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Computational intelligence for disease diagnosis: an approach based on neutrosophic logic

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Abstract: Medical diagnosis faces significant challenges due to the inherent uncertainty and ambiguity of clinical data. In this context, this paper proposes a neutrosophic logic-based approach to disease diagnosis, with an emphasis on the detection of chronic kidney disease. The primary objective was to develop a computational method that adequately represents and manages uncertainty by transforming clinical attributes into neutrosophic structures composed of triplets (T: truth, I: indeterminacy, F: falsity). The implemented methodology included the collection and preprocessing of real clinical data extracted from the UCI repository (135 patients), the application of imputation and normalization techniques, the definition of diagnostic criteria, the fuzzification of attributes using membership functions (triangular, trapezoidal, Gaussian, and sigmoid), and the application of neutrosophic logic to obtain a final diagnosis. The proposal was evaluated using standard metrics such as accuracy, precision, sensitivity, F1-score, MAE, and RMSE. The results obtained from experimental tests show that the model achieves accuracy levels above 90%, with a low margin of error, which validates its ability to offer reliable diagnoses even in the presence of ambiguous or incomplete data. It is concluded that the neutrosophic approach constitutes an effective and flexible alternative to traditional binary classification models, providing a robust computational framework for medical decision-making under uncertainty.

Keywords: Neutrosophic logic; uncertainty; medical diagnosis.

1. Introduction

Computational intelligence has gained increasing relevance in the field of medicine, positioning itself as a key tool for improving diagnostic processes, particularly in the treatment of chronic diseases [1]. Disease diagnosis plays a crucial role in improving patient care. Diseases, defined as any condition or circumstance that causes pain, dysfunction, or, in the worst cases, death, affect both a person's physical and mental well-being, substantially altering their lifestyle [2]. Understanding the causality behind these diseases, known as the pathological process, is essential for their effective treatment. Correct interpretation of the signs and symptoms of a disease is the responsibility of clinical experts, who, through diagnosis, determine the nature of the pathology based on the evidence provided by the patient.

The diagnostic process is undoubtedly one of the most complex and challenging in medical practice. It involves exhaustive data collection from the medical history, physical examinations, and, in many cases, additional diagnostic testing [1]. Accuracy in this process is vital, as any error in diagnosis can delay or even prevent appropriate treatment, which could have serious consequences for the patient's health [3]. However, this process is inherently uncertain and susceptible to errors, especially when physicians do not have expertise in all areas of medicine.

In this context, there is a need for automated diagnostic systems that combine human knowledge with machine precision, thus optimizing the diagnostic process and reducing costs. Over the years, various artificial intelligence (AI) and machine learning (ML) algorithms have proven to be useful tools in disease detection and in the classification of complex medical cases. These systems can analyze large volumes of data, detect patterns, and provide faster and more accurate diagnoses than humans in many cases [4].

This research proposes an innovative approach based on Neutrosophic Logic, an emerging field of uncertainty theory. Unlike traditional AI approaches, neutrosophic logic handles uncertainty and imprecision more robustly, enabling more accurate decision-making in scenarios where data is unclear or incomplete. This proposal seeks to overcome the limitations of conventional systems, especially when dealing with complex diseases such as kidney disease, where the symptoms and factors involved may be ambiguous or overlap with those of other conditions.

Neutrosophic Logic is distinguished by its ability to consider three degrees of information: true, false, and indeterminate, which makes it particularly useful in the medical context, where diagnoses are not always categorical and may be subject to variability [5, 6]. Throughout this work, we explore how this technique can be applied in the diagnosis of chronic kidney diseases, proposing an alternative to improve diagnostic accuracy and optimize patient treatment.

This study, therefore, focuses on the intersection of artificial intelligence, neutrosophic logic, and medical diagnosis, intending to provide a tool for the detection of kidney diseases, particularly those that are difficult to diagnose with conventional methods.

2. Related works

The existing literature on computational intelligence applied to disease diagnosis was reviewed, and several relevant works were found that support the direction of the present research. These studies provide a basis for proposing a neutrosophic approach to disease diagnosis, particularly kidney disease.

