MRF Based Contour Evolution of Non-Contrast Medical Image by Genetic Segmentation Algorithm

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Abstract: **Image Segmentation is a fundamental and challenging problem in computer vision and medical image analysis. In spite of several decades of research and many key advances and several challenges still remain in this area. The evolution of contour is governed by three types of information (i) appearance (ii) boundary edgeness and (iii) shape each of which is incorporated as clique potential into MAP-MRF problem. The evolution of the contour is performed by iteratively solving a MAP-MRF labeling problems described by the non linear function. Then a genetic algorithm is used to find the result without converting non linear to linear function.   The proposed method is a new model for segmentation contour explicitly as a chain of control point is implemented of medical image segmentation in non contrast computed tomography data.**

Keywords: **Markov random fields, active contour, genetic algorithm.**

I.   INTRODUCTION

Image segmentation is in general an ill-posed problem and additional constraints need to be imposed in order to achieve the desired segmentation result. Commonly used constraints include traditional regularization constraints and constraints based solely on image information (e.g., edges). More accurate solutions to the segmentation problem can be obtained by taking advantage of any prior information available about the class of images being segmented and about the objects of interest present in them. A significant amount of prior knowledge about the shape, appearance, and location of the organs is available that can be used to constrain the solution space of the segmentation problem. Among the various types of prior information the incorporation of prior information about shape, in particular is very challenging. However, if used it can significantly improve the segmentation results, particularly when there are neighbouring objects with similar appearance which is often the case in organ segmentation problems. In addition, it is even more challenging to unify the information from such a wide variety of sources into a single framework.

In particular, while segmenting organs in medical images which is our main concern here a significant amount of prior knowledge about the shape, appearance and location of the organs is available that can be used to constrain the solution space of the segmentation problem. However, if used it can significantly improve the segmentation results particularly when there are neighboring objects with similar appearance which is often the case in organ segmentation problems. In addition it is even more challenging to unify the information from such a wide variety of sources into a single framework. With respect to the incorporation of shape priors into the MAP-MRF framework used the distance map of the boundary of a pre aligned shape template to design a pair wise clique potential that minimizes the deviation between the boundary of the segmented object and the boundary of the shape template. Once the shape of the medical image was detected, the segmentation can be done by using genetic algorithm.

II.   RELATED WORKS

Andy Tsai et al.,[1] proposed level set the implicit representation of the segmenting curve and calculate the parameters of this implicit model to minimize the region-based energy functional for image segmentation. The resulting algorithm is found to be computationally efficient and robust to noise has an extended capture range and does not require point correspondences. The development of these techniques for two-dimensional data, this algorithm can easily be generalized to handle multidimensional data. The region-based models also used. However, it is important to point out that other region-based models are equally applicable in this framework.

Vladimir Kolmogorov et al.,[2] proposed scheme is Tree-reweighted message passing is closely related to a certain linear programming (LP) relaxation of the energy function. This relaxation has been widely studied in different contexts. Formulated this LP relaxation for arbitrary functions in their terminology the problem is called partial constraint satisfaction. This LP formulation in the context of the TRW algorithm for general energy functions of the form. Recently,showed that graph cuts have close links with this LP. Thus the LP relaxation plays a very important role in the theory of MRF optimization algorithms.

Amol Pednekar et al.,[3] The automatic segmentation of CMR data typically faces two challenges: the determination of the tissue boundaries and the delineation of the anatomical boundaries. The partial voluming effect blurs the intensity distinction between neighboring tissue types. Separability of tissues based on intensity statistics alone is not accurate. In addition, neighboring tissues though of the same type need not belong to the same anatomical structures. Thus, it is not possible to delineate the myocardium based on tissue border detection alone. The priori information regarding the geometry of the left ventricle (LV) into the intensity-based segmentation. The statistical approaches are limited by the sample size and how representative the training set.

Mark A. Horsfield et al.,[4] proposed scheme is to include prior knowledge into the fuzzy connectivity algorithm. The aims were to reduce the operator time needed as much as possible, and to reduce the computational complexity so as to produce a more general tool for assessing lesion volume. This model is used with images of different types of contrast (such as FLAIR images) without modification. Proposed scheme to produce a general tool that matched the performance of a human operator performing the measurements using an established method but with considerably less drudgery and strain caused by operating the computer mouse.

