SINGLE VALUED NEUTROSOPHIC FUZZY C-MEANS FOR MR BRAIN IMAGE SEGMENTATION

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Abstract- The image segmentation in medical field plays a vital role in early detection and diagnosing the disease. Recent days, many researchers are working on enhancing the result of segmentation, which are crucial for treatment planning. The Segmentation of brain images are challenging due to the presence of noise and intensity in-homogeneity that creates uncertainty in segmenting the tissues. The neutrosophic sets are efficient tools to address these uncertainties present in the images. In this paper, a novel single valued triangular neutrosohic fuzzy c-means algorithm is proposed to segment the magnetic resonance brain images that can effectively model the uncertainty with truth, falsity and indeterminacy regions. The experimental results reveal that the proposed work out performs the other relevant methods.

I. INTRODUCTION

Although there is tremendous improvement in medical acquisition devices, still the acquired medical images are subjected to noise and intensity in homogeneity. These artifacts are the resultant of improper acquisition device or process or the person movements during acquisition of image. These artifacts make the segmentation of medical images more challenging. The magnetic resonance(MR) brain image is often segmented into white matter(WM), gray matter(GM) and cerebro spinal fluid (CSF) and is important to study the functioning of brain, treatment arranging and quantitative examination.

Fuzzy CMean (FCM) is an effective clustering methods to segment MR brain images. Dunn [1] has designed the method and later was extended by Bezdek [2]. Fuzzy systems could not handle the pixels present in the boundary region called the indeterminacy set.

Neutrosophic sets(NS) introduce the indeterminacy set to effectively handle the boundary conditions. NS is a generalized fuzzy set and deals with origin, nature and neutrality. The NS represent the data with true t, false f and indeterminacy i, sets.

Guo *et al.*, [3] proposed NS to process the images with noise and propose a novel NS approach for image segmentation. In this method, the image is transformed into the NS and two new operations, $\alpha-$mean and $\gamma-$enhancement, are defined and applied to reduce the indeterminacy of the image, measured by the entropy of the indeterminate set. After this process the image becomes more uniform and homogeneous and more suitable for segmentation. Finally, the image in the NS domain is segmented using a $\gamma-$means clustering method.

In papers [4], [5] proposed automated brain tumor segmentation on MR images based on neutrosophic set approach. The method uses the averaging methods and based on it extracted the truth ,indeterminacy and false region that involves lots of computation. Intuisionistic fuzzy sets were also proposed in the literature [6], but the indeterminacy region is absent in the intuitionistic fuzzy sets.

The neutrosphic sets can effectively segment the image in the presence of noise, very well suited for brain image segmentation. In this paper a novel single valued triangular neutrosophic fuzzy c-Means (SVTNFCM) is proposed to extract the GM, WM and CSF from brain images.

The rest of the paper is organized as follows: Section II present the backround of neutrosophic sets and single valued triangular neutrosohic sets(SVTNS). The propose method is presented in Section III. The experimentation and discussion of the proposed method is present in Section IV and finally the conclusion is presented in Section V.

II. BACKGROUND

In the last five years MRI diffusion become important tool for learning the morphology of brain, the brain tissues unique insights into macro structure as well as micro structure. The Consortium Of Neuroimagers for the Non-invasive Exploration of brain Connectivity and Tracts (CONNECT) is introduced to combine tractography and measure of the brain to obtain the better accuracy of connectome [7].The magnetic resonance (MR) data analysis is introduced for handling very huge datasets with user friendly tools for paralleziation using R software. Compared to non parallized task, the task runned in parallized task and computation time reduced by 15 percent [8]. Imaging functional MRI is confounded by various factors, notably signal dropouts due to low signal to noise ratio and inhomogeneity of the magnetic are making difficult to make decision.However, the signal changes are identified based on nearby vessels mostly notable by BVR(Basel Vein of Rosenthal) [9].Maximizing the amount to which knowledge of human brain function extracted from the connectome results in new neuroimaging analysis algorithms and tools [10]. The fMRI used to check the non-invasively of the brain

