

Prognostic Model for the Risk of Coronavirus Disease (COVID-19) Using Fuzzy Logic Modeling

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ABSTRACT

This study formulated a model for assessing the risk of coronavirus disease (COVID-19) based on variables associated with the spread of COVID-19 infections. The study used the Mamdani fuzzy logic model based on a multiple input and single output (MISO) scheme which required 12 inputs and one output variable. Each of the input variables was identified using binary values, namely No and Yes, while the spread of COVID-19 was assessed using four nominal linguistic values. Two triangular membership functions were used to formulate each associated variable and four triangular membership functions to formulate the spread of COVID-19 using specific crisp intervals. The results of the study showed that 4096 rules were inferred from the possible combination of the binary linguistic values of the associated variables for the assessment of the spread of COVID-19. The study concluded that knowledge about variables associated with the spread of COVID-19 infection can be adopted for supporting decision-making which affects the assessment of the spread of COVID-19 by stakeholders.

KEYWORDS

Coronavirus, COVID-19, Disease Spread, Fuzzy Logic, Predictive Modeling

1. INTRODUCTION

Coronavirus is a member of the influenza virus family, which includes symptoms such as pneumonia, respiratory problems, fever, and lung infection in the victims. (Adhhikari, et al., 2020). Although it is known that these viruses are common among animals around the world, recent studies have shown that they also infect humans (Zhu, et al., 2020). According to Li et al. (2020), the World Health Organization (WHO) mentioned the type of coronavirus that affects the lower respiratory tract of patients with pneumonia in China, the new 2019 coronavirus. According to WHO (2020), the official name for the new 2019 coronavirus is coronavirus disease (COVID-19), while the reference is the severe acute respiratory syndrome of coronavirus 2 (SARS-CoV-2). Common symptoms of COVID-19 include: fever, cough, shortness of breath, sputum, muscle pain, diarrhea, sore throat, loss of smell, and abdominal pain (Centers for Disease Control and Prevention (CDC), 2020a). The

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incubation period is the delay between the moment a person becomes infected with the virus and the moment the symptoms appear. For COVID-19, the incubation period is usually five to six days, but can vary from two to 14 days, but in 97.5% of people with symptoms develop within 11.5 days after infection (Lauer *et al.*, 2020).

There are some people who are not infected but develop symptoms called asymptomatic, but their role in transmitting COVID-19 is unknown (Centers for Disease Control and Prevention (CDC), 2020b). However, preliminary evidence suggests that asymptomatic individuals contribute to the spread of COVID-19 (Bai, *et al.*, 2020). COVID-19 is mainly distributed between people during close contact and through respiratory drops from cough and sneezing is faster when people are next to each other or traveling between areas (Centers for Disease Control and Prevention, 2020c). According to Kucharsky *et al.* (2020), travel restrictions may affect the base number of reproductions from 2.35 to 1.05, which makes the epidemic more manageable. The first case of a new coronavirus for 2019 was reported by marketers in Wuhan, Hubei Province, China, on December 29, 2019, when five patients suffered from acute respiratory distress syndrome after the death of one of the hospitalized patients (Lu, Stratton & Tang, 2020; Zhao, *et al.*, 2020). Later, 41 registered patients with laboratory-confirmed COVID-19 infection were identified by January 2, 2020, of which less than half had the underlying disease, including diabetes and hypertension.

