Human brain tumors detection using neutrosophic c-means clustering algorithm

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Abstract

For the last several decades, detecting human brain tumors has evolved into one of the most difficult problems in the field of medical research. In the realm of medical image processing, the categorization of brain tumors is a difficult job to do. In this research, we offer a model for the detection of human brain tumors in magnetic resonance imaging (MRI) images that makes use of the template-depend neutrosophic c-means and is compared with the fuzzy C means method. This model is referred to as the NCM method. In this suggested method, well first of all, the pattern K-means method is used to initialize segmentation markedly through the ideal choice of a template, depending on the gray-level intensity of the image; besides which, the revised membership is calculated by the ranges from the closest centroid to cluster pieces of data by using neutrosophic C-means (NCM) method while it approaches its perfect outcomes; and at last, the NCM clustering method is used for sensing tumor positron emission tomography (PET) imaging The findings of the simulation reveal that the suggested method can produce improved identification of pathological and normal cells in the human brain despite a little separation in the intensity of the grey level.

Keywords: Human brain tumors; Neutrosophic c-means clustering; Detection; Classification; Segmentation

1. Introduction

Research on brain tumors is consistently ranked among the most discussed issues in today's academic world. In a nutshell, the separation of tumor sections and the categorization of the tumor itself make up what is known as the malignant tumor categorization. This very important organ may be found right in the middle of the nervous system. Therefore, diseases that are caused by brain tumors are life-threatening, and it is essential to have an early diagnosis in these kinds of situations. The characteristics that are going to be utilized for the categorization of brain tumors play a significant part in identifying the category that the tumor falls into. In modern times, the Convolutional Neural Network (CNN) approach is considered to be the most effective in feature extraction. In a recent work on the treatment of brain tumors, Havaei et al. advocated the use of a two-way CNN. This kind of CNN considers both the attributes of individual pixels and the possibilities provided by nearby pixels[1]. The researchers Usman et al. segmented brain cancer to compute their density, density differences, neighborhood, and wavelet patterns, and then categorize the divided brain tumors using the random forest classification algorithm. Cheng et al. increased the precision of brain tumor detection by obtaining the attributes of the tumor site by using the concentration histogram, the grey level founder matrix (GLCM), and the bag-of-words (BoW) methodologies. These features contributed to the improved accuracy of brain tumor classification. When it came to the categorization of brain tumors, Afshary et al. demonstrated that the capsule networks (CapsNets) technique had an accurate recognition rate of 86.56%[2]–[4].

Deep learning has overtaken more traditional approaches to image processing in recent times and is now the industry standard. Several different pieces of research point to the fact that deep learning algorithms are better than the more traditional approaches. When using traditional image analysis, the

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extracting features stage is the most important step in the image classification step. This stage demands expert-level expertise. Deep learning algorithms, in comparison to more traditional methods of image processing, provide several benefits, the most significant of which is the removal of the need for extracting features. When compared to more traditional approaches, CNN technology demonstrates much better performance in picture categorization and pattern identification. It has a strong performance in image identification, fragmentation, and acknowledgment, which accounts for the widespread use of the concept in the recognition of video and images[5]–[7].

Within the scope of this study, we suggest the following key contributions:

I. We present an algorithm called NCM that will identify brain cancers with a higher level of precision even if the tumor that has to be identified is extremely small.

II. Even with a noisy magnetic resonance (MR) picture, the suggested approach performs better in terms of accuracy and efficiency than competing algorithms do.

III. When it comes to detecting and designating brain tumors in an MR image, the efficiency of the suggested method is superior to that of existing algorithms such as median filter, region expanding, region splitting and merging, artificial neural network (ANN), TK-means, and NCM methods, amongst others.

2. Digital Image Processing

The topic of digital image processing (DIP) is a developing one in the biological sciences, and its applications include the detection and classification of tumors, the detection, and classification of cancer, as well as the testing and examination of important components of the human body. In the field of medical research, the identification of brain tumors automatically plays an important role. The human body is made up of many various kinds of cells, and the brain, which is also known as the body's processor, plays a very important part. The human brain is by far the most important component of our neurological system. In addition to this, it serves as the primary component of the human brain's central nervous system[8], [9].

