Spatial Regression Analysis on Factors Influencing Number of HIV/AIDS Cases in Indonesia

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ABSTRACT

HIV/AIDS cases from one region are thought to be influenced by the surrounding areas. Analysis of factors influencing HIV/AIDS cases can be done through classical Linear Regression. However, Spatial Regression analysis is a more appropriate method to use if it takes location into account. The purpose of this study was to conduct a spatial regression analysis on HIV/AIDS cases in Indonesia in 2021. Spatial dependency testing and selection of spatial regression models were carried out using Moran's I and Lagrange Multiplier (LM) tests. The Moran's index value obtained $0 < 0.52545401 \leq 1$ showed that there was a relationship between HIV/AIDS cases between provinces in Indonesia. The SAR regression model obtained using the Queen Contiguity spatial weighting matrix was $\hat{Y}_i = 0.037991 \sum_{j=1, i \neq j}^{34} W_{ij} Y_{ij} - 329.62 - 0.031408 X_2 + 15.898 X_3 + 2.5701 X_4 + 26.71 X_5$ with R^2 of 93.39%. In this model, the factors that influence the number of HIV/AIDS cases in Indonesia are the number of fertile couples using condoms (X_2), the number of hospitals (X_3), the number of HIV-positive pregnant women (X_4), and the number of drug users (X_5). The number of hospitals give positive influence in perspective that Hospitals are places where HIV/AIDS cases are recorded, so the more hospitals there are, the more cases can be recorded.

Keywords: HIV/AIDS, Moran Index, Lagrange Multiplier, Spatial Autoregressive Regression (SAR).

INTRODUCTION

The literature surrounding spatial autoregressive modeling in the context of HIV epidemiology has evolved significantly, reflecting an increasing recognition of the importance of spatial analysis in understanding disease prevalence and distribution. The foundational work by (Zulu et al., 2014) underscores the critical role of local spatiotemporal analysis in elucidating the geographic variation of HIV/AIDS prevalence in Malawi from 1994 to 2010. Their study employs inverse distance weighting within ArcGIS to produce continuous surfaces of HIV prevalence, revealing significant spatial clustering and autocorrelation. This analysis highlights a notable decline in HIV prevalence post-1999, while also identifying regional "hotspots" and "coldspots" that necessitate tailored intervention strategies. The authors advocate for improved access to health services and education in rural districts, demonstrating how spatial analysis can inform public health initiatives by targeting specific areas based on their unique epidemiological profiles.

Building on this foundation, (Okango et al., 2016) further advance the discourse by introducing spatially varying coefficients in the modeling of HIV and HSV-2 prevalence among women in Kenya. Their research challenges traditional assumptions in disease mapping by employing a random walk model of order 2 and a conditional autoregressive model, allowing for non-linear relationships and spatial variability in covariates. The findings reveal that education's impact on HIV prevalence is not uniform across regions, emphasizing the necessity of localized strategies that account for cultural and demographic differences. This approach not only enhances the accuracy of prevalence estimates but also informs targeted interventions, reinforcing the value of spatial modeling in public health research.

In a broader context, (Nazia et al., 2022) provide a systematic review of methods used in the spatial and spatiotemporal analysis of infectious diseases, including COVID-19. This review highlights the significance of spatial clustering analysis in identifying disease hotspots and the role of socioeconomic and environmental factors in shaping disease distribution. The authors discuss the utility of Bayesian spatiotemporal models, which allow for a nuanced understanding of epidemiological data across different spatial resolutions. Their work emphasizes the need for robust research designs that can address gaps in current methodologies, ultimately contributing to more effective public health responses.

Collectively, these studies illustrate the critical integration of spatial analysis in understanding HIV dynamics and the broader implications for public health interventions. They underscore the necessity of employing advanced statistical methods to capture the complexities of disease prevalence and the spatial factors that influence it.

Regression Analysis is one of the analysis methods that study the pattern of relationships between variables to estimate the value of a variable using the value of another known variable. Regression Analysis can be used to determine the relationship between factors that influence HIV/AIDS cases. In Regression analysis, there are two types of variables, namely response variables and predictor variables (Shofiyah & Sofro, 2018). In some cases, the observed response variables are related to the results of observations in different areas, especially adjacent areas (Nasir et al., 2020). The existence of spatial relationships in the response variables will cause the estimation to be inaccurate because the assumption of randomness of errors is violated (Sanusi et al., 2018). To overcome this problem, a regression model is needed that includes spatial relationships between regions in the model. Therefore, the model used is the Spatial Regression model.

