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A Proposed Model for Measuring Neutrosophic Inference of Comparative Nucleic Acids

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ABSTRACT

This paper introduces a novel neutrosophic inference model for the field of bioinformatics. The model is applied to develop a robust model for precise comparisons of human nucleic acids, where a new DNA sequence is matched against a comprehensive database of old nucleic acids. The results are analyzed in terms of accuracy, certainty, uncertainty, impartiality, and neutrality. Although the proposed model obtained an average accuracy rate of 33% in some cases, the similarities between sequences indicating its ability to accurately with a high accuracy rate of 85% for dissimilarity which highlights its effectiveness in distinguishing dissimilar sequences. However, the neutrality criterion yielding 0% in some cases may raise concerns about potential biases in the model's results towards specific samples. Further research is needed to understand the factors influencing neutrality and improve it for unbiased results. In conclusion, this study emphasizes the importance of employing neutrosophic inference models in the field of bioinformatics. It establishes a reliable benchmark for future nucleic acid comparisons, paving the way for advanced and more comprehensive applications in sequence analysis and genomic research.

Keywords: Neutrosophic, DNA, Database, Bioinformatics, Medicalinformatics.

1. INTRODUCTION

Neutrosophy is a branch of philosophy introduced by Smarandache in 1995, focusing on the study of neutrality and its interactions with various aspects of truth and falsehood. Building upon this concept, A.A. Salama extended it to introduce the theory of crisp neutrosophic crisp and various applications in computer science, information models, mathematics, statistics, and probability [1]. The main motivation of the current study indicates that the neutrosophic data science can be utilized as an emerging discipline within the field of computational and informatics sciences. Its objective is to develop tools and techniques that empower researchers and experts to manage neutrosophic information data. This data encompasses

both quantitative and qualitative information, as well as spatial and non-spatial data. Neutrosophic data science excels in handling the uncertainty and ambiguity present in data, which includes variations and contradictions in both the qualitative and quantitative values. It achieves this by introducing neutrosophic concepts, which provide a more robust representation of the intricate relationships within data. The applications of neutrosophic data science span a multitude of fields, including environmental science, agriculture, medicine, business, marketing, finance, insurance, commerce, and more [2-5]. Neutrosophic data science is instrumental in assessing the similarities and differences between DNA sequences. Nucleotides with high membership scores signify their significance and vitality. This information about shared nucleotides among various DNA sequences can be leveraged to identify conserved and crucial regions within the DNA sequence [5-8]. Regions showing high neutrosophic overlap indicate the importance of these nucleotides in the structure or function of the sequence. For instance, if a particular nucleotide at a specific position exhibits a high degree of membership across all sequences, it may imply the critical role of that position in function or structure. Consequently, neutrosophic overlap aids in identifying biologically significant regions of interest in DNA sequences by analyzing homology and variations between them.Furthermore, neutrosophic overlap can uncover interactions and associations among nucleotides located at different positions along the DNA sequence. Through the analysis of the resulting neutrosophic set, we can pinpoint nucleotides with strong affinities and minimal unaffiliated degrees at various positions within the DNA sequence. This data can be employed to identify critical interactions among nucleotides that occur across different loci. For example, when a neutrosophic overlap reveals that two nucleotides at distinct positions exhibit high degrees of affinity and low degrees of unaffiliation, this suggests that these nucleotides are functionally or structurally related. Such insights can be used to uncover functional or structural elements or understand how nucleotide interactions influence the structure or function of DNA [8-12]. In all, neutrosophic junction provides a comprehensive model for analyzing DNA sequences depending on degrees of membership and inorganicity [12-17]. Yes, advantages of neutrosophic DNA topology include its ability to handle incomplete or uncertain data:

- Neutrophil populations are used instead of exact numeric values, allowing incomplete data to be dealt with. Where an integer group includes a series of possible values.
- Neutrophil groups allow for the representation of uncertainty or ambiguity in the data. It does not require knowledge of the exact value of the data but does include a range of possible values.
- Neutrophil DNA topology can be used to identify factors with higher relevance and consistency even when there is uncertainty in the data.

Therefore, it is a very useful method for analyzing biological data which is generally characterized by uncertainty and incomplete data. Neutral group theories and fuzzy group theories can be used to represent the biological 3D structures of DNA molecules such as mRNA and siRNA. These two theories allow for the representation of uncertainty and uncertainty in the data of these structures due to their dynamic and changing nature. These structures play an important vital role in the functions of molecules and cellular processes, but traditional methods of calculating molecular topology require accurate and constant values. Using set theory, we can represent the data using neutrophil groups that include a range of values rather than exact values [18-22]. This allows us to compute fuzzy topologies of these structures that reflect variance and dynamic changes in shape, providing a better understanding of their biological functions. The topological structure of DNA can be represented and analyzed in different ways, depending on its nature as dynamic and non-deterministic structures. The theories of neutral groups and fuzzy groups are useful in this. Neutral group theory is characterized by its use of fuzzy affiliation criteria, whereby the degree of belonging of each nucleotide or base pair to the different groups constituting the topological structure is assigned. This allows for the representation of indeterminacy and inconsistency in the data due to the dynamic nature of DNA [23]. Whereas, fuzzy set theory is characterized by its use of fuzzy criteria of affiliation, which allows for the representation of uncertainty and ambiguity in data for topological structures. This is suitable for representing and analyzing dynamic changes in the structure of

DNA. Thus, the use of both theories allows for a more realistic and accurate representation and analysis of the structure of DNA, which helps to understand its vital function [24].

