

Climatic Risk Factors for the Transmission of Dengue Fever: Bangladesh Perspective

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Climatic Risk Factors for the Transmission of Dengue Fever: Bangladesh Perspective

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Abstract

Dengue fever has become a major global public health concern. A significant global public health risk is dengue disease. Predicting how climatic factors will affect the spread of vector-borne diseases is difficult. However, the link is non-linear, geographically localized, and involves considerable lag periods between predictors and disease outbreaks. This disease spreads swiftly in Bangladesh due to its dense population and complex health policy setting. It is crucial to investigate the impact of climatic risk factors on Dengue transmission because it is an infectious disease spread by mosquitoes. In anticipating the occurrence or extent of each dengue outbreak, the methodology integrates confirmed Dengue cases and seasonal variables such as precipitation, temperature, humidity, wind speed, and lag duration of up to two years. The main objective is to examine how climatic risk variables affect dengue epidemics using Bayesian inference. Bayesian inference is drawn using MCMC with Gibbs sampling, which is carried out in the WinBUGS software. According to the study, less precipitation reduces infected cases and fatalities from Dengue. Furthermore, the spread of Dengue has diminished due to high temperatures, which have also affected the virus's ability to survive and spread.

Keywords Bayesian Inferences · Markov Chain Monte Carlo · Gibbs sampling · Dengue · Bangladesh.

1 Introduction

The Dengue virus, one of the viral pathogens, predominantly affects tropical and subtropical areas where it produces classical Dengue fever (DF) and Dengue Hemorrhagic fever (DHF). Dengue fever is a mosquito-borne disorder that affects millions of people each year [21, 6]. The *Aedes aegypti* mosquito transmits Dengue illnesses. The *Aedes* mosquito may transmit the dengue virus without the need for an intermediary animal vector. Often found in metropolitan areas, the *Aedes* mosquito maintains a man-mosquito-man interaction. Bangladesh is a country that suffers the most from dengue practically every year [2] and its tropical environment has made it an excellent place for the dengue virus to spread. Bangladesh witnessed occasional dengue virus transmission from 1964 to 1999, but The country is experiencing its worst dengue outbreak since 2000, with widespread dread of fatality as the illness spreads throughout the country, disproportionately impacting children, pregnant women, and the elderly [3, 4, 11, 33] and mainly in the capital city of Dhaka. The country experienced its greatest epidemic in history in 2019, with over 100,000 reported illnesses and almost 120 deaths [14]. In the middle of the epidemic, the Directorate General of Health in Bangladesh recorded 1026 confirmed cases in 2020, and 20,000 in 2021 [14]. We again spotlight the dengue outbreak in Bangladesh in 2022, thus far is the third most cases reported in a year since the first cases were reported in 2000. The Ministry of Health & Family Welfare of Bangladesh has reported 52,807 laboratory-confirmed dengue cases overall as of 20 November 2022, with 230 deaths associated

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with the disease [1].

Dengue fever is common in tropical and subtropical regions, but the epidemic in Bangladesh warrants additional investigation. What's inflicting this unusual boom in dengue cases? The concept that weather modifications make it easier for illnesses to unfold to new populations has substantially heightened humans' worry approximately the arrival and reemergence of infectious diseases [26]. Bangladesh's outbreak is being exacerbated by way of poor water, sanitation, and hygiene structures, in addition to a congested population, climatic trade, unplanned speedy urbanization, and building, poor vector manipulation strategies, and Bangladesh's faltering healthcare gadget all contribute to the extent and severity of dengue epidemics [20, 25, 27, 34, 35]. Additional causes might be drainage issues, stagnant water and rubbish anywhere, weak immune reputation, bodily weak spot, unplanned market, wetland occupation, the habit of gardening, polluted waterbody, [13] and so on. Climate change increases the opportunity for Dengue epidemics as it strengthens the hyperlink between the vector and the virus [36, 18]. The majority of research on this topic focuses on climate-related factors (rainfall or humidity). This tendency may be detected in quite early studies, such as Moore's [28], which showed that both the amount of rain and the persistence of rainfall were good predictors since when rainfall has continued to provide the most reliable early warning indicator [5]. Geographic location peak [5, 30] and trough weather events, such as highest and lowest temperatures [30], abnormal climatic occurrence, and running averages [32] have all been added to the list of variables used in the literature. Choudhury et al. evolved a Seasonal Autoregressive incorporated transferring average (SARIMA) model, especially for Dhaka, Bangladesh. While this look stated that it does now not take into consideration weather elements, it does remember seasonality, which axiomatically captures primary climatic characteristics [10]. Karim et al. evolved models with the use of simple linear regression and Pearson's correlation, utilizing a spread of environmental parameters including month-to-month rainfall, humidity, maximum, and lowest temperature, and determined that meteorological parameters may are expecting month-to-month dengue incidence with an excessive degree of accuracy [23]. However, the predictor variable glaringly deviated from the normal distribution. In some other studies, Kanchanapairoj, McNeil, and Thammapalo provided conflicting evidence that demonstrates the connection between dengue incidence and climatic situations is still up for debate [22]. Only a small amount of research has been executed so far on how weather influences the weight of ailment, appreciably dengue in South Asia.

The latest study, in addition to addressing the topic of climatic predictors of dengue in Bangladesh, employs a broader variety of statistical tactics. Statistically, it appears that most investigations utilized either very simple correlational techniques [12, 19, 23] or regression modeling [5, 37], or both. We employed the Bayesian Regression Method in this study. This generates a vast number of factors, including seasonal aspects, that allow researchers to investigate plausible links between scientifically quantifiable climate change and dengue transmission. Moreover, Bangladesh's lack of preparedness, including weak public health infrastructure and ineffective vector-control programs, increases the impact of dengue virus importation, resulting in rising outbreaks. Anorexia, nausea, vomiting, pharyngitis, upper respiratory tract symptoms, relative bradycardia, prostration, depression, hyperesthesia, lymphadenopathy, and rash are some of the symptoms and signs of dengue [13]. Other symptoms and signs include fever, backache, arthralgia, headache, generalized pain, eye pain, lacrimation, scleral injection, and rash. Since 2000, medical professionals in Bangladesh have clinically identified dengue following WHO guidelines.

