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Materials Today: Proceedings 49 (2022) 2654–2658

Contents lists available at ScienceDirect

Materials Today: Proceedings

journal homepage: www.elsevier.com/locate/matpr

Neutrosophic sets in determining Corona virus

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ARTICLE INFO

Article history:
Available online 3 September 2021

2010 MSC:
03E72
03F55

Keywords:
Fuzzy set
Intuitionistic set
Hausdorff minimum distance
Neutrosophic set

ABSTRACT

An attempt that is made here is to apply neutrosophic sets to a medical data. By means of extended Hausdorff minimum distance we find out the core symptoms of the patients. From the minimum distance or the core symptoms we can get a clue for the type of disease affecting the patient.

Selection and peer-review under responsibility of the scientific committee of the Indo-UK International Virtual Conference on Advanced Nanomaterials for Energy and Environmental Applications (ICANEE-2020).

1. Introduction

Zadeh [1] in 1965 introduced fuzzy set to study uncertainty or vagueness and partial truth by assigning percentage to the truth value of the data. Atanassov [2,3] in 1986 proposed intuitionistic fuzzy set which is one step further than fuzzy set to studyimprecisive data since it gives percentage not only to membership value but also to non-membership value. Neutrosophic sets, which are defined by Smarandache [4] is an advanced system to intuitionistic fuzzy set. In neutrosophic set all three parameters, namely membership value, non-membership value and indeterminacy value, are given importance by assigning its due percentage. Hence it is found to be more effective than fuzzy and intuitionistic sets. In 2012, Salama, Alblowi [5] induced the concept of neutrosophic topological space.

Lellis Thivagar et al. [6,7–12] produced neutrosophic nano topology reducing theentire universe under five open sets. In this paper, we try to find out the normalised hamming minimum distance to neutrosophic sets data by applying Hausdorff minimum distance. The minimum distance is nothing but narrowing down the given medical data to a desirable result. In other words the minimum number gives us an indication for the kind of sickness affecting a sick person. By this method we can easily find out the decease of a sick person and enable the doctors to start the treatment at once. So that the life of a patient is saved without prolonging his suffering.

2. Preliminaries

To apply neutrosophic sets to a medical data we recall here a few related concepts and definitions that will enable us to apply the theory efficiently.

Definition 1. [1] Let $\Xi \neq \emptyset$. A fuzzy set Γ is an object having the form $\Gamma = \{(\varepsilon, \mu_\Gamma(\varepsilon)) : \varepsilon \in \Xi\}$, where $0 \leqslant \mu_\Gamma(\varepsilon) \leqslant 1$ represents the degree of membership of each $\varepsilon \epsilon \Xi$ to the set Γ.

Definition 2. [2,3] Let $\Xi \neq \emptyset$. An intuitionistic set Γ is of the form $\Gamma = \{(\varepsilon, \mu_\Gamma(\varepsilon), \gamma_\Gamma(\varepsilon)) : \varepsilon \in \Xi\}$, where $\mu_\Gamma(\varepsilon)$ and $\gamma_\Gamma(\varepsilon)$ represent the degree of membership and non-membership function respectively of each $\varepsilon \epsilon \Xi$ to the set Γ and $0 \leqslant \mu_\Gamma(\varepsilon) + \gamma_\Gamma(\varepsilon) \leqslant 1$ for all $\varepsilon \epsilon \Xi$.

Definition 3. [4] Let Ξ be a non-empty set. A neutrosophic set Γ having the form, where $\mu_\Gamma(\varepsilon), \sigma_\Gamma(\varepsilon)$ and $\gamma_\Gamma(\varepsilon)$ represent the degree of membership function (namely $\mu_\Gamma(\varepsilon)$), the degree of indeterminacy (namely $\sigma_\Gamma(\varepsilon)$) and the degree of non-membership (namely $\gamma_\Gamma(\varepsilon)$) respectively of each $\varepsilon \epsilon \Xi$ to the set Γ. Also $-0 \leqslant \mu_\Gamma(\varepsilon) + \sigma_\Gamma(\varepsilon) + \gamma_\Gamma(\varepsilon) \leqslant 3^+$ for all $\varepsilon \epsilon \Xi$.

