Real-Time Motion Correction for High-Resolution Imaging of the Larynx: Implementation and Initial Results

J. K. Barral[1], J. M. Santos[1], and D. G. Nishimura[1]
[1]Electrical Engineering, Stanford University, Stanford, CA, United States

Introduction: Motion is one of the main limitations to high-resolution imaging, which requires small voxels and long scan times. High-resolution imaging of the larynx is all the more challenging, as the larynx is an area particularly vulnerable to motion [1,2]. Patients present irregular breathing, frequent swallowing, and coughing (Fig. 1). The effects of sporadic motion can be mitigated using a pseudo-random k-space trajectory and Compressed Sensing (CS) [3,4]. Data corrupted by rigid motion can be effectively corrected using navigators [5]. However, respiratory motion is non-rigid, and it is the dominant type of motion in patients (Fig. 1). The Diminishing Variance Algorithm (DVA) has been used to eliminate respiratory artifacts from thoracic and abdominal images [6]. In this work, we propose to use DVA in conjunction with CS to eliminate respiratory and sporadic-motion artifacts from larynx images.

Methods: We implemented our algorithm within the framework of the real-time system RTHawk [7]. The pipeline is summarized in Fig. 2. A full dataset is first acquired using either a sequential or a pseudo-random k-space trajectory, suitable for CS. The navigator information is processed in real time to obtain a histogram of the translational shifts. A list of encodes to reacquire—based on a priority criterion—is then sent to the scanner. These reacquired encodes replace the previously corrupted ones. A new image is reconstructed, making a new frame, and the histogram of shifts is updated. This step is repeated until satisfactory image quality is obtained and the user decides to stop the acquisition.

As a proof of concept, we used a spoiled-GRE sequence and designed a 2D Cartesian readout trajectory with navigators interleaved between the two axes (Fig. 3). We first performed the following experiment on a phantom, using a pseudo-random trajectory: we started with an axial acquisition for the first half of the full acquisition, then switched to a sagittal acquisition for several seconds, then returned to the axial acquisition before the end of the full acquisition. In this way, at the end of the full acquisition, several randomly-located encodes were corrupted. This is more effective than manually moving the fluid phantom as we avoid flow effects and we are guaranteed to be back at the original position for the rest of the scan. We then scanned a healthy volunteer on a GE 1.5 T magnet using a dedicated three-channel array [6], a sequential trajectory, and the following parameters: FOV = 10 cm, slice thickness = 2 mm, matrix size = 256x256, number of navigator samples = 64, BW = ±32 kHz, TR/TE = 110/3 ms. Resolution was 0.4x0.4x2 mm^3. The subject was instructed to swallow and cough intermittently at will. For both experiments, the priority of each encode was chosen as the distance of the corresponding shift from the 2D mode of all shifts.

Results and Discussion: Figure 4 shows the results of the phantom experiment. As expected, the first frame is corrupted by motion-like artifacts. Once the corrupted encodes are reacquired, a clean image is obtained. Figure 5 presents four frames of the in vivo scan. The first one was acquired in 28 ms and each subsequent one in 3.5 ms (32 encodes were reacquired for each new frame). Image quality was considered satisfactory after 1 min 21 s. Motion artifacts heavily corrupt the initial image (first frame), whereas the thyroid cartilage and fine details in skin are nicely delineated in the last frame. Due to the processing complexity, there is a trade-off between the length of the list of encodes to reacquire and the TR (both can be changed in real time). For very short TRs, this length cannot be decreased to 1. However, for longer TRs (> 200 ms), this is possible. Optimization of the implementation will improve flexibility.

This experiment demonstrates the successful integration of our algorithm with RTHawk and its potential for high-resolution imaging of the larynx. Navigators will be refined to avoid contamination by pulsatile flow from the carotid arteries. The use of a 3D sequence, necessary to get thin contiguous slices, will allow an elaborated integration of CS to the priority criterion, which will reduce the scan time overhead.

