

Content Based Retrieval of Liver Images for Computer Aided Diagnosis



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Abstract- Liver cancer is a serious disease caused by a variety of factors that damage the liver region. Early detection of this disease is necessary to diagnose and to cure it completely. Enormous increase in medical database images has lead to development of Content Based Image Retrieval (CBIR) system to retrieve relevant liver images from medical database consisting of abdominal Computed Tomography (CT) images. In the proposed method Content Based Medical Image Retrieval (CBMIR) system is designed to search and retrieve relevant liver images from medical image database. Adaptive Region Growing Algorithm (ARGA) and Simple Linear Iterative Clustering (SLIC) are used for liver and tumor segmentation. Features are extracted using Gray Level Co-occurrence Matrix (GLCM), Average Correction High order Local Autocorrelation Coefficients (ACHLAC) and Legendre Moments (LM). Based on the distance metric, distances between extracted features of query image and images in the database are measured. Euclidean distance metric is used to retrieve relevant medical images.

Keywords - Liver tumor, Adaptive Region Growing Algorithm (ARGA), Simple Linear Iterative Clustering (SLIC), Gray Level Co-occurrence Matrix (GLCM), Average Correction High order Local Autocorrelation Coefficient (ACHLAC) and Legendre Moments (LM), Euclidean Distance.

I. INTRODUCTION

CBIR in medical domain continue to be the significant area in research over last decade. Image retrieval searches relevant images in huge medical records using characteristic features associated with images. To help radiologist in searching required image from large datasets effective Content Based Medical Image Retrieval (CBMIR) development is necessary [1]. To manage large medical database images, numerous automatic retrieval based algorithms are proposed. By retrieving similar images and case histories doctors could make a precise and accurate decision about the patient's disease stage. Generally CBIR algorithm is helpful in crime investigation, military application, intellectual property, designing and in medical applications [2], [3]. Advance and fast use of internet leads to increase in adding digital images

on web produced by scientific, educational, medical, industrial and other applications. Medical image diagnosing and rapid progress of digital images in medical field from past three decade provide exclusive way for physicians and radiologists to diagnose the diseases [4]. Medical images give anatomical and structural information of affected region which helps radiologist for diagnosing tumor. Present methods such as Digital Imaging and Communication in Medicine (DICOM), Picture Archival and Communication Systems (PACS) increase image transfer interoperability. Medical images like Magnetic Resonance (MRI), Computerized Tomography (CT), Microscopic Pathology, Single Positron Emission Computed Tomography (SPECT), histology images and Ultrasound (US) are highly complex and localized in nature. These images take various processing (image) techniques for diagnosing the disease. Many physicians or radiologists observe images in conventional ways using their individual skill and knowledge to avoid complexity [5], [6].

II. LITERATURE SURVEY

Azhar Quddus et.al [7] proposed retrieval of two dimensional MR image slices in Neurological area. This system recognizes three dimensional brain volumes from medical dataset, based upon query image and matches the slices to the dataset. Slices which resemble the dataset images are then retrieved. The system works well even in presence of noise. SVM classifies MRI brain into semantic region. MR images are registered before classification to avoid misalignment. Proposed system mainly deals with two phases, first phase identifies three dimensional brain volumes using two dimensional query slices. Second phase using SVM classify two dimensional queries into semantic region. FMR obtained is 10%, and system is robust to 10^0 rotation.

Y. Srinivasa Rao et al. [8] introduced Genetic Algorithm (GA) and Square Euclidean Distance (SED) to retrieve medical images. CBIR system extracts (low level features) query image contents to compare it with database images for searching resemblance. This method extract medical image features like texture and then SED measures similarity of medical database to recover images relevant to query images. GA generates chromosome genes using database images and then this chromosome subjected to mutation, crossover and genetic operator to generate new chromosomes. SED then measures similarity between query and new chromosome set. Chromosomes having minimum SED are retrieved. This procedure continues till similar images are achieved.

John Collins et al. [9] introduced M-CBIR using standardized Image CLEF database.

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This system provides similarity measure using BOW (Bag of Words) and SIFT (Scale Invariant Feature Transform).

SIFT extract feature vectors, position of this feature vectors is called keypoints. Before clustering feature vectors centroid, scaled and normalized using Z score. This system works in three phases, in first phase all the database image features is extracted using SIFT. Second phase represents K codebook features using KMC. In third phase k comprehensive features are transformed to single vector as normalized histogram.

