Ultra Sound Kidney Image Retrieval using Time Efficient One Dimensional GLCM Texture Feature

C.Callins Christiyana
Associate Professor, CSE
Sethu Institute of Technology,
Pulloor,Kariapatti.
Tamilnadu, India

V.Rajamani
Principal
Indra Ganesan College of Engineering, Trichy,
Tamilnadu, India

A.Usha devi
II year CSE
Sethu Institute of Technology,
Pulloor,Kariapatti,
Tamilnadu, India

ABSTRACT

Ultrasound applications are used for diagnostic applications such as visualizing muscles, tendons, internal organs, to determine its size, structures, any lesions or other abnormalities. This paper concentrates the diagnosis of abnormalities in kidney Images based on retrieving past similar images from kidney Image Database. More and more amount of ultrasound digital images are being captured and stored in clinical laboratories. In order to use this information, a time efficient retrieval technique is required. One major development in this area is content based image retrieval(CBIR) . The CBIR techniques use image features for image indexing and retrieval. The main features used for image retrieval are color, texture and shape. This Paper looks into the image retrieval technique based on texture, because of same modality ultrasound kidney images. The Most familiar Texture feature extraction technique is using the Two Dimensional Gray level Co-occurrence Matrix (2D-GLCM). But the problem with this method is Computational overhead. To overcome this difficulty, this paper experiments the texture feature extraction by Computationally efficient Gray level Co-occurrence Vector(GLCV), which is called one dimensional Gray level Co-occurrence Matrix(1D-GLCM). The 1D-GLCM Texture feature representation is the central theme of this proposed work and the Performance the system based on 1D-GLCM is compared with traditional two dimensional GLCM called 2D-GLCM. Experimental results show that this technique achieves higher Recall rates with the lesser time compared with traditional 2D-GLCM.

General Terms

Medical Image Retrieval.

Keywords

Ultra sound kidney image**,** CBIR, Texture, 1D-GLCM, 2D-GLCM, Recall.

1. INTRODUCTION

WITH the advancements in information technology, there is an great growth of image databases, which demands effective and efficient system that allow users to search through such a large collection. Traditionally, the most straightforward way to implement image database management systems is by means of using the conventional database-management systems such as relational databases or object-oriented databases. The system of these kinds is usually called Text-based, in which the images are described with keywords. As the database size gets grow larger, to retrieve a particular image with these methods becomes tedious and inadequate. To solve these problems, content-based image retrieval (CBIR) has emerged as a promising approach. In CBIR, images are indexed by their own visual contents. A comprehensive and extensive literature survey on CBIR can be found in [1]–[4].

This paper applies the concept of CBIR in Ultrasound Kidney Images. Content Based Medical Image Retrieval methods developed specifically for biomedical images could offer a solution to traditional image retrieval system specially used in clinical, research, and educational aspects of biomedicine.

Medical Image CBIR does not aim to replace a physician by predicting the disease of a particular case but to assist him/her in diagnosis. The visual characteristics of the disease carry diagnostic information and oftentimes visually similar images correspond to the same disease category. By consulting the output of a CBIR system, the physician can gain more confidence in his/her decision[5].

For any class of biomedical images, however, it would be necessary to develop suitable feature representation for the visual contents and similarity algorithms that capture the "content" in the image. Many systems were developed during the last years, both by commercial and academia. The challenge in Medical CBIR is to develop the methods that will increase retrieval accuracy and reduce the retrieval time so as to quicker diagnosis is possible.

The motivation of taking ultrasound images are as follows: Most ultrasound scanning is noninvasive (no needles or injections) and is usually painless. Ultrasound is widely available, easy-to-use and less expensive than other imaging methods such as MRI, CT. Ultrasound imaging does not use any ionizing radiation. So the ultrasound medical images are created in more number. Then there is need of efficient CBIR for ultrasound medical images in terms of time efficient. The time efficiency factor is very important in medical CBIR , because their applications are earlier diagnosis of diseases.

