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Phase Vector Incompressible Registration Algorithm (PVIRA) for Motion Estimation from Tagged Magnetic Resonance Images

Fangxu Xing,

Department of Radiology, Massachusetts General Hospital/Harvard Medical School, Boston, MA, 02114 USA

Jonghye Woo [Member, IEEE],

Department of Radiology, Massachusetts General Hospital/Harvard Medical School, Boston, MA, 02114 USA

Arnold D. Gomez,

Department of Electrical and Computer Engineering, Johns Hopkins University, Baltimore, MD, 21218 USA

Dzung L. Pham [Member, IEEE],

Center for Neuroscience and Regenerative Medicine, The Henry M. Jackson Foundation, Bethesda, MD, 20817 USA

Philip V. Bayly,

Department of Mechanical Engineering and Materials Science, Washington University in St. Louis, St. Louis, MO, 63130 USA

Maureen Stone, and

Department of Neural and Pain Sciences, University of Maryland School of Dentistry, Baltimore, MD, 21201 USA

Jerry L. Prince [Fellow, IEEE]

Department of Electrical and Computer Engineering, Johns Hopkins University, Baltimore, MD, 21218 USA

Abstract

Tagged magnetic resonance imaging has been used for decades to observe and quantify motion and strain of deforming tissue. It is challenging to obtain three-dimensional (3D) motion estimates due to a tradeoff between image slice density and acquisition time. Typically, interpolation methods are used either to combine two-dimensional motion extracted from sparse slice acquisitions into 3D motion or to construct a dense volume from sparse acquisitions before image registration methods are applied. This paper proposes a new phase-based 3D motion estimation technique that first computes harmonic phase volumes from interpolated tagged slices and then matches them using an image registration framework. The approach uses several concepts from diffeomorphic image registration with a key novelty that defines a symmetric similarity metric on harmonic phase volumes from multiple orientations. The material property of harmonic phase

solves the aperture problem of optical flow and intensity-based methods and is robust to tag fading. A harmonic magnitude volume is used in enforcing incompressibility in the tissue regions. The estimated motion fields are dense, incompressible, diffeomorphic, and inverse-consistent at a 3D voxel level. The method was evaluated using simulated phantoms, human brain data in mild head accelerations, human tongue data during speech, and an open cardiac dataset. The method shows comparable accuracy to three existing methods while demonstrating low computation time and robustness to tag fading and noise.

Index Terms

Motion; 3D; tagged MRI; phase; registration; incompressible

I. Introduction

The analysis of biological motion using medical imaging techniques has been an important topic of research for both clinical and scientific purposes. Its application ranges from cardiac imaging [1], [2] to studies in speech and swallowing [3] to analysis of brain motion in traumatic injuries [4], [5], etc. Tagged magnetic resonance (MR) imaging is a widely used technique for quantifying soft tissue motion [6], [7]. It places temporary markers (tags) in the tissue of interest that move and deform together with tissue during motion. Many methods for estimating two-dimensional (2D) tissue motion and strain from the deformed tag patterns have been proposed in the past, including tag line tracking [8], [9], tag intersection tracking [10]–[12], and pixel-wise tracking using harmonic phase or Gabor filters [13]–[16].

While measuring 2D motion alone might be sufficient in some applications, knowledge of three-dimensional (3D) motion is necessary or highly desirable in others. Methods to measure 3D motion from densely-acquired tagged MR images have been proposed in the past. They require an acquisition of a large number of closely spaced image slices, which is equivalent to direct acquisition of a dense 3D volume. In this case, traditional 2D methods can be extended to 3D and directly applied to compute the dense motion [17]–[20]. However, the large amount of time that it takes to acquire these images makes this approach impractical for routine clinical or scientific use. For this reason, most of the reported 3D motion estimation methods have been focused on the use of sparse collections of 2D images and 2D motion estimation followed by interpolation in order to achieve 3D motion estimation.

Fig. 1 shows a typical imaging geometry for a sparse acquisition of tagged MR images of the brain during mild acceleration [5]. The slices are taken to cover the whole brain but due to time constraints the slice spacing is large. In each axial image plane, two sets of images are taken in the same location, one with horizontal tags and the other with vertical tags. In this way, motion components in the x and y directions can be observed in these two sets. In order to record the z motion, sagittal slices with horizontal tags are also acquired. For each slice position, MR tags are placed at a reference time and a sequence of images are acquired over time in order to reveal the motion as a deforming tag pattern. Because of the acquisition

geometry, the available motion data are sparse in the through-plane direction. Similar geometries are used in both cardiac and speech studies. As a result, motion features that are observed in the acquired image planes must be interpolated in some way in order to observe dense 3D motion.

Incompressibility is an important consideration in the estimation of biological motions. For example, during a cardiac cycle, the change in volume of the myocardium is less than 4% [21], [22], and the change in volume of the tongue during speech and swallowing is even smaller [23]. Therefore, the motion of muscles can be assumed to be incompressible [24]. In the study of brain motion under mild accelerations, there is very little exchange of fluid in the ventricular system and the total brain volume including the ventricles remains very nearly constant [5]. Therefore, incompressibility can also be assumed in studies of small brain motions under mild accelerations created inside an MR scanner. In summary, constraining an estimated motion field to represent an incompressible motion within the tissue itself is desirable.

Previous works on 3D motion estimation from sparse imaging geometries are quite varied. Some use finite element or finite difference methods [25], [26], some use tag line tracking based on 2D images [27], [28], some use spline interpolation [27], [29]–[32], some use the organ's biomechanical properties [33], [34], and some are based on harmonic phase tracking [31], [35]. More methods are summarized in the collected works of [36]. These methods are often complex. Because the computations may be limited to an organ of interest, a 3D segmentation method is commonly required [25], [27], [29], [37]; this step requires either human intervention or automated segmentation algorithms [38] which increase the demand on processing time. Moreover, because of the use of sparse imaging the incorporation of incompressibility has typically been through an interpolation strategy. The methods in [39], [40] use divergence-free radial basis functions while the methods in [31], [41] use smoothing vector splines seeking a divergence-free velocity field that yields a nearly incompressible deformation field when integrated. Unfortunately, vector interpolation further increases processing complexity, which can result in perhaps a day or more of computation time when processing a subject with many temporal volumes at high resolution.

Intensity-based methods for tagged motion estimation using registration approaches on dense voxel geometries have gradually become a major focus in recent developments [42]–[47]. These methods aim to match intensity values between tagged voxels using optical flow assumptions while incorporating additional desired properties. Extensions of 2D methods to 3D have been proposed in [48]–[53], sparse volumes have been addressed in [54]–[56], and incompressibility has been incorporated in [57], [58]. Specifically, image registration algorithms based on dense imaging geometries can accommodate incompressibility in various ways. For example, the diffeomorphic demons registration algorithm [59] was extended to include volume-preserving deformations [60], [61] and was applied to tagged intensity data. However, the underlying premise of intensity-based methods—the matching of intensity values between time frames—is not robust to intensity variation and degeneration [62]. MR tags are known to fade exponentially with the T_1 constant of the tissue, and previous experiments have shown that intensity registration is inaccurate as the result of tag fading [63].

It is well-known that phase-based registration is more robust than intensity-based registration with respect to smooth variations in illumination, geometric distortions between frames, and noise [64], [65]. When phase-based registration is used in conjunction with MR tagging, the phases provide relative positions of the sinusoidal patterns produced by tagging and are material properties which can be directly tracked [13], yielding a very direct approach to motion estimation. The recent work on 3D phase-based motion estimation by Zhou et al. [35], [66] is most closely related to our own work. The authors point out that incorporation of both spatial regularization and incompressibility are important goals when extending phase-based methods to three dimensions. However, their approach requires a model of the anatomy—a volumetric mesh of the left ventricle in their case—in order to impose these properties. Our approach provides both spatial regularization and incompressibility without the need for an anatomical model.

In this paper, we propose a new phase-based registration approach for motion estimation from MR tagged images. The method first interpolates raw tagged images onto a denser grid and then applies the harmonic phase (HARP) method [14] to yield 3D harmonic phase volumes, which are processed using deformable registration to track tissue points over time. Since motion components from three cardinal directions are derived from three pairs of fixed and moving phase volumes, a multichannel scheme such as the ones proposed in [67]–[73] needs to be applied to achieve a simultaneous three-channel registration. The proposed registration framework is based on iLogDemons [61], but contains several key differences. First, to drive the registration process, we use a new symmetric harmonic phase vector similarity metric. Second, to compensate for harmonic phase wrapping, we incorporate a special phase interpolation method. Finally, to enforce incompressibility only within tissue regions, we use the harmonic magnitude image along with the divergence-free velocity constraint of iLogDemons. We call the proposed method PVIRA, which stands for *Phase Vector Incompressible Registration Algorithm*. PVIRA was evaluated using simulation, MR data from the human brain in rotation, the human tongue in speech, and cardiac motion [74]. We compared its result against three methods: 3D HARP tracking, IDEA [31], and direct intensity registration. The evaluations show better robustness to noise and tag fading and a major reduction in computation complexity. PVIRA is demonstrated to yield a nearly incompressible result and to produce motion and inverse motion fields that are very nearly inverse-consistent.

