HARP TRACKING REFINEMENT USING SEEDED REGION GROWING

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ABSTRACT

Tagged magnetic resonance (MR) imaging makes it possible to image the motion of tissues such as the muscles found in the heart and tongue. The harmonic phase (HARP) method largely automates the process of tracking points within tagged MR images. It works by finding spatial points in successive images that retain the same two harmonic phase values throughout the entire image sequence. Given a set of tracked points, many interesting and useful motion properties such as regional displacement or rotation, elongation, strain, and twist, can be computed. When there is a large motion between successive image frames, HARP tracking can fail, and this results in mistracked points and erroneous motion estimates. In this paper, we present a novel HARP refinement method based on seeded region growing that addresses this problem. Starting from a given seed point which is determined by the user to be correctly tracked throughout the entire sequence, this method can reliably track the motion of the whole tissue. A novel cost function is used in the region growing to assure that points that can be most reliably tracked are tracked first. Experimental results on tagged MR images of the tongue demonstrate very reliable tracking.

INDEX TERMS — MR tagging, HARP, motion tracking, region growing

1. INTRODUCTION

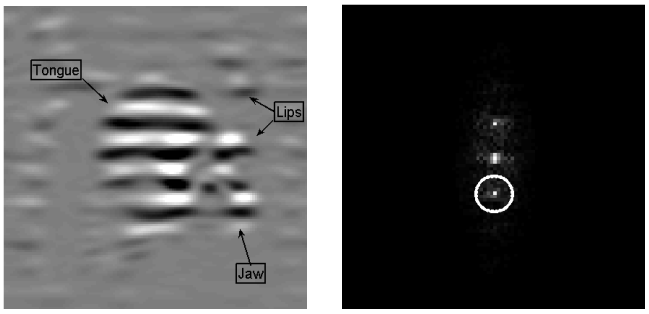
Magnetic resonance (MR) tagging creates patterns of magnetic spin systems within the tissue, yielding images that carry information about motion within homogeneous tissues. This information complements conventional anatomical images, which carry information about motion only at the boundaries of tissues. Detailed information about the motion of tissues such as the heart and tongue throughout the muscles can be imaged in this way. Displacement, velocity, rotation, elongation, strain, and twist are just some of the quantities that be computed from this data. The harmonic phase (HARP) method processes tagged MR images, enabling the automatic computation of these quantities. The HARP method [**?**, **?**] has been successfully applied in both the heart [**?**] and the tongue [**?**], and has proven to be useful for both scientific and clinical applications.

Two-dimensional (2D) in-plane motion tracking is an important part of the HARP method because other quantities are often computed using these tracking results. HARP tracking (explained below) implicitly assumes that tissue points do not move much from one time frame to the next. If the tissue moves too fast, the temporal resolution is too low, or that MR tag parameters are selected incorrectly, this assumption is violated, and HARP tracking will fail. Although such failures are relatively rare in typical well-designed applications, careful scientific studies and robust clinical applications require that the user manually identify and correct mis-tracked points. This can be very time-consuming, to the point where large reseach studies take too much time and clinical throughput is too low. In our research on tongue motion, which motivated this particular research result, there are some utterances in which parts of the tongue move quite fast relative to the temporal resolution of the scan, causing predictable HARP tracking errors. Efforts to track a very large number of points in the tongue [**?**, **?**] thereby become extremely time consuming, as manual correction is routinely required.

There have been some previous efforts to identify and automatically correct mistracked points. Khalifa et al. [**?**] recently proposed a HARP tracking error correction method on cardiac tagged MR images. This method used an active contour model to correct the tracking error on a predefined circular mesh model. The approach is limited to the circular geometry and not easily generalized for applications in the tongue. In [**?**], the idea of HARP refinement — which we expand herein — was mentioned, but it was not considered to be computationally feasible [**?**]. Refinement was also developed for circular geometries, but we show herein, it is readily generalizable to arbitrary regions, even whole images.

