



Supporting Medical Diagnostic Reasoning via a Dissimilarity Measure for Single-Valued Neutrosophic Sets

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ABSTRACT

Medical diagnosis is often carried out under incomplete, imprecise, or even conflicting clinical information. Single-valued neutrosophic sets are useful for describing this type of uncertainty, but the final diagnostic result can still depend strongly on how patient profiles are compared with disease patterns. Some available measures do not provide sufficient discrimination when the underlying component variations are different. To address this issue, this study develops a bounded dissimilarity measure for single-valued neutrosophic sets and examines its application to medical diagnosis. For each criterion, the measure first takes the minimum absolute difference among the truth, indeterminacy, and falsity components. A bounded nonlinear function is then applied, and the resulting values are aggregated across all criteria. The main properties of the measure are established theoretically, while its ability to distinguish different profiles is further examined through numerical examples and comparisons with eight existing measures. The numerical results show that the proposed measure can distinguish several cases that receive identical values under some existing approaches. Two medical examples are also considered. The minimum-dissimilarity rule identifies malaria in one case and bacterial pneumonia in the respiratory case. For the latter, the resulting ranking is consistent with those obtained using the comparison measures, while the proposed measure provides greater separation between the most plausible disease and the other candidates. Overall, the measure appears suitable for ranking uncertain medical profiles, although further testing with larger clinical datasets is needed.

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1. Introduction

Medical diagnosis often relies on observations that are incomplete, imprecise, or partly contradictory. A symptom may receive strong support from one examination but remain weakly documented by another, so forcing all available evidence into a binary judgment can conceal clinically relevant uncertainty. Zadeh [1] established the mathematical foundation for graded membership through fuzzy sets (FSs). Atanassov [2] subsequently proposed intuitionistic fuzzy sets (IFSs), which extend FSs by incorporating an explicit non-membership degree together with a derived hesitation degree, a feature that remains useful in recent expert-based decision models. Smarandache [3] later developed neutrosophic theory to accommodate indeterminate and potentially inconsistent information. To support practical computation, Wang et al. [4] formulated single-valued neutrosophic sets (SVNSs) by restricting their evaluations to the unit interval. This progression provides a flexible basis for constructing patient and disease profiles without reducing every clinical observation to simple presence or absence.

Distance measures have been studied for various fuzzy information structures [5, 6]. For intuitionistic fuzzy sets, Kumar and Kumar [7] constructed a new distance measure and applied it to a decision-making problem. Garg et al. [8] considered a symmetric distance measure and examined its use in pattern recognition, clustering, and medical diagnosis. More recently, Abraham et al. [9] developed a three-dimensional distance metric for Pythagorean fuzzy information, in which the membership, non-membership, and hesitation components are considered simultaneously. These studies indicate that the design of suitable distance measures remains important when uncertain information needs to be compared or distinguished. Representing uncertain information, however, is only the first stage of the analysis. The next task is to distinguish an unknown object from a collection of reference patterns. In an SVNS-based pattern recognition problem, the unknown object and each reference pattern are described over the same attributes, and a dissimilarity measure quantifies the separation between their profiles. A smaller value indicates a closer correspondence under the adopted comparison rule, whereas a larger value indicates greater separation. Medical diagnosis follows the same general structure: the patient constitutes the unknown pattern, the candidate diseases provide the reference patterns, and the disease with the minimum dissimilarity is regarded as the most plausible match. The construction of a suitable dissimilarity measure is therefore important not only for numerical comparison but also for the reliability of the resulting recognition or diagnostic ranking.

Pattern recognition has consequently become an important testing ground for SVNS comparison methods. Garg and Nancy [10] developed biparametric distances for both pattern recognition and medical diagnosis. Chai et al. [11] examined recognition examples when evaluating new SVNS information measures, while Zeng et al. [12] incorporated a modified Manhattan construction into recognition, decision-making, and clustering procedures. Singh and Sharma [13] applied aggregation-based divergence measures to pattern discrimination, and Bisht and Pal [14] recently used an inner-product construction in recognition and diagnostic problems. Within the medical branch of this research, Ye [15] constructed an early diagnostic comparison scheme for simplified neutrosophic information, and Shahzadi et al. [16] used SVNS evaluations to identify diseases from uncertain symptom records. Ye and Fu [17] incorporated observations collected over multiple periods, whereas Zhang et al. [18] combined SVNSs with probabilistic rough multisets over two universes to model more complex diagnostic relations. Xiao and Ding [19] further illustrated the role of divergence-based classification in a neighboring fuzzy environment. Despite their different formulations, these studies follow the same fundamental principle: classification depends on the numerical separation between an unknown profile and the available reference profiles.

Researchers have constructed SVNS dissimilarity or distance information in several ways. Broumi and Smarandache [20] used maximum component deviations in an early neutrosophic comparison

formula. Majumdar and Samanta [21] investigated Hamming- and Euclidean-type expressions and connected set comparison with entropy. Huang [22] proposed a distance designed to retain more information about the direction and distribution of SVN differences. Liu and Luo [23] introduced a weighted distance procedure for multi-attribute group decision making, thereby allowing criteria to contribute unequally. Garg and Nancy [10] added adjustable parameters to the distance construction, and Ren et al. [24] drew on chi-square normalization to rescale component deviations. These approaches show that dissimilarity is not determined merely by calculating absolute differences; it also depends on how the local differences are selected, transformed, weighted, and aggregated.

Other authors have obtained bounded comparison values through nonlinear transformations of local or aggregated deviations. Ye [25] employed a cotangent transformation in a fault-diagnosis model, whereas Mondal et al. [26] adopted a hybrid binary logarithm formulation for group decision making. Zhang et al. [27] combined ordered and average weighting for single-valued neutrosophic linguistic assessments. Garg and Nancy [28] incorporated a new distance into TOPSIS and clustering algorithms, demonstrating that the choice of dissimilarity structure can affect the subsequent decision procedure. Chai et al. [11] examined axiomatic requirements and counter-intuitive cases in SVN comparison, and Zeng et al. [12] developed a modified Manhattan construction to improve discrimination for selected data arrangements. Ali et al. [29] later extended Hausdorff distance to SVN, offering a set-level account of separation. Collectively, these studies reveal no single compulsory aggregation rule for all neutrosophic problems.

Recent research has continued to broaden both the mathematical forms and application domains of neutrosophic distance and dissimilarity. Mustapha et al. [30] used distance-based evaluations in clustering for medical data. Dasan et al. [31] introduced a sine-based distance and embedded it in a minimum-distance decision procedure, while Singh and Sharma [13] constructed divergence measures from aggregation operators for pattern recognition. Radha and Samuel [32] developed a Tan-log distance specifically for neutrosophic medical diagnosis. Mishra et al. [33] combined a Hellinger-type distance with objective weighting and ranking tools for sustainable energy-storage evaluation. Xu and Zhao [34] integrated a parameterized distance with TOPSIS and TODIM to account for both profile separation and decision attitude. Thakur [35] investigated several distances and distance-based confidence in a generalized neutrosophic environment. Bisht and Pal [14] used an inner-product construction in recognition and diagnostic problems, and Dasan et al. [36] recently developed an average-function distance for consumer selection. The continued appearance of new formulations indicates that the way a model represents dissimilarity remains an active methodological question.

