Computer-Aided Diagnosis of Liver Cirrhosis Based on Multiple Statistical Shape Models

M. Uetani, T. Tateyama, S. Kohara, X.H. Han, Y.W. Chen

Graduate School of Information Science and Engineering
Ritsumeikan University
Shiga, Japan

A. Furukawa

School of Health Sciences
Tokyo Metropolitan University
Tokyo, Japan

S. Kanasaki

Kyoto Takeda Hospital
Kyoto, Japan

X. Wei

Institute for Infocomm Research
A-STAR
Singapore

*Abstract-*In the fields of medical image analysis and computational anatomy, statistical shape models (SSMs) is usually used for organ segmentation; SSMs are statistically constructed from a population of organs. In this paper, we focus on the application of SSMs for the computer-aided diagnosis of cirrhotic livers. Since chronic liver diseases or cirrhosis will cause significant morphological changes on both the liver and spleen, we constructed multiple SSMs (i.e., liver SSM, spleen SSM, and a joint SSM of the liver and spleen) for morphological analysis. Coefficients of SSMs are used as features for the classification of normal and cirrhotic livers. Through this paper, we show that classification accuracy can be significantly improved by effective mode selection, which is based on fisher discriminant analysis, and the use of a non-linear support vector machine. Furthermore, we also construct Computer-aided Diagnosis (CAD) of liver cirrhosis system using SSMs.

Keywords-computational anatomy; statistical shape model; liver cirrhosis; computer-aided diagnosis; effective mode selection; fisher discriminant analysis; non-linear SVM

I. INTRODUCTION

In recent years, there has been an increased interest in statistical shape models (SSMs) of human anatomy. SSMs are statistically constructed from a population of organs and can capture morphological variations of human anatomy. To date, SSMs of various organs such as livers, hearts, and spleens have been constructed [2-5]. In the fields of medical image analysis and computational anatomy, SSMs are usually applied to the automatic segmentation of medical images [6-11]. However, there have been few studies for applying SSMs to computer-aided diagnosis and treatment support. In our previous study, we constructed a SSM of the liver and proved the potential application of SSMs for the classification of normal and cirrhosis livers by using a simple linear classifier [12, 13]. We also constructed multiple SSMs (i.e., liver SSM, spleen SSM and joint SSM of the liver and the spleen) for morphological analysis [14, 15]; this study is based on the fact that the chronic liver diseases and liver cirrhosis will also cause significant morphological changes in the spleen [16].

Since each mode of the SSM represents a specific morphological variation, it is important to find effective modes that contribute to cirrhotic livers. As an improvement on our previous study, we propose to use fisher discriminant analysis to select effective modes as features for the classification of chronic liver diseases. We also use a non-linear SVM for classification instead of the previously used simple linear classifier [13] and nearest neighbour (NN) [15]. Our experiments have shown that both the mode selection method and the non-linear SVM classifier significantly improved classification accuracy.

II. CONSTRUCTION AND EVALUATION OF SSMs

We construct SSMs using the method, based on Ref.[16]. In this study, we evaluate the effectiveness of the constructed SSMs compactness. Compactness is a measure of the ability to express as many shape variations as possible by using as few components as possible. We use the accumulation contribution rate (ACR) as an indicator of a compactness of the model, calculated as follows:

$$ACR = \sum_{i=1}^{m} \lambda_i \bigg/ \sum_{j=1}^{N} \lambda_j \qquad (4)$$

Where N is the number of samples, and λ_i and λ_j are the ith and jth eigen values, respectively. In Figure 1, the ACR is plotted against the number of modes used to represent the model. In the figure, the compactness of the liver and spleen is denoted by solid and dotted lines; the compactness of the joint is denoted by circles. Figure 1 shows that the top 25% of components (i.e., modes) contain more than 95% of the model's variance (i.e., information). This implies that the 3D shape can be represented well by using only a few of the top components. Because morphological changes of other components are largely irrelevant, the top leading modes containing 95% of the information—i.e., the ACR are larger than 95%—are considered as useful modes, whereas other modes are considered to be noise.
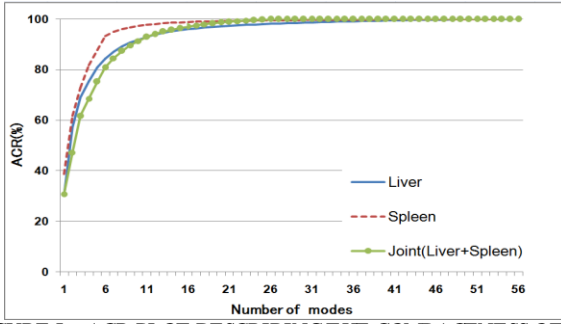
FIGURE I.   ACR PLOT DESCRIBING THE COMPACTNESS OF THE THREE MODELS.

