# SEGMENTATION OF BONE FROM ADC MAPS IN PELVIS AREA USING LOCAL LEVEL-SET AND PRIOR INFORMATION

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**ABSTRACT**

Lack of anatomical details in diffusion weighted magnetic resonance images limits their utilization and treatment response monitoring, shadowing the useful information they contain. Contemporary methods of utilizing these images are based on manual selection of region of interest, raising concerns about susceptibility of manual ROI placement to human errors, and limiting the investigation in specific spatial regions. In contrary to the whole body bone marrow segmentation with the luxury to include all the diseased bone marrow, high profile analysis could be applied. In this paper, we propose an automatic method for segmentation of pelvic bone with possible bone metastasis in apparent diffusion coefficient (ADC) maps. This method is a multi-parametric registration-segmentation method, taking advantage of prior information of the pelvic anatomy. Intensity inhomogeneity in the bone structure caused by bone marrow metastasis challenges the segmentation process on anatomical MR images. Specifically, we first build a probability map which provides shape and volume constraints for the segmentation. Then, T1-weighted MR images are rigidly registered to the probability map, and then the registered T1-weighted image is non-rigidly registered to its' corresponding ADC maps. Finally, the probability map is coupled with a local level set framework for automatic pelvic bone segmentation of the T1-weighted images. The segmented bone is used as a mask on the ADC map. The method is validated on 10 pairs of ADC/T1 images of breast cancer with bone marrow metastases patients. Both quantitative and qualitative evaluation results demonstrate the validity of the proposed method.

## 1. INTRODUCTION

Segmentation of bone in Diffusion Weighted Magnetic Resonance Images (DW-MRI), especially in Apparent Diffusion Coefficient (ADC) maps is essential in the study of malignant cancers, such as breast cancer with bone marrow metastases. In recent years, these images have shown proper results for assessment, validation and monitoring of patient response to drug therapy. It has been proposed that monitoring the intensity alterations in DW-images, and the changes of ADC values in the bone marrow over the treatment period could be a potent tool to indicate the outcome of the treatment [1]. Most widely used methods for studying these alterations are based on manual selection of the regions-of-interest (ROI)s on the bone marrow in the ADC-maps. Manual ROI-placement is irreproducible, time-consuming and susceptible to errors caused by contamination of the bone marrow with surrounding tissues. This issue compromises the detection of the true treatment-related changes on ADC maps. To overcome this problem complete bone segmentation has been suggested [2]. However, due to the low resolution nature of these images, heterogeneous nature of tumors, and presence of cystic or necrotic areas before therapy, correct and complete separation of the overall border of the bone is difficult.

Widely used image segmentation algorithms [3], [4], [5] mostly rely on intensity homogeneity. Due to the bone metastasis and the intensity inhomogeneity nature of T1-weighted images, these algorithms could not be effectively applied. The level set method has been increasingly applied to image segmentation [3], introduced in a piecewise smooth formulation which do not assume intensity homogeneity. Therefore, they can perform well on images with intensity inhomogeneity. Prior information as a probabilistic function can bring better performance to level set segmentation [6], [7], [8].

In this paper, we automatically segment the bone in ADC maps by using a registration/segmentation method. Initially, we create a probability map of the pelvis bone structure. Then, a set of registered ADC maps, T1-wieghted images and bone anatomy probability map is created. By coupling the prior knowledge into a local level set framework, the bone is segmented from the anatomical T1-weighted MR images. Finally, with using the segmented pelvis bone in T1-wieghted MRI as a mask, pelvis bone is extracted from the ADC maps.

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## 2. METHOD

### 2.1. Data Acquisition

Whole-body T1- and diffusion-weighted images of 10 breast cancer patients with bone marrow metastases under treatment, were acquired on a 1.5T MR scanner. Whole-body T1-weighted images were acquired with the following specifications: TR/TE = 171/4.76 ms, matrix size = 256×151, field of view (FOV) = 430×430 mm, slice thickness = 5mm, spaces between slices = 5.5mm. Whole-body DWI was acquired using a GE-EPI sequence with the following specifications: TR/TE = 5540/102ms, matrix size = 256×151, FOV = 430×430 mm, slice thickness = 5mm, spaces between slices = 0.5mm, at b-values of 50, and 900 sec/mm$^2$. ADC maps were then calculated from DW images.

