

# Imaging of Fluid using a Divided Inversion Recovery Technique (DIRT)

J. W. Goldfarb<sup>1</sup>, N. Reichek<sup>1</sup>

<sup>1</sup>Department of Research and Education, Saint Francis Hospital, Roslyn, NY, United States

**Introduction:** The goal of this study was to develop and test a method that provides images of only fluid. A IR SSFP method is presented which spatially displaces very long  $T_1$  species (fluid). The imaging FOV is made such that it is twice the object's size and the image is then divided into two parts (spatially displaced fluid and other tissue). Hence, the name of the technique: Divided Inversion Recovery (DIRT). The cause of the displacement of long  $T_1$  species in a segmented IR SSFP pulse sequences follows directly from the evolution of the magnetization during excitation and recovery. The transverse ( $M_x$ ) and longitudinal ( $M_z$ ) magnetizations during an IR gradient refocused pulse sequence (TR/TE/TI/FA=2.4 ms / 1.5 ms / 250 ms / 50 degree with 64 rf excitations/k-space lines per segment) with two segments were theoretically simulated and are plotted in Fig 1. Figs 1a and c  $T_1=4500$  ms  $T_2=2200$  ms (Long  $T_1$  to simulate fluid), Fig 1b and d,  $T_1 = 250$  ms  $T_2= 50$  ms (Short  $T_1$  to simulate fat). A single segment without data acquisition (DAQ) was used as preparation. A linear ramp of ten rf pulses was used for steady-state preparation before data acquisition.

When the  $T_1$  was much longer than the time between inversion pulses (Figs 1b and d), the longitudinal magnetization does not have a chance to pass through the null point ( $M_z=0$ ) and at the beginning of the next segment, the longitudinal magnetization will have an opposite sign. If phase-encoding is performed such that interleaving of the segments is done prior to image reconstruction with the discrete Fourier transform, species with long  $T_1$ s will have an alternating phase in the raw data reconstruction matrix, effectively being multiplied by  $-1$  on alternating rows. This multiplication is commonly used in MR image reconstruction and is equivalent to shifting the reconstructed image by half of the FOV.

**Methods:** All imaging experiments were performed on a 1.5T whole body MRI system (Magnetom Siemens Sonata, Erlangen, Germany). Twelve subjects participated in this study. Imaging was performed using an inversion recovery TrueFISP sequence (TR/TE/FA=2.4/1.2/50; Matrix=256x512; Voxel size=2x1.8x8mm; 128 phase encoding lines per segment; interleaved segments; 1 dummy heartbeat; BW=1180 Hz/pixel with linear filling of k-space). Region-of-interest signal intensity measurements were made in fluid regions including CSF and pericardial effusions. The ratio was calculated to determine the effectiveness of the method and signal measurements were compared using a paired student's t-test.

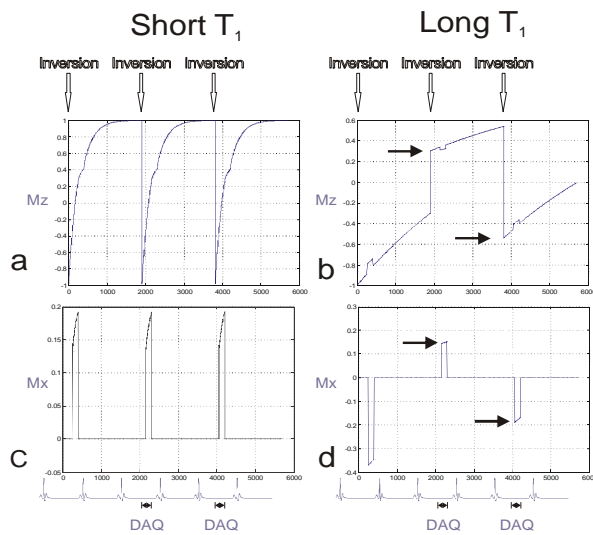


Figure 1. Plots of Bloch simulation of a segmented IR TrueFISP sequence. Three segments are shown. Data acquisition (DAQ) is done during the second and third segments. The first being a preparatory or so-called dummy segment where data is not acquired. Arrows show the alternation in polarity of the longitudinal magnetization ( $M_z$ ) and the observed magnetization ( $M_x$ ) in successive segments.

**Results:** Fig. 2 shows example acquisitions. The fluid signal intensity was suppressed by a factor of  $10.2 \pm 15$  with a min of 3.6 and a max of 56. The signal measured in the divided images was significantly different ( $p < 0.01$ ).

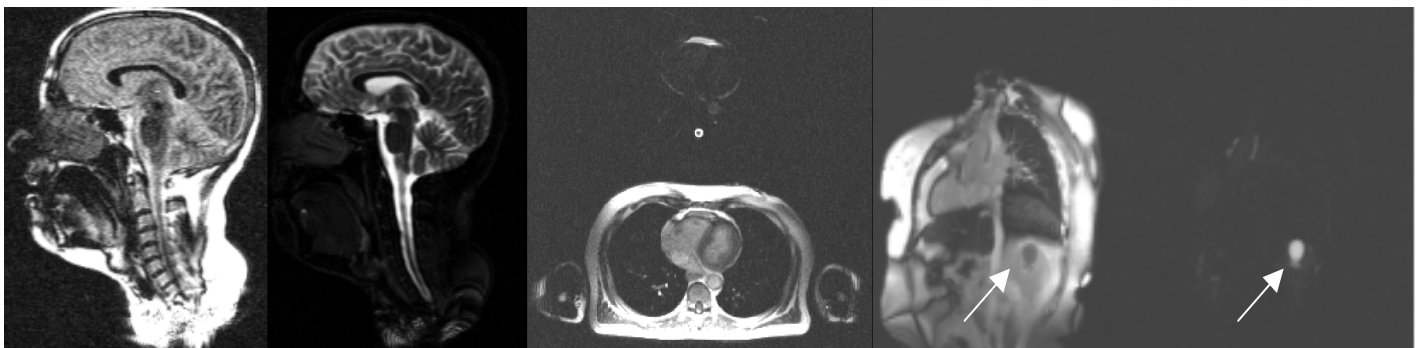


Figure 2: Example images using the Divided Inversion Recovery Technique (DIRT) for fluid separation: Images depict CSF, a pericardial effusion and a renal cyst.

**Conclusions:** A method has been presented which effectively separates fluid from other tissues based on the long  $T_1$  of fluid. Fluid imaging is usually performed exploiting the long  $T_2$  of fluid. The method presented here may be useful for easy segmentation and volume calculations of fluid structures and discrimination between fluid and fat in SSFP, which remains difficult due to the  $T_2/T_1$  weighting of the sequence.