Automatic Liver Segmentation from CT scans using Multi-Layer Segmentation and Principal Component Analysis

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Abstract. This paper describes an automatic liver segmentation algorithm for extracting liver masks from CT scan volumes. The proposed method consists of two stages. In the first stage, a multi-layer segmentation scheme is utilized to generate 3D liver mask candidate hypotheses. In the second stage, a 3D liver model, based on the Principal Component Analysis, is created to verify and select the candidate hypothesis that best conforms to the overall 3D liver shape model. The proposed algorithm is tested for MICCAI 2007 grand challenge workshop dataset. The proposed method of this paper at this time stands among the top four proposed automatic methods that have been tested on this dataset.

Key words: Liver segmentation, 3D organ reconstruction, mean shift segmentation, principal component analysis

1 Introduction

An essential part of every computer assisted minimally invasive surgery is planning which is performed prior to the surgery. The planning process involves preparing a patient specific 3D model of the organ under surgery and its surroundings in order to provide the surgeon with a better understanding of the patient specific anatomy. This 3D model is based on image data of a patient that could be acquired from different modalities such as Magnetic Resonance Imaging (MRI), Computed Tomography (CT) or Ultrasound Imaging. In order to build the 3D organ model, various segmentation/extraction algorithms are applied on the pre-operative scans. A survey of segmentation methods for computer assisted surgery can be found in [1].

Liver is one of the most common human organs to undergo minimally invasive surgeries and therefore automatic liver segmentation/extraction from pre-operative scans for the purpose of 3D patient specific model reconstruction, is a highly needed task. In this paper an automatic liver segmentation algorithm is proposed. In this algorithm a multi-layer segmentation method that incorporates mean shift segmentation [2] is utilized to generate candidate boundary hypotheses of the liver. Also the shape of the liver is modeled by Principal Component Analysis (PCA). A training set of 20 liver mask volumes are used to

generate a PCA based liver space. The liver space is used to measure the similarity of volume mask candidates to the liver's overall shape. The best volume candidate that conforms to the PCA based model is the final result of our liver segmentation algorithm. The main contribution of this paper is an algorithm that encodes overall liver shape information using PCA to determine the proper parameter settings for a segmentation algorithm that leads to the best estimate of the reconstructed 3D liver model.

1.1 Previous Work

Various methods have been proposed in the literature for automatic and semi-automatic segmentation of liver. In general these methods either solely rely on the information in the input images to extract liver masks or they rely on training sets to incorporate shape information of the liver. Information available in the input images include: liver's texture/intensity image, spatial correlation of the 2D liver masks in consecutive slices, and location of the liver in abdominal area with respect to neighboring structures such as ribs. Methods in [3–5] are examples of the group of approaches that rely only on such information available in input images. There are also active contour model based methods such as [6] that rely on the information from the input images. In addition to the approach taken for utilizing input liver image information, methods in [7–10] use training sets to incorporate liver shape knowledge. These methods are in general more successful in extracting liver boundaries. Many of these methods use Active Shape Models (ASM) [11]. ASMs are statistical representations of the object's shape, which iteratively deform to fit to an example of the object of interest in a new image. ASM is based on PCA which has proven to be a strong tool to model organ shapes. The objective of the proposed work in this paper is to combine an intensity based segmentation method with a PCA based model approach to identify liver region in CT scan volumes. Such combination fuses strong characteristics of each one of these approaches to improve the overall quality of the liver extraction problem.

The rest of this paper is organized as follows; Section 2 describes the proposed algorithm in details. In Section 3 performance related issues and quantitative results of the proposed method are reviewed followed by conclusions in Section 4.

2 Proposed Method

The proposed method in this work incorporates liver intensity values, similarity of 2D liver masks in consecutive slices and a PCA based model.

The method has two modes: offline and online. In the offline mode, a PCA based model of the liver is generated from a training set including liver masks of 20 volumes. The output of the offline mode is a series of eigenvector (we name them eigenliver) that represent the liver space.

