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Modeling the Risk of Dengue Fever Spread in Deli Serdang Regency Using the Cauchy Cluster Process Model

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ABSTRACT

Dengue fever is an infectious disease that is still a public health problem in Indonesia. The number of dengue fever cases continues to increase. One of the districts in North Sumatra with the highest dengue fever cases is Deli Serdang Regency. With the sub-district contributing the highest Dbd cases is Percut Sei Tuan with a case percentage of 16% in 2022. This study aims to determine risk modeling by involving several covariates where the comparison criteria are using the smallest BIC value. The homogeneity test results show that the dengue fever case data tends to be inhomogeneous. The spatial correlation results show that the plot results tend to form groups or clusters. The modeling results obtained by the Cauchy cluster process after elimination is the best model, where the covariates of hospital density, rainfall, temperature, and humidity have a significant effect on the spread of dengue fever in Deli Serdang Regency.

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1. INTRODUCTION

One of the infectious diseases that is still a public health problem in Indonesia is Dengue Fever (DHF). DHF is a public health problem that can cause death in a short time and often causes Extraordinary Events (KLB), causing panic in the community [1]. Dengue fever is still a health problem in both urban and semi-urban areas. The incidence of DHF in Indonesia tends to increase every year [2]. The Ministry of Health noted that in 2022, the cumulative number of dengue cases in Indonesia reached 87,501 cases. While deaths due to DHF reached 816 cases. In general, the increase in Dengue cases occurred mostly in the age group of 14-44 years as much as 38.96% and 5-14 years as much as 35.61%. This number increased compared to data throughout 2021, where a total of 73,518 cases were reported positive for DHF, but this number decreased by 32.12% when compared to 2020, where there were 108,303 cases of DHF [3].

Meanwhile, in North Sumatra Province, according to data from the North Sumatra Provincial Health Office, the cumulative number of dengue hemorrhagic fever (DHF) patients in this area reached 5,270 cases, with 24 of them died. This number has increased compared to data throughout 2021, which amounted to 2,992 cases, with 14 people dying. [4]. According to BPS data for North Sumatra Province, Deli Serdang Regency was the area that contributed the most cases of Dengue Fever in 2020, namely 1,326 cases [5]. Meanwhile, in 2022 dengue fever cases in Deli Serdang Regency were also the highest in North Sumatra Province, totaling 1211 cases, with 1 person dying. [6].

2. RESEARCH METHODE

2.1 Spatial Point Process

According to Baddeley Spatial Point Process is a random pattern of points in d-dimensional space that is useful as a statistical model of the observed point pattern, where the points represent the location of several research objects [7]. Spatial point process is an unordered set of points, so the order in which the data is recorded is ignored in the method. Spatial point process X is a set of random parts derived from a certain boundary. $W \subseteq \mathbb{R}^2$. The realized form of Spatial point process is a spatial point pattern x={x_1,.....x_n} of n ≥ 0 points located in an observation window W. Where x_i is the location of the research object represented by cartesian coordinate points u= (longitude, latitude), with $u \in W, W \subseteq \mathbb{R}^2$.

According to spatial correlation, there are 3 basic patterns in point patterns. The three patterns are shown in Figure 1.

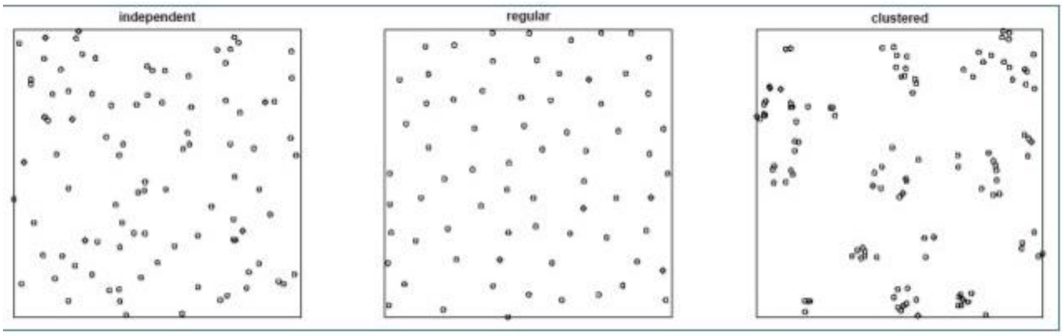

Figure 1. Basic Point Patterns Independent (left), regular (center), and group (right). All three patterns are in square units