Subrahmanyam Murala et al. [10] introduced Local Mesh Pattern (LMeP) algorithm for retrieving biomedical images. Conventional LBP (Local Binary Pattern) finds similarity between referred pixel and surrounding pixel whereas LMeP for referred pixel finds similarity relation among surrounding pixel. Proposed LMeP algorithm is more effective combined with Gabor transform. Experiment is demonstrated on three dataset OASIS-MRI, NEMA-CT and VIA/I-ELCAP dataset. LMeP outcomes are compared with Standard LBP results. Precision rate for LBP, LMeP, GLMep is 42 %, 44% and 56% respectively. Dumitru Dan Burdescu et.al [11] proposed a Semantic Based Image Retrieval (SBIR) and CBIR. Hexagonal structure based segmentation significantly used for segmenting medical images. KMC is used for clustering images. KMC generate vocabulary blobs from image features, this vocabulary blobs describe the image region. SBIR performs the annotation model like Cross Media Relevance Model (CMRM) and Continuous Space Relevance Model (CSR). The result obtained proves that CRM model is better than CMRM for SBIR and annotation tasks. Megha P. Arakeri et.al [12] proposed CBIR system to retrieve MR images. MR image helps radiologist to diagnose brain tumor. In proposed system retrieval of MR images is possible in two ways. In first way query images is discriminated into benign or malignant class based on image features and then similar MR images are retrieved. To achieve fast image retrieval clustering algorithm with Principal Component Analysis (PCA) is used with KD tree. KD tree clusters all subclass features using KMC. Proposed method provides robustness against misalignment during MRI acquisition. Camille Kurtz et.al [13] proposed image retrieval system in computer vision which helps radiologist and doctors to take decision while diagnosing patient. Proposed system retrieves images using semantic features which involve two steps. First step extract semantic features second step measure similarity using Hierarchical Semantic-Based Distance (HSBD). Proposed work evaluated on 30 dataset images using Normalized Discounted Cumulative Gain (NDCG) to retrieve and classify two dimensional images. Classification accuracy is 95 % on 75 dataset images.

III. METHODOLOGY

Many research works have been developed to carry out CBIR technique. In this work we are attempting to get efficient retrieve medical images from medical database (CBMIR). Fig. 1 depicts overall architecture of Content Based Medical Image Retrieval (CBMIR). Proposed systems require four phases to retrieve similar images. In first phase abdominal CT image is taken as input and then enhanced using

morphological operation and median filtering to reduce noise. The enhanced abdominal image is segmented using Adaptive Region Growing Algorithm (ARGA) to separate liver part. Second phase segments tumor part using Simple Linear Iterative Clustering (SLIC) Algorithm. In third phase GLCM and Histogram algorithm extracts the tumor features. Using Hamming Distance, tumor features are validated as tumor or non tumor type. After tumor validation, features of tumor region extracted by using Average Correction Higher Order Local Autocorrelation Coefficients (ACHLAC) and Legendre Moments (LM). The extracted features of tumor are stored in knowledge base by labeling. In fourth phase distance metric algorithm measures similarity between input and database images using extracted tumor features. The distance metric algorithm used in proposed method is Euclidean distance.

3.1 Pre-processing

Due to various noises in medical images the intensity distribution varies which create difficulty during segmentation without pre-processing. To address this kind of noise issues, image enhancement technique is employed in pre-processing stage which corrects the contrast of input image [14]. Tap-hat algorithm is used to enhance input image by computing the morphological operation.

Increase in image contrast helps ARGA to segment abdominal image. The segmented liver image is then transformed to gray scale image in pre-processing step and filtered by median filter to apply normalization technique. Median filtering is required to filter out the unwanted regions of the medical image that has no information about the tumor block hence reducing the complexity of SLIC method during segmentation. Pre-processing also consists of resizing of the images. Resizing of all considered images at fixed dimensions will help to generate feature vector of fixed sized. This is very necessary to maintain fixed dimensional feature vector, otherwise classifying the features will become difficult [15 - 27].

