Applied Soft Computing xxx (2017) xxx–xxx

Contents lists available at ScienceDirect

Applied Soft Computing

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

A neutrosophic recommender system for medical diagnosis based on algebraic neutrosophic measures

Mumtaz Ali[a], Le Hoang Son[b,*], Nguyen Dang Thanh[c], Nguyen Van Minh[d]

[a] University of Southern Queensland, 4300, Australia
[b] VNU University of Science, Vietnam National University, Hanoi, Vietnam
[c] People's Police University of Technology and Logistics, Bac Ninh, Vietnam
[d] Hanoi University of Natural Resources and Environment, Hanoi, Vietnam

ARTICLE INFO

Article history:
Received 8 September 2016
Received in revised form 22 August 2017
Accepted 8 October 2017
Available online xxx

Keywords:
Algebraic neutrosophic measures
Medical diagnosis
Neutrosophic set
Neutrosophic recommender system
Non-linear forecast model

ABSTRACT

Medical diagnosis is a procedure for the investigation of a person's symptoms on the basis of disease. This problem has been investigated and applied to personal healthcare systems in medicine. The relevant methods have limitations regarding neutrosophication, deneutrosophication, similarity measures, correlation coefficients, distance measure, and patients' history. In this paper, we propose a novel neutrosophic recommender system for medical diagnosis based on algebraic neutrosophic measures. Specifically, a single-criterion neutrosophic recommender system (SC-NRS) and a multi-criteria neutrosophic recommender system (MC-NRS) accompanied by algebraic operations such as union, complement and intersection are proposed. Several types of similarity measures based on the algebraic operations and their theoretic properties are investigated. A prediction formula and a new forecast algorithm using the proposed algebraic similarity measures are designed. The proposed method is experimentally validated on some benchmark medical datasets against the relevant ones namely ICSM, DSM, CARE and CFMD. The experiments demonstrate that the proposed method has better Mean Square Error (MSE) than the other algorithms. Besides, there is no large increase in computational time taken by the proposed method and other algorithms. Experiments by various cases of parameters suggest that the MSE values remain almost the same for each dataset when randomly changing the values of parameters in all the medical datasets. Lastly, the strength of all the algorithms is analyzed through ANOVA one-way test and Kruskal-Wallis test. The proposed method has better accuracy than the related algorithms. Experimental results support the advantage and superiority of the proposed method.

1. Introduction

Medical diagnosis is a procedure for the investigation of a person's symptoms on the basis of disease [19]. From modern medical technology, a large amount of uncertain, inconsistent, indeterminate information is available to medical experts for performing medical diagnoses [24]. Thus, starting with the beginning of artificial intelligence, medical diagnosis has received the full attention of both the computer science and applied computer mathematics research society [14,26,42–48]. A medical diagnosis problem often contains a huge amount of uncertain, inconsistent, incomplete, and indeterminate data which are very difficult to retrieve [21]. The neutrosophic set (NS) proposed by Smarandache [32] can handle this type of information accurately. A neutrosophic set can be characterized independently by a truth membership function, indeterminate membership function and false membership function, respectively. Many researches utilizing the neutrosophic set have been proposed for the application of medical diagnosis such as the improved cosine similarity measures [51–54],

Abbreviations: NS, neutrosophic set; RS, recommender system; NRS, neutrosophic recommender system; SC-NRS, single criterion neutrosophic recommender system; MC-NRS, multi criteria neutrosophic recommender system; RHC, right heart catheterization; DMD, duchenne muscular dystrophy; ICSM, improved cosine similarity measures; DSM, dice similarity measure; CARE, collaborative assessment and recommendation engine; CFMD, collaborative filtering in medical datasets; MSE, mean square error; Sec, seconds.

* Corresponding author at: 334 Nguyen Trai, Thanh Xuan, Hanoi, Vietnam. Tel.: +84 904 171 284.
E-mail addresses: Mumtaz.Ali@usq.edu.au (M. Ali), sonlh@vnu.edu.vn, chinhson2002@gmail.com (L.H. Son), ndthanht36@gmail.com (N.D. Thanh), nvminh@hunre.edu.vn (N.V. Minh).

https://doi.org/10.1016/j.asoc.2017.10.012
1568-4946/

the simplified NS [6,16], the extended Sanchez approach [20], the rough neutrosophic set [30], and segmentation algorithms [1,18,55]. It has been observed that NS is a good methodology for medical diagnosis.

Despite of having remarkable achievements, yet the NS still remains some disadvantages regarding the history of patients and neutrosophication processes [37,38]. Besides, the neutrosophic set approach has the problems of neutrosophication and deneutrosophication, similarity measures [50–55], correlation coefficients [6] and distance measure [7]. Mathematical properties such as the distance and similarity measures were either not examined nor was it explained why these operations were performed in medical diagnosis [50–55]. In order to handle these problems, the hybridization approach between the neutrosophic set and the recommender system (RS) was utilized for the benefit of utilizing the advantages of each standalone method. As a special type of information systems, RS can evaluate information based on the historic dataset which is the first limitation of the NS approach. The RS itself has been applied to medical diagnosis such as in [9,11,17,22,25,27,31,34,35]. Nonetheless, the RS cannot handle uncertain and indeterminate data so that the integration with other advanced fuzzy techniques is a wise choice in this regard [37,38]. It is indeed realizable that the hybrid systems could handle the issues of RS. There are many proofs of designing and using hybrid systems for medical diagnosis such as in [2,8,23,28,29,36–38,40]. Some other recent papers [3–5,12,13,39] also implied two crucial arguments: i) using hybrid systems for medical diagnosis is necessary; and ii) the combination of RS and advanced fuzzy sets, e.g. the neutrosophic set is a good choice to enhance the accuracy.

Thus, the main aim of this paper is to design a new hybrid method between RS and NS called NRS for medical diagnosis. The substantial difference with the existing works is listed as follows. *Firstly*, compared with the standalone NS and RS approaches, the new method handles the problems of the history of patients and neutrosophication processes (in NS) and uncertain and indeterminate data (in RS). *Secondly*, compared with other hybrid systems for medical diagnosis, the proposal follows the trends of combination of RS and advanced fuzzy sets. But different to the other papers, the new system is deployed on the NS which was shown to be better of modelling real-life problems than the others [33]. *Thirdly*, NRS is constructed based on the new theory – algebraic neutrosophic measures which were not existed in the previous works [6,7,20,30,51–54]. *Fourthly*, the proposal is a generalization of the other existing hybrid recommender systems which could improve accuracy of the neutrosophic set as well as the recommender system. *Lastly*, NRS is designed based on a strong mathematical foundation. It is indeed recognizable that the significance and importance of the proposed work can be seen from both theoretical and practical aspects. Moreover, the new proposal expresses a different view of hybridization with the others.

The detailed contributions are shown below. *Firstly*, we propose two different types of NRS called the single-criterion neutrosophic recommender system (SC-NRS) and the multi-criteria neutrosophic recommender system (MC-NRS). *Secondly*, we investigate the algebraic operations of NRS in the first time. *Thirdly*, we construct the neutrosophic similarity measures for NRS based on the algebraic operations. *Lastly*, we design a non-linear forecast model for NRS motivated under the light of RS. The proposed method will be experimentally validated on benchmark medical datasets against the relevant ones.

The rest of the paper is organized as follows. Section 2 presents some background for the paper including the formulation of medical diagnosis, neutrosophic sets, neutrosophication and deneutrosophication, and recommender systems. Section 3 describes the proposed method including NRS (Section 3.1), algebraic operations in NRS (Section 3.2), similarity measures based on the algebraic operations (Section 3.3), and the non-linear forecast model (Section 3.4). Section 4 validates the proposed approach on benchmark datasets. Finally, conclusions and further work are covered in the Section 5.

2. Background

In this section, we discuss some basic and fundamental concepts of medical diagnosis, neutrosophic sets and recommender systems, respectively.

2.1. Medical diagnosis

Definition 1 *([29,36–38])*. Let $\wp = \{p_1, p_2, ..., p_n\}$, $\Gamma = \{s_1, s_2, ..., s_m\}$ and $D = \{d_1, d_2, ..., d_k\}$ be three lists of patients, symptoms and diseases, respectively such that $n, m, k \in N^+$ are the numbers of patients, symptoms and diseases, respectively. Let $\Re_{\wp\Gamma} = \left\{\Re^{\wp\Gamma}\left(p_i, s_j\right) : \forall i = 1, 2, .., n; j = 1, 2, ..., m\right\}$ be the set of relations between patients and symptoms where $\Re^{\wp\Gamma}\left(p_i, s_j\right)$ is the level of the patient p_i who acquires the symptom s_j. The value of $\Re^{\wp\Gamma}\left(p_i, s_j\right)$ is either numeric number or a neutrosophic number which depends on the proposed domain of the problem. Similarly, let $\Re_{\Gamma D} = \left\{\Re^{\Gamma D}\left(s_i, d_j\right) : \forall i = 1, 2, .., m; j = 1, 2, ..., k\right\}$ be the set which represents the relationship between the symptoms and the diseases where $\Re^{\Gamma D}\left(s_i, d_j\right)$ reveals the probability that symptom s_i leads to the disease d_j. The purpose of the medical diagnosis is to determine the relationship between the patients and the diseases described as $\Re_{\wp D} = \left\{\Re^{\wp D}\left(p_i, d_j\right) : \forall i = 1, 2, .., m; j = 1, 2, ..., k\right\}$ where the value of $\Re^{\wp D}\left(p_i, d_j\right)$ is either 0 or 1 which indicates that the patient p_i acquired the disease d_j or not. Mathematically, the problem of medical diagnosis is an implication operator given by the mapping $\left\{\Re_{\wp\Gamma}, \Re_{\Gamma D}\right\} \rightarrow \Re_{\wp D}$.

2.2. Neutrosophic set

The non-standard analysis introduced by Robinson [33] in 1960s is a branch of mathematical logic that rigorously defines the infinitesimals. Informally, an infinitesimal is an infinitely small number. For instance, x is called infinitesimal if and only if for all positive integers n, one has $|x| \leq \frac{1}{n}$. Let $\varepsilon > 0$ be such infinitesimal number. The hyper-real number set is an extension of the real number set that consists of classes of infinite numbers and classes of infinitesimal numbers. Let us consider the non-standard finite numbers $1+ = 1+\varepsilon$, where "1" is its standard part and "ε" is the non-standard part, and $-0 = 0-\varepsilon$, where "0" is the standard part and "ε" is the non-standard part. Then, we call $]^{-}0, 1^{+}[$ as a non-standard unit interval. Obviously, 0 and 1, and analogously non-standard numbers infinitely small but less than 0 or infinitely small but greater than 1, belong to the non-standard unit interval.

In what follow, we recall the definition of neutrosophic set.

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Definition 2 *([32])*. Let X be a non-empty set and $x \in X$. A neutrosophic set A in X is characterized by a truth membership function T_A, an indeterminacy membership function I_A, and a falsehood membership function F_A. Here $T_A(x)$, $I_A(x)$ and $F_A(x)$ are real standard or non-standard subsets of $]0^-, 1^+[$ such that $T_A, I_A, F_A : X \to]0^-, 1^+[$. There is no restriction on the sum of $T_A(x)$, $I_A(x)$ and $F_A(x)$. The constraint is $0^- \leq T_A(x) + I_A(x) + F_A(x) \leq 3^+$ where 3^+ means $3 + \varepsilon$. From a philosophical point view, the neutrosophic set takes the value from real standard or non-standard subsets of $]0^-, 1^+[$. Thus it is necessary to take the interval $[0, 1]$ instead of $]0^-, 1^+[$ in technical applications because it is difficult to use $]0^-, 1^+[$ in real life applications such as engineering and scientific problems. If the functions $T_A(x)$, $I_A(x)$ and $F_A(x)$ are singleton subinterval/subsets of the real standard such that $T_A(x) : X \to [0, 1]$, $I_A(x) : X \to [0, 1]$, $F_A(x) : X \to \in [0, 1]$, then a simplification of the neutrosophic set A is denoted by,

$$A = \left\{ \left(x, T_A(x), I_A(x), F_A(x) \right) : x \in X \right\}, \tag{1}$$

where $0 \leq T_A(x) + I_A(x) + F_A(x) \leq 3$. In Eq. (1), $T_A(x)$, $I_A(x)$ and $F_A(x)$ mean the truth, indeterminacy and falsehood membership degrees of x in the neutrosophic set A (subscript A). It is a subclass of the neutrosophic set and called the simplified neutrosophic set. The neutrosophic set is a three-dimensional set while a fuzzy set lies in one dimension. For more details on the comparison between fuzzy sets and neutrosophic sets, we refer to [32].

