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THE GAMMA-POISSON CONJUGATE HIERARCHICAL MODEL ON THE MORTALITY RATE OF DENGUE FEVER CASES IN INDONESIA

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Abstract: Infectious dengue can be lethal if not treated immediately and effectively. To comprehend the illness and treat it, a thorough epidemiological investigation is required to ascertain the distribution pattern of dengue mortality utilizing hierarchical models. A hierarchical model is a data-driven model that depicts the relationship between groups of distributions that are thought of as samples of the original population distribution and their variations from the projected population distribution. Data on dengue fever infections and deaths were gathered for this study from the Indonesian Health Profile in 2021. The researchers utilized a hierarchical conjugate Gamma-Poisson distribution model to investigate Indonesia's dengue deaths. This distribution offers a more suitable statistical framework for analyzing variation in mortality data, which is occasionally poorly distributed. The number of cases and fatalities is among the data used, ranging for the provinces in Indonesia. The outcomes demonstrated that this distribution could describe a more precise picture of the pattern of dengue fever fatalities. The results can be applied to bolster preventative initiatives in each province with the most significant death rates and to enhance planning for health programs. In addition, applying the conjugate Gamma-Poisson distribution in the study of dengue mortality may

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provide a more substantial basis for future research in this area, which may contribute to better disease control and decreased dengue mortality in Indonesia.

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2020 AMS Subject Classification: 65C20, 62F15, 62C12.

1. INTRODUCTION

Dengue Fever is a disease that has a high morbidity and mortality rate internationally in tropical and subtropical climates. Dengue fever is transmitted through the bite of Aedes aegypti and Aedes albopictus mosquitoes that harbor the dengue virus. Global warming and environmental changes are responsible for the high incidence of dengue fever. Data from the World Health Organization (WHO) of the United Nations shows that Asia ranks first in the Integrated Rural Development Foundation (IRDF) annually, where Indonesia has the most significant dengue caseload, with an estimated 10 million cases and 3,000 deaths annually [1-2]. The study in Yogyakarta, Indonesia, found endemic dengue fever, whose peak occurs seasonally between November and May [3]. The high level of contamination in Yogyakarta is indicated by the use of these varieties of dengue fever cases hospitalized and the excessive seroprevalence of dengue virus antidote (DENV) antibodies (68%) in young children aged 1-10 years in the world [4].

The mortality rate caused by dengue fever can be analyzed using statistical methods, one of which is the Bayesian hierarchical method. Bayesian hierarchies are used to generate a joint posterior distribution of model parameters. This parameter estimator distribution is obtained by combining data models, process models, and priors [5]. Several other researchers have proposed hierarchical methods such as to infer analysis for the study of isolated cardiomyocytes [2], the use of Poisson hierarchy to detect variation in the number of rows of coverage data [3], some researchers are also using Bayesian hierarchical methods with conjugate conditional distributions [6], spatial Bayesian survival models in dengue fever cases, these are more suitable than non-spatial models [7]. The principle of applying the Bayesian Method using Markov Chain Monte Carlo (MCMC) is to evaluate segmented scan data for waste packages containing gamma-ray emitting radioactive waste [8-11]. The Poisson-Gamma model has been used for daily rainfall data without inflation, with the results of the parameters in the model helping to reduce data

overdispersion that usually occurs in the model [12]. Furthermore, in the spatial Bayesian model, there is a substantive relationship between dengue patients' age, class, and survival time. This dengue Bayesian model is still challenging to give a better description of the health care model.

There have been many Gamma-Poisson models used in several cases both in the fields of health and medical biology or other physical models. Still, there has yet to be research using the Gamma-Poisson hierarchical conjugate model for dengue fever cases. This study will discuss the death rate of dengue fever cases in several provinces in Indonesia. The model is developed by the Bayesian approach as the Gamma-Poisson hierarchical conjugate model on the mortality rate of dengue fever cases in provinces of Indonesia.

