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Analysis Of The Distribution Of Livestock Disease Cases By Region Based On Data From The Ministry Of Trade's Animal Health Center Using The Dbscan Clustering Method In Bandar District

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Abstract

Livestock farming serves as a vital economic pillar for the community in Bandar District, Simalungun Regency. However, the high intensity of livestock activities is accompanied by a significant risk of disease transmission, which has historically been managed through conventional recording methods that lack spatial integration. This research aims to analyze the spatial distribution patterns of livestock diseases by implementing the Density-Based Spatial Clustering of Applications with Noise (DBSCAN) method integrated into a web-based Geographic Information System (GIS). Using a quantitative approach, the study processed 200 case records from December 2025 to January 2026. Spatial distances were calculated using the Haversine formula to ensure geographic accuracy. The results indicate that the optimal parameters for the DBSCAN algorithm are an epsilon (ϵ) of 3.0 km and a minimum points (MinPts) of 2. These parameters successfully identified two primary clusters with zero noise, encompassing all 200 cases. Cluster 1 (98 cases) is concentrated in the west-central region, dominated by cattle and goats with diverse pathologies such as Scabies and BEF. Cluster 2 (102 cases) is located in the east-northern region and exhibits a more heterogeneous livestock profile, including rabies cases in dogs. High-density areas requiring priority intervention were identified in Pematang Kerasaan Rejo and Perdagangan II. The developed web-based GIS provides an interactive visualization platform that enhances early warning capabilities and supports data-driven decision-making for livestock disease surveillance and regional control.

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1. Introduction

The Bandar Subdistrict in Simalungun Regency is an area highly dependent on the agricultural and livestock sectors as the main sources of livelihood for its population. Approximately 45.30% of residents work in agriculture, while the agriculture, forestry, and fisheries sectors contribute around 52.99% to the Gross Regional Domestic Product (GRDP) of Simalungun Regency (Parboaboa, 2023; BPS Simalungun, 2024). Within this economic structure, the livestock subsector plays a crucial role as both an income source and a financial asset for rural households.

The high intensity of livestock activities in productive villages such as Marihat Bandar Village and Pematang Kerasaan Rejo Village increases the risk of infectious disease outbreaks (Situmorang, 2021). In 2022, Simalungun Regency recorded approximately 176,000 livestock populations (Mistar.id, 2023), and during the same period, outbreaks of symptoms resembling Foot-and-Mouth Disease (FMD) affected hundreds of cattle, causing significant economic losses and raising concerns among farmers (AnalisaDaily, 2022; Ministry of Agriculture Indonesia, 2023). These conditions highlight the urgency of implementing a spatial-based livestock disease monitoring system to support early detection and mitigation strategies.

However, current livestock disease data collection in the region is still conducted manually and has not been integrated with spatial analysis or digital mapping systems. As a result, it is difficult to identify high-risk areas, disease clustering patterns, and spatial spread tendencies. Previous studies have demonstrated that spatial approaches can support disease mapping, but most still rely on descriptive statistics and static visualization without advanced spatial clustering techniques (Tadesse & Amare, 2021; Wibowo et al., 2022). Although Geographic Information Systems (GIS) have been widely used in animal health surveillance, their application is generally limited to visualization and has not been fully integrated with density-based clustering methods for hotspot detection at the subdistrict level (Ngwira et al., 2024; Manzoor et al., 2024).

Density-Based Spatial Clustering of Applications with Noise (DBSCAN) has been proven to be effective in identifying clusters in spatial datasets with irregular distributions and noise, making it suitable for disease outbreak detection (Syahra et al., 2022; Ester et al., 1996). Furthermore, DBSCAN does not require prior specification of the number of clusters and has been successfully applied in epidemiological studies for spatial pattern detection (Hermanto & Sunandar, 2020; Liu et al., 2023). However, despite these advantages, there is still a limited number of studies that integrate DBSCAN with web-based GIS platforms for livestock disease monitoring at the subdistrict scale, particularly in rural agricultural regions such as Simalungun.

Existing studies have not yet developed an integrated system that combines DBSCAN-based spatial clustering with interactive web-GIS for real-time visualization and decision support in livestock disease monitoring at the subdistrict level. Most prior works either focus on GIS-based mapping without clustering analytics or apply DBSCAN in non-web-based analytical environments, limiting accessibility for stakeholders such as veterinarians and local livestock officers.

