3D Active Shape Model for CT-scan liver segmentation

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***Abstract*—This paper present an automatic 3D liver segmentation based on Active Shape Model . It allows us to introduce a 3D modeling feature for the target organ to lead the segmentation. This method is tested on the dataset IRCAD which containe a 20 Computed tomography exams. These exams are obtained with different scanning protocol. Thence, we used two algorithms. First, we employed the Shape Context based Corresponding Point Model with a B-spline registration to normalize the 3D dataset with the landmarks mean distance equal to 95% .Then , we applied the active shape model .The experiments demonstrate that this algorithm is efficient and it have a tolerate value of Modified Hausdorff Distance of 3D matching between surface mesh using the iso-surface reconstruction and the Active Shape Model. Its range equal to 28.95mm.**

Keywords—Active Shape Model 3D; B-Spline registration ; Modified Hausdorff Distance ; segmentation 3D.

I. INTRODUCTION

The three-dimensional medical imaging attend with the development of imaging modalities such as X-ray tomography (CT), imaging magnetic resonance and ultrasound scan . This modalities make a successive 2D slices. Only a single slice can be represented at a time. This imaging form presents some difficulties to read , to analyze and to interpret an organ. However, 3D modeling provides to the doctors a model that can be handle in the virtual space to be observed from a desired angle of view. Thus, it helps to accurate more information about anatomical structures and their volume. The application of this model is limited due to the large variation in liver shapes and its intensity from one patient to another and for the same patient before and after surgery.

The present manuscript is organized as follow: the first section present the related work. The second section expose the proposed method and finally we state the different results

II. RELATED WORKS

There are several researches propose preferment 3D modeling. In 2015, Pham The Bao et al. [1] segmented the liver on CT scans volumetric images using the intensity model and the morphological operations. In 2014, Jian-Jun Chen et al. [2] constructed a model of the intensity distribution for the surface of the liver, cysts and lesions. Then, they calculated the probability of pixel belonging to each classification of different regions using the maximum rules posteriori (MAP). However, in [3] used the "SGM growing slice method" algorithm for a 3D reconstruction of liver. In 2011, the researchers [4] did a 3D liver segmentation from CT scans using the "Support Vector Machine" algorithm and the surface distance maps. Pedro Rodrigues et al. [5] obtained a similarity coefficient equal to 87% of 274 CT images using the algorithm of watershed and MeVislab software. In[6], they used the watershed and morphological operator algorithm to segment the microtomographic trabecular bone and then they applied a zero-isosurface to make a 3D reconstruction. Furthermore in [7], the shape of radar image was detected with Fisher algorithm. Then , they applied watershed algorithm. Jin Ma et al. [8] described a new texture feature extraction method to improve image classification using K-mean.

These presented methods are semi-automatic 3D segmentation. They require intervention of an expert to set some parameters. To overcome this problem, researchers succeed in developing advanced 3D automatic segmentation techniques. There are two major contributions in our work .First, the pre-processing step of the dataset by using the Shape Context based Correspondence Point Model to extract feature for matching surface between two 3D data and a cubic interpolation using a 3D B-spline registration. Second , the adaptation of the active shape model 3D on the training and testing phase.

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III. METHODS AND MATERIALS

The proposed method includes two parts : first , a phase of pre-processing, second an Active Shape Model 3D liver segmentation. Fig.1 shows an overview of this method.

A. Pre-processing 3D dataset

Shape registration modeling have many applications in medical imaging such as analyzing the shape differences. In [9], Toon Huysmans and al. established an alignment for a population of cylindrical surface topologys. However, in [10],the author presented a new method for vertebral segmentation based on statistical shape decomposition and conditional models using Point Distribution Model(PDM)approach. In our work, in order to create the training active shape 3D model, we must insert the same size of vertices and faces to each volume data .For that, we apply the shape context correspondence point model with 3D registration handeling a B-Spline interpolation.