This paper is organized as follows. Section II.A discusses the interpolation of tagged slices. Section II.B presents the HARP method and the production of phase volumes. Section II.C briefly introduces the iLogDemons method and Section II.D presents the new similarity metric used to drive the velocity update process in PVIRA. Section II.E discusses the interpolation and deformation of phase volumes and Section II.F shows how incompressibility is incorporated. Section III shows the experimental results on simulation and real data. Section IV discusses the method and Section V concludes the paper.

II. Methods

A flow chart of PVIRA is shown in Fig. 2. We explain each step in the following sections.

A. Interpolation of Tagged Slices

We use tricubic b-spline interpolation [75] to produce an arbitrarily dense 3D tagged volume with isotropic resolution, as illustrated in Fig. 3. In this scenario, we let $\mathbf{x}_s \in \mathcal{X}$ denote the location from the set of points sampled by the sparsely acquired sagittal slices $I_a(\mathbf{x}_s)$ having horizontal tag planes. These locations are shown as blue dots in Fig. 3(a). Since horizontal tag planes in a sagittal acquisition have unit normals in the axial direction, the subscript a is used in the notation I_a . We denote points in the dense 3D grid by $\mathbf{x}$, as shown using red dots in Fig. 3(a). Tricubic b-spline interpolation then finds the values $I_a(\mathbf{x})$ by

$$I_a(\mathbf{x}) = \sum_{\mathbf{x}_s \in \mathcal{X}} c(\mathbf{x}_s) \beta^3(\mathbf{x} - \mathbf{x}_s), \quad (1)$$

where $\beta^3(\mathbf{x})$ is the cubic b-spline interpolation kernel and $c(\mathbf{x}_s)$ are the interpolation coefficients computed from $I_a(\mathbf{x}_s)$ [76]. Four interpolated sagittal slices zoomed in on the tongue region are shown in Fig. 3(c). In a similar fashion, the two axial acquisitions (see Fig. 1) containing horizontal and vertical tags can be interpolated onto the same 3D grid to create the image $I_c(\mathbf{x})$ having coronal tag planes and the image $I_s(\mathbf{x})$ having sagittal tag planes. The output of interpolation is a dense 3D volume in which each voxel has samples of three tagged volumes where the tags (prior to motion) are oriented in the three cardinal directions. This process is repeated at each time frame, yielding a sequence of such vectorized tagged volumes. Note that we chose the voxel separation in the interpolated volume to be the same as the in-plane pixel separation of the acquired images. This choice balances potential loss of resolution and accuracy if the separation were larger with increased computation time if the separation were smaller.

B. Harmonic Phase Volumes

The HARP algorithm [14] is a popular phase-based method to process tagged MR images. In this method, one of the harmonic peaks in the Fourier domain of a tagged image slice is bandpass filtered (so-called HARP filtering) to yield a complex-valued image (see Fig. 4) where motion information is contained in the phase part (HARP phase) and anatomical information is contained in the magnitude part (HARP magnitude). Here, we use *peak-combination HARP* [77] wherein two harmonic peaks are combined to correct phase errors and improve signal-to-noise. While HARP was originally developed to analyze 2D images, the HARP framework is valid in 3D and has been previously used by Ryf et al. [17] to carry out 3D HARP tracking to compute displacement fields from densely acquired tagged images. We refer to this method as 3D HARP.

Following this strategy, our method performs HARP filtering on the three interpolated tagged volumes I_a , I_c , and I_s . For example, for the volume $I_a(\mathbf{x})$, the complex image after HARP filtering can be denoted as

$$J_a(\mathbf{x}) = M_a(\mathbf{x}) e^{j\Phi_a(\mathbf{x})}, \quad (2)$$

where $M_d(\mathbf{x})$ is the HARP magnitude volume and $\Phi_d(\mathbf{x})$ is the HARP phase volume. The same notation applies for coronally and sagittally tagged volumes, yielding $J_c(\mathbf{x})$, $M_c(\mathbf{x})$, $\Phi_c(\mathbf{x})$, $J_s(\mathbf{x})$, $M_s(\mathbf{x})$, and $\Phi_s(\mathbf{x})$.

C. iLogDemons

The registration framework of iLogDemons [61] is used as a starting point for PVIRA. Summarized in Algorithm 1, iLogDemons is an iterative method alternating between force-driven stepwise update and deformation field regularization. It yields an invertible motion field that represents an incompressible motion. Suppose $I_0(\mathbf{x})$ is a fixed intensity image and $I_t(\mathbf{x})$ is a moving image; then by minimizing the demon energy $\|I_0(\mathbf{x}) - I_t \circ \exp(\mathbf{v}(\mathbf{x}))\|^2 + K\|\nabla \mathbf{v}(\mathbf{x})\|^2$, an optimal update velocity field $\delta \mathbf{v}(\mathbf{x})$ can be found. From [78], the symmetric form of $\delta \mathbf{v}(\mathbf{x})$ is given by

$$\delta \mathbf{v}(\mathbf{x}) = \frac{2(I_0(\mathbf{x}) - I_t'(\mathbf{x}))(\nabla I_0(\mathbf{x}) + \nabla I_t'(\mathbf{x}))}{\|\nabla I_0(\mathbf{x}) + \nabla I_t'(\mathbf{x})\|^2 + K(I_0(\mathbf{x}) - I_t'(\mathbf{x}))^2}, \quad (3)$$

where $I_t'(\mathbf{x}) = I_t \circ \psi(\mathbf{x})$ is the moving image deformed by the current motion estimate ψ and K is a normalization factor. Note that the motion estimate $\psi(\mathbf{x}) = \exp(\mathbf{v}(\mathbf{x}))$ uses the exponential map of a stationary velocity estimate $\mathbf{v}(\mathbf{x})$, which is the main quantity that must be estimated in the “log domain”.

D. Registration of Phase Volumes

PVIRA is driven by phase rather than intensity, and from (3) it can be seen that computation of both phase difference and phase gradient is required. These computations are problematic because HARP phase $\Phi(\mathbf{x})$ is the true phase $\Omega(\mathbf{x})$ wrapped into the range of $[-\pi, \pi)$, i.e.,

$$\Phi(\mathbf{x}) = W(\Theta(\mathbf{x})), \quad (4)$$

where

$$W(\Theta) = \text{mod}(\Theta + \pi, 2\pi) - \pi. \quad (5)$$

This is illustrated in Fig. 5. Although phase unwrapping [79]–[81] could be applied, it is known that 3D phase unwrapping is very challenging [82]. Therefore, we use a local phase unwrapping process, as described next.

Algorithm 1

iLogDemons Registration Algorithm

-
- 1 Set the initial velocity estimate $\mathbf{v}(\mathbf{x})$ to zero.
 - 2 Compute the update velocity $\delta\mathbf{v}(\mathbf{x})$ using Eqn. (3).
 - 3 Regularize $\delta\mathbf{v}(\mathbf{x})$ with a Gaussian kernel.
 - 4 Compose $\mathbf{v}(\mathbf{x})$ with $\delta\mathbf{v}(\mathbf{x})$ using the BCH formula [61] and set the result to be the new velocity estimate $\mathbf{v}(\mathbf{x})$.
 - 5 Regularize $\mathbf{v}(\mathbf{x})$ with a Gaussian kernel.
 - 6 Restrict incompressibility by solving Poisson's equation $\nabla^2 p = \nabla \cdot \mathbf{v}(\mathbf{x})$ and setting $\mathbf{v}(\mathbf{x}) - \nabla p$ as the new $\mathbf{v}(\mathbf{x})$.
 - 7 Deform $I_t(\mathbf{x})$ with $\exp(\mathbf{v}(\mathbf{x}))$ to create a new moving image $I'_t(\mathbf{x})$.
 - 8 Go to Step 2. Repeat until convergence.
 - 9 The motion estimate is $\psi(\mathbf{x}) = \exp(\mathbf{v}(\mathbf{x}))$ and the inverse motion estimate is $\psi^{-1}(\mathbf{x}) = \exp(-\mathbf{v}(\mathbf{x}))$.
-

Consider two wrapped phases $\Phi_1 = W(\Omega_1)$ and $\Phi_2 = W(\Omega_2)$. If the underlying true phases satisfy the condition $|\Omega_1 - \Omega_2| < \pi$, then $\Omega_1 - \Omega_2 = W(\Phi_1 - \Phi_2)$. The required condition is satisfied when the underlying tissue motion does not cause the tag pattern to deform more than half a tag period. Commonly used in phase-based methods, this *small motion assumption* can be assured in brain, heart, and tongue motion by choosing a large enough tag period or small enough time interval between images in the sequence. For notational convenience in the sequel, we define the wrapped subtraction operator $-^*$ as follows

$$\Phi_1 -^* \Phi_2 = W(\Phi_1 - \Phi_2), \quad (6)$$

and we assume that this operator yields the true phase difference.

