A networked GPU reconstructor within the clinical workflow for rapid fat quantification.

G. Kowalik[1,2], J. A. Steeden[1,2], D. Atkinson[2], and V. Muthurangu[1]

[1]Centre for Cardiovascular MR, UCL Institute of Child Health, London, United Kingdom, [2]Centre for Medical Image Computing, UCL Department of Medical Physics & Bioengineering, London, United Kingdom

Introduction: Myocardial fat quantification is increasingly important in studies of diabetes and obesity [1]. T2 corrected IDEAL [2] is a relatively new method that provides spatial quantification of fat. However, the requirement for multiple echoes and cardiac gating results in long breath-holds. Furthermore, reconstructions are usually time-consuming and implemented off-line. These factors limit the usefulness of T2 IDEAL in the clinical environment. In order to provide a more clinically useful technique we present a T2 IDEAL sequence accelerated with GRAPPA and partial Fourier, which is reconstructed online using a networked GPU.

Aims: The aim is to provide an image reconstruction platform to facilitate computationally intensive algorithms, such as IDEAL, within a clinical environment.

Methods: The framework is divided into three separate layers to allow porting across different MR systems. Currently it is implemented on 1.5T MR scanner (Avanto, Siemens Medical Solutions, Erlangen, Germany) with ICE VB17 software. *Client reconstruction layer* – organises reconstruction steps in form of commands and data transfers. It is implemented within the scanner's reconstruction pipeline. *Networking layer* – uses omniOrb C++ free implementation of CORBA technology. It is used to create two sides of the client-server communication pattern. *Server reconstruction layer* – provides a unified reconstruction interface. It is a set of methods through which each reconstruction is accessible.

Fig. 1. System architecture.

A phantom study of a raw meat was performed to evaluate and validate the implementation. Additionally, in-vivo quantification was performed in the heart (short axis and four chamber view). All scans were performed using standard Spoiled Gradient Echo sequences. All cardiac scans were performed within a breath-hold and were ECG gated.

The cardiac imaging has the following steps. Data were acquired undersampled by a factor of two and additionally, partial Fourier (6/8) was used. The manufacturer's native code is first used to reconstruct k-space (GRAPPA). Next data is sent over the network to the external computer. A GPU accelerated version of *homodyne* T2-IDEAL [3] is applied. The resulting water and fat images are sent back to the scanner system. A water-fat fraction image is computed as a |fat| / (|fat| + |water|).

In-vivo scan settings: FOV: 300x300mm, matrix: 128x128, TEs: 2.32, 3.76, 5.2, 6.64, 8.08, 9.52 ms, TR: 14ms, slice thickness: 8mm, bandwidth: 814 Hz/pixel, flip angle: 15°.
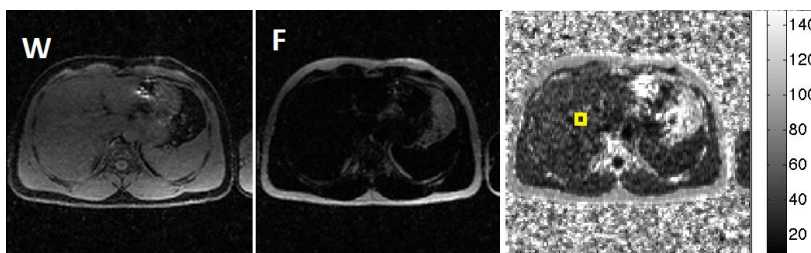

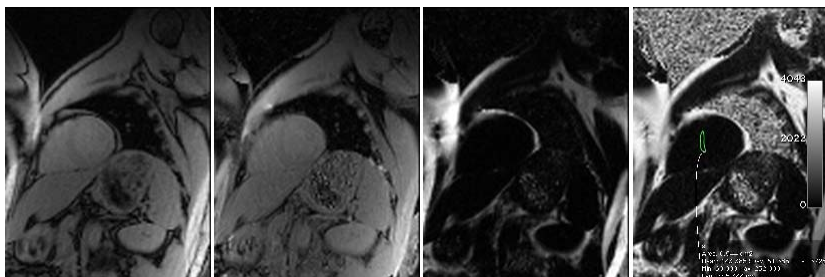Fig. 2. Liver image: water and fat images on left; T2* map on right. Selected point: 14.7ms.

Fig. 3 Short axis: echo, water, fat and fat fraction; Selected fraction: 4%.

Results: Reconstructed images of the phantom gave a good separation of water and fat. A good agreement in water-fat fraction was found between MRS and IDEAL in the meat (2% vs. 3%, respectively) and in the fat (70% vs. 76%, respectively). For a healthy population of 6 volunteers, the results of myocardial fat quantification gave consistent fat content 4.3% +/- 0.7%. Reconstruction of a single 128x128 slice, acquired with 3 coils and partial k-space acquisition, took 20ms. This time is measured from initialisation of connection to arrival of the last reconstructed image. Due to the partial k-space acquisition, the time for a breath-hold has been reduced to 9-13 sec, depending on heart rate. This makes the examination feasible for sick patients and children, who may find long breath-holds difficult.

Discussion: We have demonstrated a rapid reconstruction of a complex and time-consuming T2 IDEAL algorithm, which made it clinically attractive. Cardiac scans demand introduction of undersampling to speed up acquisition time. Resulting data sets need more time to reconstruct than their fully sampled versions. *Homodyne* version of T2 IDEAL for partially sampled k-space requires additional processing steps making it even longer to reconstruct. GPUs have been already widely used [4] to overcome this problem, but none of the studies reported a full integration with MRI system. Although, the authors of [5], presented a connection with an external reconstruction system, it is a fixed solution without data being fed back into a scanner system. Our flexible solution fully utilises the computational power of GPU and allows immediate assessment of the results. The elevated fat fraction for in-vivo examinations can be caused by T1 relaxation and image noise bias, as described in [6]. In a future, we will consider implementation of a more complex version of IDEAL [7] for more precise fat quantification.

References: [1] Sharma S. et al. FASEB J 2004(18)1692–1700; [2] Yu H. et al. JMRI, 2007(26):1153–1161; [3] Reeder S.B. et al. MRM, 2005(54):586–593; [4] Stone S.S. et al. CF 2008:261-272 ; [5] Roujol S. et al. MRM 2009(62):1658–1664; [6] Liu C.Y. et al. MRM, 2007(58)354–364; 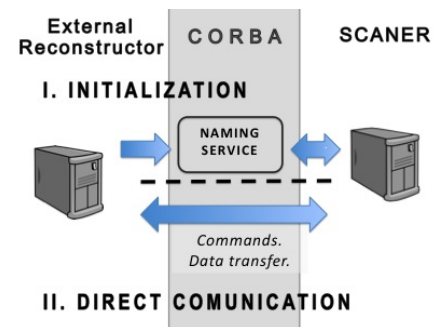[7] Yu H. et al. MRM, 2008(60)1122–1134