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Bayesian spatial modeling of malaria risk in Mozambique: a province-level analysis

Abstract

Malaria remains one of the major public health challenges in Mozambique, with substantial spatial variation in disease occurrence across provinces. Understanding the geographical distribution of malaria risk is essential for guiding targeted control strategies and improving the allocation of health resources. This study investigated the spatial distribution of malaria relative risk across the provinces of Mozambique using a Bayesian spatial modelling approach. Global and local spatial autocorrelation analyses were performed to identify spatial patterns and clustering of malaria risk. The Intrinsic Conditional Autoregressive (ICAR) model was applied to estimate province-specific relative risks. Posterior exceedance probability maps were generated to assess the statistical evidence of increased or reduced malaria risk. The results revealed significant positive spatial autocorrelation, indicating that malaria risk is spatially structured rather than randomly distributed. A high-risk spatial cluster was identified in the northern and central regions of the country, particularly encompassing the provinces of Nampula, Cabo Delgado, and Zambézia, with Nampula emerging as the main hotspot. In contrast, most provinces in the southern region and some central provinces exhibited low relative risk, with the exception of Inhambane, which showed elevated relative risk. Although Niassa presented relatively low estimated risk, its location adjacent to high-risk provinces suggests increased epidemiological vulnerability. The ICAR model provided robust estimates of relative risk, while posterior exceedance probabilities confirmed areas with strong evidence of risk exceeding the expected level. The findings demonstrate substantial spatial heterogeneity in malaria risk across Mozambique and highlight the importance of incorporating spatial dependence into disease mapping analyses. Bayesian spatial models and posterior exceedance probability maps provide valuable evidence to support geographically targeted malaria interventions.

Keywords: malaria, Mozambique, bayesian disease mapping, ICAR model, relative risk, posterior exceedance probability

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Introduction

Malaria continues to impose a substantial public health burden worldwide, disproportionately affecting populations in low- and middle-income countries. In 2023, more than 263 million malaria cases were reported worldwide, representing an increase of approximately 11 million cases compared with 2022. Nearly 52% of these cases were concentrated in five African countries, including Mozambique.[1] Furthermore, malaria is estimated to cause approximately 408,000 deaths annually, mainly affecting populations in Africa and Asia, despite being a preventable and curable disease when appropriate prevention, diagnosis, and treatment measures are implemented.[2] The disease is transmitted through the bite of infected Anopheles mosquitoes carrying Plasmodium parasites, which complete part of their life cycle in both humans and mosquitoes.[3,4]

In 2024, Mozambique reported 11,614,339 malaria cases, highlighting that malaria continues to represent one of the country's most significant public health challenges. This substantial disease burden places considerable pressure on the national healthcare system, requiring sustained investments in prevention, diagnosis, treatment, and epidemiological surveillance, while also imposing substantial economic and social costs.

Identifying high-risk areas is essential for supporting evidence-based decision-making and establishing priorities for allocating human, material, and financial resources dedicated to malaria control. Disease mapping techniques, particularly Bayesian hierarchical spatial models, provide a robust framework for estimating malaria risk by explicitly accounting for the spatial dependence that exists among neighboring provinces. Consequently, these models generate more reliable and stable risk estimates, offering valuable scientific evidence to guide targeted public health interventions. Their application can contribute to a more efficient allocation of available resources and strengthen malaria prevention and control strategies in Mozambique.

This study aims to estimate the spatial variation in malaria infection risk across the provinces of Mozambique using Bayesian hierarchical disease mapping models. Different Bayesian spatial models are compared to identify the model that best represents the observed malaria pattern and provides the most reliable estimates of relative risk. The paper is structured as follows. Section 2 introduces the study area, describes the data sources, and outlines the approach used to derive the expected number of malaria cases. In Section 3, spatial dependence is explored through the Global Moran's I and Local Moran's I (LISA) statistics. Section 4 introduces the Bayesian hierarchical disease mapping models adopted in the study, together with the estimation procedure and model fitting strategy. Section 5 presents the results of the spatial analysis, model comparison, and malaria risk estimation. The implications of the study findings for malaria surveillance and control in Mozambique are examined in Section 6. The final section highlights the key conclusions of the study and suggests areas for further research.

