In silico validation of motion-including dose reconstruction for MR-guided lung SBRT using a patient specific motion model

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Introduction

Motion-including dose reconstruction (MIDR) aims at reconstructing the actually delivered dose to the moving anatomy during radiotherapy. However, the time-resolved patient anatomy during treatment is generally unknown. Patient specific motion models (PSMM) built on MR imaging can be used to estimate the time-resolved anatomy during treatment delivery with simultaneous MR imaging on an MR-linac. In this study, a digital 4D phantom was used to validate PSMM-based MIDR for MR-guided lung SBRT.

Materials & Methods

Data. The digital XCAT phantom[1] was used to create a reference anatomy with a lung tumour and corresponding deformable vector fields (DVF) for diaphragm and chest motion traces measured *in vivo* in a volunteer. The DVFs were smoothed, inverted, and used to warp the reference anatomy to produce the ground truth time-resolved anatomy (GT-XCAT) with CT-contrast as well as with MR-constrast (fig1.a).

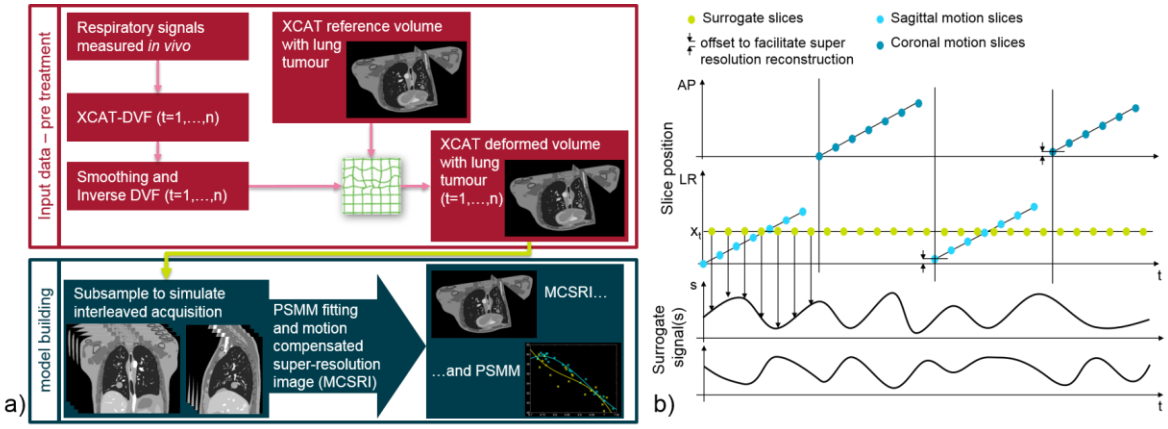


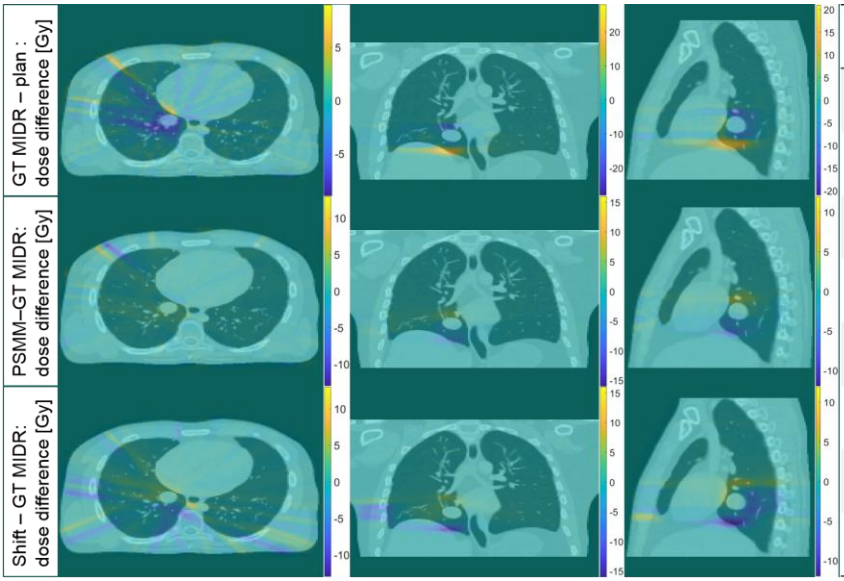
Figure 1: *(a) Pre-treatment: GT-data generation and PSMM building. (b) MR acquisition sequence.*

