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ภาคผนวก

บทความที่นำเสนอในงานการประชุมวิชาการ

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2. บทความ   Deformable Contour for Brain MR Images by Genetic Algorithm: From Rigid to Training Approaches นำเสนอในงานประชุมวิชาการ IVCNZ'99 (Image and Vision Computing '99 New Zealand) จัดที่ University of Canterbury เมืองChristchurch ประเทศนิวซีแลนด์ ระหว่างวันที่ 30-31 สิงหาคม พ.ศ. 2542

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A Multiscale Approach to Deformable Contour for Brain MR Images by Genetic Algorithm

Thosaphon Tanatipanond and Nongluk Covavisaruch
Department of Computer Engineering
Faculty of Engineering, Chulalongkorn University
Bangkok 10330, Thailand
b0688521@student.chula.ac.th, nongluk.c@chula.ac.th

Abstract

Deformable contour is an image segmentation technique in which a contour is deformed until it fits around the target object. Many researches reported that deformable contour is a feasible technique for image segmentation. Several searching techniques such as Greedy Algorithm, Hill Climbing, and Simulated Annealing are often used in the target object contour fitting process. However, these techniques often cause a stuck in the searching process and hence resulting in local maxima. In this paper, Genetic Algorithm (GA) is introduced to be applied with deformable contour to segment brain in MR images depending on the fitness function at different image scales. The segmentation algorithm starts by constructing images at several different scales depending on the standard deviation of the Gaussian kernel. At coarse scale, draft target contour is encountered because local maxima are eliminated since there are less noise and lower small gradients in the image. This draft contour is then used as the initial state for the finer scale process where image details are more apparent. As the image scale gets finer, the number of generations in GA reduces to prevent far exceeding contour from the former. By the use of GA and multiscale approach, contour closer the global maximum is encountered. The performance and the robustness of this algorithm are tested and the results show that it is possible to apply GA for the searching technique in deformable contour algorithm.

1. Introduction

It is well known that image segmentation plays an important role in image analysis and computer vision. In medical applications, doctors also use it as a tool to support their medical diagnosis and treatment planning. For a task that deals with segmenting a large set of images, such as brain MR images, manual segmentation for target objects not only requires expert's knowledge but also is a very tiring and time-consuming job. Therefore, many researchers have been attempting for automatic segmentation. In most of the previous work, techniques used include pixel classification step, followed by pixel aggregation or region growing. The disadvantage of region growing technique is that it can occasionally cause leaking across regions.

Kass et al. [1] introduced the use of deformable contour approach to identify region boundaries to segment contour objects in 2D images. Searching methods have high influences both on how to determine and on the quality of best-fitted contours. State space search methods [2] are alternative approaches for the search and selection part of region formation. Instead of finding the region validation probability on individual pixel basis as in pixel aggregation method, state space search works on a pixel-group basis. Furthermore, a typical state space search considers a large variety of possible region boundaries in wide areas

while region growing concentrates only on one boundary in a limited area that, in many cases, misses the target results. Greedy Algorithm, Hill Climbing, Simulated Annealing [3] and Iterated Conditional Modes (ICM) [4] are a few examples of state space search methods. However, with state space search methods, stuck in the searching process could happen and hence resulting in local maxima, and the target boundaries are also missed.

Over the past few years, Genetic Algorithm (GA) has been successfully used to search for good results out of a very large solution domain. GA can be found in many application areas such as automatic circuit design, pattern recognition, robotic control and synthesis on neural architectures but it is rarely found in digital image processing area. This paper presents a method that uses GA with deformable contour approach to find the best-fitted brain boundary in brain MR images. Multiscale approach is also used in combination with GA in this work as it is aimed that at coarse scale images, rough contours of overall brain part should be fast and more correctly attacked. More accurate contours will be gained at finer scales.

2. Multiscale Image Approach

Koenderink [5] has proposed to work on images at different scales simultaneously since there is no single scale that contains adequate image information. Witkin [6] proposed a coarse-to-fine tracking algorithm applied with multiscale approach based on the assumption that image features are identified at coarse scales and localized at fine scales.

In this research, multiscale images are obtained in such a way as presented by Rueckert and Burger [7]. For a 2-D image, $I(x,y)$, a multiscale representation $L(x,y,\sigma)$ can be achieved by blurring the input image. Gaussian kernel is chosen for the blurring process since it possesses several suitable properties that are linearity, rotation-, translation-, and zoom-invariance [8].

$$L(x,y,\sigma) = I(x,y) \otimes G(x,y,\sigma) \tag{1}$$

where $\otimes$ denotes spatial convolution and G is a Gaussian function with standard diviation σ.

$$G(x,y,\sigma) = \frac{1}{2\pi\sigma^2} e^{-(x^2+y^2)/2\sigma^2} \tag{2}$$

$$\sigma_i = \sigma_0 s^i \tag{3}$$

where σ_0 corresponds to the coarsest scale, s is the scale change rate and i is the order of the multiscale level.

3. GA for Deformable Contour

Sets of co-ordinate points within an input image are used as deformable contours. For the encoding scheme in terms of GA, one *population* refers to one set of deformable contours. Each set of points of a contour is considered as one *chromosome* where each point within the same set is one *gene*. The algorithm used in this work is as follows:

(1)   Initialize G = 0
(2)   Generate initial parents

(3) While G<MAX_GENERATION

    (a) Create new population from previous generation by mutation, crossover, and reproduction

    (b) Evaluate each chromosome's fitness value

    (c) Select chromosomes for regeneration based on *quality* and *diversity ranks*

    (d) G = G+1

3.1 Evolutionary Operations

Three operations that are used in GA is as follows:

3.1.1 Mutation

The process to generate new chromosomes by mutation starts at randomly select one chromosome from the parent chromosomes, I. Then generate a random number, J, to be used as the number of genes to be mutated. At this state, small numbers are high probable to be generated than high numbers. Again, pick another random number, K, that will be used as the order of the gene to be changed. At this state, the chromosome, C_I, is as follows:

$$C_I: (a_1a_2...\ a_{K-1})(a_K a_{K+1}...a_{K+J-1})(a_{K+J}...a_N)$$

Finally, the co-ordinates in the genes a_K to a_{K+J-1} are changed randomly.

3.1.2 Crossover

For this crossover operation, two chromosomes, C_1 and C_2 are randomly picked from the parent chromosome. After that, randomize two genes named I and J where I must be less than J. At this state, the chromosomes are as follows:

$$C_1: \quad (a_1a_2...a_{I-1})(a_I a_{I+1}...a_J)(a_{J+1}...a_N)$$
$$C_2: \quad (b_1b_2...b_{I-1})(b_I b_{I+1}...b_J)(b_{J+1}...b_N)$$

Finally, a new chromosome, C_{new}, is generated by combining the first and third parts of C_1 and the second part of C_2.

$$C_{new}: \quad (a_1a_2...a_{I-1})(b_I b_{I+1}...b_J)(a_{J+1}...a_N)$$

3.1.3 Reproduction

Reproduction is the process that generates chromosomes from the parent chromosome by cloning.