The human brain is a very complicated organ that is estimated to have between 50 and 100 billion neurons. It consists of a huge number of cells, each of which performs a specialized role for the organism as a whole. The vast majority of cells that are formed in the body divide to make new cells to ensure that the human body can operate properly. When naturally occurring cells develop, older or damaged cells pass away to make room for them. The old cells are eventually replaced by brand-new ones. Sometimes the body may make new cells even if it does not need them at the moment[10], [11]. In addition, damaged or old cells do not pass away as normally as they should. The formation of a mass of abnormal tissue known as a tumor is caused by the body's production of extra cells. The sensitive processes of the body get deformed as a result of a tumor that has been implanted in the area of the brain. Because of its location and its capacity to spread, it is very challenging and fraught with danger to treat. Benign and malignant brain tumors are the two primary subtypes that are distinguished by clinical characteristics. The term "benign tumor" refers to a tumor that does not include cancerous cells, whereas "malignant tumor" refers to a tumor that does contain cancerous cells[12], [13].

It is very important to identify and diagnose brain cancers in their early stages. At the moment, computer-aided diagnostic (CAD) systems are often used to conduct a comprehensive and accurate diagnosis of brain disorders. A brain tumor is an abnormal development of tissue or the central spine that has the potential to impede the brain's ability to perform its normal functions. According to the data that is published by the National Cancer Institute Statistics (NCIS), the mortality rate in the United States demonstrates that diagnosing brain tumors at more advanced stages is very important to preserve lives. In addition, the procedures of tumor identification should be carried out at a very rapid speed while maintaining a very high level of accuracy. This is only achievable by employing pictures created with magnetic resonance (MR), and suspicious areas are retrieved from complicated medical images using MR image segmentation. The diagnosis of a brain tumor is performed manually by medical professionals[14], [15].

On the other hand, there are certain drawbacks, such as the fact that it takes a substantial amount of time and the fact that the segmentation of an MR picture performed by various specialists may be rather variable. In addition, the findings of segmentation may change depending on the brightness and contrast of the display screen, as well as the conditions under which the tumor was detected by the same physician. Because of all of these factors, the automated diagnosis of brain tumors is becoming more important. It is possible to improve a patient's chances of surviving a brain tumor if the tumor is detected automatically. In the realm of medicine, there is no tried-and-true approach that can be developed to diagnose brain tumors. Multiple lines of research are now working toward the goal of developing an automated method for diagnosing brain tumors that is superior in terms of precision, exactness, and computational speed while also reducing the amount of labor that must be performed manually[16], [17].

To diagnose a brain tumor, it is necessary to determine not only the region of the brain that is afflicted but also the form, size, border, and location of the tumor itself. Imaging the brain may include the use of a wide variety of imaging modalities, including but not limited to magnetic resonance imaging (MRI), computed tomography (CT), positron emission tomography (PET), and others. MRI and CT scans are the most common types of imaging tests that may be used to investigate the structure of a brain tumor. The CT scan, on the other hand, exposes patients to radiation that is harmful to the human body, but the MRI provides an exact view of the anatomical structure of the tissues that make up the brain[17]–[19]. The magnetic resonance imaging (MRI) scanner is a piece of medical equipment that creates high-resolution pictures of inside organs and tissues by using radio waves and magnetic fields. The interpretation of MR images is exceedingly difficult, and it is under ongoing investigation by researchers to provide pathologists with a more satisfying experience while diagnosing patients.

3. K-Means Clustering

A relatively simple example of an unsupervised learning algorithm is the K-means clustering method. It makes it relatively simple to arrange a specific set of information into a predetermined number of clusters, known as S clusters; for example, a collection of data such as $a_1, a_2, \dots, a_n$ may be organized into S clusters. The primary goal of this technique is to identify S centers, one for each of the clusters in the data[20]. It is important to choose the centers of the S clusters at random. The measure of the distance plays an extremely significant role in the overall success of this method. This method supports a variety of approaches to distance measurement, including the Euclidean distance, the Manhattan distance, and the Chebychev distance, amongst others. However, the kind of data that we're going to cluster has a significant impact on how we should go about selecting the appropriate method for calculating distance. The Euclidean distance, on the other hand, will be used as the distance measure since it is quick, reliable, and straightforward to comprehend[21], [21]. Following is a step-by-step description of how the standard K-means clustering method works:

Suppose that the collection of data points is denoted by $A\ as\ a_1, a_2, a_3, \dots, a_n$, and that the set of centers is denoted by $D\ as\ d_1, d_2, \dots, d_c$.