Study area and data sources

Study area

Mozambique is a country located on the African continent, specifically in the eastern region of Southern Africa. According

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to projections from the National Statistics Institute, the country had an estimated population of 33,244,414 inhabitants in 2024. Administratively, Mozambique consists of 11 first-level units, comprising 10 provinces and Maputo City, the country's capital. These are Niassa, Cabo Delgado, Nampula, Zambézia, Tete, Sofala, Manica, Gaza, Inhambane, and Maputo Province.

Data sources

The data used to estimate the risk of malaria infection in each of the study regions, corresponding to Mozambique's provinces, were extracted from the platform of the National Statistics Institute of Mozambique. These data, pertaining to the year 2024, comprise the annual number of notified malaria cases and the resident population per province, which formed the basis for calculating the expected number of cases and the relative risk. Geospatial data were obtained from the Humanitarian Data Exchange platform, which provides shape files of Mozambique's administrative boundaries. These files were subsequently merged with the epidemiological database using the unique identifier code for each province, allowing the spatial visualisation of malaria distribution and the generation of thematic maps to represent estimated malaria risk and identify patterns of disease spread.

Calculation of the expected number of cases

The expected number of malaria cases for each province was computed according to the following:[5]

$$E_i = N_i \frac{\sum_i^n O_i}{\sum_i^n N_i} \quad (1)$$

where N_i is the population of province i and O_i is the number of reported malaria cases in province i

Spatial autocorrelation analysis

Spatial autocorrelation, understood as the lack of independence between observations located in space, constitutes one of the fundamental principles of spatial analysis and disease mapping.[6] This phenomenon arises from the tendency of geographically proximate areas to exhibit similar characteristics, resulting in spatial covariation among observations.[7]

In studies involving area-aggregated data, Blangiardo and Cameletti[8] argue that spatial dependence should be explicitly incorporated into the statistical model by using a neighbourhood structure that represents the spatial relationships between geographical units. This approach allows for a more realistic capture of the correlation between adjacent areas, leading to more robust estimates and more reliable inferences.

Spatial autocorrelation is measured through the application of global and local tests. Global tests assess autocorrelation across the entire study region. However, since global autocorrelation may sometimes be driven by local patterns, the application of local spatial autocorrelation tests is also necessary. Both global and local tests have as their null hypothesis the absence of spatial autocorrelation, against the alternative hypothesis of its presence.[9]

To test for the presence or absence of global spatial autocorrelation, Moran's I statistic was applied, as defined by Bivand et al.:[10]

$$I = \frac{n}{\sum_{i=1}^n \sum_{j=1}^n w_{ij}} \times \frac{\sum_{i=1}^n \sum_{j=1}^n w_{ij}\left(y_i - \bar{y}\right)\left(y_j - \bar{y}\right)}{\sum_{i=1}^n \left(y_i - \bar{y}\right)^2} \quad (2)$$

where y_i represents the observation (which may be any measure of interest, such as the difference between observed and expected cases, treated as residuals, or the SMR — Standardized Mortality Ratio , Taero, 2025) for province i, y_j is the same observation for province j, w_{ij} denotes the spatial weight associated with regions i and j, $\bar{y}$ is the mean of the variable under analysis, and n is the number of observations in the variable of interest.

For the local test, the local Moran's I statistic was applied, as defined by Bivand et al.:[10]

$$I_i = \frac{n\left(y_i - \bar{y}\right)\sum_{j=1}^n w_{ij}\left(y_j - \bar{y}\right)}{\sum_{i=1}^n \left(y_i - \bar{y}\right)^2} \quad (3)$$

where I_i represents the Moran's I statistic value for province i.