Therefore, this study proposes the development of a web-based Geographic Information System integrated with the DBSCAN clustering algorithm to identify livestock disease hotspots in Bandar Subdistrict, Simalungun Regency.

The novelty of this research lies in the integration of DBSCAN-based spatial clustering into an interactive web-GIS platform, enabling dynamic visualization of livestock disease clusters, identification of high-risk zones, and improved accessibility for decision-makers at the local level.

The objectives of this study are: (1) to analyze the spatial distribution of livestock disease cases in Bandar Subdistrict using GIS; (2) to implement the DBSCAN algorithm for identifying disease hotspot clusters; and (3) to design and develop a web-based GIS system that visualizes clustering results to support early warning and decision-making in livestock health management.

This study is expected to contribute to improving spatial-based livestock disease surveillance systems by combining machine learning-based clustering and web-GIS technology for more effective regional animal health monitoring.

2. Research Methodolgy

3.1 Research Design

This study employs a quantitative approach using the DBSCAN clustering method and a web-based Geographic Information System (GIS) to analyze the distribution of livestock disease cases in Bandar Subdistrict. The research data were obtained from the Trade Animal Health Center in the form of livestock disease case data along with location coordinates. The research process included data collection, preprocessing, distance calculation using the Haversine formula, the DBSCAN clustering process, and visualization of the results on a digital GIS map.

3.2 Dataset Collection and Preparation

The data used consists of livestock disease case records from the Bandar subdistrict, comprising 200 cases from December 2025 to January 2026. This data was collected from official records of relevant agencies and served as the basis for analyzing the spatial distribution of livestock diseases using the DBSCAN clustering method. The livestock disease occurrence data used in this study contains several key attributes, namely time of occurrence, animal species, disease type, location of occurrence, and location coordinate information used for spatial analysis and map visualization. This data was then processed to identify patterns of livestock disease spread based on the proximity of occurrence locations.

3.3 DBScan Method

The DBSCAN method is used to cluster livestock disease case data based on geographical proximity. DBSCAN operates using two main parameters: epsilon (ε) and minimum points (MinPts). Distances between coordinates are calculated using the Haversine formula to obtain more accurate distance measurements on the Earth’s surface (Zhang et al., 2023).

3.4 Parameter DBScan

Parameter values used:

1) ε (epsilon) = 3 km
2) MinPts = 2

Haversine formula:

$$d = 2r \cdot \arcsin\left(\sqrt{\sin^2\left(\frac{\Delta\varphi}{2}\right) + \cos\varphi_1 \cdot \cos\varphi_2 \cdot \sin^2\left(\frac{\Delta\lambda}{2}\right)}\right)$$

Notes:
d = distance between locations
r = Earth's radius (6,371 km)
ϕ = latitude in radians = latitude (degrees) × $\frac{\pi}{180}$
λ = longitude in radians = longitude (degrees) × $\frac{\pi}{180}$

3.5 Research Flow

The research process begins with the collection of livestock disease case data, data preprocessing, calculation of spatial distances, application of the DBSCAN method, and visualization of the clustering results on a web-based GIS.

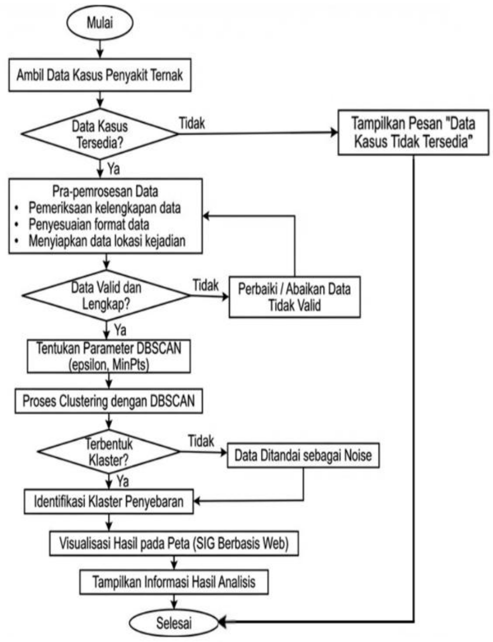

Figure 1. System Flowchart

3. Results and Discussion

3.1 Manual Calculation of DBSCAN

The following three sets of livestock disease data were used:

Point	Livestock Type	Disease Type	Village/Subdistrict	Latitude	Longitude
A	Goat	Scabies/Kurap	Pematang Kerasaan Rejo	3.11455	99.29575
B	Dog	Rabies Vaccination	Bandar Jawa	3.18818	99.28344
C	Cow	BEF/Fever	Marihat Bandar	3.12638	99.30297

A. Conversion to radians and intermediate values:

1) Point A:
   a. $\varphi_A = 3.11455 \times \frac{\pi}{180} \approx 0.054359152218$ rad
   b. $\lambda_A = 99.29575 \times \frac{\pi}{180} \approx 1.733037770737$ rad
2) Point B:
   a. $\varphi_B = 3.18818 \times \frac{\pi}{180} \approx 0.055644238146$ rad
   b. $\lambda_B = 99.28344 \times \frac{\pi}{180} \approx 1.732822920706$ rad
3) Point C:

$$\varphi_C = 3.12638 \times \frac{\pi}{180} \approx 0.054565624669 \text{ rad}$$
$$\lambda_C = 99.30297 \times \frac{\pi}{180} \approx 1.733163783509 \text{ rad}$$

B. Calculating the distance between pairs of points (step-by-step instructions):

1) Distance between Point A and Point B

i) Differences:

$$\Delta\varphi = \varphi_B - \varphi_A \approx 0.001285085928 \text{ rad}$$
$$\Delta\lambda = \lambda_B - \lambda_A \approx -0.000214850031 \text{ rad}$$

ii) Component a in the Haversine formula:

$$a = \sin^2\left(\frac{\Delta\varphi}{2}\right) + \cos\ \varphi_A \cdot \cos\ \varphi_B \cdot \sin^2\left(\frac{\Delta\lambda}{2}\right) \approx 0.000000424367$$

iii) Center Angle c:

$$c = 2 \cdot \arcsin\left(\sqrt{a}\right) \approx 0.001302868707 \text{ rad}$$

iv) Distance:

$$d(A, B) = r \cdot c \approx 6371 \times 0.001302868707 \approx 8.300576535 \text{ km}$$

2) Distance between Point A and Point C

i) Differences:

$$\Delta\varphi = \varphi_C - \varphi_A \approx 0.000206472451 \text{ rad}$$
$$\Delta\lambda = \lambda_C - \lambda_A \approx 0.000126012772 \text{ rad}$$

ii) Component a in the Haversine formula:

$$a = \sin^2\left(\frac{\Delta\varphi}{2}\right) + \cos\ \varphi_A \cdot \cos\ \varphi_C \cdot \sin^2\left(\frac{\Delta\lambda}{2}\right) \approx 0.000000014616$$

iii) Center Angle c:

$$c = 2 \cdot \arcsin\left(\sqrt{a}\right) \approx 0.000241791311 \text{ rad}$$

iv) Distance:

$$d(A, C) = r \cdot c \approx 6371 \times 0.000241791311 \approx 1.540452439 \text{ km}$$

3) Distance between Point B and Point C

i) Differences:

$$\Delta\varphi = \varphi_C - \varphi_B \approx -0.001078613478 \text{ rad}$$
$$\Delta\lambda = \lambda_C - \lambda_B \approx 0.000340862803 \text{ rad}$$

ii) Component a in the Haversine formula:

$$a = \sin^2\left(\frac{\Delta\varphi}{2}\right) + \cos\ \varphi_B \cdot \cos\ \varphi_C \cdot \sin^2\left(\frac{\Delta\lambda}{2}\right) \approx 0.000000319810$$

iii) Center Angle c:

$$c = 2 \cdot \arcsin\left(\sqrt{a}\right) \approx 0.001131035818 \text{ rad}$$

iv) Distance:

$$d(B, C) = r \cdot c \approx 6371 \times 0.001131035818 \approx 7.205829195 \text{ km}$$

C. Summary of distance results (rounded to 3 decimal places for brevity):

a. d(A,B) ≈ 8.301 km
b. d(A,C) ≈ 1.540 km
c. d(B,C) ≈ 7.206 km

1. Determining the Number of Neighbors within a Radius of ε = 3 km
   a. Point A: neighbors within a 3 km radius = {A, C} count = 2
   b. Point B: neighbors within a 3 km radius = {B} count = 1
   c. Point C: neighbors within a 3 km radius = {C, A} count = 2
2. Determining Point Type (with MinPts = 2)
   a. Point A: number of neighbors ≥ MinPts—core point.
   b. Point C: number of neighbors ≥ MinPts—core point.
   c. Point B: number of neighbors < MinPts—noise (not a core, not a border because it is not within the range of any core).
3. Cluster Formation
   a. Point A and Point C are density-connected via a distance ≤ ε and both are core points, so they are combined into a single cluster.
   b. Point B has no other neighbors within a radius of ε and is therefore categorized as noise.
4. Clustering Results (summary)
   a. Cluster 1: {A, C} indicates a concentration of livestock disease cases (goats and cattle) in adjacent areas (Pematang Kerasaan Rejo and Marihat Bandar).
   b. Noise: {B}—one dog in Bandar Jawa is categorized as an isolated case.

