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Integration between Bioinformatics Algorithms and Neutrosophic Theory

Romany M. Farag[1]*, Mahmoud Y. Shams[2], Dalia A. Aldawody[3], Huda E. Khalid[4], Hazem M. El-Bakry[5] and Ahmed A. Salama[6]

[1] Dept. of Math and Computer Science, Faculty of Science, Port Said Univ., Egypt; blackfox2100@gmail.com

[2] Dept. of Machine Learning, Faculty of Artificial Intelligence, Kafrelsheikh University, Egypt; mahmoud.yasin@ai.kfs.edu.eg

[3] Dept. of Math and Computer Science, Faculty of Science, Port Said Univ., Egypt; drdaliaawad@yahoo.com

[4] Telafer University, The Administration Assistant for the President of the Telafer University, Telafer, Iraq; https://orcid.org/0000-0002-0968-5611, dr.huda-ismael@uotelafer.edu.iq

[5] Dept. of Information Systems, Faculty of Computer and Information Sciences Mansoura University Egypt; elbakry@mans.edu.eg

[6] Dept. of Math and Computer Science, Faculty of Science, Port Said University, Egypt;drsalama44@gmail.com

Correspondence: blackfox2100@gmail.com

Abstract: This paper presents a neutrosophic inference model for bioinformatics. The model is used to develop a system for accurate comparisons of human nucleic acids, where the new nucleic acid is compared to a database of old nucleic acids. The comparisons are analyzed in terms of accuracy, certainty, uncertainty, neutrality, and bias. The proposed system achieves good results and provides a reliable standard for future comparisons. It highlights the potential of neutrosophic inference models in bioinformatics applications. Data mining and bioinformatics play a crucial role in computational biology, with applications in scientific research and industrial development. Biological analysts rely on specialized tools and algorithms to collect, store, categorize, and analyze large volumes of unstructured data. Data mining techniques are used to extract valuable information from this data, aiding in the development of new therapies and understanding genetic relationships between organisms. Recent advancements in bioinformatics include gene expression tools, Bio sequencing, and Bio databases, which facilitate the extraction and analysis of vital biological information. These technologies contribute to the analysis of big data, identification of key bioinformatics insights, and generation of new biological knowledge. Data collection, analysis, and interpretation in this field involves the use of modern technologies such as cloud computing, machine learning, and artificial intelligence, enabling more efficient and accurate results. Ultimately, data mining and bioinformatics enhance our understanding of genetic relationships, aid in developing new therapies, and improve healthcare outcomes.

Keywords: DNA; Neutrosophic Inference Model; Sequence Analysis; Artificial Intelligence.

1. Introduction

Genomics and proteomics sciences have developed rapidly in recent years, accumulating a huge amount of biological data. Therefore, this data needs complex computational analysis to draw useful conclusions from it. Computational biology or bioinformatics is an interdisciplinary discipline aimed at interpreting and analyzing biological data using computational technology and analytical tools [1-9]. Bio-data management is a crucial research area that has gained significant importance in recent years, primarily due to the rapid expansion of bioinformatics. Bioinformatics encompasses various tasks such as mapping and analyzing DNA and protein sequences, which are utilized to compare and match sequences. Additionally, 3D models can be generated to visualize protein structures. Bioinformatics employs algorithms, databases, information retrieval systems, artificial intelligence techniques, and other tools to effectively manage, analyze, and interpret biological information. The significance of this field stems from the accumulation, transmission, and growth of information within biological systems. Bioinformatics operates in parallel with disciplines like biophysics and biochemistry, focusing on the management, analysis, retrieval, and storage of biological data. Information processing is integrated into highly specialized databases designed to handle this type of data. These databases are maintained to develop and provide researchers with user-friendly interfaces for accessing existing data and contributing new data. The field of bioinformatics aims to analyze and comprehend biological information, transforming it into valuable insights for scientific research and the development of treatments and medicines [1]. The field of bioinformatics provides support for the creation, organization, and updating of databases storing biological data, as well as the necessary tools for analyzing this information. These data can be used to discover and develop gene-based drugs. Gene patterns within the genome are analyzed by comparing biological structures such as DNA and proteins and analyzing sequencing patterns. Indeed, DNA and proteins are fundamental components of every living organism. DNA carries genetic information that is passed from generation to generation, determining individual characteristics such as hair color, eye color, and skin tone, among others. Proteins, on the other hand, provide structure and function to the body, assisting in the formation of tissues and organs and regulating cellular and chemical processes in the body [2]. DNA is composed of a sequence of nucleotides strung together, carrying genetic information in its nucleotide arrangement. When this information is translated in a process called translation, chains of proteins are produced that impact the structure and function of the body. In fact, DNA can be considered a code or guide for protein molecules, as DNA contains instructions for translating and producing different proteins that influence individual traits. Thus, DNA and proteins work together in the creation and maintenance of living organisms [3]. Computer modeling plays a crucial role in studying DNA, proteins, and biological data. Static and dynamic modeling are used to analyze interactions between proteins, nucleic acids, and peptides. Various software and tools are employed to create these models and analyze biological data. The study of DNA and proteins requires collaboration between the fields of Biology, Computer Science, Statistics, Mathematics, and Physics, utilizing different tools and techniques to gather and examine data accurately and efficiently [4].

Traditional sequence alignment techniques face several challenges when dealing with large genomes such as the human genome. They consume significant central processing unit (CPU) and memory resources, as well as time, to perform computational operations. Additionally, the use of multiple sequencing analysis techniques may result in gaps in the results that need to be filled later. To minimize these gaps and handle large genomes more effectively, the shotgun sequencing approach is considered the most efficient [5]. Several sequence comparison packages have been

developed for DNA and protein sequence alignment, such as FASTX, FASTY, TFASTX, and TFASTY. A search table is used to identify matching regions between DNA and protein sequences, which are then further examined using matrices like the BLOSUM50 scoring matrix. Similar regions are merged, and gaps are filled, followed by the calculation of the optimal alignment solution. The algorithms used in DNA and protein sequence comparison include those mentioned in the research, such as BLAST and Doplots. There are multiple algorithms used for translation and comparison of sequences between proteins and DNA. Sequences can be compared based on physical similarity or evolutionary relationship. Various algorithms are employed to perform sequence alignment, such as Dotplots and BLAST, which can detect local alignments and find matching sequences in large protein databases. Several programs can be used to perform annotations for sequence analysis, which can identify genes and other biological features within DNA sequences. Dealing with complexities and repetitive regions in DNA sequences can be challenging, thus filtering techniques can be used to reduce noise and increase alignment accuracy. The mentioned research highlights BLAST and Dotplots as examples of algorithms used in sequence comparison [7]. The algorithms used for sequence comparison include local and global algorithms, which are used for sequence alignment. Sequence alignment helps identify identities and similarities between sequences, aiding in determining the relationship between different organisms and predicting the biological functions of genes and proteins. It also helps identify potential mutation sites and variations in sequences, contributing to the understanding of genetic diseases and the development of genomics-based treatments. In general, genome and sequence comparisons are employed in various biological and medical applications and are essential for understanding the genetic relationships between different organisms [8].

