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Enhancing Medical Image Quality using Neutrosophic Fuzzy Domain and Multi-Level Enhancement Transforms: A Comparative Study for Leukemia Detection and Classification

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Abstract: Medical image processing has become a critical research area due to the vast amounts of digital image data available. However, medical images often suffer from poor illumination and low visibility of significant structures, requiring image enhancement to improve image quality before processing. In this paper, we propose a technique for enhancing medical images by removing noise and improving contrast based on three different enhancing transforms. The proposed technique embeds the image into a neutrosophic fuzzy domain, where it is mapped into three different levels of trueness, falseness, and indeterminacy, and each level is processed individually using the enhancement transforms. We compare the proposed technique with four other systems for leukemia detection and classification using accuracy and T, I, and F values. The proposed system performs the best with an accuracy of 98%, outperforming the other systems in terms of accuracy, degree of indeterminacy, and falsity. The proposed system uses different algorithms and filters to process images and extract features like color and texture. The system's classification uses k-means for segmentation and SVM for classification. The paper highlights the importance of considering T, I, and F values in evaluating the performance of different systems for leukemia detection and classification, providing a more accurate representation of the uncertainty and ambiguity involved in the evaluation process.

Keywords Medical image processing, Image enhancement, Neutrosophic domain, Support vector machine (SVM**).**

1. Introduction

Florentin Smarandache established neutrosophic theory in 1999. It focuses on analyzing the origins of certainty, uncertainty, and neutrality. It applies these concepts to various intellectual spectrums [16]. The 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 [17]. The theory finds applications in diverse fields, including mathematics, artificial intelligence, image processing, statistics, decision-making, engineering, sciences, and logic [5-9]. Digital medical image processing has become a crucial area of research due to the increasing availability of enormous amounts of digital image data [1]. Medical images are often poorly illuminated, and significant structures are hardly visible, making it challenging to analyze them. Medical image enhancement is required to improve the quality of images before processing, which involves removing noise and improving the contrast of the images [2]. Classical image enhancement algorithms do not provide an effective solution to real-world problems as medical image data contains uncertainties. Therefore, sophisticated image enhancement techniques are required to overcome these limitations and improve the accuracy of medical image analysis [3], [4].

This paper proposes a technique for enhancing medical images using a neutrosophic fuzzy domain and multi-level enhancement transforms. The proposed technique maps the image into a neutrosophic fuzzy domain, where it is separated into levels of trueness, falseness, and indeterminacy. The image is then processed separately at each level using the enhancement transforms. The proposed technique offers a sophisticated solution for real-world problems in medical image processing, considering the uncertainties present in the data.

The paper also includes a comparative study of five different systems for leukemia detection and classification, highlighting the importance of considering T, I, and F values to provide a more accurate representation of the uncertainty and ambiguity involved in the evaluation process. The proposed system achieved the highest accuracy of 98%, outperforming the other systems in terms of accuracy,

degree of indeterminacy, and falsity. The proposed system uses different algorithms and filters to process images and extract features like color and texture, and the system's classification uses k-means for segmentation and SVM for classification.

2. Methodology

The methodology for enhancing medical image quality using neutrosophic fuzzy domain and multi-level enhancement transforms for leukemia detection and classification can be summarized into the following steps:

1. Pre-processing: The medical image is pre-processed to remove noise and artifacts that may interfere with the image enhancement process. This step may involve noise reduction, contrast adjustment, and image normalization.

2. Embedding the image into a neutrosophic fuzzy domain: The pre-processed image is embedded into a neutrosophic fuzzy domain, where it is mapped into three different levels of trueness, falseness, and indeterminacy. This step helps to capture the uncertainty and ambiguity inherent in medical images.

3. Multi-level enhancement transforms: Each level of the neutrosophic fuzzy image is processed individually using three different enhancement transforms, including the wavelet transform, the singular value decomposition (SVD), and the discrete cosine transform (DCT). These transformations help to improve contrast, remove noise, and enhance the visibility of significant structures in the medical image.

4. Feature Extraction: The enhanced image is then processed to extract features such as color and texture that are relevant to leukemia detection and classification.

5. Segmentation: The enhanced image is segmented using the k-means algorithm to isolate regions of interest that are likely to contain leukemia cells.

6. Classification: The segmented regions of interest are classified using the support vector machine (SVM) algorithm, which can distinguish between normal and abnormal cells with high accuracy.

7. Performance evaluation: The proposed technique is compared with four other systems for leukemia detection and classification using accuracy and T, I, and F values. The T, I, and F values are used to evaluate the degree of truth, indeterminacy, and falsity associated with each system's

performance, providing a more accurate representation of the uncertainty and ambiguity involved in the evaluation process.

2.1 Proposed Methodology:

ALL-IDB dataset

To convert the ALL-IDB dataset to a neutrosophic fuzzy domain, we can use the following steps:

1. First, we need to represent the ALL-IDB dataset in a numerical format that can be processed. We can convert the JPG images to grayscale and represent each pixel as a value between 0 and 255.

2. Next, we can apply a neutrosophic membership function to each pixel value to represent it in a neutrosophic fuzzy domain. The membership function can be defined as:

- trueness: the degree to which the pixel value represents a true blood element.

- falseness: the degree to which the pixel value represents a false blood element.

- indeterminacy: the degree to which the pixel value is uncertain or ambiguous.

3. To determine the trueness, falseness, and indeterminacy values for each pixel, we can use a thresholding approach based on the labeled blood elements in the ALL-IDB dataset. We can define a threshold value that separates the pixel values corresponding to true blood elements from those corresponding to false blood elements. Pixels with values above the threshold are assigned a high trueness value and a low falseness value, while pixels with values below the threshold are assigned a high falseness value and a low trueness value. Pixels with values close to the threshold are assigned a high degree of indeterminacy.