The visual characteristics of images are represented by a features like color, texture and shape. But for gray level medical images texture and shape features are normally preferred for diagnosis purpose. This paper extracting visual content by representing texture features in terms of second order statistics.

The Preprocessing of ultrasound kidney images such as removal of speckle noise and segmenting the organ are explained in Section 2. Section 3 and 4 describes the proposed method of retrieval using time efficient 1D GLCM texture feature and the limitations in the existing method of ultrasound kidney image retrieval. Section 5 reports the significant experimental results and the efficiency of the

proposed method is compared with the traditional 2D GLCM. Conclusions are given in section 6.

2. PREPROCESSING OF ULTRASOUND KIDNEY IMAGES

To improve the retrieval accuracy of the ultrasound images, it should be free from noise. It is well-known that speckle is a multiplicative noise that degrades the visual evaluation in ultrasound imaging[6]. The recent advancements in ultrasound instrumentation and portable ultrasound devices necessitate the need of more robust despeckling techniques for enhanced ultrasound medical imaging for both routine clinical practice and teleconsultation.

When the image is affected by the speckle noise ,the corrupted pixels are either set to the maximum value. Speckle noise follows a gamma distribution and is given in equation 1

$$f(g) = \left[\frac{g^{\alpha-1}}{(\alpha-1)!a^{\alpha}} e^{-\frac{g}{a}} \right] \qquad (1)$$

Where, variance is a^{α} and g is the gray level.

There are so many number of filters used to remove the speckle noise. It is proven that the spatial M3- filter[6] has the highest PSNR ratio to remove speckle noise from ultrasound medical images. The M3-Filter is given in equation 2, the hybridization of mean and median filter. This replaces the central pixel by the maximum value of mean and median for each sub images S_{XY}. It is expressed as M3-Filter, and it preserves the high frequency components in image. Therefore it may be suitable for de noising the speckle noise in the ultrasound medical image. It is a simple, intuitive and easy to implement method of smoothing images.

$$f(x,y) = \max\left(median_{(s,t)\in S_{XY}}\{g(s,t)\}, mean_{(s,t)\in S_{XY}}\{g(s,t)\}\right) \qquad (2)$$

The main objective of this retrieval system is to reduce the retrieval time for fast diagnosis. For achieving that it is necessary to avoid the unnecessary processing of background pixels from the ultrasound kidney image. The kidney organ should be segmented effectively by identifying its boundary. It is proven that the Cellular Automata model [7] effectively detecting boundary from the given image.

Boundary detection requires edge detection. The cellular automata mode is used to find the edge of the image. Cellular automata model is applied on binary images for that gray-scale image is converted to binary image. The basic element of a Cellular Automata is the cell. A cell is a kind of a memory element and stores Information. Each cell can have the binary states 1 or 0. In more complex simulation the cells can have more different states. The cells arranged in a spatial web form a lattice. These cells arranged in a lattice represent a static state. In cellular automata a rule defines the state of a cell in dependence of the neighborhood of the cell. In this work the Moore neighborhood method is used. In Moore neighborhood method the maximum number of neighboring pixels for any image pixel is 9 that count includes the image pixel concerned. In Figure 1, if 'P' is the image pixel then the adjacent pixels are, all 'A' pixels and 'P' pixel.

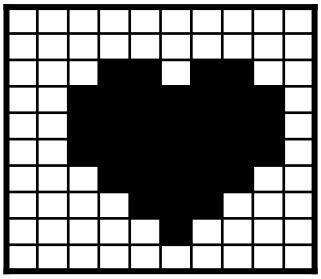

Fig. 1.Moore Neighborhood

The following steps are necessary to extract the organ.

Step 1: The cellular map is set for black and white image data for edge detection. In cellular map, black color pixels represented by '1'and white pixels represented by '0'. The cellular map and its binary representation of following heart shape image is shown in figure 2.