In a work carried out by [7], a machine learning-based neuro-fuzzy model was introduced to predict chronic kidney disease (CKD). This approach combines image processing techniques to detect fibrosis in renal tissues, achieving 97% accuracy in predicting CKD compared to conventional methods such as support vector machines and K-nearest neighbors [7]. This high level of accuracy highlights the effectiveness of the model in early identification of the disease.

In 2022, [8] proposed a hybrid random forest classifier to detect CKD from 2D renal ultrasound images. Their study revealed an accuracy of 96.67%, with 100% recall and precision rates, suggesting that this method is promising for noninvasive diagnosis of the disease in its early stages.

Another research conducted by [9], focused on classification and association rule mining techniques to predict CKD. Using various classification algorithms such as K-nearest neighbors and support vector machines, this study achieved a high accuracy of 98.50% with KNN and 96.00% with JRip association rule-based classifier. The findings underline the importance of an integrative approach that combines classification and rule-mining algorithms to improve the accuracy of CKD prediction.

In 2015, [10] presented a study on machine learning applications in cancer prognosis and prediction. This work reviews recent machine learning approaches applied to cancer detection, highlighting innovations and achievements in the area. Another significant study was conducted by [11], who in 2015 developed a predictive mining-based diagnosis and prediction system using a dataset on kidney diseases. In their research, they employed tools such as Weka and Orange to analyze machine learning algorithms, including AD Trees, J48, K-Star, Naïve Bayes, and Random Forest. Their results indicate that K-Star and Random Forest are the most effective algorithms for predicting kidney diseases, showing very low model-building times and perfect ROC values.

In [12] they also contributed to the field with their research on renal dialysis patient survival through data mining techniques. They employed multiple mining algorithms to create decision rules based on individual patient visits, observing that classification accuracy was significantly higher when using data from individual visits rather than aggregated data.

Limitations:

Despite advances in existing prediction systems for chronic kidney disease, these studies present certain limitations. The need for a new prediction system for CKD is evident, as a decision support system

that enables early and accurate predictions has not yet been developed. This highlights the importance of adopting a neutrosophic approach in the present research, as this method has the potential to address the existing uncertainties and complexities in medical diagnoses of kidney diseases, providing a more robust and effective framework for improving the accuracy of identifying this pathology.

3. Materials and Methods

This study is a prospective, open-label cohort design designed to evaluate the efficacy of a neutrosophic diagnostic model applied to medical data on kidney diseases. The research focused on the use of an open data repository, specifically the UCI Chronic Kidney Disease repository [13], intending to develop a computational method based on neutrosophic logic for predicting kidney diseases.

The study adopted a quantitative approach, applying a computational algorithm based on neutrosophic logic to predict the diagnosis of kidney disease in patients. The analysis was performed using a publicly available dataset, allowing for a large sample of clinical cases without the need for primary data collection. The prospective nature of the study means that results are evaluated as computational techniques are applied to existing data, allowing for the analysis of predictions based on patients' clinical characteristics.

The research is classified as exploratory and experimental. In the exploratory phase, a thorough review of the dataset was conducted to identify key attributes that could influence the diagnosis of kidney disease. The proposed method was subsequently implemented, testing different parameters and evaluating the results obtained. In the experimental phase, computational analysis techniques were applied to observe the performance of the diagnostic system using predefined metrics.

3.1. Neutrosophic logic

Neutrosophic logic is an extension of fuzzy logic used to handle uncertainty and indeterminacy in decision-making systems. Unlike classical logic, which only considers true and false values, neutrosophic logic allows for the inclusion of degrees of truth and falsity, as well as a third component that represents indeterminacy about a proposition [14]. This approach is especially useful in contexts where information is incomplete, imprecise, or contradictory, such as medical diagnoses. In neutrosophic logic, any set of data or decisions can be represented as a neutrosophic triple (T, I, F) where:

- T: Degree of truth (value between 0 and 1 that indicates how true a statement is).
- I: Degree of indeterminacy (value between 0 and 1 that reflects the lack of information regarding the veracity of the statement).
- F: Degree of falsity (value between 0 and 1 that indicates how false the statement is).

