Rapid M-mode MRI Using Undersampled 2D Excitation and Parallel Reconstruction

C. J. Hardy[1], L. Marinelli[1], and T. K. Foo[1]
[1]GE Global Research, Niskayuna, NY, United States

Introduction: When 2D pulses (1) are used to excite pencil regions for the purpose of M-mode MRI (2) or respiratory navigation (3), time resolution is degraded by the relatively long duration of the pulses. Parallel transmission can be used to shorten pulses, but this currently requires special hardware and software. We introduce here an alternative method for significantly reducing pulse lengths for these applications, by employing an under-sampled rectilinear excitation trajectory, and then using parallel imaging to unwrap signals from the resulting replicated excitation regions.

Methods: A pencil excitation pulse designed using a 7-line rectilinear trajectory is shown in Fig. 1A, with the corresponding 2D target profile and actual excitation profile shown in Figs. 1B and 1C respectively. Here the limited number of k-space lines has resulted in a relatively short (3.6 ms) pulse, at the cost of closely spaced replicates of the target excitation region. (Only the center 3 replicates are displayed.) Imaging was performed on a 1.5 T Echospeed (33 mT/m, 120 T/m/s) Signa scanner. Figure 2 shows coronal MR images of a uniform phantom, acquired with a linear 4-element receiver coil array (Fig. 2A), without (Fig. 2B) and with (Figs. 2C and 2D) use of the 2D excitation pulse of Fig. 1A. Each column in Fig. 2 shows images acquired with the corresponding highlighted coil, with the rightmost column showing composite images from all coils. It can be seen that the relative signal strength from each replicate is weighted by the various coils' sensitivity functions. If MR signals are acquired in the presence of a readout gradient in the direction of the pencil axis (vertical in Fig. 2C) with no phase encoding, and a 1DFFT is applied, then a scrolling "M-mode" display of magnetization along the pencil versus time is produced. In this case the signal includes combined contributions from the different excitation replicates. Parallel reconstruction can then be used to separate these contributions into separate scrolling displays from the different excitation regions, i.e., the replicated traces along the excitation column can be separated at each point in the readout by $M = (S^H S)^{-1} S^H A$, where M is the separated signal, A is the acquired signal, and S is the coil sensitivity matrix.

Results and Discussion: Figure 3A shows a coronal scout image of a normal volunteer acquired with the rf array of Fig. 2. The same view is seen in Fig. 3B, with the pencil pulse of Fig. 1A used for excitation. If phase encoding is omitted, the combined M-mode trace of Fig. 3C results (with time on the horizontal axis). Use of parallel reconstruction allows separation of the different excitation regions, resulting in the M-mode traces of Fig. 3D-F. Here the 2D excitation was 3.6 ms long, and TR was 11.0 ms, shortened from values of 10.8 ms and 18.2 ms, respectively, with a 21-line excitation pulse.

This method simultaneously improves time resolution and provides M-mode traces from multiple regions. It therefore may provide improved performance for navigator echo applications, where the use of 2D excitation rather than spin-echo crossed slices will also reduce saturation effects. It should also aid M-mode and velocity-encoded M-mode MRI of the heart and great vessels.

References: **1)** J Pauly, et al. JMR 81:43 (1989). 2) CJ Hardy, et al. JCAT 15:868 (1991). 3) RL Ehman, et al, Radiol. 173:255 (1989).

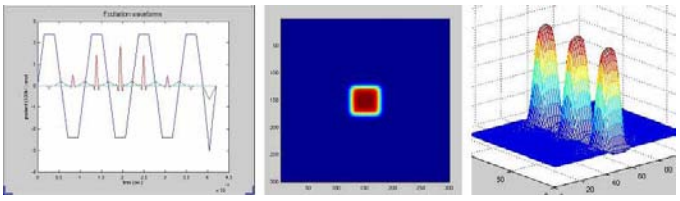

Figure 1. A) Rectilinear 2D excitation pulse (red –RF, green – Gy, blue – Gz). B) 2D target profile and C) actual excitation profile for pulse.

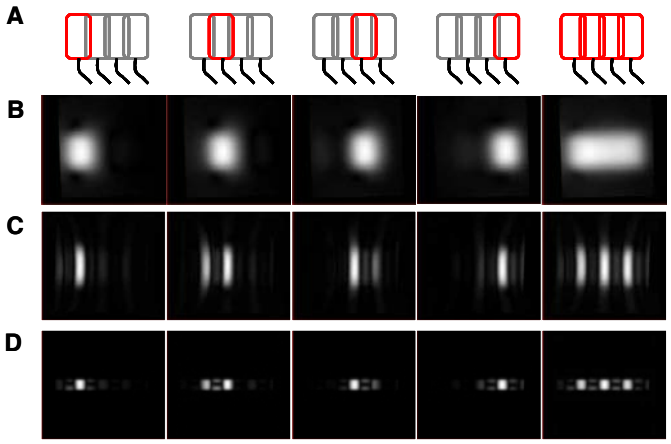

Figure 2. A) 4-element rf coil array; B) images of a uniform phantom acquired with array; C) and D) 2D excitation profiles of phantom imaged with array, as seen on the side (C) and on-end (D), showing 3 replicates of 2D target excitation region.

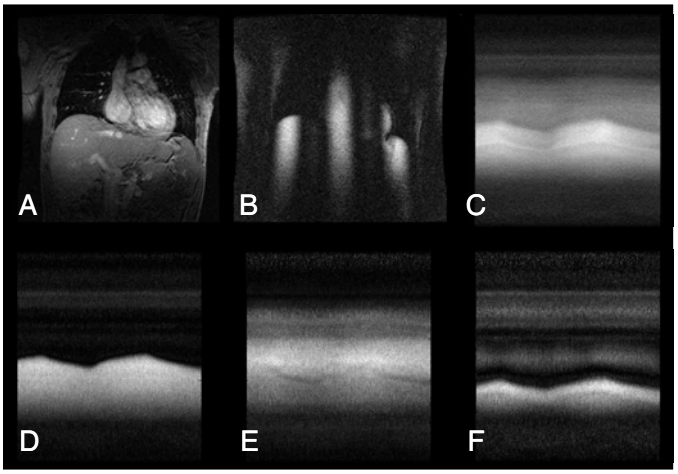

Figure 3. A) Coronal image across diaphragm, B) Same view with use of 2D excitation pulse, C-F) M-mode views from 3 excitation regions in (B), collapsed into single trace (C) and separated by use of parallel reconstruction, showing breathing motion at 3 different locations simultaneously (D-F).