### 2.2. Probability Map Construction

To construct a probability map, a reference image is selected. This image is a high resolution T1-weighted MRI of the pelvis area of a healthy adult female. Since a bone-windowed CT image can exactly exhibit the bone boundaries, it is used to accurately extract the bone form the T1-weighted reference image. Hence, the reference image is non-rigidly registered to its corresponding bone-windowed-CT image. Using the registered CT image as a mask, the T1-wieghted pelvis bone is segmented. Finally, using a Gaussian kernel the segmented bone is smoothed giving the map variability in shape and volume.

Statistical-deformation-model based bone segmentation from T1-weighted images, despite their significant result require rich data set, and complex procedures. Moreover, the segmentation quality highly depends on the accuracy of the statistical model [9]. On the other hand, providing a rough probability map, instead of a complex statistical deformation model, is sufficient for the proposed method. That is because in this method, the main step of segmentation relies on the local level set algorithm which causes independency from the probability map accuracy. Information such as the verge of bone location and its shape in an image is the required information, which a simple probability map can provide it. This can prevent the complication of creating a population atlas. Moreover, the probability map is constructed using a reference T1-weighted image. Adaptation of this map to other images is simplified when a T1-wieghted image coupled with the probability map exists. That is because instead of the time consuming and complex registration of a map to an MR image, a simple rigid registration with the least square cost function and a gradient distance optimization of the MR image and the reference image is applied. Fig. 1 shows an example of the proposed probability map.

### 2.3. Automatic Registration

For prior information adaptation, as mentioned in section 2.2 the T1-wieghted MRI is rigidly registered to the reference image. The registration has the least square cost function and a gradient distance optimization. In order to map structural information available in MR images onto ADC maps, another registration is needed. Since ADC maps have lower resolution, T1-wieghted images are non-rigidly registered to ADC maps. In this step, the thinner the MR slice thickness, the better the registration. After registration each ADC voxel will have a corresponding voxel in the T1-weighted image. There are several available software tools for registration. In this paper the SPM8 toolbox is used.

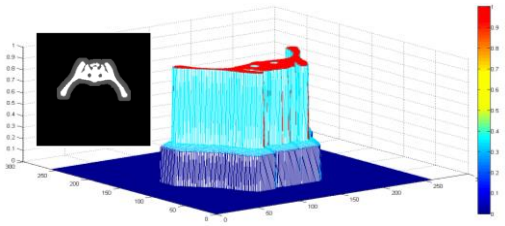


Fig. 1. Visualization of the proposed probability map for a slice in 2D and 3D.

### 2.4. Local Level Set Segmentation Integrating Probability Map

In this section, we integrate the probability maps created in section *B* into a region based local level set frame work [10]. Using the Heaviside function *H*, we use a level set function $\varphi$, to describe the bone tissue and the background. The proposed energy is defined as follows,

$$E = \alpha E^{Lankton} + \beta E^{\Pr ior}. \quad (1)$$

The Lankton energy is calculated as follows [10]:

$$E^{Lankton} = \int \delta\varphi(x) \int B(x,y).F(I(y),\varphi(y))dydx + \lambda \int \delta\varphi(x)\|\nabla\varphi(x)\|dx. \quad (2)$$

where $B(x,y)$ is used to mask the local regions, $I$ donates the original image, $\delta$ is the Dirac function, and $\lambda$ is the weight of the regularization term. $F$ is a generic internal energy measure used to present local adherence to a given model at each point along the contour. In this study $F$ is a uniform modeling energy as following:

$$F = H(\varphi(y))(I(y)-u_x)^2 + (1-H(\varphi(y)))(I(y)-v_x)^2. \quad (3)$$

*I(y)* is the local equivalent of the original image, and $u_x$ and $v_x$ are the local mean intensity. The prior energy is calculated as [11]:

$$E^{\Pr ior} = \int_r (\varphi-\varphi_0)^2 dx \quad (4)$$

where $\varphi_0$ is the shape prior, and *r* is the localization scale. The shape prior is the signed distance function of the constructed probability map explained in section 2.2.

## 3. EXPERIMENTAL RESULTS

We have applied the proposed segmentation technique to

imaging data of 10 breast cancer patients with bone marrow metastases. We have chosen following parameters for all experiments: localization scale $r$ =7 pixels, $\beta$ = 2.8 and $\alpha$ =3.

