# **SPATIAL-TEMPORAL MODEL FOR CAPTURING THE AUTOCORRELATION AND INTERACTION EFFECT IN MEASLES DATA**

#### **Habiba Danjuma, Bilkisu Maijama'a and Emmanuel Chaku Shammah**

Department of Statistics, Nasarawa State University, Keffi, Nasarawa State maijamaab@nsuk.edu.ng

## **ABSTRACT**

Spatial data are data observed from different neighboring but non-overlapping areal units. In Nigeria, measles continues to be a leading cause of morbidity and mortality in children. Numerous factors, including spatial (S.P.) and temporal trends impacting the disease's intensity and dissemination, affect the transmission dynamics of measles. Although numerous methods exist for spatially time-to-event data, most S.P. models exclude the interaction effect and spatial autocorrelation. Therefore, this study offers the most effective model for overcoming these constraints and allows researchers to flexibly represent spatial clustering in their disease data. However, this research aims to use a–temporal mode to capture the autocorrelation and interaction effects in measles data. To provide an appropriate model for capturing the autocorrelation and interaction effect in the data across the areal units and time and to determine whether the model investigated above is consistent with capturing the measles data, This work uses simulations and poison distribution to identify the substantial spatiotemporal model and interaction/ autocorrelation influence on area unit data. The findings show that the interaction between the small area unit and period decreases as time increases, while the autocorrelation increases for the five area units. The spatial-temporal model is better fitted to 5 areal units when the period is 50 (5x50); however, in 10 and 15 area units, the interaction between the areal unit and period decreases as time increases, and the autocorrelation also decreases. The spatio-temporal model was better fitted to 10 areal units when the period was 20 (10  $\times$  20) and 15 areal units when the period was 100 (15  $\times$  10).

**Keywords:** Spatial-temporal data, Simulation, Areal units, Modeling, Poison prior

## **1. INTRODUCTION**

Measles is a severe threat in many countries, including Nigeria. Numerous factors, including regional and temporal trends, impact the disease's intensity and dissemination. A comprehensive understanding of the spatiotemporal dynamics of measles is lacking, which hinders the development of effective control and prevention strategies. Measles is a severe public health threat in many countries, including Nigeria. This is because there isn't a robust modeling framework that can faithfully represent the temporal and spatial dynamics of the disease.

Meanwhile, current measles research frequently concentrates on discrete elements like disease burden or vaccine coverage but does not include these elements in a cohesive spatiotemporal model. This information gap hinders our ability to identify high-risk areas, understand transmission patterns, and develop targeted interventions to stop the spread of measles effectively. There are



additional obstacles in adequately estimating the spatial-temporal trends of measles due to a location's geographic characteristics, such as its diversified population distribution, varying accessibility to healthcare, and traditional cultural customs. These variables could be involved in localized epidemics and irregular disease transmission patterns in various places and areas.

Scan statistics, using spatio-temporal analyses, have been widely applied to explore disease patterns and detect high-risk disease clusters, particularly for diseases with limited resources for prevention (Kulldorff *et al.* 2015). Some studies have explored irregularly shaped disease clusters, which might more realistically reflect actual, albeit complicated, disease patterns (Costa and Kulldorff, 2014). Moreover, most studies have utilized relative risk (R.R.) derived from scan statistics to identify high-risk regions (Carrel *et al.* 2009, Jones *et al.* 2012, Ling *et al.*2014 and Sindato *et al.* 2014). Rare studies have measured the population-attributable risk percentage to evaluate the regional disease burden (Zhu *et al.,* 2013). Moreover, there is a lack of studies on the spatio-temporal patterns of measles, mainly in Guangxi, a region with large-scale measles outbreaks.

Lawson (2018), Rushworth *et al.* (2014), Napier *et al*. (2018) and Beraha *et al*. (2021) in their study, examined the issue of spatially dependent areal data and suggested using a finite mixture of Gaussian distributions to characterize the data gathered for every areal unit. A joint distribution for a set of vectors on the simplex, a logistic transformation of the Gaussian multivariate CAR models, is used to introduce spatial dependency.

A Bayesian model for spatiotemporal data based on a generalized linear mixed-effects model was suggested by Nicoletta *et al.* (2022) to quantify the percentage of isolation among various clusters in a given geographic area (Lee *et al*. 2018, 2021 and 2022) but did not consider interaction and autocorrelation effect.

A few of the many reasons to model these include determining the degree of segregation between two or more different groups in a town (Lee *et al*. 2018), identifying clusters of nearby area units that show an elevated risk of disease compared with neighboring areas (Anderson, Lee, and Dean 2014), and estimating the effect of a risk factor on a response. Frequently, sets of autocorrelated random effects are employed to replicate the spatio-temporal autocorrelation in these data through a Bayesian inferential technique. These random effects are typically allocated with spatiotemporal extensions of Conditional Autoregressive (CAR) priors to capture this autocorrelation. This study offers Bayesian hierarchical models using the poison distribution priors to predict the spatio-temporal data on associated simulated data and measles data.