3.2 Adaptive Region Growing Algorithm

For CT images of region R at pixel x , the homogeneity can be defined as a function h of that pixel x_i in a neighbourhood of x and inside R .

$$h(x; x_i; a_1, \dots, a_n) = \begin{cases} 1, & \text{if } x \text{ given pixels } x_i \text{ is part of } R, \\ & \text{defined by } a_1, \dots, a_n \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

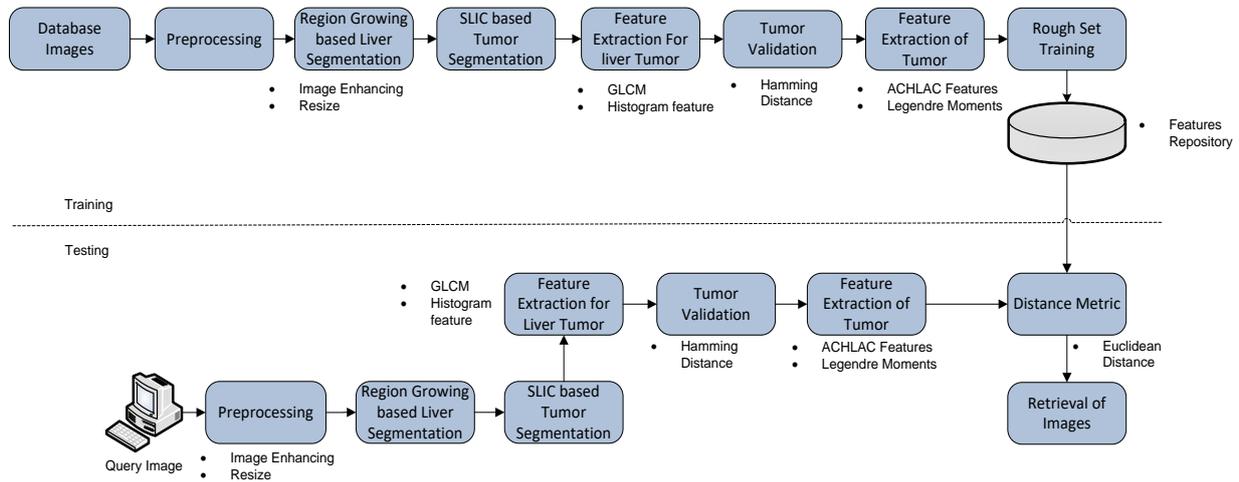


Fig 1: Architecture of CBMIR

Homogeneity defined as maximum likelihood having grey values Gaussian distribution with mean and Standard Deviation (SD). By assuming SD of grey values which is lower or higher than mean, the results of the Partial Volume Effect (PVE) is recorded in an approximate method. The homogeneity function h then becomes.

$$h(x; \mu, ud, ld) = \begin{cases} 1, & \text{if } \mu - w \cdot ld < x < \mu + w \cdot ud \\ 0, & \text{otherwise} \end{cases} \quad (2)$$

Adaptive region growing also called as segmentation process is used for finding homogeneity parameter to segment gray image. To segment specific region adaptive region algorithm initializes seed point as connecting region on condition to examine neighbor active pixel for region membership and to keep homogeneity criteria constant during learning process. Learning homogeneity criteria require calculation of mean and two standard deviation gray values. To find region membership upper threshold and lower threshold are used.

$$T_{upper} = mgv(n) + [ud(n) \cdot w + c(n)] \quad (3)$$

$$T_{lower} = mgv(n) - [ld(n) \cdot w + c(n)] \quad (4)$$

n shows pixels number. Function $c(n)$ compensate erroneous estimates of mgv , ud and ld . $c(n)$ is the inverse function value of n i.e. as the value of n increases function value decreases. In this manner the ARGGA segments the liver part in an efficient manner.

3.3 Simple Linear Iterative Clustering

In SLIC image is decomposed into homogeneous regions. SLIC works same as K-means clustering. SLIC uses two parameters for clustering, like region size and regularization. First the input image will be divided into grids. Each centre grid initializes K-Means to segment image. SLIC samples k number of cluster centres $C_k = [lk, ak, bk, xk, yk]^2$ in CEILAB color space on grid image. The images of CIELAB (Commission International de l'Eclairage) color space represents all color based on human view. Grid distance is $S = \sqrt{\frac{N}{k}}$ for equally sized 'k' numbered of pixels (cluster of pixels). To avoid centering of super pixels on edge, to avoid probability of selecting noisy pixels, all centers of cluster are send to seed location (lowest gradient position) in 3x3

- Step1. Initialize cluster centers $c_k = [lk, ak, bk, xk, yk]^2$ by inspecting pixels at general grid steps S .
- Step2. The 3x3 neighborhood sends the centre of clusters to the lowest gradient location.
- Step3. Repeat this for every group focus to c_k . Allocate the best coordinating pixels from a $2S \times 2S$ square neighborhood around the group focus as indicated by the separation measure.
- Step4. End for
- Step5. Process new cluster centers and remaining error E {L1 separation between past focuses and recomputed centers}
- Step6. Continue process until $E \leq \text{threshold}$
- Step7. Enforce connectivity.