After this event, it was noted that COVID-19 infection was largely spread due to the fact that many patients were infected in various places in the hospital by unidentified methods. Only patients who became ill were tested with the more suspected infected patients. On January 25, 2020, a total of 1975 cases with COVID-19 were confirmed in mainland China, with a total of 56 deaths, and by January 30, 2020, 7,734 cases were confirmed in China, with 90 other cases reported, including: Taiwan, Thailand, Vietnam, Malaysia, Nepal, Sri Lanka, Cambodia, Japan, Singapore, Republic of Korea, United Arab Emirates, United States (USA), Philippines, India, Australia, Canada, Finland, France and Germany (Nishiura, *et al.*, 2020; Bassetti, Vena and Giacobbe, 2020). The first human-to-human transmission of COVID-19 was recorded in the United States, which also led to the description, identification, diagnosis, clinical course, and management of COVID-19 (Holshue *et al.*, 2020). Also on January 30, 2020, WHO announced the coronavirus 2019/2020, a Public Health Emergency of International Concern (PHEIC) and pandemic March 11, 2020 (WHO, 2020b). The first case of COVID-19 in Nigeria occurred on February 27, 2020, when a citizen of Italy in Lagos had a positive result, and in the second case, in Ogun, a citizen of Nigeria working with an Italian came into contact. (Nigerian Center for Disease Control (NCDC), 2020; PM News, 2020). As of March 31, 2020, the total number of cases in Nigeria was 135 with 2 deaths and 8 collections.

Preventive measures to reduce the likelihood of infection include staying at home, avoiding places, washing your hands with soap and water for at least 20 seconds, breathing hygiene and eyes, nose, or Avoid using your mouth with a dirty hand (WHO), 2020c). The CDC also recommends covering of the mouth and nose with tissue when coughing or sneezing, using the inside of your elbow if tissues are not accessible, and good hand hygiene after any coughing or sneezing (CDC, 2019). Social distancing strategies are also recommended because they aim to reduce contact with infected people in large groups. This is ensured by the closure of schools and jobs, travel restrictions and the cancellation of public events (Maragakis, 2020). There is currently no vaccine against SARS-CoV-2, which is expected only in 2021, and a key role in combating the COVID-19 pandemic is to reduce the number of new infections. This can reduce the risk of suppressing health services, thereby improving treatment for current cases and delaying additional cases until vaccines are readily available (Anderson, Heesterbeek, Klinkenberg, & Hollingsworth, 2020).

The motivation for developing a predictive model for distributing COVID-19 was to use some new tool, such as fuzzy logic, when developing an expert system based on fuzzy logic. Fuzzy logic was used mainly to eliminate the uncertainties in human-oriented analysis as a way of processing complex, inaccurate, uncertain, and vague data. Expert systems (also known as knowledge-based systems) are computer programs that aim to achieve the same level of accuracy as human experts when

dealing with complex, poorly structured problems in a particular area, which allows non-specialists to use them for receiving answers to problems or for experts to gain decision support (Turban, Sharda, & Delen, 2010). The strength of these systems lies in their ability to use expert knowledge almost when an expert is unavailable. Expert systems make knowledge more accessible and help solve the problem of translating knowledge into practical useful results.

Fuzzy logic is an extended set of traditional (Boolean) logic designed to access the concept of partial truth (Massad, Ortega, de Barros, & Struchiner, 2008). Fuzzy logic is associated with the morphology of logical inference, which can apply the approaches of human thinking to knowledge-based systems. Fuzzy logic is a computational approach based on *degrees of truth*, and not on the classic *truth or false* Boolean logic (1 or 0). This is because it is difficult to assign a natural language in absolute terms 0 and 1. Fuzzy logic uses 0 and 1 as extreme cases of truth, but also contains various states of truth represented by the meanings that lie between them. Fuzzy Inference Systems (FIS) are widely used to model or control processes and can be developed based on expert knowledge or data. The fuzzy inference mechanism consists of three phases, namely: fuzzification for displaying numerical inputs using functions with some degree of compatibility; processing rules in accordance with the fire resistance of the inputs; and defuzzification, where subsequent fuzzy values are again converted to numerical values (Plerou, Vlamou, & Papadopoulos, 2016). This procedure allows the use of fuzzy categories in the representation of words and abstract ideas of a person in the description of decision-making procedures.