3.2 System Implementation

The web-based Geographic Information System (GIS) developed here is designed to support the analysis and visualization of livestock disease outbreaks using the DBSCAN clustering method. The system features several key components, including an administrator login page, a monitoring dashboard, a livestock disease case data entry module, a map visualization feature, a clustering process, and an automated reporting feature.

1. Dashboard View

The dashboard visually presents a summary of key information in the form of stat cards, including: the total number of livestock disease cases stored in the database, the number of clusters formed from the latest clustering results, the amount of data processed through clustering, and the amount of noise data.

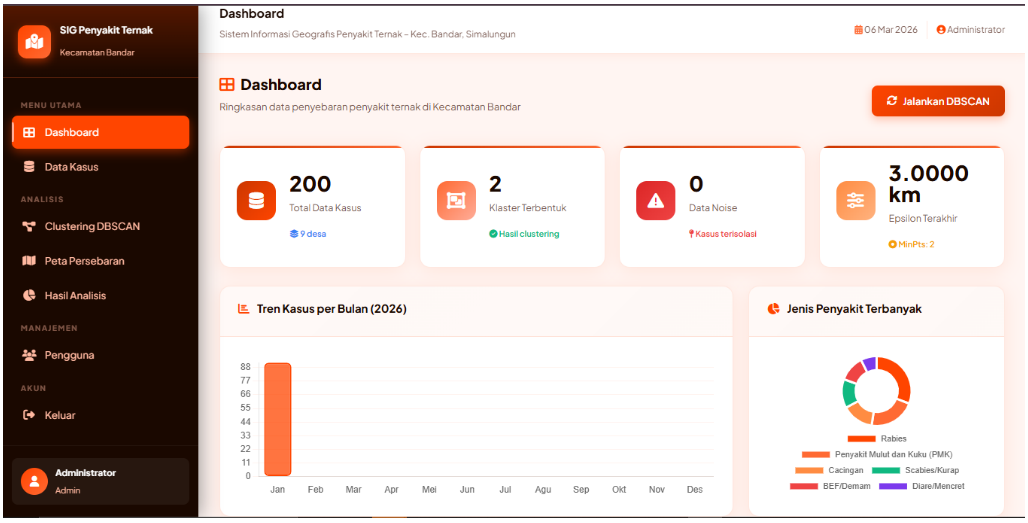

Figure 2. Dashboard View

2. Case Data View

The table includes real-time search, column sorting, and pagination features to facilitate navigation through large datasets. Each data row displays the serial number, date of occurrence, livestock type, disease type, village, number of animals, coordinates, and the cluster label from the DBSCAN analysis.

