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A FLEXIBLE SEMI-AUTOMATIC APPROACH FOR GLIOBLASTOMA MULTIFORME SEGMENTATION

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Introduction:

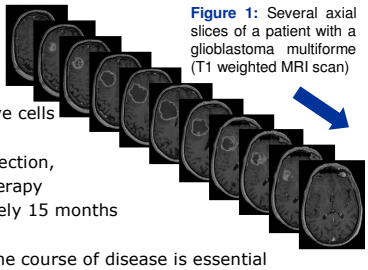

Figure 1: Several axial slices of a patient with a glioblastoma multiforme (T1 weighted MRI scan)

Gliomas
- most common primary brain tumors
- evolving from the cerebral supportive cells

Glioblastoma multiforme (GBM)
- therapy contains maximum safe resection, percutaneus radiation and chemotherapy
- survival rate is still only approximately 15 months

Clinical follow-up
- evaluation of the tumor volume in the course of disease is essential
- 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

Graph construction
- sampled points are the nodes $n \in V$ of the graph $G(V,E)$ and $e \in E$ is a set of edges
- edges between the nodes and edges that connect the nodes to source s and sink t

Extra seed points / User-defined restrictions
- rays that contain an additional user-defined seed point are set "fixed"
- binding all "following" nodes of a considered ray with maximum weight to the source
- and "previous" nodes – including the additional seed point – with maximum weight to the sink

This graph construction forces the mincut to follow the user's input for *s-t* cut!

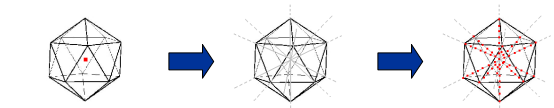

Figure 2: Principle of sampling the graph's nodes (red points in the rightmost image)

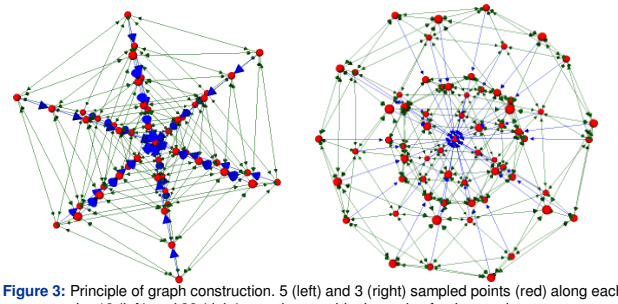

Figure 3: Principle of graph construction. 5 (left) and 3 (right) sampled points (red) along each of the 12 (left) and 32 (right) rays that provide the nodes for the graph

$$\frac{\sum_{i=1}^{s} \int_{-d/2}^{d/2} \int_{-d/2}^{d/2} \int_{-d/2}^{d/2} T(s_x + x, s_y + y, s_z + z)\,dx\,dy\,dz}{s} \quad | \; s > 0$$

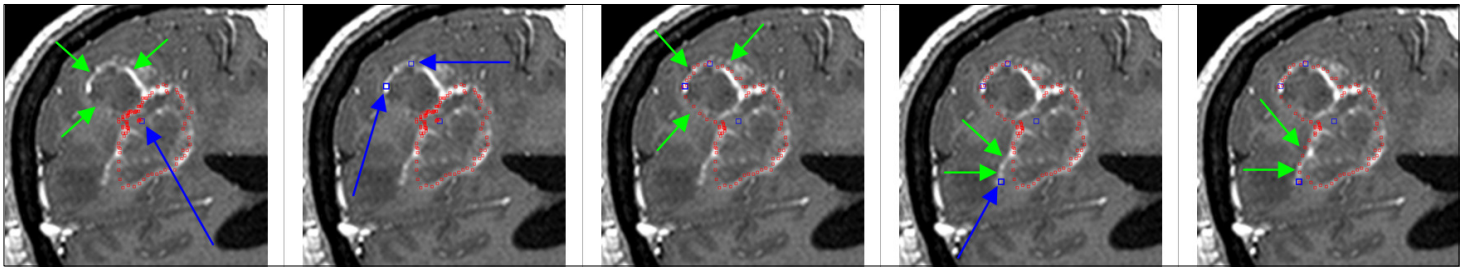

Figure 4: Principle of applying additional seed points that support the one click algorithm

Results:

The methods were implemented in C++ in the MeVisLab environment and applied to magnetic resonance imaging (MRI) datasets with GBM

One click and semi-automatic tumor Segmentation
- 12 clinical datasets were used and manual slice-by-slice segmentation was performed by experts (neurosurgeons)
- the semi-automatic approach supported the algorithm by 15 to 75 additional user-defined seed points
- the average Dice Similarity Coefficient (DSC) for all datasets was 77.72% (one click method) and 83.91% (semi-automatic approach)

TABLE I
SUMMARY OF RESULTS: MIN., MAX., MEAN AND STANDARD DEVIATION FOR 12 GLIOMAS.

	Volume of tumor (cm^3)			Number of voxels			$DSC_{oneClick}$ (%)	DSC_{semi} (%)
	manual	one click	semi	manual	one click	semi		
min	2.38	0.99	0.99	2694	993	993	53.76	72.61
max	86.91	65.6	67.51	283011	252316	252316	91.96	91.96
$\mu \pm \sigma$	21.02 ± 26.48	15.55 ± 20.18	20.31 ± 22.16	57278.33	45461.50	58196.67	77.72 ± 13.19	83.91 ± 6.91

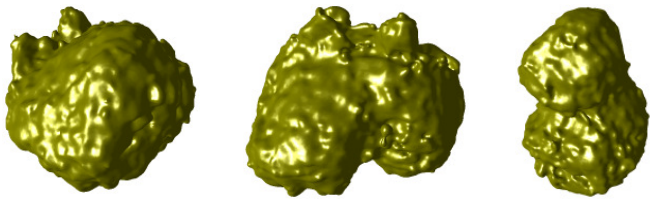

Figure 5: Three 3D models of (semi-) automatically segmented tumors

Conclusion:

In this work, a flexible semi-automatic approach for World Health Organization grade IV gliomas (Glioblastoma multiforme) has been introduced. The presented approach uses a new segmentation scheme for spherically shaped objects and creates a 3D graph in two stages: In the first stage, rays are sent through the surface points of a polyhedron, and in the second stage, the graph's nodes are sampled along the ray. Afterwards, the minimal cost closed set on the constructed graph is computed via a polynomial time s-t cut, resulting in an optimal segmentation of the tumor and therefore the also the tumor boundaries. There are several areas of future work. For example, the presented segmentation scheme can be enhanced with statistical information about shape and texture of the desired object.

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