A G-quadruplex structure formed by four guanine protons linked by hydrogen bonds. DNA containing multiple G-guanine repeats may form several different G-quads structures. Its representation thus requires a way of expressing this indeterminacy. Fuzzy set theory and neutral groups provide the solution: Each nucleotide is assigned a degree of belonging to different groups so that the same nucleotide can belong to more than one group according to different degrees of affiliation [25].

This allows a better understanding of the nature of the G-quadruplex structure as a dynamic structure that changes with time, and helps to study the pathological effects on this structure and to design drugs that are able to manipulate this indeterminacy. Fuzzy phase topological structures can increase our understanding of the structure and function of DNA:

• It allows us to represent DNA in a more accurate and consistent manner with its uncertain dynamic nature through the use of fuzzy and neutral group theories.

• Allows us to represent biological data in a way that focuses on critical elements affecting DNA structure and function, while filtering out uncertainty and noise [26].

• Helps understand how genetic changes work and how they affect the topological structures of DNA.

• May contribute to identifying drug targets for related diseases and formulating future drugs.

• Because of their suitability for the complex nature of DNA, these fuzzy phase topological representations can provide new insights into articulating its structure and function [27].

Therefore, our ability to more accurately represent and filter biological data through the use of fuzzy and neutral set theories may help enrich our understanding of complex models such as DNA, paving the way for new discoveries and innovations.

Computational biology is an interdisciplinary discipline that develops and applies mathematical methods to analyze large sets of biological data for example genetic sequences, cell populations or protein samples, in order to make new predictions or new biological discoveries. Computational biology uses quantitative methods and advanced techniques to interpret cellular processes and mechanisms, discovering new relationships and function-limiting sites in the genome or amino acid sequence. Bioinformatics uses a variety of computational mathematical techniques such as sequence and structural alignment of biomolecules, database design and data extraction, molecular engineering, phylogenetic tree construction, structure and function prediction of proteins, discovery of novel genes, and collection of expression data. These techniques help to uncover new relationships and functional locations in the genome or amino acid sequences, learning about interactions between molecules and metabolic pathways, which helps in understanding vital processes at the cellular and molecular level [4-5].

In general, neutrosophic DNA topology is a theoretical framework complementary to traditional approaches in the field since it addresses the relationship of uncertainty and indeterminacy in the analysis of the structure and function of DNA sequences. We can summarize the major contribution of the paper as follows:

1 - Identification of conserved regions in the DNA sequence: nucleotides that show high degrees of membership indicate their functional or structural significance.

2 - Determine the interactions and dependencies between nucleotides: nucleotides that have similar degrees of membership and inorganicity at different sites can be considered to be functionally or structurally related.

3- Identification of functional or structural elements in the DNA sequence: Nucleotides with high membership and stability reflect their importance.

4- Identification of nucleotide interactions important for the function or structure of DNA: the dependencies between nucleotides at different sites indicate their common role.

2. Previous works

The researchers have designed an automated model for diagnosing brain tumors using an improved discrete wavelet transform called Slantlet Transform and neutrosophic, a generalization of fuzzy logic. Statistical measurements were extracted from MRI images that were subsequently provided to neural network classification techniques for tumor prediction. The proposed model achieved a high accuracy of 98.94%, which indicates its accuracy and efficiency in diagnosing brain tumors. This reveals the effectiveness of the proposed model in identifying brain tumors using MRI images. Incorporation of Slantlet transformation with fuzzy ensemble significantly improves classification accuracy compared to other existing techniques used to detect brain tumors. Therefore, the proposed approach can be effectively used for computer assisted diagnosis of brain tumors [28]. A Z test for uncertainty under neutrophil statistics has been proposed by the researchers, which is a generalization of existing tests in classical, noise-based, and time-lapse statistics. It was found to be more efficient than existing tests in terms of information and test power. Future research could include application of the proposed test to big data, use of paired sampling, sample size estimation and other characteristics of the proposed test [29]. A new epistemological map (MS-TrNCM) based on triangular neutrosophic numbers is outperforming traditional FCMs and NCMs for multistage sequential decision problems. Results from applying the model to project records appear from its effectiveness database. Future work should explore the use of machine learning techniques for map construction [30]. The proposed paired t-test under neutrophil statistics is a modified version of the existing paired t-test under classical statistics. It gives information about the chance of indeterminacy and delivers results at indefinite time intervals rather than exact values, which makes it more flexible and useful than the existing test. The measure of indeterminacy associated with the test statistic is 0.3457 [31]. Neutrosophic sets may be used (NS) to effectively manage inaccuracies and uncertainties in medical applications. Algorithms have been proposed for tasks such as denoising, thresholding, segmentation, clustering, classification, recovery and scoring, which can help improve existing fuzzy models. NS has potential applications in medical diagnosis and can be used to construct decision diagrams for this purpose [32]. A health care model based on computer-assisted diagnosis and the Internet of Things is designed to detect and monitor patients with heart failure. By using NMCDM techniques, the model can reduce mortality and treatment cost. Future work includes improving accuracy using machine learning methods, integrating patient data clouds with block chain, and extending the model to other platforms through snap computing [33]. The Chi-square test for K counts was introduced under Neutrophil Statistics to determine whether K counts differ significantly. An example using pulse count data was used to illustrate the procedure, and it was concluded that the proposed test is effective in uncertain situations and provides more information than conventional tests. It can be used to guide cardiologists in different treatment modalities and can be expanded with big data in future research [34]. Researchers use fuzzy and cognitive maps to mathematically analyze COVID-19 symptoms, transmission patterns, and precautionary measures. The results indicate that people without symptoms, high blood pressure, diabetes, tuberculosis, cancer, and the elderly are more likely to be infected. Social distancing, mask wearing and frequent hand washing are key precautions. This research can be extended with murkier techniques [35]. The researchers also provided an overview of neutrosophic groups and their extensions, such as single-valued neutrosophic groups (SVNSs), interval neutrosophic groups (INS), bipolar neutrosophic groups (BNSs), and generalized neutrosophic groups (GINSSs) and repeating neutrosophic groups (RNSs). The theoretical and mathematical properties of these models are discussed, as well as their applications in multi-trait decision making. Decision making algorithms are reviewed with examples of their usefulness [36]. A new decision-making method called NS-DANP combines neutrophil numbers, ANP and DEMATEL to deal with non-specific and inconsistent information. The proposed method is illustrated by a case study of coastal erosion in Peninsular Malaysia and the results indicate that coastal development is the most risky factor. Comparative analysis shows that the proposed method is reliable and sensitivity analysis can be applied in the future to evaluate NRM decisions due to uncertainty