The choice of a dissimilarity measure can influence medical diagnosis, particularly when several diseases share similar symptoms. Different measures may assign different levels of separation to the same patient-disease pair or produce ties for profiles with different patterns of deviation. Previous studies have therefore continued to examine the discriminative behavior of SVN comparison methods [11, 12, 14]. These findings suggest that the way local differences are aggregated deserves further investigation. Motivated by this issue, the present study develops a minimum-based dissimilarity measure for SVN. The measure selects the smallest coordinate deviation for each criterion, applies a bounded nonlinear transformation, and then aggregates the resulting values. Rather than claiming universal superiority, this study examines the construction as an alternative way of comparing uncertain profiles and evaluates its usefulness in medical diagnostic reasoning.

The main contributions of this study are summarized as follows:

1. This study introduces a bounded SVN dissimilarity measure that combines minimum coordinate selection with nonlinear normalization.
2. It examines the basic properties and numerical behavior of the measure through examples and comparisons with existing formulas.

3. It incorporates the measure into a minimum-dissimilarity procedure for ranking candidate diseases represented by SVNS symptom profiles.
4. It explores the feasibility of the procedure through two medical diagnostic applications and a comparative evaluation of the resulting rankings.

Although many measure constructions have been studied for SVNSSs, the use of minimum coordinate selection followed by bounded nonlinear normalization remains less explored in medical diagnosis. This approach offers an alternative way to aggregate local deviations when ranking uncertain clinical profiles. Accordingly, this article introduces the proposed dissimilarity measure, examines its basic properties, and explores its diagnostic feasibility. Section 2 presents the required concepts and existing formulas, Section 3 develops the proposed measure, Section 4 describes the diagnostic procedure, Section 5 reports the applications, and Section 6 concludes the article.

2. Preliminaries

2.1 Basic Concepts

Definition 1 ([1]). Let $\Xi = \{z_1, z_2, \dots, z_n\}$ be a finite universe of discourse. A fuzzy set (FS) $\mathcal{P}$ on Ξ is defined as

$$\mathcal{P} = \{\langle z_j, \mu_{\mathcal{P}}(z_j) \rangle : z_j \in \Xi\},$$

where $\mu_{\mathcal{P}}(z_j) \in [0, 1]$ denotes the membership degree of z_j in $\mathcal{P}$.

Definition 2 ([2]). An intuitionistic fuzzy set (IFS) $\mathcal{P}$ on Ξ is defined as

$$\mathcal{P} = \{\langle z_j, \mu_{\mathcal{P}}(z_j), \nu_{\mathcal{P}}(z_j) \rangle : z_j \in \Xi\},$$

where $\mu_{\mathcal{P}}(z_j), \nu_{\mathcal{P}}(z_j) \in [0, 1]$ denote the membership and non-membership degrees, respectively, and satisfy

$$0 \leq \mu_{\mathcal{P}}(z_j) + \nu_{\mathcal{P}}(z_j) \leq 1.$$

The hesitancy degree is given by

$$\pi_{\mathcal{P}}(z_j) = 1 - \mu_{\mathcal{P}}(z_j) - \nu_{\mathcal{P}}(z_j).$$

Definition 3 ([4]). A single-valued neutrosophic set (SVNS) $\mathcal{P}$ on Ξ is defined as

$$\mathcal{P} = \{\langle z_j, T_{\mathcal{P}}(z_j), I_{\mathcal{P}}(z_j), F_{\mathcal{P}}(z_j) \rangle : z_j \in \Xi\},$$

where $T_{\mathcal{P}}(z_j)$, $I_{\mathcal{P}}(z_j)$, and $F_{\mathcal{P}}(z_j)$ denote the truth-membership, indeterminacy-membership, and falsity-membership degrees, respectively. For every $z_j \in \Xi$,

$$T_{\mathcal{P}}(z_j), I_{\mathcal{P}}(z_j), F_{\mathcal{P}}(z_j) \in [0, 1], \quad 0 \leq T_{\mathcal{P}}(z_j) + I_{\mathcal{P}}(z_j) + F_{\mathcal{P}}(z_j) \leq 3.$$

Definition 4 ([4]). Let $\mathcal{P}$ and $\mathcal{Q}$ be two SVNSSs on Ξ . Their inclusion and equality relations are defined as follows:

1. $\mathcal{P} \subseteq \mathcal{Q}$, if and only if $T_{\mathcal{P}}(z_j) \leq T_{\mathcal{Q}}(z_j), I_{\mathcal{P}}(z_j) \geq I_{\mathcal{Q}}(z_j), F_{\mathcal{P}}(z_j) \geq F_{\mathcal{Q}}(z_j), z_j \in \Xi$.
2. $\mathcal{P} = \mathcal{Q}$, if and only if $T_{\mathcal{P}}(z_j) = T_{\mathcal{Q}}(z_j), I_{\mathcal{P}}(z_j) = I_{\mathcal{Q}}(z_j), F_{\mathcal{P}}(z_j) = F_{\mathcal{Q}}(z_j), z_j \in \Xi$.

Table 1
Existing distance measures for SVNSSs

Source	Distance measure
Broumi and Smarandache [20]	$d_{BS}(\mathcal{P}, \mathcal{Q}) = \frac{1}{n} \sum_{j=1}^n \max \left\{ \begin{array}{l} T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j) , \\ I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j) , \\ F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j) \end{array} \right\}$
Majumdar and Samanta [21]	$d_{MS}^1(\mathcal{P}, \mathcal{Q}) = \frac{1}{3n} \sum_{j=1}^n (T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j) + I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j) + F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j))$ $d_{MS}^2(\mathcal{P}, \mathcal{Q}) = \sqrt{\frac{1}{3n} \sum_{j=1}^n \left[\begin{array}{l} (T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j))^2 \\ + (I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j))^2 \\ + (F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j))^2 \end{array} \right]}$
Ye [25]	$d_Y^1(\mathcal{P}, \mathcal{Q}) = 1 - \frac{1}{n} \sum_{j=1}^n \text{Cot} \left[\frac{\pi}{4} + \frac{\pi}{4} \max \left(\begin{array}{l} T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j) , \\ I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j) , \\ F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j) \end{array} \right) \right]$ $d_Y^2(\mathcal{P}, \mathcal{Q}) = 1 - \frac{1}{n} \sum_{j=1}^n \text{Cot} \left[\frac{\pi}{4} + \frac{\pi}{12} \left(\begin{array}{l} T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j) \\ + I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j) \\ + F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j) \end{array} \right) \right]$
Mondal et al. [26]	$d_M(\mathcal{P}, \mathcal{Q}) = 1 - \frac{1}{n} \sum_{j=1}^n \log_2 \left[2 - \frac{1}{3} \left(\begin{array}{l} T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j) \\ + I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j) \\ + F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j) \end{array} \right) \right]$
Mishra et al. [33]	$d_{Mi}(\mathcal{P}, \mathcal{Q}) = \frac{1}{2n} \sum_{j=1}^n \sqrt{\begin{array}{l} \left(\sqrt{T_{\mathcal{P}}(z_j)} - \sqrt{T_{\mathcal{Q}}(z_j)} \right)^2 \\ + \left(\sqrt{I_{\mathcal{P}}(z_j)} - \sqrt{I_{\mathcal{Q}}(z_j)} \right)^2 \\ + \left(\sqrt{1 - I_{\mathcal{P}}(z_j)} - \sqrt{1 - I_{\mathcal{Q}}(z_j)} \right)^2 \\ + \left(\sqrt{F_{\mathcal{P}}(z_j)} - \sqrt{F_{\mathcal{Q}}(z_j)} \right)^2 \end{array}}$
Xu and Zhao [34]	$d_{XZ}(\mathcal{P}, \mathcal{Q}) = \frac{1}{3n} \sum_{j=1}^n \left(\begin{array}{l} \frac{ T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j) }{T_{\mathcal{P}}(z_j) + T_{\mathcal{Q}}(z_j)} \\ + \frac{ I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j) }{I_{\mathcal{P}}(z_j) + I_{\mathcal{Q}}(z_j)} \\ + \frac{ F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j) }{F_{\mathcal{P}}(z_j) + F_{\mathcal{Q}}(z_j)} \end{array} \right)$

