Global Shape Analysis of the Fibrotic Liver in CT Temporal Sequence

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Abstract— It is widely known that morphological changes of the liver occur during the clinical course of liver fibrosis. The morphologic change of the liver 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 statistics shape models. We have also proved the potential application of statistical shape models in classification of normal and fibrotic livers.

I. INTRODUCTION

Chronic liver disease is one of major worldwide health problems. Liver fibrosis occurs in most types of chronic liver diseases. Serious liver fibrosis results in cirrhosis. Diagnosis and staging of liver fibrosis 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 liver fibrosis. It is widely known that morphological changes of the liver occur during the clinical course of liver fibrosis [1]. The morphologic change of the liver in liver fibrosis 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 both statistical shape model of liver and joint statistics shape model of liver and spleen [2, 3]. We have also proved the potential application of statistical shape models in classification of normal and fibrotic livers (abnormal livers).

II. STATISTICAL SHAPE MODELS

We constructed two statistical shape models for classification of normal and chronic livers. The first one is the statistical shape model of the liver. Based on the well known fact that the liver fibrosis will also cause significant morphological changes on spleen [3], the joint statistical shape model of the liver and the spleen is also constructed as the second one.

We use 47 clinical CT datasets (27 normal data and 20 abnormal data) to construct statistical shape models. In the first step, both liver and spleen are segmented manually in CT datasets. The segmentation is performed under the guidance of physician. As the second step, each segmented data is normalized for reducing translation variation between different samples. In the third step, we apply marching cube algorithm to convert the segmented volume to a triangulated mesh surface which containing \( n=1000 \) vertex points [4]. Assume \( (x^l, y^l, z^l) \) and \( (x^s, y^s, z^s) \) are the coordinates of these vertex points for liver and spleen, respectively, the shape vectors \( \mathbf{x}_{\text{Liver}} = [x^l_1, y^l_1, z^l_1, \ldots, x^l_n, y^l_n, z^l_n]^T \) and \( \mathbf{x}_{\text{Joint}} = [x^l_1, y^l_1, z^l_1, \ldots, x^s_1, y^s_1, z^s_1, \ldots, x^l_n, y^l_n, z^l_n]^T \) are used for statistical shape model of liver and joint statistical shape model of the liver and the spleen. In this research, we proposed a novel mode selection method.

In addition to the conventional Accumulated Variance Contribution Rate (AVCR) based mode selection, we newly propose a correlation based one and combine them to select the effective modes [3]. We finally select one mode from each model, and the projection coefficients of the selected modes are used as features for classification (diagnosis).

III. EXPERIMENTAL RESULTS AND CONCLUSIONS

7 normal data and 19 abnormal data are used as test data. Among 19 abnormal data, 5 temporal sequence (each sequence includes a pair CT volumes obtained from the same patient in 2006 and 2009, respectively). These temporal sequences can be used to evaluate the progress of the liver fibrosis and temporal morphological changes. Each data is projected to the subspace of two selected modes and their distribution is shown in Fig.1. The blue points are normal data and the red ones are abnormal data. From Fig. 1, we can see that most of the normal data are located in the center, while abnormal data are scattered around the normal data. The arrows express the temporal changes. We can see that if fibrosing progresses, data will move outside. The distance to the center can be used as a scaling measure of liver fibrosis. The classification accuracy for abnormal data is 85.7% with a false positive rate of 5.3%.

REFERENCES


*Research supported by the Grant-in Aid for Scientific Research from the Japanese MEXT (No. 2430076, No,24103710) and R-GIRO.

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