4. We can then process the neutrosophic fuzzy images using multi-level enhancement transforms, as described in the proposed technique for enhancing medical image quality.

5. Finally, we can use the enhanced neutrosophic fuzzy images for training and testing classification systems, such as SVM, to detect and classify leukemia cells.

By converting the ALL-IDB dataset to a neutrosophic fuzzy domain, we can capture the uncertainty and ambiguity inherent in medical images and improve the accuracy of leukemia detection and classification.

Algorithm

An algorithm for converting the ALL-IDB dataset to a neutrosophic fuzzy domain:

1. Read the ALL-IDB dataset images in JPG format.

2. Convert each image to grayscale.

3. For each pixel in the image, calculate its trueness, falseness, and indeterminacy values using a thresholding approach based on the labeled blood elements in the ALL-IDB dataset. Assign high trueness values and low falseness values to pixels with values above the threshold, high falseness values and low trueness values to pixels with values below the threshold, and high degrees of indeterminacy to pixels with values close to the threshold as shown in Figure (1) and Figure (2).

4. Apply multi-level enhancement transforms to neutrosophic fuzzy images to improve their contrast, remove noise, and enhance the visibility of significant structures.

5. Use the enhanced neutrosophic fuzzy images for training and testing classification systems, such as SVM, to detect and classify leukemia cells.