2. Previous works

Searching through a database of known modification sites makes it simple to find modification sites. But sometimes using plain database scanning isn't enough, and using neural networks yields superior outcomes. Comparable methods are applied to the prediction of active sites; the neural method makes use of nearest-neighbor classifiers and training data to predict protein modification sites. These methods provide efficient ways to determine locations that are relevant to biology and forecast the functions of proteins that have been changed [10].

2.1 Data mining in proteomics

Protein characteristics including shape, solubility, and stability have all been predicted using neural networks. Protein domain predictions can be achieved by using hierarchical clustering techniques. Numerous developments have been achieved in the field of protein secondary structure prediction through the application of data mining techniques. Furthermore, methods based on information theory, Bayesian theory, nearest neighbors, and neural networks have been developed to provide more precise statistical approaches and methods. For protein interactions, the density-based clustering technique (GDBSCAN) might be employed [11].

It is now possible to predict protein characteristics like stability, solubility, and structure using neural networks. Protein domain predictions are made using hierarchical clustering techniques. Many methods have been developed in the field of protein secondary structure prediction using data mining approaches. Moreover, preliminary statistical methods and improved methods based on

neural networks, information theory, Bayesian theory, and nearest neighbors have been described. For protein interactions, the density-based clustering technique (GDBSCAN) can be applied.

Based on both spatial and non-spatial properties, this algorithm can cluster point objects and spatial bodies. It can be applied to the design of biological catalysts, nanomachines, and drug targets' three-dimensional architectures, among other things. An atomic-level computational protocol for modeling and predicting protein structures has been devised.

In terms of protein expression analysis, sequencing and protein expression analysis are two methods used to quantify gene expression. However, because proteins typically serve as the last agents in a cell's activity chain, protein expression is thought to be one of the best measures of true gene activity. High-throughput mass spectrometry (HT-MS) measurements and protein microarray data can shed light on the proteins included in a biological sample. Understanding HT-MS and protein expression analysis data involves computational biology.

The main structure, or amino acid sequence, of a protein can be easily ascertained from the associated gene sequence to predict the protein's structure. Usually, the protein's fundamental structure is found only in its original environment. comprehension protein function requires a comprehension of this structural information. The three main categories of structural information are secondary, tertiary, and quaternary structures. Predicting the structure of proteins is one of the most important uses, along with creating new enzymes and drugs. In terms of protein-protein interactions, X-ray crystallography and Nuclear Magnetic Resonance (NMR) methods have been used to determine the three-dimensional structures of thousands of proteins over the past few decades. Biologists can predict potential interactions between proteins based on these three-dimensional structures without needing to perform actual protein interaction experiments.

Various methods have been developed to address the protein-protein docking problem [12]. Furthermore, several algorithms have been proposed to solve the multiple sequence alignment (MSA) problem in literature. These algorithms are classified based on the methodology they employ, including the Carrillo-Lipman MSA algorithm that relies on dynamic programming (DP). DP is a methodology aimed to solve complex computational problems and optimize multiple sequences in a gradual and efficient manner. There are also other algorithms that rely on heuristics and probabilities to solve the MSA problem. The choice of the appropriate algorithm depends on the nature of the problem and specific application requirements [13]. Generally speaking, the objective of DP algorithms is to break the bigger problem down into smaller subproblems and solve each subproblem independently utilizing the answers to the earlier subproblems. Pairwise alignment subproblems make up the MSA problem in the context of the Carrillo-Lipman MSA algorithm. By resolving these subproblems, the goal is to discover thorough alignment solutions for the whole problem. The majority of contemporary MSA algorithms use a progressive alignment strategy. These algorithms' primary goal is to create a guide tree by gradually adding target sequences to it using the progressive alignment technique. Through this approach, the non-aligned sequences are then sequentially aligned [14]. The alignment tool Clustal-Omega uses the profile hidden Markov model (HMM) approach in conjunction with a guide tree to align a set of sequences. Its main purpose upon development was to align protein sequences. For sequence alignment, the Fast Fourier Transform (MAFFT) method also makes use of a related idea. On the other hand, nucleic acid sequencing has

also suggested using it [15]. While MAFFT and Clustal-Omega are thought to be quicker in creating multiple sequence alignments, they are not as accurate as some other programs, such T-Coffee. Although T-Coffee requires more time to align, the precision is higher [16]. Using a position matrix rather than a distance matrix to accurately insert gaps in sequences, the PoMSA (Position-specific Scoring Matrix-based Alignment) technique stands out for increasing alignment efficiency. PoMSA's performance has been assessed with a variety of datasets, including SMART, OXBench, and BAliBASE. Studies have demonstrated that PoMSA outperforms other contemporary algorithms, such as Clustal-Omega, MAFFT, and MUSCLE, in terms of alignment precision [17].

2.2 Neutrosophic Theory in Biomedical informatics:

The proposed Neutrosophic Gaussian Mixture Model (NGMM) is aimed at classifying Breast Ultrasound images. The process involves feature extraction using a Deep Neural Network (DNN), computation of three probability functions using Neutrosophic Logic, and the development of an enhanced Expectation Maximization algorithm that incorporates this logic. The performance of NGMMs is evaluated using a new dataset that combines two public datasets, and the results indicate that NGMMs outperform DNN-based methods and Gaussian Mixture Models (GMMs) in terms of six metrics [18]. In our proposed method, the issue of missing and anomalous data was addressed by utilizing Neutrosophic Logic and inverse Lagrangian interpolation for data processing. The dataset was reshaped using these techniques. Experiments on a breast cancer dataset obtained from Al-Bayrouni Hospital were conducted by employing a Support Vector Machine (SVM) classifier with an orthogonal Legender kernel. The results of this study demonstrated an improved accuracy rate of 97%, surpassing the performance of the classical SVM algorithm [19]. A hybrid neutrosophic set of single values used to measure vector similarity. The measure is applied in the context of multiple-attribute decision-making problems. To validate its effectiveness, the proposed method is compared to existing methods using a numerical example related to medical diagnosis. The results highlight the effectiveness, simplicity, and applicability of the proposed measure. It is demonstrated that the measure can be applied to various decision-making problems in refined neutrosophic environments, including fault diagnosis, cluster analysis, data mining, and investment [20]. The simplification of two complex similarity measures proposed by Ye and Fu into more straightforward distance measures, specifically the maximum norm and arithmetic mean. The study demonstrates that these simplified measures can be effectively used in medical consultations, providing reliable results. Moreover, utilizing these simpler measures also simplifies the computational aspect of the analysis [21].

In this paper, the focus is on estimating the ratio of two means within the framework of neutrosophic theory. The study considers the uncertainty associated with an auxiliary variable, which is modeled as a neutrosophic variable. The bias and variance of the proposed estimator is further derived for a selected sample using Simple Random Sampling. The aim is to provide insights into the estimation process and assess the performance of the proposed estimator within the neutrosophic theory framework [22]. A novel Multi-Criteria Decision-Making (MCDM) method is also proposed, which utilizes single-valued neutrosophic sets in conjunction with the Decision-Making Trial and Evaluation Laboratory (DEMATEL) technique. The method is applied to a subcontractor selection problem, and the results reveal that "Experience" and "Quality" are the most influential criteria, while "Completing on Time" has no effect on the decision-making process [23].