2. MATERIAL AND METHODS

The data used is on dengue fever cases based on provinces in Indonesia that had cases of death in 2021; as much as 29 data were taken through the Indonesian Ministry of Health website from https://www.kemkes.go.id. Dengue fever case data will be modeled into the Gamma-Poisson hierarchical conjugate to describe the mortality rate of dengue fever cases in provinces of Indonesia.

The Gamma-Poisson conjugate hierarchical model is developed as the theoretical approach using gamma distribution and Poisson distribution with definitions stated as their mass functions. The Poisson distribution starts by setting up the expected value of the event in an interval of parameter λ. In that case, the probability of the event occurring k times (k is a non-negative integer, $k = 0, 1, 2, ...$), then the Poisson distribution probability mass function is defined as follows:

$$f(k \mid \lambda) = \frac{e^{-\lambda}\,\lambda^{k}}{k!}, \tag{1}$$

with e is the natural logarithm base $e \approx 2.71828$, k is the number of occurrences of an event with a given probability, and λ is the expected value [13].

A random variable is said to be a gamma distribution with parameters α and β, which is the inverse parameter denoted by $X \sim \Gamma(\alpha,\beta)$ if it has a probability density function, namely:

$$f(x \mid \alpha, \beta) = \frac{e^{-\beta x}\,\beta^{\alpha}}{\Gamma(\alpha)}\, x^{\alpha-1} \text{ for } x > 0 \text{ and } \alpha, \beta > 0, \tag{2}$$

where $\Gamma(\alpha)$ is a gamma function with $\Gamma(\alpha) = (\alpha\text{-}1)!$ [14].

The Gamma-Poisson hierarchical model is developed by assuming the number of successes of an event x_i follows a Poisson distribution with parameter λ_i denoted by $X_i \sim Poisson(\lambda_i)$ with $\lambda_i = \theta_i \times t_i$ for $i = 1, 2, \ldots, k$, and the parameter θ_i is the success rate in the i event, and t_i is time to i as explained in [15] with conditional probability and expectation as follows:

$$P(x(i) \mid \lambda_i) = \frac{e^{-\lambda_i} \lambda_i^{x_i}}{x_i!} = \frac{e^{-\theta_i t_i} (\theta_i t_i)^{x_i}}{x_i!}, \tag{3}$$

$$E(X(i)) = Var(X(i)) = \lambda_i = \theta_i. \tag{4}$$

The likelihood function of θ_i is:

$$L(\theta_i) = \prod_{i=1}^{k} \frac{e^{-\theta_i t_i} (\theta_i t_i)^{x_i}}{x_i!} \propto \prod_{i=1}^{k} e^{-\theta_i t_i} (\theta_i t_i)^{x_i} \propto e^{-k\theta_i t_i} (\theta_i t_i)^{\sum_{i=1}^{k} x_i}. \tag{5}$$

Since t_i and k are constant, where k events occur in the interval t_i, then θ_i is assumed to be mutable. In the first stage of the hierarchical model, the gamma distribution is chosen as the conjugate prior distribution for the following parameters:

$$\theta_i \sim gamma(\alpha, \beta), \tag{6}$$

when α and β are a hyper-parameter, so that we have the following probability density:

$$\begin{aligned} f(\theta_i \mid \alpha, \beta) &= \frac{e^{-\theta_i} \beta^{\alpha}}{\Gamma(\alpha)} \theta_i^{\alpha-1} \text{ for } \alpha, \beta > 0, \text{ and } 0 < \theta_i < \infty \\ &\propto e^{-\theta_i \beta} \theta_i^{\alpha-1}. \end{aligned} \tag{7}$$

The distribution of $\alpha \sim exponential(\gamma)$ is:

$$\begin{aligned} f(\alpha \mid \gamma) &= \gamma e^{-\lambda\alpha}, \text{ for } \gamma > 0 \\ &\propto e^{-\lambda\alpha}. \end{aligned} \tag{8}$$