Bayesian hierarchical disease mapping models

Statistical model

To model the relative risk of malaria across the different provinces of Mozambique, four models were considered: the ICAR (Intrinsic Conditional Autoregressive) model, the BYM (Besag-York-Mollié) model, the BYM2 model, and the Leroux model. These models were formulated within the framework of Bayesian Poisson regression, initially adopting the Poisson likelihood as a natural specification for areal count data. The models account for spatial dependence between geographical areas through spatially structured random effects, thereby capturing residual spatial variation not explained by the expected number of cases. The adequacy of the Poisson likelihood was assessed through posterior predictive checks, PIT (Probability Integral Transform) diagnostics, residual diagnostics, and sensitivity analysis using a negative binomial likelihood. For further details on Bayesian disease mapping and spatial hierarchical models, see Blangiardo and Cameletti,[8] Lawson,[11] Haining and Li,[6] and Sahu.[12]

Let y_i be the number of observed malaria cases in province i, recorded in 2024, and let E_i the expected number of malaria cases in province i. The relative risk of malaria of province i is denoted by θ_i. The data model was initially specified as

$$y_i \mid \theta_i \sim Poisson\left(E_i\theta_i\right), \qquad i = 1,2,3,\ldots,n \quad (4)$$

where $n=11$ is the total number of provinces in Mozambique. The ICAR model considers only the structured spatial component and is specified as:

$$\log\left(\theta_i\right) = \alpha + u_i \quad (5)$$

where α is the intercept, representing the logarithm of the overall mean relative risk of contracting malaria across all provinces, and the spatial structure is represented by u_i, which follows an intrinsic conditional autoregressive (ICAR) prior. Its joint distribution is given by:

$$u \mid \tau_u \sim N\left(0, \tau_u^{-1}Q^{-1}\right) \quad (6)$$

where τ_u is the precision parameter and Q is the neighbourhood matrix. This model captures only the spatial dependence between neighbouring provinces. *The BYM model extends the ICAR model by adding an unstructured random effect to account for heterogeneity not explained by spatial structure. Its formulation is:*

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$$\log(\theta_i) = \alpha + u_i + v_i \quad (7)$$

where is the unstructured spatial random effect, modelled as independently and identically distributed:

$$v_i \sim N\left(0, \sigma_v^2\right) \quad (8)$$

with precision $\tau_v = 1/\sigma_v^2$. As before, α represents the overall log-relative risk and u_i captures the spatially structured component. This model decomposes the relative risk into two sources of variation: one that is spatially dependent (modelled via the ICAR prior) and another that is independent across provinces, capturing local heterogeneity.

The BYM2 model corresponds to a reparameterisation of the BYM model, which improves parameter interpretability and estimation stability.[13] Its specification is:

$$\log(\theta_i) = \alpha + \frac{1}{\sqrt{\tau}}\left(\sqrt{1-\phi}v_i + \sqrt{\phi}u_i^*\right) \quad (9)$$

where u_i^* represents the scaled spatially structured component (i.e., the combined effect), with $\phi(0 \le \phi \le 1)$ being the proportion of spatial variance and $\tau(\tau > 0)$ the precision parameter.[14,15] *The Leroux spatial structure can be expressed as follows:*

$$\log(\theta_i) = \alpha + \varphi_i \quad (10)$$

where φ_i denotes the spatial random-effect vector, which follows a multivariate normal prior whose precision matrix is determined by the spatial neighbourhood structure.[16]

Prior distributions

For the precision parameters associated with the random effects, we used the default prior specification in R-INLA, namely a log-Gamma distribution with shape and rate parameters equal to 1 and 0.0005, respectively. This constitutes a weakly informative prior, ensuring that the likelihood dominates the posterior inference. Vague normal priors were assigned to the fixed effects, including the intercept α.