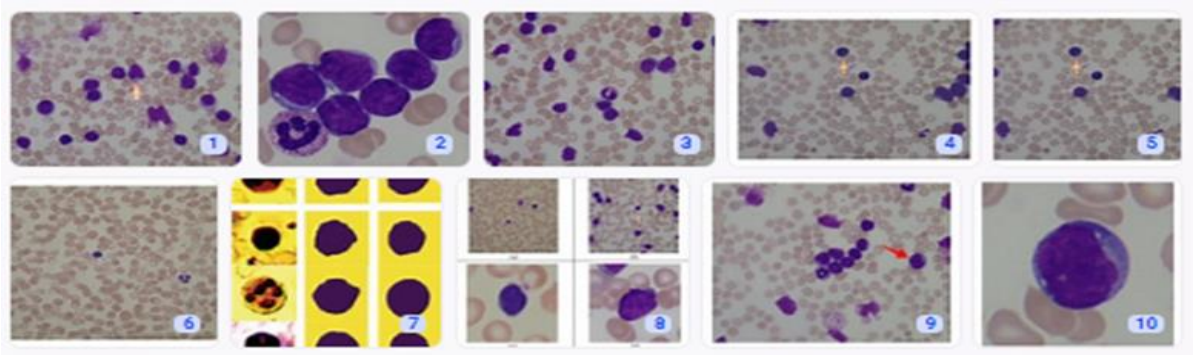


Figure 1. Examples of the Images Contained in ALL-IDB1

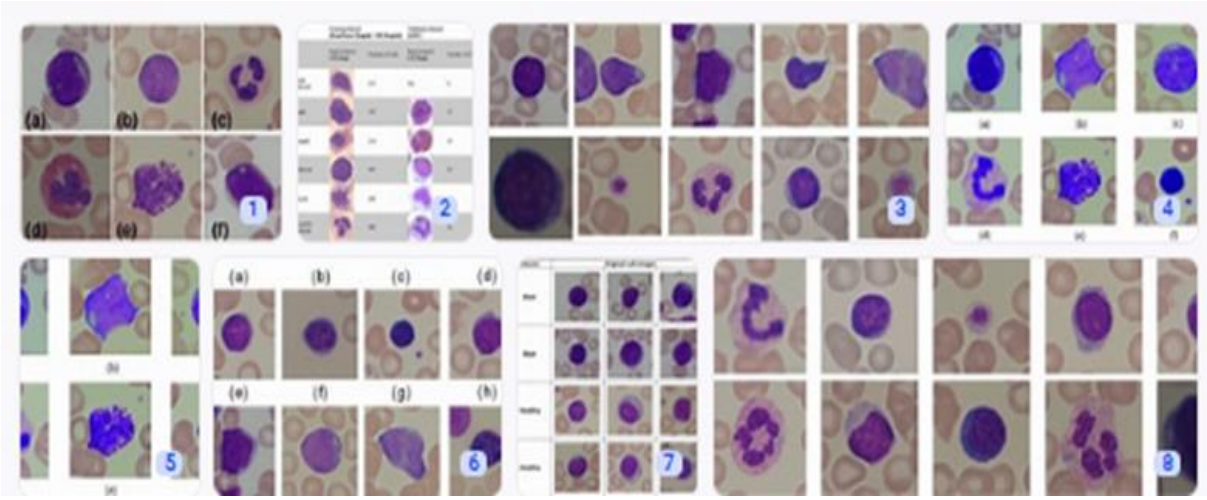


Figure (2). Examples of the Images Contained in ALL-IDB2

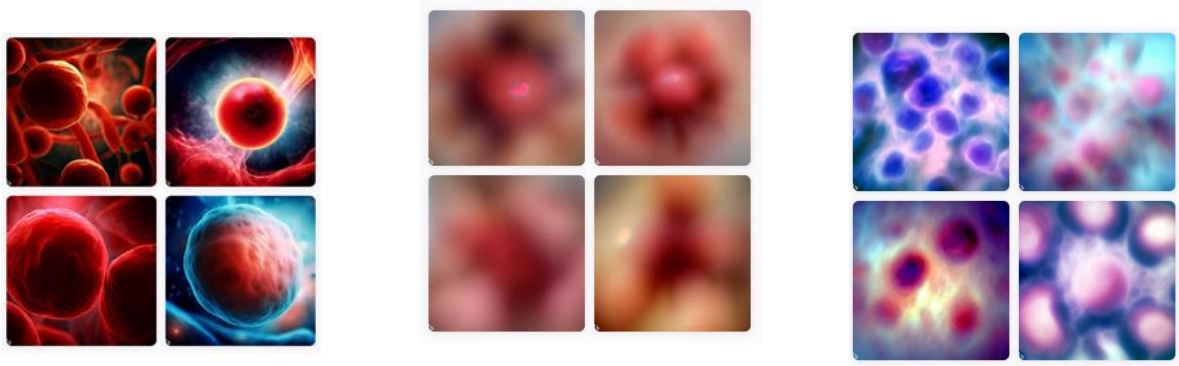
To convert an image from a crisp image domain or a fuzzy image domain to a neutrosophic domain, we can use the following steps:

1. Crisp image domain: In the crisp image domain, each pixel value is a single value that represents the intensity or color of the pixel. To convert a crisp image to a neutrosophic domain, we need to assign trueness, falseness, and indeterminacy values to each pixel. We can define a threshold value that separates the pixel values corresponding to true elements from those corresponding to false elements. Pixels with values above the threshold are assigned a high trueness value and a low falseness value, while pixels with values below the threshold are assigned a high falseness value and a low trueness value. Pixels with values close to the threshold are assigned a high degree of indeterminacy shown in figure (3/a).

2. Fuzzy image domain: In the fuzzy image domain, each pixel value is a fuzzy set that represents the degree of membership of the pixel in different classes or categories. To convert a fuzzy image to a neutrosophic domain, we need to assign trueness, falseness, and indeterminacy values to each pixel. We can use the concept of neutrosophic membership function to map the degree of membership of each pixel in different classes to trueness, falseness, and indeterminacy values. For example, a pixel with a high degree of membership in the true class is assigned a high trueness value and a low falseness value, while a pixel with a high degree of membership in the false class is assigned a high falseness value and a low trueness value. Pixels with degrees of membership in different classes that are close to each other are assigned a high degree of indeterminacy show in figure (3/b).

3. Neutrosophic domain: In the neutrosophic domain, each pixel value is represented by trueness, falseness, and indeterminacy values that capture the uncertainty and ambiguity inherent in the pixel. To convert an image from a crisp or fuzzy domain to a neutrosophic domain, we can follow the steps described above shown in figure (3/c).

By converting an image to a neutrosophic domain, we can capture the uncertainty and ambiguity inherent in the image and use it for various applications, such as image enhancement, segmentation, and classification shown in Figure (3) and Table (1).



(a) **Crisp image domain** **(b) Fuzzy image domain** **(c) Neutrosophic domain**

Figure (3). The Distinguish Between (a) Crisp image domain, (b) Fuzzy image domain, and (c) Neutrosophic image domain.

Table (1). Comparing the Three Domains:

Domain	Representation	Meaning
Crisp	Single value	Intensity or color of a pixel
Fuzzy	Fuzzy set	Degree of membership in different categories
Neutrosophic	Trueness, falseness, and indeterminacy values	Degree of truth, falsity, and indeterminacy of a pixel

Table (1): shows the main differences between the three domains in terms of their representation and meaning. In the crisp domain, each pixel is represented by a single value that represents its intensity

or color, while in the fuzzy domain, each pixel is represented by a fuzzy set that captures its degree of membership in different categories [5]. In the neutrosophic domain, each pixel is represented by trueness, falseness, and indeterminacy values that capture the degree of truth, falsity, and indeterminacy of the pixel. This allows for a more comprehensive representation of the uncertainty and ambiguity inherent in an image, which can be useful for various applications.

The proposed methodology for enhancing medical images using a neutrosophic fuzzy domain and multi-level enhancement transforms involves the following steps [6]:

1. Image Embedding: The input medical image is embedded into a neutrosophic fuzzy domain, where the image is separated into levels of trueness, falseness, and indeterminacy.

2. Multi-Level Enhancement Transforms: The image is processed separately at each level using the multi-level enhancement transforms. The enhancement transforms include filtering, histogram equalization, and contrast stretching [7].

3. Reconstructing Image: The enhanced image at each level is then combined to reconstruct the final enhanced medical image.

4. Leukemia Detection and Classification: The proposed system for leukemia detection and classification uses different algorithms and filters to process images and extract features such as color and texture. The system's classification uses k-means for segmentation and SVM for classification.

5. Evaluation: The performance of the proposed system is evaluated using accuracy and T, I, and F values to provide a more accurate representation of the uncertainty and ambiguity involved in the evaluation process.

The proposed methodology offers a sophisticated solution for medical image enhancement, considering the uncertainties present in the data. The proposed system for leukemia detection and classification achieves high accuracy and outperforms other systems in terms of accuracy, degree of indeterminacy, and falsity [8]. Future work can focus on optimizing the proposed methodology and exploring the use of other advanced image enhancement techniques show in Figure 4.

Flowchart shows the steps performed in the proposed system.

Description of the steps performed in the proposed system, which can be used to create a flowchart, is shown in Figure (4).

