

An Interactive X-Ray Image Segmentation Technique for Bone Extraction

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Abstract. Image segmentation plays a fundamental role in many medical imaging applications by facilitating the contouring of the regions of interest. In this paper, we propose an accurate interactive method which combines two image segmentation techniques. In the first step, a mean shift segmentation algorithm is used for initial segmentation, followed by an adaptive region merging process based on the maximal similarity between regions, in the second step. The proposed method is tested on a set of real X-ray images and the goal is to separate the bones from the rest of the image. The experimental results on real X-rays show that the proposed segmentation algorithm is highly effective, since it has the ability to extract the contour of the desired objects from the image.

Keywords: Biomedical imaging, digital images, X-Ray Bone Segmentation, radiography

1 Introduction

During the recent years, much attention has been focused on medical imaging due to the appearance of less invasive and more accurate medical devices. Modern medical imaging offers the potential and promise for major advances in science and medicine, as higher fidelity images are produced. Digital images are more and more used by medical practitioners to help them during the disease diagnosis and decision making process, because they display various body organs. There are several imaging technologies used in radiology to diagnose or treat diseases: X-ray radiography, ultrasound, computed tomography (CT), nuclear medicine and magnetic resonance imaging (MRI). X-ray images (radiographs) represent one of the oldest and more frequently used noninvasive medical tests that help physicians during various stages of treatment, including fracture diagnosis, skeletal maturation evaluation, hip replacement surgery, or other bone diseases.

Imaging science has expanded primarily along three distinct, but related lines of investigation: segmentation, registration and visualization [2]. One of the major challenges in medical imaging is the segmentation process, one of the most common operations in image processing. Segmentation allows the partitioning of

an image into regions with cohesive properties. Medical image segmentation is a fundamental problem in image processing and computer vision. Segmentation algorithms play a vital role in many biomedical-imaging applications, such as diagnosis and treatment planning, localization of pathology, study of anatomical structure, and computer-integrated surgery [1]. However, most of the existing articles on medical image segmentation are focused on CT and MRI and less on the segmentation of X-ray images. X-Ray image segmentation techniques are treated in [3], [4], [5], [6]. The goal in these papers is the segmentation of bone structures from the X-ray images. This task is considered challenging because this type of images are complex in nature since the regions delineated by bone contours are highly nonuniform in intensity and texture. Therefore, classical segmentation algorithms such as thresholding, clustering, region growing, watershed, classifiers, etc are not applicable because they rely on region homogeneity criteria. Deformable models (snakes, level set based models, or active shape models) can be used for X-ray image segmentation as well, but they require a good initialization of the model contour and thus, may incorrectly segment the regions. An interesting solution is to combine two or more segmentation techniques.

In this paper, we aim to segment X-ray images in order to separate the bones from the rest of the image. The proposed method automatically merges the regions that are initially segmented using the mean shift algorithm. After the merging process ends, the object of interest (the bone structure) will be extracted from the background. This method has been proposed in [7] for color image segmentation. In this paper, we adapted this method for X-ray images.

2 Segmentation scheme

A large amount of literature in the medical image analysis research domain is dedicated to the segmentation topic. Some of segmentation techniques have achieved an extraordinary success and have become popular in a wide range of applications. However, it is difficult to decide which approach is the best for a particular segmentation task. Classical image segmentation algorithms including thresholding, edge detection, or region based techniques can solve only simple medical image segmentation problems, since they are sensitive to noise or may have over-segmentation tendency.

In this paper, we will use a segmentation method based on the mean-shift algorithm and region merging. The segmentation scenario implies the following steps [8]:

1. Use an initial segmentation method to split the entire image region, R , into smaller regions, $R_i, i = 1 \dots S$ until that, for any region R_i , $P_r(R_i) = TRUE, i = 1 \dots S$, where P_r is a predicate.
2. Choose a criterion for merging two adjacent regions, R_j and R_k , for which $P_r(R_j \cup R_k) = TRUE$.
3. Merge all the adjacent regions. Stop if no further merging is possible.

There are various low level image segmentation methods that can be used for initial segmentation. However, the mean-shift algorithm is more robust and produces less over segmentation.

2.1 Mean-shift algorithm

Mean-shift algorithm is a powerful clustering procedure that estimates the gradient of a probability density function using a generalized kernel approach. It has been successfully used for image segmentation in [9], [10], and [11].

Being given a set of n points, $x_1 \dots x_n$, in the d -dimensional Euclidean space, the kernel density estimate is defined as:

$$\hat{f}(x) = \frac{1}{nh^d} \sum_{i=1}^n K\left(\frac{x - x_i}{h}\right), \tag{1}$$

where h is the window radius (bandwidth parameter) of the used kernel $K(x)$.

