

What?

This document aims to provide a summary of our research based on listing and documenting available models for our project. Available models are brain segmentation related models that should at least cover the tumor segmentation task, but not limited to it.

Each model listed should follow the format above

Model Name

Github Link: Github link of the model for reproduction, or for reference

Model: Corresponding model from model definitions

Dataset: Corresponding dataset definition from dataset definitions

Input: Expected inputs of the model, e.g., 4 types of MRI images

Output: Expected output of the model, e.g., Brain segmentation for tumor

Metrics: Metrics related to the model, if available

Additional Notes: Any additional note related to the model

We hope this document will be a good baseline for our future deep learning model related tasks.

Dataset Definitions

Medical Decathlon Brain Tumors

This dataset refers to the dataset defined in Medical Decathlon[1] as:

Target: Segmentation labels of the different glioma sub-regions

Modality: Multimodal multisite MRI data

- native (T1)
- post-contrast T1-weighted (T1Gd)
- T2-weighted (T2)
- T2 Fluid Attenuated Inversion Recovery (T2-FLAIR)

Size: 750 4D volumes (484 Training + 266 Testing)

Source: BRATS 2016 and 2017 datasets [7].

BraTS'21

Data: Multimodal multisite MRI data (T1, T1gd,T2, T2-FLAIR)

Target: Segmentation labels of the different glioma sub-regions

Modality: Multimodal multisite MRI data

- native (T1)

- post-contrast T1-weighted (T1Gd)
- T2-weighted (T2)
- T2 Fluid Attenuated Inversion Recovery (T2-FLAIR)

Size: MRI Size: 1470 3D volumes (1251 Training + 219 Validation)

Dataset used in the BraTS challenge[3, 4, 5] in 2021. See paper [The RSNA-ASNR-MICCAI BraTS 2021 Benchmark on Brain Tumor Segmentation and Radiogenomic Classification](#) for more information on BraTS 2021 challenge.

Dataset comprises of “multi-parametric MRI (mpMRI) scans of glioma, with pathologically confirmed diagnosis and available MGMT promoter methylation status”[6]

A good aspect of this dataset is that it **comprises multi-institutional images captured with different equipment and imaging protocols**. Even our small set of data collection (sent initially by Dr. Şahin) **includes samples with different resolutions and qualities**, hence this property of the dataset makes itself a great choice for us in terms of model selection and training. This also enables the possibility of **extending our work to other hospitals with possibly less fine-tuning**.

The paper also talks about the **preprocessing operations involved while transforming DICOM to NIFTI file format**. Currently, we use the corresponding **conversion function offered by MONAI**, however, we may also want to look at the operations done here to further develop our methodology. The main advantage of this conversion is getting rid of the header metadata stored by a DICOM file, thus it **removes all Patient Health Information (PHI)**. Their preprocessing pipeline is available through Cancer Imaging Phenomics Toolkit (CaPTk) [9] and Federated Tumor Segmentation (FeTS) [8] tool.

The paper also gives information about how the annotation process is done. After the preprocessing operation, they **used top-performing models on the previous challenge (BraTS'20) and fused their segmentation outputs as initial segmentation**, and post-processed these segmentations by expert neuroradiologists. Their pipeline is again available through FeTS [8] tool, though they also explain the flow:

“To facilitate the annotation process for BraTS 2021, initial automated segmentations were generated by fusing previously top-performing BraTS methods. The specific methods fused were the DeepMedic, DeepScan, and nnUNet, all trained on the BraTS 2020 dataset. The STAPLE label fusion was used to aggregate the segmentation produced by each of the individual methods, and account for systematic errors generated by each of them separately. All these segmentation methods and the exact pipeline used to generate the fused automated segmentation has been made publicly available through the Federated Tumor Segmentation (FeTS) platform.” [6]

The challenge consists of two tasks

1. Tumor Sub-region Segmentation
 - a. Produce segmentation labels of the different glioma sub-regions
 - b. The sub-regions considered for evaluation are
 - i. "enhancing tumor" (ET)