		A	A	A		
		A	P	A		
		A	A	A		

0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	1	1	0	0
0	0	1	1	1	1	1	1	1	0
0	0	1	1	1	1	1	1	1	0
0	0	1	1	1	1	1	1	1	0
0	0	0	1	1	1	1	1	0	0
0	0	0	0	1	1	1	0	0	0
0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0

Fig. 2.Cellular Representation of Black and white Heart Image

Step 2: The edge detection rule is applied in cellular representation of an image to extract boundary. The type of rules employed in this work is so called "Totalistic" Rule[7]. This rule results the neighbor matrix of image in cellular representation. That is, the state of the core cell is only dependent upon the sum of the states of the neighborhood cells, and its own present state. Each dead cell has state "0" as value, and each alive cell has state "1" as in figure 2 of cellular representation. The sum of the states of all the adjacent and diagonal neighbors cells were calculated based on moore neighborhood. The result of this step for black and white heart image is shown in figure 3.

0	0	0	0	0	0	0	0	0	0
0	0	1	2	2	2	2	2	1	0
0	1	3	5	5	5	5	5	3	1
0	2	5	8	8	8	8	8	5	2
0	3	6	9	9	9	9	9	6	3
0	2	5	8	9	9	9	8	5	2
0	1	3	6	8	9	8	6	3	1
0	0	1	3	6	7	6	3	1	0
0	0	0	1	3	4	3	1	0	0
0	0	0	0	1	1	1	0	0	0

Fig. 3. Neighbor matrix of an black and white image

Step 3: Once the Neighbor matrix for black and white image is set then the decision rule is applied to extract the boundary. The cells with 3 neighbors or less will die of loneliness, and those cells with 7 neighbors or more will die of over population. Only the cells with 5 neighbors will be born, and furthermore the cells with 4 or 6 neighbors keep its previous state. The cells with the neighbor values 4,5,6 having the boundary information. Those information are extracted for boundary detection. The Result is shown in figure 4.

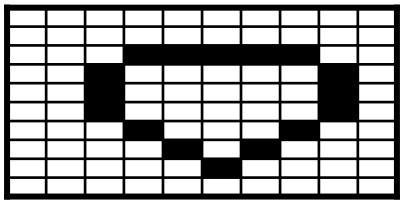

Fig. 4.Cellular Representation of Heart Image after Boundary detection

Step 4: The final result is a black and white edge detected image. The black color pixels representing the boundary. The original pixel value on the boundary line and the pixels inside the boundary are retained as the segmented image. Figure 5 and figure 6 shows the input and output of the boundary detection algorithm based on cellular automata model.

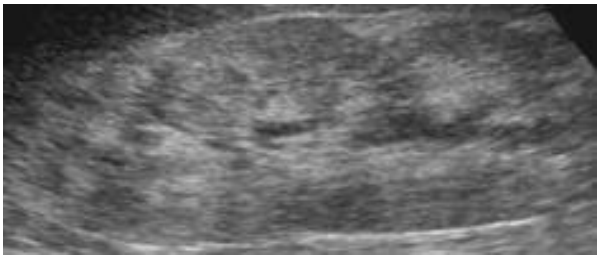

Fig. 5. Ultrasound Kidney image

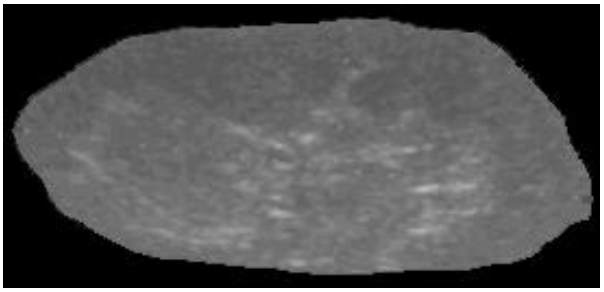

Fig. 6. Segmented image using Cellular automata model

3. ULTRASOUND KIDNEY IMAGE RETRIEVAL USING EFFICIENT 1D GLCM

The previous work of ultrasound kidney image retrieval represents the visual characteristics by means of its texture. The texture feature is calculated by computing 2D GLCM. From the matrix 14 features[1] are extracted in four directions specified by 0˚, 45˚, 90˚, 135˚. Even though the existing method yields the better retrieval accuracy the computing time of 2D GLCM matrix is infeasible. For a critical case, diagnosis and the remedial actions should be taken in the shortest time period. So that there is a need of CBIR system that should retrieves the similar images by balancing the retrieval accuracy and retrieval time.

