A Machine Learning Approach for Locating Boundaries of Liver Tumors in CT Images

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Abstract

In this paper, we propose a novel machine learning approach for locating boundaries of liver tumors in CT (Computed Tomography) images. Given a marker indicating a rough location of a tumor, the proposed solution locates its boundary. Our approach consists of training process and locating process. In training process, we train AdaBoosted histogram classifiers to classify true boundary positions and false ones on the 1-D intensity profiles of tumor regions. In locating process, we locate the boundaries by using the trained AdaBoosted histogram classifiers. The novelty of our approach is that we use AdaBoost in the training process to learn diverse intensity distributions of the tumor regions, and utilize the trained results successfully in locating process. Experimental results show our approach locates the boundaries successfully, despite the diverse intensity distributions of the tumor regions, marker location variability and tumor region shape variability. Our framework is also generic and can be applied for locating boundaries of blob-like targets with diverse intensity distributions in other applications.

1. Introduction

Liver cancer is one of the most common malignancies in the world, with approximately 1,000,000 cases reported every year [1]. X-ray computed tomography (CT) is one of sensitive imaging domains for the liver tumor analysis. The helical CT scanners greatly improved image resolution. The improved image resolution indeed helps radiologists to detect tumors more accurately. However, it also costs them more burdens because of increasing the amount of data they need to interpret. Thus, automation of the analysis with computer-assisted systems is much needed for reducing the burdens.

The goal of this paper is to locate the boundaries of liver tumors in CT images automatically based on a given marker indicating the rough position. Examples of tumor region images and their 1-D intensity profiles used in our experiments are shown in Fig. 1. If we locate the boundaries successfully, we can easily derive the information, which the radiologists need to interpret, such as tumor size, shape and intensity variance.

Snakes [2] and ASM (Active Shape Model) [3] are widely used in medical image segmentation [4][5]. The basic idea of snakes is to evolve a contour, by shrinking or expanding it to minimize the weighted sum of internal energy and potential energy. The internal energy specifies the smoothness of the contour, and the potential energy specifies image intensity edges occurring at object boundaries. Because the intensity distributions of different tumors vary from each other largely, shown in Fig.1, it is very difficult to find a proper function representing the potential energy. In ASM, researchers use statistical shape models and local appearance models of landmarks to locate object boundaries. Because shapes of liver tumors are irregular and meaningful landmarks cannot be defined, ASM is inadequate to be used.

In this paper, we propose a novel approach to locate boundaries of liver tumors automatically and robustly. To cope with the diverse intensity distributions of the liver tumors, we use AdaBoost to learn the 1-D intensity distributions of tumors. AdaBoost is a widely used machine learning method in face detection [6][7]. Here, we use AdaBoost to train AdaBoosted histogram classifiers [8] to classify true boundary positions and false ones on the 1-D intensity profiles. Then, we locate the boundaries in polar coordinate by using the trained classifiers.

2. Approach

Our approach consists of training process and locating process. In training process, we train AdaBoosted histogram classifiers to classify true boundary positions and false ones on the 1-D intensity profiles. In locating process, there are 3 processing steps. Firstly, we transform a tumor ROI (Region Of Interest) to polar coordinate. Then, we calculate the score image in polar coordinate by using the trained AdaBoosted histogram classifiers. Finally, we locate the tumor boundary by DP and transform it back to XY coordinate.

Proceedings of the 18th International Conference on Pattern Recognition (ICPR'06)
0-7695-2521-0/06 $20.00 © 2006 IEEE

2.1. Training AdaBoosted histogram classifiers

To robustly locate tumor boundaries with diverse intensity distributions, we train AdaBoosted histogram classifiers by using 1-D intensity profiles as training samples. This is similar to the method described in [8]. Firstly, we label true boundary positions on tumor regions, such as the red "+"s shown in Fig. 1. Then, we train the AdaBoosted histogram classifiers by the following steps. Intensity profile length and quantization value are determined empirically. To each labeled 1-D profile,

① Derive 1-D profiles just at the manually labeled positions from the training images as positive training samples.

② Derive 1-D profiles at positions apart from the manually labeled positions from the training images as negative training samples.

③ Normalize the length of the positive and negative samples to 20.

④ To each profile, calculate its intensity variance and quantize the intensities of the profile to 5 levels based on the intensity variance. The reason that we base on the intensity variance to quantize is to make our algorithm robust to different contrasts of different tumor regions.

⑤ Make histogram classifiers based on quantized value combinations at 3 different positions of quantized profiles. Number of bins of each histogram is 5^3.

⑥ Train theses histogram classifiers based on the training samples by using AdaBoost.

