Faster Abdominal MRI Examinations by Limiting Table Movement

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1 How to create a minimized shimming protocol.
   Modifications will be made to pulse sequences following the initial localizers (1A).
   For the second sequence in the scan protocol, ‘Shim mode’ is set to ‘Standard’, and ‘Adjust with body coil’ is selected (1B).
   For the third and subsequent sequences, ‘Positioning mode’ is set to ‘FIX’ (1C), ‘Shim mode’ is set to ‘Standard’, ‘Adjust with body coil’ is selected, and ‘Adjustment Tolerance’ is set to ‘Maximum’ (1D).
   Finally, for the third sequence, a reference is created to the table position of the second sequence (1E). The same reference is created for all subsequent sequences (1F).
Hepatic magnetic resonance imaging (MRI) is widely used for a variety of indications, including characterization of focal lesions, detection of diffuse liver disease, as well as evaluation for hepatocellular carcinoma in patients with chronic hepatitis or cirrhosis [1-8]. One of the main criticisms of hepatic MRI is scan time, both in terms of length and variability. In a small prospective study at a single center, table times in contrast-enhanced MRI of the liver were shown to vary from 19 up to 58 minutes, even when examinations were performed by an experienced technologist [9].

In a detailed analysis of MRI scanner activity during various imaging examinations, we observed that the number of adjustments performed by the scanner prior to initiating a pulse sequence was higher when imaging the liver as compared to the knee [10]. These adjustments take time, with the acquisition of shim data alone taking up to 20 s per pulse sequence. The need to acquire new adjustment data is dictated, in part, by table movement, after which field homogeneity in the scan volume must be measured, and additional adjustments made as needed. This increases the time that the MRI system spends preparing to scan but not actually acquiring image data [10].

A more recent study showed that a scan protocol in which the table moves only once during the examination achieves significant total scan time savings by obviating the need to gather new adjustment data during the course of the examination [11]. For every step in which the table moves and new shim data is acquired, this protocol change reduces the time spent collecting prescan adjustment data by approximately 30 s. In that study, a reduction in total examination time of up to 20% was observed in a non-contrast liver MRI/MRCP protocol, with no observable change in image quality.
Methods
Automated algorithms to minimize table movement have already been incorporated into MAGNETOM MRI systems under syngo MR D11 and later software versions. Under earlier software versions, a few simple steps can be performed to convert a standard MRI protocol into a minimized shimming protocol, in order to realize the time savings previously described. These changes can all be made via the Exam Explorer (Fig. 1A).

Pulse Sequence #1 – localizer
The first pulse sequence of an examination is a localizer, typically utilizing either a three-plane TrueFISP or HASTE technique. At the MRI console, under the ‘Sequence’ card, the Shim is set to ‘None’ (typically the default value), and precalibrated prescan data is used with no need to acquire new prescan data. No additional modification of this sequence is required.

Pulse Sequence #2 – first and only table move
Using the image data from the localizer sequence, the image volume for Pulse Sequence #2 is prescribed. This volume should be centered on the area of interest and rather large, covering the volume of interest for the entire examination; at our institution, we typically use a coronal HASTE sequence for this purpose. The prescan data acquired in this step, including shim data, will be carried forward for the remainder of the examination. The following modifications are made to this pulse sequence:
1. In the ‘System’ card, under the ‘Adjustments’ tab, set ‘Shim mode’ to ‘Standard’. Check the ‘Adjust with body coil’ box (Fig. 1B).

Pulse Sequences #3 and higher – no further table movements
For all subsequent pulse sequences, table movement is disallowed, and prescan adjustment data from Pulse Sequence #2 is carried forward, so that as little time as possible is spent acquiring new adjustment data. The following modifications are made:
1. In the ‘System’ card, under the ‘Miscellaneous’ tab, set ‘Position mode’ to ‘FIX’ (Fig. 1C).
2. In the ‘System’ card, under the ‘Adjustments’ tab: set ‘Shim mode’ to ‘Standard’; select ‘Adjust with body coil’; and set ‘Adjustment Tolerance’ to ‘Maximum’ (Fig. 1D).
3. From the Exam Explorer, right-click on the sequence and select ‘Properties’.

Under the ‘Copy References’ tab, check the ‘Copy reference is active’ box, then select Pulse Sequence #2 in the left-hand window and ‘Table position’ in the right-hand window (Fig. 1E). In combination with step #2 above, this ensures that the MRI system table will not move when progressing to later pulse sequences in the examination, despite different prescriptions for the imaging volume.

4. Repeat steps 1–4 for all subsequent sequences (Figure 1F).

Discussion
Preparatory adjustments made by an MRI system are essential to realize excellent image quality. In particular, adequate shimming is necessary to ensure magnetic field homogeneity. Shimming is a process whereby the magnet (B₀) is fine-tuned to compensate for field fluctuations and inhomogeneities introduced by the presence of the human body within the scanner. These adjustments are applied specifically to a volume within the bore of the magnet (based on the anticipated imaging volume), attempting to optimize magnetic field homogeneity within that volume while sacrificing field homogeneity outside of the volume.
Comparison of image convention between traditional (2A, 2C, and 2E) and minimized shimming (2B, 2D, and 2F) protocols in three different subjects. Note similar tissue contrast fat, suppression, image sharpness, and overall image quality.

A scanning protocol which prohibits table movement can reduce total table time by removing the need to repeatedly acquire adjustment data, particularly time-consuming shim data, throughout the course of the examination. Even though placing the liver at isocenter during an inspiratory breath-hold means that it would be located, on average, cranial to isocenter during free breathing sequences, the above study observed no differences in image quality in any type of pulse sequence. Note we do not suggest that patient- and position-specific shimming is unnecessary, but rather that if patient position can be maintained during the examination and adequate initial adjustment data is acquired, table movement during the examination and much of the additional adjustment data may be unnecessary. This holds true for both typical quantitative and qualitative abdominal MRI applications (Fig. 2). In addition, it may be possible to achieve the same time savings by any protocol which prevents table movement, for example a protocol where the image volumes of all pulse sequences are centered in the same location.

An overall workflow analysis of abdominal MRI acquisitions shows that shortening data acquisition times can reduce overall imaging time [10]. This is likely to be of greatest benefit in examinations where the large majority of table time is spent acquiring image data, e.g. musculoskeletal and brain examinations [10]. However, much less attention has been directed to other events which contribute to total imaging time, including time spent preparing the patient for imaging as well as scanner preparation, such as image prescription and prescan adjustments. In abdominal MRI, where preparatory activities take up a large proportion of total table time, reducing the prescan time represents an important opportunity to reduce total table time substantially [10]. Since this methodology is independent of the particular details of the imaging protocol, it could be applied to a variety of routine clinical and novel imaging techniques. In conclusion, any MRI protocol can be easily modified to minimize the time spent collecting prescan adjustment data. In certain scenarios, such modifications can reduce total scan time by as much as 20% with no sacrifice in image quality.

References

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