Workflow. Pre-treatment: GT-XCAT were generated for the first 10 minutes of the motion traces. The MR-contrast volumes were subsampled to simulate an interleaved sagittal/coronal MR acquisition with a sagittal surrogate slice (fig1.b). The skin and diaphragm motion were extracted from the surrogate slices and used as breathing signals to simultaneously fit a PSMM and reconstruct a motion-compensated super-resolution image (MCSRI)[2]. An MR-linac treatment plan for 3-fraction lung-SBRT was designed (9 beams step-and-shoot IMRT, 54 Gy to 95% of the PTV, 7MV) on a reference GT-XCAT with CT-contrast. Intra-treatment: GT-XCAT were generated for the remainder of the motion traces as for pre-treatment (fig1.a). The time-resolved deformations of the MCSRI were estimated by the PSMM using the breathing signals extracted from surrogate slices sub-sampled from GT-XCATs every 0.3s. The reference XCAT anatomy was registered to the MCSRI and deformed to obtain the time-resolved PSMM anatomy with CT-contrast. Treatment delivery was simulated in our in-house emulator[3] updated with an Elekta Unity MR-linac model.

MIDR: The treatment fluence was discretized into sub-beams, each associated with the GT or deformed MCSRI anatomy that it was delivered to. The dose on each anatomy was calculated in a TPS with a Monte Carlo dose engine (2% uncertainty per calculation) and accumulated onto the reference anatomy using GT-XCAT-DVFs or PSMM-DVFs and direct dose mapping. For comparison, shift-MIDR was calculated emulating tumour motion as sub-beam isocenter shifts on the static reference XCAT anatomy[4].

Results

The difference between GT-MIDR and the plan dose illustrates the motion-induced target underdosage as well as noticeable differences in OAR doses (fig2. top). Evaluated against GT-MIDR, PSMM-MIDR was more accurate than shift-MIDR for OAR dose estimation and similar for target dose estimation (fig2.)



DVH endpoint	plan	GT-MIDR	PSMM-MIDR	shift-MIDR
GTV $D_{98\%}$ [Gy]	70.8	67.7	69.0	67.4
GTV $D_{50\%}$ [Gy]	77.7	75.2	75.5	76.0
Heart V_{30Gy} [cc]	48.4	55.6	53.0	64.7
Liver V_{17Gy} [cc]	12.7	21.7	16.6	15.3
Lungs V_{20Gy} [cc]	239.8	227.0	230.2	220.6
Oesophagus $V_{2\%}$ [Gy]	22.6	21.7	21.7	23.1
Aorta $V_{2\%}$ [Gy]	23.4	23.3	23.8	25.0
Spinal Cord $V_{2\%}$ [Gy]	12.5	12.2	12.2	11.0

Figure 2: *Top: GT-MIDR – plan shows an underdosage of the tumour and hotspots at the heart and the liver. Middle: PSMM – GT-MIDR. Bottom: Shift – GT-MIDR. Yellow (resp. blue) colour indicates that PSMM/shift-MIDR is hotter (resp. colder) than the GT. Table: DVH endpoints for the plan and MIDR.*

Discussion & Conclusions

The presented method allows to validate MIDR for different time-resolved anatomy estimation methods. The PSMM based on interleaved MR acquisition and internal breathing signals extraction was shown to be suitable for MIDR of the target and OAR. Shift-MIDR is not intended to correctly estimate OAR dose[4] but may be used for target dose estimation with similar accuracy as PSMM-MIDR. PSMM-MIDR may be used for verification of lung-SBRT treatment delivery on the MR-linac.

References

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Acknowledgements

We thank Tom Bruijnen from UMC Utrecht for his help generating MR-contrast XCAT. We acknowledge funding from: CRUK (C33589/A19727 and /A19908); CRUK ART-NET Network Accelerator Award (A21993); NHS funding to the NIHR Biomedical Research Centre at the RMH and the ICR; Elekta AB.

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