This study examines how key meteorological variables such as precipitation, heat, moisture, and wind speed may promote Dengue incidence in Bangladesh. Here, we present the findings of a study conducted across Bangladesh, using a Bayesian regression approach to estimate the prevalence of Dengue and pinpoint significant risk variables for infection. Following are the research's main contributions. Then, using the Gibbs sampling (MCMC) algorithm to estimate the posterior distribution, future observations will be predicted. First, we will summarize measures for the location and variability of Dengue cases with additional risk factors and investigate the non-linear relationship between Dengue case counts and climatic factors for the dataset. To structure this article, there are four more sections. In Section 2, the fundamental formulation of the Bayesian model and the design of the Gibbs sampling technique, including the data sources, are discussed. In Section 3, the distributions for modeling daily Dengue cases are described, and the method's application to a specific example of daily Dengue cases data is examined. Finally, Sections 4 and Section 5 give a general discussion and conclusion, respectively. In order to develop and provide a better knowledge of the complicated relationship between climate and health, this study aims to assess the impact of climatic risk variables on dengue incidence in Bangladesh. Health

professionals who create efficient plans to enhance public health may find this material to be useful.

2 Methods and Materials

Data Sources

The weather variables of temperature (measured in ° C), humidity (measured in %), precipitation (measured in mm), and wind speed (measured in km/h) were collected from Bangladesh Meteorological Department. Data are available on the website www.timeanddate.com/weather/bangladesh/dhaka/ext. Daily dengue data were obtained from the Directorate General of Health Services (DGHS) of the Ministry of Health and Family Welfare [14].

Bayesian Poisson Regression

To represent discrete event counts that occur over predetermined intervals of time or space, the Poisson model can be employed. The Poisson model is especially useful when counts are right-skewed and cannot be reasonably approximated by a Normal model. Fitting a Bayesian Poisson regression model to the frequency of Dengue infected cases, say Y with density

$$Y_i | \lambda_i \sim \text{Poisson}(\lambda_i)$$

where, $Y_i = 0, 1, 2, \dots$ is the random variable and λ is the rate parameter, $\lambda > 0$. The mean and variance of the density are generally known to be equal to λ_i . As a result, the typical value of Y should approximately reflect its variability given the predictors X . The Poisson regression model is defined as ([7]):

$$E(Y = y/x) = \exp(\beta_0 + x_1\beta_1 + x_2\beta_2) \dots x_p\beta_p) \quad (1)$$

where y is the response variable, x 's are the independent variable, p is the number of independent variables and β 's are regression parameters.

Likelihood Distribution

Assume that λ_i can be expressed as a linear combination of X predictors, we can write

$$\text{data: } Y_i | \beta_0, \beta_1, \beta_2, \beta_3, \beta_4 \sim \text{Poisson}(\lambda_i) \quad \text{with} \quad \log(\lambda_i) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_4 X_4. \quad (2)$$

where β represents the regression coefficients and X_i 's are the covariates as X_i = precipitation, temperature, humidity, wind speed. The likelihood function $Pr(Y|X_i, \beta) = \text{Poisson}(\lambda_i)$. where, $Pr(\cdot|\cdot)$ denotes a conditional probability function. The five parameters $\beta_0, \beta_1, \beta_2, \beta_3, \beta_4$ is the intercept, precipitation, temperature, humidity and wind speed effect respectively.

Specifying the Priors Distribution

Assume the following prior distribution is applied to a parameter, where $\pi(\cdot)$ represents a prior distribution.

$$\pi(\beta_0) = \text{uniform}(0, 1) \quad \text{and} \quad \pi(\beta_1) \cdot \pi(\beta_2) \cdot \pi(\beta_3) \cdot \pi(\beta_4) = \text{normal}(0, \sigma^2)$$

To build the Bayesian model, we must express our prior knowledge of regression coefficients ($\beta_0, \beta_1, \beta_2, \beta_3, \beta_4$). Again, using Normal priors makes sense because each of these coefficients can take on any value along the real line. We'll also suppose that these priors—that is, our prior knowledge of the model coefficients—are independent. The complete Poisson regression model depiction of Y_i is as follows.

$$\begin{aligned} \text{prior: } \beta_0 &\sim U(0, 1) \\ \beta_1 &\sim N(0, \tau_1) \\ \beta_2 &\sim N(0, \tau_2) \\ \beta_3 &\sim N(0, \tau_3) \\ \beta_4 &\sim N(0, \tau_4) \end{aligned}$$

where $\tau_1, \tau_2, \tau_3, \tau_4 \sim \exp(0.1)$ are precision of priors (i.e. precision = $1/\text{variance}$). The posterior distribution of $\beta_0, \beta_1, \beta_2, \beta_3, \beta_4$ is determined by the likelihood function and prior distribution using the Bayes theorem. The likelihood and data-driven prior are multiplied to arrive at the posterior distribution. Consequently, we demonstrate the posterior distribution using the likelihood and prior distributions which are as follows:

$$P(\lambda/Y) = \exp\left[-\sum_{i=1}^n \log y_i! + n\bar{Y} \log \lambda - n\lambda\right] \times \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left[-\frac{x^2}{2\sigma^2}\right] \quad (3)$$

A prior is multiplied by a likelihood based on data to create the posterior distribution, which is then used as a prior in further modeling. Finally, these Bayesian probability distributions were employed for the data on Dengue cases in the Bayesian regression model.

Markov Chain Monte Carlo (MCMC) Method

The posterior inference result is increasingly difficult to assess and study the more variables we include in our model. The MCMC method is then utilized in this situation. The MCMC approach imitates the posterior in order to examine it. Inferences about the model and its parameters can then be made using the results. There are numerous MCMC approaches available. One of the most significant MCMC algorithms is the *Gibbs sampler*, which transformed Bayesian statistics and dramatically revived the Bayesian philosophy by offering solutions to real-world problems.

Gibbs Sampling

Using a combined probability distribution of two or more random variables, Gibbs sampling generates a series of samples as a form of probabilistic inference ([9]). In order to study the Gibbs distribution, the Gibbs sampler was first introduced in the context of image processing by [17]. The Gibbs sampler, on the other hand, didn't become well-known in the statistical community until [15] showed that it could deal with complex estimating concerns in a Bayesian fashion.