The distribution of $\beta \sim gamma(c, d)$ is:

$$\begin{aligned} f(\beta \mid c, d) &= \frac{e^{-\beta d} d^{c}}{\Gamma(c)} \beta^{c-1}, \text{ for } c, d > 0 \\ &\propto e^{-\beta d} \beta^{c-1}. \end{aligned} \tag{8}$$

The joint distribution of (θ, α, β) is:

$$f(\theta, \alpha, \beta \mid x) = \prod_{i=1}^{k} (\theta_i t_i)^{x_i} \times e^{-\theta_i \beta} \theta_i^{\alpha-1} \times e^{-\gamma\alpha} \times e^{-\beta d} \beta^{c-1}. \tag{9}$$

The Posterior distribution of θ_i is:

$$f(\theta_i \mid \alpha, \beta, x) \propto \prod_{i=1}^{k} \theta_i^{x_i} e^{-\theta_i \beta} \times e^{-\theta_i \beta} \theta_i^{\alpha-1} \tag{10}$$
$$\propto \theta_i^{\sum_{i=1}^{k} x_i} e^{-k\theta_i t_i} e^{-\theta_i \beta} \theta^{\alpha-1} = \theta_i^{\sum_{i=1}^{k} x_i + \alpha - 1} e^{-\theta(k t_i + \beta)}.$$

This equation is proportionally with a gamma distribution with parameters $(\sum x_i + \alpha, k t_i + \beta)$.

Posterior distribution of β is:

$$f(\beta \mid \gamma, c, d, \theta) \propto \prod_{i=1}^{k} e^{-\theta_i \beta} \beta^{c-1} e^{-\beta d} = e^{-\beta(\sum_{i=1}^{k} \theta_i + d)} \beta^{c-1}. \tag{11}$$

This equation is a gamma distribution with parameters $(c, \sum_i \theta_i + d)$.

The posterior distribution of α is:

$$f(\alpha \mid \gamma, c, d, \theta) \propto \prod_{i=1}^{k} \theta^{\alpha-1} e^{-\gamma\alpha}. \tag{12}$$

Assume the distribution of α and β as $\alpha \sim exponential(1.0)$ and $\beta \sim gamma(0.1, 0.1)$ respectively. Furthermore, by using Gibbs sampling through a Markov Chain Monte Carlo (MCMC) iteration process, parameter estimation can be obtained using a Bayesian approach.

The steps taken in modeling the Gamma-Poisson hierarchical conjugate model on the mortality rate of dengue fever can be described as follows:

a) Plotting the graph of dengue fever cases for each province in Indonesia as the first insight.
b) For each parameter, determine the linear random effects model.
c) Find the conjugate Gamma-Poisson distribution's likelihood function and associated prior distribution.
d) The conjugate Gamma-Poisson distribution's posterior should be known.
e) Determine the marginal posterior distribution of the conjugate Gamma-Poisson distribution.
f) Identifying the prior distribution and posterior distribution of the obtained conjugate Gamma Poisson distribution against the data.
g) Evaluating the outcomes produced by data on Indonesia's dengue disease cases on its parameter interpretation.

3. RESULT AND DISCUSSION

The Gamma-Poisson conjugate approaches in this research, which has given a strong foundation for data analysis related to the Poisson distribution, it will be discussed in this part as analysis data on mortality caused by dengue fever in Indonesia.

(A) (B)

Figure 1. (A) Number of Cases Dengue Fever, **(B)** Death Cases of Dengue Fever.