Neighborhoods. SLIC performs clustering by using (x, y) coordinates of the pixel. To speed up the algorithm, limited size of search region reduces distance calculation by using distance measure D . Distance measure finds nearest centre of clusters by computing distance between pixel and associated cluster centre. Expected super pixels region size is $S \times S$. Similar pixels are searched in the $2S \times 2S$ region size. Once each pixel forms association with centre of clusters, then cluster centre act as the mean for all the pixels associated to the cluster. L2 norm calculates the residual error E (difference between new cluster and existing cluster) by using color and intensity information and it continues to process in a linear fashion till the point, where difference between the previous and current mean pixel reached to a threshold value. At this point iteration will be stopped; therefore the name given is a simple linear iteration.

3.4 GLCM

To analyze the texture by considering pixel spatial relationship a method called gray-level co-occurrence matrix (GLCM) also known as the gray-level spatial dependence matrix is used. GLCM represents a square matrix G . Elements (i, j) in G represents the occurrence of i intensity pixels, which is adjacent (horizontal, vertical, right and left) to j intensity pixels.

Algorithm 1: Efficient super pixel segmentation

Dividing G element by total co-occurrence pairs of element in G, normalized co-occurrence matrix is obtained. Gray scale images giving small change in brightness over large distance, appears as smooth. Other gray scale image show large change over short distances appears as rough. Given $K \times K$ image size, GLCM of $G \times G$ elements is defined in Eq. (5). The GLCM characterize image texture by extracting information from this matrix.

$$M_{co} = \sum_{x=1}^K \sum_{y=1}^K \left\{ \begin{matrix} 1 & \text{if } I(x,y) = i \text{ and } I(x+d_x, y+d_y) = j \\ 0 & \text{otherwise} \end{matrix} \right\} \quad (5)$$

3.5 Histogram Features

Histogram plots grey values of image or intensity distribution value versus pixel number at that value. Histogram gives detail information of image like narrow histogram shows low contrast image and high histogram shows bright image. Generally histogram features are statistical features which give intensity level information of the image. Histogram features are skew, entropy, variance and energy. High mean indicate high image brightness. High variance shows high image contrast. Skew measures asymmetry of the mean intensity level distribution. Histogram of small area having the rectangle or circle shape extracted from main image is calculated to get better information. Histogram of small block size area is increased which intern removes the shadow effect. The bin values are used to separate pixels of small areas in the histogram. The histogram uses bilinear method for reducing aliasing effect. Based on the illumination information final features are calculated here. These features with GLCM features are used in our proposed method for the segmentation purpose. The accumulated features would increase the accuracy of the system.

3.6 Hamming Distance

To validate tumor and non tumor region based on tumor features hamming distance is used. Hamming distance also called as matching or distance metric algorithm which measures the tumor features to identify tumor or non tumor region. Since different region have similar texture by using thresholding algorithm it may result false match. Hence during matching process distance between tumor features is calculated using hamming distance. After evaluation output decision is validated as tumor or non tumor region. Hamming distance gives measure of how much similarity exist between two bit patterns. Decision is concluded based on whether two patterns obtained is from different tumor or from the same one using the Hamming distance of two bit patterns. If patterns are generated from same tumor then Hamming distance becomes near to 0.0, since patterns are highly correlated. The Hamming distance of bit patterns (binary integers) shows corresponding number of bit positions that differ to each other.

