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BAYESIAN SPATIAL TEMPORAL TREND ANALYSIS FOR DECISION MAKING AND RISK ASSESSMENT IN DENGUE INCIDENCE STUDIES: A CASE OF TAMILNADU

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Abstract

This study presents a Bayesian spatial-temporal analysis for studying Dengue incidence in Tamil Nadu, aiming to provide insights into decision-making and risk assessment strategies. Statistical models that allow a more accurate depiction of true disease rates by borrowing information from neighboring regions will help mitigate the effects of sparsely populated regions and deliver better inference. Perhaps the most conspicuous manner of modeling spatial dependence is to introduce spatially associated random effects within a Bayesian hierarchical setting. The Bayesian modeling and inferential framework are flexible and extremely rich in its capabilities to accumulate various scientific hypotheses and assumptions. The spatial and spatial temporal epidemiology is concerned with the description and analysis of spatial and spatial temporal variations in disease risk with respect to risk factors. As the primary aim of this work is to quantify the spatial disease pattern of dengue incidences apart from the mapping of disease modelling the disease and finding spatial clusters/hotpots is one important aspect in epidemiology is to find the temporal trends in or outside of clusters. In this study, a spatial-temporal trends model is fitted using the Leroux CAR prior's set up for studying the spatial-temporal disease patterns with the estimation of the temporal trends with reference to dengue incidences in Tamil Nadu, India.

Keywords: Spatial temporal, Bayesian modeling, Bayesian hierarchical modeling, Leroux CAR prior

I. Introduction

In spatial epidemiology, the main interest is to describe the spread of a disease or infection through models that attempt to summarize the spatial and temporal effects. After detecting disease clusters, further analysis about those clusters leads to the finding of the temporal trend of the cluster. The Bayesian methodology is highly useful to study this behaviour which may be better than the classical procedure, because of the fact that the procedure of Bayesian inference combines prior distribution of model parameters and the data likelihood, for deriving the posterior distribution of parameters which portray the behaviour of the parameter in a better manner. The Bayesian hierarchical model that involves time and regional effects yield more information to the problem of study based on the neighbourhood structures of the regions and adjacent times.

But a model developed so would be quite complex in nature. However, the computational procedures based on MCMC methodology are very much useful to approximate the posterior distribution in Bayesian hierarchical models. In this article, a Bayesian model is used to describe the spatial patterns with the estimation of the temporal trends with reference to dengue incidences in Tamil Nadu, India. The spatio-temporal model was proposed to study the spatial and temporal patterns which allows for spatial temporal discontinuities between areas [12] by using this model the study has been made to address the climatic variability of dengue cases in Makassar Indonesia [1]. The rate of cases in neighborhood i and time j, mosquito density data, fixed scaling factors, lagged time for specific variables and different weighting functions between neighborhood effects which consists of economic value of the neighborhood, population density and travel distance between neighborhoods are included. The nearest-neighborhood effects, (local) and all between-neighborhood effects (global) are compared in order to predict the association between mosquito density and human cases of dengue. Models that preferred were contains global between-neighborhood effects and the covariates mosquito density and human cases of dengue and their interaction. In this study we have used the district wise dengue incidences data collected from the Government of Tamil Nadu over the period of 2007 – 2018.

II. The Spatial and Temporal Models

The Bayesian methodology is highly useful to study this behaviour which may be better than the classical procedure, because of the fact that the procedure of Bayesian inference combines prior distribution of model parameters and the data likelihood, for deriving the posterior distribution of parameters which portray the behaviour of the parameter in a better manner. As already stated, a large number of models have been proposed for estimating the Spatio-temporal trends in disease risk and as our disease outcome variable is a count they have the general form,

$$Y_{it} \sim \text{Poisson}(E_{it}R_{it}) \qquad \text{for } i = 1, \dots, N, t = 1, \dots, T \tag{1}$$

$$\text{In}(R_{it}) = \beta_0 + \beta_1 \text{Rainfall}_{it} + \beta_2 \text{Temperature}_{it} + \psi_{it} \tag{2}$$