3.2 Fitness Function

In GA, fitness function resembles energy function in digital image processing except that, for the concept of fitness function, the higher value is the better.

In this problem, *quality* of deformable contour is evaluated by fitness value. The fitness function composes of several terms that depend on the contour's properties and the force acting upon the contour. Fitness function of a chromosome, C, can be written as follows:

$$F_{total}(C,\sigma) = \sum_{i=1}^{n} F_{internal}(C,i) + F_{external}(C,i,\sigma) \tag{4}$$

where n is the number of genes in one chromosome.

The internal function forces the contour to conform to the pre-defined characteristics based on the knowledge of the problem.

$$F_{internal}(C,i) = \alpha F_{cont}(C,i) + \beta F_{curve}(C,i) \tag{5}$$

where α and β are parameters used to control the relative influences of F_{cont} and F_{curve}.

The objective of continuous function, F_{cont}, is to prevent all genes to get clustered in small areas in an image. This function value is calculated by the distance between two genes.

$$F_{cont}(C,i) = \|C(a_i) - C(a_{i-1})\| \tag{6}$$

Curve function, F_{curve}, prevents rapid changes in angle between two consecutive points. The value of curve function increases if the angle gets closer to $\dfrac{n}{n+2} * \pi$.

The external function forces the deformable contour towards the desired target contour.

$$F_{external}(C,i,\sigma) = \gamma \sum_{(x,y)\in C(a_i)} \nabla L(x,y,\sigma) \tag{7}$$

where $\nabla L(x,y,\sigma)$ is the Kircsh spatial gradient of the intensity image at position (x,y) with scale σ. And γ is a parameter used to control the relative influence of $F_{external}$.

3.3 Chromosome Selection Criteria

The criteria to select chromosomes for regeneration is based on *quality* and *diversity values*. The selection procedure is as follows:

(1)   Evaluate each chromosome's *quality value* that is its fitness value.
(2)   Sort and rank chromosomes by *quality values* and assign rank number to *quality rank*
(3)   Three highest quality ranked chromosomes are selected
(4)   N=3
(5)   While N<NUMBER_OF_POPULATION

(a)   Evaluate chromosome differences by summing corresponding genes Euclidean distances of the pre-selected chromosome and each one from the rest. Then keep the sum as *diversity value*

(b)   Sort and rank chromosomes' diversity values. The more difference is the more diversity, and hence the higher rank

(c)   Select the best chromosome for regeneration based on the sum of *quality* and *diversity ranks*

(d)   N=N+1

3.4 GA Applied with Multiscale Approach

In this research of brain MR image segmentation, GA is applied with multiscale to take advantages from both approaches. As mentioned above, at coarse scale, brain image feature can be extracted and resulted in rough contour. At this state, the number of generations of GA used is set to a high number in order to increase the probability of obtaining global maxima in fitness space. The selected results of deformable contours at coarser scales are used as the parent chromosomes at finer scales. However, too many generations generally cause too much chromosome deviation as selected chromosomes and their parents tend to be too independent. Therefore, number of generations used should decrease as image scales get finer.

In summary, this research proposes an approach of using many generations of GA at coarse scales to increase probability to encounter global maxima which is the target object. For finer scales, image features are more apparent and less number of GA generations is more suitable to prevent far exceeding deformable contour from the former ones, which means that the deformable contours deform closer around the target object.

4. Experiments, Results and Discussion

The proposed algorithm is applied to a set of brain MR images. The target object for segmentation is the brain area that includes white matter, gray matter and Cerebro Spinal Fluid (CSF).

4.1 Experiments

In the experiments, the test image set composes of 60 coronal view, T1, 256 x 256, 8-bit images of 3 mm. thickness. The number of image scale is set to 5. Number of generations of GA is set to 100 for the coarsest scale, and decreases linearly for finer scales. Each generation composes of 465 chromosomes, 300 of which are from mutation, 150 from crossover and 15 from reproduction. At each generation, 15 chromosomes are selected.

4.2 Results

Test results are observed and presented in 2 categories.
1.   Results at different image scales.
2.   Final results.

4.2.1 Results at Different Image Scales

The results of image segmentation at different image scales are observed and presented in Figure 1. Figure 1(a) is the brain MR image number 30 of the test set. Figure 1(b), 1(c) and 1(d) are the results from applying the proposed approach to images at coarse scales with $\sigma = 8$, $\sigma = 4$, and to the original image which is the finest scale, respectively.

From the results, it is quite clear that the draft target contour is encountered at coarse scale and the result contours in the following finer states deform towards the target contour.

4.2.2 Final Results

Final results of applying the proposed approach to a test set in Figure 2 are revealed in Figure 3. Figure 2 (a), 2 (b), 2 (c) and 2 (d) are images number 25, 30, 35 and 40 of the test set respectively. Figure 3 (a), 3 (b), 3 (c) and 3 (d) are the corresponding results of Figure 2.

It can be noticed that, for all images, final contour results surround the right target objects with different degrees of correctness.

4.3 Discussion

From the experiments, the results of the proposed technique are closed to the targets. The quality of the results depends not only on the features of an individual image but also on the designed fitness function. It is observed that the result contour in each program run varies within the range of the targets. The reason is that GA has a characteristic of randomness dependence. Therefore, the criterion to stop generating new result contours is still a problem to be explored.

5. Conclusion

Applying GA and mutiscale to be used with deformable contour technique is a feasible and promising approach for image segmentation. Both multiscale and GA have strong points in increasing the probability of obtaining global maxima, therefore, the result contours correctly surround target objects. However, from this research, it should be pointed out that quality of results does not depend only on the searching method. The chance of success depends highly on the fitness function that is based on the knowledge of the target object in specific problems.

