



Enhanced Geometric Active Contour Segmentation Model (ENGAC) For Medical Image Segmentation

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ABSTRACT

Segmentation is an aspect of computer vision that deals with partitioning of an image into homogeneous region. Medical image segmentation is an indispensable tool for medical image diagnoses. This work built on Geometric active contour (GAC) segmentation which is one of the outstanding model used in machine learning community to solve the problem of medical image segmentation. However, GAC has problem of deviation from the true outline of the target feature and it generates spurious edge caused by noise that normally stop the evolution of the surface to be extracted.

In this paper, an enhanced Geometric active contour was formulated by hybridizing Kernel Principal Component Analysis(KPCA) with the existing Geometric active contour segmentation model . KPCA was used to analyse shape variability in trans-axial human brain medical images collected from University College Hospital Ibadan. The enhanced model was used to segment selected feature from registered normal and pathological Magnetic Resonance Image (MRI) scan and Computed Tomography (CT) scan medical image. Finally, the caudate nucleus from normal human brain and tumour from pathological human brain was detected and segmented using our enhanced model. The segmentation time, volume area segmented and the hausdorff distance was calculated for the new model.

General terms

Image analysis, Medical image processing.

Keywords

Geometric active contour, MRI, CT, segmentation.

1. INTRODUCTION

Image segmentation is an aspect of computer vision that deals with the partitioning an image into regions having homogeneous meaning. It is used to separate an object from its background and extracts meaningful objects lying in images either by dividing images into contiguous semantic regions, or by extracting one or more specific objects in images such as medical structures. However, we have different types of image segmentation methods which are not suitable for medical images since medical images are diverse, complex and vary from natural images.

Medical image segmentation which is the process of outlining relevant anatomical structures in an image dataset is a problem that is central to a variety of medical applications including image enhancement and reconstruction, surgical planning, disease classification, data storage and compression, and 3-Dimensional (3D) visualization. Some of the methods used for medical image

segmentation fall under deformable models. The use of deformable model was popularized by Kass et al. (1990), snake model was used to develop active contour model that minimizes energy functional under the influence of forces which are internal force, image force and external constraint force. Deformable models can be classified into three categories which are Free-form, Parametric and Geometric active contour model.

Geometric active contour make use of level set method that represent contour or surfaces as Zero level set of a higher dimensional function usually called a level set function Chunming *et al.*, (2011). Level set can handle topological changes in curve evolution which is not possible with the classical active contour model. Osher and Sethian (1998) offer a natural and numerical implementation of curve evolution equation using level set. Readers are refer to Neithammer and Tannenbum (2004) for some previous work on Geometric active contour model. Xiao *et al.*, (2003) gave the numeric scheme used for GAC model, which is describe in the following equation.

Let $x = (x, y)$ denote a point in a curve C which is a member in image domain Ω and let the curve be represented by Lipchitz-continuous function using signed distance function $\phi : \Omega \rightarrow \mathfrak{R}$.

A parameterized differentiable curve C is a differential map

$$C : [a, b] \subset \mathfrak{R} \rightarrow \Omega = [x(p), y(p)]^T = x(p) \quad (1)$$

The rule that determine how each point C moves starting from initial curve C_0 is

$$\frac{dC(P, t)}{dt} = v(C(P, t), t) \quad (2)$$

$$\frac{dC}{dt} = v \quad (3)$$

Equation (2) gives a partial differential equation that determines how curve C evolves and often called flow. Minimized the energy below

$$E_{image}(\phi, T) = \|H\phi - G(T)\|^2 = \int_{\Omega} (H\phi(x) - G(T, I(x)))^2 \quad (4)$$

Where E_{image} is the energy that represents distance between the shape of the region defined by the interior of the curve C and the shape G extracted from the image. Effectiveminimization of the energy in (4) amount to realizing a trade-off between segmented object and the background.