activity with high spatial resolution.However the number of problems needs to be addressed. In statistical analysis needs many preprocessing steps, like slice time correction and compensation of motion are applied. [11]. The modern neuroimaging research signifies a multifactorial and data broad ranging becomes challenging, the growth of the data and logsticaland sociological issues. Multi data type and multisite becomes infrastructural challenge. The neuroimaging further advances in genetics,aging,diseases releated to age are required new vision to process the data while organizing of the resourecs into novel results [12]. The REstingstate based SCALing of parameter Estimates (RESCALE) uses the local information to determine the the compute voxelwise scaling factor based on correlaeation structure of fALFF. The RESCALE method pro posed here and easy to adapt to all taska based fMRI group studies in case of the resting state data for the same group group is correspondingly acquired [13]. A novel distributed rank one dictionary model is introduced for fMRI big data analysis.The model with sparsity constraint which loading the coefficient input data in every learning step.Spark engine with RDD (resilient distributed dataset) deployed to perform the operation in distributed manner. The Human Connectome Project (HCP) used in this model and proposed D-r1DL model is more scalable and efficient towards the bigdata analytics [14].

A. Neutrosophic sets

Neutrosophic Sets (NS) are proposed by Florentin Smarandache [15] with a new idea for dealing with the origin, nature and scope of neutralities. In neutrosophic set theory, every element is represented with a degree of truth, degree of false and an indeterminacy degree uniquely . Thus, a data, event, concept, element or entity A is considered as truth with its opposite Anti-A and the neutrality Neutral-A. Neutral-A is element not in A nor Anti-A. The Neutral-A and Anti-A are referred to as Not-A. As per the neutrosophic theory, every element A is neutralized and stabilized by Anti-A and Not-A. NS provides a powerful tool to deal with the indeterminacy [15].

Consider U as an universe and NS(A) is specified over U. An element x_i in set A is denoted as (t, i, f), where, t varies in $T(truth)$, i varies in $I(indeterminacy)$ and f varies in $F(false)$. Here, T, I and F are neutrosophic components varying in $]0^-, 1^+[$.

The element $x_i(t, i, f)$ belongs to A with $t\%$ true, $i\%$ indeterminacy and $f\%$ false. Statically, T, I and F are membership sets, but dynamically T, I and F are functions/operators depending on known and/or unknown parameters [15]. There are no constraints on the sum of T, I and F, so $0 \leq$ sup $T(X)+$ sup $I(X)+$sup $F(X)3^+$

B. Single valued netrosophic sets

A single valued netrosophic set N over X is defined as

$[0,1], I(x_i) : X \rightarrow [0,1] and F(x_i) : X \rightarrow [0,1]$ with $0 \leq T(x_i) + I(x_i) + F(x_i) \leq 3$ for all $x_i \in X$

1) Single valued triangular netrosophic sets : The SVTNS is defined as $\bar{N} = \{x_i, \bar{T}(x_i), \bar{I}(x_i), \bar{F}(x_i) \mid x \in X\}$ where

$$\bar{T}(x_i) = \begin{cases} \alpha\frac{(x_i - n_1)}{(n_2 - n_1)} & (n_1 \leq x_i \leq n_2) \\ \alpha & (x = n_2) \\ \alpha\frac{(n_3 - x_i)}{(n_3 - n_2)} & (n_2 < x_i \leq n_3) \\ 0 & otherwise \end{cases} \quad (1)$$

$$\bar{I}(x_i) = \begin{cases} \frac{(n_2 - x_i + \beta(x_i - n_1))}{(n_2 - n_1)} & (n_1 \leq x_i \leq n_2) \\ \theta & (x = n_2) \\ \frac{(x_i - n_2 + \beta(n_3 - x_i)}{(n_3 - n_2)} & (n_2 < x_i \leq n_3) \\ 1 & otherwise \end{cases} \quad (2)$$

$$\bar{F}(x_i) = \begin{cases} \frac{(n_2 - x_i + \theta(x_i - n_1))}{(n_2 - n_1)} & (n_1 \leq x_i \leq n_2) \\ \beta & (x = n_2) \\ \frac{(x_i - n_2 + \theta(n_3 - x_i)}{(n_3 - n_2)} & (n_2 < x_i \leq n_3) \\ 1 & otherwise \end{cases} \quad (3)$$

where n_1, n_2 and n_3 are neutrosophic numbers and α, β and θ determine the upper degree of truth, lower degrees of indeterminacy and falsity respectively.