2.3. Neutrosophication and deneutrosophication

Definition 3 *([49])*. The main purpose of **neutrosophication** is to map input variables to neutrosophic sets. If x is a crisp input then

$$\mathrm{T}(x) = \begin{cases} \dfrac{x - a_1}{a_2 - a_1}, & a_1 \leq x < a_2, \\ \dfrac{a_3 - x}{a_3 - a_2}, & a_2 \leq x < a_3, \\ \dfrac{x - a_3}{a_4 - a_3}, & a_3 \leq x < a_4 \\ 0, & otherwise. \end{cases} \quad \mathrm{I}(x) = \begin{cases} \dfrac{b_2 - x}{b_2 - b_1}, & b_1 \leq x < b_2, \\ \dfrac{x - b_2}{b_3 - b_2}, & b_2 \leq x < b_3, \\ \dfrac{b_4 - x}{b_4 - b_3}, & b_3 \leq x < b_4, \\ 1, & otherwise. \end{cases} \quad \mathrm{F}(x) = \begin{cases} \dfrac{c_2 - x}{c_2 - c_1}, & c_1 \leq x < c_2, \\ \dfrac{x}{c_3} & c_2 \leq x < c_3, \\ \dfrac{c_4 - x}{c_4 - c_3}, & c_3 \leq x < c_4 \\ 1, & otherwise. \end{cases}, \tag{2}$$

are the truth, indeterminacy and falsehood memberships for the crisp input $x \in X$ and $a_j \leq x \leq a_k$ for truth membership, $b_j \leq x \leq b_k$ for indeterminacy membership and $c_j \leq x \leq c_k$ for falsehood membership, respectively, and $j, k = 1, 2, 3, 4$.

Definition 4 *([49])*. Deneutrosophication

This step is similar to defuzzification of George and Bo [15]. This step involves in the following two stages:

Stage 1: Synthesization

In this stage, we transform a neutrosophic set A into a fuzzy set B by the following function:

$$f\left(T_A(y), I_A(y), F_A(y)\right) : [0, 1] \times [0, 1] \times [0, 1] \to [0, 1]. \tag{3}$$

$$T_B(y) = \alpha T_A(y) + \beta \frac{F_A(y)}{4} + \gamma \frac{I_A(y)}{2}, \tag{4}$$

where $0 \leq \alpha, \beta, \gamma \leq 1$ such that $\alpha + \beta + \gamma = 1$.

Stage 2: Typical neutrosophic value

In this stage, we can calculate a typical deneutrosophicated value $den\left(T_B(y)\right)$ by the centroid or center of gravity method which is given below:

$$den\left(T_B(y)\right) = \frac{\int_a^b T_B(y)\, y dy}{\int_a^b T_B(y)\, dy} \tag{5}$$

where the integrand is a continuous function.

2.4. Recommender systems

Definition 5 *([31])*. Single-criterion recommender systems (SC-RS)

Suppose U is a set of all users and Ω is the set of items in the system. The utility function $\Re$ is a mapping specified on $U_1 \subset U$ and $\Omega_1 \subset \Omega$ as follows:

$$\begin{matrix} \Re : U_1 \times \Omega_1 \to \wp \\ (u_1; \omega_1) \mapsto \Re(u_1; \omega_1) \end{matrix}, \tag{6}$$

where $\Re(u_1; \omega_1)$ is a non-negative integer or a real number within a certain range (set of real numbers R). $\Re$ is a set of available ratings in the system. Thus, SC-RS is the system that provides two basic functions below.

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(a) Prediction: determine $\Re(u^*;\omega^*)$for any $(u^*,\omega^*) \in \left(U,\Omega\right)\setminus\left(U_1;\Omega_1\right)$;
(b) Recommendation: choose $\omega^* \in \Omega$ satisfying $\omega^* = arg\max_{i\in I}\Re(u,\omega)$, u $\in U$

Definition 6 *([31]).* Multi-criteria recommender systems (MC-RS)

MC-RS provides similar basic functions with SC-RS but follows multiple criteria.

$$\begin{array}{l}\Re : U_1\times\Omega_1 \to \wp_1\times\wp_2\times\ldots\times\wp_k,\\ (u_1;\omega_1)\mapsto(\Re_1,\Re_2,\ldots,\Re_k)\end{array}, \tag{7}$$

where $\Re_i\,(i=1,2,\ldots,k)$ is the rating of user $u_1\in U_1$ for item $\omega_1\in\Omega_1$ following by criteria i in this case, the recommendation is performed according to a given criteria.

3. Neutrosophic recommender system

In this section, we propose two variants of the Neutrosophic Recommender System (NRS) called SC-NRS and MC-NRS in Section 3.1. Further, we propose some algebraic operations of the neutrosophic recommender system in Section 3.2. Then, we present some novel similarity measures based on these algebraic operations in Section 3.3. Finally, a non-linear forecast model is designed in Section 3.4.

3.1. SC-NRS and MC-NRS

Let $\wp=\{p_1,p_2,\ldots,p_n\}$, $\Gamma=\{s_1,s_2,\ldots,s_m\}$ and $D=\left\{d_1,d_2,\ldots,d_k\right\}$ be three lists of patients, symptoms and diseases, respectively such that $n, m, k\in N^+$ be the numbers of patients, symptoms and diseases, respectively where p_i and s_j have some features and characteristics, respectively and $i=1,2,\ldots,n$ and $j=1,2,\ldots,m$. Further, we consider that the features of the patient and characteristics of the symptoms are denoted by X and Υ which consist of s neutrosophic linguistic labels. Similarly, disease d_i also has s neutrosophic linguistic labels where $i=1,2,\ldots,k$.

Definition 7. Single-criterion Neutrosophic recommender System (SC-NRS)

The (SC-NRS) is a utility function $\Re$ which is a mapping defined on (X,Υ):

$$\Re : X\times\Upsilon\to D$$

$$\begin{array}{l}\langle\begin{array}{l}(T_{1X}(x),I_{1X}(x),F_{1X}(x)),\\ (T_{2X}(x),I_{2X}(x),F_{2X}(x)),\\ \ldots\\ (T_{sX}(x),I_{sX}(x),F_{sX}(x))\end{array}\rangle\times\langle\begin{array}{l}(T_{1\Upsilon}(y),I_{1\Upsilon}(y),F_{1\Upsilon}(y)),\\ (T_{2\Upsilon}(y),I_{2\Upsilon}(y),F_{2\Upsilon}(y)),\\ \ldots\\ (T_{s\Upsilon}(y),I_{s\Upsilon}(y),F_{s\Upsilon}(y))\end{array}\rangle\to\langle\begin{array}{l}(T_{1D}(d),I_{1D}(d),F_{1D}(d)),\\ (T_{2D}(d),I_{2D}(d),F_{2D}(d)),\\ \ldots\\ (T_{sD}(d),I_{sD}(d),F_{sD}(d))\end{array}\rangle,\end{array} \tag{8}$$

where $T_{iX}(x), I_{iX}(x), F_{iX}(x)$ are the truth membership function, indeterminate membership function and false membership function of the patient with the linguistic label ith of the feature X such that $i=1,2,\ldots,s$ and $T_{iX}(x), I_{iX}(x), F_{iX}(x)\in[0,1]$. Similarly, $T_{j\Upsilon}(y), I_{j\Upsilon}(y), F_{j\Upsilon}(y)$ are the truth membership function, indeterminate membership function and false membership function of the symptom with the linguistic label jth of the feature Υ where $j=1,2,\ldots,s$ and $T_{j\Upsilon}(y), I_{j\Upsilon}(y), F_{j\Upsilon}(y)\in[0,1]$. Additionally, $T_{lD}(d), I_{lD}(d), F_{lD}(d)$ are the truth membership function, indeterminate membership function and false membership function of the disease D with the linguistic label lth such that $l=1,2,\ldots,s$ and $T_{lD}(d), I_{lD}(d), F_{lD}(d)\in[0,1]$. SC-NRS depicts the following assertions:

1. Prediction: Compute the values of $(T_{lD}(d), I_{lD}(d), F_{lD}(d))$ for all $l=1,2,\ldots,s$.
2. Recommendation 1: select $\overset{*}{i}\in\left\{1,2,\cdots,s\right\}$, which satisfies

$$\overset{*}{i}=\underset{i=1}{\overset{s}{arg\max}}\left\{T_{lD}(d)+T_{lD}(d)(3-T_{lD}(d)-I_{lD}(d)-F_{lD}(d))\right\}$$

3. Recommendation 2: select $\overset{*}{i}\in\left\{1,2,\cdots,s\right\}$ which satisfies

$$\overset{*}{i}=\underset{i=1}{\overset{s}{arg\max}}\left\{T_{lD}(d)+T_{lD}(d)(2(1-T_{lD}(d))-I_{lD}(d)-F_{lD}(d))\right\}$$

The formulae of recommendation 1 and recommendation 2 give different results for $\overset{*}{i}\in\left\{1,2,\cdots,s\right\}$, which means that NRS has the ability of depicting more than one choice for a recommendation. In this definition, d stands for the type of disease in the disease set D. Recommendations 1 and 2 are different from each other which are due to the neutrosophic set components. They are different combinations of the neutrosophic set components that lead to different recommendation choices. The recommendation is often selected based on priority basis. It is an advantage of neutrosophic set that provides two types of possible recommendations.

Remark 1. a) It is clear from Definition 7 that the medical diagnosis denoted by the implication $(Patient, Symptom)\to Disease$ is identical to that of Definition 1. Consequently, SC-NRS is another form of medical diagnosis which follows the philosophy of the recommender system.

b) SC-NRS in Definition 7 could be seen as the extension of RS in Definition 5 if there exists i such that:

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- $T_{iX}(x) = 1 \wedge I_{iX}(x) \wedge F_{iX}(x) = 0; \forall j \neq i; T_{jX}(x) = 0 \wedge I_{jX}(x) \wedge F_{jX}(x) = 1,$
- $T_{i\Upsilon}(y) = 1 \wedge I_{i\Upsilon}(y) \wedge F_{i\Upsilon}(y) = 0; \forall j \neq i; T_{j\Upsilon}(y) = 0 \wedge I_{j\Upsilon}(y) \wedge F_{j\Upsilon}(y) = 1,$
- $T_{iD}(d) = 1 \wedge I_{iD}(d) \wedge F_{iD}(d) = 0; \forall j \neq i; T_{jD}(d) = 0 \wedge I_{jD}(d) \wedge F_{jD}(d) = 1,$
- $T_{iX}(x) = 1 \wedge I_{iX}(x) = 0; \forall j \neq i; T_{jX}(x) = 0 \wedge I_{jX}(x) = 1,$
- $T_{iX}(x) = 1 \wedge F_{iX}(x) = 0; \forall j \neq i; T_{jX}(x) = 0 \wedge F_{jX}(x) = 1,$
- $T_{i\Upsilon}(y) = 1 \wedge I_{i\Upsilon}(y) = 0; \forall j \neq i; T_{j\Upsilon}(y) = 0 \wedge I_{j\Upsilon}(y) = 1,$
- $T_{i\Upsilon}(y) = 1 \wedge F_{i\Upsilon}(y) = 0; \forall j \neq i; T_{j\Upsilon}(y) = 0 \wedge F_{j\Upsilon}(y) = 1,$
- $T_{iD}(d) = 1 \wedge I_{iD}(d) = 0; \forall j \neq i; T_{jD}(d) = 0 \wedge I_{jD}(d) = 1,$
- $T_{iD}(d) = 1 \wedge F_{iD}(d) = 0; \forall j \neq i; T_{jD}(d) = 0 \wedge F_{jD}(d) = 1.$