2.2 Existing Distance Measures for SVNSSs

Various distance measures have been developed to quantify the difference between SVNSSs. Let $\mathcal{P}$ and $\mathcal{Q}$ be two SVNSSs on $\Xi = \{z_1, z_2, \dots, z_n\}$. The existing distance measures are summarized in Table 1.

3. Methodology

This section develops and validates the proposed dissimilarity measure for SVN_Ss. First, the new measure is defined and its fundamental properties are established. Subsequently, four numerical examples are presented to verify these properties and compare the proposed measure with existing measures under different numerical settings.

3.1 A New Dissimilarity Measure for SVN_Ss

Definition 5. Let $\mathcal{P}$ and $\mathcal{Q}$ be two SVN_Ss on Ξ . The new dissimilarity measure between $\mathcal{P}$ and $\mathcal{Q}$, denoted by $d(\mathcal{P}, \mathcal{Q})$, is defined as follows

$$d(\mathcal{P}, \mathcal{Q}) = \frac{1}{n} \sum_{j=1}^n \left(\frac{2 \min(|T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j)|, |I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j)|, |F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j)|)}{1 + \min(|T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j)|, |I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j)|, |F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j)|)} \right). \quad (1)$$

Unlike a direct sum of the three component differences, Eq. (1) retains the least component-wise deviation at each z_j and then applies a nonlinear normalization. This construction produces a bounded value without altering the order of the local deviation.

Theorem 1. Consider three LDFSs $\mathcal{P}$, $\mathcal{Q}$, and $\mathcal{R}$ on the UOD Ξ , the proposed measure satisfies the following properties:

1. $0 \leq d(\mathcal{P}, \mathcal{Q}) \leq 1$;
2. if $\mathcal{P} = \mathcal{Q}$, then $d(\mathcal{P}, \mathcal{Q}) = 0$;
3. $d(\mathcal{P}, \mathcal{Q}) = d(\mathcal{Q}, \mathcal{P})$;
4. if $\mathcal{P} \subseteq \mathcal{Q} \subseteq \mathcal{R}$, then $d(\mathcal{P}, \mathcal{Q}) \leq d(\mathcal{P}, \mathcal{R})$ and $d(\mathcal{Q}, \mathcal{R}) \leq d(\mathcal{P}, \mathcal{R})$.

Proof. 1. For convenience, denote the minimum component difference at z_j by

$$\delta_j(\mathcal{P}, \mathcal{Q}) = \min(|T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j)|, |I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j)|, |F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j)|).$$

Because every membership degree belongs to $[0, 1]$, each absolute difference, and hence its minimum, lies in the same interval:

$$0 \leq \delta_j(\mathcal{P}, \mathcal{Q}) \leq 1.$$

Let

$$h(x) = \frac{2x}{1+x}, \quad 0 \leq x \leq 1.$$

Since $h(0) = 0$, $h(1) = 1$, and

$$h'(x) = \frac{2}{(1+x)^2} > 0,$$

the function h maps $[0, 1]$ onto $[0, 1]$ and is strictly increasing. Eq. (1) is the arithmetic mean of $h(\delta_j(\mathcal{P}, \mathcal{Q}))$ over all $z_j \in \Xi$. Therefore, $0 \leq d(\mathcal{P}, \mathcal{Q}) \leq 1$, which proves Property 1.

2. If $\mathcal{P} = \mathcal{Q}$, the corresponding truth, indeterminacy, and falsity membership degrees are equal for every z_j . Thus, $\delta_j(\mathcal{P}, \mathcal{Q}) = 0$ for all j , and Eq. (1) gives $d(\mathcal{P}, \mathcal{Q}) = 0$. Property 2 follows.

3. The equality $|a - b| = |b - a|$ holds for each component difference. Hence,

$$\delta_j(\mathcal{P}, \mathcal{Q}) = \delta_j(\mathcal{Q}, \mathcal{P}),$$

and substituting the above equation into Eq. (1) establishes Property 3.

4. Assume that $\mathcal{P} \subseteq \mathcal{Q} \subseteq \mathcal{R}$. By the inclusion rule for SVNss, each $z_j \in \Xi$ satisfies

$$T_{\mathcal{P}}(z_j) \leq T_{\mathcal{Q}}(z_j) \leq T_{\mathcal{R}}(z_j), I_{\mathcal{P}}(z_j) \geq I_{\mathcal{Q}}(z_j) \geq I_{\mathcal{R}}(z_j), F_{\mathcal{P}}(z_j) \geq F_{\mathcal{Q}}(z_j) \geq F_{\mathcal{R}}(z_j).$$

The component difference between either pair of adjacent sets is no greater than the corresponding difference between $\mathcal{P}$ and $\mathcal{R}$. Consequently,

$$\delta_j(\mathcal{P}, \mathcal{Q}) \leq \delta_j(\mathcal{P}, \mathcal{R}), \quad \delta_j(\mathcal{Q}, \mathcal{R}) \leq \delta_j(\mathcal{P}, \mathcal{R}).$$

The function h is strictly increasing on $[0, 1]$, so it preserves both inequalities. Applying h first and then taking the mean over $j = 1, 2, \dots, n$ yields $d(\mathcal{P}, \mathcal{Q}) \leq d(\mathcal{P}, \mathcal{R})$ and $d(\mathcal{Q}, \mathcal{R}) \leq d(\mathcal{P}, \mathcal{R})$. These are the two assertions in Property 4. □

3.2 Numerical Validation

Example 1. For an arbitrary element $z_j \in \Xi$, denote the component-wise deviations between $\mathcal{P}$ and $\mathcal{Q}$ by

$$\Delta T = |T_{\mathcal{P}}(z_j) - T_{\mathcal{Q}}(z_j)|, \quad \Delta I = |I_{\mathcal{P}}(z_j) - I_{\mathcal{Q}}(z_j)|, \quad \Delta F = |F_{\mathcal{P}}(z_j) - F_{\mathcal{Q}}(z_j)|.$$

Taking $\Delta F = 1$ and allowing ΔT and ΔI to vary over $[0, 1]$ gives the boundary surface

$$d(\mathcal{P}, \mathcal{Q}) = \frac{2 \min\{\Delta T, \Delta I, 1\}}{1 + \min\{\Delta T, \Delta I, 1\}}.$$

The resulting values are displayed in Figure 1.