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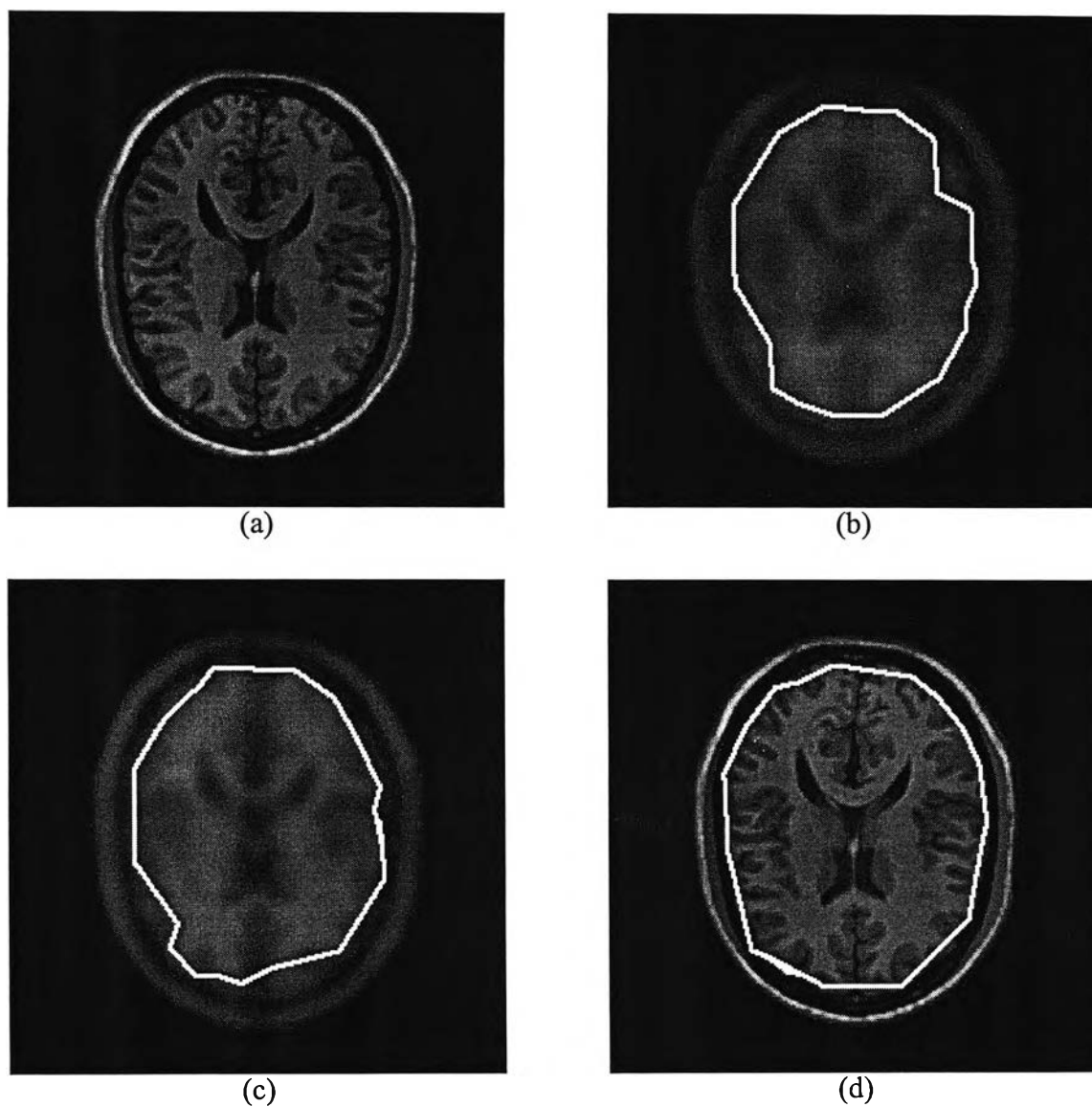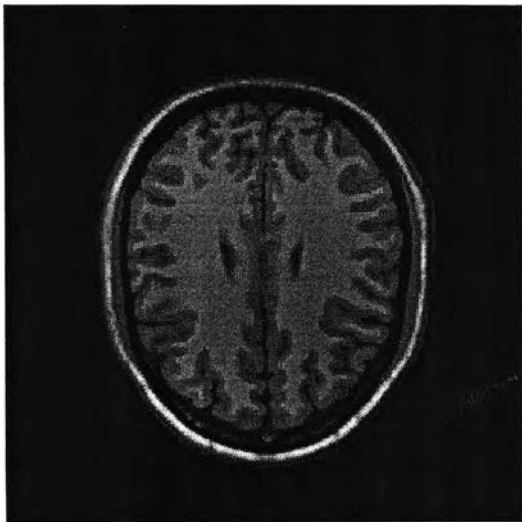
Figure 1: Results at different image scales. (a) Brain MR image number 30. (b), (c) and (d) Segmentation results of images with $\sigma = 8$, $\sigma = 4$, and of the original image.
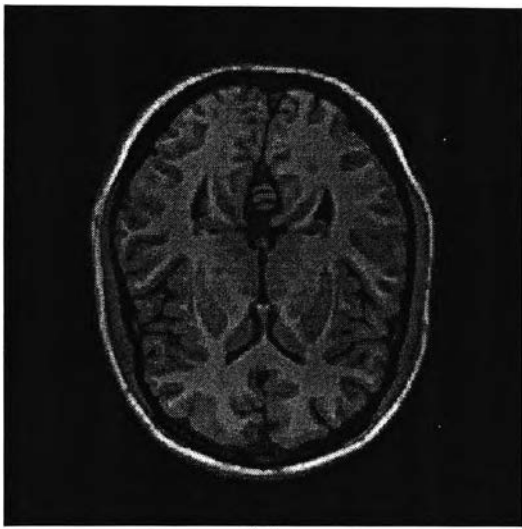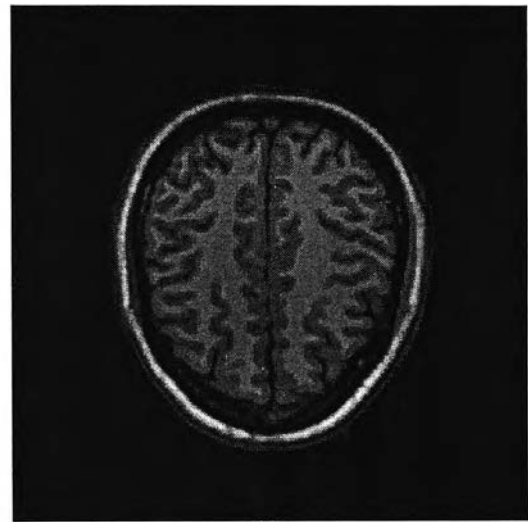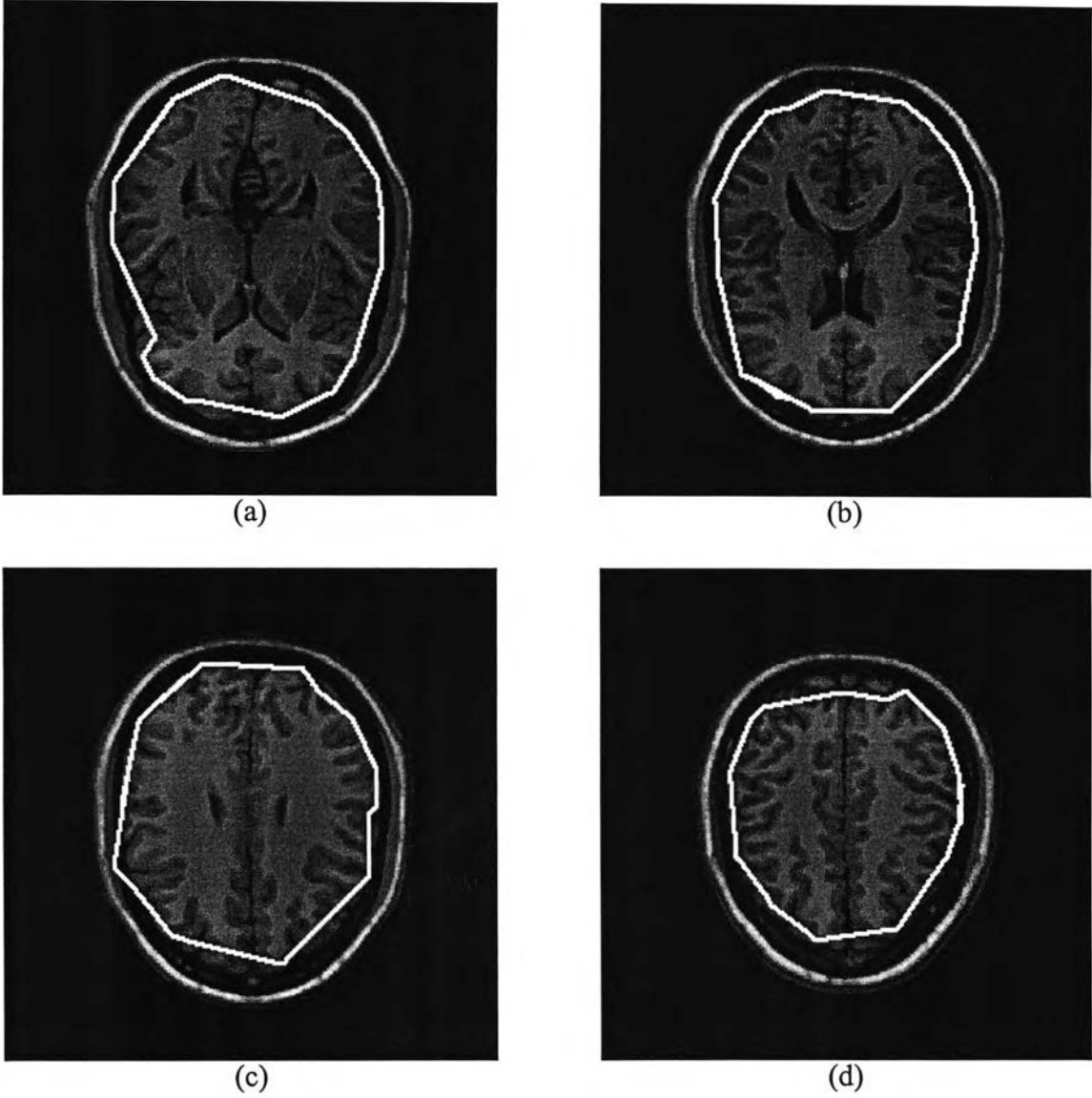
(a)

