Liver Tumor Detection and Segmentation using Kernel-based Extreme Learning Machine*

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Abstract—This paper presents an approach to detection and segmentation of liver tumors in 3D computed tomography (CT) images. The automatic detection of tumor can be formulized as novelty detection or two-class classification issue. The method can also be used for tumor segmentation, where each voxel is to be assigned with a correct label, either a tumor class or non-tumor class. A voxel is represented with a rich feature vector that distinguishes itself from voxels in different classes. A fast learning algorithm Extreme Learning Machine (ELM) is trained as a voxel classifier. In automatic liver tumor detection, we propose and show that ELM can be trained as a one-class classifier with only healthy liver samples in training. It results in a method of tumor detection based on novelty detection. We compare it with two-class ELM. To extract the boundary of a tumor, we adopt the semi-automatic approach by randomly selecting samples in 3D space within a limited region of interest (ROI) for classifier training. Our approach is validated on a group of patients' CT data and the experiment shows good detection and encouraging segmentation results.

I. INTRODUCTION

Liver tumor is one of the highest causes of death due to cancer. An accurate detection and proper segmentation of liver tumor from CT image is of high significance especially for early detection and diagnoses of cancer. Liver tumor segmentation can be formulized as a pattern recognition problem, where a given voxel is to be assigned a label, either a tumor or non-tumor class. A semi-automatic approach of liver tumor segmentation is applied in this paper. Previously, detection or segmentation of liver tumor is done by experienced clinicians, but it is too time consuming and subjective depending on the skills and experiences of the clinicians. Thus minimal user involvement with reliable detection and segmentation of liver tumors is highly aspired.

Researchers in the past have investigated this topic. Masuda et al. [1] showed that by enhancing contrast levels and using the expectation maximization of the posterior marginal algorithm as well as a shape constrain, liver tumors can be detected even in poor CT images. Pescia et al. [2] proposed the use of advanced non-linear machine learning techniques to determine the optimal features, as well as the hyperplane that uses these features to separate tumor voxels from healthy liver tissues. Bilello et al. [3] showed that liver

tumor detection can be done by using intensity-based histogram method to find central lesions, followed by liver contour refinement to identify peripheral lesions. Hong et al. [4] proposed an automatic system to perform the liver tumor detection. Shape information is used to identify and recognize a lesion adjacent to the border of the liver and the lesion is extracted by means of Fuzzy C-means clustering technique. The proposed system performs a 3D consistency check based on three dimensional diagnoses to increase the recognition rate. Mala et al. [5] also adopted Fuzzy C-Means for tumor extraction followed by a tumor type classification. There are also works done by using other imaging devices. For example Optical imaging using Diffuse Reflectance Spectroscopy (DRS) can distinguish different tissue types (tumor/non-tumor) through a specific "optical fingerprint" [6]. A miniaturized optical needle was developed for the imaging. It is not based on conventional CT scan but in an intrusive way image tumor tissues directly.

In tumor segmentation, Zhou et al. [7] had developed a semi-automatic approach using Support Vector Machine SVM) and propagational learning. In their method, a tumor contour of the initial slice is extracted by learning a SVM using randomly selected samples in a ROI from a 2D CT slice. With the morphological operations (dilation and erosion), the contours after dilation and erosion are projected to its neighboring slices. The region within the dilation contour gives the suspicious tumor region and the region within the erosion region serves as the positive tumor samples to train the SVM classifier. After the tumor region of the neighboring slices is detected, the algorithm is applied recursively on the next neighboring slice. In this way, the SVM classifier is trained and updated through propagational learning. Wong et al. [8] developed another method where a seed point is selected and its feature is generated. Then 2D region growing technique is deployed for liver tumor segmentation. Some knowledge-based constraints are taken into consideration to ensure the size and the shape of the segmented tumor can be properly accepted. Chen et al. [9] also proposed a Detect Before Extract system, which will automatically find the liver boundary. A neural network classifier is trained by using specially designed feature descriptor to distinguish normal liver and two types of tumor: hepatoma and hemageoma. Instead of locating and segmenting tumors using the texture features, it classified two types of liver tumors in relatively big 16x16 blocks.

