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Group sparse reconstruction for image segmentation

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ABSTRACT

Image segmentation is a fundamental problem in computer vision and image analysis. Specially, the segmentation of medical images can assist doctors in making decisions. Due to the lack of distinctive features to describe the boundary of an organ and match function with high performance for features, medical image segmentation is difficult to be achieved with high accuracy. In this paper, an one-class classifier is proposed as the match function to decide whether the pixel belongs to the boundary or not. The proposed method is comprised of two steps. At first, a feature vector space is built with the gradient feature and its statistical information in the training stage. In the test image, a feature vector of one candidate probably being located on the boundary is reconstructed by sparse coding with the feature vector space. After reconstruction, the candidate is classified belonging to boundary or non-boundary via the reconstruction based one-class classifier. Then, in order to maintain the consistency between the candidates which are neighbors to each other, the neighboring candidates are coded using group lasso with the same dictionary. Compared to the traditional methods, the proposed one has three advantages. Firstly, it solves the non-Gaussian distribution problem of the positive samples. Secondly, it avoids large variation among the negative samples. Thirdly, the relationship of the neighboring candidates is considered and used in classification, which is ignored in other methods. The proposed method is validated on 52 MR images of prostate and outperforms Mahalanobis distance, which is considered as one of the state-of-the-art match functions. The experimental results show that the segmentation accuracy can be significantly improved by the proposed method with one-class classification.

1. Introduction

Image segmentation plays an important role in computer vision and image analysis [1–4]. It serves as the assistance to many tasks such as object recognition [5] and image understanding [6,7], especially in medical images [8–10]. The segmentation of medical images can be helpful to the diagnosis and surgical planning of the disease [11], *e.g.*, prostate cancer [12–14].

The external beam radiotherapy for the prostate cancer has evolved tremendously. In radiotherapy planning, the goal is to treat the prostate a high radiation dose while minimizing the dose to its surrounding tissues, *e.g.*, the bladder and the rectum [15]. To achieve this goal, the accurate delineation of the prostate is an important task and therefore in urgent need. With the techniques of computer vision and machine learning, the prostate can be segmented automatically and accurately to alleviate the burdensome work and inter-observer variations for the doctors or the experts.

With the increasing medical imaging modalities, several methods have been employed to segment the medical images [16], including the *statistical shape model* (SSM) [17], *Markov random field* models (MRF) [18], and atlas-guided approaches [19]. Due to the incorporation of the prior knowledge and the generation of the plausible shapes limited in the training shape space (see Fig. 1), SSM based methods have been widely used in medical image segmentation. In Fig. 1, the principal modes of variation for an SSM of the prostate are shown. The blue and the red dashed lines are the mean shape and the deformed shape with principal modes of variation, respectively.

Active shape model (ASM) [20], as one of the SSM based methods [21], has performed well in medical image segmentation. In ASM, the shape prior is learned from a collection of training images, which are the MR images of the prostate in our work. The shape prior is comprised of the mean shape and the shape variation when *principal component analysis* (PCA) is used to train the shape model. After constructing the shape model, the image appearance model is employed to guide the shape deformation. For ASM, the image appearance model is based on the normalized first order derivative profiles and the Mahalanobis distance, which measures the distance between the testing profile and the training

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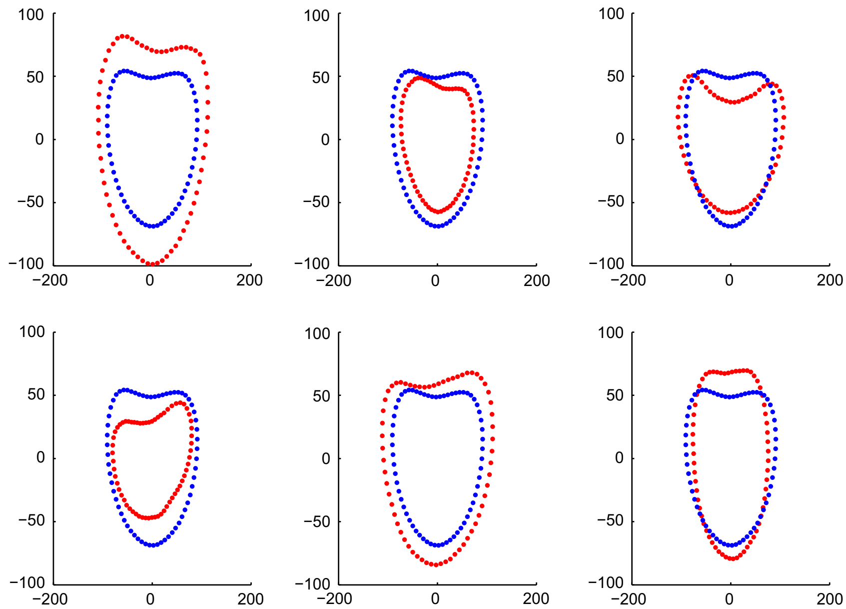