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https://doi.org/10.1016/j.matpr.2021.08.290
2214-7853/
Selection and peer-review under responsibility of the scientific committee of the Indo-UK International Virtual Conference on Advanced Nanomaterials for Energy and Environmental Applications (ICANEE-2020).

Definition 4. [8] The Hausdorff distance is defined as $d_H(\alpha,\beta) = H(\alpha,\beta)$ for the two sets $\alpha = \{a_1, a_2\}$ and $\beta = \{b_1, b_2\}$ in a real space R.

Remark 5. [8] The Hausdorff distance $d_H(a,b) = H(a,b)$ between α and β satisfies the following properties:

$(D1)$ $0 \leqslant d_H(\alpha,\beta) \leqslant 1$
$(D2)$ $d_H(\alpha,\beta) = 0$ if and only if $\alpha = \beta$, for all α, β
$(D3)$ $d_H(\alpha,\beta) = d_H(\beta,\alpha)$
$(D4)$ if $\alpha \subseteq \beta \subseteq \gamma$, then and $d_H(\alpha,\gamma) \geqslant d_H(\beta,\gamma)$

Definition 6. [8] Based on the Hausdorff metric, Szmidi and Kacprzyk defined new distance between intuitionistic fuzzy sets and/or interval valued fuzzy sets taking into account three parameter representations (membership, non-membership values and the hesitation margins) of a intuitionistic fuzzy set which fulfill the properties of the Hausdorff distances. The distance is defined by

$$H_{IFS}(\alpha,\beta) = \frac{1}{n}\int_{i=1}^{n} \text{Max}\{|\mu_\alpha(\varepsilon_i) - \mu_\beta(\varepsilon_i)|, |\gamma_\alpha(\varepsilon_i) - \gamma_\beta(\varepsilon_i)|, |\pi_\alpha(\varepsilon_i) - \pi_\beta(\varepsilon_i)|\},$$

where $\alpha = \{< \varepsilon, \mu_\alpha(\varepsilon), \gamma_\alpha(\varepsilon), \pi_\alpha(\varepsilon) >\}$
And $\beta = \{< \varepsilon, \mu_\beta(\varepsilon), \gamma_\beta(\varepsilon), \pi_\beta(\varepsilon) >\}$.

3. Neutrosophic sets in the diagnosing system

Based on Neutrosophic Hamming distance we develop an application to find the core attribute of the disease. By the core attribute one can conclude whether the patient is affected by Viral fever or Malaria or Typhoid or Chicken gunya or Corona virus.

Definition 1. Let $\Xi = \{\varepsilon_1, \varepsilon_2, \varepsilon_3, ..., \varepsilon_n\}$ be a discrete finite set. Consider a neutrosophic set ω in Ξ where $T_\omega(\varepsilon_i), I_\omega(\varepsilon_i), F_\omega(\varepsilon_i) \in [0,1]$ for every $\varepsilon_i \in \Xi$ representing membership, indeterminacy, and non-membership values respectively. Let it be denoted by $\omega = \{< \varepsilon, \mu_\omega(\varepsilon), \gamma_\omega(\varepsilon), \pi_\omega(\varepsilon) >\}$

The distance between two neutrosophic sets, say ω and σ, is defined as follows: $d_{HNS}(\omega,\sigma) = \frac{1}{n}\int_{i=1}^{n} \max\{|T_\omega(\varepsilon_i) - T_\sigma(\varepsilon_i)|, |I_\omega(\varepsilon_i) - I_\sigma(\varepsilon_i)|, |F_\omega(\varepsilon_i) - F_\sigma(\varepsilon_i)|\}$ where $d_{HNS}(\omega,\sigma) = H(\omega,\sigma)$ denotes the extended Hausdorff distance between two neutrosophic sets (NS) ω and σ.

