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Interactive Liver Tumor Segmentation from CT Scans Using Support Vector Classification with Watershed

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***Abstract*— In this paper, we present an interactive method for liver tumor segmentation from computed tomography (CT) scans. After some pre-processing operations, including liver parenchyma segmentation and liver contrast enhancement, the CT volume is partitioned into a large number of catchment basins under watershed transform. Then a support vector machines (SVM) classifier is trained on the user-selected seed points to extract tumors from liver parenchyma, while the corresponding feature vector for training and prediction is computed based upon each small region produced by watershed transform. Finally, some morphological operations are performed on the whole segmented binary volume to refine the rough segmentation result of SVM classification. The proposed method is tested and evaluated on MICCAI 2008 liver tumor segmentation challenge datasets. The experiment results demonstrate the accuracy and efficiency of the proposed method so that indicate availability in clinical routines.**

I. INTRODUCTION

Liver cancer is the third most leading cause of death from cancer worldwide and accounted for 700,000 deaths (around 9% of all cancer deaths) in 2008. Accurate Liver tumor detection is an important issue in liver disease diagnosis and liver surgical planning (e.g., oncologic resections and liver transplantation). Moreover, the subsequent quantitive analysis of liver tumor can help physician evaluate therapy effect on tumors. Tumor volume is a precise representation of tumor size for deciding the stage of cancer and therapy evaluation. Due to the fuzzy boundary between tumor and healthy parenchyma, inhomogeneous structures and noise, the large variability of tumor shapes and intensities, liver tumor segmentation becomes a challenging problem which attracts much research attention in recent years. Especially, MICCAI 2008 Workshop on 3D Liver Tumor Segmentation Challenge provides a platform for testing and comparing different approaches for the topic. In the competition, an interactive method that combines graph-cuts with a watershed low-level segmentation [1] achieved the best performance, and a semi-automatic method using supervised voxel classification strategy in 2D slice [2] ranked second. Other approaches applied in liver tumor detection include AdaBoost [3], thresholding and morphological processing [4], etc.

Some related work on liver tumor segmentation from CT scans proved that the supervised classification methods are effective for this topic [2], [5]. Due to large inter-individual intensity variability of different liver tumors, the supervised learning methods are more robust than the unsupervised clustering methods. In the proposed classification method, the training samples are designated from user-selected seeds to distinguish tumors and healthy parenchyma. Support vector machines (SVM) is a supervised learning method that have been successfully applied in discriminative classification and regression problems. In the domain of 2D image classification, SVM is trained and predicted on pixel level. However, when generalized to 3D volume data, the SVM classifier will take a long time to train and predict as a result of a mass of voxels. In order to improve efficiency while not affected the accuracy of classification, we use the SVM classifier on region level which is produced by watershed over-segmentation.

II. METHODS

The liver tumor segmentation workflow consists of the following steps: 1) Pre-processing: Liver region segmentation and contrast enhancement; 2) Watershed transform of the liver region; 3) Region-based classification using SVM training and prediction; 4) Refined segmentation using connected region detection and morphological operation.

A. Pre-processing

1) Liver Segmentation: The liver region is separated from the abdominal CT scans using a statistical shape model with optimal surface detection strategy [6]. The original CT slice and the segmented orthogonal liver slice from an abdominal CT volume are shown as Fig. 1.

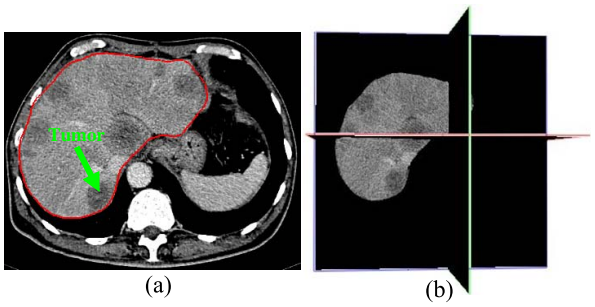

Fig. 1. The original CT slice and the segmented orthogonal liver slice from an abdominal CT volume.