$$\beta \sim N(\mu_\beta, \Sigma_\beta) \tag{3}$$

where the number of observed disease count is denoted by $Y = (Y_1, \dots, Y_N)_{i \times T}$, where $Y_t = (Y_{1t}, \dots, Y_{it})$ denoted by $i \times 1$ column vector of observed disease count for all regions i for time t, E_{it} is the expected number of disease cases, R_{it} is the relative risk of dengue disease in area i and time t. The vector of covariate regression parameters is denoted by $\beta$and a multivariate Gaussian prior is assumed with mean μ_β and diagonal dispersion matrix Σ_β, ψ_{it} is the random effect for the study region i and time t. Taking $\psi_{it} = \rho_T \psi_{t-1} + \epsilon_t$. The temporal autocorrelation is thus induced through the mean $\rho_T \phi_{t-1}$, while spatial autocorrelation is induced by the variance $\tau^2 Q(W, \rho_s)^{-1}$. The precision matrix is given by,

$$Q(W, \rho_s) = \rho_s(\text{diag}[W1] - W) + (1 - \rho_s)I \tag{4}$$

where $(1, I)$ is a $N \times 1$ vector of ones and the $N \times N$ identity matrix respectively. Hence, the spatial autocorrelation is induced by the neighbourhood matrix W defined above, and if $\omega_{ij} = 1$ then the random errors $(\epsilon_{kt}, \epsilon_{jt})$ are modelled as spatially autocorrelated, while if $\omega_{ij} = 0$ then $(\epsilon_{it}, \epsilon_{jt})$ are assumed to be conditionally independent. Thus ρ_s, ρ_T respectively control the levels of spatial and temporal autocorrelation, with values of 0 corresponding to independence while a value 1

corresponds to string autocorrelation. The precision matrix $Q(W, \rho_s)$ corresponds to the conditional autoregressive (CAR) prior proposed by Leroux [15], given by,

$$\epsilon_{it}|\epsilon_{-it}, W \sim N\left(\frac{\rho_s \sum_{j=1}^{N} \omega_{ij}\epsilon_{jt}}{\rho_s \sum_{j=1}^{N} \omega_{ij}+1-\rho_s}, \frac{\tau^2}{\rho_s \sum_{j=1}^{N} \omega_{ij}+1-\rho_s}\right) \quad (5)$$

With the temporal informative priors $\tau^2 \sim$Inverse Gamma$(1, 0.01)$ $\rho_s, \rho_T \sim$Uniform$(0, 1)$ and $\epsilon_{-it} = (\epsilon_{1t}, \ldots, \epsilon_{i-1t}, \epsilon_{i+1t}, \ldots, \epsilon_{Nt})$. If $\rho_s = 1$ the model simplifies to the intrinsic CAR prior proposed Besag et al.,[3] and if $\rho_s = 0$ the errors ϵ_{kt} are independent and normally distributed with mean zero and a constant variance τ^2.

III. Results

The analysis was performed using the model assumed in the previous section. As the primary aim of this work is to quantify the spatial disease pattern of dengue incidences risk over time the spatially autoregressive model is used. The MCMC samples are generated from the three independent Markov chains and each chain was run for 20,000 samples. To check whether the Markov chains are converged the trace plot of the samples for each parameter are observed and since the samples show no trend in their means or variances, convergence is assured. These trace plots are presented in Figure:1