Definition 2. Let L, M and N be three neutrosophic sets. Then the distance between L and M is denoted as $d_{HNS}(L,M) = H(L,M) = \max\{|T_L(\varepsilon_i) - T_M(\varepsilon_i)|, |I_L(\varepsilon_i) - I_M(\varepsilon_i)|, |F_L(\varepsilon_i) - F_M(\varepsilon_i)|\}$. Similarly the distance between L and N can be written as: H (L, N) = $\max\{|T_L(\varepsilon_i) - T_N(\varepsilon_i)|, |I_L(\varepsilon_i) - I_N(\varepsilon_i)|, |F_L(\varepsilon_i) - F_N(\varepsilon_i)|\}$. The distance between M and N is written as: H (M, N) = $\max\{|T_M(\varepsilon_i) - T_N(\varepsilon_i)|, |I_M(\varepsilon_i) - I_N(\varepsilon_i)|, |F_M(\varepsilon_i) - F_N(\varepsilon_i)|\}$.

Definition 3. Let $\Gamma 1 = \{< \varepsilon_i, \mu_{\Gamma 1}(\varepsilon_i), \sigma_{\Gamma 1}(\varepsilon_i), \gamma_{\Gamma 1}(\varepsilon_i) > | \varepsilon_i \in \Xi\}$ and $\Gamma 2 = \{< \varepsilon_i, \mu_{\Gamma 2}(\varepsilon_i), \sigma_{\Gamma 2}(\varepsilon_i), \gamma_{\Gamma 2}(\varepsilon_i) > | \varepsilon_i \in \Xi\}$ be two neutrosophic sets of the universe of discourse $\Xi = \{\varepsilon_1, \varepsilon_2, \varepsilon_3, ..., \varepsilon_n\}$. Then the neutrosophic Hamming distance defined as: $d_{NH}(\Gamma 1, \Gamma 2) = \int_{i=1}^{n} \max\{|\mu_{\Gamma 1}(x_i) - \mu_{\Gamma 2}(x_i)|, |\sigma_{\Gamma 1}(x_i) - \sigma_{\Gamma 2}(x_i)|, |\gamma_{\Gamma 1}(x_i) - \gamma_{\Gamma 2}(x_i)|\}$.

The neutrosophic normalized Hamming distance is given as: $l_{NNH}(\Gamma 1, \Gamma 2) = \frac{1}{n}\int_{i=1}^{n} \max\{|\mu_{\Gamma 1}(x_i) - \mu_{\Gamma 2}(x_i)|, |\sigma_{\Gamma 1}(x_i) - \sigma_{\Gamma 2}(x_i)|, |\gamma_{\Gamma 1}(x_i) - \gamma_{\Gamma 2}(x_i)|\}$.

Application: Finding the core attribute of corona virus utilising neutrosophic normalised Hamming distance formula:

When a person is affected by a particular disease that person will have more than one symptoms such as Temperature, Cough, Throat infection, Headache, Sneezing etc. Also each viral disease will have more than one symptoms. For example Malaria, Typhoid, Chicken gunya will have various symptoms, like temperature, body pain, cough etc. A person who is affected by corona virus also will have the symptoms of temperature, cough, sneezing, body pain etc. Now to find out the core symptom of corona virus we will use neutrosophic normalized Hamming distance method. By Neutrosophic Normalised Hamming distance we can **find the lowest/minimum distance or core symptom by which we can conclude the kind of sickness affecting the person or the patient suffering from**.

Let us take eight patients for our case study, i.e., $P = \{P_1, P_2, P_3, P_4, P_5, P_6, P_7, P_8\}$. Each patient is experiencing more than one symptoms say, S={Temperature, Headache, body pain, Cough, Sneezing}. Now using the neutrosophic data we want to find out the kind of disease affecting the person from the common prevalent diseases say, d = {Viral fever, Malaria, Typhoid, Chicken gunya, Corona virus}. For this purpose we need two kinds of observations:

(i) In each patient the multiple symptoms found.