Another aspect of the paper focuses on the lattice structures of neutrosophic theories. It is demonstrated that Zhang-Zhang's Pinang bipolar fuzzy set can be considered as a subclass of the Single-Valued Bipolar Neutrosophic Set. Furthermore, the pair structure is shown to be a specific case of refined neutrosophy, which allows for any finite or infinite number of neutralities or sub-indeterminacies.

In the brain tumor segmentation study, the use of wavelet transform as an auxiliary element in deep learning networks was investigated. The results indicated that the Daubechies1 wavelet function was the most effective in improving network performance while managing computational overload. The choice of wavelet function should be based on specific problem requirements and considerations such as computational load, processing time, and performance [25]. In this work, a Neutrosophic Cognitive Map (NCM) model was presented to aid clinical judgments on the management of pregnant patients with cardiovascular disorders. The use of Triangular Neutrosophic Numbers led to improved diagnosis and treatment accuracy by measuring the degrees of truth, indeterminacy, and falsity in experts' choices. The model was evaluated by professionals based on its accuracy in interpreting results and its capacity to interrelate various concepts. It was validated using data from the Cardiovascular and Pregnancy National Service/Gynecology and Obstetrics Hospital Ramón Gonzales Coros. Future work aims to expand the application of this model to other diseases and construct the map using machine learning techniques [26]. The novel outranking method for bipolar neutrosophic environments: multi-attribute decision-making difficulties. The method consists of defining outranking relations for bipolar neutrosophic numbers based on ELECTRE, going into great depth into the features of these relations, and creating a ranking scheme based on these relations. An actual case is used to demonstrate the approach's efficacy. Furthermore, a straightforward, practical, and efficient multi-criteria decision-making approach based on outranking relations is created for bipolar neutrosophic sets in order to minimize the loss of evaluative information. Subsequent investigations will delve into more effective techniques for making decisions and broaden the utilization of these ideas in the domains of engineering, game theory, multi-agent systems, and decision-making [27]. A diagnostic decision-making strategy for viral disease diagnosis is presented, which utilizes Interval-valued trapezoidal neutrosophic fuzzy numbers (IVTrNFN) and Multiple Attribute Decision Making (MADM). The proposed framework incorporates information entropy to determine attribute weights, grey relational analysis, and projection method to assess the relative closeness of Preferred Interval Sets (PIS) and is verified using an example of viral disease [28]. There are six methods for finding the correlation between fingerprint images using the neutrosophic technique, these methods involve the comparison of fingerprint images with a focus on basic neutrosophic operations, fuzzy concepts, and minutiae matching. The proposed methods demonstrate good accuracy across all image sizes and provide additional information when detecting relationships at high-level images. Future work involves applying machine learning techniques to classify biometric images [29]. Fingerprint matching is a challenging task due to the variations in fingerprint images of the same finger and the similarities between fingerprint images from different fingers. These variations are referred to as intraclass variations and interclass similarity. One of four methods is usually used by fingerprint-matching algorithms: phase matching, minutiae matching, picture correlation, and skeleton matching. Although the fuzzy idea has been applied to fingerprint matching in the past, the neutrosophic model—a sophisticated mathematical framework—expands

its application to practical issues. It is feasible to find correlation patterns in fingerprint photos by taking use of their neutrosophic link. This article analyzes fingerprint photos using the neutrosophic technique and suggests six ways to build associations in the image domain using the neutrosophic approach. Three different analysis approaches are used in the paper. The first methodology is the same as that found in [46]. The concept of probabilistic linguistic term sets (PLTSs) is a powerful tool for modeling qualitative assessment information using linguistic terms associated with probabilities or weights. The authors highlighted the lack of research on correlation coefficient and clustering analysis for PLTSs and proposed correlation coefficient formulas to measure the relationship between two PLTSs. These formulas are then utilized to develop two novel clustering algorithms for grouping PLTSs [30]. The proposed methodology put an analogical reasoning framework for mining negative patterns of life events (NLE-LPs) from psychiatric consultation documents. The framework combines word representation approaches (skip-gram and continuous bag-of-words) with pattern inference methods (cosine similarity and cosine multiplication similarity) to extract precise NLE-LPs. Experimental results demonstrate the framework's superiority over traditional methods (positive pairwise mutual information and hyperspace analog to language). The superior results are obtained using CBOW with cosine similarity. The proposed framework's word embedding, and inference engine can also enhance the HAL model. Overall, the framework offers a simple matching function that improves the HAL model's mining performance [31]. The authors of [31] develop a disease risk analysis and prediction model for schizophrenia patients using an automatic Analytic Hierarchy Process (AHP) framework called Auto AHP. The model utilizes over 15 million follow-up records and integrates mental health information and intelligent data processing. Key factors for risk prediction are identified, including changes in mental health policy, public support, regional differences, patient gender, compliance, and social function. The Auto AHP framework achieves high precision, recall, and F1 scores and outperforms general models in risk prediction. It can assist in the clinical analysis of disease risk factors and support decision-making in chronic disease management for schizophrenia patients [49].

Fuzzy systems are widely used in decision-making problems to handle uncertain information. Evolutionary fuzzy systems have been developed using various fuzzy representations such as intuitionistic fuzzy, hesitant fuzzy, and neutrosophic representations. Complex numbers are also utilized to capture compound features and convey multifaceted information in fuzzy and intuitionistic fuzzy sets. However, the existing order relations in these systems have limitations, such as not being total order relations or being defined based on intermediate functions. These limitations make it challenging to build and ensure important properties of logical systems [32]. The introduction of the paper discusses the distinctions between inter-, trans-, multi-, and cross-disciplinary research, both theoretically and in the context of rural and mountain tourism. The main section of the paper presents a detailed presentation, starting with the research methodology and results in various disciplines such as economics, statistics, econometrics, sociology, demography, psychology, anthropology, linguistics, ethnography, folklore, and culture. The section also highlights the specific approaches used in programs, projects, and tourism policies. The central question throughout the main section and the conclusion of the article revolves around the current state of Romanian rural and mountain tourism and proposes solutions to enhance the economic development of Romania through the promotion of rural and mountain tourism [33]. The first algorithm is a fuzzy clustering

