Fuzzy logic and mathematical theory of evidence to detect the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1

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Abstract

This research presents Fuzzy Logic and mathematical theory of evidence implement to detect the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1. This research has considered population changes in an area to detect the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1. Population density in the area include very low, low, medium, high and very high. The result reveals that the system has successfully identified the risk of disease spreading, moreover the maps can be displayed as the visualization. The highest percentage of the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 is 20%. Fuzzy Logic and mathematical theory of evidence have shown good results to detect the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1. The risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 in areas which include Batang, Kendal, Kota Magelang, Kota Salatiga, Kota Semarang, Magelang, Semarang, Temanggung, Wonosobo.

1. Introduction

Based on Cumulative Number of Confirmed Human Cases of Avian Influenza (H5N1) Reported to World Health Organization (WHO) in the 2013 from 15 countries, Indonesia has the largest number of death because of Avian Influenza which are 160 deaths1. Avian Influenza results from infection by viruses in the influenza virus A genus and influenza A species of the family Orthomyxoviridae. These viruses are also called type A influenza viruses2. The idea to study the risk of disease spreading was motivated by research published about mapping the risk of spread of Highly Pathogenic Avian Influenza H5N1 in Indonesia3. Glanville et al. using map layer of Indonesian major cities represents those cities in Indonesia that have a population greater than 50,000. It is expected that such cities are likely to have at least one poultry market. The density of cities was calculated over an area of 100 km, and the risk of spread classified according to this density (higher density=higher risk). In this research, the risk of disease spreading of

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Highly Pathogenic Avian Influenza H5N1 is not classified according to higher density which is equal to higher risk. We consider population changes in area to find the risk of disease spreading. Population density is usually shown as the number of people per square kilometer. Disease spreading and population density are highly correlated.

Fuzzy Logic can handle problems with imprecise data and give more accurate results. Professor L.A. Zadeh introduced the concept of Fuzzy Logic. The formalisation of Fuzzy sets started in the 1960s with the works of Zadeh in Fuzzy sets and Dempster in belief functions, set functions which generalise additive probability measure. Belief functions offer a non-Bayesian method for quantifying subjective evaluations by using probability. In the 1970s, it was further developed by Shafer, whose book Mathematical Theory of Evidence remains a mathematical framework in which assessments of evidence can be represented by belief functions, or the so-called Theory of Evidence. This research presents Fuzzy Logic and mathematical theory of evidence implement to detect the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1. Dempster-Shafer mathematical theory of evidence is a powerful tool for combining accumulative evidence and changing prior knowledge in the presence of new evidence. It also allows for the direct representation of uncertainty of system responses where an imprecise input can be characterized by a set or an interval and the resulting output is a set or an interval. Fuzzy Logic deals with truth values between 0 and 1, and these values are considered as intensity or degrees of truth. Dempster-Shafer mathematical theory of evidence, a probabilistic reasoning technique, is designed to deal with uncertainty and incompleteness of available information. Dempster-Shafer mathematical theory of evidence allows one to combine evidence from different sources and arrive at a degree of belief which is represented by a belief function that takes into account all the available evidence.

2. Evidence Combination

Mathematical theory of evidence provides a method to combine the previous measures of evidence of different sources. This rule assumes that these sources are independent. The combination: \( m = m_1 \oplus m_2 \), also called orthogonal sum, is defined according to the Dempster’s rule of combination, given in equation 1. It can be applied repetitively when the sources are more than two. After the combination, a decision can be made among the different hypotheses according to the decision rule chosen.

\[
(m_1 \oplus m_2)(A) = \begin{cases} 
0; & A = 0 \\
\sum_{B_i \cap B_j = A} m_1(B_i)m_2(B_j); & A \neq 0 \\
1 - \sum_{B_i \cap B_j \neq 0} m_1(B_i)m_2(B_j) & 
\end{cases}
\]

(1)

Where \( A \in 2^\Theta \), \( B_i \in 2^\Theta \) and \( B_j \in 2^\Theta \).

