Purpose: To assess errors in online localization of deforming and regressing target structures, and to evaluate potential error reduction using rigid registration of individual featurelets distributed on the target surface.

Methods: Fifteen patients with locally advanced non-small-cell lung cancer received weekly CT scans throughout treatment under active breathing control. The primary gross tumor volume (GTV) was contoured on each image by a physician, including two GTVs for one patient. To eliminate patient setup errors during image acquisition, secondary images were manually registered to the reference image using bony anatomy. Initial errors were computed as the distance between centroids of the GTV from reference and secondary images in this alignment. Six separate rigid registrations were then performed to align featurelets contained by the left, right, anterior, posterior, superior, and inferior subvolumes of the GTV, including a 1 cm margin. A final translation was computed by averaging the two registrations along each patient axis. Residual errors were defined as the remaining distance between centroids of the GTV from reference and secondary images are gauged relative to bony alignment and to standard whole-target registration.

Results: The mean (standard deviation) of the absolute value of initial errors was 3.0 (2.7) mm, 3.8 (3.7) mm, and 3.6 (3.4) mm in the lateral, anterior-posterior, and superior-inferior directions, respectively. Whole-target registration reduced corresponding errors to as low as 1.6 (1.5) mm, 1.8 (2.0) mm, and 2.4 (2.3) mm. Featurelet registration provided the lowest absolute mean residual errors of 1.5 (1.3) mm, 1.4 (1.2) mm, and 1.9 (1.6) mm.

Conclusions: Featurelet registration demonstrated improved tumor centroid reproducibility compared to bony-anatomy and whole-target alignments. Future work includes automation and optimization of featurelet detection and subvolume definition.

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