Figure 1. (A) depicts the number of dengue fever cases in Indonesia, with West Java province having the highest number of cases and Maluku province having the lowest number of cases. In contrast, **Figure 1. (B)** depicts the number of dengue fever deaths in Indonesia, with West Java province having the highest death rate and Bengkulu province having the lowest rate. Based on the data distribution, it is not appropriate to say that West Java province has the most significant fatalities because the data also provide the number of cases in each province with various proportions of death cases. Analysis of the data for better interpretation is therefore required. In this analysis, it is necessary to determine the model; if the stationary or equilibrium requirements apply and whether the target distribution is the previous distribution of the computed parameters, then the model is well-built [16]. Besides this model, the case data for dengue fever are frequently discontinuous and sparse, consistent with a Poisson distribution. However, in actual circumstances, the frequency of occurrences may change over time or between different places. For these cases, we can address this fluctuation by using a gamma distribution as a prior for the incidence rate in the conjugate Gamma-Poisson model.

3.1 Trace Plot of Gamma-Poisson Hierarchical Model

Trace plots are used to evaluate the progress of parameter estimates in the model for dengue disease using the conjugate Gamma-Poisson approach. A trace plot is a Bayesian statistical

analysis graph showing how parameter values change across MCMC process iterations. It aids in the verification of convergence and the identification of difficulties in statistical analysis [17].

Figure 2. Trace Plot for each parameter of Dengue Fever.

Figure 2 shows a long-term pattern of stability. This signifies that the posterior distribution of specific parameters has converged to the target distribution, which means that all parameter values are in an area with no periodic pattern, indicating that the sample meets the strongly ergodic character of MCMC.

3.2 Kernel Density of Gamma-Poisson Hierarchical Model

Kernel density is one of the statistical analysis methods used to depict data distribution more smoothly and continuously. The conjugate Gamma-Poisson model can display the posterior distribution of the model's parameters in the context of dengue disease [17].