In online mode the PCA based model from the offline mode is used to assess and verify the quality of several liver mask that are generated through segmentation. The algorithm has two stages in this mode. In the first stage, several segmentation hypotheses are generated using an algorithm based on mean shift segmentation [2]. In the second stage of the proposed algorithm, the knowledge of the liver space is used to determine the similarity of generated liver hypotheses to the actual liver. The main idea at this stage is inspired by [12] where PCA was used to build a face space and measure the similarity of an input image to a face image. Here, every volume candidate is projected into the liver space (generated in the offline mode) and then reconstructed using the eigenlivers. The distance between each volume candidate and its reconstruction version by the liver space is a measure of shape fidelity of each volume candidate to overall liver shape and is used to identify the best candidate.

Details of the offline mode and stages of online mode are described in following subsections. In section 2.1 stage 1 of online mode is explained. In section 2.2 the offline mode where the PCA based liver model is created is described. In section 2.3 the second stage of online mode part of the algorithm is described.

2.1 Stage 1: Multi-Layer Segmentation and Candidate Generation

In the first stage, the process starts from the middle slice of the CT scan volume where liver has its largest 2D surface. Mean shift segmentation [2] is used to extract the largest segment at this slice (our assumption in here is that the largest segment in this slice always corresponds to the liver). The remaining slices are then processed in two batches. Both batches start from the aforementioned middle slice but move in opposite directions. Every newly visited slice is segmented and the segment with the largest area overlap with the liver segment from the previous slice is marked as liver.

At each slice, the quality of segmentation is controlled by two parameters [2]: spatial resolution and intensity resolution. These parameters are usually set manually. Often a single set of values for each parameter will not be sufficient for a complete segmentation. Therefore in this stage the mean shift segmentation is applied over each slice several times using a range of different values for spatial and intensity resolution parameters. The range for spatial resolution is between 5 and 11 and the range for intensity resolution is between 3 and 25. We noticed that values outside these ranges would lead to either under segmentation or over segmentation of the liver region. We call each set of parameters for mean shift segmentation s. After applying the mean shift segmentation for each set, the boundary edges of all the segmented areas are extracted forming an edge map called EM. Different EM for each slice are added together to form one accumulative edge map (AEM) for each slice. The contrast of AEM is enhanced using Log transform. Constrast enhanced AEM is then thresholded to form an Enhanced Edge Map (EEM) which includes isolated connected regions. The threshold applied here is called β and is the variable parameter of the algorithm at stage 1. Naturally a fixed parameter would not provide the best results across

all volumes. Therefore, different values of β are utilized to generate a number of EEM images. This is described by equations 1 and 2:

$$AEM = \sum_{s} EM \tag{1}$$

$$EEM_{\beta}(x,y) = \begin{cases} 1 & Log(AEM(x,y)) > \beta \\ 0 & otherwise \end{cases} \tag{2}$$

At this point the segment (in EEM) with the largest area overlap with the liver segment from the previous slice is identified as liver segment. This segment is first morphologically opened by a small structuring element (a disk with radius of 4 pixels) to remove any excess small parts around its boundary. This procedure is followed by a morphological hole filling process to fill any small gaps within this segment. Sample EEM results with their corresponding segmented liver regions at different β values are shown in Fig. 1.

It must be noted that in the transverse direction, the 2D liver mask at each slice may consist of two or more pieces. Therefore, processing the CT volume at this direction could lead to missing liver components. For this reason the segmentation is performed at coronal and sagittal directions since it is observed that 2D liver masks at these two directions consist of one single piece.

After extracting all masks of a volume for a β value, these masks are stacked up together to form a candidate 3D liver mask volume. This implies that for each β value, one mask volume hypothesis is generated. The range of β used for this stage is empirically chosen from the set 1.5, 1.6, 1.7, ..., 3.5. Fig. 2 shows three examples of 3D volumes generated for different values of β.