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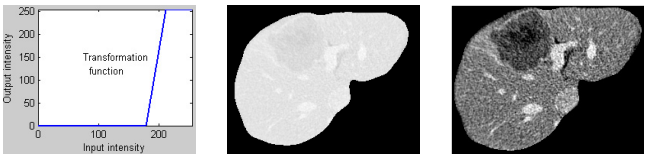
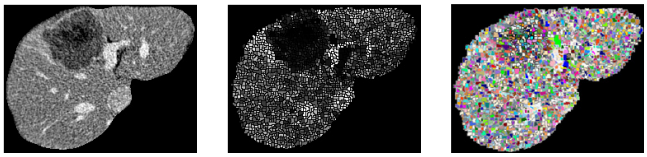


(a) (b) (c)

Fig. 2. Contrast enhancement of CT volume. (a) Transformation function; (b) The original CT slice; (c) The contrast-enhanced CT slice by histogram stretching.



(a) (b) (c)

Fig. 3. Watershed transform based on immersion analogy [7]. (a) Original transversal slice of liver before watershed pre-segmentation; (b) Transversal slice of liver after watershed pre-segmentation; (c) Pseudo-color image of catchment basins produced by watershed pre-segmentation.

2) Contrast Enhancement: Low contrast between liver tumor and parenchyma makes tumor detection a difficult problem. It is necessary to enhance contrast within liver region to identify tumors in CT images. One of the most widely used methods for contrast enhancement of image is histogram processing. The original histogram of liver region is stretched from zero to the maximum intensity of the liver, as illustrated in Fig . 2.

B. Watershed Transform

Watershed transform [7] is one of the classical topographical methods that is commonly used in image segmentation, feature extraction and surface visualization. Under conventional watershed transform, an image is partitioned into different catchment basins according to immersion or drainage simulation [7]. However, watershed usually suffers from over-segmentation due to noise or irrelevant local minima in the gradient image. Instead of training or predicting on voxels using classification method, watershed transform is employed as a pre-segmentation step to improve efficiency. The liver mask CT volume is partitioned into a large number of small regions, which locate edges accurately and reduce the number of training and predicting samples distinctly in the succedent SVM classification. The original transversal slice and the corresponding watershed pre-segmentation result based on immersion analogy [7] are shown as Fig. 3. The implementation of watershed transform has linear-time complexity with respect to the number of voxels.

C. SVM Classification

Support vector machines (SVM) is a popular machine learning technique which have been successfully applied in classification, regression and other learning tasks [8]. SVM formulation embodies the Structural Risk Minimization (SRM) principle which enhances the generalization ability [8]. Since limited number of training samples obtained by an interactive manner in medical image segmentation, SVM can effectively solve this small sample size problem due to its superior generalization ability compared with some traditional classification methods.

To obtain training samples, we interactively label tumors and healthy parenchyma on traversal slice using a 3D brush. For each catchment basin R_i produced by watershed over-segmentation, a feature vector is constructed which consists of four values: the mean I_{mean}, the standard deviation I_{std}, the minimum I_{min} and the maximum intensity I_{max} of the catchment basin. Prior to the training process, each feature vector $\mathbf{x} = [I_{mean}, I_{std}, I_{min}, I_{max}]$ is normalized to [0, 1].