Although there are numerous methods for dealing with spatial (S.P.) time-to-event data (e.g., Banerjee and Carlin, 2004. Choi and Lawson, 2011; Zhou *et al*., 2020; Lee and Pettersson, 2021), Conversely This Study, therefore, extends the work of Lee and Pettersson, 2021 where existing S.P. models either ignore spatial autocorrelation and interaction effect altogether. Thus, we shall present the best model that has the power to overcome these limitations as well as the flexibility for researchers to model spatial clustering in their disease data. This study, therefore, provides Bayesian hierarchical models for estimating the spatio-temporal data from related simulated data.



This study is significant because of its wide applications. The model consideration will help investigate, measure, analyze, and model spatial data features, such as places, characteristics, and their connections, that disclose the geometric or geographic characteristics of measles infections and other relevant data. The findings will assist in supplying the data that pinpoints the locations of features and boundaries where cases of measles are much more prevalent over time. Furthermore, this study will allow experts in the fields of science, sociology, psychology, epidemiology, biology, business, and marketing (among others) to understand better human behaviors, environmental factors, and relationships between people and a location.

## **1.1. Research Question**

There is an urgent need for a comprehensive study that addresses the following research questions:

- i. Is the Bayesian Hierarchical spatio-temporal model appropriate for capturing the autocorrelation and interaction effect in the data for poison prior across the areal units and periods?
- ii. Is the model investigated above consistent with capturing the measles data simulated from different regions at consecutive periods and distribution

# **1.2 Aim and Objectives**

The objectives of the study are

- i. To provide an appropriate for capturing the autocorrelation and interaction effect in the data for poison prior across the areal units and periods
- ii. To determine whether the model investigated above is consistent in capturing the measles data simulated from different regions at consecutive periods and distribution

# **2. RESEARCH METHODOLOGY**

The model's effectiveness described in the preceding section is evaluated using a simulation procedure, focusing on the models' capacity to accurately estimate the varying degrees of temporal trend and geographical variability. Simulated measles incidence data are generated from binomial, poison and negative binomial distributions for the  $K = 5$ , 10 and 15 areal units and t = 20, 50, 100 and 200 time periods. The areal units and periods are varied to assess the models' performance. The logit probability surface is generated from multivariate normal distributions.

The K × K neighborhood matrix  $W = (w_{ki})$  where W is K x K matrix,

$$
W = (w_{kj}) = \begin{pmatrix} w_{11} & \cdots & w_{1k} \\ \vdots & \ddots & \vdots \\ w_{k1} & \cdots & w_{kk} \end{pmatrix}
$$

It is used in all models in this study to induce spatial autocorrelation into the response data Y through the latent component M. W typically consists of binary elements, where the value of  $w_{ki} = 1$  if areal units  $(S_k, S_j)$  share a common border (i.e., are spatially close) and is zero otherwise. Additionally, when the value of  $w_{ki} = 0$ . This indicates that spatially adjacent areal units  $(S_k, S_j)$ ,  $(M_{kt}, M_{jt})$  are spatially auto-correlated. In contrast, values for non-neighboring areal units are conditionally independent given the remaining {Mit} values. This binary specification of W based on sharing a



common border is the most commonly used for areal data, but CARBayesST only requires that W be symmetric and contain non-negative elements. Similarly, the model S.T.CARanova () employs a binary N × N temporal neighborhood matrix  $D = (d_{tj})$ , where  $d_{tj} = 1$ , if  $|j - t| = 1$  and  $d_{tj} = 0$ , otherwise.

## **2.1 Research Design**

This study will partition the region into  $K = 1...k$  (Where  $k = 5$ , 10 and 15 areal units). The areal units studied constitute different communities, and data on generated measles susceptibility was obtained over time periods T (where T= 20, 50, 100, and 200). Bayesian hierarchical logistic regression models with poison prior were used to fit and evaluate its performance on the simulated data to get the best among them.

#### **2.2 Population, sample and sample technique of the study**

The population of this study will comprise local government areas in Taraba state of Nigeria, and three local government areas will be considered from each of the three senatorial districts in Taraba state to make a total number of nine samples. Sample data on measles across the local governments were considered using random sampling. The data shall be collected across the region for 30 years or 30 months.

#### **2.3Method of data collection**

The data collection method will be simulations based on different distributions. Secondary data on measles cases will also be obtained from the general hospital across the selected local government area. The research will cover the following Local government areas in Taraba state: Bali, Zing, Wukari, Donga, Gassol, Jalingo, Gashaka, Takum and Lau.

