Computer Assisted Branch Cut Placement for Computing 3D+t Biventricular Strain from Tagged MRI

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TARGET AUDIENCE: Cardiologists, cardiovascular physiologists, scientists and engineers with research interests in cardiovascular MRI.

PURPOSE: Myocardial strain is an important parameter of cardiac mechanical function. Tagged magnetic resonance imaging (tMRI) is used to assess myocardial function by analyzing strain reconstructed from tag lines applied to the heart before imaging. In a recent paper [1], a three-dimensional biventricular strain throughout cardiac cycle was reconstructed using a discrete model-free (DMF) method [2] with dense displacement measurements obtained from tMRI harmonic phase unwrapping [3]. Ideally, multiples of 2π can be added to regions to unwrap a phase image, but noise and artifacts can create inconsistencies in the phase map and cause unwrapping methods to fail. In [3], manually-placed branch cuts were used to resolve phase inconsistencies (mSUP). Manual branch cuts, however, are time consuming. In this abstract, we present and validate a computer-assisted branch cut method to compute 3D+time biventricular strain from unwrapped phase (caSUP).

METHODS

Residues and Branch Cuts: Inconsistencies in a phase image can be identified by computing a residue, which is the sum of phase differences around a 2x2 pixel loop. If the phase is consistent, this sum is zero. Phase inconsistencies result in a sum <0 (negative residue) or >0 (positive residue). Branch cuts connect either a positive to a negative residue or any residue to the border of the region being unwrapped (in this case, the myocardium).

Automated Branch Cut Placement: Branch cuts were automatically placed using one of two methods. The first uses an exhaustive search over all possible branch-cut connections when there are <7 residues in the phase image. Otherwise, the second method of simulated annealing [4] is utilized. Both of methods minimize an energy function composed of a weighted sum of the following four terms:

Term 1: Sum of phase differences around closed loops around the myocardium. The left ventricle (LV) and right ventricle (RV) walls were segmented in all short-axis images. Closed loops around the LV and RV cavities were generated. Term 1 penalized phase inconsistencies around these holes.

Term 2: Consistent deformation. Incorrect branch cuts can result in displacement measurements with large, rapid spatial changes. Term 2 penalized such non-physical changes in displacement by penalizing the squared difference of the area between consecutive phase wraps in consecutive time frames.

Term 3: Correctly-placed branch cuts should be short and approximately aligned in the tag line direction. Term 3 penalized long and misaligned branch cuts.

Term 4: Branch cuts effectively remove pixels from the myocardium segmentation so that the unwrapping path will result in a unique unwrapped phase. However, removing pixels can sometimes remove large regions of the myocardium. Term 4 penalized the number of pixels removed from the segmentation.

Branch Cut Correction: Branch cuts that could not be successfully placed by the above algorithm were automatically detected by identifying large spatial gradients in the phase map. This automatic detection allowed the user to only interact with certain images instead of inspecting each image for branch cut accuracy.

Patient Population: A group of 40 patients with different pathologies underwent tMRI. A subset of 10 studies (4 normal volunteers, 3 hypertensive patients, and 3 patients with isolated mitral regurgitation) was selected to optimize weighting factors of the energy function. The remaining studies (10 normal volunteers (NL), 7 patients with pulmonary arterial hypertension (PAH), 8 patients with resistant systemic hypertension (HTN), and 5 diabetic patients with myocardial infarction (DMI)) were used to validate the caSUP method by comparing it with manually-placed branch cuts (mSUP) [1] and 2D harmonic phase (HARP) [5].

MRI Protocol: tMRI was acquired in 8-12 slices of a short axis view and 6 slices of 360° radial long axis view were acquired with a prospectively ECG gated fast gradient echo cine sequence with grid tags spaced 7mm apart. Scanning parameters were: FOV = 40x40cm, scan matrix = 256x128, 8mm slice thickness, flip angle = 10°, TE = 4.2ms, TR = 8.0ms, 20 frames per cardiac cycle, typical temporal resolution 50ms.

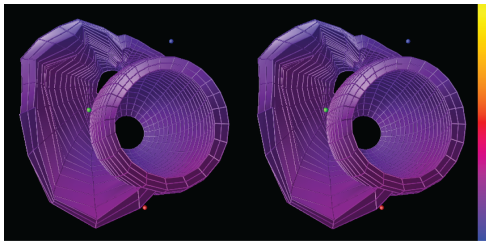

Fig. 1: Maps of end-systolic maximal shortening strains using mSUP (left) and caSUP (right) for a representative normal subject (NL). Strain ranges from blue = -25% to yellow = 25%

RESULTS/DISCUSSION: The caSUP algorithm was implemented in MATLAB on a computer with a dual core 2.67GHz processor. The average time required for fully-automated branch cut placement and phase unwrapping of both short and long-axis images was ~11 sec per image or ~59min for a typical 320 image study. 96% of the images were unwrapped successfully without manual correction. ~ 5min per study were required to manually correct branch cuts automatically identified by the caSUP algorithm. No significant differences were found between end-systolic LV and RV strains computed using caSUP and mSUP. Coefficients of variation in strains ranged from 1.2% (minimum principal strain - Emin) to 2.2% (longitudinal strain – Ell) in the LV and from 1.8% (Emin) to 5.7% (circumferential strain) in the RV. Fig. 1 shows maps of end-systolic Emin using mSUP and caSUP for a representative normal volunteer (NL). Fig. 2 shows excellent agreement between mid-ventricular strains throughout the cardiac cycle computed using caSUP and HARP.

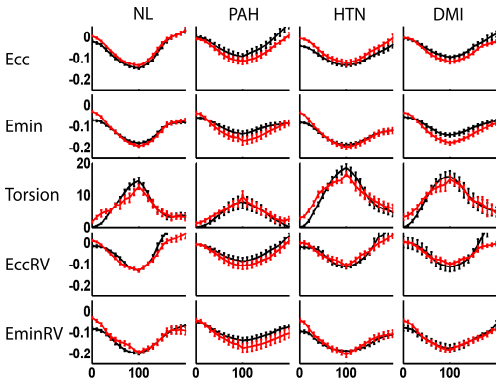

Fig. 2: Averaged mid-ventricular strains and torsions for patient groups of normal (NL), pulmonary hypertension (PAH), hypertension (HTN) and diabetics (DMI) from caSUP (red) and 2D HARP (black). Error bars represent standard deviation.

CONCLUSION: Computer-assisted branch cut placement in both short and long-axis images can accurately reconstruct biventricular 3D strain throughout the cardiac cycle with a minimum of user interaction.

REFERENCES: [1] Ambale, et al. *JMRI* 2011; 34:799-810; [2] Denney and McVeigh. *JMRI* 1997; 7:799-810; [3] Ambale, et al. *JMRI* 2010; 31:854-862; [4] Ambale, et al. *ISBI* 2009; pp 466-469; [5] Osman and McVeigh. *IEEE Trans Med Imaging* 2000; 19:186-202