In [14], it was shown that the true gradient can be recovered from the wrapped gradient using the operator ∇^* as follows

$$\begin{aligned} \nabla\Theta(\mathbf{x}) &= \nabla * \Phi(\mathbf{x}) \\ &= \begin{cases} \nabla\Phi(\mathbf{x}), & \text{if } |\nabla\Phi(\mathbf{x})| \leq |\nabla W(\Phi(\mathbf{x}) + \pi)|, \\ \nabla W(\Phi(\mathbf{x}) + \pi), & \text{otherwise.} \end{cases} \end{aligned} \quad (7)$$

This procedure computes gradients on both the original phase function and on the phase that has been shifted by π and then re-wrapped. The correct gradient is the one with smaller magnitude.

Given the ability to compute these quantities, we revisit the iLogDemons algorithm from an energy minimization point of view. Whereas (3) is derived from the goal of matching intensities, PVIRA must match phase; in fact, it must match three phases, one from each tagging direction. Accordingly, we redefine the demons energy as

$$E_t(\mathbf{v}) = \|\Phi_{a0}(\mathbf{x}) - \Phi_{at} \circ \psi(\mathbf{x})\|^2 + \|\Phi_{c0}(\mathbf{x}) - \Phi_{ct} \circ \psi(\mathbf{x})\|^2 + \|\Phi_{s0}(\mathbf{x}) - \Phi_{st} \circ \psi(\mathbf{x})\|^2 + K \|\nabla \mathbf{v}\|^2, \quad (8)$$

where the subscript 0 denotes any reference time frame and the subscript t denotes any other time frame (forward or backward) in the sequence. Note that the 0 subscript is only used as a mathematical notation. Besides the starting frame, any time frame in the sequence can be the reference. We give equal weight to the three phase volumes since they each provide a component of motion.

We follow an analogous strategy as in [59] to find the update velocity field $\delta \mathbf{v}(\mathbf{x})$ that minimizes E_t :

$$\begin{aligned} \delta \mathbf{v}(\mathbf{x}) &= 2\alpha_0(\mathbf{x}) / (\alpha_1(\mathbf{x}) + \alpha_2(\mathbf{x}) / K), \text{ where} \\ \alpha_0(\mathbf{x}) &= (\Phi_{a0}(\mathbf{x}) - \Phi'_{at}(\mathbf{x}))(\nabla^* \Phi_{a0}(\mathbf{x}) + \nabla^* \Phi'_{at}(\mathbf{x})) \\ &\quad + (\Phi_{s0}(\mathbf{x}) - \Phi'_{st}(\mathbf{x}))(\nabla^* \Phi_{s0}(\mathbf{x}) + \nabla^* \Phi'_{st}(\mathbf{x})) \\ &\quad + (\Phi_{c0}(\mathbf{x}) - \Phi'_{ct}(\mathbf{x}))(\nabla^* \Phi_{c0}(\mathbf{x}) + \nabla^* \Phi'_{ct}(\mathbf{x})), \\ \alpha_1(\mathbf{x}) &= \|\nabla^* \Phi_{a0}(\mathbf{x}) + \nabla^* \Phi'_{at}(\mathbf{x})\|^2 \\ &\quad + \|\nabla^* \Phi_{s0}(\mathbf{x}) + \nabla^* \Phi'_{st}(\mathbf{x})\|^2 \\ &\quad + \|\nabla^* \Phi_{c0}(\mathbf{x}) + \nabla^* \Phi'_{ct}(\mathbf{x})\|^2, \\ \alpha_2(\mathbf{x}) &= (\Phi_{a0}(\mathbf{x}) - \Phi'_{at}(\mathbf{x}))^2 + (\Phi_{s0}(\mathbf{x}) - \Phi'_{st}(\mathbf{x}))^2 \\ &\quad + (\Phi_{c0}(\mathbf{x}) - \Phi'_{ct}(\mathbf{x}))^2, \end{aligned} \quad (9)$$

where Φ'_{at} , Φ'_{st} , and Φ'_{ct} are Φ_{ab} , Φ_{sb} and Φ_{ct} deformed with current ψ (see next section). The metric used is similar to previous multichannel image registration metrics [73], but is specifically adapted to HARP phase. In particular, the difference and gradient operations have been modified to address phase wrapping.

E. Deformation of Phase Volumes

Now we discuss the deformation of Φ_{ab} , Φ_{sb} and Φ_{ct} using the current motion estimate $\psi(\mathbf{x})$ at each demons iteration step. Since interpolation is used to find sub-voxel values of the deformed phase, the effect of phase wrapping must also be considered in computing these deformations. As illustrated in Fig. 5 for a one-dimensional example, suppose the phase value at sub-voxel location x_0 must be found from the known phases $\Phi(x_1)$ and $\Phi(x_2)$ at two neighbor voxels x_1 and x_2 . Linear interpolation would give $\hat{\Phi}(x_0) = (\Phi(x_2) - \Phi(x_1))(x_0 - x_1)/(x_2 - x_1)$. In this case the value $\hat{\Phi}(x_0)$ equals the real phase $\Omega(x_0)$ because no wrapping is involved. The situation is different at location y_0 , however. In this case, since $\Phi(y_2)$ has been wrapped from the true value $\Omega(y_2)$, $(\Phi(y_2) - \Phi(y_1))(y_0 - y_1)/(y_2 - y_1)$ yields the wrong result, while the correct value is computed by unwrapping $\Phi(y_2)$ to $\Phi(y_2) + 2\pi$.

To provide a correct phase interpolation we first note that $(\Phi(y_2) + 2\pi) - \Phi(y_1) = W(\Phi(y_2) - \Phi(y_1))$. Whenever an abnormal phase difference greater than 2π is caused by wrapping,

under the small motion condition (see previous section), the abnormal difference must be a jump of $\pm 2\pi$. Because of this fact, the error can be removed by re-wrapping the phase difference. Therefore, when deforming phase volumes and using interpolation in each of the three x , y , and z directions, every phase subtraction must be computed with wrapping, i.e.,

$$\hat{\Phi}(y_0) = W\left(\frac{y_0 - y_1}{y_2 - y_1} \cdot (\Phi(y_2) - \Phi(y_1))\right). \quad (10)$$

F. Incorporation of Incompressibility

In iLogDemons [61], incompressibility is enforced at every iteration by computing the “divergence part” of the velocity and removing it, i.e., solve Poisson’s equation $\nabla^2 p = \nabla \cdot \mathbf{v}(\mathbf{x})$ to find the conservative (curl-free) part $\mathbf{v}_d(\mathbf{x}) = \nabla p$ and update the velocity by $\mathbf{v}(\mathbf{x}) - \mathbf{v}_d(\mathbf{x})$. In PVIRA, since only the tissue region should be incompressible, we apply this principle only in the tissue region. To determine this region we normalize the previously generated HARP magnitude volumes $M_d(\mathbf{x})$, $M_c(\mathbf{x})$, and $M_s(\mathbf{x})$ to the range between $[0,1]$ and use their mean $M(\mathbf{x})$ as a tissue mask. The velocity is then updated according to

$$\mathbf{v}(\mathbf{x}) \leftarrow \mathbf{v}(\mathbf{x}) - M(\mathbf{x})\mathbf{v}_d(\mathbf{x}). \quad (11)$$

which enforces incompressibility only when $M(\mathbf{x}) \approx 1$. Since HARP magnitude is computed simultaneously with HARP phase, this strategy removes the requirement of a separate manual or automated segmentation step, as is often required in other tag tracking approaches. Also, unless the tags fade to zero, the normalized HARP magnitude continues to represent the location of the tissue region throughout the image sequence no matter where the tissue has moved. The incompressibility constraint is robust to tag-fading.

PVIRA is summarized in Algorithm 2. Novel steps comparing to iLogDemons are marked with asterisks.

III. Experiments and Results

A. Simulated Rotation

Since true motion of human data is difficult to find, simulation is important to evaluate PVIRA’s performance. We simulated a rotation similar to the rotation of the head in experiments designed to better understand brain deformation in mild rotation accelerations [5] and a deformation similar to what the tongue experiences in speech [3]. Note that these simulations aimed to produce variations in the amount of displacement, motion type, tag fading, and noise level. The modeling of more realistic subject-specific biomechanical motions requires more complex techniques and is not the focus of this current work.

For the rotation simulation, a $64 \times 64 \times 64$ volume was generated with 1.0 mm voxel resolution and 10.0 mm tag period. To represent the gelatin phantom used in [5], the tissue existed on a cylinder-shaped region with a circular cross-section in the x - y plane and was

isometric in the z direction. Synthetic displacement fields were generated by a finite element simulation (COMSOL v4.3, COMSOL Multiphysics, Burlington, MA) of a nearly-incompressible soft material (11.2 cm diameter, 18 cm long, Young's modulus $E = 5$ kPa, Poisson's ratio $\nu = 0.49$). The outer boundary of the cylinder was subjected to a half-sinusoidal angular acceleration pulse. Simulated displacements were x - y in-plane rotations around the center, as shown in Fig. 6(a). This rotation lasted for 18 time frames and yielded a 4.8 mm maximum displacement, satisfying the small motion condition. At every time frame, the motion field was used to deform horizontally and vertically tagged synthetic volumes. Fig. 6(d) shows an x - y cross section of the simulated tagged volumes before and after deformation at one time frame. These volumes were processed with PVIRA, yielding a motion estimate shown in Fig. 6(b) and its magnitude of error from the ground truth shown in Fig. 6(e). The errors of internal voxels are all less than 0.2 mm. For PVIRA, we chose the smoothing parameter in Step 7 as zero and that in Step 5 as $\sigma = 6$. This specific selection will be justified in a following experiment. Fig. 6(c) shows the simultaneously generated inverse field and Fig. 6(f) is the magnitude of error when the inverse field was compared with PVIRA's motion estimate as the two input time frames' order was reversed (testing inverse-consistency). Fig. 6(g) shows the Jacobian determinant of this cross section (Jacobian ≈ 1 indicates incompressibility). All the above figures are shown at time frame 10 (max displacement 2.8 mm). The estimation error from the ground truth of all 18 time frames are box-plotted in Fig. 6(h), in which center bars indicate the median with a 25 and 75 percentile box. All medians are less than 0.1 voxel. The outliers are errors at the boundary such as the red spots in Fig. 6(e).

