Free-Breathing Cardiac Cine MRI using the Diminishing Variance Algorithm

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Target Audience MR physicists and clinicians interested in pulse sequence design, image reconstruction, cardiac imaging, and ventricular function.

Purpose Breath-held cardiac cine MRI is considered to be the gold-standard technique for ventricular function assessment. However, some patients are unable or unwilling to perform the series of 5-15 second breath holds, resulting in severe degradation of image quality. Recently, a free-breathing cardiac cine approach was developed that utilized diaphragm navigator gating[1]. Diaphragm navigators require the interruption of the steady-state signal used for cine imaging, and they require additional scan time and sequence modifications to avoid transient signal artifacts. Alternatively, respiratory bellows gating has been shown to be well correlated with diaphragm navigation in cardiac MRI while requiring no disruption of the main imaging sequence[2]. In this work, we develop a technique for free-breathing cardiac cine MRI, which uses the respiratory bellows signal for motion tracking and the diminishing variance algorithm (DVA)[3] for reacquisition of motion-corrupted data. The technique uses the same protocol as standard breath-held cine MRI, but it employs DVA to facilitate imaging during free breathing.

Methods The proposed free-breathing cine application was implemented using the RTHawk Research platform (HeartVista, Inc., CA), which enabled real-time monitoring of the respiratory bellows signal and on-the-fly updating of the view table[4]. Sequential slice-by-slice acquisition was employed using a balanced steady-state free precession (bSSFP) imaging sequence. DVA was applied to each slice independently to determine a list of motion-corrupted heartbeats (k-space segments) to be reacquired immediately following the initial full acquisition for the respective slice. Four DVA iterations were acquired for each slice. The first iteration consisted of a full segmented cine acquisition, which used an initial heartbeat of dummy views to reach steady state, followed by ten heartbeats of segmented cine imaging. During this period, the respiratory bellows signal was monitored, and the mode position was calculated and used as the end-expiratory reference location for DVA (Fig. 1). At the end of the first DVA iteration, the mean deviation from this reference location was computed for each of the ten k-space segments. The five segments with the greatest deviation were reacquired during the second DVA iteration, following a period of dummy views to maintain steady state. The segment ordering was re-computed at the end of the second and third iterations, and two segments with the greatest deviation were reacquired during the final two DVA iterations (Fig. 2).

In-vivo bSSFP scans were performed on a GE 1.5 T TwinSpeed scanner using an 8-channel cardiac receive array. A segmented 2DFT acquisition with 11 views per segment (42-ms temporal resolution) was used with the following parameters: FOV = 32x32 cm^2, resolution = 1.6x2.0 mm^2, flip angle = 65°, slice thickness = 6 mm, TR = 3.8 ms, parallel imaging acceleration factor = 1.6x, 10 k-space segments. SPIRiT was used to reconstruct images at 20 cardiac phases for each slice location[5].

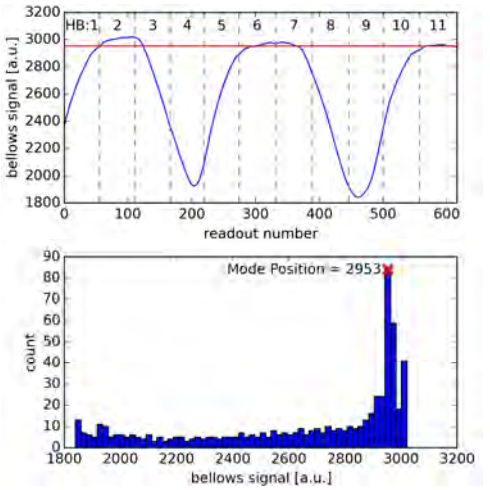

Figure 1. Respiratory bellows signal (top) and associated histogram-based mode detection (bottom). Mode detection is performed separately for each slice during the initial 11-heartbeat DVA iteration.