The surface remains between 0 and 1 for all $\Delta T, \Delta I \in [0, 1]$. Its minimum value is 0, and it reaches 1 only when $\Delta T = \Delta I = \Delta F = 1$. When $\Delta F < 1$, the distance remains within the same interval. Therefore, the average over all elements also lies between 0 and 1, satisfying Property 1.

Example 2. Let $\Xi = \{z_1, z_2, z_3\}$ and consider

$$\begin{aligned} \mathcal{P} &= \mathcal{Q} = \{\langle z_1, 0.20, 0.60, 0.70 \rangle, \langle z_2, 0.40, 0.50, 0.50 \rangle, \langle z_3, 0.55, 0.25, 0.35 \rangle\}, \\ \mathcal{R} &= \{\langle z_1, 0.30, 0.50, 0.60 \rangle, \langle z_2, 0.60, 0.30, 0.30 \rangle, \langle z_3, 0.80, 0.00, 0.10 \rangle\}. \end{aligned}$$

Since $\mathcal{P} = \mathcal{Q}$, the proposed measure gives

$$d(\mathcal{P}, \mathcal{Q}) = 0, \quad d(\mathcal{P}, \mathcal{R}) = d(\mathcal{R}, \mathcal{P}) = 0.3051.$$

The zero value obtained for the identical sets verifies Property 2, while the equal distances for $\mathcal{P}$ and $\mathcal{R}$ verify Property 3.

Example 3. Consider the following SVNss on Ξ :

$$\begin{aligned} \mathcal{P} &= \{\langle z_1, 0.20, 0.70, 0.80 \rangle, \langle z_2, 0.30, 0.60, 0.70 \rangle, \langle z_3, 0.40, 0.50, 0.60 \rangle\}, \\ \mathcal{Q} &= \{\langle z_1, 0.35, 0.55, 0.65 \rangle, \langle z_2, 0.45, 0.45, 0.55 \rangle, \langle z_3, 0.55, 0.35, 0.45 \rangle\}, \\ \mathcal{R} &= \{\langle z_1, 0.60, 0.30, 0.40 \rangle, \langle z_2, 0.70, 0.20, 0.30 \rangle, \langle z_3, 0.80, 0.10, 0.20 \rangle\}. \end{aligned}$$

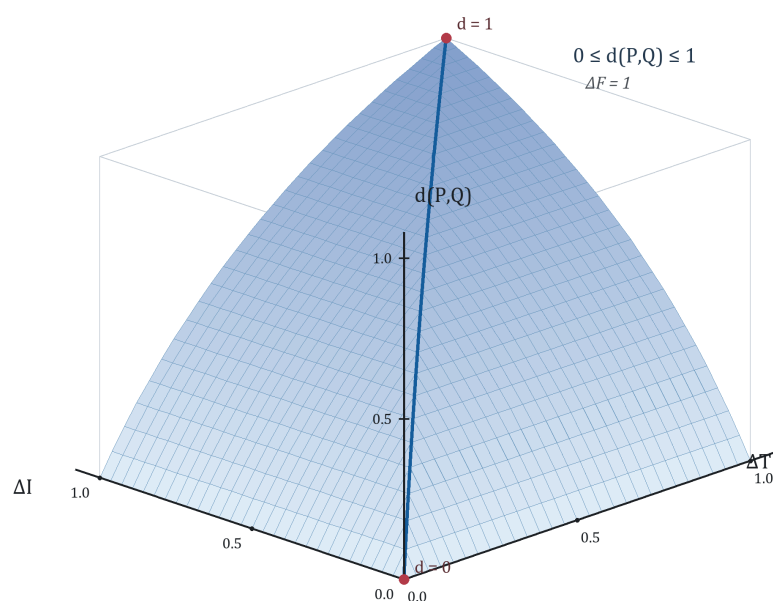


Fig. 1. The boundedness of the proposed dissimilarity measure

It is clear that $\mathcal{P} \subseteq \mathcal{Q} \subseteq \mathcal{R}$. The proposed measure gives

$$d(\mathcal{P}, \mathcal{Q}) = 0.2609, \quad d(\mathcal{Q}, \mathcal{R}) = 0.4000, \quad d(\mathcal{P}, \mathcal{R}) = 0.5714.$$

Therefore,

$$d(\mathcal{P}, \mathcal{Q}) \leq d(\mathcal{P}, \mathcal{R}), \quad d(\mathcal{Q}, \mathcal{R}) \leq d(\mathcal{P}, \mathcal{R}),$$

which verifies Property 4.

Example 4. The proposed measure is compared with the eight existing measures listed in Table 1. Let $\Xi = \{z_1, z_2, z_3\}$, and consider the four cases presented in Table 2.

The values produced by the nine measures are reported to four decimal places in Table 3.

As shown in Table 3 and Fig. 2, several existing measures cannot distinguish between cases with different component structures. In particular, d_{BS} , d_{MS}^1 , d_Y^1 , d_{Mi} , and d_{XZ} return the same values for Cases 1 and 2, whereas d_{MS}^1 , d_{MS}^2 , d_Y^2 , d_M , and d_{XZ} remain unchanged for Cases 3 and 4. In comparison, the proposed measure gives 0.2913, 0.3239, 0.3683, and 0.3440 for the four cases, respectively, and therefore distinguishes all of them. This outcome demonstrates its stronger sensitivity to variations in the component-wise deviations and highlights its advantage when finer discrimination among SVNSSs is required.

4. Dissimilarity-Based Medical Pattern Recognition

This section develops a dissimilarity-based algorithm for medical pattern recognition with SVNSS information.

Problem statement: Let $\mathcal{S} = \{s_1, s_2, \dots, s_n\}$ denote the clinical criteria and $\mathcal{C} = \{C_1, C_2, \dots, C_q\}$ the candidate diseases.

The classification procedure consists of the following steps, and its overall workflow is illustrated in the flowchart in Fig. 3.

