## Highly Accelerated Free-Breathing Whole Heart T1/T2/Proton Density Mapping

Jing  $\bar{\text{Liu}^1}$  and David Saloner 1,2

<sup>1</sup>Radiology and Biomedical Imaging, University of California San Francisco, San Francisco, CA, United States, <sup>2</sup>Radiology Service, VA Medical Center, San Francisco, CA, United States

### INTRODUCTION

Tissue characterization through parametric mapping of relaxation parameters is useful in a broad range of applications. Simultaneous parametric mapping (T1/T2/proton density) by using an inversion pulse followed with a bSSFP acquisition has been proposed [1]. This approach requires full recovery of magnetization after each inversion pulse and data acquisition train, which is very time consuming, especially for tissues with long T1

relaxation times. Fast T1 mapping has been achieved based on incomplete inversion recovery with a continuous bSSFP acquisition [2]. However, it requires prior knowledge of T2 values of the tissues and has limited applications. In this study, we explored the idea of using incomplete inversion recovery with bSSFP acquisition as well as dictionary matching of acquired data to the evolution curves derived from Block simulations with the same acquisition scheme, aiming to achieve highly accelerated free-breathing 3D T1/T2/proton density mapping in the heart.

## MATERIALS AND METHODS

Highly accelerated free breathing 3D cardiac cine bSSFP imaging [3] was achieved based on a pseudo-random undersampling strategy named CIrcular Cartesian UnderSampling (CIRCUS) [4] combined with a joint multicoil compressed sensing reconstruction k-t SPARSE-SENSE [5,6]. The sequence was modified by turning on inversion pulse every N TRs, where Tiny=N•TR is the time interval between two inversion pulses (called inversion recovery cycle). N readouts are continuously acquired during each inversion recovery cycle before next inversion pulse runs. Fig1 shows the evolution of transverse magnetization from Bloch simulations using this IR-bSSFP sequence. The evolution of magnetization between inversion pulses is consistent after the 2<sup>nd</sup> inversion recovery cycle. Given scan parameters (flip angle FA, TR, N), we can generate a dictionary containing the evolution curves with a range of T1 and T2 values. With the acquired data, we can derive the voxel-based signal change

throughout inversion times (TIs) and find the best match in the dictionary, which provides the T1 and T2 values for that voxel. Data was acquired on a 3.0T MR scanner (GE Medical Systems, Milwaukee, WI) with an 8-channel cardiac coil. A 3D gradient-echo sequence (bSSFP) using CIRCUS was applied for 2 mins 20s, with FOV=340mm, TR/TE=3.8/1.4ms, FA=30°, BW= ±62.5kHz, slice thickness of 8mm, and image matrix= $192\times160\times16$  (75% in  $k_v$  and  $k_z$ ). A non-selective inversion pulse was applied at every Tinv=3.5s (N=916). ECG triggers were saved for retrospective cardiac gating, and bellows signals were saved for respiratory gating (50% gating efficiency was applied). Data was resorted into a matrix of cardiac phases and TI phases. In this preliminary study, we reconstructed cardiac phases and TI phases with a relatively low temporal resolution of 200ms, due to the 3D coverage and limited scan time.

# RESULTS AND DISCUSSION

The best cardiac phase was chosen for generating the parametric mappings. Fig.2 shows our preliminary results of T1, T2, and proton density mappings, as well as the synthetic image at steady states.

Compared to the conventional method that requires full recovery, our proposed approach largely reduces the scan time.

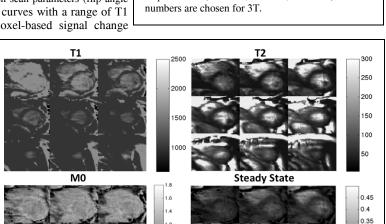


Fig.2 Highly accelerated free-breathing whole heart T1, T2 and proton density mappings, and synthetic image of steady state signals.

The method based on complete recovery does not differentiate the tissues of the same T1/T2 ratio, however, the incomplete recovery curves are always unique with different T1 and T2 values.

The timing of the inversion pulses of this method does not depend on the ECG triggers as most of other cardiac T1 mapping methods do. In addition, the variation of the cardiac cycles spreads the distribution of the TI phases to the cardiac cycle. The current preliminary results show an underestimation of T1 values of myocardium. Further investigations will be conduct.

A method based on inversion recovery and bSSFP acquisition has been developed. Our preliminary results have shown its great potential for freebreathing whole heart T1/T2/proton density mapping.

## REFERENCES

1. Schmitt P, et al, MRM, 51:p661, 2004. 2. Gai ND, et al, MRM, 35:p1437, 2012. 3. Liu J, et al. ISMRM, p429, 2014. 4. Liu J, et al. QIMS, 4(1):57-67, 2014. 5. Otazo R et al. MRM 64(3):767-76, 2010. **6**. Feng L et al, MRM 70(1):64-74, 2013.

Myocardium T<sub>4</sub>=1500ms, T<sub>0</sub>=50ms

Blood

myocardium and blood by applying inversion pulse every Tinv=3s followed with continuous bSSFP acquisitions (TR=4ms, N=750, FA=30°). T1/T2

0.3

0.25 0.2

0.15

0.1

0.05