algorithm, while the second algorithm is an orthogonal clustering algorithm. To validate their proposed clustering algorithm, the authors provide a practical example involving the analysis of general higher education levels in different regions of China. The results demonstrate the usability and effectiveness of their approach. The neutrosophic theory was established in 1998 by Florentin Smarandache, focusing on analyzing the origins of certainty, uncertainty, and neutrality. It uses these ideas to address different intellectual spectra [34, 35]. The neutrosophic theory analyzes the aspects of reality, such as contradiction, compatibility, and incompatibility, by studying the interactions between entities. It identifies and analyzes compatibility, incompatibility, and neutrality between these entities [35]. The theory finds applications in diverse fields, including mathematics, artificial intelligence, image processing, statistics, decision-making, engineering, sciences, and logic [36]. DNA topology refers to the shape and arrangement of DNA molecules and is important for biological processes like transcription and recombination [37]. Topoisomerases are enzymes that alter DNA topology, influencing its function [38] [39]. Neuronal DNA topology applies neutrosophic theory to analyze DNA sequences [40]. It represents DNA sequences as neutrosophic groups, where each nucleotide has degrees of belonging, non-affiliation, and indeterminacy [41] [42]. Neutrosophic crosstalk in neuronal DNA topology helps identify important and stable nucleotides across different DNA sequences [43]. It analyzes the intersection of neutrosophic groups to identify significant nucleotides [44] [45]. The neutrosophic intersection is useful for identifying conserved and critical regions in DNA sequences. Nucleotides with high membership scores indicate their significance [46] [47]. Neutrosophic junction identifies interactions and associations between nucleotides at different positions in the DNA sequence [49]. It helps identify functionally or structurally related nucleotides [50] [51]. Neutrosophic junction is a valuable tool for identifying important properties in DNA sequences, including conserved regions, nucleotide interactions, and functional or structural elements [52]. Neutrosophic junction allows the handling of uncertain and incomplete data in DNA analysis [53]. It uses neutrosophic populations and groups to represent uncertainty and ambiguity [54,55]. Neutral group theory and fuzzy set theory can represent the 3D structures of DNA molecules and accommodate their dynamic nature and uncertain data [56] [57] [58]. Fuzzy phase topological structures, such as nucleosomes and G-quadruplex structures, play vital roles in DNA function. Representing them using neutral and fuzzy groups helps understand their organization, effects of mutations, and potential drug targets [59] [60] [61-67].

3. Results (examples/case studies related to the proposed work)

Through previous studies, an algorithm was designed relying entirely on bioinformatics algorithms with the neutrosophic theory, in a precise sense, the algorithm of integration of bioinformatics techniques with the neutrosophic theory, and the results were quite impressive in relation to the bioinformatics algorithms that were mentioned in previous works.

3.1 Algorithm design method

Where the algorithm was designed to compare nucleic acids, where the nucleic acid is compared to a group of nucleic acids, as shown in Figure 1, where the new DNA is compared to the existing nucleic acids inside the data warehouse.

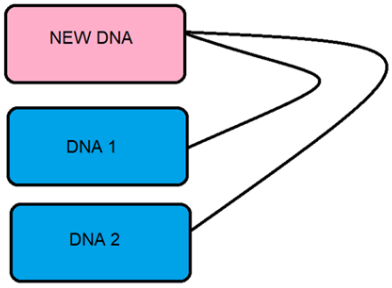

Figure 1. The new DNA from the data warehouse DNA1 and DNA2.

Then the three values are extracted, and they are similarity, neutrality, and dissimilarity (T & I & F) then the results are printed in a table, and then the degrees of accuracy are calculated for the three values, and Figure No. 2 shows the design method.

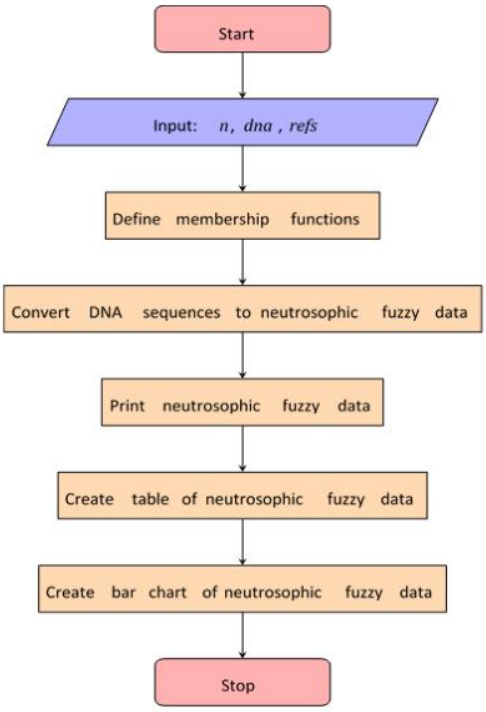

Figure 2. The flow chart of the proposed methodology.

3.2 Algorithm working

DNA Sequence Comparison

Require: new sequence: the new DNA sequence

Require: input file: the path to the text file

1. Procedure Read Sequences from File (file path):
   - Open the file at the specified file path.
   - Read the sequences from the file.
   - Split the sequences into individual strings.
   - Return the sequences.

2. Procedure Insert Gaps (sequences):
   - Create an empty list called modified sequences.
   - Calculate the maximum length as the maximum length of the sequences.
   - For each sequence (seq) in the sequences:
     - If 'C' exists in seq, replace 'C' with 'C-'.
     - If 'G' exists in seq, replace 'G' with 'G-'.
     - Append '-' characters to seq to make its length equal to the maximum length.
     - Append seq to modified sequences.
   - Return modified sequences.

3. Procedure Compare Sequences (seq1, seq2):
   - Initialize match count, mismatch count, and gap count as 0.
   - For each corresponding character (char1, char2) in seq1 and seq2:
     - If char1 is equal to char2, increment the match count by 1.
     - Else if char1 or char2 is '-', increment the gap count by 1.
     - Otherwise, increment the mismatch count by 1.
   - Return the match count, mismatch count, and gap count.

4. Procedure Calculate Similarity (seq1, seq2):
   - Calculate the total length as the sum of the lengths of seq1 and seq2.
   - Invoke the Compare Sequences procedure to get the match count, mismatch count, and gap count.
   - Calculate the similarity percentage as (total length - mismatch count) × 100 / total length.
   - Calculate the mismatch percentage as (total length - match count) × 100 / total length.
   - Calculate the neutrality percentage as (total length - gap count) × 100 / total length.
   - Calculate the similarity accuracy as total length - match count.
   - Calculate the mismatch accuracy as total length - mismatch count.
   - Calculate the neutrality accuracy as total length - gap count.

- Return the similarity percentage, mismatch percentage, neutrality percentage, similarity accuracy, mismatch accuracy, and neutrality accuracy.

5. If the input file exists, perform the steps between lines 46 and 48.

This algorithm is designed to compare DNA sequences. It includes procedures for reading sequences from a file, inserting gaps in sequences, comparing sequences to calculate numbers of matches, numbers of mismatches, and numbers of gaps, and calculating similarity and precision information. The algorithm relies on the basic concepts of DNA sequences and uses mathematical operations to compare and analyze them. Figure 3 shows the flow chart of the pseudo-code of the algorithm.

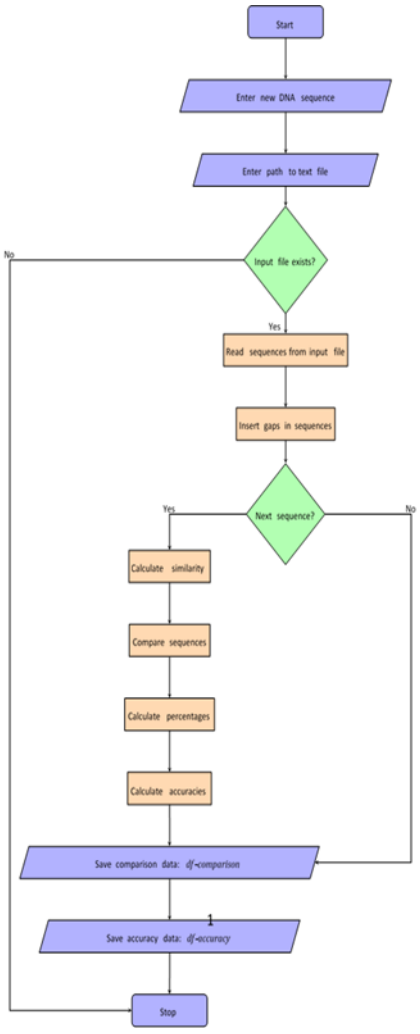

Figure 3. The flow chart steps of the pseudo-code of DNA sequences with neutrosophic.