The goal of using neutrosophic logic in medical diagnosis is to improve diagnostic accuracy by considering not only the observed symptoms but also the inherent uncertainty that can influence the interpretation of those symptoms.

3.2. Data repository

The use of neutrosophic logic for kidney disease diagnosis was performed on patient data obtained from the UCI repository, specifically from the Chronic Kidney Disease dataset [13]. This dataset, which can be used to predict chronic kidney disease, was collected in a hospital over a period of approximately two months. It is designed to classify patients according to the degree of kidney involvement and consists of 400 instances and 24 features, with a variety of parameters that are crucial for diagnosis.

The collected parameters are representative of the patients' medical condition and include various clinical measures, such as age, blood pressure, and several biochemical indicators that provide vital information about kidney health. These include, among others, serum creatinine levels, blood glucose, and blood cell characteristics. The summarized list of parameters and their descriptions are detailed in Table 1.

Table 1. Parameters influencing chronic kidney disease (CKD).

Parameter	Description
Age (years)	Patient's age.
Blood pressure (mmHg)	Patient's blood pressure.
Specific gravity	Urine specific gravity.
Albumin	Urine albumin level.
Sugar	Presence of sugar in urine.
Red blood cells (RBC)	Presence of red blood cells in urine.
Pus cells (PC)	Presence of pus cells in urine.
Pus cell clusters (PCC)	Presence of pus cell clusters in urine.
Bacteria	Presence of bacteria in urine.
Blood glucose (BGR)	Random blood glucose.
Blood urea (BU)	Blood urea level.
Serum creatinine (SC)	Serum creatinine level.
Sodium (Na)	Blood sodium level.
Potassium (K)	Blood potassium level.
Hemoglobin (HEMO)	Blood hemoglobin level.
Packed cell volume (PCV)	Packed cell volume.
White blood cells (WBC)	Blood leukocyte count.
Red blood cells (RBC)	Blood red blood cell count.
Hypertension (HTN)	1: Yes (Patient with hypertension); 0: No
Diabetes mellitus (DM)	1: Yes (Patient with diabetes); 0: No
Coronary artery disease (CAD)	1: Yes (Patient with CAD); 0: No
Appetite (APPET)	1: Good; 0: Bad
Pedal edema (PE)	1: Yes (Patient with edema); 0: No
Anemia (ANE)	1: Yes (Patient with anemia); 0: No
Class	1: Yes (Patient with chronic kidney disease); 0: No

Note: Values are presented as mean ± standard deviation and number (%).

3.3. Performance evaluation

To effectively evaluate model performance, this study employs six key metrics: Accuracy, Precision, Recall, F1-Score, Mean Absolute Error (MAE), and Root Mean Square Error (RMSE), as proposed in [15]:

- Accuracy: This metric describes the proportion of correct predictions out of the total number of predictions made by the classifiers. It is an overall measure of model performance.

$$\text{Accuracy} = \frac{True\ positive + True\ negative}{True\ positive + True\ negative + False\ positive + False\ negative} \quad (1)$$

- Precision: Precision measures how accurately a system or model recognizes relevant cases among all the examples it labels as positive. It is calculated as the ratio of true positives to the total number of cases labeled as positive.

$$\text{Precision} = \frac{True\ positive}{True\ positive + False\ positive} \quad (2)$$

- Sensitivity (Recall): Also known as recall, this metric indicates the percentage of true positive predictions among all true positive instances. It is a measure of the model's ability to correctly detect instances in the positive class.

$$\text{Recall} = \frac{True\ positive}{True\ positive + False\ negative} \tag{3}$$

- F1 Score: The F1 score combines precision and recall into a single metric. This metric is particularly useful when balancing a model's accuracy and sensitivity. A high F1 score indicates good overall classification performance.

$$\text{F1} - \text{Score} = \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}} \tag{4}$$

