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Generalized Distance Measures of Neutrosophic Sets for Coronavirus Disease Analysis

Norzieha Mustapha[1,*], Nur Elini Jauhari[2], Suriana Alias[3] and Roliza Md Yasin[4]

[1,2,3,4]Faculty of Computer and Mathematical Sciences, Universiti Teknologi MARA Kelantan, Bukit Ilmu, Machang, Kelantan, Malaysia

[*]norzieha864@uitm.edu.my

Abstract: The world is currently facing an infectious disease caused by the SARS-CoV-2 virus which is known as coronavirus disease 2019. There are a few symptoms that are linked significantly to the disease. The symptoms and disease relationship can be represented by neutrosophic set values. In general, neutrosophic set give remarkable contributions in denoising, clustering, segmentation, and classification in handling data of many real applications including in the medical field. This study aims to analyse the coronavirus disease risks together with viral fever, malaria, typhoid and chikungunya by several generalized distance measures. An analysis is conducted by using the data on the severity level of five symptoms found in eight different patients. The neutrosophic data are analysed to determine the possibility of patients having any one or a combination of several types of diseases, including coronavirus. A comparative study involving four distance measures is conducted. The results show that the distance measures for all patients were less than 0.5, but the distance measures for all patients for coronavirus were higher than other diseases. From this situation, it can be further concluded that there is a possibility that the patients are not suffering from coronavirus.

Keywords: Coronavirus, Distance measures, Neutrosophic set.

1 Introduction

The coronavirus disease 2019 (COVID-19) pandemic is the world's largest shock in decades, touching every facet of life. Officially known as Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2), the virus was previously known as 2019 novel coronavirus (2019-nCoV). The disease is highly contagious and has been declared a global public health emergency by the World Health Organization (WHO) [1]. Most of the infected patients will develop mild to moderate respiratory illness and recover without the need for special treatment. However, some will fall ill and need medical treatment. Some of the COVID-19 symptoms are fever, headache, cough, sneezing, body pain, tiredness and sore throat. Due to the severity of COVID-19, it is crucial to make the correct diagnosis so that proper treatment can be provided to the patients.

The invasive or non-invasive medical diagnosis methods are used as guidelines by doctors to provide appropriate treatments. There is a non-invasive method in the mathematical branch which is able to reduce the possibility of making imprecise diagnosis in spite of incomplete or uncertain information. The area uses fuzzy mathematics concepts in defining the set theory where it evolves from fuzzy set [2] to many more advanced sets such as intuitionistic fuzzy set [3] and neutrosophic set [4]. In 1995, Smarandache proposed the notion of neutrosophic logic and, in 1999, its founder unified and generalised it [5]. Since then, neutrosophic logic has been employed in a variety of computer science domains, including pattern recognition, image segmentation, processing and it has helped to solve many real-world problems in medicine, economics, and agriculture [6]. Studies on the development of more advanced neutrosophic sets and its applications in medical or clinical diagnosis are found in [7-12].

Thus far, the application of neutrosophic set theory is considerably noticeable in decision-making studies. The outstanding advantage of the set is its ability to handle uncertainty and incompleteness of the data. Neutrosophic set is an imperative set for denoising, clustering, segmentation, and classification of real data in many areas including the medical field. For successful diagnosis systems, the neutrosophic set has been integrated with clustering techniques to reduce vagueness for proficient diagnosis. Habib et al. [13] proposed the neutrosophic clinical decision-making system using explainable artificial intelligence approaches for a proper diagnosis of cardiovascular disease risk. Then, Habib et al. [14] extended the same approach to help physicians in early diagnosis and identifying the type of treatment. Deli et al. [8] focused on the heart disease diagnosis problem as an application of neutrosophic refined set using distance measure while Alias et al. [9] analysed the medical diagnosis for rough neutrosophic set using Dice and Cosine similarity measures.

