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ENHANCING TUMOR DETECTION IN BRAIN MRI: A HYBRID CLUSTERING APPROACH WITH DEEP LEARNING AND PROBABILISTIC NEURAL NETWORKS

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Abstract

The process of partitioning into different objects of an image is segmentation. In different major fields like face tracking, Satellite, Object Identification, Remote Sensing and majorly in medical field segmentation process is very important to find the different objects in the image. To investigate the functions and processes of human boy in radiology magnetic resonance imaging (MRI) will be used. MRI technique is using in many hospitals for the diagnosis purpose widely in finding the stage of a particular disease. In this paper, we proposed a new method for detecting the tumor with enhanced performance over traditional techniques such as K-Means Clustering, fuzzy c means (FCM). Different research methods have been proposed by researchers to detect the tumor in brain. To classify normal and abnormal form of brain, a system for screening is discussed in this paper which is developed with a framework of artificial intelligence with deep learning probabilistic neural networks by focusing on hybrid clustering for segmentation on brain image and crystal contrast enhancement. Feature's extraction and classification are included in the developing process. Performance in Simulation of proposed design has shown the superior results than the traditional methods.

Keywords: K-Means Cluster, MRI, FCM.

I. INTRODUCTION

Magnetic resonance imaging (MRI) [1] is a technique used in radiology to study human body processes and organ functions. Magnetic fields and radio waves can be used to create these visuals. This technology has been widely used in hospitals for medical diagnosis, illness staging, and follow-up without exposing patients to ionising radiation. MRI offers a wide range of uses in medical diagnostics, and there are over 25,000 scanners in operation across the world. It affects diagnosis and treatment in a wide range of disciplines, while the influence on improved health outcomes is unknown. When either modality might provide the same information, MRT is preferred over computed tomography (CT) because it does not require ionising radiation. The continued rise in MRI demand in the healthcare business has raised concerns regarding cost effectiveness and over diagnosis.

An attempt to organise comparable colours or parts of an image into a cluster or group is known as segmenting a picture. Clustering, which divides the number of colours or elements into many clusters based on the similarity of colour intensities and grey intensities in an image, is one way to accomplish this. The extraction of dominating colours from photographs is the main goal of clustering.

Image segmentation may be particularly useful for simplifying by extracting information from photos like as texture, colour, shape, and structure. Because it extracts information from images, segmentation has been utilised in a variety of domains, including image enhancement, compression, retrieval systems (such as search engines), object detection, and medical image processing [2].

There have been numerous ways to picture segmentation developed over the years. Among these, Fuzzy c-means (FCM) is a well-known and often used clustering approach that divides an image into many portions using a membership function [4] and [5]. Following FCM, the K-means method was introduced as a way to lower FCM's computational cost. K-means has been widely employed in numerous applications [4], [7], [8], and [9] due to its capacity to cluster large data points quickly. Hierarchical clustering has been frequently used for picture segmentation in recent years [12], [13],



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Volume : 53, Issue 4, No. 2, April : 2024

and [14]. The images were then segmented using the Gaussian Mixture Model and its version Expectation Maximization [17] and [18].

In this paper, a hybrid clustering with estimate arguing algorithm is suggested for recognising various tissues in brain pictures with better accuracy than traditional segmentation techniques such as fuzzy c means (FCM), K-means, and even manual segmentation. Preprocessing, segmentation, feature extraction, and estimate arguing are the four primary modules in this system. Median filtering is used for pre-processing. Unified iterative partitioned clustering is used to segment the data (U-IPC). Calculating the tissue area and the number of cells it occupied is used to estimate the area.

II. LITERATURE SURVEY

The automatic brain tumour segmentation (ABTS) method was created by Idanis Diaz to separate the various components of a brain tumour. The approach was used to four magnetic resonance image modalities to determine the edoema and gross tumour volume (GTV). The ABTS segmentation algorithm uses morphological operations such geodesic transformations and a histogram multi-thresholding approach, as well as a histogram multi-thresholding technique. The registered pictures using the typical MR sequence were utilised as input. The initial phase was thresholding, followed by skull segmentation, edoema, and gross tumour volume (GTV). The method is rapid and accurate for images produced by various scanners since it automatically selects thresholds based on histograms. Meiyan Huang came up with a new classification system.

The local independent projection was incorporated into the standard classification paradigm in this paper. Local independent projections are calculated for the LIPC (independent projection-based classification) approach, with locality as a key parameter. By learning a model termed soft max regression, the LIPC approach additionally takes into account the data distribution of distinct classes. This may aid in further improving categorization performance.