1. The ET is described by areas that show hyper-intensity in T1Gd when compared to T1, but also when compared to “healthy” white matter in T1Gd.
- ii. “tumor core” (TC)
 1. The TC describes the bulk of the tumor, which is what is typically resected. The TC entails the ET, as well as the necrotic (NCR) parts of the tumor. The appearance of NCR is typically hypo-intense in T1-Gd when compared to T1.
- iii. “whole tumor” (WT)
 1. The WT describes the complete extent of the disease, as it entails the TC and the peritumoral edematous/invaded tissue (ED), which is typically depicted by hyper-intense signal in FLAIR.

2. Brain Tumor Radiogenomic Classification

- a. “predict the MGMT [promoter methylation](#) status”[6] what is it? Why is it important?

*“The release of the current revised World Health Organization (WHO) classification of Central Nervous System (CNS) tumors highlighted the appreciation of integrated diagnostics, and transitioned the clinical tumor diagnosis from a purely morphological histopathologic classification to integrating molecular-cytogenetic characteristics. O-methylguanine-DNA methyltransferase (MGMT) is a DNA repair enzyme that the **methylation of its promoter** in newly diagnosed Glioblastoma (GBM) has been identified as a **favorable prognostic factor** and a **predictor of chemotherapy response**. Thus, determination of MGMT promoter methylation status in newly diagnosed GBM **can influence treatment decision making**.”[6]*

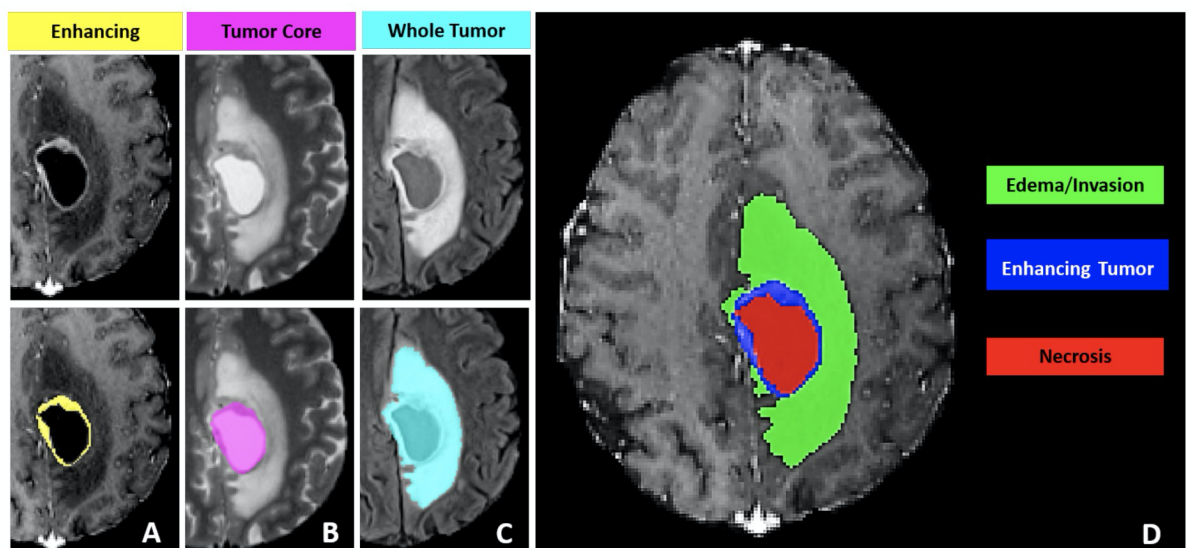


Image from paper above.

All BraTS mpMRI scans are available as

- NIfTI files (.nii.gz) for Task 1 (Segmentation)
- DICOM (.dcm) files for Task 2 (Classification)

Scans were acquired with different clinical protocols and various scanners from multiple institutions.