Research using the Spatial Regression method was conducted by (Puspita & Yanti, 2022) about the influence of breastfeeding on the number of stunted babies in West Nusa Tenggara, the best model used was the Spatial Autoregressive Model (SAR) with the smallest Root Mean Square Error (RMSE) value. Previously a research by (Ulvatunnisa, 2017) found a similar fact with the study conducted on young people who had their first marriage at less than 15 years according to Province with the method used being the Spatial Autoregressive Model (SAR).

Spatial autoregression models have shown significant contributions to HIV prediction by incorporating spatial and temporal correlations. These models outperform linear mixed models in predicting HIV cases, particularly in areas with limited temporal data but abundant spatial information (Shand et al., 2018). Mobile phone data has also been utilized to extract mobility and connectivity features, which correlate strongly with HIV prevalence rates and can serve as proxies for epidemic monitoring (Brdar et al., 2016). Spatial analysis techniques, such as structural equation modeling, have revealed that socioeconomic factors and maternal mortality significantly impact child HIV/TB mortality in rural areas. Spatial prediction maps derived from these analyses can guide targeted interventions in areas with the greatest need (Musenge et al., 2013).

Human Immunodeficiency Virus(HIV) is a virus that attacks or infects white blood cells which causes a decrease in the human immune system so that it is very susceptible to several infections and other diseases, while Acquired Immune Deficiency Syndrome (AIDS) is a symptom of a disease that arises due to a decrease in the immune system caused by the HIV (Mardalena & Apriani, 2020). The HIV/AIDS virus is transmitted through several transmission methods such as the use of non-sterile medical equipment, repeated use of injection needles, sexual intercourse with people infected with HIV/AIDS, breastfeeding mothers of HIV/AIDS patients, and tattooing with non-sterile sharp objects (Azizah & Budiantara, 2020). A person infected with HIV will lose their immune system over time and can progress to the stage of AIDS if they continue to suffer from symptoms of the disease and other problems for a long period. (Hariadi & Sulantari, 2019).

The number of HIV/AIDS sufferers is increasing rapidly and spreading to almost all regions in Indonesia. The Ministry of Health reported that HIV cases found in Indonesia in 2021 were 36,902 people. The number of cases found in Indonesia continues to increase and the victims come from various groups, both rich and poor (Yusuf, 2016). Indonesian society must know the causes of HIV well to prevent the spread of the virus and reduce the percentage of HIV-positive sufferers in each province (Azizah & Budiantara, 2020). HIV/AIDS

sufferers from one area are thought to be able to be affected by the surrounding areas (Rohimah & Riyantobi, 2019). HIV cases in each region have different influencing factors, so an analysis is needed that can identify the factors that influence HIV cases in a region by considering the influence of adjacent areas.

Researchers tried to use Spatial Regression Analysis in determining the factors that influence HIV/AIDS cases, it is hoped that the results of this study can be used in determining appropriate policies for dealing with the spread of HIV/AIDS.

DATA AND METHODS

Data on the number of HIV/AIDS cases in Indonesia in 2021 was obtained from the Ministry of Health of the Republic of Indonesia's website https://kemkes.go.id/id/profil-kesehatan-indonesia-2021. The variables used are the number of HIV/AIDS cases (Y), the number of poor people (X1), the number of fertile couples using condoms (X2), the number of hospitals (X3), the number of HIV-positive pregnant women (X4), and the number of drug users (X5).

The outline of the work is described as follows.

1. Presents a descriptive analysis of the variables studied.
2. The Spatial Dependency Test is conducted in two ways, namely:
a. Determining the Morans Index value
b. Conducting the Lagrange Multiplier (LM) test which has two tests, namely SAR modeling and SEM modeling. If the value of $LM_{tag} > \chi^2_{(\alpha,1)}$ or p-value $< \alpha$ then there is a spatial lag dependency or Spatial Autoregressive (SAR). If $LM_{error} > \chi^2_{(\alpha,1)}$ or p-value $< \alpha$ then there is a spatial error dependency or Spatial Error Model (SEM).
4. If there is no spatial dependency, then modeling can only be done with multiple linear regression. If it is met, then it is continued with spatial regression analysis using Spatial Autoregressive Model (SAR) modeling with the following equation
y = $Wy + αι + Xβ + ε (LeSage & Pace, 2009)
5. Calculate the estimated values of the SAR model parameters.
6. Conducting spatial regression model assumption tests consisting of normality tests, multicollinearity tests, normally distributed residual tests, and homoscedasticity tests.
7. Analysis and interpretation of results.