Pre-processing, tumour segmentation using the LIPC approach, feature extraction, and post-processing with spatial constraints are the four primary stages of the proposed method.

To cut down on computing expenses, a multi-resolution framework was built in.

For both Synthetic Data and Image Data, experimental findings were obtained. This method addressed the issues of tumour segmentation methods that arise due to the complex characteristics presented by brain tumour MRI images, such as great variation in the appearance of the tumour and ambiguous tumour boundaries.

Jin Liu went over the various imaging modalities and MRI-based tumour segmentation algorithms in detail. The pre-processing techniques as well as the most up-to-date state-of-the-art methodologies for MRI-based brain tumour segmentation were comprehensively discussed. The results of the MRI-based tumour segmentation were then analysed and confirmed. Finally, utilising MR images, an objective appraisal of future advancements and trends in brain tumour segmentation approaches was presented.

Many segmentation tactics have helped to solve the problems that semiautomatic and fully automatic systems have. Dr Mohd Fauzi Bin Othman gave an overview of MRI brain tumour classification utilising Field Programmable Gate Array (FPGA) implementation.

Field Programmable Gate Arrays are the greatest choice for real-time study of image processing algorithms since they can be customised and are adaptable.

They cut down on the time and cost of implementing new segmentation algorithms on hardware. Using a sophisticated kernel-based technology called Support Vector Machine (SVM), the MRI data images are categorised as normal (without a brain tumour) or abnormal (with a brain tumour) (with a brain tumour). The inverse wavelet transform is used to create a noise-free image after the wavelet transform is performed to eliminate noise. As a result, we do a wavelet-based feature extraction.



ISSN: 0970-2555

Volume : 53, Issue 4, No. 2, April : 2024

III. IMAGE SEGMENTATION

Segmentation in computer vision involves dividing a digital image into distinct parts or sets of pixels, commonly referred to as super pixels. The primary objective of segmentation is to enhance the interpretability and analysis of an image by simplifying or altering its representation. This process facilitates the identification of objects and boundaries within images. Technically, image segmentation entails assigning a label to each pixel in an image, ensuring that pixels with the same label exhibit similar visual attributes.

The outcome of image segmentation can manifest as either a collection of segments covering the entire image or a series of contours derived from the image (referred to as edge detection). Each pixel within a region can be compared based on certain characteristics or computed features, such as color, intensity, or texture. Adjacent regions typically exhibit significant differences in these traits.

- Edge finding
- Thresholding
- Mathematical morphology in binary form
- Mathematical morphology based on grey values

It is critical to be able to discriminate between the objects of interest and "the remainder" while analysing objects in photographs.

This second group is also known as the background. Segmentation techniques - separating the foreground from the background - are commonly employed to find the objects of interest. In this section, we'll go over two of the most prevalent segmentation techniques: thresholding and edge finding, as well as techniques for enhancing segmentation quality. It's critical to realise that:

1. No segmentation technique is generally applicable to all images, and

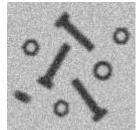
2. No segmentation technique is flawless.

Thresholding:

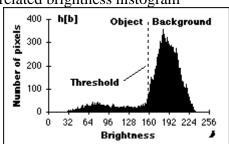
This method is based on a straightforward premise. The brightness threshold is chosen and applied to the image a [m, n] in the following way: This version of the algorithm thinks we're looking for light objects against a dark backdrop. We'd use the following for dark objects on a light background: The output is the label "object" or "background," which can be represented as a Boolean variable "1" or "0" due to its dichotomous character. The test condition might theoretically be based on something other than brightness (for example, If (Redness a [m, n] \geq red), but the concept is apparent.

There is no universal threshold selection process that is guaranteed to operate on all photos, but there are a number of options. Fixed threshold - Using a threshold that is set independently of the image data is an option. If it is known that one is working with very high-contrast photos with objects that are very dark and a homogeneous and very light background, a constant threshold of 128 on a range of 0 to 255 may be sufficient. By accuracy, we mean that the number of pixels that have been incorrectly identified should be maintained to a minimum.

Thresholds obtained from the brightness histogram of the region or image to be segmented - In most circumstances, the threshold is calculated from the brightness histogram of the region or image to be segmented. Figure 2 depicts an image and its related brightness histogram

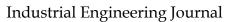


(a) Image to be threshold



(b) Brightness histogram of the image

Figure 1 : Pixels below the threshold (a $[m, n] < \theta$) will be labelled as object pixels; those above the threshold will be labelled as background pixels.