In our work, we propose to use the kernel based Extreme Learning Machine to detect and segment liver tumor voxels in CT scans. The kernel based ELM achieves a better performance compared to traditional ELM, and it is faster than SVM [10][13]. In the ELM training and testing, each voxel is associated with a feature vector which consists of a

set of image features, namely the mean and variance, entropy, Law's features [11] and sum-and-difference histograms [12]. Minimal user involvement is designed to segment the liver tumor in a given CT volume. The user is required to select the tumor samples (positive samples) and/or the non-tumor samples (negative samples) at the beginning. Given those samples, an ELM classifier is learned for voxel classification, followed with morphological smoothing (erosion and dilation), a suspicious region of tumor is detected or segmented using this classifier. To ease the selection of tumor training samples, one class ELM is proposed for tumor detection where the user only needs to select healthy liver samples. We also apply the two-class ELM classifier for automatic liver tumor detection assuming some training tumor samples are available. Experiment testing shows encouraging results.

II. BRIEF OF EXTREME LEARNING MACHINE

A. Introduction

Extreme Learning Machine [13] is designed as a single hidden layer feed forward networks (SLFN). It is shown that the learning speed is much faster compared to other learning algorithms such as SVM. The brief idea of ELM is illustrated in the following. Given N training samples $\{(\mathbf{x}_i, t_i)\}_{i=1}^N$ where $\mathbf{x}_i$ is the input feature vector and $t_i \in \{-1,1\}$ is the corresponding target vector, the output of a SLFN network with L hidden nodes can be expressed as the following:

$$f_L(\mathbf{x}_j) = \sum_i^L \beta_i g(\mathbf{w}_i \cdot \mathbf{x}_j + b_i), \quad j = 1,...,N . \quad (1)$$

It can be written as $f(\mathbf{x}) = \mathbf{h}(\mathbf{x})\boldsymbol{\beta}$. Here $\mathbf{w}_i$ and b_i denote the input weights and biases to the hidden layer respectively, β_i is the output weight linking the i-th hidden node to the output layer and $g(\cdot)$ is the activation function of the hidden nodes. Equation (1) can be written in a matrix form as $\mathbf{H}\boldsymbol{\beta} = \mathbf{T}$, where

$$\mathbf{H} = \begin{bmatrix} g(w_1 \times x_1 + b_1) & \cdots & g(w_L \times x_1 + b_L) \\ \vdots & \ddots & \vdots \\ g(w_1 \times x_N + b_1) & \cdots & g(w_L \times x_N + b_L) \end{bmatrix},$$

$$\boldsymbol{\beta} = [\beta_1 ... \beta_N]' \text{ and } \mathbf{T} = [t_1 ... t_N]'.$$

The input weights and hidden biases can be assigned arbitrarily so that $\mathbf{H}$ does not need to be tuned. To train such an SLFN is simply equivalent to finding a least-square solution by using Moore-Penrose generalized inverse:

$$\hat{\boldsymbol{\beta}} = \mathbf{H}\dagger\mathbf{T}, \quad (2)$$

where $\mathbf{H}\dagger = (\mathbf{H}'\mathbf{H})^{-1} \mathbf{H}'$ or $\mathbf{H}' (\mathbf{H}\mathbf{H}')^{-1}$, depending on the singularity of $\mathbf{H}'\mathbf{H}$ or $\mathbf{H}\mathbf{H}'$.