In order to accommodate problems related with COVID-19 diagnosis, Hezam et al. [15] used neutrosophic Analytic Hierarchy Process (AHP) and TOPSIS methods to determine which groups should get COVID-19 vaccination doses first. They found that health staff, people with pre-existing medical conditions, the elderly, essential employees, and pregnant and breastfeeding mothers are among the first to receive vaccination. Contribution of a progressive mathematical model for the investigation of COVID-19 and the recovery of COVID-19 victims under certain conditions has been done by Hashmi et al. [16] where they were investigating innovative approach of m-polar neutrosophic set (MPNS) and the results showed the updated operators can readily tackle real-life impediments and decision-making problems, according to a comparative investigation. Khalifa et al. [6] sought to look at how neutrosophic settings affect three deep transfer learning models conducted over x-ray samples of patients with COVID-19, normal, pneumonia bacterial and pneumonia virus. They concluded that the use of neutrosophic set with deep learning models results in better testing accuracy, especially in the case of limited datasets.

Other than the neutrosophic set, there are various methods used in investigating several concerned issues on COVID-19. Basst et al. [17] recommended a model that uses the best-worst method (BWM) and techniques in order of preference (TOPSIS) based on how close they are to the optimal answer. They discussed how intelligent the Internet of Things technology is in guiding doctors in tracking the COVID-19 spread. In all five situations, the suggested model has successfully identified COVID-19, with detection accuracy of up to 98%. Albahri et al. [1] used Entropy-TOPSIS approach in finding a novel framework to handle the problems of prioritising COVID-19 infected individuals using multi-laboratory criteria based on integrated MCDM and TOPSIS. The patients were divided into four groups of similar sizes, with substantial differences in their scores. The framework is useful for recognising patients’ health status before their discharge, supporting hospitalisation features, monitoring patient care, and optimising clinical prediction rules.

Grida et al. [18] evaluated the impact of COVID-19 epidemic preventive policies in three supply chain aspects which are supply, demand and logistics for industries of food, electronics, pharmaceutical and textile. They applied MCDM, BWM and TOPSIS based on plithogenic set. The result shows that the COVID-19 preventive strategies have the greatest impact on demand in the supply chain. In collaboration with many stakeholders, Ahmad et al. [19] presented a potential use of the approach MCDM to prioritise criteria while dealing with the new coronavirus COVID-19 epidemic. The technique focused on rating factors for controlling the COVID-19 epidemic based on the choices of health professionals, social workers, academics, and the public.

In neutrosophic sets, distance measures are significant in numerous scientific research fields such as in decision making, pattern identification, and market forecasting. The use of distance measure has a significant role in data clustering process and a work by Ye [20] has proven that single-valued neutrosophic set (SVNS) clustering algorithm improved the accuracy in representing the indeterminate or inconsistent information. Strength relation between the information given can be identified by the distance measure.

The most widely used distance measures are Hausdorff distance, Hamming distance and Euclidean distance. A new distance-based similarity measure proposed by [21] for a refined neutrosophic set is applied in medical diagnosis of few diseases with a common set of symptoms. Further, Liu et al. [22] developed a new hybrid distance-based similarity measure for refined neutrosophic sets. Antonysamy et al. [7] studied Hausdorff distance in order to analyse patients and COVID-19 symptoms.

Based on the related studies stated above, there are less studies that focus on COVID-19 using neutrosophic sets with a comparison between several generalized distance measures. Due to the very uncertain nature of infectious diseases and incomplete data, this is crucial. Thus, the present study aims to evaluate the severity of Coronavirus disease in eight patients as well as four other diseases, such as viral fever, malaria, typhoid and chikungunya. The present study applies the distance formula from Mustapha et al. [12], normalized Hamming distance and Euclidean distance measures, and compares the results with those of extended Hausdorff distance [7]. The study presents significant results on the medical diagnosis of five diseases for eight patients including COVID-19. The description of the diseases together is well defined in Section 2. The section also provides the definition of SVNS that contains three membership functions (MFs) that are truth (T), indeterminacy (I), and falsity (F) together with several distance measures which were used in subsequent sections.

2 Preliminaries

This section introduces some preliminary notions which will be applied in the analysis of medical diagnosis data.

A *Single Valued Neutrosophic Set*

A neutrosophic set which can be used in real scientific and engineering applications is known as single valued neutrosophic sets (SVNS).

