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# A Comparative Study of Brain Tumour Detection Using K- Harmonic Means, Expectation Maximization and Hierarchical Clustering Algorithms

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**ABSTRACT:** Brain is the centre of human Central nervous system. The brain is a complex organ as it contains 50-100 billion neurons forming a gigantic neural network. Detection of anatomical brain structures with their exact location is important for treatments like radiation therapy and surgery. Radiologists perform the diagnosis of brain tumour manually on MRI images but it being time consuming and error prone as large no of image slices and the large variations between them. DICOM (Digital Imaging and Communications in Medicine) plays a key role as it is the standard for handling, storing, reading, viewing and writing, printing information for medical Imaging.

**KEY WORDS:** Brain tumour, Clustering, Harmonic Means, Maximization, MRI, Nervous system, DICOM

## I. INTRODUCTION

Brain tissue and tumour segmentation in images have been an active research area. Extraction of good features is fundamental to successful image segmentation. Due to complex structures of different tissues such as the gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF) in the MRI brain images, extraction of useful features is a challenging task.

Variability in tumour location, shape, size, and texture properties further complicates the search for robust features. Posterior fossa (PF) tumour is usually located near the brain stem and cerebellum. About 55–70% paediatric brain tumours arise in the PF. Due to narrow confinement at the base of the skull, complete removal of PF tumours poses nontrivial challenges. Therefore, accurate segmentation of PF tumour is necessary.

The techniques like MRI (Magnetic Resonance Imaging), NMRI (Nuclear Magnetic Resonance Imaging), MRT (Magnetic Resonance Tomography) and CT (Computed Tomography) Scan are being widely used to get the images for processing to detect the tumour, out of which MRI is widely used as it provides much greater contrast between the different soft tissues of the body compared to computed tomography (CT). Segmentation techniques like K means clustering, Fuzzy C means, Hierarchical, Watershed Algorithms, and Self Organizing Maps are widely implemented depending on which methodology is required as it can be Region growing, frequency domain based or thresholding based which classifies the MRI Images.

***Tumour:***

A tumour is an acronym for a neoplasm or a solid lesion formed by an abnormal growth of cells (termed neoplastic) which looks like a swelling. Brain Tumours are composed of the cells that exhibit abnormal and unrestrained cell division. Brain tumour can be benign or malignant, benign being non-cancerous and malignant are cancerous. Malignant tumours are classified in to two types like Primary and Secondary tumours.

Benign tumours are less harmful compared to malignant as in malignant tumours it spreads rapidly invading other tissues of brain, progressively worsening the condition causing death.

MRI images to detect brain tumour classifies the tumour depending on whether the brain is an abnormal tissue containing normal volume brain tissues like white matter, gray matter and CSF (cerebro-spinal fluid) but also have

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some slices contain pathology like edema and necrosis hence making them abnormal brain tissues. Based on the CSF Symmetry on the vertical axis through the brain centre a normal volume brain tissue and an abnormal volume brain tissue could be classified. The MRI images can be of T1, T2 weighted type of which T2 weighted Images are being widely used in Medical Imaging as in this case of cerebral and spinal study, the CSF (cerebrospinal fluid) are lighter in T2 weighted images as they are acquired using fast echo spin sequence whereas the T1 weighted images are acquired using a spin echo sequence. Primary focus on exact brain tumour's location and its extraction with parameters like area and time to yield faithful and error free output.

