

## Automated Registration of Multiple Single Breath-hold Cardiac MRI Images

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**PURPOSE:** Cine cardiac MRI (cMRI) images are typically acquired as multiple slices with one slice position and/or orientation per breath-hold. These multiple images are often misaligned due to patient motion. We developed a novel image processing technique, which allows registering multi breath-hold short-axis (SA), 2-chamber (2CH), and 4-chamber (4CH) cMRI views into common 3D spatial coordinates. **MATERIALS AND METHODS:** Studies from 20 consecutive patients (10 males, 10 females) undergoing cMRI exams, with 2CH, 4CH, and SA cine (20 phases), each acquired in separate breath-holds, with pixel size 1.3-1.8 mm were analyzed retrospectively. 2CH, 4CH and SA image planes were brought into common 3D coordinates by dynamic profile registration technique. Profiles with voxel image intensities were extracted from the images at plane intersections using bilinear interpolation. A cost function for the alignment quality based on the combination of correlation coefficients from all cine phases was iteratively maximized by a simplex optimization. Anisotropic stretching of SA profiles was implemented as a proxy for the SA 3D plane rotations with respect to the long axis planes. Automatic alignment was compared to the manual alignment performed by 2 observers, performed at 1mm increments with sub-voxel translations. **RESULTS:** The automatic processing time was < 20 seconds per case on a 3.0 GHz Pentium computer and approximately 16-20 minutes per case for the manual correction. Average plane displacement identified by 2 observers was  $2.8 \pm 1.8$  mm with maximum displacement of 14 mm and 32% of slices needing corrections. The overall accuracy of the automatic algorithm was  $1.0 \pm 0.9$  mm for the 2CH to 4CH registration, and  $1.1 \pm 1.0$  mm,  $1.1 \pm 1.2$  mm, and  $2.0 \pm 1.8$  mm for SA registration in midventricular, basal and apical regions respectively. Automatic variability (algorithm vs. human observers) and inter-observer variability were comparable (ANOVA,  $p = \text{NS}$ ), with the exception of the apical region where automatic variability is higher ( $2.3 \pm 1.8$  mm vs.  $1.6 \pm 1.5$  mm). Example of automatic alignment is shown in Figure 1. **CONCLUSION:** The alignment algorithm can be used as a completely automated and accurate pre-processing step in the analysis of cMRI data reducing the spatial misregistration between planes acquired at different breath-holds and allowing integrated 3D spatial visualization of multiple planes.

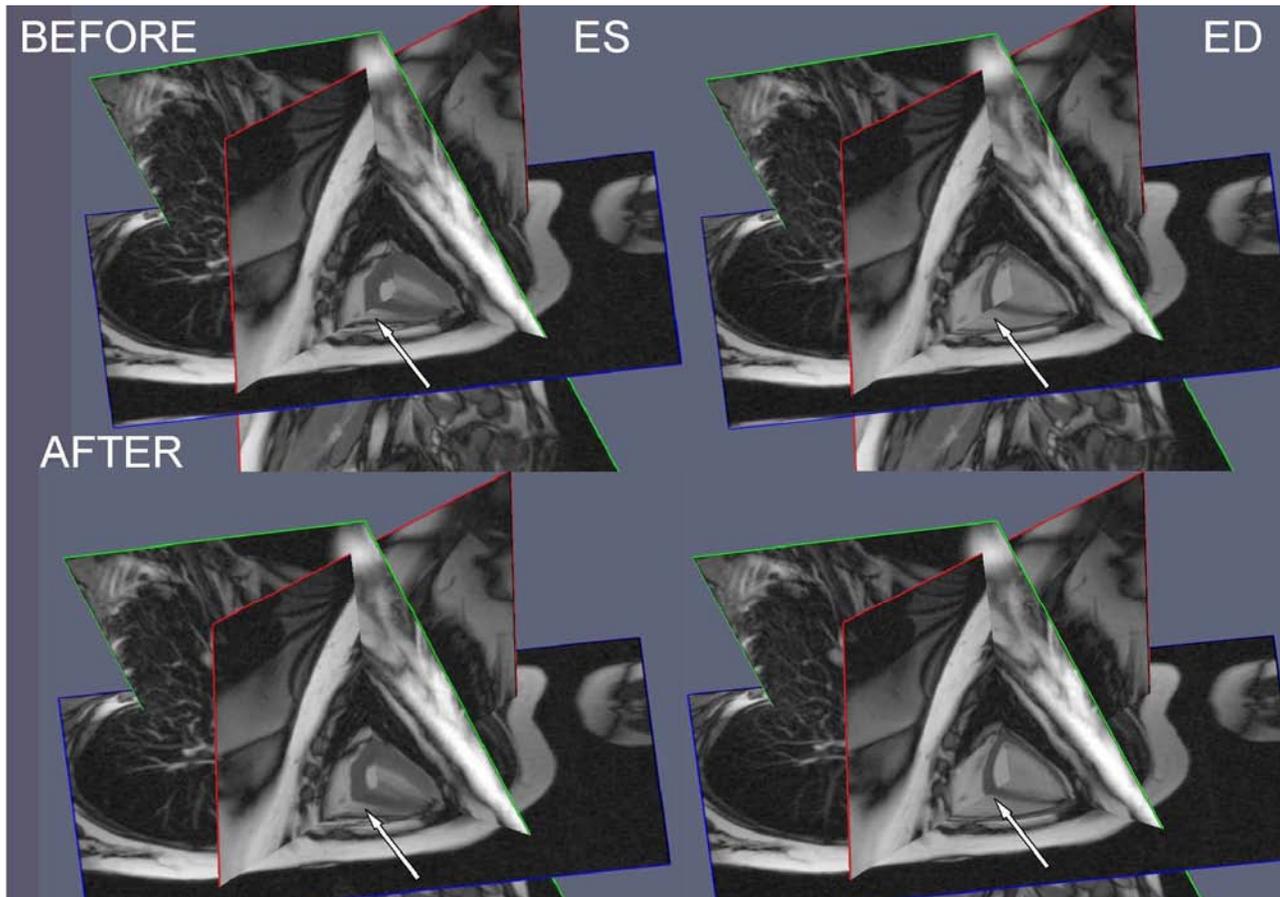


Figure 1. Example of automatic alignment for End Systolic (ES) and End diastolic (ED) frames.