Jean Provost et al.,[5] In previous reports high frame rates were obtained using ECG gating. The analysis of diseases such as ventricular tachycardia the ECG may not be regular. Presented the new technique of motion-matching that is based on local incremental displacements used to co-register those sectors. Incremental displacements were previously used to map the EMW. While this approach provides a higher signal-to-noise ratio, it may be affected by the presence of rigid motion. Graded ischemia was obtained by gradually by gradually obstructing the LAD flow to generate an ischemic region of increasing size and severity, in order to test the EWI performance in depicting the ischemic region size as the coronary flow decreases.

Nikos Komodakis et al.,[6] A novel MRF-optimization scheme is proposed in this paper. It is called DD-MRF (from Dual Decomposition MRF) and unlike existing message-passing techniques. The theoretical setting of our method rests on the technique of dual decomposition. This is an extremely general technique which is well known to people in optimization as it has been used with great success for solving many different kinds of problems up to now. More generally demonstrate that one can use the proposed framework to easily design algorithms that are tailored to any particular class of MRFs. The derived methods can take full advantage of the structure in that class e.g., allow the use of efficient inference techniques such as graph-cut based approaches.

Pradeep Kumar et al., [7] To focus on addressing the other type of errors consistent bias. Biases are systematic errors mostly caused by mistranslating manual segmentation protocols into the criteria followed by the automatic segmentation method. By definition bias occurs consistently across different segmentation trials when certain conditions are met a manual segmentation protocol may assign a specific label. Hence, one can detect bias via capturing the correlated patterns. In reality, the bias may appear in more complexes and less intuitive patterns. Although it may be difficult for the human to identify such bias, most machine learning techniques are capable of providing satisfactory solutions.

III.   PROPOSED SYSTEM

An explicit shape-constrained MAP-MRF-based contour evolution method for the segmentation of organs in 2-D medical images was used. With respect to the incorporation of shape priors into the MAP-MRF framework used the distance map of the boundary of a pre aligned shape template to design a pair wise clique potential that minimizes the deviation between the boundary of the segmented object and the boundary of the shape template. Once the shape of the medical image was detected, the segmentation can be done by using genetic algorithm.
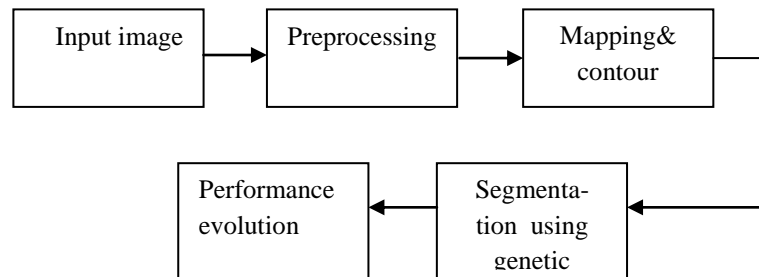
Fig 1.1 Block diagram for the proposed system

In this paper first we have to give the input as medical image of non contrast computed tomography data it reads the image and its stores the image value .After that Preprocess is used to remove the presence of noise in the image. It enhances the visual appearance of an image and improves the manipulation datasets. Median filter is used to enhance the image to remove the noise. The 3*3 sub region is scanned over the entire image. At each position the centre pixel is replaced by the median value it preserves edges. The normal outline or configuration of the body or of a part. To shape a solid along certain desired lines. A contour is represented as a collection of control points. MRF based contour evolution is undergone here. Uses available information to explicitly choose the control points.

Mapping and contour evolution:

The segmentation problem as a contour evolution problem wherein the evolution of the contour is performed by iteratively solving a MAP-MRF labeling problem .The explicit representation of the segmentation contour provides direct control over its evolution. The incorporation of three types of prior information that are commonly available while segmenting organs in medical images.

