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BIO SIGNAL

International Biosignal Processing Conference Humboldt University of Berlin, Charité, July 14-16, 2010, Berlin, Germany

PITUITARY ADENOMA SEGMENTATION

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Introduction:

Sellar tumors

- approximately 10-15% among all intracranial neoplasms
- most common sellar lesion is the pituitary adenoma
- **Pituitary adenoma**
- lesions can be classified according to size or hormone-secretion
- surgery is in most cases possible via a transsphenoidal approach
- Clinical follow-up
- in cases of continuous (mostly one-year) MRI follow-up, tumor-volume should be rigidly registered over the time so that a progress is not missed
- volumetric assessment of a tumor using manual segmentation is a time-consuming process

Methods:

Novel segmentation scheme for spherical objects

- sending rays through the surface points of a polyhedron
- sampling the graph's nodes along every ray

After graph construction

minimal cost closed set on the graph is computed via a polynomial time s-t cut • arcs A_r between nodes of different rays enforce smoothness via the parameter Δ_r



Figure 2: Principle of a cut of edges between two rays for Δr=1. Left and middle: Same cost for a cut (2•∞). Right: Higher cost for a cut (4•∞)



Figure 4: Segmentation results for a pituitary adenoma data set with user-defined seed point (blue)

Results:

Methods were implemented in C++ in the MeVisLab environment. Results were applied to magnetic resonance imaging (MRI) datasets with pituitary adenoma 10 clinical datasets were used and manual segmented by experts (neurosurgeons)

- the average Dice Similarity Coefficient for all ten datasets was 77.49%

SUMMARY OF RESULTS: MIN., MAX., MEAN AND STANDARD DEVIATION FOR 10 PITUITARY ADENOMAS.						
	Volume of tumor (cm3)		Number of voxels		DSC (%)	manual segmentation
	manual	algorithm	manual	algorithm	DSC (%)	time (min)
min	0.84	1.18	4492	3461	71.07	3
max	15.57	14.94	106151	101902	84.67	5
$\mu \pm \sigma$	6.30 ± 4.07	6.22 ± 4.08	47462.7	47700.6	77.49 ± 4.52	3.91 ± 0.54





Axial slice of a pituitary adenoma (left). 3D mask of a segmented pituitary adenoma (right)





Figure 3: Principle of graph construction. 5 (left) and 3 (right) sampled points (red) along each of the 12 (left) and 32 (right) rays that provide the nodes for the graph



Figure 5: Different views of sagittal slices with segmented pituitary adenoma

Conclusion:

In this paper, a method for pituitary adenoma segmentation was presented. 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 and provided an average Dice Similarity Coefficient (DSC) of 77%. For automatic and adequate adenoma 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 is hereby user-defined and located inside the adenoma. Then, the minimal cost closed set on the graph is computed via a polynomial time s-t-cut, creating an optimal segmentation of the adenomas boundary and volume.

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