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Hierarchical Spatio-Temporal Modeling of Malaria Incidence in Kenya.

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Abstract: Malaria remains a significant public health challenge in Kenya, with substantial spatial and temporal variability in incidence and mortality rates across the country. Despite the growing availability of disease surveillance data, existing analyses often overlook the joint spatial and temporal dependencies that characterize malaria epidemiology. This study addresses this by applying spatial and spatio-temporal Bayesian models to analyze malaria incidence rates in Kenya over the period 2010–2021. Using integrated nested Laplace approximations (INLA) within a hierarchical modeling framework, the study proposed a skewed spatio-temporal (SKEW ST) model and compared its performance to the intrinsic conditional autoregressive (ICAR) and Besag-York-Mollié (BYM) models in modelling malaria incidence rates in Kenya. Model diagnostics were based on WAIC, lppd, and pWAIC which indicated superior performance of the BYM model. Spatial trend analysis revealed significant regional disparities, with high incidence clusters observed in Lake Victoria and coastal regions. The temporal trend demonstrated fluctuating malaria patterns with notable surges in 2015 and 2021. Exceedance probability and relative risk maps further highlighted hotspots with persistent transmission intensity in Northern Kenya, thereby validating spatially structured vulnerability. These findings emphasize the necessity of integrating spatial and temporal patterns in malaria surveillance to guide data-driven policy.

Keywords: Hierarchical Modeling, Malaria Incidence, Spatio-Temporal, Bayesian Analysis, Integrated Laplace Approximation and Skew Spatio-Temporal Model.

Introduction

Malaria, a life-threatening disease caused by *Plasmodium* parasites and transmitted by female *Anopheles* mosquitoes, remains a major public health concern globally, particularly in Sub-Saharan Africa where the burden is most pronounced (Ayele *et al*., 2024; Bhamani *et al*., 2024). Agboka *et al*., 2024 and Gondwe *et al*., 2021 highlight that the region accounts for over 94% of global malaria cases and 95% of related deaths, with children under five and pregnant women among the most vulnerable groups. Kenya continues to face a substantial malaria burden, although intensified interventions have contributed to notable progress in both prevention and control (Frings *et al*., 2018; Muriithi *et al*., 2024). In 2023, Kenya reported approximately 3.29 million malaria cases, a decrease from 3.42 million in 2022, alongside a 93% reduction in malaria-related deaths since 2015—from 15,061 to 1,060 deaths (Adegbite *et al*., 2023; Hollowell *et al*., 2023). Despite these achievements, the spatial and spatio-temporal distribution of malaria incidence remains uneven. (Frings *et al*., 2018; Ayele *et al*., 2024).

Given this spatial and temporal heterogeneity, the need for spatio-temporal modeling techniques to accurately characterize and predict malaria patterns is paramount as noted by Agboka *et al*. (2024). It's in this regard that this study aimed to uncover the spatial and temporal dynamics of malaria incidence in Kenya by first developing a skew spatio-temporal model in a Bayesian hierarchical framework and then comparing the model's performance to the intrinsic conditional autoregressive (ICAR) and Besag-York-Mollié (BYM) models.

Literature Review

Gaussian conditional autoregressive (CAR) priors are widely used in mapping areal data to capture spatial correlation (John *et al.*, 2021). Extensions of CAR models have been proposed to address various challenges as with Alfelt *et al*. (2023) who introduced the Singular Conditional Autoregressive

Wishart (SCAW) model for high-dimensional financial data, while Shen *et al*. (2021) demonstrated CAR's utility in genetic association studies. Mucheri *et al*. (2024) applied Bayesian spatial modeling with CAR and Poisson Lognormal (PLN) models for mapping tuberculosis incidence in Kenya. Similarly, Soroori *et al*. (2019) developed local CAR models for zonal crash prediction, and Tessema *et al*. (2023) systematically reviewed Bayesian CAR models in health research.

