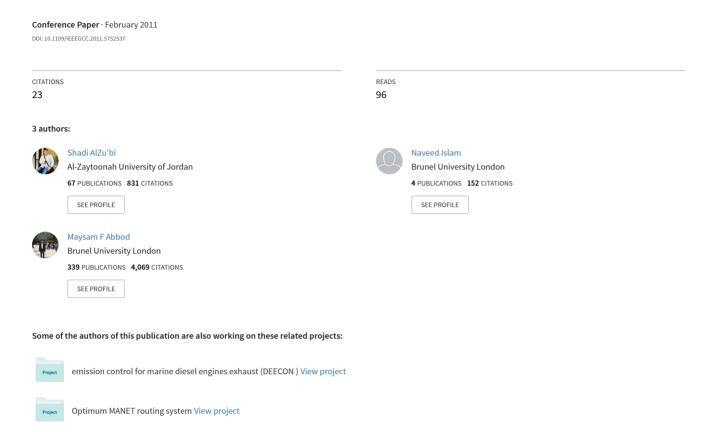
# Enhanced Hidden Markov Models for accelerating medical volumes segmentation



## ENHANCED HIDDEN MARKOV MODELS FOR ACCELERATING MEDICAL VOLUMES SEGMENTATION

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#### **ABSTRACT**

A fully automated unsupervised image segmentation method using Hidden Markov Models (HMMs) is proposed to segment medical volumes. The application of this system to medical volumes has been evaluated using NEMA IE body phantom and a comparison study has been carried out to evaluate HMM and other segmentation techniques which reveal thatHMMdelivers promising results in terms of accurate region of interest detection. Computational time is the main issue to tackle in HMMs, a solution has been proposed and evaluated with respect to the effects of the accelerators on the system accuracy.

*Index Terms*— Segmentation, Feature Reduction, Hidden Markov Models, PCA.

#### 1. INTRODUCTION

Image segmentation is the process of classifying each pixel of an image into a set of distinct classes, where the number of classes is much smaller than the number of unique pixel values. Existing work completed by Collet and Murtagh [1] [2] focused on the segmentation of astronomical multiband imagery using a similar statistical model, however, resolution analysis is supplied via a quadtree structure where decimation is required. Similar work in this area has been performed by Stanford and Raftery [3] [4]. Which is applied only to 2D imagery in a spatial context using analogous model.

Thresholding and clustering based methods are used in image segmentation by classifying each pixel in the image into the proper cluster, and then mapping the clusters to display the segmented images. A certain clustering criterion can be adopted to group each pixel into a specific number of clusters depending on the image type [5]. When images contain different structures with contrasting intensities, thresholding provides a simple but effective means for obtaining segmentation. Generally, the thresholds are generated based on visual assessment of the resulting segmentation [6].

Statistical model describes the behavior of an object of study in terms of random variables and the associated probability distribution. From a medical imaging perspective, this kind of analysis is useful as most pixels can be categorized into the same class as their neighbors.

This paper is focusing on the implementation of a robust system for volume segmentation using Hidden Markov Models (HMMs) and exploring Feature Reduction (FR) techniques to speed up the segmentation process. The rest of this paper is structured as follows: The proposed segmentation system is described in section 2. In section 3, HMMs are defined for segmenting 2D medical images and the process performance is evaluated. Process acceleration using FR techniques is presented in section 4. Conclusions are listed in section 5.

#### 2. PROPOSED SYSTEM

HMM is a statistical model which observes a sequence of emissions with hidden sequence of states that the model went through to generate the emissions [7]. HMM states are not directly visible to the observer but the variables influenced by the states are visible. Each state in HMM has a probability distribution over the other states which evaluate the state sequence. The challenge in HMM is to determine the hidden parameters from the observable parameters to be used in performing further analysis [8]. Fig. 1 illustrates the proposed medical volume segmentation system using HMMs. The system input is a 3D phantom or real volume from a scanner acquisition system. Statistical approaches using HMMs can be applied to obtain a segmented slice. All segmented slices are grouped together to form the segmented medical volume which includes the object of interest. This segmentation method can be applied on the reduced features of each medical slice using different FR techniques to accelerate the segmentation process.

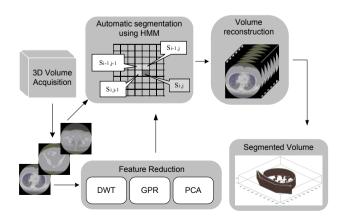


Figure 1. Enhanced segmentation system

## 3. HMM FOR MEDICAL IMAGE SEGMENTATION

HMM comprises of four elements which are *states*, *possible observations*, *state transition probability matrix* [A], and *emission probability matrix* [B]. The system is assumed to be in one of a finite set of states at any discrete unit of time. Transitions between states take place according to a fixed probability depending only on the system state [9]. At each unit of time, a single possible observation which is a set of the observation that generated from the current state according to a probability distribution is dependent on the state itself.

