Interactive and Scale Invariant Segmentation of the Rectum/Sigmoid

via User-Defined Templates

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Introduction

Among all types of cancer, gynecological malignancies belong to the 4th most frequent type of cancer among women. Besides chemotherapy and external beam radiation, brachytherapy is the standard procedure for the treatment of these malignancies. In the progress of treatment planning, localization of the tumor as the target volume and adjacent organs of risks by segmentation is crucial to accomplish an optimal radiation distribution to the tumor while simultaneously preserving healthy tissue. Segmentation is performed manually and represents a time-consuming task in clinical daily routine. This study focuses on the segmentation of the rectum/sigmoid colon as an Organ-At-Risk in gynecological brachytherapy. The proposed segmentation method uses an interactive, graphbased segmentation scheme with a user-defined template. The scheme creates a directed two dimensional graph, followed by the minimal cost closed set computation on the graph, resulting in an outlining of the rectum. The graphs outline is dynamically adapted to the last calculated cut. Evaluation was performed by comparing manual segmentations of the rectum/sigmoid colon to results achieved with the proposed method.

Results

For evaluation of the introduced approach, datasets have been used where the appearance of the rectum/sigmoid colon strongly varies. From each dataset to another, its shape, size, slice thickness and grey value distribution alter in no predictable manner. The data used for this experiment is a set of seven MRI datasets acquired during gynecological interstitial brachytherapy cases⁶⁻⁸. For comparison of the algorithmic computed segmentation result, a medical doctor experienced in radiological segmentations of gynecological brachytherapy manually outlined the rectum/sigmoid two times with a time difference of several months (Figure 3). Computation was performed in MeVisLab⁹ on a personal computer with an Intel® Core[™] i3 CPU M330 with 2.13 GHz dual core, which enabled the interactive algorithm to run smoothly without any delay or interruptions. In addition, the time in seconds for the segmentation of each dataset was acquired by screen capture recordings. The comparison of the algorithmic to manual results yielded to a Dice Similarity Coefficient (DSC) value of $83.85 \pm 4.08\%$, in comparison to $83.97 \pm 8.08\%$ for the comparison of two manual segmentations of the same physician. Utilizing the proposed methodology resulted in a median time of 128 seconds per dataset, compared to 300 seconds needed for pure manual segmentation.

Methods

The methodology is based on a graph network and has been developed during a German diploma thesis. The approach is a consistent further development of previous publications where different templates have been used to create a graph¹⁻⁵. However, in these publications fixed pre-defined shapes have been used for the segmentation process, e.g. a square template for 2D vertebra segmentation in sagittal slices. Thus, these approaches were not able to handle segmentations of structures that vary in anatomy shape from patient to patient. In summary, we solve this problem by letting the user define an individual template by simply outlining the structure contour in the first slice (Figure 1). Thereafter, this initial information is used to automatically construct a specific graph to segment consecutive slices (Figure 2). After the complete object is segmented, slices that have been skipped by the user have to be interpolated in order to generate an object contour in each image slice. Thereafter, the set of object contours is used for voxelization of the object and to generate a 3D Object. The set of object contours is stored as cso file, while the voxelized 3D object is stored as nrrd file for further use in treatment planning.



Figure 3 – Segmentation results for two datasets (1), (2). Red shows the interactive and green the manual segmentations, and brown the overlap. On the right side the 3D result of an interactive segmentation is shown (3).

Conclusions

The objective of this contribution was the development of a novel interactive graph-based segmentation methodology for the rectum/sigmoid colon as an Organ-At-Risk in the context of interstitial gynecological brachytherapy. The clinical gold standard for segmentation tasks is given by time and resource consuming slice-by-slice manual outlining of the region of interest. Although various fully automatic segmentation tools have been developed up to date, none of these have found their way into clinical practice. One drawback of automatic approaches is their complexity, limited flexibility and little provided user influence on the computed segmentation result where the algorithm is challenged. Thus, manual refinement of the computed segmentation is desirable and the motivation for the development of interactive segmentation approaches that allow direct and intuitive control over the segmentation result. Evaluation of the algorithm was performed by comparing the computer assisted segmentation results with manual expert segmentations of the rectum/sigmoid colon. There are several areas of future work: due to the star-like graph node distribution with the seed point at its origin, the algorithm was challenged where the object shape was particularly concave or convex. For future approaches multiple, equally distributed seed points could be utilized to guarantee an ideal areal sampling of the object and thus enhance the segmentation quality. Finally, the approach can be used to segment other longitudinal/tubular structures, like fiber tracts¹⁰⁻¹² or the aorta to support the time-consuming analysis of aortic aneurysms¹³⁻¹⁶, which then can be used for virtual stenting^{17,18}.



Figure 1 – The rectum is manually outlined (yellow) to define a user-defined template for a segmentation graph.



Figure 2 – Graph construction via a user-defined template: the manually outlined rectum (yellow) is used to calculate the graph's center point (blue, left image), next the graph's nodes are sampled (red, middle image) and finally the whole graph is constructed (red, right image).

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