Definition 2.1 [23]. Let X be a space of points (objects) with a generic element in X denoted by x. A single valued neutrosophic set A in X is characterized by a truth membership function, $T_A(x)$, an indeterminacy membership function, $I_A(x)$, and a falsity membership function $F_A(x)$. Here $[T_A(x), I_A(x), F_A(x)]$ are the real subsets of [0,1].

$$A = \{\langle x, T_A(x), I_A(x), F_A(x)\rangle | x \in X\}$$

B *Distance Measures of Neutrosophic set*

Definition 2.2 [24]. Normalized Hamming distance measure $d_{NS}^{NH}(A, B)$ operator between neutrosophic set A and B is defined as follows:

$$d_{NS}^{NH}(A, B) = \frac{1}{3n}\sum_{i=1}^{n}(|T_A(x_i) - T_B(x_i)| + |I_A(x_i) - I_B(x_i)| + |F_A(x_i) - F_B(x_i)|) \quad (1)$$

Definition 2.3 [24]. Normalized Euclidean distance measure$d_{NS}^{NE}(A, B)$ operator between neutrosophic set A and B is defined as follows:

$$d_{NS}^{NE}(A, B) = \sqrt{\frac{1}{3n}\sum_{i=1}^{n}((T_A(x_i) - T_B(x_i))^2 + (I_A(x_i) - I_B(x_i))^2 + (F_A(x_i) - F_B(x_i))^2)} \quad (2)$$

Definition 2.4 [25]. An extended Hausdorff Distance $d_{NS}^{EH}(A,B)$ operator between neutrosophic set A and B is defined as follows:

$$d_{NS}^{EH}(A,B) = \frac{1}{n}\sum_{i=1}^{n} max\{|T_A(x_i) - T_B(x_i)|, |I_A(x_i) - I_B(x_i)|, |F_A(x_i) - F_B(x_i)|\} \tag{3}$$

Definition 2.5 [12]: Let $X = \{x_1, x_2, \ldots, x_n\}$ be the universe of discourse. Let $A = \{x_i, T_A(x_i), I_A(x_i), F_A(x_i)): x_i \in X\}$ and $B = \{x_i, T_B(x_i), I_B(x_i), F_B(x_i)): x_i \in X\}$ be two neutrosophic sets. A distance measure can be defined as:

$$d_{New}^{N}(A,B) = \frac{2}{n}\sum_{i=1}^{n} \frac{sin\left\{\frac{\pi}{10}|T_A\,(x_i) - T_B\,(x_i)|\right\} + sin\left\{\frac{\pi}{10}|I_A\,(x_i) - I_B\,(x_i)|\right\} + sin\left\{\frac{\pi}{10}|F_A\,(x_i) - F_B\,(x_i)|\right\}}{1 + sin\left\{\frac{\pi}{10}|T_A\,(x_i) - T_B\,(x_i)|\right\} + sin\left\{\frac{\pi}{10}|I_A\,(x_i) - I_B\,(x_i)|\right\} + sin\left\{\frac{\pi}{10}|F_A\,(x_i) - F_B\,(x_i)|\right\}} \tag{4}$$

Proposition 2.6: The distance measures for neutrosophic set $d_{NS}(A,B)$ in Eqs. (1-4) satisfies the following properties:

(C1) $0 \leq d_{NS}(A,B) \leq 1$;
(C2) $d_{NS}(A,B) = 0$ if and only if $A = B$;
(C3) $d_{NS}(A,B) = d_{NS}(B,A)$;
(C4) $d_{NS}(A,C) \leq d_{NS}(A,B)\ \ and\ d_{NS}(A,C) \leq d_{NS}(B,C)$ if C is neutrosophic set in X and $A \subseteq B \subseteq C$;

All the proof of the proposition are shown in [12, 24].

C Types of diseases

COVID-19 – is a disease caused by a type of coronavirus which is known as SARS-CoV-2. It causes respiratory tract infections which can spread through infectious droplets, and the behaviour and environmental factors associated with the infected individuals. Signs and symptoms include respiratory symptoms and fever, cough and shortness of breath. In more severe cases, infection causes pneumonia, severe acute respiratory syndrome and death.

Viral Fever – is a group of viral infections that affect the health of the body and cause high fever, burning sensation in the eyes, headache, body aches and sometimes nausea and vomiting.