[37]. The researchers designed a new local binary pattern (LBP) method based on neutrophil populations, called LBP NZ. It is more resistant to noise and can calculate edge information more accurately than the original input image. Experimental results show that this method increases the classification accuracy of the LBP method by about 11% without increasing feature dimensions, which makes it a viable solution for real-time applications such as classification, semantic segmentation, and object tracking [38]. An investigation into the uses of single-value neutrophil pools for logistics center site selection was established to improve reliability and suitability. A numerical example is used to demonstrate the effectiveness of the model in making multi-trait group decisions. The proposed strategy can be applied to a variety of problems, such as pattern recognition, medical diagnosis, and personnel selection [39]. A technique called neutrosophic fuzzy TOPSIS is designed for multi-criteria decision-making that uses a scale Space to arrange and choose different options. We show its accuracy by applying it to production industry and the MCDM problem with single-value neutrophil information. We also give a graphical model of the technology and use the example of selecting suppliers in the production industry to show its validity. This technique should be useful for problem solving and scaling investigations of decision making under uncertain environments [40]. An improved segmentation method for liver tumor segmentation from abdominal CT images using neutrophil clustering (NS), watershed algorithm, and fast fuzzy C-modal (FFCM) algorithm was presented. Intensity values in CT images are adjusted to increase contrast followed by image conversion to NS domain. This is reinforced by adaptive thresholding and morphological operators before being passed to the watershed algorithm for subsequent segmentation. Evaluation of the results showed that the overall accuracy provided by the NS method used was accurate, less time consuming, and performed better on non-uniform CT images with an overall accuracy of 95% [41]. An overview of neutrophil populations and their different extensions, such as SVNSs, INSs, BNSs, RNSs, and TFNNs, was done. It discusses the theoretical properties of NS and their related counterparts, and reviews decision-making algorithms and applications in multi-criteria decision-making problems. Examples of personnel selection and medical diagnosis are provided [42]. A proposal has been made to study a new mathematical tool, the Neutrophil Hyper plasticity Probability Set (pNHs set), to address the limitations of decision-making. The proposed pNHs array algorithm was used to modify the Sanchez method for medical diagnosis using real data from the Cleveland Cardiology dataset. The results show that this approach provides more flexibility and reliability than the current methods. It can be applied in areas such as soft computing, fuzzy logic, artificial intelligence, theoretical computer science, and pattern recognition [43]. This study proposes a new, higher-order approach to multi-trait decision-making problems in a bipolar neuroscience environment. External relations based on ELECTRE and the classification method are being developed, and the effectiveness of the proposed method is illustrated with an example. The proposed approach is simple and effective, and can be extended to engineering, game theory, multifactor models and decision making [44]. This study explores the use of neutrosophic ambiguous TOPSIS to assist decision-makers in uncertain environments. An example of supplier selection is used in the production industry to demonstrate its consistency and ease of use. Future research will focus on applying this technology in unstudied settings in areas such as medicine, robotics, artificial intelligence, pattern recognition, and economics [45]. A fuzzy new TOPSIS Fuzzy Technique article is presented as a multi-criteria decision-making method for selecting suppliers and proposes a GNRCS model for diagnosing COVID-19 patients based on chest X-ray images. The results show that both approaches are robust and accurate, and promise for further investigation of current issues related to MCDM [46]. The researchers also presented a new two-stage MADM framework study based on neutrosophic fuzzy groups to measure smart e-tourism applications. It uses NS-FWZIC for attribute weighting and NS-FDOSM for full performance measurement, with three processes used for evaluation. Limitations include binary assessment based on assumption, lack of significance measure and use of a single clustering factor and method of de-cluttering. Future studies could explore other ways to improve the relevance of the framework in addressing uncertainty [47]. A new axiomatic definition was proposed

