

Bladder Segmentation for Interstitial Gynecologic Brachytherapy with the Nugget-Cut Approach

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Purpose

Gynecologic malignancies, which include cervical, endometrial, and vaginal/vulvar cancers, are the 4th leading cause of death in women in the US, with 83,750 new cases in the US in 2010 and 26,930 deaths per year [1]. Treatment consists of concurrent chemotherapy and external beam radiation followed by brachytherapy. The clinical practice of brachytherapy is well characterized using five components: 1) Applicator Choice and Insertion Techniques 2) Imaging Protocol 3) Contouring Protocol 4) Treatment Planning 5) Dose and Fractionation. Details of each institutional experience are provided in the textbook of Viswanathan et al. [2] and its references. With this work we want to support the time consuming Contouring Protocol, more precise the segmentation of the bladder.

Methods

Our overall method starts by setting up a directed 3D graph from a user-defined seed point that is located inside the bladder. To set up the graph, the method samples along rays that are sent through the surface points of a polyhedron with the seed point as the center (Fig. 1).

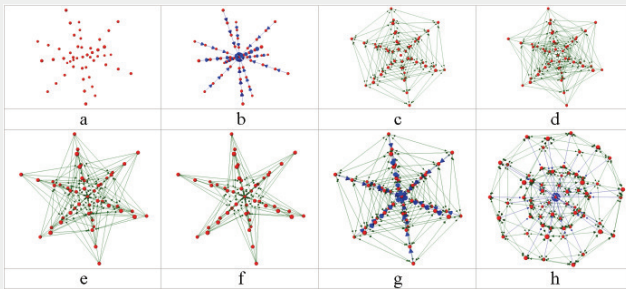


Figure 1: Principle of graph construction. a) five sampled points (red) along each of the 12 rays that provide the nodes for the graph. b) edges between the nodes belonging to the same ray. c) edges between nodes of different rays for $\Delta_r=0$, d) $\Delta_r=1$, e) $\Delta_r=2$ and f) $\Delta_r=3$. g) complete graph for $\Delta_r=0$. h) complete graph with 32 surface points, 3 nodes per ray and $\Delta_r=0$.

The sampled points are the nodes $n \in V$ of the graph $G(V,E)$ and $e \in E$ is the corresponding set of edges. There are edges between the nodes and edges that connect the nodes to a source s and a sink t . After the graph has been constructed, the minimal cost closed set on the graph is computed via a polynomial time s-t cut [3], creating the segmentation of the object (Fig. 2).

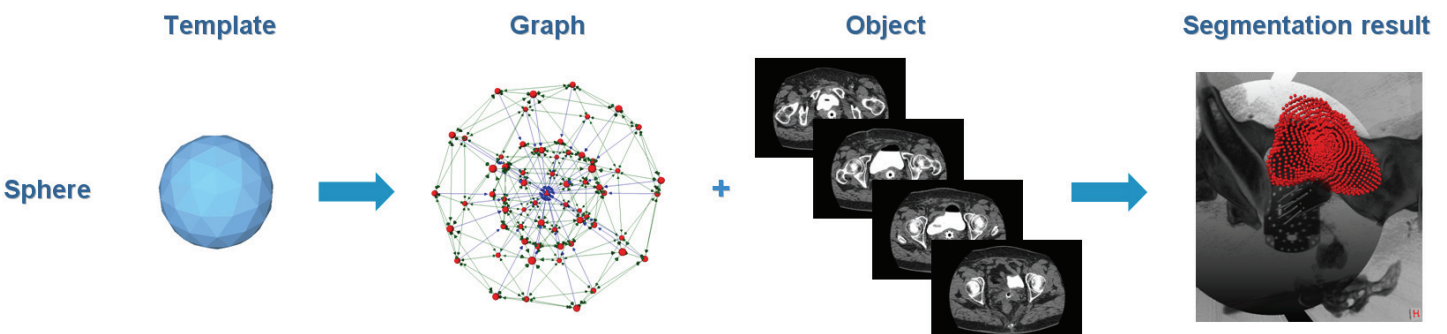


Figure 2: Overall workflow of the presented segmentation approach. A Sphere (left) is used to construct directed 3D graph from a user-defined seed point that is located inside the bladder (middle). Then, the minimal cost closed set on the graph is computed via a polynomial time s-t cut, creating an optimal segmentation of the bladder's boundary and volume (right).

Results

For testing the presented segmentation method we used a C++ implementation within the medical prototyping platform MeVisLab (see <http://www.mevislab.de>). The overall segmentation – sending rays, graph construction and mincut computation – in our implementation took about one second on an Intel Core i5-750 CPU, 4x2.66 GHz, 8 GB RAM, Windows XP Professional x64 Version, Version 2003, SP 2. The left image of Figure 3 shows the segmentation result of a bladder (red) on a 2D slice with the user-defined seed point (blue) located inside the bladder. The image in the middle visualizes a triangulated model of the segmented bladder (yellow/green) faded into the Computed Tomography (CT) dataset. The image on the right displays the 3D mask of the bladder (red).

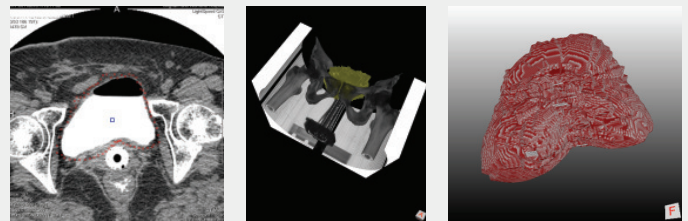


Figure 3: Left: segmentation result of a bladder (red) on a 2D slice with the user-defined seed point (blue) located inside the bladder. Middle: triangulated model of the segmented bladder (yellow/green) faded into the Computed Tomography (CT) dataset. Right: 3D mask of the bladder (red).

Conclusions

In this contribution, we present a segmentation method for the bladder. The method is based on an algorithm we developed recently in a previous work where the novel segmentation scheme was successfully used for segmentation of glioblastoma multiforme (GBM) and provided an average Dice Similarity Coefficient (DSC) of 80% [4]. For bladder segmentation, the original scheme was used, creating a directed 3D-graph within two steps: sending rays through the surface points of a polyhedron and sampling the graph's nodes along every ray. The center of the polyhedron was user-defined and located inside the bladder. Then, the minimal cost closed set on the graph is computed via a polynomial time s-t cut, creating an optimal segmentation of the bladder's boundary and volume.

References

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