An Auto-Contouring Method for Kidney based on SVM

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Abstract. In adaptive radiotherapy planning, the contour map of the treatment target area is still the most difficult problem. Usually this work is done by a professional radiologist oncologist, which is very time-consuming and labor-intensive. In order to solve this problem, this paper proposes an automatic contour method based on support vector machine. Experiments were conducted on the lower abdomen MR data set of eight patients. In the experiment, the simulated data was only used to train the classifier, and the treatment day images were used to evaluate the performance of the classifier. DSI was used to compare the manual contour and automatic contour of the kidney. The experiment showed that, The automatic contour method based on support vector machine has better classification performance than most classification algorithms. Among the eight sets of results, the DSI value of the six sets of results is 1, and the smallest DSI value is also greater than 9.423.

1. Introduction

With the maturity and continuous progress of radiotherapy technology, radiotherapy tends to be more precise. Clinically, due to better target dose conformity, tumors can obtain higher doses while ensuring low doses for normal tissues. Anatomical changes during radiotherapy include tumor size reduction, weight loss, and muscle shape changes. These changes may cause important organs to move into high-dose areas and tumor target areas to move out of high-dose areas, resulting in insufficient target areas and excess organs at risk (OARS) [1], ultimately leading to a decrease in the local tumor control rate and an increase in the incidence of complications.

The emergence of adaptive radiation therapy is to solve this problem. Adaptive radiation therapy (ART) is a self-responsive, self-correcting dynamic closed-loop system from diagnosis positioning, planning design, treatment implementation to verification. ART uses image-guided radiation technology (IGRT) to evaluate patient anatomical and physiological changes, or feedback information during treatment such as tumor size, shape, and position changes, and analyze the difference between fractional treatment and the initial plan design [2]. So as to guide the redesign of the subsequent fractionated treatment plan. ART aims to improve the accuracy of tumor radiotherapy, achieve high-dose irradiation to the tumor target area, and maximize the protection of surrounding normal tissues. In this way, the local control rate of the tumor is increased while the probability of radiological complications is reduced.
During the radiotherapy process, the radiotherapy plan is constantly changed as the tumor shrinks. Generally, the radiotherapy plan is re-designed according to the tumor situation every week or every day. During this period, the imaging needs to be automatically loaded online, and the radiotherapy plan is automatically generated [3].

The drawing of the radiation position contour is still the most important part of ART. Although the manual contour drawn by an experienced expert is more accurate, it has great variability and non-reproducibility. At present, manual contours are mainly used to evaluate the segmentation performance of self-contouring methods. It is very meaningful to develop an automatic contouring algorithm. This article will use voxel-based features and support vector machines (SVM) for a priori knowledge of MRI. The image data set is automatically contour drawn, and the difference between SVM and other algorithms is compared.

2. Related work

2.1. Introduction to the data set

The data set used in the experiment is the image data of the lower abdomen of 8 patients with unresectable abdominal malignant tumors collected by professional doctors. The data sets of the 8 patients are represented as sub1~8. For each piece of data, extract the voxel values and 3D position coordinates of its four MR sequences, and combine the two for classification.

2.2. Data preprocessing

In order to further improve the separability of the data, we use Kalman filter to improve the dimensionality of the data. Kalman filter [4] is an algorithm that uses the linear equation of state and the observation data of the system to optimize the estimation of the system state. We can use Kalman filter in any dynamic system with uncertain information to make an educated prediction for the next step of the system. Even with interference, Kalman filtering can always point out what actually happened.

2.3. Main method

We mainly use the automatic contour algorithm based on SVM in the experiment. For SVM, we can describe it as:

Given a training set $T = \{(x_1,y_1),(x_2,y_2),\ldots,(x_N,y_N)\}$, where $x_i \in \mathbb{R}^n$, $y_i \in \{1, -1\}$

The conventional dual form of SVM formula can be expressed as:

$$\min_{\alpha} \frac{1}{2} \sum_{i=1}^{N} \sum_{j=1}^{N} \alpha_i \alpha_j y_i y_j K(x_i,x_j) - \sum_{i=1}^{N} \alpha_i$$

s.t. $\sum_{i=1}^{N} \alpha_i y_i = 0$

$0 \leq \alpha_i \leq C, \quad i = 1, 2, \ldots, N$ (1)

Where $\alpha$ is the Lagrange multiplier, $y_i \in \{1, -1\}$ is the label of $x_i$, $k$ is a $N \times N$ matrix and $k(\cdot, \cdot)$ is the kernel function, $C$ is an appropriate parameter.

