Template Matching Can Accurately Track Tumor Motion in Cine MRI Images from Lung Cancer Patients

Xiutao Shi[1], Tejan Diwanji[1], Karen E Mooney[1], Warren D D'Souza[1], and Nilesh Mistry[1]
[1]*Department of Radiation Oncology, University of Maryland School of Medicine, Baltimore, MD, United States*

INTRODUCTION: Respiratory motion management during the treatment of thoracic tumors is extremely challenging[1]. The development of new hybrid MRI-Linear Accelerator systems may eventually enable real-time imaging of tumor motion. Recently, Cervino *et al.* demonstrated that it is possible to use template matching to determine the position of vascular structures in the lungs as they move with respiration[1]. However, the utility of the technique in tracking thoracic tumors was not validated. Here we extend the use of the template matching technique to automatically track tumor motion in lung cancer patients. Furthermore, we compare the performance of this technique to manual estimates of tumor position.

METHODS: Five patients with lung tumors of various sizes (Table 1) were recruited in a prospective study. MRI imaging was performed in 3 time sessions: before treatment, 1-2 weeks into treatment, and 4-5 weeks into treatment. One patient (Patient 3) withdrew from this study after the 1st session. Patients were instructed to breathe normally during the imaging sessions. True FISP (fast imaging in steady state) cine-images were obtained in the sagittal plane with the following parameters: TE/TR/Flip/Matrix-size/Slices of 1.29ms/2.57ms/60/176x256/5. In-plane spatial resolution was ~1.95 mm, and slice thickness ranged from 9 mm-16 mm to ensure complete tumor coverage. The total acquisition time was ~8 min for each session. One representative slice was selected from each dataset to create a series of ~200 frames with a temporal resolution of ~2.5 s. All further analysis was conducted on this series.

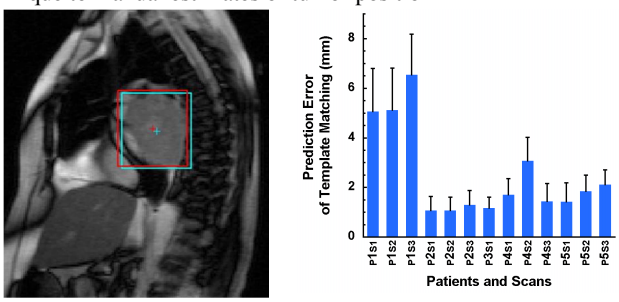

Figure 1: a) Sample illustration of the surrounding boxes and the corresponding tumor centers as determined by the manual (cyan) and automatic (red) method. b) Prediction error of the automatic method – template matching – for all patients and scans. Error bars mean one standard deviation.

Ground truth was established by determining the tumor location ($\vec{x}_{man}$) and size manually by drawing the smallest box that enclosed the tumor on each frame (Fig. 1a, cyan). Subsequently, an automated template matching algorithm was used to estimate frame-by-frame tumor position (Fig. 1a, red). The manually contoured box on the first frame served as the starting position and template for the automated algorithm. Template matching was performed by calculating the cross-correlations between this template and the targets in subsequent frames using MATLAB (MathWorks Inc., MA). In each frame, multiple cross-correlations were calculated within an established "search window" that allowed for ~2.73 cm of motion in the AP and SI dimensions. The point of maximum correlation was selected as the position of the tumor in the new frame ($\vec{x}_{auto}$). In order to compare the results, the difference in the determined positions between the two methods was calculated using the following equation: $\vec{x}_{dif} = \vec{x}_{auto} - \vec{x}_{man}$. The prediction error was defined as $e = \sqrt{x_{difAP}^2 + x_{difSI}^2}$ for each frame. The performance of template matching was examined by comparing the mean errors and standard deviations among patients and scans.

Table 1: Patient information (L: Lower, M: Middle, U: Upper, A: Anterior, P: Posterior).

	Sex	Age (yr)	Tumor Size (APxSI, mm)	Tumor Position
Pat. 1	F	66	73x80	LP
Pat. 2	F	75	47x47	MP
Pat. 3	M	64	14x29	MP
Pat. 4	F	64	34x29	UA
Pat. 5	M	58	19x20	MP

RESULTS: The mean prediction error of template matching for each patient and their repeat sessions was plotted in Fig. 1b (with error bars signifying 1 std dev). For Patient 2, Patient 3, Patient 4 (Session 1 and Session 3), and Patient 5 (Session 1 and Session 2), the prediction error with the automated template matching method was less than 1 pixel (1.95 mm). Patient 4 (Session 2) and Patient 5 (Session 3) had prediction errors of less than 2 pixels. Patient 1 had the biggest prediction errors, ranging from 5.06 mm to 6.55 mm (~3 pixels). The prediction error was positively correlated with the size of the tumors (Table 1, $R^2 = 0.73$, $p < 0.001$).

DISCUSSION: Accurate tracking of the tumor in lung cancer is crucial for the safe and effective delivery of radiation treatment. In the current study, an automated template matching technique has been applied to track respiration induced tumor motion based on cine MRI images. For tumors smaller than 50 mm in the longest dimension, the prediction error is within two pixels. This error is close to the order of intra-operator or inter-operator variability during manual tracking. While further verification is necessary, these results suggest template matching could be used to automate the laborious process of manual tracking in order to establish ground truth when testing other motion management techniques.

Cervino *et al.*[1] successfully applied this technique to track vascular structures in the lung. In their study, the diaphragm was used as a surrogate to help determine the position of the vascular structure in the event of severe out-of-plane motion. However, in our study, tumors have sufficiently distinctive patterns from the surrounding tissue, which enables consistent results and obviates the need to utilize surrogates.

The biggest error occurred in Patient 1 where the tumor was very large. When the size of the tumor increases substantially, its motion is restricted due to abutment with other solid structures, i.e. chest wall, diaphragm, and heart. These restrictions not only limit motion in those directions, but also induce a significant component of rotational and out-of-plane motion. These factors are likely to contribute to the increase in prediction error for template matching.

CONCLUSION: The effectiveness of template matching to estimate tumor position during respiratory motion was tested in patients with lung cancer. The prediction error is often less than two pixels when compared to a manual tracking technique. With further development, this technique could be utilized not only with on-board imaging, but also to replace the laborious manual tracking process necessary to establish the ground-truth when evaluating external surrogates of tumor motion.

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REFERENCES: [1] Cervino L. et al. PMB 2011 56:3773-3785.