ISSN: 0970-2555

Volume : 53, Issue 4, No. 2, April : 2024

A variety of techniques have been devised to automatically choose a threshold starting from the gray-value histogram, $\{h[b] | b = 0, 1, 2^{B}-1\}$.

Many of these algorithms can benefit from a smoothing of the raw histogram data to remove small fluctuations but the smoothing algorithm must not shift the peak positions. This translates into a zero-phase smoothing algorithm given below where typical values for W are 3 or 5:

Image Segmentation By Clustering

Segmentation By clustering

It is a method to perform Image Segmentation of pixel-wise segmentation. In this type of segmentation, we try to cluster the pixels that are together. There are two approaches for performing the Segmentation by clustering.

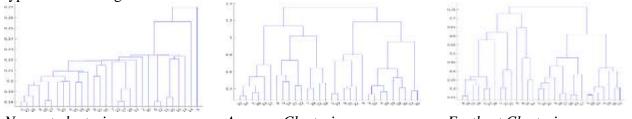
- Clustering by Merging
- Clustering by Divisive

Clustering by merging or Agglomerative Clustering:

In this approach, we follow the bottom-up approach, which means we assign the pixel closest to the cluster. The algorithm for performing the agglomerative clustering as follows:

- Take each point as a separate cluster.
- For a given number of epochs or until clustering is satisfactory.
- Merge two clusters with the smallest inter-cluster distance (WCSS).
- Repeat the above step

The agglomerative clustering is represented by Dendrogram. It can be performed in 3 methods: by selecting the closest pair for merging, by selecting the farthest pair for merging, or by selecting the pair which is at an average distance (neither closest nor farthest). The dendrogram representing these types of clustering is below:



Nearest clustering

Average Clustering

Farthest Clustering

Clustering by division or Divisive splitting

In this approach, we follow the top-down approach, which means we assign the pixel closest to the cluster. The algorithm for performing the agglomerative clustering as follows:

- Construct a single cluster containing all points.
- For a given number of epochs or until clustering is satisfactory.
- Split the cluster into two clusters with the largest inter-cluster distance.
- Repeat the above steps.
- In this article, we will be discussing how to perform the K-Means Clustering.

K-Means Clustering

K-means clustering stands as a widely embraced algorithm for clustering tasks, particularly beneficial when dataset labels are absent. Its primary objective is to discern distinct groups within the data, with the number of groups denoted by 'K'. This method finds application across diverse domains including market and customer segmentation. However, its utility extends to image processing, where it can effectively segment objects based on pixel values.

The process for image segmentation using this algorithm unfolds as follows:

- 1. First, we need to select the value of K in K-means clustering.
- 2. Select a feature vector for every pixel (color values such as RGB value, texture etc.).

3. Define a similarity measure b/w feature vectors such as Euclidean distance to measure the similarity b/w any two points/pixel.

4. Apply K-means algorithm to the cluster centers



ISSN: 0970-2555

Volume : 53, Issue 4, No. 2, April : 2024

5. Apply connected component's algorithm.

6. Combine any component of size less than the threshold to an adjacent component that is similar to it until you can't combine more.

Following are the steps for applying the K-means clustering algorithm:

- Select K points and assign them one cluster center each.
- Until the cluster center won't change, perform the following steps:
- Allocate each point to the nearest cluster center and ensure that each cluster center has one point.
- Replace the cluster center with the mean of the points assigned to it.
- End

The optimal value of K?

In a specific category of clustering algorithms, a parameter known as 'K' determines the number of clusters to identify. When we possess domain knowledge about the data, we may have a predetermined value for K, reflecting the known number of categories within the dataset. However, prior to determining the optimal value of K, it is imperative to establish the objective function for the aforementioned algorithm. This objective function can be expressed as:

$$J = \sum_{j=1}^{k} \sum_{i=1}^{n} |x_i^j - c_j|^2$$

Where j is the number of clusters, and i will be the points belong to the jth cluster. The above objective function is called within-cluster sum of square (WCSS) distance.

A good way to find the optimal value of K is to brute force a smaller range of values (1-10) and plot the graph of WCSS distance vs K. The point where the graph is sharply bent downward can be considered the optimal value of K. This method is called the Elbow method.