The estimate of the density gradient is defined as the gradient of the kernel density estimate:

$$\hat{\nabla}f(x) = \nabla\hat{f}(x) = \frac{1}{nh^d} \sum_{i=1}^n \nabla K\left(\frac{x - x_i}{h}\right). \tag{2}$$

The kernel $K(x)$ is a function of $\|x\|^2$: $K = c_{k,d}k(\|x\|^2)$. $k(x)$ is called the profile of $K(x)$ and $c_{k,d}$ is a normalization constant, which makes $K(x)$ integrate to one. This class of kernels are called radially symmetric kernels.

The density estimator can be rewritten as:

$$\hat{f}_{h,K}(x) = \frac{c_{k,d}}{nh^d} \sum_{i=1}^n k\left(\left\|\frac{x - x_i}{h}\right\|^2\right), \tag{3}$$

Two commonly used kernels are the multivariate Gaussian kernel:

$$K_G(x) = (2\pi)^{-d/2} e^{-\frac{1}{2}\|x\|^2} \tag{4}$$

and the Epanechnikov kernel:

$$K_E(x) = \begin{cases} \frac{1}{2}c_d^{-1}(d+2)(1-\|x\|^2), & 0 \leq \|x\| \leq 1 \\ 0, & \|x\| > 1 \end{cases} \tag{5}$$

The density gradient estimator of $\hat{f}_{h,K}(x)$ is obtained as:

$$\hat{\nabla}f_{h,K}(x) = \nabla\hat{f}_{h,K}(x) = \frac{2c_{k,d}}{nh^{d+2}} \sum_{i=1}^n (x - x_i)k'\left(\left\|\frac{x - x_i}{h}\right\|^2\right), \tag{6}$$

We denote: $g(x) = -k'(x)$. Using $g(x)$ for profile, the kernel $G(x)$ is defined as:

$$G(x) = c_{k,g} \cdot g \cdot \|x\|^2, \tag{7}$$

where $c_{k,g}$ is a positive constant (the normalization coefficient). The kernel $K(x)$ is called the shadow of $G(x)$. The estimate of the density gradient becomes:

$$\hat{\nabla} f_{h,K}(x) = \frac{2c_{k,d}}{nh^{d+2}} \sum_{i=1}^n g\left\|\frac{x-x_i}{h}\right\|^2 \frac{\sum_{i=1}^n g\left(\left\|\frac{x-x_i}{h}\right\|\right)x_i}{\sum_{i=1}^n g\left(\left\|\frac{x-x_i}{h}\right\|\right)} - x, \quad (8)$$

The density estimator computed with the kernel $G(x)$ can be written as:

$$f_{h,G}(x) = \frac{c_{k,g}}{nh^d} \sum_{i=1}^n g\left(\left\|\frac{x-x_i}{h}\right\|\right), \quad (9)$$

The mean shift vector (or sample mean shift) is defined as the difference between the weighted mean using kernel $G(x)$ and x , as the center of the kernel:

$$m(x) = \frac{\sum_{i=1}^n g\left(\left\|\frac{x-x_i}{h}\right\|\right)x_i}{\sum_{i=1}^n g\left(\left\|\frac{x-x_i}{h}\right\|\right)} - x, \quad (10)$$

The mean shift segmentation is an advanced and versatile technique for clustering based segmentation. The parameters of the mean shift segmentation are: the spatial resolution parameter, (σ_r), the range resolution parameter, (σ_s) and M , the size of the smallest segment. The use of the mean-shift algorithm for image segmentation requires the selection of (σ_r) and (σ_s).

2.2 Region merging technique

The initial segmentation produces a number of small regions. In the following, a region growing/merging algorithm [12] is used to merge these small regions to larger ones. Region merging techniques consider two regions to be merged if they are similar and adjacent or connected to each other. The main segmentation criterion in region growing is the homogeneity of regions. The criteria for homogeneity include: gray level, color, texture, shape, model, region size, etc. The region descriptor is compared to the descriptor of an adjacent region. If they match, they are merged into a larger region, if not, the regions are marked as non-matching. The merging process of adjacent regions continues between all neighbors, including newly formed ones. If a region cannot be merged with any of its neighbors, it is marked as "final". The merging process stops when all regions are marked.