A simulation study was carried out to evaluate the effect of poison, binomial, and negative binomial distributions described in the next sections, particularly the accuracy in estimating the varying degrees of temporal trend and spatial variability. Simulated measles incidence data are generated from poison distribution for the  $k = 5$ , 10 and 15 areal units and T= 20, 50, 100 and 200 times period. The population sizes are varied to assess the models' performance in case simulation.

#### **2.4 Technique for Simulation and Data Analysis**

The technique for the data analysis is Bayesian hierarchical logistic regression models with poison prior, which was used to model the simulated data and determine when the best is fitted across areal units and time periods. Our Bayesian hierarchical model has the following prior distribution.

$$
Y_{kt} \sim pois(N_t, \theta_{kt})
$$

$$
\ln\left(\frac{\theta_{kt}}{1 - \theta_{kt}}\right) = Y_{kt}'\beta + \delta_t + e_t
$$
(1)

The measles susceptibility logit probabilities are represented as a linear mixture of two random effects, a px1 vector Y<sub>kt</sub> of covariates and their corresponding regression parametersβ,  $\delta_t$  and  $e_t$ . Upon the regression parameters  $\beta$ , a multivariate normal prior distribution is applied,



# $\beta \sim N(0,I)$

Where Ipxp is the identity matrix, after the covariate effects are considered, the random effects δt and et are added to the data to represent the temporal and spatial trends and autocorrelation. The temporal random effects come first. The random walk of order one prior distribution for  $e_t=e_1 e_2, \ldots$ ,  $e_N$  is provided as follows.

$$
e_t \sim N(e_{t-1}, \sigma^2), t = 1, 2, ..., N
$$

The  $e_t$  will be varied for different prior distributions as follows

$$
e_t \sim Unif(e_{t-1}, \sigma^2), t = 1, 2, ..., N
$$
  
\n $e_t \sim exp(e_{t-1}, \sigma^2), t = 1, 2, ..., N$   
\n $\sigma^2 \sim inversegamma(0.1, 0.1)$ 

The effect at the prior time period,  $e_{t-1}$ , is the mean of the temporal random effect at time period t. Thus, the temporal random effects capture the overall temporal trend in the region's vulnerability to measles.

## **2.5 Spatio-Temporal Interaction Effect for areal unit data**

The most common modeling approaches utilize a main effect, interaction effect or an autoregressive structure (Rushworth *et al.*, 2014). Different levels of this effect will be examined in the model. Data simulation techniques are used to estimate the number of susceptible measles cases  $(y_{it})$  per year and the number of children visiting the hospital  $(n_{it})$ . The interaction effect  $(\gamma_{kt})$  is incorporated in (1) to five (2) as follows

$$
\ln\left(\frac{\theta_{kt}}{1-\theta_{kt}}\right) = X'_{kt}\beta + \delta_t + \gamma_{kt} + e_t \tag{1}
$$

 $\gamma_{kt/\mu_t \sim N(0,\mu_t^2)}$ 

Where  $\theta_{kt}$  Is the estimated likelihood of having measles at a particular region and time? The remaining terms in the linear predictor are  $\delta = (\delta_1, \delta_2, \ldots, \delta_N)$  and  $e = (e_1, e_2, \ldots, e_N)$ . What are the overall spatial and temporal trends in the estimated probability? $\theta_{kt}$ .

 $\gamma_{kt/\mu_t \sim N(0,\mu_t^2)}$  As an interaction effect, its mean values also varied in the simulations to investigate the strength of the spatio-temporal interaction effect on the data.

## **2.6 Spatio-Temporal Models for Mkt**

Using a K  $\times$  K neighborhood matrix W = (w<sub>ki)</sub>, all models in this study produce spatial autocorrelation in the response data Y through the latent component M. W typically contains binary elements, where  $w_{ki} = 0$  otherwise and one if areal units  $(S_k, S_j)$  are spatially close to one another or share a shared border. Furthermore,  $w_{kk} = 0$ . This indicates that while values for non-neighboring areal units are conditionally independent given the remaining  ${M_{it}}$  values, those for geographically nearby areal units  $(S_k, S_j)$  have a spatial auto-correlated relationship  $(M_{kt}, M_{it})$ . The most popular binary specification of W for areal data is this one, which is based on having a shared boundary; however, CARBayesST requires that W be symmetric and have non-negative elements.

The spatial and temporal main effects and space-time interaction model Knorr-Held (2000) put forth are similar to the S.T.CARanova model. The model is considered to fit our simulated data of



different distribution categories, parameter values/ levels, levels of an interaction effect, autocorrelation levels and sample sizes to estimate the susceptibility of measles across the regions. The details of the model's description are given below.