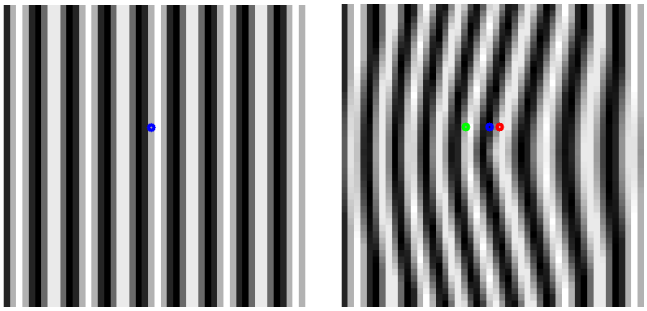
In this paper, we proposed a refinement method for HARP tracking that is based on seeded region growing[**?**]. It can reliably track every point (pixel) inside a given tissue (or even the whole image) and does not require a circular geometry or organized mesh of points defined on the region. This approach, which is computationally fast, extends the original HARP tracking method making Lagrangian strain computa-

This research was supported by NIH grants R01 HL047405 and R01 DC001758



(a) (b)

Fig. 1. (a) A tagged MR image of a mid-sagittal image of the lower-half of the head and (b) the magnitude of its Fourier transform.



(a) (b)

Fig. 2. This example illustrates how HARP tracking fails. (a) is the image at first time frame, and (b) is the image at the second time frame. In both images, the blue dot is the point being tracked. In (b), the green dot is where the point actually moves, and the red dot is the result of HARP tracking. The HARP tracking fails because the red dot is the closest point to the blue dot that has the same phase value at the second time frame.

tions between arbitary points feasible. Experiment results on MR tagged images of the tongue are used to demonstrate the effectiveness of this method.

2. METHOD

2.1. HARP method and motion tracking

The Fourier transform of a SPAMM-tagged MR image has two harmonic peaks, as shown in Fig. 1. In the HARP method, a bandpass filter is used to extract just one of the harmonic peaks, and its inverse Fourier transform is given by [**?**]

$$I(\mathbf{x},t) = D(\mathbf{x},t)e^{j\phi(\mathbf{x},t)}, \tag{1}$$

where $D(\mathbf{x},t)$ is the harmonic magnitude image, and $\phi(\mathbf{x},t)$ is the harmonic phase (HARP) image. The magnitude image reflects the tissue anatomy, and the HARP image contains the tissue motion information.

The harmonic phase is a material property of tagged tissue. Thus, the phase value $\phi(\mathbf{x}(t)) = \phi(\mathbf{x}_0)$ of a material point $\mathbf{x} = \mathbf{x}(t)$, and $\mathbf{x}(0) = x_0$, does not change as the point moves. The HARP value is the principal value of the corresponding phase value

$$\alpha_{(1,2)}(\mathbf{x},t) = W(\phi_{(1,2)}(\mathbf{x},t)) \tag{2}$$

where $W(\cdot)$ is the wrapping function defined as:

$$W(\phi(\mathbf{x},t)) = \mod(\phi+\pi, 2\pi) - \pi \tag{3}$$

such that $\alpha_{(1,2)}(\mathbf{x},t) \in [-\pi,\pi)$, and (1,2) gives one of the two tag orientations.

It is observed that the HARP value is also a material property and therefore does not change as $\mathbf{x}$ moves either. This is called phase invariance property and is the basis of HARP motion tracking. For 2D tracking, two tag orientations are required to track the apparent motion of a material point. The HARP tracking method is described in detail in [**?**]. Briefly, when given the position of a material point $\mathbf{x}$ at some time frame t_i, the HARP method searches its neighborhood at next time frame t_{i+1} in both tag orientations to find the closest point $\mathbf{x}(t_{i+1})$ such that

$$\alpha_{(1,2)}(\mathbf{x}(t_i),t_i) = \alpha_{(1,2)}(\mathbf{x}(t_{i+1}),t_{i+1}) \tag{4}$$

If the tissue moves more than half of the tag separation between two successive time frames, HARP tracking will fail. To be clear, the HARP tracking algorithm will converge in all cases, but in the case of large motion, it will converge to a point having the same pair of HARP values but is fully one tag period away from the true corresponding point. Fig. 2 shows such an example that 1D HARP tracking fails for large motion.