Region merging techniques usually work with a statistical test to decide the merging of regions. Some examples of statistical test are the Euclidean distance, the Bhattacharyya coefficient, the Kullback Leibler divergence, or the log-likelihood ratio. Many researchers have used the Bhattacharyya similarity measure and found it advantageous. Bhattacharyya coefficient correlates images using histograms [13] and gives a measure of similarity between the probability density functions of two populations. Being given $p(i)$ and $q(i)$, two multinomial populations of N classes, the Bhattacharyya coefficient is defined as:

$$\rho(p, q) = \sum_{i=1}^N N \sqrt{p(i)q(i)}, \quad (11)$$

where $p(i)$ and $q(i)$ are probability distributions:

$$\sum_{i=1} Np(i) = \sum_{i=1} Nq(i) = 1. \quad (12)$$

The Bhattacharyya measure can be used to compare the similarity between two histograms. If two regions have similar contents, their histograms will be very similar. We consider two regions Q and R . If H_{Q_i} is the normalized histogram of the first region, Q , and H_{R_i} is the normalized histogram of the second region, R , with i representing the i th element of them, $\rho(R, Q)$ is defined as:

$$\rho(R, Q) = \sum_i \sqrt{H_{R_i}} \sqrt{H_{Q_i}}, \quad (13)$$

is a measure of the similarity between the two regions. The higher the Bhattacharyya coefficient between two images is, the higher the similarity between them is.

The proposed region merging method starts with marking the object and background. After object marking, each region will be labeled as object marker region, background marker region, or non-marker region. The object/background marker regions represent a small part of the object/background. The regions that are not marked by the user should be identified and merged with the corresponding regions, based on the similarity between regions. Two regions will be merged if the similarity between them is maximal (the Bhattacharyya coefficient has the highest value).

Briefly, considering Q a region of the image and S^Q the set of all adjacent regions of Q , we compute the similarity between Q and all its adjacent regions (the Bhattacharyya coefficient). Q will be merged with the region having the highest similarity [7]. This means:

$$\rho(R, Q) = \max_{i=1\dots q} \rho(Q, S_i^Q), \quad (14)$$

then R and Q will be merged.

From the initial marker regions, all the non-marker regions will be gradually labeled as either object region or background region. In the end, each region will be labeled as object or background. This is equivalent with extracting the object contour from the background.

3 Segmentation results

In the following, we will show the segmentation results of the previously presented algorithm. We applied the algorithm on nine real X-ray images collected from a local public hospital. The results for three of them are shown in Fig. 1, Fig. 2 and Fig. 3. Green markers are used to mark the object, while blue markers are used to represent the background. The initial segmentation using mean-shift algorithm and the positioning of markers are presented in the left image of each figure, while the results after region merging are shown in the right image.

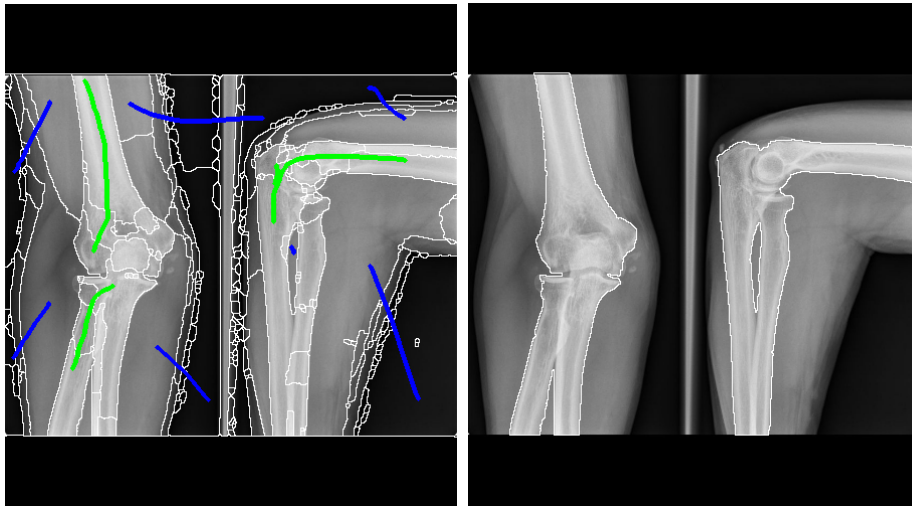


Fig. 1. Test 1: The initial segmentation using the mean-shift algorithm and the markers placed by the used (left) and the segmentation results after region merging procedure (right).

