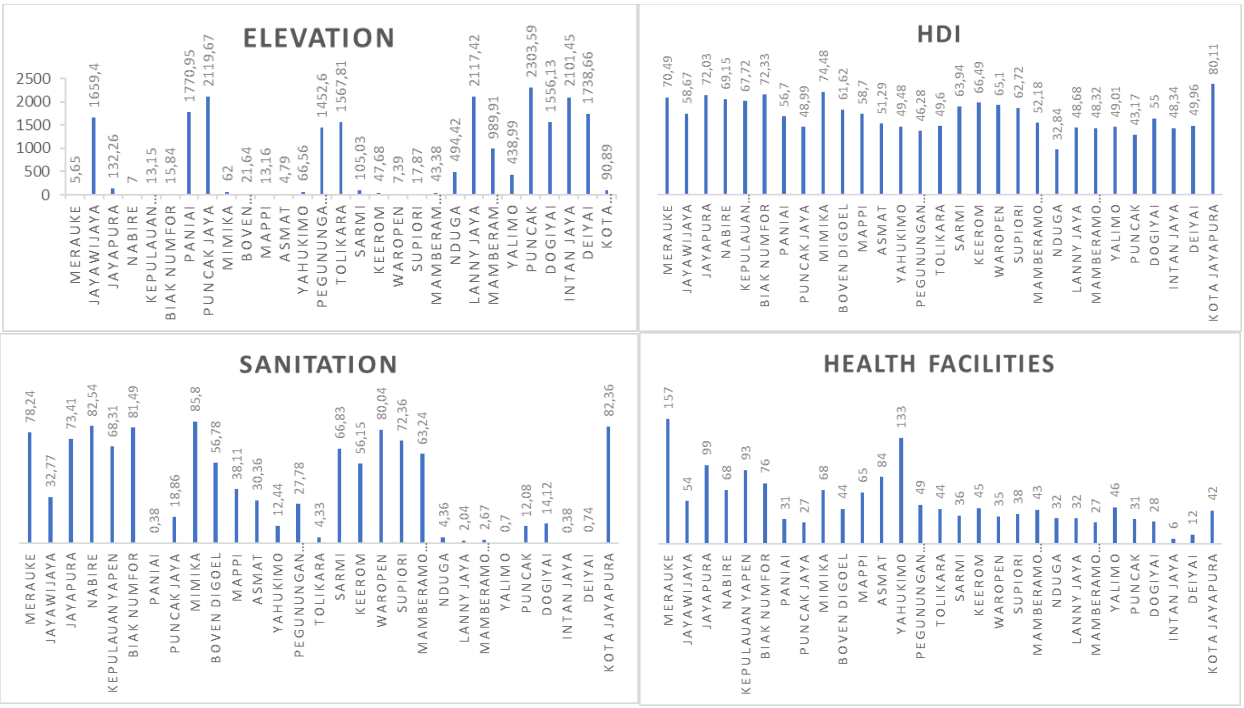

Figure 3. Data on elevation, human development index (HDI), sanitation, and health facilities.

The analysis stages are as follows:

1) Data exploration to determine the characteristics of malaria suspect data in Papua.
2) Forming spatial regression models of order 1 and order 2. Also carrying out the inference process using INLA.
3) Obtain posterior summaries and inferences for the model parameters, such as mean, standard deviation, and credible intervals.
4) Comparing first order and second order model using Root Mean Square Error (RMSE) as follows:

$$RMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}$$

Where:
n = Number of data
y_i = Actual value of i-th data
$\hat{y}_i$ = Predicted value of i-th data

Model evaluation based on the smallest RMSE. The smallest RMSE has high accuracy for predicting malaria suspect cases.

RESULTS AND DISCUSSION

Spatial Regression Model Besag-York-Mollie 2

Spatial regression is a model that is shown by the existence of a dependency relationship between a set of observations that get spatial influence (location). The result of spatial regression

calculation is a mixed model that allows fixed effects and random effects. The following is the general form of the spatial regression equation:

$$\widehat{y_i} = \alpha + \beta_1 x_{1i} + \beta_2 x_{2i} + \cdots + \beta_n x_{ni} + \frac{1}{\sqrt{\tau_b}}(\sqrt{1-\phi}\boldsymbol{v}_* + \sqrt{\phi}\boldsymbol{u}_*) \quad (1)$$

where $\widehat{y_i}$ is the number of suspected malaria cases in the i-th region, α is the intercept, β_n as coefficients to measure the effect of predictors x_1, x_2, x_3, x_4. Meanwhile, the size of the random effect is represented by u_* and v_*. The precision parameter $\tau_b > 0$ controls the marginal variance contraction of the weighted sum of u_* and v_*. The mixing parameter $0 \leq \phi \leq 1$ measures the proportion of marginal variance explained by the structured effect u_*. Thus, the BYM2 model is the same as the single spatial model when $\phi = 1$ and the unstructured spatial model.

