ABSTRACT

Helium-3 tagged magnetic resonance imaging has demonstrated potential for calculating pulmonary deformation from medical imagery. Such measurements are useful for determining the biomechanical properties of the lung. Unfortunately, the relative facility of visually tracking deformation via the high contrast tag lines has not transferred readily to the algorithmic domain of automatically establishing tag-line correspondences. We proffer a solution to this dilemma by translating the problem into a unique point-set registration scenario. Not only does this permit capitalizing on certain spectral aspects of tagged MRI but registration can be performed within a deterministic annealing framework for decreased susceptibility to local minima.

Index Terms— B-splines, free-form deformation, Gabor filter bank, Jensen-Shannon entropy, point-set registration

1. INTRODUCTION

Introducing our previous research [6], we outlined the comparative maturity of myocardial tagged MRI analysis and the reliance on that research field for forwarding analysis of tagged helium-3 MRI. The current research we present constitutes a step towards more automated analysis of generic tagged MR imagery although, in this paper, we specifically apply our methodology to tagged helium-3 MRI of the lung.

2. METHODOLOGY

Given two configurations of a deformable body (such as the lung), extraction of salient biomechanical quantities requires establishing a continuous mapping between the configurations. Assuming the reliable permanency of the tagging fiducials, we can establish that continuous mapping by finding the correspondence between the sets of tag planes in the two configurations via an underlying continuous mapping defined over the entire transformation domain. The general algorithmic workflow for calculating this mapping is summarized as follows:

1. Images are preprocessed which includes an automated coarse segmentation of the lungs and inhomogeneity correction of the image.

2. A separate Gabor filter bank is applied to the preprocessed images for each set of tag planes. Those voxels within the coarse segmentation with a high response are thresholded to produce candidate points providing a sampling of the tag planes.

3. Convert each of the three point sets from each configuration into separate probability density functions.

4. For each of the three sets of tag planes, minimize the Jensen-Shannon entropy using a specified transformation model and minimization technique. Each of the three sets of corresponding tag planes provides the deformation field in one of the three canonical Cartesian directions.

5. Conjoin the results to provide a full 3-D continuous mapping which establishes correspondence between the two configurations. From this mapping, kinematic measures can be calculated.

Elaboration of the algorithmic details is provided in subsequent sections.

2.1. Gabor Filter Banks for Tag Points Extraction

After preprocessing the images, we extract the sampled tag plane points using a Gabor filter bank [3]. The Gabor function is complex sinusoid modulated by a Gaussian envelope formulated (in 1-D) as

\[ g(x) = \frac{1}{\sqrt{2\pi\sigma}} \exp\left(-\frac{x^2}{2\sigma^2}\right) \cdot \exp\left(-j2\pi\omega x + \theta\right). \]  (1)
2-D and 3-D extensions of the Gabor filter have found use in different areas of computer vision research (e.g., [5]). Although the tag planes have such structure, due to the deformation of the lung during the respiratory cycle, the tag plane surfaces will also deform which necessitates the use of multiple Gabor filters for enhancing the local planar structure. For each image, the Gabor filter bank is applied three times—once for each of the three sets of mutually orthogonal tag planes. The user selects the number of Gabor filters in the filter bank by sampling both in terms of the orientation of the filters as well as the tag spacing. A user-selected threshold percentage determines the number of voxels included as candidate tag plane points. Note that it is expected that some true tag plane sample points will be excluded from the results and that outliers will inevitably be included in the result. Such misclassification relies on the robustness of the subsequent registration step for accurate results. Using typical values given in [3], sample results are provided in Figure 1.

2.2. Minimizing the Jensen-Shannon Entropy for Point-Set Registration

Wang et al. [9] present recent research for point-set registration which employs the Jensen-Shannon (JS) entropy divergence measure and a thin-plate spline transformation model. Each point-set is represented as a probability density function through the use of a Gaussian mixture model (GMM) where each point, \( x_i \), specifies a Gaussian center with a constant isotropic covariance.