Accuracy of bone segmentation in ADC maps has been validated by comparing manual and automatic segmentations of the corresponding T1-weighted image. Manual segmentations on T1-weighted images were obtained by accurately identifying points on the bone boundaries and by reconstructing the bone using a deformable surface which does not use any prior information on the bone shape. Then, the bone was extracted from the ADC map using the corresponding manually segmented T1-weighted image. Segmentation accuracy has been evaluated using boundary-based and volume-based measures. Results of ten patients are reported in Table 1.

Table 1. Segmentation quality evaluated using Dice, Sensitivity, Hausdorff distance (H) and the Hausdorff distance with 5% outlier elimination (H95).

| Dice | Sensitivity | H | H95 |
|---|---|---|---|
| 0.83 ±0.06 | 0.81±0.08 | 5.55±1.4 | 2.78±0.65 |

Fig. 2 presents an example of ADC map segmentation, based on manual and automatic T1-wieghted segmented images, and shows an example of T1/ADC registration where the T1-wieghted MRI is superimposed on the ADC map.

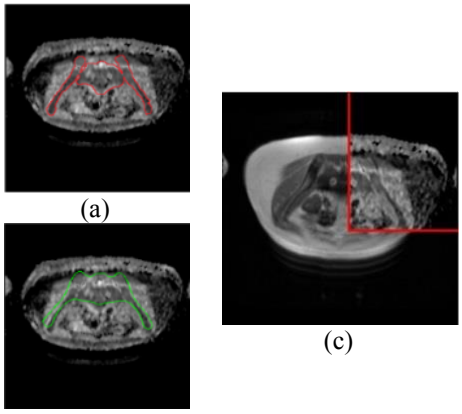



Fig. 2. a) Manual segmentation, b) Automatic segmentation, c) T1/ADC registration where the T1-wieghted MRI is superimposed on the ADC map. Portions of the images are shown to illustrate their relation.

Fig. 3 shows the segmentation results of different methods for a typical subject on the T1-weighted images. We compare the proposed method with Chan-Vese global level set segmentation method [3] and Li, et al method [12], both coupled with prior information. The original intensity images and the results by Li, Chan-Vese, and the proposed method are shown from left to right in the first four columns of Fig. 3. To better compare the results by different methods, the label differences compared with the manual segmentation are also presented in the next three columns, which qualitatively demonstrate the advantage of the proposed method.

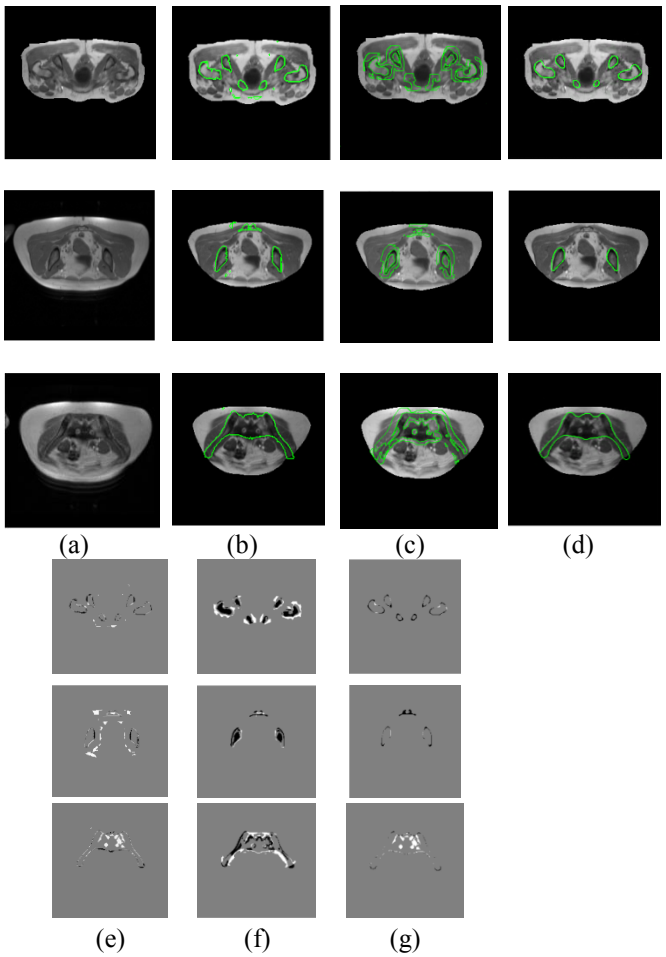



Fig. 3. Comparison of different methods: (a) Original image, (b) Li, et al method, (c) Chan-Vese method, (d) Proposed method, (e) Difference of Li, et al. method and manual, (f) Difference of Chan-Vese method and manual, (g) Difference of the proposed method and manual.