(b)

(c)

(d)

Figure 2: Images of the test set. (a), (b), (c) and (d) Images number 25, 30, 35 and 40 respectively.

Figure 3: Segmentation results of images in figure 2 (a), (b), (c) and (d) respectively.

Deformable Contour for Brain MR Images by Genetic Algorithm: From Rigid to Training Approaches

N. Covavisaruch and T. Tanatipanond

Department of Computer Engineering
Faculty of Engineering, Chulalongkorn University
Bangkok 10330, Thailand
nongluk.c@chula.ac.th, b0688521@student.chula.ac.th

Abstract

This paper presents rationales for the alteration of our approaches to segment brain MR images by deformable contour. Our previous work, "A Multiscale Approach to Deformable Contour for Brain MR Images by Genetic Algorithm", resulted in rough brain contour that correctly surrounded target object. The quality of results does not depend only on searching method but also on the fitness function that is set too rigidly. Hence, details of a contour cannot be located as the fitness function does not closely match image problem. As a result, "training" with a previously segmented brain contour can help the system acquire more relevant knowledge about the target's pre-selected features used in the fitness function. Experimental results reveal that, with an appropriate contour representation and a problem-oriented trained system, not only better contours of target objects are obtained, but segmentation of other images of the same manners, such as adjacent image slices of the same MR dataset, can also be encountered.

Keyword: Training, Deformable Contour, MRI, Genetic Algorithm

1 Introduction

Brain MR image segmentation has been a popular research topic in the field of image processing. Referring to the survey of Clarke et al. [1] on the image processing techniques for segmenting the brain, the techniques used can be divided into several groups. The first one is brain extraction using automatic thresholding. Another group is to get a brain contour by refinement of a rough one. "Snakes" and several deformable shape model algorithms are used in the refinement process. Brain segmentation based on both supervised and unsupervised statistical methods is another group of techniques in use. The last group is region growing and boundary detection.

Our research adopts deformable contour approach to segment brain MR images. This technique has been introduced by Kass et al. [2] to segment target brain contours in 2D MR images. Grzeszczuk and Levin [3] have adapted this technique by using "crack edges" as a contour represented in the form of line segments between pixels. The deformable contour with lowest energy is selected with Simulated annealing (SA). Rueckert and Burger [4] have presented a multiscale contour fitting process based on energy minimizing deformable models. SA optimization is also used in this approach. It has been reported that more accurate segmentation results than classic contour fitting process are achieved.

2 Our Previous Work

Our previous work, *"A Multiscale Approach to Deformable Contour for Brain MR Images by Genetic Algorithm"* [5] has proposed to use genetic algorithm (GA) as a searching method applied with deformable contour to segment brain MR images. Multiscale approach has been used in order to help accelerating brain area identification at coarse scales and localizing more accurate brain contours at finer scales.

2.1   Contour Representation

In this work, a deformable contour is represented as a set of orderly control points connected by straight lines. In addition, it must be closed curve and should not intersect. Hence, for the encoding scheme in terms of GA, one *population* refers to one set of deformable contours. Each set of points of a contour is considered as one *chromosome* where each point within the same set is one *gene*.

2.2   Fitness Function

The quality of deformable contour in this work is evaluated by fitness value. The fitness function of each chromosome composes of two feature groups, *internal* and *external*. *Internal* features force a contour to conform to the pre-defined characteristics of contour's properties that are *continuity* and *curvature*. The *continuity* feature means to prevent all genes to get too clustered in small areas. The *curvature* feature means to avoid rapid changes in angle between two consecutive control points. The *external* features force the contour towards the desired target contour by using the *gradient* of the image intensity.

2.3   Multiscale Approach

As Koenderink [6] has pointed out that, in the absence of any a-priori information, no single scale contains adequate image information. Therefore, he proposed to work with images at different image scales simultaneously. A coarse-to-fine tracking algorithm has been proposed later by Witkin [7] to work with multiscale approach based on the assumption that image features are identified at coarse scales and localized at fine scales.

Multiscale images in our research are obtained by the same method as used by Rueckert and Burger [4]. A multiscale representation of a 2-D image is the blurred image obtained by convoluting input image with Gaussian function with standard deviation. With different values of standard deviation, σ_i, multiscale images can be achieved.

$$\sigma_i = \sigma_0 s^i \qquad \qquad ...(1)$$

where σ_0 corresponds to the coarsest scale, s is the scale change rate and i is the order of the multiscale level.

2.4   GA Applied with Multiscale Approach

Instead of using several other searching techniques such as Greedy Algorithm, Hill Climbing, and Simulated Annealing, we proposed to use GA applied with multiscale approach. At coarse scales, brain image feature can be extracted. This results in rough contours and hence, number of generations of GA is set to a high number in order to increase probability of obtaining global maxima in fitness space. The best set of deformable contours at coarser scales is used as parent chromosomes at finer scales. However, too many generations generally cause chromosomes to deviate too much since the chromosomes and their parents become very independent. Therefore, fewer generations of GA are used as image scale gets finer in order that new contours are not too much different from those of their previous generation and deform closer around target contour.