for a measure of divergence of single-value neutrosophic groups, as well as a corresponding maximization divergence method and single-value TOPSIS to solve multi-criteria decision-making with incomplete weight information. A numerical example was used to demonstrate the effectiveness of the proposed approach [48]. Research has been done on the use of neutrophil groups and their hybrid combinations to assist in medical diagnostic problems. It investigates how uncertainty, inconsistency, and non-specificity can be used to assess a person's symptoms and proposes an effective method for making a diagnosis based on these combinations and combinations [49]. We have shown that Neutrosophic Statistics is an extension of interval statistics, and not all cases of indeterminacy can be represented by intervals. We compared neutrosophic and interval statistics, and showed that NS is more general than IS. We also forwarded Woodall et al. to plethyogenic probability and generated statistics as the most general forms of multivariate probability and multivariate statistics respectively [50]. The authors present a novel concept study, the Simplified Neutrosophic Indefinite Collection (SNIS), to express the hybrid information of both Simplified Neutrosophic Sets (SNS) and Neuronal Numbers (NNs). It is then used to create a multi-attribute decision-making approach with unspecified ranges of decision makers. This approach is applied in an example of selecting a suitable slope design scheme to demonstrate its applicability and suitability. They feature degree, precision, and certainty functions for ranking SNIEs, as well as SNIEWAA and SNIEWGA operators for grouping SNIEs [51]. A proposal was made for a new neutrosophic approach to reduce noise and errors in signal transmission. Three organic functions have been identified to explain truth, indeterminacy, and falsehood in the model. Experiments showed a 1% decrease in noise loss with PAM and 0.1% with FSK when shifting the frequency to a higher range, indicating the feasibility and applicability of the method [52]. A new technique is designed to segment the liver using CT images. It involves pre-treatment, transformation into Neutrosophic Clusters, and post-treatment through morphological processes and the fast-march method. The proposed algorithm is evaluated using measures based on area and distance, which can help in diagnosing liver diseases and performing liver transplants [53]. A new approach was designed to assess the risk of prostate cancer using hybrid information of fuzzy digits with an interval value and heterogeneous unspecified/neutrophil digits. A cubic reciprocating neutrosophic number ensemble has been proposed, along with generalized distance and similarity metrics for CHFSs. Sixteen clinical cases are presented as examples to demonstrate the effectiveness of this method [54]. This paper presents a new type of hybrid array called BQSVNR, which is an extended version of QSVN array, bipolar array and approximate array. She has greater abilities to deal with uncertain situations than any other group in existence due to her ability to deal with ambiguity, incompleteness, ambiguity, blurring, compactness, and bipolarity. It discusses basic theoretical terms, algebraic operations, measures of similarity, properties, and application to the problem of medical diagnosis. Future research can apply this ensemble to model real-life problems and explore the possibilities of extending it to include unipolar and multi-partition neutrosophic value approximate ensembles [55]. A model was designed to do a multi-criteria group decision-making (MCGDM) strategy, which uses linguistically refined neutrosophical groups to evaluate alternatives. The entropy method is used to calculate The weights of the unknown criteria, and an example is presented to demonstrate the applicability of the approach [56]. A proposal was presented to make a new grouping procedure for segmentation of the mammogram image in the field of neutrophil collection. It compares the proposed method with existing algorithms and shows better results both quantitatively and qualitatively. The algorithm uses three features—gradient, standard deviation, and pixel value—and Shannon entropy and standard deviation to determine the indefinite score. Future work will include feature extraction and classification of mammograms using optimization algorithms [57]. Two models were designed to predict the risk of drug toxicity. Both models use Rough Set-based methods to determine the most discriminating traits, followed by three different sampling algorithms (Random Under-Sampling, Random Over-Sampling, and SMOTE) to obtain balanced data. Neural Rule Based Classification Model (NRCS) and Genetic NRCS (GNRCS) are used in the final stage of classification. Experimental results show that the

proposed models have high sensitivity (89-93%), specificity (91-97%), and GM (90-94%) for all toxic effects, which indicates that they can be used to predict drug toxicity in the early stages of drug development. medication [58]. A novel tangential similarity proposal based on single-valued neutrosophic groups for multi-criteria best-worst decision-making, together with an algorithm to select best- and worst-criteria, is presented. A mathematical model is proposed to define a single-valued consistent preference relationship, and its effectiveness is shown in an example of problems of appointment registration models. The optimal feature weight vector and consistency ratio are used to calculate the final score for the alternative. This method will be extended to separating neutrophil populations in further work [59]. A model was designed to make a method for stratification of breast tumors in ultrasound images using a combination of neutrophil group (NS) scores and homogeneity value calculations, an Otsu-based adaptive threshold approach, an adaptive zone growth approach, and a deep convolutional neural network. Results show that this method outperforms current methods of breast tumor segmentation on BUS images, especially for tumors with blurry borders and low contrast. The proposed method achieves 81.6% and 84.4% dice coefficient, 77.0% and 84.3% true positive ratio, 11.2% and 15.2% false positive ratio, and 57.5 pixels and 52.8 pixels Hausdorff distance for benign and malignant images, respectively [60]. From above stated work, we found that the neutrosophic sets are a generalization of fuzzy logic that can be used to model uncertainty and indeterminacy in medical data. Neutrosophic sets have been used to develop a variety of new methods for medical diagnosis, including: automated brain tumor detection using MRI images [61], improved decision-making in heart failure management, enhanced liver tumor segmentation from abdominal CT images [62]. Hence, the research on neutrosophic sets in medical applications is still in its early stages, but the results are promising. Neutrosophic sets have the potential to improve the accuracy, efficiency, and reliability of medical diagnosis and decision-making. Neutrosophic sets for brain tumor detection: Researchers have developed an automated model for diagnosing brain tumors using an improved discrete wavelet transform called Slantlet Transform and neutrosophic sets. The model achieved a high accuracy of 98.94%, which indicates its potential for use in clinical practice. Neutrosophic sets for heart failure management: Researchers have developed a new neutrosophic multicriteria decision-making (NMCDM) model to assist clinicians in making decisions about the treatment of heart failure patients. The model considers a variety of factors, including the patient's medical history, symptoms, and treatment options. Neutrosophic sets for liver tumor segmentation: Researchers have developed a new image segmentation method for liver tumor segmentation from abdominal CT images using neutrosophic clustering (NS), watershed algorithm, and fast fuzzy C-means (FFCM) algorithm. The method was shown to be effective in segmenting liver tumors from non-uniform CT images, with an overall accuracy of 95%. Neutrosophic sets are a powerful tool for modeling and reasoning about uncertainty and indeterminacy in medical data. As the research in this area continues to mature, we can expect to see neutrosophic sets applied to even more medical applications. The main advantages includes:

- Neutrosophic sets can model uncertainty and indeterminacy in medical data more effectively than traditional fuzzy sets. This is important because medical data is often noisy, incomplete, and ambiguous.
- Neutrosophic sets can be used to develop new methods for medical diagnosis and decision-making that are more accurate, efficient, and reliable.
- Neutrosophic sets are still a relatively new area of research, which means that there is a lot of potential for innovation and development in this area.

