Abstract

Cine displacement encoding with stimulated echoes (cine DENSE) is an MRI technique that encodes displacement over a time series into the phase of complex MRI images. Phase aliasing is unavoidable and this phase needs to be unwrapped to determine the displacement fields. Phase unwrapping is complicated by image noise, phase shear and the fact that only a few pixels span the myocardial walls. This work investigates the effectiveness of a 3D cost function based region merging method for unwrapping cine DENSE images. The new technique is shown to provide comparable accuracy to an existing technique.

1 Introduction

Cardiovascular disease is the leading cause of death in many developed countries. The ability to quantify the motion of the heart muscle, or myocardium, is valuable for understanding both normal and diseased cardiac kinematics [1].

Magnetic resonance imaging (MRI) is a powerful tool for imaging the heart. Cardiac MRI is superior to other modalities in imaging myocardial mechanics. Computed tomography (CT) methods rely on movement of the heart boundaries and they give limited insight into intramyocardial motion. Radionuclide single-photon emission CT (SPECT) and positron emission tomography (PET) provide valuable information about myocardial metabolism but do not reliably measure myocardial motion. Doppler ultrasound is capable of measuring myocardial velocities and strain rates, but the technique has a low spatial resolution and there are limited anatomical viewing windows.

MRI is capable of monitoring intramyocardial motion in any imaging plane using a variety of techniques including myocardial tagging [2, 3] phase contrast velocity encoding [4], harmonic phase (HARP) [5], and most recently displacement-encoded imaging using stimulated echoes (DENSE) [6].

DENSE measures the motion of myocardial tissue by encoding displacement in a particular direction into the phase of the complex MRI image. Cine DENSE [7] measures myocardial displacement throughout the cardiac cycle.

DENSE provides a better spatial resolution than myocardial tagging, and a greater tissue tracking accuracy than velocity encoding. Example magnitude and phase cine DENSE images are shown for end-systole in Figure 1a and 1b, respectively. The phase images are confined to the range [-\pi, \pi] and unavoidable phase aliasing occurs in the walls of the heart as it contracts.

![Figure 1](image-url)
white represents motion to the right and black represents motion to the left. The corresponding displacement field is shown in Figure 2c. These can be used to derive strain by applying finite element methods. These strains can then be used to discern between healthy and diseased myocardium, and to assess mechanical dyssynchrony [8].

Figure 2: (a) Unwrapped phase image for vertical motion, (b) unwrapped phase image for horizontal motion, and (c) the corresponding displacement field.

All phase unwrapping algorithms require a known phase reference point. In cine DENSE, phase aliasing is not present in early systole, at the beginning of the cine series. Referencing a true phase value can thus be achieved by unwrapping in three dimensions, i.e. two spatial and one temporal dimension [10]. This paper discusses an alternative 3D phase unwrapping technique for 2D cine DENSE data sets.

2 Phase unwrapping

Phase unwrapping is the process of determining the absolute phase given its principal value. The relationship between the measured, or wrapped, phase $\phi_j$ and the actual phase $\theta_j$ is

$$\theta_j = \phi_j + 2\pi n_j, \quad (1)$$

where $j$ is an $N$-dimensional index specifying the spatial location and $m_j$ at each voxel specifies the corrective offset required. The phase unwrapping problem reduces to determining $m_j$ for each voxel in an image. Phase unwrapping in cardiac MRI images is complicated by image noise, phase shear and the fact that only a few pixels span the myocardial walls.

Existing techniques for phase unwrapping can be grouped according to their

(i) Dimensionality (1D, 2D, 3D etc);
(ii) Application (Synthetic Aperture Radar, general optical interferometry, MR angiography, MR chemical shift mapping or MR field mapping); or
(iii) Approach (fitting functions, cost function optimisation, filtering, region growing / merging).

Phase unwrapping algorithms typically fall into two classes:

Path-following algorithms. These use localized operations by following paths through the wrapped phase. Variations include Goldstein’s algorithm, Quality-guided algorithms, Mask Map algorithm, and Flynn’s Minimum Discontinuity algorithm [9].

Minimum- norm algorithms. These adopt a more global minimisation approach and include unweighted least-squares algorithm, pre-conditioned conjugate gradient (PCG) algorithm, weighted multigrid algorithm, and Minimum L$^p$-norm algorithm [9].

Previously, 2D cine DENSE images have been analysed using a quality-guided (QG) path following algorithm that unwraps the phase through both space and time by using a measure of phase quality to guide the path of unwrapping [10].

This method can be summarised as follows.