#### **2.7 S.T.CARanova**

The model is a modification of that proposed by Knorr-Held (2000) and is given by

$$
M_{kt} = \emptyset_k + \delta_t + \gamma_{kt}
$$
\n
$$
\emptyset_k \sim N\left(\frac{\rho_S \sum_{j=1}^k w_{kj} \emptyset_j}{\rho_S \sum_{j=1}^k w_{kj} \emptyset_j + 1 - \rho_S}, \frac{\tau_S^2}{\rho_S \sum_{j=1}^k w_{kj} \emptyset_j + 1 - \rho_S}\right)
$$
\n
$$
\delta_k \sim N\left(\frac{\rho_T \sum_{j=1}^k w_{kj} d_{tj} \delta_j}{\rho_T \sum_{j=1}^k d_{tj} + 1 - \rho_T}, \frac{\tau_T^2}{\rho_T \sum_{j=1}^k d_{tj} + 1 - \rho_T}\right)
$$
\n
$$
\tau_S^2, \tau_T^2, \tau_I^2 \sim Inverse - Gamma(a, b),
$$
\n
$$
\rho_S, \rho_T \sim Uniform(0, 1),
$$
\n
$$
\gamma_{kt} \sim N(\mu_\alpha, \tau_I^2).
$$
\n(11)

In this case, the CAR prior suggested by Leroux et al. (2000) models both the spatio-temporal autocorrelation and a standard set of spatial random effects,  $\phi = (\phi_1,...,\phi_k)$ , and a standard set of temporal random effects,  $\delta = (\delta_1,...,\delta_k)$ . Furthermore, the model can optionally include a collection of separate space-time interactions  $\gamma = (\gamma_{11} \ldots \gamma_{kt})$ , which can be indicated in the function call by passing in the argument interaction=TRUE (the default). Every random effect set has a mean center. For the remaining parameters, fixed uniform  $(\rho_S, \rho_T)$  and conjugate  $(\tau_S^2, \tau_T^2, \tau_I^2 I)$  priors are supplied; default values for the latter are  $(a = 1, b = 0.01)$ . Alternatively, instead of estimating the dependence parameters  $(\rho_s, \rho_T)$  in the model, they can be fixed at values in the unit interval [0, 1]

#### **4. ANALYSIS AND RESULTS**

# **4.1. Model Fitting and Summary of the Numerical Results on 5-Areal unit when there is Interaction and Autocorrelation effect**

The simulation for 5-arealUnit at different periods is carried out to fit the spatial-temporal model and to illustrate the appropriateness of the model fitting across the arealUnit and period to establish the objective. We assume here that the data comes from Poisson likelihood. Before making an inference from the model, we have to ensure the Markov chains appear to have converged, and a single chain diagnostic is the Z-score proposed by Geweke (2022) and given in the model summary in the table.1 (Geweke. diag), where convergence is suggested if the Z-score lies within (−1.96, 1.96). Table 1 includes parameter estimates (Mean values), 95% credible intervals (2.5% and 97.5%) of the parameter and convergence diagnostics (n effective and Geweke. diag) for specific parameters, as well as overall model fit measures such as the DIC. We assume here that the interaction terms γkt are absent and that the data come from a Poisson likelihood. Where  $\tau_s$  and  $\tau_T$ The estimated probability of having measles is at a particular region and time.  $\rho_s$  and  $\rho_T$  These are the interactions between an areal unit and time period and the autocorrelation effect.



K x T	T	Mean	2.5%	97.5%	n.effec	Gewek	<b>DIC</b>	p.d	<b>LMPL</b>
					tive	e.diag			
	Intercept	4.0377	4.0316	4.0437	4787.8	0.6			
	$\tau_{S}$	0.0094	0.0065	0.0130	5200.9	1.7			
5X20	$\tau_T$	0.0132	0.0070	0.0243	5000.0	0.3	13911.7	96.237	$-6958.89$
	$\rho_{\rm s}$	0.9281	0.7949	0.9940	4544.9	$-1.1$			
	$\rho_T$	0.7169	0.3050	0.9654	5000.0	$-0.7$			
	Intercept	3.9600	3.9522	3.9679	5000.0	0.1			
	$\tau_s$	0.0092	0.0055	0.0206	4860.3	$-0.3$			
5X50	$\tau_{T}$	0.0116	0.0102	0.0244	4607.9	$-1.0$	8674.58	68.489	$-4341.8$
	$\rho_{\rm s}$	0.6957	0.0689	0.9247	4553.3	1.6			
	$\rho_T$	0.8176	0.5829	0.9624	4733.8	0.5			
	Intercept	3.8549	3.8491	3.8608	5000.0	0.7			
5X100	$\tau_{s}$	0.0090	0.0049	0.0160	5000.0	1.6			
	$\tau_T$	0.0088	0.0061	0.0124	4600.3	$-1.4$	16833.6	108.01	$-8418.3$
	$\rho_{\rm s}$	0.6393	0.2085	0.9570	5000.0	1.1			
	$\rho_T$	0.9507	0.8822	0.9905	4457.5	0.4			
	Intercept	3.9603	3.9560	3.9644	4138.0	$-1.6$			
	$\tau_{s}$	0.0078	0.0042	0.0137	5000.0	0.4			
	$\tau_{T}$	0.0068	0.0077	0.0123	4597.5	1.0			
5X200	$\rho_{\scriptscriptstyle S}$	0.6127	0.1758	0.9524	4817.2	$-1.0$	34135.9	198.57	$-17069.3$
	$\rho_T$	0.9864	0.9688	0.9971	5000.0	$-0.8$			