1: Describe the term "a number of clusters" (abbreviated as "S").

2: At random, define the cluster centers designated by the letter 'c'

3. Determine the distance that separates each data point from the centers of the clusters.

4. A data point is allotted to the cluster center whose distance from the cluster is the shortest of all the distances between cluster centers.

5: After that, the new center of the cluster is computed as shown below.

$$d_i = \frac{1}{c_i} \sum_{j=1}^{c_i} a_i \qquad (1)$$

where 'c_i' refers to the number of data points included in the $i - th$ cluster

6. Recompute the distance that separates each data point from the newly obtained cluster centers.

7: If there was no reassignment of data points, then this process is complete; otherwise, return to stages three through six.

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Calculations are done to determine the distance, known as the Euclidean distance, between every pixel and the centers of every cluster. Using the distance function, each pixel in the image is evaluated on its own with the centers of each cluster. The pixel will be sent to one of the groups that are the shortest distance away out of all of them. After then, a new calculation for the center is performed. After then, each pixel is matched to all of the centroids once again. This procedure will continue until the center converges, at which point the convergence will be assessed using the highest possible number of iterations. The effectiveness of this algorithm's clustering is improved by repeatedly using the K-means clustering technique with a variety of various initializations to locate the optimal centroids.

In addition, it enables vectors with many dimensions and offers better computing efficiency. Therefore, the purpose of this technique is to reduce an objective function called the squared error function, which may be expressed as:

$$J_d = \sum_{i=1}^{c} \sum_{j=1}^{c_i} \left(\lVert a_i - d_j \rVert \right)^2 \tag{2}$$

4. Fuzzy C-Means Clustering

Suppose that the collection of data points is denoted by $A\ as\ a_1, a_2, a_3, \ldots, a_n$, and that the set of centers is denoted by $D\ as\ d_1, d_2, \ldots, d_c$.[22]–[25]
1. Change the number of clusters to $2 \le c \le n$, where n is the total number of elements in the data set. Find the value of m where $1 < m < \infty$. Pick any integral inspired norm metric |.|| from the options.
2. Start with the initialization of the fuzzy c segment $U^{(0)}$.
3: When you get to step b, set b to any value between 0 and 1, then go to step 4.
4: Compute the fuzzy joining function U_{ij} by

$$U_{ij} = \sum_{k=1}^{c} \left(\frac{\lVert a_j - d_i \rVert}{\lVert a_i - d_s \rVert} \right)^{-\frac{2}{m-1}} \tag{3}$$

5: After that, determine the fuzzy centers labeled"D_i" by

$$D_i = \frac{\sum_{j=1}^{N} (U_{ij})^m \times J}{\sum_{j=1}^{N} (U_{ij})^m} \tag{4}$$

6: Steps 2 and 3 should be repeated until the required minimum value for 'J' is reached or until the following condition is satisfied: $||U_{ij}^{k+1} - U_{ij}^{k}|| < \varepsilon$

5. Neutrosophic C-Means Clustering

Cluster analysis, also known as data clustering, is an important study field in patterns and machine learning. It aids in the better comprehension of a data structure, which is necessary for the development of various applications. The clustering process is often managed by first splitting the data into several clusters, to maximize similarity within each cluster while simultaneously maximizing dissimilarity across each cluster. The K-means clustering method is widely recognized as a pioneering technique in this field and has a wide range of potential applications. There have been many different iterations of the K-means clustering technique suggested up to this point. The K-means method gives precise memberships to each data point based on the characteristics of the point itself. Instead of utilizing crisp affiliations, Zadeh's fuzzy set theory made it possible to use partial subscriptions that were characterized by membership functions in cluster analysis. This made sense once the fuzzy set theory was first presented. The fuzzy notion was first used by Ruspini in the data clustering process. Dunn created the widely used fuzzy c means (FCM) technique, in which an existing goal function was rethought, and memberships were modified following the distance. Bezdek presented a generalized FCM as his contribution. Although FCM has been successfully used in a wide variety of applications, it does have a few limitations. For instance, the FCM methodology considers all data points to be of equal significance. In addition to this problem, FCM is unable to deal with noisy data points or outliers. In the past, there have been several efforts made to mitigate the negative effects of these disadvantages. When analyzing the influence that varying cluster shapes have, the authors took into account the