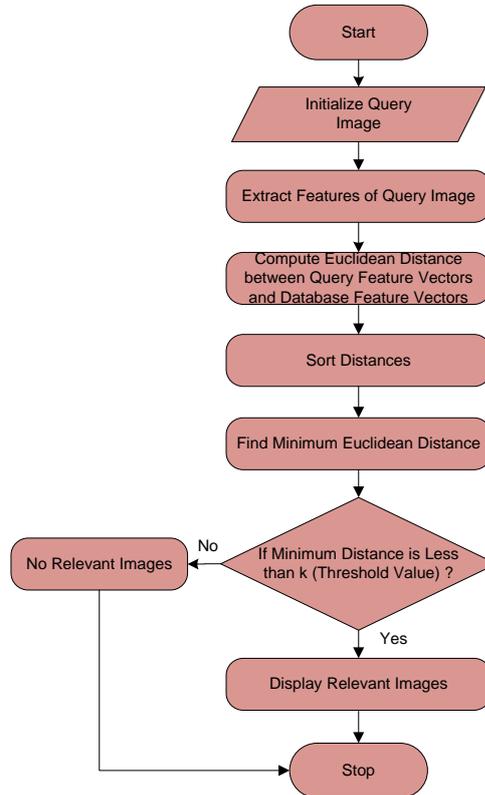


Fig 2: Flowchart of Distance Metric Algorithm

3.7 ACHLAC

Conventional HLAC directly multiplies gray valves which cannot give image information (information is lost, multiplication is similar but gray pixel value intensity distribution is different). To address drawbacks of HLAC, ACHLAC is introduced. In ACHLAC whole image gray pixel values are averaged. The difference between current gray pixel and average gray pixel value is calculated to update current pixel. Updated image shows variation in gray value. Finally HLAC features are calculated using updated image. Major difference between HLAC and ACHLAC is HLAC used on local information but ACHLAC combines both local and global average gray value information.

3.8 Legendre Moments

Two dimensional and three dimensional orthogonal moments are also called Legendre Moments (LM). LM is used for image analysis. Legendre moments are continuous moments and require long multiplication and addition operation for calculation. Eq. (6) defines Legendre moments for digital image.

$$L_{pq} = \frac{(2p+1)(2q+1)}{(N-1)(N-1)} \sum_{x=0}^{N-1} \sum_{y=0}^{N-1} P_p(x_i) P_q(y_j) f(x,y) \quad (6)$$

Where $P_p(x_i)$ and $P_q(y_j)$ denotes the order p and q Legendre polynomials respectively. Normalized coordinates are denoted by x_i and y_j which ranges within [-1, 1]. The transformation of image coordinates into is done as follows,

$$x_i = \left(\frac{2x}{N} \right) - 1; \quad (7)$$

$$y_j = \left(\frac{2y}{N} \right) - 1; \quad (8)$$

With defining Legendre polynomial as,

$$P_p(x_i) = \sum_{k=0}^p \frac{1}{2^p} \frac{(-1)^{\frac{p-k}{2}} (p+k)! x_i^k}{k! (\frac{p+k}{2})! (\frac{p-k}{2})!} \quad (9)$$

Where $|x_i| \leq 1$ and $(p - k)$ are even.

3.9 Distance and Similarity Measures

Basically classifiers uses feature vectors to classify object since this feature vectors provide higher-level of image information. To represent and to classify object minimum two features are needed. To compare feature vectors for classification similarity measure algorithms are used. Vectors which are closed and similar to one other will have small difference, small distance and large similarity. Large distance between feature vectors shows larger difference and dissimilarity. Euclidean distance commonly used to measure the min distance (nearer distance) exist between the two feature vectors a_k and b_k given in Eq. (10). Fig. 2 depicts the flowchart of distance metric algorithm. Euclidean distance used is quite appropriate for small and exact matches. Similarity measure compares the similarity of two feature vectors; two vectors that are close in feature space will have large similarity measure. The common types of similarity measure are vector inner product and Tanimoto metric.

$$D(a, b) = \sqrt{\sum_k (a_k - b_k)^2} \quad (10)$$

3.10 Rough-ANN

Image processing based on rough set can be divided into 3 parts: formation of decision table, descritization of attribute values followed by its reduction in order to remove any unwanted or redundant attribute so as to decision making process easier. The rough set is weak for error data processing and rough set always deal with unknown information. The attribute reduction consists of decision making attribute and condition attribute. The rough set neuron is constituted by traditional neuron and rough set. Rough set neural network have slight edge on the traditional neural network regarding operating on a range of input values apart from singular inputs. Traditional neural network has a tendency to create more errors when trained with the range of input values. The major difference between rough neural network and conventional neural network is in terms of input layer, hidden layer and output layer.

IV. EXPERIMENTAL RESULTS & DISCUSSION

Experimental results of proposed system are demonstrated by considering publicly available medical data. Fig. 3(a) and Fig. 3(b) depict the retrieve of images for input Hepatic *Haemangioma tumor*. Fig. 4(a) and Fig. 4(b) depict retrieve images for input Hepatocellular tumor using distance metric algorithm.