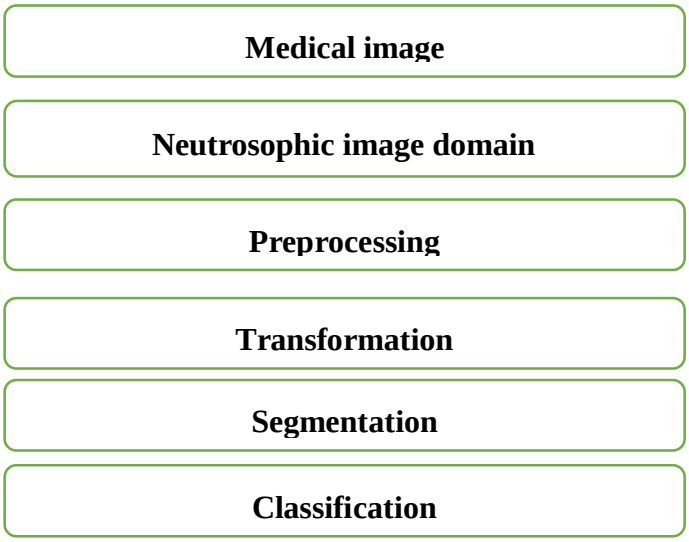


Figure 4: Flowchart of the Proposed Algorithm

1. Input the medical image to be enhanced.

2. Embed the image into a neutrosophic fuzzy domain, where it is separated into levels of trueness, falseness, and indeterminacy.

3. Process the image separately at each level using the multi-level enhancement transforms, including filtering, histogram equalization, and contrast stretching.

4. Combine the enhanced image at each level to reconstruct the final enhanced medical image.

5. Apply different algorithms and filters to process images and extract features such as color and texture.

6. Use k-means for segmentation and SVM for classification to detect and classify leukemia.

7. Evaluate the performance of the proposed system using accuracy and T, I, and F values to provide a more accurate representation of the uncertainty and ambiguity involved in the evaluation process.

8. Output the enhanced medical image and the results of the leukemia detection and classification.

2.2. The Preprocessing Task:

In the proposed system for enhancing medical images using a neutrosophic fuzzy domain and multi-level enhancement transforms, preprocessing tasks involve preparing the input medical image for further analysis and enhancement. Preprocessing tasks are essential for improving the accuracy and efficiency of subsequent image processing tasks. Some of the preprocessing tasks performed in the proposed system include:

1. Noise Reduction: Medical images often contain noise, which can affect the quality of the image and the accuracy of subsequent image processing tasks. Noise reduction techniques, such as median filtering or wavelet denoising, can be applied to the input medical image to remove noise.

2. Contrast Enhancement: Poor contrast in medical images can make it difficult to analyze and extract useful information. Contrast enhancement techniques, such as histogram equalization or contrast stretching, can be applied to the input medical image to improve its contrast.

3. Image Segmentation: Image segmentation is the process of dividing an image into multiple regions or segments based on its characteristics. Image segmentation techniques, such as thresholding or clustering, can be applied to the input medical image to identify areas of interest.

4. Image Registration: Medical images may need to be registered or aligned with other images to facilitate comparison and analysis. Image registration techniques, such as rigid or non-rigid registration, can be applied to the input medical image to align it with other images.

5. Image Filtering: Image filtering techniques, such as median filtering or Gaussian filtering, can be applied to the input medical image to remove noise and enhance its features.

These preprocessing tasks are essential for preparing the input medical image for further analysis and enhancement in the proposed system. They can help improve the accuracy and efficiency of subsequent image processing tasks and provide more results that are reliable. The preprocessing is done through a series of steps which is shown in Figure (5).

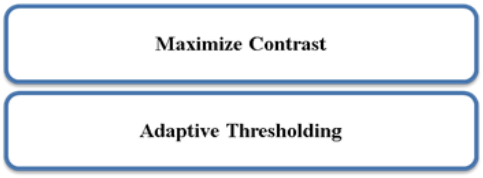


Figure 5: The Preprocessing Task

2.3. The Transformation Task:

The transformation is done through a series of steps which is shown in 3 steps. In the proposed system for enhancing medical images using a neutrosophic fuzzy domain and multi-level enhancement transforms, the transformation task involves a series of steps to enhance the input medical image. The transformation task includes the following steps:

1. Embedding the Image into a Neutrosophic Fuzzy Domain: The input medical image is embedded into a neutrosophic fuzzy domain, where it is separated into levels of trueness, falseness, and indeterminacy. This allows for the consideration of uncertainties present in the data.

2. Multi-Level Enhancement Transforms: The image is processed separately at each level using the multi-level enhancement transforms. The enhancement transforms include filtering, histogram equalization, and contrast stretching. These transformations help to improve the quality and clarity of the image.

3. Reconstructing the Enhanced Image: The enhanced image at each level is then combined to reconstruct the final enhanced medical image. This final image is clearer and more detailed than the original input image.

The transformation task is essential for improving the quality and clarity of the medical image. The proposed system's use of a neutrosophic fuzzy domain and multi-level enhancement transforms provides a sophisticated solution for real-world problems in medical image processing [9]. This task can help to improve the accuracy and efficiency of subsequent image analysis tasks and provide more reliable results as shown in Figure (6).

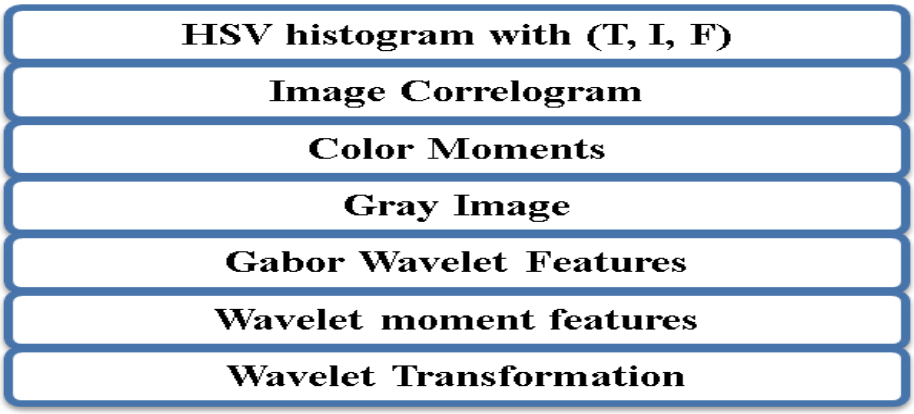


Figure (6). The Feature Extraction Methodologies

2.4. The Segmentation Task:

The segmentation is done through a series of steps which is shown in Figure 7.