III. PROPOSED METHOD

This section describes the flow of complete algorithm for segmentation of brain MR images using triangular neutrosophic fuzzy set.

A. Representation of image in triangular neutrosophic set

The observed image with size $M * N$ be denoted as $X = \{x_i / x_i$ is the value of the ith pixel in the image $\}$ where $1 \leq i \leq M * N$. The image X is represented in triangular neutrosophic fuzzy set as

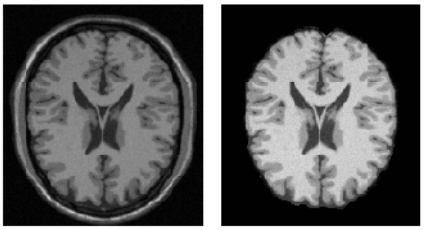
$$A = \{\bar{T}(x_i), \bar{I}(x_i), \bar{F}(x_i)) \mid x_i \in X\} \quad (4)$$

where $\bar{(T)}(x_i)$ is the membership value indicating truth , $(\bar{F})(x_i)$ is the non membership value indicating the falsity and $\bar{(I)}(x_i)$ indicates the indeterminacy value of x_i pixel.

B. Region determination using triangular neutrosophic fuzzy set

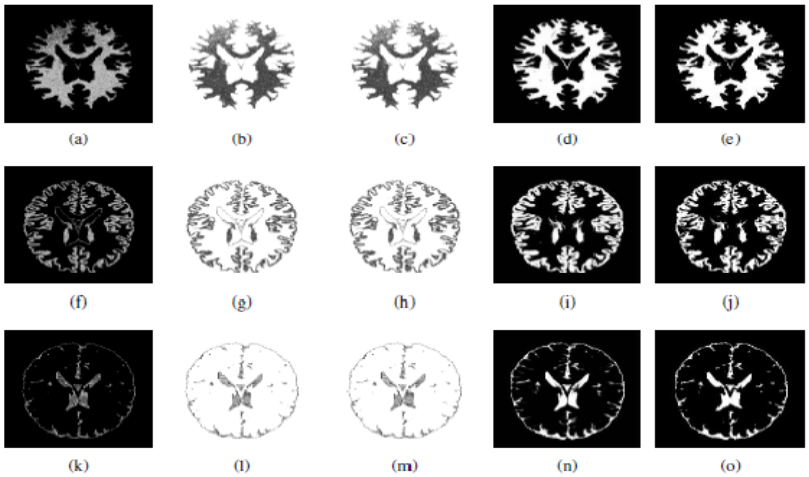
In order to determine the regions for brain image, the neutrosphic numbers need to be defined. The numbers $n1$,$n2$and $n3$ are obtained on experimentation on BrainWeb database.Different tissues WM,GM and CSF need to be extracted for better analysis. Hence, we consider three clusters to determine these tissues. Every cluster indeed is represented with triangular netrosophic fuzzy set. In order to extract the WM the values of n1=0.7, n2=0.8, n3=1, to extract CSF n1=0.2, n2=0.3,n3=0.4 , and to extract GM n1=0.5,n2=0.6, n3=0.7 are used on empirical experimentation.The $\alpha = 0.8$ to increase the truth intensity and $\beta = 0.2$, $\theta = 0.2$ are used for lowering the indeterminacy and falsity. Figure 1 (a) shows the Phantom image from BrainWeb with 20% INU and 3% noise and (b)skull stripped image. Figure 2 shows the regions extracted with the SVTNS.