In malaria modeling, Agboka *et al*. (2024) predicted insecticide resistance trends in Anopheles gambiae, and Anwar *et al*. (2024) assessed Plasmodium vivax models through a scoping review. Socio-economic and environmental factors in malaria transmission were considered by Ayele *et al*. (2024) using multilevel logistic regression. Targeted intervention strategies were reviewed by Bhamani *et al*. (2024) while Gondwe *et al*. (2021) studied malaria trends among children in Malawi. Haq *et al*. (2024) linked climatic and topographical factors to malaria incidence in Pakistan. Equally, John *et al*. (2021) and Karekezi *et al*. (2024) examined spatial malaria risks in Kenya and Rwanda, respectively.

Machine learning and advanced modeling have furthered malaria prediction as with Komugabe *et al*. (2024) who integrated AI and geospatial models in Uganda while Kouame *et al*. (2024) conducted joint spatial modeling of malaria incidence and vector abundance. In this regard, Lacey *et al*. (2023) reviewed collaborative health education initiatives in Kenya while Li *et al*. (2024) provided a broad overview of malaria control efforts in Africa. Muriithi *et al*. (2024) applied machine learning for malaria prediction, and Musyoka *et al*. (2023) used Bayesian spatio-temporal models to analyze malaria incidence with time-dependent covariates. while Ouédraogo *et al*. (2020) assessed malaria case fatality trends in Burkina Faso.

Similarly, Panzi *et al*. (2022) projected malaria morbidity trends in the DRC. Taheri *et al*. (2024) modeled malaria spatial risk based on Anopheles maculipennis distribution. Wang *et al*. (2023) examined climate-malaria relationships across Africa and Asia-Pacific.

Methodology

3.1: ICAR and BYM Modeling

This study used the ICAR and the Besag, York, and Mollié, 1991 models to model the spatial dependence of Malaria Incidence. The ICAR model was obtained as;

$$O_i \mid \lambda_i, \log(\lambda_i), \phi_i \sim \text{Poisson}(\lambda_i E_i),$$
$$\lambda_i = \exp(\alpha + \phi_i),$$
$$\phi_i \sim \text{ICAR}\left(W, \frac{1}{\tau_\phi}\right)$$

for which the random effects denoted by ϕ model spatial dependence. Equally, the BYM model on the other hand was obtained as;

$$O_i \mid \lambda_i \sim \text{Poisson}(\lambda_i E_i),$$
$$\log(\lambda_i) = \alpha + \theta_i + \phi_i,$$
$$\theta_i \sim N\left(\frac{0,1}{\tau_\theta}\right),$$
$$\phi \sim \text{ICAR}\left(W, \frac{1}{\tau_\phi}\right).$$

The elements of the adjacency matrix W in these models' matrix W were defined as;

$$w_{ij} = \begin{cases} 1, & \text{if } j \in \partial i, \\ 0, & \text{otherwise}, \end{cases}$$

where ∂i is the set of neighbors of i.

3.2: Skew Hierarchical Modeling

In order to model skewness and sparseness of malaria incidence data, this study proposes a skew spatio-temporal model. In this case, the study lets Y_i to be malaria incidence rates in county i $(i = 1, \dots, 47)$. The hierarchical representation of the skew spatio-temporal model was proposed as;

$$Y_i \sim \text{Poisson}(\boldsymbol{\mu_i} = E_i R_i)$$
$$R_i = \theta_i \times h_i; h_i = \exp(\beta_0 + u_i + v_i + g_{jk} + \psi_{s,t,k})$$
$$\log(\mu_i) = \log(E_i) + \log(\theta_i) + \log(h_i)$$
$$v_i \sim N(0, \sigma_v^2); \psi_{s,t,k} \sim N(0, \sigma_\psi^2); \theta \sim \text{Gamma}(a, b)$$
$$g_{jk} \sim ICAR(\sigma_g^2); u_i | u_i, \sigma_u^2, \delta_u, w_i \sim N\left(\frac{\sum_{j\sim i} s_j}{m_i} + \delta_u w_i, \frac{\sigma_s^2}{\eta \times m_i}\right)$$
$$s_i | s_{-i} \sim N\left(\frac{\sum_{j\sim i} s_j}{m_i}, \frac{\sigma_s^2}{m_i}\right); w_i \sim N(0, I)\mathbb{I}(w_i > 0); \eta \sim \text{gamma}\left(\frac{k}{2}, \frac{k}{2}\right)$$