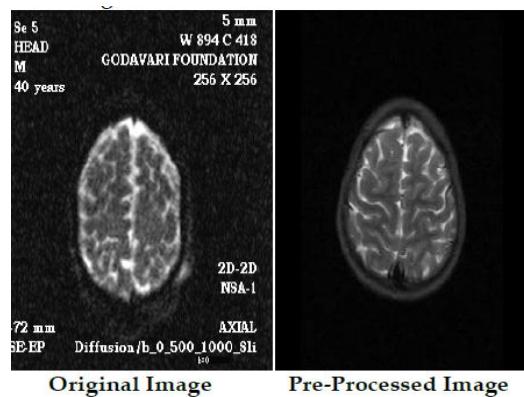


Figure 1  
 TUMOUR DETECTION PROCESS

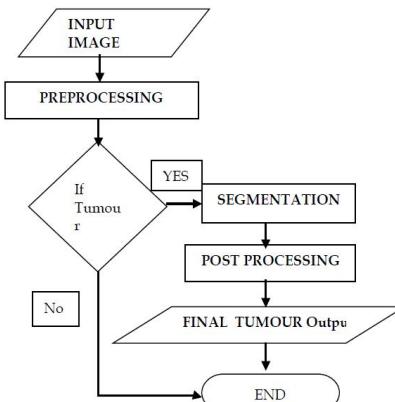


Figure 2

*Input Data sources: (Collected from Hospital (A Patient Record))  
 Images Listed Below*

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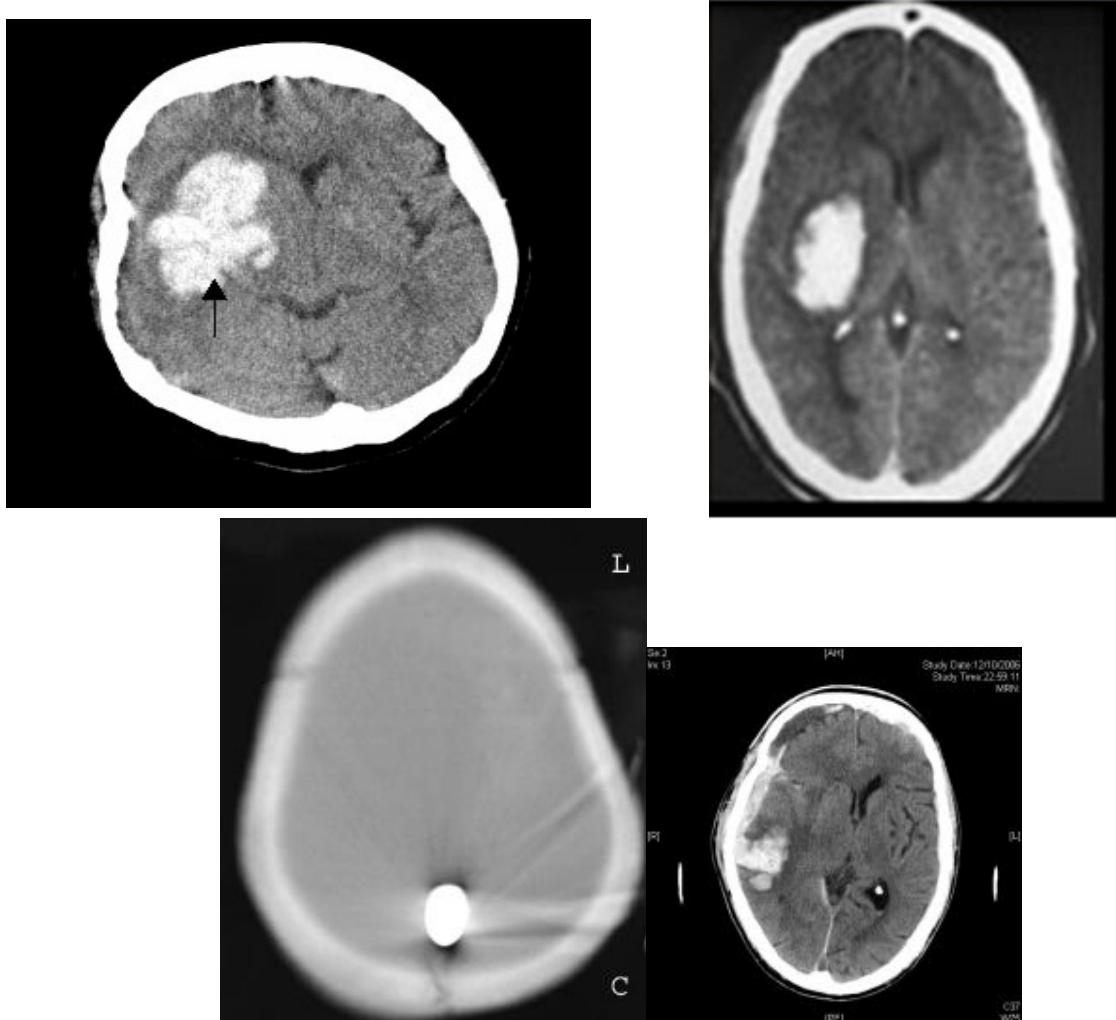
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## II. LITERATURE SURVEY