2.2 Cauchy Cluster Process

Cauchy Cluster Process is one type of spatial point process in spatial statistics that is used to model the pattern of points that form clusters or groups in an area. The Cauchy Cluster Process assumes that the points in the cluster are generated from the Cauchy distribution, while the points outside the cluster are generated from the Poisson distribution [8].

In the Cauchy cluster process, the probability density of the offspring is the Cauchy distribution. The k-density function is shown in the following equation.

$$k(u;\omega) = \frac{1}{2\pi\omega^2}\left[1 + \frac{||u||^2}{\omega^2}\right]^{\frac{3}{2}} \tag{1}$$

where ω is the scale parameter. The spatial extent of a cluster is proportional to ω. The Cauchy density is very heavy-tailed, so the derivative can be very far from the parent [9].

The pair correlation function and K-function of the Cauchy cluster process are shown in equations 2 and 3 respectively.

$$\mathrm{g}(\mathrm{r};\varphi) = 1 + \frac{1}{8\pi\mathrm{k}\omega^2}\left[1 + \frac{||\mathrm{r}||^2}{4\omega^2}\right]^{\frac{3}{2}} \tag{2}$$

$$\mathrm{k}(\mathrm{r};\varphi) = \pi\mathrm{r}^2 + \frac{1}{\mathrm{k}}\left[1 - \frac{1}{\sqrt{1 + \frac{\mathrm{r}^2}{4\omega^2}}}\right] \tag{3}$$

2.3 Homogenitas Test with Chi-squared

Chi-squared is a statistical test used to determine whether there is a significant relationship between two categorical variables, which measures the difference between the observed and expected frequencies of the variable and then calculates a value based on this difference [10] .

The Chi-square test is conducted to test whether the observation data used in the study has a homogeneous pattern or not [11]. The goal is to ensure that the groups being compared have the same characteristics or properties so that the results of the analysis can be considered valid [12]. Before testing the homogeneity of the data, the observation window is divided into quadrat counts where $n_1,n_2,....,n_n$ is the number of points in each section box [13]. Homogeneity testing uses the Chi-Squared test with the following test hypothesis.

$H_\circ$: $\rho(u)=\rho(v);u,v \in W$ (i.e. the population variances between groups are equal, or in other words, the groups are homogeneous).

H_1: $\rho(u)\neq\rho(v);u,v \in W$ (i.e., the variances of the populations between groups are not equal, or in other words, the groups being compared are not homogeneous).

The test statistic used is shown in Equation 4.

$$X^2{}_{hit} = \sum_{j=1}^{m} \frac{(n_j - e_j)^2}{e_j} = \sum_{j=1}^{m} \frac{(\frac{n_j - n}{m})^2}{\frac{n}{m}} \tag{4}$$

with,
n_j: number of points in the jth quadrat count.
e_j: expected number of points in the jth quadrat count.
m: number of square sections/quadrature boxes
Test result Reject $H_\circ$ if $X^2{}_{hit} > X^2_{(\alpha,df)}$ with $df = m - 1$ or $\rho - value < \alpha$ [14]

2.4 Population Density

Population density can be one of the factors causing the spread of dengue fever in the community. Population density is an indicator of population pressure in an area [15] . The density in an area compared to the land area occupied is expressed by the number of inhabitants per square kilometer [16] .