For which $\beta_i \sim N(\beta_0, \Lambda), i = 0,1,2, \dots, k$ where k is the number of covariates, $\sigma_v^2 \sim \text{IG}(\Omega, v), \delta_u \sim N(0, \Gamma), \sigma_s^2 \sim \text{IG}(\Omega, u)$ and $k \sim \text{Exp}(k_0)\mathbb{I}(k > 2)$ where p_i is the weighted prevalence corresponding to Y_i^*; $i = 1,2, \dots, 13$, σ_u^2 and σ_v^2 are variance of the spatial and the heterogeneous random component and $\mathbb{I}(w_i > 0)$ is an indicator function, IG is inverse gamma, Exp is exponential.

3.3: Parameter Estimation and Model Diagnostics

The parameter estimation was based on Integrated Nested Laplace Approximation approaches. In order to check the goodness of fit for the fitted distributions in the modeling of malaria incidence, the study Watanabe Information Criterion, Posterior Predictive Loss and Exceedance Probabilities.

Results and Discussions

This study used spatial temporal data for malaria incidence in the data analysis by first obtaining the descriptive statistics and the fitted model results.

4.1 Descriptive Statistics

Table 1 presents the descriptive statistics for the malaria incidence rate (IR) for which malaria incidence rate ranged from a minimum of 0.00 to a maximum of 367.00 with a median value of 40.00 that lied below the mean (64.57) indicating a right-skewed distribution for the data as shown in Figure 1. This skewness of the study data motivated the development of a skew spatio-temporal model for the modeling of malaria incidence in relation to the ICAR and BYM models in the literature.

Table 1: Descriptive Statistics of Malaria Incidence Data.

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
IR	0.00	23.00	40.00	64.57	72.00	367.00

Figure 1 presents a histogram and overlaid density curve illustrating the distribution of malaria incidence rates across Kenyan counties. The shape of the distribution was highly right-skewed, which gave an indication that the majority of counties experienced relatively low malaria incidence with a long tail extending toward higher values.

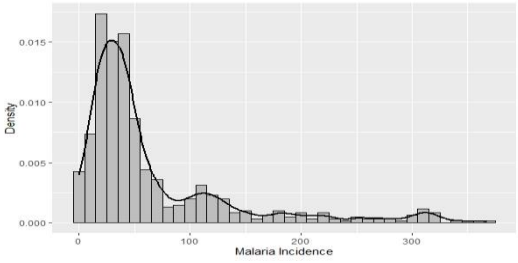

Figure 1: Histogram and Density of Malaria Incidence in Kenya

Figure 2 illustrates the spatial distribution of malaria incidence rates (IR) across Kenya at the county level. The western region of Kenya, particularly areas bordering Lake Victoria, exhibits the highest malaria incidence, represented by the darkest shades on the map.

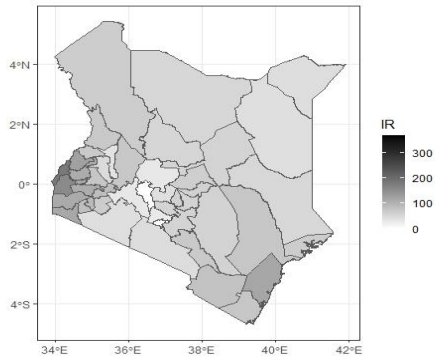

Figure 2: Distribution of Malaria incidence in Kenya

In contrast, counties in the central and northern parts of the country generally show much lower incidence rates, with many areas depicted in lighter shades. These regions tend to be more arid or high-altitude, environments less conducive to sustained malaria transmission. Coastal areas display moderate levels of incidence, reflecting a transitional malaria ecology.

This distributional pattern underscores the importance of developing heterogenous models that can be used to model the spatio-temporal pattern of malaria incidence in Kenya.

4.2 ICAR and BYM Modeling of Malaria Incidence

This study first estimates the spatial trend of malaria incidence using the ICAR and BYM models. The model parameter estimates for the Intrinsic Conditional Autoregressive (ICAR) model are presented in Table 2 as;

Table 2: ICAR Model Parameter Estimates.