IV. METHODOLOGY

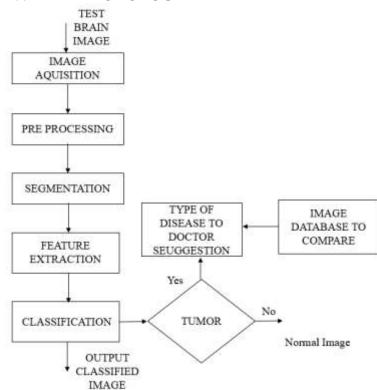


Fig.2 Proposed structure algorithm block diagram



ISSN: 0970-2555

Volume : 53, Issue 4, No. 2, April : 2024

PRE-PROCESSING

The image from acquired images will be considered for further step of pre-processing, which includes background information and noise. To remove this needless information in the image, it is need to apply noise removing techniques before processing further. It is used to eliminate irrelevant information which includes noise, unwanted background part, pectoral muscle on the skin image and other artifacts. The noise of different types occurred in the skin images are Salt and Pepper, Gaussian, and Speckle and Poisson noise [8]. The different intensity will be shown by the image, whenever noise occurred in the image instead of actual pixel values of the image. Therefore, it is compulsory to choose and apply a filtering method to remove the noise as first stage. The system here has applied median filtering technique as shown in figure 5 and median filtered output images are in figure 8, which eradicates the noise from the image. These filters can effectively can detect, remove noise and thin hairs from the image. Later, Bi Histogram equalization works on the whole image and enhances the image, whereas adaptive histogram equalization divides the whole image and works on the small regions called tiles. Each tile is typically 8*8 pixels and within each tile, histogram is equalized and thus it enhances the edges of the lesion. Contrast limiting is applied to limit the contrast, a level below the specific limit to limit the noise. Bi histogram equalization is applied which is focused on the average input image intensity threshold [9-10] by following the calculation of the brightness of mean and the pixels are separated into classes or sub-vector images dependent on the value of mean [8][11].

P				• • ••			•••••	[0][].
124	112	116	127	112	115	114	117	
112	110	113	118	112	119	120	121	
119	117	115	119	120	127 -	116 -	127	Values 115 119 120 123
112	116	123	124	125	118	113	118	124 125 126 127 150
110	113	125	127	150	116	114	116	Median Value is 124
117	114	116	112	116	127	116	127	
110	113	118	110	113	118	113	118	
117	114	116	117	114	116	114	116	1

Figure 3: Median Filter

 $I_H = \{I(u, v) | (u, v) \ge I_m\}$

$$I_L = \{ I(u, v) | (u, v) < I_m \},$$
(1)

Besides, the two groups create two cumulative density functions, that is,

$$C_L(i) = \sum_{j=0}^{l} h(j), \quad i = 0 \dots \dots I_m - 1.$$

 $C_H(j) = \sum_{k=I_m}^{i} h(k), \quad j = I_m \dots \dots L - 1$ (2) Where $\sum i^c L(i) = \sum j^c H(j) = 1$ each sub-image is processed to provide improved contrast performance,

$$I_L, enh(i) = (I_m - 1) \times C_L(i)$$

$$I_{H}, enh(j) = I_{m} + (L - 1 - I_{m}) \times C_{H}(j)$$
(3)
From the set of sub-images, the output and enhanced image.

From the set of sub-images, the output and enhanced image are obtained.

 $I_{enh} = I_L, enh \cup I_H, enh.$ (4)

The average image brightness is the average value of the average luminosity of sub-images. The output is differed from the average input brightness as shown in figure 6 and Figure 7 is the changed histogram of crystal contrast enhanced images to input images.

SEGMENTATION

After the pre-processing stage, segmentation of lesion was carried out to get the transparent portion of the affected area of skin. On performing transformation, Hybrid clustering technique is applied on the processed image to segment the skin lesion area based on Fuzzy C-Means clustering and K-Means techniques. In K-means technique, Segmentation is the preliminary process of this technique, at the cluster centres, cost junction must be minimized which randomly varies with respect to memberships of user inputs. Dividing an image into multiple clusters is the main function of



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Volume : 53, Issue 4, No. 2, April : 2024

segmentation and this is based on region of interest to identify the skin cancer. As described in figure 9, In this proposed system, K-Means clustering technique is applied first after detecting the specific edges and later fuzzy c means clustering is applied.