With GA applied with multiscale approach, brain area can be correctly identified at coarse scales and at finer scales, contour can be more localized with moderate details. It has been concluded that it is possible to apply GA for the searching technique in deformable contour algorithm. However, this work reveals that quality of results does not depend only on the searching method. The success prospect depends highly on the fitness function that is based on the knowledge of the target object in specific problems.

3   An Improved Approach

In our previous work, the knowledge in fitness function has been rigidly pre-defined based on some general knowledge about the brain. This causes unimpressive results even when working with images of the same manner like those of an MR dataset. Therefore, our next step aims to improve the fitness function to possess more problem-oriented knowledge. This objective can be reached by gathering selected features of the target object from a known answer which, in this case, is a previously segmented brain contour. The representation of contour also needs changing in order to support this new fitness

function. More details can be found in "An Improvement of Multiscale Approach to Deformable Contour for Brain MR Images by Genetic Algorithm" [8].

3.1 Training the Fitness Function

This new fitness function also consists of *external* and *internal* features. In order to make the fitness function more problem-oriented, the information of both *internal* and *external* features is *trained* from a previously segmented brain contour. In the process of segmenting brain in an MR dataset, the *internal* features are dynamic as they are trained from slice to slice while the *trained external* features are static as they are kept unchanged for the same entire MR dataset.

3.1.1 External Features

External features consist of *intensity relationship* and *gradient* of each contour point and its connected outer neighbor(s). The *intensity relationship* represents the relationship of intensity levels of each contour pixel and its connected outer neighbor(s). The data is kept in terms of frequencies in 2D accumulator space. When evaluating this feature value, a 5x5 mean filter is applied to this accumulator space. A *gradient* is the intensity difference between a contour pixel and its connected outer neighbor(s). The data, ranges from –255 to 255, is also kept in terms of frequencies and forms a histogram.

3.1.2 Internal Features

Internal features are the *contour's length* and *contour's center*. A *contour's length* is simply the number of points on the contour while a *contour's center* is defined as ($\bar{x}$, $\bar{y}$).

$$\bar{x} = \frac{1}{L}\sum_{x=0}^{N-1}\sum_{y=0}^{N-1}xC(x,y) \qquad\qquad ...(2)$$

$$\bar{y} = \frac{1}{L}\sum_{x=0}^{N-1}\sum_{y=0}^{N-1}yC(x,y) \qquad\qquad ...(3)$$

where N is the height and width of image
          L is the contour's length
          $C(x,y) = 1$ if pixel at *(x,y)* is on the contour, and
             $= 0$ otherwise

3.2 A New Contour Representation

Representation of a contour and a fitness function are closely related. In order to get a finer contour and better fitness value evaluation, the contour representation from our previous work must be changed. As mentioned before, the contour results from our previous work are rough. This is because only less than 10 percents of all actual brain contour are used as control points. Therefore, in this new approach, all contour points are used as a new representation. Only minor change of the encoding scheme in terms of GA is that a gene refers to a point on the contour instead of a control point.

3.3 Applying the Improved Approach

It is our main target in this research to segment brain of the whole MR dataset. We, therefore, *train* the fitness function with one previously segmented, i[th], slice of an MR dataset. Brain MR image segmentation process starts at segmenting the ith image slice by applying the multiscale and GA approach with the *trained* fitness function, and the internal features used in fitness function are updated afterwards. The segmentation process continues by progressing on to the adjacent slices, (i-1)[th] and (i+1)[th] slices respectively. Setting up with the result from previous slice as an initial contour makes multiscale technique no longer needed.

4   Rigid Versus Training Approaches

The two proposed approaches were tested with a test brain MR dataset. In this work, quantitative validation was studied in order to evaluate the improvements.

The two proposed approaches, *"rigid"* and *"training"*, were tested with a brain MR dataset composed of 60 coronal view, T1, 256x256, 8-bit images of 3-mm. thickness. Our target brain contour covers white matter, gray matter, and Cerebro Spinal Fluid (CSF).

Multiscale approach was applied in the segmentation process for all image slices in the *rigid* approach and it was used only for the first segmentation slice in the *training* approach. The number of multiscale in the experiments for both methods was set to 5.

The number of generations of GA for *rigid* approach was set to 100 at the coarsest scale and decreased linearly at finer scales while it was fixed at 100 for *training* approach. For both approaches, each generation consisted of 465 chromosomes, 300 of which were from mutation, 150 from crossover, and 15 from reproduction. At each generation, 15 chromosomes were selected.

Apart from comparisons of the segmented areas, *similarity index (S)* was also used in this work as a quantitative validation for both approaches. According to Zijdenbos [9], who has proposed *similarity index* that is derived from a reliability measure known as the kappa statistic, *similarity index* between two measurements is defined as the ratio of twice the common area to the sum of the individual areas. It is sensitive to both differences in size and location. Consider a set A to be a binary segmentation that consists only of pixels of the same classification. The similarity of two segmentations, A1 and A2, is given by a real number, $S \in [0,1]$, as follows:

$$S = 2 \frac{|A_1 \cap A_2|}{|A_1| + |A_2|} \qquad \qquad ...(4)$$

Two segmentations can be said to be more similar as S gets closer to 1. Referring to Zijdenbos, although $S > 0.7$ indicates excellent agreement, the absolute value of S is difficult to interpret.

4.2   Results

Fig. 1 illustrates 4 pairs of the contour results from image slices number 25, 30, 35, and 40 of the test dataset respectively. The results in the upper row, (a) to (d), are from the *rigid* approach, while those in the lower row, (e) to (h), are the results of the same images from the *training* approach.
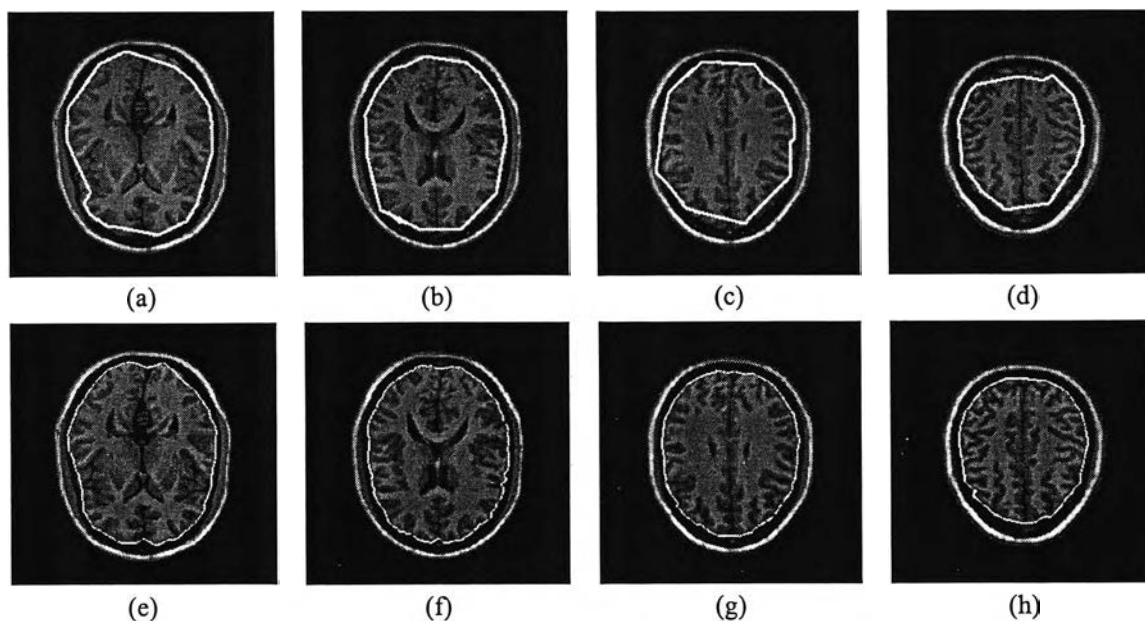

(a)   (b)   (c)   (d)

(e)   (f)   (g)   (h)

Fig. 1.   Results of image slices number 25, 30, 35, and 40 from the two proposed approaches.
Images (a) to (d) illustrate the results from rigid approach
while (e) to (h) are those of the consecutive slices from training approach.