Parameter	Mean	SD	2.5% Percentile	97.5% Percentile
Alpha	-2.0597	-2.0586	-2.2825	-1.8523
Phi	9.5610	9.1434	5.6380	15.6162
SIR	0.1282	0.1276	0.1020	0.1569

The posterior mean of the intercept parameter (α) was estimated at -2.0597, with a narrow range between the 2.5% and 97.5% credible intervals (−2.2825 to −1.8523), indicating a high degree of certainty around the baseline log-risk of malaria incidence in the absence of spatial effects. The spatial precision parameter (φ) was estimated at 9.5610 with a standard deviation of 9.1434. The wide credible interval (5.6380 to 15.6162) for φ reflected substantial variability in spatial dependence across locations. The standardized incidence ratio (SIR) had a posterior mean of 0.1282, with a 95% credible interval ranging from 0.1020 to 0.1569 which gave an indication that on average, the observed malaria incidence was considerably lower than what would be expected under a null spatial model, further emphasizing the importance of incorporating spatial structure in the analysis.

For the BYM model, Table 3 presents the posterior parameter estimates as;

Table 3: BYM Model Parameter Estimates.

Parameter	Mean	SD	2.5% Percentile	97.5% Percentile
Alpha	-2.0791	0.2179	-2.5393	-1.6489
Phi	1.6991	3.4802	0.0031	11.3702
Theta	1.8169	0.9718	0.0060	3.4948
SIR	0.1280	0.0282	0.0789	0.1923

The intercept parameter (α) had a posterior mean of -2.0791, with a standard deviation of 0.2179 and a 95% credible interval ranging from -2.5393 to -1.6489 reflecting the log-baseline risk of malaria incidence, accounting for both structured and unstructured spatial variability. The spatial precision parameter (φ), associated with the structured component of the model, had a mean of 1.6991 and a notably large standard deviation of 3.4802. The wide credible interval (0.0031 to 11.3702) for φ indicated considerable uncertainty regarding the strength of spatial autocorrelation for the BYM model. This variability was attributed to differential clustering of malaria incidence across counties, where some counties exhibited strong spatial dependencies while others did not.

The unstructured random effect precision parameter for the BYM model (θ) had a posterior mean of 1.8169 and a standard deviation of 0.9718, with a 95% credible interval spanning from 0.0060 to 3.4948 suggesting the presence of substantial unstructured heterogeneity in malaria incidence, potentially reflecting localized factors or measurement noise that are not captured by the spatial structure model. The standardized incidence ratio (SIR) was estimated at 0.1280, with a standard deviation of 0.0282 and a credible interval of 0.0789 to 0.1923 consistent with estimates from the ICAR model and indicated a generally low observed-to-expected malaria incidence ratio.

Figure 3 presented the spatial distribution of the standardized incidence ratio (SIR) for malaria under the ICAR and BYM models, alongside their corresponding posterior exceedance probabilities. Both the ICAR and BYM models showed high exceedance probabilities (Pr(SIR > 1) ≥ 0.75) in several counties, particularly in the northeastern region, providing strong statistical evidence of elevated malaria burden in these areas as given in Figure 3. The similarity in spatial patterns between these two models reinforces the robustness of the findings, despite differences in model specifications.

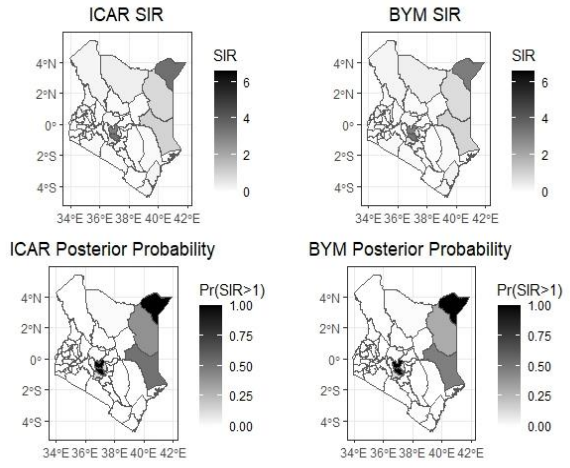

Figure 3: SIR for ICAR and BYM Models and Respective Posterior Probability.