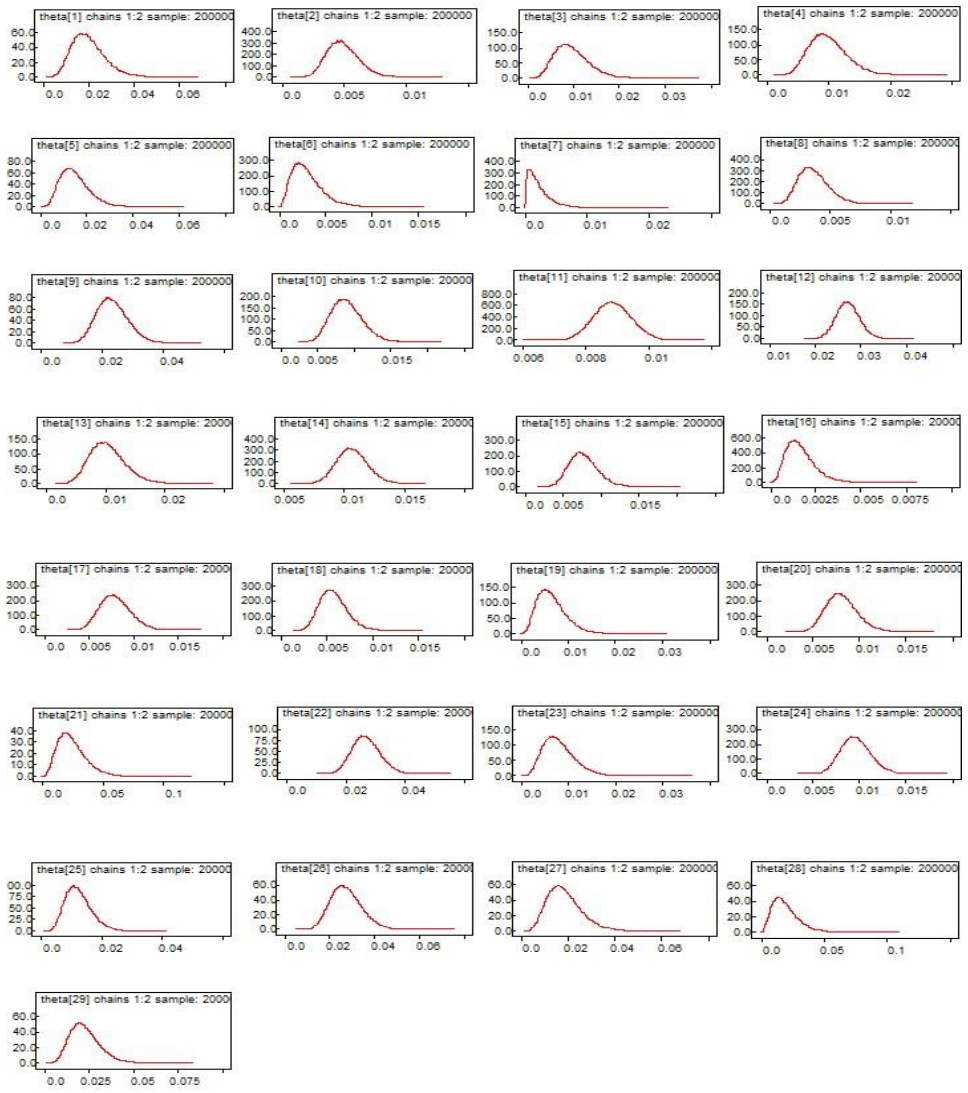

Figure 3. Density Plot for Each Parameter of Dengue Fever.

Based on **Figure 3**, it can be concluded that the parameter estimation process of dengue case kernel density plots follows a standard curve, showing that the overall distribution of dengue data is comparable to the normal distribution. A dengue data distribution that follows a standard curve will exhibit symmetry around its apex. The dengue incidence or prevalence rate tends to cluster symmetrically around its center or mean value.

3.3 Quantiles Plots of Gamma-Poisson Hierarchical Model

A statistical model's generated sample distribution can be seen visually via a quantile plot. This graph aids in evaluating how closely the sample distribution resembles the predicted

distribution. The model's ability to fit the data and validate distributional assumptions can be done using quantile plots.

