Automated Cardiac Strain Estimation from 2D Cine DENSE MRI

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Introduction: Displacement encoding with stimulated echoes (DENSE) directly encodes tissue displacement into the phase of MR images, providing access to important physiological information such as cardiac strain [1], [2]. Unfortunately, the quantification of tissue displacement and cardiac strain from cine DENSE imagery continues to rely upon the time-consuming manual delineation of cardiac anatomy. Recent work has reduced this segmentation burden, but still requires some user defined anatomy [3]. A fully automated analysis solution could potentially improve measurement throughput, simplify data interpretation, and provide access to important physiological measurements at acquisition. In this study, we present the first fully automated solution to estimate tissue displacement and cardiac strain from 2D cine DENSE data.

Methods: 2D short-axis cine DENSE imagery was acquired in five healthy volunteers and five patients with heart disease using a 1.5T MR system (Avanto, Siemens), obtaining 3-4 short-axis slices per subject extending from base to apex. All imaging was performed in accordance with protocols approved by our Institutional Review Board and after obtaining informed consent. DENSE phase pixels are proportional to displacement values indicating the prior location of underlying tissue when the DENSE encoding pulses were applied. Large displacements produce phase wrapping artifacts as MR phase is inherently confined to [-π,π]. Regions devoid of tissue contain unpredictable phase information.

Our analysis used the noisy, wrapped, and un-segmented DENSE phase data to automatically track individual elements of tissue through time. Consider a set of candidate targets to be tracked, initially located at pixel centers with unknown underlying tissue presence. For each frame, we first predicted current target positions guided by prior target motion. We then unwrapped the raw DENSE displacement observations consistent with nearby predictions, discarding inconsistent observations likely devoid of tissue. We next estimated true target positions from the unwrapped observations via compact support radial basis functions [4]. We lastly assessed the probability of tissue presence via proximity to valid observations, discarding targets likely devoid of tissue. This multi-step process was replicated for every frame of the cine DENSE dataset. We repeated the entire procedure to further refine target motion, replacing position predictions with the current position estimates. Finally, principle strain values were derived from the assessed target motion.

Results: Principle cardiac strain values were derived from DENSE imagery using both the proposed automated algorithm and a standard semi-manual method [2]. Figs. 1 and 2 provide illustrative examples of principle shortening strain values at the mid-plane of a normal heart, respectively depicting end-systolic strain patterns and selected segmental strain-time curves. Validation of the automated method against the standard method was performed using a standard 17-segment model (excluding the apical cap). For principle shortening strain (Fig. 3), linear regression reveals a slope of 0.968 and R^2=0.933, and Bland-Altman analysis reveals a difference of -0.002±0.026. For principle lengthening strain (not shown), linear regression reveals a slope of 1.147 and R^2=0.82, and Bland-Altman analysis reveals a difference of 0.045±0.126. The proposed algorithm produces strain estimates for a 20 frame [128x128] pixel image sequence in 2-4 minutes. Using outer volume suppression during image acquisition reduces the algorithm runtime to less than 30 seconds.

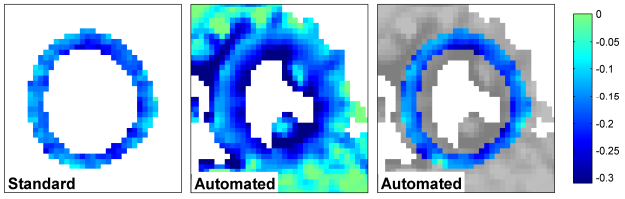

Fig. 1. End-systolic principle shortening strain in a normal heart. (a) Standard [2] and (b) automated analyses; (c) automated analysis with highlighted cardiac region.

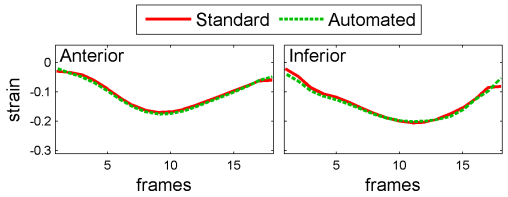

Fig. 2. Principle shortening strain versus time for selected mid-plane cardiac segments in a normal heart.

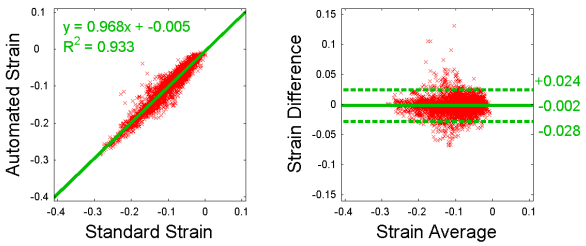

Fig. 3. Linear regression and Bland-Altman comparison for principle shortening strain: standard vs. automated.

Conclusion: This research presented the first fully automated solution to estimate tissue displacement and cardiac strain from 2D cine DENSE data. Results indicate good agreement between the proposed automated algorithm and a traditional semi-manual analysis. This innovative solution has the potential to both improve measurement throughput and simplify data interpretation. Ongoing algorithm enhancements have the potential to produce nearly real-time measurements of tissue strain.

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