Prostate Central Gland Segmentation Using a Spherical Template Driven Graph Approach

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Purpose – Prostate cancer is the most abundant cancer in men, with over 240,000 expected new cases and around 28,000 deaths in 2012 in the US alone [1]. Accurate risk stratification for each individual cancer is central to a successful treatment strategy, especially because of the high incidence rate of less aggressive prostate cancers, and the high complication rate of radical prostatectomy. Diagnostic prostate magnetic resonance imaging (MRI) and MRI guided prostate biopsies have demonstrated improved diagnostic discrimination rates of the different types of cancer [2]. Our goal is to enhance the state of the art in automated segmentation (i.e. delineation) of organ limits for the prostate, a step that has been shown to facilitate efficient MR-guided biopsy.

Methods – The *Nugget-Cut* scheme [3] was used for prostate center gland segmentation on 5 datasets [4]. It sets up a directed 3D-graph $G(V,E)$ in two steps: (I) sending rays through the surface points of a polyhedron and (II) sampling the graph's nodes $n \in V$ along every ray (Figure 1). Additionally, a corresponding set of edges $e \in E$ is generated, which consists of edges
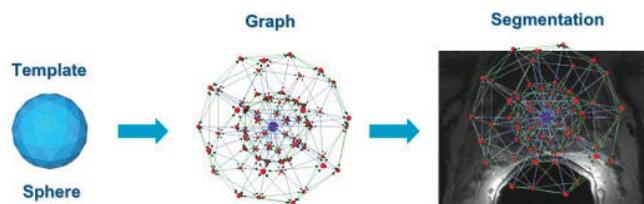

Fig 1. Nugget-Cut Scheme: A template is used as a basic structure for the segmentation graph

between the nodes and edges that connect the nodes to a source s and a sink t. After graph construction – the center of the polyhedron was defined by the user and located inside the prostate center gland – the minimal cost closed set on the graph is computed via a polynomial time *s-t-cut* [5], which results in the segmentation of the prostate center gland's boundaries and volume. A C++ module was implemented within the medical prototyping platform MeVisLab (see http://www.mevislab.de) for evaluation. Results were compared to an expert segmentation using the Dice Similarity Coefficient (DSC).

Results – A DSC of 85 ± 6.0% overlap was achieved compared to expert segmentation. This is an improvement on recent 80% DSC reported in the literature [6]. In our C++ implementation the overall segmentation: (1) sending rays, (2) graph construction and (3) *mincut* computation, took about one second on *an Intel Core i7 CPU, 4x2.50 GHz, 8 GB RAM*. Figure 2 shows the segmentation result of a prostate central gland (red) on an axial and a sagittal 2D slice with the typical user-defined seed point position on the axial slice (blue arrow) located inside the organ.
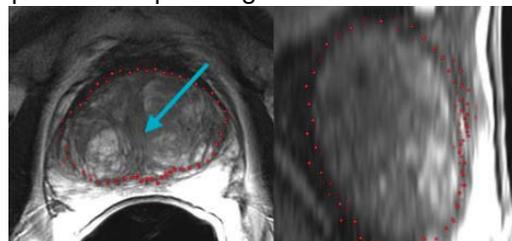

Fig 2. Segmentation results in axial and sagittal reformatting (blue arrow: seed point)

Conclusions – In this abstract, we present segmentation results for the prostate gland in MRI data using a recently developed method. A graph driven method has been used that is based on a spherical template. The algorithm prefers spherically- and elliptically-shaped 3D objects and has already been evaluated with glioblastoma multiforme, pituitary adenoma and cerebral aneurysm data [7]. There are several areas of future work including comparison with level-set based prostate segmentation methods such as [8], extensions for automatic segmentation of structures adjacent to the central prostate gland, such as the peripheral prostatic zone. An immediate next application for MR-guided biopsy is the generation of regions of interest towards automatic registration of preoperative to intraprocedural images.

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