Fig. 1. Principal modes of variation for an SSM of the prostate: The left column shows the variation of the largest eigenmode between $\pm 3\sqrt{\lambda_1}$, the medium and the right columns show the variation of the second and the third largest eigenmode, respectively.

profiles. The image appearance model assumes that the normalized first derivative profiles is of Gaussian distribution. However, the assumption does not always hold.

To be more general, van Ginneken et al. [22] proposed to employ a nonlinear *k-nearest neighbors* (*k* NN) classifier to compute the displacement for each landmark during optimization. The *k* NN classifier with weighted voting replaces the Mahalanobis distance for the segmentation of several types of data. In the works of [23,24], the true and false boundary examples are sampled and then weak classifiers are trained. Probabilistic boosting trees are employed to combine them into a strong classifier. With the classifier for boundary detection but not in SSM framework, Gao et al. [25] proposed a *sparse representation based classifier* (SRC) to determine whether the test sample is the object. The SRC is used to segment prostate from *computed tomography* (CT) images. High-quality image segmentation increasingly relies on the boundary detection [26,27].

In [23–25], both the positive and the negative samples are required from training images. Based on the positive and the negative samples, a two-class classifier is trained to determine whether a pixel belongs to the object (or belongs to the boundary in the boundary-detection methods) or not. However, when the negative samples vary enormously and share little characteristics, two-class classification for segmentation does not work well. In medical images, it always occurs when the texture of the organ is complex. In Fig. 2, crosses and asterisks denote the positive and the negative samples, respectively. The negative samples are represented with different colors showing large variation among them. The classifier is difficult to learn to distinguish the positive samples from the negative samples.

In order to solve the problem of large variation among the negative samples, the one-class classification is proposed as the match function in this paper. When one sample is reconstructed by the positive samples with large reconstruction error, the one-class classifier detects it as an outlier. In addition, the threshold is not required in decision-making for the reason that the target position is based on searching. In the searching process, a set of candidates is assessed and one candidate is selected by comparing their reconstruction error based on the one-class classifier.

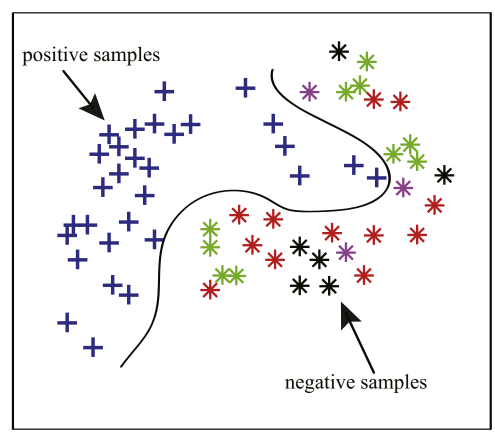

Fig. 2. Crosses and asterisks represent the positive and the negative samples, respectively. The points of negative samples are represented by asterisks, which mean that the negative samples show large variation in some cases.

In our work, one-class classification [28] is proposed for the segmentation of the prostate. The reconstruction method in one-class classification is selected and the reconstruction error indicates the probability that the pixel is located on the boundary. When computing the reconstruction error, the reconstruction weights are given using sparse coding. In order to maintain the consistency between the candidates which are neighbors to each other, the candidates probably being located on the boundary can be coded using *group lasso* [29,30] with the same dictionary. The theory is that the representations of the neighboring pixels by one dictionary should be similar. In the experiments, the proposed method is evaluated on 52 MR images of prostate. The segmentation results show that the proposed method outperforms the Mahalanobis distance, which is considered as one of the state-of-the-arts when constructing the image appearance model.

There are three contributions in our work. Firstly, it solves the non-Gaussian distribution problem of the positive samples. Secondly, it avoids large variation among the negative samples.