Segmentation Of 3D Brain Using an Adaptive K-means Algorithm

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ABSTRACT

To segment the 3D medical image using K-Means clustering algorithm for 3-dimensional and multi-valued images that can be better for large datasets and to find initial centroid. In order to compare the performance an algorithm is described for segmenting 3D MR brain image into *K* different tissue types, which include gray, white matter and CSF, and maybe other abnormal tissues.MR images considered can be either scaled or multi-valued.

Keywords:

MR, Barycenter, Segmentation, low frequency coefficient.

1.INTRODUCTION:

With the evolution of new imaging sensors there arises the need of a meaningful combination of all employed imaging sources. The actual fusion process can take place at different levels of information representation such as signal, pixel, feature and symbolic level. This paper focuses on the so-called pixel level fusion process[1], where a composite image has to be built of several input images. In pixel-level image fusion, some generic requirements can be imposed on the fusion result. The fusion process should preserve all relevant information of the input imagery in the composite image.The fusion scheme should not introduce any artifacts or inconsistencies which would distract the human observer or following processing stages.This fused image undergoes segmentation process where the Segmentation refers to the process of partitioning a digital image into multiple regions (sets of pixels). The goal of segmentation is to simplify and/or change the representation of an image into something that is more meaningful and easier to analyze. Image segmentation is typically used to locate objects and boundaries (lines, curves, etc.) in images.The result of image segmentation is a set of regions that collectively cover the entire image, or a set of contours extracted from the image (see edge detection). Each of the pixels in a region are similar with respect to some characteristic or computed property, such as color, intensity, or texture. Segmentation is done using clustering technique, which separates the vessel structure from background.Thus the output image is contrast enhanced and more accurate than the source image and it also contains the exact features of the source image.

2. PROBLEMS AND SOLUTIONS:

In the existing system they have discussed with only 2-D images as input, but 2-D image is not enough for finding the Brain tumor.Initial centroid value is assumed. This system fails in large data sets. The objective of the present study is to use the improved K-means algorithm which is a solution to handle large scale data, which can select initial clustering center purposefully, reduce the sensitivity to isolated point and to avoid dissevering big cluster.

By using this technique locating the initial seed point is easy and which will give more accurate and high-resolution result.

Initial centroid algorithm is useful to avoid the formation of empty clusters, as the centroid values are taken with respect to the intensity value of the image.The advantages of theproposed systemis that the input image will be illustrated as a 3-D image. So Brain tumor can be detected easily with low image distortion[8]. Thus the Proposed algorithm is better for large datasets and to find initial centroid and also in cryptography and image hiding process.

2.1 Image Fusion:

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Image fusion is a image processing technique where more than one input image is fused to produce a single output image [2][6].

PCA is a powerful tool for analyzing data.It is a way of identifying patterns in data, and expressing the data in such a way as to highlight their similarities and differences[9].At first, multi-resolution wavelet decomposition on each source image is performed, and then the energy of the each 3*3 matrix region is calculated.The frequency coefficients of the source image are compared and the low frequency coefficient acts as a visible part.Finally, by applying the inverse wavelet transform the final fused image is obtained.

2.1.1.Principal Components Analysis:

It is a way of identifying patterns in data, and expressing the data in such a way as to highlight their similarities and differences. Since patterns in data can be hard to find in data of high dimension, where the luxury of graphical representation is not available, PCA is a powerful tool for analyzing data [9]. The other main advantage of PCA is that once you have found these patterns in the data, and you compress the data, i.e. by reducing the number of dimensions, without much loss of information.

 Method:

Step 1: Get some data.
Step 2: Subtract the mean.
Step 3: Calculate the covariance matrix.
Step 4: Calculate the eigen vectors and eigen values of the covariance matrix.
Step 5: Deriving the new data set.

2.1.2. Wavelet Transform:

Wavelets are mathematical functions defined over a finite interval and having an average value of zero that transform data into different frequency components, representing each component with a resolution matched to its scale. Calculating wavelet coefficients at every possible scale is a fair amount of work, and it generates an awful lot of data. If the scales and positions are chosen based on powers of two, the so-called dyadicscales and positions, then calculating wavelet coefficients are efficient and just as accurate[6]. This is obtained from discrete wavelet transform(DWT).