Brain tumour is an abnormal mass of tissue in which some cells grow and multiply uncontrollably, apparently unregulated by the mechanisms that control normal cells. The growth of a tumour takes up space within the skull and interferes with normal brain activity. So detection of the tumour is very important in earlier stages. Various techniques were developed for detection of tumour in brain. This paper focused on survey of well-known brain tumour detection algorithms that have been proposed so far to detect the location of the tumour. The main concentration is on those techniques which use image segmentation to detect brain tumour. These techniques use the MRI Scanned Images to detect the tumour in the brain. Differences between some well-known techniques are also considered in this paper[1]. During past few years, brain tumour segmentation in magnetic resonance imaging (MRI) has become an emergent research area in the field of medical imaging system. Brain tumour detection helps in finding the exact size and location of tumour[2]. An efficient algorithm is proposed in this paper for tumour detection based on segmentation and morphological operators. Firstly quality of scanned image is enhanced and then morphological operators are applied to detect the tumour in the scanned image.

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In this paper, modified image segmentation techniques were applied on MRI scan images in order to detect brain tumours. Also in this paper, a modified Probabilistic Neural Network (PNN) model that is based on learning vector quantization (LVQ) with image and data analysis and manipulation techniques is proposed to carry out an automated brain tumour classification using MRI-scans. The assessment of the modified PNN classifier performance is measured in terms of the training performance, classification accuracies and computational time. The simulation results showed that the modified PNN gives rapid and accurate classification compared with the image processing and published conventional PNN techniques. Simulation results also showed that the proposed system out performs the corresponding PNN system presented in, and successfully handle the process of brain tumour classification in MRI image with 100% accuracy when the spread value is equal to 1[3]. These results also claim that the proposed LVQ-based PNN system decreases the processing time to approximately 79% compared with the conventional PNN which makes it very promising in the field of in-vivo brain tumour detection and identification

**III. METHODOLOGY*****K-Harmonic Means:***

The computation starts with an initialization of the centre positions and followed by iterative refinement of these positions. Many experimental results show that KHM is essentially insensitive to the initialization of the centres than KHM and EM. The dependency of the K-Means performance on the initialization of the centres is a major problem; a similar issue exists for an alternative algorithm, Expectation Maximization (EM), although to a lesser extent. Many papers have been published to find good initializations for KM. This paper takes a totally different approach by changing MIN () used in KM to HA () (Harmonic Average), which is similar to MIN () but “softer”, to make the performance function “easier to optimize” by an algorithm that is essentially insensitive to initialization. More explanation will be given later.

***Algorithm***

1. Initialize the algorithm with guessed centres C
2. For each data point  $x_i$ , compute its membership  $m(c_j|x_i)$  in each centre  $c_j$  and its weight  $w(x_i)$ .
3. For each centre  $c_j$ , re compute its location from all data points  $x_i$ , according to their membership and weights
4. The solution is then a set of k cluster centres, which is located at the centroid of the data for which it is the closest centre
5. KM has a hard membership function, so each data point belongs only to its nearest cluster. This way a Voronoi partitioning of the data is created. The membership function is defined
6. KM has a constant weight function, that gives all data points equal importance in each iteration. The weight function is defined.

***Expectation Maximization Algorithm:***

An expectation–maximization (EM) algorithm is an iterative method for finding maximum likelihood or maximum a posteriori (MAP) estimates of parameters in statistical models, where the model depends on unobserved latent variables. The EM iteration alternates between performing an expectation (E) step, which creates a function for the expectation of the log-likelihood evaluated using the current estimate for the parameters, and maximization (M) step, which computes parameters maximizing the expected log-likelihood found on the E step. These parameter-estimates are then used to determine the distribution of the latent variables in the next E step.