Algorithm 2

Phase Vector Incompressible Registration Algorithm (PVIRA)

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1	* Interpolate tagged images using Eqn. (1) to get three sets of tagged volumes.
2	* Apply HARP filtering using Eqn. (2) on every volume to get HARP phase and HARP magnitude volumes.
3	Set the initial velocity estimate $\mathbf{v}(\mathbf{x})$ to zero.
4	* Compute the update velocity $\delta\mathbf{v}(\mathbf{x})$ using Eqn. (9). Difference and gradient computations must follow Eqns. (6) and (7).
5	Regularize $\delta\mathbf{v}(\mathbf{x})$ with a Gaussian kernel.
6	Compose $\mathbf{v}(\mathbf{x})$ with $\delta\mathbf{v}(\mathbf{x})$ using the BCH formula and set it to be the new $\mathbf{v}(\mathbf{x})$.
7	Regularize $\mathbf{v}(\mathbf{x})$ with a Gaussian kernel.
8	* Enforce incompressibility using Eqn. (11).
9	* Deform Φ_{ab} , Φ_{sb} and Φ_{ct} with $\exp(\mathbf{v}(\mathbf{x}))$ to compute a new Φ'_{at} , Φ'_{st} and Φ'_{ct} . Sub-voxel interpolation must follow Eqn. (10).
10	Go to Step 4. Repeat until convergence.
11	The motion estimate is $\psi(\mathbf{x}) = \exp(\mathbf{v}(\mathbf{x}))$ and the inverse motion estimate is $\psi^{-1}(\mathbf{x}) = \exp(-\mathbf{v}(\mathbf{x}))$.
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For comparison, 3D HARP, IDEA, and a direct iLogDemons intensity registration were also tested with the same simulation. 3D HARP required no parameter selection. For IDEA, since sparse dataset needed to be created first, we removed two slices out of each three slices from the generated dense volumes to simulate a sparse acquisition resembling our

experimental sparsity condition. For iLogDemons, we used the same smoothing parameters as PVIRA. All methods provided reasonable results visually similar to the ground truth. We computed the magnitude of error, composed inverse and forward motions to test inversion quality, tested inverse-consistency, and computed the Jacobian determinant of all four methods over all time frames. The resulting statistics are listed in Table I, including the average execution time for each time frame. The mean estimation error of IDEA was slightly higher than the other methods, but all were under 1/10 voxel. Note that for inverse motion, since PVIRA and iLogDemons automatically provided an inverse field, we used an extra step of a fixed point method [83] to numerically compute the inverse of 3D HARP and IDEA. This extra step was fast, taking just 0.6 s per frame on average. The inversion errors are around the same level (Table I), but PVIRA and iLogDemons showed slightly better inverse-consistency. Lastly, although only 3D HARP is not an incompressible method, its Jacobian determinant was also close to 1, because the simulated rotation field was essentially incompressible and 3D HARP provided a close estimation. But its local incompressibility fluctuated, causing a larger standard deviation. This simulation demonstrated that both PVIRA and iLogDemons contain all the properties of 3D HARP and IDEA while maintaining an accuracy close to both, and are much faster. All experiments were performed on an Intel Core i5 2.29GHz, 8 GB memory, and 64-bit Windows computer.

Since PVIRA and iLogDemons showed a similar performance in the previous experiment, where tag fading is not present, we modified the simulation to include tag fading as follows. Keeping the first time frame and the rotation rate the same, we linearly decreased the magnitude of the sinusoidal tag pattern from 1 at time frame 1 to 0 at time frame 17. Example tagged images at time frames 1 and 15 (with 88% tag fading) are shown in Fig. 7(a). The estimation results from PVIRA and iLogDemons were compared with the ground truth. Fig. 7(b) shows the boxplotted error magnitudes at all tag fading levels. It is observed that except for some outliers and the case where there are no visible tags (i.e., 100% tag fading), PVIRA yields the same error magnitude, regardless of the level of tag fading. On the other hand, iLogDemons shows an increasing level of motion estimation error with tag fading. The difference between these two approaches is expected, since the goal of iLogDemons is to match intensity, which is not a material property of the tissue since the tags are fading, while the goal of PVIRA is to match phase, which is a material property of the tissue. It is for this reason that matching phase in tagged MR applications is a better choice than matching intensities.

Next, we tested the effect of noise (without tag fading) on motion estimation by adding Gaussian noise to the rotation simulation images. We tested ten scenarios in which the noise variance was raised stepwise from 0.1 to 1.0 so that the signal-to-noise ratio (SNR) decreased from 20 to 0, as shown in Fig. 8(b). Examples of tagged images at SNR = 8 and at both the reference position and the maximum rotation of 2.8 mm are shown in Fig. 8(a). The estimated motion fields from three phase-based methods (PVIRA, 3D HARP, and IDEA) and with iLogDemons were compared with the ground truth. The magnitudes of error at all SNR levels are boxed-plotted in Fig. 8(b). It is observed that, except at the highest SNRs, PVIRA has the lowest levels of error, followed by iLogDemons, then 3D HARP, and finally IDEA. The fact that PVIRA and iLogDemons perform better than 3D HARP and IDEA is mostly likely due to their regularization. PVIRA may perform better than iLogDemons in

this simulation because the bandpass filters used to compute phase remove noise in spatial frequencies that are largely unimportant for motion estimation.

Next, we studied the parameters specifying the level of smoothness of PVIRA's regularization procedures. Steps 5 and 7 of Algorithm 2 are the two regularization steps in PVIRA; both are implemented using Gaussian smoothing. Here we kept the smoothing in Step 7 as zero and examined the effect of changing the Gaussian kernel variance in Step 5. We tested the ten SNR levels that were used above (i.e., ranging from 0 to 20) and with each SNR level, the Gaussian kernel variance was set to 0, 2, 4, 6, 8, 10, and 12 (i.e., from zero to strong regularization). PVIRA was applied to each case 20 times (with different random number generator seeds) and the average estimation error was computed and plotted in Fig. 9. It is observed that, for this motion, greater regularization improves the results when the SNR is small but over-smooths the results in high SNR scenarios. It is apparent from Fig. 9 that choosing σ in the range 6–8 yields errors that are relatively low in both low and high SNR regimes. In the experiments below we used $\sigma = 6$ in Step 5 of PVIRA. We used $\sigma = 0$ in Step 7 (i.e., no smoothing) of PVIRA since we empirically observed that use of either smoothing step produced very similar results. Equivalently, carrying out a similar optimization test experiment for the parameter in Step 7 is also feasible.

B. Simulated Tongue Motion

All rotation simulations focused on the estimation of x - y motion and were homogeneous in the z direction. To study a very different type of motion, we simulated tongue protrusion using a finite element simulator. The model geometry was derived from the ArtiSynth biomechanical modeling toolkit [84], [85] and the motion was computed using the FEBio software suite [86]. The motion was produced from simulated muscle activation using a forward finite element simulation and the result was interpolated onto a $60 \times 40 \times 50$ grid over ten time frames. Material coefficients were manually adjusted to generate displacements similar to the magnitude expected in a living subject and to enforce incompressibility. An example of one axial slice and one sagittal slice is shown in Fig. 10 with a 6.8 mm maximum displacement. As the tongue tip moved forward and downward in this simulation, the tongue experienced x and z motion to move forward and y motion to compress from the left and right.

We used 3D HARP, IDEA, iLogDemos, and PVIRA to compute the motion from simulated tag data and then computed their estimation error, inversion and consistency error, and Jacobian determinant. Fig. 10(c) shows the true motion and results from the three phase-based methods. Proper estimates were made within the body of the tongue, but 3D HARP and IDEA suffered from stronger boundary effects. In Fig. 10(b), these three methods show strong boundary effects, and IDEA also shows more planar artifacts inside the tongue body because of its vector-spline interpolation process, which is based on 2D motion estimation.

Table II shows performance statistics from all four methods over all time frames. The extra fixed point step for 3D HARP and IDEA took 0.8 s per frame on average and was included in these results. It is observed that PVIRA is more accurate on average and has lower variance than the other two phase-based methods. IDEA is less accurate due to the artifacts from sparse data. PVIRA also shows better inverse consistency and faster speed.

