Whole-Body STIR Diffusion-Weighted MRI in One Third of the Time

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Introduction: Whole body (WB) short TI inversion-recovery (STIR) diffusion weighted (DW) echo-planar imaging (EPI) is becoming increasingly important as a contrast agent free method for screening and treatment monitoring [1, 2]. The selective IR pulse and the associated acquisition module (excitation of a single slice, diffusion preparation, and EPI readout) are often played out sequentially with TI times between 170 ms (1.5T) and 240 ms (3 T). This results in long acquisition times for WB-DWI, typically in the order of 5–7 min per station (25-cm coverage, 2b-values, and multiple averages/diffusion directions). Hence more than 20 minutes are needed for scanning from head to pelvis. Reducing scan times in WB-STIR-DW-EPI is therefore desirable.
In fluid (CSF) attenuated IR of the brain, with significant longer TI times, interleaved IR is used to shorten scan time. If the duration of the acquisition module is shorter than the TI fill time (idle time between IR module and acquisition module) the same interleaving techniques can be used to shorten acquisition times of STIR-DW-EPI. This work describes a recently developed DW-EPI sequence, which utilizes an efficient interleaving scheme [3], and to report first results with this sequence on a clinical WB scanner with high gradient performance.

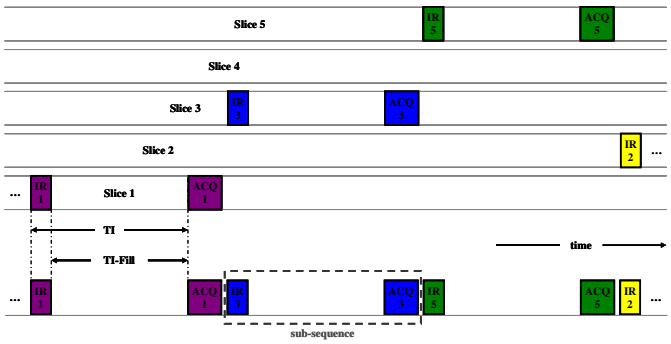

Figure 1: Sequential IR acquisition scheme of the old sequence for 5 slices. Only the inversion and acquisition of the three odd numbered slices and the inversion of the first even numbered slice are shown due to limited space. On the bottom of the figure the IR and acquisition modules of all slices are drawn in a single row to illustrate the time intervals not used for imaging. A sub-sequence is defined as one IR module and the following acquisition module. Here IR and acquisition module of a particular sub-sequence belong to the same slice.

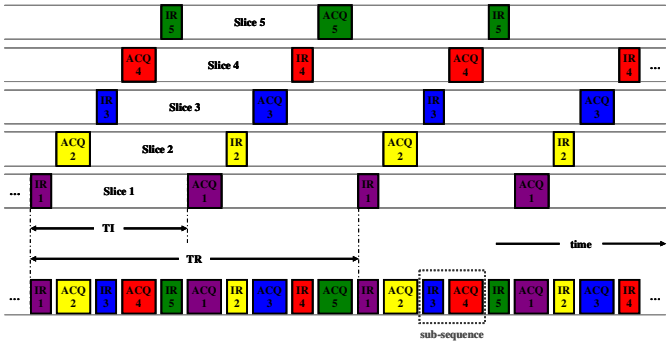

Figure 2: Interleaved IR acquisition scheme of the new sequence for 5 slices. IR and acquisition modules that belong to the same slice are drawn in the same color. On the bottom of the figure the IR and acquisition modules of all slices are drawn in a single row.
In the example shown here the IR pulse of a sub-sequence belongs to the acquisition module of the sub-sequence after next.

