

Abstract 750

A topological method for automatic segmentation of glioblastoma in MR FLAIR for radiotherapy

Session Type: Scientific Session

Topic: Clinical Applications / Brain (excluding functional and MRS)

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Purpose / Introduction

Glioblastoma (GBM) is an intracranial tumor composed of infiltrating necrotic masses. GBM appears hyperintense in postoperative FLAIR, and it is possible to distinguish two compartments: tumor, and vasogenic edema, having slightly different histograms. Automatic segmentation of GBM constitutes an active research field [1,3,4,5]. We propose a novel, fully-automated method, employing recent developments in spatial model checking [2,6,7], permitting automated identification of image regions via machine-executable specifications. Such specifications exploit topological features (proximity, connectedness, distance, reachability, ...) and texture similarity operators.

Subjects and Methods

The method has been assessed using datasets of 7 patients affected by GBM that have undergone radiotherapy from 2014 to 2017. The datasets consist of skull-stripped postoperative FLAIR and CT and contours used for planning in radiotherapy. The method we define consists of the following steps, directly performed on the whole 3D image volume. Step 1 is an external pre-processing, whereas steps 2-4 are done via spatial model checking.

- 1) Affine co-registration of FLAIR and CT volumes.
- 2) Identification of anomalies in FLAIR via statistical texture analysis, selecting brain voxels in an area with different histogram (cross-correlation < 0.3) from that of the whole brain.
- 3) Automatic selection, in the ROI from step 2, of regions satisfying the pattern: "two hyperintense regions with different mean intensity connected to each other".
- 4) Expansion of the ROI from step 3 to include sub-clinical disease spread.

Results

Segmentation results were evaluated using the DICE coefficient (DICE) and the percent (0.95) Hausdorff distance (HD) between our segmented volumes and the Clinical Target Volume (CTV) manually delineated on CT by an expert radiotherapist for planning. Tests were performed on a machine with an intel i7 CPU and 8GB of RAM. Average execution time per patient (3D image size: 256x256x40) was 10min, improving the state of the art (see e.g. [5]). Results are shown in table 1. In figures 1,2 we show the result of our segmentation (blue+green ROI) and the CTV (yellow ROI).

Table 1. Score of comparison with manual segmentation

	Mean	Std. Dev.	Median	Range(min-max)
DICE(%)	87	2	87	78-89
HD(mm)	3.50	1.20	3.18	2.47-5.45