References:

[1] Larkman, ISMRM 2002, p. 75
[2] Chan, JMRI 29: 211-216, 2009
[3] Lustig, MRM 58:1182-1195, 2007
[4] Barral, ISMRM 2009, p. 4593
[5] Ehman, MRI 173:255-263, 1989
[6] Sachs, MRM 34: 412-422, 1995
[7] Santos, IEEE-EMBS 2:1048-1051, 2004

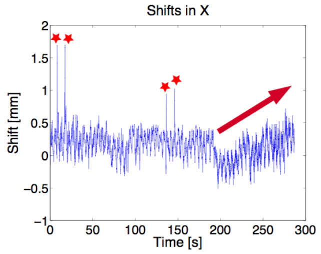

***Figure 1**: Translational shifts in X occurring during the scan of a patient with laryngeal cancer, obtained from Cartesian navigators. Some outliers (stars) corresponding to sporadic motion are found, and a drift (arrow) is observed toward the end of the scan. The high-frequency content corresponds to non-rigid respiratory motion (14 beats/min).*

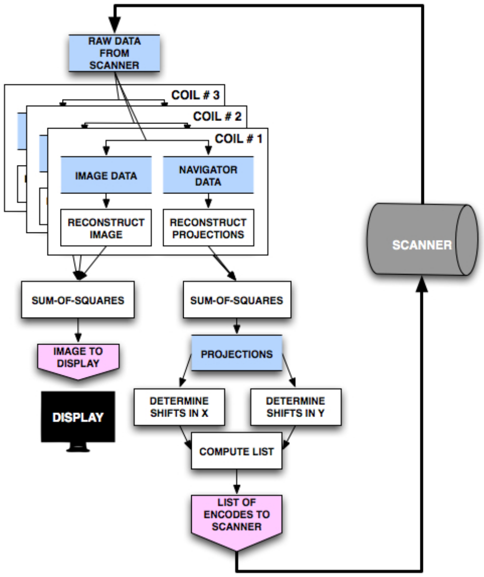

***Figure 2**: Flow chart of the real-time algorithm. Coils are processed in parallel (block). Navigator data is processed in real time to determine which encodes need to be reacquired. A stopping criterion can be defined, or the user stops the acquisition when image quality is satisfactory.*

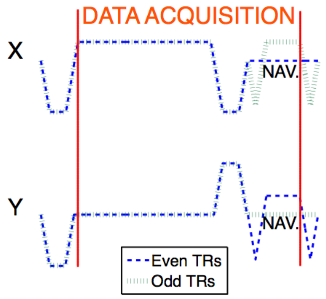

***Figure 3**: 2D readout trajectory. Navigators (NAV.) alternate between the two axes.*

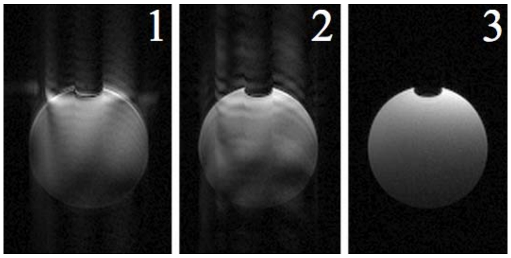

***Figure 4**: Phantom experiment. The three frames (1, 2, 3) obtained are shown. The first frame corresponds to a full acquisition (256 encodes) and is corrupted by motion-like artifacts. As corrupted encodes are reacquired, these artifacts are removed. Two additional frames, each corresponding to 32 encodes reacquired, are needed to get a clean image. The processing happens in real time.*

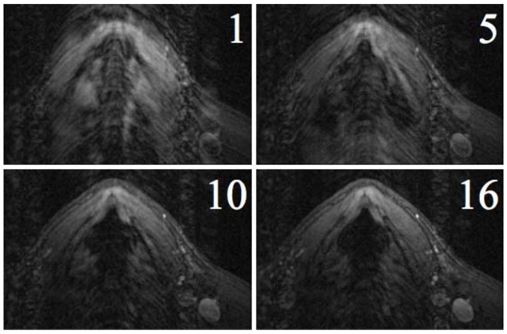

***Figure 5**: Larynx imaging experiment. Sixteen frames were acquired (frames 1, 5, 10, and 16 are shown). The first frame corresponds to 256 encodes acquired and each consecutive one to 32 encodes reacquired. Motion artifacts are very effectively removed.*