The BYM2 specification employed penalised complexity (PC) priors following the framework of Simpson et al.[17] Specifically, the following priors were set for the parameters τ and φ:

$$P\left(\frac{1}{\sqrt{\tau}} > 0{,}02\right) = 0{,}01$$

and

$$P(\phi < 0{,}5) = \frac{2}{3}$$

Model fitting and parameter estimation

Posterior inference for the four spatial specifications described in Section 4.1 was performed using R-INLA.[18] The INLA framework provides approximate inference for latent Gaussian models without requiring conventional MCMC sampling, offering an efficient computational strategy for the fitted models. The response variable in all models was the number of malaria cases recorded in each province of Mozambique, and a Poisson likelihood was adopted to account for the count nature of the data. The model formula specified in R-INLA included the fixed and random effects defined for each of the four models, allowing for the estimation of all relevant parameters and the computation of the linear predictors. For further details on model fitting and parameter estimation, see Blangiardo and Cameletti,[8] Wikle et. al.,[19] and Moraga,[14,15] who also provide R code examples for this purpose.

Model Comparison Criteria

Model adequacy and relative performance were assessed using the Deviance Information Criterion (DIC) and the Watanabe–Akaike Information Criterion (WAIC). The DIC, introduced by Spiegelhalter et al.,[20] is defined as:

$$DIC = 2E_{\theta|y}\left(D(\theta)\right) - D\left(E_{\theta|y}(\theta)\right) \quad (11)$$

Through mathematical manipulation,[11] equation (11) can be rewritten as:

$$DIC = \bar{D} + pDIC \quad (12)$$

where pDIC is the effective number of parameters. The WAIC, introduced by Watanabe (2010), is defined as follows:[21]

$$WAIC = lppd - pWAIC \quad (13)$$

where $lppd$ *is the log pointwise predictive density and* $pWAIC$ *is the effective number of parameters. The decision to consider both criteria was motivated by the need to evaluate the behaviour of each model with respect to the data. Both DIC and WAIC are automatically available in R-INLA. Other evaluation measures may also be used as alternatives to DIC, such as the Log Pseudo-Marginal Likelihood (LPML) (Wang et al., 2018), defined as:*

$$LPML = \sum_{i=1}^{n} \log CPO_i \quad (14)$$

where CPO_i is conditional predictive ordinate for i data.

Results

To explore the presence of spatial autocorrelation in malaria cases, the global Moran's I test was applied, and the results are presented in Table 1.

The result presented in Table 1 indicates the presence of positive spatial autocorrelation in the data, suggesting that neighbouring provinces tend to exhibit similar levels of malaria cases. The local Moran's test was applied in order to identify local patterns of spatial autocorrelation among Mozambican provinces. The results obtained are presented in Table 2.

Table 1 Global Moran's I test results

Moran I statistic	p-value
0.38384334	0.01335

Source: Elaborated by the author (results generated using R)

Table 2 Local Moran's I test results for malaria cases by province

Province	Moran's I	p-value
Cabo Delgado	0.37432477	0.299757
Gaza	0.53952442	0.169729
Inhambane	0.21160865	0.28375
Manica	0.22472108	0.260794
Maputo	0.83315993	0.135096
Cidade de Maputo	0.86447633	0.312266
Nampula	1.33504773	0.032446
Niassa	-0.49461406	0.006774
Sofala	-0.04509125	0.575967
Tete	-0.11607128	0.375468
Zambézia	0.49519041	0.148647

Source: Elaborated by the author (results generated using R)

As shown in Table 2, only two provinces presented statistically significant local spatial autocorrelation at the 5% significance level. Nampula province exhibited a positive and significant Moran's I statistic, while Niassa province showed a negative and significant

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value. These results suggest, preliminarily, that Nampula tends to have neighbours with similar behaviour, whereas Niassa tends to have neighbours with dissimilar behaviour, in terms of malaria relative risk. For the remaining provinces, the results did not provide statistically significant evidence of local spatial autocorrelation (p-value > 0.05). The map presented in Figure 1 is the result of an empirical test, adopting a significance level of 0.05, aimed at assessing the statistical significance of the local Moran's I indices obtained for each province.

