Modelling Respiratory Motion for Optimisation of Lung Cancer Radiotherapy Using Fast MR Imaging and Intensity-Based Image Registration

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Introduction

Despite recent improvements to the delivery of treatment for lung cancer, such as conformal and intensity-modulated radiotherapy, management of the disease continues to be difficult. These new radiotherapy techniques require accurate target definition and patient positioning in order to deliver the desired dose to the target volume while minimizing normal tissue exposure [1]. Irradiation of normal lung tissue causes pneumonitis, which is the major dose-limiting toxicity of lung cancer radiotherapy. This is a significant problem and is contributory to non-cancer related deaths in patients receiving radiotherapy [2,3]. Respiratory motion of the lung is a major factor in the design of radiotherapy planning target volumes. In current clinical practice, uncertainties due to tumour motion are inadequately dealt with by treating with radiation fields that are larger than would otherwise be necessary [4]. Various approaches to overcome the problem of respiratory motion include Active Breathing Control systems [5], respiratory gating techniques [6] and tracking the moving lung using implanted markers and X-ray imaging [7] have been used with only modest success. More recent studies have used cine CT data acquired throughout the breathing cycle to illustrate more accurate tumour localization [8]. Using fast imaging in conjunction with a parallel acquisition technique such as SENSE [9] it is possible to obtain sample images of the entire lung volume at a sufficient frequency to analyze motion and deformation over the breathing cycle. We are developing a system that makes use of these rapidly acquired images to model and predict motion and deformation of the lungs due to breathing during treatment, thereby reducing margins on radiotherapy planning target volumes, and ultimately improving the therapeutic ratio.

Methods

MR Imaging: Ten volunteers (7 male, 3 female) aged 25-47 (median 31.5 years) were imaged using MRI. Scanning was carried out on a 1.5T Philips Intera. in the XMR suite. Two fast sequences were used in conjunction with SENSE to image the right lung. The first was a multi-slice breath-hold Steady State Free Precession sequence: 25-27 slices, SENSE factor 2, flip angle 5-20°, TE 1.75-3 ms, TR=2×TE, slice thickeness 6 mm, rFOV 70%, resolution 224×256, sacn % 105. Flip angle and TE were adjusted for each volunteer to improve the signal of the distal blood vessels in order to facilitate the automatic registration process. Volunteers were asked to hold their breath at the maximum number of positions they could fit throughout their breathing cycle. The second was a dynamic 3D free-breathing FFE-EPI sequence (TE 3.3 ms, TR 6.8 ms, 25-27 slices, slice thickness 7 mm, resolution 128×256×25-27, flip angle 20°, EPI factor 5, rFOV 70%, 52 dynamic scans). The series of free-breathing 3D volumes was acquired twice.

Model Construction: Models were constructed using an intensity-based affine image registration technique [10] to coregister MR images acquired throughout the breathing cycle. Anatomical landmarks of interest were identified in the breath-hold image acquired at maximum exhale, which was selected as a subject-specific reference image, and transferred to the corresponding positions throughout the rest of the cycle using the affine transformations calculated as a result of registration. Models of the respiratory motion of these landmarks, distributed over the surface of the lung, were formed from four different subsets of the MR data for each volunteer: A - free breathing volumes going from exhale to inhale (on the inhaling trajectory), B - free-breathing volumes going from inhale back to exhale on the same cycle (on the exhaling trajectory), C - free-breathing volumes going from exhale to inhale (on the inhaling trajectory) on a different breathing cycle and D - multislice images acquired at different breath-hold positions between exhale and inhale and retrospectively ranked according to diaphragm position. The motion was parameterised in terms of diaphragm position (in the head-foot direction) by fitting polynomials to the coordinates of each landmark point and storing the coefficients of these functions. Comparisons were then made between models: A and B (free-breathing inhaling and exhaling trajectories from the same cycle), A and C (free-breathing inhaling trajectories from two different cycles) and A and D (free-breathing inhaling trajectory compared with a series of breath-holds between exhale and inhale) across the overlapping range of diaphragm positions which were represented by all four models.

Results and Discussion

Subject-specific lung motion models were formed for each of ten volunteers as described above. Comparison of the different model construction techniques was carried out by generating instances of the lung surface landmark set, using each of the four models in turn, at five different points over the breathing cycle as parameterised in terms of diaphragm position. For each point in the breathing cycle, the difference in position of each corresponding lung surface landmark was calculated to give an error measure. Typical results for one volunteer are shown in tables 1-3. The results are displayed in terms of a normalised range, where diaphragm position is represented on a range where 0.0 is the position closest to exhale and 1.0 is the position closest to inhale within the range of diaphragm positions represented in the data used to construct the motion models. In general, errors are smallest when comparing models built from inhale and exhale parts of the same free-breathing cycle (RMS values of 0.6-2.9mm), and only a little larger (RMS values of 1.1-2.5mm) when comparing models built from inhale parts of two separate free-breathing cycles. Errors are considerably larger when comparing a model constructed with free-breathing data to one formed from breath-hold images (RMS values of 4.2-6.8mm).

Table 1 *Comparison of inhale free-breathing and exhale free-breathing models, same cycle*

Diaphragm position (% of range)	*0*	*25*	*50*	*75*	*100*
RMS error (mm)	*0.62*	*0.66*	*1.13*	*2.40*	*2.92*
Max error (mm)	*1.33*	*1.26*	*1.80*	*5.01*	*6.64*

Table 2 *Comparison of inhale free-breathing models from two different cycles*

Diaphragm position (% of range)	*0*	*25*	*50*	*75*	*100*
RMS error (mm)	*2.42*	*1.98*	*1.18*	*2.50*	*1.11*
Max error (mm)	*3.57*	*4.21*	*1.81*	*6.21*	*2.15*

Table 3 *Comparison of inhale free-breathing model and model from series of breath-holds*

Diaphragm position (% of range)	*0*	*25*	*50*	*75*	*100*
RMS error (mm)	*4.15*	*4.89*	*5.50*	*6.19*	*6.81*
Max error (mm)	*6.17*	*8.00*	*9.28*	*11.26*	*12.69*

Conclusion

Our findings demonstrate the potential for the use of respiratory motion models in providing vital information on motion and deformation of the lungs and thus further improving radiotherapy planning and delivery of treatment. The comparison of different image acquisition protocols suggests that models formed using breath-hold data do not accurately represent the motion and deformation which occurs when the subject is breathing freely as they would be during radiotherapy treatment. However, affine registration of rapidly acquired free-breathing MR volumes has been shown to yield reproducible models of breathing motion, which could be combined with CT images for radiotherapy dose calculations.

References

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