Using the Geometric active contour model described in segmenting a particular feature in an image has a



shortcoming of generating a spurious edges and delineation from true outline of the segmented feature. Due to this problem, Leventon *et al.*(2000) represented shapes to be segmented by signed distanced functions (SDFs) and perform Principal Component Analysis on the set of training SDFs. The learnt shape information was incorporated into a Geodesic Active Contour active contour model as an additional shape force to drive the embedding function to the likely exact shape. Chen *et al.*(2001) used average shape to get shape variability for geometric active contour model and this gave ambiguous result because average shape cannot capture total variability in a given shape. Wang and Staib(1998) used a statistical point model for the segmenting curve and applied Principal Component Analysis to the covariance matrices that capture the statistical variation of the landmark points. Tsai *et al.*(2003) also use Principal Component Analysis on signed distance function of shapes and then optimized the PCA coefficient of the first few Eigen modes directly. Using Principal Component Analysis on Signed distanced function of spaces has many shortcomings since features in consideration are not linear and PCA is use for linear analysis. Dambreville *et al.*(2008)

is closely related to our work in that Kernel Principal Component Analysis (KPCA) was used to model the shape variability and the distance between the shapes in the feature space and the initial constraint until the feature is extracted. Kernel Principal Component Analysis allows the extraction of nonlinear structure in the spaces of Signed distance functions and therefore performs better than linear Principal Component Analysis.

2. METHODOLOGY

The enhanced model (ENGAC) was formulated using Kernel Principal Component Analysis (KPCA) and Geometric active contour (GAC) segmentation model. In this paper, KPCA was used to get shape variability within the Geometric active contour segmentation model. The training set of MRI and CT scan of tran-axial medical images were gotten from University College Hospital, Ibadan, Oyo state. The medical images were registered using appropriate registration method to pre-process the medical images. Figure 1 gives the conceptual view of the enhanced geometric active contour model.

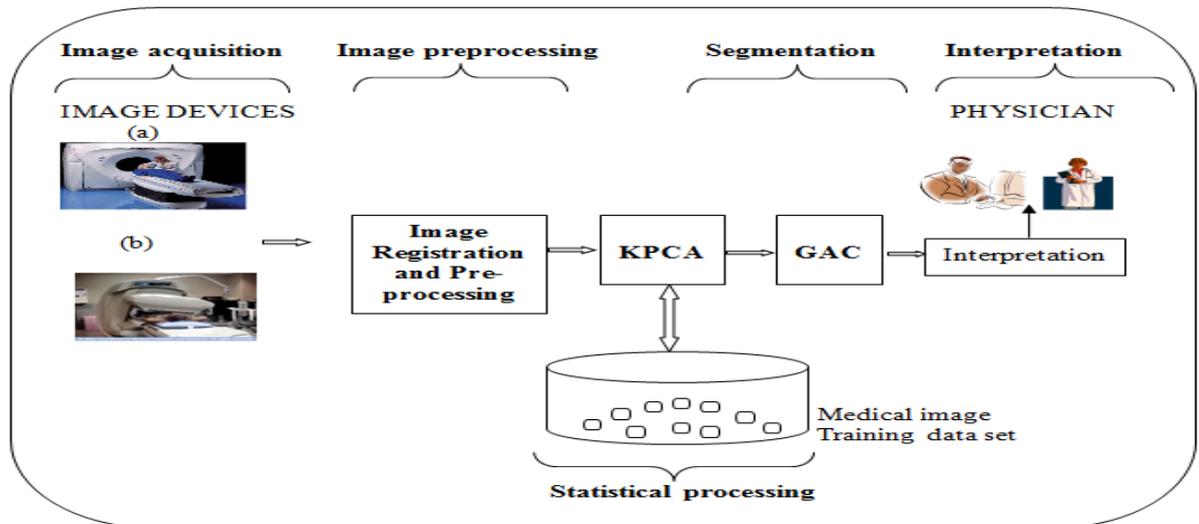


Figure 1: Conceptual view of Enhanced Geometric Active Contour model (ENGAC)

The hybridized segmentation model for the conventional Geometric Active Contour segmentation model and Kernel Principal Component Analysis (KPCA) process was discussed in this section. The shape variability was extracted to form the feature space for medical image features to be extracted and segmented. These are the steps involved to derive the model;

