A Novel Framework for Deformable Registration Evaluation and Quality Assurance

S Pirozzi, BS[1], JW Piper, BS[1], AS Nelson, MD[1], M Duchateau, MSc[2], D Verellen, PhD[2], M De Ridder, MD, PhD[2]

[1]MIM Software Inc., Cleveland, OH • [2]Universitair Ziekenhuis Brussel, Brussels, Belgium

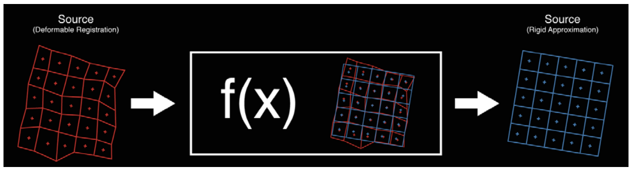
Purpose

Deformable registration is now routinely used at many radiation oncology centers not only for automatic contouring, but also for diagnostic image registration and dose accumulation. In these applications, it is essential that these registrations are not only characterized with phantom studies, but also be checked on a per-patient basis around the regions where the deformable registration is guiding the clinical decisions. Here we test a novel framework for evaluation of deformable registration using a real-patient point-validated pixel-based breathing thorax model.

Materials/Methods

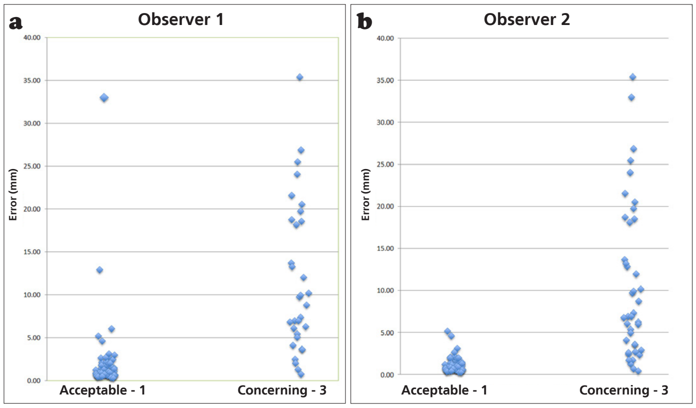
A novel framework, Reg Reveal, is proposed, wherein a variety of evaluation tools are provided to inspect different properties of a deformable registration between two volumes. The primary mode, and the only one used for this study, is an interactive visual display of a rigid fusion between the two volumes. This rigid fusion is computed as the best approximation to the local deformable registration, in a least squares sense, constrained such that the center of the rigid fusion is the exact transform defined by the deformable vector field at that point (See Figure 1). The 4D dataset used is Patient 2 of the POPI-model (4) in order to result in a distribution of registration errors which could be evaluated within the new framework. The average motion of 100 points of interest was 14.0 +/- 7.2 mm between the 0% and 50% phases which has been shown to be a challenge to deformable registration algorithms. After deformable registration with a commercially available algorithm provided in MIM 5.6 (MIM Software Inc), there was an average of 5.1 +/- 7.5 mm residual registration error. Two users independently reviewed the locally approximated rigid fusions centered at the points of interest. The users then rated their confidence using a binary scale that the approximated rigid registration represented an accurate alignment of the local anatomy within approximately 3 mm. These ratings were then compared to the measured error in the deformable registration and compared to each other.

Figure 1
Deformable QA Method



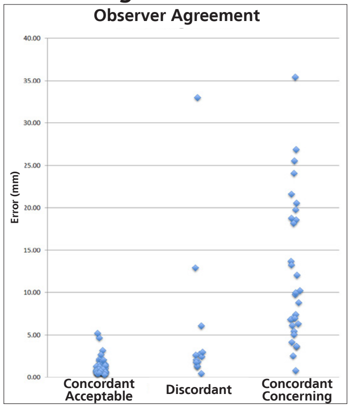
The best fit rigid registration is found, in a least squares sense, to the deformable registration that occurred within the sampling box. The registration is constrained so that the rigid vector at the center is exactly equal to the deformation vector.

Figure 2
Observer Ratings



Acceptable and concerning registration ratings versus the actual error at each point. Observers were advised displacements > 3mm would be concerning and < 3mm would be acceptable as estimated using Reg Reveal.

Figure 3
Oberver Agreement



Agreement in acceptable versus concerning registration ratings for each point. Points are plotted relative to the degree of error that was present at that point.

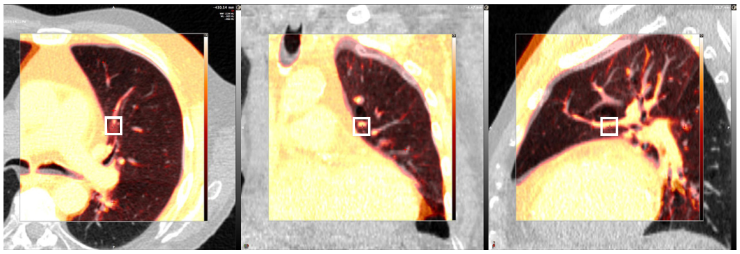
Results

The two users achieved a separation between good and concerning registrations with 91% and 92% accuracy, at a threshold of 3.1 mm and 2.4 mm respectively, (T-test, $p < 0.0000001$ for each user). Sensitivity for detecting errors greater than 5 mm was 86% and 97%, respectively. There was good agreement between the two observers, with a kappa of 0.72.

Conclusion

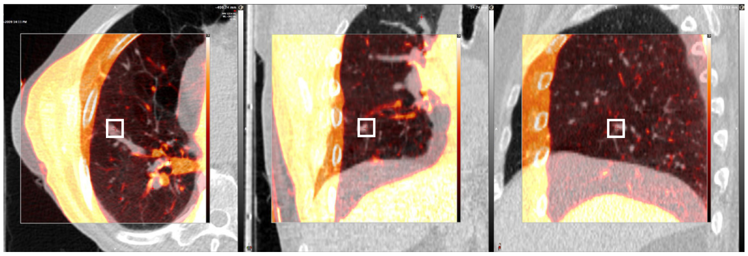
To the authors' knowledge, this framework is the first of it's kind to offer ad hoc evaluation of patient-specific deformable registration with no known ground truth. With an excellent detection rate for significant deformable registration errors and good agreement between observers, this framework shows promise for quality assurance evaluation of deformable image registration.

Figure 4
Acceptable Registration



Example of a good deformation resulting in good point to point correspondence between source and target images as well as demonstrating proper matching of anatomy within the sampling box.

Figure 5
Concerning Registration



Example of poor deformation resulting in no closely matching points between source and target image and improper matching of anatomy within the sampling box.

References

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