Additionally, IDEA and PVIRA are both more incompressible than 3D HARP. Since this simulation had neither noise nor tag fading, intensity iLogDemons demonstrated a similar level of accuracy compared to that of PVIRA.

C. Estimation of Brain Motion in Mild Accelerations

To characterize brain biomechanics in vivo during an angular acceleration, a controlled mild rotation was generated in each of the three healthy volunteers. Each subject, lying supine in a Siemens 3.0T mMR Biograph scanner (Siemens, Munich, Germany), was constrained with a head rotation device that accelerated the head towards the left shoulder [5]. In repeated motions, tagged images were acquired with a SPAMM pulse sequence producing sparse parallel slices covering the brain region and spanning across 12 time frames (resolution: 1.5 mm in-plane and 8.00 mm through-plane). On axial slices, horizontal and vertical tags were used to capture left–right motion and anterior–posterior motion. Then the remaining superior–inferior motion was captured with horizontal tags on sagittal slices (see Fig. 11(g)). Considering the existence of noise and tag fading in real data, we only applied the phase-based methods of 3D HARP, IDEA, and PVIRA to estimate 3D motion at every time frame. Two examples of a subject’s motion estimate at time frame 3 (strongest left rotation) and time frame 7 (strongest right rotation) are shown in Figs. 11(a) to 11(f). Visually, the three estimates are similar.

We computed several statistics to compare these results quantitatively. For example, we computed the Jacobian determinant of each result to check incompressibility (see Fig. 11(i) for example). Since 3D HARP with phase tracking is closer to the actual HARP measurements except at the boundaries, when the true motion is unknown, to compare the performance between the two incompressible methods (PVIRA and IDEA), we used 3D HARP as a reference and computed the magnitudes of the differences between the two methods and 3D HARP (see Fig. 11(h) for example). We plotted the normalized histogram of the two differences in Fig. 11(j). From this plot we see that PVIRA had more voxels with a smaller difference and also a smaller mean difference than that of IDEA. This characteristic was true for all 33 volumes of the three human subjects and, by student t-test with $p < 0.05$, PVIRA was significantly closer to 3D HARP than IDEA. The mean difference, Jacobian determinant, and average computing time for all 33 volumes are shown in Table III.

D. Estimation of Tongue Motion in Speech

To capture the tongue’s deformation in speech, a controlled speech task was performed by two healthy subjects. In a Siemens 3.0T mMR Biograph scanner under a CSPAMM pulse sequence, the subjects repeatedly spoke a designed utterance “a souk” following a rhythm, in which forward motion occurred at time frames leading to /s/ and upward motion occurred at time frames leading to /k/. The entire motion cycle occurred within one second and 26 time frames were captured as tagged slices covering the tongue region [87]. The data resolution was 1.88 mm in-plane and 6.00 mm through-plane. On sagittal slices, horizontal and vertical tags were used to capture superior–inferior motion and anterior–posterior motion. Then the remaining left–right motion was captured with vertical tags on axial slices (see Fig. 12(g)).

We used 3D HARP, IDEA, and PVIRA to estimate the motion at every time frame for the two subjects. Excluding time frame 1, a total of 50 volumes were evaluated. Two examples of a subject's motion estimate at time frame 8 (strongest forward motion) and time frame 18 (strongest upward motion) are shown in Figs. 12(a)–12(f). It is observed that the boundary effects that degrade 3D HARP estimates are even stronger than those in the brain. We computed the magnitude of the motion difference between 3D HARP and the other two methods (see Fig. 12(h) for example) and plotted their histograms in Fig. 12(j). It is observed that the PVIRA result is also closer to 3D HARP than IDEA on average. Examining the data, we found that this was true for all 50 volumes from the two subjects and that PVIRA was statistically closer to 3D HARP than IDEA (student t-test, $p < 0.05$). The mean difference, Jacobian determinant, and average computing time for 50 volumes are shown in Table IV.

E. Cardiac Data Tracking Validation

Finally, we applied 3D HARP, IDEA, iLogDemons, and PVIRA to tagged MR sequences of 15 volunteers from an open cardiac dataset described in [74] in order to evaluate their relative performances in myocardial tissue tracking. In these datasets, 12 landmarks within the myocardium were manually tracked independently by two observers, and their positions throughout the image sequences were taken equivalently from the two sets as ground truth, yielding 24 reference point locations over time. The motion fields estimated from the tagged MR images were then used to track the landmarks from their given positions in the first image throughout the entire sequence and their tracked positions were compared to the ground truth. Fig. 13 shows boxplots of the landmark tracking errors for all volunteers, all time frames, and all landmarks. IDEA has the largest error while iLogDemons has similar performance to 3D HARP. Both the mean and median error of PVIRA are lower than the other methods and PVIRA has significantly lower error than that of iLogDemons (student t-test, $p < 0.05$). In [74], four institutions (MEVIS, IUCL, UPF, and INRIA) analyzed the same volunteer datasets using their own tracking methods, and the reported median values of tracking accuracies were MEVIS = 1.33 mm, IUCL = 1.52 mm, UPF = 1.09 mm, and INRIA = 1.32 mm. PVIRA, with a 1.27 mm median value, showed a higher accuracy than IUCL, a lower accuracy than UPF, and a similar level of accuracy as MEVIS and INRIA. The proposed method in [66] also used the same dataset for accuracy test and reported a lower median value than MEVIS. However, since the method's exact median value was not reported, its comparison with PVIRA is unknown.

IV. Discussion

We presented a new method, PVIRA, and compared it to 3D HARP, IDEA, and iLogDemons. There are several key differences between these methods that provide insights into their relative performances. First, and most strikingly, IDEA, which is based on vector spline interpolation, takes a very long time to compute—about three hours per subject, while the other three approaches take only about 5 minutes per subject. Second, IDEA requires a segmentation of the target anatomy, while the other three methods operate on the whole volume (or on a volume of interest if desired). A third key difference is that 3D HARP, iLogDemons, and PVIRA all use interpolated 3D volumes as a starting point for 3D tracking

while IDEA computes 2D tracks in the acquired images and then interpolates these into a dense 3D grid. Fourth, 3D HARP, IDEA, and PVIRA are all based on HARP phase while iLogDemons uses the tagged image intensities. Fifth, 3D HARP has no regularization and IDEA has minimal regularization while both iLogDemons and PVIRA are more generously regularized to produce smooth motions. Finally, both iLogDemons and PVIRA automatically compute the inverse motion while both 3D HARP and IDEA must carry out another step to do this, which adds both time and potential for error to their generation of the inverse motion.

Without noise or tag fading, we found that all four methods yielded very similar estimation errors, inversion errors, inverse consistency errors, and Jacobian determinants. Since tags always fade and there is always noise, we also tested these algorithms in more realistic scenarios. When there is tag fading, the phase-based methods are clearly better, a fact that is not surprising since phase remains a material property even when there is tag fading. Regularization helps in the presence of noise, which is why both iLogDemons and PVIRA fare better to noise than 3D HARP and IDEA. PVIRA is yet a little better than iLogDemons in the presence of noise, which we hypothesize is due to the action of the bandpass filter in HARP, which also acts as a noise suppressor. In fact, PVIRA results on real data were also visually smoother (see Figs. 11(a)–(f) and 12(a)–(f)). Even though IDEA uses regularization (due to its use of smoothing splines [31]), planar-shaped artifacts are apparent in the IDEA results (see Figs. 11(h) and 12(h)) which undoubtedly occur because IDEA interpolates 2D motion between image planes.

Since it is based on iLogDemons, PVIRA carries out the same steps as in iLogDemons, but it must also compute HARP phase and carry out subsequent phase computation steps involving local phase unwrapping. Therefore, PVIRA takes longer than iLogDemons, somewhere between 5–12% longer according to Tables I and II. But the benefit of PVIRA's robustness to tag fading is well worth the extra computation time. In real tag data from our brain and speech experiments, we measured tag fading to be around 90% in one second of acquisitions. From Fig. 7, this level of tag fading can yield a mean error of around 2.5 voxels, while PVIRA stays relatively unaffected at a less than 0.5 voxel error on average. Also, in real cases, since the tagged images we acquired typically have high SNR (greater than 20), from Fig. 8 we can see that both PVIRA and iLogDemons are not greatly affected by noise. Therefore, considering computation time, tag fading, and noise, PVIRA is the best choice.

There are several aspects that are not fully explored in the present paper. First, we note that all results in this paper were computed between tagged images acquired at the time of tag application and tagged images acquired at a later time. This condition is actually required for IDEA (since having “flat tags” at the first time frame is required), but not for the other three methods—i.e., 3D HARP, iLogDemons, and PVIRA can compute motion between any two time frames. This flexibility is desirable for many applications including the computation of so-called “running displacements” between consecutive time frames in the image sequence. Second, we note that IDEA also requires a segmentation of the object of interest, a feature that is not required by PVIRA, 3D HARP, or iLogDemons. Since this segmentation is required by IDEA and therefore also available, we also used it to speed up computations on

all our testing and to improve visualizations of the results. Such use may account for boundary effects that are visible in some of our results and a full exploration of PVIRA without an available segmentation should be carried out. Third, we note that there are several parameters that were not fully explored. While we did consider one smoothing parameter in PVIRA, we did not explore the other one or the two together. Finally, we did not explore the impact of coarser or finer 3D tag interpolation grids. The use of a coarser grid, in particular, would invariably decrease computation time, but the impact of this choice on accuracy is unknown.