B. Kernel ELM

In a newly developed kernel ELM [13], a positive regularization coefficient is introduced into the learning system to make it more stable. Assume $\mathbf{H}'\mathbf{H}$ is nonsingular, the coefficient $1/\lambda$ is added to the diagonal of $\mathbf{H}'\mathbf{H}$ in the calculation of the output weights $\boldsymbol{\beta}$. The resultant solution is more stable and with better generalization performance. We then can have $\boldsymbol{\beta} = \mathbf{H}'(\frac{\mathbf{I}}{\lambda} + \mathbf{H}\mathbf{H}')^{-1}$. The corresponding function of the regularized ELM is:

$$f(\mathbf{x}) = \mathbf{h}(\mathbf{x})\boldsymbol{\beta} = \mathbf{h}(\mathbf{x})\mathbf{H}'(\frac{\mathbf{I}}{\lambda} + \mathbf{H}\mathbf{H}')^{-1}\mathbf{T} . \quad (3)$$

It has been shown [13] that a kernel matrix for ELM can be defined as follows. Let $\boldsymbol{\Omega}_{\text{ELM}} = \mathbf{H}\mathbf{H}'$ $\boldsymbol{\Omega}_{\text{ELM}i,j} = \mathbf{h}(\mathbf{x}_i)\mathbf{h}(\mathbf{x}_j) = K(\mathbf{x}_i, \mathbf{x}_j)$. The output function of ELM can be written compactly as:

$$f(\mathbf{x}) = \mathbf{h}(\mathbf{x})\mathbf{H}'(\frac{\mathbf{I}}{\lambda} + \mathbf{H}\mathbf{H}')^{-1}\mathbf{T}$$

$$= \begin{bmatrix} K(\mathbf{x}, \mathbf{x}_1) \\ \vdots \\ K(\mathbf{x}, \mathbf{x}_N) \end{bmatrix}' (\frac{\mathbf{I}}{\lambda} + \boldsymbol{\Omega}_{\text{ELM}})^{-1}\mathbf{T} \quad (4)$$

In this implementation, the hidden layer feature mapping $\mathbf{h}(\mathbf{x})$ need not to be known to users, instead its corresponding kernel $K(\mathbf{u},\mathbf{v})$ can be computed. Here the Gaussian kernel is used, $K(\mathbf{u},\mathbf{v}) = \exp(-\gamma \|\mathbf{u}-\mathbf{v}\|^2)$.

III. LIVER TUMOR DETECTION AND SEGMENTATION

A. Preprocessing

Since the texture features of liver tumor vary from slice to slice and tumors of different patients have different characteristics, in this paper, different from previous works where only the voxels on a certain slice is used to construct the training dataset, we select the voxels from three planes: coronal, sagittal, and transversal planes. Then the features of the voxels on these three planes are generated and a training dataset is constructed using these features for ELM classifier training. With a proper selection of threshold for the outcome of the classification results, each voxel is labeled as either tumor and or non-tumor class. We tested this classifier on the region of suspicious tumor of each slice. This method mainly consists of four parts: pre-processing of the CT image scans, feature generation of the positive and negative samples (for tumor detection with one class ELM, only healthy liver voxels are used), training and testing of ELM, and post-processing to refine the segmentation result.

The original CT images of different sessions may have different contrast and CT images also contain procedure noise. The contrast adjustment is done simply by normalizing the window level and range around liver intensity histogram. Following that, we adopted a noise suppression procedure based on Block Matching 3D Sparse Transform Domain Collaborative Filtering (BM3D) [14]. The filtered blocks are then returned to their original positions. Because these blocks overlap with each other, many different estimates were obtained for each pixel. These estimations are combined together later. The result is a 3D estimate that consists of the jointly filtered grouped image blocks. Here, aggregation as a particular averaging procedure is exploited to take advantage of this redundancy.

B. Feature Extraction

For each voxel sample, its texture features are generated in terms of its neighborhood mean and variance, intensity, intensity power, entropy, intensity co-occurrence, Law's texture [11], and Sum and Difference Histogram [12]. These features are generated in 3D volume that makes them more representative. For example, a cubic of 5x5x5 voxels is used to calculate the corresponding feature vector for the center voxel in the cubic. For each positive or negative voxel sample, 22 different image features were generated. Both positive and negative data are prepared in the same way. ELM classifiers are subsequently trained using these samples.