The main disadvantages includes

- Neutrosophic sets are more complex than traditional fuzzy sets, which can make them difficult to implement and use.

- There is a lack of standardized methods for using neutrosophic sets in medical applications. This can make it difficult to compare the results of different studies and to apply neutrosophic set-based methods to clinical practice.
- More research is needed to evaluate the effectiveness of neutrosophic set-based methods in real-world medical settings.

3. Proposed model.

We will do a comparison process between the nucleic acids, where we will have a group of nucleic acids inside the database. The comparison process will be done through the proposed algorithm, which is neutrosophic phase for comparison, where the results will be extracted from similarity, dissimilarity, and neutrality, and we will calculate the accuracy standard as it is shown in Figure 1, and it shows how the model works. The results will be output and placed in separate tables for accuracy, as well as a separate table for the comparison process, making statistics and representing them on graphs. We will explain the algorithm and write it next to the flowchart diagram in Figures 2.

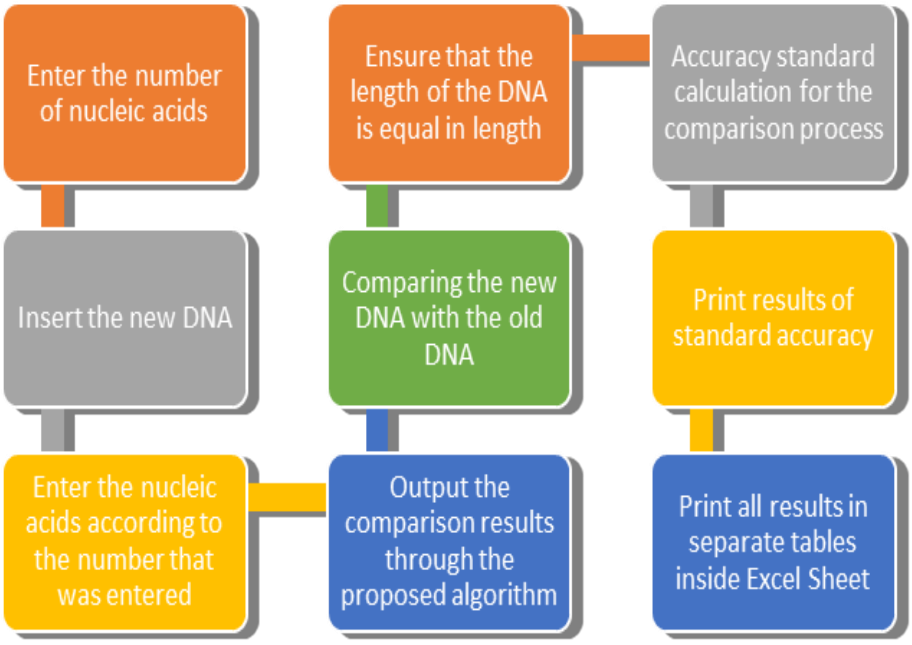

Figure 1. The steps of the proposed method.