Given a set of N training samples $(\mathbf{x}_i, y_i)$, $i = 1, \cdots N$, $\mathbf{x}_i \in R^4$, $y_i \in \{+1, -1\}$, while +1 denotes liver tumor and -1 denotes healthy liver parenchyma. As shown in Fig. 4, there are many possible hyperplanes that can separate the two classes with the given formation:

$$\langle \boldsymbol{\omega}, \boldsymbol{x} \rangle + b = 0 \tag{1}$$

Among all possible hyperplanes, there is only one optimal hyperplane that maximizes the distance between the closest vectors of each class, which is illustrated as the black real line in Fig. 4. The margin between support vectors is given as $2/\|\boldsymbol{\omega}\|$. To maximize the margin, we solve the following quadratic problem with inequalities constraints:

$$\begin{aligned} &\min \ \tfrac{1}{2}\|\boldsymbol{\omega}\|^2 \\ &s.t. \ y_i\left[\langle \boldsymbol{\omega}, \boldsymbol{x_i} \rangle + b\right] \geq 1, \quad \forall i \end{aligned} \tag{2}$$

where $\boldsymbol{\omega}$ is normal of the hyperplane, $|b|/\|\boldsymbol{\omega}\|$ is the perpendicular distance from the hyperplane to the origin.

With the Lagrange multiplier method, the optimization problem of Eq. (2) is given as the saddle point of the unconstrained objective function:

$$L_P(\boldsymbol{\omega}, b, \alpha) = \frac{1}{2}\|\boldsymbol{\omega}\|^2 - \sum_{i=1}^{N} \alpha_i \left(y_i\left[\langle \boldsymbol{\omega}, \boldsymbol{x_i} \rangle + b\right] - 1\right) \tag{3}$$

where α_i denotes the Lagrange multiplier. The Lagrangian L_P has to be minimized with respect to $\boldsymbol{\omega}$, b and subject to the constraints $\alpha_i \geq 0$. The primal problem L_P can be transformed to its dual formulation L_D which can be optimized via easier solution. The dual problem is given as follows:

$$L_D(\alpha) = \frac{1}{2}\sum_{i=1}^{N}\sum_{j=1}^{N} \alpha_i \alpha_j y_i y_j \left\langle \boldsymbol{x_i}, \boldsymbol{x_j} \right\rangle - \sum_{i=1}^{N} \alpha_i \tag{4}$$

Finally, the optimal decision function is defined as:

$$f(\boldsymbol{x}) = sign\left(\langle \boldsymbol{\omega}, \boldsymbol{x} \rangle + b\right) = sign\left\{\sum_{i \in SV_S} \alpha_i K(\boldsymbol{x_i}, \boldsymbol{x}) + b\right\} \tag{5}$$

where $\boldsymbol{x_i}$ is support vector, α_i denotes Lagrange multiplier corresponding to each support vector. When generalized the optimal separating hyperplane to linearly non-separable training samples, a kernel function K is employed to map the training data to a high-dimensional space. We can use kernel

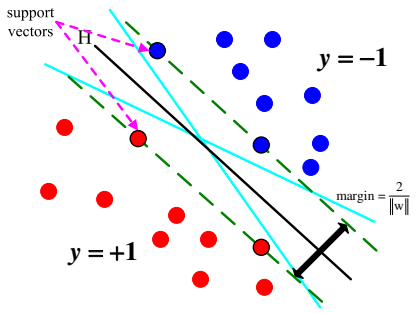


Fig. 4. Optimal separating hyperplane for binary classification.

functions [9] such as linear function, polynomial function and radial basis function. From the training process, the support vectors $\boldsymbol{x}_i$, the corresponding coefficients α_i and the classification threshold b can be obtained for subsequent SVM prediction of unlabeled catchment basins.

For each unlabeled catchment basins in a CT data, after computing the feature vector $\mathbf{x}$ and linearly scaling to [0, 1] in previous step, we predict classification result of all unlabeled regions via the decision function given in Eq. 5.

D. Post-processing

The SVM classifier usually yields classification error for tumor segmentation. In the proposed method, the misclassified result takes the form of isolated regions scattered across the entire CT volume. For the classified binary volume produced by the previous step, we take two steps to refine SVM classification result. First, the false positive tumor regions are removed by connected region detection with seeds in each tumor. Second, a morphological opening operator followed by a closing operator with the same sphere structure element is performed on the binary volume to smooth contour and fill holes.