To use Dempster-Shafer mathematical theory of evidence, there must be the feasible measures to determine basic probability assignment. The Fuzzy theory also requires basic probability assignment. Basic probability assignment which is called the primitive function is the fundamental and important object of the mathematical theory of evidence. The membership function of a Fuzzy set is a generalization of the indicator function in classical sets. In Fuzzy Logic, it represents the degree of truth as an extension of valuation. Fuzzy Logic is a logic operation method based on many-valued logic rather than binary logic or two-valued logic. Two-valued logic often considers 0 to be false and 1 to be true. Fuzzy Logic deals with truth values between 0 and 1, and these values are considered as the intensity or degrees of truth. Dempster-Shafer mathematical theory of evidence, a probabilistic reasoning technique, is designed to deal with uncertainty and incompleteness of available information. Dempster-Shafer mathematical theory of evidence allows one to combine evidence from different sources and arrive at a degree of belief which is represented by a belief function that takes into account all the available evidence. The Degree of belief is expecting a truth value which is the relation between Fuzzy Logic and Dempster-Shafer mathematical theory of evidence.
3. Fuzzy Logic and Mathematical Theory of Evidence to The Risk of Disease Spreading of Highly Pathogenic Avian Influenza H5N1

The set of linguistic variables and their meanings is compatible and consistent with the set of conditional rules used, the overall outcome of the qualitative process is translated into objective and quantifiable results. Fuzzy mathematical tools and the calculus of Fuzzy IF-THEN rules provide a most useful paradigm for the automation and implementation of an extensive body of human knowledge heretofore not embodied in the quantitative modelling process. These mathematical tools provide a means of sharing, communicating, and transferring this human subjective knowledge of systems and processes. On the basis of the description of input and output variables, this research has constructed 25 rules for the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1. The Fuzzy rules are nearly a series of if-then statements. These statements are derived by an expert to achieve optimum results. Following is the description of the rules of the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1:

1. IF Area1 Density is [Very Low] AND Area2 Density is [Very High] THEN The Risk of Disease Spreading should be [Medium]
2. IF Area1 Density is [Low] AND Area2 Density is [Very High] THEN The Risk of Disease Spreading should be [Low]
3. IF Area1 Density is [Medium] AND Area2 Density is [Very High] THEN The Risk of Disease Spreading should be [Very Low]
4. IF Area1 Density is [High] AND Area2 Density is [Very High] THEN The Risk of Disease Spreading should be [Very Low]
5. IF Area1 Density is [Very High] AND Area2 Density is [Very High] THEN The Risk of Disease Spreading should be [Very Low]
6. IF Area1 Density is [Very Low] AND Area2 Density is [High] THEN The Risk of Disease Spreading should be [High]
7. IF Area1 Density is [Low] AND Area2 Density is [High] THEN The Risk of Disease Spreading should be [Very Low]
8. IF Area1 Density is [Medium] AND Area2 Density is [High] THEN The Risk of Disease Spreading should be [Very Low]
9. IF Area1 Density is [High] AND Area2 Density is [High] THEN The Risk of Disease Spreading should be [Very Low]
10. IF Area1 Density is [Very High] AND Area2 Density is [High] THEN The Risk of Disease Spreading should be [Very Low]
11. IF Area1 Density is [Very Low] AND Area2 Density is [Medium] THEN The Risk of Disease Spreading should be [High]
12. IF Area1 Density is [Low] AND Area2 Density is [Medium] THEN The Risk of Disease Spreading should be [High]
13. IF Area1 Density is [Medium] AND Area2 Density is [Medium] THEN The Risk of Disease Spreading should be [Medium]
14. IF Area1 Density is [High] AND Area2 Density is [Medium] THEN The Risk of Disease Spreading should be [Very Low]
15. IF Area1 Density is [Very High] AND Area2 Density is [Medium] THEN The Risk of Disease Spreading should be [Very Low]
16. IF Area1 Density is [Very Low] AND Area2 Density is [Low] THEN The Risk of Disease Spreading should be [Very High]
17. IF Area1 Density is [Low] AND Area2 Density is [Low] THEN The Risk of Disease Spreading should be [Very High]
18. **IF** Area1 Density is [Medium] **AND** Area2 Density is [Low] **THEN** The Risk of Disease Spreading should be [High]

19. **IF** Area1 Density is [High] **AND** Area2 Density is [Low] **THEN** The Risk of Disease Spreading should be [Low]

20. **IF** Area1 Density is [Very High] **AND** Area2 Density is [Low] **THEN** The Risk of Disease Spreading should be [Very Low]

21. **IF** Area1 Density is [Very Low] **AND** Area2 Density is [Very Low] **THEN** The Risk of Disease Spreading should be [Very High]

22. **IF** Area1 Density is [Low] **AND** Area2 Density is [Very Low] **THEN** The Risk of Disease Spreading should be [Very High]