First Order Model

First order modelling of suspected malaria cases produces variable values for each predictor as presented in Table 2. Negative coefficient values indicate an inverse relationship between the predictor variable and suspected malaria cases, while positive coefficients indicate a direct relationship between the predictor variable and suspected malaria cases.

Table 2. First Order Spatial Modelling

	mean	sd	Credibility Intervals
Intercept	4.014	1.545	(0.966, 4.008)
Elevation (x_1)	-0.038	0.034	(-0.106, 0.030)
HDI (x_2)	-0.023	0.034	(-0.089, 0.043)
Sanitation (x_3)	0.013	0.013	(-0.014, 0.039)
Health Facilities (x_4)	0.005	0.007	(-0.008, 0.019)

The results of first-order modelling can be expressed in regression equations, namely:

$$\widehat{y_i} = log(p_i) = 4{,}014 - 0{,}038x_{1i} - 0{,}023x_{2i} + 0{,}013x_{3i} + 0{,}005x_{4i} + \frac{1}{\sqrt{\tau_b}}(\sqrt{1-\phi}v_* + \sqrt{\phi}u_*) \quad (2)$$

The value for τ_b is expressed as $2{,}59 \times 10^4$. We define the mixing parameter ϕ as $1{,}31 \times 10^{-1}$. Equation (2) utilizes a spatial regression model with a log link function; hence it needs to be transformed back to its original values. The elevation and HDI variables have a negative effect on the number of suspected malaria cases. Each increase of 100 meters in elevation reduces the number of infected people by 49, while a 1 unit increase in HDI leads to a decrease of 50 cases. On the other hand, sanitation and health facilities have a positive impact on malaria cases. For every unit increase in sanitation, there is an increase of 52 cases, and each additional health facility contributes to an increase of 51 cases. It is important to note, however, that while all these variables have some influence, they are not significant factors in determining the number of malaria cases.

Second Order Model

Second order modelling of suspected malaria cases produces variable values for each predictor as presented in Table 3. Negative coefficient values indicate an inverse relationship between the predictor variable and suspected malaria cases, while positive coefficients indicate a direct relationship between the predictor variable and suspected malaria cases.

Table 3. Second Order Spatial Modelling

	mean	sd	Credibility Intervals
Intercept	3,934	1,519	(0,933, 6,936)
Elevation (x_1)	-0,037	0,034	(-0,105, 0,031)
HDI (x_2)	-0,022	0,033	(-0,087, 0,043)
Sanitation (x_3)	0,012	0,013	(-0,014, 0,039)
Health Facilities (x_4)	0,006	0,007	(-0,007, 0,019)

The results of second order modelling can be expressed in regression equations, namely:

$$\hat{y}_i = log(p_i) = 3.934 - 0{,}037x_{1i} - 0{,}022x_{2i} + 0{,}012x_{3i} + 0{,}006x_{4i} + \frac{1}{\sqrt{\tau_b}}(\sqrt{1-\phi}\boldsymbol{v}_* + \sqrt{\phi}u_*) \quad (3)$$

The value for τ_b is expressed as $2{,}46 \times 10^4$. We define the mixing parameter ϕ as $1{,}48 \times 10^{-1}$. Equation (3) utilizes a spatial regression model with a log link function; hence it needs to be transformed back to its original values. The elevation and HDI variables have a negative effect on the number of suspected malaria cases. Each increase of 100 meters in elevation reduces the number of infected people by 53, while a 1 unit increase in HDI leads to a decrease of 54 cases. On the other hand, sanitation and health facilities have a positive impact on malaria cases. For every unit increase in sanitation, there is an increase of 56 cases, and each additional health facility contributes to an increase of 56 cases. It is important to note, however, that while all these variables have some influence, they are not significant factors in determining the number of malaria cases.

Random Effect

Random effects using the BYM2 model which is a new parametrization of the BYM model that uses a spatially structured random component u_* and an unstructured random component v_*. The structured random effect u_* and the unstructured random effect v_* in equation (4) are summed up and summarized in the combined random effect value b. The precision parameter τ_b controls the random effects u_* and v_*.

$$\boldsymbol{b} = \frac{1}{\sqrt{\tau_b}}(\sqrt{1-\phi}\boldsymbol{v}_* + \sqrt{\phi}\boldsymbol{u}_*) \quad (4)$$

The summation of the random effects results in random effects map as shown in Figure 3.

