

Semantic segmentation of brain tumor MRI scans

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Abstract

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I. MOTIVATION

Gliomas, and in particular glioblastomas, are the most common and aggressive types of malignant tumor that affects the central nervous system in adults. Glioma patients do not have favorable prognoses, and the current standard for treatment is surgery in combination with radiotherapy and chemotherapy. Glioblastomas present with a wide heterogeneity in appearance, shape and histology, and the diagnosis typically is formulated after a magnetic resonance imaging (MRI) of the patient's brains. A problem in diagnosing a glioblastoma is due to the low pixel intensity differences in the boundaries of the tumor, as well as the wide range of shapes it can manifest in. These factors result in a difficult precise identification of the boundaries of the tumor within the brain, even for expert diagnosticians.

For these reasons it is apparent that automated techniques of tumor detection are needed in order to improve patient prognoses and make the diagnostician's job easier.

II. OBJECTIVES

The main goal of this project is to benchmark methods to automatically produce segmentation labels for sub-regions of brain MRI scans where a glioma is present. The diagnostically relevant segmentation labels that need to be produced are the "enhancing tumor", "non-enhancing tumor", "edema" and "background", which describe the three main regions of a tumor and the surrounding healthy brain tissue.

Secondarily, the goal is to compare the different image segmentation methods, between each other as well as between themselves with varied parameters.

III. DATASET

For this task the BraTS 2021 dataset [1] was used, which is a collection of 484 multi-parametric MRI (mpMRI) scans of brains whose diagnosis of glioma was pathologically confirmed. The dataset is split into a set of mpMRI scans and a set of labels associated to them. All files are stored in NIfTI format (.nii.gz), which is a standard commercial format for MRI scans.

An mpMRI scan contains a 4D array of dimension (240,240,155,4), whose first three dimensions are the x, y and z coordinates of each voxel in the 3D volume, while the fourth dimension represents one among four possible pixel intensity enhancements that were applied to the voxel:

- 0: FLAIR (Fluid Attenuated Inversion Recovery)
- 1: T1w (T1-weighted)
- 2: T1gd (T1-weighted with contrast enhancement)
- 3: T2w (T2-weighted)

A label file contains a 3D integer array of dimension (240,240,155) whose values are the four possible labels:

- 0: Background
- 1: Edema
- 2: Non-enhancing tumor
- 3: Enhancing tumor

Having access to 484 fully labeled images, 80% (i.e. 388) of the dataset was used as training data, while 20% (i.e. 96) of it was used for validation.

IV. METHODOLOGY

V. EXPERIMENTS AND RESULTS

VI. CONCLUSIONS

REFERENCES

- [1] U.Baid, et al., "The RSNA-ASNR-MICCAI BraTS 2021 Benchmark on Brain Tumor Segmentation and Radiogenomic Classification", arXiv:2107.02314, 2021.