4.3: Skew Hierarchical Modeling

In order to account for skewness and sparseness of malaria incidence in Kenya, this study used the proposed hierarchical skew spatio-temporal model.

The parameter estimates for this model are presented in Table 4 as;

Table 4: Skew Modeling of Malaria Incidence Rates Parameter Estimates.

Parameter	Mean	SD	2.5% Percentile	97.5% Percentile
a0	-1.8880	0.1227	-2.0000	-1.6865
gg	0.3321	0.0980	0.1948	0.5046
vv	0.8090	0.1676	0.5803	1.2659
uu	1.3436	0.1960	1.0224	1.7200
psi	0.4221	0.0586	0.3349	0.5446
mspe	147.8399	39.7327	113.4087	256.9304

The intercept term (a0) had a posterior mean of -1.8880, with a standard deviation of 0.1227 and a 95% credible interval ranging from -2.0000 to -1.6865 reflecting a consistently low baseline log-risk of malaria incidence across the study domain, with high precision and low uncertainty surrounding the estimate. The temporal trend parameter (gg) had a posterior mean of 0.3321 and a 95% credible interval spanning from 0.1948 to 0.5046 indicating a statistically significant positive temporal trend. The spatial random effects were decomposed into the uncorrelated heterogeneity (vv) and the spatially correlated (structured) component (uu). The parameter vv, with a posterior mean of 0.8090 (95% CI: 0.5803 to 1.2659), captured spatial variation that was independent across locations while uu represented the spatially structured variation, with a higher mean of 1.3436 and a credible interval from 1.0224 to 1.7200, indicating substantial spatial autocorrelation, whereby neighboring areas tend to exhibit similar malaria risk levels. The spatio-temporal interaction parameter Psi was estimated at 0.4221 (95% CI: 0.3349 to 0.5446), indicating a moderate degree of spatio-temporal interaction, supporting the presence of spatial temporal dependencies in the data. The mean squared prediction error (MSPE) was estimated at 147.8399, with a relatively wide 95% credible interval ranging from 113.4087 to 256.9304 which indicated variability in predictive reliability of the proposed model across space and time, emphasizing the need for models that accommodate both structured and unstructured sources of spatio-temporal heterogeneity in modeling malaria incidence data.

Figure 4 illustrates the temporal trend of malaria incidence rates in Kenya from 2010 to 2022, as estimated by the proposed spatio-temporal model.

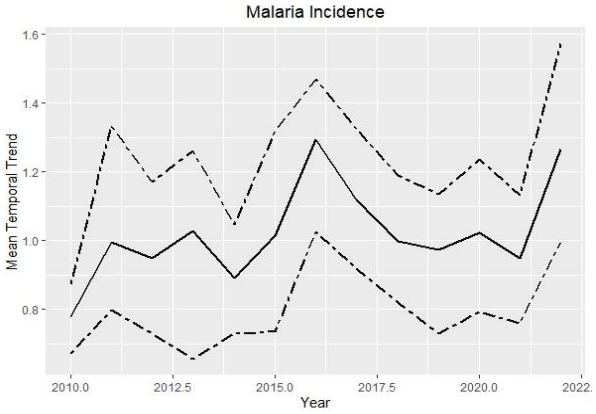

Figure 4: Temporal trend for Malaria Incidence Rate in Kenya.

The temporal trend shows a general upward trajectory, particularly pronounced from 2014 onward, with a notable surge in incidence observed in 2021 and 2022.

Figure 5 gave the spatial trend of malaria incidence across Kenya, derived from the fitted skew spatio-temporal model. There was notable spatial heterogeneity, with pronounced spatial trends concentrated in the counties of western Kenya, the Lake Victoria basin, and southern counties. In contrast, central and northeastern counties show lower spatial trend translating to reduced malaria endemicity in these counties.