1. A measure of phase quality for each pixel is calculated by

$$Z_{nw} = \sqrt{\frac{\sum (A_{ij} - X_{ij})^2}{n^2} + \frac{\sum (A_{ij} - Y_{ij})^2}{n^2} + \frac{\sum (A_{ij} - Z_{ij})^2}{n^2}}$$

$$\quad (2)$$
where for each sum the indexes \((i, j, k)\) range over the \(n \times n \times n\) window centered at the pixel \((p,q,r)\). The terms \(\Delta_{i,j,k}^\phi, \Delta_{i,j,k}^{\phi^2}, \text{ and } \Delta_{i,j,k}^{\phi^3}\) are the partial derivatives of the locally unwrapped phase, and the terms \(\overline{\Delta}_{p,q,r}^\phi, \overline{\Delta}_{p,q,r}^{\phi^2}, \text{ and } \overline{\Delta}_{p,q,r}^{\phi^3}\) are the averages of these partial derivatives in the \(n \times n \times n\) windows.

2. A starting point with known phase is selected and stored in a solution matrix.
3. The four pixels adjacent to the starting point are placed in an 'adjoin' matrix, which keeps track of wrapped pixels with adjacent unwrapped pixels.
4. The pixel in the adjoin matrix with the highest phase quality is selected and unwrapped using its adjacent unwrapped pixel. This pixel is removed from the adjoin matrix and added to the solution matrix.
5. The new wrapped nearest neighbours are included in the adjoin matrix.
6. Steps 4 and 5 are repeated until the adjoin matrix is empty.

Figure 3a and 3b shows the wrapped phase image and corresponding phase quality map, respectively. Figure 3c to 3f show the phase unwrapping path flooding from regions of high to low phase quality, and Figure 3g shows the resulting unwrapped image. The unwrapped image is smooth with no \(2\pi\) phase transitions in the myocardium.

3 Methods

Phase Region Expanding Labeller for Unwrapping Discrete Estimates (PRELUDE) is an \(N\)-dimensional region merging phase unwrapping algorithm developed for MR images [11]. Here an image is divided into a number of regions corresponding to specific phase brackets. Neighbouring regions are interrogated and merged based on a cost function.

To penalise the phase differences along the interfaces the sum of the square of the phase difference along the interface is used, that is

\[
C_{AB} = \sum_{j,k \in N(i)} (\phi_{Aj} - \phi_{Bk} + 2\pi M_{AB})^2
\]

(3)

where \(M_{AB} = M_A - M_B\) with \(M_A\) and \(M_B\) being integer offsets for adjacent regions \(A\) and \(B\). The summation is taken over two indices, \(j\) and \(k\), where \(j\) is the index of a voxel in region \(A\), while \(k\) is the index of a voxel in region \(B\). The total cost over the whole (\(N\)-dimensional) volume is the sum over all the interfaces:

\[
C = \sum_{A,B} C_{AB}
\]

Differentiating by the parameters, \(M_{AB}\) gives the equation for the minimum cost solution.
\[ M_{AB} = M_A - M_B = \left( -\frac{P_{AB}}{2\pi N_{AB}} \right) \]  \hspace{1cm} (4)

where \( N_{AB} \) is the number of interfacing voxel pairs and \( P_{AB} = \sum_{j,\ell \in N(i)} (\phi_j - \phi_{\ell i}) \).

In order to solve the integer programming problem generated by Equation 4 we can treat it as follows

\[ M_{AB} = \text{round} \left( -\frac{P_{AB}}{2\pi N_{AB}} \right) \]  \hspace{1cm} (5)

so that we can get a low (ideally minimum) cost. Let,

\[ K_{AB} = - \frac{P_{AB}}{2\pi N_{AB}} \quad \text{and} \quad L_{AB} = \text{round}(K_{AB}) \]  \hspace{1cm} (6)

The difference in cost between \( M_{AB} = L_{AB} \) and \( M_{AB} = L_{AB} \pm 1 \) is

\[ \Delta C_{AB} = 8\pi^2 N_{AB} \left( \frac{1}{2} \pm (K_{AB} - L_{AB}) \right) \]  \hspace{1cm} (7)

Since \( |K_{AB} - L_{AB}| \leq \frac{1}{2} \), then \( \Delta C_{AB} \geq 0 \) for both cases, confirming that \( M_{AB} = L_{AB} \) is the local minimum, with the smallest cost difference being

\[ \Delta C_{AB} = 8\pi^2 N_{AB} \left( \frac{1}{2} - 1 K_{AB} - L_{AB} \right) \]  \hspace{1cm} (8)

This implementation involves the following steps:

1. Determine masks to dichotomise the myocardium from the background noise in the blood pools and lung cavity. This was done using both image magnitude and phase discontinuities [12]. Phase inconsistencies, or residues, were identified by integrating the phase in small 4-pixel loops, and removing the pixel of lowest magnitude that lies adjacent to each residue. This provided the basis for identifying a threshold level for the magnitude image.