2. RELATED WORKS

Deepak, Divya, Suyash and Mayank (2020), worked on the application of fuzzy logic modeling for the prediction of COVID-19. The study identified eleven (11) variables associated with the prediction of COVID-19 namely: fever, cough, age, diabetes, travel history, breathing problems, flu, hearing problems, loss of smell, body aches and sore throat. The study formulated the fuzzy logic model using triangular membership functions to fuzzify the identified variables following which fifteen (15) inference rules were used to represent the association between the variables and the risk of COVID-19. The results revealed that a relationship between the identified variables and the risk of COVID-19 can be established using fuzzy logic inference rules. The number of inference rules adopted in the study did not capture all the possible combination of the values of the associated variables identified.

Arji *et al.* (2019), in their study performed a methodical evaluation, review and classification of studies covering the use of fuzzy logic modeling for the diagnosis of infectious disease. The study assessed over forty (40) papers which were published between 2005 to 2019 covering areas related to human infectious diseases. The papers were retrieved from indexing sources such as: Scopus, PubMed, Science Direct and Web of Sciences from an initial value of 300 articles. The results of the study revealed the wide application of fuzzy logic rule modeling to diseases such as: dengue fever, hepatitis and tuberculosis to mention a few. The results showed that the fuzzy approaches adopted included: fuzzy inference systems, fuzzy set theory, rule-based fuzzy logic, fuzzy expert system, and fuzzy decision support system to mention a few with the most popular been fuzzy inference systems. The study suggested a need for intensive efforts on the application of fuzzy logic modeling to infectious disease research.

Renu, Tiwari, & Ranjit (2018), applied fuzzy logic modeling to the modeling of the spread of Influenza virus. The study formulated fuzzy membership functions for the contact rate, death-induced mortality and virus load. The study assumed that the contact rate and the death-induced mortality rate were both functions of the viral load. The study adopted the use of trapezoidal membership function for the formulation of the contact and death-induced mortality rate while triangular membership functions were used to formulate the viral load. The results of the study showed that the spread of the Influenza virus can be controlled due to proper management of the the contact rate and the

death-induced mortality rate of the population. The study was limited to the modeling of the spread of influenza virus.

Scrobota, *et al.* (2017), worked on the application of fuzzy logic modeling to the risk assessment of oral cancer. The study adopted the use of the Mamdani fuzzy logic model for estimating the oxidative stress related-cancerization risk of oral potentially malignant disorders. Two biochemical parameters, namely: the serum total malondialdehyde (MDA) and serum proton donor capacity (DONORS_PROTONS) were formulated as the input variables alongside the risk of oral cancer as the output variable. Five fuzzy triangular membership functions were used to formulate the linguistic variables of each input parameter following which 25 IF-THEN rules were inferred from the input and output variables. The result showed that fuzzy logic is appropriate for prediction since it can reach general solutions by using limited data and even uncertain verbal information characteristic to human logic. The study was limited to the assessment of the risk of oral cancer.

Idowu, Aladekomo, & Balogun, (2015), applied fuzzy logic modeling to the survival of sickle-cell anaemia (SCA) among pediatric patients in Nigeria. The study adopted the use of the Mamdani fuzzy model for the estimation of the level of survival. The study identified three variables to be associated with the survival of SCA among pediatrics, namely: level of fetal haemoglobin, genotype and the degree of anaemia. Triangular membership functions were used to formulate the linguistic values of the variables following which 18 IF-THEN rules were inferred from the possible combination of the linguistic values of the variables. The results of the study showed the ability of fuzzy logic to capture human reasoning required for assessing the survival of SCA.

3. MATERIALS AND METHODS

In this study, fuzzy logic model was adopted for the development of a predictive model required for the assessment of the risk of the spread of COVID-19 from an individual to another individual. Therefore, an attempt was made at the identification of the various risk factors/symptoms which are associated with the risk of COVID-19 spread from individual to individual. Information was sought from the website of the Philippines Department of Health (DOH) located at www.doh.gov.ph. The variables identified consisted of clinical and epidemiological variables and are presented in Table 1 alongside their respective linguistic values and weighted values. Unlike variables identified in related works which had equal weights assigned, the variables in this study possess varying weighted values to their relative association with the spread of COVID-19. Therefore, clinical variables were assigned weighted values of 1 and 2 while the epidemiological variables were assigned weighted values of 3.