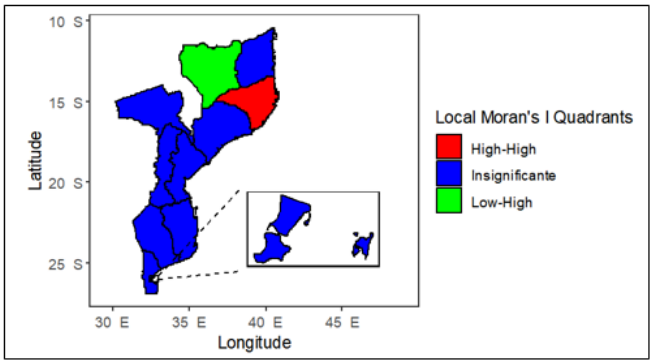

Figure 1 Empirical test results for the local moran's I.

The map in Figure 1 visually corroborates the findings presented in Table 2, reinforcing the spatial patterns identified by the local Moran's test. Table 3 presents the model-fit criteria, namely the DIC and WAIC, used to compare the four fitted spatial models.

The four fitted models produced very similar DIC and WAIC values (Table 3), indicating comparable model fit and predictive performance. In particular, the ICAR and BYM models yielded identical DIC and WAIC values. Thus, based solely on these criteria, there is no evidence of clear superiority of any of the four models. Table 4 presents the Log Pseudo Marginal Likelihood (LPML) values obtained for the fitted models.

Table 3 Model comparison measures for the fitted models

Model	DIC	WAIC
ICAR	185.145	181.769
BYM	185.145	181.769
BYM2	185.145	181.77
Leroux	185.145	181.77

Source: Elaborated by the author (results generated using R)

Table 4 Estimated LPML values for the fitted models

Model	LPML
ICAR	-101.235
BYM	-101.235
BYM2	-101.237
Leroux	-101.239

Source: Elaborated by the author (results generated using R)

Table 4 shows that the LPML values were also very similar across the four models, with negligible differences. In particular, the difference in LPML between the ICAR and BYM models was only 0.0002, further supporting the similarity in their predictive performance. Examination of the BYM components also showed that the unstructured component contributed very little additional variation compared with the structured spatial component.

To further assess the adequacy of the Poisson likelihood, posterior predictive checks and predictive diagnostics were performed for the selected Poisson–ICAR model. Posterior predictive checks showed no substantial discrepancies between the observed data and the fitted model. The posterior predictive p-values for the total number of cases, variance, and maximum were 0.4920, 0.4928, and 0.4916, respectively. No zero counts were observed, and none of the 5,000 posterior predictive replicates contained zero counts. The PIT values ranged from 0.449 to 0.480, providing no indication of a pronounced systematic predictive discrepancy.

Given the similarity in model-fit and predictive criteria, the ICAR model was retained as the primary specification because of its parsimonious formulation and direct interpretation of spatial dependence, rather than because of clear superiority over the alternative models. These findings were further supported by the sensitivity analysis comparing the Poisson and negative binomial likelihoods. The Poisson model yielded DIC = 185.14 and WAIC = 181.77, compared with DIC = 322.74 and WAIC = 323.38 for the negative binomial model. Figure 2 presents the spatial distribution of the estimated relative risk for malaria in Mozambique in 2024.

Figure 2 reveals a heterogeneous spatial distribution of relative risk, with values ranging from 0.0354 to 1.711. The lowest risk was observed in Maputo City, while the highest occurred in Cabo Delgado. In the South and Central regions, most provinces exhibit risk below 1.0, with the exception of Inhambane and Zambézia, which present values above this threshold. In the North region, the opposite pattern is observed, with most provinces showing risk above 1.0, except for Niassa, which presents a value below this level. Table 5 presents the detailed estimates of relative risk, standard deviation, and confidence intervals for each province.