2.2 PCA Based Model Generation

The objective of this section is to create a model that represents the general shape of the liver volume. One approach for extracting shape information in a series of training liver mask volumes is to find the principal components of the distribution for the training set. This is equivalent to computing the eigenvectors of the covariance matrix of the set of liver mask volumes. Each volume contributes more or less to each eigenvector. Each eigenvector looks like a ghostly liver mask and therefore it is named eigenliver. Each new liver volume candidate can be approximated using a linear combination of the eigenlivers. The model is reconstructed as follows:

Let each 3D liver mask volume be a X by Y by Z array of 0s and 1s or equivalently a 1D vector of size $X \times Y \times Z$. If L_1, L_2, ... L_n, are 1D vectors that represent liver mask volumes in the training set and ψ is their average then the distance of each volume to the average is defined by $\phi_i = L_i$ - ψ_i. Here we look for the set of n orthonormal vectors u_i that best describe the distribution of the volume data. These vectors are the result of applying PCA over the entire training volumes and are eigenvectors of covariance matrix below:

$$C = \frac{1}{n} \sum_{i=1}^{n} \phi_i \phi_i^T = AA^T \tag{3}$$

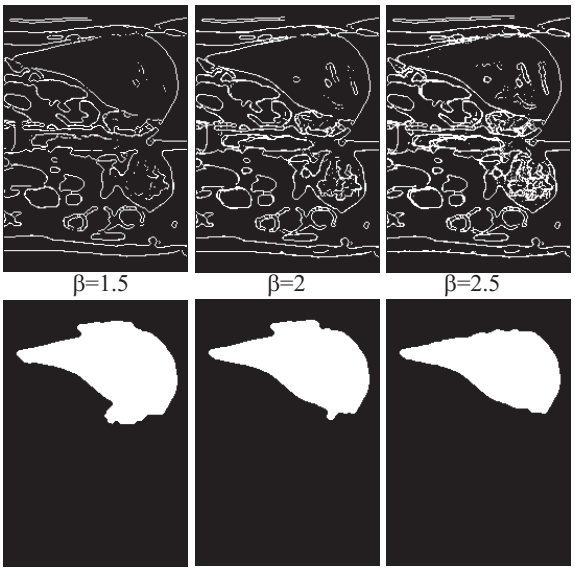

Fig. 1. Sample EEM for different β values (top row) with the corresponding extracted mask candidate (bottom row).

Where $A = [\phi_1\ \phi_2\ ...\ \phi_n]$. Matrix C is however very large and computing its eigenvectors is exhaustive. [12] introduces a computationally effective way to compute these vectors. Once eigenvectors/eigenlivers u_i are approximated, they are used to represent the liver space. This model is used (as explained in the next subsection) to measure the similarity of each volume candidate to the overall liver shape.

2.3 Stage 2: Candidate Selection Based on Liver Shape Fidelity

As proposed by [12], where the face space knowledge is used to detect faces, we can use the liver space to measure the similarity of a liver mask volume to an actual liver shape. For this purpose, first mean adjusted input volume $\phi = L$ - ψ is projected onto the liver space. The result of this projection is vector [η_1, η_2, ... η_n] where each η_i represents the contribution of each eigenliver in reconstructing the projected liver volume. The reconstructed liver is then computed as:

$$\phi_{rec} = \sum_{i=1}^{n} \eta_i u_i \tag{4}$$

For all candidate volume generated at stage 1, the Euclidean distance between their mean adjusted volume ϕ, and their reconstruction ϕ_{rec} is computed. The liver volume candidate with the minimum Euclidean distance is the volume with most fidelity to overall liver shape and therefore is chosen as the best representing liver mask by the proposed algorithm. Fig. 3 shows some 2D examples of the