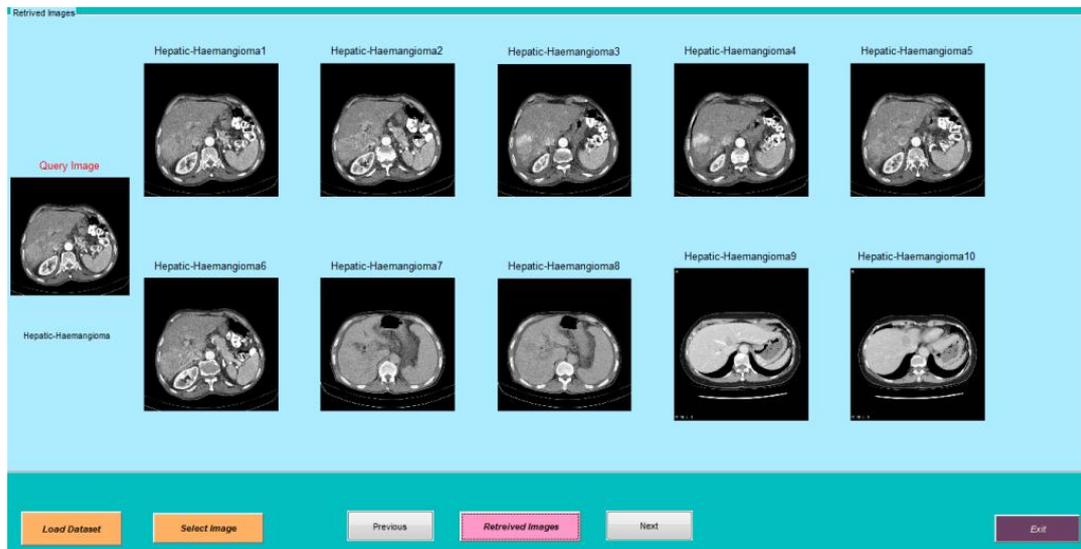




Fig. 3(b) 2/2 Retrieved Images of Hepatic Haemangioma

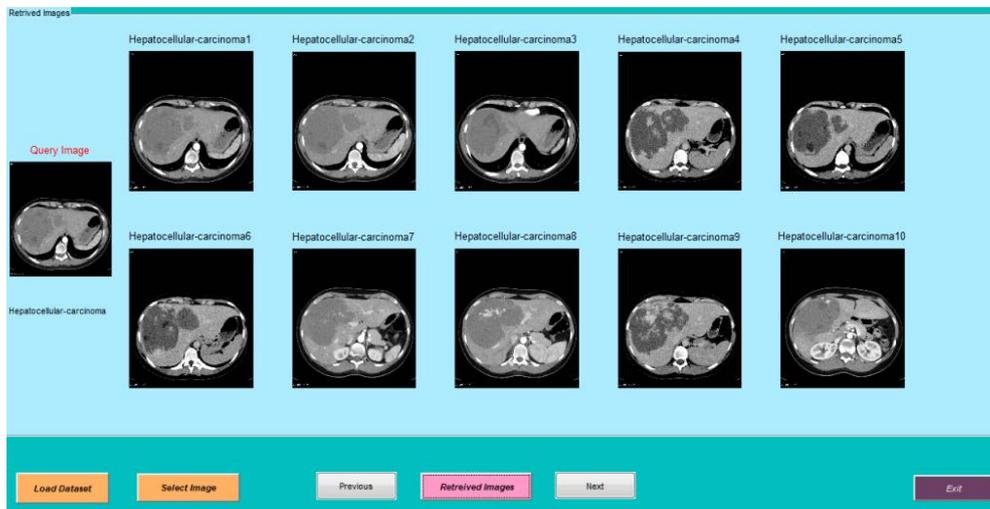


Fig. 4(a) 1/2 Retrieved Images of Hepatocellular Carcinoma

Table 1: Comparison Table of Proposed and Existing System

Sl.No	Paper	Methods	Precision	Recall
1	B Syam et.al [8]	Genetic Algorithm and Euclidian Distance	78%	78%
2	Ashish Oberoi et.al [16]	Haar Wavelet and Euclidian Distance	80%	82%
3	Abdalla Mostafa Zidan et.al [17]	Region Growing, Watershed and SVM	84.33%	73.05%
4	Proposed Method	Legendre Moments, GLCM and R-ANN	95%	95%

The Results are demonstrated by considering 50 samples with T_p , T_n score are 42 and 4. F_p is 2, F_n is 2. Table 1 depicts comparison for existing and proposed system. Fig.5 and fig.6 Shows the respective precision and recall rate

comparison graphs. The proposed system achieved the accuracy of 92%, precision of 95% and recall rate of 95%.

