

# Respiratory motion models built using MR-derived signals and different amounts of MR image data from multi-slice acquisitions

E.H. Tran<sup>1†</sup>, B. Eiben<sup>1</sup>, A. Wetscherek<sup>2</sup>, U. Oelfke<sup>2</sup>, G. Meedt<sup>3</sup>, D.J. Hawkes<sup>1</sup> and J.R. McClelland<sup>1</sup>

<sup>1</sup>Centre for Medical Image Computing, University College London, UK. <sup>2</sup>Joint Department of Physics, the Institute of Cancer Research and the Royal Marsden NHS Foundation Trust, UK. <sup>3</sup>Elekta, Medical Intelligence Medizintechnik GmbH, Germany

## Introduction

An MR-Linac can acquire 2D cine-MR images capturing respiratory motion of the internal anatomy before and during radiotherapy treatment. However, 3D information is required for dose calculations and for accurate guidance if there are multiple targets or organs-at-risk that cannot be seen in the 2D plane(s) being imaged. Surrogate-driven respiratory motion models use respiratory signals, in this case extracted from the 2D cine-MR images, to estimate the 3D motion of the internal anatomy [1]. Such models usually require high quality 3D images, but these are obtained by sorting data acquired from different breathing cycles and rely on the assumption of regular breathing and/or long acquisition times. Conversely, this study employs a recently developed unified motion modelling framework which can fit the model directly to the unsorted 2D images, model breath-to-breath variations, and can produce a motion-compensated super-resolution reconstruction (MCSR) [2]. Some of the limiting factors for the potential application of the motion models in MR-guided radiotherapy are long image acquisition and processing times. To overcome these limitations, we investigated the effect of the amount of data used to build 3D respiratory motion models with MR-derived signals.

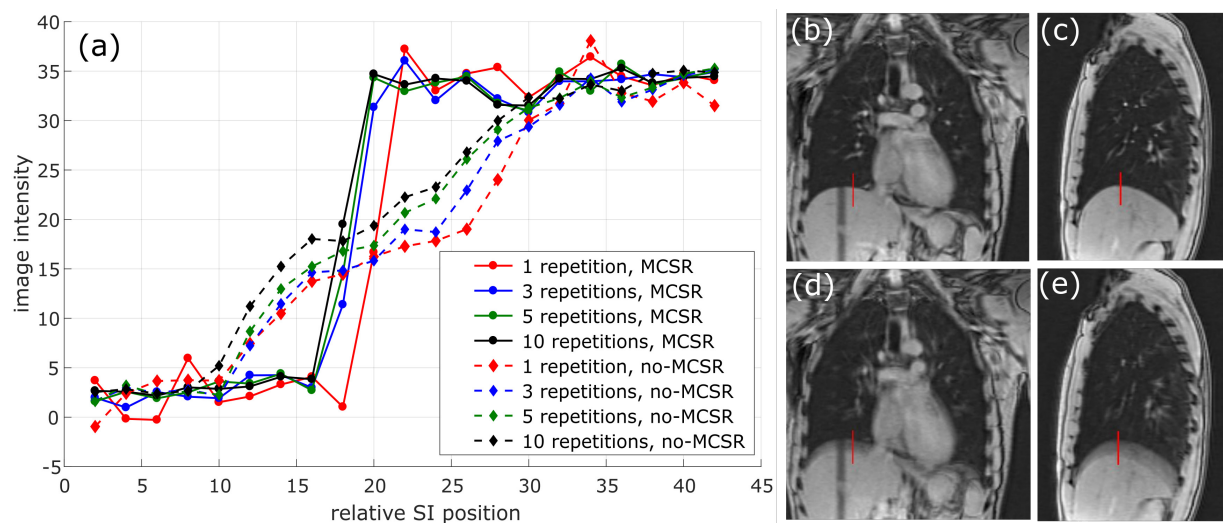
## Materials & Methods

Four volunteers were scanned on a Siemens Aera 1.5T MR scanner using a spoiled gradient-echo sequence. For each volunteer an interleaved multi-slice acquisition was used to acquire surrogate and motion images (resolution  $2 \times 2 \times 10 \text{mm}^3$ ): surrogate images from a fixed slice location with sagittal orientation, motion images covering the thorax with sagittal and coronal orientations, and 8-mm overlap between adjacent slices enabling a  $2 \times 2 \times 2 \text{mm}^3$  MCSR.  $\sim 280$  motion images and  $\sim 280$  surrogate images were acquired in  $\sim 3$  minutes. This acquisition was repeated 10 times with a total acquisition time of  $\sim 30$  minutes. For each volunteer we built motion models using data from 1, 3, 5, and 10 repetitions. Two surrogate signals were generated by applying principal component analysis to the deformation fields obtained from deformable registration of the surrogate images. To compare the image quality of the MCSRs obtained from different amounts of data, we computed the intensity profiles along the boundary between diaphragm and lung. To assess the models' ability to reproduce the motion seen in the original motion images, we deformed the MCSRs using the model estimated motion, and then simulated 10-mm thick slices at the same locations as the motion images. The mean absolute difference (MAD) was calculated between the motion images used to build the models and the simulated images. We could show the improvements when using the models by performing similar analyses on the super-resolution reconstructions obtained without any motion compensation (no-MCSR).

## Results

Fig. 1(a) shows the intensity profiles obtained from the MCSRs and no-MCSRs for 1, 3, 5 and 10 repetitions and Fig. 1(b-e) shows the MCSR and no-MCSR from 3 repetitions, from one volunteer. These show that

the majority of the motion has been compensated for in the MCSRs. The MCSRs from 1 repetition appeared noisier than the MCSRs from 3, 5, and 10 repetitions which had a similar image quality. The estimated respiratory motion visible when animating the MCSRs appeared plausible with breath-to-breath variations. Deep-inhalations, however, were not well-modelled especially when using data from 1 repetition only. Some artifacts were present due to sliding motion, which cannot currently be modelled. Similar results were obtained for all volunteers. The mean MAD (calculated over all images used to build the models and all volunteers) increases as the number of repetitions increases (2.10, 2.25, 2.28, 2.33 for 1, 3, 5, 10 repetitions). This is likely due to the longer acquisition times capturing more variability in the respiratory motion. Higher mean MADs were obtained without motion compensation (2.40, 2.49, 2.51, 2.56 for 1, 3, 5, 10 repetitions). Computational times to build the models without optimized code or GPU implementation were ~30, ~90, ~190, ~380 minutes for 1, 3, 5, 10 repetitions.



**Figure 1:** Line profiles (a) from MCSRs (b-c) and no-MCSRs (d-e) for different repetitions. Coronal and sagittal slice of the MCSR (b-c) and no-MCSR (d-e) for 3 repetitions with line profile position in red.

## Discussion & Conclusions

We built 3D respiratory motion models for four volunteers using MR-derived signals and different amounts of data. Promising results indicate that clinical feasible acquisition and processing times may be possible with a more efficient implementation. Future works will investigate alternative MR-derived surrogate signals and thoroughly assess the MCSRs and models on patient data.

## References

- [1] McClelland et al. Medical Image Analysis 17, 19-42, 2013.
- [2] McClelland et al. Physics in Medicine & Biology 62, 4273-4292, 2017.

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†Corresponding Author: elena.tran.16@ucl.ac.uk