Fast and Robust HARP Tracking Using Region Growing

X. Liu[1], and J. L. Prince[1,2]

[1]Computer Science, Johns Hopkins University, Baltimore, MD, United States, [2]Electrical and Computer Engineering, Johns Hopkins University, Baltimore, MD, United States

Introduction: MR tagging is widely used for visualization of myocardial motion. The harmonic phase (HARP) method ([1-2]) automatically estimates motion from tagged MR images by computing the phase values of harmonic images, which are in turn computed by extracting the vertical and horizontal harmonic peaks in the Fourier domain. These phase values are material properties, which can be tracked to reveal tissue motion. Conventional HARP tracking, however, suffers from mistracking due to variety of reasons: large motion, poor temporal resolution, noise, artifacts, or through-plane motion. In most current HARP software, mistracked points are manually identified and corrected, which can be very time-consuming, especially when a dense motion field is required, as in zHARP [3] and other applications. The HARP refinement idea for correcting mistracked points was mentioned in [1] but was not considered to be computationally feasible. Other efforts [4-5] were more recently explored to automatically identify and correct mistracked points; however, these methods are computationally complex and/or require a predefined mesh geometry. In the present work, we revisited the HARP refinement idea and developed a new method based on region growing that can rapidly, robustly, and accurately compute myocardial motion, virtually removing the problem of mistracked points, even when there is severe temporal undersampling. It is also shown that this new approach extends HARP tracking capability right up to the myocardial borders, which was previously impossible.

Methods: The proposed method is based on seeded region growing [6]. It is observed that at least one region within the myocardium – often the posterior septal region – has pixels with relatively small displacements, and they can be correctly tracked throughout the entire cardiac cycle using conventional HARP tracking. Accordingly, one or more points are manually selected within such a region, and these points become seed points from which the fully automatic algorithm proceeds. Because myocardial motion is relatively smooth, the pixels comprising neighbors of the seed point(s) are the first candidates for tracking. When tracking from time frames t_0 to t_1, these neighbors are examined one by one and put on a sequentially sorted list (SSL) in the following fashion: the neighbor y_i^0 is moved to location y_i^1 at time t_1 by assuming the same amount of displacement as its seed point. Then the phase values $p_{(1,2)}^1(y_i^1)$ of the estimated location at t_1 are calculated. For each neighbor, a cost function is defined as
$C(y_i^0) = |p_1^0(y_i^0)-p_1^1(y_i^1)| + |p_2^0(y_i^0)-p_2^1(y_i^1)|$, where $p_{(1,2)}^{(0,1)}$ is the HARP value at the two tagging directions at t_0 and t_1. The neighbors are inserted on the SSL so that the neighbor with the smallest cost is always the next to be taken off the list. The algorithm then proceeds by taking the first point off the list, tracking it (using conventional HARP tracking initialized with its seed point's estimated displacement), and then places the newly tracked point's neighbors onto the SSL. This process continues until the SSL is empty (implying that the entire image is tracked).

Results: The HARP refinement method was implemented in C and compiled and run in Matlab 7 (Mathworks, Natick MA). On a computer with Intel Core Duo 1.83GHz processor and 1G Ram, our implementation takes 0.2 second to track a 128 by 128 image over one time frame. It was applied on real tagged cardiac images, and compared with the traditional HARP method. The imaging parameters are: FOV=280mm, image size=256x256, tag separation=14mm, time frames = 22, temporal resolution=30ms. To evaluate the effectiveness of the method on large motion/low temporal resolution, experiments were done using subsets of the available data obtained by evenly dropping intermediate images: (A) all 23 images; (B) 11 images + last image; (C) 8 images + last image; and (D) 6 images + last image). (The last image was always included so the final computed displacements could be directly compared.) The results are shown in Figure 1 (A-D is shown left-right). All images shown are cropped to display the left ventricle only. The first row is the displacement magnitude map calculated by tracking every point using conventional HARP tracking. The second row is the region growing HARP refinement result. The last row displays regions where conventional HARP is effective/correct (blue) and regions where region growing HARP refinement method is also effective/correct (blue+red). Note the red regions are correctly tracked by region growing HARP refinement method only, while the blue regions are correctly tracked by both methods. It is observed that region growing HARP tracking expands the region of valid tracking to include the myocardial boundaries and produces nearly identical results whether severely undersampled in time or not.
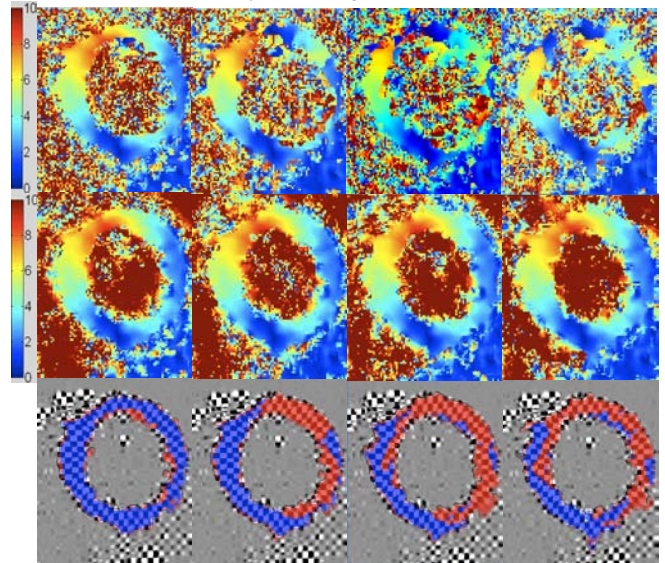
Table 1 quantitatively compares correctly tracked pixels for the two methods. It can be seen that when the temporal resolution decreases the traditional HARP method fails in more points, while region growing HARP refinement almost always tracks every point inside the LV correctly regardless of temporal resolution.

Conclusion: Region growing HARP refinement can robustly track all points within the myocardium despite poor temporal resolution. Improved tracking near myocardial boundaries is also observed. The method is also computationally fast and makes it feasible to compute the Lagrangian strain computation between arbitrary points.

Figure 1

Time Frames \ # Correctly Tracked Points	22+1	11+1	8+1	6+1
Traditional HARP	1808	1190	934	1039
HARP Refinement	2256	2262	2374	2301
Ratio	0.8014	0.5261	0.3933	0.4515

Table 1

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