- (i) Let $T = \{ X_1, X_2, \dots, X_N \}$ be a training set of registered medical images.
- (ii) Selected feature was represented with high dimensional function (Signed distance function) and mean offset map was calculated using

$$\bar{\varphi} = \frac{1}{N} \sum_{i=1}^N \varphi(X_i) \quad (5)$$

(iii) Centered kernel matrix for the points was calculated

$$\tilde{K}(i, j) = \langle (\varphi(X_i) - \bar{\varphi}), (\varphi(X_j) - \bar{\varphi}) \rangle$$

$$\tilde{K}(X_i, X_j) = \langle \tilde{\varphi}(X_i), \tilde{\varphi}(X_j) \rangle \quad (6)$$

with $\tilde{\varphi}(X_i) = \varphi(X_i) - \bar{\varphi}$



Since \tilde{K} is symmetric, it was decomposed as

$$\tilde{K} = MSM^T$$

Where

S= diagonal matrix $(\alpha_1, \dots, \alpha_n)$ containing the eigenvalues of \tilde{K}

M= orthonormal matrix (M_{11}, \dots, M_{iN}) containing the eigenvector

M^T = column vectors containing the eigenvectors corresponding to the eigenvalues α_1

Let C denote the Covariance matrix of element in the training set, then the eigenvector of the covariance matrix in the feature space was represented and calculated as V_k .

$$V_k = \sum_{i=1}^N \frac{M_{ki}}{\sqrt{\alpha_k}} \tilde{\varphi}(X_i) \quad (7)$$

Then the subspace of the feature space F spanned by the first l eigenvectors of C was refers to as KPCA space. i.e the kernel PCA space is the subspace of F obtained from learning the training data.

Let X be any element of the input space I, then the projection of $\varphi(X)$ onto the subspace spanned by the first l eigenvectors was calculated as

$$Z^l \varphi(x) = \sum_{k=1}^l B_k V_k + \bar{\varphi} \quad (8)$$

Where

$$B_k = \frac{1}{\sqrt{\alpha_k}} \sum_{i=1}^N M_{ki} \tilde{K}(X, X_i) \text{ i.e the coordinate of}$$

$Z^l \varphi(x)$ on the kth component V_k

The square distance d_F^2 between $\varphi(X)$ and its projection on the KPCA space was calculated using

$$d_F^2[\varphi(X), Z^l \varphi(X)] = \|\varphi(X) - Z^l \varphi(X)\|^2 \quad (9)$$

$$= K(X, X) - 2\langle \varphi(X) \rangle + \langle Z^l \varphi(X), Z^l \varphi(X) \rangle$$

but the square distance between the projection $Z^l \varphi(x)$ and a specific (mapped) element of the training set

$\varphi(X_i)$ was calculated as

$$\|\varphi(X_i) - Z^l \varphi(X)\|^2 = \|Z^l \varphi(X)\|^2 + \|\varphi(X_i)\|^2 - 2\langle Z^l \varphi(X), \varphi(X_i) \rangle$$

(10) The distance measures the discrepancy between a mapped element $\varphi(x)$ and the learnt space, and was minimized to introduce shape knowledge in the contour evolution process.

To segment a specific object or feature from particular medical image, the initial constraint was placed on the region of interest and represented with Signed Distance functions(SDF) such that the constraint have positive values at point x inside the constraint and negative values at point x outside the constraint.

- (i) Nonlinear PCA was performed on the constraint SDF using Polynomial kernel function.

$$K_{\varphi_o}(X_i, X_j) = \langle \phi_i \bullet \phi_j \rangle^d \quad (11)$$

Using an implicit direct generalization of a result proved by Poggio (1975, lemma 2.1) in the context of polynomial approximation equation (11) become

$$\langle \phi_i \bullet \phi_j \rangle^d = \langle C_d(X), C_d(Y) \rangle = C_d(X, Y)$$

Where C_d maps X to the vector $C_d(X)$ whose entries are all possible n^{th} degree ordered products of the entries of X. The energy between the initial constraint and the feature in the feature space was minimized

$$E_{shape}^F(x) = d_F^2[C_d(X, Y), Z^l \varphi(X)] \quad (12)$$

$$\text{using } \frac{\delta \Phi}{\delta \mathcal{I}} = -\nabla_{\Phi} E_{energy}^F = -\nabla_x E_{energy}^F \cdot \frac{dx}{d\Phi}$$

where E_{energy}^F denotes the facts that the shape knowledge is expressed as a distance in

However, for the purpose of this work, the projection of the current Signed distance function was deliberately used to drive the evolution because of different object in the training set. The energy between the test shape and the shape in the Kernel PCA space need to be minimized so that outside of the initial constraint matches the background and the inside of the curve matches the boundary of feature to be extracted.