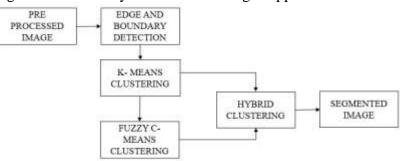


Figure 4: Segmentation with Hybrid Clustering method

K-Means Clustering

The key structure of K-Means Clustering technique is discussed in this section. Let $Y = \{y_i | i=1,...,P\}$ be features of P-dimensional vectors and $Z=\{zj \mid j=1,...,N\}$ be each data of Y. K-means clusters which Z is $TP = {Ti | I 1, d..., = k}$. The image is separated into clusters and every cluster will have average centre value. K-Means clustering contains the subsequent phases as discussed below

1. At first, generate with centroids C, the random starting points.

2. Separation between pixel and centre has to discover by Euclidean distance i.e. from X to C.

(5)

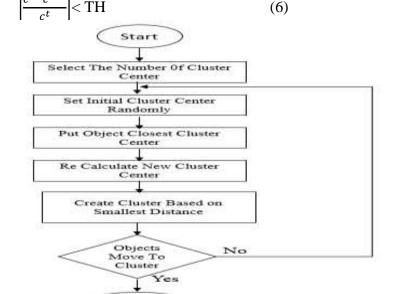
3. From the partition of Xi for 1=1---- N Determine the base d(zi,C).

4. Discovering cluster centre which is new Ci for i=1...k is defined as:

$$\operatorname{Ci} = \frac{1}{mi} \sum_{i=1}^{n(si)} mij \in si$$

5. The procedure need be repeated from step 2 for all the clusters.

$$\left|\frac{c^t - c^{t-1}}{c^t}\right| < \mathrm{TH}$$





Stop

The centroids are said to be converged if they are not changing their position and they may stop in any particular cluster 't' with a threshold TH, then the positions have to be refreshed by considering the threshold value TH. The figure 10 represents the step-by-step procedure for K-Means clustering. Fuzzy C-Means Clustering

In general, segmentation fuzzy c-mean algorithm is one which will be used for dividing the images with space of image to numerous cluster areas with parallel image pixel values. It is very useful for



ISSN: 0970-2555

Volume : 53, Issue 4, No. 2, April : 2024

medical image analysis, as it is fuzzified type of the k-means segmentation technique. The Fuzzy C-Means (FCM) clustering algorithm introduced first in [12] and then it was improved in [13]. The procedure is an iterative clustering technique which produces an ideal C partition by lessening the weighted inside group sum of squared error and is extensively used in pattern recognition and segmentation of images. This algorithm will have the following steps traditionally.

$$\forall x \left(\sum_{k=1}^{num.clusters} u_k(x) = 1 \right)$$
(7)

The algorithm centroids with a cluster of all the points is shown as

$$Center_{k} = \frac{\sum_{x} u_{k}(x)^{m} x}{\sum_{x} u_{k}(x)^{m}}$$
(8)

The distance between the cluster to centre in relation with above equations is:

$$u_k(x) = \frac{1}{d(center_k, x)} \tag{9}$$

Then coefficient is a proper parameter to proper distribution > 1 So there is 1.

$$u_k(x) = \frac{1}{\sum_j \left(\frac{d(center_k, x)}{d(center_j, x)}\right)^{2/(m-1)}}$$
(10)

The equivalent of 2m for a linear normalization of coefficients equalling their quantity to 1. When 1 m is closer, the cluster is much weighted more than other clusters at this stage and is similar to the K-means algorithm [14].

Fuzzy C-Means clustering technique looks almost similar to K-Means clustering and contains the subsequent phases as discussed below

- Need to select the cluster randomly in number
- Repeat the algorithm as discussed in each step of equations 7,8,9,10
- Calculate the centre using the above equation 8
- Calculate the coefficients by using canter value from 8 using equations 9 and 10.

• Figure 12 represents the segmented image using this algorithm and figure 13 shows the segmented images of input using hybrid clustering technique.

FEATURE EXTRACTION

From the basic and raw information, extracting of required image data is important and it should be most relevant for further procedure like classification. The information dimensionality of the data may be reduced while extracting the features. It is done here due to technical limits in time for computation and memory. A normal and quality feature extraction technique should have the capability to enhance and uphold the features of input image raw data which makes difference patterns from each other. At the same time, while acquiring the image, it should be capable to process by human being. Three major features are extracted: Texture features using Gray Level Cooccurrence Matrix (GLCM), Low level features using Discrete Wavelet Transform (DWT), Colour features. These are the most common features used for the extraction of features, though the performance of three techniques dependent on the image raw data.