Malaria – caused by mosquitoes infecting a person's blood with the parasite. In fact, a single mosquito bite can be fatal if malaria is not diagnosed and treated properly. Symptoms include high fever, headache, muscle aches, diarrhea, and vomiting.

Typhoid – is a foodborne infection caused by the bacterium *Salmonella typhi*. This bacterium is found in the blood, urine and feces of patients as well as carrier feces. Symptoms of typhoid are high fever, headache, digestive disorders, stomach ache, nausea and vomiting.

Chikungunya – is a viral disease that infects humans through the bite of an infected mosquito. Infected people may experience the following symptoms such as fever, coolness, headache, nausea and vomiting.

3 Methodology

There are three steps to complete the medical diagnosis focusing on COVID-19 risk analysis using distance measures of the neutrosophic set. This study used the extended Hausdorff distance [7], Mustapha et al. [12], normalized Hamming distance and normalized Euclidean distance [24] for comparative analysis. The steps to complete the analysis are as follows:

Step 1: The extraction of data.
Data on the symptoms experienced by patients were given in the form of single valued neutrosophic numbers (SVNN). Due to the presence of symptoms, they are initially being suspected as COVID-19 patients but were eventually tested negative for coronavirus after treatments [6]. Furthermore, the relationships between the symptoms and diseases are displayed in SVNN form too which can easily be used as reference in determining which disease puts the patients at a high risk.

Step 2: The calculation of distance measures.
The distance measures of SVNS for each patient were calculated using four different distance measures in Eqs. (1 - 4). The Matlab coding was used to ease the process of calculation.

Step 3: Discussion of complete data analysis
Finally, based on the calculated distance measures value resulted in step 2, the conclusion on how close the patients' symptoms are to the diseases. A patient is possibly suffering from one disease when the value of distance measure is lower than 0.5. Meanwhile, the patient may not be suffering from a disease when the value of distance measure is bigger than 0.5.

4 Results and Discussions

This section discusses the case study of eight patients having five similar symptoms such as temperature, headache, body pain, cough and sneezing. The patients' data on the severity degree of the symptoms together with experts' consensus on the symptoms-diseases relations are presented in SVNN form. COVID-19 was analysed together with other diseases such as viral fever, malaria, typhoid and chikungunya. The data considered the degree of truth membership, indeterminacy membership and falsity membership for each element in the set. Let $P = \{p_1, p_2, p_3, p_4, p_5, p_6, p_7, p_8\}$ is a set of patients and $S = \{s_1, s_2, s_3, s_4, s_5\}$ is a set of symptoms. Table 1 shows the data relation between patients and symptoms as discussed in [7]. Besides, the relation among diseases and symptoms is presented in Table 2.

Table 1: The relation between patients and symptoms

	Temperature, s_1	**Headache, s_2**	**Body Pain, s_3**	**Cough, s_4**	**Sneezing, s_5**
Patient 1	(0.6,0.3,0.3)	(0.5,0.2,0.4)	(0.3.0.5,0.2)	(0.4,0.4,0.4)	(0.3,0.4,0.5)
Patient 2	(0.1,0.6,0.4)	(0.4,0.6,0.3)	(0.3,0.5,0.4)	(0.3,0.5,0.4)	(0.3,0.6,0.7)
Patient 3	(0.6,0.3,0.4)	(0.6,0.2,0,4)	(0.4,0.5,0.5)	(0.2,0.5,0.5)	(0.2,0.4,0.3)
Patient 4	(0.4,0.3,0.2)	(0.4,0.4,0.4)	(0.2,0.4,0.5)	(0.5,0.2,0.4)	(0.4,0.3,0.4)
Patient 5	(0.2,0.4,0.6)	(0.2,0.4,0.0)	(0.7,0.6,0.1)	(0.2,0.4,0.7)	(0.3,0.2,0.7)
Patient 6	(0.3,0.4,0.5)	(0.6,0.4,0.3)	(0.6,0.3,0.1)	(0.5,0.4,0.7)	(0.5,0.4,0.6)
Patient 7	(0.4,0.5,0.3)	(0.6,0.5,0.1)	(0.6,0.4,0.4)	(0.5,0.3,0.4)	(0.6,0.5,0.4)
Patient 8	(0.6,0.3,0.7)	(0.6,0.2,0.3)	(0.6,0.3,0.6)	(0.4,0.3,0.4)	(0.7,0.1,0.2)