4. The Results

The data set was obtained from the International Gen Bank (NPCI), where 50 nucleic acids were obtained, and each acid contains 49 letters of DNA. Table 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:

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

Following completing the comparison process, the following results were produced. Table 1 presents the results of the comparison process alongside the results of the three ratios. Table 2 shows the results of the accuracy standard.

Table 1. The evaluation of total length with gap amount and determination of neutrality (F).

Total Length	Match Count	Mismatch Count	Gap Count	Similarity (T)%	Mismatch (I)%	Neutrality (F)%
118	9	25	14	78.8135593	92.37288136	88.13559322
121	12	21	15	82.6446281	90.08264463	87.60330579
116	10	22	16	81.0344828	91.37931034	86.20689655
124	7	24	17	80.6451613	94.35483871	86.29032258
119	7	25	16	78.9915966	94.11764706	86.55462185
120	11	22	15	81.6666667	90.83333333	87.5
118	8	23	17	80.5084746	93.22033898	85.59322034
124	8	22	18	82.2580645	93.5483871	85.48387097
115	5	29	14	74.7826087	95.65217391	87.82608696
112	6	30	12	73.2142857	94.64285714	89.28571429
120	9	24	15	80	92.5	87.5
119	11	22	15	81.512605	90.75630252	87.39495798
116	9	25	14	78.4482759	92.24137931	87.93103448
124	3	29	16	76.6129032	97.58064516	87.09677419
116	10	24	14	79.3103448	91.37931034	87.93103448
112	8	27	13	75.8928571	92.85714286	88.39285714
127	12	18	18	85.8267717	90.5511811	85.82677165
121	4	28	16	76.8595041	96.69421488	86.7768595
115	6	29	13	74.7826087	94.7826087	88.69565217
127	8	22	18	82.6771654	93.7007874	85.82677165

111	12	25	11	77.4774775	89.18918919	90.09009009
128	5	24	19	81.25	96.09375	85.15625
120	4	28	16	76.6666667	96.66666667	86.66666667
111	7	29	12	73.8738739	93.69369369	89.18918919
123	7	24	17	80.4878049	94.30894309	86.17886179
114	12	22	14	80.7017544	89.47368421	87.71929825
121	10	21	17	82.6446281	91.73553719	85.95041322
117	5	29	14	75.2136752	95.72649573	88.03418803
114	3	31	14	72.8070175	97.36842105	87.71929825
125	10	20	18	84	92	85.6
123	6	25	17	79.6747967	95.12195122	86.17886179
119	6	27	15	77.3109244	94.95798319	87.39495798
113	14	23	11	79.6460177	87.61061947	90.26548673
124	3	29	16	76.6129032	97.58064516	87.09677419
119	8	24	16	79.8319328	93.27731092	86.55462185
121	10	23	15	80.9917355	91.73553719	87.60330579
120	9	22	17	81.6666667	92.5	85.83333333
131	9	19	20	85.4961832	93.12977099	84.73282443
121	9	21	18	82.6446281	92.56198347	85.12396694
119	8	25	15	78.9915966	93.27731092	87.39495798
115	8	27	13	76.5217391	93.04347826	88.69565217
111	9	28	11	74.7747748	91.89189189	90.09009009
122	10	22	16	81.9672131	91.80327869	86.8852459
122	12	20	16	83.6065574	90.16393443	86.8852459
112	7	30	11	73.2142857	93.75	90.17857143
118	12	22	14	81.3559322	89.83050847	88.13559322
113	13	20	15	82.300885	88.49557522	86.72566372
114	15	20	13	82.4561404	86.84210526	88.59649123
124	10	21	17	83.0645161	91.93548387	86.29032258

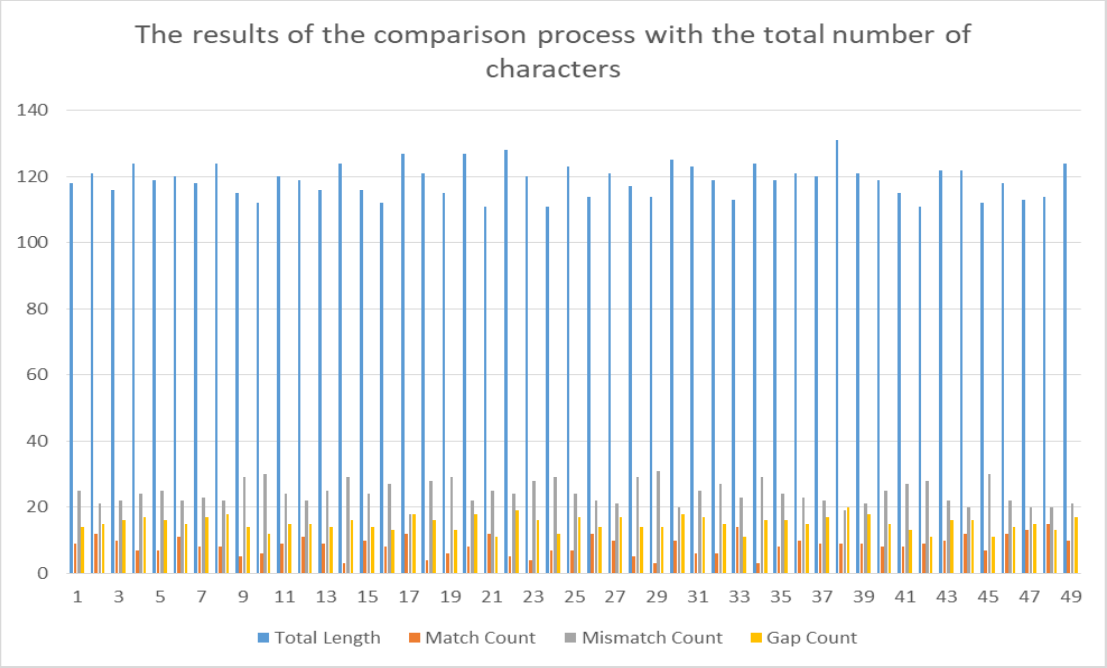

Figure 4. the results of the comparison process with the total number of characters.

