Landmark-Based Assessment of Human Lung Motion Analysis via Registration of Sagittal 2-D MR Images

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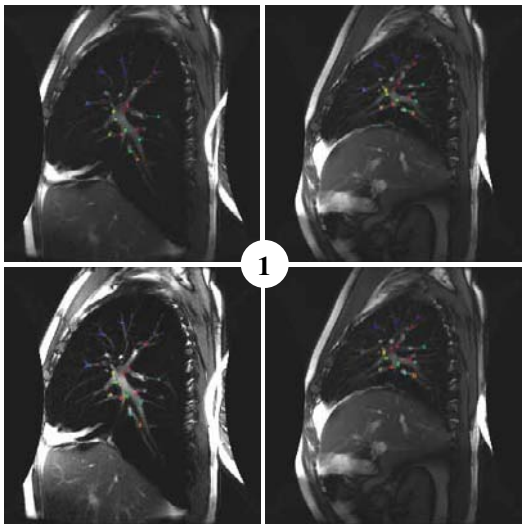
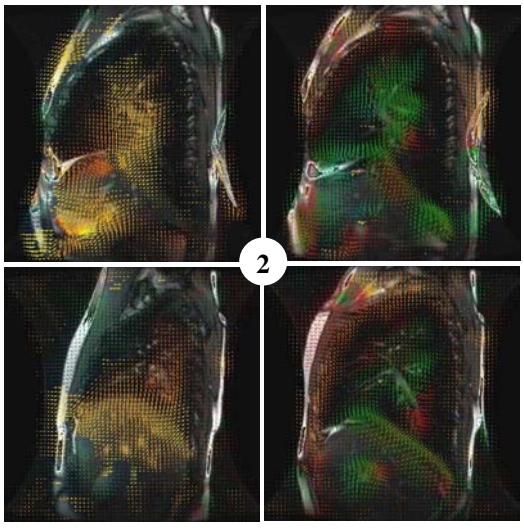
Introduction: In order to effectively characterize whole-lung motion, it is logical to analyze whole-lung (3-D) images. However, it is difficult to acquire whole-lung images in real-time that are of sufficient spatial and temporal resolution. Furthermore, it is clinically advantageous to image patients as quickly as possible, and with as few breath-holds as necessary. Plathow et al. found that 2-D estimates of lung capacity were sensitive to changes in lung dimension before and after chemotherapy in mesothelioma patients [3]. Koch et al. determined that surface fiducials did not effectively reflect intraparenchymal motion during respiration [2]. As a result, when choosing landmarks for validation of lung motion estimates, it is necessary to select both intraparenchymal and surface markers. Motion measured on the surface of the lungs may not accurately reflect the internal deformation of the tissues, nor the regional variation in motion patterns. In this work, we explore the quantitation of lung motion with real-time 2-D MR imaging of healthy human volunteers.



Methods: We use two sets of 2-D sagittal, free-breathing images of the right lung obtained using fast imaging (GE FIESTA, TR=3.22 ms, TE=1.45 ms, slice thickness=15 mm, FOV=35 cm, 256x256 matrix). Healthy volunteers are instructed to breathe slowly and deeply as they lie supine in the scanner; images are continuously acquired every 1.4 seconds. Sequence N6 contains 21 images from end-inspiration through end-expiration to the subsequent end-inspiration. Sequence N7 contains 43 images, starting with end-expiration and spanning a complete inspiration and expiration. Landmarks are identified by two raters at vessel bifurcations that are clearly identifiable in the end-expiratory image of each sequence. Each collection of points to identify is chosen in consensus, while each rater independently labels the landmarks on each image. 19 landmarks are placed on the images in N6, and 13 landmarks are placed on the images in N7. In a few instances, image frames do not contain the full complement of landmarks because raters are unable to identify particular points with absolute certainty due to image noise and parenchymal compression. Landmarks that cannot be labeled correctly are omitted from the error analysis. Sample landmarks from rater A (figure 1, top) and rater B (figure 1, bottom) are shown; the first image of each pair is inspiratory and the second image is expiratory.

Lung motion is estimated using sequential pairwise registration with the diffeomorphic algorithm discussed in [1]. Registrations are run with a small step size at the half- and full-resolution for 80 and 60 iterations, respectively. We assess the performance of the registration against both raters. We wish to compare the registration-derived displacement to the "ground truth" provided by the landmarks. At each anatomic location, we establish a "true" landmark—a common origin for the landmark displacements—as the average location of the two raters' points. Two landmark displacements are computed, one to each rater's point in the subsequent image. The registration-derived displacement is determined by evaluating the displacement field at this centroid location. Hence, at every landmark, three vector endpoint errors are compared: registration vs. rater A, registration vs. rater B, and rater A vs. rater B.

Results: Figure 2 shows sample inspiratory (left) and expiratory (right) displacement fields overlaid on the first image in the registered pair for N6 (top) and N7 (bottom). The maps are color-coded according to the direction of motion. In both phases, a great deal of motion is captured in the lung bases. There is also motion concentrated over the hilar vasculature; these vessels serve as natural features that can be registered. Rater-registration errors are calculated over each landmark throughout the respiratory cycle, as well as within each image pair for all landmarks. Ideally, the rater-registration errors are less than the inter-rater variability. This is primarily true in N7, although there are some landmarks at which the rater-registration error exceeds the inter-rater error. In most cases, however, the discrepancy is relatively small. When examining individual image pairs, there are two that have higher errors ($\geq$ 3 pixels). Both of these occur at the start of expiration, when the lungs deform significantly more than they do as an individual reaches the end of inspiration. It is possible that the deformation of the lung between these image pairs is higher than between adjacent neighbors, and requires additional iterations to be effectively matched. Over all landmarks and image pairs in sequence N6, there is an average inter-rater disagreement of 1.59±1.58 pixels. The average rater-registration errors are 1.61±1.37 and 1.49±1.25 pixels, respectively. Though one is slightly higher, both rater-registration errors closely match the inter-rater errors. In sequence N7, the overall errors are less than those in N6; there is much greater consensus between the raters and the registrations. Over all landmarks and image pairs in sequence N7, the average inter-rater error is 1.04 ± 0.68 pixels. The average rater-registration errors are 0.82±0.70 and 0.85±0.74 pixels, respectively.



Discussion & Future Work: The results of these experiments suggest that with the appropriate registration parameters, we can quantify regional lung motion using 2-D sagittal MR images with accuracy to within 1-2 pixels. The source of this error is likely multifactorial, a combination of through-plane motion as well as the inherent limitations of the registration. Regardless, it is useful to be aware of the precision that can be achieved when processing these sequences. These results are important in light of the fact that real-time imaging of the lung is clinically valuable but not yet practical in 3-D. Motion analysis in 2-D sequences is a readily available technique that can rapidly provide regional information about parenchymal deformation with reasonable accuracy despite the issues described above. Acquiring real-time data with many samples during a single breath further allows us to explore the path of a particular anatomic location throughout the respiratory cycle. It is important to sample the respiratory cycle at more than its endpoints in order to effectively characterize lung kinematics. However, further work is necessary to determine if there is an optimal sampling frequency for both image acquisition and subsequent motion quantitation.

References: [1] B. Avants et al. *Neuroimage* Suppl. 1:S139-150, 2004. [2] N. Koch et al. *Int'l J. Rad. Onc.* 5(1):1459–1472, 2004. [3] C. Plathow et al. *Invest. Radiol.* 41(5):443–448, 2006.