Table 2: The relation among diseases and symptoms

	Viral Fever	**Malaria**	**Typhoid**	**Chikungunya**	**COVID-19**
Temperature, s_1	(0.6,0.3,0.3)	(0.2,0.5,0.3)	(0.2.0.6,0.4)	(0.1,0.6,0.6)	(0.1,0.6,0.4)
Headache, s_2	(0.4,0.5,0.3)	(0.2,0.6,0.4)	(0.1,0.5,0.4)	(0.2,0.4,0.6)	(0.1,0.6,0.4)
Body Pain, s_3	(0.1,0.6,0.3)	(0.0,0.6,0,4)	(0.2,0.5,0.5)	(0.8,0.2,0.2)	(0.1,0.7,0.1)
Cough, s_4	(0.4,0.4,0.4)	(0.4,0.1,0.5)	(0.2,0.5,0.5)	(0.1,0.7,0.4)	(0.4,0.5,0.4)
Sneezing, s_5	(0.1,0.7,0.4)	(0.1,0.6,0.3)	(0.1,0.6,0.4)	(0.1,0.7,0.4)	(0.8,0.2,0.2)

According to the data collected in Table 1, the truth membership degree for five symptoms of all patients was between 0.1 and 0.7, the indeterminacy membership degree for all patients was between 0.1 and 0.6 and the falsity membership degree for all patients was between 0.1 and 0.7. It is obvious that the value of the truth membership degree of body pain for patient 5 and sneezing symptom for patient 8 was 0.7. This indicates a high possibility for both patients to be categorized as suffering from any one of the diseases. As for patient 2 and patient 5, their sneezing symptom falls into the category of less suffering with 0.7 falsity membership degree. As can be seen for patient 2, the temperature data set (0.1,0.6,0.4) indicates patient 2 had a low temperature. Meanwhile, the relation for temperature with COVID-19 data was also (0.1, 0.6, 0.4) which indicates that COVID-19 has an indeterminate influence of 0.6 with low temperature 0.1 and middle temperature 0.4. The same description is indicated for each data.

By using the data in Table 1 and Table 2, four distance measures discussed in Section 2 were calculated. Then, the results are displayed in Tables 3-6. Table 3 depicts the extended Hausdorff distance measures given by [7]. In Table 4, the distance measure follows the formula in [12]. Meanwhile, Tables 5 and 6 show the distance measures calculated by normalized Hamming and normalized Euclidean formula [23], respectively. Each distance measure has been proven to satisfy all the properties needed.

Table 3: Extended Hausdorff distance measures between patients and diagnosis [7]

	Viral Fever	**Malaria**	**Typhoid**	**Chikungunya**	**COVID-19**
Patient 1	**0.1600**	0.3200	0.3000	0.3800	0.3400
Patient 2	0.2400	0.2800	**0.1800**	0.3000	0.2400
Patient 3	**0.2400**	0.3600	0.2600	0.3600	0.4400
Patient 4	0.2200	**0.2000**	0.2600	0.4200	0.3400
Patient 5	0.4200	0.4200	**0.3400**	0.4000	0.4000
Patient 6	0.3400	0.3800	0.3600	**0.3200**	0.3800
Patient 7	**0.300**	0.3800	0.3800	0.3800	0.3600
Patient 8	0.380	0.4400	0.4200	0.4600	**0.3600**

It can be seen that, from Table 3, only patient 8 were detected to have coronavirus disease. Meanwhile, patients 1, 3 and 7 were suffering from viral fever, patients 2 and 5 had typhoid, patient 4 had malaria, and patient 6 had chikungunya.