- $T_{iX}(x) = 1 \wedge I_{iX}(x) \wedge F_{iX}(x) = 0; \forall j \neq i; T_{jX}(x) = 0 \wedge I_{jX}(x) \wedge F_{jX}(x) = 1,$
- $T_{i\Upsilon}(y) = 1 \wedge I_{i\Upsilon}(y) \wedge F_{i\Upsilon}(y) = 0; \forall j \neq i; T_{j\Upsilon}(y) = 0 \wedge I_{j\Upsilon}(y) \wedge F_{j\Upsilon}(y) = 1,$
- $T_{iD}(d) = 1 \wedge I_{iD}(d) \wedge F_{iD}(d) = 0; \forall j \neq i; T_{jD}(d) = 0 \wedge I_{jD}(d) \wedge F_{jD}(d) = 1,$
- $T_{iX}(x) = 1 \wedge I_{iX}(x) = 0; \forall j \neq i; T_{jX}(x) = 0 \wedge I_{jX}(x) = 1,$
- $T_{iX}(x) = 1 \wedge F_{iX}(x) = 0; \forall j \neq i; T_{jX}(x) = 0 \wedge F_{jX}(x) = 1,$
- $T_{i\Upsilon}(y) = 1 \wedge I_{i\Upsilon}(y) = 0; \forall j \neq i; T_{j\Upsilon}(y) = 0 \wedge I_{j\Upsilon}(y) = 1,$
- $T_{i\Upsilon}(y) = 1 \wedge F_{i\Upsilon}(y) = 0; \forall j \neq i; T_{j\Upsilon}(y) = 0 \wedge F_{j\Upsilon}(y) = 1,$
- $T_{iD}(d) = 1 \wedge I_{iD}(d) = 0; \forall j \neq i; T_{jD}(d) = 0 \wedge I_{jD}(d) = 1,$
- $T_{iD}(d) = 1 \wedge F_{iD}(d) = 0; \forall j \neq i; T_{jD}(d) = 0 \wedge F_{jD}(d) = 1.$

Alternatively, the mapping in Eq. (8) can be written as

$$\Re : \wp \times \Gamma \rightarrow D$$

$$((p, X), (s, \Upsilon)) \rightarrow \Re_{\wp D}$$

Next, we extend SC-NRS to the multi-criteria neutrosophic recommender system (MC-NRS) which can handle multiple diseases $D = \{d_1, d_2, \cdots, d_k\}$.

Definition 8. The MC-NRS is a utility function $\Re$ which is a mapping defined on (X, Υ) as follows.

$$\Re : X \times \Upsilon \rightarrow D_1 \times D_2 \times \cdots \times D_k$$

$$\begin{matrix} (T_{1X}(x), I_{1X}(x), F_{1X}(x)), & (T_{1\Upsilon}(y), I_{1\Upsilon}(y), F_{1\Upsilon}(y)), & (T_{1D}(d_1), I_{1D}(d_1), F_{1D}(d_1)), & (T_{1D}(d_2), I_{1D}(d_2), F_{1D}(d_2)), & (T_{1D}(d_k), I_{1D}(d_k), F_{1D}(d_k)), \\ \langle (T_{2X}(x), I_{2X}(x), F_{2X}(x)), \rangle \times \langle & (T_{2\Upsilon}(y), I_{2\Upsilon}(y), F_{2\Upsilon}(y)), \rangle \langle & (T_{2D}(d_1), I_{2D}(d_1), F_{2D}(d_1)), \rangle \times \langle & (T_{2D}(d_2), I_{2D}(d_2), F_{2D}(d_2)), \rangle \times \cdots \times \langle & (T_{2D}(d_k), I_{2D}(d_k), F_{2D}(d_k)), \rangle, \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ (T_{sX}(x), I_{sX}(x), F_{sX}(x)) & (T_{s\Upsilon}(y), I_{s\Upsilon}(y), F_{s\Upsilon}(y)) & (T_{sD}(d_1), I_{sD}(d_1), F_{sD}(d_1)) & (T_{sD}(d_2), I_{sD}(d_2), F_{sD}(d_2)) & (T_{sD}(d_k), I_{sD}(d_k), F_{sD}(d_k)) \end{matrix} \quad (9)$$

MC-NRS can effectively explain the judgement of multiple diseases simultaneously in an accurate way by considering the truth membership function, the indeterminate membership function and the falsity membership function. It defines the following functions:

1. Prediction: Compute values of $(T_{lD}(d_i), I_{lD}(d_i), F_{lD}(d_i))$ for all $l = 1, 2, ..., s$ and $i = 1, 2, ..., k$

2. Recommendation 1: select $\overset{*}{i} \in \{1, 2, \cdots, s\}$ which satisfies

$$\overset{*}{i} = \underset{i=1}{\overset{s}{argmax}} \left\{ \sum_{j=1}^{k} w_j \left(T_{iD}\left(d_j\right) + T_{iD}\left(d_j\right) \left(3 - T_{iD}\left(d_j\right) - I_{iD}\left(d_j\right) - F_{iD}\left(d_j\right)\right)\right) \right\},$$

where w_j is the weight of d_j which belongs to [0, 1] and satisfies $\sum_{j=1}^{k} w_j = 1$.

3. Recommendation 2: select $\overset{*}{i} \in \{1, 2 \cdots s\}$ which satisfies

$$\overset{*}{i} = \underset{i=1}{\overset{s}{argmax}} \left\{ \sum_{j=1}^{k} w_j \left(T_{iD}\left(d_j\right) + T_{iD}\left(d_j\right) \left(2\left(1 - T_{iD}\left(d_j\right)\right) - I_{iD}\left(d_j\right) - F_{iD}\left(d_j\right)\right)\right) \right\},$$

where w_j is the weight of d_j which belongs to [0, 1] and satisfies $\sum_{j=1}^{k} w_j = 1$.

Example 1. Consider 4 patients who have age (feature X) which consists of 3 linguistic labels $\{young, middle, old\}$ where $s = 1, 2, 3$. Similarly, the "Temperature" is a symptom (characteristic) Υ which is comprised of 3 linguistic labels $\{cold, medium, hot\}$. The disease $\{d_1\}$ is $\{Fever\}$ which is also comprised of 3 linguistic levels $\{L_1, L_2, L_3\}$. We use the trapezoidal neutrosophic number –*TNN* [36] to find which ages of patients and temperatures are identified with the relevant disease. The truth membership functions, indeterminate membership functions and false membership functions of the patients to the linguistic label *ith* of the age (feature X) are defined, respectively:

Please cite this article in press as: M. Ali, et al., A neutrosophic recommender system for medical diagnosis based on algebraic neutrosophic measures, Appl. Soft Comput. J. (2017), https://doi.org/10.1016/j.asoc.2017.10.012

$$T_{young}(x)\begin{cases}1 & if \quad 5\le x<25,\\ 45-x/20 & if \quad 25\le x<45,\\ 0 & if \quad 45\le x>50\end{cases},\quad I_{young}(x)\begin{cases}0 & if \quad 5\le x<25,\\ 35-x/30 & if \quad 25\le x<35,\\ 1 & if \quad x>35,\end{cases}\quad F_{young}(x)\begin{cases}0 & if \quad 5\le x<25,\\ x-25/20 & if \quad 25\le x<35,\\ 1 & if \quad x>35,\end{cases} \tag{10}$$

$$T_{middle}(x)\begin{cases}0 & if \quad x>70,\\ x-25/20 & if \quad 25<x\le 35,\\ 1 & if \quad 35\le x<50,\\ 70-x/20 & if \quad 50\le x\le 70\end{cases},\quad I_{middle}(x)\begin{cases}1 & if \quad x>70,\\ 35-x/20 & if \quad 25<x\le 35,\\ 70-x/50 & if \quad 35<x\le 50,\\ 0 & if \quad 50<x\le 70\end{cases},\quad F_{middle}(x)\begin{cases}1 & if \quad x>70,\\ 40-x/20 & if \quad 25<x\le 35,\\ 0 & if \quad 35<x\le 50,\\ x-50/20 & if \quad 50<x\le 70,\end{cases} \tag{11}$$

$$T_{old}(x)\begin{cases}0 & if \quad 25<x\le 70,\\ x-35/20 & if \quad 45<x\le 50,\\ 1 & if \quad 35<x\le 45,\\ x-35/50 & if \quad 50<x\le 70\end{cases},\quad I_{old}(x)\begin{cases}1 & if \quad 50<x\le 70\\ 50-x/25 & if \quad 25<x\le 35\\ 0 & if \quad 35<x\le 50\end{cases},\quad F_{old}(x)\begin{cases}1 & if \quad 25<x\le 45,\\ 60-x/20 & if \quad 45<x\le 50,\\ 0 & if \quad x<25, 55<x\ge 70,\\ x-35/25 & if \quad 50<x\le 55,\end{cases} \tag{12}$$

From Eqs. (10)–(12), we calculate the following information about the patients:

$$Alex(30t)=\langle old(0,0.8,1);middle(0.25,0.25,0.5),young(0.75,0.16,0.25)\rangle, \tag{13}$$

$$Linda(40t)=\langle old(1,0,1);middle(1,0.6,0);young(0.25,1,1)\rangle, \tag{14}$$

$$Bill(50t)=\langle old(0.75,0,0.5);middle(1,0.4,0);young(0,1,1)\rangle, \tag{15}$$

$$John(55t)=\langle old(0.4,1,0.8);middle(0.75,0,0.25);young(0,1,1)\rangle. \tag{16}$$

Similarly, the membership functions of the symptoms to the linguistic label *jth* of characteristic Υ are given below.

$$T_{cold}(x)\begin{cases}20-x/25 & if \quad x\le 5,\\ x-5/15 & if \quad 5<x\le 15,\\ 30-x/15 & if \quad 15<x\le 30,\\ 0 & if \quad x>30\end{cases},\quad I_{cold}(x)\begin{cases}10-x/15 & if \quad x\le 5,\\ x-5/15 & if \quad 5<x\le 15,\\ x-15/30 & if \quad 15<x\le 30,\\ 1 & if \quad x>30\end{cases},\quad F_{cold}(x)\begin{cases}5-x/10 & if \quad 5\le x<10,\\ x-5/20 & if \quad 10\le x<20,\\ 30-x/20 & if \quad 20\le x\le 30,\\ 1 & if \quad x>30,\end{cases} \tag{17}$$

$$T_{medium}(x)\begin{cases}15-x/15 & if \quad 5\le x<10,\\ 20-x/20 & if \quad 10\le x<20,\\ 30-x/10 & if \quad 20\le x\le 30,\\ 0 & if \quad x>30,\end{cases}\quad I_{medium}(x)\begin{cases}9-x/15 & if \quad 5\le x<9,\\ x-5/18 & if \quad 9\le x<18,\\ 30-x/30 & if \quad 18\le x\le 30,\\ 1 & if \quad x>30,\end{cases}\quad F_{medium}(x)\begin{cases}7-x/5 & if \quad 5\le x<7,\\ x-7/14 & if \quad 7\le x<14,\\ 30-x/14 & if \quad 14\le x\le 30,\\ 1 & if \quad x>30,\end{cases} \tag{18}$$

$$T_{hot}(x)\begin{cases}10-x/10 & if \quad 5\le x<10,\\ x-7/17 & if \quad 10\le x<17,\\ 30-x/17 & if \quad 17\le x\le 30,\\ 0 & if \quad x>30,\end{cases}\quad I_{hot}(x)\begin{cases}8-x/5 & if \quad 5\le x<8,\\ x-8/16 & if \quad 8\le x<16,\\ 30-x/16 & if \quad 16\le x\le 30,\\ 1 & if \quad x>30,\end{cases}\quad F_{hot}(x)\begin{cases}5-x/11 & if \quad 5\le x<11,\\ x-11/18 & if \quad 11\le x<18,\\ 30-x/18 & if \quad 18\le x\le 30,\\ 1 & if \quad x>30,\end{cases} \tag{19}$$

From Eqs. (17)–(19), we can compute the information about the symptoms as follows.

$$(4^{\circ}C)=\langle cold(0.64,0.4,0.1);medium(0.73,0.33,0.6);hot(0.6,0.8,0.09)\rangle, \tag{20}$$

$$(15^{\circ}C)=\langle cold(0.66,0.66,0.5);medium(0.25,0.55,0.57);hot(0.47,0.43,0.22)\rangle, \tag{21}$$

$$(22^{\circ}C)=\langle cold(0.53,0.23,0.4);medium(0.8,0.26,0.57);hot(0.47,0.5,0.44)\rangle, \tag{22}$$

$$(28^{\circ}C)=\langle cold(0.13,0.43,0.1);medium(0.2,0.06,0.14);hot(0.11,0.12,0.11)\rangle. \tag{23}$$

Eqs. (13)-(16), (20)-(23) can be written in Table 1.