III. EXPERIMENTS AND RESULTS

The proposed method is tested on the training datasets of MICCAI 2008 liver tumor segmentation challenge (`http://lts08.bigr.nl`). There are a total of ten tumors in four training datasets and the corresponding ground truth segmentation result for each tumor. We implemented our method based on the *Medical Imaging Toolkit* (MITK `www.mitk.net`) [11] developed by our group on a 32-bit desktop PC (2.33GHz Core 2, 2GB RAM). The SVM classification step in the segmentation chain is implemented based on the LIBSVM toolkit [12] developed by Lin et al.

After the pre-processing step, the CT volume is partitioned into numerous small regions under watershed transform using 6-neighborhood. The number of regions is reduced by a factor of about 18 compared to the number of voxels. In the SVM classification process, we select seed points by painting tumor and healthy parenchyma in the CT volume using a 3D brush. Each liver tumor needs at least one seed for the subsequent connected region detection. We use the linear function as kernel function in SVM classifier. In the post-prossing step, a sphere of radius 2mm is used as structural element to perform morphological operation.

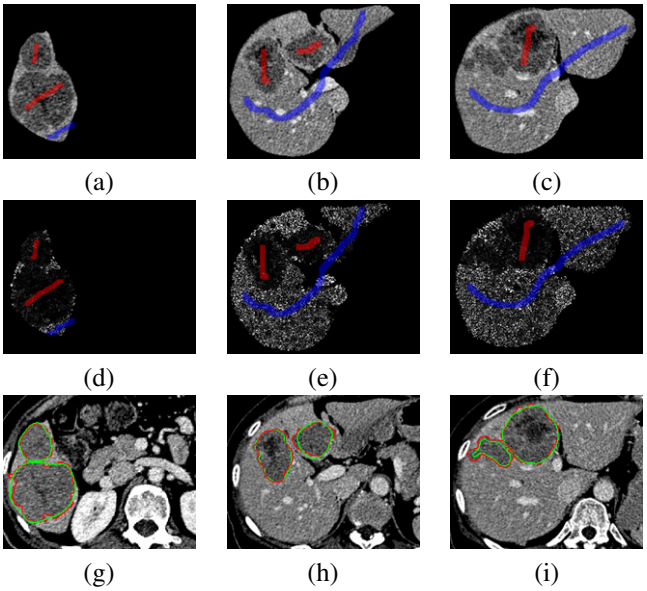


Fig. 5. Segmentation process and result of four tumors in data LTS_IMG04. (a), (b) and (c) Interactive labeling of four tumors on transversal slice of data LTS_IMG04; (d), (e) and (f) Synchronous labeling on watershed pre-segmentation images; (g), (h) and (i) The contour of the corresponding segmentation result is in red while the reference result is in green.

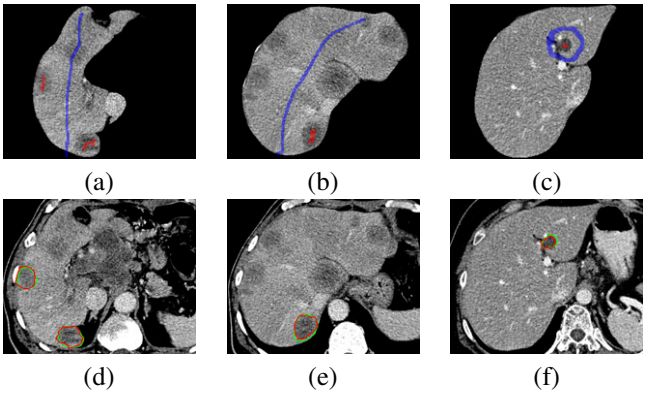


Fig. 6. Segmentation process and result of tumors in data LTS_IMG02 and LTS_IMG03. (a) and (b) Interactive labeling of three tumors on transversal slice of data LTS_IMG02; (c) Interactive labeling of one tumor on transversal slice of data LTS_IMG03; (d), (e) and (f) The contour of the corresponding segmentation result is in red while the reference result is in green.