#### 3.1. Technical background

The problem with applying HMM on 2D images is the double dependency of  $S_{i,j}$  on its two neighbors,  $S_{i-l,j}$  and  $S_{i,j-l}$  as illustrated in Fig. 1. This does not allow the factorization of computation as in 1D, where  $S_{i,j}$  must only depends on one neighbor at a time which can be the horizontal  $S_{i,j-l}$  or the vertical  $S_{i-l,j}$  [8][10][11].

Each slice from the acquisition system is a two dimensional matrix which can be classified by an optimum set of states with maximum probability; these states are mapped into classes or segmented objects. Segmentation using HMM can be applied using three main steps which are illustrated in Fig. 2 [7][10].

#### Defining HMM initial states

- An initial state is chosen according to the initial state distribution.
- Choose an observation sequence according to the probability distribution.
- Transit to a new state according to the state transition probability matrix for the current state.

#### Training HMM

- Divide the image into non-overlapping equal size blocks
- Extract a feature vector for each block.
- Each block and its feature vector evaluates the observation.
- [A] and [B] are generated by HMM training process.
- The model parameters are estimated based on the blocks statistics.
- Pixels which belong to the same class are grouped together to evaluate a segmented image.

#### **Testing HMM**

- Generates the feature vectors for a testing image.
- Finds the set of classes with maximum posteriori according to the trained HMM.

**Figure 2.** HMM steps

The basic assumption of applying HMM to medical images is using an embedded-HMM that is based on defining a set of Markovian superstates. There is a set of simple Markovian states within each superstate. Superstate is first chosen using a first order Markov state transition probability based on the previous superstate. A simple Markov chain is then used to generate observations in this superstate. Thus, superstates are related to rows (or any equal size blocks) and simple states are related to columns (or smaller blocks).

#### 3.2. Segmentation performance using HMM

The proposed approach has been tested using NEMA IEC body phantom data which consists of an elliptical water filled cavity with six spherical inserts suspended by plastic rods of inner diameters: 10, 13, 17, 22, 28 and 37 mm [12]. NEMA IEC body phantom has been utilized to perform the experimental study using HMMs for medical image segmentation. Table 1 compares the proposed segmentation technique with other available results on NEMA IEC phantom according to their accuracy in detecting the Region Of Interest (ROI).

 Table 1. Error percentages for NEMA spheres segmentation

Diameters (mm)	10	13	17	22	28	37
Thresholding [1]	3.0	3.1	0.6	0.9	1.1	1.8
K-means [5]	13.6	11.5	5.77	5.51	5.1	5.01
MRFM [5]	7.41	8.69	4.28	4.06	3.9	3.89
HMM	1.5	0.89	0.1	0.8	0.04	1

From Table 1, it can be seen that underestimated diameters have been achieved using k-means classifications [5] and with the two small spheres in MRFM [5]. The other available technique over estimate the spheres diameters between (0.6% - 4.28%).

Promising results have been achieved using HMM in the spatial domain for segmenting the experimental data. Image segmentation using HMMs is more automated than many other available techniques, but suffer a long computation time for its calculations. The process of training HMM is based on the dependency of each pixel on its neighbors which leads to the long computation time.

### 4. PROCESS ACCELERATION USING FEATURE REDUCTION

The weakness of HMMs is the long processing time, which is much smaller in the other available techniques. Many approaches have been used to overcome this issue, HMMs can be applied on a reduced dimensionality images using different FR techniques for acceleration.

One of the problems with high dimensional data is the redundancy of information through the measurement of dozens of features that represent the similarity of data. FR techniques provide efficient methods of simplifying multidimensional data. The new images have reduced dimensionality hence it is an efficient way for reducing computation time and storage demands for medical image segmentation algorithms.

#### 4.1. Mathematical background for FR techniques

This section presents some FR techniques which are developed in the proposed system:

#### 4.1.1. Discrete Wavelet Transform (DWT)

DWT is a multiresolution analysis technique which has many applications in the field of medical imaging, DWT decomposition at different levels provides the capabilities of transforming high dimensional image into reduced dimensional image yet preserving most of the important features. Thus the decomposition method can be utilized as one of the most robust dimension reduction techniques in image processing [5].

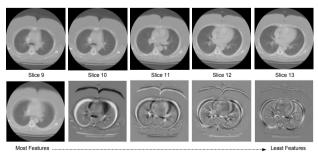
#### 4.1.2. Gaussian Pyramids Reduction (GPR)

GPR is a hierarchical structure of low-pass filter transformed images of the input image. At each level, average image of the upper level is achieved with each pixel containing a local average that corresponds to a pixel neighborhood on a lower level of the pyramid. GPR reduces image dimensions at each level by half while retaining the most image features thus allowing segmentation algorithms to perform faster. The limitations of GPR start when the image begins to lose features from the second level of reduction. It may not affect the simple images with fewer features but complex images with various features may suffer from the loss of information.

#### 4.1.3. Principal Components Analysis (PCA)

PCA is the most conventionally used technique for dimensionality reduction in the field of image processing. It is widely used in face recognition for its ability to reduce the dimensionality of a data set while retaining as much characteristic features as possible. In PCA, while discarding a large number of minor components, a small number of principal components are retained on a linear and low dimensional subspace.