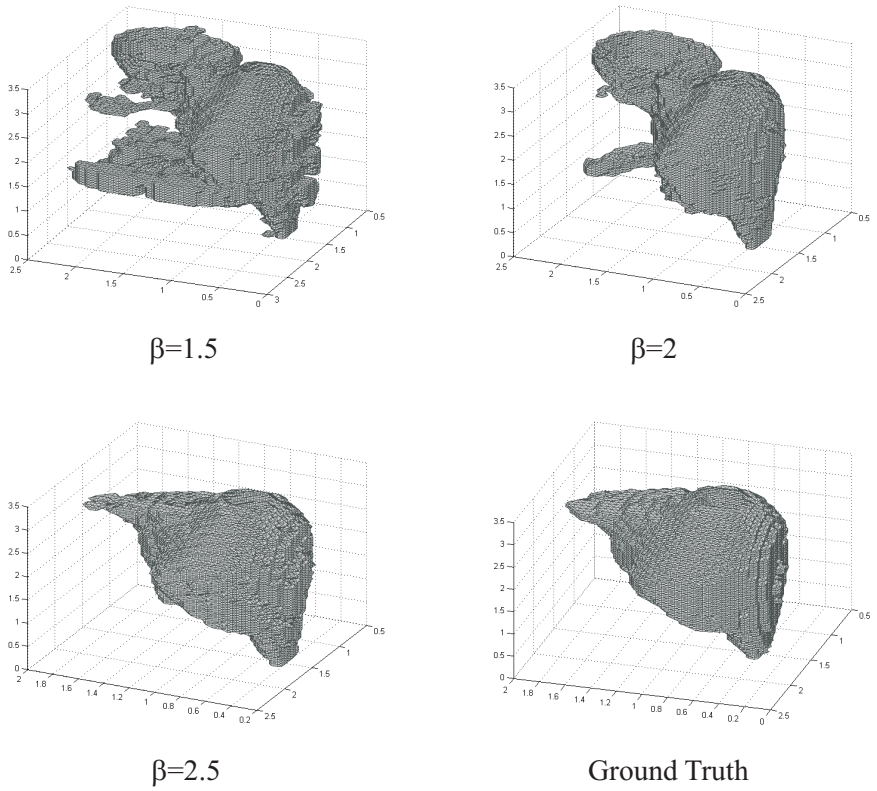

Fig. 2. Sample 3D volume mask representation for different β values.

detected liver mask boundaries along with their corresponding ground truth segmentation.

3 Results and Discussions

To evaluate the proposed method, the datasets and evaluation metrics from MICCAI 2007 grand challenge workshop [13] are adopted. The dataset includes 20 training and 10 test volumes. Each volume consists of CT scans of size 512 by 512. For faster simulation the size of the images are rescaled to 256 by 256. The results for the test volumes are shown in Table 1. The definition of the metrics applied can be found in [13]. Brief descriptions of these metrics are as follows.

1. Volumetric Overlap Error, in percent. This is the number of voxels in the intersection of segmentation and ground truth divided by the number of voxels in their union, subtracted from 1 and multiplied by 100.
2. Relative Volume Difference, in percent. This is the total volume difference between segmentation and ground truth divided by total volume of ground truth multiplied by 100.