RESULTS AND DISCUSSION

Data Description

HIV/AIDS cases have long been spread throughout all provinces in Indonesia. Figure 1 shows seen from the distribution of the highest number of HIV/AIDS cases in Java. In Java, only Banten Province has HIV/AIDS cases of less than 2000, other provinces have more than 4000 cases. The highest cases are in East Java at 5872 and the lowest in West Sulawesi Province at 31 cases.
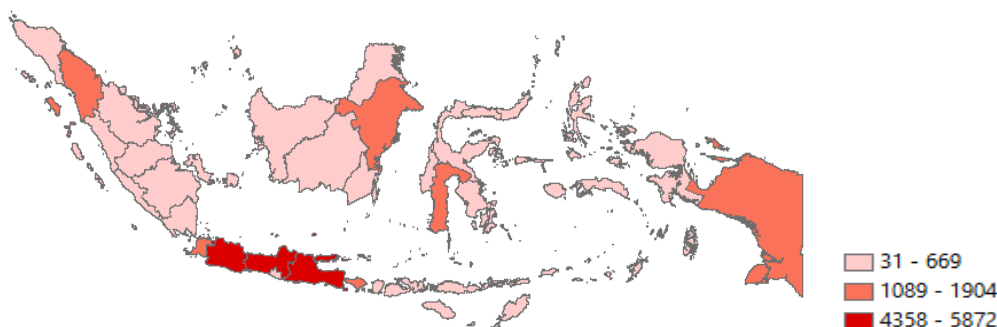

	31 - 669
	1089 - 1904
	4358 - 5872

Figure 1. Map of the distribution of the number of HIV/AIDS 2021 cases in Indonesia

The highest number of poor people is in East Java Province at 4259.60 thousand people and the lowest number is in North Kalimantan Province at 49.49 thousand people. The highest number of fertile couples using condoms is in Central Java Province at 93683 couples. The highest number of hospitals is in West Java Province at 329 units and the lowest number is in North Kalimantan Province at 12 hospitals. The highest number of HIV-positive pregnant women is in Central Java Province at 1328 cases and the lowest number is in Bengkulu Province at 1 case. The highest number of drug users is in DKI Jakarta Province at 34 cases.

Queen Contiguity Matrix

Indonesia, which has territories separated by oceans, creates irregular polygons. Using this matrix means that all provinces in Indonesia have adjacent neighbors. Separated inter-island areas such as Java and other islands still have access to interact and be neighbors. Indonesia has 34 provinces, so the Queen Contiguity weighting matrix (LeSage & Pace, 2009) will form a 34×34 matrix. Based on neighboring areas, the W matrix is obtained. The W matrix obtained is transformed into a standardized form, then multiplied by the matrix of the Y variable and called the Wy matrix. The Wy matrix will be used for the calculation of spatial regression models containing lag dependencies.

Moran's I Test

Moran's index is an important spatial statistical measure used to determine the presence or absence of spatial autocorrelation, thereby determining the selection orientation of spatial statistical methods (Chen, 2023). Moran' index is calculated as follows.

$$I = \frac{n}{\sum_{i=1}^{n}\sum_{j=1}^{n} w_{ij}} \frac{\sum_{i=1}^{n}\sum_{j=1}^{n} w_{ij}(x_i - \bar{x})(x_j - \bar{x})}{\sum_{i=1}^{n}(x_i - \bar{x})^2}$$

(LeSage & Pace, 2009; Oyana & Margai, 2015). With n = 31, R output of the Moran test is presented in Table 1.

Table 1. The result of Moran's Test I

Moran I statistic standard deviation = 3.9353, p-value = 4.154e-05		
alternative hypothesis: greater		
Sample estimates:		
Moran I statistics	Expectation	Variance
0.52545401	-0.03030303	0.01994374

In this study, the significance level $\alpha = 0.05$ is used so that with p-values., then H_0 is rejected, So it can be concluded that there is spatial autocorrelation between one region and another for the Y variable. The Moran's I value obtained on the Y variable is equal to 0,525454010 and is in the range of $0 < I \leq 1$ values indicating that the number of HIV/AIDS cases in Indonesia has positive spatial autocorrelation. This means that provinces that are close together have almost the same number of HIV/AIDS cases or indicate that the number of HIV/AIDS cases tends to be clustered.