Table 4: Mustapha et al. [12] distance measures between patients and diagnosis

	Viral Fever	**Malaria**	**Typhoid**	**Chikungunya**	**COVID-19**
Patient 1	**0.1616**	0.3053	0.2943	0.3785	0.3274
Patient 2	0.2306	0.2394	**0.1676**	0.2972	0.2475
Patient 3	0.2369	0.3117	**0.2193**	0.3669	0.3756
Patient 4	**0.2180**	0.2587	0.2629	0.3986	0.3293
Patient 5	0.3706	0.3677	**0.3234**	0.3260	0.3546
Patient 6	**0.3236**	0.3740	0.3532	0.3518	0.3621
Patient 7	**0.2639**	0.2990	0.3135	0.3801	0.3484
Patient 8	**0.3310**	0.4245	0.4208	0.4367	0.3620

Table 5: Normalized Hamming distance measures between patients and diagnosis

	Viral Fever	**Malaria**	**Typhoid**	**Chikungunya**	**COVID-19**
Patient 1	**0.3000**	0.1933	0.1867	0.2533	0.2200
Patient 2	0.1467	0.1467	**0.1000**	0.1933	0.1733
Patient 3	0.1467	0.2000	**0.1400**	0.2467	0.2533
Patient 4	**0.1333**	0.1600	0.1667	0.2733	0.2133
Patient 5	0.2467	0.2467	**0.2133**	**0.2133**	0.2333
Patient 6	**0.2133**	0.2533	0.2333	0.2333	0.2400
Patient 7	**0.1667**	0.1933	0.2000	0.2533	0.2333
Patient 8	**0.2333**	0.3000	0.2933	0.3067	0.2600

However, in Tables 4-6, no patient has been detected to suffer from the coronavirus disease. Table 4 and 5 show consistent results for two groups of patients. Patients 1, 4, 6, 7 and 8 were suffering from viral fever and patients 2, 3 and 5 were suffering from typhoid. On the other hand, from Table 6, all of the patients were suffering from viral fever except for patient 2.

Table 6: Normalized Euclidean distance measures between patients and diagnosis

	Viral Fever	**Malaria**	**Typhoid**	**Chikungunya**	**COVID-19**
Patient 1	**0.1438**	0.2324	0.3162	0.2898	0.2769
Patient 2	0.1966	0.1932	**0.1390**	0.2324	0.2503
Patient 3	**0.1751**	0.2530	0.2145	0.2745	0.3162
Patient 4	**0.1751**	0.1789	0.2944	0.3235	0.2477
Patient 5	**0.1633**	0.3066	0.2608	0.2781	0.2955
Patient 6	**0.2530**	0.2875	0.2671	0.2620	0.2828
Patient 7	**0.2266**	0.2620	0.3559	0.2989	0.2720
Patient 8	**0.3152**	0.3512	0.3307	0.3521	0.3235

A lower distance measure value implies higher possibility of one patient having a particular disease. The slight difference of symptoms shown in all the eight patients results in a distinct conclusion on the types of diseases that they experienced. Concurrently, it is apparent that most of the distance measure values in Tables 3-6 were less than 0.5 for all the diseases. Hence, it is probable to conclude that the eight patients were possibly suffering from at least one of these diseases. As can be seen from Tables 3-6, patients 1 and 7 had the highest severity degree of symptoms for viral fever. Meanwhile, patient 2 was more likely to be diagnosed with having typhoid. These results are consistent with [7] and also other distance formulas that have been used [12].