These extracted regions act as input for clustering.



(a) (b)

Fig. 1. (a)Phantom image of brain web database with 1mm thickness 20% INU and 3% noise (b) skull stripped image.



(a) (b) (c) (d) (e)

(f) (g) (h) (i) (j)

(k) (l) (m) (n) (o)

Fig. 2. (a)(b)(c)(d)(e) Truth, indeterminacy , false regions Ground truth, SVTNSFCM result of WM. (f)(g)(h)(i)(j) Truth, indeterminacy , false regions Ground truth, SVTNSFCM result of GM. (k)(l)(m)(n)(o) Truth, indeterminacy , false regions Ground truth, SVTNSFCM result of CSF.

C. Single valued triangular neutrosophic fuzzy C-Means clustering(SVTNFCM

The fuzzy C-mean partitions the data set X in to n clusters by minimizing the below objective function J [16].

$$J = \sum_{i=1}^{n}\sum_{j=1}^{n}(u_{ij})^m || x_i - C_j ||^2 \quad (5)$$

u_{ij} is the membership value with i^{th} pixel and j^{th} centroid. C_j is the mean value of the cluster j, m is the fuzzifier value defined by the user. The fuzzy value m if closes to 1 the membership function becomes more crisp and binary, if m increases the membership function becomes increasingly fuzzy and blurred [17]. The m value $1.5 < m < 3$ gives good results for most of data and generally 2 is taken [16], [18], [19], [20]. The objective function is modified fro nuetrosophic sets a

$$J = \sum_{i=1}^{n}\sum_{j=1}^{n}\mu_{NS}(x_i)^m || \bar{T}(x_i) - C_j ||^2 \quad (6)$$

The SVTNSFCM is performed by calculating the cluster centroids and partition matrix using the below equation.

$$C_j = \frac{\sum_{x_i \in X}(\mu_{NS}(x_i))^m(1-\bar{I}(x_i))\bar{T}(x_i)\bar{F}(x_i)}{\sum_{x_i \in X}(\mu_{NS}^m(1-\bar{I}(x_i))} \quad (7)$$

$$\mu_{NS}(x_i) = \frac{1}{\sum_{c=1}^{n}\left(\frac{||\bar{T}(x_i)-C_j||}{||\bar{T}(x_i)-C_c||}\right)^{\frac{2}{m-1}}} \quad (8)$$

Like other clustering algorithms the neturosophic fuzzy c-means is also iterative and stops when the clusters are stable.

IV. EXPERIMENTATION AND DISCUSSION

A. Experimental setup

In order to find the efficacy of the proposed algorithm NFCM, brain databases: (i) Simulated Brain Web database [21] (ii) IBSR database [22] are used. The Brain Web database images are in MINC format, IBSR images are of .hrd or .bit8 format and BRATS images are .mha format. The databases and their image sizes are indicated in Table I. These images are converted to MATLAB readable format using the software (medical image processing, analysis and visualization) MIPAV[23]. Pre-processing is performed to separate the non brain image from the MR images before segmentation using the same MIPAV software. The proposed algorithm is implemented in MATLAB 10.1 on 1.8 GHz Intel core i3 processor.

TABLE I
DATA SETS USED FOR SIMULATION

Dimension	Dataset	Number of Images	Image Size
2D	Brain Web	20	181*217
2D	IBSR	20	256*128

In the experimental setup for all images to apply proposed segmentation GRIFCM algorithm, the number of clusters is taken as n = 4 (pertaining to GM, WM, CSF and back-ground). The initial $\mu_{NS}(x_i)$ is initalized with zeros,fuzzifier constant is set as m = 2 and the exit criteria is set as 0.01.

CONCLUSIONS

The novel and automatic segmentation approach for brain images has been proposed. SVTNFCM is a generalization of FCM that uses SVTNS to represent the image and applies the modified neutrosophic fuzzy c-means for clustering. The proposed method efficiently handle the uncertainty in the boundary region of the image with indeterminacy region.

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