Given \( K \) probability densities \( \{ P_1, \ldots, P_K \} \), the JS divergence is given by

\[
JS(P_1, \ldots, P_K) = H \left( \sum_{k=1}^{K} \pi_k P_k \right) - \sum_{k=1}^{K} \pi_k H(P_k) 
\]

where \( H(\cdot) \) is the Shannon entropy and the set of weights \( \{ \pi_1, \ldots, \pi_K \mid \pi_k > 0, \sum_{k=1}^{K} \pi_k = 1 \} \) determines the relative contribution of the corresponding probability density function to the divergence measure. Associating each \( P_k \) with a mapping function, \( T_k \), allows for the determination of the parameters of the respective mapping functions which map each point set to an unbiased average atlas. Please note that in our case, we are not interested in calculating an average atlas but wish to map the deformed configuration (end-expiration) to the undeformed configuration (end-inspiration). This is done by maintaining \( T_{\text{undeformed}} = I \) throughout the minimization process where \( I \) is the identity transformation.

Using the core algorithm presented above, we made several improvements to enhance the performance of our algorithm when applied to tagged MR images. Two major differences are the construction of a structurally-based probability density function from each point-set and the employment of an enhanced B-spline deformation model within a deterministic annealing framework. These two improvements are described below.

2.2.1. Manifold Parzen Windowing for Structurally-Based Density Functions

Given that point-sets often represent a sampling of an underlying structure, we modify the conversion process transforming a point-set to its corresponding probability density function to capture that local structure. Whereas previous work used isotropic Gaussians, we use the local point-set neighborhood to estimate an appropriate covariance matrix where the local structure is reflected in the anisotropy of that covariance [8]. For each point, \( x_i \), the associated weighted covariance matrix, \( C_{K_i} \), is given by

\[
C_{K_i} = \frac{\sum_{x_j \in N_i, x_j \neq x_i} K(x_i; x_j)(x_i - x_j)(x_i - x_j)^T}{\sum_{x_j \in N_i, x_j \neq x_i} K(x_i; x_j)}
\]

where \( N_i \) is the local neighborhood of the point \( x_i \) and \( K \) is a user-selected neighborhood weighting kernel. We use an isotropic Gaussian for \( K \) as well as a k-d tree structure for efficient determination of \( N_i \).

For the optimization routine the inverse of each covariance matrix is required. Determination of \( C_{K_i} \) from Equation (3) could potentially result in an ill-conditioned matrix. For this reason, we use the modified covariance, \( C_i = C_{K_i} + \sigma^2 I \) where \( I \) is the identity matrix and \( \sigma \) is a user-provided parameter denoting added isotropic Gaussian noise (this parameter is used in our annealing scheme discussed in a later section). Thus, the \( k^{th} \) probability density function calculated from the \( k^{th} \) point-set is given by the GMM

\[
P_k(s) = \frac{1}{N_k} \sum_{i=1}^{N_k} G(s; x_i^k, C_i^k)
\]

where \( G(s; x_i^k, C_i^k) \) is a normalized Gaussian with mean \( x_i^k \) and covariance \( C_i^k \) evaluated at \( s \).
2.2.2. B-spline Transformation Model

Thus far we have described how distinct point-sets extracted from tagged helium-3 MR images are converted into probability density functions which allows their dissimilarity to be quantified by the $JS$ divergence measure. Associating each point-set (i.e. probability density function) with a continuous mapping function, $T_k$, and minimizing the $JS$ divergence with respect to the parameters of all $K$ transformation models brings the point-sets into correspondence.

Optimization requires evaluation of Equation (2) in addition to the corresponding gradient with respect to the transformation model parameters. Both evaluations require the generation of a set of sample points from each of the $K$ probability density functions (further details are given in [9]). We designate the number of sample points generated for each of the $K$ probability density functions as $\{M_1, \ldots, M_K\}$ and the $k^{th}$ set of samples as $\{s_1^k, \ldots, s_{M_k}^k\}$.

Calculation of the gradient of the $JS$ divergence with respect to the transformation parameters is slightly different than that given in [9] and so we reproduce our gradient formulation for the benefit of the reader. The partial derivative of Equation (2) with respect to the $l^{th}$ parameter, $\beta^l_k$, of $T_k$ is given by

$$\frac{\partial JS}{\partial \beta^l_k} = \frac{\partial T_k}{\partial \beta^l_k} \cdot \sum_{i=1}^{N_k} \left[ \frac{1}{MN} \sum_{k'=1}^{K} \sum_{j=1}^{M_{k'}} G(s_j^{k'}, x^k, C^k) (C^k)^{-1} (x^k_j - s_j^{k'}) \right] - \frac{1}{M_k N} \sum_{j=1}^{M_k} G(s_j^{k}, x^k, C^k) (C^k)^{-1} (x^k_j - s_j^{k}) \right] P^*(s^k_j) \right)$$