As shown in Table 1, there are twelve variables/symptoms which are associated with the risk of the spread of the COVID-19 infection from individual to individual. All the identified variables are binary values with values, Yes and No respectively. Also, for each identified variables associated with the spread of COVID-19 infection, there is a weighted value. The first seven variables have a weighted value of 1, namely: presence of cough, colds, diarrhea, sore throat, body aches, headaches, and fever. The next two variables have a weighted value of 2, namely: difficulty breathing and fatigue. The last three variables have a weighted value of 3, namely: travelled last fortnight, travel history to COVID-19 infected area and direct contact with COVID-19 patient.

As a result of this, whenever the linguistic value of a variable is No then a value of 0 is assigned else its respective weighted value. Thus showing the degree of importance of the association of variables with the risk of the spread of COVID-19 infection. Therefore, variables with a higher association with the spread of COVID-19 infection have higher weighted values while those with lower association with COVID-19 infection have lower weighted values. The total sum of the weighted values of the variables based on the linguistic values were used to estimate the risk of the spread of COVID-19 infection from individual to individual. Table 2 shows the various linguistic values that were used to assess the risk of the spread of COVID-19 infection based on the sum of the weighted values of the identified variables.

Table 1. Identification of Factors associated with COVID-19 Spread

S/N	Variable Name	Linguistic Values	Weighted Value
V1	Presence of Cough	Yes No	1
V2	Presence of Colds	Yes No	1
V3	Presence of Diarrhea	Yes No	1
V4	Presence of Sore Throat	Yes No	1
V5	Presence of Body Aches	Yes No	1
V6	Presence of Headaches	Yes No	1
V7	Presence of Fever (above 37.8 degrees Celcius)	Yes No	1
V8	Difficulty Breathing	Yes No	2
V9	Fatigue	Yes No	2
V10	Travelled last Fortnight	Yes No	3
V11	Travel History to COVID-19 Infected Area	Yes No	3
V12	Direct contact with COVID-19 Patient	Yes No	3

Table 2. Level of Risk of Spread of COVID-19 Infection

Output Variable	Linguistic Value	Crisp Interval	Remarks
Spread of COVID-19 Infection	No Risk	Below 3	Stress related, observe
	Low Risk	3 – 5	Hydrate properly and maintain proper hygiene
	Moderate Risk	6 – 12	Seek a consultation with doctor
	High Risk	Above 12	Call the COVID-19 Response Hotline

As shown in Table 2, it can be observed that there were four classification of the level of the risk of spread of COVID-19, namely: No, Low, Moderate and High risk of COVID-19 spread. A total weighted score below 3 implies a no risk of spread, a total weighted score between the closed interval [3, 5] implies a low risk of spread, a total weighted score between the closed interval [6, 12] implies a moderate risk of spread while a total weighted score above 12 implies a high risk of spread. Following the identification of the risk factors/symptoms associated with the spread of COVID-19, fuzzy membership functions were used to fuzzify the linguistic values (fuzzification of variables) of the identified variables associated with COVID-19 spread.

