Fast Feature Based Multi Slice to Volume Registration Using Phase Congruency

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Abstract—Slice to volume registration is very useful in many medical imaging applications, for example, fusing static high resolution three dimensional (3D) image volumes to dynamic two dimensional (2D) slice data for deriving motion information in 3D. Though information theoretic registration methods such as Mutual Information are usually robust, they are time intensive and typically require a high level of field-of-view correspondence between the source and target images. In single slice to volume registration scenarios, where such correspondence is limited, registration accuracy and robustness often deteriorate. In this paper, we present a novel registration method that maintains robustness and accuracy while significantly increasing registration speed. Our approach employs multiple slice (as opposed to single slice) to volume registration, which increases the amount of potential matching information while maintaining a small number of slices hence facilitating often necessary high speed dynamic image acquisition. Our proposed registration approach first extracts phase congruency information from the slices/volume using oriented 2D Gabor wavelets. Using local non maximum suppression, we then automatically obtain a robust and accurate set of feature points that are subsequently matched using an Iterative Closest Point (ICP) approach. Validation on BrainWeb simulated magnetic resonance imaging (MRI) data showed significant gains in speed (~40-fold increase) when compared to conventional Mutual Information based volumetric registration while maintaining comparable robustness and accuracy levels.

I. INTRODUCTION

Image registration is a commonly needed step in medical image analysis tasks which facilitates fusion of data captured using varying imaging modalities or alignment of same-modality data captured at different time points. Registration also plays an important role in atlas based segmentation methods [13]. Numerous techniques have been reported for medical image registration [1][2]. Most state-of-the-art approaches cater to registration of image volumes, i.e. three dimensional (3D) to 3D image registration, however, two dimensional (2D) to 3D data registration is important in many medical imaging applications. Examples include registration of volumetric data to projection images, e.g. fluoroscopy to computed tomography (CT), and registration of single image slices to volumetric data, e.g. 2D magnetic resonance imaging (MRI) to 3D MRI. The latter is generally referred to as ‘slice-to-volume registration’.

Slice to volume registration can be used to fuse static high resolution 3D image volumes to dynamic 2D slice data in order to obtain motion information in 3D. This is of great utility in a number of applications, especially in the area of computer aided surgical procedures, where registration needs to be real time as well as being robust.

Slice-to-volume registration is limited, though it has been used for registering ultrasound (US) slices to MRI volumes [4], for interventional MRI guided radio frequency ablation of prostate cancer [5], for motion correction of fMRI volumes [3] and for registering 2D MR brain scout (planning) scans to complete 3D MR brain images. Most of these applications used information theoretic similarity metrics in the registration process such as mutual information (MI) [10],[11] and normalized mutual information (NMI) [12] which are more robust to data contrast differences and noise than other methods such as direct correlation. However, since they use the entire information in the datasets, they are typically time consuming and prone to deterioration in accuracy if there isn’t enough correspondence between target and source data. Accordingly, robustness of such methods is typically reduced in single 2D image slice to 3D image volume registration scenarios. Xu et al tackled this problem by using multiple slices to volume registration in an MR-TRUS (Trans-rectal ultrasound) image-guided prostate biopsy application [16]. However, the metric they use is the sum of squared differences (SSD) for which they use all the information in the datasets. Hence the method is time consuming.

In this paper, we propose increasing registration robustness by employing multiple slices (as opposed to single slice) to volume registration, as proposed by Xu et al [14]. This increases the amount of potential matching information while simultaneously keeps the number of needed slices small, thus facilitating high speed image acquisition, often a seriously limiting constraint. However, instead of using all the information in the data, our approach extracts phase congruency image features that are then robustly matched using an iterative closest point matching (ICP) approach. We validate our method on sample MRI volumes and slices taken from the BrainWeb simulated database [15] and demonstrate a significant improvement in speed when compared to registration using traditional MI based methods.

II. METHODS

Our proposed method comprises three steps: First, after preprocessing, phase congruency measures of both reference
and target images are calculated. Second, robust feature points are identified in the phase congruency images using non maximum suppression. Third, the feature points are robustly matched using ICP to generate point pairs of correspondence and a transformation is calculated. The use of multiple, as opposed to single, slices allows enough features to be obtained for robust and accurate registration. Moreover, unlike previous registration methods which use all the information in the data, feature based registration leads to considerably fast registration, which can be implemented in real-time.

Since slices in low resolution data are typically thicker than high resolution 3D volume data (e.g. a typical 3 mm vs. 1 mm), we start by averaging groups of N slices in the 3D volume (e.g. N=3) to equate the thickness of the slices taken during the multi-slice imaging. For example, a 90 slices high resolution volume becomes a 30 slice volume of thick slices since we group 3 slices at a time.

The next step involves the calculation of local image phase features where phase congruency (PC) [7] is used to detect robust feature points for subsequent registration. Phase is congruent when its values are the same or similar at a specific point in the signal. PC enjoys robustness across modalities; furthermore, it corresponds to features believed to be important in human vision. Since some physiological evidence [7] has indicated that the human visual system responds strongly to points of high phase congruency in an image, it stands to reason that PC filtered images will give a large number of meaningful features that can accurately correspond across modalities even in the presence of noise.

