Achieving 3D CINE from free breathing multi-slice 2D acquisitions via Simultaneous Groupwise Manifold Alignment

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Introduction: Multislice 2D CINE MRI is a common approach for assessing cardiac function and anatomy. This approach requires multiple breath-holds and usually suffers from slice-misalignments due to motion between the acquisitions. To overcome these problems, free-breathing respiratory-gated 3D CINE MRI has been proposed. However, these methods require long acquisition times and suffer from poor contrast between blood and myocardium compared to 2D acquisitions[1]. In this work, we propose to combine the contrast of 2D acquisitions with the coverage of the 3D scans by generating a "simulated 3D" scan. This is achieved by addressing the issue of slice misalignment using manifold learning[2] based self-gated *Simultaneous Groupwise Manifold Alignment* (SGA)[3] technique. This technique estimates respiratory navigator signals from real time images of each slice such that all the slices are always corrected to the same reference respiratory position. Prospective golden radial cardiac MR acquisitions, performed in 3 volunteers, demonstrate the feasibility of proposed framework to achieve gated "simulated 3D" CINE from free-breathing multi-slice 2D acquisitions.

Theory: Standard Manifold Learning (ML) techniques[2,4,5] have been successfully applied in MRI to extract underlying, low dimensional (usually 1-D) respiratory motion from a sequence of real time higher dimensional MR images. Simultaneous groupwise manifold alignment (SGA)[3,5] further extends the ML concept to align the respiratory signals from all the slices in a common space. Starting from the 2D real time images corresponding to each of the slices, this method establishes relations between the low dimensional manifolds of neighbouring slice positions by embedding them simultaneously in overlapping groups of two. For two high dimensional data sets X_p and X_q in a group, the aligned low dimensional embeddings Y_p and Y_q can be obtained by minimizing the cost function given as: $\phi_{tot}(Y_p, Y_q) = \phi_p(Y_p) + \phi_q(Y_q) + \mu\,\phi_{pq}(Y_p, Y_q)$, where p and q are neighbouring slice positions and ϕ_p and ϕ_q are derived via a ML technique such as Local Linear Embedding (LLE) [5]. The mixed cost term ϕ_{pq} draws similar slices together in the common embedded space based on their similarity in image space, and μ governs the influence of this term. The volume is covered by G = S − 1 overlapping groups, where S is the number of slice positions. Since, each slice position p (except the outermost ones) is embedded in two neighbouring groups 'g-1' and 'g', there are two low-dimensional embeddings Y_g^P and Y_{g-1}^P of the same data. Group 'g −1' can be transformed into the space of group 'g' by minimizing least squares function: $\arg\min_{a,b} \left\| \left(aY_{g-1}^P + b\right) - Y_g^P \right\|_2^2$. In order to transport all navigators into a common reference frame, we choose a reference slice position 'r' in the middle of the volume, and transform all groups into the space of the group containing 'r' by going from group to group via a series of transformations.

Method: A multi-slice golden angle radial acquisition[6] is performed to ensure the k-space sample locations for any specific cardiac phase and respiratory position are mutually exclusive in subsequent R-R intervals allowing flexibility in the reconstruction. Data corresponding to all the slices are retrospectively combined to reconstruct N cardiac phases of simulated 3D CINE as follows: low temporal resolution real time images (one 2D image per cardiac cycle) are reconstructed using gridding from free breathing data acquired for each slice. Using SGA, respiratory signals are generated for all the slices such that all signals are aligned from end-expiration to end-inspiration. Based on the aligned respiratory signals, a global respiratory gating acceptance window (one third of the full extent of respiratory motion) is defined such that it has the most amount of data for all the slices. The data corresponding to all the slices that lie within the acceptance window were combined using k-t Sparse[7] reconstruction with 4D x-y-z-f space (z indicates the slice encoding direction) as sparse representation. For comparison, a respiratory signal is generated for each slice independently using standard ML approach with LLE embedding. A local gating acceptance window is defined for each slice and reconstruction is done from acquired data in the gating acceptance window with x-y-f space as sparse representation (Fig.1).