3.2. Some algebraic operations of NRS

In this section, we propose some algebraic operations of NRS and their properties. Suppose we have three subsets of $NRS=\{X,Y,\{D_k\}\,|k=1,2,...,n\}$ given below.

$$NRS_1=\{X_1;Y_1;\{D_i^1\}|i=1,2,\ldots,n\};\quad NRS_2=\{X_2;Y_2;\{D_i^2\}|i=1,2,\ldots,n\};$$

$$NRS_3=\{X_3;Y_3;\{D_i^3\}|i=1,2,\ldots,n\};$$

$$X_i\subset X;Y_i\subset Y;D_i^j=\left\{R_i^j;T_i^j;F_i^j;I_i^j\right\}=\left\{\left(R_{iq}^j;T_{iq}^j;F_{iq}^j;I_{iq}^j\right)\,|\,q=1,2,\ldots,r;j=1,2,3;\right\}.$$

The Union, Intersection and Complement operations of NRSs are defined:
(a) Union: $NRS_1\cup NRS_2=NRS_{12}$, where

$$NRS_{12}=\{X_{12};Y_{12};\{D_l^{12}\}|\,l=1,2,\ldots,k\}$$

$$X_{12}=X_1\cup X_2$$

$$Y_{12}=Y_1\cup Y_2$$

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Table 1
A neutrosophic recommender system for medical diagnosis.

Age	Temperature	Fever Level 100 M/l
$Alex(30t) = \langle \begin{matrix} old(0, 0.8, 1); \\ middle(0.25, 0.25, 0.5); \\ young(0.75, 0.16, 0.25) \end{matrix} \rangle$	$(4^{\circ}C) = \langle \begin{matrix} cold(0.64, 0.4, 0.1); \\ medium(0.73, 0.33, 0.6); \\ hot(0.6, 0.8, 0.09) \end{matrix} \rangle$	$L_1 = \langle 0.5, 0.3, 0.5 \rangle$, $L_2 = \langle 0.4, 0.7, 0.1 \rangle$, $L_3 = \langle 0.7, 0, 0 \rangle$
$Linda(40t) = \langle \begin{matrix} old(1, 0, 1); \\ middle(1, 0.6, 0); \\ young(0.25, 1, 1) \end{matrix} \rangle$	$(15^{\circ}C) = \langle \begin{matrix} cold(0.66, 0.66, 0.5); \\ medium(0.25, 0.55, 0.57); \\ hot(0.47, 0.43, 0.22) \end{matrix} \rangle$	$L_1 = \langle 0.9, 0.1, 0.3 \rangle$, $L_2 = \langle 0, 0, 0.8 \rangle$, $L_3 = \langle 0.7, 0, 0.5 \rangle$
$Bill(50t) = \langle \begin{matrix} old(0.75, 0, 0.5); \\ middle(1, 0.4, 0); \\ young(0, 1, 1) \end{matrix} \rangle$	$(22^{\circ}C) = \langle \begin{matrix} cold(0.53, 0.23, 0.4); \\ medium(0.8, 0.26, 0.57); \\ hot(0.47, 0.5, 0.44) \end{matrix} \rangle$	$L_1 = \langle 0.15, 0.03, 0.01 \rangle$, $L_2 = \langle 0.24, 0.75, 0.16 \rangle$, $L_3 = \langle 0.8, 0.3, 0.1 \rangle$
$John(55t) = \langle \begin{matrix} old(0.4, 1, 0.8); \\ middle(0.75, 0, 0.25), \\ young(0, 1, 1) \end{matrix} \rangle$	$(28^{\circ}C) = \langle \begin{matrix} cold(0.13, 0.43, 0.1); \\ medium(0.2, 0.06, 0.14); \\ hot(0.11, 0.12, 0.11) \end{matrix} \rangle$	$L_1 = \langle 0.55, 0, 0 \rangle$, $L_2 = \langle 0, 0.7, 0.9 \rangle$, $L_3 = \langle 0.4, 0.4, 0.4 \rangle$

$$\begin{aligned} &\{D_l^{12}\} = (R_l^{12}; T_l^{12}; F_l^{12}; I_l^{12}) = \{(R_{lq}^{12}; T_{lq}^{12}; F_{lq}^{12}; I_{lq}^{12}) |\ q = 1,2,\ldots,r, l \in N;\ k \in N\} \\ &T_{lq}^{12} = \max\{T_{lq}^1; T_{lq}^2\}; F_{lq}^{12} = \min\{F_{lq}^1; F_{lq}^2\}; I_{lq}^{12} = \min\{I_{lq}^1; I_{lq}^2\} \end{aligned} \tag{24}$$

where k is a non-zero positive integer that belong to set N (set of integers).

(b) Intersection: $NRS_1 \cap NRS_2 = NRS_{12}$, where

$$\begin{aligned} &NRS_{12} = \{X_{12}; Y_{12}; \{D_l^{12}\} |\ l = 1,2,\ldots,k\} \\ &X_{12} = X_1 \cap X_2 \\ &Y_{12} = Y_1 \cap Y_2 \\ &\{P_l^{12}\} = \{R_l^{12}; T_l^{12}; F_l^{12}; I_l^{12}\} = \{(R_{lq}^{12}; T_{lq}^{12}; F_{lq}^{12}; I_{lq}^{12}) |\ q = 1,2,\ldots,r, l \in N;\ k \in N\} \\ &T_{lq}^{12} = \min\{T_{lq}^1; T_{lq}^2\}; F_{lq}^{12} = \max\{F_{lq}^1; F_{lq}^2\}; I_{lq}^{12} = \max\{I_{lq}^1; I_{lq}^2\} \end{aligned} \tag{25}$$

(c) Complement: $NRS_1^c = \{X_1^C; Y_1^C; \{D_i^{1^C}\} |\ i = 1,2,\ldots,n\}$; where

$$\begin{aligned} &X_1^C = X \backslash X_1, \\ &Y_1^C = Y \backslash Y_1, \\ &\{D_i^{1^C}\} = \{R_i^{1^C}; T_i^{1^C}; F_i^{1^C}; I_i^{1^C}\} = \{\left(R_{iq}^{1^C}; T_{iq}^{1^C}; F_{iq}^{1^C}; I_{iq}^{1^C}\right) |\ q = 1,2,\ldots,r;\ i = 1,2,\ldots,n\} \\ &T_{iq}^{1^C} = F_{iq}^1; F_{iq}^{1^C} = I_{iq}^1; I_{iq}^{1^C} = T_{iq}^1 \end{aligned} \tag{26}$$

These operations are used to define some new algebraic operations between NRSs such as the probabilistic sum (Definition 9), bold sum (Definition 10), bold intersection (Definition 11), bounded difference (Definition 12), symmetrical difference (Definition 13), convex linear sum (Definition 14) and the Cartesian product (Definition 15). The algebraic operations are bases for determining the similarity measures of NRS stated in Section 3.3.

Here we study some properties of these algebraic operations.

(a) Commutative:

$$\begin{aligned} &NRS_1 \cup NRS_2 = NRS_2 \cup NRS_1, \\ &NRS_1 \cap NRS_2 = NRS_2 \cap NRS_1. \end{aligned} \tag{27}$$

(b) Associative:

$$\begin{aligned} &(NRS_1 \cup NRS_2) \cup NRS_3 = NRS_1 \cup (NRS_2 \cup NRS_3), \\ &(NRS_1 \cap NRS_2) \cap NRS_3 = NRS_1 \cap (NRS_2 \cap NRS_3). \end{aligned} \tag{28}$$

(c) Distributive:

$$(NRS_1 \cup NRS_2) \cap NRS_3 = (NRS_1 \cap NRS_2) \cup (NRS_2 \cap NRS_3) \tag{29}$$

Proof. We first prove the commutative property in Eq. (27). Other properties can be proved analogously. We define

$$NRS_1 \cup NRS_2 = NRS_{12},$$

$NRS_{12} = \{X_{12}; Y_{12}; \{D_l^{12}\} | \ l = 1,2,...,k\}$,where

$X_{12} = X_1 \cup X_2$

$Y_{12} = Y_1 \cup Y_2$

$\{P_l^{12}\} = \{R_l^{12}; T_l^{12}; F_l^{12}; I_l^{12}\} = \{(R_{lq}^{12}; T_{lq}^{12}; F_{lq}^{12}; I_{lq}^{12}) | \ q = 1,2,...,r, l \in N; \ k \in N\}$

$T_{lq}^{12} = \max\{T_{lq}^1; T_{lq}^2\}; F_{lq}^{12} = \min\{F_{lq}^1; F_{lq}^2\}; I_{lq}^{12} = \min\{I_{lq}^1; I_{lq}^2\}.$

Similarly, we have

$NRS_2 \cup NRS_1 = NRS_{21}$,

$NRS_{21} = \{X_{21}; Y_{21}; \{D_l^{21}\} | \ l = 1,2,...,k\}$

$X_{21} = X_2 \cup X_1$

$Y_{21} = Y_2 \cup Y_1$

$\{P_l^{21}\} = \{R_l^{21}; T_l^{21}; F_l^{21}; I_l^{21}\} = \{(R_{lq}^{21}; T_{lq}^{21}; F_{lq}^{21}; I_{lq}^{21}) | \ q = 1,2,...,r; l = 1,2,...,k\}$

$T_{lq}^{21} = \max\{T_{lq}^2; T_{lq}^1\}; F_{lq}^{21} = \min\{F_{lq}^2; F_{lq}^1\}; I_{lq}^{21} = \min\{I_{lq}^2; I_{lq}^1\}.$

Thus,

$NRS_{12} = NRS_{21}$,

such that

$NRS_2 \cup NRS_1 = NRS_1 \cup NRS_2$

are the subsets of

$X = \{x_1; x_2; x_3\}; Y = \{y_1; y_2; y_3\}; X_1; X_2 \subset X; Y_1; Y_2 \subset Y.$

Definition 9. Let NRS_1 and NRS_2 be two neutrosophic recommender systems. The **probabilistic sum** of NRS_1 and NRS_2 denoted as $NRS_1 \hat{+} NRS_2$ is:

$$NRS_1 \hat{+} NRS_2 = \left\{X_{12}; Y_{12}; \{D_l^{12}\}\right\}, X_{12} = X_1 \cup X_2; Y_{12} = Y_1 \cup Y_2. \tag{30}$$

$$\{D_l^{12}\} = \{R_l^{12}; T_l^{12}; F_l^{12}; I_l^{12}\} = \{(R_{lq}^{12}; T_{lq}^{12}; F_{lq}^{12}; I_{lq}^{12}) | \ q = \overline{1; r}, l \in N; \ k \in N\} \tag{31}$$

$$\begin{aligned} T_{lq}^{12} &= T_{lq}^1(x) + T_{lq}^2(x) - T_{lq}^1(x).T_{lq}^2(x); \\ I_{lq}^{12} &= I_{lq}^1(x) + I_{lq}^2(x) - I_{lq}^1(x).I_{lq}^2(x); \\ F_{lq}^{12} &= F_{lq}^1(x) + F_{lq}^2(x) - F_{lq}^1(x).F_{lq}^2(x) \end{aligned} \tag{32}$$

where $T_{lq}^{12}; I_{lq}^{12}; F_{lq}^{12}$ are their truth membership functions, indeterminacy membership functions and falsity membership functions, respectively.