The EM algorithm is used to find the maximum likelihood parameters of a statistical model in cases where the equations cannot be solved directly. Typically these models involve latent variables in addition to unknown parameters and known data observations. That is, either there are missing values among the data, or the model can be formulated more simply by assuming the existence of additional unobserved data points. (For example, a mixture model can be described more simply by assuming that each observed data point has a corresponding unobserved data point, or latent variable, specifying the mixture component that each data point belongs to.)

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**Toc H Institute of Science & Technology, Arakunnam, Kerala, India during 16th - 18th July -2014***Algorithm*An iterative algorithm, in the case where both  $\theta$  and  $Z$  are unknown:

1. First, initialize the parameters  $\theta$  to some random values.
2. Compute the best value for  $Z$  given these parameter values.
3. Then, use the just-computed values of  $Z$  to compute a better estimate for the parameters  $\theta$ . Parameters associated with a particular value of  $Z$  will use only those data points whose associated latent variable has that value.
4. Iterate steps 2 and 3 until convergence.

The algorithm as just described monotonically approaches a local minimum of the cost function, and is commonly called hard EM. The k-means algorithm is an example of this class of algorithms.

*Hierarchical Clustering Algorithm:*

The hierarchical clustering is a method of cluster analysis which seeks to build a hierarchy of clusters. Strategies for hierarchical clustering generally fall into two types:

*Agglomerative:* This is a "bottom up" approach: each observation starts in its own cluster, and pairs of clusters are merged as one moves up the hierarchy.

*Divisive:* This is a "top down" approach: all observations start in one cluster, and splits are performed recursively as one moves down the hierarchy in general, the merges and splits are determined in a greedy manner. The results of hierarchical clustering are usually presented in a dendrogram.

*Algorithm*

1. The sum of all intra-cluster variance.
2. The decrease in variance for the cluster being merged (Ward's criterion).
3. The probability that candidate clusters spawn from the same distribution function.
4. The product of in-degree and out-degree on a k-nearest-neighbour graph.
5. The increment of some cluster descriptor (i.e., a quantity defined for measuring the quality of a cluster) after merging two clusters.

**IV. EXPERIMENTAL RESULTS**

Computational Costs of KHM in Each Iteration In each iteration, calculating all the pair wise distances from N data points to K centres (of dimensional vectors) costs  $O(N*K*D)$ . KM and EM (linear mixing) share the same cost on this part. After getting the coefficients  $p_{i,k}$ , calculating the linear combinations,  $m_k = \sum p_{i,k}x_i$ , costs another  $O(N*K*D)$ . EM costs the same on this part. KM costs less ( $O(N*D)$ ) on this due to the partitioning but an additional  $O(N*K)$  comparison and assignment (marking) operations are used to do the partitioning. After calculating the distances, all quantities used in the algorithm no longer depend on the dimension and all other costs are  $O(N*K)$ . The leading asymptotic term for all three algorithms are the same,  $O(N*K*D)$ . The asymptotic computational complexity per iteration for KM, KHM and EM (linear mixing model) are all  $O(N*K*D)$ . It is the convergence rate and the convergence quality (dependency on the initialization) which differentiate them in real world applications.

The quantity inside is the linear mixing of the bell-shape functions the EXP()'s. Comparing with EM's performance function, we can look at the performance functions of KM and KHM also as mixings of bell-shape functions. (The extra factor,  $1/\sqrt{2\pi D}$ , does not have any real impact because it only change the performance function by adding a constant, which does not change the locations of the optima of the function. It is OK to either add the factor to KM and KHM's performance functions, or remove the factor from the EM's. They choose not to change any of them.

For both MIN-Mixing and Harmonic Mixing, the maximums of the components (the individual bells) match the maximums of the mixture. This can be proved easily by setting the gradient of the mixing functions to zero. It is also shown in Figure 4 for a particular example. But for linear mixing, they do not match -- the maximums of the mixture shift towards of the maximums of the components as shown. When Linear Mixing EM is used, the centres of the bell

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shape functions are biased from the true centres of the local densities of data because the maximums of the mixture are intended to match the local densities of data.

This shows the quality of the three algorithms on the BIRCH data set when the “correct” number of centres is used. All three algorithms started from the same random initialization the centres under EM is “more mobile” than under KM. They are most mobile under KHM. From the plots (given at the end of this paper), eight pairs of centres are trapped under KM (two centres found in one cluster) after it has already converged to a local optimum. Only one pair of centres is trapped under KHM; and 4 pairs under EM. The results are comparable under many different random initializations used.