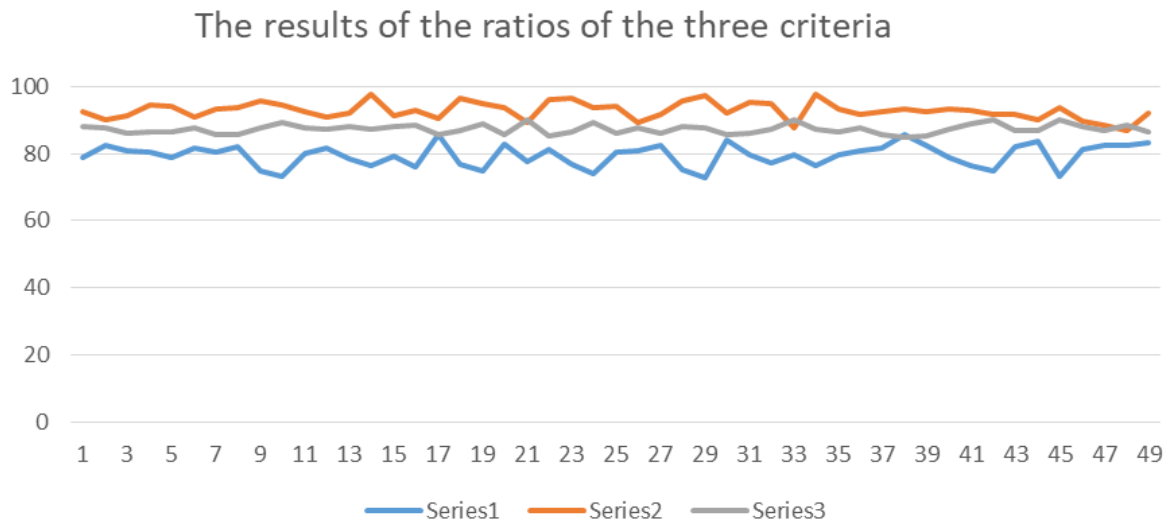

Figure 5. The results of the ratios of the three criteria

Table 2. The similarity accuracy with the mismatch and neutrality determination

Similarity Accuracy%	Mismatch Accuracy	Neutrality Accuracy%
78.81355932	92.37288136	88.13559322
82.6446281	90.08264463	87.60330579
81.03448276	91.37931034	86.20689655

80.64516129	94.35483871	86.29032258
78.99159664	94.11764706	86.55462185
81.66666667	90.83333333	87.5
80.50847458	93.22033898	85.59322034
82.25806452	93.5483871	85.48387097
74.7826087	95.65217391	87.82608696
73.21428571	94.64285714	89.28571429
80	92.5	87.5
81.51260504	90.75630252	87.39495798
78.44827586	92.24137931	87.93103448
76.61290323	97.58064516	87.09677419
79.31034483	91.37931034	87.93103448
75.89285714	92.85714286	88.39285714
85.82677165	90.5511811	85.82677165
76.85950413	96.69421488	86.7768595
74.7826087	94.7826087	88.69565217
82.67716535	93.7007874	85.82677165
77.47747748	89.18918919	90.09009009
81.25	96.09375	85.15625
76.66666667	96.66666667	86.66666667
73.87387387	93.69369369	89.18918919
80.48780488	94.30894309	86.17886179
80.70175439	89.47368421	87.71929825
82.6446281	91.73553719	85.95041322
75.21367521	95.72649573	88.03418803
72.80701754	97.36842105	87.71929825
84	92	85.6
79.67479675	95.12195122	86.17886179
77.31092437	94.95798319	87.39495798
79.6460177	87.61061947	90.26548673
76.61290323	97.58064516	87.09677419
79.83193277	93.27731092	86.55462185
80.99173554	91.73553719	87.60330579
81.66666667	92.5	85.83333333
85.49618321	93.12977099	84.73282443

82.6446281	92.56198347	85.12396694
78.99159664	93.27731092	87.39495798
76.52173913	93.04347826	88.69565217
74.77477477	91.89189189	90.09009009
81.96721311	91.80327869	86.8852459
83.60655738	90.16393443	86.8852459
73.21428571	93.75	90.17857143
81.3559322	89.83050847	88.13559322
82.30088496	88.49557522	86.72566372
82.45614035	86.84210526	88.59649123
83.06451613	91.93548387	86.29032258

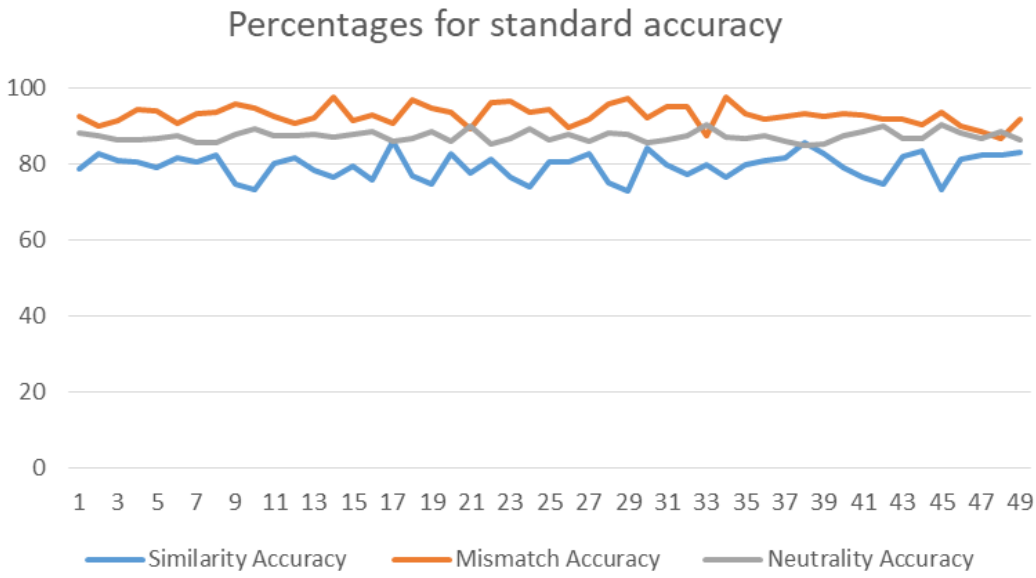

Figure 6. Accuracy standard of similarity, mismatch, and neutrality

5. Conclusion and future work

The neutrosophic has been applied to determine the measurement of similarity, dissimilarity, and neutrality, and the results have been good due to the experiment was highly fruitful since the accuracy standard for similarity and dissimilarity was measured. The similarity was encoded as "T" and dissimilarity as "F". Artificial intelligence techniques, such as deep learning and random forest, could be integrated with neutrosophic for optimal use in biomedical informatics. The paper presents the accuracy of standard similarity of the DNA sequence analysis indicating the mismatch account as well as the neutrality accuracy based on neutrosophic theory. As future work, more standard

datasets can be used to represent more patients and cases in order to determine the suitable drug based on DNA sequence analysis and alignment.