Definition 10. The **bold sum** of NRS_1 and NRS_2 is defined as following.

$$NRS_1 \oplus NRS_2 = \left\{X_{12}; Y_{12}; \{D_l^{12}\}\right\}, X_{12} = X_1 \cup X_2; Y_{12} = Y_1 \cup Y_2, \tag{33}$$

$$\{D_l^{12}\} = \{R_l^{12}; T_l^{12}; F_l^{12}; I_l^{12}\} = \{(R_{lq}^{12}; T_{lq}^{12}; F_{lq}^{12}; I_{lq}^{12}) | \ q = 1,2,...,r, l \in N; k \in N\}, \tag{34}$$

$$T_{lq}^{12}(x) = \min\{1; T_{lq}^1(x) + T_{lq}^2(x)\}; I_{lq}^{12}(x) = \min\{1; I_{lq}^1(x) + I_{lq}^2(x)\}; \ F_{lq}^{12}(x) = \min\{1; F_{lq}^1(x) + F_{lq}^2(x)\} \tag{35}$$

Definition 11. The **bold intersection** of NRS_1 and NRS_2 is:

$$NRS_1 \cap NRS_2 = \left\{X_{12}; Y_{12}; \{D_l^{12}\}\right\}, X_{12} = X_1 \cap X_2; Y_{12} = Y_1 \cap Y_2, \tag{36}$$

$$\{D_l^{12}\} = \{R_l^{12}; T_l^{12}; F_l^{12}; I_l^{12}\} = \{(R_{lq}^{12}; T_{lq}^{12}; F_{lq}^{12}; I_{lq}^{12}) | \ q = 1,2,...,r, l \in N; k \in N\}, \tag{37}$$

$$T_{lq}^{12}(x) = \max\{0; T_{lq}^1(x) + T_{lq}^2(x) - 1\}; I_{lq}^{12}(x) = \max\{0; I_{lq}^1(x) + I_{lq}^2(x) - 1\}; \ F_{lq}^{12}(x) = \max\{0; F_{lq}^1(x) + F_{lq}^2(x) - 1\} \tag{38}$$

Definition 12. The **bounded difference** of NRS_1 and NRS_2 is:

$$NRS_1 | - | NRS_2 = \left\{X_{12}; Y_{12}; \{D_l^{12}\}\right\}, X_{12} = X_1 \backslash X_2; Y_{12} = Y_1 \backslash Y_2 \tag{39}$$

$$\{D_l^{12}\} = \{R_l^{12}; T_l^{12}; F_l^{12}; I_l^{12}\} = \{(R_{lq}^{12}; T_{lq}^{12}; F_{lq}^{12}; I_{lq}^{12}) | \ q = 1,2,...,r, l \in N; k \in N\}, \tag{40}$$

$$T_{lq}^{12}(x) = \max\{0; T_{lq}^1(x) - T_{lq}^2(x)\}; I_{lq}^{12}(x) = \max\{0; I_{lq}^1(x) - I_{lq}^2(x)\}; \quad F_{lq}^{12}(x) = \max\{0; F_{lq}^1(x) - F_{lq}^2(x)\} \tag{41}$$

Definition 13. The **symmetrical difference** of NRS_1 and NRS_2 is:

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$$NRS_1 \nabla NRS_2 = \left\{X_{12}; Y_{12}; \{D_l^{12}\}\right\}, X_{12} = X_1 \cup X_2; Y_{12} = Y_1 \cup Y_2, \tag{42}$$

$$\{D_l^{12}\} = \{R_l^{12}; T_l^{12}; F_l^{12}; I_l^{12}\} = \{(R_{lq}^{12}; T_{lq}^{12}; F_{lq}^{12}; I_{lq}^{12}) | \ q = 1,2,\ldots,r, l \in N; k \in N\}, \tag{43}$$

$$T_{lq}^{12}(x) = |T_{lq}^1(x) - T_{lq}^2(x)|; I_{lq}^{12}(x) = |I_{lq}^1(x) - I_{lq}^2(x)|; \ F_{lq}^{12}(x) = |F_{lq}^1(x) - F_{lq}^2(x)| \tag{44}$$

Definition 14. The **convex linear sum** of min and max of NRS_1 and NRS_2 is:

$$NRS_1 ||_\lambda NRS_2 = \left\{X_{12}; Y_{12}; \{D_l^{12}\}\right\}, X_{12} = X_1 \cup X_2; Y_{12} = Y_1 \cup Y_2, \tag{45}$$

$$\{D_l^{12}\} = \{R_l^{12}; T_l^{12}; F_l^{12}; I_l^{12}\} = \{(R_{lq}^{12}; T_{lq}^{12}; F_{lq}^{12}; I_{lq}^{12}) | \ q = 1,2,\ldots,r, l \in N; k \in N\}, \tag{46}$$

$$\begin{aligned} T_{lq}^{12}(x) &= \lambda \min\{T_{lq}^1(x); T_{lq}^2(x)\} + (1-\lambda) max\{T_{lq}^1(x); T_{lq}^2(x)\}, \\ I_{lq}^{12}(x) &= \lambda \min\{I_{lq}^1(x), I_{lq}^2(x)\} + (1-\lambda) max\{I_{lq}^1(x); I_{lq}^2(x)\}, \qquad \lambda \in [0;1] \\ F_{lq}^{12}(x) &= \lambda \min\{F_{lq}^1(x), F_{lq}^2(x)\} + (1-\lambda) max\{F_{lq}^1(x); F_{lq}^2(x)\}, \end{aligned} \tag{47}$$

Definition 15. The **Cartesian product** of NRS_1 and NRS_2 is:

$$NRS_1 \times_1 NRS_2 = \left\{X_{12}; Y_{12}; \{D_l^{12}\}\right\}, X_{12} = X_1 \times X_2; Y_{12} = Y_1 \times Y_2, \tag{48}$$

$$D_l^{12} = \left\{\langle (x;y), T_{lq}^1(x) T_{lq}^2(y), F_{lq}^1(x).F_{lq}^2(x), I_{lq}^1(x).I_{lq}^2(x)\rangle | X_{12}; y \in Y_{12}\right\}, \tag{49}$$

$$\begin{aligned} NRS_1 \times_2 NRS_2 &= \left\{X_{12}; Y_{12}; \{D_l^{12}\}\right\}, X_{12} = X_1 \times X_2; Y_{12} = Y_1 \times Y_2, \\ D_l^{12} &= \left\{ \begin{array}{ll} (x;y), min\{T_{lq}^1(x), T_{lq}^2(y)\}, & \\ \langle min\{F_{lq}^1(x), F_{lq}^2(x)\}, & \rangle | x \in X_{12}; y \in Y_{12} \\ max\{I_{lq}^1(x), I_{lq}^2(x)\} & \end{array} \right\} \end{aligned}$$

Remark 2. a) By the same proof as that for Eqs. (27)–(29), all the operators satisfy the commutative and associative properties.

b) The meanings of the operations related to the proposed method are given as follows. The *probabilistic sum* operation in Definition 9 is the combination of addition, subtraction and multiplication between the two neutrosophic recommender systems. It can be seen as an extended form of ordinary addition operations. Since we are working with approximations, these extended operations are different types of approximations based on the classical set theoretic operations such as addition, multiplication, union, intersection, etc. Indeed, the probabilistic sum gives close results between two neutrosophic recommender systems. This is the reason for using these operations to develop similarity measures for the proposed method. The *bold sum* operation in Definition 10 is another type of extended operation based on the addition but in combination with the minimum operation. We also developed a similarity measure based on this operation. The *bold intersection* in Definition 11 is based on addition and subtraction with the maximum operation to approximate the truth, indeterminate and falsehood membership functions of the neutrosophic recommender system. The *bounded difference* operation in Definition 12 is the combination of subtraction and maximum operations which is used to develop a similarity measure. The *symmetrical difference* in Definition 13 is the combination of subtraction with the absolute operation to obtain positive values. The *convex linear sum* in Definition 14 is the operation of min, max, and addition with convex operations between two neutrosophic recommender systems. Lastly, the *Cartesian product* in Definition 15 is the usual Cartesian product defined for the neutrosophic recommender system.

3.3. Similarity measures of NRS based on the algebraic operations

In this section, we define the similarity measures based on the algebraic neutrosophic operations in Section 3.2.

Definition 16. Let $F(NRS)$ be a family of neutrosophic recommender systems. Then, the similarity measure based on the **union and intersection operations** of NRS_i and NRS_j denoted as $\$_{NRS_{ij}}$ is:

$$\$_{NRS_{ij}} = \bigcup_{i,j=1}^{n} \left\{\left(\cap\left(S_{X_{ij}}, S_{\Upsilon_{ij}}\right)\right) \cup \left(\cap\left(S_{\Upsilon_{ij}}, S_{D^{ij}}\right)\right)\right\}, \tag{51}$$

$$S_{X_{ij}} = \frac{1}{r}\sum_{i,j=1}^{n}\left[\frac{|T_{X_i}(x) - T_{X_j}(x)| \vee |I_{X_i}(x) - I_{X_j}(x)| \vee |F_{X_i}(x) - F_{X_j}(x)|}{2}\right], \tag{52}$$

$$S_{\Upsilon_{ij}} = \frac{1}{r}\sum_{i,j=1}^{n}\left[\frac{|T_{\Upsilon_i}(y) - T_{\Upsilon_j}(y)| \vee |I_{\Upsilon_i}(y) - I_{\Upsilon_j}(y)| \vee |F_{\Upsilon_i}(y) - F_{\Upsilon_j}(y)|}{2}\right], \tag{53}$$

$$S_{D^{ij}} = \frac{1}{r}\sum_{i,j=1}^{n}\left[\frac{|T_{D^i}(d) - T_{D^j}(d)| \vee |I_{D^i}(d) - I_{D^j}(d)| \vee |F_{D^i}(d) - F_{D^j}(d)|}{2}\right].$$

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Table 2
Similarity measures of patients, symptoms and diseases.

$S_{X_{ij}}$	$S_{\Upsilon_{ij}}$	$S_{D^{ij}}$
$S(Alex, Linda) = 0.4316,$	$S(4^\circ C, 15^\circ C) = 0.20833,$	$S(L_{Alex}, L_{Linda}) = 0.2666,$
$S(Alex, Bill) = 0.39833,$	$S(4^\circ C, 22^\circ C) = 0.11166,$	$S(L_{Alex}, L_{Bill}) = 0.15833,$
$S(Alex, John) = 0.29,$	$S(4^\circ C, 28^\circ C) = 0.2866,$	$S\left(L_{Alex}, L_{John}\right) = 0.28333,$
$S(Linda, Bill) = 0.15833$	$S(15^\circ C, 22^\circ C) = 0.2$	$S(L_{Linda}, L_{Bill}) = 0.31666,$
$S(Lind, John) = 0.30833$	$S(15^\circ C, 28^\circ C) = 0.23$	$S\left(L_{Linda}, L_{John}\right) = 0.25833,$
$S(Bill, John) = 0.2333$	$S(22^\circ C, 28^\circ C) = 0.23$	$S\left(L_{Bill}, L_{John}\right) = 0.25666,$

Table 3
Similarity measures of NRS_i and NRS_j based on the union and intersection (bold values imply the most analogous NRSs).

$\cup$	$\$_{NRS_{i1}}$	$\$_{NRS_{i2}}$	$\$_{NRS_{i3}}$	$\$_{NRS_{i4}}$	$\$_{NRS_{i5}}$	$\$_{NRS_{i6}}$
$\$_{NRS_{1j}}$	0.20833	0.11166	**0.2866**	0.2	0.23	0.23
$\$_{NRS_{2j}}$	0.11166	0.11166	**0.2866**	0.2	0.23	0.23
$\$_{NRS_{3j}}$	**0.2866**	**0.2866**	**0.2866**	**0.2866**	**0.2866**	**0.2866**
$\$_{NRS_{4j}}$	0.2	0.2	**0.2866**	0.2	0.23	0.23
$\$_{NRS_{5j}}$	0.23	0.23	**0.2866**	0.23	0.23	0.23
$\$_{NRS_{6j}}$	0.23	0.23	**0.2866**	0.23	0.23	0.23

Eq. (51) is the similarity measure of the neutrosophic recommender systems whereas $\bigcup$, $\bigcap$ are the union and intersection algebraic operations, respectively. Eqs. (52)-(54) are the similarity measures of features of the patients X_i, X_j, items or characteristics of the symptoms Υ_i, Υ_j and the diseases D^i, D^j respectively. The variable 'r' is the number of linguistic labels and $i, j \in \{1, 2, \cdots, n\}$.