In step ⑥, let training samples be $(x_1, y_1),(x_2, y_2),...,(x_N, y_N)$, where x_i is the training sample and y_i is the label for the sample (+1 for positive samples and –1 for negative samples). The AdaBoost algorithm trains weak histogram classifiers $f_m(x)$ so that the sum $F_M = \sum_{m=1}^{M} f_m(x)$ will have high classification accuracy. To archive this, we have to optimize the following objective function:

$$J(F(x)) = \sum_i e^{-y_i F(x_i)} \tag{1}$$

We minimize (1) by adding new histogram weak classifiers one at a time. Given the current classifier $F_{M-1} = \sum_{m=1}^{M-1} f_m(x)$, the new classifier $f_M(x)$ is chosen as:

$$f_M(x) = \arg\min_f J(F_{M-1}(x) + f(x)) \tag{2}$$

It can be shown that the minimizer is

$$f_M(x) = \frac{1}{2}\ln\frac{P(y=+1 \mid x, w^{M-1})}{P(y=-1 \mid x, w^{M-1})} \tag{3}$$

where w^{M-1} are the weights given at time M and updated by using the following function:

$$w^M = w^{M-1} e^{-y f_M(x)} \tag{4}$$

The final function is $F(x) = \mathrm{sgn}\left(\sum_{m=1}^{M} f_m(x)\right)$, which should be positive for positive samples and negative for negative samples.

2.2. Locating tumor boundaries

Since diameters of tumor regions differ from 5 pixels to 100 pixels and the length of 1-D profiles for training is fixed, we locate tumor boundaries on the pyramid images of different scales derived from an original image. The following in this section only describes the process on one scale. After we get one boundary from every scale, we select the boundary with the highest cumulative score as output. An illustration of locating process is shown in Fig. 2.

2.2.1. Transforming ROI to polar coordinate

To avoid troublesome coordinate transformations, we transform the ROI of a tumor to polar coordinate, where the center position is the given location of the marker. The size of the transformed polar image is 32x50 pixels, whose X-axis represents angle information ranging from 0 to 360 degree.

2.2.2. Calculating boundary-like scores

We use formula (5) to calculate a boundary-like score on every pixel of the polar image, where the trained AdaBoosted histogram classifiers are used. A higher boundary-like score shows higher possibility that the location is on a tumor boundary.

$$s(x,y) = \sum_{i=1}^{32} \max_j \left(AdaS((x,y),(i,j))\right) \tag{5}$$
$$i \neq x, \quad j = 1,...,36$$

$$AdaS((x,y),(i,j)) = \begin{cases} if \quad \sum_{m=1}^{M} f(p((x,y),(i,j))) > 0, \\ \qquad \sum_{m=1}^{M} f(p((x,y),(i,j))) \\ else \quad 0 \end{cases} \tag{6}$$

(x,y) and (i,j) are coordinates of 2 positions of polar image. $p((x,y),(i,j))$ is a "combined" profile of (x,y) and (i,j). The relationship among (x,y), (i,j) and the given marker location in XY coordinate is shown in Fig. 3, and $p((x,y),(i,j))$ is combined by the two half intensity profiles shown by the two black lines intersecting at the maker location.

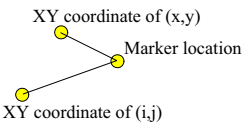

Fig. 3 An illustration of $p((x,y),(i,j))$ in XY coordinate.

$\sum_{m=1}^{M} f(p((x,y),(i,j)))$ is the AdaBoost score of $p((x,y),(i,j))$ calculated by the following 3 steps.

① Normalize the length of the profile to 20.
② Apply the same quantization in training to the profile.
③ Calculate its AdaBoost score by using the AdaBoosted histogram classifiers based on the quantized intensities.

In formula (6), if the score is lower than 0, which means that the profile is not on the boundary, we set the AdaBoost score $AdaS((x,y),(i,j))$ to 0.

The most important thing of calculating the boundary-like score is how to use the classifiers trained based on 1-D intensity profiles to locate the boundary of a 2-D tumor region. We successfully solved this problem in formula (5). If both (x,y) and (i,j) are on the tumor boundary, the AdaBoost score $AdaS((x,y),(i,j))$ should be a high positive value. Since the intensity distributions of the 1-D profiles are independent of the angles (X-axis coordinate in the polar image), we calculate $\max_j(AdaS((x,y),(i,j)))$ at different angles by changing the value of *i* and then sum them up. Because there should be a boundary location at every column of the polar image, if (x,y) is on the tumor boundary, the boundary-like $s(x,y)$ should be a high positive value.