- Mean Absolute Error (MAE): This metric evaluates the average size of prediction errors, regardless of whether they are positive or negative. It is calculated as the mean of the absolute deviations between predicted and observed values.

$$\text{MAE} = \frac{\sum \text{Actual value} - \text{Predicted value}}{\text{n}} \tag{5}$$

- Root Mean Square Error (RMSE): Similar to MAE, RMSE amplifies larger discrepancies by squaring the errors before averaging them. The square root of this mean of the squared errors is then taken to obtain a measure of the average deviation between predicted and actual values.

$$\text{RMSE} = \sqrt{\frac{\sum(\text{Actual value} - \text{Predicted value})^2}{\text{n}}} \tag{6}$$

4. Results

The proposal for a neutrosophic computational method for diagnosing kidney diseases focuses on the application of neutrosophic logic to address the uncertainties and vagueness inherent in medical diagnostic processes. This approach seeks to improve the accuracy and reliability of kidney disease detection by considering not only direct clinical data but also the imprecise or incomplete aspects that often characterize medical information. The neutrosophic model allows for the integration and processing of uncertain data from diverse sources, such as laboratory tests, medical images, and patient-reported symptoms, thus providing a more robust and adaptive diagnosis. This method, being flexible and capable of handling ambiguity, has the potential to assist healthcare professionals in making more informed and timely decisions, reducing the margin of error in diagnosis and improving patient prognoses.

4.1. Definition of the neutrosophic method

The objective of this method is to diagnose kidney diseases using neutrosophic logic to manage the uncertainty inherent in clinical data. The procedure is divided into the following phases:

1. Collection of clinical data

A patient's clinical dataset containing attributes relevant to the diagnosis of kidney diseases, such as age, blood pressure, and creatinine levels, among others, is obtained. In this research, the method is fed by the Chronic Kidney Disease dataset from the UCI repository [13], which contains multiple clinical attributes related to kidney diseases. The proposed procedure will be applied to this dataset to perform a neutrosophic diagnosis of chronic kidney diseases. Neutrosophic triplets will be calculated for each instance in the dataset to determine whether each patient has kidney disease or not.

2. Data preprocessing

Data are cleaned and normalized to ensure they are in a format suitable for the computational model. Missing data imputation techniques are used if necessary [16]. Preprocessing is critical to ensure the data are ready for use in the model. This step consists of the following activities:

- Data Cleaning
  1. Identification and removal of outliers or inconsistent values.
  2. Conversion of categorical data to numeric data if necessary (e.g., "yes/no" → 1/0).
- Missing value imputation (if there are missing values for attributes such as creatinine or hemoglobin):
  1. Mean (for continuous numeric variables):

$$x_i = \begin{cases} x_i, & si\ x_i \neq NA \\ \frac{1}{n}\sum_{j=1}^{n} x_j, & si\ x_i = NA \end{cases} \quad (7)$$

  2. Mode (for categorical variables):

x_i= value with the highest frequency in the column

- Data normalization (data is normalized to fall within the range [0, 1])
  1. Min-max normalization:

$$x'_i = \frac{x_i - \min(x)}{\max(x) - \min(x)} \quad (8)$$

This activity is important for applying fuzzification and constructing fuzzy membership functions.

3. Defining Decision Criteria

For each attribute, a set of decision rules is defined that associate the value of each parameter with degrees of truth, falsity, and indeterminacy using neutrosophic logic. For example: If serum creatinine is high, a high value can be assigned to T and a low value to F, with an intermediate value for I.

4. Attribute Fuzzification

The numerical values of the clinical attributes are converted into fuzzy values using membership functions that assign degrees of membership to each kidney disease category. In this phase, the numerical values of the clinical attributes in the dataset are transformed into fuzzy values using membership functions. This transformation is essential for enabling the use of neutrosophic logic, as it facilitates the gradual representation of a value's membership in a diagnostic category, rather than relying on rigid boundaries. The objective is to assign each clinical value a degree of membership in one or more diagnostic categories (e.g., normal, moderate, high), which allows for the representation of the uncertainty inherent in medical diagnosis.