III.   COMPUTER-AIDED DIAGNOSIS OF LIVER CIRRHOSIS USING SSMS

A.   Selection of Effective Modes for Liver Cirrhosis

Liver cirrhosis is one of liver disease; it can cause left lobe's hypertrophy and right lobe's atrophy [17]. Further, liver cirrhosis often causes spleen hypertrophy [13]. These features impact the shape of the liver and spleen. Coefficients of the SSMs are used as morphological features to classify normal and abnormal livers. The modes, which have large class variations between the normal and abnormal classes and small variations within each of the classes, can be considered as effective modes for computer-aided diagnosis. We therefore apply fisher discriminant analysis (FDA) to select effective modes by Eq.(5) below and rank modes from larger to smaller values. Eq.(5) is as follows:

$$f_i = \sigma_{b,i}^2 / \sigma_{w,i}^2 \tag{5}$$

$$\sigma_{b,i}^2 = \frac{n_{Normal} n_{Abnormal} (\overline{m}_{Normal,i} - \overline{m}_{Abnormal,i})}{n_{Normal} + n_{Abnormal}} \tag{6}$$

$$\sigma_{w,i}^2 = \frac{n_{Normal} \sigma_{Normal,i}^2 + n_{Abnormal} \sigma_{Abnormal,i}^2}{n_{Normal} + n_{Abnormal}} \tag{7}$$

Where

$$\overline{m}_{Normal,i} = \frac{1}{n_{Normal}} \sum_{j=1}^{n_{Normal}} b_{i,j} \tag{8}$$

$$\overline{m}_{Abnormal,i} = \frac{1}{n_{Abnormal}} \sum_{j=1}^{n_{Abnormal}} b_{i,j} \tag{9}$$

$$\sigma^2_{Normal,i} = \frac{1}{n_{Normal}} \sum_{j=1}^{n_{Normal}} (b_{i,j} - \overline{m}_{Normal,i})^2 \tag{10}$$

$$\sigma^2_{Abnormal,i} = \frac{1}{n_{Abnormal}} \sum_{j=1}^{n_{Abnormal}} (b_{i,j} - \overline{m}_{Abnormal,i})^2 \tag{11}$$

Eq.(6) shows class variations between the normal and abnormal classes. Eq.(7) shows variations within each of the classes. In these equations, i is the evaluated mode, n is the number of samples, m is each mode's mean, and σ is each mode's variance. In this study, only the top modes containing 95% of the information are used for mode selection.

B.   Classification Experiments

To improve classification accuracy, we use a non-linear SVM [19] as a classifier instead of our previous simple linear classifier [13] and NN[15]. In our classification experiments, two classifiers, nonlinear SVM and our previous NN, and two feature selection methods, the proposed FDA-based mode

selection and conventional ACR-based mode selection, are used. Further, we use the leave-one-out method in our experiments. We randomly select one CT data as a test image, whereas the other CT data are used for training. For each method, a total of 57 experiments (i.e., 28 for normal data and 29 for cirrhosis data) with a different test image are performed. Classification accuracy is defined as N_c / N, where N_c and N represent the number of correctly classified data and overall number of test data, respectively.

Figure 2 shows the classification accuracy of livers using three, six, and nine modes, respectively. We compare four experimental results—i.e., SVM with our proposed FDA mode selection, SVM with conventional ACR mode selection, NN with our proposed FDA mode selection, and NN with conventional ACR mode selection—for each case. As shown in Figure 2, our proposed FDA mode selection demonstrates better results than the conventional ACR mode selection for both SVM and NN; further, non-linear SVM is superior to NN. Figure 3 shows the dependence of classification accuracy (SVM with FDA mode selection) on the number of modes. The best result was obtained by the use of the selected top six modes.
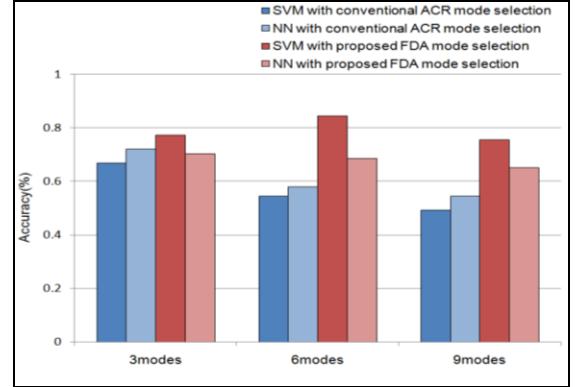