Therefore the minimization of E_{energy} for any arbitrary contour results in the deformation of the contour towards a familiar shape. To summarize all the steps involve in the formulated model, an algorithm which is general was designed for ENGAC model for medical image segmentation.



3. DISCUSSION OF RESULTS

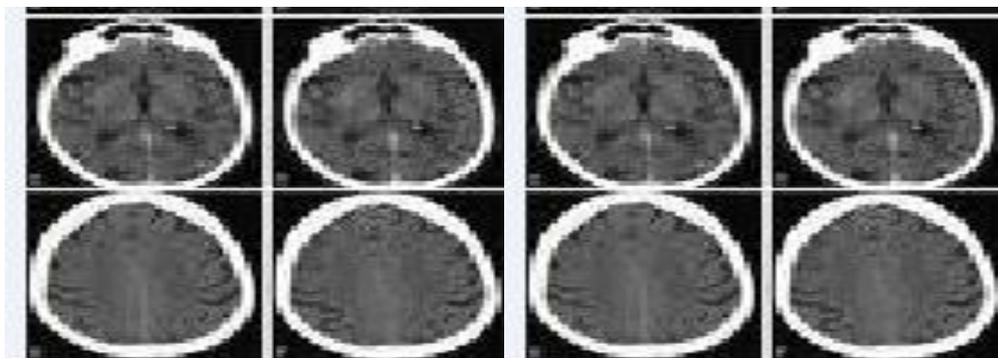
The training sets used for the ENGAC model were obtained from University College Hospital Ibadan (UCH). Figure 3(a) gives few samples of human brain medical images used for the training. Trans-axial Human Brain medical images for both Computed tomography (CT) and Magnetic Resonance Imaging (MRI) were used. Figure 3(b) is a MRI scan of a human brain that serves as the test image for the registration, while Figure 3(c) is a CT scan of a human brain that was used as the reference image for the registration. Figure 3(d) is a registered image for both CT and MRI

Figure 4(a) shows a region of interest or an initial constraint for the region to be segmented. The constraint then evolved according to specified time steps (0.005s). During the process, embedding functions continues to change the topology little by little according to the given time steps. The embedding function then reconstructed after each set of the time-steps using incremental solver. The evolving energy stops when the initial constraint minimized the energy functional to reach the shape in kernel space.

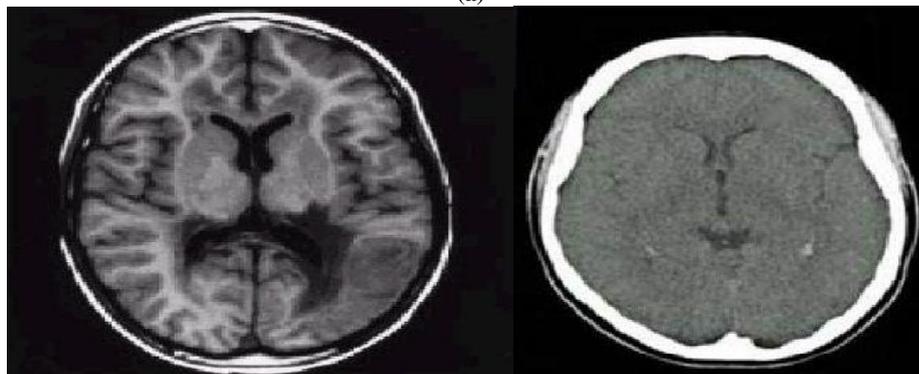
Figure 4(b) and Figure 4(c) depict intermediate results of ENGAC Segmentation model at iteration equal 100 and 250 respectively. Figure 4(c) gives the final segmentation result at iteration equal 350. The caudate nucleus in trans-axial human brain was fully extracted using the model. Figure 4(e) gives the magnitude of Eigen value and isovalues for ENGAC image segmentation that results in a set of shape parameter vectors. From this set, the mean parameter vector and the covariance matrix as well as the Eigen vector and Eigenvalues were interpreted as mode of shape variation. At

different points in the feature space on the co-ordinates x and y, x represents 0.002 and y represents 0.039. The nine (9) vectors found were represented as shown in the graph and the non-linearity of these Eigen vectors was what kernel identifies by keeping the Eigen vectors higher than tolerance of $1e^{-18}$ and by normalizing these Eigen vectors to get the exact shape. Figure 4(f) gives the 3D view of the final segmentation of the specified region of interest. This could help the physician to locate the position of caudate nucleus in the entire image domain.