Proposition 1. The similarity measure $\$_{NRS_{ij}}$ defined in Eq. (51) satisfies:

1. $0 \leq \$_{NRS_{ij}} \leq 1$;
2. $\$_{NRS_{ij}} = 0$ if and only if $i = j$;
3. $\$_{NRS_{ij}} = \$_{NRS_{ji}}$;
4. If NRS_k is another subset in $F(NRS)$ such that $NRS_i \leq NRS_j \leq NRS_k$, then $\$_{NRS_{ik}} \leq \$_{NRS_{ij}}$ and $\$_{NRS_{ik}} \leq \$_{NRS_{jk}}$ where $i, j, k = 1, 2, ..., n$.

Proof. This can be proved easily.

Example 2. Consider Table 1. The similarity measures of patients-$S_{X_{ij}}$, symptoms- $S_{\Upsilon_{ij}}$ and diseases- $S_{D^{ij}}$ are calculated in Table 2. Using Eq. (51), we compute the similarity matrix as in Table 3 where $\cup$ is the algebraic union operation, $\$_{NRS_{ij}}$ is the similarity measure of NRS_i and NRS_j where $i, j = 1, 2, 3, 4, 5, 6$. The main advantage of this similarity measure is that it provides an identical value among all the rows in Table 1 because of the algebraic union operation used in the similarity measure. However, we are unable to obtain largest distinct values of the similarity measure between two rows in Table 1 when predicting several diseases of a patient. This similarity measure may not give accurate results, as it lacks evidence to provide broad value. It can be used in the datasets having several patients with the same disease.

Definition 17. Let $\$_{NRS_{ij}}$ be a similarity measure of NRS_i and NRS_j in Eq. (51) which is based on the algebraic union and intersection operations. The **weighted similarity measures** can be defined as follows:

$$\$_{w(NRS_{ij})} = \bigcup_{i,j=1}^{n} \left\{ \left(w_1 \times \left(\cap \left(S_{X_{ij}}, S_{\Upsilon_{ij}} \right) \right) \right) \cup \left(w_2 \times \left(\cap \left(S_{\Upsilon_{ij}}, S_{D^{ij}} \right) \right) \right) \right\}, \tag{54}$$

$$w_1 + w_2 = 1; i, j = 1, 2, \ldots, n.$$

Definition 18. We define the following additional similarity measures based on algebraic operations.

1. The similarity measure based on the **union, intersection and probabilistic sum** is defined as:

$$\$_{NRS_{ij}} = \sum_{i,j=1}^{n} \left\{ \left(\left(S_{X_{ij}} + S_{\Upsilon_{ij}} - S_{X_{ij}}.S_{\Upsilon_{ij}} \right) \right) \cap \left(\left(S_{\Upsilon_{ij}} + S_{D^{ij}} - S_{\Upsilon_{ij}}.S_{D^{ij}} \right) \right) \right\}. \tag{55}$$

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Table 4
Similarity measures of NRS_i and NRS_j based on the intersection and probabilistic sum (bold values imply the most analogous NRSs).

$\sum$	$\$_{NRS_{i1}}$	$\$_{NRS_{i2}}$	$\$_{NRS_{i3}}$	$\$_{NRS_{i4}}$	$\$_{NRS_{i5}}$	$\$_{NRS_{i6}}$
$\$_{NRS_{1j}}$	0.83878	0.67171	**0.90812**	0.74606	0.84832	0.82904
$\$_{NRS_{2j}}$	0.67171	0.50464	**0.74105**	0.57899	0.68124	0.66197
$\$_{NRS_{3j}}$	0.90812	0.74105	**0.97746**	0.8154	0.91765	0.89838
$\$_{NRS_{4j}}$	0.74606	0.57899	**0.8154**	0.65334	0.75559	0.73632
$\$_{NRS_{5j}}$	0.84832	0.68124	**0.91765**	0.75559	0.85784	0.83857
$\$_{NRS_{6j}}$	0.82904	0.66197	**0.89838**	0.73632	0.83857	0.8193

2. The weighted similarity measure of Eq. (55) is defined below:

$$\$_{w(NRS_{ij})} = \sum_{i,j=1}^{n} \left\{ \left(w_1 \times \left(S_{X_{ij}} + S_{\Upsilon_{ij}} - S_{X_{ij}}.S_{\Upsilon_{ij}} \right) \right) \cap \left(w_2 \times \left(S_{\Upsilon_{ij}} + S_{D^{ij}} - S_{\Upsilon_{ij}}.S_{D^{ij}} \right) \right) \right\}. \tag{56}$$

3. The similarity measure based on the **intersection and bold sum** of NRS_i and NRS_j is:

$$\$_{NRS_{ij}} = \prod_{i,j=1}^{n} \left\{ \left(\min\left(1, S_{X_{ij}} + S_{\Upsilon_{ij}}\right) \right) \cap \left(\min\left(1, S_{\Upsilon_{ij}} + S_{D^{ij}}\right) \right) \right\}. \tag{57}$$

4. The weighted similarity measure of Eq. (57) is as following:

$$\$_{w(NRS_{ij})} = \prod_{i,j=1}^{n} \left\{ \left(w_1 \times \left(\min\left(1, S_{X_{ij}} + S_{\Upsilon_{ij}}\right) \right) \right) \cap \left(w_2 \times \left(\min\left(1, S_{\Upsilon_{ij}} + S_{D^{ij}}\right) \right) \right) \right\}. \tag{58}$$

5. The similarity measure based on the **union and bounded difference** of NRS_i and NRS_j is:

$$\$_{NRS_{ij}} = \sum_{i,j=1}^{n} \left\{ \left(\max\left(0, S_{X_{ij}} - S_{\Upsilon_{ij}}\right) \right) \cup \left(\max\left(0, S_{\Upsilon_{ij}} - S_{D^{ij}}\right) \right) \right\}. \tag{59}$$

6. The weighted similarity measure of Eq. (59) can be defined as following:

$$\$_{w(NRS_{ij})} = \sum_{i,j=1}^{n} \left\{ \left(w_1 \times \left(\max\left(0, S_{X_{ij}} - S_{\Upsilon_{ij}}\right) \right) \right) \cup \left(w_2 \times \left(\max\left(0, S_{\Upsilon_{ij}} - S_{D^{ij}}\right) \right) \right) \right\}. \tag{60}$$

7. The similarity measure based on the symmetrical difference of NRS_i and NRS_j is:

$$\$_{NRS_{ij}} = \sum_{i,j=1}^{n} \left\{ \left(S_{X_{ij}} - S_{\Upsilon_{ij}} \right) + \left(S_{\Upsilon_{ij}} - S_{D^{ij}} \right) \right\}. \tag{61}$$

8. The weighted similarity measure of Eq. (61) can be defined as following:

$$\$_{w(NRS_{ij})} = \sum_{i,j=1}^{n} \left\{ w_1 \times \left(S_{X_{ij}} - S_{\Upsilon_{ij}} \right) + w_2 \times \left(S_{\Upsilon_{ij}} - S_{D^{ij}} \right) \right\}. \tag{62}$$

$\$_{NRS_{ij}}$ denotes the similarity measure between NRS_i, NRS_j and $S_{X_{ij}}$, $S_{\Upsilon_{ij}}$, $S_{D^{ij}}$ are calculated from Eqs. (52)-(54), respectively.

Proposition 2. The similarity measure $\$_{NRS_{ij}}$ defined in Eqs. (55), (57), (59), (61) satisfies the following conditions.

1. $0 \leq \$_{NRS_{ij}} \leq 1$;
2. $\$_{NRS_{ij}} = 0$ if and only if $i = j$;
3. $\$_{NRS_{ij}} = \$_{NRS_{ji}}$;
4. If NRS_k is another subset of $F(NRS)$ such that $NRS_i \leq NRS_j \leq NRS_k$, then $\$_{NRS_{ik}} \leq \$_{NRS_{ij}}$ and $\$_{NRS_{ik}} \leq \$_{NRS_{jk}}$ where $i, j, k = 1, 2, ..., n$.

Example 3. Consider $S_{X_{ij}}$, $S_{\Upsilon_{ij}}$ and $S_{D^{ij}}$ calculated in Table 2. From Eqs. (55), (57), (59), (61) we calculate the following similarity matrix in Tables 4–7, respectively. The symbol $\sum$ refers to the aggregation operator in Tables 4,6,7 while $\prod$ refers to the geometric operator in Table 5. The bold values indicate the largest similarity measures in these tables. The similarity measure in Table 4 provides the largest distinct values compared to all other similarity measures in Tables 5–7. Furthermore, this similarity measure in Eq. (55) provides us an accurate result and will be used in the prediction formula for calculating the levels of diseases of the patients in the subsequent sections.

3.4. A new non-linear prediction model

In this section, we will present a non-linear prediction model that utilizes the similarity measure in Eq. (55) for the medical diagnosis problem.

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Table 5
Similarity measures of NRS_i and NRS_j based on the intersection and bold sum (bold values imply the most analogous NRSs).

$\prod$	$\$_{NRS_{i1}}$	$\$_{NRS_{i2}}$	$\$_{NRS_{i3}}$	$\$_{NRS_{i4}}$	$\$_{NRS_{i5}}$	$\$_{NRS_{i6}}$
$\$_{NRS_{1j}}$	0.22555	0.12822	**0.27067**	0.17018	0.23192	0.22003
$\$_{NRS_{2j}}$	0.12822	0.07289	**0.15387**	0.09674	0.13184	0.12508
$\$_{NRS_{3j}}$	0.27067	0.15387	**0.32482**	0.20422	0.27831	0.26404
$\$_{NRS_{4j}}$	0.17018	0.09674	**0.20422**	0.12840	0.17498	0.16601
$\$_{NRS_{5j}}$	0.23192	0.13184	**0.27831**	0.17498	0.23846	0.22624
$\$_{NRS_{6j}}$	0.22003	0.12508	**0.26404**	0.16601	0.22624	0.21464

Table 6
Similarity measures of NRS_i and NRS_j based on the union and bounded difference (bold values imply the most analogous NRSs).

$\sum$	$\$_{NRS_{i1}}$	$\$_{NRS_{i2}}$	$\$_{NRS_{i3}}$	$\$_{NRS_{i4}}$	$\$_{NRS_{i5}}$	$\$_{NRS_{i6}}$
$\$_{NRS_{1j}}$	0.44654	**0.50994**	0.22667	0.2237	0.3016	0.22657
$\$_{NRS_{2j}}$	0.50994	**0.57334**	0.29007	0.28667	0.365	0.28997
$\$_{NRS_{3j}}$	0.22667	**0.29007**	0.0068	0.0034	0.08173	0.0067
$\$_{NRS_{4j}}$	0.2237	**0.28667**	0.0034	0	0.07833	0.0033
$\$_{NRS_{5j}}$	0.3016	**0.365**	0.08173	0.07833	0.15666	0.08163
$\$_{NRS_{6j}}$	0.22657	**0.28997**	0.0067	0.0033	0.08163	0.006

Table 7
Similarity measures of NRS_i and NRS_j based on the symmetrical difference (bold values imply the most analogous NRSs).