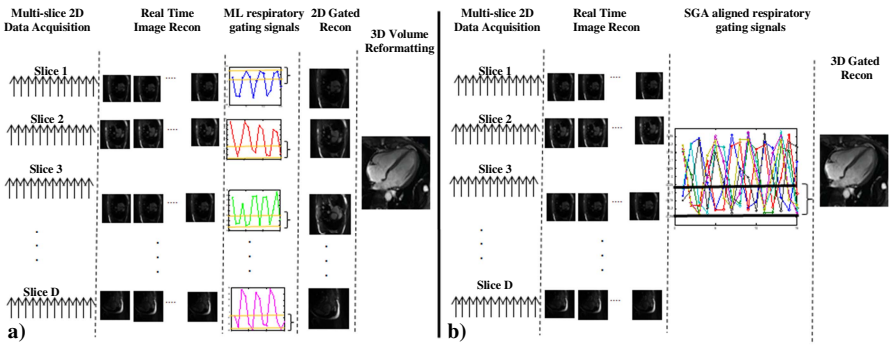
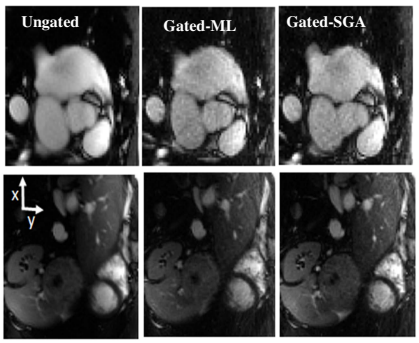


Fig.1: Diagram of gated reconstructions using ML and SGA techniques a) *Standard gated reconstruction using respiratory signals obtained for each slice with ML. Gated reconstruction is done independently for each slice based on the corresponding respiratory signal. Slice misalignment can occur when reformatted into a volume as reference respiratory position can be different for different slices (see the reference positions selected for different slices)* ***b)*** *Reconstruction using respiratory navigator signals from all slices that have been aligned using proposed SGA method. SGA addresses any slice misalignment issue as gating is now based on a global acceptance window for all the slices.*

Experiment: Multislice ECG-gated free breathing golden radial acquisition was performed on Philips 1.5T in 3 volunteers (b-SSFP, TR/TE=4/1.46 ms, matrix size =160x160, FOV: 320x320 mm^2, number of slices: 10-12, slice thickness: 8-10 mm, 120-240 radial profiles per cardiac cycle, scan time=3.5 min). The acceleration factor within the gating window was 4. Twenty cardiac phases were retrospectively reconstructed. Reconstructions using proposed SGA method were compared with those using ML method without alignment.



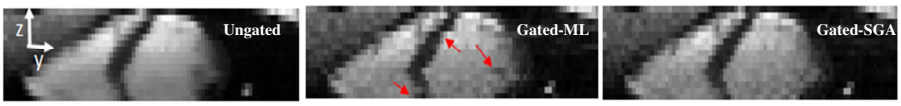


Fig.2: Comparison of gated reconstructions using respiratory navigator signals obtained with ML and SGA techniques. *In-plane reconstruction quality was similar for both techniques (see diastolic images for two slices on the left). Through-plane slice misalignment can be seen above with ML method (see areas pointed by red arrows). The SGA method ensured that slices are aligned globally. Ungated reconstructions are also shown for reference.*

Results and Discussion: The diastolic ungated and respiratory gated reconstructions using standard manifold learning (Gated-ML) and the proposed SGA method (Gated-SGA) are shown in Fig 2 (left three columns). Here, two slices are shown that were not gated at the global reference respiratory position with the ML method. This results in slice misalignment that can be seen in Fig. 2 three right columns (see the region pointed by the arrows). The gated reconstruction using the proposed SGA method ensured that all slices were aligned globally. Our proposed method ensures that slices are always reconstructed at a common respiratory position without the need to perform 3D acquisition. Moreover since sparsity is exploited in 3D instead of 2D, our method should be able to achieve higher acceleration factors than the multislice 2D. Future works include integrating the group alignment based method to motion correction technique[8,9] to achieve 3D motion corrected CINE reconstruction.

References: [1] Nehrke et al, ISMRM 2005 [2] Belkin et al, MIT Press,2001 [3] Baumgartner et al, IPMI, 2013 [4] Wachinger et al, MedIA 2012 [5] Roweis et al, Science, 2001 [6] Winkelmann et al, IEEE TMI,2007 [7] Lustig et al, ISMRM 2007 [8] Hansen et al, MRM 2011 [9] Usman et al, MICCAI 2012