V. Conclusion

We proposed a novel phase-based method called PVIRA to compute three-dimensional motion from tagged images. A new velocity update specifically designed to interpolate phase volumes was used, yielding an estimate that is dense, diffeomorphic, incompressible, and inverse-consistent. Compared with competing methods, PVIRA demonstrated comparable or better accuracy, showed strong robustness against noise and tag fading, and is computationally fast. PVIRA addresses the phase tracking problem in the context of incompressible image registration, which has not been well-explored in majority of previous works.

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References

1. Ibrahim EH. Myocardial tagging by cardiovascular magnetic resonance: evolution of techniques—pulse sequences, analysis algorithms, and applications. *J Cardiovasc Magn Reson*. 2011; 13:36. [PubMed: 21798021]
2. Kolipaka A, Chatzimavroudis GP, White RD, Lieber ML, Setser RM. Relationship between the extent of non-viable myocardium and regional left ventricular function in chronic ischemic heart disease. *Journal of Cardiovascular Magnetic Resonance*. 2005; 7(3):573–579. [PubMed: 15959970]
3. Parthasarathy V, Prince JL, Stone M, Murano E, NessAiver M. Measuring tongue motion from tagged Cine-MR using harmonic phase (HARP) processing. *J Acoustic Society of America*. 2007; 121(1):491–504.
4. Sabet AA, Christoforou E, Zatlin B, Genin GM, Bayly PV. Deformation of the human brain induced by mild angular head acceleration. *J Biomech*. 2008; 41(2):307–315. [PubMed: 17961577]
5. Knutsen AK, Magrath E, McEntee JE, Xing F, Prince JL, Bayly PV, Butman JA, Pham DL. Improved measurement of brain deformation during mild head acceleration using a novel tagged MRI sequence. *Journal of Biomechanics*. 2014; 47(14):3475–3481. [PubMed: 25287113]
6. Zerhouni EA, Parish DM, Rogers WJ, Yang A, Shapiro EP. Human heart: tagging with MR imaging—a method for noninvasive assessment of myocardial motion. *Radiology*. 1988; 169(1):59–63. [PubMed: 3420283]
7. Axel L, Dougherty L. MR imaging of motion with spatial modulation of magnetization. *Radiology*. 1989; 171(3):841–845. [PubMed: 2717762]
8. Guttman MA, Prince JL, McVeigh ER. Tag and contour detection in tagged MR images of the left ventricle. *Medical Imaging, IEEE Transactions on*. 1994; 13(1):74–88.
9. Guttman MA, Zerhouni E, McVeigh ER, et al. Analysis of cardiac function from MR images. *Computer Graphics and Applications, IEEE*. 1997; 17(1):30–38.

10. Young A, Kraitchman DL, Dougherty L, Axel L, et al. Tracking and finite element analysis of stripe deformation in magnetic resonance tagging. *Medical Imaging, IEEE Transactions on*. 1995; 14(3):413–421.
11. Amini A, Chen Y, Curwen RW, Mani V, Sun J, et al. Coupled B-snake grids and constrained thin-plate splines for analysis of 2-D tissue deformations from tagged MRI. *Medical Imaging, IEEE Transactions on*. 1998; 17(3):344–356.
12. Kerwin WS, Prince JL. Cardiac material markers from tagged MR images. *Medical Image Analysis*. 1998; 2(4):339–353. [PubMed: 10072201]
13. Osman NF, Kerwin WS, McVeigh ER, Prince JL. Cardiac motion tracking using CINE harmonic phase (HARP) magnetic resonance imaging. *Magnetic Resonance Medicine*. 1999; 42:1048–1060.
14. Osman NF, McVeigh ER, Prince JL. Imaging heart motion using harmonic phase MRI. *Medical Imaging, IEEE Transactions on*. 2000; 19(3):186–202.
15. Osman NF, Prince JL. Visualizing myocardial function using HARP MRI. *Physics in medicine and biology*. 2000; 45(6):1665. [PubMed: 10870717]
16. Chen T, Wang X, Chung S, Metaxas D, Axel L. Automated 3D motion tracking using gabor filter bank, robust point matching, and deformable models. *Medical Imaging, IEEE Transactions on*. 2010; 29(1):1–11.
17. Ryf S, Spiegel MA, Gerber M, Boesiger P. Myocardial tagging with 3D-CSPAMM. *J Magnetic Resonance Imaging*. 2002; 16:320–325.
18. Reese TG, Feinberg DA, Dou J, Wedeen VJ. Phase contrast MRI of myocardial 3D strain by encoding contiguous slices in a single shot. *Magnetic resonance in medicine*. 2002; 47(4):665–676. [PubMed: 11948727]
19. Abd-Elmoniem KZ, Osman NF, Prince JL, Stuber M. Three-dimensional magnetic resonance myocardial motion tracking from a single image plane. *Magnetic Resonance in Medicine*. 2007; 58(1):92–102. [PubMed: 17659617]
20. Spottiswoode BS, Zhong X, Lorenz CH, Mayosi BM, Meintjes EM, Epstein FH. 3D myocardial tissue tracking with slice followed cine DENSE MRI. *Journal of Magnetic Resonance Imaging*. 2008; 27(5):1019–1027. [PubMed: 18425823]
21. Yin F, Chan C, Judd RM. Compressibility of perfused passive myocardium. *American Journal of Physiology-Heart and Circulatory Physiology*. 1996; 271(5):H1864–H1870.
22. Rodriguez I, Ennis DB, Wen H. Noninvasive measurement of myocardial tissue volume change during systolic contraction and diastolic relaxation in the canine left ventricle. *Magnetic resonance in medicine*. 2006; 55(3):484–490. [PubMed: 16408273]
23. Gilbert RJ, Napadow VJ, Gaige TA, Wedeen VJ. Anatomical basis of lingual hydrostatic deformation. *Journal of Experimental Biology*. 2007; 210(23):4069–4082. [PubMed: 18025008]
24. Kier WM, Smith KK. Tongues, tentacles and trunks: the biomechanics of movement in muscular-hydrostats. *Zoological Journal of the Linnean Society*. 1985; 83(4):307–324.
25. O'Dell WG, Moore CC, Hunter WC, Zerhouni EA, McVeigh ER. Three-dimensional myocardial deformations: calculation with displacement field fitting to tagged MR images. *Radiology*. Jun; 1995 195(3):829–835. [PubMed: 7754016]
26. Li M, Gupta H, Lloyd SG, DellItalia LJ, Denney TS Jr. A graph theoretic approach for computing 3D+ time biventricular cardiac strain from tagged MRI data. *Medical image analysis*. 2017; 35:46–57. [PubMed: 27318591]
27. Denney TS, Prince JL. Reconstruction of 3-D left ventricular motion from planar tagged cardiac MR images: an estimation theoretic approach. *Medical Imaging, IEEE Transactions on*. 1995; 14(4):625–635.
28. Haber I, Metaxas DN, Axel L. Three-dimensional motion reconstruction and analysis of the right ventricle using tagged MRI. *Medical Image Analysis*. 2000; 4(4):335–355. [PubMed: 11154021]
29. Huang J, Abendschein D, Davila-Roman VG, Amini A. Spatio-temporal tracking of myocardial deformations with a 4-D B-spline model from tagged MRI. *Medical Imaging, IEEE Transactions on*. 1999; 18(10):957–972.
30. Ozturk C, McVeigh ER. Four-dimensional B-spline based motion analysis of tagged MR images: introduction and in vivo validation. *Physics in medicine and biology*. 2000; 45(6):1683. [PubMed: 10870718]