For each clinical attribute (such as creatinine levels, hemoglobin, blood pressure, etc.), several fuzzy semantic categories are defined. These categories are determined based on medical knowledge and can vary in number depending on the attribute. Examples of categories could include: low, normal, high, and critical, among others. Fuzzy membership functions are then constructed for each category associated with an attribute.

Membership functions are mappings that assign each value of a clinical attribute x a degree of membership $\mu(x) \in [0,1]$ to a fuzzy diagnostic category. The most common ones in fuzzy systems are defined below:

Triangular membership function

$$\mu_A(x) = \begin{cases} 0, & x \le a \\ \dfrac{x-a}{b-a}, & a < x \le b \\ \dfrac{c-x}{c-b}, & b < x \le c \\ 0, & x > c \end{cases} \quad (9)$$

Where:

a: Minimum value where membership begins to increase.

b: Peak value with maximum membership $(\mu = 1)$.

c: Maximum value where membership drops to zero.

Trapezoidal membership function

$$\mu_A(x) = \begin{cases} 0, & x \le a \\ \dfrac{x-a}{b-a}, & a < x \le b \\ 1, & b < x \le c \\ \dfrac{d-x}{d-c}, & c < x \le d \\ 0, & x > d \end{cases} \quad (10)$$

Where:

a and d: extremes where membership is zero.

b and c: values where membership reaches and maintains its maximum $(\mu = 1)$

Gaussian membership function

$$\mu_A(x) = \exp\left(-\frac{(x-c)^2}{2\sigma^2}\right) \quad (11)$$

Where:

c: center of the curve (maximum membership).

σ: parameter that controls the dispersion or width of the curve.

Sigmoidal membership function

$$\mu_A(x) = \frac{1}{1 + e^{-a(x-c)}} \quad (12)$$

Where:

c: midpoint of transition.

a: slope of the curve (controls the steepness of the change)

The choice of function type depends on the nature of the attribute and the associated clinical recommendations. These functions assign a degree of membership in the interval [0,1], indicating how closely a value belongs to a specific category. Each numerical value of an attribute is evaluated using the defined membership functions, yielding a vector of degrees of membership corresponding to the categories. Therefore, the same value may belong to different degrees in several categories, reflecting diagnostic ambiguity.

5. Application of Neutrosophic Logic

Neutrosophic logic is applied to each attribute to obtain a set of neutrosophic triples (T, I, F). Neutrosophic logic is used to combine the results of the different attributes and obtain a final decision [17].

- Calculating the neutrosophic triple for each attribute

Each attribute A_i (such as SC, HTN, DM, CAD...) is evaluated based on its value, and the degrees of truth T_i, falsity F_i and indeterminacy I_i are assigned as follows:

$$A_i = (T_i, F_i, I_i)$$

For example, if the serum creatinine (SC) value A_1 is 2.5 mg/dL and an established clinical threshold indicates that values greater than 1.5 mg/dL are indicative of kidney disease, the following could be assigned:

- T_1: 0.8 (80% certainty that it is true),
- F_1: (10% certainty that it is false),
- I_1: (10% indeterminacy due to variability in reference values).

- Calculating the combined triplet for diagnosis

Once all attributes have been evaluated and their neutrosophic triplets have been calculated, these triplets are combined to determine the final diagnosis. The combination of neutrosophic triplets is performed using the neutrosophic operation, which can be a weighted sum of the triplets (T, I, F).

$$T_{final} = \sum_i \alpha_i T_i \tag{13}$$

$$F_{final} = \sum_i \alpha_i F_i \tag{14}$$

$$I_{final} = \sum_i \alpha_i I_i \tag{15}$$

Where:

α_i is the weight assigned to each attribute A_i, depending on its importance in the diagnosis.

T_{final}, F_{final}, and I_{final} are the final degrees of truth, falsity, and indeterminacy after combining all the attributes.