where

$$P^*(s) = \frac{1}{N} \sum_{k=1}^{K} \sum_{i=1}^{N_k} G(s; x^k_i, C^k)$$

$$N = \sum_{k=1}^{K} N_k, \quad M = \sum_{k=1}^{K} M_k.$$  

Traditional gradient approaches, which are intrinsically susceptible to hemstitching during the gradient descent, calculate $\frac{\partial T_k}{\partial \beta^l_k}$ as

$$\frac{\partial T_k}{\partial \beta^l_k} = \prod_{j=1}^{D} B_{ij, dj}(u_j)$$

whereas we calculate a preconditioned version

$$\frac{\partial T_k}{\partial \beta^l_k} = \prod_{j=1}^{D} B_{ij, dj}(u_j) \cdot \prod_{j=1}^{D} B_{ij, dj}(u_j) \cdot \frac{1}{\sum_{u_j} \prod_{j=1}^{D} B_{ij, dj}(u_j)}$$

(9)

where $D$ is the parametric dimensionality of the B-spline object, $d$ is the degree of B-spline used, and the set of $B(\cdot)$ are the B-spline basis functions governing $T_k$. Additional details discussing the deficiency of traditional gradient approaches as well as the derivation of Equation (9) can be found in [7].

2.2.3. Deterministic Annealing

The core of the optimization by conjugate gradient descent is relatively standard [2]. However, we have placed this minimization routine within a deterministic annealing framework [4], both in terms of the transformation model as well as the $JS$ divergence, which decreases the susceptibility to local minima. This is extremely important since, at the local level, determination of correct tag correspondence is difficult.

At the initial stage of the optimization, the B-spline transformation model is defined by a low-resolution mesh to determine more global correspondence. At each subsequent level, the mesh-resolution is doubled [7] for increased local, refined registration. In coordination with this hierarchical registration, we specify an annealing schedule for the isotropic gaussian noise discussed in Section 2.2.1. At the $p^{th}$ level the covariance is calculated as $C_i = C_i + \lambda^p \sigma^2 I$ where $\lambda$ is the annealing rate. This also has the effect of increasing the localization during the course of the optimization.

3. EXPERIMENTATION

To demonstrate the methodology described above, sample registration results are acquired using the tagged helium-3 images shown in Figure 2. MR imaging was performed using a 1.5 T whole-body scanner (Siemens Sonata), and helium-3 gas was polarized to approximately 40% using a commercial system (Model 9600, MITI). Following inhalation of a 1 L mixture of $\sim$400 ml hyperpolarized helium-3 and $\sim$600 ml $N_2$, 3-D tagging grids were created at breath hold by applying sinc-modulated RF-pulse trains consecutively along all three principal axes. Tag spacing was 22 mm. The grid-tagging preparation was applied first, followed by a FLASH-based 3D image acquisition at full inspiration with the following parameters: TR/TE = 2.0/ 0.7 ms; FOV= 340x280x198 mm; matrix = 64x64x22; flip angle = 1. The subject was then instructed to exhale completely, and the FLASH-based acquisition was repeated following a pause of 2-3 s. Total scan time is 7.4s. The short TE of the FLASH sequence was achieved by using the asymmetric readout, yielding a partial k-space acquisition.
The acquired images were then processed to extract point sets (one set from each set of tag planes from each image). Extracted points were then manually refined to remove spurious sample points. The results are provided in Figure 2. A cubic B-spline transformation domain was then defined over the image domain. Starting from an initial mesh resolution of one B-spline element, four levels were used during the course of the optimization where the B-spline mesh resolution was doubled at each level. The resulting displacement field and corresponding principal strain field are shown in Figure 3(a) and Figure 3(b), respectively.

4. DISCUSSION

We have presented a potentially useful framework for analyzing pulmonary biomechanics from tagged helium-3 MRI with possible application to other tagged MR imagery. Equally as important, we implemented this framework using the Insight Toolkit [1] which allows for open-source dissemination and efficient portability of useful components of our research. This allows others in relevant areas of research to apply and build upon our methods.

5. ACKNOWLEDGMENTS

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6. REFERENCES