$\sum$	$\$_{NRS_{i1}}$	$\$_{NRS_{i2}}$	$\$_{NRS_{i3}}$	$\$_{NRS_{i4}}$	$\$_{NRS_{i5}}$	$\$_{NRS_{i6}}$
$\$_{NRS_{1j}}$	0.33	**0.405**	0.17167	0.00667	0.215	0.14164
$\$_{NRS_{2j}}$	0.405	**0.48**	0.24667	0.08167	0.29	0.21664
$\$_{NRS_{3j}}$	0.17167	**0.24667**	0.01334	−0.15166	0.05667	−0.01669
$\$_{NRS_{4j}}$	0.00667	**0.08167**	−0.15166	−0.31666	−0.10833	−0.18169
$\$_{NRS_{5j}}$	0.215	**0.29**	0.05667	−0.10833	0.1	0.02664
$\$_{NRS_{6j}}$	0.14164	**0.21664**	−0.01669	−0.18169	0.02664	−0.04672

Definition 19. Let S_h be the symptoms of the patient p_i whose diseases are $(d_1, d_2, \ldots., d_k)$ in a multi-criteria neutrosophic recommender system (MC-NRS) where $i = 1, 2, 3, ..., n$ and $h = 1, 2, 3, ..., m$. The linguistic labels of the patient p_i can be predicted by the following formulae:

$$T_{D_l}{}^{p_i}(d_h) = \frac{\sum_{j=1}^{n} \$_{NRS_{ij}} \times T_{D_l}{}^{p_j}(d_h)}{\sum_{j=1}^{n} \$_{NRS_{ij}}}, I_{D_l}{}^{p_i}(d_h) = T_{D_l}{}^{p_i}(d_h) + \frac{\sum_{j=1}^{n} \$_{NRS_{ij}} \times I_{D_l}{}^{p_j}(d_h)}{\sum_{j=1}^{n} \$_{NRS_{ij}}}, F_{D_l}{}^{p_i}(d_h) = I_{D_l}{}^{p_i}(d_h) + \frac{\sum_{j=1}^{n} \$_{NRS_{ij}} \times F_{D_l}{}^{p_j}(d_h)}{\sum_{j=1}^{n} \$_{NRS_{ij}}} \quad (63)$$

where $\$_{NRS_{ij}}$ is the similarity measure in Eq. (55) and for $h = 1, 2, 3, ..., m$, $i = 1, 2, 3, ..., n$ and $l = 1, 2, 3, ..., s$. The components $T_{D_l}{}^{p_i}(d_h)$, $I_{D_l}{}^{p_i}(d_h)$ and $F_{D_l}{}^{p_i}(d_h)$ refer to the predictive truth membership, predictive indeterminate membership, and predictive false membership function of the linguistic labels of the patientp_i, respectively.

Theorem 1. The predictive values in Eq. (63) are neutrosophic values.

Theorem 2. The maximum value is the best optimum of the proposed method in the (n − 1) iterations.

We illustrate the non-linear prediction model for the prediction task in Fig. 1. Moreover, we use the neutrosophication and deneutrosophication to convert crisp data to neutrosophic sets and again from neutrosophic sets to crisp inputs, respectively.

4. Results and discussions

4.1. Experimental environments

- *Experimental tools*: The proposed algorithm has been implemented in addition to the methods of CARE [9], CFMD [17], ICSM [51] and DSM [54]. We run the algorithms in the Matlab 2015a programming language and execute them on a PC Intel(R) Core (TM) 2 Dual CPU T6400@2.00 GHz (2CPUs), 2048 MB RAM and the operating system is windows7 Professional 32 bits.
- *Datasets:* The benchmark dataset HEART has been taken from the UCI Machine Learning Repository [41] while the remaining 4 benchmark datasets (RHC, Diabetes, Breast Cancer, DMD) have been taken from [10]. Table 8 provides a description of the experimental medical datasets.
- *Experimental objectives:* (a) Compare the performance of algorithms through MSE values and computational time; (b) Validate the stability of algorithms for various sets of parameters.

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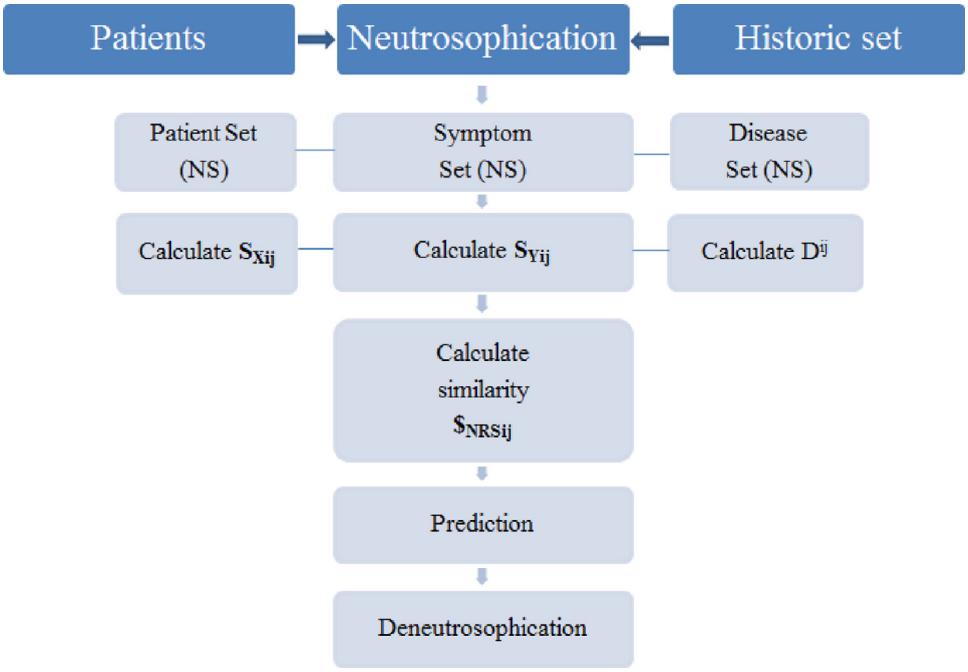

Fig. 1. The non-linear regression model.

Table 8
The descriptions of experimental datasets.

Dataset	No. elements	No. attributes	No. classes
RHC	5736	5	3
Diabetes	404	4	2
Breast	3304	5	3
DMD	201	3	1
Heart	271	4	2

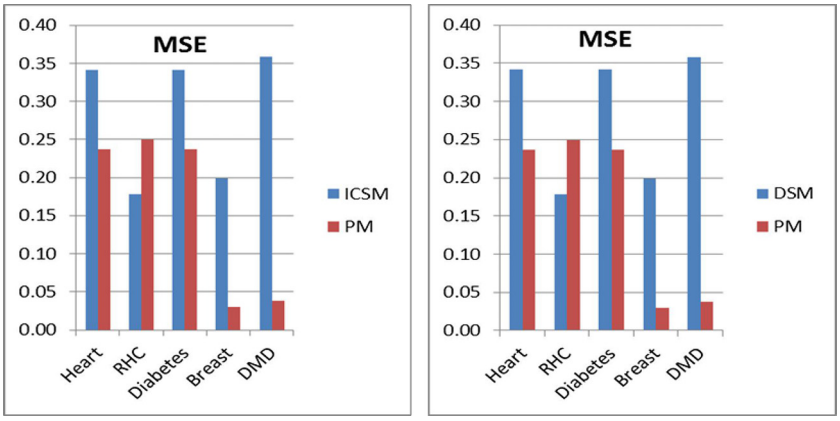

Fig. 2. MSE values of the proposed method (PM) and (a) ICSM; (b) DSM.

4.2. The comparison of performance

Figs. 2 and 3 present a comparison of MSE values for the proposed method and the relevant algorithms (ICSM, DSM, CARE and CFMD) on the medical datasets of Heart, RHC, Diabetes, Breast and DMD. It is clearly seen that MSE of the proposed method is better than ICSM, DSM, CARE and CFMD on the Heart dataset. The MSE of the proposed algorithm (0.25) is clearly better than CARE (0.366) on RHC but it does not provide a significant improvement when compared to ICSM (0.178), DSM (0.178) and CFMD (0.189) due to the natural complexity of the data. Analogously, the proposed method has better MSE values for Diabetes than ICSM, DSM and CARE with the MSE values being 0.086, 0.108, 0.108 and 0.125, respectively. Similarly, the proposed algorithm is advantageous for the remaining two datasets (Breast and DMD). The MSE values of the proposed algorithm, ICSM, DSM, CARE and CFMD calculated for Breast dataset are 0.03, 0.198, 0.198, 0.149 and 0.191, respectively. These numbers in cases of DMD are 0.039, 0.359, 0.359, 0.244 and 0.047, respectively. Overall, the average MSE values output by the proposed algorithm are better than those of the other algorithms.

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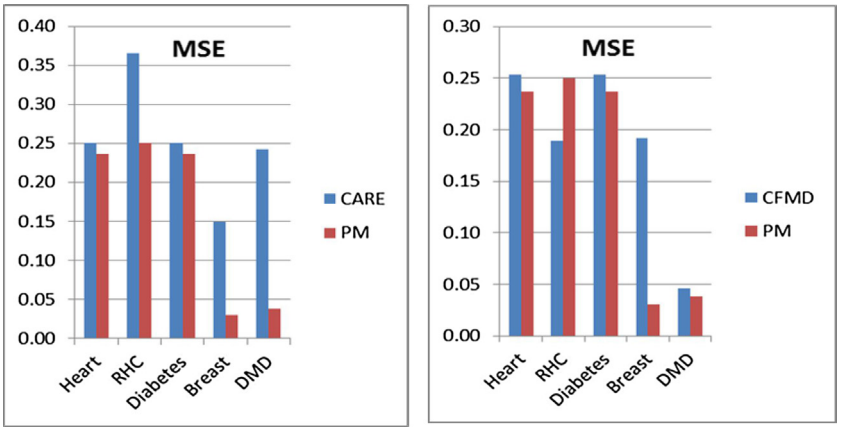

Fig. 3. MSE values of the proposed method (PM) and (a) CARE; (b) CFMD.

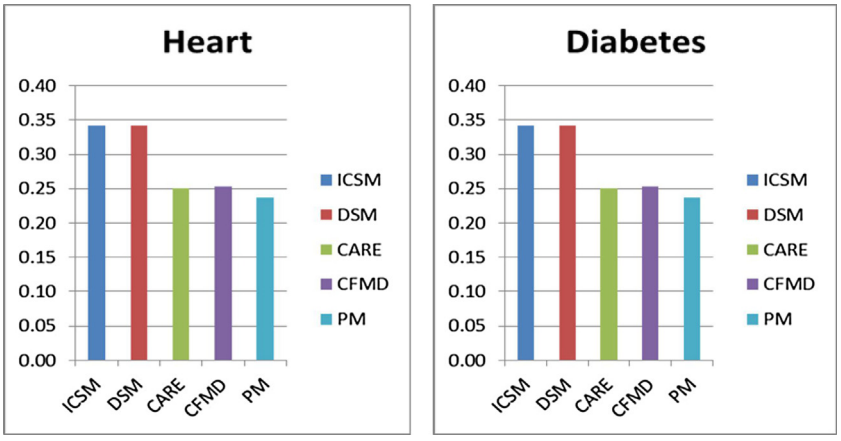

Fig. 4. MSE of all algorithms on (a) Heart and (b) Diabetes datasets.

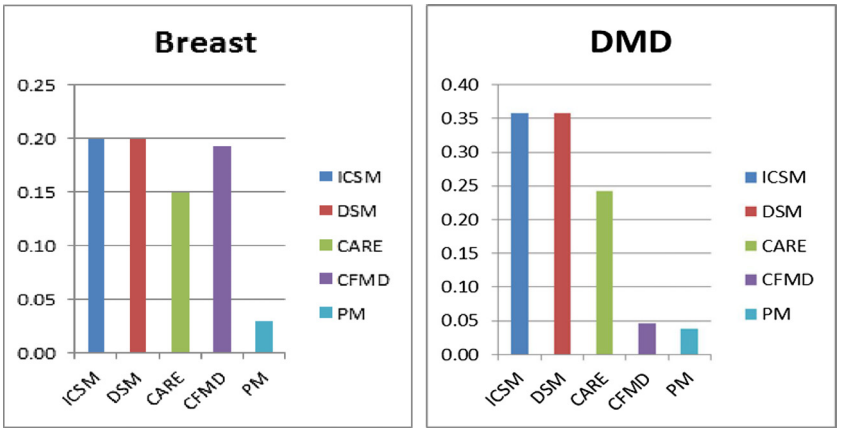

Fig. 5. MSE of all algorithms on (a) Breast and (b) DMD datasets.

In Fig. 2, we see the MSE values of ICSM, DSM and the proposed method (PM) on the datasets of Heart, RHC, Diabetes, Breast and DMD. The MSE values of the proposed algorithm on each dataset in the case of DSM is better (smaller) while there is some variation in the values of MSE of DSM and proposed method on the datasets of RHC and Diabetes. However, overall, out of 5 data sets, the MSE of our proposed algorithm is better in 3 data sets than DSM. Again it is clear that the MSE of the proposed algorithm on each dataset is better (smaller) than the MSE of CARE and CFMD in Fig. 3. Similar results for CFMD are drawn on to clearly demonstrate this fact.