23. **IF** Area1 Density is [Medium] **AND** Area2 Density is [Very Low] **THEN** The Risk of Disease Spreading should be [Very High]

24. **IF** Area1 Density is [High] **AND** Area2 Density is [Very Low] **THEN** The Risk of Disease Spreading should be [High]

25. **IF** Area1 Density is [Very High] **AND** Area2 Density is [Very Low] **THEN** The Risk of Disease Spreading should be [Medium]

There are two input variables which include Area1 and Area2 taken in this Fuzzy system. These variables use different membership functions. Area1 functions which include Area1very low, Area1low, Area1medium, Area1high, Area1very high. Area2 functions which include Area2very low, Area2low, Area2medium, Area2high, Area2very high. Area1 is a Fuzzy range of population density in Kendal and Area2 is a Fuzzy range of population density in Temanggung. Fuzzy ranges of population density of two areas in Central Java to detect the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 can be defined as follows:

Area1very low = 8,000; Area1low = 11,000; Area1medium = 14,000; Area1high = 17,000; Area1very high = 20,000

Area2very low = 6,000; Area2low = 8,000; Area2medium = 10,000; Area2high = 12,000; Area2very high = 14,000

**Area1very low** is used to define the variable very low. The weight is calculated by the following formula:

$$
\mu(Area1_{low}[x]) = \begin{cases} 
1, & x \leq 8,000 \\
\frac{11,000-x}{11,000-8,000}, & 8,000 \leq x \leq 11,000 \\
0, & x \geq 11,000 
\end{cases} \quad (2)
$$

**Area1low** is used to define the variable low. The weight is calculated by the following formula:

$$
\mu(Area1_{low}[x]) = \begin{cases} 
0, & x \leq 8,000 \text{ or } x \geq 14,000 \\
\frac{x-8,000}{11,000-8,000}, & 8,000 \leq x \leq 11,000 \\
\frac{14,000-x}{14,000-11,000}, & 11,000 \leq x \leq 14,000 
\end{cases} \quad (3)
$$

**Area1medium** is used to define the variable medium. The weight is calculated by the following formula:

$$
\mu(Area1_{medium}[x]) = \begin{cases} 
0, & x \leq 11,000 \text{ or } x \geq 17,000 \\
\frac{x-11,000}{14,000-11,000}, & 11,000 \leq x \leq 14,000 \\
\frac{17,000-x}{17,000-14,000}, & 14,000 \leq x \leq 17,000 
\end{cases} \quad (4)
$$

**Area1high** is used to define the variable high. The weight is calculated by the following formula:
$$\mu(Area_{1\text{high}}[x]) = \begin{cases} 
0, & x \leq 14,000 \text{ or } x \geq 20,000 \\
\frac{x-14,000}{20,000-14,000}, & 14,000 \leq x \leq 17,000 \\
\frac{17,000-x}{20,000-17,000}, & 17,000 \leq x \leq 20,000 
\end{cases}$$ (5)

$Area_{1\text{very high}}$ is used to define the variable very high. The weight is calculated by the following formula:

$$\mu(Area_{1\text{very high}}[x]) = \begin{cases} 
0, & x \leq 17,000 \\
\frac{x-17,000}{20,000-17,000}, & 17,000 \leq x \leq 20,000 \\
1, & x \geq 20,000 
\end{cases}$$ (6)

**Area2 of Highly Pathogenic Avian Influenza H5N1**

$Area_{2\text{very low}}$ is used to define the variable very low. The weight is calculated by the following formula:

$$\mu(Area_{2\text{very low}}[y]) = \begin{cases} 
1, & y \leq 6,000 \\
\frac{8,000-y}{8,000-6,000}, & 6,000 \leq y \leq 8,000 \\
0, & y \geq 8,000 
\end{cases}$$ (7)

$Area_{2\text{low}}$ is used to define the variable low. The weight is calculated by the following formula:

$$\mu(Area_{2\text{low}}[y]) = \begin{cases} 
0, & y \leq 6,000 \text{ or } y \geq 10,000 \\
\frac{y-6,000}{10,000-6,000}, & 6,000 \leq y \leq 8,000 \\
\frac{8,000-y}{10,000-8,000}, & 8,000 \leq y \leq 10,000 
\end{cases}$$ (8)