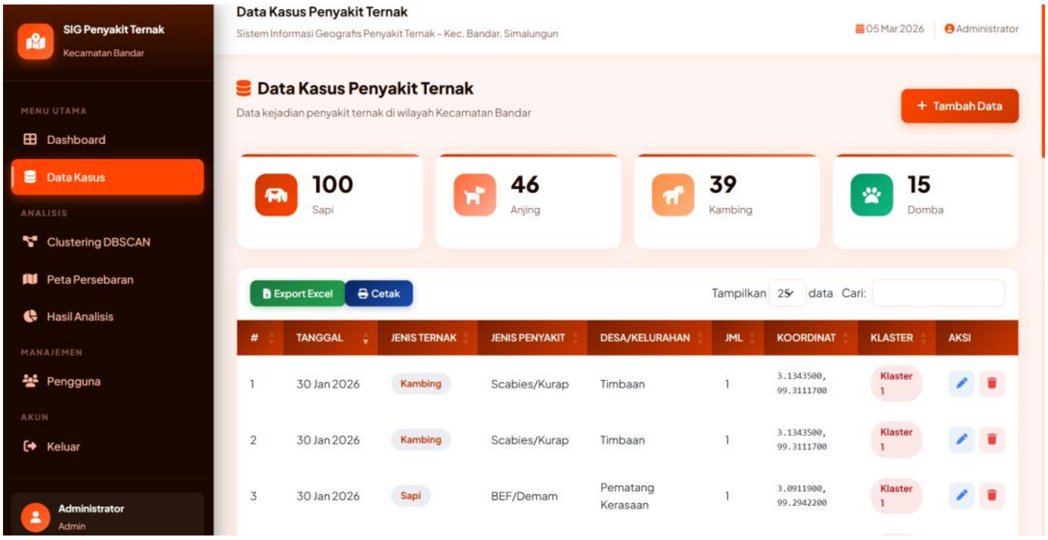

Figure 3. Case Data View

3. Distribution Map View

The distribution map visualizes all livestock disease case coordinates on an interactive map. Each case point is displayed as a colored circle marker that distinguishes the clusters resulting from the DBSCAN analysis. Cluster 1 is marked in red, Cluster 2 in orange, while noise data is marked in gray.

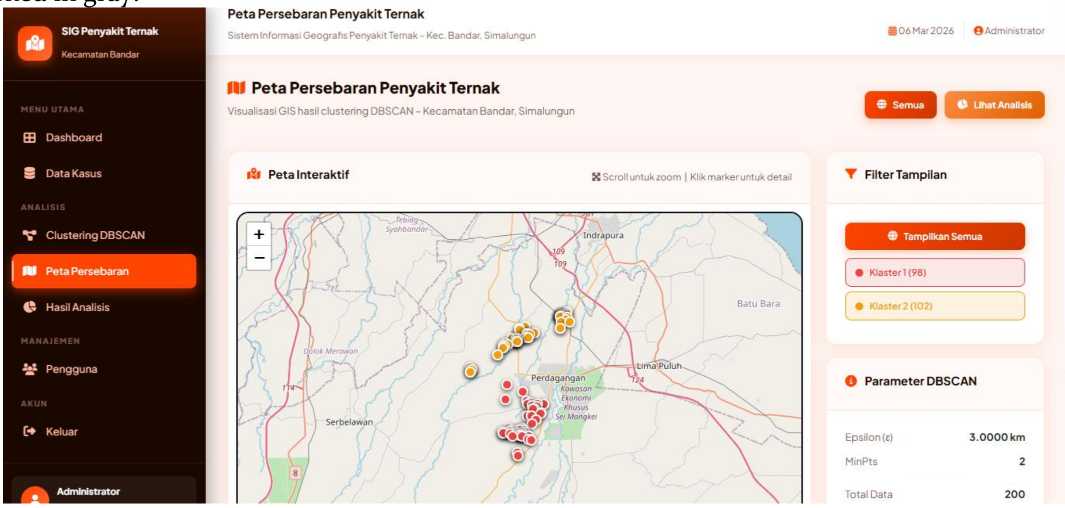

Figure 4. Distribution Map View

4. DBSCAN Clustering Display

The clustering process is executed on the server side using PHP. The method reads all coordinate data from the `kasus_ternak` table, calculates the distance between points using the Haversine formula, and then classifies each point as a core point, border point, or noise based on the specified parameters.