The observable data (Y) is the beginning condition for the Gibbs sampler. Gibbs sampling necessitates the usage of an unnamed vector of pertinent variables. Gibbs sampling seeks estimates for the parameters of interest (Y) to ascertain how well the observable data fits the model of interest and whether or not data independent of the observed data matches the model given by the observed data ([31]). The Gibbs sampler method does not compute the density before selecting random variables from a distribution. The Gibbs sampler needs very large sets (on the order of 15 or more sequences) for poorly preserved patterns to reach statistical significance ([31]). In order to avoid the considerably more challenging calculations, we can instead build a succession of simpler ones.

Basic Algorithm of Gibbs Sampling: Assuming a starting location $\beta^0 = (\beta_0^0, \beta_1^0, \beta_2^0, \dots, \beta_d^0)^T$, The multivariate Gibbs sampler uses an iterative technique, as seen below. The sampling process performs the following d steps at iteration $(k+1)$:

- (1). Sample β_0^{k+1} from $p(\beta_0|\beta_1^k, \beta_2^k, \dots, \beta_{d-1}^k, \beta_d^k, \mathbf{y})$;
- (2). Sample β_1^{k+1} from $p(\beta_1|\beta_0^{k+1}, \beta_2^k, \beta_3^k, \dots, \beta_d^k, \mathbf{y})$;
-
- (d). Sample β_d^{k+1} from $p(\beta_d|\beta_0^{k+1}, \beta_1^{k+1}, \dots, \beta_{d-2}^{k+1}, \beta_{d-1}^{k+1}, \mathbf{y})$.

The conditional distributions $p(\beta_j|\beta_0^k, \beta_1^k, \beta_2^k, \dots, \beta_{j-1}^k, \beta_{j+1}^k, \dots, \beta_{d-1}^k, \beta_d^k, \mathbf{y})$ are referred to as full conditional distributions, because β_j depends on all other parameters.

The open-source MCMC application WINBUGS makes it straightforward to implement the Gibbs sampling algorithm. It can handle models with both common and unusual parameters because it is flexible enough. It can therefore be used in a variety of contexts, such as with insurance claim data, and is easy adaptable to enable more distributions (see [24]).

3 Results

Exploratory Data Analysis

Table 1 and Figure 3 shows the daily mean rainfall, temperature, humidity, wind speed readings, and dengue incidence in Bangladesh, respectively. Dengue incidences in Bangladesh ranged from 0 to 1224 over a two-year period (1st January 2020 to 31st December 2021), with the peak incidence (1224 cases) occurring in December 2020. The daily mean precipitation ranged from 0 to 118 millimeters, with the maximum recorded measurement in April 2020. The daily mean temperature ranged from 15.10°C to 34.0 °C, with the maximum recorded temperature being in May 2020. The daily mean humidity ranged from 27% to 100%. The highest temperature ever recorded was in June 2021. The daily mean wind speed values ranged from 0.00 to 32.0 units. The fastest recorded speed occurred in May 2020. These findings indicate that all climatic parameters contribute to a conducive environment, increasing mosquito breeding and dengue transmission rates which is also supported by [30].

Table 1 Descriptive statistics of Number of Dengue-infected people, precipitation, temperature, humidity, and wind speed for January 01, 2022, to 31 December 2022.

Variables	Infected case	Precipitation	Temperature	Humidity	Wind speed
Mean (SD)	274.80 (287.51)	5.08 (12.26)	26.94(4.23)	73.67(15.06)	4.02 (4.32)
Skewnwss	1.69	4.11	-0.73	-0.64	2.10
25th Percentile	41.50	0.00	23.50	63.50	1.00
Median	232.0	0.00	28.40	76.50	2.50
75th Percentile	357.00	3.40	30.30	85.50	5.50
90th Percentile	607.00	16.00	31.30	91.00	8.50
99th Percentile	1209.00	59.10	32.65	97.35	19.50
Min	0.00	0.00	15.10	27.00	0.00
Max	1224.0	118.00	34.00	100.0	32.00

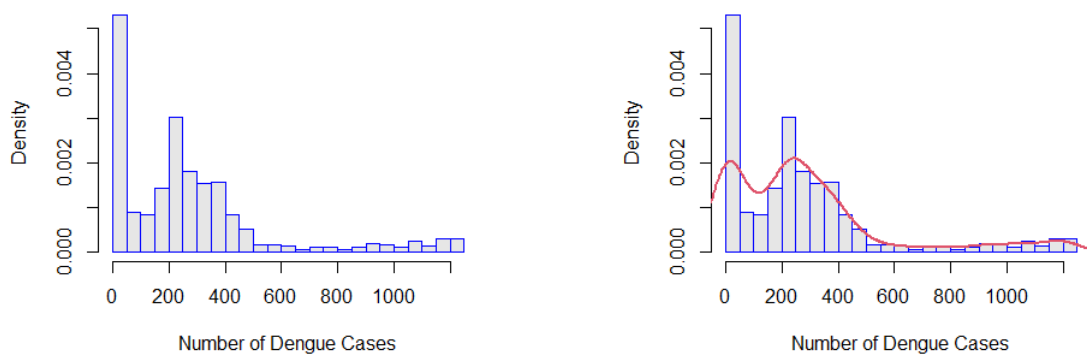


Fig. 1 (a).Histogram of Number of Infected Dengue Cases ; (b). Distribution of the number of Dengue Cases, during the period 1st January 2020– 31st December 2021.

A kernel density plot of the infected dengue cases brought on by dengue fever is shown on a histogram in Figure 1. It demonstrates that one of the most accurate probabilistic models for this variable is the bell-shaped distribution by showing that the number of confirmed Dengue cases appears to have a symmetric distributional form. It is hypothesized that a skewed distribution would be more accurate in forecasting the values of this variable based on a comparison of the distributional shape of the number of Dengue cases.