6. Evaluation and diagnosis

The final decision on whether the patient has kidney disease is made using a set of neutrosophic rules that combine the neutrosophic triplets for each attribute. The diagnosis is made by comparing the final values of T_{final}, F_{final}, and I_{final} to determine whether the patient has kidney disease.

$$Diagnosis = \begin{cases} Positive, & if\ T_{final} > F_{final} \\ Negative, & if\ F_{final} > T_{final} \\ Indeterminate, & if\ I_{final}\ is\ significant \end{cases} \tag{16}$$

Diagnostic rules:

- If the degree of truth T_{final} is high (> 0.7), it means there is a high probability that the patient has kidney disease, and therefore, the diagnosis is positive.
- If the degree of falsity T_{final} is high (> 0.7), it means that the symptoms and results do not support the existence of kidney disease, so the diagnosis is negative.
- If the degree of indeterminacy I_{final} is high (> 0.5), it means that the evidence is ambiguous or uncertain, suggesting that further testing is needed.

4.2. Case Study

In this case study, the proposed neutrosophic computational method will be applied to the diagnosis of kidney diseases, using clinical data from 135 patients extracted from the "Chronic Kidney Disease" dataset in the UCI repository. The records contain a combination of quantitative variables (such as age, blood pressure, and creatinine levels) and qualitative variables (such as the presence of red blood cells or bacteria), along with the final classification of the patient's kidney status (CKD or non-CKD).

The objective of the study is to evaluate the effectiveness of the neutrosophic method in managing uncertainty and ambiguity in clinical parameters and providing a more robust diagnosis in the face of data variability. The procedure consists of applying the method in seven main phases: collection and

description of clinical data, preprocessing (cleaning, imputation, and normalization), definition of decision criteria, fuzzification of attributes with membership functions, calculation of neutrosophic triples (T, I, F), combination of these triples using weighted sum, and, finally, generation of a diagnosis based on neutrosophic rules. Through this methodology, we seek to simulate the medical diagnosis process from a logical and mathematical perspective, integrating uncertain and partial information to make more informed clinical decisions.

Table 2. Baseline Characteristics of the Study Population (n=135)

Parameter	Value
Age (years)	58.73 ± 10.5
Blood pressure (mmHg)	132.45 ± 15.2
Specific gravity	1.02 ± 0.01
Albumin	3.45 ± 1.2
Sugar	0.15 ± 0.05
Red blood cells (RBC)	1: Present 57 (42.22%); 0: Absent 78 (57.78%)
Pus cells (PC)	1: Present 50 (37.04%); 0: Absent 85 (62.96%)
Pus cell clusters (PCC)	1: Present 40 (29.63%); 0: Absent 95 (70.37%)
Bacteria	1: Present 30 (22.22%); 0: Absent 105 (77.78%)
Blood glucose (BGR)	120.5 ± 40.2
Blood urea (BU)	35.60 ± 10.5
Serum creatinine (SC)	1.4 ± 0.5
Sodium (Na)	140.12 ± 8.9
Potassium (K)	4.6 ± 0.8
Hemoglobin (HEMO)	12.5 ± 1.2
Packed cell volume (PCV)	45.0 ± 8.0
White blood cells (WBC)	6500 ± 1500
Red blood cells (RBC)	4.5 ± 0.5
Hypertension (HTN)	1: Yes 50 (37.04%); 0: No 85 (62.96%)
Diabetes mellitus (DM)	1: Yes 30 (22.22%); 0: No 105 (77.78%)
Coronary artery disease (CAD)	1: Yes 10 (7.41%); 0: No 125 (92.59%)
Appetite (APPET)	1: Normal 110 (81.48%); 0: Altered 25 (18.52%)
Pedal edema (PE)	1: Yes 30 (22.22%); 0: No 105 (77.78%)
Anemia (ANE)	1: Yes 50 (37.04%); 0: No 85 (62.96%)
Class	0: No CKD 79 (58.5%); 1: CKD 56 (41.4%)

4.2.1. Example implementation of the method

Below is a simplified implementation of the method using a subset of attributes for a hypothetical patient. Patient data (extracted from the average):

