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Tracking tumor boundary using point correspondence for adaptive radio therapy



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ABSTRACT

Background and objective: Tracking mobile tumor regions during the treatment is a crucial part of imageguided radiation therapy because of two main reasons which negatively affect the treatment process: (1) a tiny error will lead to some healthy tissues being irradiated; and (2) some cancerous cells may survive if the beam is not accurately positioned as it may not cover the entire cancerous region. However, tracking or delineation of such a tumor region from magnetic resonance imaging (MRI) is challenging due to photometric similarities of the region of interest and surrounding area as well as the influence of motion in the organs. The purpose of this work is to develop an approach to track the center and boundary of tumor region by auto-contouring the region of interest in moving organs for radiotherapy.

Methods: We utilize a nonrigid registration method as well as a publicly available RealTITracker algorithm for MRI to delineate and track tumor regions from a sequence of MRI images. The location and shape of the tumor region in the MRI image sequence varies over time due to breathing. We investigate two approaches: the first one uses manual segmentation of the first frame during the pretreatment stage; and the second one utilizes manual segmentation of all the frames during the pretreatment stage.

Results: We evaluated the proposed approaches over a sequence of 600 images acquired from 6 patients. The method that utilizes all the frames in the pretreatment stage with moving mesh based registration yielded the best performance with an average Dice Score of 0.89 ± 0.04 and Hausdorff Distance of 3.38 ± 0.10 mm.

Conclusions: This study demonstrates a promising boundary tracking tool for delineating the tumor region that can deal with respiratory movement and the constraints of adaptive radiation therapy.

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1. Introduction

Image-guided radiotherapy (IGRT) is an important treatment option for treating mobile tumors, which promises improved targeting and delivery of highly conformal radiation dose [1]. Currently, many different indirect tumor tracking methods using internal or external tumor surrogates are used to treat mobile tumors [2–4]. Despite the variety of tracking techniques, however, reliance on surrogates has been shown to be sub-optimal due to (1) in-

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https://doi.org/10.1016/j.cmpb.2018.08.002 0169-2607/© 2018 Elsevier B.V. All rights reserved. ternal surrogates require invasive procedures, and the surrogates may migrate from the initial locations [5], (2) external surrogates must rely on ambiguous correlations between internal tumor motion and external surrogates displacement [6]. More importantly, any tumor shape deformation is completely unknown during treatment. To compensate for these inaccuracies, a margin around the tumor is assigned and irradiated, which may results in (1) unacceptable medical complications due to excessive healthy tissue irradiations, or (2) poor disease control due to limiting the necessary therapeutic dose to avoid those complications [7,8].

Recently, hybrid radio-therapy MR-systems, called Linac-MR, have been proposed by several groups for intra-fractional tumor motion management [9–13] without the need for surrogates,

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which may overcome those difficulties. With Linac-MR, one can directly image the tumor during irradiation and use them in real time to adjust therapeutic radiation to track changes in tumor position and shape. The first and most important step of real-timein tumor tracking is the accurate delineation of the tumor region in each intra-fractional MRI image. Manual contouring to obtain such delineation is time-consuming, thus is not an option. Therefore, a precise and fast auto-contouring algorithm is critical to perform real-time tumor tracking during radiation therapy. With a reliable algorithm, the dosage of the beam delivery can be significantly increased which will lead to a better treatment of patients

Auto-contouring of mobile tumors in MR images is challenging due to the low contrast between the tumor region and their surrounding anatomies. The problem becomes more challenging with large range of tumor motion and deformation; this type of problems arises occasionally, for instance, when tumors are located in lung regions [14]. Lung tumors are often difficult to treat due to the large ranges of motion and deformation produced by breathing. Several studies have shown that lung tumors may move up to 40 mm in superior-inferior (SI), 15 mm in anterior-posterior (AP), and 10 mm in left-right (LR) directions during normal breathing [15–18]. To delineate tumors in lung region, Yun et al. [19] recently have proposed a neural network based auto-contouring algorithm.

This study proposed to use a non-rigid registration with moving meshes as a framework to track tumor region boundaries. The imaging for lung tumor treatment consists of two stages: (1) pretreatment stage; and (2) treatment stage [14]. In the pretreatment stage, the algorithm requires an expert oncologist to manually contour tumor regions of MR slices. Whereas in the treatment stage, the algorithm is expected to produce automatic contours to track the tumor region. Two approaches were proposed in this context: (1) first frame registration approach that uses the manual segmentation of the first frame of the pretreatment stage; and (2) best frame registration approach that uses manual segmentation of all the frames from the pretreatment stage to find the best frame, which was decided based on a minimum L_2 -norm between the selected treatment image and the pretreatment images. We also tested both first frame and best frame methods using a publicly available RealTITracker registration algorithm¹.