$Area_{2\text{medium}}$ is used to define the variable medium. The weight is calculated by the following formula:

$$\mu(Area_{2\text{medium}}[y]) = \begin{cases} 
0, & y \leq 8,000 \text{ or } y \geq 12,000 \\
\frac{y-8,000}{12,000-8,000}, & 8,000 \leq y \leq 10,000 \\
\frac{10,000-y}{12,000-10,000}, & 10,000 \leq y \leq 12,000 
\end{cases}$$ (9)

$Area_{2\text{high}}$ is used to define the variable high. The weight is calculated by the following formula:

$$\mu(Area_{2\text{high}}[y]) = \begin{cases} 
0, & y \leq 10,000 \text{ or } y \geq 14,000 \\
\frac{y-10,000}{12,000-10,000}, & 10,000 \leq y \leq 12,000 \\
\frac{10,000-y}{12,000-10,000}, & 12,000 \leq y \leq 14,000 
\end{cases}$$ (10)

$Area_{2\text{very high}}$ is used to define the variable very high. The weight is calculated by the following formula:

$$\mu(Area_{2\text{very high}}[y]) = \begin{cases} 
0, & y \leq 12,000 \\
\frac{y-12,000}{14,000-12,000}, & 12,000 \leq y \leq 14,000 \\
1, & y \geq 14,000 
\end{cases}$$ (11)
Assume that the population density for inputs to detect the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 can be defined as follows:

\[ \begin{align*}
Area_{1\text{very low}} &= 9,500; \\
Area_{1\text{low}} &= 12,500; \\
Area_{1\text{medium}} &= 15,500; \\
Area_{1\text{high}} &= 16,000; \\
Area_{1\text{very high}} &= 19,000 \\
Area_{2\text{very low}} &= 7,000; \\
Area_{2\text{low}} &= 9,250; \\
Area_{2\text{medium}} &= 10,750; \\
Area_{2\text{high}} &= 11,500; \\
Area_{2\text{very high}} &= 12,950
\end{align*} \]

Membership value of Area1 density to detect the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 can be calculated as follows:

\[ \begin{align*}
\mu(Area_{1\text{very low}}[9,500]) &= \frac{11,000 - 9,500}{11,000 - 8,000} = 0.50 \\
\mu(Area_{1\text{low}}[12,500]) &= \frac{14,000 - 12,500}{14,000 - 11,000} = 0.50 \\
\mu(Area_{1\text{medium}}[15,500]) &= \frac{17,000 - 15,500}{17,000 - 14,000} = 0.50 \\
\mu(Area_{1\text{high}}[16,000]) &= \frac{16,000 - 14,000}{17,000 - 14,000} = 0.666 \\
\mu(Area_{1\text{very high}}[19,000]) &= \frac{19,000 - 17,000}{20,000 - 17,000} = 0.666
\end{align*} \]

Membership value of Area2 density to detect the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 can be calculated as follows:

\[ \begin{align*}
\mu(Area_{2\text{very low}}[7,000]) &= \frac{8,000 - 7,000}{8,000 - 6,000} = 0.50 \\
\mu(Area_{2\text{low}}[9,250]) &= \frac{10,000 - 9,250}{10,000 - 8,000} = 0.375 \\
\mu(Area_{2\text{medium}}[10,750]) &= \frac{12,000 - 10,750}{14,000 - 12,000} = 0.625 \\
\mu(Area_{2\text{high}}[11,500]) &= \frac{11,500 - 10,000}{12,000 - 10,000} = 0.75 \\
\mu(Area_{2\text{very high}}[12,950]) &= \frac{12,950 - 12,000}{14,000 - 12,000} = 0.475
\end{align*} \]

From the above, membership values to detect the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 are shown as follows:

\[ \begin{align*}
Area_{1\text{very low}} &= 0.50; \\
Area_{1\text{low}} &= 0.50; \\
Area_{1\text{medium}} &= 0.50; \\
Area_{1\text{high}} &= 0.666; \\
Area_{1\text{very high}} &= 0.666 \\
Area_{2\text{very low}} &= 0.50; \\
Area_{2\text{low}} &= 0.375; \\
Area_{2\text{medium}} &= 0.625; \\
Area_{2\text{high}} &= 0.75; \\
Area_{2\text{very high}} &= 0.475
\end{align*} \]

The result of Highly Pathogenic Avian Influenza H5N1 Fuzzy rules between Area1 versus Area2 are shown in Figure 1. The similarity between Fuzzy membership function to get the basic probability assignment can be calculated by the equation 12:

\[
Bel(\text{variables}) = \frac{\sum_{i=1}^{n} \min_{u} [\mu_{A_i}(u) \land \mu_{A_i}(u), \max_{v} [\mu_{B_i}(v) \land \mu_{B_i}(v)]](\text{variables})}{n(\text{variables})} \tag{12}
\]
The risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 describes five interpretations which include the risk of disease spreading should be very low, the risk of disease spreading should be low, the risk of disease spreading should be medium, the risk of disease spreading should be high, and the risk of disease spreading should be very high. The following will shown the detection process of the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1.