Population density can be calculated using the formula in equation 12 as follows.

$$KP = \frac{P}{A} \tag{5}$$

where

KP	: Population Density
P	: Total Population
A	: Area (Km^2)

2.5 Parameter Estimation

In this study, parameter estimation was carried out to estimate the value of the β parameter and also the cluster model parameters (ω and κ).

a. Maximum Composite Likelihood 1st Order

This method is used as an estimation of the parameter β in the first order. In the Inhomogeneous Poisson model with intensity ρ(u;β) there is a parameter denoted by β. The ¬log-likelihood function is used to estimate β [17]. This is shown in equation 6.

$$\log L(\boldsymbol{\beta}) = \sum_{i=1}^{n} \log \rho(\boldsymbol{\beta}; \boldsymbol{u}_i) - \int_W \rho(\boldsymbol{\beta}; \boldsymbol{u}_i) d\boldsymbol{u} \tag{6}$$

Based on equation 5, it is known that the log-likelihood function of the inhomogeneous Poisson process involves the integral of the observation window W. Therefore, the estimation of parameters with the likelihood function cannot be calculated precisely, so numerical calculations are needed [18] . The numerical quadrature method was developed for the inhomogeneous Poisson Point Process so that its likelihood function is close to the likelihood function of the Generalized Linear Poisson Model [19]. Using the numerical quadrature approach, the $\int_w \rho(u;\beta)\,du$ can be approximated by $\sum_{i=1}^{n+q} \rho(u;\beta)w$, where w is the quadrature weight and ρ is the number of dummy points so that equation 6 can be written as equation 7.

$$\log L(\boldsymbol{\beta}) = \sum_{\boldsymbol{i=1}}^{\boldsymbol{n+q}} (I, \log \rho(\boldsymbol{\beta}; \boldsymbol{u}_{\mathrm{i}}) - \rho(\boldsymbol{u}_{\mathrm{i}}; \boldsymbol{\beta}) w_{\mathrm{i}}) \tag{7}$$

The value of I_i is 1 if w is a data point, while for w which is a dummy point, I_i is 0. Equation 6 can also be written as in equation 7 [20]

$$\log L(\boldsymbol{\beta}) = \sum_{i=1}^{n+q} (y, \log \rho(\boldsymbol{\beta}; \boldsymbol{u}_{\mathrm{i}}) - \rho(\boldsymbol{u}_{\mathrm{i}}; \boldsymbol{\beta})) w_{\mathrm{i}} \tag{8}$$

Where $y_i = \frac{I}{W}$, equation 8 is equivalent to the Weighted Poisson likelihood function weighted by w_i. The estimate of β can be found using Maximum Likelihood Estimation (MLE) [21]

b. Maximum Composite Likelihood 2nd Order

Maximum Composite Likelihood Order 2 is one of the methods for estimating the parameters of the clustered point process model $\boldsymbol{\theta} = (\kappa; \boldsymbol{\omega})^{\boldsymbol{T}}$ [22]. In equation 8, the 2nd Order Composite Likelihood function built from all data points $u_i u_j$ is written.

$$\log CL(\boldsymbol{\theta}) = \sum_{i} \sum_{j \neq i} w\,(\boldsymbol{u}_{\mathrm{i}}, \boldsymbol{u}_{\mathrm{j}}) \left[\log \rho^{(2)}\,(\boldsymbol{u}_{\mathrm{i}} \boldsymbol{u}_{\mathrm{j}}; \boldsymbol{\theta}) \right. \\ \left. - \log \int_W \int_W w(\boldsymbol{u}_{\mathrm{i}}, \boldsymbol{u}_{\mathrm{j}}) \rho^{(\mathbf{2})}(\boldsymbol{u}_{\mathrm{i}}, \boldsymbol{u}_{\mathrm{j}}; \boldsymbol{\theta}) d\boldsymbol{u} d\boldsymbol{u} \right] \tag{9}$$

The value of W in equation 8 is a weighting function, to facilitate the calculation, the value of W is the weighting function. $w(\boldsymbol{u}_{\mathrm{i}} \boldsymbol{u}_{\mathrm{j}}) = \{\| \boldsymbol{u}_{\mathrm{i}} - \boldsymbol{u}_{\mathrm{j}} \| \le R\}$ with R>0 is the upper limit of the correlation of the model. The composite score function which is the first derivative of the likelihood function on θ, can be written as in equation 9 [23].