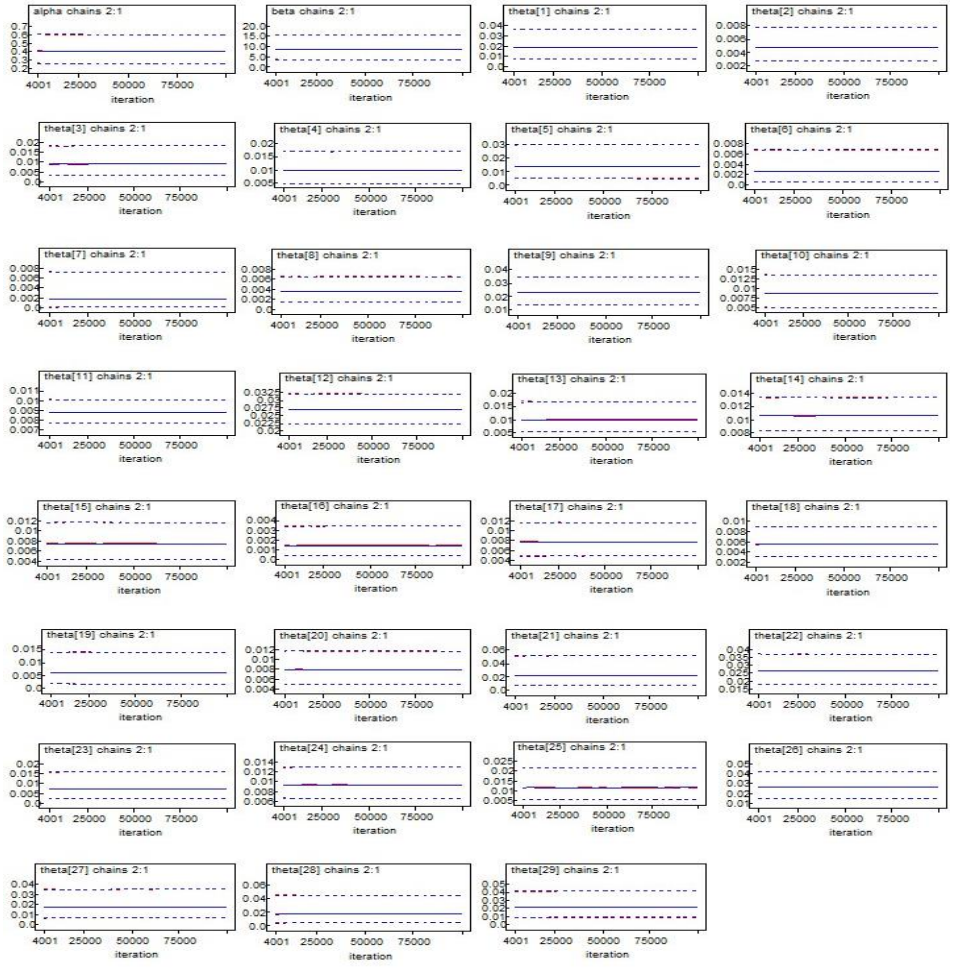

Figure 4. Quantiles Plot for Each Parameter of Dengue Fever.

Figure 4 shows that all of the points on the quantiles plot are along or near the horizontal straight line, indicating that the distribution of data or samples is very close to the expected distribution or that the data or samples are consistent with the expected distribution assumptions. The ergodic mean value for each parameter has stabilized, and all sample values are within a reasonable interval, indicating that the sample collected satisfies the MCMC characteristics.

3.4 Autocorrelation function of Gamma-Poisson Hierarchical Model

A statistical analysis called the autocorrelation function (ACF) examines time series or observed data correlation patterns. The degree of sample correlation can be understood using ACF

plots, which can also shed light on the stability and effectiveness of the MCMC method used for data processing.