This shows that when the initialization is very bad, both KM and EM converges very slowly (if converge to anything meaningful at all). All three algorithms started from the same bad initialization. KHM moves the centres out “layer-by-layer” like peeling an onion. KHM converges very fast and reached a configuration that is close to the global optimum in about 40 iterations.

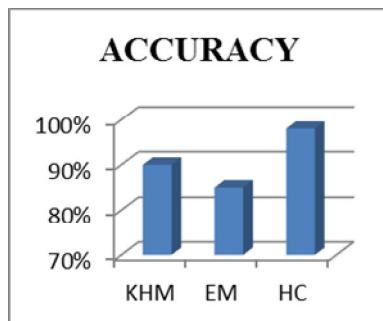
EM does not work well when the centres are close to each other (the reason was given earlier the individual bell shape functions lose their identity and are merged into a big bell shape function with a ghost centre). Most centres out of the 2000 centres merged with others. The problem could be fixed by allowing the variance (“diameter”) of the bell-shape functions to change. But that will introduce a lot more parameter(s), which cause new convergence problems. The third one shows that KHM can start from really bad initializations. In the Bad Initialization, 400centres are linearly spread out on a small line segment out the region occupied by data. KHM converged nicely. KM and EM do not work under this bad initialization. A random initialization is used for them.

Next we repeat the same experiment as but with a bad initialization instead of the random initialization. In the Bad Initialization, 100 centres are linearly spread out on a small line segment in the centre of all data. KHM converged nicely in 90iterations with only two pairs trapped. KM and EM do not converge well even after 300 iterations.

The first parameter is accuracy and hierarchical clustering outperforms the other methods as shown.

Table 1

FACTORS	KHM	EM	HC
ACCURACY	90%	85%	98%



The next is about the convergence of the iterations and EM takes less iterations, while KHM and HC are more.

Table 2

DETAILS	KHM	EM	HC
ITERATIONS	21	15	42

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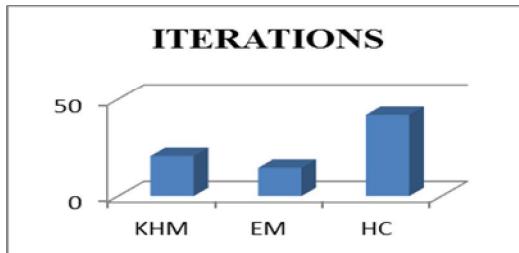
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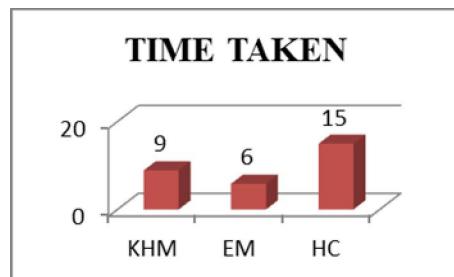
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Therefore it may be concluded that EM takes lesser time due to the lesser number of iterations.

Table 3

DETAILS	KHM	EM	HC
TIME TAKEN IN SEC	0.009	0.006	0.015



Accuracy Measured by the following criterias:

- (i) Segmentation of image
- (ii) Edge of the image
- (iii) Comparison of Pre-processed images
- (iv) Extraction of the image

### V. CONCLUSION

A new system that can be used as a second decision for the surgeons and radiologists is proposed. In this system brain tumours have been segmented with the help of three methods. The accuracy for Hierarchical clustering was high compared to the other methods and also the segmentation was intended. Thus tumour segmentation has a promising future as the universal segmentation algorithm and has become the focus of contemporary research. In spite of several decades of research up to now to the knowledge of authors, there is no universally accepted method for image segmentation, as the result of image segmentation is affected by lots of factors, such as: homogeneity of tumour's, spatial characteristics of the image continuity, texture, image content. The study has focused on segmentation by k harmonic means; expectation maximization and hierarchical clustering based detection techniques and has made its observations. Thus there is hierarchical clustering method for accuracy which can be considered good for all type of images, and other methods equally good for time and iterations.

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