Figs. 4–6 present the results on each dataset; herein we observe the MSE values of all the algorithms to allow interpretation of the results in a more detailed and comprehensive way. Figs. 4 and 5 show that the proposed method is better than others on the datasets of Heart, Diabetes, Breast and DMD while on the RHC dataset the proposed algorithm is not as effective compared to ICSM, DSM and CFMD due to the natural complexity of the data.

Table 9 compares the computational time of the algorithms in seconds (sec). It is obvious that there is no large increase in computational time taken by the proposed method and other algorithms. The computational time of ICSM, DSM, CARE, CFMD and the proposed method

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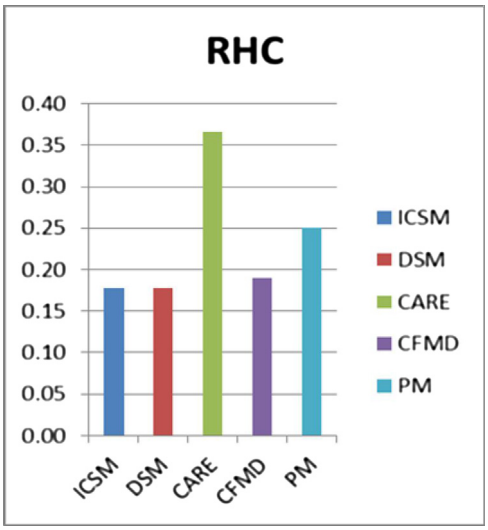

Fig. 6. MSE of all algorithms on RHC dataset.

Table 9
The computational time of algorithms (sec).

	ICSM	DSM	CARE	CFMD	Proposed method
Heart	0.152517	0.076999	0.139614	204	0.192975
RHC	0.325134	0.222736	56	3064	420
Diabetes	0.189302	0.093844	0.302440	334	1.4231
Breast	0.468686	0.155074	19	1004	71
DMD	0.113384	0.021726	0.078052	565	1.17265

on the Heart dataset are 0.152517, 0.076999, 0.139614, 204.127803 and 0.192975sec, respectively. This scenario can also be seen in the datasets of Diabetes and DMD. This shows the effectiveness of the proposed method when dealing with the small and medium datasets since a small number of parameters in neutrosophication and deneutrosophication have to be invoked. On the other hand, on a large and complex dataset such as RHC, the time taken by the proposed method is quite large (420.05 s) compared to ICSM (0.325134), DSM (0.222736) and CARE (56.976828). An analogous situation appeared with the Breast dataset. Nonetheless, the computational time of the proposed method is acceptable in most of the cases.

4.3. The experiments by various cases of parameters

Table 10 shows the MSE values and the computational time of the proposed method for various cases of parameters of the deneutrosophication process (Section 2.3, Eq. (4)). It is clear that the MSE values remain almost the same for each dataset when randomly changing the values of parameters (α, β and γ) in all the medical datasets. For example, the MSE values are approximately the same (0.236009, 0.235996, 0.030184, 0.236010, 0.236043, 0.236036), respectively in the Heart dataset by taking the values of $\alpha = 0.2, 0.3, 0.5, 0.5, 0.3, 0.2$, $\beta = 0.3, 0.2, 0.3, 0.2, 0.5, 0.5$ and $\gamma = 0.5, 0.5, 0.2, 0.3, 0.2, 0.3$. However, in the computational time (sec.), some noticeable changes can be seen (0.331406, 0.231169, 0.206800, 0.212506, 74.391425, 0.196846). The analogous scenario can be seen on the other 4 datasets of RHC, Diabetes, Breast and DMD where the values of MSE remains the same in each datasets while the computational time (sec.) varies by changing the values of parameters which can be checked in the above. This shows the stability of the proposed method in comparison to the results in Section 4.2.

4.4. Analyzing the strength of algorithms by ANOVA test

Next, we have tested all algorithms using one-way ANOVA and the Kruskal-Wallis test of variance by considering the MSE values among all algorithms on the same dataset. This scenario can be seen in Fig. 7 and Tables 11 and 12, respectively. With regards to the ANOVA one-way test, in Fig. 7, the blue bar represents the comparison interval for mean strength for our proposed algorithm while the red bar represents the comparison interval for mean strength for the rest of all the algorithms. There is no overlap between the blue bar and red bar which indicates that the mean strength for the proposed algorithm is significantly different from the rest of the algorithms.

The ANOVA Table 11 shows the between-group variation (column) and within-groups variation (error). Here *df* denotes the total degrees of freedom which means the total number of observations minus 1. In this case we have $df = 5-1 = 4$. *SS* is the sum of squares due to each source which is 0.05711 whereas, *MS* represents the mean squared error which is equal to $MS = SS/df = 0.01428$. $F = F$-statistic which is the ratio of mean square and we have 1.35. Finally Prob > F means the probability that the *F*-statistic can take a value greater than the computed test-statistic value. In this case, we have the probability of 0.2857. Table 11 summarizes all the results of the ANOVA tests.

In the Kruskal-Wallis test, the *F*-statistic value in the one-way ANOVA test is replaced by the Chi-square statistic. The results of the Kruskal-Wallis test can be seen in Table 12 below for the analysis of all the algorithms.

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Table 10
The results of the proposed method by parameters of deneutrosophication.

A. Heart				
α	β	γ	**MSE**	**Time (sec)**
0.2	0.3	0.5	**0.236009**	**0.331406**
0.3	0.2	0.5	**0.235996**	**0.231169**
0.5	0.3	0.2	**0.236031**	**0.206800**
0.5	0.2	0.3	**0.236010**	**0.212506**
0.3	0.5	0.2	**0.236043**	**0.184897**
0.2	0.5	0.3	**0.236036**	**0.196846**
B.RHC				
0.2	0.3	0.5	**0.250000**	**71.887356**
0.3	0.2	0.5	**0.250000**	**72.612241**
0.5	0.3	0.2	**0.250000**	**73.629676**
0.5	0.2	0.3	**0.250000**	**77.334187**
0.3	0.5	0.2	**0.250000**	**74.391425**
0.2	0.5	0.3	**0.250000**	**73.131208**
C.Diabetes				
0.2	0.3	0.5	**0.055733**	**0.409223**
0.3	0.2	0.5	**0.038069**	**0.402370**
0.5	0.3	0.2	**0.030184**	**0.414937**
0.5	0.2	0.3	**0.042295**	**0.421679**
0.3	0.5	0.2	**0.042529**	**0.399683**
0.2	0.5	0.3	**0.034698**	**0.391552**
D.Breast				
0.2	0.3	0.5	**0.033555**	**35.283942**
0.3	0.2	0.5	**0.033579**	**36.248034**
0.5	0.3	0.2	**0.033472**	**36.425809**
0.5	0.2	0.3	**0.033522**	**35.224594**
0.3	0.5	0.2	**0.033464**	**35.228633**
0.2	0.5	0.3	**0.033488**	**36.703062**
E.DMD				
0.2	0.3	0.5	**0.250000**	**0.136135**
0.3	0.2	0.5	**0.250000**	**0.126467**
0.5	0.3	0.2	**0.250000**	**0.117475**
0.5	0.2	0.3	**0.250000**	**0.132521**
0.3	0.5	0.2	**0.250000**	**0.111520**
0.2	0.5	0.3	**0.25000**	**0.127623**

Table 11
Result of analyze one-way variance for all algorithms by ANOVA test.

Source	SS	df	MS	F	Prob > F
Columns	0.05711	4	0.01428	1.35	0.2857
Error	0.21121	20	0.01056		
Total	0.26832	24			

Table 12
Result of analyze Kruskal-Wallis test.

Source	SS	df	MS	Chi-sq	Prob > Chi-sq
Columns	226.3	4	56.575	4.19	0.3812
Error	1070.7	20	53.535		
Total	1297	24			

5. Conclusions

This paper focused on the development of a novel neutrosophic recommender system (NRS) based on the hybridization of neutrosophic set and recommender system for medical diagnosis to guarantee the ability to predict more accurately during the diagnosis process. The contribution of this paper included two variants of NRS namely the single-criterion neutrosophic recommender system (SC-NRS) and the multi-criteria neutrosophic recommender system (MC-NRS). Then, we presented some new algebraic operations of NRS for the first time such as the union, complement and intersection. We showed that these algebraic operations satisfy the commutative, associative and distributive properties. In addition, we proposed several types of algebraic similarity measures which are based on these algebraic operations. A non-linear prediction model using those similarity measures was developed. We finally designed a new algorithm for medical diagnosis based on the neutrosophic recommender system. The experiments on the benchmark medical datasets demonstrated that the proposed method has better accuracy than the other algorithms. The proposed algorithm can be effectively used for personal healthcare systems in medicine.

However, the proposed method requires large computation times to perform the calculations. This is due to the representation of information in the three dimensions of the neutrosophic model. A distributed/parallel computational paradigm is hence required in this case to accelerate the computation speed of the algorithm. Another limitation of the proposed method relates to the number of parameters used in the neutrosophication and deneutrosophication processes. As shown in the experiments, a vast number of parameters are used in the construction of the model. We are planning to develop a parameter estimation method for the neutrosophic recommender system using

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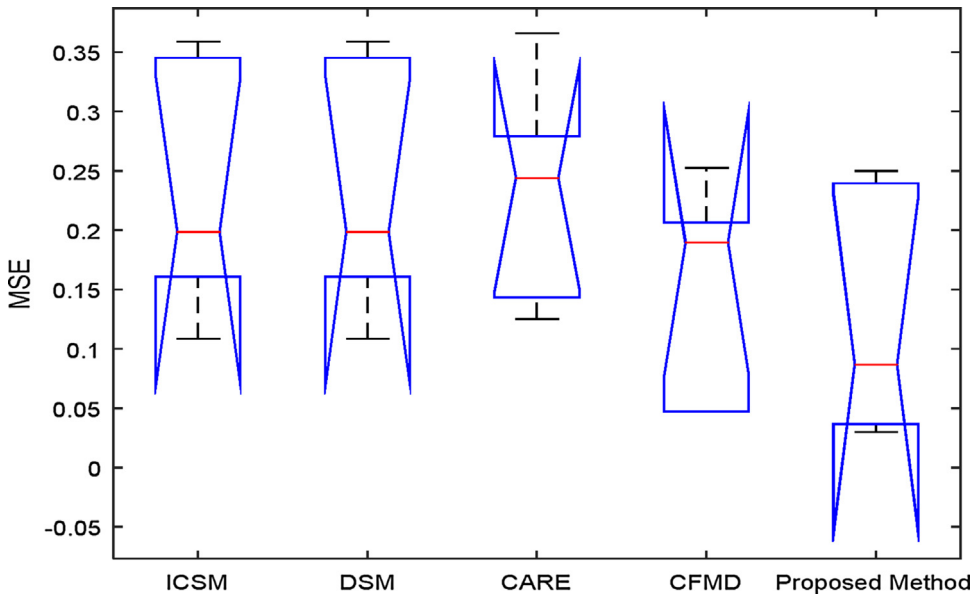

Fig. 7. Analysis of one-way ANOVA for all algorithms.

the Bayesian approach. The third limitation of the NRS system is that it does not utilize multiple sets of data for patients and symptoms in the entire computation process. For example, a patient can have various personal data such as age, income, location and province, etc. Analogously, there can be many patients' symptoms such as vomiting, illness, etc. Those additional data should be treated concurrently in the computing process. This leads to the design of a new multi-characteristic neutrosophic recommender system for medical diagnosis. Lastly, a hybrid algorithm between the proposed algorithm and neutrosophic clustering methods should be proposed to investigate the structure of the NRS system and enhance the similarity level through patient data.

Acknowledgement

This research is funded by Vietnam National Foundation for Science and Technology Development (NAFOSTED) under grant number 102.01-2017.02.

Appendix A.

The source codes and the experimental datasets can be retrieved at this link: http://se.mathworks.com/matlabcentral/fileexchange/55239-a-neutrosophic-recommender-system-for-medical-diagnosis-based-on-algebraic-neutrosophic-measures.

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