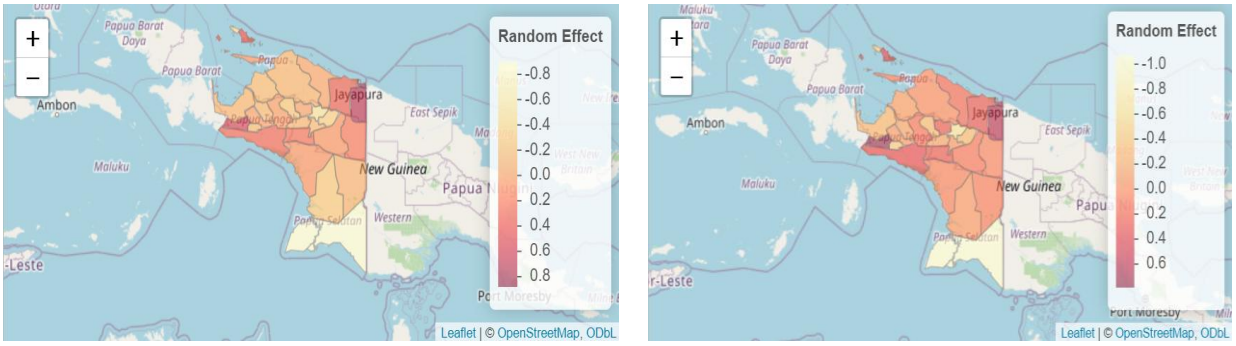

Figure 3. Random effect for the first order model (left) and random effect for the second model (right)

Random effects in statistical analysis are variations that cannot be explained by the observed variables in the model. Random effects consider additional factors that influence the variation in data that cannot be explained by the model. The random effects of neighboring areas do not always have similar colors. Figure 3 shows that there is a pattern on the map shown in the orange areas and a red pattern. This can be interpreted as the proximity of a neighboring region influencing the risk of malaria spread in a similar way. The influence of neighboring areas also has an impact on the difference in the number of malaria cases between neighboring areas.

If the value of the random effect $b > 0$, then the suspected cases in the regency are above average and vice versa if $b < 0$. The magnitude of the random effects at first order and second order has a small difference. There are 16 districts with $b > 0$ while there are 13 districts with $b < 0$. Regency with low random effects ($b < -1$) are Deiyai, Memberamo Tengah, Merauke, Supiori, and Yalimo. Keerom, Mimika, Nduga and Jayapura City have large random effect values ($b > 0.9$). This increases the potential risk of malaria cases. Regencies with large b values indicate that they are

endemic. All regencies need to be aware of the spread of malaria, but regencies that are direct neighbors to endemic areas need to make more efforts to prevent the spread of malaria. This is because the risk of contracting malaria is greater than in areas that are not direct neighbors.

In previous studies, modeling was conducted using first-order neighbor elements. However, modeling endemic infectious diseases would be better if using second-order neighbors to get a more accurate representation of complex spatial patterns and spatial interactions. In Figure 3, it can be seen that the random effects in the second-order model are more complex than the random effects in the first-order model. This happens because the neighbor diversity of the second-order is more widespread than that of the first-order.

CONCLUSION

Modeling of malaria cases in Papua Province using the INLA method was conducted to determine the causes of high malaria cases. The results of the modeling show that elevation and HDI are inversely proportional to malaria cases, while sanitation and health facilities are directly proportional. The modeling results show the influence of each variable, but the results are not significant. The region with the highest predicted suspects is Mimika Regency, while the region with the lowest predicted suspects is Mamberamo Tengah Regency. This is because fixed effects and random effects support the size of the prediction of malaria cases. Regions with large random effect values are influenced by their neighbors who also have great potential for malaria transmission. The same thing happens in areas with small random effects that have little potential for malaria transmission.

Based on the previous discussion, it can be concluded that the model of suspected malaria cases in Papua for 2021 has the best equation of second order. The first order model has a RMSE value of $1{,}078 \times 10^{-4}$ and the second order model has a RMSE value of $1{,}067 \times 10^{-4}$. Model evaluation based on the smallest RMSE value. The second order model is more accurate in predicting suspected malaria cases because its RMSE value is smaller than the first order model. The second order spatial modelling in the case of malaria tends to be better than first-order modelling because it accounts for more complex spatial interactions between different geographic locations. By using the second order, the model can capture more complicated spatial patterns and offer a deeper understanding of how the spread of a disease like malaria can be affected by complex spatial factors. As such, second order modelling is likely to provide more accurate and informative results in understanding and forecasting the spread of malaria.

AUTHOR CONTRIBUTIONS

Each author of this article played an important role in the process of method conceptualization, simulation, and article writing.

CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest.

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