Accelerating 3D Molecular MR Imaging using Compressed Sensing

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INTRODUCTION: Molecular MR imaging is an emerging technique for the assessment of cardiovascular risk [1-3]. This technique provides molecular differentiation among tissues (rather than anatomical differences) by using target-specific MR contrast agents (CA) leading to regionally modified relaxation rates. Molecular images using gadolinium based CAs are characterized by very localized and high T1-contrast enhancement, which, in most of the applications, results in sparse images. However, molecular MRI suffer from relatively long acquisition times to provide high spatial resolution together with sufficient signal to noise ratio (SNR). Considering the SNR constraint and the sparse nature of the desired images, here we propose to accelerate the acquisition of molecular MRI by using the recently introduced SparseMRI technique [4]. SparseMRI is a reconstruction technique based on the Compressed Sensing (CS) theory, which exploits the fact that sparse (or compressible) images can be recovered from randomly undersampled data via a non-linear reconstruction.

CS, using a L_1 norm minimization and the image itself as the sparsity domain, was implemented in Matlab and applied to two 3D preclinical studies: a) detection of venous thromboembolism (mouse model), and b) atherosclerosis and ventricular ablation (swine model). The effect of undersampling on SNR, contrast-to-noise ratio (CNR), wall sharpness (WS) and vessel wall thickness (WT) were analyzed.

METHODS: CS reconstruction, using L_1 norm minimization and sparsity in the image domain, is given by: *Min* $\|\mathbf{m}\|_1$, s.t. $\mathbf{F_u m} = \mathbf{B}$, where $\mathbf{m}$ denotes the reconstructed image, $\mathbf{B}$ is the acquired *k*-space data and $\mathbf{F_u}$ is the undersampled Fourier operator. This reconstruction was implemented in Matlab with a non-linear conjugate approach [4], and retrospective random undersampling in both phase-encoding planes (k_y-k_z) was performed for different undersampling factors *Q*.

a) Venous thromboembolism mouse model: A 3D segmented gradient-echo inversion recovery sequence (3D IR-TFE) was performed on a 3T Philips scanner using a fibrin-binding contrast agent, (EP-2104R, EPIX Pharmaceuticals), and a dedicated small animal surface coil. Relevant scan parameters include: FOV = *45×45×15mm*, matrix size = *768×768×30*, resolution = *0.1×0.1×1mm*, TR/TE/flip angle = *42/13ms/30°*, dose of *8 µmol/kg* EP-2104R, acquisition time ≈ *20 minutes*.

b) Aortic vessel wall and ablation lesions in a swine model: 3D IR-TFE imaging was performed on a 1.5T Philips MR scanner using an elastin-binding contrast agent (BMS-753951, Lantheus Medical Imaging) and a 5-array receiver coil. Relevant scan parameters include: FOV = *320×320×45mm*, matrix size = *512×512×30,* resolution = *1.25×1.25×3mm*, TR/TE/flip angle = *4.9/1.47ms/30°*, dose of *0.1 mmol/kg* BMS-753951, acquisition time ≈ *8 minutes*. SNR, CNR, WS and WT were computed for the fully sampled and undersampled reconstructions with *Q = 4 to 7* (using the Soap-Bubble tool [5]). SNR and CNR were computed for the aortic vessel wall (between the aortic wall and the surrounding blood pool) and liver (between the liver and the blood pool), measuring signal and noise in the same region of interest for both cases.

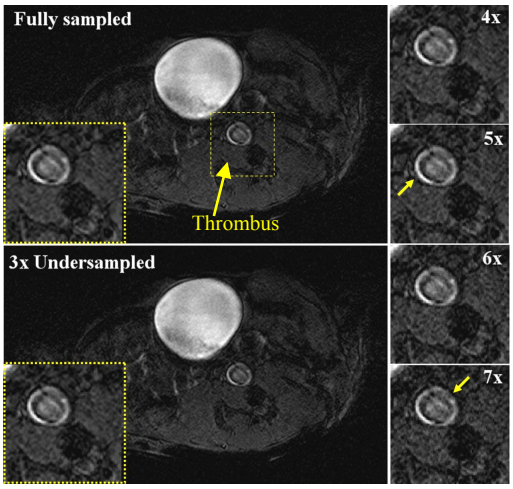

Fig1: Venous thromboembolism mouse model: fully sampled and 3x CS reconstruction. Enlarged view of the thrombus for CS reconstructions with Q= 4 to 7 are also included.