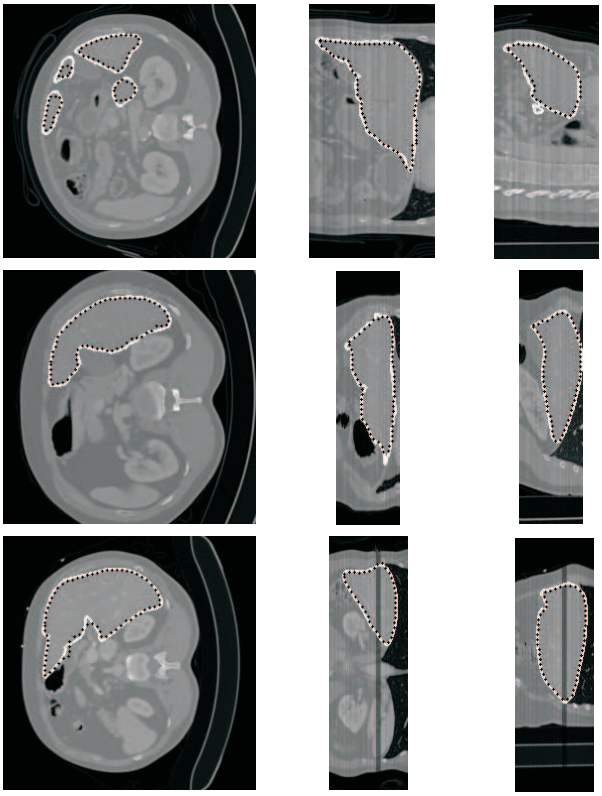

Fig. 3. Sample results of segmentation in transverse direction (left column), coronal direction (center column) and sagittal direction (right column), from training volumes of MICCAI 2007 dataset (white contours: ground truth boundaries, dotted contours: boundaries by the proposed algorithm).

3. Average Symmetric Surface Distance, in millimeters. First the Euclidean distance between every bordering voxel in segmentation and the closest bordering voxel in ground truth is determined. Then the Euclidean distance between every bordering voxel in ground truth and the closest voxel in ground truth is determined. These two sets of distances are stored. The average of all these distances gives the Average Symmetric Absolute Surface Distance.
4. Symmetric RMS Surface Distance, in millimeters. This measure is similar to the previous measure but here the squared distances are used and the root of the average value is taken.
5. Maximum Symmetric Absolute Surface Distance, in millimeters. This measure is similar to the two previous measures but only the maximum of all the distances is considered.

The average runtime for extracting one liver mask using the proposed algorithm is 2 minutes using MATLAB 7.6.0.324 environment on a PC with an Intel Core 2 Duo (2 GHz) processor.

Presented results in Table 1 at this time stand among the top four automatic segmentation algorithms that have been tested on MICCAI 2007 dataset ([7], [9] and [10]) in terms of segmentation accuracy. Our method is also comparable to those by some of the interactive methods.

Table 1. Quantitative results for the proposed method.

Data set No.	Vol overlap error%	Score	Ave symm diff%	Score	Ave symm surface dist [mm]	Score	RMS symm surface dist [mm]	Score	Max symm surface dist [mm]	Score	Total
1	8.95	65.03	-4.69	75.04	1.32	66.98	2.52	65.06	18.37	75.83	69.59
2	9.90	61.32	-6.16	67.42	1.33	66.75	2.44	66.14	18.23	76.02	67.53
3	7.37	71.20	4.09	78.25	1.58	60.51	3.16	56.07	25.00	67.11	66.63
4	10.01	60.91	0.30	98.42	2.01	49.68	4.27	40.73	39.54	47.98	59.54
5	8.69	66.04	-5.28	71.92	1.45	63.71	2.83	60.73	23.73	68.78	66.24
6	8.12	68.28	-1.82	90.32	1.26	68.45	2.41	66.53	15.06	80.18	74.75
7	6.29	75.41	-2.81	85.08	0.86	78.41	1.67	76.85	12.99	82.91	79.73
8	7.83	69.40	-4.35	76.86	1.13	71.75	2.12	70.54	20.71	72.75	72.76
9	7.33	71.38	-1.03	94.54	0.90	77.39	1.78	75.23	20.77	72.67	78.24
10	10.90	57.41	-2.64	85.95	1.69	57.71	3.03	57.86	29.28	61.48	64.08
Mean	8.54	66.64	-2.44	82.38	1.35	66.14	2.62	63.57	22.37	70.57	69.86

4 Conclusions

In this paper an automatic algorithm for extracting liver masks of CT scan volumes from abdominal area is proposed. The algorithm starts scanning the CT volumes in the coronal and sagittal directions to extract 2D liver mask candidates based on a multi-layer segmentation scheme that relies on mean shift segmentation. Multiple 3D liver mask candidates are generated as a result and the best candidate is chosen according to its similarity with its reconstructed version through a PCA based 3D liver model. This algorithm is novel in the way that it encodes overall liver shape information using PCA to determine the proper parameter setting for a segmentation algorithm that leads to the best estimate of the 3D reconstructed liver model. The idea of eigenliver can be utilized by previously proposed non-model based approaches to determine an optimal set of parameters that could potentially lead to better segmentation results.

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