Similarity index values were calculated in comparison with the manual segmented contours. Areas of results from manual and the two proposed automatic segmentation approaches, as well as the overlapped, excess, and shortage areas were reported as number of pixels. Table 1 shows all the quantitative data.

Table 1
Quantitative validations of both *rigid* and *training* approaches
(All figures are compared with manual segmentation)

Slice number	Approach	Area (pixels)					Similarity index
		Manual Seg.	Auto. Seg.	Overlapped	Excess	Shortage	
25	*Rigid*	19410	19844	18880	434	530	0.97511
	Training	19410	20292	19356	882	54	0.97639
30	*Rigid*	19100	19223	18540	123	560	0.98191
	Training	19100	19292	19082	192	18	0.99453
35	*Rigid*	16909	17350	16079	441	830	0.96198
	Training	16909	17463	16880	554	29	0.98302
40	*Rigid*	13013	13291	12388	278	625	0.96484
	Training	13013	14094	13012	1081	1	0.96008

4.3 Discussion

The objective of the experiments is to compare, and thus, evaluate the improvement of the two proposed approaches. From Fig. 1, it is clearly seen in the upper row that all the results from *rigid* approach identify brain correctly but details at the contours are not detected. The contours appear to be formed by connection of straight lines and thus, needs refinement. The results from *training* approach also correctly identify brain and the contours are much more localized closely to the brain contours.

For quantitative validation measurements, *similarity index values (S)* of both approaches are all above 0.95, with higher values from *training* approach than those from *rigid* approach except for the 40th slice. It is noticed that, the most S value in Table 1, 0.99453, comes from *training* approach of the 30th slice which is the same slice used at the beginning of the training process. In addition, the S values slightly decrease as the slices are further from the 30th.

It is noticed that the overlapped areas from *training* approach are greater than those from *rigid* approach while the shortage areas are much smaller. The excess areas from *training* approach are in the range of 1% to 9% of the manual segmented areas. This is due to the fact that the concave on the contours are still not reached, and hence, indicates that the algorithm needs more improvement.

From both qualitative and quantitative validation methods, it can be concluded that both the *rigid* and the *training* approaches can result in correct identification of target. With *training* approach, details of a contour can be more localized. The closer knowledge to the specific problem is acquired, the better results can be encountered. It should be noticed that human error has been excluded as all the quantitative data in our experiments is calculated based on manual segmented contours.

5 Conclusion

From our research, it is apparent that GA applied with deformable contour algorithm is a high potential brain MR image segmentation approach. Quality of segmentation results depend on several factors, i.e. contour representation, searching method and fitness function. These factors are closely related and can affect one another. A suitable contour representation is needed for a designated fitness function. The more relevant knowledge to a specific problem, the better fitness function, and hence, the better evaluation and selection of the searching method. It should be pointed out that "*training*" with a "*known answer*" shown in this research is a good way of acquiring problem-oriented features to be used in fitness function. For a problem like segmenting brain in an MR dataset, *training* with a previously known contour of an image slice can result in better segmentation in other slices than those of the *rigidly* parameter set up approach.

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An Improvement of

Multiscale Approach to Deformable Contour for

Brain MR Images by Genetic Algorithm

Thosaphon Tanatipanond and Nongluk Covavisaruch
Department of Computer Engineering
Faculty of Engineering, Chulalongkorn University
Bangkok 10330, Thailand
b0688521@student.chula.ac.th, nongluk.c@chula.ac.th

Abstract

This paper presents an improvement of multiscale approach to deformable contour for brain MR images by genetic algorithm (GA). Fitness function used in selection process is trained with one previously segmented image in order that the system can learn the target's pre-selected features. Hence, the system possesses enough knowledge about target's characteristics and is capable of segmenting the target in other images of the same manner. Contour representation is also changed in the way that more details are considered in the selection process. In the experiments, a set of brain MR images is used. It is found that the features "learned" from the training process are adequate for good brain segmentation and that the "trained" system can efficiently segment brain in other MR images of the same dataset.

Index Terms: Image segmentation, deformable contour, fitness function, genetic algorithm, multiscale, brain MR images.

1. Introduction

Automatic segmentation is one of the most challenging tasks in image processing and computer vision. In most of the previous works, techniques used include pixel classification step followed by pixel aggregation or region growing. The disadvantage of region growing technique is that it can occasionally cause leaking across regions.

Kass et al. [1] introduced the use of deformable contour approach to identify region boundaries to segment target objects in 2D images. Grzeszczuk and Levin [2] adapted this technique by using "crack edges" as a contour represented in the form of line segments between pixels. Simulate annealing (SA) was used to select the deformable contour with lowest energy. It was reported that global or nearly global minimum of the energy contour could be automatically found.

Rueckert and Burger [3] presented a multiscale contour fitting process which was based on the assumption that there was no single scale that contained adequate image information [4]. The segmentation process started by tracking the object contour in scale-space from coarse to fine scales. At coarse scales, the selected contours were closer to global maxima and at finer scales, they became nearer to actual contour. SA was also used in this research.

It was concluded that this technique provided more accurate segmentation results than the classic contour fitting process and was very robust to noise and random initialization.

Our previous work, *"A Multiscale Approach to Deformable Contour for Brain MR Images by Genetic Algorithm"* [5], introduced a new searching technique by using genetic algorithm (GA) to segment brain MR images at multiscale with deformable contour. In the encoding scheme of this research, a contour was encoded as a set of control points connected by straight lines. Most suitable contours were selected based on quality values evaluated from fitness function and diversity values, from the differences among pre-selected contours. It was concluded that this technique was a feasible and promising approach for image segmentation. Both multiscale and GA possessed strong advantageous properties in increasing probability of obtaining global maxima, and therefore, the result contour surrounded correct target. However, it was pointed out that the quality of result depended highly on the fitness function that was based on the characteristics of target object.

2. An Improved Approach

Several alterations have been achieved to improve our previous work. The first change starts at the encoding scheme for GA. Instead of representing a contour as a set of control points connected by straight lines, all points on a contour are used. Hence, more fine details about the specific contour are considered and evaluated in fitness function.