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Mahalanobis distance in FCM. Dave and his colleagues came up with a novel clustering approach that they called "fuzzy c-shell." It worked well on datasets that were both circular and elliptic in form. On the other hand, research was done to look at the disadvantages that the FCM algorithm has while dealing with noise. A method known as possibilistic c-means (PCM) was suggested by the author. This algorithm was implemented by removing the condition that FCM summation must equal 1. In this study, Pal et al. took into consideration the possibility of taking into consideration both absolute and relative similarities to cluster centers. This is because the PCM and FCM methods are combined in this study.

Recent years have seen the development of a plethora of new clustering methods, all of which take into account the fact that a single data point might concurrently belong to a number of different sub-clusters. The evidential theory served as the foundation for the adoption of these techniques. The evidential c-means method was first suggested by Masson and Denoeux (ECM). After that, the authors created a method known as the relational ECM (RECM). Clustering techniques known as neutrosophic c-means (NCM) and neutrosophic evidential c-means (NECM) were proposed by Guo and Sengur. Both of these algorithms are based on neutrosophic logic. To compensate for the shortcomings of the FCM approach while dealing with distortion and aberrant data points, a new cost mechanism was designed for the NCM. In the NCM method, two new kinds of rejection have been devised; these rejections may be used for either noise or outliers.

The objective function can be computed as:

$$\begin{aligned} J_{NCM}(T, I, F, c) = & \\ & \sum_{i=1}^{N} \sum_{j=1}^{C} \left(w_1 T_{ij}\right)^m \left\| a_i - c_j \right\|^2 + \\ \langle & \sum_{i=1}^{N} (w_2 I_i)^m \| a_i - c_{imax} \|^2 + \rangle \\ & \varepsilon \sum_{i=1}^{N} (w_3 F_i)^m \end{aligned} \tag{5}$$

6. Results and Discussion

This research presents a database consisting of 40 different photos of brain tumors. The database was created by compiling several separate high-resolution photos of complicated brain tumors. These photos were acquired from earlier research and pre-processed so that they could be used more effectively in the algorithmic program that we developed. After that, we used Python to analyze these photographs, and then we created a database for our ultimate usage of them. The tumors shown in these photographs are of such a severe kind that it would be quite difficult for the average person to identify them.

It is quite important to do MR image pre-processing to improve the picture's visual effect before continuing to process it. In most cases, the photos that have been gathered for the collection have such a low quality that it is necessary to filter out the noise and enhance the image. During the pre-processing stage, the obtained picture from the dataset is transformed into a two-dimensional matrix, and its color space is changed from RGB to grayscale. A midrange filter is applied to the picture to get rid of the noise in it. After that, the picture is improved by carrying out an adjusted operation, a template-matching procedure, and an adaptive template-matching operation. In most cases, when we talk about enhancing a picture, we mean boosting the contrast in the image. Following that, many traits are first extracted implicitly.
Following that, a variety of characteristics are first retrieved implicitly. Even a relatively little part of the brain tumor cannot be bypassed; it is necessary to pick the whole of the malignant growth. The first step involves passing the picture that was provided as input through a filter. After that, there is a first segmentation of the picture using framework K-means (TK), which is segregated on the premise of their grey level brightness and temper of color, with S equal to 8. After that, the tumor goes through a second round of the median filter. After that, the tumor is found by using an updated FCM method that is based on the Distance measure from the centroids to every data point. This distance is mostly determined by the various attributes. The tumor is then highlighted as a red line. Understanding the significance of this altered and included strategy may depend on having this information.

The NCM is carried out for 13 clusters, with the number of clusters determined by the intensity of the grey level. A picture is said to be clustered if it has the lowest possible grey level and its pixels are differentiated from one another by increasing levels of color intensity. For example, a large number of photographs grouped for input image no. 10 of database 2. Here, the tumor component along with other portions of the picture are exhibited in an individualized image, and from this, the tumor is selected based on the traits that it has.