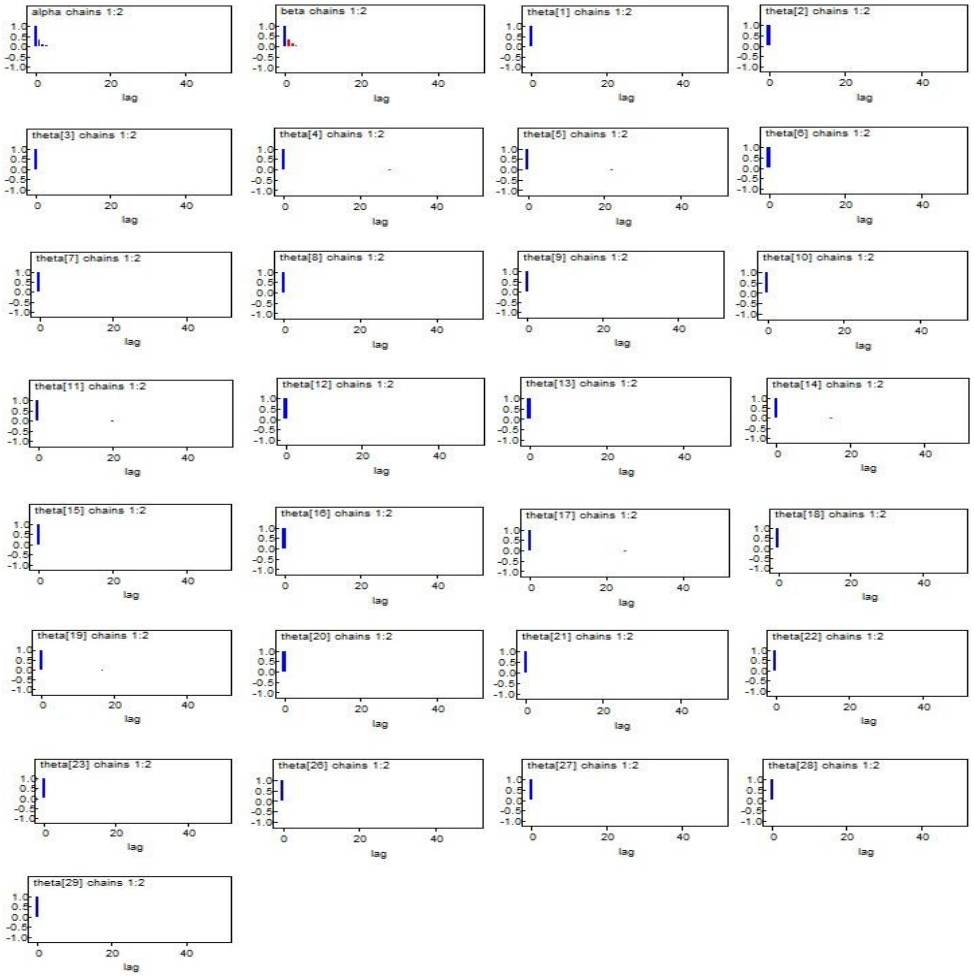

Figure 5. Autocorrelation Plot for Each Parameter of Dengue Fever.

Based on **Figure 5**, it can be seen that the autocorrelation value of the sample data for each MCMC parameter is close to zero. The convergence pattern runs fast so that the sample has fulfilled the strongly ergodic properties.

Parameter samples in the Markov Chain are taken after the equilibrium condition is reached so that the samples obtained are guaranteed to be samples from the target distribution, namely the prior distribution of the parameters. The equilibrium condition is reached if the sample obtained has fulfilled the nature of the Markov Chain, which is strongly ergodic. All parameters have fulfilled the strongly ergodic condition, so the equilibrium condition is achieved, and the model is good to use.

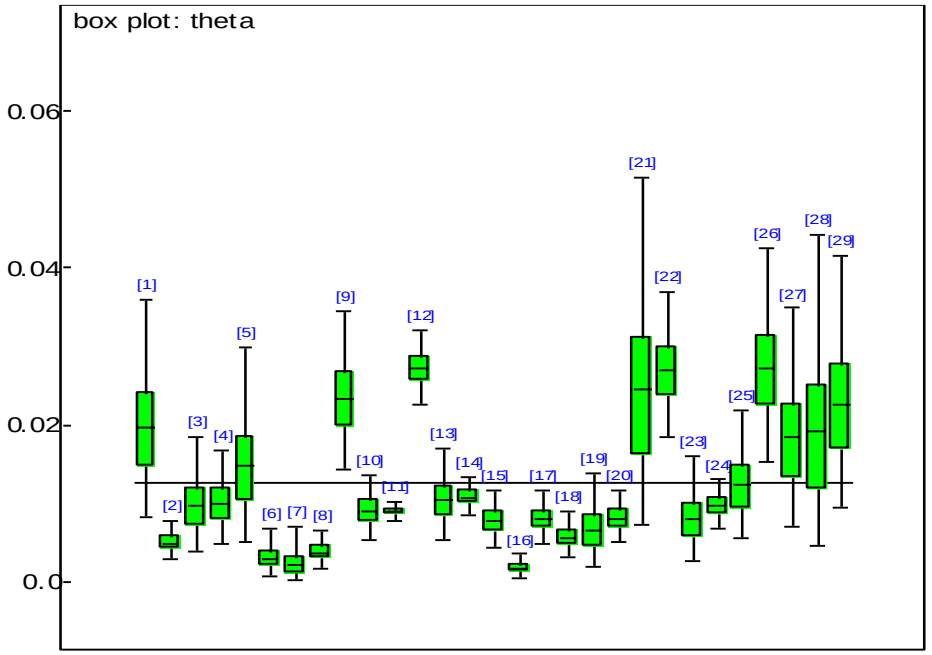

Figure 6. Box Plot Mortality Rate of Dengue Fever Cases.