2. Method

2.1. Non-rigid image registration

A two-dimensional moving mesh is applied in order to obtain a point-to-point correspondence between *i*th image T_i and *k*th image T_k defined over $\Omega \subset \mathbb{R}^2$. To reduce the time in computing the moving mesh, only a part of the image is used with enough margin to ensure the region of interest is included. Finding the points correspondence can be formulated as the following optimization problem [20]:

$$\hat{\phi}_{k,i} = \|T_i(\xi) - \phi(T_k(\xi))\|_2$$
(1)

where for each pixel location $\xi \in \Omega \subset \mathbb{R}^2$, $\phi: \Omega \to \Omega$ is a transformation function and $\|\cdot\|_2$ denotes the L_2 -norm. To get a unique solution to the problem, we introduced a deformation field using a Jacobian transformation μ and curl of end velocity field γ , where $\mu: \Omega \to \mathbb{R}$ and $\gamma: \Omega \to \mathbb{R}$.

2.1.1. Moving mesh generation

In order to generate a moving mesh, we first define a continuous monitor function $\mu(\xi)$ which is used to obtain a vector field [21]:

$$\int_{\Omega} \mu = |\Omega|, \tag{2}$$

Our goal is to find a transformation $\phi: \Omega \to \Omega, \partial\Omega \to \partial\Omega$ with

$$J_{\phi}(\xi) = \mu(\xi), \tag{3}$$

where J_{ϕ} denotes the Jacobian of the transformation. To find a transformation ϕ which satisfies (2) and (3), let a vector field $\rho(\xi)$ be such that:

$$\operatorname{div} \rho(\xi) = \mu(\xi) - 1 \tag{4}$$

and

$$\operatorname{curl} \rho(\xi) = \gamma(\xi), \tag{5}$$

with null boundary condition $\rho(\xi) = 0 \forall \xi \in \partial \Omega$, where $\gamma(\xi)$ is a continuous function over Ω . Let a velocity vector field from $\rho(\xi)$ be:

$$\nu_t(\xi) = \frac{\rho(\xi)}{t + (1 - t)\mu(\xi)}, \qquad t \in [0, 1], \tag{6}$$

where *t* is an artificially introduced time parameter.

Then ϕ is obtained using:

$$\frac{d\psi(\xi,t)}{dt} = v_t(\psi(\xi,t)), \qquad t \in [0,1], \, \psi(\xi,t=0) = \xi, \tag{7}$$

where $\phi(\xi) = \psi(\xi, t = 1)$.

The above optimization problem is solved using a *step-then-correct* approach [20]. We refer the reader to Chen et al. [20] for derivation and numerical implementation details. We computed a sequence of corresponding points along a window surrounding the border of the tumor region in all the frames using a transformation function $\hat{\phi}$, given the segmentation in one frame.

In contrast to registering images sequentially [22], we took the following approaches to reduce the accumulative error of the algorithm.

2.1.2. First frame registration based technique

We used the above moving mesh point correspondence method between the first image in pretreatment stage T_1 and each *k*th image in treatment stage T_k to obtain a sequence of points over time.

2.1.3. Best frame registration based technique

In this approach, we use the pretreatment images as the training set. For each image in the treatment stage, we select the closest image base on L_2 -norm between the selected treatment image and the pretreatment images from the pretreatment stage and compute point correspondence between them. Let N_q be the number of frames in the pretreatment images. The typical number of manually segmented frames in pretreatment is 30. The best frame T_q (among T_j for $j \in (1, ..., N_q)$) for any image in the treatment frame T_k can be found by:

$$T_{q} = \arg\min_{T_{i}} \left\| T_{j}(\xi) - T_{k}(\xi) \right\|_{2}.$$
(8)

Then a points correspondence between T_q and T_k is computed to obtain the segmentation on T_k .

3. Results

3.1. Experimental protocol

The data consists of free-breathing 3T MRI images acquired from six patients with lung cancer. An additional image noise was added to reflect the image noise at 0.5T which will be used during radiation treatment. Each data set consists of 130 images that include 30 images from pretreatment stage and 100 images from the

¹ The RealTITracker is available at: http://bsenneville.free.fr/RealTITracker/.

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