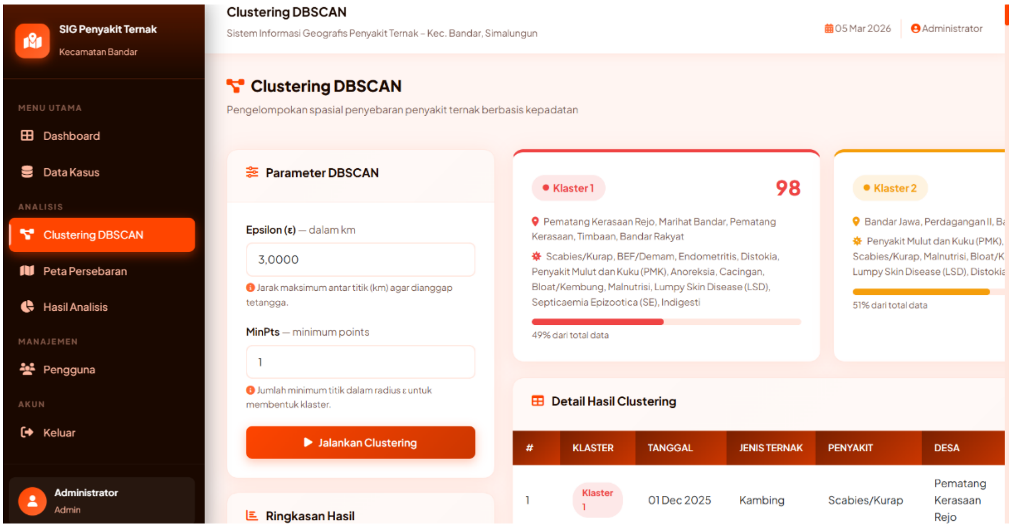

Figure 5. DBSCAN Clustering Display

5. Analysis Results Display

This page is divided into several main sections: (1) A summary statistics card displaying the total number of cases, the number of formed clusters, the number of data points in each cluster, and the number of noise points; (2) A cluster distribution map visualizing the clustering results; (3) Details of each cluster containing information on the region, disease type, and livestock type within it; and (4) An early warning system that automatically identifies villages with above-average case density.

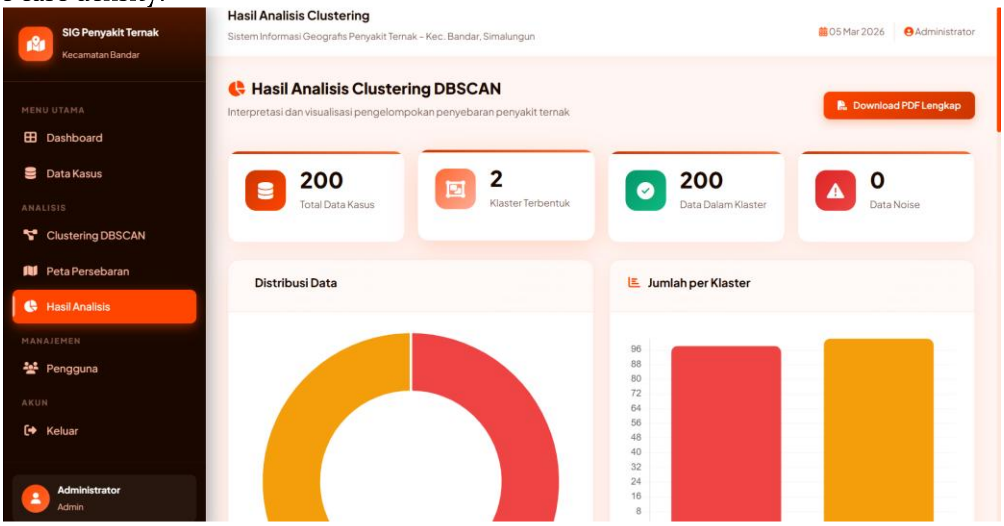

Figure 6. Analysis Results Display

6. PDF Report Feature Interface

The PDF Report Download feature automatically generates official report documents from data stored in the system. The reports are built using the jsPDF library on the client side with a native drawing API approach.