(ii) For each disease, in a normal given circumcisions, the kind of symptoms found. Both these observations are recorded in a neutrosophic set form, namely describing the percentage of membership function μ, percentage of indeterminacy function σ and percentage of non-membership function γ etc. To find the core attribute by utilising neutrosophic normalised Hamming distance formula for every symptoms of i^{th} patient from k^{th} diagnosis is:

$$l_{NNH}(S(P_i), d_k) = \frac{1}{n}\int_{j=1}^{n} \max\{|\mu_j(p_i) - \mu_j(d_k)|, |\sigma_j(p_i) - \sigma_j(d_k)|, |\gamma_j(p_i) - \gamma_j(d_k)|\}.$$

Algorithm to detect core attribute or the minimum distance

Step 1: The characteristic symptoms observed in every patient (Table 1).

Step 2: For each disease the type of symptoms usually found so that we can obtain symptom-disease relation (Table 2).

Step 3: The computed values are tabulated for each person as per diseases (Table 3).

Step 4: Finally, the minimum value for each person is identified from Table 3 to find the kind of sickness from which the patient is suffering from.

Execution of the algorithm

The required inputs are P_i i.e. the number of patients i = 1,2,3,4,5,6,7,8.

S_j Denotes the symptoms where j = 1, 2,3,4,5.

d_k Denotes the kind of diagnosis i.e. k = 1, 2,3,4,5 and Tables 1 and 2 are the required observations. Computing the algorithm as per the given input i.e.

$$l_{NNH}(S(P_1), d_1) = \tfrac{1}{5}[\max\{|\mu_1(p_1) - \mu_1(d_1)|, |\sigma_1(p_1) - \sigma_1(d_1)|, |\gamma_1(p_1) - \gamma_1(d_1)|\} + \max\{|\mu_2(p_1) - \mu_2(d_1)|, |\sigma_2(p_1) - \sigma_2(d_1)|, |\gamma_2(p_1) - \gamma_2(d_1)|\} + \max\{|\mu_3(p_1) - \mu_3(d_1)|, |\sigma_3(p_1) - \sigma_3(d_1)|, |\gamma_3(p_1) - \gamma_3(d_1)|\} + \max\{|\mu_4(p_1) - \mu_4(d_1)|, |\sigma_4(p_1) - \sigma_4(d_1)|, |\gamma_4(p_1) - \gamma_4(d_1)|\} + \max\{|\mu_5(p_1) - \mu_5(d_1)|, |\sigma_5(p_1) - \sigma_5(d_1)|, |\gamma_5(p_1) - \gamma_5(d_1)|\}].$$

From the above calculation we get the output for the patient P_1 with respect to diagnosis k = 1. Similarly computing for k = 2,3,4 and 5 we get the entire output for P_1 from which the required minimum distance or the core attribute is obtained. The core attribute or the minimum distance is the desired diagnosis of the patient. Continuing the process for $P_2, P_3, ..., P_8$ we complete Table 3.

```
'Extended Hausdorff - Neutrosophic Normalizied Hamming Distance/Core Attribute
Calculation Starts here

        For Each Key In diagnosisData.Keys
            'diagKey = diagnosisData(Key)
            If sympData.Exists(Key) Then
              'If sympData(Key) = diagnosisData(Key) Then
                maxData = 0
                dataArray = Split(sympData(Key), ",")
                diagArray = Split(diagnosisData(Key), ",")
                For j = LBound(dataArray) To UBound(dataArray)
                    If WorksheetFunction.IsNumber(CDbl(diagArray(j))) = True And _
                       WorksheetFunction.IsNumber(CDbl(dataArray(j))) = True Then
                       result = Abs(dataArray(j) - diagArray(j))
                       If maxData < result Then maxData = result
                    Else
                        MsgBox "Check for Numeric values in Symptoms and Diagnosis"
                        dataMisMatch = True
                        Exit For
                    End If
                Next
                If dataMisMatch = True Then Exit For
                distData = distData + maxData
             'Else
               ' MsgBox "Symptom - " & Key & " ordering mismatch with Diagnosis ordering"
               'dataMisMatch = True
               'Exit For
             'End If
           Else
              MsgBox "Symptom " & sympData.Keys(Key) & " not found in Diagnosis"
              dataMisMatch = True
              Exit For
            End If
            dLoop = dLoop + 1
        Next Key
'Extended Hausdorff - Neutrosophic Normalizied Hamming Distance/Core Attribute
Calculation Ends here
```

Table 1
Symptoms characteristic for the patients considered.