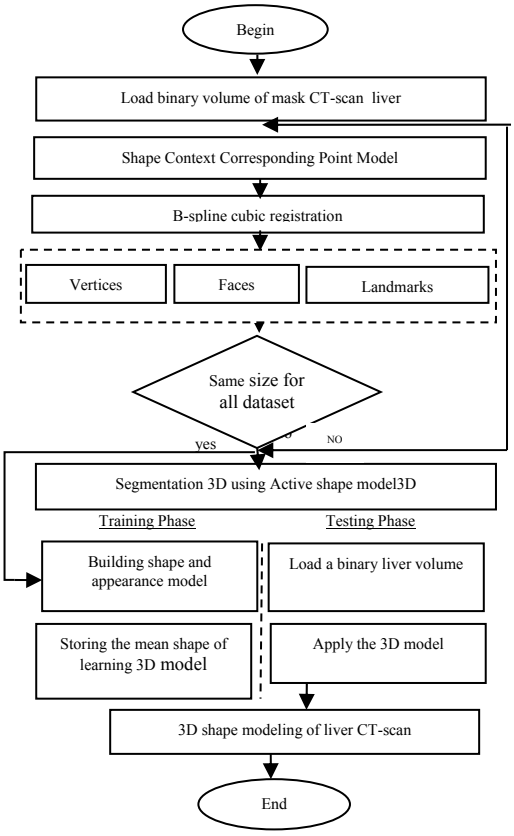


Fig. 1. Proposed method

- Shape Context Corresponding Point Model

The Shape Context is one of the ways to describe a shape. Its basic idea is to select the "n" points on the contour of an object . We count the matching for each point p_i on the shape and a point q_j on the second shape by minimizing total cost matrix C_{ij}[11]. Then, we apply a modeling transformation [12], T(p) between the two shapes P and Q.In[13]the autors used a new method to find matches between feature from two different sides by using a match point growing algorithm l.However , In our work, we will make a 3D B-spline interpolation to maxims similarities between the two shapes.

- 3D B-spline registration

Registration could play an important role to reduce the distortion of medical imaging. As Olivier Commowick [14] mentioned that there are many various transformation models and registration approaches have been proposed. These models [15] depend in class of feature spaces and types of transformation methods like an intensity-based methodology, the Iterative Closest Point algorithm[16] and a non parametric local intensity[17]. Fig.2 shows the different steps of a non rigid B-Spline registration used in our work. It is based on surface matching betwen two points x, y and a spatial transformation noted T(r) which can be written as :

$$T:\mathbb{R}^3 \to \mathbb{R}^3 \; ; T(r) = r + d(r). \quad (1)$$

where r =(x,y,z) and d(r) is the smooth deformation method[18].

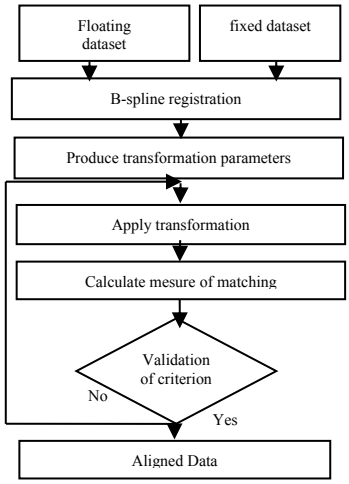


Fig. 2. Registration B-Spline

B. Active Shape Model 3D automatic segmentation

The Active Shape Model (ASM) is an iterative algorithm, developed by Cootes and Taylor in 1998. It contains the average shape and the main modes of variations of form. The Shape and its variations are represented by the Distribution Point Model algorithm (PDM).This algorithm [19] is a form of Statistical Model that generate from a set of data by principal analyzing components (PCA). It tags manually a number of interesting points of a dataset to approximate the geometry of the shape. The authors in [20] hybridized the ASM3D with a probabilistic filtering to segment the left ventricle. In [21], the segmentation of mandibular canal from cone beam CT images is based on 3D Active Appearance Models and Shape Context registration. Fig.3 presents the ASM3D algorithm[22]which is composed of two phases: a training phase and a test phase.