As shown in Fig. 5 and Fig. 6, the red label indicates tumor and the blue label indicates healthy parenchyma. The corresponding final segmentation result in comparison with the expert manual reference segmentation result is displayed as the third row of Fig. 5 and the second row of Fig. 6. Surface distance maps from the segmentation result to the reference result of three training datasets are illustrated as Fig. 7.

The average runtime for each step in segmentation chain of 10 tumors in training datasets is given in Table I. The total runtime of the segmentation chain takes about 30 seconds compared to 7 minutes with a slice-by-slice voxel-based SVM classification method in previous work[2].

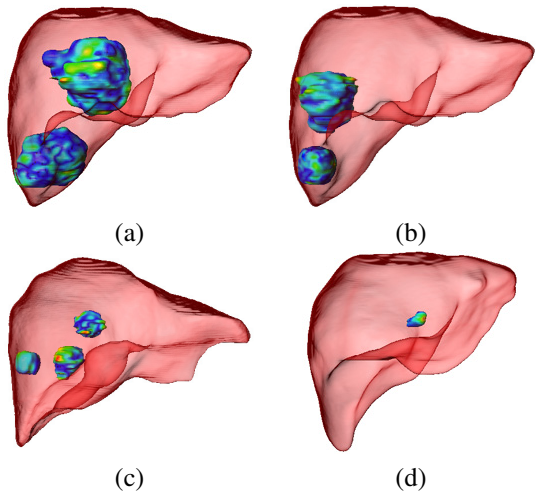


Fig. 7. Surface distance map from the segmentation result to the reference result. (a) and (b) Surface distance map of four tumors in LTS_IMG04; (c) Surface distance map of three tumors in LTS_IMG02; (d) Surface distance map of one tumor in LTS_IMG03.

TABLE I
AVERAGE RUNTIME OF EACH STEP IN SEGMENTATION CHAIN

Process step	Watershed	SVM	Post-process
Runtime (seconds)	5.54	8.34	16.19

Segmentation results produced by our method are compared to the reference results according to the following five metrics: volumetric overlap error (OE), absolute relative volume difference (AVD), symmetric average surface distance (D_{Avg}), symmetric roots mean square (RMS) surface distance (D_{RMS}) and maximum surface distance (D_{Max}). The five evaluation metrics of 10 tumors segmented by the proposed method are summarized in Table II. The proposed method achieves an averaged overlap error of 31.14%, compared to 29.49% by the method [1] on the testing datasets from liver segmentation workshop.

IV. CONCLUSIONS AND FUTURE WORKS

We have presented an interactive approach for 3D liver tumor segmentation which combines watershed transform and SVM classification. This method is tested on abdominal CT volume with ten liver tumors and five quantitative metrics are computed, and the averaged overlap error for 10 tumors is 31.14%. The experiment results demonstrate our method is accurate and efficient for a wide variety of tumor types so that indicate availability in clinical routines.

TABLE II
RESULTS OF FIVE EVALUATION METRICS FOR ALL TEN TUMORS

Tumor	OE [%]	AVD [%]	D_{Avg} [mm]	D_{RMS} [mm]	D_{Max} [mm]
IMG01_L1	40.09	27.13	2.61	3.35	11.58
IMG01_L2	51.91	24.26	2.47	3.21	8.87
IMG02_L1	42.68	7.57	1.97	2.66	9.51
IMG02_L2	33.39	43.45	1.58	2.11	6.95
IMG02_L3	42.51	39.19	1.70	2.16	6.48
IMG03_L1	28.97	22.90	0.56	0.94	3.95
IMG04_L1	16.81	7.23	1.25	1.77	9.72
IMG04_L2	12.05	0.45	0.36	0.64	3.17
IMG04_L3	23.25	17.40	1.94	2.55	12.48
IMG04_L4	19.71	6.12	1.12	1.51	6.33
Average	31.14	19.57	1.56	2.09	7.90

The proposed method has three advantages. First, the supervised classification method incorporates prior knowledge through training samples from users via interactive labeling tumors and healthy liver. The classification approach is more robust than the unsupervised clustering approach. Second, the classification feature vector for SVM is computed within catchment basins obtained from the previous watershed transform, which is more efficient compared with the time-consuming voxel-based SVM method. Finally, the proposed method only has few parameters to set therefore improve robustness of the method.