	Temperature	Headache	Body Pain	Cough	Sneezing
P1	(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)
P2	(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)
P3	(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)
P4	(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)
P5	(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)
P6	(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)
P7	(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)
P8	(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
Symptoms characteristic for the diagnoses considered.

	Viral fever	Malaria	Typhoid	Chicken gunya	Corona virus
Temperature	(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	(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	(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	(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	(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)

Table 3
The minimum distance or core number table.

	Viral fever	Malaria	Typhoid	Chicken gunya	Corona virus
P1	**0.1600**	0.3200	0.3000	0.3800	0.3400
P2	0.2400	0.2800	**0.1800**	0.3000	0.2400
P3	**0.2400**	0.3600	0.2600	0.3600	0.4400
P4	0.2200	**0.2000**	0.2600	0.4200	0.340
P5	0.4200	0.4200	**0.3400**	0.4000	0.4000
P6	0.3400	0.3800	0.3600	**0.3200**	0.3800
P7	**0.3000**	0.3800	03,800	0.3800	0.3600
P8	0.3800	0.4400	0.4200	0.4600	**0.3600**

Remark 4. The above sample data as well as symptoms sample for our study are collected from Fatima Medical College Kadapa run by a private trust, which is also one of the corona quarantine centre for Kadapa district in Andhra Pradesh, India. Kadapa district had number of suspected cases but fortunately many after quarantine treatment have come out successfully and tested negative results for corona.

The following sample code of EXCEL programme, for finding the possible minimum number or the core symptom, is used to simplify our calculation work. The output is tabulated in Table 3.

The above Excel programme is designed to find the Hausdorff minimum distance that indicates the core number of the patient

In the above table with bold letters are the **minimum distance or core attribute** acquired by using Hausdorff Hamming distance as per the given neutrosophic data.

The above histogram indicates **the minimum distance or the core attribute** of the particular patient in a graph.

4. Conclusion

As a result by executing the neutrosophic extended Hausdorff normalised Hamming distance programme for each patient we observer that patients $\boldsymbol{P}_1, \boldsymbol{P}_3$ and $\boldsymbol{P}_7$ have got their minimum number under the column **Viral fever**. Hence, by this minimum number (distance) method, we conclude that in all likelyhood they will be suffering from viral fever. Following this pattern we can say that patients $\boldsymbol{P}_2$ and $\boldsymbol{P}_5$ will have **Typhoid**, patient $\boldsymbol{P}_4$ will have **Malaria**, patient $\boldsymbol{P}_6$ will have **Chicken Gunya** and patient $\boldsymbol{P}_8$ will be affected by **Corona virus**. Further we hope that this application can open up a lot of scope for future study which may be very useful for the common people.

Abbreviations

d_H - Hausdorff distance, H_{IFS} - Hausdorff intuitionistic fuzzy set, *NS* - neutrosophic sets, d_{HNS} - Extended Hausdorff distance, d_{NH} - neutrosophic Hamming distance, l_{NNH} - neutrosophic normalized Hamming distance, max - maximum.

Declarations

Availability of data and materials: It is just examples to illustrate the results in examples.

Funding: This research received no external funding.

Authors' contributions: All authors have contributed equally to this paper. The idea of this paper was put forward by VA and MT. VA and MT completed the preparatory work of the paper, SJ analyzed the existing work. The revision of the paper was completed by VA and SJ and the submission of this paper was completed by VA.

CRediT authorship contribution statement

V. Antonysamy: Writing - original draft, Software. **M. Lellis Thivagar:** Conceptualization. **S. Jafari:** Writing – review & editing. **Abdulsattar Abdullah Hamad:** Methodology, Visualization, Investigation, Supervision.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

The authors would like to thank the referees for providing very useful comments and suggestions that helped in improving the quality of the paper.

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