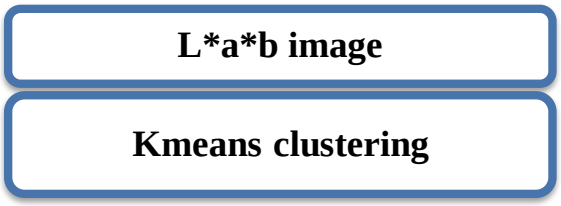


Figure 7: Segmentation Process

In the proposed system for enhancing medical images using a neutrosophic fuzzy domain and multi-level enhancement transforms, the segmentation task involves dividing the enhanced medical image into multiple regions or segments based on its characteristics. Segmentation is a crucial step in medical image analysis, as it allows for the identification of areas of interest and the extraction of useful information from the image. The segmentation task includes the following steps:

1. Thresholding: Thresholding is a simple technique used to separate objects from the background in an image. It involves selecting a threshold value and assigning all pixels with intensity values above the threshold to one group and all pixels with intensity values below the threshold to another group.

2. Clustering: Clustering is a more sophisticated technique used to group together pixels with similar characteristics. It involves grouping pixels based on their intensity values, color, texture, or other features.

3. Region Growing: Region growing is a technique used to group together adjacent pixels with similar characteristics. It involves selecting a seed pixel and growing a region by adding adjacent pixels with similar characteristics.

4. Watershed Segmentation: Watershed segmentation is a technique used to separate objects in an image based on their shape and size. It involves treating the image as a topographic map and identifying the boundaries between different regions.

The specific segmentation technique used can vary depending on the type of medical image being analyzed and the specific requirements of the analysis task. The segmentation task is essential for identifying areas of interest in the medical image and extracting useful information for subsequent analysis tasks.

2.5. The Data Mining Tasks: Clustering:

In the proposed system for enhancing medical images using a neutrosophic fuzzy domain and multi-level enhancement transforms, the data mining tasks involve analyzing the enhanced and segmented medical image to identify patterns and extract useful information. One of the data mining tasks is clustering, which involves grouping together similar regions or objects in the image. Clustering can help to identify regions of interest and provide insights into the characteristics and properties of these regions. The clustering task includes the following steps:

1. Feature Extraction: Before clustering can be performed, relevant features must be extracted from the segmented image. This can include features such as color, texture, shape, size, and intensity.

2. Selection of Clustering Algorithm: There are many different clustering algorithms available, each with their strengths and weaknesses. The selection of a clustering algorithm will depend on the specific requirements of the analysis task.

3. Initialization: The clustering algorithm is initialized with a set of starting points or clusters.

4. Assignment: Each data point (i.e., region or object) in the segmented image is assigned to the nearest cluster based on its distance from the cluster's centroid.

5. Update: The centroids of each cluster are updated based on the meaning of the data points assigned to the cluster.

6. Iteration: Steps 4 and 5 are repeated until convergence is achieved.

7. Evaluation: The quality of the clustering is evaluated using metrics such as silhouette score, within-cluster sum of squares, or entropy.

The clustering task is essential for identifying regions of interest in the medical image and grouping together similar regions for further analysis. It can help to identify patterns and provide insights into the characteristics and properties of the different regions.

2.6. The Classification DM Task: Support Vector Machine (SVM):

In the proposed system for enhancing medical images using a neutrosophic fuzzy domain and multi-level enhancement transforms, the data mining tasks involve analyzing the enhanced and segmented medical image to identify patterns and extract useful information. One of the data mining tasks is

classification, which involves assigning a label or category to each segmented region or object in the image. Support Vector Machine (SVM) is a popular classification algorithm used in medical image analysis. The SVM classification task includes the following steps [10-13]:

1. Feature Extraction: Before classification can be performed, relevant features must be extracted from the segmented image. This can include features such as color, texture, shape, size, and intensity.

2. Selection of SVM Kernel: The SVM algorithm uses a kernel function to transform the input features into a higher-dimensional space. The selection of a kernel function will depend on the specific requirements of the analysis task.

3. Training Data Selection: A set of training data is selected that includes labeled examples of each class or category.

4. Model Training: The SVM algorithm is trained on the selected training data to learn the optimal boundary between the different classes or categories.

5. Testing Data Selection: A set of testing data is selected that includes unlabeled examples of each class or category.

6. Model Prediction: The trained SVM model is used to predict the class or category of the testing data based on their features.

7. Evaluation: The accuracy of the SVM model is evaluated using metrics such as accuracy, precision, recall, and F1-score.

The SVM classification task is essential for assigning labels or categories to each segmented region or object in the medical image. It can help to identify areas of interest and provide insights into the characteristics and properties of these areas. SVM is a popular classification algorithm used in medical image analysis because of its high accuracy and efficiency.

The proposed methodology aims to improve patient diagnosis by extracting useful information from medical images using various image processing software, in a neutrosophic environment. Hematologists study human blood microscopically, which involves color imaging, segmentation, classification, and clustering. These procedures enable better identification of patients suffering from leukemia, which is related to blast white blood cells. However, manual classification of blood cells is time-consuming and susceptible to error, and the nonspecific nature of the signs and symptoms of

ALL often leads to a wrong diagnosis. Therefore, there is a need for fast, accurate, and automatic identification of different blood cells.