$$\frac{\vartheta}{\vartheta \boldsymbol{\theta}} \log CL(\boldsymbol{\theta}) = \sum_{i} \sum_{j \neq i} w\,(u_{\mathrm{i}}, u_{\mathrm{j}}) \frac{\kappa_2(u_{\mathrm{i}}, u_{\mathrm{j}}; \boldsymbol{\theta})}{\rho^{(\mathbf{2})}(\boldsymbol{u}_{\mathrm{i}} \boldsymbol{u}_{\mathrm{j}}; \boldsymbol{\theta})} - \sum_{i} \sum_{j \neq i} w\,(u_{\mathrm{i}}, u_{\mathrm{j}}) \frac{\kappa_2, w)}{\rho^{(\mathbf{2})}, \boldsymbol{w})} \tag{10}$$

Where $\mathrm{K}^2(\mathrm{u_i u_j}; \theta) = \frac{\vartheta}{(\vartheta\theta)\rho^{(2)}(\mathrm{u_i u_j}; \theta)}$

and $(\mathrm{I}, \mathrm{w}) = \int_{\mathrm{w}} \int_{\mathrm{w}} \mathrm{w}(\mathrm{u_i}, \mathrm{u_j})\, \mathrm{I}(\mathrm{u_i}, \mathrm{u_j}; \theta) \mathrm{du_i du_j}$ [24].

2.6 Eksponensial

The expression exp(koef) represents an exponential function where "exp" is the exponential function and "koef" is the coefficient (usually a numerical value) that is the exponent. In a broader context, this expression is often related to mathematical or statistical models, especially in exponential regression or exponential growth modeling [25] .

In general, an exponential function is defined as follows.

$$\exp(koef) = e^x \tag{11}$$

Where e is the Euler number, and x is the exponent.

2.7 Z-value

Z-value usually refers to z-score or z-value, which is a standardized measure that expresses how far an individual value is from the mean value in a sample or population in standard deviation units. This concept is related to statistics and the normal distribution [26].

In general, the z-value (z-score) can be calculated using the following formula:

$$Z = \frac{(X - \mu)}{\sigma} \tag{12}$$

Where:

Z = Z-value or z-score,
X = Individual Score
μ = The mean value of the population or sample,
σ = Standard deviation of the population or sample.

3. RESULT AND ANALYSIS

3.1 Data Description

The data used in this study are data on confirmed cases of dengue fever in 2022, patient addresses and hospitals or clinics in Deli Serdang Regency taken from the Deli Serdang District Health Office, as well as data on population density, temperature, rainfall, humidity data taken from the Central Bureau of Statistics.

The following is a percentage of the number of dengue fever cases in each sub-district in Deli Serdang Regency.

