Whole-Lung Parenchymal Dynamics: Evaluation of Motion Estimation Using Non-Rigid Registration

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Introduction

Quantification of pulmonary deformation is useful in characterizing normal lung motion as well as the changes that occur as a result of pathological processes. Diseases such as emphysema typically disrupt the intricate architecture of the alveolar air spaces and disrupt the lung's ability to effectively expand and contract [4]. Medical imaging can be applied to observe such morphological changes and their effects on normal lung motion. We have previously demonstrated and validated our 2-D non-rigid image registration algorithm for computing the deformation between successive magnetic resonance (MR) images of the lung [1,2,5]. The algorithm incrementally computes a deformation field that seeks to minimize the total potential energy Π, which is composed of the image similarity and the constitutive response (isotropic linear elasticity). The constitutive response treats each image as an elastic body in a first order approximation to true parenchymal behavior. The resulting deformation field represents an estimate of the pulmonary motion between two sequential images. Explicit correspondences between images are not required; the extensive pulmonary vasculature and other parenchymal features are treated as natural sources of spatial markers that are tracked between the configurations given by the image data. In previous work, we have demonstrated this method on one coarse 3-D MR dataset (15 mm slices) and 2 high-resolution CT datasets. Here, we quantify the algorithm's performance by using the inherent pulmonary vasculature to evaluate the success of the motion estimation using high-resolution 3-D MR images. We also investigate the advantage of pre-processing the data to exclude all structures except the pulmonary parenchyma and associated vessels. The results provide regional information about volumetric deformation of the lung through the respiratory cycle, and can be used to study the effects of pathological processes on the expected deformation of the lung, as well as to make regional comparisons within or between individuals.

Methods

MR imaging was conducted using a 1.5 T body MR scanner (Signa Twinspeed, General Electric Medical Systems, Milwaukee, WI) with an 8-channel torso coil and the subject in the supine position. To reproducibly locate the imaging region, a coronal localizer scan was first performed in which the entire thorax was identified using multi-slice FIESTA with breath-holding at end-expiration. On the scout images, a three-dimensional field of view (FOV = 30x24x83 cm) encompassing the entire right lung was carefully selected to avoid artifacts due to cardiac motion. Sagittal images were subsequently acquired with a 3-D FIESTA sequence, yielding 54 contiguous images with 1.3 mm slice thickness. All images were obtained using pulse repetition and echo times of 4.2 ms and 1.6 ms, respectively, a flip angle of 25º, and a 224x160 image matrix, with a total scan time of approximately 15 seconds. Image volumes were acquired while two healthy volunteers held their breath at four respiratory phases. The motion between three of these phases (end-expiration, mid-inspiration, and end-inspiration) is evaluated in this work. To accommodate existing hardware and software limitations, image volumes are interpolated into isotropic voxels and scaled to half the original data resolution. Sequential image volumes are registered for each individual using a multi-resolution scheme that matches coarser image features at lower image resolutions and finer detail at the higher resolutions. Registrations are performed on both whole-chest image volumes and lung-only image volumes, in which the lungs have been extracted from the original data via semi-automated segmentation (figure 1a-c) [3]. The registrations are evaluated by computing the squared intensity difference between the expected and achieved images.

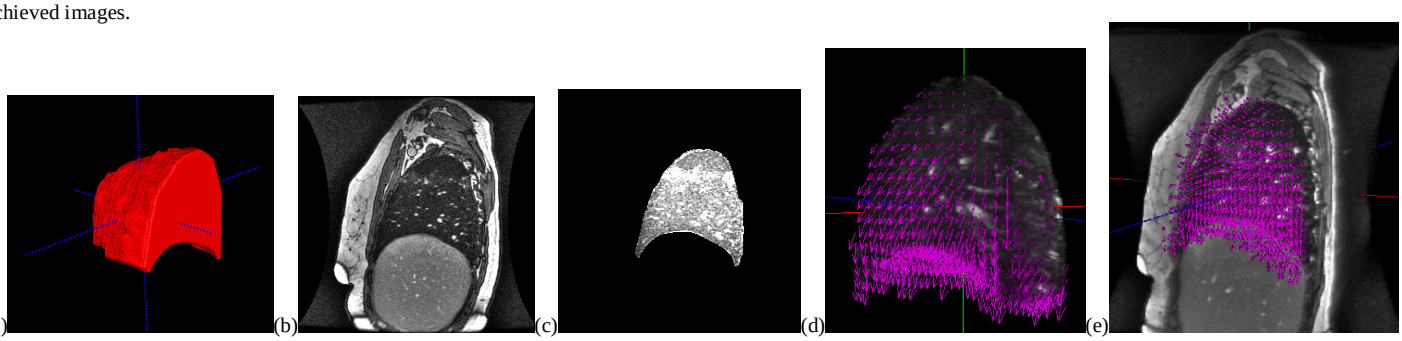

Figure 1: (a) Segmentation mask used to extract pulmonary parenchyma from whole-chest image volume. (b) Coronal slice from whole-chest image volume. (c) Corresponding slice after segmentation, containing only pulmonary parenchyma and associated vasculature. Note the increase in image contrast once the high signal regions outside the lung have been removed. (d) Whole-lung motion field computed using volumes in (c) and depicting the deformation between end-expiration and an intermediate point during inspiration. (e) A whole-body motion field masked to show only parenchymal displacements.

Results

Registration error is computed in table 1 as the percentage reduction in mismatch (represented by the squared intensity difference) between the expected and computed images. The lung-only registrations perform slightly better than the whole-chest registrations, especially when there is a large amount of deformation to recover, as between the mid-inspiratory and end-inspiratory images of volunteer #1.

Table 1	#1	#2
Whole chest (end-exp to mid-insp)	78.51	72.98
Lung only (end-exp to mid-insp)	77.29	74.30
Whole chest (mid-insp to end-insp)	63.10	74.78
Lung only (mid-insp to end-insp)	73.78	80.63

Discussion & Future Work

We explore registration-based motion quantitation using image volumes containing only pulmonary parenchyma as opposed to the whole chest. Extracting and matching the pulmonary parenchyma is advantageous not only from the perspective of reducing registration error, but also by increasing parenchymal contrast within the image and reducing the number of displacement vectors produced. Future work includes regional quantitation of the differences between these approaches, particularly with tracking of vascular bifurcations and investigation of matching of the pulmonary vascular tree, as well as extensions into atlas construction, whole-cycle motion quantitation, and the evaluation of regional parenchymal deformation in healthy individuals and patients with pulmonary pathologies.

References

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