Improved Cardiac Strain Estimation from DENSE using Automatic Outlier Rejection

S. N. Gupta[1], A. Aletras[2], M. N. Hood[3], V. B. Ho[3], E. J. Schmidt[4], and P. Aksit[5]

[1]Visualization and Computer Vision Lab, GE Global Research, Niskayuna, NY, United States, [2]LCE, NHLBI, NIH, Bethesda, MD, United States, [3]NNMC and USUHS, Bethesda, MD, United States, [4]Applied Science Lab, GE Healthcare, Boston, MA, United States, [5]Applied Science Lab, GE Healthcare, Bethesda, MD, United States

Introduction: Displacement Encoding with Stimulated Echoes (DENSE) is a promising technique for measuring regional cardiac function with high spatial resolution. DENSE encodes displacement in a given direction into the phase of the MR signal using stimulated echoes with a bipolar gradient in this direction [1]. Tissue strain is calculated from spatial derivatives of displacement data, which is directly obtained from the phase signal. From the 2D displacement data, it is possible to determine the principal directions of deformation and the principal strains (the eigen-vectors and eigen-values, respectively, of the strain tensor). For short-axis acquisitions with in-plane encoding, these vectors can then be projected along the myocardial circumferential and radial directions to determine the pixel-wise percent circumferential shortening (CS) and radial thickening (RT).

Objective: The decomposition of the strain tensor into principal strains may be numerically unstable due to insufficient SNR or image artifacts [2], which can lead to a large variability in the estimated eigen-values and eigen-vectors. This variability is compounded when these eigen-vectors are projected along the radial and circumferential directions, yielding large variations in pixel-wise strain values. We present a novel, automatic method for detecting pixels with unstable strain values, and thereafter eliminating them from analysis, thereby greatly reducing the variability in strain calculation. This may be particularly useful in patients with limited breath-holding capacity (e.g. patients with heart failure), or those in which multiple cardiac cycles are rejected due to arrhythmia.

Methods:

Acquisition: Imaging was performed on 5 healthy subjects with a 1.5T MRI system (GE, Waukesha WI) using an 8-channel cardiac coil under an IRB-approved study. Single-phase (systolic), single-slice (mid-ventricular), ECG-gated DENSE was used [parameters: 16-24 ETL Fast Spin Echo readout (meta-DENSE), 128 x 128, 36 x 27cm FOV, 8mm slice width, 4-6 mm/pi encoding strength].

Processing: DENSE raw data files were processed offline using IDL-based (ITTVIS) custom software (Denseviewer, GE). In all subjects, the left-ventricular epicardial and endocardial contours were manually traced, and then the myocardium was automatically divided into 6 sectors and data was processed using two methods. In Method A, conventional strain map processing was carried out with averages and standard deviations recorded for CS and RT strains in each sector and in each subject. In Method B, the DENSE data was processed using outlier rejection as follows: the regional strain data was median filtered and a difference map between median filtered data and the original strain data was computed. A threshold was applied to this difference map, to detect and mask those pixels where the difference exceeded a preset threshold. These pixels were eliminated from subsequent analysis and CS and RT strains were recomputed from the refined set of myocardial pixels. Means and standard deviations were quantified, as in Method A.

Results: Average CS and RT strains across all sectors, and for all subjects, was 28.3% and 15.6%, respectively, with Method A, and was 23.2% and 29.3% with outlier rejection (Method B). The average intra-sector variability of CS data for all subjects was 50.9% in Method A and this reduced to 17.0% after outlier rejection. Similarly, the average intra-sector variability of RT data dropped from 59.2% to 13.5% after outlier rejection. Inter-sector CS variability reduced from 8.1% to 4.7% and inter-sector RT variability reduced from 15.9% to 6.4% after outlier rejection. Note that the intra-sector variabilities are larger than inter-sector as expected due to the transmural variation of strain within each sector. Figure 1 shows the myocardial shortening and stretching and CS and RT maps for one subject, before and after outlier rejection processing. It can be seen that the regions with incorrect strain estimation are eliminated from processing, yielding more uniform CS and RT strain maps (arrows). Figure 2 shows the reduction in variability of CS and RT data for all subjects. It can be seen that all the strain errors near the edges of the myocardial walls have been eliminated. We verified that the method does not affect measurement of strain in infarcted tissue. Average CS and RT strain in known infarcted myocardial territory in a sheep study was 3.2% and 4.0% respectively with no outlier rejection, and 2.7% and 4.0% respectively after outlier rejection.

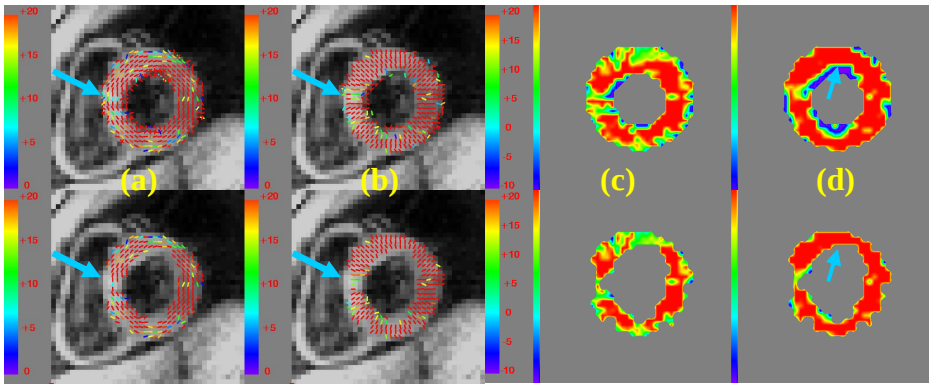

Fig.1: Myocardial shortening (a), thickening (b), CS (c), and RT (d) maps with standard Method A (top row) and new outlier rejection Method B (bottom row). Note changes in variability in (c) and (d).

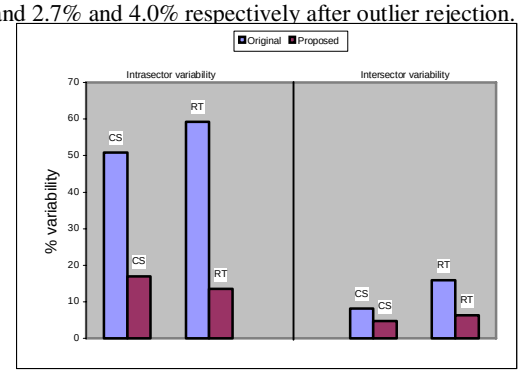

Fig. 2: Comparison of intra- and inter-sector variability in CS and RT between no outlier removal Method A and proposed outlier rejection Method (B).

Conclusion: We have presented a new method for automatic detection of outlier pixels in cardiac strain estimation and their removal from analysis. The proposed method results in a 3-fold reduction in variability of CS and RT strains, making automatic quantification of regional strain from DENSE processing more robust. It allows robust strain quantification even with suboptimal myocardial segmentation. Finally, it has the promise of allowing DENSE processing to be performed in very sick patients, such as those with significant congestive heart failure. Optimizing the rejection filter thresholds to ensure minimal loss of "good" strain pixels is the subject of ongoing human and animal experiments.

References:

[1] *MRM* 46:523-534; 2001. [2] *JMRI* 24:1432-1438; 2006.