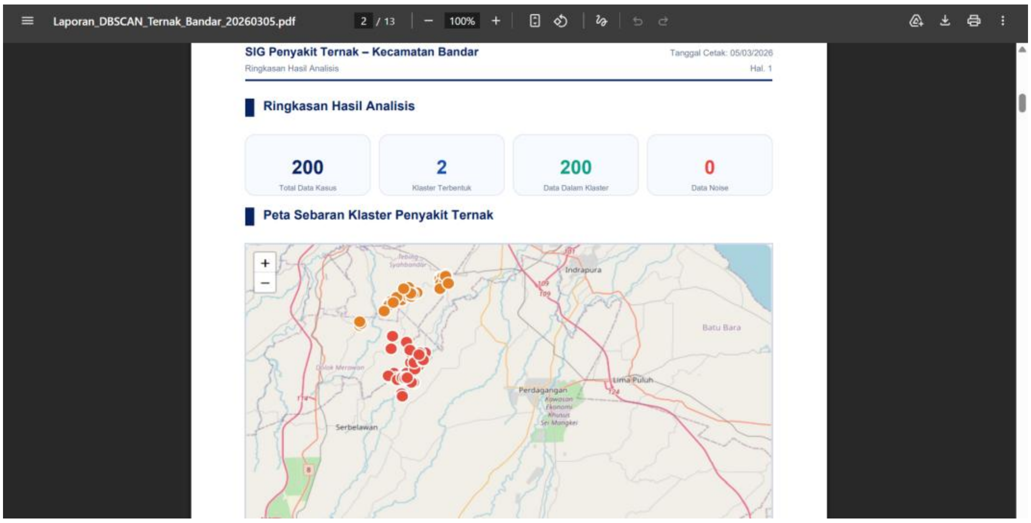

Figure 7. PDF Report Feature Interface

3.3 DBSCAN Analysis Results

The clustering results show that the distribution of livestock disease cases in Bandar Subdistrict forms concentrations in specific areas and does not occur randomly. Cluster 1 is dominated by cases in goats and cattle with a wider variety of diseases, while Cluster 2 has a more heterogeneous mix of livestock, including rabies cases. The differences in characteristics across each cluster indicate that disease management must be tailored to the specific conditions of each region.

RINGKASAN ANALISIS DBSCAN PENYAKIT TERNAK			
Wilayah	Kecamatan Bandar, Kabupaten Simalungun		
Parameter DBSCAN	Epsilon = 3,00 km | MinPts = 2 | Jarak = Haversine		
Validasi Hasil Analisis		**Sorotan Temuan**	
Total kasus	200.0 kasus	**Klaster 1**	98 kasus (49.0%)
Klaster terbentuk	2.0 klaster	**Klaster 2**	102 kasus (51.0%)
Data dalam klaster	200.0 kasus	**Zona perhatian tertinggi**	Pematang Kerasaan Rejo
Data noise	0.0 kasus	**Kasus tertinggi**	54
Jumlah desa terdampak	9.0 desa	**Catatan**	Zona perhatian ditetapkan untuk desa dengan kasus di atas rata-rata kasus per desa
Rata-rata kasus per desa	22.2 kasus/desa		
Konsistensi data			
Total kasus = Cluster 1 + Cluster 2	VALID		
Semua data masuk klaster	VALID		
Noise = 0	VALID		

Figure 8. Analysis Summary

The analysis also generated early warnings for areas with high case densities, namely Pematang Kerasaan Rejo with 54 cases and Perdagangan II with 41 cases. Both areas were categorized as priority zones because they had the highest number of cases in their respective clusters. This indicates that the DBSCAN method not only clusters data but also helps identify areas requiring greater attention in the surveillance and management of livestock diseases.

Desa	Jumlah Kasus	Status	Penyakit Dominan	Jenis Ternak Domina	Catatan
Pematang Kerasaan Rejo	54	Zona Perhatian	BEF/Demam	Sapi	Kasus di atas rata-rata desa
Perdagangan II	41	Zona Perhatian	Rabies	Anjing	Kasus di atas rata-rata desa
Bandar Jawa	30	Zona Perhatian	Rabies	Anjing	Kasus di atas rata-rata desa
Timbaan	25	Zona Perhatian	Cacingan	Sapi	Kasus di atas rata-rata desa

Figure 9. Case Conclusions

3.4 Setting DBSCAN Parameters

The selection of DBSCAN parameter values was based on the geographical characteristics of the Bandar subdistrict and an analysis of the distance distribution between data points. The two main parameters that need to be set are:

Table 1. DBSCAN Parameters

Epsilon (km)	MinPts	Cluster Form	Data in a cluster	Data noise
1.00	1	8	200	0
1.00	2	8	200	0
1.00	3	6	196	4
2.00	1	4	200	0
2.00	2	4	200	0
2.00	3	4	200	0
3.00	1	2	200	0
3.00	2	2	200	0
3.00	3	2	200	0

Based on the results of testing on 200 livestock disease case data points, the most appropriate DBSCAN parameters are ε = 3.0 km and MinPts = 2. The value of ε = 3.0 km was chosen because it corresponds to the distance between regions in Bandar Subdistrict, thereby effectively representing location-based spread patterns. This combination of parameters produced two noise-free clusters, allowing all data to be clearly grouped and easily interpreted. Meanwhile, the value MinPts = 2 was used so that the cluster formation would indicate a correlation between location points. Compared to a smaller epsilon, this parameter produced clusters that were more stable and representative of the livestock disease distribution pattern at the subdistrict level.

3.5 DBSCAN Computation

The DBSCAN method is implemented using PHP with coordinate data retrieved from a database. Distance calculations between points are performed using the Haversine formula because the data consists of geographic coordinates. Once the distance matrix is formed, the system identifies points within a radius of epsilon (ε). Points that meet the MinPts requirement are designated as core points and used to form clusters. The iteration process continues until all points have been processed and grouped.