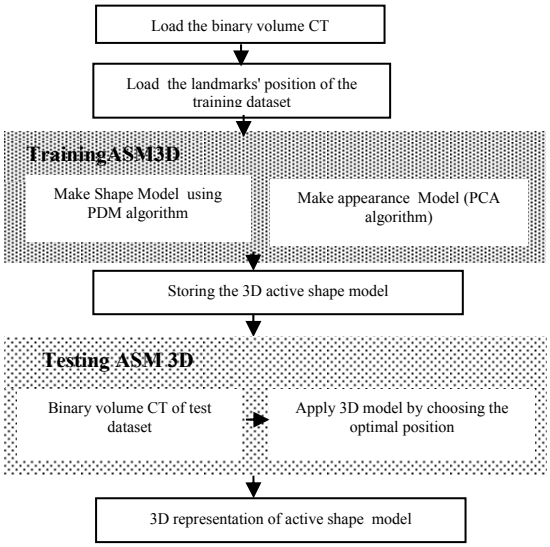


Fig. 3. A schematic of active shape model 3D

In the training phase, a manual tracing is done to describe the contour of the object defined by a set of landmarks "n" followed by PCA to calculate the mean shape and its variance. For a 3D space the landmarks (x, y,z) are grouped into a vector X.

$$X = (x_1, x_2, \dots, x_n, y_1, y_2, \dots, y_n, z_1, z_2, \dots, z_n)^T \quad (2)$$

After making the shape model with a PDM algorithm, a normal's contour and covariance matrix are determined to make the 3D appearance model of the vertices' shape noted $\hat{X}$. $\hat{X} = \bar{X} + \phi_s b_s$. (3) ; bs= ϕsTX−X . (4) With : $\bar{X}$: the aligned shape in the training set; b: the shape parameter vector of the mode; ϕs: the matrix of the principale componements from the variance matrix "S".

In fact, the PCA algorithm determines the average shape. It sets the geometric and statistics transformations to determine the variations in the shape. To measure the PCA, we must identify the eigenvectors "x_i" and the eigenvalues of the covariance matrix "S" [23]. To adapt the generated appearance model with the new dataset, Cootes proposed to calculate the Mahalanobis Distance [24] between the sample and the mean value.

The size of vertices, faces and landmarks must be the same for all volume binary dataset to be used like a prior knowledge for training phase of ASM3D. For this reason, the pre-processing data consists of two parts. First, we extract a set of point of a reference liver volume and a second volume dataset . Then, we establish a vertex correspondence using the Shape Context Corresponding Point Model between a 3D reference liver and an another 3D binary liver volume. For the input 3D liver , a new mesh topology is generated by a diffeomorphic and B-spline cubic registration . Its steps are described as the following:

Algorithm1 Shape Context Corresponding Points Model and B-spline registration.

1: In put : A mastery data volume with their landmarks

2: for i=1 to n dataset 3D

{/* Read the volume dataset */}

3: ← Volume data

4 : Surface← V.surfaces

5 : Facen← V.surface.faces

6 : Verticen← V.surface.vertices

7 : {/*Convert the segmented volume data to contour data*/}

8 : Cost← cost matrix

9 : for i=1 to n-1

10 : l= distance mean of landmark

11 : While (l>0) do

12 : {/* warp the new -spline grid */}

13 : end While

14 : end for

15 : end for.

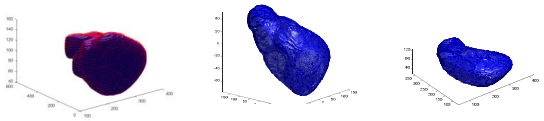
16 : Output: A new size of vertices and faces as the mastery volume data.

Once , the vertices size are all the same, we begin the training phase of ASM3D introducing some parameters mentioned below.

TABLE I. ASM3D PARAMETER

Parameters	Length of landmarks:k	Search length in pixels:ns	Resolution scales :nscales	Limit shape to bs:m	Numbre of iteration: nsearch
VALUE	8	6	2	3	60

Then , we train the ASM3D using 10 dataset 3D of binary liver slices to create the mean Shape which will be applied on the testing phase. Fig.5 shows the results founded.