Table 2
SVNS data for the four illustrative cases

Case	Element	$\mathcal{P}$	$\mathcal{Q}$
1	z_1	$\langle 0.35, 0.30, 0.45 \rangle$	$\langle 0.65, 0.70, 0.55 \rangle$
	z_2	$\langle 0.41, 0.41, 0.39 \rangle$	$\langle 0.59, 0.59, 0.61 \rangle$
	z_3	$\langle 0.38, 0.28, 0.28 \rangle$	$\langle 0.62, 0.72, 0.72 \rangle$
2	z_1	$\langle 0.38, 0.30, 0.41 \rangle$	$\langle 0.62, 0.70, 0.59 \rangle$
	z_2	$\langle 0.29, 0.28, 0.34 \rangle$	$\langle 0.71, 0.72, 0.66 \rangle$
	z_3	$\langle 0.45, 0.39, 0.41 \rangle$	$\langle 0.55, 0.61, 0.59 \rangle$
3	z_1	$\langle 0.38, 0.38, 0.29 \rangle$	$\langle 0.62, 0.62, 0.71 \rangle$
	z_2	$\langle 0.34, 0.37, 0.32 \rangle$	$\langle 0.66, 0.63, 0.68 \rangle$
	z_3	$\langle 0.25, 0.31, 0.41 \rangle$	$\langle 0.75, 0.69, 0.59 \rangle$
4	z_1	$\langle 0.45, 0.31, 0.29 \rangle$	$\langle 0.55, 0.69, 0.71 \rangle$
	z_2	$\langle 0.37, 0.34, 0.32 \rangle$	$\langle 0.63, 0.66, 0.68 \rangle$
	z_3	$\langle 0.36, 0.28, 0.33 \rangle$	$\langle 0.64, 0.72, 0.67 \rangle$

Table 3
Comparison of the existing and proposed dissimilarity measures

Measure	Case 1	Case 2	Case 3	Case 4
d_{BS}	0.3533	0.3533	0.4267	0.4067
d_{MS}^1	0.2778	0.2778	0.3222	0.3222
d_{MS}^2	0.3015	0.3006	0.3363	0.3363
d_Y^1	0.4390	0.4390	0.5154	0.4966
d_Y^2	0.3599	0.3582	0.4107	0.4107
d_M	0.2171	0.2178	0.2536	0.2536
d_{Mi}	0.2195	0.2195	0.2344	0.2505
d_{XZ}	0.2778	0.2778	0.3222	0.3222
d (proposed)	0.2913	0.3239	0.3683	0.3440

Step 1. Construct the SVNS profiles. The disease profiles and the patient's symptom profile are assumed to be available before the distance evaluation. For $\mathcal{C}_k$, write

$$\mathcal{C}_k(s_j) = \langle \tau_{kj}, \iota_{kj}, \phi_{kj} \rangle, \quad j = 1, 2, \dots, n, \quad k = 1, 2, \dots, q,$$

while the patient profile on the same criterion set is expressed as

$$\mathcal{A}(s_j) = \langle a_j, b_j, c_j \rangle, \quad j = 1, 2, \dots, n,$$

where all membership components belong to $[0, 1]$.

Step 2. Calculate the diagnostic dissimilarities. For each pair $(\mathcal{A}, \mathcal{C}_k)$, set

$$\rho_{kj} = \min \{ |a_j - \tau_{kj}|, |b_j - \iota_{kj}|, |c_j - \phi_{kj}| \}. \quad (2)$$

Collecting these values for all candidates and criteria gives the deviation matrix

$$\mathbf{R} = [\rho_{kj}]_{q \times n} = \begin{bmatrix} \rho_{11} & \rho_{12} & \cdots & \rho_{1n} \\ \rho_{21} & \rho_{22} & \cdots & \rho_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ \rho_{q1} & \rho_{q2} & \cdots & \rho_{qn} \end{bmatrix}.$$

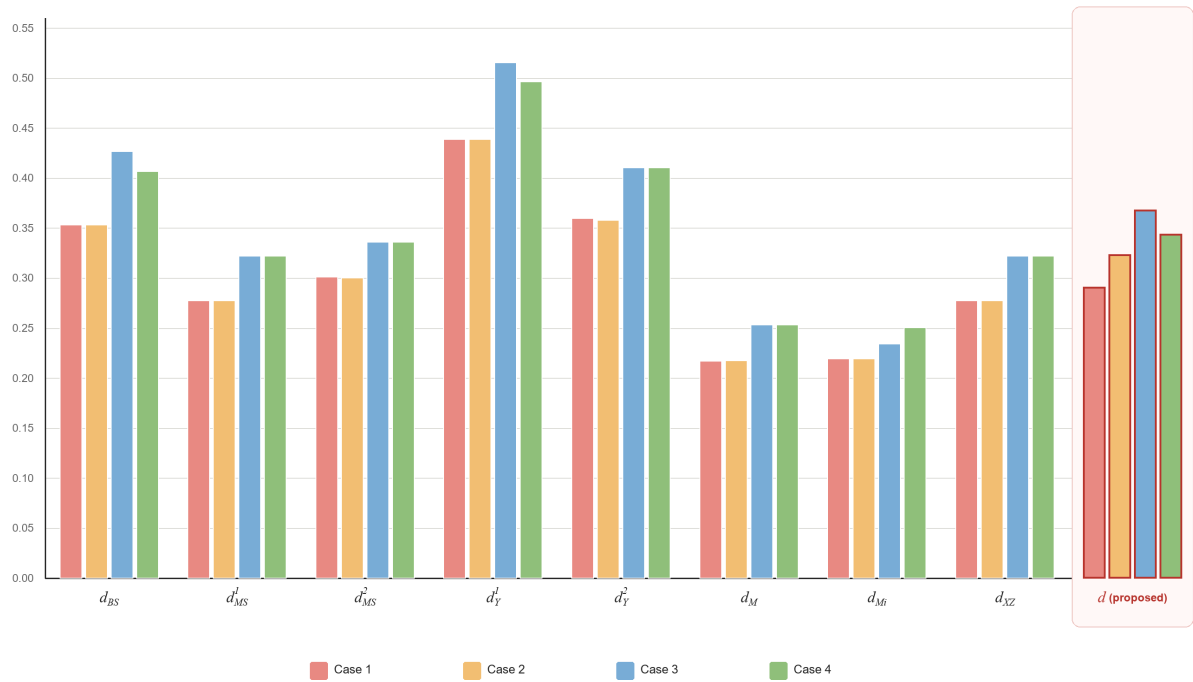


Fig. 2. Comparison of the existing and proposed measures across the four illustrative cases

The k th row of $\mathbf{R}$ is then aggregated to obtain the diagnostic distance

$$\Lambda_k = d(\mathcal{A}, \mathcal{C}_k) = \frac{1}{n} \sum_{j=1}^n \frac{2\rho_{kj}}{1 + \rho_{kj}}, \quad k = 1, 2, \dots, q. \quad (3)$$

Step 3. Rank the candidates and determine the diagnosis. Arrange $\{\Lambda_1, \Lambda_2, \dots, \Lambda_q\}$ in ascending order and determine

$$k^* \in \arg \min_{1 \leq k \leq q} \Lambda_k, \quad \hat{\mathcal{C}} = \mathcal{C}_{k^*}. \quad (4)$$

Hence, the candidate attaining the lowest distance is selected.

