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## Respiratory motion model derived from CBCT projection data

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### Introduction

Respiratory induced organ motion is one of the primary sources of tumour localisation uncertainty, which can cause error and uncertainty during radiotherapy. 4DCT can be used to measure motion such that it can be taken into account during planning, but the magnitude and pattern of breathing can vary from day to day, thus 4DCT may not give a good representation of the motion at the time of treatment. 4DCBCT can be used to monitor motion just prior to treatment delivery, but this requires a longer acquisition (compared to 3DCBCT) and hence more dose to the patient. In addition, 4DCBCT can suffer from poor image quality, and therefore may not give a good representation of the true motion and its variability.

Patient specific motion models can potentially provide accurate estimates of the respiratory motion, including modelling breath to breath variability. McClelland et al. [1] proposed a framework unifying Deformable Image Registration (DIR) and motion modelling. This framework can fit a motion model directly to ‘unsorted’ dynamic data, e.g. multi-slice data (from CT or MR) or projection data (from CBCT). Previously published results demonstrated good performance for CT and MR slice data. Here we apply this approach for the first time to CBCT projection data.

It is very difficult to evaluate the motion model accuracy using real patient data as the true motion is unknown. Therefore, we have used an anthropomorphic software phantom (XCAT)[2] to simulate CBCT projection data and evaluate the method as a proof-of-concept.

### Materials & Methods

The XCAT anthropomorphic software phantom was used to generate the data for this study. The motion of the XCAT was driven by real respiratory signal measured from a patient, and hence included both intra- and inter-cycle variations. A full 3D volume (with CT like intensity values) of the thoracic region, including a 1.5 cm diameter spherical “tumour” in the right lung, was generated for each time point corresponding to each CBCT projection. 683 CBCT projections were simulated over 60s, corresponding to a real 3D CBCT acquisition. RTK [3] was used for the forward projections (and was also used for the forward and back-projections required to fit the motion model below). The voxel size in the 3D volumes was 1.76 x 1.76 x 2 mm<sup>3</sup>, and the pixel size in the CBCT projections was 2.3 x 2.3 mm<sup>2</sup>.

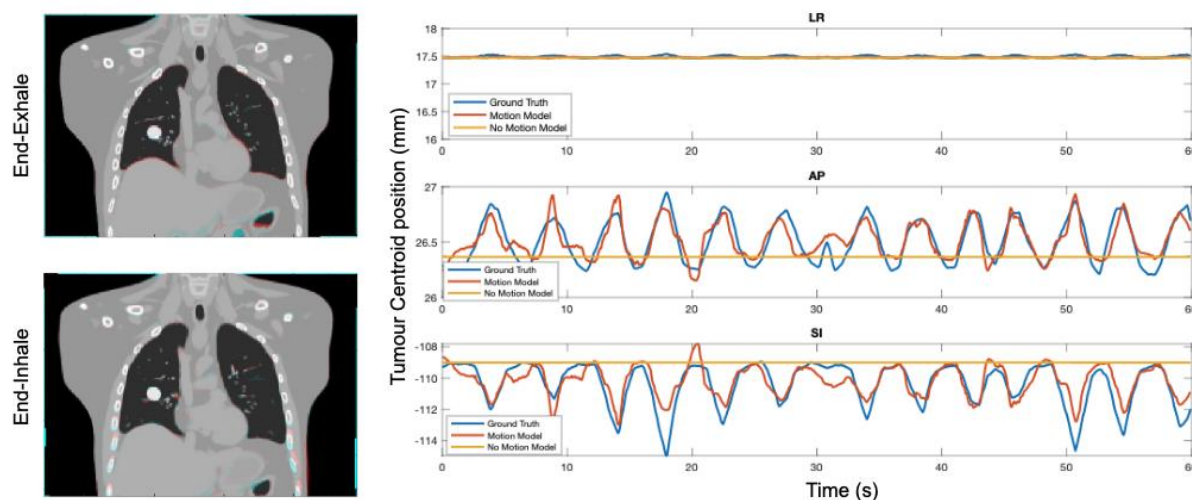
The unified framework of McClelland et al.[1] directly optimizes the motion model parameters on the unsorted dynamic image data, in this case the CBCT projections. In the approach used here, the model deforms an existing ‘reference-state’ volume, so that projections simulated from the deformed volumes best match the input projection data. In a clinical setting, this reference-state volume could be one of the 4DCT volumes used for planning. Here it was the 3D XCAT volume corresponding to end-exhalation. The motion model relates the deformation of the reference-state volume to the current value and gradient of a respiratory surrogate signal, which enables both intra- and inter-cycle variation to be modelled. A B-spline transformation model was used for the deformations. The surrogate signal was generated from the input projections using a method based on principal component analysis proposed by Akintonde et al.[4]. The fitting procedure minimised the Sum of Square Differences (SSD) between the model generated projections and input projections.

To evaluate the results the fitted model was used to deform the reference-state volume to estimate the full 3D volume at the time of each CBCT projection. These were visually compared to the ground-truth (GT) 3D XCAT volumes. To quantitatively assess the results, the Centre Of Mass (COM) of the tumour

was compared between the estimated and GT volumes, and the Dice overlap was calculated between the tumour in the two volumes. In addition, the estimated volumes were used to simulate CBCT projections, and these were compared to the input projections visually and by calculating the SSD. For comparison, the metrics above (using both 3D volumes and projections) were also calculated using the static reference-state volume instead of the estimated volumes.

## Results

Shown on the left of figure 1 are colour overlays between the GT volume and the deformed reference-state volume using the model. The volumes corresponds to an End-Exhale (EE) and End-Inhale (EI) from an exemplar cycle. The red/blue regions indicates area of disagreement between the model and the GT. The right of figure 1 shows the tumour centroid position along the left-right (LR), anterior-posterior (AP), and the superior-inferior (SI), directions, while the 90<sup>th</sup> percentile error of the tumour centroid position was 0.04, 0.13 and 0.76 mm respectively for each direction. The SSD between the input projections and the model estimated projections was reduced by a factor of 2 when compared to the projections from the reference static volume relative to the input projections. A mean Dice coefficient of 0.912 was obtained between the estimated tumour and the GT data, compared to 0.821 when the reference-state volume was used.



**Figure 1:** (Left) Colour overlay of the estimated and the GT volume at EE and EI. (Right) Difference in tumour centroid position between the model and the case where no motion model was applied relative to the GT motion.

## Discussion & Conclusions

In this initial simulation study, qualitative and quantitative evaluation suggests that the modelled motion closely matches the GT motion. The good agreement between the model and the GT suggests that the model can be used to accurately estimate motion throughout the respiratory cycle. Future work is needed to test this method on more simulated data and patient data.

## References

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