Table 2. Illustration of the DBSCAN Iteration Process (Sample of 7 Iterations out of 200)

Point	Lat	Lon	Neighbour (e=3km)	Total neighbour	Type	Action	Cluster
P1	3.11455	99.29575	P1–P8 (radius 3 km)	≥ 1	Core Point	Cluster 1 formed	1
P2	3.11455	99.29575	P1, P2, P3, ...	≥ 1	Core Point	Join Cluster 1	1

P9	3.12638	99.30297	P9, P10, P47, P48, ...	≥ 1	Core Point	Expanded Cluster 1	1
P17	3.21331	99.33181	P17–P41 (radius 3 km)	≥ 1	Core Point	Klaster 2 Formed	2
P18	3.21331	99.33181	P17, P18, P19, ...	≥ 1	Core Point	Join Cluster 2	2
...	...	...	...	...	...	...	...
P200	3.13435	99.31117	P55, P56, P96–P100, ...	≥ 1	Core Point	Expanded Cluster 2	1

3.6 Clustering Results

After running the DBSCAN algorithm with parameters Epsilon = 3.0 km and MinPts = 2 on 200 coordinate data points, the following results were obtained:

Table 2. Summary of DBSCAN Clustering Results

Cluster	Total cases	Percentage	Village Area	Type of Disease	Type of Livestock
1 (Red)	98	49%	Pematang Kerasaan Rejo, Pematang Kerasaan, Marihat Bandar, Bandar Rakyat, Timbaan	Scabies, BEF/Fever, PMK, Worm Infection, Dystocia, Endometritis, Indigestion, LSD, Malnutrition, SE, Bloat, Anorexia	Cow, Goat
2 (Orange)	102	51%	Perdagangan II, Bandar Jawa, Bahlias, Bandar Pulo	Rabies, Foot-and-Mouth Disease (FMD), Intestinal Parasites, LSD, Diarrhea, Bloat, Dystocia, Malnutrition, Scabies	Dog, Cow, Goat, Sheep
Noise	0	0%	-	-	-

The analysis yielded 2 (two) clusters with a total of 200 cases, all of which were successfully grouped (0 noise). Cluster 1 consists of 98 cases (49%) concentrated in the west-central region of Bandar Subdistrict, while Cluster 2 consists of 102 cases (51%) spread across the northeast region. These results indicate that the distribution of livestock disease cases in Bandar Subdistrict is not random but forms specific regional clustering patterns based on the proximity of the incident locations.

4. Conclusion

This study successfully implemented a web-based DBSCAN clustering approach to analyze the spatial distribution of livestock disease cases in Bandar Subdistrict. The optimal parameters were determined at ε = 3.0 km and MinPts = 2, resulting in the formation of two main clusters without noise data points. The clustering evaluation, based on internal validation indicators, shows a stable cluster structure with good spatial compactness and clear separation between clusters. These results indicate that DBSCAN is an effective method for identifying livestock disease hotspot areas in the study region. The spatial analysis reveals that livestock disease cases are concentrated in specific high-density areas, particularly in Pematang Kerasaan Rejo, Perdagangan II, Bandar Jawa, and Timbaan Villages. These findings demonstrate the presence of distinct spatial patterns that are not easily identified using conventional manual reporting methods. In addition, the developed web-based Geographic Information System (GIS) provides interactive visualization of disease distribution, enabling faster, more structured, and more accessible monitoring for stakeholders compared to traditional data recording approaches. The integration of DBSCAN with GIS contributes significantly to supporting spatial-based decision-making in livestock disease surveillance and control. The system allows local authorities and animal health officers to identify potential hotspot areas more efficiently and supports more targeted intervention strategies. However, this study has several limitations. The analysis is based solely on static spatial data and does not include temporal dynamics of disease spread, which limits the ability to analyze outbreak progression over time. In addition, the model has not yet incorporated other relevant epidemiological or environmental factors such as livestock movement patterns, climate conditions, or biosecurity practices that may influence disease transmission. Future research is recommended to extend the system by integrating spatio-temporal analysis to capture disease evolution more comprehensively. Furthermore, incorporating additional predictive variables and advanced machine learning models could enhance early warning capabilities. Developing a real-time data integration system from field surveillance officers would also improve the practical applicability of the system for continuous livestock disease monitoring.

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