1) Appearance prior*: Each organ is composed of a set of tissues which in turn, have a characteristic appearance or texture in medical images whose knowledge can be used to improve the segmentation.

$$E^A(f|D) = A_x\big(x(s), y(s)\big)(\hat{N}_{e_{ij}}, \hat{\imath}\,)\, \mathrm{d}s \qquad\qquad (3.1)$$

2) Boundary edgeness prior: The energy function *EB* (**f** /**D**) models the prior information that an object boundary is more likely to be located in the areas where there is high intensity gradient. Since higher intensity gradient corresponds to a stronger edgeness, refer to this information as the boundary edgeness prior.

$$E^B(f|D) = \sum_{\{i,j\}\in C_2} V_{ij}^B (f_i, f_j|D) \qquad\qquad (3.2)$$

3) Label Regularization Prior: The energy function $E^R(\mathbf{f}\,/\mathbf{D})$ in   models a simple regularization prior on the labels/displacements assigned to consecutive points on the contour. Specifically, $E^R(\mathbf{f}\,/\mathbf{D})$ is defined in the form of a second-order clique potential as shown in the following equation

$$E^R(f|D) = \sum_{\{i,j\}\in C_2} V_{ij}^R (f_i, f_j|D) \qquad\qquad (3.3)$$

Where V_{ij}^R is defined as follows

$$V_{ij}^R(f_i, f_j|D) = ||d_{f_i} - d_{f_j}|| \qquad\qquad (3.4)$$

4) Shape Prior: The energy function *ES* (**f** /**D**) models prior information about the shape of the object being segmented. Where **s***ijk* is the shape descriptor of the triangle formed by the triplet of the three control points *i*, *j* and *k* after the

application of the displacements corresponding to the labels fi, fj, fk and $\mathbf{p}ijk$ is the learned probability density function of the shape descriptor corresponding to this triplet.

$$E^s(f|D) = \sum_{\{i,j,k\}\in c_3} V_{ijk}^S(f_i, f_j, f_k|D) \qquad\qquad (3.5)$$

Segmentation using genetic algorithm:

Genetic algorithm is a heuristic search or optimization technique for obtaining the best possible solution in a vast solution space.

Selection:

The fitness function is defined over the genetic representation and measures the quality of the represented solution. The fitness function is always problem dependent. The fitness of the solution is the sum of values of all objects in the knapsack if the representation is valid or 0 otherwise

Cross over:

In genetic algorithms, crossover is a genetic operator used to vary the programming of a chromosome or chromosomes from one generation to the next. Cross over is a process of taking more than one parent solutions and producing a child solution from them.

Mutation:

Mutation is a genetic operator used to maintain genetic diversity from one generation of a population of genetic algorithm chromosomes to the next. Mutation alters one or more gene values in a chromosome from its initial state. Hence GA can come to better solution by using mutation.

FLOW OF GENETIC ALGORITHM PROCESS
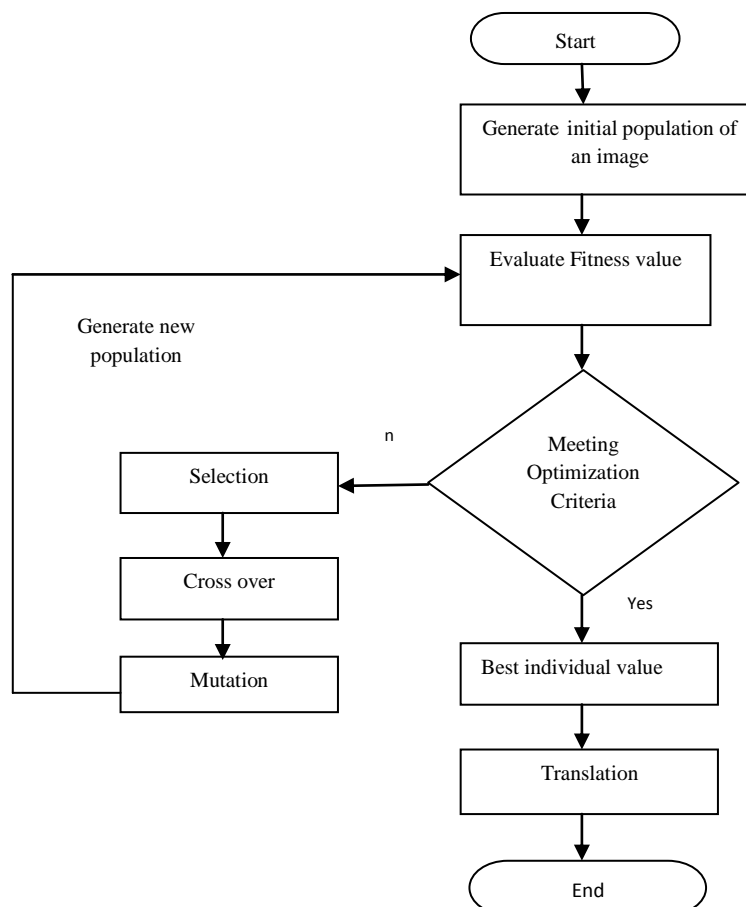
A brief outline of the steps involved in our segmentation algorithm is given as follows:

1. Functional Optimization of Non linear Function using Genetic Algorithm.

2. To encode the each parameter of the contour images by using binary coding.

3. This binary coding is done by using the position of each binary bit.

4. Generating Non Linear Function The binary bit positions are interchanged by using swapping method.

5. Crossover contains parent region and child region(Parent region is the majority segmented region and child region is the minority segmented region.