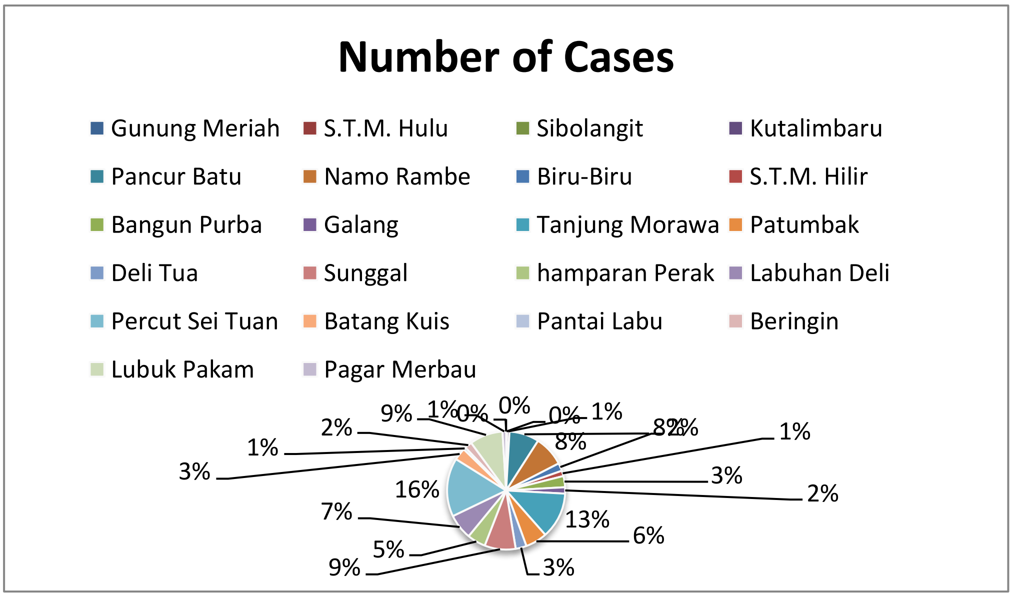

Figure 2. Percentage of Dengue Fever Cases in Each Deli Region Serdang

It can be seen from Figure 2 above that Percut Sei Tuan Sub-district is the largest contributor of confirmed dengue fever cases in Deli Serdang Regency with a percentage of the number of cases of 16%. Next, we will show a plot of the spread of dengue fever in each sub-district in Deli Serdang Regency.

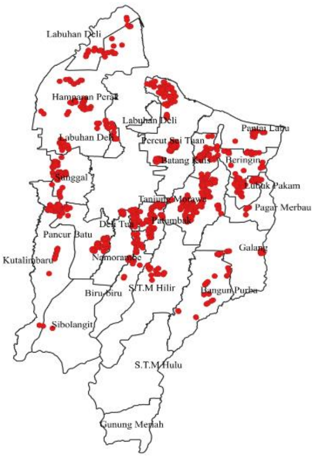

Figure 3. Map Plot of the Distribution of Dengue Fever cases in Deli Serdang District

It can be seen that dengue fever cases in Deli Serdang Regency tend to spread and form a group (Cluster).

3.2 Homogeneity Test

After knowing the characteristics of the data, the next step is to conduct a homogeneity test using the Chi-squared test. It aims to determine whether the data on dengue fever cases in Deli Serdang Regency follow a homogeneous or inhomogeneous pattern using the formula in equation 4 with data on cases of dengue fever patients in Deli Serdang Regency, the statistical value is obtained as in table 1 below.

Table 1. Chi-squared Test of Dengue Fever Case Data

Chi-Squared **Test**	
X^2hit	14,11084394
df	19
$X^2 tabel$	30,143527

The results of the test obtained are x^2hit 14.11084394 < x^2 table 30.143527 with a significance level of 0.05%. Then the decision can be obtained to reject Ho. This shows that the data on dengue fever cases in Deli Serdang Regency tends to be inhomogeneous with a 95% confidence interval, which means that there are other factors that cause a very large difference in the number of dengue fever cases between one sub-district and another. This is clarified in Figure 4 where it is shown that the spread of dengue fever tends to be not equally large.

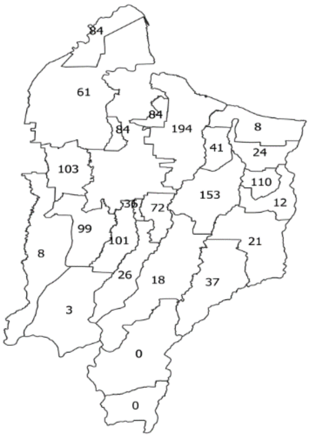

Figure 4. Map of the Number of Dengue Fever Cases in Each Subdistrict

3.3 Modeling the Risk of Dengue Fever Case Spread in Deli Serdang Regency Using the Inhomogeneous Cauchy Cluster Process Model

1.Parameter Estimation of Cauchy Cluster Model

Modeling the risk of dengue fever spread using the inhomogeneous Cauchy cluser process is shown in Table 2 below.