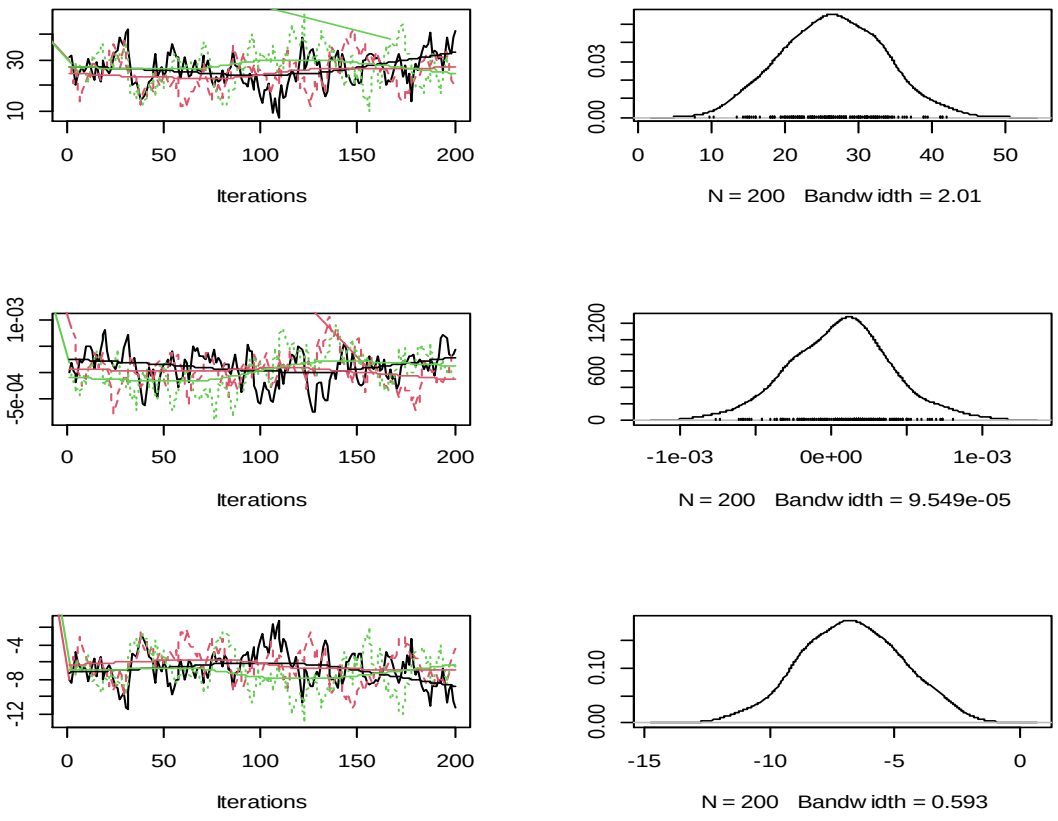

Figure 1: *Trace plots of the MCMC samples from each chain*

The Gelman and Rubin diagnostic [7] is used as an additional check for testing the between to within chain variation reduction in the MCMC samples. It is observed that the samples are well mixed both separately and then jointly as the values of the point estimates are less than 1.1.

Table1: *Gelman-Rubin statistic*

MCMC Chain	Point Estimates	Upper Credible Interval
Chain 1	1.04	1.13
Chain 2	1.07	1.25
Chain 3	1.04	1.14

Table 2: *Posterior Quantities for Selected Parameters and DIC of the Autoregressive CAR Model (Chain 1)*

Model paramters	Median	2.5%	97.5%	n.effective	Geweke.diag
Intercept	26.1415	14.3764	39.2920	22.9	-0.2
Rainfall	0.0001	-0.0006	0.0007	29.3	1.5
Temperature	-6.7187	-10.6279	-3.1630	22.3	0.1
tau2	2.2096	1.8642	2.6795	231.0	-1.5
rho.S	0.9083	0.8233	0.9542	200.0	-2.0
rho.T	0.6794	0.5806	0.7782	91.1	-2.0

DIC=2365.255

The above Table.2 provides the parameter summaries and posterior median point estimates with 95% credible intervals. The Deviance Information Criterion is given at the bottom. It is observed that the covariate temperature has a negative relationship with dengue incidences and all other covariates have a positive relationship. The spatial and temporal parameters ρ_s and ρ_T exhibit the presence of spatial and temporal autocorrelation after adjusting for the effects of covariates. It is observed that the condition for convergence according to Geweke diagnostic [8] is satisfied as the corresponding values lie between -2 to +2.

Table 3: *Posterior Median Relative Risk for Covariates*

Credible Interval	50%	2.5%	97.5%
Temperature	1.0	0.999	1.002
Rainfall	1.004	0.780	1.437

The estimated relative risk of the covariates obtained from MCMC samples for the regression parameters β_1 and β_2 are obtained and given in Table.3 It is seen that the covariate temperature is not significantly related to dengue incidence risk as 95% credible interval consist of the null risk of 1. A similar thing is observed for the variable rainfall.

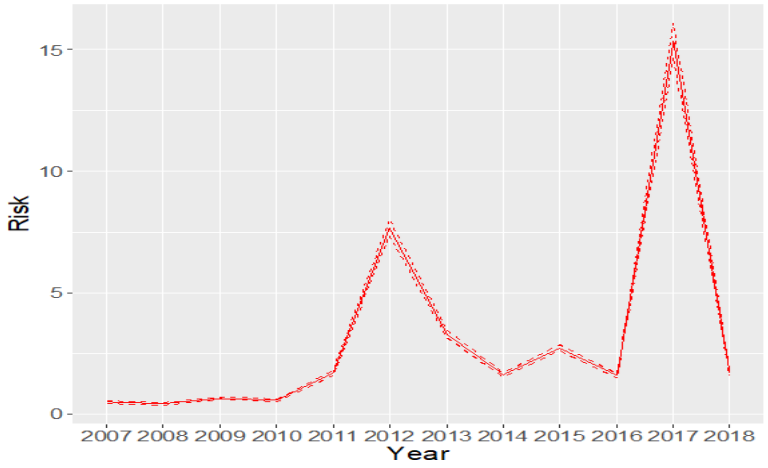

Figure 2: *Posterior Median and 95% Credible Interval for the Temporal Trend in Dengue*