Equation (1) is a quadratic programming problem, and its optimal solution can be obtained. Through its optimal solution $\alpha^*$ it can be calculated $b^*$.

$$b^* = y_j - \sum_{i=1}^{N} \alpha^*_i y_i k(x_i, x_j)$$ (2)

Then, the final classification decision function of the support vector machine can be expressed as:

$$f(x) = \text{sign}\left(\sum_{i=1}^{N} \alpha^*_i y_i k(x, x_i) + b^*\right)$$ (3)
3. Experimental details

All experiments in this article are run on a computer with Intel(R) Core(TM)i5-8500 CPUX 3.00GHz, 12GB memory and 64-bit Windows10 operating system. The simulated data is used to train the model, and the treatment day data is used to test the classification effect of the model. We divide the kidney area into the first type of data, and the organs and skin other than the kidney are defined as the second type of data. SVM is used to train this second classification model. The typical calculation time using the SVM training phase is about 3 seconds. Due to the limitation of the experimental equipment, on the trained classification model, the average segmentation time of the treatment day image in the daily processing process is about 1 minute.

3.1. Evaluation index

This article uses dice similarity index (DSI) [5] to evaluate our image segmentation effect, and DSI uses Dice distance to calculate the similarity of two contours. Dice distance is mainly used to calculate the similarity of two sets. It has been widely used in various medical segmentation algorithms. The Dice coefficient is defined as follows:

\[ s = \frac{2|A \cap B|}{|A| + |B|} \] (4)

Where A and B are the two sets we use to compare, we compare the contour generated by the algorithm with the manual contour drawn by a professional doctor. Value of 1 means that the manual contour and the contour generated by the algorithm completely overlap.

3.2. Experimental comparison

In order to compare the performance of the SVM method on this data set, we have selected 7 methods that can be used for classification for comparative experiments, which are the linear discriminant analysis (LDA) [6] and the quadratic discriminant analysis (QDA) [7] that are commonly used in classification problems, and the semi-supervised SVM algorithm TSVM [8] and S4VM [9], random subspace (RSM)[10] for integrated learning, naive Bayes (NB)[11], radial basis neural network (RBF)[12]. All experiments are in the same data set, and the respective algorithm parameters are adjusted to the best.

3.3. Analysis of results

Generally speaking, in medical segmentation algorithms, only DSI value greater than 0.7 is acceptable. The table 1 shows the DSI value when inputting the same image data of treatment day on eight well-trained classifiers, first of all, you can see that the DSI values of RSM and LDA are basically based on 0.3, indicating that these two algorithms have poor segmentation effects on this data set. S4VM, TSVM, RBF and NB have large numerical fluctuations. The performance of these four algorithms fluctuates greatly between different samples. The full Range is respectively 0.1924, 0.4719, 0.270, 0.2107.

SVM and QDA are the two best-performing algorithms, especially SVM. The minimum value of DSI has reached 0.9423±0.0127. Six of the eight patients achieved complete overlap of automatic and manual contours. Although QDA has a high DSI value, none of the eight patients has a DSI value of 1, and we can compare the automatic contours generated by SVM and QDA on the same MR abdominal cross-sectional image, through the Figure 1 can be seen that the automatic contour generated based on SVM is completely overlapped, while the automatic contour generated based on QDA is circled, but there are still some wrong points on the kidney.

Table 1. Average Dice similarity index (DSI) for kidneys using the Classification algorithms.

| Datasets   | SVM     | LDA     | S4VM    | QDA     |
|------------|---------|---------|---------|---------|
| Enter as part of a complete treatment day image |         |         |         |         |
| Datasets | RSM       | TSVM      | NB        | RBF      |
|----------|-----------|-----------|-----------|----------|
| Sub1     | 0.2157±0.0021 | 0.4267±0.0153 | 0.7510±0.0189 | 0.5976±0.0213 |
| Sub2     | 0.3078±0.0012 | 0.6127±0.0483  | 0.8298±0.0220 | 0.6624±0.0176 |
| Sub3     | 0.1724±0.0031 | 0.6925±0.0221  | 0.8528±0.0176 | 0.6768±0.0229 |
| Sub4     | 0.2226±0.0012 | 0.8986±0.0318  | 0.9220±0.0304 | 0.7633±0.0318 |
| Sub5     | 0.1862±0.0016 | 0.8318±0.0430  | 0.9111±0.019  | 0.7796±0.0174 |
| Sub6     | 0.2543±0.0021 | 0.6811±0.0194  | 0.8363±0.0343 | 0.6717±0.0312 |
| Sub7     | 0.2784±0.0011 | 0.5653±0.0236  | 0.8968±0.0308 | 0.6602±0.0158 |
| Sub8     | 0.1748±0.0016 | 0.7168±0.0297  | 0.7113±0.0352 | 0.8681±0.0153 |

Figure 1. MR images of the lower abdomen under four conditions, four MR images of the lower abdomen, original image (A), manual circle drawing (B), automatic contour based on SVM (C), automatic contour based on QDA (D). In the automatic contour based on QDA, there are wrong points in the left kidney (a)

4. Conclusion
In this article, we use an automatic contour algorithm based on SVM to draw the contour of the kidney. The experimental results show that the SVM algorithm has a very good classification performance for lower abdomen MR data. Future research can be further explored, such as using deep learning to extract features, using Multiple Kernel Learning (MKL) [13] to further improve classification performance, and verifying in different data sets.

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