References

1. Christine. (March 2011). Bioinformatics–The application of the different technologies for gathering and analyzing information. [Online]. Available: http://www.ismb2008.org/bioinformatics-the-application-of-the-differ ent-technologies-for-gathering-and-analyzing-information
2. P. E. Gary, W. A. Reynolds, and R. Reynolds, "DNA: The key to life," Programmed Biology Series, Educational Methods, Chicago, 1977.
3. Genetic Science Learning Center. (August 6, 2012). Tour of the Basics. Learn. Genetics. [Online]. Available: http://learn.genetics.utah.edu/ content/begin/tour
4. P. H. Searls and B. David, "The roots of bioinformatics in theoretical biology," PLoS Computational Biology, vol. 7, no. 3, 2011.
5. W. R. Pearson, T. Wood, Z. Zhang, and W. Miller, "Comparison of DNA sequences with protein sequences," Genomics, vol. 46, issue 1, pp. 24-36, 1997.
6. A. Elumalai, "An overview of bioinformatics," Journal of Science – Biological Science, vol. 2, Issue 2, pp. 71-80, 2012
7. Shamsi F, Memon ZA, Soomrani AR, Khand QU. Comparative Study of Different Computational Systems for Analysis of DNA and Protein Sequences. International Journal of Bioscience, Biochemistry and Bioinformatics. 2014 Mar 1;4(2):86.
8. Mount, D. W., "Bioinformatics: Sequence and genome analysis". Spring Harbor Press, (2002).
9. Whishart, D.S., "Tools for protein technologies", In: Sensen, C.W. (Ed.), Biotechnology, Vol 5b, Genomics and Bioinformatics, Wiley-VCH. pp. 325-344, 2002
10. Sander, J., Ester, M., Kriegel, P.-H. and Xu, X., "Density-based clustering in spatial databases: The algorithm GDBSCAN and its applications", Data Mining and Knowledge Discovery, Vol. 2, issue 2, pp. 169-194, 1998.
11. Lee, K., "Computational study for protein-protein docking using global optimization and empirical potentials", International Journal of Molecular Science, Vol. 9, pp. 65-77, 2008.
12. Katoh, Kazutaka, and Daron M. Standley. "MAFFT multiple sequence alignment software version 7: improvements in performance and usability." Molecular biology and evolution 30, no. 4 (2013): 772- 780.
13. Thompson, Julie D., Desmond G. Higgins, and Toby J. Gibson. "CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice." Nucleic acids research 22, no. 22 (1994): 4673-4680.
14. Katoh, Kazutaka, and Daron M. Standley. "MAFFT: iterative refinement and additional methods." Multiple Sequence Alignment Methods (2014): 131-146.
15. Notredame, Cédric, Desmond G. Higgins, and Jaap Heringa. "T-Coffee: A novel method for fast and accurate multiple sequence alignment." Journal of molecular biology 302, no. 1 (2000): 205-217.
16. Shehab S, Shohdy S, Keshk AE. Pomsa: An efficient and precise position-based multiple sequence alignment technique. arXiv preprint arXiv:1708.01508. 2017 Aug 3.
17. Huang K, Xu M, Qi X. NGMMs: Neutrosophic Gaussian Mixture Models for Breast Ultrasound Image Classification. In2021 43rd Annual International Conference of the IEEE Engineering in Medicine & Biology Society (EMBC) 2021 Nov 1 (pp. 3943-3947). IEEE.
18. Alshikho M, Jdid M, Broumi S. A Study of a Support Vector Machine Algorithm with an Orthogonal Legendre Kernel According to Neutrosophic logic and Inverse Lagrangian Interpolation. Journal of Neutrosophic and Fuzzy Systems (JNFS) Vol. 2023;5(01):41-51.
19. Pramanik S, Dey PP, Giri BC. Hybrid vector similarity measure of single valued refined neutrosophic sets to multi-attribute decision making problems. Infinite Study; 2018.
20. Chou JC, Lin YF, Lin SS. A further study on multiperiod health diagnostics methodology under a single-valued neutrosophic set. Computational and Mathematical Methods in Medicine. 2020 Aug 1;2020.

21. Bouza-Herrera CN, Subzar M. Estimating The Ratio Of A Crisp Variable And A Neutrosophic Variable. International Journal of Neutrosophic Science (IJNS) Volume 11, 2020.:9.
22. Abdullah, L., Ong, Z. and Mahali, S.M., 2021. Research Article Single-Valued Neutrosophic DEMATEL for Segregating Types of Criteria: A Case of Subcontractors' Selection.
23. Smarandache F. Refined neutrosophy and lattices vs. pair structures and YinYang bipolar fuzzy set. Mathematics. 2019 Apr 16;7(4):353.
24. Hajiabadi M, Alizadeh Savareh B, Emami H, Bashiri A. Comparison of wavelet transformations to enhance convolutional neural network performance in brain tumor segmentation. BMC Medical Informatics and Decision Making. 2021 Dec;21(1):1-1.
25. Al-subhi SH, Rubio PA, Pérez PP, Papageorgiou EI, Vacacela RG, Mahdi GS. A New Neutrosophic Clinical Decision Support Model for The Treatment of Pregnant Women with Heart Diseases. Infinite Study.
26. Yildiz I, Sahin M. A new approach for multi-attribute decision-making problems in bipolar neutrosophic sets. Neutrosophic Sets and Systems. 2018; 23:142-59.
27. Touqeer M, Rasool E. Multiple Attribute Decision Making Based on Interval-Valued Neutrosophic Trapezoidal Fuzzy Numbers and its Application in the Diagnosis of Viral Flu. International Journal of Emerging Multidisciplinaries: Mathematics. 2022 May 14;1(2):124-44.
28. Devarasan E. Neutrosophic Based Image Relationship Analysis for Fingerprint Image Pattern Recogniton and Matching. Available at SSRN 4047124.
29. Lin M, Wang H, Xu Z, Yao Z, Huang J. Clustering algorithms based on correlation coefficients for probabilistic linguistic term sets. International Journal of Intelligent Systems. 2018 Dec;33(12):2402-24.
30. Wu JL, Xiao X, Yu LC, Ye SZ, Lai KR. Using an analogical reasoning framework to infer language patterns for negative life events. BMC Medical Informatics and Decision Making. 2019 Dec;19(1):1-2.
31. Tan W, Weng H, Lin H, Ou A, He Z, Jia F. Disease risk analysis for schizophrenia patients by an automatic AHP framework. BMC Medical Informatics and Decision Making. 2021 Nov;21(9):1-2.
32. Ngan RT, Ali M, Fujita H, Abdel-Basset M, Giang NL, Manogaran G, Priyan MK. A new representation of intuitionistic fuzzy systems and their applications in critical decision making. IEEE Intelligent Systems. 2019 Aug 30;35(1):6-17.
33. Manea C, SAVOIU G, Siman II, TAICU M. Inter-, trans-and multidisciplinarity, and some ideas or remarks on cultural tourism. Anuarul Institutului de Cercetari Economice" Gheorghe Zane"-Iasi. 2014;23(Supplement):133.
34. Smarandache F. Neutrosophy, a new Branch of Philosophy. Infinite Study; 2002 Jan.
35. Smarandache F. A unifying field in Logics: Neutrosophic Logic. InPhilosophy 1999 (pp. 1-141). American Research Press.
36. Smarandache F. A unifying field in logics: neutrosophic logic. Neutrosophy, neutrosophic set, neutrosophic probability: neutrsophic logic. Neutrosophy, neutrosophic set, neutrosophic probability. Infinite Study; 2005.
37. Luscombe NM, Greenbaum D, Gerstein M. What is bioinformatics? A proposed definition and overview of the field. Methods of information in medicine. 2001;40(04):346-58.
38. Russell PH, Johnson RL, Ananthan S, Harnke B, Carlson NE. A large-scale analysis of bioinformatics code on GitHub. PloS one. 2018 Oct 31;13(10):e0205898.
39. Gaur L, Solanki A, Wamba SF, Jhanjhi NZ, editors. Advanced AI techniques and applications in bioinformatics. CRC Press; 2021 Oct 17.
40. Belal Amin, A. A. Salama, I. M. El-Henawy, Khaled Mahfouz, Mona G. Gafar, "Intelligent Neutrosophic Diagnostic System for Cardiotocography Data", Computational Intelligence and Neuroscience, vol. 2021, Article ID 6656770, 12 pages, 2021.
41. Ibrahim Yasser, Aya A. Abd El-Khalek, Abeer Twakol, Mohy-Eldin Abo-Elsoud, A. A. Salama, Fahmi Khalifa, A hybrid Automated Intelligent COVID-19 Classification System Based on Neutrosophic Logic and Machine Learning Techniques Using Chest X-ray Images, Studies in Systems, Decision and Control,

Advances in Data Science and Intelligent Data Communication Technologies for COVID-19, Vol.378, Springer Nature.