The lengthiest computational time in 2D GLCM occurs because 2D GLCM involves extensive calculations to derive the texture features. Normally 2D GLCM is generated with all the 256 gray levels. Then the size of the matrix become 256x256. When deriving texture features all the elements in the matrix are involved, so for larger size of the matrix , more computations are performed.

To reduce the lengthiest computational time in 2D GLCM, there are two approaches[8]. The first approach reduce the matrix size where as the second approach reduce the matrix dimension. When reducing the matrix size the smallest amount of gray level is considered instead of all 256 gray levels. In real world, the same objects will have a different gray value due to orientation and lightening condition during image acquisition. When group of gray values are grouped into single gray value attempting to reduce the matrix size the retrieval accuracy will be degraded.

This paper concentrates the reduction of lengthiest computational time by reducing the 2D GLCM matrix dimension to one dimension by combining certain values of the matrix. The resultant structure is called as co-occurrence vector instead of matrix. This one dimensional GLCM focuses the differences of the gray level, so the size of this vector is 2xN-1, where N is the number of gray levels. By reducing the dimension size of GLCM, the calculations of texture features will be faster because of fewer values in the calculation.

In the conventional 2D GLCM, Cd(m,n) represents the total pixel pair value where d represents the spatial distance between the pixels m and n, m represents the reference pixel value and n represents the neighboring pixel value with the specified spatial distance and direction defined. The probability density function normalizes the 2D GLCM by dividing every set of pixel pairs with the total number of pixel pairs used and is represented using p(m,n) as shown in Equation 3 [9]. The one-dimensional GLCM is similar, but focus only on the differences of gray value between the pixel pairs, therefore, x shows the differences of gray value between the two pixels of the pixel pairs, as shown in Equation. 4.

$$p(m,n) = \left[\frac{1}{All\_Pairs\_of\_pixels\_used} C_d(m,n) \right] \quad (3)$$

$$p(x) = \left[\frac{1}{All\_Pairs\_of\_pixels\_used} C_d(x) \right] \quad (4)$$

The feature formulas for deriving the texture features must be modified to be suitable to the one-dimensional GLCM, this must be done as the original feature extraction functions involved two dimensional data from the GLCM as shown in Equation 5. [10].

$$Energy = \sum_{m=0}^{G-1}\sum_{n=0}^{G-1} p(m.n)^2$$

$$Entropy = \sum_{m=0}^{G-1}\sum_{n=0}^{G-1} p(m,n)\log p(m,n)$$

$$Contrst = \frac{1}{(G-1)^2}\sum_{m=0}^{G-1}\sum_{n=0}^{G-1}(m-n)^2 p(m,n)$$

$$Homogenity = \sum_{m=0}^{G-1}\sum_{n=0}^{G-1}\frac{p(m,n)}{(1+|m-n|)} \quad (5)$$

For the modification of the textural features, the summation function that involves every value in the 2D GLCM is only one dimension in the 1D GLCM, and the probability density p(m,n) is replaced by p(x) in the 1D GLCM. The calculations of (m-n) that represents the differences of gray value in the 2D GLCM is represented by x that represents the same thing in the 1D GLCM. After the modification, the values of contrast and homogeneity will be identical but the values of energy and entropy will be different with the 2D GLCM. The modified texture features are listed below in Equation 6.

$$Energy = \sum_{x=-(L-1)}^{L-1} p(x)^2$$

$$Entropy = \sum_{x=-(L-1)}^{L-1} - p(x)\log p(x)$$

$$Contrast = \frac{1}{(L-1)^2}\sum_{x=-(L\_1)}^{L-1}(x)^2 p(x) \quad (6)$$

$$Homogeneity = \sum_{x=-(L-1)}^{L-1}\frac{p(x)}{(1+|x|)}$$

Similar to the 2D GLCM method , the 1D GLCM method is also derives the texture feature from four directions specified by 0˚, 45˚, 90˚, 135˚. The feature vector length in 1D GLCM is 16. This is because of 4 features from four directions. The sample feature value for query image 1 in 1D GLCM and 2D GLCM is listed below.

