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Similarity-driven motion-resolved reconstruction for ferumoxytol-enhanced whole-heart MRI of congenital heart disease patients

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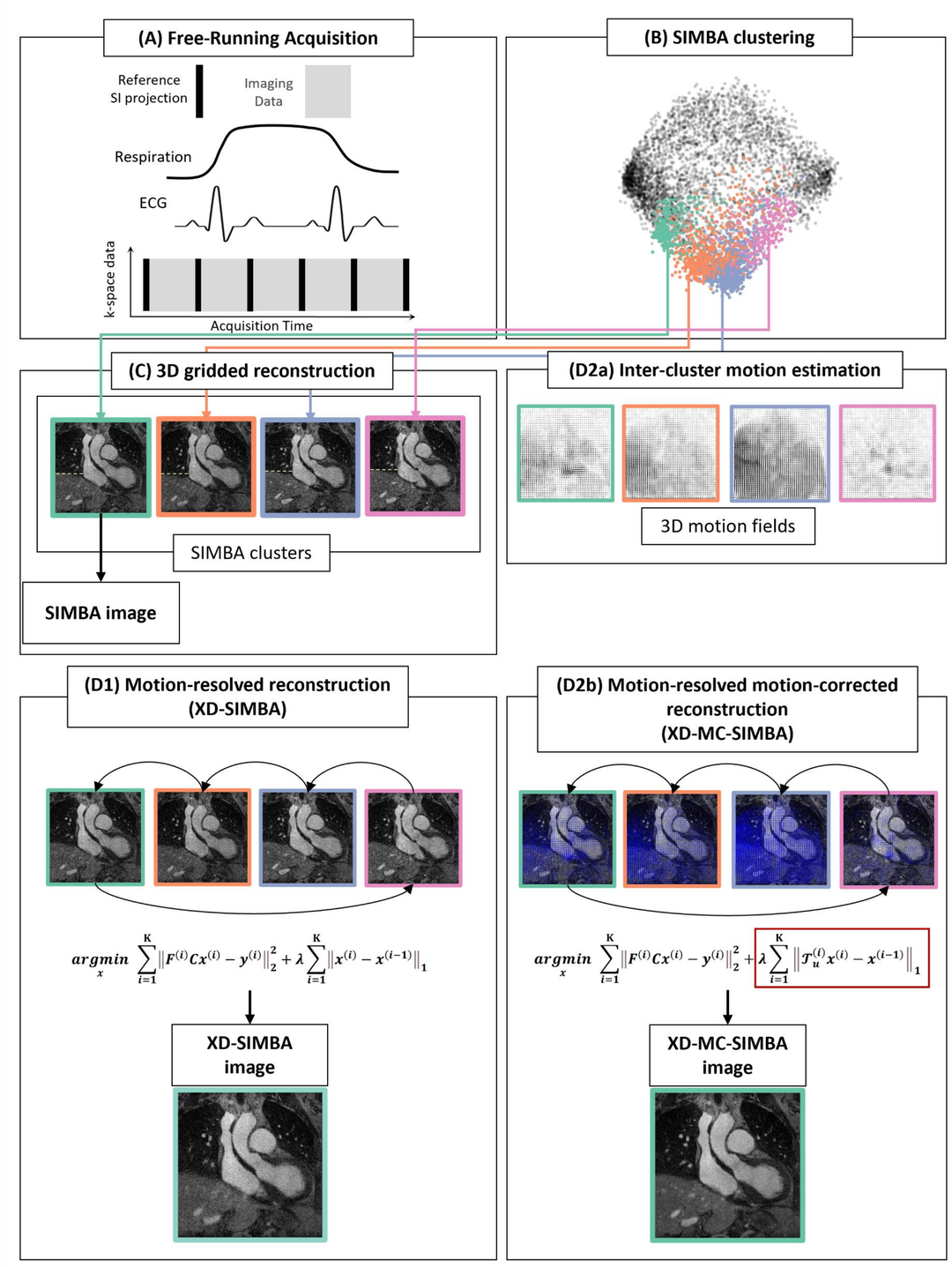
BACKGROUND

Ferumoxytol-enhanced whole-heart MRI enables accurate evaluation of the whole 3D cardiac anatomy, including origin and course of the coronary arteries in patients with congenital heart disease (CHD)[1]. In combination with free-running acquisitions[2] it allows for robust self-gated physiological signal extraction and dynamic XD-GRASP 3D reconstructions[3]. A computationally efficient, static reconstruction of the same free-running data can be obtained using a similarity-driven multi-dimensional binning algorithm (SIMBA)[4], without any assumptions on physiology.