Five DICOM slices (9-13) of real human chest images [13] have been used for the experiments. Each image is converted into a column vector (X) by concatenating successive transposed rows. According to the algorithm in [14][15], each of the image vectors is stacked into a training matrix X, where  $X = x_1, x_2, \ldots, x_5$ . PCA is applied to the data X which returns principal components based on the eigenvectors corresponding to the highest eigenvalues. Fig. 3 illustrates the input slices and the reduced features slices.



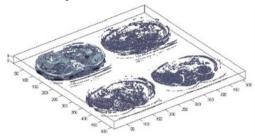
**Figure 3.** PCA for 3D volume feature reduction

It can be seen from the output slices in Fig. 3 that the first principal component image has significant portion of

contrast/feature details and it decreases rapidly from the second image. This is due to the eigenvalues of this data, as the first image in Fig. 3 has very large eigenvalue and it decreases rapidly after that. Looking at the perspective of dimensionality reduction of such large data it can be used as a 3D FR technique to reduce the number of tested slices. However segmentation algorithms using HMM is applied on a single slice rather than the whole volume.

#### 4.2. Results for acceleration using feature reduction

Fig. 4 illustrates real chest volume after FR using PCA followed by 3D-DWT to illustrate how the reduced features volume looks like after reduction. The dimensionality has been reduced from  $512 \times 512 \times 62$  to  $256 \times 256 \times 5$  which is the dimensionality of the low-pass wavelet filter output.



**Figure 4.** Chest volume after applying PCA followed by 3D-DWT.

Different FR techniques have been applied on a CT medical image [13] and HMMs used to segment the reduced features images as illustrated in Fig. 5. Table 2 illustrates the required time for segmenting the reduced features real chest image using HMM for one slice. Applying 2-levels of DWT or GPR reduces the image dimensions into the quarter and the segmentation processing time into less than 2%. The required time for segmenting the whole volume can be calculated by multiplying the required time for each slice by the number of slices comprising the full volume. PCA is applied on 5 slices where ROI is predefined, HMM is then applied on the reduced features slice which includes all the required features instead of applying it on 5 slices.

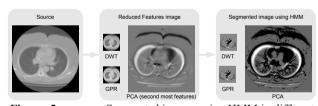


Figure 5. Segmented images using HMM in different transforms

**Table 2.** Computational time using FR techniques (sec)

Tuble 20 computational time using 110 committee (500)						
FR	Time	Time for	Time for	Time for		
Technique	for FR	HMM	each slice	full volume		
Spatial	0	1355.24	1355.24	84024.88		
domain						
DWT	0.695	22.17	22.87	1417.94		
(2-levels)						
GPR	0.628	19.03	19.66	1218.92		
(2-levels)						
PCA	0.957	1104.8	1105.76	13269.12		
(2-levels)						

From Table 2, it can be seen that the best computational time is achieved using HMM on GPR, but as mentioned before GPR is affected by data loss problem as well as DWT. PCA reduce the computational time by ~84% but still longer than the achieved time using other FR techniques. The point is PCA can be generalized to be more efficient if applied on large number of slices such compressing the whole volume into one slice. PCA compressing NEMA phantom into one slice (illustrated in Fig. 6) to reflect the effects on the proposed system accuracy, NEMA phantom has been tested and the detected spheres diameters have been measured.



**Figure 6.** The fifth PCA slice which includes most of the required features.

Table 3 illustrates the segmentation quality using HMM after FR techniques. Because of the overlapping in the spheres edges after compressing the volume into one slice using PCA, outer diameters have been measured instead of the inners and illustrated in Table III.

**Table 3.** NEMA spheres diameters error percentages detected using HMM on reduced features volume with the required time

Diameters	10	13	17	22	28	37	Time (sec)
Spatial	1.5	8.0	0.1	8.0	0.04	1	84024.88
DWT	4.9	4.3	3.1	2.6	2.13	1.74	800.45
GPR	5.2	4.7	3.5	3.2	2.93	1.88	688.1
PCA*	1.8	1.1	0.85	0.59	0.34	0.22	1108.1

<sup>\*</sup> using outer diameters

From Table 3, it can be seen that accelerating the process is affecting the quality of the proposed system by different percentages. The errors achieved using both DWT and GPR reduction are around the triple of the spatial HMM but the required computational time is still less than 1%. Errors achieved using PCA are close to the spatial HMM and the time is  $\sim 1.3\%$  which is a very good reduction with acceptable accuracy.

#### 5. CONCLUSIONS AND FUTURE WORK

Segmentation is very important for medical image processing, to detect tumours and ROI for radiotherapy planning and cancer diagnosis. A sophisticated system has been developed for volume segmentation. Statistical models using HMMs have been used for segmentation. The weakness of HMMs is the long computation time for its calculations, which is much smaller in other evaluated

techniques. This system commonly reduces the percentage error achieved using other segmentation techniques. In order to speed up computation, FR techniques have been used to reduce the dimensionality of the images. Graphical Processing Unit (GPU) using parallel processing can be investigated to achieve real time processing. Higher dimensional HMMs will also be implemented for a more accurate and automatic volume segmentation system.

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