With reference to Spatio-temporal trends in disease risk, the following graph (Figure: 2) has been plotted based on posterior risk distributions, in which the samples of fitted values are divided by the fixed expected number of disease cases.

Table 4: *Posterior Median and 95% credible interval for the Temporal Trend in Dengue Disease Risk.*

Year	Median	Lower Credible Interval	Upper Credible Interval
2007	0.0133	0.0119	0.0147
2008	0.0171	0.0152	0.0192
2009	0.0168	0.0154	0.0184
2010	0.0137	0.0124	0.0152
2011	0.0417	0.0391	0.0445
2012	0.2014	0.193	0.2101
2013	0.1064	0.1015	0.1115
2014	0.0437	0.0412	0.0463
2015	0.0155	0.0719	0.0794
2016	0.0475	0.0448	0.0504
2017	0.5473	0.5252	0.5712
2018	0.0505	0.0477	0.0535

To estimate the average temporal trend, the average risk across the study areas for each year is estimated which yields the posterior distribution of spatial averages for each year. The corresponding posterior median and 95% credible intervals are given in the following Table 4. The estimated temporal trend in disease risk is plotted in the following Figure 3. The figure clearly shows a downward trend in dengue incidences over 12 years study period. The peaks of risk are observed in 2012 and 2017.

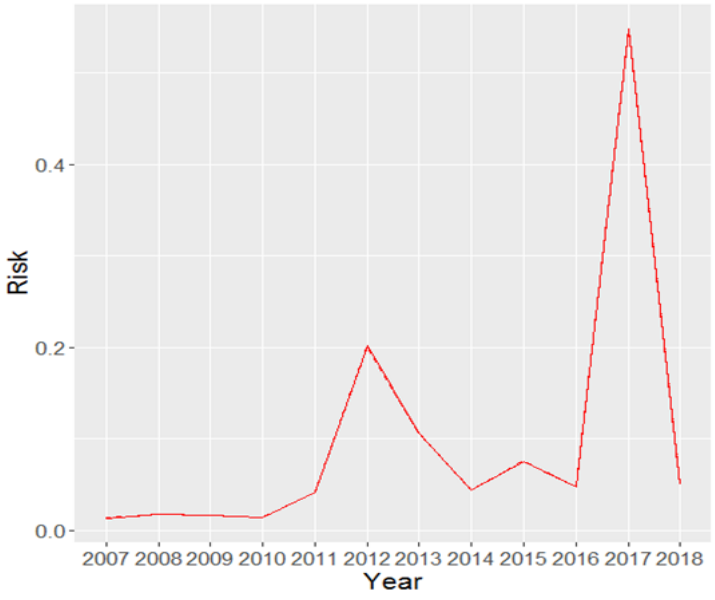

Figure 3: *Estimated temporal trend in Temporal Trend in Dengue incidence risk as measured by The Spatial Interquartile Range*

The measure of variations in disease risk over the study region called "Total Inequality" is measured by the interquartile range (IQR) variation for each year and is given in Table 4. and the corresponding plot is given in Figure 3 The figure clearly shows that the total inequality in Dengue incidences when using the interquartile range has increased over the years till 2017 and decreased in 2018 which suggest that the population is becoming uneven in terms of later years.

Table 4: Inter Quartile Ranges

Year	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018
IQR	0.008	0.013	0.009	0.005	0.015	0.142	0.096	0.036	0.078	0.038	0.475	0.038

The spatial pattern is computed in two ways, the one is with reference to the posterior median risk surface and the one is the posterior exceedance probability. The maps of posterior exceedance probability and the median risk have been generated and shown in figures: 4 and 5.