FIGURE II.   COMPARISON OF CLASSIFICATION ACCURACY OF FOUR DIFFERENT METHODS.
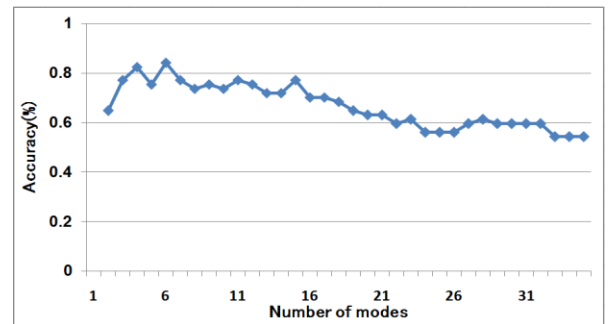

FIGURE III. CLASSIFICATION ACCURACY VERSUS THE NUMBER OF MODES.

C.   Computer-Aided Diagnosis of Liver Cirrhosis

In this study, we will aim to put our research to practical use in medical fields. So, We construct CAD of liver cirrhosis system using SSMs. This system can diagnose liver cirrhosis automatically. Figure 4 shows execution screen of this system. For visually understanding diagnostic results, we classify liver

using linear discriminant analysis in this system at present. In addition, this system can link to electronic health record and compare input case's 3D liver shape with three similar cases' 3D liver shape in datasets. Since doctors diagnose liver cirrhosis by liver shape using CT images (2D images), this function can understand liver shape easily. In our future study, we will attempt to switch from linear discriminant analysis to non-linear SVM.
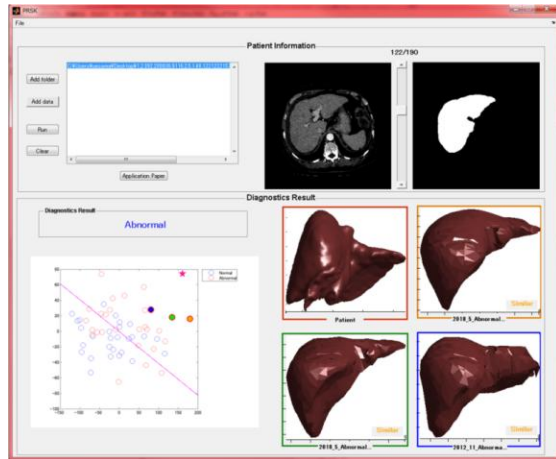

FIGURE IV. CAD OF LIVER CIRRHOSIS SYSTEM.

IV. CONCLUSION

In this study, we constructed three SSMs: one for the liver, one for the spleen and one for the joint. Next, we selected effective modes for classification by using FDA. We compared classification accuracy between using effective modes and eigen values in the decreasing order in non-linear SVM and NN. We classified livers normal and abnormal by non-linear SVM while changing modes for classification one by one. Results indicated that selecting effective modes using FDA is necessary for classification. Furthermore, we also construct CAD of liver cirrhosis system using SSMs. In our future study, we will attempt to increase our datasets and construct more accurate models by using other statistical methods, such as sparse coding.

REFERENCES

[1] H. Kobatake, Y. Masutani, Y. Sato, H. Fujita, N. Niki, K. Mori, A. Shimizu, S. Kido, M. Hashizume, H. Haneishi, J. Hasegawa and T. Sato, "The project "Computational Anatomy", funded by MEXT Grant-in-Aid for Scientific Research on Innovative Areas: What is aimed at? What is expected? ," IEICE Technical Report, Vol.109, No.407, pp. 205-210, 2010. In Japanese.

[2] P.M. Tompson, et. al., "Mathematical and computational challenges in creating deformable and probabilistic atlases of the human brain," Hum Brain Mapp. Vol.9, pp.81-92, 2000.