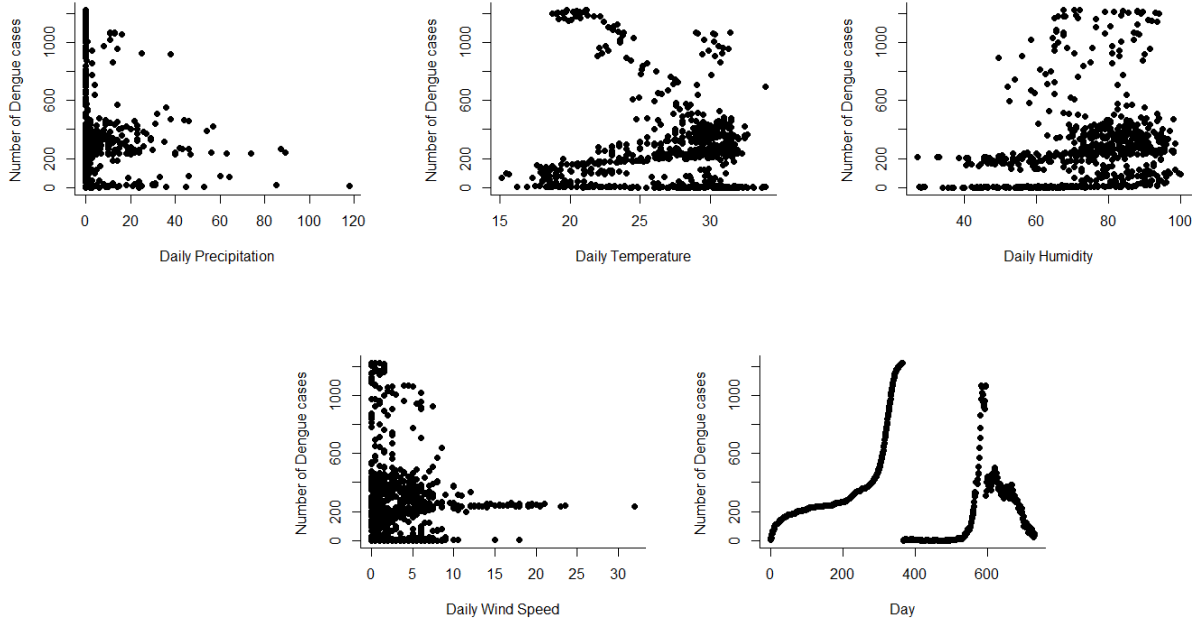


Fig. 2 Scatter diagram (a). The daily number of Dengue Cases vs. Daily Precipitation; (b). The daily number of Dengue Cases vs. Daily Precipitation; (c). The daily number of Dengue Cases vs. Daily Temperature; (d). The daily number of Dengue Cases vs. Daily Humidity; (e). The daily number of Dengue Cases vs. Daily Wind Speed during the period 1st January 2020– 31st December 2021.

3.1 Bayesian Poisson Regression Model

To carries our Bayesian inference on the statistical problems using MCMC methods, we used the most popular Bayesian software. Three *WinBUGS* tools are required to obtain posterior samples: (a) the specification tool, (b) the sample monitor tool, and (c) the update tool. Since our model had four initial values, we set the *number of chains* = 4 in order to get the appropriate posterior information. Furthermore, the MCMC iteration is specified as 30,000 in the update tool. In the sampling monitor tool, we specified *beg* from 10,000 and ended with 30,000 for updating the model. However the *thin* number was taken as 10 out there. We have got the summary statistics, trace, and density plot by clicking the option of these toolbars. The posterior summary measurements are displayed using the density and stat settings. Table 2 gives the sample, start iteration, posterior mean and SD, MC error, 2.5%, 50%, and 97.5% posterior quantiles. Hence the estimated model is

$$\log(\lambda_i) = 3.781 - 0.007 \times \text{precipitation}_{i-19} + 0.015 \times \text{temperature}_i + 0.021 \times \text{humidity}_i - 0.037 \times \text{wind speed}_i. \quad (4)$$

Table 2 Summary statistics of the posterior distribution.

Parameter	mean	SD	MC error	2.5%	median	97.5%	start	samples
β_0	3.781	0.02108	2.882×10^{-4}	3.74	3.781	3.822	10000	8000
β_1	-0.006777	2.135×10^{-4}	2.568×10^{-6}	-0.0072	-0.006774	-0.006356	10000	8000
β_2	0.01527	5.724×10^{-4}	6.822×10^{-6}	0.01415	0.01527	0.01639	10000	8000
β_3	0.02116	1.731×10^{-4}	2.20×10^{-6}	0.02082	0.02115	0.0215	10000	8000
β_4	-0.03779	6.406×10^{-4}	7.275×10^{-6}	-0.03906	-0.0378	-0.03654	10000	8000
τ_1	15.22	12.52	0.139	1.1	11.94	47.03	10000	8000
τ_2	14.84	12.06	0.1311	1.153	11.73	46.53	10000	8000
τ_3	15.2	12.49	0.1529	0.9981	11.94	47.49	10000	8000
τ_4	14.83	12.2	0.1445	1.077	11.72	47.95	10000	8000

3.1.1 Interpreting the Posterior

To simulate the Poisson posterior regression model, we employ MCMC trace graphs, density plots, and autocorrelation plots 4 and show that our simulation has stabilized. From 1 January 2020 to 31 December 2021, only nine posterior simulations of Dengue case data had ACF histograms with skew, range, and trend that match the observed data. Think about the precipitation coefficient β_{α_1} , which has a posterior median that is roughly -0.007. This suggests that we should expect roughly one time as much precipitation if it increases by one mm or 0.993% more, anti-discrimination laws: $e^{-0.007} = 0.993$ and the posterior median is around 0.015 for the temperature coefficient β_{α_2} . It implies that if the temperature rises by one unit, we might anticipate 1.02 times as many anti-discrimination measures, or 1.02 percent more: $e^{0.0152} = 1.0153$. The posterior median for the humidity coefficient β_{α_3} is around 0.02115. This means that if the humidity increases by one unit, we should expect it to have 1.02 times as many, or 1.02 percent, more, likewise for the posterior median of the wind speed coefficient β_{α_4} , which is -0.0378. This means that if the wind speed increases by one km/h, we should anticipate 0.96 times as many, or 0.96 percent, more.