ENGAC model was applied to segment tumor from pathological medical image of trans-axial Human Brain. Figure 5(a) shows a region of interest or an initial constraint for tumor to be segmented. Figure 5(b) and Figure 5(c) depict intermediate results of ENGAC Segmentation model at iteration equal 100 and 350 respectively. Figure 5(d) gives the final segmentation result at iteration equal 450. The tumor in pathological trans-axial human brain was fully extracted using the model. Figure 5(e) gives the 3D view of the final segmentation of the specified region of interest. This could help the physician to locate the position of tumor in the pathological medical image. Enhanced model outperformed the existing Geometric active contour segmentation model and this has been tested and published by Ajala F.A and Emuoyibofarhe O.J (2012).

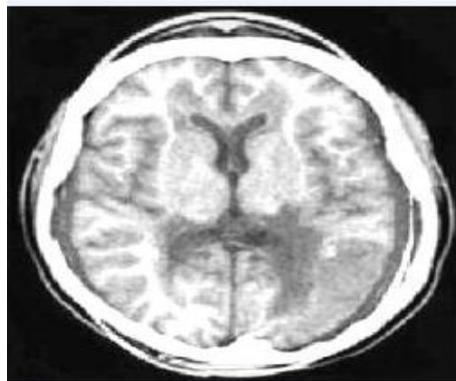


(a)



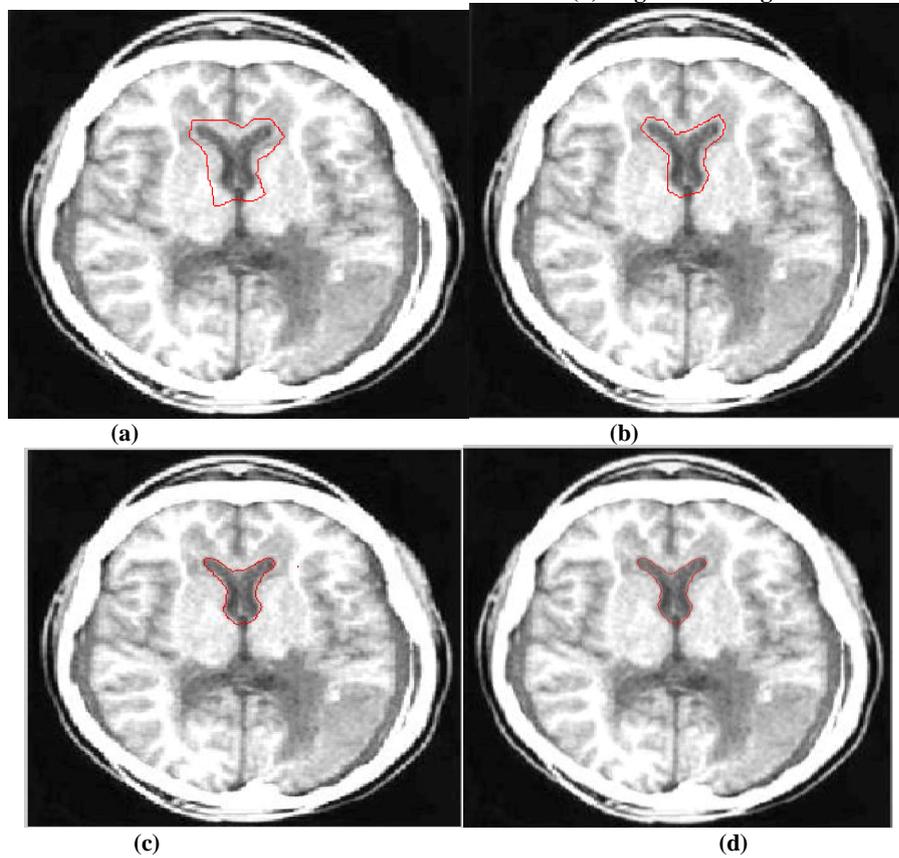
(b)