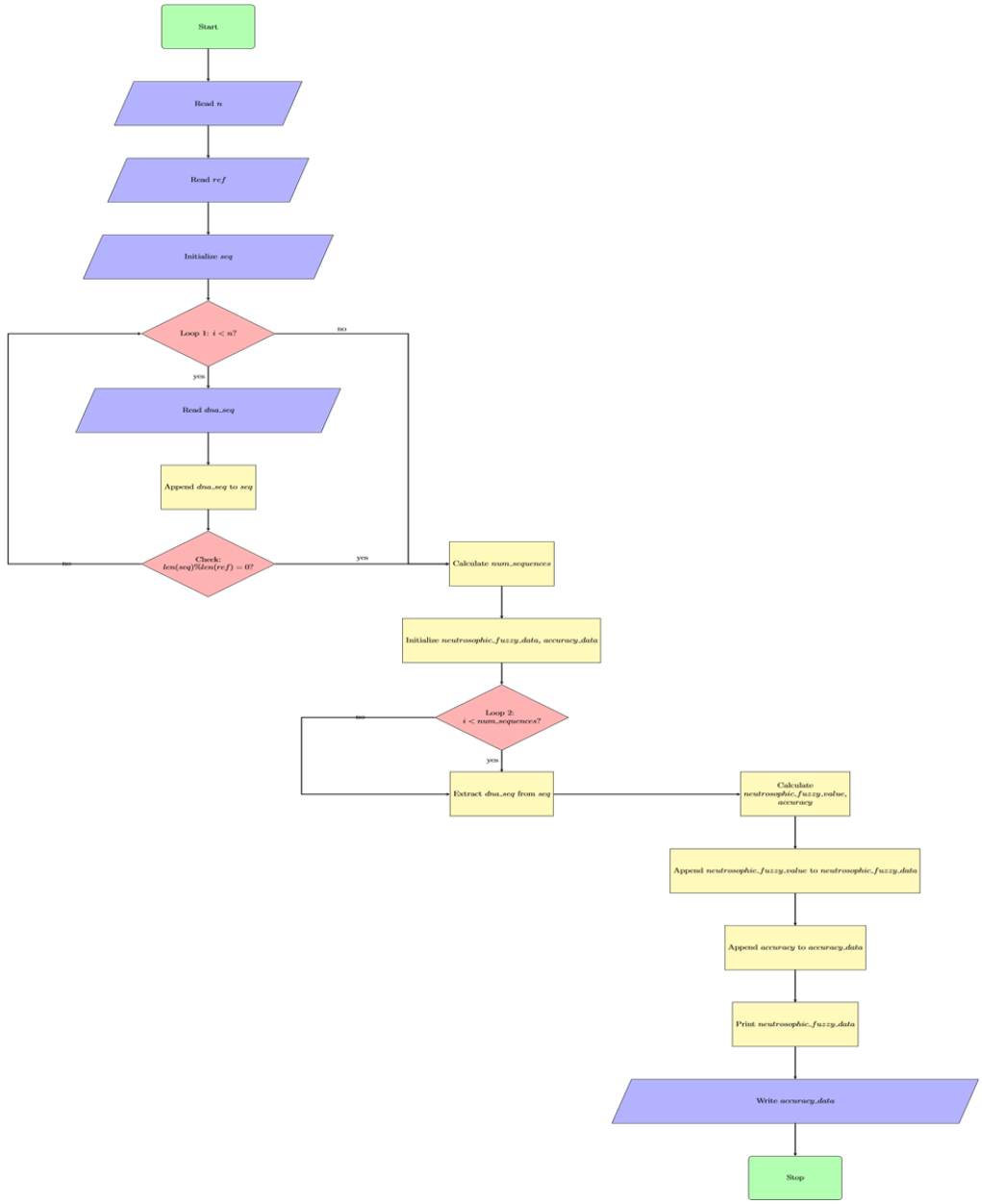

Figure 2. The flow chart of the proposed algorithm

4. RESULTS AND DISCUSSION

The data set was obtained from the National Center of Biotechnology Information (NCBI) [63], where 51 nucleic acids were obtained, and each acid contains 50 letters of DNA, and Table No. 1 shows the data set on which the experiment was conducted, where DNA No. 1 is the new DNA, and the rest of the acids Nuclear are already inside the database.

The new DNA:

TTGCCGACCCATCTGTACAAGAACTTCACTGTCCAGGAGCTGGCCTTG

Ancient nucleic acids:

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AAAAATACAAGTGGGTGGTGGCAAGGAGAGTTACAGGCCAGAGGAAAA
AAACTGAAGGGCAAGAATCAGGAGTTCTGCCTGACCGCCTTCATGTCG
AAGCGACAGAAAGGATGGTTTCCTGCCAGTCATGTTAAACTTTTGCTA
AAGGAGAGTGACTGGAACCAGCACAAGGAGCTGGAGAAATGCCGGGGC
AAGGAGGGATATGTTCCACGTAACTTGCTGGGACTGTACTACCAGTAC
AATGGCTATAATGAAACCACAGGGGAAAGGGGGGACTTTCCGGGAACT
ACGCCAGTCGGAGTCATTTATGCGCTTTGGGATTATGAACCTCAGAAT
ACTCCCGGCGATCTGCTCGAACTGCAGATCTGCCCGCTCAACGGATAT
AGAGAGAAGAAAGCTCCCCAGACTATTACAGAACTATGTTCGGAATAT
AGAGCGCTGTATGATTATAAAAAGGAAAGAGAAGAAGATATTGACTTG
AGGGAAGACGAAGATGAAATCGAATGGTGGTGGGCGCGCCTTAATGAT
ATCCAGTCTCTGGAAGTTATCGGTAAAGGCACTCACTGCAACCAGGTT
CAAAAGTCAGAGATTGCTCAGGTAACTTCAGCATATGTTGCTTCTGGT
CAAGTGGTGTATGTCTTCTCCAAGCTGAAGGGCCGTGGGCGGCTCTTC
CACTTGGGTGACATATTGACTGTGAATAAAGGGTCCTTAGTAGCTCTT
CAGAAAAAAGCCATTGAAAGGATGAAGGACACATTAAGAATCACATAT
CAGGACTACATGGCCCCCGACTGCCGATTCCTGACCATTCACCGGGGC
CCAGTTTGGAAAGGACCAGCAAAGCTTCTGTGGAAAGGTGAAGGGGCA
CCCAATTCAATTGCGGCAATCAGTATGAAAAACAACCTTTTCGTTGCA
CCCTTCCAGAACCCGGAGGAGCAGGATGAAGGCTGGCTCATGGGCGTG
CGCAACACACAAATATATACGATAAATGACAAGATACTATCATATACG
CTCAAGAGCCGGATCGCGCTGACGGTGGAAGACTCGCCGTATCCGGGC
CTCCGTTGCCTGTGCATCAAAACTACTTCTGGGATCCACCCGAAAAAC
CTGACCGAGACCAAAATTGATAAATTATGTGTATGGAATAATAAAACC
CTGGGCTATTTCCCCAGTAGCATTGTCCGAGAGGACGAGCCATACGTC
CTGTATGATTTTGTGGCCAGTGGAGATAACACTCTAAGCATAACTAAA
GAAGCCCAAACCAAAAATGGCCAAGGCTGGGTCCCAAGCAACTACATC
GAAGTTATCGCTACTCTGAAAGACGGTCGTAAAATCTGTCTAGATCCG
GAATCGATGGCAGGCAAAAGAGAAATGGTTATCATTACATTTAAGAGC
GACACGGATGAGCTGCAGCTCAAGGCTGGGGATGTGGTGCTGGTGATC
GACACGTGGTTCGACACCATGCTTGGCTTTGCCATATCCGCGTATGCG
GACGCTCCACGTATCAAGAAGATCGTTCAGAAAAAACTGGCTGGTGAC
GAGAAAGATGCTCCAAAAGAATTATTAGACATGTTAGCAAGAGCAGAA
GAGGGTGAAGCTGTTGAGGTCATTCACAAGCTCCTGGACGGCTGGTGG
GATGATGAGCTGCCCATGAAAGAAGGAGACTGCATGACAATCATCCAC
GCAAAAATCATTTTCAAGGTGCAGGCCCAGCACGACTACACGGCCACT
GCCATCAAGGCCTACACTGCTGTGGAGGGGGACGAGGTGTCCCTGCTC
GGATTCAGTGATGGACAGGAAGCCAGGCCTGAAGAAATTGGCTGGTTA
GGCAGAAGCCTGGTCCGGGCGTGCCTGTCCGACGCGGGACACGAGCAC
GGCGAAACATTTCAGGTCGAAGTCCCGGGCAGTCAACATATAGACTCC
GGTGAAAAGCTCCGGGTCTTAGGCTATAATCACAATGGGGAATGGTGT
GTAGACACTTCAAAGATAAAGAAGGTTTGGAGAGTAGGCAAAATGGTG
GTAGTAATACAAGATAATAGTGACATCAAAGTAGTGCCAAGAAGAAAA
GTCATCAGGAAAGACGACGTCACAGGCTACTTCCCGTCCATGTACCTG
GTCTTCCCTGAGAACTTTACCGAGCGAGTATCCATGGCTGTGGCCCTT
TACGTAGAATATATTAATTTTCGGGTTTATTACAGGGACAGCAGAGAT
TCCTTTACCTATGACGACAATGGTAAGACAGGTAGAGGAGCTGTAAGC
TCTGAACAACTTAGCCTTGCACCAGGACAGTTAATATTAATTCTAAAG
TGCGAAATGGTGAAGGTAAAGTTCAAGTATAAGGGTGAAGAGAAAGAA
TGGGGAGGCAGCGTTCAGGGAGATTACTATGGAGATCTGGCTGCTCGC
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After the comparison process was completed, the following results were produced. First, the results of the comparison process as shown in Table 1 and Figure 3. Second, the results of the standard accuracy are shown in Table 2 and Figure 4. The neutropsohic analysis of the data stated that truth, indeterminacy and falsity of DNA sequences with a satisfied results reached to 33% of the truth.