1. The risk of disease spreading should be Very Low (RSVL)

\[ m_1[RSVL] = 0.5424, \quad m_1[\theta] = 1 - 0.5424 = 0.4576 \]

2. The risk of disease spreading should be Low (RSL)

\[ m_2[RSL] = 0.45, \quad m_2[\theta] = 1 - 0.45 = 0.55 \]

The calculation of the combined \( m_1 \) and \( m_2 \) is shown in Table 1. Each cell of the table contains the intersection of the corresponding propositions from \( m_1 \) and \( m_2 \) along with the product of their individual belief.
Table 1. The first combination of the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1

|   | [RSVL] | 0.5424 | θ 0.45 | 0.55 | [RSVL] | 0.2983 |
|---|---|---|---|---|---|---|
| θ | 0.4576 | [RSL] | 0.2059 | θ 0.2517 |

Table 2. The second combination of the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1

|   | [RSM] | 0.4917 | θ 0.5083 | [RSVL] | 0.2006 |
|---|---|---|---|---|---|
| [RSVL] | 0.3946 | θ 0.1940 | [RSVL] | 0.1339 | [RSL] | 0.1385 |
| [RSL] | 0.2724 | θ 0.1637 | [RSM] | 0.1693 |
| θ | 0.3330 | [RSM] | 0.1181 |

Table 3. The third combination of the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1

|   | [RSH] | 0.4687 | θ 0.5313 | [RSVL] | 0.1586 |
|---|---|---|---|---|---|
| [RSVL] | 0.2985 | θ 0.1399 | [RSVL] | 0.1095 |
| [RSL] | 0.2061 | θ 0.0966 | [RSL] | 0.1294 |
| [RSM] | 0.2436 | θ 0.1142 | [RSM] | 0.1338 |
| θ | 0.2519 | [RSH] | 0.1181 |

The first two bpas \( m_1 \) and \( m_2 \) are calculated to yield a new bpa \( m_3 \) by a combination rule as follows:
\[
m_3\{RSVL\} = 0.2983 \frac{1}{1-0.2441} = 0.3946, \quad m_3\{RSL\} = 0.2059 \frac{1}{1-0.2441} = 0.2724, \quad m_3\{θ\} = 0.2517 \frac{1}{1-0.2441} = 0.3330
\]

3. The risk of disease spreading should be Medium (RSM)

\[m_4\{RSM\} = 0.4917, \quad m_4\{θ\} = 1 - 0.4917 = 0.5083\]

The calculation of the combined \( m_3 \) and \( m_4 \) is shown in Table 2. Each cell of the table contains the intersection of the corresponding propositions from \( m_3 \) and \( m_4 \) along with the product of their individual belief.

The second two bpas \( m_3 \) and \( m_4 \) are calculated to yield a new bpa \( m_5 \) by a combination rule as follows:
\[
m_5\{RSVL\} = 0.2006 \frac{1}{1-0.1940+0.1339} = 0.2985, \quad m_5\{RSL\} = 0.1385 \frac{1}{1-0.1940+0.1339} = 0.2061,
\]
\[
m_5\{RSM\} = 0.1693 \frac{1}{1-0.1940+0.1339} = 0.2436, \quad m_5\{θ\} = 0.1693 \frac{1}{1-0.1940+0.1339} = 0.2519
\]

4. The risk of disease spreading should be High (RSH)

\[m_6\{RSH\} = 0.4687, \quad m_6\{θ\} = 1 - 0.4687 = 0.5313\]

The calculation of the combined \( m_5 \) and \( m_6 \) is shown in Table 3. Each cell of the table contains the intersection of the corresponding propositions from \( m_5 \) and \( m_6 \) along with the product of their individual belief.