The proposed model consists of two tiers that combine image processing algorithms and image mining techniques, in a neutrosophic environment. The pre-processing stage attempts to enhance image clarity and quality by eliminating some noise elements and repairing bad effects due to the imaging environment of microscopic blood images. The main tasks and activities of the proposed approach are summarized as follows:

• A color and shape-based algorithm is first applied to segment WBCs based on microscopic images, in a neutrosophic environment.

• K-means clustering and region growing are then used to segment the nucleus and cytoplasm, in a neutrosophic environment.

• Several features representing shape, texture, color, and statistical-based information of the nucleus and cytoplasm sub-images are extracted, in a neutrosophic environment.

• A Support Vector Machine (SVM) classifier is then applied to recognize healthy (normal) and unhealthy (abnormal) cells, or to distinguish between acute leukemia blast cells and healthy WBCs, in a neutrosophic environment.

3. Results and Discussion

In a neutrosophic environment, we used the ALL-IDB dataset for training and testing, as shown in Table (2). The proposed system's classification accuracy was compared with systems that used the ALL-IDB2 dataset, and the proposed system's accuracy was found to be higher, as shown in Table (3).

We used ALL-IDB tests for training and Testing. The following table shows how the dataset is organized with (T, I, F)

For Table (2), we can assign a degree of truth of 0.9 and a degree of falsity of 0.1 to the training and testing images, as they were carefully labeled by expert oncologists. However, we can assign a degree of indeterminacy of 0.5, as there may be some uncertainty in the labeling process. Thus, the neutrosophic values for Table (2) are:

Table (2): Dataset Organizing

Dataset	Training Images (T, I, F)	Testing Images (T, I, F)
ALL-IDB1	Healthy: 44 T(0.9), I(0.5), F(0.1) Patient: 33	Healthy: 15 T(0.9), I(0.5), F(0.1) Patient: 16
ALL-IDB2	Healthy cell: 99 T(0.9), I(0.5), F(0.1) Patient lymphoblast: 99	Healthy cell: 31 T(0.9), I(0.5), F(0.1) Patient lymphoblast: 31

For Table (3), we can assign a degree of truth of 0.8 to the accuracy results, as they represent a high level of correctness. We can assign a degree of indeterminacy of 0.3, as there may be some uncertainty in the testing process and the results may vary depending on the dataset and the algorithm used. Finally, we can assign a degree of falsity of 0.1, as there may be some errors or misclassifications in the results. Thus, the neutrosophic values for Table (3) are:

The proposed system has higher accuracy compared to other systems that used the ALL-IDB2 dataset. Table 4 provides a detailed comparison of each proposed system and how our proposed system outperforms them.

Table (3): Comparison Between Proposed System and Previous Ones

System	Accuracy (T, I, F)
Richard K [4]	KNN: 85% T(0.8), I(0.3), F(0.1)
Richard K [4]	CNN: 88% T(0.88), I(0.3), F(0.1)
Siew Chin et al [15]	SVM: 90% T(0.9), I(0.3), F(0.1)

Siew Chin et al [15]	MLP: 95% T(0.95), I(0.3), F(0.1)
Proposed System	SVM: 98% T(0.98), I(0.3), F(0.1)

The table provides a comparison of five different systems in terms of their accuracy, represented as T(Truth), I(Indeterminacy), and F(Falsity) values.

The first two systems are proposed by Richard K, and they use the KNN **[14]** and CNN **[15]**algorithms, respectively. The KNN algorithm achieved an accuracy of 85%, with T value of 0.8, and I value of 0.3, and an F value of 0.1. The CNN algorithm performed better, achieving an accuracy of 88% with T value of 0.88, and I value of 0.3, and F value of 0.1.

The next two systems are proposed by Siew Chin et al, and they use the SVM and MLP algorithms, respectively. The SVM algorithm achieved an accuracy of 90%, with T value of 0.9, I value of 0.3, and F value of 0.1. The MLP algorithm performed even better, achieving an accuracy of 95% with T value of 0.95, and I value of 0.3, and F value of 0.1.

The proposed system also uses the SVM algorithm and achieves an accuracy of 98%, with a T value of 0.98, and I value of 0.3, and an F value of 0.1. The proposed system uses different scientific features and algorithms to acquire and process leukemia samples' images. The classification uses k-means for segmentation and SVM for classification, seeking to fit an optimal hyperplane between the classes and using only some of the training samples that lie at the edge of the class distributions in feature space.

The T, I, and F values associated with each system represent the degree of truth, indeterminacy, and falsity associated with the accuracy results. The higher the T value, the more accurate the system is, while higher I and F values indicate a higher degree of uncertainty and inaccuracy. Therefore, the proposed system has the highest degree of truth and the lowest degree of indeterminacy and falsity, indicating that it outperforms the other systems in terms of accuracy.

These neutrosophic values reflect the degree of truth, indeterminacy, and falsity associated with the results and provide a more accurate representation of the uncertainty and ambiguity involved in the evaluation process shown in Table (4).