Table 5 Relative risk, standard deviation, and 95% credible intervals for each province

Province	Relative risk	Standard deviation	Confidence intervals	
			2.50%	97.50%
Cabo Delgado	1.711	0.001312	1.7084	1.7136
Gaza	0.1722	0.000576	0.1711	0.1733
Inhambane	1.0969	0.001402	1.0941	1.0996
Manica	0.5645	0.000827	0.5628	0.5661
Maputo	0.0462	0.000231	0.0458	0.0467
Cidade de Maputo	0.0354	0.000302	0.0348	0.036
Nampula	1.209	0.000713	1.2076	1.2104
Niassa	0.8609	0.001041	0.8588	0.8629
Sofala	0.8966	0.000966	0.8948	0.8985
Tete	0.6975	0.000782	0.696	0.6991
Zambézia	1.6193	0.000868	1.6176	1.621

Source: Elaborated by the author (results generated using R)

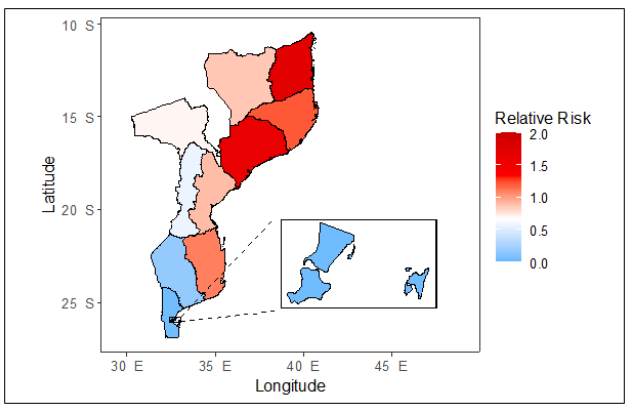

Figure 2 Spatial distribution of the estimated malaria relative risk in Mozambique.

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Figure 3 presents the maps of the Posterior Exceedance Probability (PEP) for the relative risk across the provinces of Mozambique. The map on the left shows the probability that the relative risk is below 1, whereas the map on the right displays the probability that the relative risk exceeds 1. The results reveal spatial heterogeneity in the distribution of probabilities, highlighting differences among provinces regarding their likelihood of exhibiting relative risks lower or higher than the reference level.

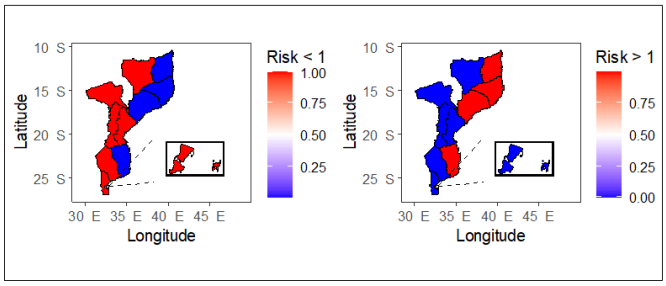

Figure 3 Posterior exceedance probabilities of the relative risk across the provinces of Mozambique: (left) probability that the relative risk is below 1; (right) probability that the relative risk is above 1.

Discussion

Mozambique is a country that, decades after independence, continues to be profoundly affected by malaria, a disease that remains one of the major public health challenges facing the nation. In this context, the integration of research findings into health authorities' decision-making processes is crucial for guiding and strengthening malaria control and elimination initiatives.

The presence of positive spatial autocorrelation (Table 1) demonstrates that malaria distribution in Mozambique is not random but rather spatially structured, with geographically neighbouring provinces exhibiting similar levels of risk. This pattern is not merely a statistical finding; it reflects the reality of a territory where environmental conditions, healthcare infrastructure, and population dynamics are regionally interconnected. Therefore, incorporating spatial dependence into statistical modelling is essential, as ignoring such structures may lead to biased estimates and underestimated uncertainty, as highlighted by Blangiardo and Cameletti[8] and Haining and Li.[6] The spatial approach adopted in this study is thus not only methodologically appropriate but also indispensable for achieving a more realistic understanding of malaria transmission patterns and for designing geographically targeted intervention strategies.