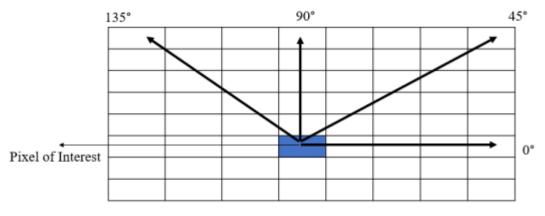
To continue the developments in image processing, computer vision extraction of features is having a large role as it has a rich history of fields of classifying images, medical imaging, remote sensing, visual human perceptions. Word texture depends always on human perception as interpretations of individual will vary based on that particular texture. It provides a meaningful result as a quantify we can define it as texture. In an image, pivotal component is always texture and it uses to explain about spatial differences in a raw segmented image at particular point, to define brightness, regularity and coarseness of the image. Especially in diagnosis analysis of texture, it is very important to give a

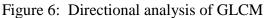


ISSN: 0970-2555

Volume : 53, Issue 4, No. 2, April : 2024

solution to a problem by performing manipulations on digital images which can be easy for a human expert eye. The system here extracts three features as discussed earlier. First, the GLCM features are given importance and extracted in the proposed work: Gray levels, Energy, Contrast, Inverse Difference and entropy. In [15] Haralick et al have proposed different texture features of characteristics complexity information. It has become wide for many applications since the authors proposed their own work features. Moreover, GLCM characteristic features with image enhancement focus was discussed in [16]. The procedure of GLCM is explained in following figures. Different four directions of GLCM for the same image or image sub-regions are shown in the figure 14. Figure 15 shows the test image and figure 16 is the general structure of GLCM, figure 17 (a), (b), (c), (d) are GLCM with relative distance ' δ ' and with different inclinations.





1	0	1	2
2	0	1	3
1	2	3	1
1	1	0	3

Figure 7: Test Image

m/n	0	1	2	3
0	#(0,0)	#(0,0)	#(0,0)	#(0,0)
1	#(0,0)	#(0,0)	#(0,0)	#(0,0)
2	#(0,0)	#(0,0)	#(0,0)	#(0,0)
3	#(0,0)	#(0,0)	#(0,0)	#(0,0)

Figure 8: General form of GLCM

0	2	0	0		0	1	1	0	1	0	0	1	
1	0	2	1		1	2	0	0	0	2	2	1	(a)
1	1	0	0	(b)	0	0	1	0	1	1	0	0	(a) (c)
0	0	0	1	(d)	1	1	0	1	0	2	1	0	(0)

0	2	0	1
1	1	2	1
1	0	0	1
0	1	0	0

Figure 9: GLCM for (a) $\delta=1$, $\theta=135^{\circ}$ (b) $\delta=1$, $\theta=45^{\circ}$ (c) $\delta=1$, $\theta=90^{\circ}$ (d) $\delta=1$, $\theta=0^{\circ}$ *Texture feature based on GLCM*

Analysis of texture will concentrate on qualities of an image like smoothness, silky, rough or bumpy as described as function with spatial variations in gray levels. GLCM is a regularity matrix by which its level is known by image gray level values. GLCM produces a matrix with distance between pixels and different inclinations as shown in figures 14, 15, 16, 17 and to extract as texture features with eloquent statistics from the generated matrix. To compose GLCM, main property is probability value which can be defined as $P(m, n|\delta, \theta)$ to express the probability of pixels at θ inclination and δ



ISSN: 0970-2555

Volume : 53, Issue 4, No. 2, April : 2024

interval. $P(m, n | \delta, \theta)$ is represented by P(m, n) when θ and δ are known [17-18]. The equation for the Elements to compute is

$$P(m, n|\delta, \theta) = \frac{P(m, n|\delta, \theta)}{\sum_{m} \sum_{n} P(m, n|\delta, \theta)}$$
(11)

Usually, GLCM describes all the texture features, however here the system mainly focusses on entropy, energy, inverse difference and contrast as features.

Entropy

Randomness of image texture while co-occurrence matrix is equal for all the values and the maximum entropy depends on random distribution of gray levels as

$$S = -\sum_{x} \sum_{y} p(x, y) \log p(x, y)$$
(12)

Energy

Homogeneity texture measures the changes in reflection while distribution gray level uniformity in the image as

$$E = \sum_{m} \sum_{n} P(x, y)^2 \tag{13}$$

Inverse difference

Changes in texture image number is calculated by inverse difference. While p(x, y) considering as gray level at a particular point and co-ordinate (x, y) inverse difference is as

(14)

$$H = \sum_{X} \sum_{Y} \frac{1}{1 + (x - y)^2} p(x, y)$$

Contrast

Local number changes with the value distributed which reflects in image clarity and shadow depth can be calculated by Contrast as

$$I = \sum \sum (x - y)^2 p(x, y)$$
(15)

Then, level 2 DWT is also used to extract the low-level features and initially on the segmented output DWT is applied, it yields the outputs as LL1, LH1, HL1 and HH1 bands respectively. Then entropy, energy and correlation features are calculated on the LL band. Then, on the LL output band again DWT is applied, and it provides the outputs as LL2, LH2, HL2 and HH2 respectively. Again entropy, energy and correlation features are calculated on the LL2 band respectively as shown in figure.