3.1.2 Graphically Checking

Initially, the Markov chain distribution's trace and autocorrelation plots were used to visually assess convergence. 10,000 iterations of each of the four chains were investigated. For all parameters except β_{α_0} , the trace plots 3 show a horizontal strip indicating stationarity and well mixing of the chains which indicates slow mixing of the chains.

Initially, convergence was evaluated visually using the trace and autocorrelation plots of the Markov chain distribution. We looked at 10,000 iterations of each of the four chains. The trace plots given in 3 display a horizontal strip suggesting stationarity and well mixing of the chains for all parameters except β_{α_0} , which indicates slow mixing of the chains. Furthermore, the autocorrelation plot 4 indicates that the current position of the chains does not predict the future position of the chains, indicating that the posterior distribution for parameters is extensively investigated. According to the autocorrelation plots in the 4, there is a decreased correlation between lengthy lags, which indicates that the chains were poor mixed.

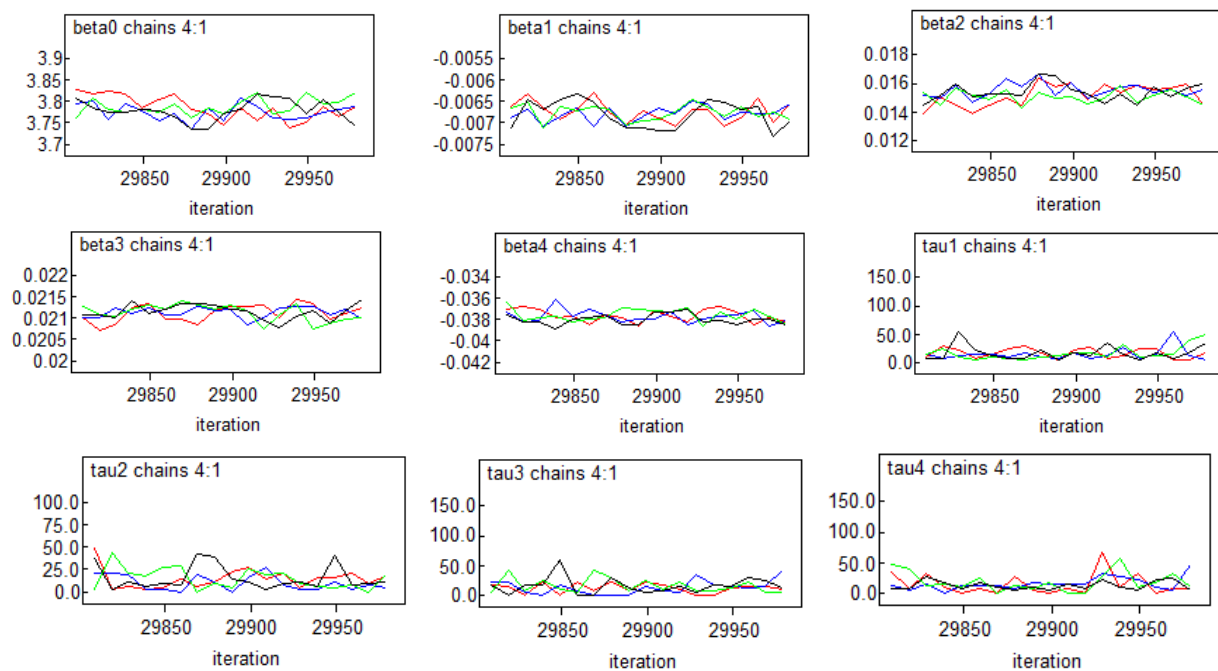


Fig. 3 Trace plots of parameters (β) and variance of random effects

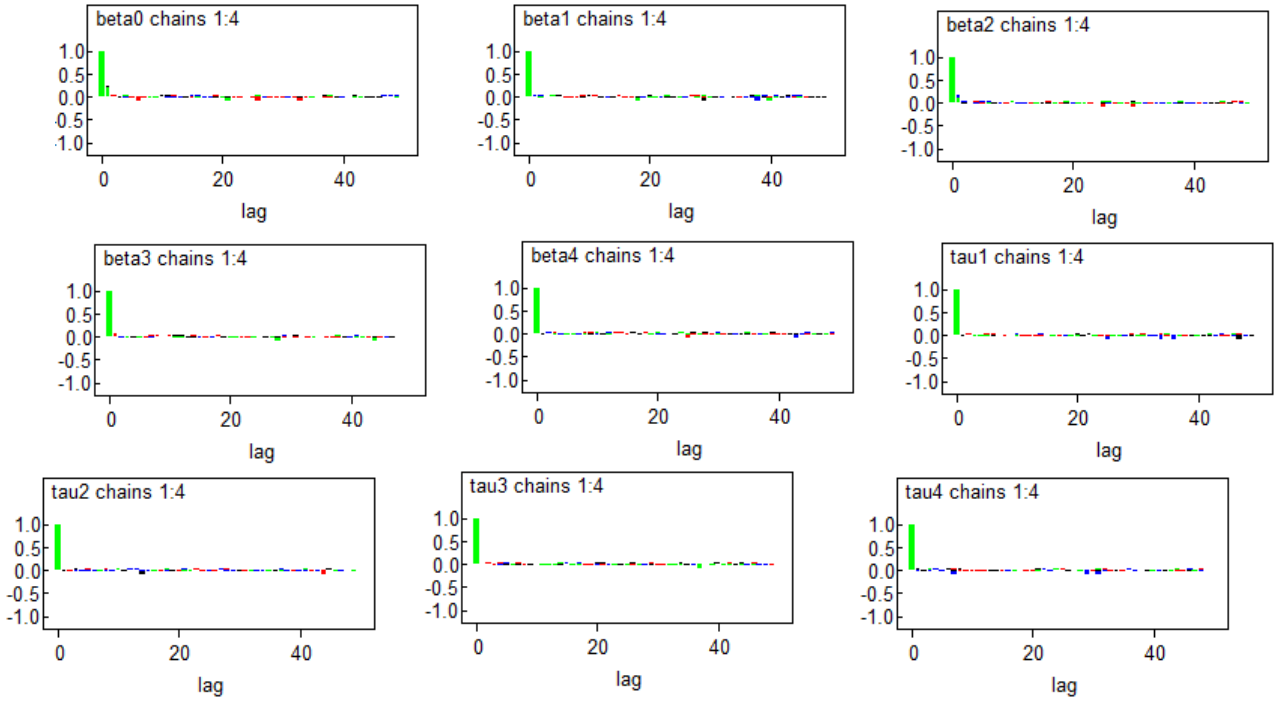


Fig. 4 Auto-correlation plots of parameters (β) and variance of random effects

Formal Diagnostic Test

Three diagnostic tests are performed in order to confirm the stationarity, accuracy, and convergence: the Brooks-Gelman-Rubin (BGR) diagnostic approach developed by Geweke, HeidelbergerWelch, and. Table 3 details the official diagnostic tests for the 4 model with random intercept and slope.