6. Population (increasing level) means number of pixel values increases in non negative region.

7. Mutation is performed correct segmented region is selected. The segment region is select negative or positive regions. Mutated parameter is uniformly selected from the row and column value.

Performance evaluation:

The performance analysis of segmentation using genetic algorithm was evaluated by the following performance metrics.

Dice Similarity Coefficient:

DSC value is very simple and useful accuracy in image segmentation. To examine the statistical validation of segmentation. It can be used to measure how similar two strings are in terms of common bigrams.

$$\text{DSC} = \frac{2*|\,A(S) \cap A(G)\,|}{|\,A(S)| + |A(G)|}$$

Sensitivity:

Sensitivity is the measure of the quality of an image in terms of smallest detail or discontinuity that may be detected. It is dependent on the combined effects of two independent sets of variables. One set of variables affects the contrast and the other set of variables affects the definition of the image.

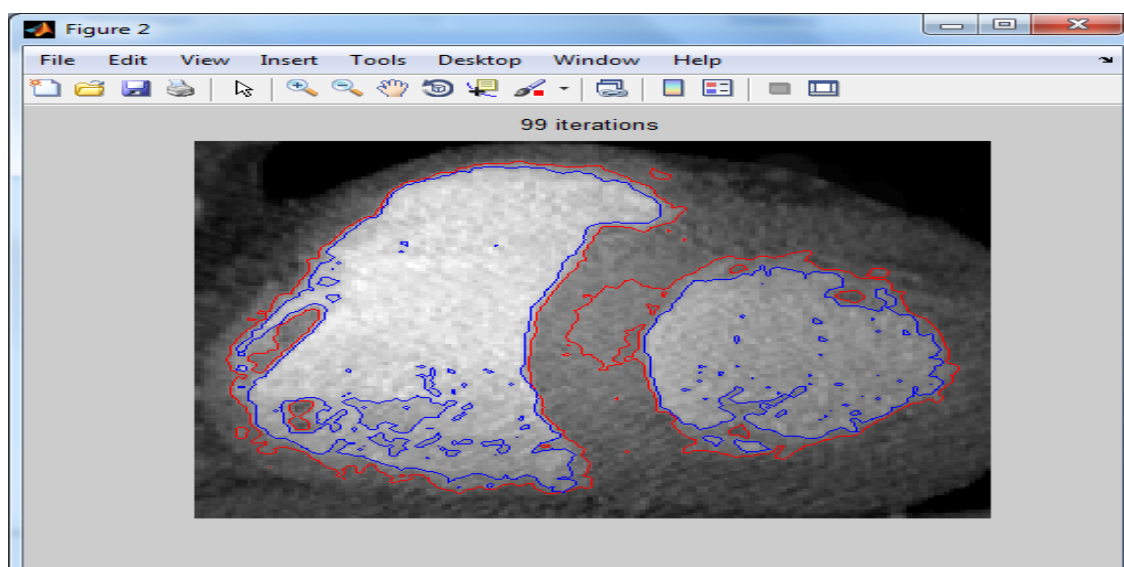$$\text{S} = \frac{|\,A(S) \cap A(G)\,|}{|\,A(G)\,|}$$
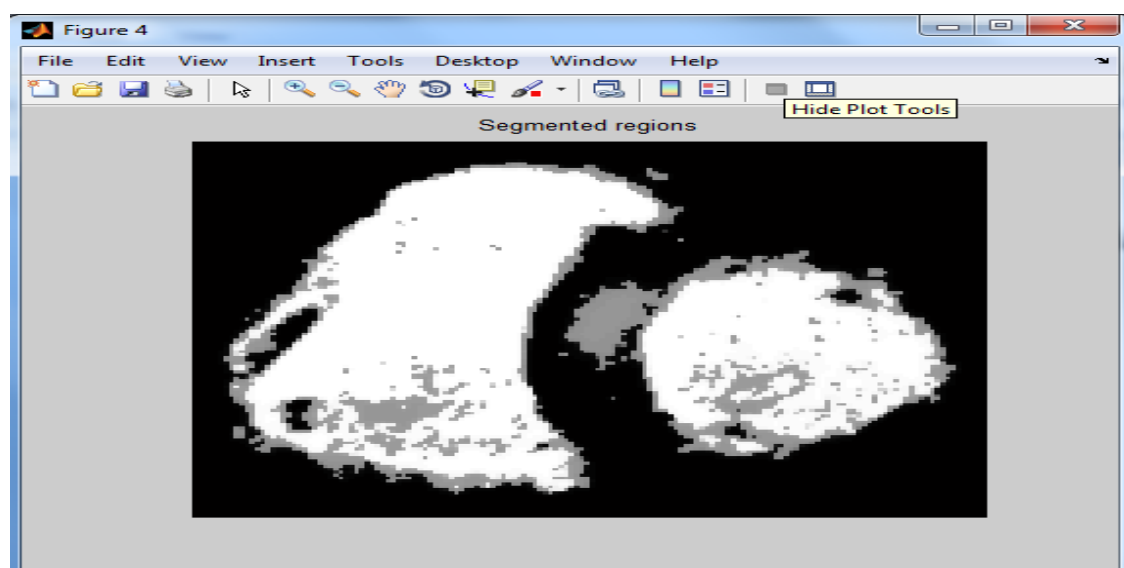
IV. RESULTS & DISCUSSION
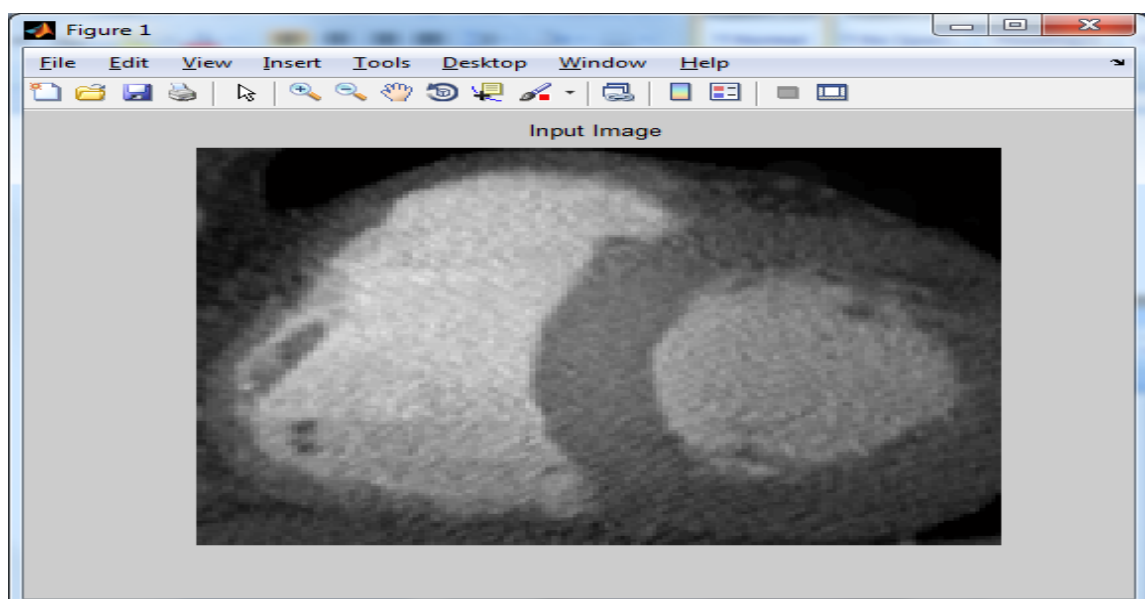
This figure is the non contrast CT data of heart image for the process as an input image.
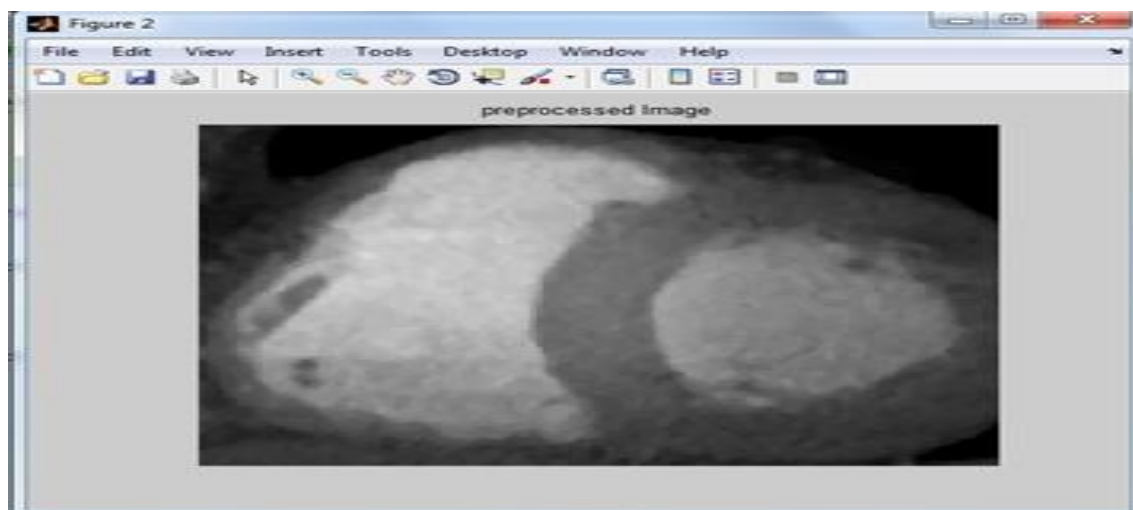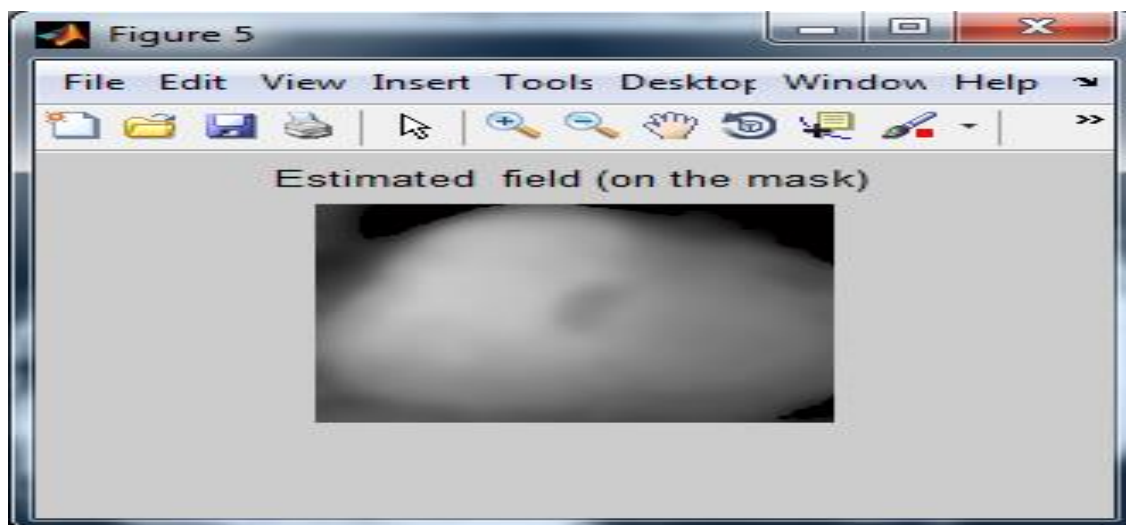
The 3*3 sub region is scanned over the entire image. At each position the centre pixel is replaced by the median value
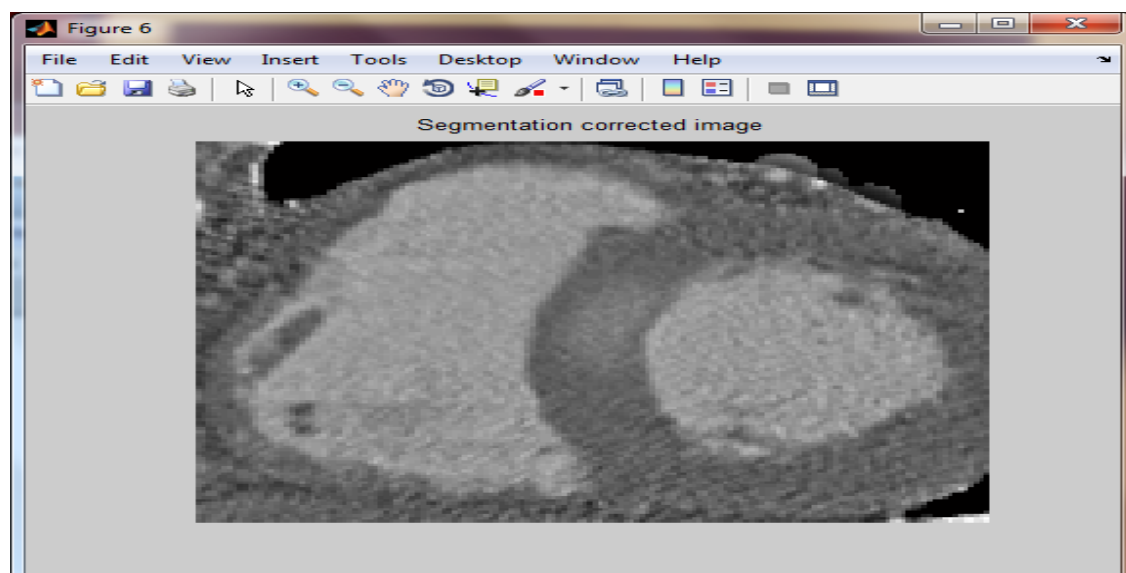