Table 2. Parameter Estimation of Inhomogeneous Cauchy Cluster Process Model

Parameter	**Estimasi**	**Exp(koef)**	**Z-Value**
$\hat{\kappa}$	6,597510		
ω	2,781340		
β_0	6,695112	808,44447	14,15662
β_1 (Rumah Sakit)	3,58961	36,21994	8,114595
β_2 (Curah Hujan)	7,63551	2.070,42669	17,21163
β_3 (Suhu)	4,53612	93,32798	20,145183
β_4 (Kelembapan)	5,39628	220,584314	10,54721
β_5 (Kepadatan Penduduk)	7,63402	2.067,34406	0,51589

In the table above, it can be seen that the population density variable has no significant effect. Therefore, an elimination process is carried out to obtain significant estimation results as in Table 3 below.

Table 3. Parameter Estimation of Inhomogeneous Cauchy Cluster Process Model After Elimination

Parameter	**Estimasi**	**Exp(koef)**	**Z-Value**
$\hat{\kappa}$	6,59362		
ω	2,78114		
β_0	6,695112	814,219511	14,26593
β_1 (Rumah Sakit)	3,59072	36,26017	8,126123
β_2 (Curah Hujan)	7,64381	2.087,68275	17,37742
β_3 (Suhu)	4,54821	94,463167	20,476141
β_4 (Kelembapan)	5,41372	224,46504	10,81127

Based on Table 3, modeling dengue fever cases in Deli Serdang Regency with a significance level of 5% shows that all variables have a significant effect on the risk of spreading dengue fever in Deli Serdang Regency with a confidence level of 95%. Thus, modeling the risk of dengue fever spread in Deli Serdang Regency can be modeled as follows.

$$(u) = 6{,}59362 \times \exp\left(6{,}695112 + 3{,}59072\,(u) + 7{,}64381\,(u) + 4{,}54821\,(u) + 5{,}41372(u)\right)$$

The Exp(koef) value is the magnitude of the risk of spreading dengue fever cases in Deli Serdang Regency. Where every increase in temperature, rainfall, and humidity of 1 object, the risk of spreading dengue fever cases increases respectively 2087.6, 94.4 and 224.46 times when compared to no additional objects.

3.4 Model Fitness Evaluation

After obtaining the modeling of the Cauchy Cluster Process model, the next step is to evaluate the goodness of the model using the BIC value. Keep in mind that the smaller the BIC value, the better the model. Table 4 will show a comparison of BIC values before and after elimination.

Table 4. BIC Value of Inhomogeneous Cauchy Cluster Process Modeling

Model	**BIC**
Model *Cauchy Cluster Process*	13,5877181851746
Model *Cauchy Cluster Process* After Elimination	10.168881213641392

From Table 4.7 it can be seen that the BIC value of the Cauchy Cluster Process Model after is smaller, compared to the BIC value of the Cauchy Cluster Process Model before elimination. This means that the model after elimination is better than before elimination.

4. CONCLUSION

a. Based on data on the number of dengue fever cases in 2022, Percut Sei Tuan Subdistrict became the highest contributor to dengue fever cases in Deli Serdang Regency when compared to other Subdistricts. The results of homogeneity testing using the chi-squared test showed that the data on dengue fever cases in Deli Serdang Regency followed a homogeneous pattern. In addition, the results of spatial correlation with the spatial point process and also the distribution plot show that the data tends to form groups (clusters).

b. The results of modeling with the inhomogeneous Cauchy Cluster Process model obtained that the best model is the inhomogeneous Cauchy Cluster Process model after elimination. This is because the inhomogeneous Cauchy Cluster Process after elimination has the smallest BIC value to model the risk of spreading dengue fever in the Deli Serdang Regency. The estimates and equations obtained from the inhomogeneous Cauchy Cluster Process model are as follows.

$$(u) = 6{,}59362\times \exp\,(6{,}695112 + 3{,}59072\ (u) + 7{,}64381\ (u) + 4{,}54821\ (u) + 5{,}41372\ (u)$$

c. The model equation above shows that the variables that have a significant effect on the risk of spreading dengue fever cases are the variables of hospital/clinic density, rainfall, temperature, and humidity.

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