Algorithm 1: Dissimilarity-based medical pattern recognition

Input : Candidate disease profiles $\mathcal{C}_1, \dots, \mathcal{C}_q$ and patient profile $\mathcal{A}$ on $\mathcal{S}$

Output: The candidate ranking and selected disease pattern $\hat{\mathcal{C}}$

Form $\mathcal{C}_k(s_j) = \langle \tau_{kj}, \iota_{kj}, \phi_{kj} \rangle$ and $\mathcal{A}(s_j) = \langle a_j, b_j, c_j \rangle$;

for $k = 1$ **to** q **do**

for $j = 1$ **to** n **do**

 Compute ρ_{kj} using Eq. (2);

 Compute $\Lambda_k = d(\mathcal{A}, \mathcal{C}_k)$ using Eq. (3);

Rank $\mathcal{C}_1, \dots, \mathcal{C}_q$ in ascending order of Λ_k ;

Determine k^* using Eq. (4);

Set $\hat{\mathcal{C}} = \mathcal{C}_{k^*}$;

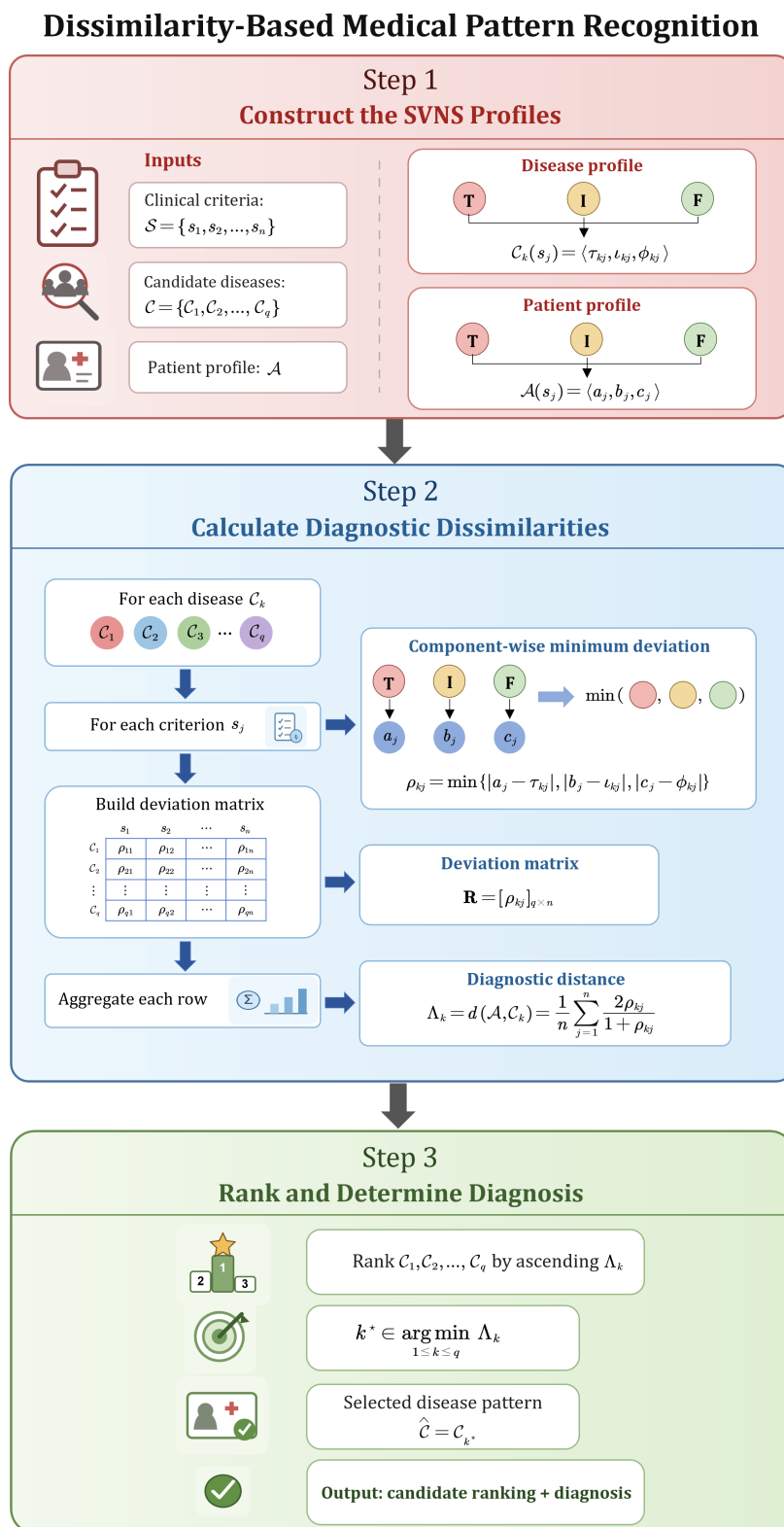


Fig. 3. Workflow of the proposed method

5. Applications in Medical Diagnosis

This section applies Algorithm 1 in two settings: symptom-based diagnosis and respiratory differential diagnosis.

5.1 Diagnosis from Symptom Profiles

The SVNS assessments reported by Ye [15] are used to examine the proposed diagnostic procedure.

Step 1. Construct the SVNS profiles. Let

$$\mathcal{C} = \{C_1 \text{ (viral fever)}, C_2 \text{ (malaria)}, C_3 \text{ (typhoid)}, C_4 \text{ (gastritis)}, C_5 \text{ (stenocardia)}\},$$

$$\mathcal{S} = \{s_1 \text{ (fever)}, s_2 \text{ (headache)}, s_3 \text{ (stomach pain)}, s_4 \text{ (cough)}, s_5 \text{ (chest pain)}\}.$$

The five disease profiles are listed in Table 4.

Table 4
SVNS profiles of the candidate diseases

Candidate	s_1	s_2	s_3	s_4	s_5
C_1	$\langle 0.4, 0.6, 0.0 \rangle$	$\langle 0.3, 0.2, 0.5 \rangle$	$\langle 0.1, 0.3, 0.7 \rangle$	$\langle 0.4, 0.3, 0.3 \rangle$	$\langle 0.1, 0.2, 0.7 \rangle$
C_2	$\langle 0.7, 0.3, 0.0 \rangle$	$\langle 0.2, 0.2, 0.6 \rangle$	$\langle 0.0, 0.1, 0.9 \rangle$	$\langle 0.7, 0.3, 0.0 \rangle$	$\langle 0.1, 0.1, 0.8 \rangle$
C_3	$\langle 0.3, 0.4, 0.3 \rangle$	$\langle 0.6, 0.3, 0.1 \rangle$	$\langle 0.2, 0.1, 0.7 \rangle$	$\langle 0.2, 0.2, 0.6 \rangle$	$\langle 0.1, 0.0, 0.9 \rangle$
C_4	$\langle 0.1, 0.2, 0.7 \rangle$	$\langle 0.2, 0.4, 0.4 \rangle$	$\langle 0.8, 0.2, 0.0 \rangle$	$\langle 0.2, 0.1, 0.7 \rangle$	$\langle 0.2, 0.1, 0.7 \rangle$
C_5	$\langle 0.1, 0.1, 0.8 \rangle$	$\langle 0.0, 0.2, 0.8 \rangle$	$\langle 0.2, 0.0, 0.8 \rangle$	$\langle 0.0, 0.0, 0.8 \rangle$	$\langle 0.8, 0.1, 0.1 \rangle$

The patient profile on the same symptom set is

$$\begin{aligned}\mathcal{A}(s_1) &= \langle 0.8, 0.2, 0.1 \rangle, & \mathcal{A}(s_2) &= \langle 0.6, 0.3, 0.1 \rangle, \\ \mathcal{A}(s_3) &= \langle 0.2, 0.1, 0.8 \rangle, & \mathcal{A}(s_4) &= \langle 0.6, 0.5, 0.1 \rangle, \\ \mathcal{A}(s_5) &= \langle 0.1, 0.4, 0.6 \rangle.\end{aligned}$$