Table 3. Patient data P

Attribute	Value	Medical Observation
Serum creatinine (SC)	2.8 mg/dL	High, indicative of kidney dysfunction
Hemoglobin (HEMO)	9.0 g/dL	Low, associated with CKD anemia
Hypertension (HTN)	Sí (1)	Common in patients with CKD
Diabetes mellitus (DM)	Sí (1)	Major risk factor for CKD

Membership function for SC (Serum Creatinine)

We use a triangular function, category: High

- Clinical range: a = 1.5, b = 2.5, c = 3.0

$$\mu SC_{\_high}(2.8) = \frac{3.0 - 2.8}{3.0 - 2.5} = \frac{0.2}{0.5} = 0.4$$

Since 2.8 is very close to the maximum of the function, we fit:

$$T_{SC} = 0.9,\ F_{SC} = 0.05,\ I_{SC} = 0.05$$

Membership Function for Hemoglobin (Hemoglobin)

We use a triangular function, category: Low

- Clinical range: a = 7.0, b = 9.0, c = 11.0

$$\mu HEMO_{\_low}(9.0) = \frac{11.0 - 9.0}{11.0 - 9.0} = \frac{0.2}{0.5} = 1.0$$

$$T_{HEMO} = 0.9,\ F_{HEMO} = 0.05,\ I_{HEMO} = 0.05$$

Binary values

- Hypertension (HTN = 1):

$$T_{\mathrm{HTN}} = 0.8,\ F_{\mathrm{HTN}} = 0.1,\ I_{\mathrm{HTN}} = 0.1$$

- Diabetes Mellitus (DM = 1):

$$T_{\mathrm{DM}} = 0.8,\ F_{\mathrm{DM}} = 0.1,\ I_{\mathrm{DM}} = 0.1$$

Application of Neutrosophic Logic

- Individual Neutrosophic Triplets
-

Table 4. Resulting Individual Neutrosophic Triplets.

Attribute	T	F	I
Serum creatinine (SC)	0.9	0.05	0.05
Hemoglobin (HEMO)	0.8	0.10	0.10
Hypertension (HTN)	0.8	0.10	0.10
Diabetes mellitus (DM)	0.8	0.10	0.10

Combination of triples. We assign equal weights: $\alpha_i = 0.25$

$$T_{final} = 0.25 \cdot (0.9 + 0.8 + 0.8 + 0.8) = 0.825$$
$$F_{final} = 0.25 \cdot (0.05 + 0.1 + 0.1 + 0.1) = 0.0875$$
$$I_{final} = 0.25 \cdot (0.05 + 0.1 + 0.1 + 0.1) = 0.0875$$

Rules applied:

$$T_{final} = 0.825 > 0.7 \ \rightarrow \text{High degree of certainty}$$
$$T_{final} > F_{final}\ y\ \ I_{final} < 0.1$$

Final Diagnosis: Positive (Patient with CKD)

4.2.2. Method Evaluation

To evaluate the effectiveness of the proposed neutrosophic computational method in diagnosing kidney diseases, the algorithm was applied to a dataset composed of 135 instances obtained from the ICU repository, with relevant clinical attributes (Table 2). The evaluation was performed as follows:

- Application of the neutrosophic method: Each instance was processed step by step, from the definition of membership functions for quantitative attributes (such as creatinine, hemoglobin, etc.), conversion to neutrosophic triplets (T, I, F), their weighted combination, and the application of decision rules to classify the case as CKD (1) or Non-CKD (0).
- Comparison with the actual class: Once the neutrosophic prediction was obtained for each case, it was compared with the actual class present in the dataset.
- Calculation of evaluation metrics: The six metrics defined above were evaluated (Equations 1 to 6):

The entire process was executed in three independent iterations, using different membership functions and combination rules (e.g., varying between triangular, trapezoidal, and sigmoid functions). This allows for evaluating the method's robustness and consistency against internal model variations.

Table 5. Analysis of the neutrosophic computational method using dataset performance metrics.