Table 3 Formal diagnostic tests for a bayesian regression model with random intercept and slope

parameter	Geweke	Heidelberger-Welch	BGR	effective sample size
Intercept (β_0)	0.285	0.850	1.000	3353.017
Precipitation (β_1)	0.827	0.387	1.000	3000.000
Temperature (β_2)	0.113	0.230	1.000	3816.157
Humidity (β_3)	-0.928	0.775	1.000	3000.000
Wind Speed (β_4)	0.348	0.060	1.000	3000.000
Deviance (σ^2)	1.425	0.567	1.000	3000.000

With default settings of 10% (first part of a chain) and 50% (second part of a chain), the Geweke diagnostic test demonstrated stationarity for all parameters with the exception of the estimated variance of the random intercepts, presuming that all Z-values for the parameters are constrained between -1.96 and 1.96. Heidelberger-diagnostic Welch's also showed that every parameter passed the convergence test, leading to the conclusion that the length of the chain is sufficient to ensure the accuracy of the posterior means of the parameters. Figure 3 shows the Brooks-Gelman-Rubin (BGR) diagnostic, which is the sole convergence diagnostic test based on the four chains.

Poor chain mixing was discovered to be the cause of the huge sample size disparity between the effective sample size and the MCMC simulation sample size (totaling 30,000). Additionally, it was found that β_{22} had a large discrepancy, which suggested considerable autocorrelation. Significant results suggest non-randomness when evaluating the correlation between a variable's most recent and previous values using autocorrelation.

For model evaluation purposes, different measures to check the model's fit are shown in table 4. It is clear that the model has a larger posterior predictive value (PD), a discrepancy metric that indicates

complexity. In Table 4 \bar{D} is the posterior mean of $-2\log L$ and $\hat{D} = -2\log L$ at a posterior mean of stochastic parameters.

Table 4 Measure of fit for the Poisson regression model

Y	\bar{D}	\hat{D}	P_D	DIC
Cases	186650.0	186645.0	5.123	186656.0
Total	186650.0	186645.0	5.123	186656.0

In figure 5, The model's intercept, slope, and precision density plots are shown. The distribution of posterior information appears to be normally distributed.