The triangular membership function was used to formulate the linguistic vales associated with each identified variable. This is because the triangular membership function was appropriate for specifying crisp values used for describing each linguistic value. Therefore, since each variables had

two linguistic variables, namely: Yes and No; two triangular membership functions were described for each variable associate with the risk of COVID-19. Equation (1) shows the relationship between the crisp interval [a, b, c] of each linguistic value suggested for this study and their respective fuzzified values.

$$linguistic_value; [x : a, b, c] = \begin{cases} 0; x \leq a \\ \frac{x-a}{b-a}; a < x \leq b \\ \frac{c-x}{c-b}; b < x \leq c \\ 0; x > c \end{cases} \quad (1)$$

For this study, the crisp interval [a, b, c] that was formulated for the linguistic values of the identified variables associated with the spread of COVID-19 infection, namely: No and Yes were [-0.5, 0, 0.5] and [0, 5, 1, 1.5] respectively with centers 0 and 1 respectively. Also, the crisp interval [a, b, c] that was formulated for the linguistic values of the level of the risk of spread of COVID-19 infection, namely: No Risk, Low risk, Moderate Risk and High Risk were [-0.5, 0, 0.5], [0, 5, 1, 1.5], [1.5, 2, 2.5] and [2.5, 3, 3.5] respectively with centers 0, 1, 2 and 3 respectively. Table 3 shows the linguistic value and their respective crisp interval [a, b, c] for each identified variable alongside the level of the risk of COVID-19 considered for this study. For each of the identified variables associated with the risk of the spread of COVID-19 infection from individual to individual, the crisp values of 0 and 1 is mapped to a full degree of membership of the linguistic values named No and Yes respectively. Thus, the selection of the linguistic value 1 for any of the identified variables initiates the weighted values associated with each of the identified variables as identified in Table 2.

Table 3. Fuzzification of Associated Variables and Spread of COVID-19

Variables	Linguistic Value	Crisp Interval
Associated Variables	No	[-0.5, 0, 0.5]
	Yes	[0.5, 1, 1.5]
Risk of Spread of COVID-19 Infection	No Risk	[-0.5, 1, 0.5]
	Low Risk	[0.5, 1, 1.5]
	Moderate Risk	[1.5, 2, 2.5]
	High Risk	[2.5, 3, 3.5]

Finally, the inference rules for the inference engine of the fuzzy model was formulated based on the combination of the possible linguistic values of the 12 identified variables associated with the risk of the spread of COVID-19 infection. This was done by determining the permutation of the two linguistic values for the 12 variables which resulted in 2^{12} (= 4096) rules in total. Therefore, 4096 rules were inferred for determining the risk of the spread of COVID-19 infection based on the selected linguistic value (Yes or No) for the 12 identified variables. The rules were inferred by using IF-THEN statements which used the combination of the possible linguistic values (Yes or No) of the identified variables as the antecedent and their respective output linguistic value of the spread of COVID-19 infection as the consequent part of the rules.

4. RESULTS

This section presents the results of this study which includes the fuzzification of the linguistic values of each identified variables associated with the spread of COVID-19 infection. As stated earlier, the two linguistic values of the identified variables namely: No and Yes were formulated using triangular membership functions with crisp closed intervals $[-0.5, 0, 0.5]$ and $[0.5, 1, 1.5]$ respectively. Equations (2a) and (2b) shows the equations that were used to formulate the triangular membership functions that were proposed for each identified variables associated with assessing the spread of COVID-19 infection from individual to individual.

$$No; [x : -0.5, 0, 0.5] = \begin{cases} 0; x \leq -0.5 \\ \frac{x + 0.5}{0.5}; -0.5 < x \leq 0 \\ \frac{0.5 - x}{0.5}; 0 < x \leq 0.5 \\ 0; x > 0.5 \end{cases} \quad (2a)$$

$$Yes; [x : 0.5, 1.0, 1.5] = \begin{cases} 0; x \leq 0.5 \\ \frac{x - 0.5}{0.5}; 0.5 < x \leq 1 \\ \frac{1.5 - x}{0.5}; 1 < x \leq 1.5 \\ 0; x > 1.5 \end{cases} \quad (2b)$$

The results of the simulation of the triangular membership functions used to formulate the linguistic values of the identified variables associated with the spread of COVID-19 infection is presented in Figure 1. As shown in Figure 1, the two triangular membership functions were formulated as function of the values of a, b and c as identified in their respective interval $[a, b, c]$. For each linguistic value, the value of a was used to define the left base point (-0.5 and 0.5 for No and Yes respectively), c to identify the right base point (0.5 and 1.5 for No and Yes respectively) and b to identify the central apex point at which the full degree of membership is assigned as 0 and 1 for No and Yes respectively.