**Table 1: Spatio-temporal models for five areal unit data over 20, 50, 100 and 200 time periods with interaction and autocorrelation effect** 





Fig.1a: Estimated parameter values of measles from 5 areal units over some time



Fig.1b: Estimated interaction and autocorrelation of 5 areal units and periods

The table above shows the output describing the model fitted on five areal unit data at  $t = 1, 2, 3...$ 20; 50; 100 and 200 time periods, and a summary of the numerical results. The estimated Values of the measles susceptibility at a particular region and time ( $\tau_s$  and  $\tau_T$ ) is presented in Figure 1a, while the correlation between an areal unit and period and autocorrelation effect, respectively ( $\rho_s$  and $\rho_T$ ) is displayed in Figure 1b. From Figure 1a, both values of  $\tau_s$  and  $\tau<sub>T</sub>$  These decrease as the period increases by five units. Indeed, the estimated measles susceptibility decreases over time. Figure 1b shows that the  $\rho_s$  decreases while  $\rho_T$  Increases over the period. This shows that the interaction between small arealUnit and period decreases as time increases while the autocorrelation increases. The spatial-temporal model is more fitted to 5 areal units when the period is 50 (5x50) due to its minimum DIC and P.D. and maximum value of LMPL.



# **4.2 Model Fitting and Summary of the Numerical Results on 10-Areal unit when there is Interaction and Autocorrelation effect**

The simulation for 10-arealUnit at different periods is carried out to fit the spatial-temporal model and to illustrate the appropriateness of the model fitting across the arealUnit and period to establish the objective. We assume here that the data comes from Poisson likelihood. Before making an inference from the model, we have to ensure the Markov chains appear to have converged. A single chain diagnostic is the Z-score proposed by Geweke(2022) and given in the model summary in Table 2 (Geweke. diag), where convergence is suggested if the Z-score lies within (−1.96, 1.96). Table 2b includes parameter estimates (Mean values), 95% credible intervals (2.5% and 97.5%) of the parameter and convergence diagnostics (n effective and Geweke. diag) for specific parameters, as well as overall model fit measures such as the DIC. We assume here that the interaction terms γkt are absent and that the data come from a Poisson likelihood. Where  $\tau_s$  and  $\tau_T$  are estimated probability of having measles at a particular region and time, respectively  $\rho_s$  and  $\rho_T$  Are interactions between an areal unit and period and autocorrelation effect, respectively?

<b>KXT</b>	T	Mean	2.5%	97.5%	n.effec	Gewek	<b>DIC</b>	p.d	<b>LMPL</b>
					tive	e.diag			
	Intercept	4.221	4.2151	4.2268	5000.0	1.0			
	$\tau_{\scriptscriptstyle S}$	0.012	0.0087	0.0170	5000.0	0.6			
10X20	$\tau_{T}$	0.014	0.0073	0.0287	4795.4	0.2	14233.6	103.68	$-7119.0$
	$\rho_{\rm s}$	0.868	0.6593	0.9863	4409.0	$-0.8$			
	$\rho_T$	0.955	0.8480	0.9973	4036.7	0.1			
	Intercept	4.241	4.2384	4.2454	3692.5	$-0.4$			
	$\tau_s$	0.017	0.0087	0.0168	5000.0	$-0.8$			
10X50	$\tau_{\scriptscriptstyle T}$	0.012	0.0078	0.0179	5000.0	$-0.3$	35667.6	142.00	$-17836.9$
	$\rho_{\rm s}$	0.744	0.4627	0.9615	5000.0	$-1.7$			
	$\rho_T$	0.864	0.6786	0.9751	4726.2	$-0.3$			
	Intercept	4.241	4.2384	4.2454	3692.5	$-0.4$			
10X10	$\tau_{s}$	0.018	0.0087	0.0168	5000.0	$-0.8$			
$\boldsymbol{0}$	$\tau_T$	0.011	0.0078	0.0179	5000.0	$-0.3$	35667.6	142.00	$-17836.9$
	$\rho_{\scriptscriptstyle S}$	0.634	0.4627	0.9615	5000.0	$-1.7$			
	$\rho_T$	0.864	0.6786	0.9751	4726.2	$-0.3$			
	Intercept	4.241	4.2384	4.2454	3692.5	$-0.4$			
	$\tau_{s}$	0.018	0.0087	0.0168	5000.0	$-0.8$			
10X20	$\tau_T$	0.009	0.0078	0.0179	5000.0	$-0.3$	35667.6	142.00	$-17836.9$
$\boldsymbol{0}$	$\rho_{\scriptscriptstyle S}$	0.511	0.4627	0.9615	5000.0	$-1.7$			
	$\rho_T$	0.864	0.6786	0.9751	4726.2	$-0.3$			