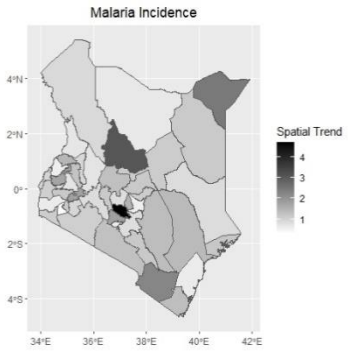

Figure 5: Spatial trend for Malaria Incidence in

Kenya.

Figure 6 presents a spatial map of exceedance probabilities for malaria incidence in Kenya.

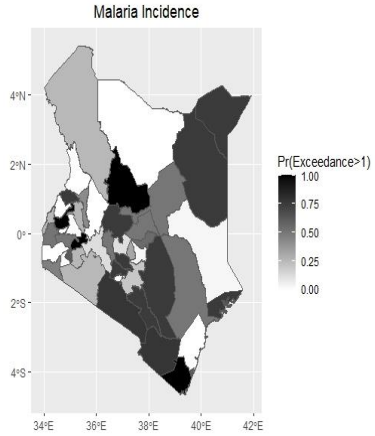

Figure 6: Exceedance Probabilities for Malaria Incidence in Kenya.

Notably, several counties in the western and coastal regions exhibit elevated exceedance probabilities, which aligns with known malaria-endemic zones characterized by favorable climatic and ecological conditions for vector proliferation. In contrast, areas in the central and northeastern parts of the country show lower exceedance probabilities. This spatial exceedance mapping provides critical insights for malaria surveillance and control, enabling health authorities to prioritize high-risk regions for targeted interventions.

4.4: Evaluation of Fitted Models

Table 5 provided the goodness of fit results for the proposed skew spatial temporal model (SKEW ST) against the SKEW ST (ICAR) and Besag-York-Mollié (BYM) models using the Watanabe-Akaike Information Criterion (WAIC), the log pointwise predictive density (lppd), and the effective number of parameters (pWAIC).

Table 5: Model Diagnostics for Fitted Models.

	WAIC	lppd	pWAIC
ICAR	206.3522	-81.2885	21.8876
BYM	201.6452	-80.6584	20.1642
SKEW ST	4761.224	-1890.332	490.2802

The BYM model exhibited the lowest WAIC value (201.6452), indicating superior predictive performance among the three models. This was closely followed by the ICAR model (WAIC = 206.3522), while the SKEW ST model recorded a substantially higher WAIC of 4761.224. In terms of the fitted model's predictive accuracy on malaria incidence data, the BYM model again performed best with a lppd of -80.6584, slightly better than the ICAR model (-81.2885). The proposed SKEW ST model had a markedly poor lppd value of -1890.332, reinforcing its relatively poor fit to the data. For the effective number of parameters, the ICAR and BYM models were comparably parsimonious, with pWAIC values of 21.8876 and 20.1642, respectively. In contrast, the SKEW ST model had high complexity (pWAIC = 490.2802), which contributed to its overfitting and suboptimal performance despite the model's flexibility.

Conclusion and Recommendations

1.1 Conclusion

This study set out to develop a flexible spatio-temporal model for analyzing malaria incidence by introducing a skew spatio-temporal framework capable of addressing the skewness and heavy tails commonly observed in malaria incidence data. The model was designed to improve upon traditional Intrinsic Conditional Autoregressive (ICAR) model, which often assume normality and does not adequately capture extreme values or spatial heterogeneity in disease distribution. Parameter estimation using Markov Chain Monte Carlo (MCMC) simulations provided robust inference and allowed for a detailed assessment of uncertainty in the model estimates.

The findings demonstrate that the skew spatio-temporal model did not outperform the ICAR and BYM model in terms of model fit and predictive performance despite its rich theoretical review. The BYM model stroke the most favorable balance between goodness-of-fit and parsimony, rendering it the most appropriate for modeling the spatial distribution of malaria incidence in Kenya.

1.2 Recommendations

The skew-t spatio-temporal model effectively addressed data skewness and heavy tails but was not fit for the univariate data. Future research

should consider applying this model to multivariate data. Also, while the comparison with the ICAR and BYM models demonstrated the superior performance of the ICAR model, future studies should broaden model comparisons to include more advanced spatial models such as Gaussian Processes and machine learning-based approaches.

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