Certain locations are grouped more specifically using the Local Indicator of Spatial Association (LISA). To see areas with the number of HIV/AIDS cases High-High, Low-High, Low-Low, and High-Low, the Queen Contiguity weighting matrix is used in Figure 2.
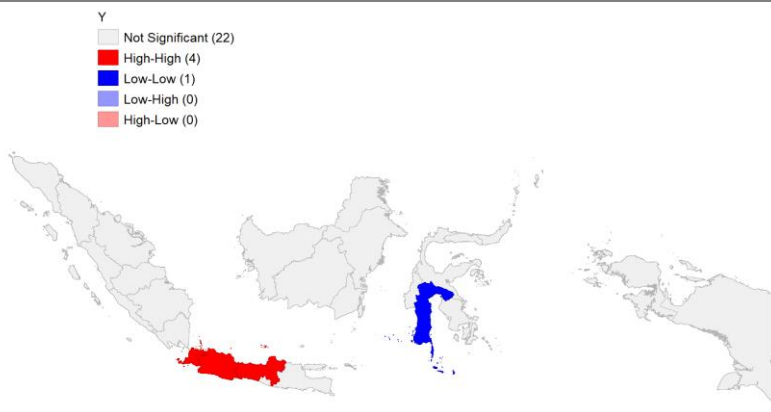
Figure 2. Cluster LISA for HIV cases

DKI Jakarta, Banten, West Java, and Central Java are at the High-High level, meaning that the region has a high number of HIV cases and is surrounded by provinces with high scores as well. South Sulawesi is at the Low-Low level, meaning that the region has a low number of HIV cases and is surrounded by provinces with low scores (Figure 3).
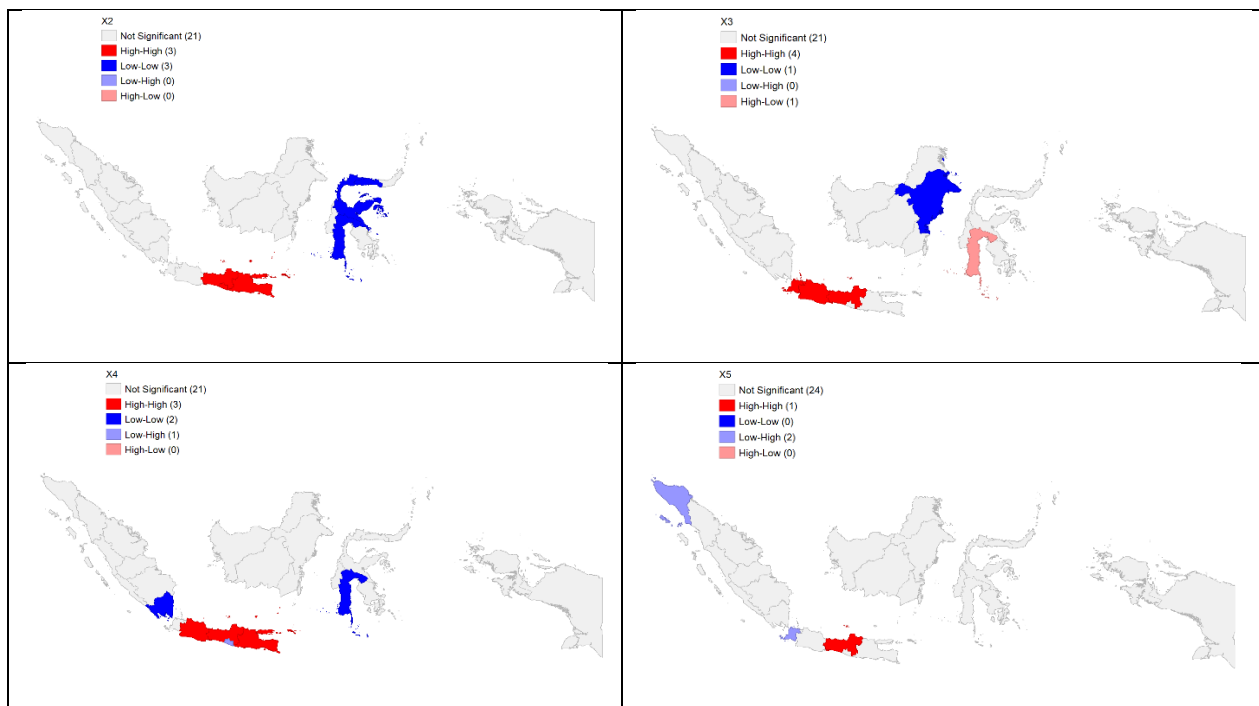

Figure 3. Cluster of LISA for Fertile couples using condoms, Number of hospital, Pregnant women with HIV, and Number of drug users.