The hierarchical conjugate Gamma-Poisson model has better performed to describe the mortality rate of dengue fever cases in provinces of Indonesia. However, it is necessary to discuss the implication of the model and the spread of dengue fever and its causes. Dengue fever is transmitted by mosquitoes that are distributed in some tropical areas in endemic countries. Mosquitoes can survive at low temperatures (10°C), but their metabolism decreases or stops when they drop below the critical temperature of 45°C. At temperatures higher than 35°C, there are also changes in the sense of slower physiological processes. The optimal average temperature for mosquito growth is 25°C-30°C. Air temperature affects virus development within the mosquito body, biting speed, resting and mating behavior, dispersal, and duration of the gonotropic cycle [18-19].

Figure 6 shows that the highest mortality rate of dengue fever cases occurred in Gorontalo province, with 557 cases and 15 deaths. Meanwhile, the lowest mortality rate occurred in Bali Province, with 2673 dengue cases and four deaths. Dengue is a tropical infection caused by an arboviru which spread widely throughout Indonesia.

Sporadic emergence of dengue cases has also occurred in Kalimantan due to forest and land burning, resulting in increased temperature and humidity that affect the dynamics of large mosquito populations in the surrounding environment. Likewise, in Java, due to increasing

population density resulting in ecological transformation, humans and their populations are highly vulnerable to dengue virus infection transmission [20]. Optimal air temperature can increase reproduction, while low humidity can reduce the effectiveness of mosquito life. Variations in humidity, rainfall, and temperature also play an important role and affect mosquito populations.

Dengue fever frequently involves an immunological response to dengue virus infection in which the human immune system responds and fights the virus, which can result in severe symptoms. Prevention and therapy in vaccine development; awareness of drugs that can be used to treat dengue symptoms [21]. Understanding dengue fever requires understanding the dengue virus life cycle, which reproduces in humans and vector mosquitoes. This involves the virus's multiplication in human cells and the transmission mechanism back to the mosquito when the insect bites an infected person. Also, disease vectors such as Aedes aegypti and Aedes albopictus are mosquitoes that act as vectors (carriers) of dengue viruses due to their behavior, habitat, and life cycle, as well as how they transmit dengue viruses from one individual to another. Many factors influence the occurrence of Dengue Fever deaths in each region, which may cause different death cases in each province, such as the availability of medicines, proper treatment given, and many more factors that cause dengue fever deaths.

Case data for dengue fever is frequently discontinuous and sparse, consistent with a Poisson distribution. However, in actual circumstances, the frequency of occurrences may change over time or between different places. The conjugate Gamma-Poisson model handles these fluctuations by employing the gamma distribution as a prior for the incidence rate. The conjugate Gamma-Poisson model helps describe how often this condition occurs. Due to its ability to precisely predict critical variables, such as case incidence rates, this model offers a solid foundation for decision-making in dengue control and prevention.

4. CONCLUSION

A key metric for assessing the severity of the disease's effects on the population at risk is the fatality rate in dengue cases. Planning public health measures, enhancing medical care, and developing a deeper understanding of the risk factors that might affect death rates are all made possible by thorough research and monitoring of mortality rates. The model for the case fatality of

dengue fever was created using a compound Poisson process, in which the number of dengue fever cases has a gamma distribution, and the patient case fatality rate has a Poisson distribution. In Gorontalo Province, there were 557 cases of dengue fever and 15 fatalities, the highest case fatality rate. Bali Province had 2673 Dengue infections, four fatalities, and the lowest mortality rate. This demonstrates that dengue fatality rates are not always highest in dengue-endemic regions. A more accurate model to explain dengue data than a single Poisson distribution is one of the significant ramifications of research on Gamma-Poisson conjugates of dengue data in epidemiological data analysis and statistical model creation. Epidemiologists and health researchers may better understand the incidence of dengue fatality rates by region due to this. Health officials can make better judgments based on solid empirical facts by using the conjugate Gamma-Poisson approach to manage dengue fever cases. However, it's crucial to constantly include the most recent data in the analysis and consider the local context when making decisions.

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CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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