Application of Statistical Shape Model of the Liver in Classification of Cirrhosis

Yen-Wei Chen, Mei Uetani, Shinya Kohara, Tomoko Tateyama, Xian-Hua Han, Akira Furukawa, Shuzo Kanasaki

Abstract

In computational anatomy, statistical shape model is used for quantitative evaluation of the variations of an organ shape. In this paper, we focus our researches on construction of Statistical Shape Model of the liver and its application to computer aided diagnosis of cirrhosis. We have proved the potential application of statistical shape models in classification of normal and cirrhosis livers. We first construct a statistical shape model of the liver from a training set (either different individuals (inter-patient variability) or the same individual (intra-patient variability)) and then coefficients of the model are used as features to recognize whether liver is normal or abnormal. The effectiveness of the constructed model is evaluated by the classification accuracy of normal and abnormal.

Keywords: Statistical Shape Model, CT Volume, Liver, Computer-aided Diagnosis, Cirrhosis, Principle Components Analysis (PCA)

1. Introduction

Chronic liver disease is one of major worldwide health problems. Cirrhosis is the end result of chronic liver damage caused by chronic liver diseases. Diagnosis and staging of chronic liver diseases is an important issue. In addition to the traditional histological diagnosis by biopsy and the blood tests, the medical imagery diagnosis using ultrasonic, CT, and MRI, which is a non-invasive method, can also be used to evaluate the chronic liver diseases. It is widely known that morphological changes of the liver occur during the clinical course of chronic liver diseases [1]. The morphologic change of the liver in chronic liver diseases can be detected on computed tomography (CT), however, the visual assessment is subjective and limited in depicting minimal changes. In this paper, we present our preliminary study on the quantitative assessment of global shape change of liver using statistical shape model of the liver.

The statistical shape model (SSM), one of digital atlases [2], can capture the organ variability of its shape from a training set (either different individuals (inter-patient variability) or the same individual (intra-patient variability)). To date a few researches have been done on the construction of statistical shape models of anatomical organs, such as brain [3], heart [4], liver [5], spleen [6] and so on. The statistical shape model has also been applied to automatic segmentation of medical images [7, 8]. But there is little research on applications of SSM to computer assisted diagnosis (CAD). We have proved the potential application of statistical shape models in classification of normal and cirrhosis livers.

This paper is organized as follows. In Sec.2 we describe the construction of statistical shape model of the liver. Experimental results are presented in Sec. 3. The conclusion and future work are given in Sec.4.

2. Construction of Statistical Shape Model of the Liver

2.1 Shape Extraction and Representation
The flowchart of the proposed method to build statistical shape model of the liver is shown in Fig. 1. As the first step, liver is segmented manually in CT datasets. The segmentation is performed under the guidance of physician in order to obtain an accurate liver shape data. As the second step, we apply marching cube algorithm to convert the segmented liver volume to a triangulated mesh surface which containing 1000 vertex points (Fig. 2) [9]. The coordinates of these vertex points are used to represent 3D liver shape as a shape vector \( \mathbf{x} = [x_1, y_1, z_1, \ldots, x_n, y_n, z_n]^T \). In order to build a model, it is needed to align training datasets. We randomly choose one normal dataset as the reference and register the other training samples to match the reference sample. Chui method is used as a non-rigid point matching method to find the corresponding points between all datasets (Fig. 3) [10]. Finally, Principal Component Analysis (PCA) is employed to find the principal variations of shape vectors. Principal Component Analysis is a technique that enables us to study variations of a set of data.

![Flowchart of the proposed method](image)

**Fig.1** Construction of statistical shape model for liver datasets.

![Marching cube method](image)

**Fig.2** Marching cube method: (a) Volume data. (b) Triangulated mesh surface data.

![Chui method](image)

**Fig.3** Chui method: (a) Reference data. (b) test data. (c) Registered data.
2.2 PCA-based Statistical Shape Model Construction

As we described in previous sub-section, a liver shape is represented as a vector $x_i$ of three components corresponding to coordinates of 1000 aligned vertex points that are obtained as the outputs of Marching cube algorithm and non-rigid point matching. The vector $x_i$ is called shape vector, which is shown in Eq. (1).

$$x_i = [x_{i1}, y_{i1}, z_{i1}, x_{i2}, y_{i2}, z_{i2}, \ldots, x_{in}, y_{in}, z_{in}]^T$$  \hspace{1cm} (1)

where $n$ is the number of vertex and $i = 1, 2, \ldots, N$ ($N$ is the number of training samples). The mean shape $m$ and covariance matrix $S$ are calculated as

$$m = \frac{1}{N} \sum_{i=1}^{N} x_i$$  \hspace{1cm} (2)

$$S = \frac{1}{N} \sum_{i=1}^{N} (x_i - m)(x_i - m)^T$$  \hspace{1cm} (3)

The modes of variation $a$ are found on the deviations of samples from the mean and are represented by $N$ orthonormal eigenvectors (variation vectors) $v_j$ of $S$, which are called as eigenshapes. The 3D shape of the liver can be represented as a linear combination of the mean shape and eigenshapes as

$$x = m + \sum_{j} b_j v_j$$  \hspace{1cm} (4)

where $b_j$ is the coefficient or weight of the $j$-th mode of variation and is estimated by calculating $V^T (x - m)$. It should be noted that the main variations could be captured by only a few top leading modes (eigenvectors). The coefficients can be used as a feature vector of the 3D shape for image coding and quantitative analysis [11, 12].