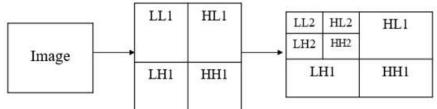


Figure 10: Level DWT coefficients.

And finally, Mean, and standard deviation based Statistical Colour features are extracted from the segmented image and specified in the below equations,

Mean
$$(\mu) = \frac{1}{N^2} \sum_{i,j=1}^{N} I(i,j)$$
 (16)
Standard Deviation $(\sigma) = \sqrt{\frac{\sum_{i,j=1}^{N} [I(i,j)-\mu]^2}{N^2}}$ (17)

Later, all these features are combined using array concatenation and it produces the output as hybrid feature matrix.

CLASSIFICATION

Neural networks have been effectively applied across a range of problem domains like finance, medicine, engineering, geology, physics, and biology. From a statistical viewpoint, neural networks are interesting because of their potential use in prediction and classification problems. PNN is a method developed using emulation of birth neural scheme. The neurons are connected in the



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Volume : 53, Issue 4, No. 2, April : 2024

predefined architecture for effectively performing the classification operation. Depending on the hybrid features, the weights of the neurons are created. Then, the relationships between weights are identified using its characteristic hybrid features. The quantity of weights decides the levels of layers for the proposed network. Figure represents the architecture of artificial neural networks. PNN basically consists of two stages for classification such as training and testing. The process of training will be performed based on the layer based architecture. The input layer is used to perform the mapping operation on the input dataset; the hybrid features of this dataset are categorized into weight distributions.

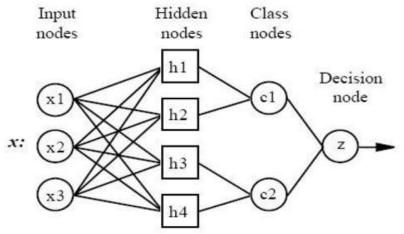


Fig.11 Layered architecture of PNN model.

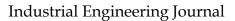
The PNN architecture has four hidden layers with weights. The first convolutional2D hidden layer of the net takes in 224 * 224*3 pixels skin lesion images and applies 96 11×11 filters at stride 4 pixels, followed by class node activation layer and decision normalization layer. Then the classification operation was implemented in the two levels of class nodes hidden layer. The two levels of hidden layer hold individually normality and abnormalities of the skin cancer characteristic information. Based on the segmentation criteria, it is categorized as normal and abnormal classification stage. These two levels are mapped as labels in output layer. Again the hidden layer also contains the abnormal cancer types separately; it is also holds the benign and malignant cancer weights in the second stage of hidden layer. Similarly, these benign and malignant weights are also mapped as label into output layer. When the test image is applied, its hybrid features are applied for testing purpose in the classification stage. Based on the maximum feature matching criteria utilizing Euclidean distance manner it will function. If the feature match occurred with hidden layer 11abels, then it is classified as normal skin image. If the feature match occurred with hidden layer C1 labels with maximum weight distribution, then it is classified as benign effected cancer image. If the feature match occurred with hidden layer C2 labels with minimum weight distribution, then it is classified as malignant affected cancer image.

Finally based on features and classification the type of disease will be predicted by comparing with the existed database. Hence, we can represent the segmented output image as a summation of total number of white and black pixels.

$$M = \sum_{x=1}^{L} \sum_{y=1}^{L} [f_{x,y}(0) + f_{x,y}(1)]$$

where L=1, 2, 3...256 $f_{x,y}(0) =$ black pixel having the value of zero, $f_{x,y}(1)$ = white pixels having the value of one

$$P = \sum_{i=1}^{L} \sum_{j=1}^{L} f_{x,y}(1)$$





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Where, P = number of white pixels

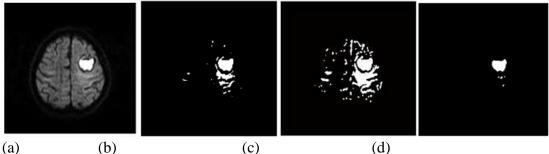
Now, by using the above equation, we can calculate the area of the segmented tumor based on the typography and digital imaging units [20], where one pixel is equal to 0.264583 millimeters. i.e., 1 pixel = 0.264583 mm