The third two bpas \( m_5 \) and \( m_6 \) are calculated to yield a new bpa \( m_7 \) by a combination rule as follows:
\[
m_7\{RSVL\} = 0.1586 \frac{1}{1-(0.1339+0.0966+0.1142)} = 0.2420, \quad m_7\{RSL\} = 0.1095 \frac{1}{1-(0.1339+0.0966+0.1142)} = 0.1671,
\]
Table 4. The fourth combination of the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1

|      | [RSVL] | 0.4583 | θ | 0.5417 |
|------|--------|--------|---|--------|
| [RSVL] | 0.2420 | ø      | 0.1109 | [RSVL] | 0.1311 |
| [RL]  | 0.1671 | ø      | 0.0766 | [RL]  | 0.0905 |
| [RSM] | 0.1975 | ø      | 0.0905 | [RSM] | 0.107  |
| [RSH] | 0.1802 | ø      | 0.0826 | [RSH] | 0.0976 |

\[
m_7[RSM] = \frac{0.1294}{1 - (0.1339 + 0.0966 + 0.1142)} = 0.1975, \quad m_7[RSH] = \frac{0.1181}{1 - (0.1339 + 0.0966 + 0.1142)} = 0.1802, \]

\[
m_7[\theta] = \frac{0.1338}{1 - (0.1339 + 0.0966 + 0.1142)} = 0.2042
\]

5. The risk of disease spreading should be Very High (RSVH)

\[
m_8[RSVH] = 0.4583, \quad m_8[\theta] = 1 - 0.4583 = 0.5417
\]

The calculation of the combined \(m_7\) and \(m_8\) is shown in Table 4. Each cell of the table contains the intersection of the corresponding propositions from \(m_7\) and \(m_8\) along with the product of their individual belief.

The fourth two bpas \(m_7\) and \(m_8\) are calculated to yield a new bpa \(m_9\) by a combination rule as follows:

\[
m_9[RSVL] = \frac{0.1311}{1 - (0.1109 + 0.0766 + 0.0905 + 0.0826)} = 0.20, \quad m_9[RL] = \frac{0.0905}{1 - (0.0550 + 0.1099 + 0.0722 + 0.0671)} = 0.141,
\]

\[
m_9[RSM] = \frac{0.107}{1 - (0.0550 + 0.1099 + 0.0722 + 0.0671)} = 0.167, \quad m_9[RSH] = \frac{0.0976}{1 - (0.0550 + 0.1099 + 0.0722 + 0.0671)} = 0.153,
\]

\[
m_9[RSVH] = \frac{0.0936}{1 - (0.0550 + 0.1099 + 0.0722 + 0.0671)} = 0.146, \quad m_9[\theta] = \frac{0.1106}{1 - (0.0550 + 0.1099 + 0.0722 + 0.0671)} = 0.173
\]

Finally, in Kendal and Temanggung, the highest basic probability assignment value is \(m_9[RSVL]\) which is equal to 0.20. This means the possibility of the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 include very low, low, medium, high, and very high is very low. The risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 in areas which include Batang, Kendal, Kota Magelang, Kota Salatiga, Kota Semarang, Magelang, Semarang, Temanggung, Wonosobo. Figure 2 shows the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1.

4. Conclusion

In the absence of empirical data, experts in related fields provide necessary information. The fundamental objects of this theory of evidence are called focal elements, and the primitive function associated with it is called basic probability assignment. Focal elements are usually crisp subsets of some universal set. However, in certain situations focal elements may also be represented by Fuzzy numbers. There are many situations where human often face at the same time Fuzzy and non Fuzzy uncertainties. This suggests to combine mathematical theory of evidence and Fuzzy sets frameworks. Thus, the goal of this work is to estimate basic probability assignments using Fuzzy membership functions which capture vagueness. The advantage of this method is a new method to obtain basic probability assignment proposed based on the similarity measure between membership function. This thesis proposes integrating Fuzzy Logic and mathematical theory of evidence by calculating the similarity between Fuzzy membership function.

Fuzzy logic and mathematical theory of evidence contribute new ideas to detect the risk of disease spreading. The risk of disease spreading is not classified according to higher density which is equal to higher risk. This research considers population changes in an area to detect the risk of disease spreading. Population density in areas which
include very low, low, medium, high and very high. The result reveals that in areas which are in close proximity to Kendal and Temanggung, the highest basic probability assignment value of the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 is very low which is equal to 0.20. It means the risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 is very rare but cannot be excluded. The risk of disease spreading of Highly Pathogenic Avian Influenza H5N1 in areas which include Batang, Kendal, Kota Magelang, Kota Salatiga, Kota Semarang, Magelang, Semarang, Temanggung, and Wonosobo.

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