There is a certain mistake rate involved, and it is dependent on whether or not any aberrant tissue is detected in every brain tumor MRI scan. These can be evaluated based on the ratio of true positives to false positives, true negatives to false negatives, and true positives to false positives. In this article, each picture in the database was put through a series of tests to determine the precision, sensitivity, and specificity of the system. The following four characteristics are included in the measurement to provide an accurate picture of the system's sensitivity, specificity, and accuracy.

TP stands for "True Positive," which indicates that the test result indicates the presence of the objective anomaly and that it was identified accurately.

TN stands for "true negative," which means that the test result indicates that the objective anomaly does not exist and that it was not recognized properly.

FP stands for "false positive," which describes a situation in which the test result is optimistic despite the actual abnormality not being present.

The test outcome is negative for the presence of objective abnormalities but it was not identified properly. This result is referred to as a false negative.
Sensitivity is the assessment of the accurate identification of the MRI picture that does not include a tumor. This may be characterized as the exact opposite of specificity. The term "sensitivity" has the following definition:

$$Sen = \frac{TP}{TP+TN} \tag{6}$$

Specificity is the assessment of exactly identifying the MRI picture that does not include a tumor, and it may be characterized as such using the word "specific."

$$Spe = \frac{TN}{TN+FP} \tag{7}$$

The assessment of actual categorization is one definition of accuracy. [Clarification needed]

$$Acc = \frac{TP+TN}{TP+TN+FP+FN} \tag{8}$$

Figure 1 shows the performance parameter under the K-means and NCM. There are 40 images used in this paper. The k-means produced 20 images in TP, 12 in TN, 3 in FP, and 5 in FN. In the NCM method, there are 39 in TP, 1 in FP, 1 in FN, and 1 in TN. Figure 2 shows the performance matrix for NCM and k-Means. The k-means have a 0.80 accuracy, 0.625 sensitivity, and 0.80 specificity. The NCM has a 0.95 accuracy, 0.9736 sensitivity, and 0.50 specificity.

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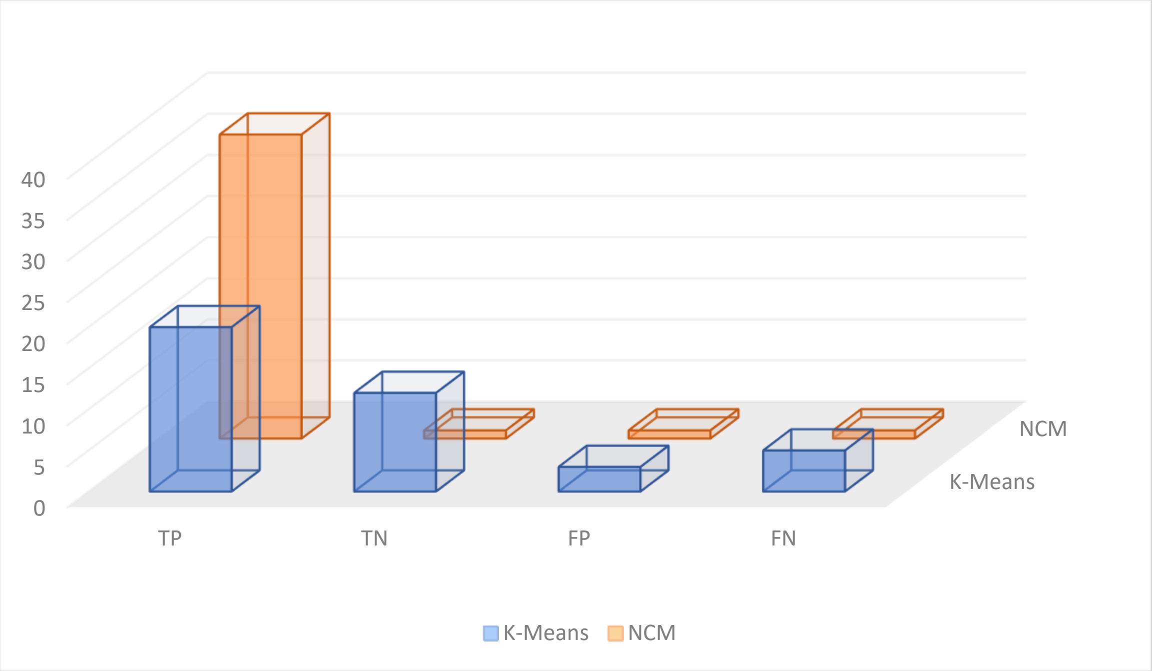

Figure 1: The performance analysis by the NCM.