(a) (b) (c)

Fig. 1. (a) 3D grid B-spline for liver shape , (b) The mean shape of liver in the training phase (c) ; The ASM3D testing model

IV. RESULTS AND DISCUSSIONS

The proposed method was evaluated on a public liver CT dataset "IRCAD , which contains 20 patients. Each volume slice is a DICOM image with a number of slices ranging from 70 to 154 slices and a spacing between slice range from 1 mm to 2 mm.

The IRCAD database includes only 15 exams with binary masks of liver among them 11 patients with the same thickness between slices equal to 1.6 mm have been used in the training ASM3D phase. To generate the liver model. Second, we standardize the number of slices for all patients to have the same volume of training data. Then, we handle the Shape Context Corresponding Points Model. The results show that the extracted landmarks and the B-spline registration can give a good geometry characters with a landmark distance mean equal to 95.7266% and a standard deviation between pixel equal to 0.250412mm. The new 3D volume will be used on the training phase of the ASM3D.Finally ,We apply the 3D active shape model to the rest of exams without making any changes to the test data. The table below shows the grouping of the IRCAD datasets between the training and the testing phase of ASM3D.

TABLE II. IRCAD DATASET

Training phase ASM3D									
Number of slice befor pre-processing									
P1	**P5**	**P6**	**P7**	**P8**	**P10**	**P11**	**P13**	**P14**	**P15**
129	139	135	151	124	122	132	122	113	125
Number of slice after pre-processing 155									
Testing phase ASM3D									
Number of slice									
P_3	P_4	P_9	P_{17}	P_{16}					
200	91	111	155	118					
Thickness									
1,25	2	2	1,6	1,6					

In order to validate the results of the ASM3D process, It's necessary to establish how the results will be evaluated. We opt to make a comparison between the surface mesh 3D of the testing data using the iso-surface and the 3D surface mesh obtained by ASM3D for the same five patients .Thus, many metrics [25] such as the modified hausdorff distance (MHD) are calculated for comparative purposes with other methods. It is a shape comparison metric of binary images..For a given two finte sets point M={m1,m2,...,mp}representing a model in the dataset and T={t1,t2,...,tq}representing. a test image, for P a number of point in M, we note the MHD like the h(M,T)

$$h(M,T) = \frac{1}{P}\sum_{M_i \in_M} min\|m_i - t_j\| \ . (5))$$

TABLE III. MODIFIED HAUSDORFF DISTANCE

Patient	**P3**	**P4**	**P9**	**P16**	**P17**
MHD(mm)	44.2994	25.4799	30.7909	26.4564	17.721

The MHD determines the most mismatched point in the 3D surface mesh using iso-surface and 3D surface mesh achived by ASM3D showed . Fig6 shows the results of 3D liver mesh for one testing volume. Its average rate is about 28.945mm. These results are better compared with the synaps challenge [26] using the Statistical Shape to segment the liver with a rate of Hausdorf Distance equal to 50.2434mm.

(a) (b)

Fig. 2. (a) The first column: the 3D mesh using iso-surface. (b) ; The 3D mesh of ASM3D

V. CONCLUSION

The 3D segmentation is still a big challenge for many problems .In this paper we used the Active Shape Model for liver 3D segmentation. We also mentioned that the major demanding is on the preprocessing of the training dataset. In the beginning we rescale and register the dataset using a Shape Context Corresponding Point Model mixed to a B-slpline cubic interpolation with the landmarks mean distance equal to 95%. The 3D ASM mesh founded are performed by two expert radiologys also the results showed that we achieve the adaptation of Active Shape Model 3D for the IRCAD dataset to create a 3D model of liver CT-scan with an acceptable rate of Modify Hausdorff Distance equal to 28 mm. For Future works will extend the pre-processing steps of the proposed method to improve the ASM3D segmentation and we will focus on accuring more training and testing sets to cover all variability between the shape of liver.

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