**Table 2: Spatio-temporal models for ten areal unit data over 20, 50, 100 and 200 time periods with interaction and autocorrelation effect from poison prior**





Fig.2a: Estimated parameter values of measles from 10 areal units over some time



Fig.2b: Estimated interaction and autocorrelation of 10 areal units and periods

Table 2 shows the output that describes the model fitted on ten areal unit data at  $t = 1, 2, 3... 20$ ; 50; 100 and 200 time periods, and a summary of the numerical results. The estimated values of the measles susceptibility at a particular region and time ( $\tau_s$  and  $\tau_T$ ) is presented in Figure 2a, while interaction between an areal unit and period and autocorrelation effect, respectively ( $\rho_s$ and $\rho_T$ ) is displayed in Figure 2b. From figure 2a, values of  $\tau_s$  is increasing while  $\tau_T$  They decrease as the period increases unit. Units Indeed, the estimated measles susceptibility increases over time. Figure 2b shows that both values of  $\rho_s$  and  $\rho_T$  Decreases over period. This shows that the interaction between small arealUnit and period decreases as time increases, and the autocorrelation also



decreases. The spatial-temporal model is more fitted to 10 areal units when the time period is 20 (10x20) due to its minimum DIC and p.d and maximum value of LMPL.

# **4.3. Model Fitting and Summary of the Numerical Results on 15-Areal Unit data over 20, 50, 100 and 200 time periods with interaction and autocorrelation effect**

The simulation for 15-arealUnit at different periods is carried out to fit the spatial-temporal model and to illustrate the appropriateness of the model fitting across the arealUnit and period to establish the objective. We assume here that the data comes from Poisson likelihood. Before making an inference from the model, we have to ensure the Markov chains appear to have converged. A single chain diagnostic is the Z-score proposed by Geweke(2022) and given in the model summary in Table 3 (Geweke. diag), where convergence is suggested if the Z-score lies within (−1.96, 1.96). Table 3 includes parameter estimates (Mean values), 95% credible intervals (2.5% and 97.5%) of the parameter and convergence diagnostics (n effective and Geweke. diag) for specific parameters, as well as overall model fit measures such as the DIC. We assume here that the interaction terms γkt are absent and that the data come from a Poisson likelihood. Where  $\tau_s$  and  $\tau_T$  Are estimated probability of having measles at a particular region and time respectively.  $\rho_s$  and  $\rho_T$  The interaction between an areal unit and period and the autocorrelation effect are as follows:

<b>KXT</b>	T	Mean	2.5%	97.5%	n.effec	Gewek	<b>DIC</b>	p.d	<b>LMPL</b>
					tive	e.diag			
	Intercept	4.178	4.174	4.1816	4790.8	$-1.2$	31701.2	189.29	$-15851.7$
	$\tau_{S}$	0.007	0.0057	0.0093	4380.9	$-1.7$			
	$\tau_T$	0.010	0.0055	0.0185	5000.0	1.7			
	$\rho_{\rm s}$	0.839	0.6480	0.9744	4423.0	$-0.6$			
15X20	$\rho_T$	0.570	0.1251	0.9233	4584.4	$-0.8$			
15X50	Intercept	4.074	4.1555	4.3683	4534.2	0.7			
	$\tau_{S}$	0.008	0.0523	0.0825	5000.5	$-1.6$			
	$\tau_T$	0.010	0.1567	0.0131	4054.8	0.9	25849	123.76	$-12894.1$
	$\rho_{\rm s}$	0.822	0.6259	0.9107	3815.1	$-0.5$			
	$\rho_T$	0.557	0.0362	0.4249	4275.4	$-0.7$			
	Intercept	3.953	3.9474	3.9596	4554.5	0.6			
15X100	$\tau_{S}$	0.009	0.0066	0.0130	5000.0	$-1.3$			
	$\tau_{T}$	0.006	0.0034	0.0116	5000.0	1.8	5778.90	287.17	$-2598.6$
	$\rho_{\rm s}$	0.816	0.6049	0.9014	4012.0	0.4			
	$\rho_T$	0.513	0.0768	0.9047	4000.0	$-0.4$			
	Intercept	4.035	4.0261	4.0444	4703.7	1.6	6921.44	148.61	$-3457.63$