AIMS

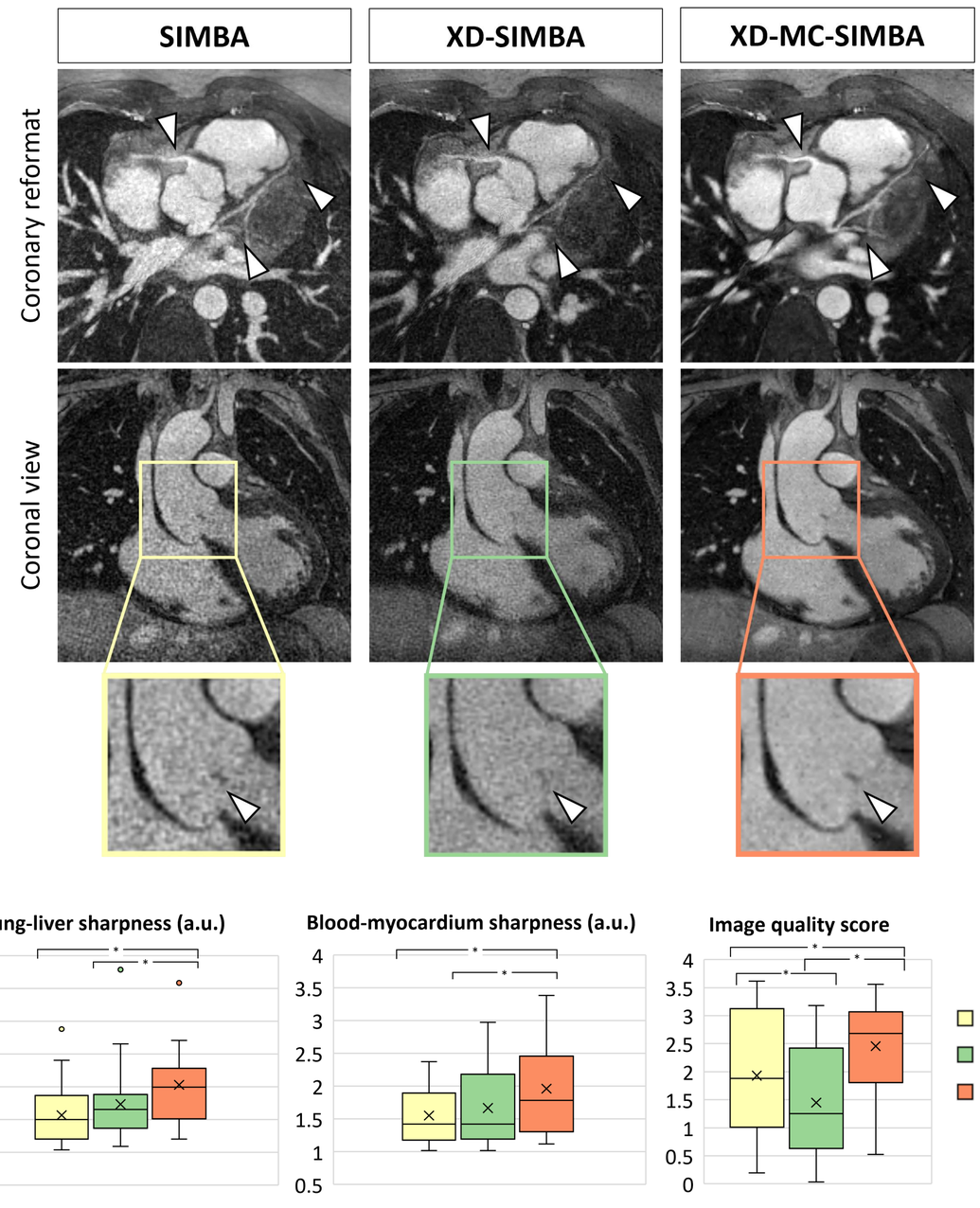
The goal of this work is to explore how SIMBA can be extended to use the redundant information that is shared among the clusters, and ultimately to improve the image quality.

METHODS



- Motion-consistent clusters were integrated as a new dimension in a compressed sensing (CS) reconstruction, with non-rigid inter-cluster motion-fields registration to maximize sparsity.
- 27 CHD patients were scanned on a 1.5T clinical MRI scanner (MAGNETOM Sola, Siemens Healthcare), after injection of ferumoxytol (2-4mg/kg) using a free-running GRE research sequence[2,5].
- We computed the blood-myocardium and lung-liver sharpness, the coronaries visible length and sharpness[6], and assigned an image quality score[7].

RESULTS



CONCLUSION

We developed an improved SIMBA reconstruction (XD-MC-SIMBA) that better exploits the inherent abundancy of information from a free-running acquisition by using the SIMBA clustering as a new dimension of sparsity for CS reconstruction. When combined with a non-rigid inter-cluster motion-field registration, we conclude that XD-MC-SIMBA leads to improved image quality in a cohort of CHD patients.

FREE-RUNNING

SIEMENS Healthineers

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