2.2. HARP Refinement

For normal tissue motion, two facts are observed. Firstly, the motion field within the tissue is smooth. In another words the motions of neighboring tissue points are similar, e.g.: for two neighboring 2D points $\mathbf{x}(t_0), \mathbf{y}(t_0)$ at time frame t_0,if at next time frame t they move to $\mathbf{x}(t)$and $\mathbf{y}(t)$, then the difference between their motion

$$\Delta(\mathbf{x},\mathbf{y},t_0,t)) = |(\mathbf{x}(t)-\mathbf{x}(t_0)) - (\mathbf{y}(t)-\mathbf{y}(t_0))| \tag{5}$$

is small. So if $\mathbf{x}(t)$ can be tracked correctly from $\mathbf{x}(t_0)$, a good estimation of $\mathbf{y}(t)$ is

$$\mathbf{y}'(t) = \mathbf{y}(t_0) + (\mathbf{x}(t)-\mathbf{x}(t_0)). \tag{6}$$

Therefore $\mathbf{y}'(t)$ can be used as the starting point when tracking $\mathbf{y}(t_0)$ to prevent failure of HARP tracking.

Secondly, some part of the tissue has relatively small motion, and can always be tracked correctly using HARP over

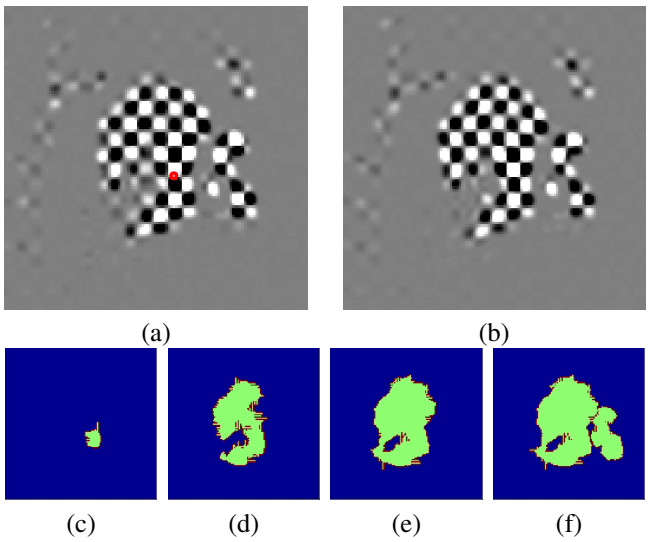


Fig. 3. Illustration of the region growing process. (a) is the checkoard image at the first time frame by overlaying the two tagged images with different orientations, (b) is the checkboard imge at the second time frame. The red dot in (a) is the manually selected seed point. (c)-(d) shows how the region grows. The green color means tracked points, brown means boundary points, and blue means points that are not tracked and not boundary points.

all time frames. For example the bottom part of the tongue usually moves much less than the tip of the tongue. This indicates that it is possible and easy to manually identify a few seed points that HARP tracking succeeds.

Based on these two facts we proposed the HARP refinement method based on seeded region growing. Our algorithm starts with one or more manually identified seed points that can be correctly tracked over all time frames using conventional HARP method. Then from every time frame to the next, the neighbor points of the seeds are identified and stored in a sequentially sorted list (SSL). Then iteratively that every point in the SSL is tracked and its neighbors are inserted into the SSL. The process is repeated until the list is empty. Note that the tracking between different neighboring time frames is independent, and from now on we consider only the tracking from time t_i to t_{i+1}.