C. Tumor detection

Two-class ELM training and testing: In tumor detection with cross-validation, the ELM is trained with training samples from two classes i.e., tumor and non-tumor, of which the ground truth data are annotated by clinicians. We have CT data from 7 patients, total 20 tumors. In cross validation, one of the patient CT data is excluded while the rest patients' CT data are used for the two-class ELM training. In testing, automatic tumor detection using the ELM is applied to the patient's CT. All detection results will be summarized (as in Table 1).

One-class ELM for tumor detection: For each patient, only healthy liver voxels are randomly selected from his/her CT data as the normal liver class. Hopefully it can characterize the healthy liver voxels effectively so at the same time it is able to detect lesion voxels, i.e., tumors as abnormal ones. As we have no tumor samples for training, the performance of tumor segmentation may degrade, compared to two-class ELM. But it could be useful to detect tumors that may not fulfill the features of the trained tumors. Although the training dataset is incomplete, the work shown here proves that the learnt one-class ELM is capable of detecting most of the tumors. We have tested the tumor detection using conventional ELM and kernel ELM for one-class classifier training. Results show that kernel ELM performs better in characterizing the healthy liver voxel. Consequently, it detects more tumors without increasing the false positive errors.

ELM was designed for two class classification and regression. However when only one class data is used for ELM training, we show that it can be considered as a one-class classifier. By examining Equation (1) and (2), we see that f(x) is the least mean square solution for given input g(x) and **T**. Let's assume t_j=1, which means only one class data is used for training. The result **β** becomes a linear approximation mapping g(·) to **T**. In geometry, it is a hyper plane approximation. Then it can be shown that the difference |f(x)-1| is the distance of any point (a sample, in either class) to the hyper plane constructed by the ELM. Thus if the hyper plane can be used to represent one class, any point away from the plane will indicate that it is not in the same class, which means we can use it to detect novelty.

In the original ELM, as it is only a linear transformation, the one-class mapping is not represented accurately using the hyper plane. The detection result is thus not satisfying. With the kernel transform [10] the data is mapped to a higher dimension space, similar to many other kernel methods, the two-class data are actually separated. By measuring the distance |f(x)-1|, it shows that the ELM is able to detect tumor based on the one-class training.

D. Tumor segmentation

Tumor segmentation extracts the boundary of a tumor, which is useful for tumor volume estimation, tumor diagnosis, treatment and prognosis.

Fully automatic tumor detection method using generic features and ELM classifier cannot achieve satisfied segmentation results. The boundary is far from accurate although most of the tumors can be detected because part of their voxels can be detected as tumors. In this paper we propose an alternative approach to semi-automatic tumor segmentation. Instead of using 3D propagation of segmentation [7], we apply the tumor sampling in 3D space and increase the feature representation of the voxels. With the scheme, we reduce the user intervention without the requirement of resampling and retraining at some slices in the 3D propagation step [7].

Cross the experiments, we found that the regularization parameter λ in (4) is not very sensitive. In our experiments, the regularization parameter is given as λ =1. We use Gaussian kernel with γ=100.

IV. RESULTS AND DISCUSSION

We use the sensitivity (S) and false positive (FP) error to measure the performance of tumor detection. To measure the segmentation performance, the metrics proposed in [15] are used: Volume Overlapped (VO), Volume Difference (VD), Average Symmetric Surface Distance (ASD) and Root Mean Square Symmetric Surface Distance (RMSD) and Maximum Surface Distance (MSD).

Fig. 1 shows tumor detection results by one-class ELM. The corresponding ELM output of the image is shown in the second row. It can be seen that with a proper threshold (the distance to the hyperplane), the tumors can be detected.
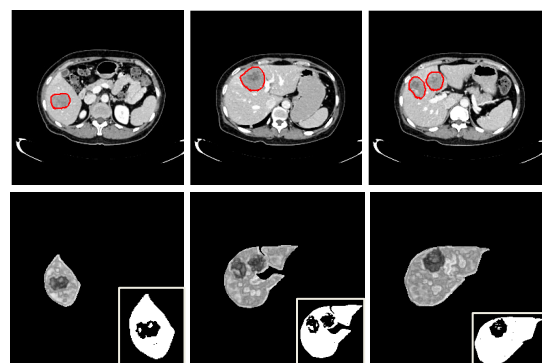

Fig. 1. Tumor Detection using One-Class Kernel ELM. Top row shows the original CTs with ground truth tumor labels. Bottom is the ELM map and the detection results.