Figure 1. Fuzzification of Variables associated with Spread of COVID-19



Also, the four linguistic values of the output spread of COVID-19 infection namely: No risk, Low risk, Moderate risk and High risk were formulated using triangular membership functions with crisp closed intervals [-0.5, 0, 0.5], [0.5, 1, 1.5], [1.5, 2, 2.5] and [2.5, 3, 3.5] respectively. Equations (3a) to (3d) shows the equations that were used to formulate the triangular membership functions that were proposed for each linguistic values that were used to describe the spread of COVID-19 infection from individual to individual. The results of the simulation of the triangular membership functions used to formulate the linguistic values of the spread of COVID-19 infection is presented in Figure 2.

$$\text{No Risk; } [x : -0.5, 0.0, 0.5] = \begin{cases} 0; x \leq -0.5 \\ \frac{x + 0.5}{0.5}; -0.5 < x \leq 0 \\ \frac{0.5 - x}{0.5}; 0 < x \leq 0.5 \\ 0; x > 0.5 \end{cases} \quad (3a)$$

$$\text{Low Risk; } [x : 0.5, 1.0, 1.5] = \begin{cases} 0; x \leq 0.5 \\ \frac{x - 0.5}{0.5}; 0.5 < x \leq 1 \\ \frac{1.5 - x}{0.5}; 1 < x \leq 1.5 \\ 0; x > 1.5 \end{cases} \quad (3b)$$

$$\text{Moderate Risk; } [x : 1.5, 2.0, 2.5] = \begin{cases} 0; x \leq 1.5 \\ \frac{x - 1.5}{0.5}; 1.5 < x \leq 2 \\ \frac{2.5 - x}{0.5}; 2 < x \leq 2.5 \\ 0; x > 2.5 \end{cases} \quad (3c)$$

$$\text{High Risk; } [x : 2.5, 3.0, 3.5] = \begin{cases} 0; x \leq 2.5 \\ \frac{x - 2.5}{0.5}; 2.5 < x \leq 3 \\ \frac{3.5 - x}{0.5}; 3 < x \leq 3.5 \\ 0; x > 3.5 \end{cases} \quad (3d)$$

As shown in Figure 2, the four triangular membership functions were formulated as function of the values of a, b and c as identified in their respective interval [a, b, c]. For each linguistic value, the value of a was used to define the left base point (-0.5, 0.5, 1.5 and 2.5 for No, Low, Moderate and High Risk respectively), c to identify the right base point (0.5, 1.5, 2.5 and 3.5 for No, Low, Moderate and High Risk respectively) and b to identify the central apex point at which the full degree of membership is assigned as 0, 1, 2 and 3 for No, Low, Moderate and High Risk respectively. The results of the 4096 rules that were inferred for the spread of COVID-19 is presented in Figure 3.