RESULTS: *a) Venous thromboembolism mouse model:* Reconstruction results for an undersampling factor of *3* are shown in Fig.1. Enlarged views of the thrombus are also included for *Q = 4 to 7*. Good overall image quality is achieved for *Qs* up to *4*. A slight increase in noise in the surrounding tissues is observed with *Q = 5* and *6*, however good depiction of the thrombus is still achieved. Increased artifacts errors are observed in the thrombus for *Q = 7*.

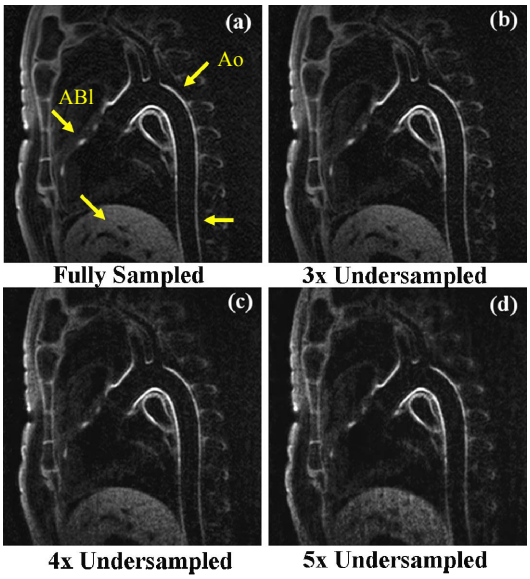

Fig2 Aortic vessel wall (Ao) and ablation lesions (ABl): fully sampled and CS reconstructions for Q = 3 to 5. CS recons preserve intensity and sharpness of the Ao wall and ABl.

b) Aortic vessel wall and ablation lesions in a swine: Reconstruction results for *Q = 3 to 5* are shown in Fig.2 in a reformatted plane. Quality measurements for all the undersampling factors are shown in Fig.3. Good overall image quality is observed for undersampling factors up to *4*. For a *Q* of *5* (Fig2.d) noise and reconstructions artifacts are observed for some anatomic areas such as the liver, while the areas of interest (aortic vessel wall and ablation lesions) demonstrate preservation of high signal intensities and image sharpness. SNR and CNR of the aortic vessel wall were almost constant for *Q* up to *4*, while an immediate drop in SNR and CNR was observed for the liver. High levels of vessel sharpness (>60%) were achieved for all acceleration factors and average wall thickness was preserved for *Qs* up to *5*.

CONCLUSIONS: Molecular MRI can be highly accelerated exploiting the sparsity in the image domain by using Compressed Sensing. Good overall image quality was achieved with acceleration factors up to *4* in 3D preclinical studies of venous thromboembolism and aortic vessel wall, which would result in acquisition times of *5* and *2* minutes respectively. This technique may be especially useful for small animal studies due to limited availability of multiple channel-coils. Quality measurements showed high SNR in the areas of interest.

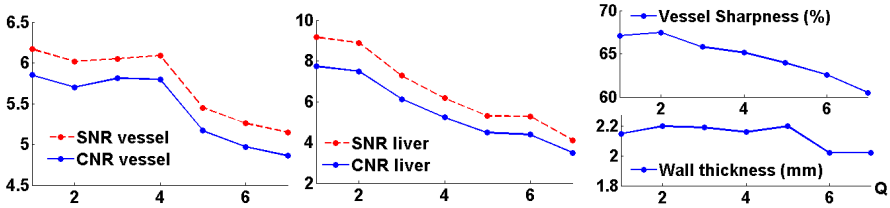

Fig3: Quality measurements for aortic vessel wall, comparison between fully sampled (Q = 1) and CS reconstructions with undersampled factors from 2 to 7.

REFERENCES: [1] Botnar et al, Circulation 2004,[2] Spuentrup et al, Circulation 2008, [3] Sosnovik et al, TMRI 2008, [4] Lustig et al, MRM 2007, [5] Etienne et al, MRM 2002