**Table 3: Spatio-temporal models for 15 areal unit data over 20, 50, 100 and 200 time periods with interaction and autocorrelation effect from poison prior.** 

Umaru Ali Shinkafi Polytechnic Sokoto, Nigeria







Fig.3a: Estimated parameter values of measles from 15 areal units over some time



Fig.3b: Estimated interaction and autocorrelation of 15 areal units and periods

Table 3 shows the output that describes the model fitted on 15 areal unit data at  $t = 1, 2, 3... 20; 50;$ 100 and 200 time periods, and a summary of the numerical results. The estimated values of the



measles susceptibility at a particular region and time ( $\tau_s$  and  $\tau_T$ ) is presented in Figure 3a, while interaction between an areal unit and period and autocorrelation effect, respectively ( $\rho_s$ and $\rho_T$ ) is displayed in Figure 3b. From Figure 4.3a, both values of  $\tau_s$  and  $\tau_{\tau}$  Are increasing as the period increases by 15 areal units. Indeed, the estimated measles susceptibility increases over time. Figure 4.3b shows that both values of  $\rho_s$  and  $\rho_T$  Decreases over period. This shows that the interaction between small arealUnit and period decreases as time increases, and the autocorrelation also decreases. The spatial-temporal model is more fitted to 15 areal units when the period is 100 (15x100) due to its minimum DIC and p.d and maximum value of LMPL.

## **5. CONCLUSION**

This study provided an appropriate model for capturing the autocorrelation and interaction effects in the spatiotemporal data for poison prior across the areal units and periods. It determined a suitable model for measles-generated data from non-overlapping regions at consecutive periods. The distributions through simulation with the following result achieved. The findings show that the interaction between small area units and periods decreases as time increases while the autocorrelation increases for 5 area units. The spatial-temporal model is more fitted to 5 areal units when the period is 50 (5x50) due to its minimum DIC and P.D. and maximum value of LMPL. Also, in 10 area units, the interaction between small area units and periods decreases as time increases, and autocorrelation decreases. The spatial-temporal model is more fitted to 10 areal units when the period is 20 (10x20). Finally, under 15 areal units, the interaction between small areal Unit and period decreases as time increases, and the autocorrelation also decreases. The spatial-temporal model is more fitted to 15 areal units when the period is 100 (15x100) due to its minimum DIC and p.d and maximum value of LMPL.

# **6. LIMITATIONS OF THE STUDY**

This study is limited to areal units partitioned into  $K = 1... k$  (Where  $k = 5, 10, 15$  areal units). The region under study constitutes different communities with data obtained over periods t (where  $t =$ 1, 2, 3…). To get the best among them, Bayesian hierarchical logistic regression models with only poison prior were used to model the simulated measles data. The simulations based on the earlier distribution were carried out, and the model was assessed.

# **7. IMPORTANCE OF FINDINGS**

This study is significant because of its wide applications. To identify the geometric or geographic characteristics of measles diseases and other relevant data, the model under consideration will assist in investigating, assessing, evaluating, and modeling spatial data features, such as locations, qualities, and their interactions. The outcomes will help provide information that explains the characteristics and boundaries of the areas where measles cases are much more prevalent over time. Furthermore, this study will allow experts in the fields of science, sociology, psychology, epidemiology, biology, business, and marketing (among others) to understand better human behaviors, environmental factors, and relationships between people and a location.



# **8. FURTHER RESEARCH**

Further research can use spatiotemporal model for fitting and forecasting in a real life data of measles from different areal units and regions at different time periods.