The SSL is maintained throughout the algorithm. The points in the SSL are called boundary points. Each node of the list contains the following information: the point's 2D coordinate $\mathbf{y}(t_i)$ in time t_i, the initial estimation of its location in next time frame $\mathbf{y}'(t_{i+1})$, and a cost value $c(\mathbf{y}(t_i))$. $\mathbf{y}'(t_{i+1})$ is calculated as defined in (6) by assuming that $\mathbf{y}(t_i)$ has the same amount of motion as one of its neighbor points that has already been tracked. The list is sorted in the ascending order of the cost value that is defined later. At each itertation, the first node of the list is fetched and removed from the list. The point in this node ($\mathbf{y}(t_i)$) is then tracked using HARP with the starting location of $\mathbf{y}'(t_{i+1})$. This means the tracked point $\mathbf{y}(t_{i+1})$ has the same HARP values as and is the closest point to $\mathbf{y}'(t_{i+1})$ (comparing with $\mathbf{y}(t_i)$ in the conventional HARP method) (ref. (4)). After that, its neighbor points that are neither tracked yet nor boundary points are inserted into the list based on the cost value. The inserted neighboring point's estimated location at time t_{i+1} is calculated and stored with the node.

As discussed before the HARP phase value is consistent and smooth inside the interested tissue. In the air among tissues the HARP values are inconsistent and random. Therefore HARP tracking in those regions is meaningless and will cause error if those regions were visited before all points inside the tissue were tracked. So it is desirable to limit the tracking inside the tissue of interest until every point in the tissue of interest is tracked. We novelly define a cost function that is used to sort the boundary points in the SSL as:

$$c(\mathbf{y}(t_i)) = \sum_{i=1}^{2} |W(\alpha_i(\mathbf{y}(t_i), t_i) - \alpha_i(\mathbf{y}'(t_{i+1}), t_{i+1}))| \quad (7)$$

Here $W(\cdot)$ and $y'(\cdot)$ are as defined previously. For a point in the region with smooth motion at time t_{i+1}, the estimated location $\mathbf{y}'(t_{i+1})$ is close to the true location $\mathbf{y}(t_i), t_i)$. So the wrapped difference between the actual phase $(\alpha_i(\mathbf{y}(t_i), t_i)))$ and the phase at the estimated location $\alpha_i(\mathbf{y}'(t_{i+1}), t_{i+1}))$ is small, and the cost function has small vaue. Therefore the point is put at the front of the SSL and is visited early.

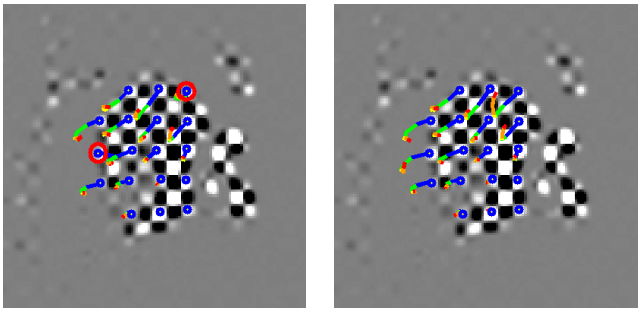
2.3. Implementation of HARP refinement algorithm

Our algorithm can be implemented as follows:

Manually select seed point(s)$\mathbf{s}_0$ and track over all time frames using HARP
  For each time frame t_i
    Find neighbors of the seed(s), and create the SSL
      While the SSL is not empty
        Remove the first node $\mathbf{x}(t_i)$ from SSL
        Find $\mathbf{x}(t_{i+1})$ using HARP
        Label $\mathbf{x}(t_i)$ as tracked point
        For ever neighbor point $\mathbf{y}_k(t_i)$ of $\mathbf{x}(t_i)$
          If not tracked point and not boundary point
            Calculate $\mathbf{y}'_k(t_{i+1}$, and the cost $c(\mathbf{y}(t_i))$
            Insert $\mathbf{y}_k(t_i)$ in the SSL based on $c(\mathbf{y}(t_i))$
            Label $\mathbf{y}_k(t_i)$ as boundary point