Figure 3 presents the cluster of Fertile couples using condoms, Number of hospital, Pregnant women with HIV, and Number of drug users. These variables have almost similar cluster with that of HIV cases. In modelling HIV cases, these variables should be considered as influent factor of HIV cases.

Lagrange Multiplier (LM) Test

The Lagrange (LM) tests are build upon the distribution of stochastic Lagrange multipliers, obtained from the solution of maximizing the likelihood function in a constrained optimization problem (Astaiza-Gómez, 2020). LM is used to test the existence of spatial autoregressive and spatial lag in spatial regression (Anselin, 1988).

In the Lagrange Multiplier test, the hypotheses tested are:
1.   Hypothesis for Spatial Autoregressive (SAR) model
$H_0: \rho = 0$ (no spatial lag dependency)

H_1 : $\rho \neq 0$ (there is a spatial lag dependency)

2.   Hypothesis for Spatial Error Model (SEM)

H_0 : $\lambda = 0$ (no spatial error dependency)

H_1 : $\lambda \neq 0$ (there is a spatial error dependency)

The results of the Lagrange Multiplier test using the modified Queen Contiguity weighting matrix are presented in Table 2 as follows.

Table 2. The Result of Lagrange Multiplier Test

LM Test	p-value	Conclusion
LM_{lag}	0.1980	Accept H_0
LM_{eror}	0.8929	Accept H_0

Decision-making based on p-value, reject H_0 if the p-value $< \alpha$ (0.05). The Lagrange Multiplier test on the lag and error dependencies in Table 2 shows a value greater than the significance level used, indicating that there is no dependency on either the spatial lag or error.

Spatial Autoregressive Model (SAR) Modeling

Based on the real results of the Moran I test, although the lag test in the LM test is not significant, the spatial model used for this data is SAR. The results of the SAR full model parameter estimation on HIV/AIDS cases in Indonesia in 2021 using the Queen Contiguity weighting matrix content X_1 which is not significant.

Table 4 is the result of SAR model with the variables $X_2, X_3, X_4, and X_5$, have a p-value of < 0.05. This means that the number of fertile couples using condoms, the number of hospitals, the number of HIV-positive pregnant women and the number of drug users have a significant influence on the number of HIV/AIDS cases in Indonesia.

Table 4. SAR Model Parameter Estimates of Significant Variables

Variables	Estimate	Standard Error	p-value
Intercept	$-329{,}62$	101,46	$1{,}159 \times 10^{-3}$
X_2	$-0{,}031408$	0,0081192	$1{,}096 \times 10^{-4}$
X_3	15,898	2,0076	$2{,}442 \times 10^{-6}$
X_4	2,5701	0,57601	$8{,}121 \times 10^{-5}$
X_5	26,710	10,894	$1{,}422 \times 10^{-2}$
$\hat{\rho}$	0,037991		

The Spatial Autoregressive Model using the Queen Contiguity weighting matrix is as follows:

$$\hat{Y}_i = 0{,}037991 \sum_{j=1, i \neq j}^{34} W_{ij}Y_j - 329{,}62 - 0{,}031408X_2 + 15{,}898X_3 + 2{,}5701X_4 + 26{,}710X_5$$

This model is significant at the level of 0.05 ($F_{calculated} = 102.5072$) > ($F_{(0.1;4;30)} = 2.14$). With a pseudo-$R^2$ value of 93.39%, it means that 93.39% of the diversity of HIV/AIDS cases in Indonesia can be explained by the variables of the number of fertile couples using condoms, the number of hospitals, the number of HIV-positive pregnant women and the number of drug users simultaneously.

Spatial Regression Model Assumption Test

Spatial Regression Model Assumption have 3 assumption which are multicollinearity, residual Normality, and homoscedasticity. Multicollinearity assesment aims to determine whether there is a correlation between predictor variables. It uses the Variance Inflation Factor (VIF). If the VIF value is less than 10, there is no multicollinearity. Since all the VIF results are less than 10, the predictor variables are not correlated with each other or are independent of each other in the regression model.