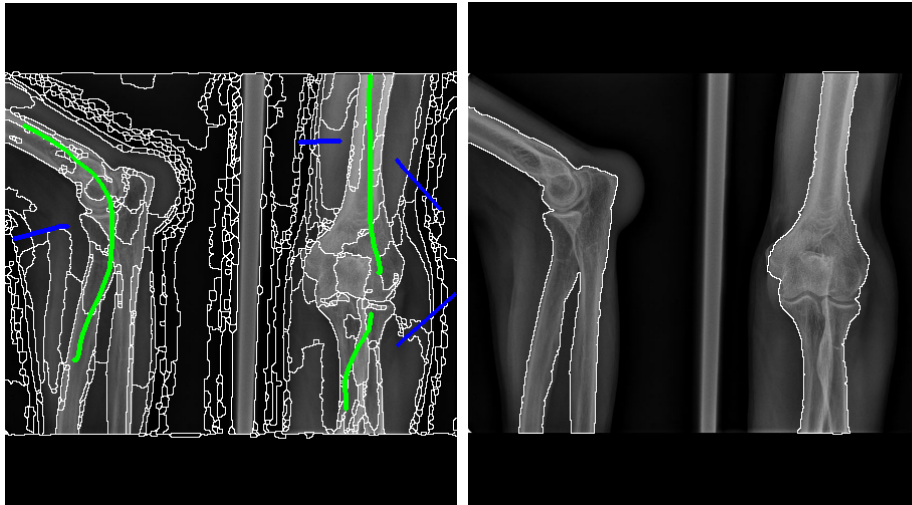


Fig. 2. Test 2: The initial segmentation using the mean-shift algorithm and the markers placed by the used (left) and the segmentation results after region merging procedure (right).

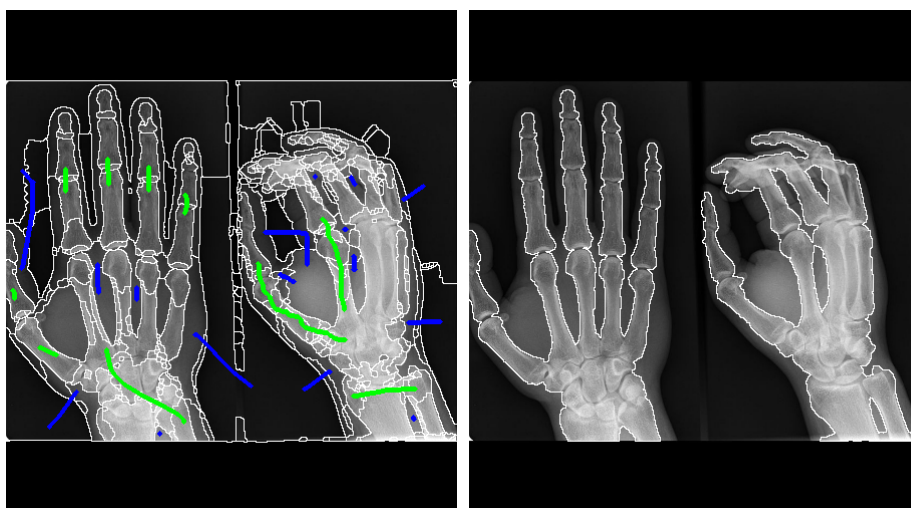


Fig. 3. Test 3: The initial segmentation using the mean-shift algorithm and the markers placed by the user (left) and the segmentation results after region merging procedure (right).

The proposed method is useful if the user is interested in separating a selected object from the rest of the image (background). Analyzing Fig. 1, Fig. 2 and Fig. 3, we can observe that the bones are perfectly extracted from the background. In [14], we compared various segmentation techniques, starting with the most simple and fast methods and increasing the computational complexity and the processing time with each presented method. By visual inspection we can conclude that the results reported in this paper are more accurate than the ones presented in [14].

4 Conclusions

The goal of this paper was to separate the bone structures from a set of X-ray images, as X-ray bone segmentation is a vital step in the X-Ray images analysis. The method proposed for this task is based on the mean-shift algorithm, followed by a region merging process, based on the maximal similarity between regions. This method is very simple but it can successfully extract the objects of interest from the image. The method has been proposed in [7], where the authors used this segmentation scheme to extract desired objects from a set of testing color images. In this paper, we adapted the method proposed in [7] for medical images.

In this paper, the algorithm (both initial segmentation and merging process) has been implemented in MATLAB R2008a. The proposed segmentation method is interactive, as the user places the markers. More, the whole segmentation process is guided by the markers input by the user. The execution time also

depends on the markers positioning, but also on the initial segmentation (based on the mean-shift algorithm), and the content of the image.

Our work has revealed that the proposed method successfully and accurately separates the bones from the background. This research work thus contributes to solving the difficult and challenging problem of segmenting X-ray images. As future work, we aim to reduce the computational speed of segmentation, as well as the amount of manual interaction.

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