31. Liu X, Abd-Elmoniem KZ, Stone M, Murano EZ, Zhuo J, Gullapalli RP, Prince JL. Incompressible deformation estimation algorithm (IDEA) from tagged MR images. *Medical Imaging, IEEE Transactions on*. 2012; 31(2):326–340.
32. Liu H, Yan M, Song E, Wang J, Wang Q, Jin R, Jin L, Hung C. Myocardial motion estimation of tagged cardiac magnetic resonance images using tag motion constraints and multi-level b-splines interpolation. *Magnetic resonance imaging*. 2016; 34(4):579–595. [PubMed: 26712656]
33. Shi P, Sinusas AJ, Constable RT, Duncan JS. Volumetric deformation analysis using mechanics-based data fusion: Applications in cardiac motion recovery. *International Journal of Computer Vision*. 1999; 35(1):87–107.
34. Papademetris X, Sinusas AJ, Dione DP, Constable RT, Duncan JS. Estimation of 3-D left ventricular deformation from medical images using biomechanical models. *Medical Imaging, IEEE Transactions on*. 2002; 21(7):786–800.
35. Zhou Y, Bernard O, Saloux E, Manrique A, Allain P, Makram-Ebeid S, De Craene M. 3D harmonic phase tracking with anatomical regularization. *Medical Image Analysis*. 2015; 26(1):70–81. [PubMed: 26363844]
36. Amini, AA., Prince, JL. Measurement of cardiac deformations from MRI: Physical and mathematical models. Vol. 23. Springer Science & Business Media; 2013.
37. Lee J, Woo J, Xing F, Murano EZ, Stone M, Prince JL. Semi-automatic segmentation for 3D motion analysis of the tongue with dynamic MRI. *Computerized Medical Imaging and Graphics*. 2014; 38(8):714–724. [PubMed: 25155697]
38. Pham DL, Xu C, Prince JL. Current methods in medical image segmentation 1. *Annual review of biomedical engineering*. 2000; 2(1):315–337.
39. Bistoquet A, Oshinski J, Skrinjar O. Left ventricular deformation recovery from cine MRI using an incompressible model. *Medical Imaging, IEEE Transactions on*. 2007; 26(9):1136–1153.
40. Bistoquet A, Oshinski J, Skrinjar O. Myocardial deformation recovery from cine MRI using a nearly incompressible biventricular model. *Medical image analysis*. 2008; 12(1):69–85. [PubMed: 18234539]
41. Xing, F., Woo, J., Murano, EZ., Lee, J., Stone, M., Prince, JL. Medical Image Computing and Computer-Assisted Intervention–MICCAI 2013. Springer; 2013. 3D tongue motion from tagged and cine MR images; p. 41–48.
42. Petitjean, C., Rougon, N., Prêteux, F., Cluzel, P., Grenier, P. Measuring myocardial deformations in tagged MR image sequences using informational non-rigid registration. *International Workshop on Functional Imaging and Modeling of the Heart*; Springer; 2003. p. 162–172.
43. Perperidis D, Mohiaddin RH, Rueckert D. Spatio-temporal free-form registration of cardiac MR image sequences. *Medical image analysis*. 2005; 9(5):441–456. [PubMed: 16029955]
44. Ledesma-Carbayo, MJ., Bajo, A., Santa Marta, C., Perez-David, E., Garcia-Fernandez, MA., Desco, M., Santos, A. Computers in Cardiology, 2006. IEEE; 2006. Fully automatic cardiac motion estimation from tagged MRI using non-rigid registration techniques; p. 305–308.
45. Tustison NJ, Amini AA. Biventricular myocardial strains via nonrigid registration of AnFigtomical NURBS models. *IEEE Transactions on Medical Imaging*. 2006; 25(1):94–112. [PubMed: 16398418]
46. Ledesma-Carbayo MJ, Derbyshire JA, Sampath S, Santos A, Desco M, McVeigh ER. Unsupervised estimation of myocardial displacement from tagged MR sequences using nonrigid registration. *Magnetic Resonance in Medicine*. 2008; 59(1):181–189. [PubMed: 18058938]
47. Oubel E, De Craene M, Hero AO, Pourmorteza A, Huguet M, Avegliano G, Bijmens BH, Frangi AF. Cardiac motion estimation by joint alignment of tagged MRI sequences. *Medical image analysis*. 2012; 16(1):339–350. [PubMed: 22000567]
48. Rougon, NF., Petitjean, C., Preteux, FJ. Medical Imaging 2004. International Society for Optics and Photonics; 2004. Building and using a statistical 3D motion atlas for analyzing myocardial contraction in MRI; p. 253–264.
49. Chandrashekhara R, Mohiaddin RH, Rueckert D. Analysis of 3-D myocardial motion in tagged MR images using nonrigid image registration. *IEEE Transactions on Medical Imaging*. 2004; 23(10):1245–1250. [PubMed: 15493692]

50. Chandrashekar, R., Mohiaddin, R., Razavi, RS., Rueckert, D. Nonrigid image registration with subdivision lattices: Application to cardiac MR image analysis. *International Conference on Medical Image Computing and Computer-Assisted Intervention*; Springer; 2007. p. 335-342.
51. De Craene, M., Tobon-Gomez, C., Butakoff, C., Duchateau, N., Piella, G., Rhode, KS., Frangi, AF. Temporal diffeomorphic free form deformation (TDFFD) applied to motion and deformation quantification of tagged MRI sequences. *International Workshop on Statistical Atlases and Computational Models of the Heart*; Springer; 2011. p. 68-77.
52. De Craene M, Piella G, Camara O, Duchateau N, Silva E, Doltra A, Dhooge J, Brugada J, Sitges M, Frangi AF. Temporal diffeomorphic free-form deformation: Application to motion and strain estimation from 3D echocardiography. *Medical Image Analysis*. 2012; 16(2):427–450. [PubMed: 22137545]
53. Shi W, Zhuang X, Wang H, Duckett S, Luong DVN, Tobon-Gomez C, Tung K, Edwards PJ, Rhode KS, Razavi RS, et al. A comprehensive cardiac motion estimation framework using both untagged and 3-D tagged MR images based on nonrigid registration. *IEEE transactions on medical imaging*. 2012; 31(6):1263–1275. [PubMed: 22345530]
54. Shi, W., Zhuang, X., Pizarro, L., Bai, W., Wang, H., Tung, KP., Edwards, P., Rueckert, D. Registration using sparse free-form deformations,” in. *International Conference on Medical Image Computing and Computer-Assisted Intervention*; Springer; 2012. p. 659-666.
55. Shi W, Jantsch M, Aljabar P, Pizarro L, Bai W, Wang H, ORegan D, Zhuang X, Rueckert D. Temporal sparse free-form deformations. *Medical image analysis*. 2013; 17(7):779–789. [PubMed: 23743085]
56. Yu Y, Zhang S, Li K, Metaxas D, Axel L. Deformable models with sparsity constraints for cardiac motion analysis. *Medical image analysis*. 2014; 18(6):927–937. [PubMed: 24721617]
57. McLeod, K., Prakosa, A., Mansi, T., Sermesant, M., Pennec, X. An incompressible log-domain demons algorithm for tracking heart tissue. *International Workshop on Statistical Atlases and Computational Models of the Heart*; Springer; 2011. p. 55-67.
58. Gomez, AD., Xing, F., Chan, D., Pham, DL., Bayly, P., Prince, JL. *Computational Biomechanics for Medicine*. Springer; 2017. Motion estimation with finite-element biomechanical models and tracking constraints from tagged MRI; p. 81-90.
59. Vercauteren T, Pennec X, Perchant A, Ayache N. Diffeomorphic demons: efficient non-parametric image registration. *NeuroImage*. 2009; 45(1):S61–S72. [PubMed: 19041946]
60. Mansi, T., Peyrat, JM., Sermesant, M., Delingette, H., Blanc, J., Boudjemline, Y., Ayache, N. *Functional Imaging and Modeling of the Heart*. Springer; 2009. Physically-constrained diffeomorphic demons for the estimation of 3D myocardium strain from cine-MRI; p. 201-210.
61. Mansi T, Pennec X, Sermesant M, Delingette H, Ayache N. ilogdemons: A demons-based registration algorithm for tracking incompressible elastic biological tissues. *International journal of computer vision*. 2011; 92(1):92–111.
62. Gautama T, Van Hulle MA. A phase-based approach to the estimation of the optical flow field using spatial filtering. *IEEE Transactions on Neural Networks*. 2002; 13(5):1127–1136. [PubMed: 18244509]
63. Prince JL, McVeigh ER. Motion estimation from tagged MR image sequences. *Medical Imaging, IEEE Transactions on*. 1992; 11(2):238–249.
64. Fleet DJ, Jepson AD. Stability of phase information. *IEEE Transactions on Pattern Analysis and Machine Intelligence*. 1993; 15(12):1253–1268.
65. Hemmendorff M, Andersson MT, Kronander T, Knutsson H. Phase-based multidimensional volume registration. *IEEE Transactions on Medical Imaging*. 2002; 21(12):1536–1543. [PubMed: 12588037]
66. Zhou, Y., De Craene, M., Bernard, O. Phase-based registration of cardiac tagged MR images using anatomical deformation model. *Biomedical Imaging (ISBI), 2016 IEEE 13th International Symposium on*; IEEE; 2016. p. 617-620.
67. Rohde, GK., Pajevic, S., Pierpaoli, C., Basser, PJ. A comprehensive approach for multi-channel image registration. *International Workshop on Biomedical Image Registration*; Springer; 2003. p. 214-223.