Then the area of tumor can be expressed as follows:

 $A_{Tumor} = (\sqrt{P})^* 0.2646 mm^2$

V. EXPERIMENTAL RESULTS

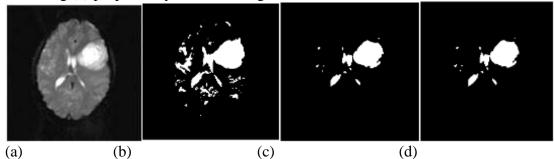
We had given an overview of conventional and proposed segmented outcomes with the tumour area in this section. All of the experiments were run using a 64-bit version of MATLAB 2016b with 4GB of RAM. We looked at five distinct sets of photos with varied sizes, such as 400x400, 512x512, and 600x600 pixels, that depicted different stages of tumours. The new hybrid clustering technique was then compared to the performance of traditional systems such as fuzzy c means, K-means, and manually segmented algorithms for detecting single and multi-tissues in MR brain pictures. The following graphs illustrate the experimental results of MRI tumour identification utilising the proposed hybrid algorithm and existing techniques. Our proposed method is more effective and accurate since it compares the findings. The segmented outputs of single tissue of MR brain images with manual segmentation, FCM clustering, K-means clustering, and proposed hybrid clustering techniques are shown in Figures 5.1 and 5.2. We can see from the results that the proposed hybrid clustering technique has recognised the tumour more effectively and accurately. Although our suggested technique will take longer to execute than k-means clustering, the accuracy of the segmented output will be higher, i.e., tumour area will be approximated more precisely to aid in diagnosis.





(e)

Fig.12 (a) Original Image (b) manual segmentation (c) Fuzzy C Means clustering (d) K-means clustering (e) proposed hybrid clustering



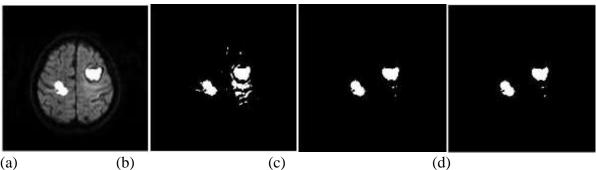


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(e)

Fig. 13 (a) original image (b) manual segmentation (c) fuzzy C means clustering (d) K-means clustering (e) proposed hybrid clustering

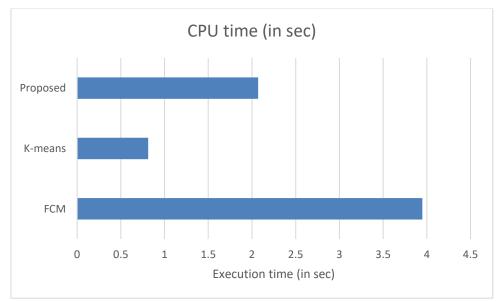


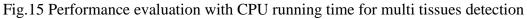
(a)



(e)

Fig.14 Segmented multi tissues obtained (a) original image (b) manual segmentation (c) FCM clustering (d) K-means clustering and (e) proposed hybrid clustering





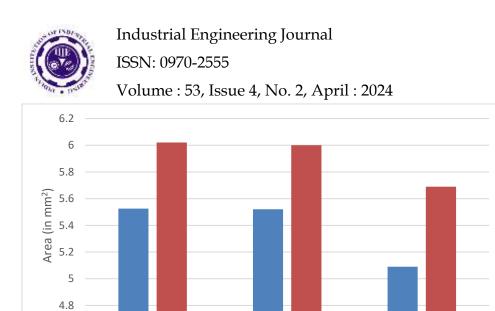


Fig. 16 Estimated area of segmented tissues T1 = tissue 1 and T2 = tissue 2

K-means

The performance evaluation of the suggested hybrid clustering algorithm in contrast to the traditional clustering algorithms provided in the literature is shown in the figures above.

Proposed

We calculated the execution time in seconds and the tissue area in millimetres squared.

CONCLUSION

4.6

FCM

The detection of single and multi-tissues in MR brain images, as well as the estimation of tissue area, has been done with better accuracy and reduced computing time. The use of U-IPC and the calculation of the area in terms of mm2 based on typography and digital imaging units worked well. The simulation results were also compared to current algorithms. With more effective and precise clustering methods, this can also be applied to 3D multimodal medical image segmentation.

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