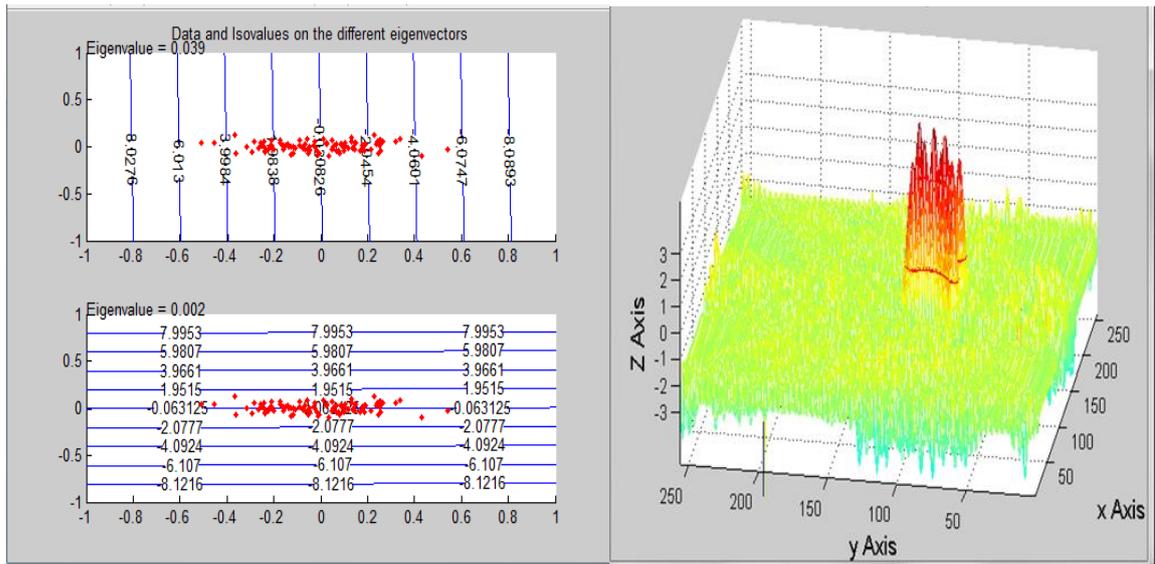
(c)



(d)

Figure 3: Medical image Registration (a) Sample training data set (b) MRI scan of trans-axial Human Brain (c) CT scan of trans-axial Human Brain (d) Registered image

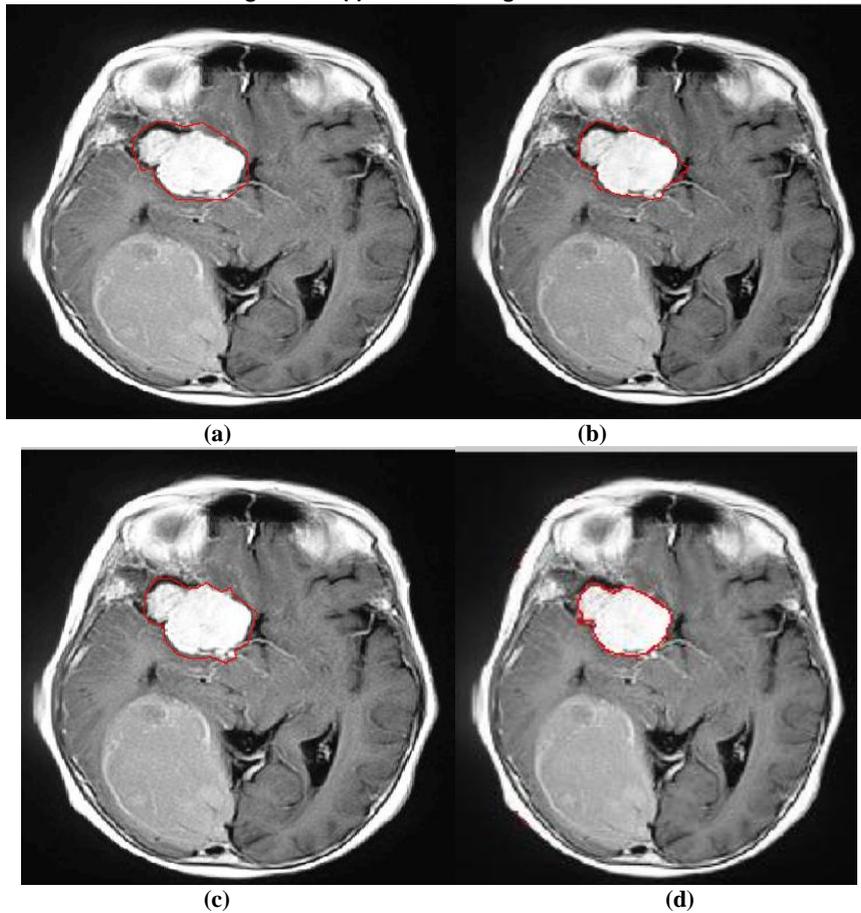




(e)