Figure 2. Fuzzification of the Spread of COVID-19

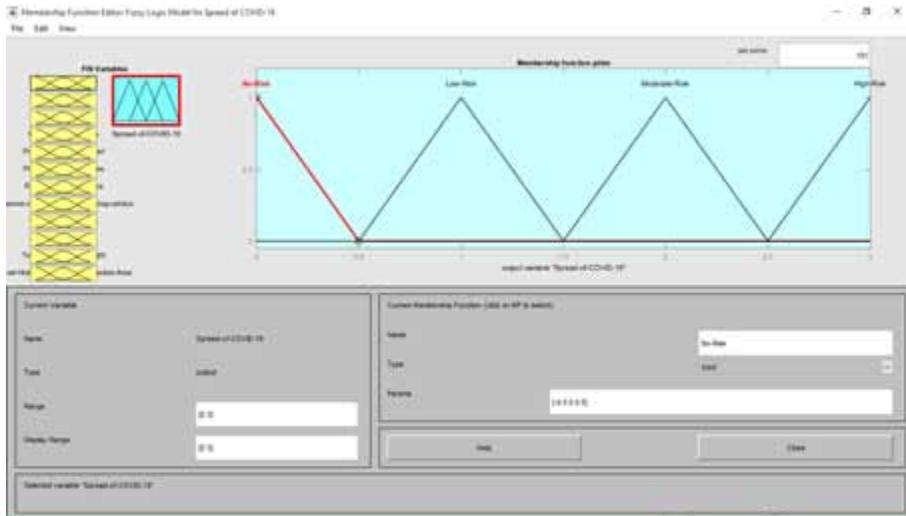
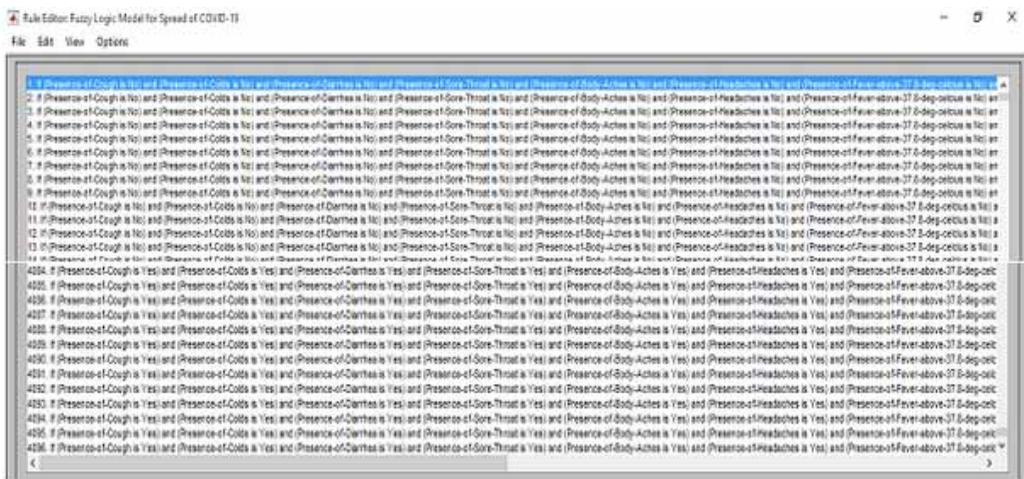
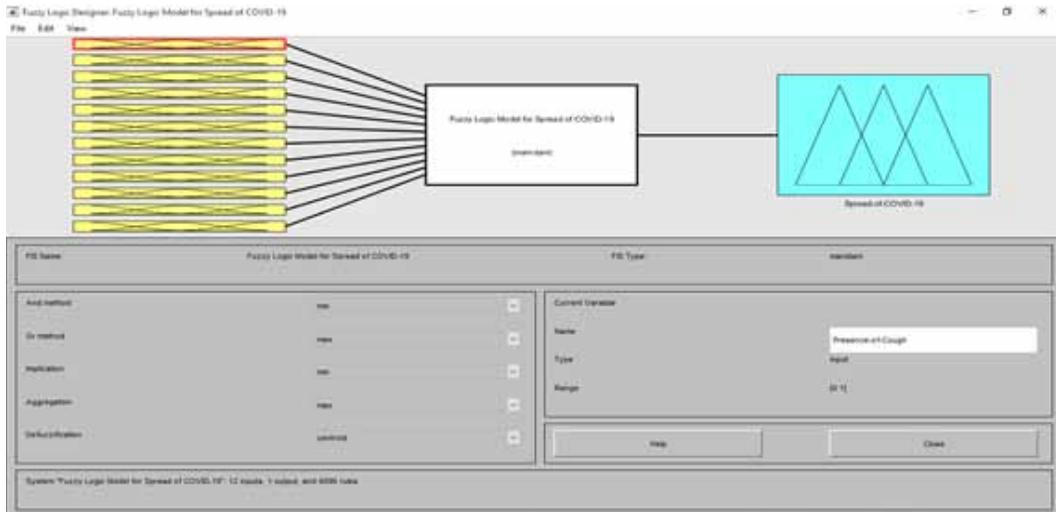