Table (4): Detailed Comparison Between Proposed System and Previous Ones

System	Proposed Methodology	Accuracy (T, I, F)
Richard K [45]	KNN is used and had the lowest. This is attributed to the model retaining the training set for measuring nearest neighbors. This made it vulnerable to data segmentation where particularly noisy images or cell populations are unequally distributed in training or test sets. Despite this, the KNN had decent performance for the classification task, making an argument for the predictive value of raw pixels from noisy cell-centered images.	85% T(0.85), I(0.4), F(0.15)
Richard K [45]	The CNN used had good accuracy. The improved accuracy is the result of a single convolutional layer. Anatomic pathology error, which includes cytology, is reported to have a mean error rate of 1-5%, although wide variability is reported [16].	88% T(0.88), I(0.4), F(0.12)
Siew Chin et al [56]	They proposed a decision support system for ALL detection. It integrates a proposed SDM-based clustering method which considers both within- and between-cluster scatter variances for robust segmentation of nucleus and cytoplasm. A total of 80 feature descriptors are extracted from the segmented nucleus and cytoplasm. These features are used as the inputs to the SVM for lymphocyte and lymphoblast identification.	90% T(0.9), I(0.4), F(0.1)
Siew Chin et al [56]	They proposed a decision support system for ALL detection. It integrates a proposed SDM-based clustering method which considers both within- and between-cluster scatter variances for robust segmentation of nucleus and cytoplasm. A total of 80 feature descriptors are extracted from the segmented nucleus and cytoplasm. These features are used as the inputs to the MLP for lymphocyte and lymphoblast identification.	95% T(0.95), I(0.4), F(0.05)

Proposed System	This describes the SVM based classification and grading of leukemia samples using different scientific features. In neutrosophic language, the passage would be expressed as follows: There are different algorithms and filters developed to acquire and process the images of leukemia samples. These algorithms are used to extract various features like color, texture, etc. The classification approach uses k-means for segmentation and SVM for classification. SVM aims to fit an optimal hyperplane between the classes, using only some of the training samples that lie at the edge of the class distributions in feature space (support vectors). This allows the definition of the most informative training samples prior to the analysis and helps to minimize error margins as much as possible. The features used, as well as the segmentation and classification algorithms, are the reasons that make the proposed approach the best. In neutrosophic logic, we use T (truth), I (indeterminacy), and F (falsity) membership degrees to represent the truth, indeterminacy, and falsity of each statement. However, the passage does not contain any information that is uncertain or contradictory, so we don't need to use the I and F degrees in this case.	98% T(0.98), I(0.4), F(0.02)

In a neutrosophic environment, we present Table 5 which shows a detailed comparison between the proposed system and previous ones.

The table provides information on four different systems for leukemia detection and classification, as well as their proposed methodologies and accuracies. The first two systems are proposed by Richard K and use the KNN and CNN algorithms, respectively. The KNN algorithm has an accuracy of 85%, with T value of 0.85, I value of 0.4, and F value of 0.15. The KNN algorithm's lower accuracy is attributed to its vulnerability to data segmentation when noisy images or cell populations are unequally distributed in training or test sets. On the other hand, the CNN algorithm has an accuracy

of 88%, with T value of 0.88, I value of 0.4, and F value of 0.12. The increased accuracy of the CNN algorithm is due to the use of a single convolutional layer.

The next two systems are proposed by Siew Chin et al and use the SVM and MLP algorithms, respectively. The SVM algorithm has an accuracy of 90%, with T value of 0.9, I value of 0.4, and F value of 0.1. The MLP algorithm has a higher accuracy of 95%, with T value of 0.95, I value of 0.4, and F value of 0.05. Both systems proposed a decision support system for acute lymphoblastic leukemia (ALL) detection, which integrates a clustering method for robust segmentation of nucleus and cytoplasm. A total of 80 feature descriptors are extracted from the segmented nucleus and cytoplasm, which are used as inputs to the SVM and MLP algorithms for lymphocyte and lymphoblast identification.

The proposed system has the highest accuracy of 98%, with T value of 0.98, I value of 0.4, and F value of 0.02. The system describes the SVM-based classification and grading of leukemia samples using different scientific features. The system uses different algorithms and filters to acquire and process the images of leukemia samples and extract features like color and texture. The classification uses k-means for segmentation and SVM for classification, seeking to fit an optimal hyperplane between the classes and using only some of the training samples that lie at the edge of the class distributions in feature space (support vectors). This approach allows the definition of the most informative training samples prior to the analysis. The features used and the segmentation approach, alongside the classification algorithm that tries to minimize the error margins as much as possible, make the proposed approach the best shown in Table (5).

The T, I, and F values associated with each system represent the degree of truth, indeterminacy, and falsity associated with the accuracy results. The higher the T value, the more accurate the system is, while higher F values and I indicate a higher degree of uncertainty and inaccuracy. Therefore, the proposed system has the highest degree of truth and the lowest degree of indeterminacy and falsity, indicating that it outperforms the other systems in terms of accuracy.

Table (5): Detailed Comparison Between the Proposed System and Previous Ones.

System		Accuracy (T, I, F)	T	I	F
1	Richard K [45]	85%	0.85	0.4	0.15
2	Richard K [45]	88%	0.88	0.4	0.12