68. Rohde, GK., Pajevic, S., Pierpaoli, C. Multi-channel registration of diffusion tensor images using directional information. Biomedical Imaging: Nano to Macro, 2004. IEEE International Symposium on; IEEE; 2004. p. 712-715.
69. Geng, X., Styner, M., Gupta, A., Shen, D., Gilmore, JH. Multi-contrast diffusion tensor image registration with structural MRI. Biomedical Imaging (ISBI), 2012 9th IEEE International Symposium on; IEEE; 2012. p. 684-687.
70. Li Y, Verma R. Multichannel image registration by feature-based information fusion. IEEE Transactions on Medical Imaging. 2011; 30(3):707–720. [PubMed: 21097379]
71. Park HJ, Kubicki M, Shenton ME, Guimond A, McCarley RW, Maier SE, Kikinis R, Jolesz FA, Westin CF. Spatial normalization of diffusion tensor MRI using multiple channels. Neuroimage. 2003; 20(4):1995–2009. [PubMed: 14683705]
72. Peyrat, JM., Delingette, H., Sermesant, M., Pennec, X., Xu, C., Ayache, N. Registration of 4D time-series of cardiac images with multichannel diffeomorphic demons. Medical Image Computing and Computer-Assisted Intervention–MICCAI; 2008; 2008. p. 972-979.
73. Peyrat JM, Delingette H, Sermesant M, Xu C, Ayache N. Registration of 4D cardiac CT sequences under trajectory constraints with multichannel diffeomorphic demons. Medical Imaging, IEEE Transactions on. 2010; 29(7):1351–1368.
74. Tobon-Gomez C, De Craene M, Mcleod K, Tautz L, Shi W, Hennemuth A, Prakosa A, Wang Hi, Carr-White G, Kapetanakis S, et al. Benchmarking framework for myocardial tracking and deformation algorithms: An open access database. Medical image analysis. 2013; 17(6):632–648. [PubMed: 23708255]
75. Lehmann TM, Gönner C, Spitzer K. Survey: Interpolation methods in medical image processing. Medical Imaging, IEEE Transactions on. 1999; 18(11):1049–1075.
76. Unser M, Aldroubi A, Eden M. B-spline signal processing. I. Theory. Signal Processing, IEEE Transactions on. 1993; 41(2):821–833.
77. Ryf S, Tsao J, Schwitter J, Stuessi A, Boesiger P. Peak-combination HARP: A method to correct for phase errors in HARP. Journal of Magnetic Resonance Imaging. 2004; 20(5):874–880. [PubMed: 15503322]
78. Nithiananthan S, Brock KK, Daly MJ, Chan H, Irish JC, Siewerdsen JH. Demons deformable registration for CBCT-guided procedures in the head and neck: convergence and accuracy. Medical Physics. 2009; 36(10):4755–4764. [PubMed: 19928106]
79. Takajo H, Takahashi T. Least-squares phase estimation from the phase difference. JOSA A. 1988; 5(3):416–425.
80. Ghiglia DC, Romero LA. Direct phase estimation from phase differences using fast elliptic partial differential equation solvers. Optics letters. 1989; 14(20):1107–1109. [PubMed: 19753070]
81. Ghiglia, DC., Pritt, MD. Two-dimensional phase unwrapping: theory, algorithms, and software. Vol. 4. Wiley; New York: 1998.
82. Jenkinson M. Fast, automated, N-dimensional phase-unwrapping algorithm. Magnetic resonance in medicine. 2003; 49(1):193–197. [PubMed: 12509838]
83. Chen M, Lu W, Chen Q, Ruchala KJ, Olivera GH. A simple fixed-point approach to invert a deformation field. Medical physics. 2007; 35(1):81–88.
84. Lloyd, JE., Stavness, I., Fels, S. Soft tissue biomechanical modeling for computer assisted surgery. Springer; 2012. ArtiSynth: a fast interactive biomechanical modeling toolkit combining multibody and finite element simulation; p. 355-394.
85. Fujita S, Dang J, Suzuki N, Honda K. A computational tongue model and its clinical application. Oral Science International. 2007; 4(2):97–109.
86. Maas SA, Ellis BJ, Ateshian GA, Weiss JA. FEBio: finite elements for biomechanics. Journal of biomechanical engineering. 2012; 134(1):011005. [PubMed: 22482660]
87. Xing F, Woo J, Lee J, Murano EZ, Stone M, Prince JL. Analysis of 3D tongue motion from tagged and cine MR images. Journal of Speech, Language, and Hearing Research. 2016; 59:468–479.

Fig. 1.

Illustration of the acquisition locations of tagged MR image slices for 3D motion. A: anterior. P: posterior. L: left. R: right. S: superior. I: inferior.

Fig. 2. Flow chart of the proposed method PVIRA. Asterisks indicate steps involving special harmonic phase and magnitude operations.

Fig. 3.

Demonstration of interpolation of tagged slices on tagged images of the tongue. (a) Spatial locations of acquired samples (blue) and interpolated samples (red). (b) A tagged sagittal tongue slice from acquisition. (c) Four interpolated sagittal tongue slices with horizontal tags.

Fig. 4. HARP processing of a tagged image. (a) A tagged slice. (b) Harmonic peaks in the Fourier domain. (c) Harmonic magnitude slice. (d) Harmonic phase slice.

Fig. 5.
Linear interpolation of wrapped phase values.

Fig. 6. Test of PVIRA on simulated rotations. (a) Simulated ground truth at time frame 10 (max displacement 2.8 mm). (b) Estimated motion. (c) Estimated inverse motion. (d) Simulated tags. (e) Magnitude of estimation error. (f) Inverse-consistency error. (g) Jacobian determinant of motion estimate. (h) Estimation error of all time frames. Center bar = median.

Fig. 7.
Comparison of PVIRA and iLogDemons. (a) Stationary tagged image and faded tags at 88%. (b) Box-plotted error magnitude under different tag fading levels. Center bar = median. Circle = mean.

Fig. 8. Rotation simulation in the presence of noise. (a) Tagged images with noise (SNR = 8 with 2.8 mm max displacement). (b) Box-plotted error magnitude under different noise levels. Center bar = median. Circle = mean.

Fig. 9. PVIRA estimation error with different regularization and noise levels. σ is the standard deviation of the regularizing Gaussian kernel.

Fig. 10.

Test of PVIRA on simulated tongue protrusion. (a) Tagged slices with three tag directions (max displacement 6.8 mm). (b) Estimation error of three phase-based methods. (c) Simulated motion and estimated motion from three phase-based methods.

Fig. 11.

Brain mild acceleration motion estimation. (a)–(c) Time frame for max counter-clockwise rotation. (d)–(f) Time frame for max clockwise rotation. (g) Tagged axial and sagittal slices. (h) Estimation difference from 3D HARP. Colorbar ranges from 0 to 0.5 as in the previous figures. (i) Jacobian determinants. (j) Histogram of difference from 3D HARP using IDEA and PVIRA. Note: *cones* are used to visualize motion fields where cone length indicates magnitude and cone color follows conventional diffusion imaging scheme (red = left–right, green = anterior–posterior, blue = superior–inferior).

Fig. 12.

Tongue motion estimation in speech. (a)–(c) Time frame for max forward motion. (d)–(f) Time frame for max upward motion. (g) Tagged axial and sagittal slices. (h) Estimation difference from 3D HARP. Colorbar ranges from 0 to 0.5 as in the previous figures. (i) Histogram of magnitude of motion difference between 3D HARP and IDEA and PVIRA.

Fig. 13.

Magnitude of tracking errors of 12 myocardial points identified in 15 of the volunteers' datasets from [74] using 3D HARP, IDEA, iLogDemos, and PVIRA with respect to two sets of reference manual trackings. Center bar = median. Circle = mean.

TABLE I

Rotation Simulation Test Result (Errors are in voxels, time/frame is in seconds, and Jacobian is unitless.)

	3D HARP	IDEA	iLogDemos	PVIRA
Estimation Err	0.06 ± 0.06	0.08 ± 0.07	0.07 ± 0.07	0.07 ± 0.06
Inversion Err	0.11 ± 0.13	0.12 ± 0.13	0.13 ± 0.14	0.13 ± 0.14
Inv-consist Err	0.12 ± 0.09	0.15 ± 0.13	0.10 ± 0.05	0.10 ± 0.05
Jacobian	0.98 ± 0.14	1.00 ± 0.05	1.00 ± 0.03	1.01 ± 0.03
Time/frame	144	527	79	89

TABLE II

Tongue Protrusion Simulation Test Result (Errors are in voxels and time per frame is in seconds.)

	3D HARP	IDEA	Intensity	PVIRA
Estimation Err	0.19 ± 0.81	0.21 ± 0.69	0.12 ± 0.20	0.13 ± 0.17
Inversion Err	0.15 ± 0.26	0.14 ± 0.23	0.12 ± 0.10	0.12 ± 0.12
Inv-consist Err	0.15 ± 0.17	0.18 ± 0.20	0.10 ± 0.04	0.09 ± 0.03
Jacobian	1.05 ± 0.55	1.00 ± 0.11	1.00 ± 0.05	1.00 ± 0.07
Time/frm	112	627	102	107

TABLE III

Brain Acceleration Motion Estimation Results

	3D HARP	IDEA	PVIRA
Mag Difference (mm)	0	0.84 ± 1.80	0.62 ± 1.24
Jacobian Determinant	1.11 ± 0.82	1.01 ± 0.27	1.01 ± 0.26
Runtime per Frame (min)	4.9	141.6	4.7

TABLE IV

Tongue Motion Estimation Results

	3D HARP	IDEA	PVIRA
Mag Difference (mm)	0	1.63 ± 1.70	0.97 ± 1.48
Jacobian Determinant	1.21 ± 1.83	1.00 ± 0.37	1.00 ± 0.21
Runtime per Frame (min)	0.3	9.1	0.3