2.1.3.One-Stage Filtering:

For many signals, the low-frequency content is the most important part. It is the identity of the signal. The high-frequency content, on the other hand, imparts details to the signal. In wavelet analysis, the approximations and details are obtained after filtering. The approximations are the high-scale, low frequency components of the signal. The details are the low-scale, high frequency components. The filtering process is schematically represented as in the fig.1.
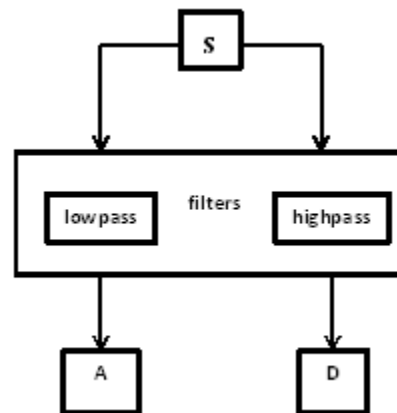

Fig.1. Single stage filtering

The original signal, S, passes through two complementary filters and emerges as two signals. Unfortunately, it may result in doubling of samples and hence to avoid this, downsampling is introduced. The process on the right, which includes downsampling, produces DWT coefficients.

2.1.4. Multiple-level Decomposition:

The decomposition process can be iterated, with successive approximations being decomposed in turn, so that one signal is broken down into many lower resolution components. This is called the wavelet decomposition tree.

2.1.5. Wavelet Reconstruction:

The reconstruction of the image is achieved by the inverse discrete wavelet transform (IDWT). The values are first upsampled and then passed to the filters.

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The wavelet analysis involves filtering and downsampling, whereas the wavelet reconstruction process consists of upsampling and filtering. Upsampling is the process of lengthening a signal component by inserting zeros between samples as shown in Fig.3.
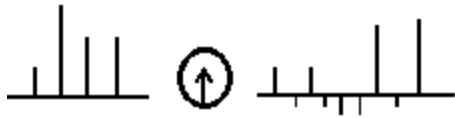

Fig.3.Reconstruction using upsampling

2.1.6. Reconstructing Approximations and Details:

It is possible to reconstruct the original signal from the coefficients of the approximations and details. The process yields a reconstructed approximation which has the same length as the original signal and which is a real approximation of it.

The reconstructed details and approximations are true constituents of the original signal. Since details and approximations are produced by downsampling and are only half the length of the original signal they cannot be directly combined to reproduce the signal. It is necessary to reconstruct the approximations and details before combining them.

2.2. Preprocessing

Pre-process technology enhances class 1 semantic content immediately before images are sent to an 3D Segmentation process. Semantic content in a class 1 refers to the correct classification of a blob of pixels, a line, a part of an image, or noise by implementing several powerful and proprietary noise removal and pixel grouping enhancement algorithms.

2.3.Centroid Calculation

K-means clustering algorithm is an easy way to classify a given data set through a certain number of clusters.The main idea is to define k centroids, one for each cluster. The next step is to take each point belonging to a given data set and associate it to the nearest centroid. At this point we need to re-calculate k new centroids as barycenters of the clusters resulting in loop.As a result of this loop the centroids do not move any more.Finally, this algorithm aims at minimizing an objective function, in this case a squared error function.

2.4.Segmentation

Segmentation refers to the process of partioning a digital image into multiple regions(sets of pixels).The goal of segmentation is to simplify and/or change the representation of an image into something that is more meaningful and easier to analyze.Image segmentation is typically used to locate objects and boundaries (lines, curves, etc.) in images[10]. The result of image segmentation is a set of regions that collectively cover the entire image.Each of the pixels in a region is similar with respect to some characteristic such as color, intensity, or texture.