Methods: Figure 1 shows the inversion and acquisition of 3 slices using the old scheme. A sub-sequence consists of an inversion module, a wait time TI-Fill and an acquisition module. The inversion and acquisition module of the sub-sequence belongs to the same slice. Sub-sequences of different slices are executed sequentially. Figure 2 shows the interleaving scheme of the new sequence. The time period between the inversion and acquisition of a particular slice is used to invert or acquire up to four different slices. Again, the sequence can be composed of sub-sequences consisting of a single inversion and acquisition module. However, the idle time between inversion and acquisition module of the sub-sequence is shorter and the acquisition module of a particular sub-sequence does not belong to the inversion pulse of the same sub-sequence but to the inversion pulse of a foregoing sub-sequence. Since the total number of sub-sequences does not change, the total scan time is approximately halved or reduced to one third depending on whether one or two sub-sequences fit between the inversion and acquisition of a particular slice.

Results & Discussion: Figure 3 shows MIP images of a 25-year-old healthy female volunteer acquired with a 3T Siemens MAGNETOM Prisma whole body scanner (maximum gradient amplitude 80 mT/m, slew rate 200 T/m/s), which is not yet commercially available . Before the MIP operation the 50 axial b=800 s/mm^2 trace weighted images of a single step were grey scale inverted and coronal reformatted. The scan for the left image used the old sequential scheme of Figure 1 and was performed in 6:34 min:s (including the acquisition of the b = 50 s/mm^2 images). The scan for the right image used the new scheme of Figure 2 and was performed in 2:11 min:s. TR was 16410.5 ms (1 concatenation) versus 2735.25 ms (2 concatenations). Further imaging parameters were: matrix: 150; acquired resolution: 2.87×2.87 mm^2; slice thickness: 5 mm with zero gap; TI = 240 ms; TE = 65ms; Stejskal-Tanner diffusion preparation with b = 50/800 s/mm^2, 3 diffusion directions (trace weighted), 2/5 averages for low/high b-value; PAT acceleration factor 2; free-breathing; total: 24 excitations per slice.
At the time of abstract submission the new scheme was only tested in volunteers. In some volunteers the dense scheme of Figure 2 could not be realized due to SAR constraints. In these subjects we used a less compact scheme with only one sub-sequence between the inversion and acquisition of a particular slice (TR = 4102.75 ms; TA = 3:17 min:s). Parts of the saved scan time can be invested to improve the image quality. For example, using partial slice overlap (slice distance less than slice thickness) leads to smooth appearance of the nerves in the coronal MIP. For the right image of Figure 3 the sequence acquired the slices in two concatenations (acquisition of the odd slices is finished completely before the acquisition of the even slices is started) to reduce cross-talk. This additionally shortens the minimum TR. The T1 value of some malignant hepatic lesions is relatively long. Clinical evaluations are necessary to determine if the inherent shorter TR of the fast scheme has a negative impact on lesion visibility.

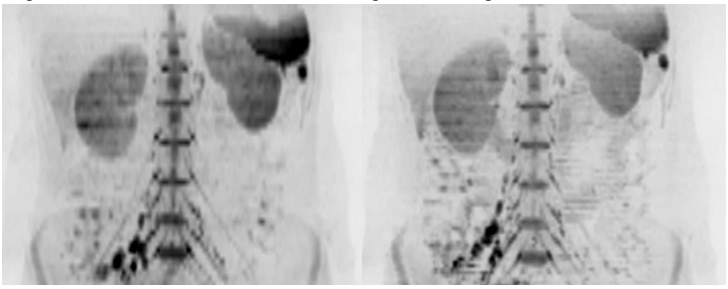

Figure 3: MIP images of a healthy female volunteer. Before the MIP operation the 50 axial, trace weighted b=800 s/mm^2 images were grey scale inverted and reformatted into the coronal plane. The scan for the left image used the old sequential scheme of Figure 1 and was performed in 6:34 min:s (including the acquisition of the b=50 s/mm^2 images). The scan for the right image used the new scheme of Figure 2 and was performed in 2:11 min:s.

References: [1] Takahara et al. Radiat Med 2004; 22(4):275-282; [2] Padhani et al. Radiology 2011; 261(3):700-718; [3] Oh et al. MRI 1991; 9:903-908.