Direct Virtual Coil (DVC) for bone tumor temperature mapping

Yuxin Hu[1], Shuo Chen[2], Bingyao Chen[3], Jiafei Yang[3], Xing Wei[3], Shi Wang[2], and Kui Ying[2]

[1]Tsinghua University, Beijing, Beijing, China, [2]Engineering Physics, Tsinghua University, Beijing, China, [3]Department of Orthopedics, First Affiliated Hospital of PLA General Hospital, Beijing, China

Target audience: Radiologists and MR scientists working on MR thermometry and fast imaging.

Introduction: The long scan time of MR thermometry has limited its application on bone tumor thermotherapy, where high speed and temperature accuracy are required. While parallel imaging can speed up the acquisition, the corresponding reconstruction usually requires significant computation, especially when large coil arrays are used. Direct Virtual Coil (DVC) is a method that combines parallel imaging and coil combination into one step to reduce the reconstruction time [1]. This work evaluates the feasibility of DVC for MR thermometry on bone tumor thermotherapy compared to traditional parallel imaging methods like GRAPPA [2].

Methods and materials: GRAPPA is a coil-by-coil auto-calibrating parallel imaging method. Individual coils are usually combined together after GRAPPA reconstruction. DVC combines these two steps into one, and targets to directly reconstruct a virtual coil instead of individual coils, where the virtual coil resembles the SOS coil combination. The pipelines of GRAPPA and DVC are shown in Fig.1.
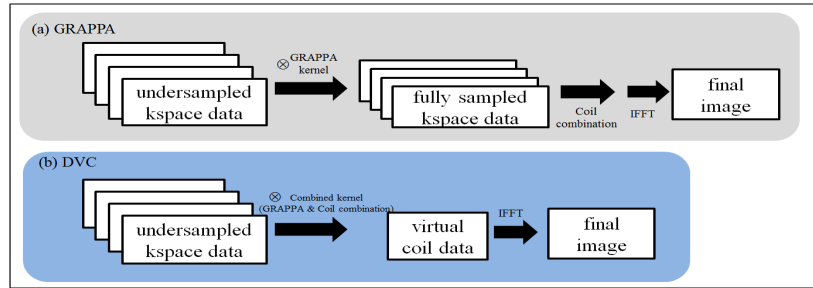

Fig.1 *Flowcharts of GRAPPA and DVC.*

To compare the performance of DVC and GRAPPA on MR thermometry, a fully-sampled dataset collected on a Philips 3 Tesla system (Philips, Best, the Netherlands) with a 15-channel coil was used. The dataset was acquired with the following imaging parameters: TR = 18 ms, TR = 13 ms, flip angle = 15°, acquisition matrix size = 480×480, FOV = 240mm × 240mm, slice thickness = 4mm. The scan time for one frame is 8.6s. The dataset was retrospectively undersampled by factors of 2, 3, and 4 with 30 auto-calibrating lines. DVC and GRAPPA were performed to reconstruct the undersampled dataset. Temperature maps were estimated in each reconstruction using proton resonance frequency (PRF) with the fully sampled dataset as reference [3].

Results: The fully sampled images and reconstruction results of GRAPPA and DVC with an acceleration factor of 2 are shown in Fig.2. The reconstruction speed of DVC is as twice as GRAPPA. The reconstruction time of GRAPPA and DVC for each frame is 82.6 seconds and 38.2 seconds, respectively. Both reconstructions had negligible error compared to the reference. The corresponding temperature error maps for these two reconstructions were estimated and shown in Fig 3. Spinal cord was manually segmented (Fig 2d) for the bone tumor temperature mapping. For acceleration factor of 2, GRAPPA achieved slightly better temperature mapping accuracy than DVC and the error of DVC is about 0.1℃ higher. Fig.4 shows the temperature error of these DVC and GRAPPA with different acceleration factors. In general, DVC and GRAPPA had similar temperature mapping accuracy. The largest error was within 1.5 degree.

Discussion and conclusion: It has been demonstrated that DVC could be potentially used for MR thermometry in bone tumor thermotherapy. DVC can achieve similar temperature mapping accuracy compared to traditional parallel imaging method under different acceleration factors while it can be about twice faster than GRAPPA.

References: [1] Philip J. Beatty et al. MRM, 2014. [2] Griswold M A et al. MRM, 2002. [3] Ishihara Y et al. MRM, 1995.
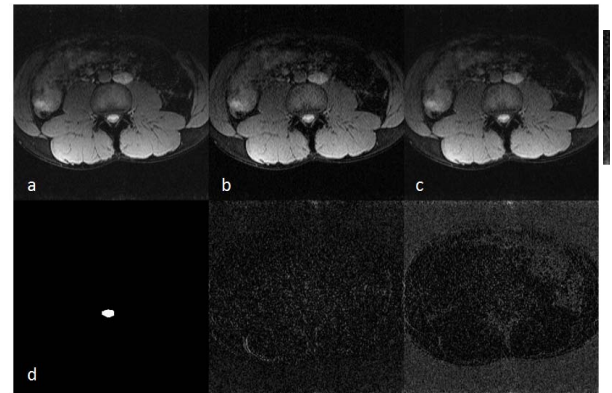
Fig.2 *Comparison of fully sampled image(a) and images reconstructed by GRAPPA(b) and DVC(c) at a reduction factor of 2. Spinal cord is manually segmented in (d). 5x error maps were shown in second row.*
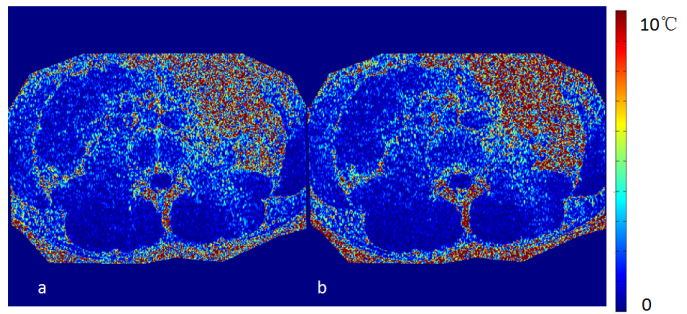

Fig.3 *Comparison of temperature error maps reconstructed by GRAPPA(a) and DVC(b) at a reduction factor of 2 with the fully sampled image as the reference.*
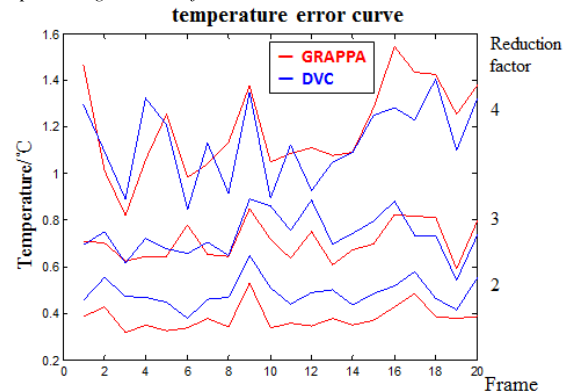

Fig.4 *The temperature error curves of two different reconstruction methods (GRAPPA (red line) and DVC (blue line)) for the under-sampled data when the reduction factor is 2, 3 and 4.*