Another major change that has high influences on the result in this work is the fitness function. Rather than assigning some fixed feature values that are used in the fitness function, training the new function with a previously segmented image makes the fitness function more flexible. With this approach, better target's contour features can be obtained for future use. In this research, four features of brain contours are taken into account as follows: *intensity relationship* and *gradient* of each contour point and its connected outer neighbor, and *contour's length* and *center*. Quality values from fitness function are calculated from the combination of these four features weighted at different scales depending on their importance related to the characteristic of brain image.

The "trained" system is tested in order to ensure that it is dependable. The test starts at initializing a dummy contour by a randomized set of points. Multiscale approach is applied at this stage to enlarge the probability of obtaining global optimal contour. The system's result contour of the brain MR image used in the training phase and the previously segmented one must be nearly the same to verify that the system is trained to work properly.

Our next goal approaches for obtaining brain segmented contours in other image slices of the same MR dataset by the "trained" system. The brain result contour of the training image slice, i^{th}, is used as an initial contour for next consecutive, $(i+1)^{th}$ and $(i-1)^{th}$, image slices and so on. Multiscale approach is not necessary in this phase as it is assumed that, at this point, the formerly segmented brain result contour of connected slice is closely surrounding the target object in current image.

3. Extracting the Optimal Contour

A. A New Representation of Deformable Contours

From our previous work, deformable contours were rough as only less than 10 percents of all actual brain contour points were used in the contour representation. Therefore, the feature information of these control points extended to searching process was very limited. Hence, in order to acquire more fine details of a brain contour, all points in each contour are used as our new representation.

B. Training the Fitness Function

Many approaches applied *energy function* as a means to evaluate and to select contours [6]. Two possible features, which can be assigned as parameters of energy function, are the intensities of nearby pixels and the contour's geometry [2]. These feature values are very often pre-defined and fixed. This makes the system very rigid and causes unimpressive results when applying to different images of the same manner.

The fitness function in our previous work followed the above concept. In this research, training the fitness function with a known previously segmented contour of target object is applied in order that the fitness function is adapted to be more problem-oriented. Dominant features around the contour, which are acquired and used in fitness function, can be categorized into 2 groups as follows:

External Features: This type of features is related to intensities of image pixels. In this research, *intensity relationship* and *gradient* of the contour pixel and its connected outer point(s) are chosen.

Internal Features: This type of features is determined purely by geometry characteristics of the contour. *Contour's length* and *center* are used in this research.

• Intensity Relationship

Frequencies of intensity relationship of the contour pixel and its connected outer neighbor(s) are determined and plotted on an accumulator space as shown in Figure 1. The x- and y-axes, ranged from 0 to 255, represent the intensities of contour and their connected neighbors respectively. In order to specify the contour intensity relationship area in the accumulator space, a mean filter of size 5x5 is applied.

Fig. 1 An example of contour intensity relationship

• Gradient

Gradient is the intensity difference between the contour pixel and its connected outer neighbor(s) and hence, ranges from –255 to 255. Frequencies of gradient values are also determined and a gradient histogram is created.

• Contour's Length

The length of a contour is simply defined by the number of points on the contour.

• Contour's Center

In this research, a contour's center is defined as ($\bar{x}$, $\bar{y}$).

$$\bar{x} = \frac{1}{L}\sum_{x=0}^{N-1}\sum_{y=0}^{N-1} xC(x,y) \qquad (1)$$

$$\bar{y} = \frac{1}{L}\sum_{x=0}^{N-1}\sum_{y=0}^{N-1} yC(x,y) \qquad (2)$$

Where N is the height and width of image

  L is the contour's length

  $C(x,y) = 1$ if pixel at (x,y) is on the contour, and

   = 0 otherwise

Fitness function uses all four features, weighted differently depending on their importance, to calculate the quality values.

C. Details of GA

Encoding Scheme

In the GA encoding scheme, a set of deformable contours is encoded as one *population*. A contour, which consists of a set of co-ordinate points, is encoded as a *chromosome*. Finally, each co-ordinate point is encoded as a *gene*.

Evolutionary Operations

In this research, three operations in GA are as follows:

● Mutation

Generating a new chromosome by mutation starts at randomly select one chromosome from its parent chromosomes. Randomly pick one gene, G_i, and at some certain distances, pick two more genes on both sides of G_i to be used as two endpoints. Define a small square to surround G_i. Move G_i randomly within the square and connect it to the formerly selected two endpoints. A sample of mutation operation is shown in Figure 2.
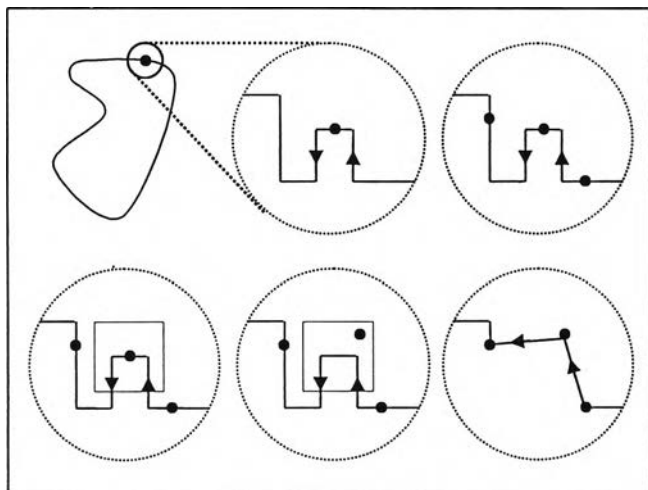
Fig. 2 Steps in mutation operation

● Crossover

For crossover operation, two chromosomes, C_1 and C_2, are randomly chosen from their parent chromosomes. Pick two genes from C_1. Search in C_2 for two genes whose positions are closest to the ones previously picked in C_1. Divide each chromosome at the positions of the two genes. A new chromosome is then generated by combining one portion from C_1 with another portion of the opposite side from C_2. Connecting lines between the two portions are often needed to make a complete contour.

● Reproduction

Reproduction is the process that generates chromosomes from the parent chromosomes by cloning.

Chromosome Selection Criteria

The criteria to select chromosomes are based on quality values evaluated from fitness function. A number of chromosomes with highest quality values are selected as parent chromosomes.

4. Experiments, Results and Discussion

A. Experiments

A test brain MR image set used in the experiments composes of 60 coronal view, T1, 256x256, 8-bit images of 3-mm. thick. The target object is the brain area which includes white matter, gray matter and Cerebro Spinal Fluid (CSF). Number of generations is set to 100 which also applies to every image scale in the single image test. There are 620 chromosomes in each generation; 500 from mutation, 100 from crossover and 20 from reproduction. Only 20 of all 620 chromosomes are selected to be parents in the next generation.

Experiments in this research can be divided into 2 parts as follows:

Single image test: This test is set up to confirm that fitness function and the whole system are dependable. It is tested by segmenting the brain image used in training process at 6 different image scales from coarsest to finest. The system is verified to be dependable when the final result contour and the training contour are nearly the same.