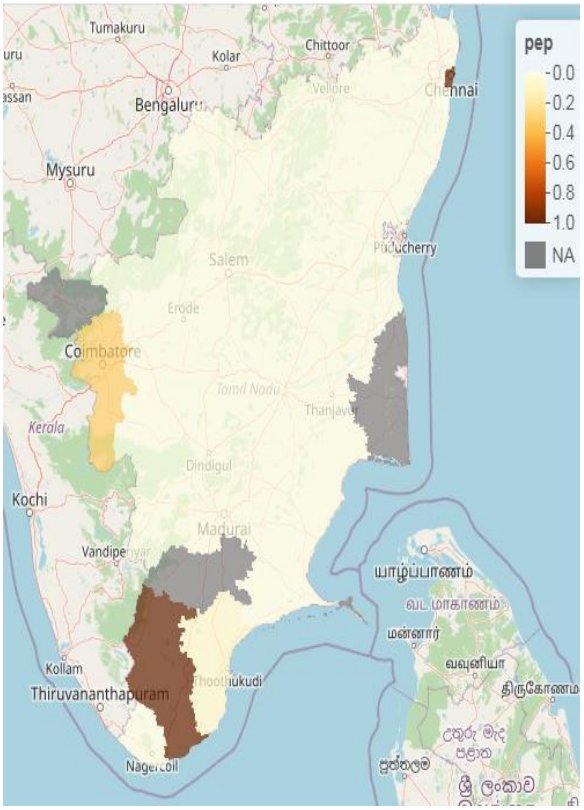

Figure 4: *Estimated (Posterior Median) Risk Surface for 2017*

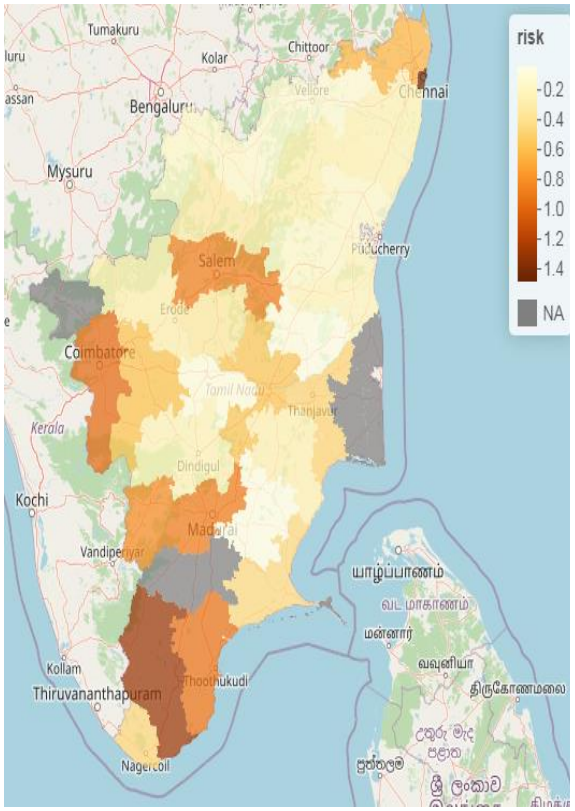

Figure 5: *The Posterior Exceedance Probabilities that the risk in 2017 is greater than 1*

From figure: 5, it is observed that the areas of highest risk are found in Chennai and the next level of higher risk is observed in Tirunelveli. Moderate levels of risk are found in Coimbatore, Thoothukudi, Madurai, Theni, Salem and Thiruvallur. Lower levels of risk are found in Tiruppur, Tiruchirapalli, Thanjavur, Ramanathapuram and Kanyakumari. The Posterior Exceedance Probabilities map shows that the majority of areas have zero probability of exceeding the risk of 1, except the areas Chennai and Tirunelveli.

IV. Discussion

Spatial-temporal disease mapping is a familiar approach for studying disease patterns in an effective manner. In this article, a spatial-temporal trends model is fitted using the Leroux CAR prior's set up for studying the spatial-temporal disease patterns of Dengue incidences are over the 12 years. From the analysis, a downward trend of dengue incidences is observed and the peaks of risk is observed in 2012 and 2017. Areas of highest risk are found in Chennai and the next level of higher risk is observed in Tirunelveli. Moderate levels of risk are found in Coimbatore, Thoothukudi, Madurai, Theni, Salem and Thiruvallur. These results are observed both spatially and temporally. If sufficient preventive measures are taken up by the health authorities on the areas quoted above the disease incidences may get lower and even null.

Conflict of Interest

The Authors declare that there is no conflict of Interest.

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