Fig. 2 shows some of the detection results using cross-validation. The detection (in green contour) is superimposed to the original CT image, with the tumor ground truth in red.
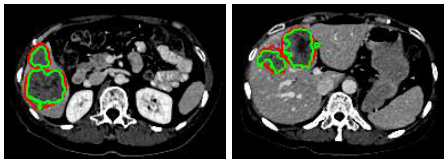
Fig. 2. Images with tumor detection using two-class kernel based ELM.

To show the overall performance, we plot the figure of FP-S for both one-class and two-class kernel based ELM tumor detection results (Fig. 3). From the figure we can see that although two-class detection performs better, one-class ELM provides a way for tumor detection which does not need the tumor samples. Further test shows that one-class ELM can only be properly trained using kernel ELM. It outperforms the conventional ELM in one-class tumor detection as the output for the later is not able to distinguish the tumor and non-tumor voxels.
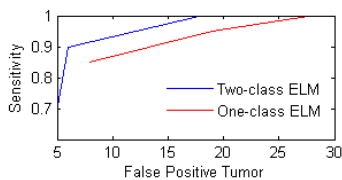

Fig. 3. ROC curves for tumor detection by kernel based ELM.

Given a detected tumor, we can further applied the semi-automatic tumor segmentation method based on the kernel ELM by selecting the training samples from 3D views per tumor. The table below summarizes the result over all the tumors. Fig. 4 shows some segmentation results (green) using two-class ELM overlapped with ground truth (red) of tumors. The poorly segmented tumors are mainly those with voxels that look like vessels (white voxels in the tumor).

Table 1. Metrics of tumor segmentation by two-class ELM.

Metrics	VO (%)	VD (%)	ASD (mm)	RMSD (mm)	MSD (mm)
mean	67.15	14.16	2.27	2.47	8.46
max	85.72	50.39	11.92	12.35	20.62
min	20.49	1.36	0.98	1.03	3.5

The mean VO of tumor segmentation is 67.15%. The improvement over traditional ELM in mean VO is 5%. Compared with [7], the performance degrades slightly. One possible reason is due to that the algorithm used here does not involve further user interaction to correct any poorly performed segmentation for each slice. The advantage is that our method does not need to supervise the segmentation slice by slice.

V. CONCLUSION

We have proposed approaches to automatic liver tumor detection and semi-automatic segmentation from CT scans using the kernel based Extreme Learning Machine. We also investigated different methods for the detection. We have showed that the method proposed has a promising segmentation and detection performance. Due to the nature of ELM, the training speed is very fast. In tumor detection, we proposed to adopt the ELM as one class learning machine. We showed that the mapping function f(x) is a specific regression function that approximates a hyper plane in the

high dimensional space mapped by ELM. The distance between f(x) and the label indicates the class type. The one-class ELM shows that it is possible to detect tumors even there is no tumor data for training. We have also compared the performance of one class tumor detection and two-class ELM using cross validation detection. The latter showed a relatively higher accuracy due to more tumor information available. The advantage of one-class ELM is that it could serve as a preliminary detection scheme, particularly in the case some unknown or new tumor is not well trained or represented by a two-class classifier.
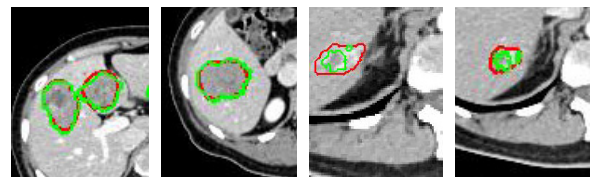

Fig. 4. Tumor segmentation result. Left two show the good segmentation. Right two shows the results of the tumors that have 'vessel' like voxels.

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