Consider a one dimensional signal (1D) signal \( f(t) \). At a location \( x \) in the signal, the local Fourier components will have an amplitude component \( A_n(x) \) and a phase component \( \phi_n(x) \), where \( n \) is the nth sinusoidal component of the signal at location \( x \). If these local Fourier components are considered as complex vectors and are then added head to tail, then a local energy, \( |E(x)| \) can be calculated using the magnitude of the summing vector (Figure 1).

\[
E(x) = \sum |A_n(x)\exp(i\phi_n(x))|
\]

Using this method for calculating local energy, Morrone et al [7] developed a measure of phase congruency (1):

\[
PC(x) = \frac{|E(x)|}{\sum_n A_n(x)}
\]

This simple measure of PC is a function of the cosine of the deviation of each phase component from the mean. Using this property, Kovesi [8] developed a modified measure that incorporates the difference of the cosine and the magnitude of the sine of the phase deviation and also introduces a term that models noise (2).

\[
PC(x) = \frac{\sum_n W_n A_n(x)\cos(\phi_n(x) - \overline{\phi}(x))}{\sum_n A_n(x) + \epsilon}
\]

The parameter \( T \) is a noise threshold and \( \epsilon \) is a small constant added to avoid division by zero. An example PC image of an MRI slice is shown in Figure 2.

In our registration scheme, we start by calculating the PC images for both the slice and volume data that are to be registered. In our current implementation, PC of the image volume is obtained by concatenating PC of its individual slices for simplicity. The parameters in (2) are currently empirically determined. In the second step we perform a non maximum suppression (with a certain radius) in order to find the locally maximal points of PC. This gives us a pool of features for matching purposes. Once the PC images are obtained, they are subsequently matched using iterative closest point matching (ICP) [9]. This gives the parameters to correct the misregistration which are then applied to the original volume to register it to the slices. Since we are considering rigid deformation, this is a linear, rigid transform.

III. EXPERIMENTS

The proposed method was validated on five 3D MRI volumes (of 181×217×181 voxel resolution) from the publicly available MNI simulated BrainWeb database [15]. Each volume was registered to five (low resolution) slices, each having a thickness equaling 3 slices of the high resolution volume. This increased thickness, as previously explained, simulates typical dynamic imaging slice resolution and was obtained by averaging 3 slices across the transverse direction. Rigid transformations for misregistration were synthetically introduced and were in the range of ±10º for rotations and ±10 pixels for translations. Registration accuracy was then measured as the difference between the misaligning (known) rotation and translation values and the corresponding resulting values obtained by our registration scheme. For comparison purposes, the slices and volumes were also registered using multi slice to volume registration employing MI and Powell’s optimization which uses all the information in the datasets [5] (for which the step sizes for rotations and translations were 0.5º and 0.5 pixels, respectively). Both registration algorithms were implemented in MATLAB.
IV. RESULTS

Quantitative results illustrate that our proposed method gave registration accuracy levels comparable to those obtained using intensity based slice to volume registration using MI and Powell’s optimization. Both methods resulted in translational errors in the range of ~0.25-0.3 pixels and rotational errors in the range of ~0.15-0.2 degrees. Qualitative results using checkerboard image display showed no discernible misregistration (an example is shown in Figure 3-e). However, in terms of speed, our proposed registration proved to be significantly faster than the MI based method, averaging ~14.9 seconds to register the datasets as opposed to ~610.7 seconds for MI. Given the fact that programs typically run an order of magnitude faster in low level languages like C as compared to MATLAB, we anticipate it to be feasible to use our registration approach in real time applications such as computer assisted surgery in the future.

Fig. 2. Example of phase congruency image of an MRI slice and extracted features. (a) Original thick slice (1 of 5) from the test set. (b) Corresponding phase congruency image. (c) The phase congruency image with extracted features.

Fig. 3. Results of proposed 2D-3D registration approach. (a) Original thick slice (1 of 5) from the test set. (b) Misregistered volume (cross slice having same z coordinate as the slice in (a)). (c) Checkerboard of (a) and (b). (d) Corrected volume registered using our proposed method (cross slice). (e) Checkerboard of (a) and (d).
V. DISCUSSION AND CONCLUSIONS
We presented a novel feature-based method for rigid registration of multiple slices to volume image data. Our approach utilizes a small number of slices which provides more information than one slice based approaches but can still be feasibly acquired using current imaging technology speeds. Our technique employs PC to obtain meaningful and stable images features which are then used to robustly match the data using ICP.

Quantitative results on simulated MRI data demonstrated the high efficiency of the proposed method reflected in the very fast registration times which were up to 40 times faster when compared to intensity based slice to volume registration using MI and Powell’s optimization while maintaining similar accuracy.

Future work will focus on assessing in noisy data and extension to non-rigid registration. Applications of interest which we are currently testing include multi-modal image registration of CT and MR data, and real time operation in computer assisted surgery tasks.

REFERENCES