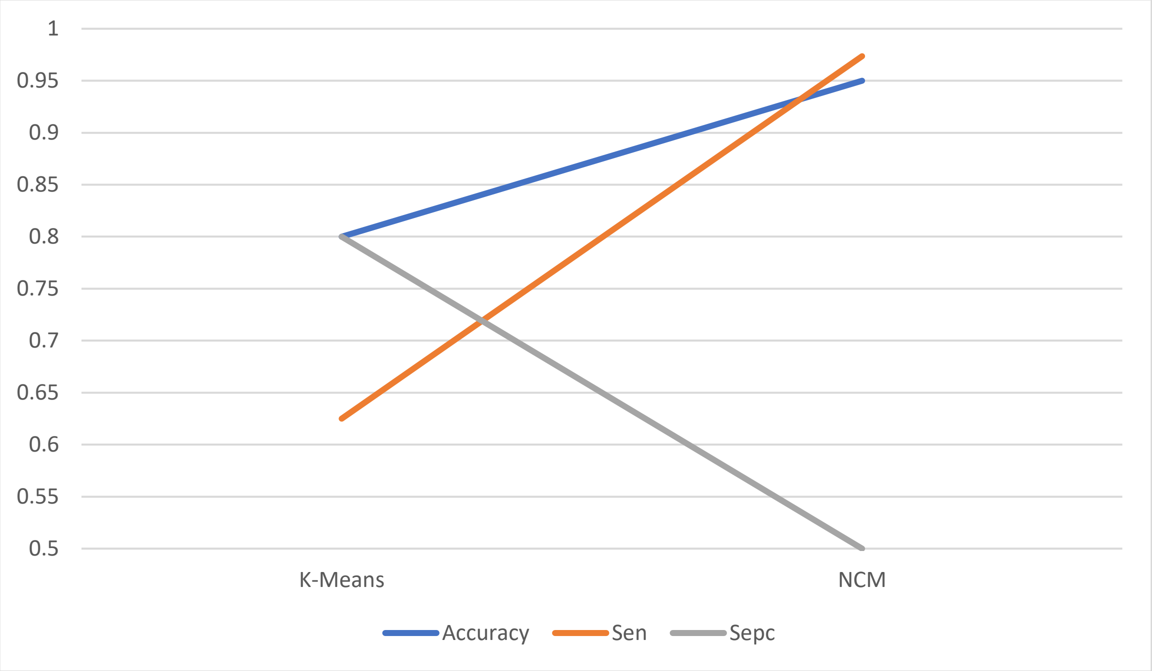

Figure 2: The accuracy value for the NCM.

This study made a comparison between fuzzy c-means clustering and neutrosophic c-means clustering. This comparison shows the robustness of this model. The comparison was made on 40 images in the dataset. Table 3 shows this comparison.

Table 1: The comparison between NCM and NCM.

	FCM	NCM
Accuracy	0.85	0.95
Sensitivity	0.7058	0.9736
Specificity	0.9090	0.50

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4. Conclusion

The primary objective of this study is to develop a reliable automated brain tumor segmentation system, with the secondary objective being to categorize brain tumors as either benign or malignant. NCM is the approach that was used to segment brain tumors.

In this article, a powerful clustering algorithm known as the neutrosophic c-means clustering algorithm (NCM) has been provided as a method for partitioning data, particularly data that is ambiguous and difficult to distinguish. The conventional approaches only describe the degree of each category. It might be challenging to establish which category a particular sample belongs to if it falls on the boundary between two or more categories. In addition, calculating membership levels might lead to erroneous estimates of the centers of various organizations. NCM was developed as a solution to address the shortcomings of the conventional ways of dividing data.

The effectiveness of the NCM method that was devised is evaluated using applications including data clustering as well as picture segmentation. For the experimental works, we made use of widely known data sets and photos of brain tumors. The NCM model has the highest accuracy compared to the FCM and k-means.

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