2.2.3. Locate tumor boundary by DP

The maximal score path through the score image obtained in 2.2.2 can be easily selected by DP (Dynamic Programming) as:

$$Su(0,y) = s(0,y)$$
$$Su(x+1,y) = \max_{-2\le k\le 2} Su(x,y+k) + s(x+1,y) \quad (7)$$

Firstly, we calculate cumulative scores using formula (7). To prevent the boundaries from bending too much, we set the range of parameter *k* from *–2* to *2*. Then, we trace back and find the path of the maximal score. Finally, we transform the polar coordinates of this path to the XY coordinates, and use it as the tumor boundary at the scale where the ROI image was obtained.

3. Experimental results

In our experiments, we used 30 liver tumor region images as training images, and 30 liver tumor region images as test images. Test results show that our approach works well, despite the diverse intensity distributions of the tumor regions, marker location variability and tumor region shape variability. Some located boundaries are show in Fig. 4. Average process time for locating one tumor boundary is about 1.2 seconds without any optimization to speedup, using Pentium 2.4GHz CPU.

4. Conclusion

This paper proposed a robust machine learning approach to locate boundaries of liver tumors in CT images. There are two contributions in this work. The first is that we introduced the AdaBoost learning to classify true boundary positions and false ones on the 1-D intensity profiles. The second is that we successfully solved the problem of how to locate a 2-D tumor boundary by the classifiers trained based on 1-D profiles. Our approach is also generic. Because machine learning is used, we can apply it to other applications easily. In future, we will apply our approach to locate pulmonary nodules and brain tumors.

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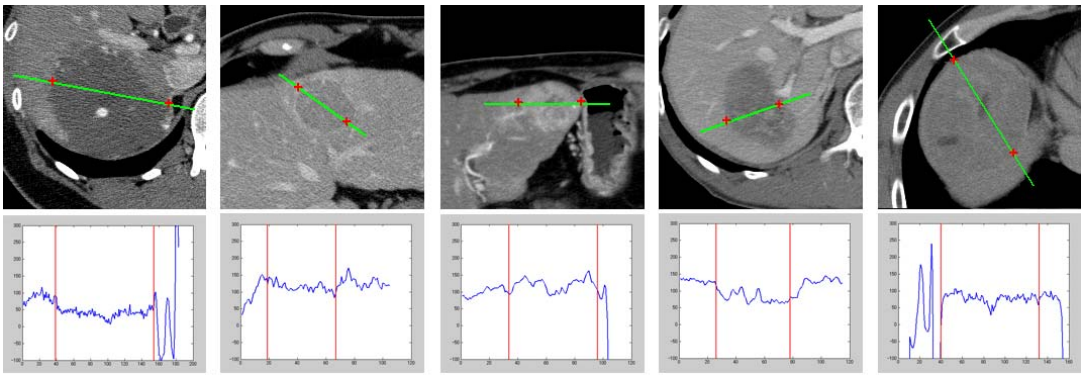

Fig. 1 An illustration of liver tumor examples. Upper row: liver tumors. Lower row: 1-D intensity distributions of the green line shown in upper row, red lines showing the positions of red "+"shown in upper row.

Fig. 2 An illustration of locating process. (a): ROI of a tumor, (b): ROI in polar coordinate, (c): score image obtained by using Trained AdaBoosted histogram classifiers, (d): located boundary in polar coordinate, (e): located boundary in XY coordinate. Green "+"s show the position of the given marker.

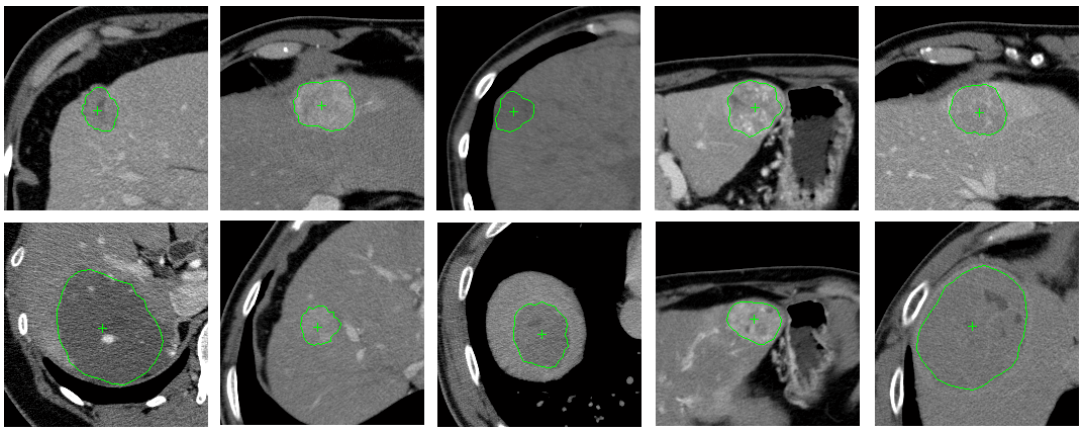

Fig. 4 Experimental results. Green "+"s show the position of the given marker.