[3] J.M. Peyrat, et. al., "Towards a statistical atlas of cardiac fiber structure: A computational framework for the statistical analysis of cardiac diffusion tensors: application to a small database of canine hearts," IEEE Trans Med Imaging, Vol.26, pp.1500-1514, 2007.

[4] T. Okada et. al., "Construction of hierarchical multi-organ statistical atlases and their application to multi-organ segmentation from CT images," Lecture Notes in Computer Science, LNCS5541 (Proc. MICCAI 2008, Part 1), pp.502-509, 2008.

[5] T. Tateyama, A.H. Foruzan, Y.W. Chen, "2D-PCA based Statistical Shape Model from few Medical Samples," Proc. of 2009 Fifth International Conference on Intelligent Information Hiding and Multimedia Signal Processing, pp.1266-1269, 2009.

[6] A. Shimizu, Y. Sato, "Construction of Statistical Atlas of Abdominal Organs and its Application to Multi-organ Segmentation," MEDICAL IMAGING TECHNOLOGY, Vol.24, No.3, pp153-160, 2006. In Japanese.

[7] A. Shimizu, "Construction of Statistical Atlas of Abdominal Organs and its Application to Multi-organ Segmentation," MEDICAL IMAGING TECH-NOLOGY, Vol.27, No.3, pp147-152, 2009. In Japanese.

[8] H. Park, P.H. Bland, C.R. Meyer, "Construction of an Abdominal Probabilistic Atlas and its Application in Segmentation," IEEE TRANSACTIONS ON MEDICAL IMAGING, Vol.22, No.4, pp483-492, 2003.

[9] T. Okada, R. Shimada, M. Hori, M. Nakamoto, Y.-W. Chen, H. Nakamaura, Y. Sato, "Automated segmentation of the liver from 3D CT images using probabilistic atlas and multi-level statistical shape model," Academic Radiology, V63.15, pp.1390-1403, 2008.

[10] K. Yokoyama, T. Kitasaka, K. Mori, Y. Mekada, J. Hasegawa, J. Toriwaki, "Liver region extraction from 3D abdominal X-ray CT images using distribution features of abdominal organs," Journal of Computer Aided Diagnosis of Medical Images, Vol.7, No.4-3, 2003. In Japanese.

[11] T. Kitagawa, X. Zhou, T. Hara, H. Fujita, R. Yokoyama, H. Kondo, M. Kanematsu, H. Hoshi, "Generation of a Probabilistic Liver Atlas and Its Application to Automated Liver Segmentation Method in Non-contrast X-Ray Torso CT Image, " IEEE, Vol.J91-D, No.7, pp.1837-1850, 2008. In Japanese.

[12] S. Kohara, T. Tateyama, et al., "Preliminary Study on Statistical Shape Model Applied to Diagnosis of Liver Cirrhosis," Proc. of 2011 IEEE International Conference on Image Processing (IEEE ICIP2011), pp.2978-2981, 2011.

[13] Y.W. Chen, M. Uetani, et al., "Application of Statistical Shape Model of the Liver in Classification of Cirrhosis," *International Journal of Digital Content Technology and its Applications*, Vol. 7, No. 9, pp. 477-484, 2013.

[14] J. Luo, Y.W. Chen, et al., "Pilot Study of Applying Shape Analysis of Liver Cirrhosis Diagnosis," Proc. of 2013 IEEE International Conference on Image Processing (IEEE ICIP2013), pp.3537-3541, 2013.

[15] Y.W. Chen, J. Luo, et al., "Computer-Aided Diagnosis and Quantification of Cirrhotic Livers Based on Morphological Analysis and Machine Learning," *Computational and Mathematical Methods in Medicine*, Volume 2013, Article ID 264809, 8 pages, 2013.

[16] M.Uetani, T.Tateyama, et al., "Statistical Shape Model of the Liver and Its Application to Computer Aided Diagnosis of Liver Cirrhosis, " IEEJ Trans. on Electronics, Information and Systems, Vol.133, No.11, pp.2037-2043, 2013(in Japanese)

[17] P.P. Anthony et al., "The Morphology of Cirrhosis," Journal of Clinical Pathology, Vol.31, pp.395-414, 1978.

[18] Vapnik V.N., The Nature of statistical Learning Theory, Springer, 1995.