# **9. REFERENCES**

- Anderson, C., Lee D., Dean, N. (2014)*. "Identifying Clusters in Bayesian Disease Mapping." Biostatistics,15:457–469.*
- Banerjee and Carlin B. P. (2004). *Parametric spatial cure rate models for interval-censored timeto-relapse data. Biometrics, 60(1):268–275.*
- Beraha, M., Pegoraro, M., Peli, R. and Guglielmi A. (2021). *Spatially dependent mixture models via the logistic multivariate CAR prior. Spatial Stat. 46, 100548*
- Carrel, M., Emch, M., Streatfield, P.K., Yunus, M.(2009)*. Spatio-temporal clustering of Cholera: the impact of flood control in Matlab, Bangladesh, 1983–2003. Health Place. 2009; 15(3):771–82.*
- Costa, M.A, Kulldorff, M. (2014). *Maximum linkage space-time permutation scan statistics for disease outbreak detection. Int J Health Geogr. 2014; 13:20.*
- Choi, J and Lawson, A.B. (2011)*.Evaluation of Bayesian Spatial-Temporal Latent Models in* Costa MA, Kulldorff M. (2014). *Maximum linkage space-time permutation scan statistics for Disease outbreak detection. Int J Health Geogr. 13:20.*
- Geweke J (2022). *"Evaluating the Accuracy of Sampling-Based Approaches to the Calculation of Posterior Moments." In Bayesian Statistics: 169–193. University Press*
- Jones, S.G.,Conner,W.,Song,B.,Gordon,D.,Jayakaran,A.(2012)*. Comparing spatio-temporal*
- *Clusters of arthropod-borne infections using administrative medical claims and state-reported surveillance data. Spat Spatio Temporal Epidemiol. 2012;3(3):205–13.*
- Knorr-Held, L.and Best, N.G.(2000). *A shared component model for detecting joint and selective clustering of two diseases. J. Roy. Statst.Soc., Ser. A, 164:73-85.*
- Kulldorff , M.(2015). *SaTScan user guide for version 9.4. Boston: Department of Ambulatory Care and Prevention, Harvard Medical School; 2015.*
- Lawson,A.B.(2018).*Bayesian Disease Mapping: Hierarchical Modeling in Spatial Epidemiology, 3rd ed. Chapman and Hall/CRC.*
- Lee, D., Rushworth, A., Napier, G. (2018). *"Spatio-Temporal Areal Unit Modeling in R with Conditional Autoregressive Priors Using the CARBayesST Package." Journal of StatisticalSoftware, Articles,84(9),1–39.doi:10.18637/jss.v084.i09.*
- Lee, D., Meeks, K., and Pettersson, W. (2021). *"Improved inference for areal unit count data Using graph-based optimization." Statistics and Computing, 31, 51.*
- Lee, D., Robertson, C. and Marques, D. (2022)*. "Quantifying the small-area spatio-temporal*
- *dynamics of the Covid-19 pandemic in Scotland during a period with limited testing capacity." Spatial Statistics, to appear, [https://doi.org/10.1016/j.spasta.2021.100508.](https://doi.org/10.1016/j.spasta.2021.100508)*

Umaru Ali Shinkafi Polytechnic Sokoto, Nigeria

- Leroux BG, Lei X, Breslow N (2000). Statistical Models in Epidemiology, the Environment, and Clinical Trials, chapter Estimation of Disease Rates in Small Areas: A new Mixed Model for Spatial Dependence, pp. 179–191. Springer-Verlag, New York.
- Ling, C.Y., Gruebner, O, Krämer,A., akes,T.(2014)*. Spatio-temporal patterns of dengue in Malaysia: combining address and sub-district level. Geospatial Health. 2014;9(1):131–40. 16.*
- Napier, G., Lee, D., Robertson, C. and Lawson, A.( 2018)*. A Bayesian space-time model for clustering areal units based on their disease trends. Biostatistics 20 (4), 681–697.*
- Nicoletta, V., Guglielmi, A., Ruiz, A., Bélanger, V. and Lanzarone, E.( 2022)*. Bayesian spatial-Temporal modeling and prediction of areal demands for ambulance services. IMA J. Manag. Math. 33 (1):101–121.*
- Rushworth, A., Lee, D., Mitchell, R. (2014)*. "A Spatio-Temporal Model for Estimating the Long-Term Effects of Air Pollution on Respiratory Hospital Admissions in Greater London." Spatial and Spatio-temporal Epidemiology, 10, 29–38.*
- *Sindato, C., Karimuribo,E.D., Pfeiffer, D.U., Mboera, L.E.G., Kivaria, F., Dautu,G.(2014). Spatial And the temporal pattern of Rift Valley fever outbreaks in Tanzania from 1930 to 2007. PLoS ONE.2014; 9(2):e88897*
- Zhang, W.Y., Wang, L.Y., Liu, Y.X., Yin, W.W., Hu, W.B., Magalhaes, R.J.S.(2014). *Spatiotemporal transmission dynamics of hemorrhagic fever with renal syndrome in China, 2005–2012. PLoS Negl Trop Dis. 2014;8(11):e3344.*
- Zhou, H., Hanson, T. and Zhang, J. (2020).*spBayesSurv: Fitting Bayesian spatial survival models using R. Journal of Statistical Software, 92(9):1–33.*
- Zhu, Y., Xu, Q., Lin, H., Yue, D., Song, L., Wang, C.(2013)*. Spatiotemporal analysis of infant*
- *Measles using population attributable risk in Shandong Province, 1999–2008. PLoS ONE. 2013; 8(11):e79334. 8. Zhuo J, Geng W, Hoekstra EJ, Zhong G, Liang X, Zhang J. Imp*