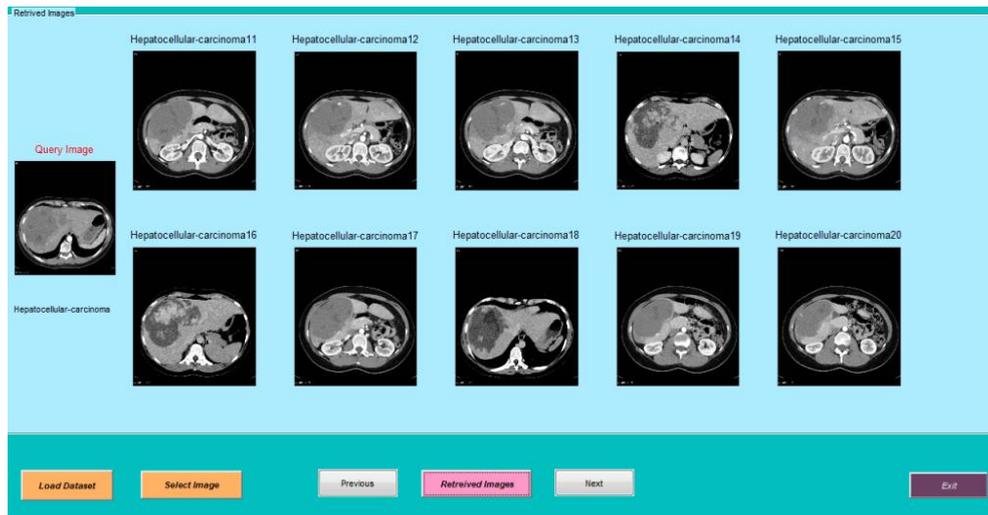


Fig. 4(b) 2/2 Retrieved Images of Hepatocellular Carcinoma

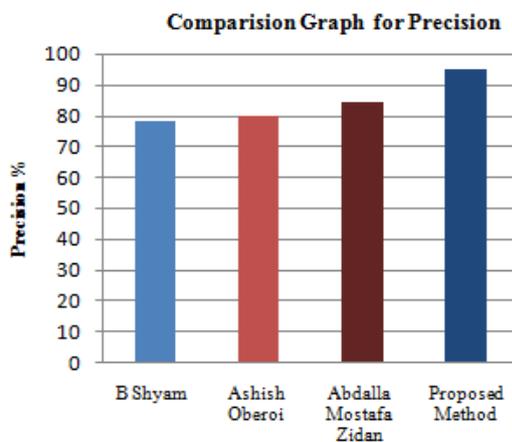


Fig.5: Precision Comparison Graph

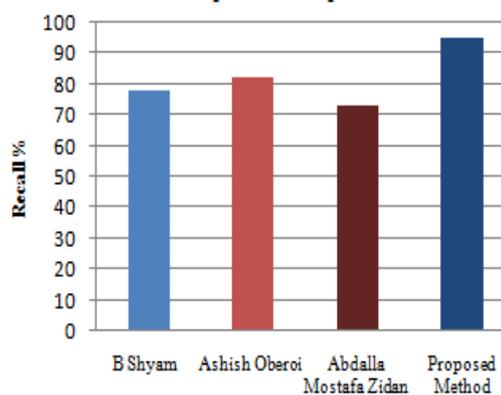


Fig.6: Recall Rate Comparison Graph

V. CONCLUSION

The proposed system is implemented in the working platform MATLAB R2010a by using publically available data. CBMIR system is implemented for retrieving relevant image from large set of medical database images. Searching relevant medical image based on texture is very difficult; hence medical images are first segmented using ARG and enhanced using morphological operations. Tumor region is segmented using SLIC. To extract tumor features GLCM and histogram features are used. Extracted features are validated as tumor and non tumor region using Hamming distance.

Tumor region features are then extracted using ACHLAC and LM. Finally similar images are retrieved using distance metric algorithm based on extracted features. Proposed CBMIR system in medical application helps radiologist and physician to diagnose and cure disease at early stage.

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