This figure shows the object boundary of an image after completion of contour process by 99 iteration.
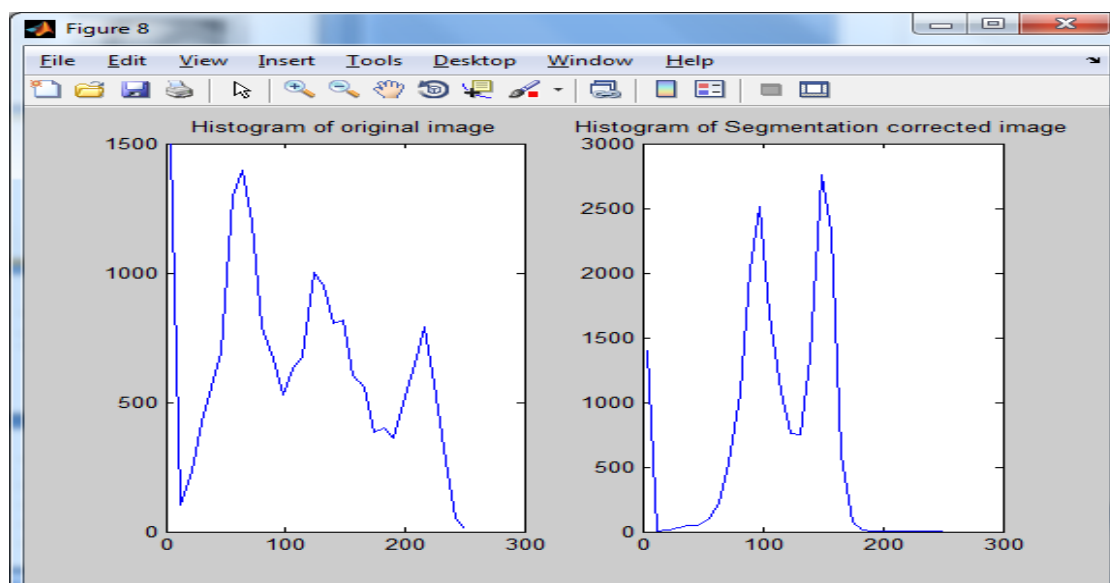