42. Kawther F. Alhasan, A.A. Salama, & Florentin Smarandache. (2021). Introduction to Neutrosophic Reliability Theory. International Journal of Neutrosophic Science, 15(1), 52–61.
43. Ibrahim Yasser, Abeer Twakol, A. A. Abd El-Khalek, Ahmed Samrah and A. A. Salama, COVID-X: Novel Health-Fog Framework Based on Neutrosophic Classifier for Confrontation Covid-19, Neutrosophic Sets and Systems, vol. 35, 2020, pp. 1-21.
44. A.A. Salama, Ahmed Sharaf Al-Din, Issam Abu Al-Qasim, Rafif Alhabib and Magdy Badran, Introduction to Decision Making for Neutrosophic Environment "Study on the Suez Canal Port, Egypt", Neutrosophic Sets and Systems, vol. 35, 2020, pp. 22-44.
45. Alhabib, Rafif, A. A. Salama. "The Neutrosophic Time Series-Study Its Models (Linear-Logarithmic) and test the Coefficients Significance of Its linear model." Neutrosophic Sets and Systems 33.1 (2020) pp105-115.
46. Rafif Alhabib, Ahmad Salama, Studying Neutrosophic Variables, Neutrosophic Theories in Communication, Management and Information Technology, Series: Mathematics Research Developments Mathematics,, ISBN: 978-1-53617-485-4, Categories: Nova, 2020.
47. Salama A.A., Eisa M., ElGhawalby H., Fawzy A.E. (2019) A New Approach in Content-Based Image Retrieval Neutrosophic Domain. In: Kahraman C., Otay İ. (eds) Fuzzy Multi-criteria Decision-Making Using Neutrosophic Sets. Studies in Fuzziness and Soft Computing, vol 369 (pp.361-369),Springer,Cham.
48. Elwahsh, H., Gamal, M., Salama, A., & El-Henawy, I. (2018). A novel approach for classifying MANETs attacks with a neutrosophic intelligent system based on genetic algorithm. Security and Communication Networks, vol.2018, pp1-7.
49. ElWahsh, H., Gamal, M., Salama, A., & El-Henawy, I. (2018). Intrusion detection system and neutrosophic theory for MANETs:A comparative study, Neutrosophic Sets and Systems, 23, pp16-22.
50. Salama, A., Smarandache, F., ElGhawalby, H. (2018). Neutrosophic approach to grayscale images domain. Neutrosophic Sets and Systems, 21, pp13-19.
51. A. A. Salama, Rafif Alhabib.(2018). Some neutrosophic probability distributions. Neutrosophic Sets and Systems, 22, 30-38.
52. Haitham ELwahsha , Mona Gamala, A. A. Salama, I.M. El-Henawy.(2017). Modeling Neutrosophic Data by Self-Organizing Feature Map: MANETs Data Case Study, Procida Computer, Vol.121, pp152-157, 2017.
53. A. Salama, Hewayda ElGhawalby, Shimaa Fathi Ali. (2017). Topological Manifold Space via Neutrosophic Crisp Set Theory, Neutrosophic Sets and Systems, Vol.15, 2017, pp.18-21.
54. A A Salama, Mohamed Eisa and A. E. Fawzy. (2017) A Neutrosophic Image Retrieval Classifier. International Journal of Computer Applications 170 (9):1-6, July 2017.
55. A. A. Salama, I. M. Hanafy, Hewayda Elghawalby, M. S. Dabash. (2016). Neutrosophic Crisp α-Topological Spaces, Neutrosophic Sets and Systems, vol. 12, 2016, pp. 92-96.
56. A. A. Salama. (2015). Basic Structure of Some Classes of Neutrosophic Crisp Nearly Open Sets & Possible Application to GIS Topology, Neutrosophic Sets and Systems, vol. 7, 2015, pp. 18-22.
57. A. A. Salama, F.Smarandache (2015). Neutrosophic Crisp Set Theory, Educational. Education Publishing 1313 Chesapeake, Avenue, Columbus, Ohio 43212, https://digitalrepository.unm.edu/math_fsp/153/
58. A. A. Salama, Florentin Smarandache, Valeri Kroumov.(2014). Neutrosophic Crisp Sets & Neutrosophic Crisp Topological Spaces, Neutrosophic Sets and Systems, vol. 2, 2014, pp.25-30. doi.org/10.5281/zenodo.571502
59. A.A. Salama, Haitham A. El-Ghareeb, Ayman M. Manie, Florentin Smarandache. (2014). Introduction to Develop Some Software Programs for Dealing with Neutrosophic Sets, Neutrosophic Sets and Systems, vol. 3, 2014, pp. 51-52.doi.org/10.5281/zenodo.571453,
60. A. A.Salama and S.A. Alblowi, Neutrosophic Set and Neutrosophic Topological Space, ISOR J. mathematics (IOSR-JM), Vol. (3). Issue (4), (Sep-Oct. 2012). pp 31-35.

61. Huda E. Khalid, "An Original Notion to Find Maximal Solution in the Fuzzy Neutrosophic Relation Equations (FNRE) with Geometric Programming (GP)", Neutrosophic Sets and Systems, vol. 7, 2015, pp. 3-7.
62. Huda E. Khalid, "The Novel Attempt for Finding Minimum Solution in Fuzzy Neutrosophic Relational Geometric Programming (FNRGP) with (max, min) Composition", Neutrosophic Sets and Systems, vol. 11, 2016, pp. 107-111.
63. Huda E. Khalid, F. Smarandache, A. K. Essa, (2018). The Basic Notions for (over, off, under) Neutrosophic Geometric Programming Problems. Neutrosophic Sets and Systems, 22, 50-62.
64. Huda E. Khalid, (2020). Geometric Programming Dealt with a Neutrosophic Relational Equations Under the ($\boldsymbol{max-min}$) Operation. Neutrosophic Sets in Decision Analysis and Operations Research, chapter four. IGI Global Publishing House.
65. Huda E. Khalid, "Neutrosophic Geometric Programming (NGP) with (max-product) Operator, An Innovative Model", Neutrosophic Sets and Systems, vol. 32, 2020.
66. Huda E. Khalid, F. Smarandache, A. K. Essa, (2016). A Neutrosophic Binomial Factorial Theorem with their Refrains. Neutrosophic Sets and Systems, 14, 50-62.
67. Huda E. Khalid, Ahmed K. Essa, The Duality Approach of the Neutrosophic Linear Programming, Neutrosophic Sets and Systems, vol. 46, 2021, pp. 9-23. DOI: 10.5281/zenodo.5553469

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