The residual normality assumption is an assumption used to test the error generated by the model, where the error generated must be normally distributed to meet the assumption. The residual normality test in this study uses the Kolmogorov-Smirnov test. Based on the R output using the Kolmogorov-Smirnov test, it produces a D value = 0.14375 with a p-value = 0.4423. It can be concluded that the residual is normally distributed

The homoscedasticity test aims to see the distribution or variance of the points of the residual value. Based on the R output, the Breusch Pagan test produces with $BP_{calculated} = 3,131 \ with \ p-value = 0,8016$. This $p-value > 0.05$ so it is concluded that the residual values are homoscedastic.

Interpretation of Results

Based on the model that has been obtained and the results of the conclusion about the existence of spatial autocorrelation in HIV/AIDS cases in Indonesia in 2021, it can be interpreted that the number of HIV/AIDS sufferers in a location or region is influenced by fertile couples who use condoms, the number of hospitals, the number of HIV-positive pregnant women and the number of drug users. The regression model formed in HIV/AIDS cases using the Spatial Autoregressive Model (SAR) is as follows.

$$\hat{Y}_i = 0,037991 \sum_{j=1,i \neq j}^{34} W_{ij}Y_j - 329,62 - 0,031408X_2 + 15,898X_3 + 2,5701X_4 + 26,710X_5$$

HIV cases in province i will decrease by 0.031408 cases if the number of fertile couples using condoms in province-i increases by one case where other variables are considered constant. HIV cases in province-i will increase by 15,898 cases if the number of hospitals in province-i increases by one case where other variables are considered constant. This is because the recording of HIV/AIDS cases is mostly done in hospitals. The more hospitals there are, the easier it is to record HIV/AIDS cases, so the number can increase. HIV cases in province-i will increase by 2.5701 cases if the number of HIV-positive pregnant women in province-i increases by one case where other variables are considered constant. HIV cases in province-i will increase by 26,710 cases if the number of drug users in province-i increases by one case where other variables are considered constant.

In general, based on the SAR model above, it can be interpreted that HIV cases in the province-i will increase by 0.037991 if there is an increase in HIV cases of one case in the neighboring province-j, where other factors are considered constant. Here is an example of a SAR model in South Sumatra Province. The province has 4 neighbors: Jambi, Bengkulu, Lampung, and the Bangka Belitung Islands. The similarities are:

$$\hat{Y}_6 = 0,00949775Y_5 + 0,00949775Y_7 + 0,00949775Y_8 + 0,00949775Y_9 - 329,62 - 0,031408X_2 + 15,898X_3 + 2,5701X_4 + 26,710X_5$$

Many HIV/AIDS cases in South Sumatra Province are also influenced by neighboring provinces, namely Jambi, Bengkulu, Lampung, and the Bangka Belitung Islands, so if the number of HIV/AIDS cases in Jambi Province increases by 100 units, then HIV/AIDS cases in South Sumatra Province will increase by 0.949775

cases. This means that the number of cases in Jambi is not large enough to affect the number of cases in South Sumatra.

CONCLUSIONS

Based on the results of the analysis of the number of HIV/AIDS cases using the Spatial Autoregressive Model (SAR), the following conclusions can be drawn:

1. HIV/AIDS cases in Indonesia are related between provinces based on the Morans index value which is in the interval between$0 < 0,52545401 \leq 1$. There is also a positive autocorrelation which means that there is a clustering pattern. Provinces that are close together tend to have the same number of HIV/AIDS cases. DKI Jakarta Province, which has a high number of HIV/AIDS cases, is close to West Java Province, which also has a high number of HIV/AIDS cases (High-High).

2. The Spatial Autoregressive Model (SAR) model using the Queen Contiguity matrix is obtained

$$\hat{Y}_i = 0,037991 \sum_{j=1,i\neq j}^{34} W_{ij}Y_j - 329,62 - 0,031408X_2 + 15,898X_3 + 2,5701X_4 + 26,710X_5$$

3. Based on the Spatial Autoregressive Model (SAR), the factors that influence the number of HIV/AIDS cases in Indonesia (Y) are the number of fertile couples using condoms (X_2), the number of hospitals (X_3), the number of HIV-positive pregnant women (X_4), and the number of drug users (X_5).

Based on the research that has been conducted, the suggestion that the author can give is that in this study, the author uses the Spatial Autoregressive Model (SAR) and the Queen Contiguity weighting matrix, in further research, other spatial models and weighting matrices can be used and it is hoped that more other variables can be used that are suspected of influencing HIV/AIDS cases in Indonesia.

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CONFLICTS OF INTEREST

The authors affirm that there are no conflicts of interest.

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