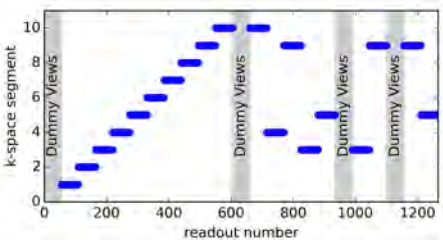

Figure 2. View segment ordering for a representative slice from a cine acquisition covering the LV. A full acquisition consisting of 10 k-space segments is initially acquired, followed by three DVA iterations in which 5, 2, and 2 segments are reacquired. Dummy views are played between iterations to maintain steady state while a new DVA view ordering is computed.

Results Figure 1 shows the respiratory bellows signal from a volunteer scan acquired during free breathing. Histogram analysis automatically locates the end-expiratory position (red line) within the initial 11-heartbeat DVA iteration. For each slice, the initial DVA iteration is used to compute a new DVA reference location, reducing the sensitivity to respiratory drift during multi-slice scans. Figure 2 shows the view segment ordering used for a representative slice from a free-breathing scan covering the entire left ventricle (LV). Figure 3 shows end-systolic and end-diastolic images from four slices of a free-breathing scan. A stack of 16 short-axis slice locations covering the entire LV was acquired in approximately nine minutes, approximately equivalent to the time for standard breath-held imaging given ~20s recovery between breath holds.

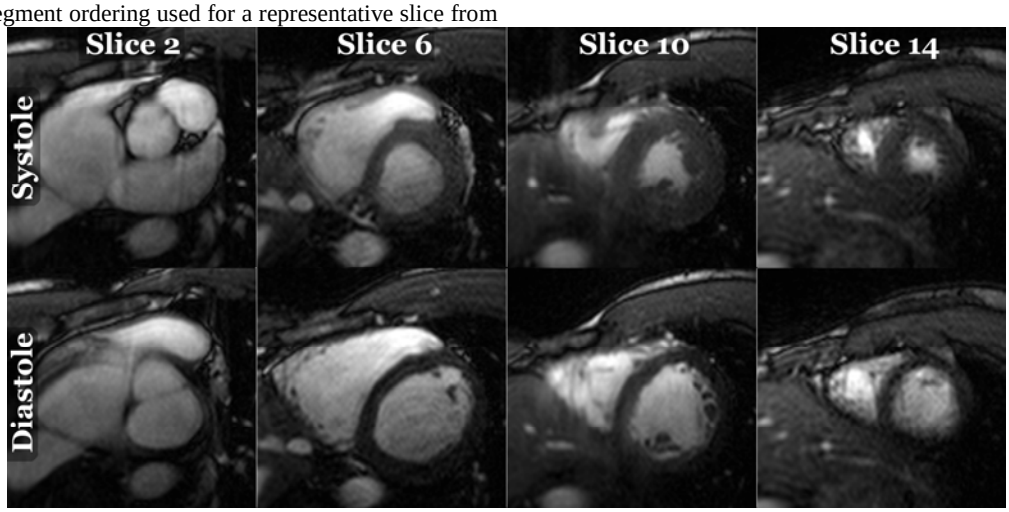

Figure 3. Four slices from a stack of 16 short-axis locations covering the LV. Slices were acquired in free breathing, and DVA was used to reacquire heartbeats that were corrupted by respiratory motion. With DVA, each slice was acquired using twice the acquisition time of a standard breath-held cardiac cine acquisition.

Discussion & Conclusion Preliminary in-vivo results have demonstrated the efficacy of free-breathing cardiac cine imaging using the respiratory bellows and diminishing variance algorithm for motion artifact reduction. Additional volunteer and patient studies will be conducted for qualitative and quantitative comparison of the proposed technique with conventional breath-held cine imaging. In conclusion, the proposed DVA cine application has enabled whole-heart free-breathing cardiac cine imaging in a moderate scan time.

References [1] Moghari MH, *et al.*, MRM 2014, early view. [2] Santelli C, *et al.*, MRM 65:1098-1103, 2011. [3] Sachs TS, *et al.*, MRM 34:412-422, 1995. [4] Barral JK, *et al.*, MRM 66:174-179, 2011. [5] Lustig M, *et al.*, MRM 64:457-471, 2010.