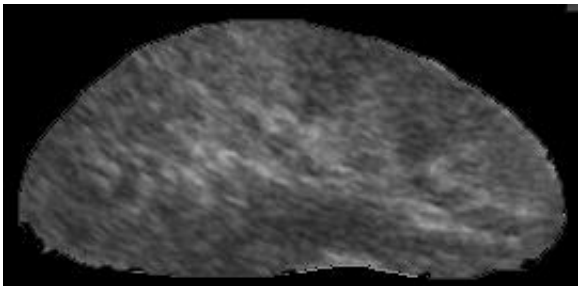

Fig. 7. Data base image 1

Table 1 Feature values of Data base image 1 in both 2D GLCM and 1D GLCM

Feature Name	Direction	Feature Name	2D GLCM	1D GLCM
F1	0˚	Energy	0.078189992	0.11285280
F2		Entropy	0.078189992	-3.2045253
F3		Contrast	0.078189992	-1413.4003
F4		Homogenity	0.078189992	0.0032023058
F5	45˚	Energy	0.077933859	0.11620083
F6		Entropy	-6.2219376	-3.1421444
F7		Contrast	151.21890	-1343.2622
F8		Homogenity	0.44996124	0.0032163353
F9	90˚	Energy	0.081541574	0.55553671
F10		Entropy	-6.0004333	-0.63653376
F11		Contrast	90.978630	-340.65222
F12		Homogenity	0.48412010	0.0039011831
F13	135˚	Energy	0.077705203	0.10377484
F14		Entropy	-6.4308816	-3.419006

				2
F15		Contrast	213.68785	-1469.3050
F16		Homogenity	0.41437720	0.0031921416

4. SIMILARITY MATCHING

Medical CBIR calculates the visual similarities between a query image and images in a database instead of exact matching for diagnosis purpose . Accordingly, the retrieval result is not a single image but a list of images ranked by their similarities with the query image. Many similarity measures have been developed for image retrieval based on empirical estimates of the distribution of features in recent years. Different similarity distance measures will affect the retrieval performances of an image retrieval system significantly. The Euclidean distance measure is best for the same modality images [11]. As our database is same modality of ultrasound kidney images, the Euclidean distance measure is taken so for similarity matching.

The similarities between two images are computed as follows. The difference between the Euclidean distance of two images texture feature values are calculated. If the distance is minimum then the images are retrieved as similar.

To calculate Euclidean distance between the images the following formula is used.

$$\sqrt{(p_1-q_1)^2+(p_2-q_2)^2+.....+(p_n-q_n)^2}=\sqrt{\sum_{i=1}^{n}(p_i-q_i)^2} \qquad (7)$$

In the above equation , where p and q are Feature vectors of database image and the query image respectively.

5. EXPERIMENTAL RESULTS

Database consist of 100 ultrasound kidney images of different categories (like Normal, CC, MRD) are taken for performance Analysis. The efficiency of 1D GLCM method is compared with the traditional 2D GLCM. Normally the performance of the CBIR system is evaluated by two familiar measures Precision and Recall [12-14] which is defined as follows.

$$\Pr ecision = \frac{No\_of\_Relevant\_images\_retrived}{Total\_no\_of\_images} \qquad (8)$$

$$Recall = \frac{No\_of\_Relevant\_images\_retrieved}{Total\_no\_of\_images} \qquad (9)$$

In this work Recall parameter is taken for performance analysis. This is because the efficiency of the proposed system is evaluated on different category of images (Normal, CC, MRD) separately. The Database consists of different category of ultra sound Kidney images like Normal, CC, MRD. The success of the method is confirmed with the different category images separately. The success rate of the system with MRD images in terms of recall rate is shown in figure 8.