Figure 3. Rules inferred for the Spread of COVID-19



Following the fuzzification of the input and output variables identified in this study, the 4096 rules that were inferred for the fuzzy inference system were implemented. As stated earlier, the rules were inferred as IF-THEN statements which adopted the combination of all possible linguistic values of the 12 variables associated with the spread of COVID-19 infections from individual to individual. Figure 4 shows the fuzzy inference system which was developed in this study for the estimation of the spread of COVID-19 infection from individual to individual based on information about the variables which are associated with the spread of COVID-19. As shown in Figure 4, there are 12 input variables on the left, followed by the inference engine in the center which contains the 4096 rules inferred while on the right is the output spread of COVID-19 infection.

Figure 4. Fuzzy Inference System for the Spread of COVID-19



5. DISCUSSIONS

Based on the results of this study, the assessment of the risk of the spread of COVID-19 infection from an individual to individual can be assessed based on knowledge about associated variables. In this study, a weighted system for assessing the spread of COVID-19 was developed based on the development of a multiple input and single output (MISO) Mamdani fuzzy logic-based model. The study showed that the various variables associated with the spread of COVID-19 have varying levels of association which was assigned based on weighted values. Thus, the degree of impact of the variables on the spread of COVID-19 were identified as a function of the value of the weight assigned which laid between values of 1 to 3. Also, the study revealed that the presence of the variables associated with the spread of COVID-19 was used to prompt their respective weight which determined the spread of COVID-19 based on the sum of the associated variables.

Unlike the study conducted by Deepak, Divya, Suyash and Mayank (2020) in which 15 rules were used to construct the IF-THEN rules from 11 variables, this study compiled an exhaustive list of 4096 IF-THEN rules based on all the possible combination of the values of 12 variables associated with the risk of the spread of COVID-19. Thus providing a more reliable and accurate estimation of the assessment of the spread of COVID-19. In addition, the results of this study further revealed that the higher the value of the weight assigned to each variables then the more important is the variables regarding the assessment of the spread of COVID 19. Thus, clinical variables were assigned weighted values of 1 and 2 while epidemiological variables were assigned weighted values of 3. Therefore, the spread of COVID-19 was determined by the interval to which the total sum of the weighted values of the presence of variables associated with the spread of COVID-19 belonged to.

6. CONCLUSIONS

The study concluded that based on the information retrieved from the Philippines' Department of Health about the variables associated with the spread of COVID-19 infection from individual to individual, it is possible to adopt fuzzy logic model for the estimation of the spread of COVID-19 infection. The study concluded that there are 12 symptoms and risk factors that are associated with the spread of COVID-19 infection. The study also concluded that each associated variables had their own respective level of impact of the spread of COVID-19 which was measured as a weighted value.

Therefore, variables with a larger impact on the assessment of the spread of COVID-19 had higher weighted values while those with smaller impact had lower weighted values. The study also conclude that a total of 4096 rules can be inferred from the combination of the possible linguistic values of the variables associated with the risk of COVID-19 spread. Also, the fuzzy logic model proposed in this study can be integrated into existing health information systems to aid as a decision support or expert system which can aid the early detection of COVID-19 especially in resource limited settings like sub-Saharan Africa. Future works will be aimed at collecting relevant data containing information about the variables identified to this study with the aim of adopting the use of machine learning and deep learning algorithms for the formulation of an improved predictive model required for assessing the spread of COVID-19.

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