Table 1. The comparison results of the DNA sequence analysis.

DNA NO	Truth	Indeterminacy	Falsity	DNA NO	Truth	Indeterminacy	Falsity
1	0.2708	0	0.7292	**26**	0.3125	0	0.6875
2	0.3333	0	0.6667	**27**	0.2292	0	0.7708
3	0.2292	0	0.7708	**28**	0.2083	0	0.7917
4	0.3125	0	0.6875	**29**	0.2500	0	0.7500
5	0.3125	0	0.6875	**30**	0.2292	0	0.7708
6	0.2083	0	0.7917	**31**	0.3750	0	0.6250
7	0.2500	0	0.7500	**32**	0.2292	0	0.7708
8	0.3333	0	0.6667	**33**	0.3125	0	0.6875
9	0.3125	0	0.6875	**34**	0.2292	0	0.7708
10	0.4375	0	0.5625	**35**	0.3125	0	0.6875
11	0.2083	0	0.7917	**36**	0.1875	0	0.8125
12	0.1875	0	0.8125	**37**	0.3125	0	0.6875
13	0.2292	0	0.7708	**38**	0.2500	0	0.7500
14	0.4167	0	0.5833	**39**	0.2917	0	0.7083
15	0.2292	0	0.7708	**40**	0.3125	0	0.6875
16	0.2083	0	0.7917	**41**	0.2917	0	0.7083
17	0.1458	0	0.8542	**42**	0.2708	0	0.7292
18	0.1458	0	0.8542	**43**	0.2917	0	0.7083
19	0.2292	0	0.7708	**44**	0.3333	0	0.6667
20	0.3333	0	0.6667	**45**	0.3125	0	0.6875
21	0.2292	0	0.7708	**46**	0.2292	0	0.7708
22	0.2917	0	0.7083	**47**	0.3125	0	0.6875
23	0.2917	0	0.7083	**48**	0.1250	0	0.8750
24	0.2708	0	0.7292	**49**	0.2292	0	0.7708
25	0.2708	0	0.7292	**50**	0.2917	0	0.7083

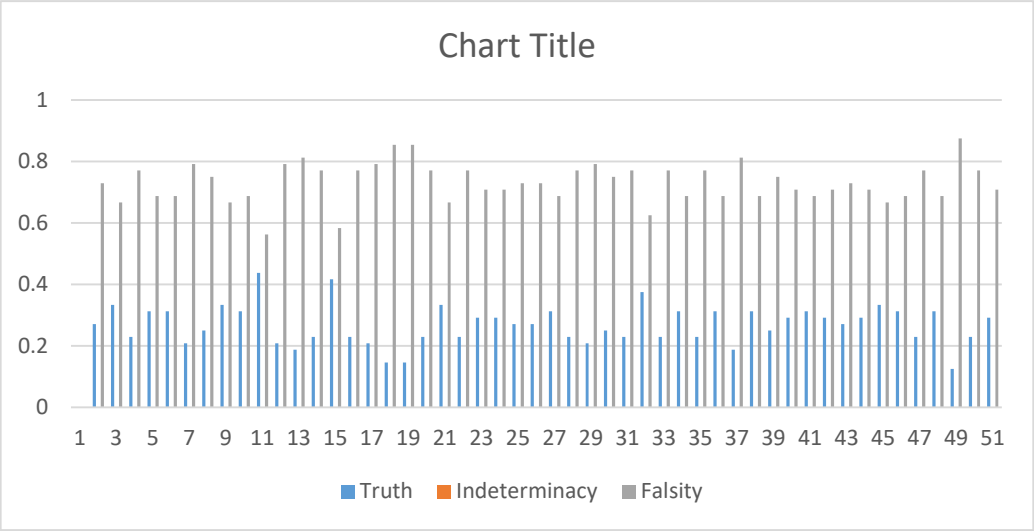

Figure 3. The comparison results chart.