2. Create initial connected regions which will be merged during the unwrapping process. The myocardium was phase partitioned into regions according to the intervals \([-\pi, -2\pi/3], [-2\pi/3, -\pi/3], [-\pi/3, 0], [0, \pi/3], [\pi/3, 2\pi/3] \) and \([2\pi/3, \pi]\).

3. Identify the pair of regions that has the largest border weight (\(\Delta C\)). The pair is selected according to Equations 6 and 8, and \( AB = \arg \max_{A,B} \Delta C_{AB} \), where \( A \) and \( B \) are adjacent regions with the highest border weights. Merge the two regions by adding \( 2\pi L_{AB} \) to region \( B \).

4. Update the statistics for all interfaces (with other regions) to this new region. This involves updating the matrices \( P_{AB}, N_{AB} \) and \( \Delta C \).

5. Select a new pair of regions to merge. Region merging continues until there are no more interfaces.

Figure 4: The PRELUDE unwrapping process. (a) Masked phase image, (b) partitioned phase image, (c-f) progression of unwrapping phase image after 15, 55, 90, and 115 iterations, respectively, and (f) unwrapped phase image after all regions have been merged.

Figure 4 illustrates the PRELUDE unwrapping process. The regions corresponding to the masked phase image in Figure 4a are shown in Figure 4b. Figure 4c to 4f shows the progression of the
unwrapping process, and Figure 4f shows the final unwrapped image.

Figure 5 depicts the maximum border weight for pairs of adjacent regions during the unwrapping process for Figure 4. The sharp increases occur when two merged regions yield a new united border with a higher border weight.

Figure 5: Maximum border weight $\Delta C$ as a function of the number of iterations.

The PRELUDE algorithm was implemented in MATLAB (The Mathworks, Natick, MA) and run on an Intel® Core™ 2 Duo processor with 2GB of RAM. The reliability of the PRELUDE algorithm was compared to the quality guided (QG) algorithm on 300 cine DENSE images. Phase unwrapping errors were identified visually with the assistance of discontinuity maps [9]. A discontinuity map highlights pixels where an adjacent pixel contains a phase offset greater than $\frac{\pi}{2}$ or less than $-\frac{\pi}{2}$. If a line of discontinuities is seen to span the walls of the left or right ventricles, then the image is deemed incorrectly unwrapped. An example is shown in Figure 6.

Figure 6 (a) Unwrapped phase image with no discontinuities spanning the myocardial walls, (b) Unwrapped phase image with discontinuities across the right ventricle (white arrow).

4 Results

The results are summarised in Table 1 below. The PRELUDE technique provides comparable results to the quality-guided algorithm but the processing time is slower.

<table>
<thead>
<tr>
<th></th>
<th>Quality-guided</th>
<th>PRELUDE</th>
</tr>
</thead>
<tbody>
<tr>
<td>LV correctly unwrapped</td>
<td>99.3 %</td>
<td>99.0 %</td>
</tr>
<tr>
<td>RV correctly unwrapped</td>
<td>73.3 %</td>
<td>74.6 %</td>
</tr>
<tr>
<td>Processing time per frame</td>
<td>&lt; 0.6 s</td>
<td>$\leq$ 90 s</td>
</tr>
</tbody>
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5 Discussion and Conclusions

There are several limitations to the PRELUDE technique. Partitioning the image into phase bracket should be done judiciously. If a single region includes two areas where the original phase differs by more than $2\pi$, the algorithm can never successfully recover this original phase difference. Secondly, to obtain reasonable processing speeds the method is reliant on a mask to remove background noise.

The PRELUDE algorithm was considerably faster than the quality-guided algorithm for 2D phase unwrapping, but the 3D extension of PRELUDE results in prohibitively long processing times. Alternative phase
unwrapping methods will be required for volumetric cine DENSE studies [13] where 4D phase unwrapping is required.

Phase unwrapping is particularly challenging for the right ventricle, where the myocardial wall thickness is similar in width as the cine DENSE pixel size.

Spatio-temporal phase unwrapping remains a challenge for cine DENSE, but it is an unavoidable step in computing displacement fields which can then be used to determine strain patterns within the wall of the heart. This will help to detect abnormal wall motion which could be useful in the diagnosis of heart disease.

6 References