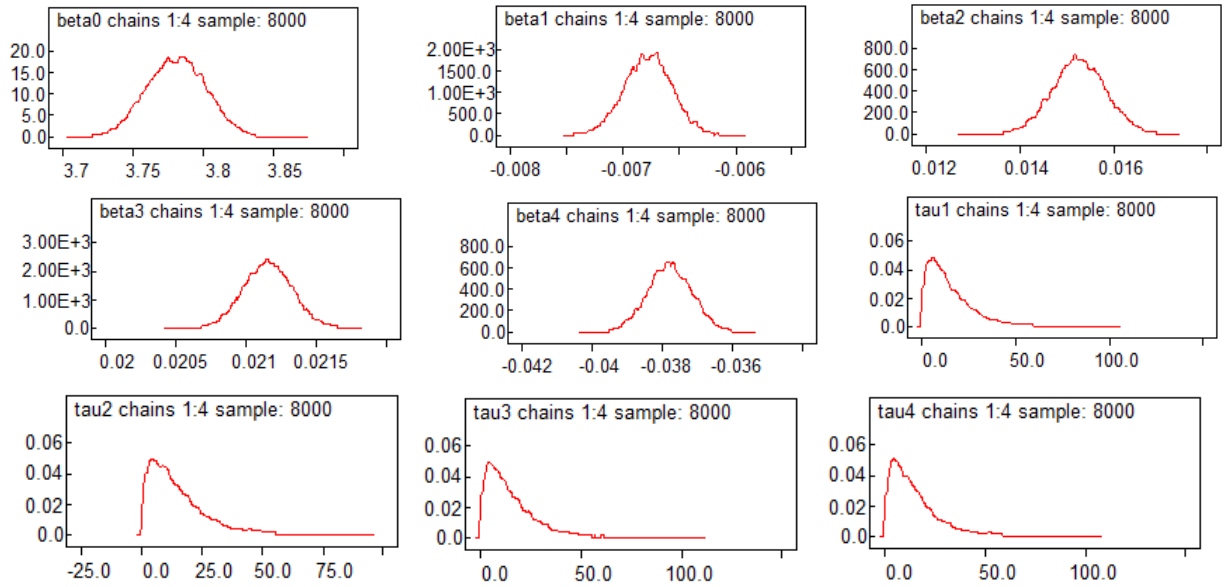


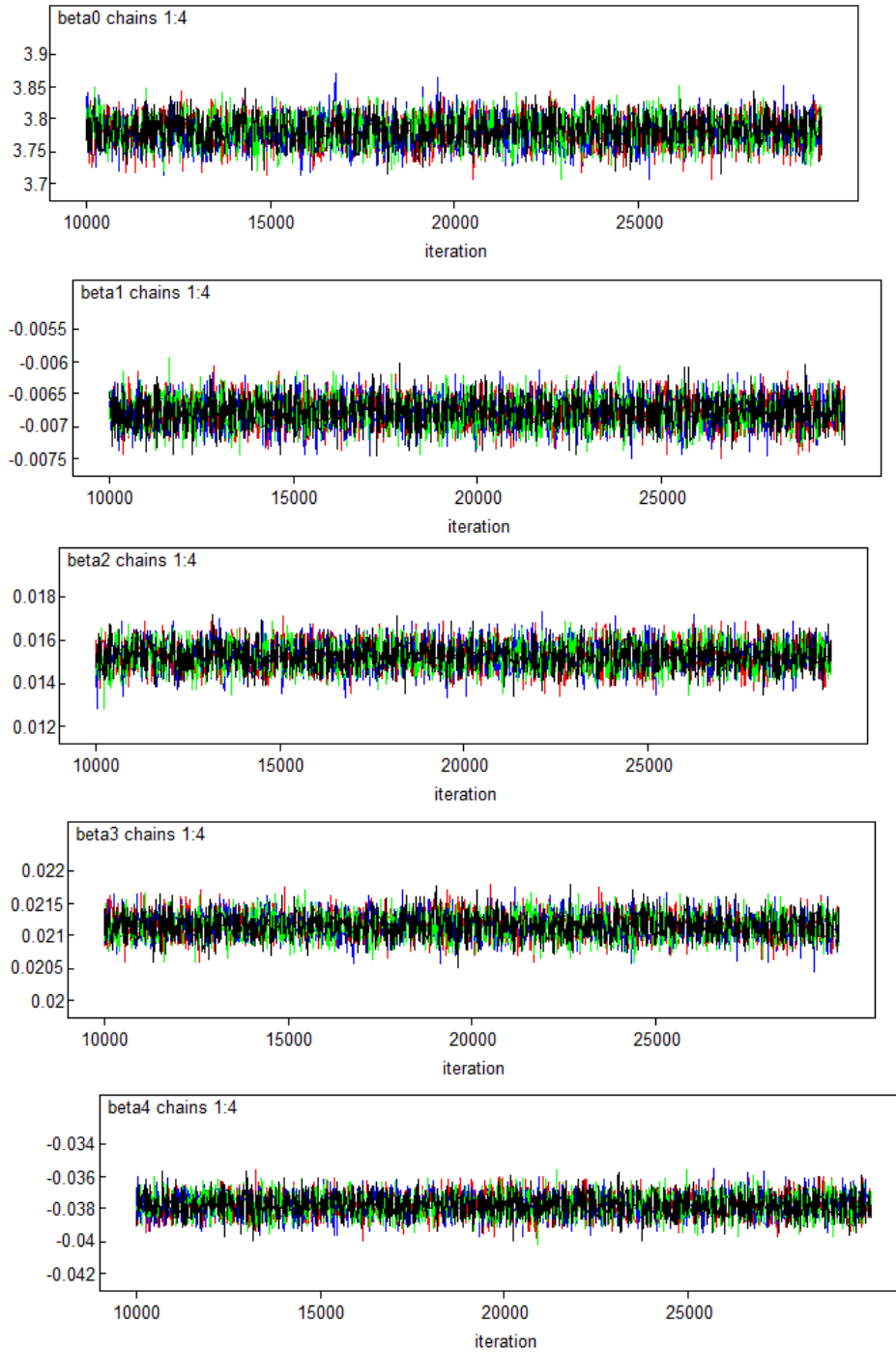
Fig. 5 Density plots for posterior distribution of parameters (β 's) and precision

In the history plot in figure 6, the well-mixed initials values have very small differences which indicates that the initial values of coefficients $\beta_0, \beta_1, \beta_2, \beta_3, \beta_4$ got convergence.

4 Discussion

Dengue is a major hazard to public health and a significant economic burden in Bangladesh. An increasing body of evidence indicates that dengue imposes a massive socioeconomic cost on households, healthcare systems, and government health expenditures in endemic nations, particularly during outbreaks. An increasing number of initiatives are being made to relate relatively local-area factors like rainfall, humidity, and temperature to dengue incidence in order to increase public health relevance.

Since Dengue fever is a growing public health concern in Bangladesh, its identification of alterations in the climatic factor pattern will enhance case-finding from an environmental standpoint. Consequently, the purpose of this study was to provide insight into the altering climatic manifestation of dengue infections in Bangladesh. In this study, we examined the effect of meteorological risk factors on the severity of dengue transmission using the dengue confirm cases. However, we must employ Bayesian methods such as Markov Chain Monte Carlo (MCMC) in order to use the informative prior ([16]). For Bayesian regression modeling, we built the Poisson regression model using the Normal distribution as the prior. The aim of Bayesian Regression is not to find the single "best" value of the model parameters but rather to determine the posterior distribution for the model parameters. Not only is the response generated



from a probability distribution but the model parameters are assumed to come from a distribution as well. In this respect, an attractive class of sampling algorithm, called MCMC method is explored to solve the practical problem in a Bayesian manner. This study demonstrated that the Gibbs sampling, a highly computationally efficient MCMC method [29], can generate accurate estimates of Bayesian regression coefficients for Dengue counts. In order to assess how well the observable data fits the model of interest and whether or not data independent of the observed data fit the model given by the observed data, Gibbs sampling is used to find estimates for the parameters of interest ([31]).

We proved the Bayesian discrete Poisson model's applicability to data on medical domain counts. We examined data on the total number of afflicted cases caused by Dengue fever in order to generate statistical proof of the impact of climatic conditions on Dengue transmission. In the instances given, we concentrated on a daily count of all 731 Dengue causes from January 1, 2020, to December 31, 2021, which is discrete and has a right-skewed distribution, making the full conditional distribution of interest.

