

4<sup>th</sup> International conference on Recent Trends in Computer Science & Engineering

## Investigation on Abnormal Tissues Detection Methods for MRI Image

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### Abstract

Magnetic resonance imaging (MRI) provides detailed information about the soft tissues of the brain to identify tumors, cancer or any abnormal conditions in brain. Usually these images contain a significant amount of noise caused by operators or some external factors. De-noising is essential before detection of any abnormal areas from these images. There are several de-noising methods. In this paper, wavelet denoising techniques are considered for denoising the MRI image. The quality of the image is assessed using Peak Signal to Noise Ratio (PSNR), Squared Error Mean (SEM) and Absolute Mean Error (AME). These de-noised images are very useful for the segmentation process to easily extract the abnormal area from the image. Segmentation plays a crucial role for detection of any abnormal areas, tumors and irregularities in brain images. For this process two unsupervised algorithms are proposed for the detection of abnormal area from de-noised image. Both Expectation Maximization and K-means segmentation algorithms are used to identify the abnormal tissues in a given MRI. The performance of both methods are analyzed with suitable parameters like Entropy, Area and Perimeter. These parameters show the performance of the algorithms for the segmentation process and hence a suitable algorithm can be applied.

*Keywords: MRI image, PSNR, MSE, SEM, Entropy, Area, Perimeter.*

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### 1. INTRODUCTION

Bio-medical image processing techniques are used to take the information of human anatomy. Now a days in the field of medical there are several technological developments occurred in diagnosis systems out of them most commonly available images are X-ray, CT, MRI. These images give the information about hard and soft tissues of the body. This information is used to identify any abnormal cases, tumors, cancers etc. In this process MRI scan is very useful and it is harmless because there will be no radiation. This scan is based on magnetic field and radio waves, and it is more comfortable than other scans<sup>2</sup>. These images provide detailed information about the abnormal areas, tumor type, position and size. For this reason, MRI imaging study is chosen for this work. These images corrupted with some type of noise during transmission process. De-noising the image is very essential before detection of abnormal areas<sup>6</sup>. This noise can be removed by using different filtering methods or some other techniques. In this paper different wavelet technique are used for de-noising the MRI. A wavelet is a “small wave”, which has its

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energy concentrated in time to give a tool for the analysis of transient, non-stationary, or time-varying phenomena about analyzing signal with short duration finite energy functions<sup>8,7</sup>. There are two types of wavelet techniques continuous wavelet transforms and discrete wavelet transforms. There several types of DWT, out of them db2, bior3.3 and sym6 are considered here. By using these wavelets MRI image can be de-noised. This de-noised images helps the segmentation process to easily extract the abnormal areas from the image.

In digital image processing different segmentation methods are used for the subtraction of the region of interests from the images. Segmentation plays vital role in medical image processing, where clustering technique widely used in medical application particularly for brain tumor detection in magnetic resonance imaging (MRI)<sup>9,10</sup>. In this paper considering two unsupervised algorithms, Expectation maximization (EM) and K-means method has been taken in to consideration, both algorithms are used to find the natural clusters with in given data base<sup>4</sup>. These two clustering methods can be based on pixel intensity, texture or some combination of these<sup>5</sup>. This paper MRI abnormal image is considered and above mention segmentation methods are developed to extract abnormal area from the background. The parameters area, perimeter, entropy are calculated on both segmentation methods, based on these parameters performance of the algorithm are analysed.

## 2. Proposed Methods

### 2.1 K-means algorithm

K-means is the clustering approach method. Clustering is the method of dividing set of data points. Each cluster can be characterized by single reference point. The variance is used in clustering it's indicate the quality of partitioning and the error is measured sum of all variance is given by.

$$D = \sum_{i=1}^k \sum_{j=1}^{m_i} \|x_{ij} - r_i\|^2 \quad (1)$$

Where  $x_{ij}$  is the  $j^{\text{th}}$  point of the  $i^{\text{th}}$  cluster,  $r_i$  is the reference point of the  $i^{\text{th}}$  cluster and  $m_i$  is the no of points in the cluster.  $\|x_{ij} - r_i\|$  indicates the distance between the  $x_{ij}$  and  $r_i$ . Error indicates the over all spread points about the reference point and its value should be small as possible<sup>1,5</sup>. In this cluster N no of clusters, partition can be considered as  $L=(L_1, L_2, \dots, L_k)$  for a given points and corresponding centers are  $C=(C_1, C_2, \dots, C_k)$ . The assignment of cluster is keep repeating until the point assignment stabilises that is no more rearrangement of points are left<sup>1</sup>.

1. Initially intensity mean value of the each region is defined
2. Determine the number of clusters and set it as N
3. The number of patterns is selected as N corresponding to N centroid for N clusters.
4. Compute the new centroid classifies each pattern to the closest cluster centroid.
5. This process is repeated until the desired result is achieved.

### 2.2 Expectation Maximization algorithm

This is unsupervised algorithm it is used to find the estimated parameters of maximum likelihood or posterior probability. When the data are incomplete are missing. This method provides a systematic approach to find the maximum likelihood model<sup>3</sup>. The EM algorithm is parameterizing based on classes, while at the same time determining parameters describe the bias field<sup>4</sup>. With an iteration of the EM algorithm, the mixture model parameters and the bias field parameters are updated and perform the classification. In this method parameter estimation into two steps first E step calculate that is expected value and second step M step computes the parameters for maximizing value based on E value. First step i.e E step estimation of parameter vector  $\phi_0$  is initially estimated<sup>4,5</sup>. The posterior probability which determines the class of the voxel is given by.

$$p(y_i | \gamma_i = j, \theta_j) = G_{\sigma_j}(y_i - \mu_j) \quad (2)$$

Where  $G_{\sigma_j}$  is Gaussian modeling class  $j$ ,  $\gamma_i$  is class of  $i^{\text{th}}$  voxel,  $\mu_j$  is mean intensity of the  $j^{\text{th}}$  class,  $\sigma_j$  is standard deviation of the  $j^{\text{th}}$  class

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