

# Robust Free-Breathing Whole-Heart Cine MRI using Multi-Slab 3D Acquisition with Isotropic Resolution and Offline Reformattability

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## Purpose:

Cardiac cine MRI has become a routine exam for assessment of cardiac function and anatomy. Conventional 2D cine requires separate scouting scans to localize different views and at each orientation multiple breathholds are required with patient recuperation time in-between breathholds. 2D cine scans easily consume more than 10 minutes, require greater technologist skill, and significantly slow down workflow. Also, due to inconsistent breathholding position, 2D cine images are intrinsically not reformattable even with thin slices. Recent developments in fast imaging have enabled 3D cine with whole ventricle coverage in one breathhold [1,2], and have demonstrated consistent quantitative volume and EF evaluations compared to 2D cine. However, it is infeasible for breathhold (BH) 3D cine to provide isotropic resolution for reformatting due to limited patient breathhold capacity. Furthermore, compared to 2D cine, 3D cine normally shows less blood-myocardium contrast due to reduced in-flow blood enhancement and also is more susceptible to SSFP banding artifacts because of less localized whole-volume shimming. These disadvantages are more prominent near the cardiac apex and at 3T. The purpose of this work was to develop a robust whole-heart 3D cine technique with near-isotropic resolution for arbitrary offline reformatting.

## Methods:

A new sequence was developed for whole-heart 3D cine imaging.

**Multi-slab (mslab) acquisition:** The proposed sequence performs a multi-slab free-breathing 3D cine acquisition, as shown in Fig. 1 (left). Each slab covers a thin 3D volume such that there is still sufficient inflow enhancement for bright blood imaging. Also, localized shimming is performed for each slab individually to reduce SSFP banding artifacts. Combining all 3D slabs, the entire heart is covered with a few overlapping slices in-between adjacent slabs to facilitate 3D reformatting. During the scan, the 3D cine slabs are collected sequentially from cardiac base to apex with minimum delays in-between. A variable density sampling scheme with random k-t shifting (VDR k-t) [3] is used for highly accelerated data acquisition. For motion robustness, a rewinding radial vieworder was used, as shown in Fig. 1 (right). Specifically, k-space sampling transits from center to outer k-space and then rewinds back to center k-space for smooth k-space transition and thus minimum eddy-current effects. Also, with this view order, data acquisition revisits center k-space during the entire scan. Therefore, the effects of patient heart rate variation and respiratory drifting should be smoothed out across slabs such that misregistration between adjacent slabs is minimized.

**Soft respiratory gated reconstruction:** A compressed sensing [4] algorithm was used to reconstruct images from the highly undersampled data with TV as the sparsification transform along time. Also, to suppress respiratory motion artifacts, the data consistency constraint was enforced using a soft gating scheme [5] with the weight determined by the respiratory position from simultaneously recorded bellow signal. Specifically, a large weight is used for data collected at near end-expiration and a small weight is used for off-expiration positions.

**Post-processing:** imperfect slice profile due to B1 inhomogeneity along slices could induce shading at peripheral slice locations and thus produce periodic signal level changes across slices. Signal alignment along the slice direction was performed to reduce the undesirable signal oscillations. Basically, a local scaling factor is determined to compensate RF shading by comparing the signal level in a small local  $[x, y]$  block across adjacent slices and this block is slid along  $x, y$  and  $z$  to align the entire image.

To validate the proposed method, 3 healthy volunteers were scanned on a GE 3T with a 32-channel cardiac coil without contrast agent. Typical imaging parameters were:  $380 \times 270 \text{ mm}^2$  FOV,  $1.8 \times 1.8$  resolution, 7 slabs covering the entire heart, 20 slices with 2mm slice thickness in each slab, 4 overlapping slices from one slab to the next, 45 degree flip angle, 16 views/segment, 5x acceleration, ~4.6min total scan time during free breathing. To obtain maximum in-flow enhancement, the 3D cine slabs were placed with short-axis orientations. For comparison, 2D cine and single-breathhold 3D cine [3] images were also collected at short axis.

**Results:** Fig 2 compares different acquisitions on the same volunteers. Clearly, 2D cine (a, d) shows superior contrast vs. BH 3D cine (b, e), especially in RV and near apex. Mslab 3D cine (c, f) provides high contrast similar to 2D cine and does not suffer from banding artifacts apparent at apex in BH 3D cine (e). As shown in Fig 3, the reformat of 2D cine slices shows discontinuous anatomy along slices. Also, both 2D and 3D cine (a, b) reformats show coarse anatomy depiction due to large slice thickness. In comparison, with near isotropic resolution, mslab 3D cine enables reformatting in arbitrary views (c: 4ch & d: 2ch) in offline processing.

## Conclusions:

This work developed a novel technique for free-breathing whole-heart 3D cine MRI that generates 3D cine images with isotropic resolution. Our preliminary results show the mslab 3D cine acquisition is more robust than BH 3D cine with higher contrast and reduced susceptibility to banding artifacts, especially on 3T. Also, the proposed method enables arbitrary offline reformatting to different cine views and thus can substantially simplify cardiac workflow and shorten cardiac exam time.

**References:** [1] Tsao, MRM 2003:1031; [2] Huang, MRM 2005:1172; [3] Lai, ISMRM 2013:4379; [4] Lustig, MRM 2007:1182; [5] Cheng, ISMRM 2015

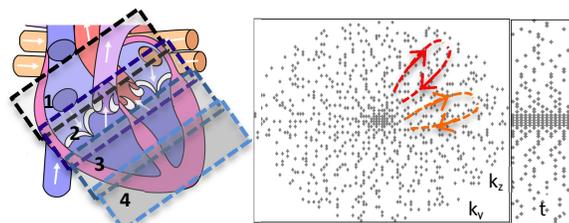


Fig. 1. Left: sequential multi-slab 3D cine on whole heart. Right: VDR kt sampling with rewinding radial vieworder.

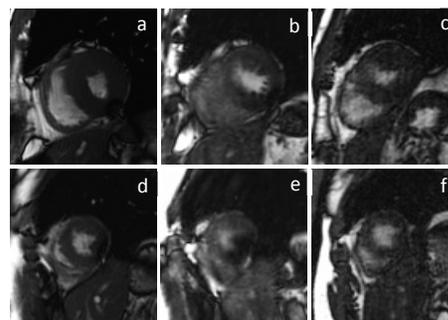


Fig. 2. 3T short-axis slices from 2D cine (a, d), BH 3D cine (b, e) & mslab 3D cine (c, f).

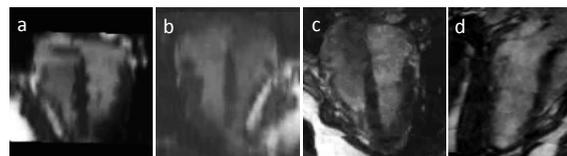


Fig. 3. Reformatted 4ch images from 2D cine (a), BH 3D cine (b) and 4ch (c) & 2ch (d) reformats from mslab 3D cine.