Table 2. The accuracy results of DNA sequence analysis

DNA NO	Accuracy T (%)	Accuracy F (%)	DNA NO	Accuracy T (%)	Accuracy F (%)
1	0.2708	0.7292	26	0.3125	0.6875
2	0.3333	0.6667	27	0.2291	0.7708
3	0.2292	0.7708	28	0.2083	0.7916
4	0.3125	0.6875	29	0.2500	0.7500
5	0.3125	0.6875	30	0.2291	0.7708
6	0.2083	0.7917	31	0.3750	0.6250
7	0.2500	0.7500	32	0.2291	0.7708
8	0.3333	0.6667	33	0.3125	0.6875
9	0.3125	0.6875	34	0.2291	0.7708
10	0.4375	0.5625	35	0.3125	0.6875
11	0.2083	0.7917	36	0.1875	0.8125
12	0.1875	0.8125	37	0.3125	0.6875
13	0.2292	0.7708	38	0.2500	0.7500
14	0.4167	0.5833	39	0.2916	0.7083
15	0.2292	0.7708	40	0.3125	0.6875
16	0.2083	0.7917	41	0.2916	0.7083
17	0.1458	0.8542	42	0.2708	0.7291
18	0.1458	0.8542	43	0.2916	0.7083
19	0.2292	0.7708	44	0.3333	0.6666
20	0.3333	0.6667	45	0.3125	0.6875
21	0.2292	0.7708	46	0.2291	0.7708
22	0.2917	0.7083	47	0.3125	0.6875
23	0.2917	0.7083	48	0.1250	0.8750
24	0.2708	0.7292	49	0.2291	0.7708
25	0.2708	0.7292	50	0.2916	0.7083

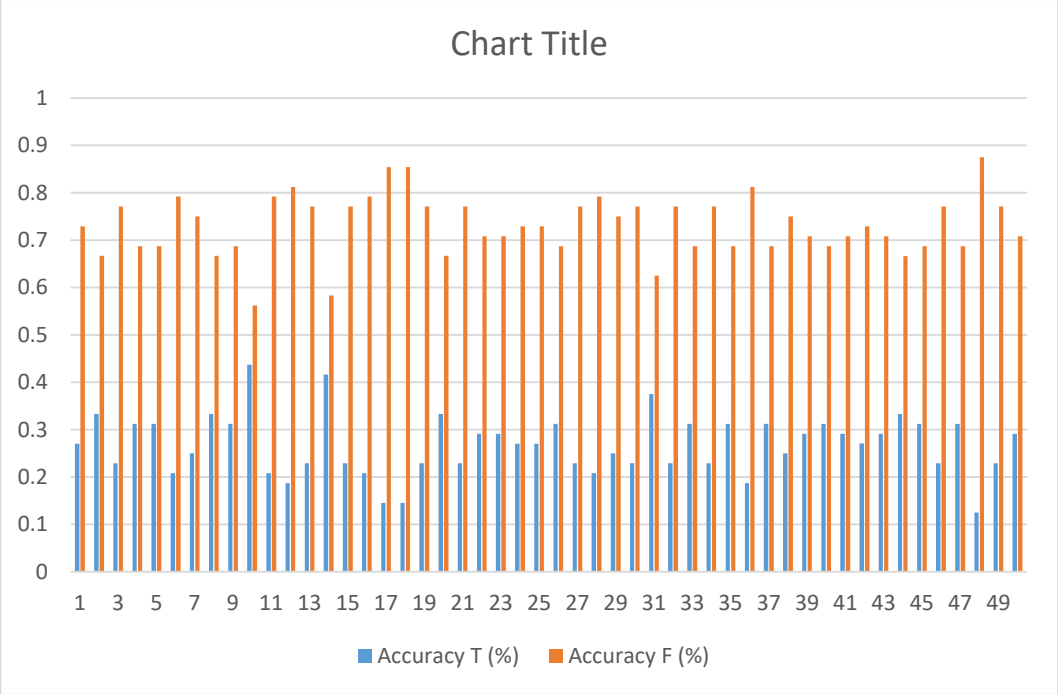

Figure 4. The charts indicate the accuracy results.

5. CONCLUSION

The application of neutrosophic theory to ascertain measures of similarity, dissimilarity, and neutrality has proven to be highly effective. The conducted experiment yielded fruitful outcomes, demonstrating a robust accuracy standard for both similarity and dissimilarity measurements. The encoding of similarity as "T" and dissimilarity as "F" resulted in excellent outcomes, highlighting the efficacy of the neutrosophic approach in capturing nuanced relationships. However, the potential of neutrosophic theory extends beyond its current applications, and there exists significant room for further development. Future endeavors will involve refining the theory and devising innovative algorithms to enhance its practical utility. To achieve this, we propose the integration of advanced artificial intelligence techniques, including deep learning and random forest methodologies, synergistically with neutrosophic theory. This amalgamation aims to optimize the theory's application in the field of biomedical informatics, fostering more nuanced and accurate insights into complex datasets. The fusion of these cutting-edge technologies holds promise for advancing the boundaries of knowledge and contributing to the evolution of sophisticated tools for data analysis in biomedical research.

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