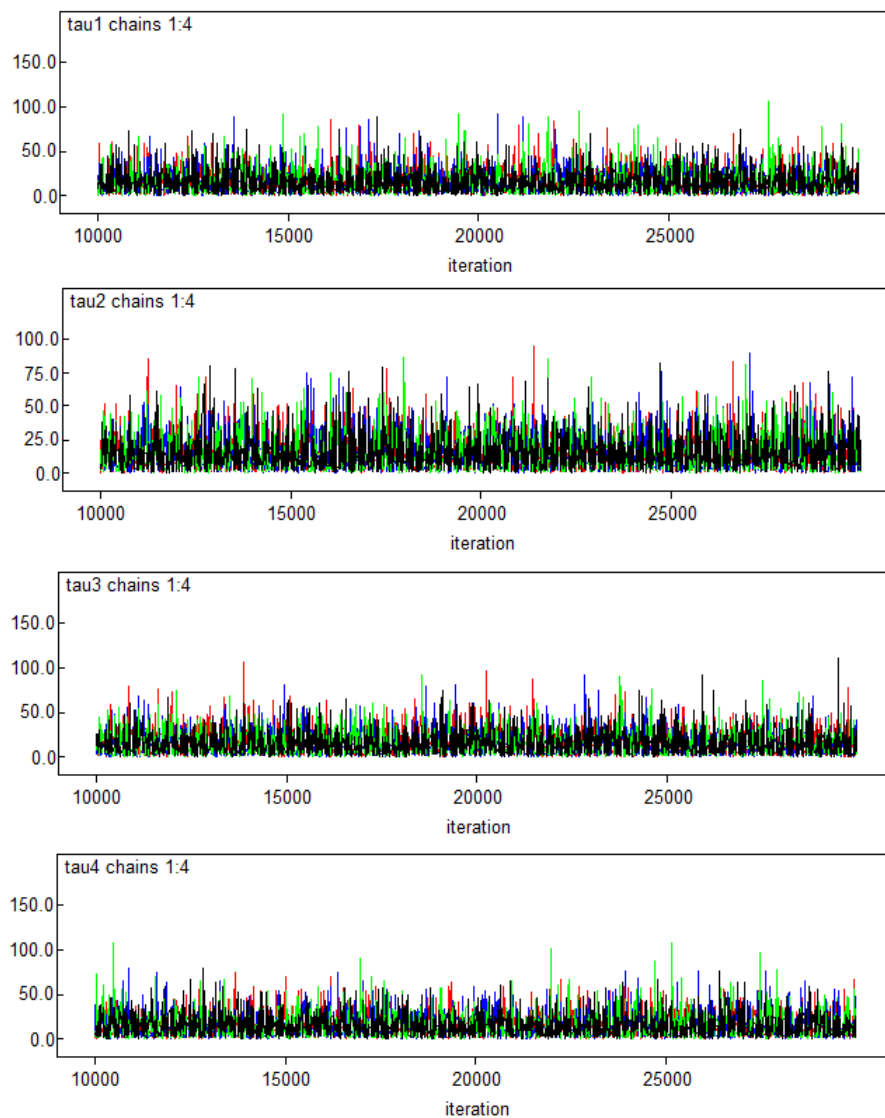


Fig. 6 History plots of parameters (β 's) Obtained from WinBUGS after 30,000 iterations

The important posterior knowledge of the parameters is obtained by assuming the previous information. Furthermore, Figure 5 shows that the posterior distribution for the parameters is well examined and that they appear to be regularly distributed. The model, which exhibits the presence of autocorrelation, likewise revealed a higher discrepancy. Additionally, we used a variety of diagnostic tests to evaluate the inference technique on actual data, demonstrating both the results' stationary nature and their convergence. In this regard, the diagnostic outcomes are also demonstrated, demonstrating the precision of the posterior parameters. The model also exhibits higher posterior density (HPD) with poor mixing convergence beginning values. Low precipitation increases the propagation of dengue, according to empirical research. Dengue has been demonstrated to spread less frequently in high temperatures, which reduces the virus's ability to survive and spread. Instead, freezing conditions give coronaviruses a secure haven that hastens their survival and spread. It may be concluded that the climate has a substantial impact on the risk factors for virus transmission in Bangladesh. We came to the conclusion that the Bayesian technique performed well and is easier to understand than traditional regression approaches in the literature on the basis of a variety of information criteria and the selection of influential elements.

Moreover, it is critical to investigate and describe these additional potential variables since they may have a significant influence on the frequency with which certain infectious diseases manifest and the long-term health and well-being of the general populace. Additionally, more study is needed to determine the genetic variations of dengue that are most prevalent as well as the effects of climate change on the biology of the vectors that spread these infectious diseases.

5 Conclusions

To sum up, we have given an overview of the Bayesian regression models used in count data analysis. Despite the fact that the majority of recent studies have concentrated on a correlation approach between meteorological parameters and pandemic data. Unfortunately, there haven't been any direct tests with dengue outbreaks in different environmental contexts. Our research revealed striking similarities in the effects of precipitation, temperature, humidity, and wind speed on the seasonal viability and severity of dengue fever. This study used a number of statistical techniques, and the model revealed a substantial causal link between climatic variables and the spread of dengue.

As it is throughout the world, dengue fever, an emerging disease, will continue to pose a serious threat to public health in Bangladesh. So, developing preventative and control measures is urgently needed in Bangladesh. Communities must take part in community-based initiatives to get rid of mosquito breeding sites. Every healthcare facility needs to have the necessary equipment, including diagnostic lab capabilities, to make an early diagnosis of dengue illness. In order to reduce fatality rates, professionals in Bangladesh must receive training in the management of severe dengue disease. To stop the spread of an outbreak, institutions, non-governmental groups, policymakers, and government officials must launch short-term national measures. Important mosquito breeding places should be eliminated and pesticides sprayed. Water logging should be addressed, and canals, water tanks, rainwater collection tanks, down-pipes, and gutters should be cleaned. In remote regions, the distribution of dengue detection kits to health centers and the training of health facilitators would be advantageous. Because personal apparel serves as a preventive strategy, schoolchildren should be given specific attention through the enhancement of school uniforms. The media might help by broadcasting information on dengue stages, the use of bed nets and insect repellents, and the wearing of light-colored, loose-fitting, long-sleeved, and breathable clothing [27]. Furthermore, a dengue virus vaccine could be introduced in the country, as it has been demonstrated to lower severity and hospital admissions by 80-90% in Asian youngsters [8].

We urge the creation of a nationwide dengue control program for clinical management of the virus, in addition to the already-existing national recommendations from the Directorate General of Health Services in Bangladesh, together with a broad community awareness campaign for better responses. Although the Bangladeshi government has launched various short-term initiatives, mostly in Dhaka, nationwide comprehensive action initiatives have fallen short. To stop preventable deaths and lessen the epidemic's disease burden, the government, and relevant stakeholders should give priority to this dengue outbreak and implement a comprehensive dengue control program. To entirely eradicate the *Aedes* mosquito, numerous community-based awareness programs need to be launched and maintained. To address the catastrophic health burden caused by dengue infections, a number of social protection programs, including "Shasthyo Surokhsha Karmasuchi (SSK)" may be implemented in metropolitan cities for poor and vulnerable households.

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