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My Thesis

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To the infinity and beyond

Abstract

Contents

Chapter 1

Introduction

Image segmentation (IS) is the process of partitioning an image into multiple image segments or objects. The goal of segmentation is to simplify the representation of an image into something that is more meaningful and easier to analyze. IS is a critical task in medical image analysis: it is often the first step to transform raw biomedical image into structured, valuable information ready to be used both for scientific discoveries and clinical applications including early diagnosis during preclinical phase, therapy planning, intraoperative assistance and tumor growth monitoring. Brain tumor segmentation is the process of isolating the tumor from healthy brain tissue; however, it is still a challenging task due to the irregular form and confusing boundaries of tumors.

Simply put, one major challenge is the lack of open datasets for designing and testing new algorithms, while private datasets may differ for so many aspects that comparing the result obtained by different solutions has no relevance and it's often inconclusive. On the other hand, with the availability of large common datasets, as the ones used in public challenges focused on medical images, more structured and comparable researches can be done. With the abundance of these data and the advent of the Vision Transformer (ViT) architecture in late 2020, a new trend in the field of medical image segmentation has spread quickly: the proposed algorithms have become more complex both in term of capacity (estimated in number of parameters), sometimes neglecting simpler, yet promising solutions.

Being conscious of my hardware limitations, the impracticability of training very large models and even the difficulties of making continuous training sessions, I had to devise a clever way to train a "good enough model" in the most effective and reproducible way, while tracking the training processes in a fashion s.t. results of different experiments were easily comparable. For this reason I leveraged deep learning frameworks for professional AI researchers for code organization and accelerating research in Medical Imaging, with the intent to create a personal baseline to confront with, and flexibly expand my solution with new parts. Many official guides, as well as research papers present long training sessions (from hundreds to thousands epochs) and the few that show how the training process evolved, share the fact that the learning curves are very noisy for most of the time and only at the very end they reach a convergence point. The only exception seems to be the ViT based architectures, but they incur more easily into overfitting. What I tried to obtain

was a flexible, relatively small model capable of learning without overfitting even with little data and in few epochs, so to have as quickly as possible a considerable amount of different "prototypes" to refine.

The work is organized as follow: ...

Chapter 2

The Challenge

The International Multimodal Brain Tumor Segmentation (BraTS) challenge is an event held in conjunction with the Medical Image Computing for Computer Assisted Intervention (MICCAI) conference. In it, prominent computational scientist and clinical researchers present their work on glioma, sclerosis and other brain injuries from every kind of point of view, but with a major focus on segmentation, prognosis and other applications for the clinical context.

Every year (from 2012), BraTS make publicy available a manually annotated dataset of preoperative brain tumor scans from different international institutions to assess the advances in the automated brain tumor segmentation task, using multiparametric MRI (mpMRI) scans. It is worth to be noted that from 2021, the challenge focuses also on a second task: the evaluation of classification methods to predict the MGMT promoter methylation status at preoperative baseline scans, since it has been identified as a strong and independent predictive factor of favorable survival in glioblastoma patients undergoing chemotherapy with alkylating agents.

Amongst brain tumors, glial tumors comprise 60% of the tumors. They are a common cause of mortality in both young and old people, with a substantial male dominance for the higher grades gliomas. Within the gliomas, Glioblastoma (GBM) and diffuse astrocytic glioma (WHO Grade 4 astrocytoma) are the most common and aggressive primary malignant brain tumors, comprising more than 16% of all primary brain and central nervous systems neoplasms. The typical survival range (prognosis) for these kind of tumors is about 1 year and the current standard of care treatment comprises surgery, followed by radiotherapy and chemotherapy. The use of MRI and diffusion tensor imaging (DTI) in preoperative planning, as well as ultrasound, CT scans, and MRI with direct stimulation during surgery, has allowed for multimodal neuronavigation and the integration of patient-specific anatomic and functional data. Despite these technologies, differentiating between normal brain and residual tumor continues to be a major challenge, and the use of an appropriate dye for fluorescence guidance has been found to be more effective then conventional neuronavigation-guided surgery alone.

The challenge requires to develop new method (or improve an existing one) being able to produce segmentation labels of the different glioma sub-regions considered for the evaluation: "enhancing tumor" (ET), "tumor core" (TC) and "whole tumor" (WT). ET is a region showing hyper-intensity in T1Gd w.r.t. healthy white matter,

but also T1 modality; TC is the bulk entailing the ET and the necrotic (NCR) parts of the tumor, and it is the section that is typically resected: surgical removal of as much of a tumor as possible (tumor debulking) has the double benefit of enhancing the effects of chemo and radiation therapies and alleviating the pain due to the symptoms. The WT covers the entire extent of the tumor, entailing TC and the accumulation of fluid in the intracellular or extracellular spaces (cerebral edema, ED).

Chapter 3

Fundamentals of magnetic resonance imaging

3.1 Nuclear Magneic Resonance

Before deep dive into my work, let's have a small digression about the physics behind MRI in order to have an intuition on how MRI images are generated, and understand the the type of data I have worked on. Differently from computed tomography (TC) and PET scans, MRI does not use neither X-rays not ionizing radiation: it applies nuclear magnetic resonance (NMR), producing better contrast in images of soft-tissue, like the tissue in the brain. The core idea behind NMR is to immerse the area to be imaged in a strong and constant magnetic field, then perturbate the nuclei in that area with by a weak magnetic field, capture their response emitted under the form of an electromagnetic signal with a receiving coil. The contrast between different tissues is determined by the rate at which excited atoms return to the equilibrium state. The whole process occurs near resonance, when the oscillation frequency matches the intrinsic frequency of the nuclei, which depends on the strength of the static magnetic field, the chemical environment and the magnetic properties of the isotope involved. Hydrogen isotope ^{1}H (protium) is the most commonly used nucleus for clinical MRI due to its abundance in biological system and the possibility of fast acquisition given by its short relaxation time (see 3.2).

3.2 Relaxation

Chapter 4

Related Works

Chapter 5

SOTA Architectures and Procedures

Chapter 6

The Data

Chapter 7

Experimental Design and Result

Chapter 8

Conclusions and Future Work