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 Chuming 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 $\Omega$ and let the curve be represented by Lipschitz-continuous function using signed distance function $\phi: \Omega \rightarrow \mathbb{R}$ A parameterized differentiable curve $C$ is a differential map $C: [a, b] \subset \mathbb{R} \rightarrow \Omega = \{(x, y) \; | \; x(p), y(p) \}^2 = x(p)$ (1)

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

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

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

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

$$E_{image}(\phi, T) = \frac{1}{T} \int_\Omega \|H\phi - G(T)\|^2 = \frac{1}{T} \int_\Omega (H\phi(x) - G(T, I(x)))^2$$ (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 distance 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
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 distance function of spaces has many
shortcomings since features in consideration are not linear
and PCA is used 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.

![Conceptual view of Enhanced Geometric Active Contour model (ENGAC)](image)

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 \( T = \{ X_1, X_2, \ldots, X_N \} \) 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

\[
\bar{\phi} = \frac{1}{N} \sum_{i=1}^{N} \phi(X_i)
\]

(iii) Centered kernel matrix for the points was calculated

\[
\tilde{K}(i, j) = \left( \phi(X_j) - \bar{\phi} \right) \left( \phi(X_j) - \bar{\phi} \right)
\]

\[
\tilde{K}(X_i, X_j) = \left\langle \tilde{\phi}(X_i), \tilde{\phi}(X_j) \right\rangle
\]

with

\[
\tilde{\phi}(X_i) = \phi(X_i) - \bar{\phi}
\]
Since $\tilde{K}$ is symmetric, it was decomposed as

$$\tilde{K} = \text{MSM}$$

Where

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

$M$ = orthonormal matrix $(M_1, \ldots, M_n)$ containing the eigenvector

$M^T$ = column vectors containing the eigenvectors corresponding to the eigenvalues $\alpha_i$

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 $V_k$

$$V_k = \sum_{i=1}^{N} \frac{M_{ik}}{\sqrt{\alpha_k}} \phi(X_i)$$

Then the subspace of the feature space $F$ spanned by the first $l$ eigenvectors of $C$ was referred 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 $\phi(X)$ onto the subspace spanned by the first $l$ eigenvectors was calculated as

$$Z^\prime \phi(x) = \sum_{k=1}^{l} B_k V_k + \bar{\phi}$$

(8)

Where

$$B_k = \frac{1}{\sqrt{\alpha_k}} \sum_{i=1}^{N} M_{ik} \tilde{K}(X, X_i)$$

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

$$d^2_F[\phi(X), Z^\prime \phi(X)] = \|\phi(X) - Z^\prime \phi(X)\|^2$$

$$= K(X, X) - 2 \langle \phi(X), Z^\prime \phi(X) \rangle + \langle Z^\prime \phi(X), Z^\prime \phi(X) \rangle$$

(9)

but the square distance between the projection $Z^\prime \phi(x)$ and a specific (mapped) element of the training set $\phi_i$ was calculated as

$$\|\phi_i - Z^\prime \phi(X)\|^2 = \|\phi(X) - Z^\prime \phi(X)\|^2 + \|\phi_i - Z^\prime \phi(X)\|^2 - 2\langle \phi_i, Z^\prime \phi(X) \rangle$$

(10)

The distance measures the discrepancy between a mapped element $\phi(x)$ 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.

$$K_{\phi_i}(X_i, X_j) = \langle \phi_i \cdot \phi_j \rangle^d$$

(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

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

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

$$E^F_{\text{shape}}(X) = d^2_F[C_d(X, Y), Z^\prime \phi(X)]$$

(12)

where $E^F_{\text{shape}}$ 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 $E^F_{\text{shape}}$ 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 continue 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 $1\times10^{-18}$ 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).
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
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.
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). Haudsorff 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 likert scale 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>
<thead>
<tr>
<th>No of Users</th>
<th>Segmentation time(sec)</th>
<th>Segmented area volume(cm³)</th>
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<tbody>
<tr>
<td>1</td>
<td>100.27</td>
<td>3.02</td>
</tr>
<tr>
<td>2</td>
<td>100.53</td>
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<tr>
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<td>4</td>
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<td>5</td>
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<td>3.01</td>
</tr>
<tr>
<td>Average</td>
<td>100.43</td>
<td>3.01</td>
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</tbody>
</table>

**Table 2: Tumor Segmentation Result**

<table>
<thead>
<tr>
<th>No of Users</th>
<th>Segmentation time(sec)</th>
<th>Segmented area volume(cm³)</th>
</tr>
</thead>
<tbody>
<tr>
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<td>2.56</td>
</tr>
<tr>
<td>Average</td>
<td>83.60</td>
<td>2.56</td>
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</table>

**Table 3: Medical Expert’s Assessment.**

<table>
<thead>
<tr>
<th>Model</th>
<th>Ease of use response mean</th>
<th>Segmentation Quality response means</th>
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</thead>
<tbody>
<tr>
<td>ENGAC</td>
<td>3.42</td>
<td>4.26</td>
</tr>
</tbody>
</table>
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.

5. REFERENCES