2.5. Clustering

Clustering deals with finding a structure in a collection of unlabeled data.Acluster is a collection of objects which are "similar" between them and are "dissimilar" to the objects belonging to other clusters.Among the various clustering algorithm, overlapping clustering algorithm is used.The overlapping clustering, uses fuzzy sets to cluster data, so that each point may belong to two or more clusters with different degrees of membership.In this case, data will be associated to an appropriate membership value.

3. ILLUSTRATION:

Step 1: Get some data:

Let us consider some 2-dimensional datasfound in Figure 3.1, along with a plot of that data.

Step 2: Subtract the mean:

The mean subtracted is the average across each dimension. So, all the $<$ values have $<\_$ (the mean of the $<$ values of all the data points) subtracted, and all the $=$ values have $=\_$ subtracted from them. This produces a data set whose mean is zero.
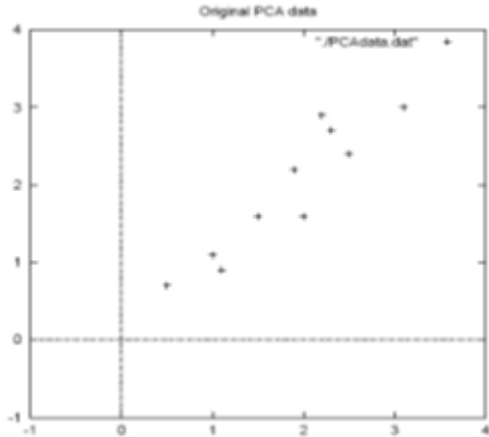
Data

X	Y
2.5	2.4
0.5	0.7
2.2	2.9
1.9	2.2
3.1	3.0

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2.3	2.7
2	1.6
1	1.1
1.5	1.6
1.1	0.9

Data Adjust

X	Y
.69	.49
-1.31	-1.21
.39	.99
.09	.29
1.29	1.09
.49	.79
.19	-.31
-.81	-.81
-.31	-.31
-.71	-1.01

Fig 3.1: PCA example data, original data on the left, data width the means subtracted on the right, and plot of the

data.

Step 3: Calculate the covariance matrix:

Since the datais 2 dimensional, the covariance matrix will be a 2×2 matrix.

Step 4: Calculate the eigenvectors and eigenvalues of the covariance matrix:

Since the covariance matrix is square, we can calculate the eigenvectors and eigenvalues

for this matrix. It is important to notice that these eigenvectors are both *unit* eigenvectors i.e. Theirlengths are both 1. This is very important for PCA. So, by this process of taking the eigenvectors of the covariance matrix, we have been able to extract lines that characterise the data.

Step 5: Deriving the new data set:

This is the final step in PCA, and is also the easiest. Once we have chosen the components(eigenvectors) that we wish to keep in our data and formed a feature vector, we simply take the transpose of the vector and multiply it on the left of the original data set transposed.

Final data=RowFeatureVector × RowDataAdjust.

Where RowFeatureVector is the matrix with the eigenvectors in the columns transposed so that the eigenvectors are now in the rows, with the mostsignificant eigenvector at the top, and RowDataAdjust is the mean-adjusted data transposed, i.e. the data items are in each column, with each row holding a separate dimension.

4.IMPLEMENTATION:

Load CT and MRI scan:
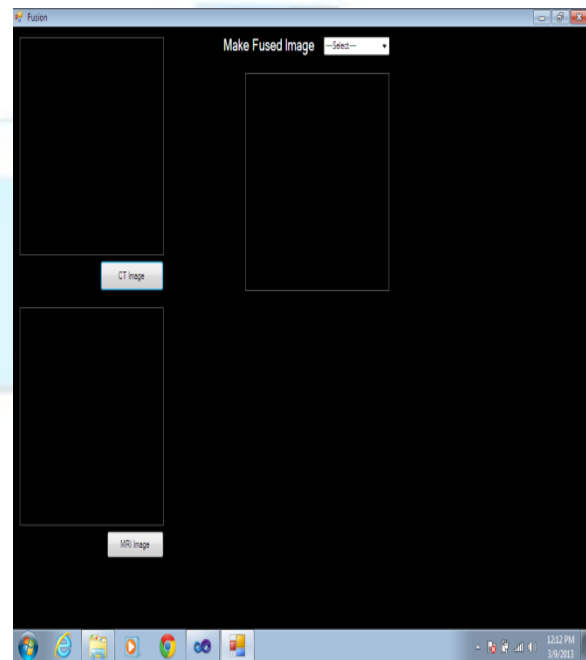
Load CT scan:
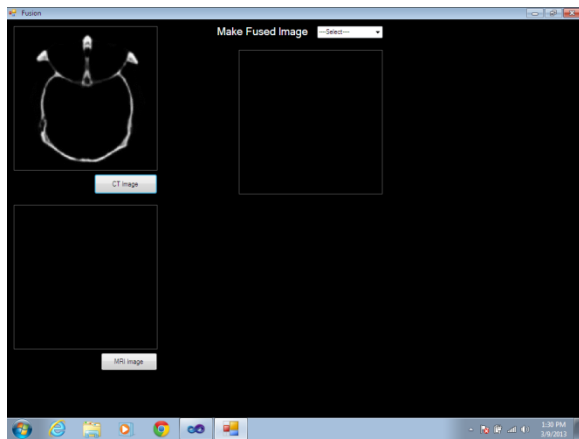
Load MRI scan:
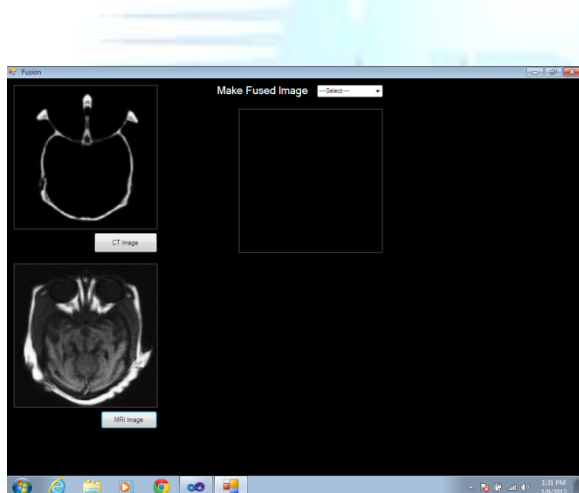
Fused image:

5.CONCLUSION:

Vessel segmentation methods have been a heavily researched area in recent years. Even though many promising techniques and algorithms have been developed, it is still an open area for more research. This algorithm does not require any user interaction, not even to identify a start point. Here seed points are selected randomly which determines the main branches of the vessel structure. Random selection of seed points does not yield accurate segmentation. Accuracy of the segmentation process is essential to achieve more precise and repeatable radiological diagnostic systems. Accuracy can be improved by incorporating a priori information on vessel anatomy and let high level knowledge guide the segmentation algorithm. k-means algorithm is a popular clustering algorithm applied widely, but the standard algorithm which selects **k** objects randomly frompopulation as initial centroids cannot always give a good and stable clustering. Experimental results show that selecting centroids by our algorithm can lead to abetter clustering.

Along with the fast development of database and network, the data scale clustering tasks involved in which becomes more and more large. K-means algorithm is a popular partition algorithm in cluster analysis, which has some limitations when there are some restrictions in computing resources and time, especially for huge size dataset. The improved K-means algorithm presented in this paper is a solution to handle large scale data, which can select initial clustering center purposefully, reduce the sensitivity to isolated point, avoid dissevering big cluster, and overcome deflexion of data in some degree that caused by the disproportion in data partitioning owing to adoption of multi-sampling.

6. FUTURE ENHANCEMENT:

The improved K-means algorithm is a solution to handle large scale data, which can select initial clustering center purposefully, reduce the sensitivity to isolated point, avoid dissevering big cluster. By using this technique locating the initial seed point is easy and which will give more accurate and high-resolution result. By using various techniques we can study or compare the results and find out which technique gives higher resolution.

7.ACKNOWLEDGEMENT:

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