Future works will include some pre-processing and post-processing steps of the proposed method. Previous to the watershed transform, a 3D nonlinear diffusion filter would be applied to a CT volume to reduce noise while preserving tumor contour. Since the region-based classification will produce rough tumor surface, an energy function that incorporates smoothness of tumor will be employed to refine the SVM classification result.

REFERENCES

[1] J. Stawiaski, E. Decenciere and F. Bidault, "Interactive Liver Tumor Segmentation Using Graph-cuts and Watershed", *in MICCAI Workshop. 3D Segmentation in the Clinic: A Grand Challenge*, 2008.

[2] J. Zhou, W. Xiong, Q. Tian, Y. Qi, J. Liu, W.-K. Leow, T. Han, S. Venkatesh and S.-C. Wang, "Semi-automatic Segmentation of 3D Liver Tumors from CT Scans Using Voxel Classification and Propagational Learning", *in MICCAI Workshop. 3D Segmentation in the Clinic: A Grand Challenge*, 2008.

[3] A. Shimizu, T. Narihira, D. Furukawa, H. Kobatake, S. Nawano and K. Shinozaki, "Ensemble Segmentation Using AdaBoost with Application to Liver Lesion Extraction from a CT Volume", *in MICCAI Workshop. 3D Segmentation in the Clinic: A Grand Challenge*, 2008.

[4] J.-H. Moltz, L. Bornemann, V. Dicken and H.-O. Peitgen, "Segmentation of Liver Metastases in CT Scans by Adaptive Thresholding and Morphological Processing", *in MICCAI Workshop. 3D Segmentation in the Clinic: A Grand Challenge*, 2008.

[5] M. Freiman, O. Cooper, D. Lischinski and L. Joskowicz, "Liver Tumors Segmentation from CTA Images Using Voxels Classification and Affinity Constraint Propagation", *Int J Comput Assist Radiol Surg.*, vol. 6, no. 2, 2010, pp. 247-255.

[6] X. Zhang, J. Tian, K. Deng, W. Wu and X. Li, "Automatic Liver Segmentation Using a Statistical Shape Model With Optimal Surface Detection", *IEEE Trans. Biomed. Eng.*, vol. 57, no. 10, 2010, pp. 2622-2626.

[7] L. Vincent and P. Soille, "Watersheds in Digital Spaces: An Efficient Algorithm based on Immersion Simulations", *IEEE Trans. Pattern Anal. Mach. Intell.*, vol. 13, no. 6, 1991, pp. 583-598.

[8] S. R. Gunn, "Support Vector Machines for Classification and Regression", *Tech. Rep.*, 1998.

[9] C. J. C. Burges, "A Tutorial on Support Vector Machines for Pattern Recognition", *Data Min. Knowl. Discov.*, vol. 2, no. 2, 1998, pp. 121-167.

[10] C. Cortes and V. Vapnik, "Support-Vector Networks", *Mach. Learn.*, vol. 20, no. 3, 1995, pp. 273-297.

[11] J. Tian, J. Xue, Y.-K. Dai, J. Chen and J. Zheng, "A Novel Software Platform for Medical Image Processing and Analyzing", *IEEE Trans. Inf. Technol. Biomed.*, vol. 12, no. 6, 2008, pp. 800-812.

[12] C.-C. Chang and C.-J. Lin, "LIBSVM: a Library for Support Vector Machines", Software available at `http://www.csie.ntu.edu.tw/~cjlin/libsvm`, 2001