Multiple image test: The main objective of this test is to explore the performance of the proposed algorithm when applied on other MR images of the same dataset. In this research, the test starts at the 30th image slice, which is done by the same method as the "single image test". The next consecutive image slices, the 31st up to the 42nd, and the 29th down to the 18th, are segmented with the "trained" fitness function without applying the multiscale approach. The result contour of each image is used as the initial contour of the next consecutive slice. By the same token, the internal feature values of each result contour are also used in the fitness function to segment brain area in the next consecutive slice.

B. Results

The final result from applying the proposed approach with multiscale in the "single image test" is shown in Figure 3. It can be noticed that the result contour is nearly the same as the one used in the training process.
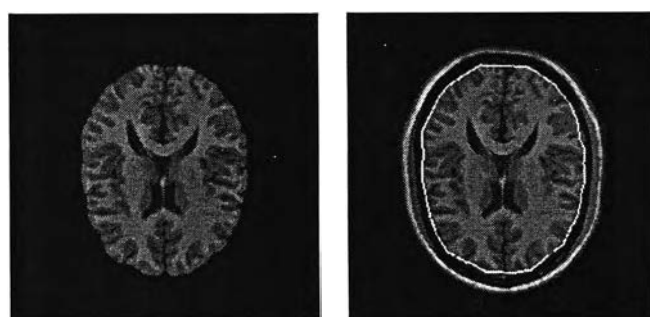

Fig. 3 Previously segmented brain image used for training process and the result from single image test of the 30th image slice are shown respectively.

Figure 4 shows the results from the "multiple image test". This figure consists of the result contours from image slices number 20, 25, 26, 34, 35, and 40 respectively. It can be seen that all the result contours are close to the brain no matter how far the slices are from the 30th, or the first segmented, image slice.
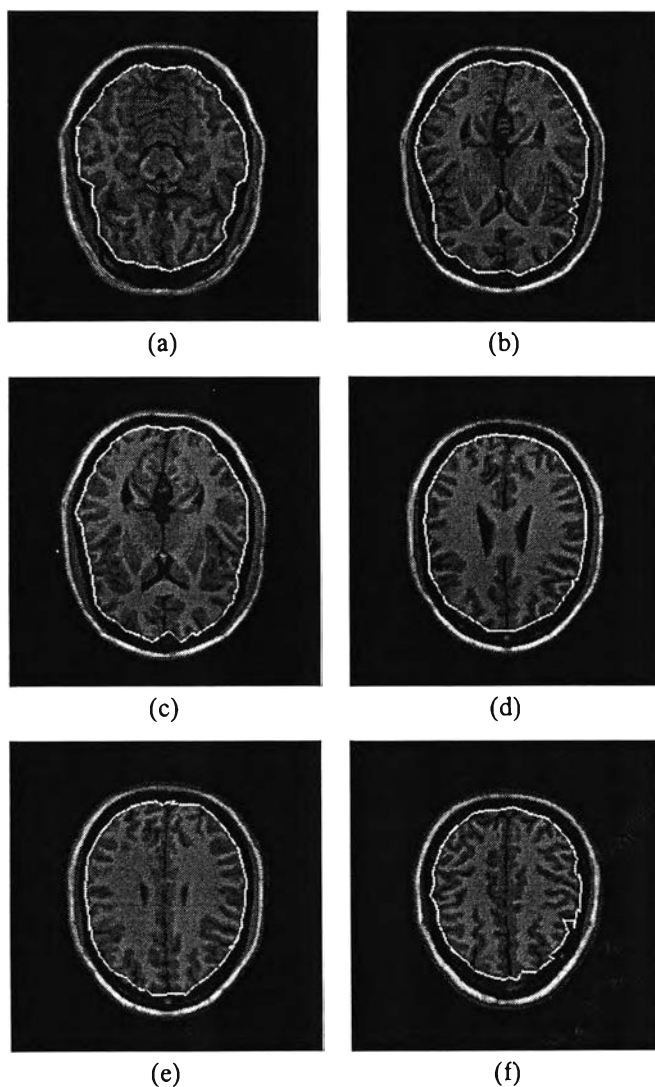
Fig. 4 Results from multiple image test of images number 20, 25, 26, 34, 35 and 40 are shown in (a) to (f) respectively.

The overall results from this research are much improved compared to those from our previous work as they are more fitted to the brain in all images. Figure 5 shows a result example from our previous work compared with the one from this research.
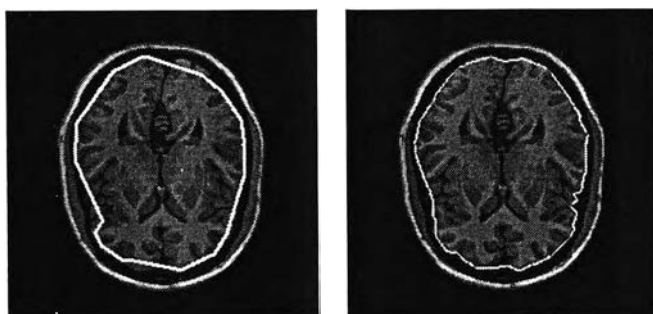

Fig. 5 Results of image number 25 from our previous work and from this research respectively.

C. Discussion

The fact that the result from the "single image test" closely resembles the training contour indicates that the fitness function works more effectively as it is trained in a problem-oriented manner. The result contour also verifies that the 4 chosen features provide enough information for the selection process.

From the "multiple image test", it can be seen that all results are closer to brain's contours. These data indicate that the result contour of an image can be used as a good initial contour for the next consecutive slice. Therefore multiscale approach is no longer necessary. As a result, processing time is greatly reduced. It is observed that results from the image slices that are far from the first segmented slice are still close to brain. Therefore, it can be concluded that, the internal features, which are barely changed slice by slice, and the unchanged external features, which are "learned" earlier from the training process, can be suitably used on other MR images of the same dataset.

5. Conclusion

Compared to our previous work, this present research is improved in several ways. Better result contours can be obtained. It is because training the fitness function with a previously segmented image assists the system to be more problem-oriented. Finally, it can be concluded that, for a problem like MRI dataset, training the system with a known-segmented image enables the "trained" system to segment the same target in other images of the same manner.

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ประวัติผู้วิจัย

      นายทศพล ธนะทิพานนท์ เกิดวันที่ 4 มกราคม พ.ศ. 2520 ที่จังหวัดกรุงเทพมหานคร สำเร็จการศึกษา
ระดับปริญญาตรีวิศวกรรมศาสตรบัณฑิต สาขาวิศวกรรมคอมพิวเตอร์ ภาควิชาวิศวกรรมคอมพิวเตอร์ จุฬา
ลงกรณ์มหาวิทยาลัย ในปีการศึกษา 2540 และเข้าศึกษาต่อในหลักสูตรวิศวกรรมศาสตรมหาบัณฑิต สาขา
วิศวกรรมคอมพิวเตอร์ ภาควิชาวิศวกรรมคอมพิวเตอร์ จุฬาลงกรณ์มหาวิทยาลัย ในปีการศึกษา 2541 และ
เป็นผู้นำเสนอผลงานวิจัยด้านการประมวลผลภาพทั้งในระดับชาติและระดับนานาชาติ ในช่วงปีพ.ศ. 2541
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