(f)

Figure 4: Segmentation Results for segmenting Caudate nucleus from trans-axial Human Brain (a) Initial constraint (b) contour at iteration = 100 (c) contour at iteration = 250 (d) Final segmentation contour at iteration =350 (e) magnitude of Eigenvalue (f) 3D view of segmented area.

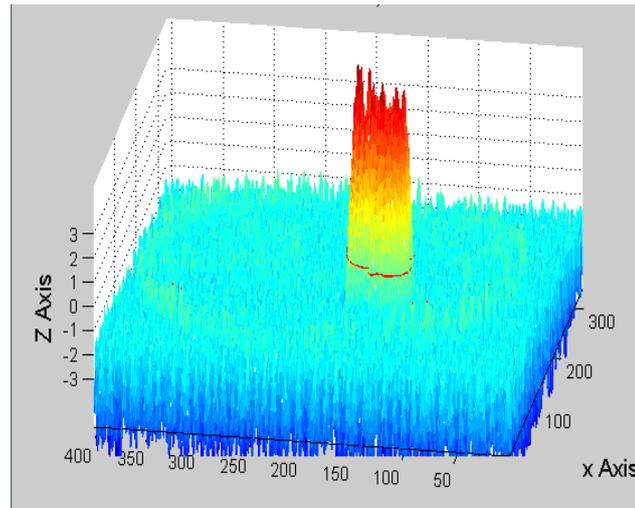


(a)

(b)

(c)

(d)



(e)

Figure 5: Segmentation Results for segmenting tumor from Pathological Human Brain(a)Initial constraint (b) contour at iteration = 100 (c) contour at iteration = 250 (d) Final segmentation contour at iteration =350 (e) magnitude of Eigenvalue (f) 3D view of segmented area.

The segmentation time was calculated using the computer system time which is Compaq Presario CQ60 notebook PC with AMD Athlon Dual-core QL-62 2.00 GHz processor. The segmented area volume was calculated by multiplying number of voxel by the volume of each voxel (Lauren, 2001). Hausdorff distance before and after segmentation was also calculated for the segmented features. Five Users were used to segment the two samples that were used to validate the model; Table 1 and Table 2 show the results of segmentation time and segmented area volume for each

user for caudate nucleus segmentation and tumor segmentation in Human Brain respectively. The system for ENGAC model was evaluated using likertscale method based on two formulated criteria which are System Ease of Use (SEU) and System Segmentation Quality (SSQ). The scale was from 1 to 5, with 5 being the highest. The response means of the methods were calculated Table 3 depicts the Medical expert’s assessment for the features segmented.

Table 1: Caudate Nucleus Segmentation Result **Table 2: Tumor Segmentation Result**

No of Users	Segmentation time(sec)	Segmented area volume(cm ³)
1	100.27	3.02
2	100.53	3.01
3	99.99	3.00
4	100.85	3.03
5	100.49	3.01
Average	100.43	3.01

No of Users	Segmentation time(sec)	Segmented area volume(cm ³)
1	83.54	2.55
2	83.40	2.57
3	83.77	2.57
4	83.65	2.55
5	83.64	2.56
Average	83.60	2.56

Table 3: Medical Expert’s Assessment.

Model	Ease of use response mean	Segmentation Quality response means
ENGAC	3.42	4.26



4. CONCLUSION

An enhanced Geometric Active Contour model (ENGAC) that produced better segmentation results over the Geometric Active Contour (GAC) model is presented. Kernel Principal Component Analysis using Polynomial kernel function was used to get the shape variability before segmentation. This enhanced the model to accurately segment the selected feature or ROI (region of interest) and the model was validated by segmenting caudate nucleus and tumor from trans-axial Human Brain. Five users were used to segment the features. The segmentation time, segmented area volume that measure its accuracy and Medical expert's assessment that measure its quality was presented.

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