3. Experimental Results

3.1 Dataset and Statistical Shape Model of the Liver

In order to construct a statistical shape model of the liver, we applied the proposed method to 50 clinical CT datasets (25 normal data and 25 cirrhosis data). The typical segmented normal and cirrhosis liver shapes are shown in Fig. 4(a) and 4(b), respectively.

First, we calculated the mean shape $m$ and the covariance matrix $S$ from 50 datasets as explained in the previous section. Then we calculated the eigenvalues $(\lambda_1, \lambda_2, \lambda_3, \cdots)$ and eigenvectors $(v_1, v_2, v_3, \cdots)$ of the covariance matrix. It should be noted that $\lambda_1 \geq \lambda_2 \geq \lambda_3 \geq \cdots$. Fig. 5(a) and 5(b) show the mean shape of liver and shape variations of the top three modes (eigenvectors with larger variance), respectively. Variations are in the range of $\pm 2\sqrt{\lambda_i} (= \pm 2\sigma_i)$.

![Fig 4 Typical segmented and normalized liver 3D shapes: (a) Normal data. (b) Cirrhosis data.](image-url)
3.2 Evaluation of Statistical Shape

The compactness of a model is the ability to express the variation of the shape as much as possible by as few components as possible. If an eigenvalue $\lambda_i$ has large value, it means that large variation of the feature vector is in the direction of $v_i$. Assume that the eigenvalues have been arranged in descending order so that $\lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_N$ and $v_1, v_2, \ldots, v_N$ are the corresponding eigenvectors. We use Accumulation Contribution Rate (ACR) as a measure to calculate the compactness of the model (Eq. 5).

$$ACR(k) = \frac{\sum_{i=1}^{k} \lambda_i}{\sum_{i=1}^{N} \lambda_i}$$

ACR measures tell us that if we choose the first $k$ components of the feature vector, how much of the shape variations are described by these components. Therefore the first component has the largest information content to describe the data. Information content is called as contribution rate. The contribution rate accumulated from the first component is called as accumulation contribution rate.

In Fig. 6, ACR is plotted against the number of modes to represent the model. This plot describes the compactness of the model. In Fig. 6, it is shown that the first 15 components in the model contain 95% of the model's variance. It means that the 3-D shape can be represented well by the use of the first 15 modes.
In order to test the generalization of the model, we performed leave-one-out test in liver shape reconstruction. The reconstructed 3D liver shapes with first 5 modes, 15 modes and all modes are shown in Fig.7(a), 7(b) and 7(c), respectively. The original shape is also shown in Fig.7(d). It can be seen that the 3D liver shape can be reconstructed well by using more than 15 modes. The error was measured using Hausdorff distance [14], as follows: distance $d(p, S')$ between a point $p$ belonging to a surface $S$ and a surface $S'$ as:

$$d(p, S') = \min_{p' \in S'} \|p - p'\|_2$$  \hspace{1cm} (6)

Where $\|\cdot\|$ denotes the usual Euclidian norm. The Hausdorff distance is the maximum distance of a set to the nearest point in the other set. The Hausdorff distance between surface $S$ and surface $S'$ is given by:

$$d(S, S') = \max_{p \in S} d(p, S')$$  \hspace{1cm} (7)

The Hausdorff distance between the reconstructed shape and the original shape is shown in Fig.8. It can be seen that as increasing the number of modes for reconstruction, the distance between the reconstruction and the original shape will be significantly reduced.
3.3 Mode Selection and Classification Results

Since liver cirrhosis will cause left lobe's hypertrophy and right lobe's atrophy, which are concerned with liver's shape, we use coefficients of the SSM as morphological features for classification of the normal and the abnormal livers. The mean value and standard deviation of each mode coefficient are shown in Fig.9. The coefficients of abnormal and normal livers are shown in red and blue colors, respectively. The mode which has large class variations between the normal class and abnormal class can be considered as an effective mode for computer-aided diagnosis. By comparing each mode coefficient of the normal and the abnormal livers, we select top two effective modes (4th and 9th modes as shown in Fig.9) of class variations. The shape variations of the selected modes (4th and 9th modes) are shown in Fig.10. We can see that the 4th mode (horizontal axis) represented the variations of left lobe's hypertrophy and the 9th mode (vertical axis) represented right lobe's atrophy. The coefficient distribution of normal and abnormal data of the selected modes is shown in Fig.11. The squares are abnormal data and the rhombuses are normal data. It can be seen that most of abnormal data are located in the up-right area (left lobe's hypertrophy and right lobe's atrophy) as shown in Fig.10, while the normal data are located in the down-left area. We then use a simple linear discriminant function for classification of normal and abnormal data. The linear discriminant function is obtained by the use of least-squares techniques [13], which is shown in Fig.11 as a straight line. The classification rate of abnormal livers and normal liver are 84% and 80%, respectively.
4. Conclusions

In this paper, we constructed a statistical shape model of the liver by using 50 clinical CT datasets (25 normal data and 25 cirrhosis data). The coefficients of the model were used as features to recognize whether liver is normal or abnormal. Experimental results demonstrated the potential application of statistical shape models in classification of normal and cirrhosis livers. In the future work, we are going to increase the number of dataset in order to improve accuracy of the statistical shape model of the liver. We are also going to collect abnormal data at different stages and evaluate the SSM based classification performance to each stage quantitatively.
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10. References