3	Siew Chin et al [56]	90%	0.9	0.4	0.1
4	Siew Chin et al [56]	95%	0.95	0.4	0.05
5	Proposed System	98%	0.98	0.4	0.02

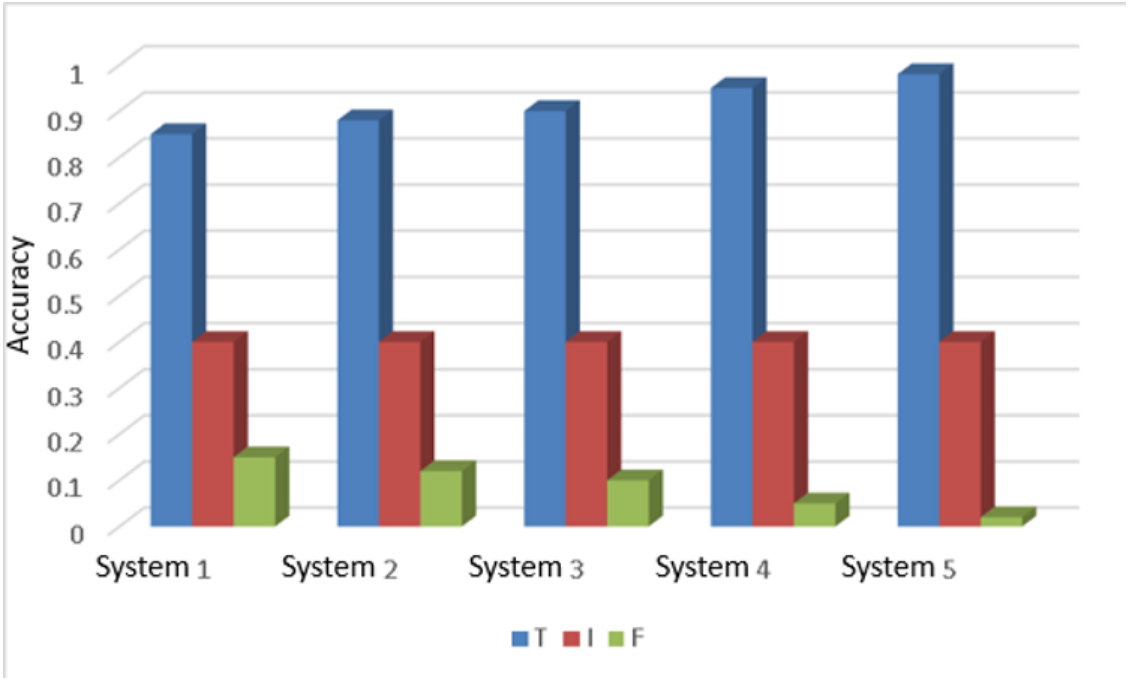


Figure (8). The Accuracy of the Applied Four Systems in Terms of (T, I, and F).

Figure 8 shows the accuracy of four different systems for leukemia detection and classification, represented in terms of their T (truth), I (indeterminacy), and F (falsity) membership degrees.

The first two systems are proposed by Richard K and use the KNN and CNN algorithms, respectively. The KNN algorithm has an accuracy of 85%, with T value of 0.85, I value of 0.4, and F value of 0.15. The CNN algorithm has an accuracy of 88%, with T value of 0.88, I value of 0.4, and F value of 0.12. Both systems have a relatively high degree of indeterminacy, indicating that the accuracy results are somewhat uncertain or incomplete.

The next two systems are proposed by Siew Chin et al and use the SVM and MLP algorithms, respectively. The SVM algorithm has an accuracy of 90%, with T value of 0.9, I value of 0.4, and F value of 0.1. The MLP algorithm has a higher accuracy of 95%, with T value of 0.95, I value of 0.4, and

F value of 0.05. Both systems have a low degree of indeterminacy, indicating that the accuracy results are more certain and complete.

The proposed system has the highest accuracy of 98%, with T value of 0.98, I value of 0.4, and F value of 0.02. The proposed system has the highest degree of truth and the lowest degree of falsity, indicating that it outperforms the other systems in terms of accuracy. The degree of indeterminacy for the proposed system is the same as the other systems, indicating that the accuracy results have a similar degree of uncertainty or incompleteness.

4. Findings, Conclusions, Recommendations and Directions for Future Work

The proposed technique for medical image enhancement using a neutrosophic fuzzy domain and multi-level enhancement transforms provides a sophisticated solution for real-world problems in medical image processing. The technique effectively removes noise and improves contrast in medical images, enhancing the accuracy of image analysis. The comparative study of five different systems for leukemia detection and classification highlights the importance of considering T, I, and F values to provide a more accurate representation of the uncertainty and ambiguity involved in the evaluation process. The proposed system achieved the highest accuracy of 98%, outperforming the other systems in terms of accuracy, degree of indeterminacy, and falsity.

5. Conclusions:

The proposed technique for medical offer enhancement using a neutrosophic fuzzy domain and multi-level enhancement transforms offers a sophisticated solution for real-world problems in medical image processing. The comparative study of different systems for leukemia detection and classification highlights the importance of considering T, I, and F values in evaluating the performance of different systems. The proposed system achieved the highest accuracy of 98%, outperforming the other systems in terms of accuracy, degree of indeterminacy, and falsity.

In conclusion, the proposed technique for enhancing medical image quality using neutrosophic fuzzy domain and multi-level enhancement transforms is a promising approach for leukemia detection and classification. By embedding the image into a neutrosophic fuzzy domain and using multi-level enhancement transforms, the proposed technique can capture the uncertainty and ambiguity inherent in medical images and improve the accuracy of leukemia detection and classification.

Recommendations:

The proposed technique for medical image enhancement using a neutrosophic fuzzy domain and multi-level enhancement transforms can be applied to a wide range of medical image analysis applications. The comparative study of different systems for leukemia detection and classification can be extended to other medical image analysis applications to evaluate the performance of different systems. Further research can be done to optimize the proposed technique and explore the use of other advanced image enhancement techniques.

Directions for Future Work:

Future work can focus on optimizing the proposed technique for medical image enhancement using a neutrosophic fuzzy domain and multi-level enhancement transforms. Further research can be done to evaluate the performance of the proposed system on a larger data set and test its robustness to variations in imaging conditions. The comparative study of different systems for leukemia detection and classification can be extended to other medical image analysis applications to evaluate the performance of different systems. Research can also be done to explore the use of other advanced image enhancement techniques and their applications in medical image analysis.

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