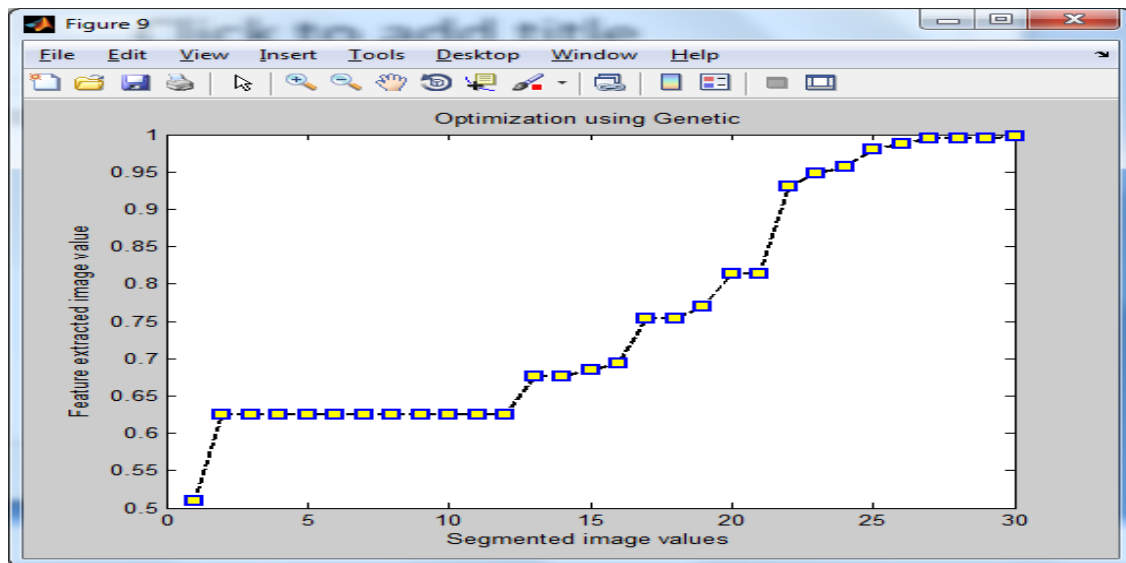After finding the contour the image has been segmented into small regions.