CANDI

Dataset created by The Child and Adolescent NeuroDevelopment Initiative (CANDI). It is a series of structural brain images, as well as their **anatomic segmentations**, demographic and behavioral data and a set of related morphometric resources (static and dynamic atlases).[13]

OASIS

A curation of 5 different datasets, namely

- OASIS-1: Cross-sectional MRI Data in Young, Middle Aged, Nondemented and Demented Older Adults
- OASIS-2: Longitudinal MRI Data in Nondemented and Demented Older Adults
- OASIS-3: Longitudinal Multimodal Neuroimaging, Clinical, and Cognitive Dataset for Normal Aging and Alzheimer's Disease
- OASIS-3 TAU: OASIS-3 Flortaucipir F18 (AV1451) PET
- OASIS-4: Clinical Cohort

A **subset of OASIS-1 used for testing** the wholeBrainSeg UNEST model.

OASIS-1 consists of a cross-sectional collection of 416 subjects aged 18 to 96. For each subject, 3 or 4 individual T1-weighted MRI scans obtained in single scan sessions are included. The subjects are all right-handed and include both men and women. 100 of the included subjects over the age of 60 have been clinically diagnosed with very mild to moderate Alzheimer's disease (AD). Additionally, a reliability data set is included containing 20 nondemented subjects imaged on a subsequent visit within 90 days of their initial session.[14]

Colin 27

Stereotaxic average of 27 T1-weighted MRI scans of the same individual. [16]

Model Definitions

SegResNet

arXiv: [1810.11654](https://arxiv.org/abs/1810.11654)

This model does not contain the variational autoencoder (VAE)

Description and guide is available in MONAI Model Zoo[12]

SegResNetVAE

arXiv: [1810.11654](https://arxiv.org/abs/1810.11654)

Same with the SegResNet, but contains the variational autoencoder (VAE).

UNETR

arXiv: [2103.10504](#)

Swin UNETR

arXiv: [2201.01266](#)

Uses Swin Vision Transformers (ViT)

State-of-the-art[11]

Description and guide is available in MONAI Model Zoo

UNEST

arXiv: [2203.02430](#)

Description and guide is available in MONAI Model Zoo

Available Models

Brain tumor 3D segmentation with MONAI

Github Link: [brats_segmentation_3d.ipynb](#)

Model: SegResNet

Dataset: Medical Decathlon Brain Tumors

Input: Multimodal multisite MRI data (T1, T1gd,T2, T2-FLAIR)

Metrics: DICE (mean): 0.7914 on the notebook

3D Brain Tumor Segmentation with Swin UNETR (BraTS'21 Challenge)

Github Link: [tutorial notebook](#), [implementation](#)

Model: Swin UNETR

Dataset: BraTS'21 and BTCV (implementation)

Input: Multimodal multisite MRI data (T1, T1gd,T2, T2-FLAIR)

Metrics: 10 model ensemble, 800 epoch

- BraTS'21 Test Set - DICE (mean): 0.876
- DICE (mean): 0.7828 on the notebook

UNETR

Github Link: [implementation](#)

Model: UNETR
Dataset: BTCV
Metrics: N/A

wholeBrainSeg UNEST

Github Link: [implementation](#)

