# **Iowa Initiative for Artificial Intelligence**

## **Final Report**



## **Brief summary of accomplished results:**

We developed and validated a WNET model to automatically segment brain tumors into multiple subcomponents (enhancing, edema and necrotic) with mean Intersection-over-Union (IoU) 0.98.

## **Research report:**

## **Aims (provided by PI):**

To perform deep learning-based segmentation of brain tumors into multiple subcomponents (enhancing, edema and necrotic).

#### **Data:**

317 patients image sets were collected from UIHC and corresponding segmentation masks of subcomponents (enhancing, edema and necrotic) were created. In addition, external 84 patients datasets were collected for external validation.

## **AI/ML Approach:**

A W-net model was trained for segmentation of the brain tumors. Training/validation/test split was 177/64/76.

## **Experimental methods, validation approach:**

## **Image preprocessing**

Following image anonymization, the DICOM images were first converted to NIfTI format. All

MRI images were subsequently pre-processed using a series of image processing steps:

- (a) resampling to a voxel size of  $1x1x1$  mm<sup>3</sup>;
- (b) reorientation to the left-posterior-superior (LPS) coordinate system;
- (c) alignment of T1 pre-contrast images to the SRI24 atlas (8) using an affine registration technique;
- (d) co-registration of all MRIs sequences of each patient to corresponding T1 pre-contrast images using affine registration;
- (e) skull stripping;
- (f) denoising to reduce the effects of noisy high-frequency features using the SUSAN technique [1]; and
- (g) intensity normalization to [0,255].

The resampling, reorientation, registration, and normalization steps were implemented using ANTsPy version 0.2.9, a python library that wraps the C++ biomedical image processing library Advanced Normalization Tools (ANTs).[2] The Nipype python package version 1.7.0 [3] provides an interface to the FSL [4-6] implementations of the skull stripping techniques.[7] Cancer Imaging Phenomics Toolkit (CaPTk), which is an NIH-funded open-source research software was used from GitHub repository [\(https:// github.com/CBICA/CaPTk\)](https://github.com/CBICA/CaPTk) for SUSAN denoising.[8].

## **Tumor Segmentation**

Three-dimensional (3D) volumetric tumor segmentation was performed on axial T1-CE and FLAIR images by three radiologists (N.S., S.P. and G.B.) in consensus using an in-house developed semi-automatic tool, Layered Optimal Graph Image Segmentation for Multiple Objects and Surfaces (LOGISMOS).[9] In patients with multiple lesions, a maximum of five largest lesions were segmented since multiplicity of lesions could potentially affect model performance. Two regions of interests (masks) were segmented using T1-CE and FLAIR images:

- (a) Tumor (WT, enhancing plus necrotic/ hemorrhagic on T1-CE images) and
- (b) Whole edema (entire region of FLAIR abnormality, including tumor and peritumoral edema [PTE]).

One tumor mask was created for each patient. (0: not tumor; 1: necrotic/core; 2: edema; 3: enhancing).

## **Image Segmentation**

The W-Net architecture is shown in Figure 1. It consists of two parts:

- U-Encoder: Outputs image segmentations from the original images.
- U-Decoder: Outputs the reconstruction images from the segmentations.



Figure 1. The architecture of WNET model [10].

## **Results:**

Mean IoU between AI-predicted segmentation and manual segmentation were 0.99 for training images, 0.98 for test images and 0.98 for external validation images.

## **Reference:**

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- 8. Davatzikos, C., et al., *Cancer imaging phenomics toolkit: quantitative imaging analytics for precision diagnostics and predictive modeling of clinical outcome.* J Med Imaging (Bellingham), 2018. **5**(1): p. 011018.
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- 10. Xia, X., & Kulis, B. (2017). W-Net: A Deep Model for Fully Unsupervised Image Segmentation. *ArXiv, abs/1711.08506*.