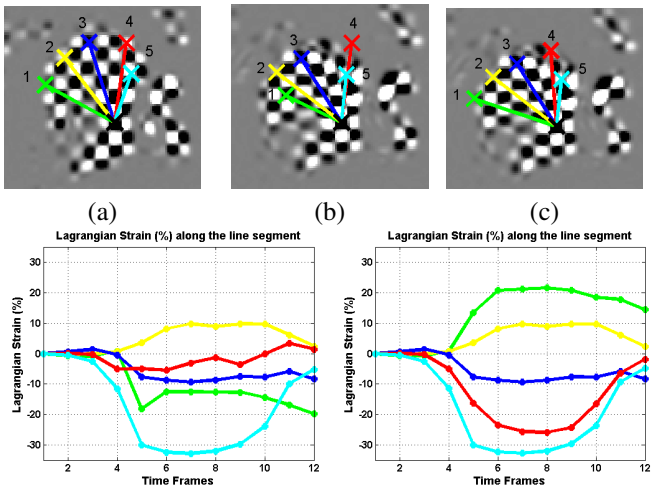
3. EXPERIMENT RESULTS

Our mehod was applied on the tagged MR images of the tongue. The images were collected on a 1.5T Maconi scanner when the subject uttered "eeoo" repeatedly. 6 sagittal slices were acquired in 12 time frames, with a temporal resolution of 66 msec. The interpolated spatial resolution was 1.09 mm x



(a) (b)

Fig. 4. The trajectory of some points on tagged MR image over 12 time frames. (a) is the HARP tracking results. The points in the circle were mistracked. (b) is the HARP refinement results.



(a) (b) (c) (d) (e)

Fig. 5. The action of Genioglossus (GG). (a) shows five segments of GG at the first time frame. They are then tracked using both conventional HARP method and our HARP refinement method throughout all the time frames, The tracked position at the last time frame is shown in (b) and (c) respetctively. (d) and (e) shows the Lagrangian strains of the 5 line segments change with time. (d) is the result of conventional HARP method, and (e) is the result of HARP refinement.

1.09 mm x 7 mm. Four sets images were collected: horizontal tagging with [$+90^0$ $+90^0$] tagging pulse and [$+90^0$ -90^0] tagging pulse, and vertical tagging with [$+90^0$ $+90^0$] and $+90^0$ -90^0] tagging pulses. As preprocessing, the MICSR ([**?**]) images were reconstructed from these 4 sets of data. Our method was implemented in C, and compiled in Matlab 7. On a computer with Intel Core Duo 1.83 GHz processor with 1.0G ram, our implementation took about 0.2 second to track an 128 by 128 image for one time frame.

Fig. 3 shows the intermediate results of the region growing process on the mid-sagittal slice. Starting from the seed point, the points inside the tongue were tracked first. The outside points were tracked only after all points inside the tongue were tracked.

In Fig. 4 a grid of points was placed inside the tongue and tracked. When using the tradiontal HARP tracking method, some points were misttracked (Fig. 4(a)). However they were all tracked correctly using our HARP refinement method.

Our HARP refinement method also helps improve the calculation of Lagrangian strain. Fig. 5 shows the lines of action for a muscle called genioglossus (GG). The Lagrangian strain is calculated as the length change of line segments with respect to the length at first time frame. It has positive value when stretching, and negative value when contracting. In Fig. 5(b), the number 1 and number 4 line segments were mistracked using conventional HARP method, which made the Lagrangian strain calculation wrong (Fig. 5(d). These line segments can be tracked correctly using HARP refinement method (Fig. 5(c)). The Lagrangian strain calculated based on the HARP refinement result is shown in Fig. 5(e).

4. CONCLUSION

In this paper we presented a semi-automatic HARP refinement method. Starting from one seed point, this method can reliably track the 2D interiortissue motion using 1-1 SPAMM tagged images. Experimental results show that comparing with conventional HARP method, this method can correctly track all points inside the tissue even the motion is larger than half of the tag separation. Besides, this method is fast and can be run in real-time. The success of this method makes the estimation of dense 2D/3D motion field easier, as well as other things that relies on reliable motion estimation, for example Lagrangian strain calculation.