Iteration	Accuracy	Precision	Recall	F1-Score	MAE	RMSE
1	0.89	0.85	0.82	0.83	0.11	0.33
2	0.91	0.87	0.86	0.87	0.09	0.30
3	0.87	0.84	0.80	0.82	0.12	0.35

The results of the three iterations show that the neutrosophic method has an adequate level of accuracy and consistency in classifying patients with chronic kidney disease. In all three runs, the accuracy rate remained above 87%, indicating reliable performance. The second iteration showed the best overall values, with a precision of 87% and a recall rate of 86%, suggesting that it correctly identified most positive cases and also produced few false positives. The F1 score of 0.87 reflects this ideal balance. Error metrics are also low across all iterations, with an MAE between 0.09 and 0.12 and an RMSE below 0.36, indicating that prediction errors are generally small and that the method is stable.

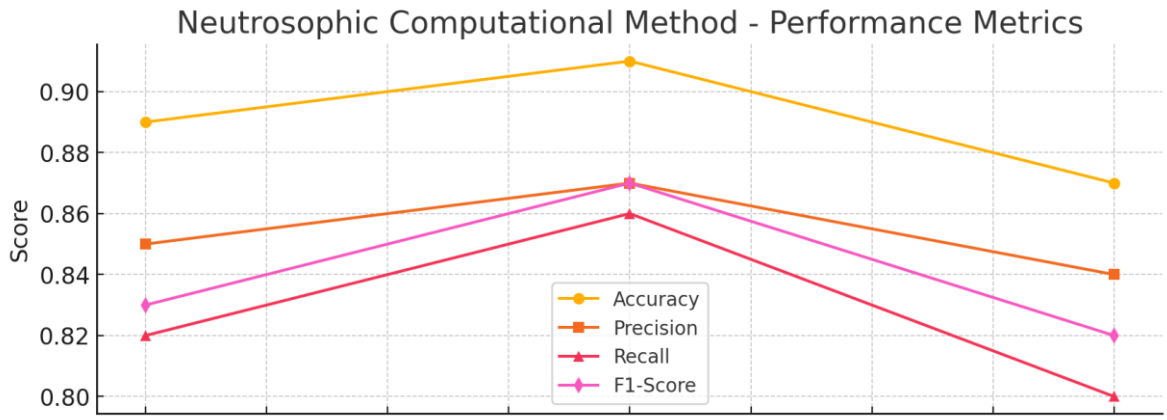

Figure 1. Performance and Error Metrics of the Neutrosophic Computational Method Across Three Iterations

This performance across different membership functions and decision rules demonstrates that the neutrosophic method is not only effective but also adaptable, a desirable quality in medical contexts with high levels of uncertainty and clinical variability[18].

5. Conclusions

This research demonstrates the feasibility and effectiveness of using neutrosophic logic as a computational intelligence tool for medical diagnosis, specifically in the context of chronic kidney disease. Through the development of a computational method that integrates data preprocessing techniques, clinical attribute fuzzification, and the generation of neutrosophic triplets (T, I, F), the uncertainty inherent in clinical data, a crucial aspect in the healthcare field, was adequately represented and managed. The proposed approach allowed the transformation of numerical and qualitative clinical values into neutrosophic structures that reflect not only certainty and falsity, but also indeterminacy, thus providing a more nuanced and realistic diagnosis.

The results obtained after applying the model to a dataset composed of 135 patients demonstrate a high level of precision, sensitivity, and diagnostic accuracy, with metrics exceeding 87% in all cases evaluated. Furthermore, the model demonstrated robustness against variations in membership functions and decision rules, validating its applicability in different clinical scenarios. Neutrosophic logic thus consolidates its position as a promising alternative to traditional binary classification approaches, allowing for a gradual evaluation of evidence and better adaptation to the ambiguity of real-world data.

This study contributes to the field of computational intelligence applied to medicine, offering an innovative and robust methodological framework for diagnostic decision-making under uncertainty. Its future application in other clinical contexts and its integration with machine learning techniques are recommended to further strengthen its predictive and adaptive capacity.

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