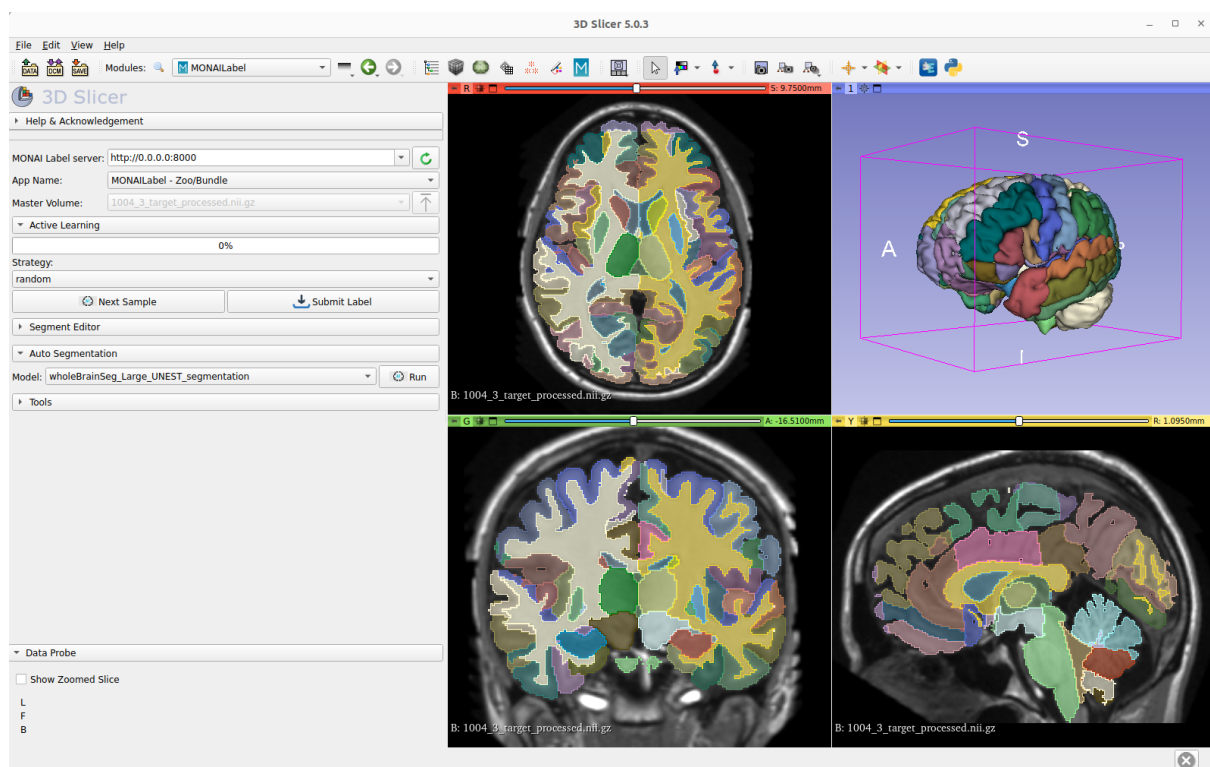
Model: UNEST

Dataset: CANDI and OASIS (training), Colin 27 (test), **133 classes in total in the whole brain segmentation[15]**

Input: 1-weighted (T1w) 3D volumes

Metrics: N/A

The previous models are only focused on the segmentation of tumors, while this model focuses on predicting the segmentation labels for a huge variety of different classes.



(Image taken from [15])

References

1. Medical Decathlon, <http://medicaldecathlon.com/>
2. <https://docs.monai.io/en/stable/networks.html>
3. Multimodal Brain Tumor Image Segmentation Benchmark (BRATS), <https://ieeexplore.ieee.org/stamp/stamp.jsp?arnumber=6975210>
4. <http://braintumorsegmentation.org/>
5. <https://www.med.upenn.edu/cbica/brats/>

6. <https://www.med.upenn.edu/cbica/brats2021/>
7. <https://sites.google.com/site/braintumorsegmentation/>
8. <https://www.med.upenn.edu/cbica/fets/>
9. <https://www.med.upenn.edu/cbica/captk/>
10. <https://arxiv.org/pdf/2103.15954.pdf>
11. https://github.com/Project-MONAI/research-contributions/tree/main/SwinUNETR/BTC_V
12. <https://monai.io/model-zoo.html>
13. https://www.nitrc.org/projects/candi_share/
14. <https://www.oasis-brains.org/>
15. https://github.com/Project-MONAI/model-zoo/tree/dev/models/wholeBrainSeg_Large_UNEST_segmentation
16. <https://www.mcgill.ca/bic/software/tools-data-analysis/anatomical-mri/atlasses/colin-27>

Appendix

Models Focused on Neural Architecture Search Strategies

DiNTS: Differentiable Neural Network Topology Search for 3D Medical Image Segmentation

Github Link: [repository link](#)

Arxiv: [2103.15954](#)

Dataset: BraTS'19