Step 2. Calculate the diagnostic dissimilarities. Equations (2) and (3) give

$$\mathbf{R} = \begin{bmatrix} 0.1 & 0.1 & 0.1 & 0.2 & 0.0 \\ 0.1 & 0.1 & 0.0 & 0.1 & 0.0 \\ 0.2 & 0.0 & 0.0 & 0.3 & 0.0 \\ 0.0 & 0.1 & 0.1 & 0.4 & 0.1 \\ 0.1 & 0.1 & 0.0 & 0.5 & 0.3 \end{bmatrix}.$$

For example, the dissimilarity associated with malaria is

$$\Lambda_2 = \frac{1}{5} \left[\frac{2(0.1)}{1.1} + \frac{2(0.1)}{1.1} + \frac{2(0.0)}{1.0} + \frac{2(0.1)}{1.1} + \frac{2(0.0)}{1.0} \right] = 0.1091.$$

The complete results are presented in Table 5.

Step 3. Rank the candidates and determine the diagnosis. The ascending order is

$$C_2 \prec C_3 \prec C_1 \prec C_4 \prec C_5,$$

According to Eq. (4),

$$k^* = 2, \quad \hat{C} = C_2.$$

Since $\Lambda_2 = 0.1091$ is the unique minimum, the patient is assigned to C_2 , corresponding to malaria.

The case above illustrates a direct application of the proposed measure. The following case examines whether the same decision is retained under other SVNS dissimilarity measures.

Table 5
Dissimilarity-based diagnostic results

Candidate disease	Λ_k	Rank
Viral fever (C_1)	0.1758	3
Malaria (C_2)	0.1091	1
Typhoid (C_3)	0.1590	2
Gastritis (C_4)	0.2234	4
Stenocardia (C_5)	0.2984	5

5.2 Respiratory Differential Diagnosis

Patients with respiratory diseases often share several common symptoms, which can make early differential diagnosis difficult. For example, fever and cough can be found in patients with acute bronchitis, influenza, bacterial pneumonia, and pulmonary tuberculosis. Symptoms such as shortness of breath or chest discomfort may also appear in asthma. According to clinical guidelines, respiratory tract infections, asthma, and pneumonia are among the conditions that should be considered when evaluating adults with cough [37]. Dyspnea is also not specific to a single disease and may occur in various cardiopulmonary conditions [38]. Therefore, relying only on the symptoms reported during the first clinical visit may not provide enough information to distinguish one respiratory disease from another. Previous outpatient studies have shown that the assessment of pneumonia usually requires a combined consideration of symptoms, vital signs, and physical examination findings [39]. In addition, symptom duration and severity vary from patient to patient, while information obtained from self-reports, clinical examinations, and preliminary tests may contain different degrees of uncertainty. For these reasons, respiratory differential diagnosis provides an appropriate example for Algorithm 1, where a patient is classified according to the disease profile that produces the minimum dissimilarity value.

Step 1. Construct the SVNS profiles. The candidate set contains acute bronchitis, influenza, bacterial pneumonia, pulmonary tuberculosis, and asthma, denoted by C_1 , C_2 , C_3 , C_4 , and C_5 , respectively. The assessment uses four clinical criteria:

$$\mathcal{S} = \{s_1 \text{ (fever)}, s_2 \text{ (cough)}, s_3 \text{ (dyspnea)}, s_4 \text{ (chest discomfort)}\}.$$

The corresponding disease data and the observations for patient $\mathcal{A}$ are listed in Table 6.

Table 6
SVNS assessments of the respiratory diseases and patient

Criterion	C_1	C_2	C_3	C_4	C_5	$\mathcal{A}$
Fever (s_1)	$\langle 0.11, 0.65, 0.10 \rangle$	$\langle 0.36, 0.41, 0.38 \rangle$	$\langle 0.41, 0.31, 0.48 \rangle$	$\langle 0.68, 0.11, 0.70 \rangle$	$\langle 0.28, 0.17, 0.29 \rangle$	$\langle 0.44, 0.33, 0.46 \rangle$
Cough (s_2)	$\langle 0.17, 0.61, 0.06 \rangle$	$\langle 0.62, 0.37, 0.27 \rangle$	$\langle 0.55, 0.27, 0.35 \rangle$	$\langle 0.75, 0.07, 0.11 \rangle$	$\langle 0.68, 0.47, 0.55 \rangle$	$\langle 0.53, 0.30, 0.37 \rangle$
Dyspnea (s_3)	$\langle 0.30, 0.52, 0.57 \rangle$	$\langle 0.74, 0.29, 0.34 \rangle$	$\langle 0.64, 0.23, 0.27 \rangle$	$\langle 0.45, 0.45, 0.50 \rangle$	$\langle 0.51, 0.05, 0.40 \rangle$	$\langle 0.66, 0.20, 0.25 \rangle$
Chest discomfort (s_4)	$\langle 0.14, 0.79, 0.14 \rangle$	$\langle 0.56, 0.51, 0.52 \rangle$	$\langle 0.49, 0.39, 0.47 \rangle$	$\langle 0.70, 0.68, 0.69 \rangle$	$\langle 0.62, 0.28, 0.57 \rangle$	$\langle 0.46, 0.42, 0.44 \rangle$

Step 2. Calculate the diagnostic dissimilarities. Using Eq. (2), the criterion-level deviations between $\mathcal{A}$ and the five disease profiles are

$$\mathbf{R} = \begin{bmatrix} 0.32 & 0.31 & 0.32 & 0.30 \\ 0.08 & 0.07 & 0.08 & 0.08 \\ 0.02 & 0.02 & 0.02 & 0.03 \\ 0.22 & 0.22 & 0.21 & 0.24 \\ 0.16 & 0.15 & 0.15 & 0.13 \end{bmatrix}.$$

Each row of $\mathbf{R}$ is then aggregated by Eq. (3). This gives

$$\Lambda_1 = 0.4761, \quad \Lambda_2 = 0.1438, \quad \Lambda_3 = 0.0440, \\ \Lambda_4 = 0.3639, \quad \Lambda_5 = 0.2569.$$

Step 3. Rank the candidates and determine the diagnosis. The ascending order is

$$\mathcal{C}_3 \prec \mathcal{C}_2 \prec \mathcal{C}_5 \prec \mathcal{C}_4 \prec \mathcal{C}_1.$$

According to Eq. (4),

$$k^* = 3, \quad \hat{\mathcal{C}} = \mathcal{C}_3.$$

Thus, the patient is assigned to the bacterial pneumonia profile.

Comparison with existing measures. The same profiles are evaluated using the proposed measure and eight existing measures. Here, d_r denotes the r th measure, $r = 1, 2, \dots, 9$, and $\mathcal{C}_{j_0}$ denotes the candidate disease attaining the minimum dissimilarity under d_r . The degree of confidence (DoC) [35] is calculated as

$$\text{DoC}(d_r) = \sum_{\substack{k=1 \\ k \neq j_0}}^5 |d_r(\mathcal{A}, \mathcal{C}_k) - d_r(\mathcal{A}, \mathcal{C}_{j_0})|. \quad (5)$$

The DoC is the total difference between the selected candidate and the other four candidates. A larger value means that the selected profile is more clearly separated in the calculation.