The observed global spatial autocorrelation is further supported by the local spatial patterns presented in Table 2, which reveal geographically clustered risk structures. In particular, Nampula Province exhibits a high–high spatial association, indicating an area of elevated malaria risk surrounded by neighbouring provinces with similarly high risk. In contrast, Niassa Province shows a distinct spatial configuration, with relatively low malaria risk but neighbouring high-risk provinces, namely Cabo Delgado and Nampula. This corresponds to a low–high spatial association and highlights the importance of considering the spatial context when interpreting malaria risk. These local patterns are also illustrated by the empirical maps based on the Local Moran's I statistic (Figure 1).

Following the confirmation of spatial dependence, spatial models incorporating the neighbourhood structure among provinces were fitted. The model adopted in this study—the Intrinsic Conditional Autoregressive (ICAR) model, that is a fully spatial Bayesian approach that allows for more robust estimation of relative risk by accounting for spatial correlation. The results indicate that Inhambane, Zambézia, Nampula, and Cabo Delgado provinces present relative risks greater than 1, meaning that malaria incidence in these regions exceeds the expected level based on the population at risk. This pattern is also supported by the posterior exceedance probability maps (Figure 3), which provide additional evidence regarding the likelihood that the relative risk is above the reference value.[22,23] These provinces should therefore receive priority in malaria prevention and control strategies. This prioritisation does not imply neglecting other provinces, but rather reflects the need for differentiated interventions according to the spatial distribution of risk revealed by the model.

Variation in malaria burden across Mozambique may reflect differences in environmental conditions, climate, and sociodemographic characteristics. Studies undertaken in the country[24,25] have reported associations between climatic conditions and patterns of malaria transmission. In particular, temperature plays a fundamental role in the malaria transmission cycle by affecting mosquito development rates and parasite maturation processes.[24] Consequently, spatial variations in climatic conditions may contribute significantly to the observed heterogeneity in malaria risk across provinces. In this sense, the relatively high risk observed in some provinces may be influenced by climatic factors, although these factors were not considered in this study due to limitations in accessing this type of data from the platforms of the relevant institutions.

The posterior exceedance probability maps (Figure 3) complement this analysis by introducing an essential additional dimension: uncertainty quantification. While the estimated relative risk provides information about the magnitude of malaria risk, the posterior exceedance probability indicates the level of statistical support for whether this risk differs from the reference value. Provinces with a high posterior probability of relative risk greater than 1 represent areas where there is strong statistical evidence that malaria risk exceeds the expected level, and therefore where public health interventions should be prioritised based on more reliable evidence. Conversely, provinces with a high posterior probability of relative risk below 1 provide consistent evidence of reduced or controlled malaria risk.

Conclusion

This study analysed the spatial distribution of malaria relative risk in Mozambique, revealing well-defined regional patterns. The presence of positive spatial autocorrelation confirmed that malaria occurrence is not randomly distributed across the country. A significant spatial cluster was identified, comprising the provinces of Nampula (the main hotspot), Cabo Delgado, and Zambézia, whereas the southern region of the country exhibited lower risk, with the exception of Inhambane Province. Although Niassa presented relatively low risk, its location among high-risk neighbouring provinces highlights its epidemiological vulnerability and the need for continuous surveillance.

The ICAR model and posterior exceedance probability maps proved to be valuable tools not only for providing more robust estimates of relative risk but also for supporting evidence-based public health decision-making. The findings highlight the need for geographically targeted interventions, with priority given to high-risk areas in the northern region and strengthened surveillance in transitional areas. Future studies should incorporate more spatially detailed data at the district level, together with environmental and climatic factors, to improve understanding of malaria transmission dynamics.

This study reinforces the importance of spatial modelling approaches in health planning and resource allocation, contributing to more effective and targeted malaria control strategies in Mozambique.

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Conflicts of interest

The author declares there is no conflicts of interest.

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