The average Dice coefficient for the proposed method and Chan-Vese and Li, et al methods are 0.83, 0.76, and 0.67, respectively (see Fig. 4). The proposed method is statistically significantly superior to the other two methods with p-values of 0.013 and 0.000006, respectively.

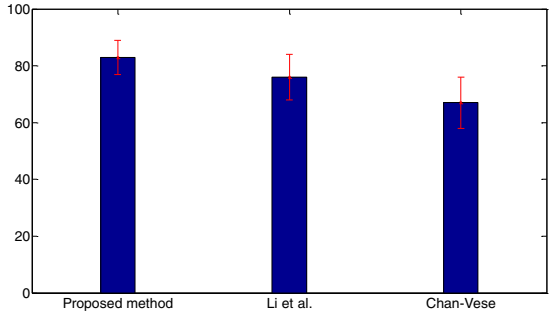
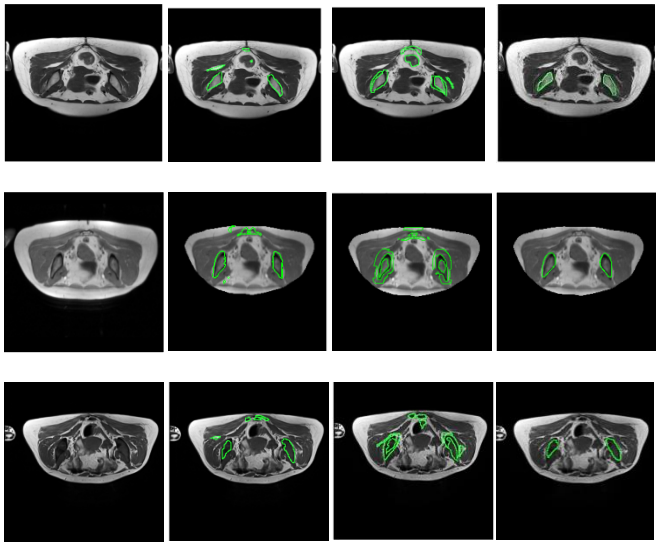



Fig. 4. Mean and standard deviations of Dice coefficients of different methods.

Qualitatively, the segmentations for all subjects were visually inspected by experts, confirming the good quality of segmentation results. Here we randomly showed 3 segmentation results in Fig. 5, observing the results of the proposed method demonstrate better segmentation accuracy than those of the Chan-Vese, and Li, et al.

In order to test the reference image affect, three different reference images where tested for the segmentation, the Dice coefficient had only 1.75% variation which can exhibit the independency of the method to the reference image.



(a) (b) (c) (d)

Fig. 5. (a) Original image, results of (b) Li method, (c) Chan-Vese method, and (d) proposed method on three different patients.

## 4. Discussion and Conclusion

In this paper, we have proposed an automatic bone segmentation method in ADC maps based on the non-rigid registration of anatomical T1-weighted MR image, and local level set method coupled with prior information. The presented approach, validated on 10 couples of T1/ADC images, is robust to yield more accurate information extraction from the DW-MRI than ROI-based methods. Although the presence of bone metastasis complicates the segmentation process and decreases its accuracy, the information extracted in each patient can easily be used in follow ups and can increase the effectiveness of these images for future clinical applications. To the best of our knowledge, there has been no direct presented method for bone extraction in ADC maps, hence the comparisons made in this paper are based on the most common methods used for image segmentation.

A remaining issue is that the poor initial positioning of the level set contour can lead to false anatomical mapping. Hence, using a statistical deformation model instead of the probability map as the prior information can highly enhance the segmentation. A further aspect we must point out is that lower average of Dice coefficients should be expected as the number of the patients increase.

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