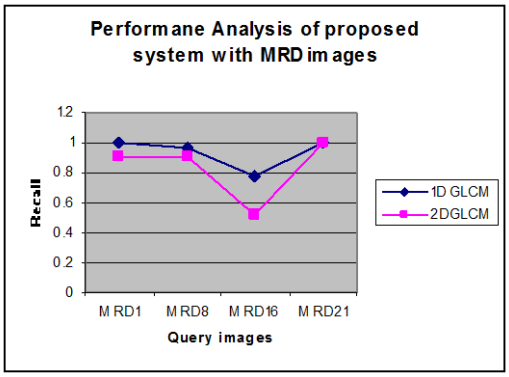

Fig.8. Performance of 1D GLCM with 2D GLCM considering MRD images.

The performance of the system with CC images in terms of recall rate is shown in figure 9.

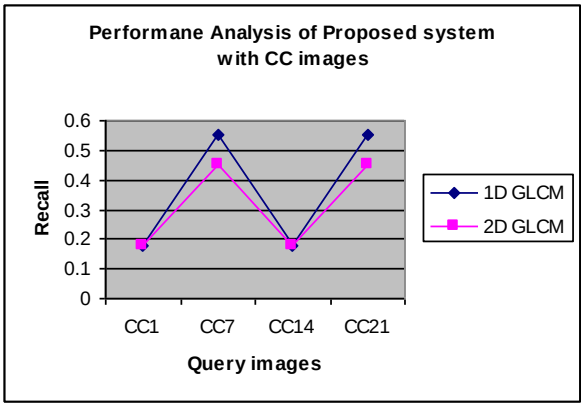

Fig.9. Performance of 1D GLCM with 2D GLCM considering CC images.

The success rate of the system with Normal images in terms of recall rate is shown in figure 10.

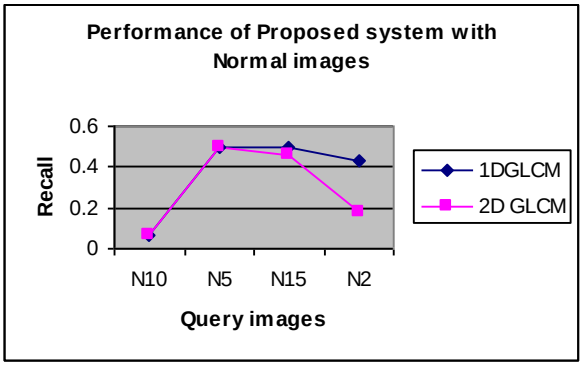

Fig.10. Performance of 1D GLCM with 2D GLCM considering Normal images.

The very important analysis of this paper is time efficiency [15] analysis. The time complexity of 1D GLCM method is O(G), Where as the time complexity of 2D GLCM O(G2). 'G' is the number of gray levels in an image. This is Shown in Table 2.

Table 2 Time Complexity Analysis of 1D GLCM with 2D GLCM

Method	Dimension / Size of the Matrix	Time complexity (G=256)
1D GLCM	1 / 511	O(G)
2D GLCM	2 / 256X256	$O(G^2)$

6. CONCLUSION

The proposed technique of 1D GLCM method compared with 2D GLCM method, not only retrieves more similar images effectively but also retrieves the similar images in a lesser amount of time. The minimum amount of time requirement is proved in time complexity analysis. So this work, suggested that 1D GLCM is the best alternative of 2D GLCM texture feature representation of Ultrasound Kidney images . The main application of medical image retrieval is to assist the diagnosis. The time factor is very important in medical diagnosis. All the physician wants to get the knowledge from the past history in quicker time. So, according to the time complexity analysis and retrieval accuracy , it is concluded that 1D GLCM is best suited for clinical purpose.

7. REFERENCES

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