The comparative results and DoC values calculated using Eq. (5) are presented in Table 7, while the DoC comparison is visualized in Fig. 4. The minimum value in each row is shown in bold.

Table 7
Diagnostic values for the patient profile

Measure	$\mathcal{C}_1$	$\mathcal{C}_2$	$\mathcal{C}_3$	$\mathcal{C}_4$	$\mathcal{C}_5$	Ranking	Result	DoC
d_{BS}	0.3625	0.0925	0.0300	0.2525	0.1650	$\mathcal{C}_3 \prec \mathcal{C}_2 \prec \mathcal{C}_5 \prec \mathcal{C}_4 \prec \mathcal{C}_1$	$\mathcal{C}_3$	0.7525
d_{MS}^1	0.3317	0.0858	0.0250	0.2392	0.1558	$\mathcal{C}_3 \prec \mathcal{C}_2 \prec \mathcal{C}_5 \prec \mathcal{C}_4 \prec \mathcal{C}_1$	$\mathcal{C}_3$	0.7125
d_{MS}^2	0.3325	0.0863	0.0255	0.2397	0.1564	$\mathcal{C}_3 \prec \mathcal{C}_2 \prec \mathcal{C}_5 \prec \mathcal{C}_4 \prec \mathcal{C}_1$	$\mathcal{C}_3$	0.7128
d_Y^1	0.4528	0.1356	0.0460	0.3346	0.2305	$\mathcal{C}_3 \prec \mathcal{C}_2 \prec \mathcal{C}_5 \prec \mathcal{C}_4 \prec \mathcal{C}_1$	$\mathcal{C}_3$	0.9693
d_Y^2	0.4209	0.1265	0.0385	0.3194	0.2190	$\mathcal{C}_3 \prec \mathcal{C}_2 \prec \mathcal{C}_5 \prec \mathcal{C}_4 \prec \mathcal{C}_1$	$\mathcal{C}_3$	0.9318
d_M	0.2616	0.0633	0.0181	0.1838	0.1171	$\mathcal{C}_3 \prec \mathcal{C}_2 \prec \mathcal{C}_5 \prec \mathcal{C}_4 \prec \mathcal{C}_1$	$\mathcal{C}_3$	0.5531
d_{Mi}	0.2794	0.0652	0.0201	0.1890	0.1255	$\mathcal{C}_3 \prec \mathcal{C}_2 \prec \mathcal{C}_5 \prec \mathcal{C}_4 \prec \mathcal{C}_1$	$\mathcal{C}_3$	0.5786
d_{XZ}	0.4759	0.1095	0.0343	0.3190	0.2288	$\mathcal{C}_3 \prec \mathcal{C}_2 \prec \mathcal{C}_5 \prec \mathcal{C}_4 \prec \mathcal{C}_1$	$\mathcal{C}_3$	0.9959
d (proposed)	0.4761	0.1438	0.0440	0.3639	0.2569	$\mathcal{C}_3 \prec \mathcal{C}_2 \prec \mathcal{C}_5 \prec \mathcal{C}_4 \prec \mathcal{C}_1$	$\mathcal{C}_3$	1.0649

The agreement in both the diagnosis and the complete ranking with the existing measures supports the consistency and reliability of the proposed measure in this application. Moreover, the proposed measure achieves the highest DoC among the nine measures, indicating a stronger ability to distinguish bacterial pneumonia ($\mathcal{C}_3$) from the remaining candidate diseases. It therefore provides clearer disease separation, less diagnostic ambiguity, and greater confidence in the obtained diagnosis.

6. Conclusions

This study proposed a bounded dissimilarity measure for SVNPs and applied it to medical diagnostic reasoning. Theoretical and numerical analyses showed that the measure is symmetric, bounded in $[0, 1]$, and monotonic under set inclusion. In the two medical applications, the method identified malaria with a dissimilarity value of 0.1091 and bacterial pneumonia with a value of 0.0440.

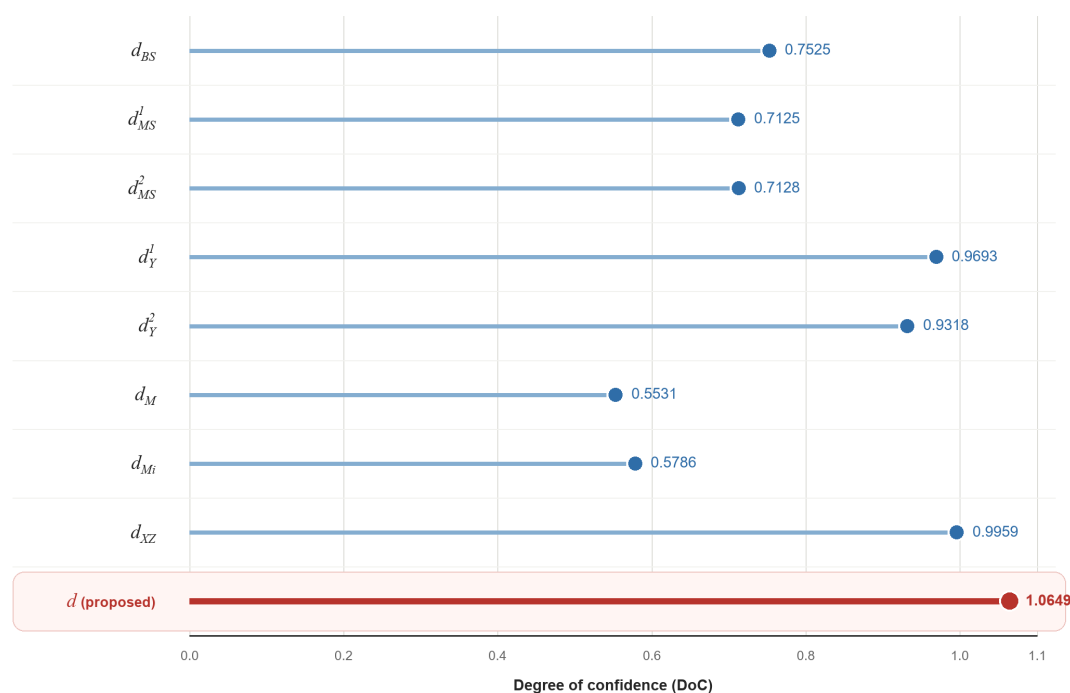


Fig. 4. Comparison of the degree of confidence obtained by the nine dissimilarity measures

For the respiratory case, the proposed measure produced the same disease ranking as the eight existing measures and achieved the highest degree of confidence, 1.0649. This result indicates that the proposed method provided clearer separation between bacterial pneumonia and the other candidate diseases for the examined data. Therefore, it offers a feasible approach for ranking uncertain medical profiles represented by single-valued neutrosophic information. Future studies should test the method on larger clinical datasets and examine the possible information loss caused by selecting only the minimum component difference.

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Conflicts of Interest

The authors declare no conflicts of interest.

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