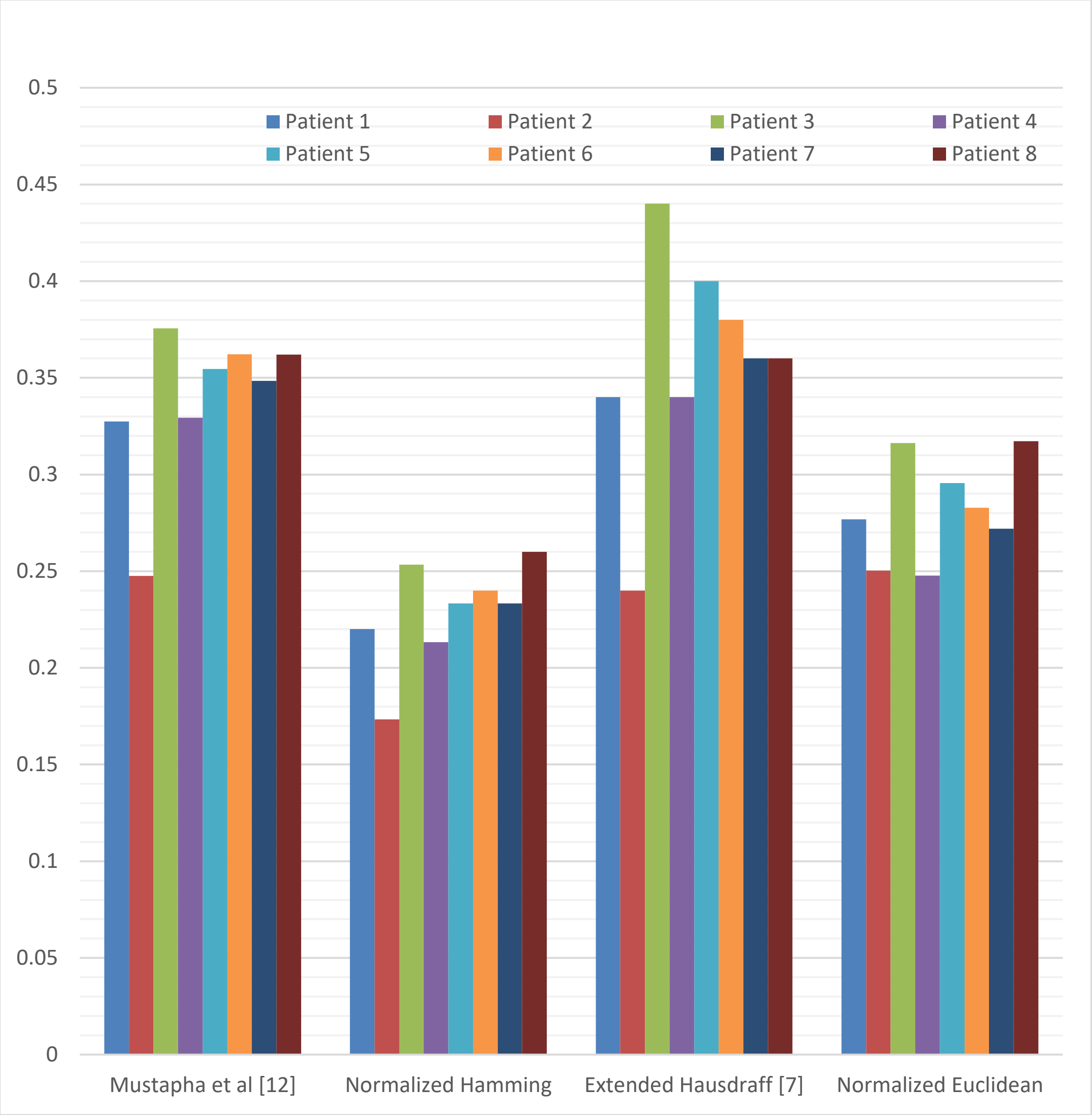

Figure 1: Distance Measure Summary of COVID-19 Amongst Patients

Meanwhile, Figure 1 shows the summary for distance measures of coronavirus disease amongst patients. It can be seen that the distance values for patient 2 were the lowest in each different measure formula indicating the same conclusion, i.e. he/she was having the coronavirus disease. Besides, the highest distance values resulted from patient 3 for each type of distance measures shows that he/she was less likely to suffer from coronavirus disease.

5 Conclusion

This research analysed the risk of having coronavirus disease by using four distance measures for a single value neutrosophic set. The distance values were found to be consistent for certain patients with distance measures of the four distance measures i.e. distance measure from Mustapha et al. [12], extended Hausdorff distance [7], normalized Hamming distance and normalized Euclidean distance [24]. The analyses show that the generalized distance measures are well executed in the case of truth membership, indeterminacy membership and falsity membership functions. In future studies, it is recommended that one might consider additional significant symptoms and other distance or similarity measures to increase the accuracy level in diagnosing a patient with COVID-19. Other than that, the integrated ANP–DEMATEL method [25] under neutrosophic environments can be considered to analyse COVID-19 disease. Entropy measure is also an important tool in measuring uncertain information and can be applied to diagnose COVID-19 [26].

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