

Geometric accuracy of surrogate-driven respiratory motion models for MR-guided lung radiotherapy

B. Eiben¹, J. Bertholet², E.H. Tran¹, A. Wetscherek², U. Oelfke², and J.R. McClelland¹

¹Centre for Medical Image Computing, University College London, UK; ²Joint Department of Physics, the Institute of Cancer Research and the Royal Marsden NHS Foundation Trust, UK

Introduction

MR-Linacs offer unprecedented motion monitoring potential during radiotherapy treatment. While the soft-tissue contrast is excellent, high-resolution 3D images of the moving anatomy show motion artefacts due to long acquisition times. Therefore, respiratory motion is commonly observed using 2D cine-MR images. Although it is possible to monitor the 2D motion of lung tumours with these images, they do not provide information outside the imaging plane. However, accurate temporally resolved volumetric patient information is an essential requirement for some downstream analysis and adaption methods such as motion-including dose reconstruction. Surrogate-driven motion models (SDMMs) can provide this information with high spatiotemporal resolution. Our group developed a methodology to build a 3D SDMM from multi-slice 2D images, which also produces a motion-compensated super-resolution reconstruction (MCSR) of the patient anatomy [1]. As the ground-truth motion and 3D images are unknown, quantifying the accuracy of SDMMs is difficult using real data. To overcome this, here we quantify the SDMM's geometric accuracy using the XCAT anthropomorphic phantom [2].

Materials & Methods

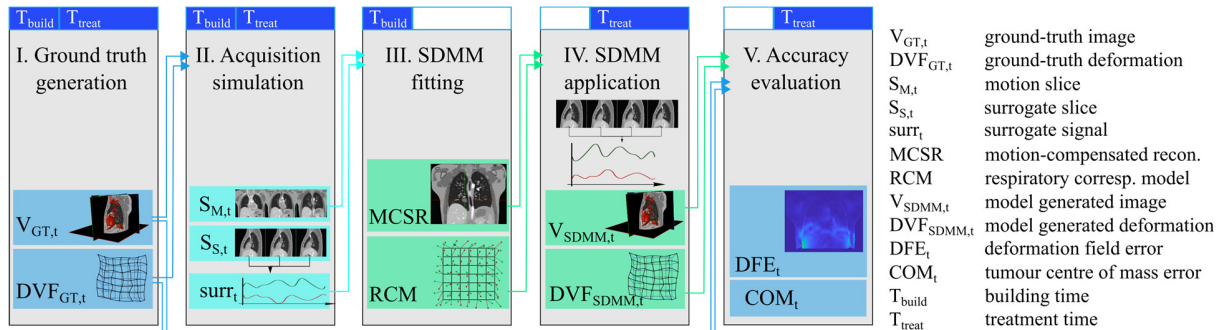


Figure 1: Flow-chart of the ground-truth data generation, model building and evaluation scheme.

Figure 1 shows the data generation, model building, and accuracy evaluation workflow. (I) An XCAT patient anatomy with a tumour in the lower right lung was animated using a volunteer's breathing trace. An MR-like image was generated ($2 \times 2 \times 2 \text{mm}^3$) and transformed to every time point with ground-truth deformation vector fields (DVF) obtained by sliding-preserving folding correction and inversion of the XCAT-generated DVFs. (II) From the transformed ground-truth images an acquisition pattern of interleaved motion slices (fig. 2a-c) and surrogate slices (fig. 2d-f) was simulated ($2 \times 2 \times 10 \text{mm}^3$). Motion slices capture the anatomy from left to right and anterior to posterior in sagittal and coronal slices. These overlap by 8mm to facilitate super-resolution image reconstruction. From the surrogate slices the skin and diaphragm motion was measured to generate two respiratory surrogate signals. (III) An SDMM was built from the motion slices and surrogate signals, and an MCSR generated [1]. For the model building phase 993 surrogate and 990 motion slices were simulated, resulting in a 3-fold sampling of each motion slice

position. With a realistic imaging frequency of 0.3s per 2D image, acquisition of this data would take just under 10 minutes. RT treatment delivery was simulated on a later part of the breathing trace. (IV) For the application phase surrogate slices were simulated, the corresponding surrogate signals were calculated, and input to the SDMM. (V) The model DVFs were compared against the ground-truth DVFs and the deformation field error (DFE) was measured for representative instances during the simulated treatment, weighting each instance based on its relative occurrence at beam-on-time. The centre of mass (COM) of the tumour was compared between the ground-truth and the model in the same way as the DFE. For comparison, errors were also evaluated for the no-motion case, i.e. DFE and COM were measured between the ground-truth DVF and the mid-position image.

Results

Figure 2 shows examples of the motion (a-c) and surrogate (d-f) slices, the MCSR (g) and the corresponding ground-truth anatomy (h). The mean weighted DFE error within the simulated anatomy without the SDMM was 3.1mm (i) and was reduced to 1.1mm through application of the SDMM (j). The weighted COM error for the tumour was 3.9mm without and 0.7mm with the SDMM.

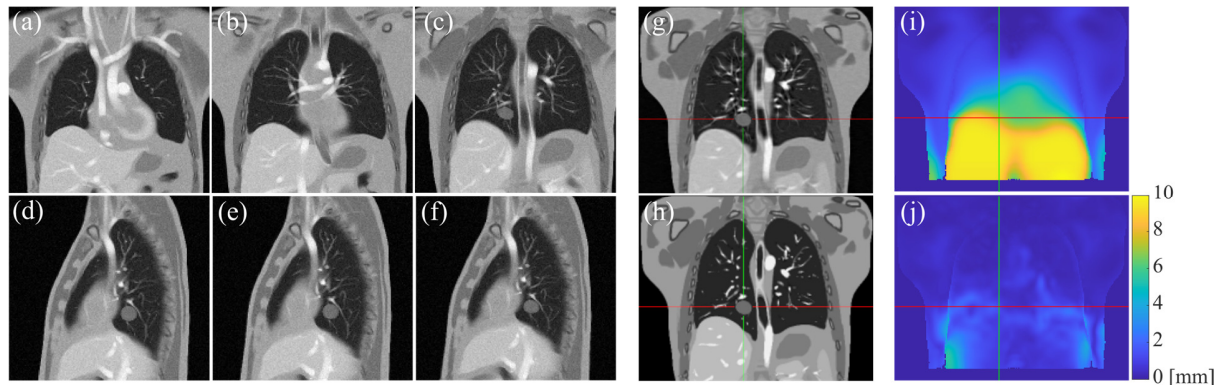


Figure 2: (a-c) Motion and (d-f) surrogate slices used to fit the SDMM, (g) coronal slice of the MCSR image, and (h) ground-truth XCAT anatomy. Mean DFE without (i) and with (j) motion model.

Discussion & Conclusions

The geometric accuracy of our SDMM was quantified using the XCAT phantom, overcoming the lack of ground-truth motion in real subjects. The mean DFE and COM error were reduced below the voxel size highlighting the potential to produce volumetric patient information of high spatial and temporal resolution.

References

[1] McClelland et al. Phys. Med. Biol. 62, 4273–4292 (2017); [2] Segars et al Med. Phys. 37, 4902–4915 (2010)

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†Corresponding Author: b.eiben@ucl.ac.uk