Masking is responsible for eliminating the noise after preprocessing.

After finding the segmented regions genetic algorithm is responsible to obtain segmented corrected image.

Histogram plots the pixel value of the input and the output image.

This shows the optimization view of the output image by genetic algorithm.

V.   CONCLUSION

The image has been segmented by genetic segmentation algorithm based on contour evolution and performance metrics has been calculated for sample images.A significant decrease in computational time can be achieved by the proposed method.

REFERENCES

[1]   Amol Pednekar, Uday Kurkure and Ioannis(2006), 'Automated Left Ventricular Segmentation in Cardiac MRI' IEEE transactions on biomedical engineering, vol.53,No.7.

[2]   Jean Provost ,Wei-Neing Lee, Kana Fujikura and Elisa E. Konofagou (2010),'Electromechanical Wave Imaging of Normal and Ischemic Hearts In Vivo' IEEE transactions on medical imaging, vol.29, No.3.

[3]   Mark A.Horsfield, Rohit Bakshi, Macro Rovaris, Mara A.Rocca, Venkata S.R.Dandamudi, Paola Valsasina(2007), 'Incorporating Domain Knowledge Into the Fuzzy Connectedness Framework :Application to Brain Lesion Volume Estimation in Multiple Sclerosis'IEEE transactions on medical imaging, vol.26,No.12.

[4]   Mohammed Talebi, Ahamd Ayatollahi, Ali Kermani(2011), 'Medical ultrasound Image Segmentation using Genetic Active contour' IEEE transaction on medical imaging.

[5]   Nikos Komodakis, Nikos Paragios and Georgios Tziritas(2011), 'MRF Energy Minimization and Beyond via Dual Decomposition' IEEE transactions on pattern analysis and machine intelligence, vol.33, No.3.

[6]   Pradeep Kumar , Rajat Chaudhary, Ambika Aggarwal, Prem Singh, Ravi Tomar(2012) 'Improving Medical Image Segmentaion Techniques Using Multiphase Level Set Approach Via Bias Correction'.

[7]   Rafael C.Gonzalez and Richard E.Woods, 'Digital Image Processing', Pearson Education, Third Edition.

[8]   Uday Kurkure, Amol Pednekar, Raja Muthupillai(2009), 'Localization and Segmentation of Left Ventricle in Cardiac Cine-MR Images' IEEE transactions on biomedical engineering, vol.56, No.5.

[9]   Vladimir Kolmogorov(2006), 'Convergent Tree-Reweighted Message Passing For Energy Minimization' IEEE transactions on pattern analysis and machine intelligence, vol. 28, No.10.

[10]   Yuri Boykov, Olga Veksler and Ramin Zabih(2001), 'Fast Approximate Energy Minimization via Graph Cuts IEEE transactions on pattern analysis and machine intelligence, vol.23, No.11.