

ATLAS-BASED SEGMENTATION: EVALUATION OF A MULTI-ATLAS APPROACH FOR PROSTATE CANCER

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Purpose

Manual contouring for prostate IMRT can be tedious and time consuming, making automatic segmentation approaches essential. In a previous study we demonstrated the time required to contour and edit a patient was reduced by 46% on average using a single best matched (SBM) atlas subject.¹ While offering significant time savings, a new multi-atlas approach has been shown to provide greater accuracy than SBM for cancer of the head and neck, liver, and lung.^{2,3,4} The goal of this study was to compare automatic segmentation results from a SBM atlas to the combined segmentation results from multiple atlas matches (multi-atlas) using a 98 subject prostate atlas containing targets and normal structures.

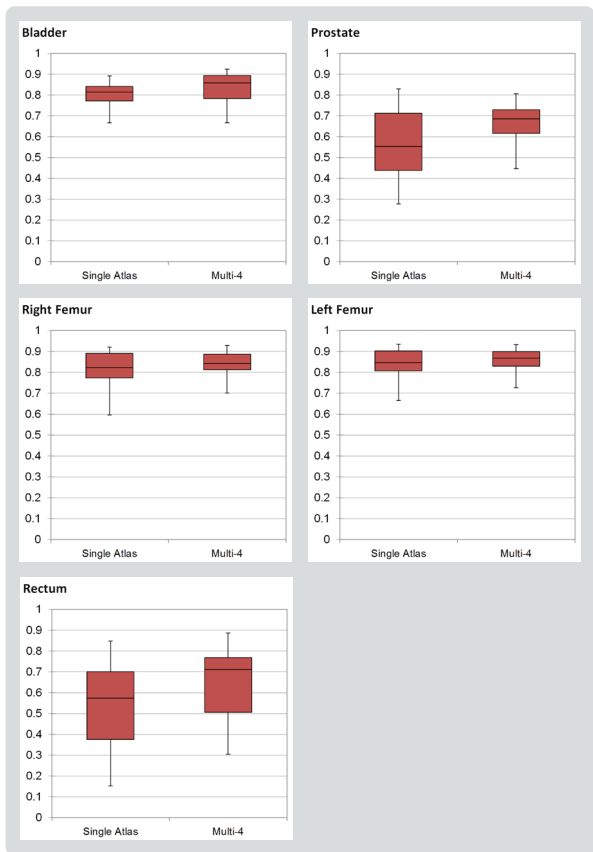
Materials/Methods

A prostate atlas containing 98 subjects was developed by a separate institution and utilized for atlas-based segmentation. Fifteen atlas subjects were selected for evaluation using a leave-one-out methodology. Atlas subjects contained manually defined contours for the bladder, left and right femur, prostate, and rectum. Automatic atlas contours were created using SBM and multi-atlas approaches. SBM used the automatically determined single best match for segmentation. Multi-atlas involved using multiple automatically determined best matches: Multi-3, Multi-4, and Multi-5. The final segmentation for multi-atlas was generated using Majority Vote which comprises the area of overlap for at least half of the individual segmentations (2 of 3, 2 of 4, and 3 of 5, respectively). Results were compared to manually defined "gold" standard contours using the average Dice Similarity Coefficient (DSC) for each structure. Overall percent improvement was calculated as the proportion of the error corrected by the method, or % difference on 1-DSC.

Results

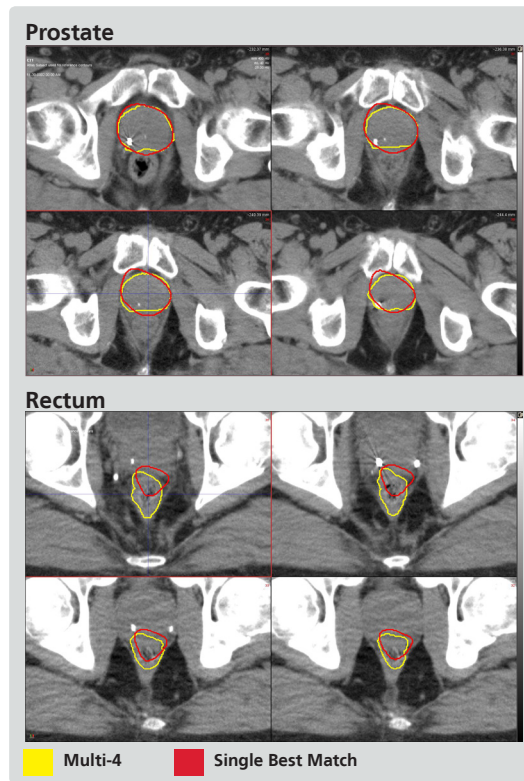
All multi-atlas methods were more accurate than SBM (p-value < 0.03) with average DSC of 0.752 +/- 0.165, 0.748 +/- 0.183, 0.743 +/- 0.177 for Multi-4, Multi-5, and Multi-3 respectively compared to 0.718 +/- 0.190 for SBM. Overall, Multi-4 and Multi-5 demonstrated the greatest improvement in accuracy over SBM with a 12% and 11% improvement respectively. Multi-3 showed an overall improvement of 9%. No statistically significant differences were observed between multi-atlas methods.

Figure 1
Average Dice Similarity Coefficient Comparison



Box and Whisker plots comparing the dice similarity coefficients for 1 and 4 atlas matches.

Figure 2
Patient Image



Comparison of segmentation results for the prostate and rectum for 1 and 4 atlas matches. Note the improved segmentation results with the greater number of atlas matches.

Table 1
Average Dice Similarity Coefficient

Structure	Single Atlas	Multi-3	Multi-4	Multi-5
Bladder	0.805	0.832	0.832	0.841
Prostate	0.597	0.629	0.650	0.640
Rectum	0.561	0.612	0.631	0.602
Right Femur	0.798	0.805	0.812	0.817
Left Femur	0.826	0.837	0.834	0.842
Overall	0.718	0.743	0.752	0.748

Average Dice Similarity Coefficient across 15 subjects using segmentation results from 1,3,4, and 5 best matches. Majority voting was used to combine segmentation results for multi-atlases.

Conclusions

The multi-atlas approach was more accurate than SBM for automatic contouring for prostate treatment planning. Although editing is still required, the multi-atlas method demonstrates further potential to decrease contouring time for prostate treatment planning.

Reference

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- 2 Pirozzi S, Piper J, Nelson AS. Atlas-based Segmentation: Comparison of Multiple Segmentation Approaches for Lymph Level Targets and Normal Structures in Head and Neck Cancer (HNC). International Journal of Radiation Oncology* Biology* Physics. 2011; 81 (Supplement): Page S828.
- 3 Horvat M, Pirozzi S, Nelson AS et al. Atlas-based Segmentation: A Comparison of Single and Multiple Atlas Matches for Automatic Liver Segmentation. Accepted for presentation at RSNA 2012.
- 4 Pirozzi S, Horvat M, Piper J, Nelson AS. Atlas-based Segmentation: Evaluation of a Multi-Atlas Approach for Lung Cancer. Med Phys 2012; 39:3677.