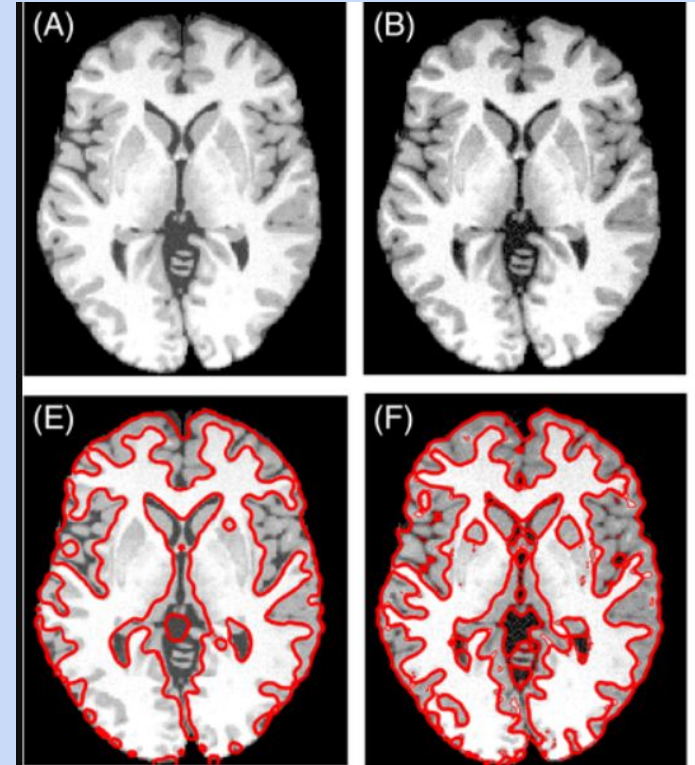


BME 3053C Final Project

Bane Elizabeth, Denning Katherine, Filippone Bianca, Lafayette Lauren,
Ramanand Ananya, Wagner Kasey

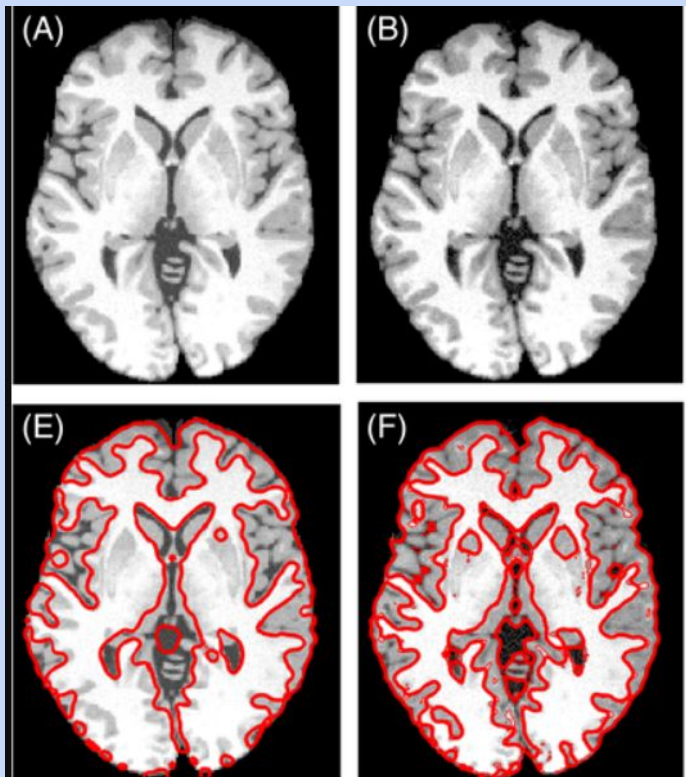
Project Overview

- Segmentation of 3D scans is used to isolate structures and render 3D models.
- Unsupervised machine learning that receives .mat files of MRI brain images, segments them to illuminate foreign masses such as tumors in the brain, and returns a new version of the file with the mass visible as an easily downloadable image file (.jpeg)



[1] Segmented Brain Slides

Problem



[1] Segmented Brain Slides

- Manual segmentation of large data sets are time consuming and has inconsistent outcomes. Hand drawing the segmentations (even with various brushes with software such as Dragonfly and ITK SNAP) has variations between people performing segmentation.
- Existing MATLAB thresholding functions are inaccessible to research settings that use Python.

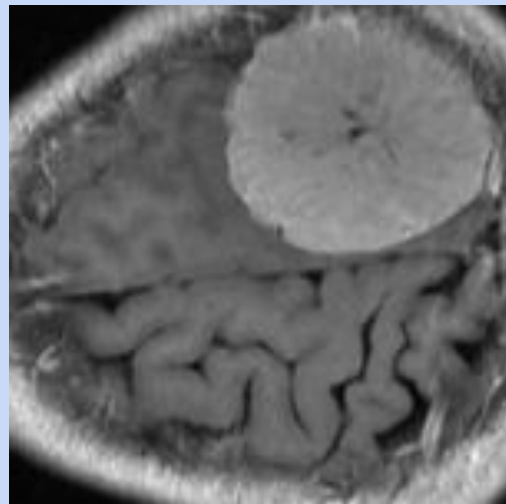
Data

brain tumor dataset

The dataset utilized for this project is a store of 3064 contrast-enhanced T1-weighted MRI slices from 233 patients with brain tumors of varying types.

Each scan is stored in a .mat file, which also contains tumor class, patient identification, and masking data.

Using this dataset, our team can explore the applications of AI in mapping tumors.



1.mat

10.mat

100.mat

101.mat

102.mat

103.mat

104.mat

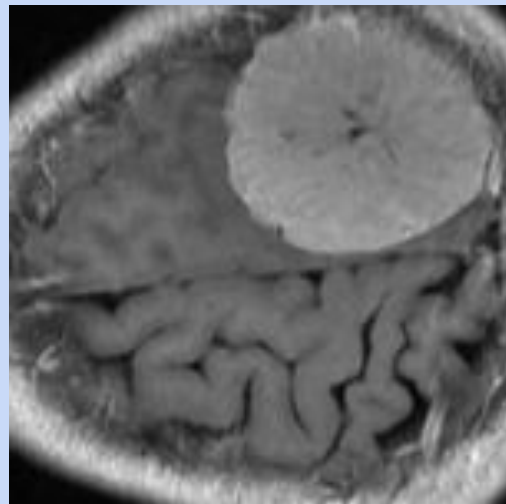
Data

brain tumor dataset

Tumor class (1 = meningioma, 2 = glioma, 3 = pituitary tumor)

Imaging Details:

- Resolution: 512×512 pixels
- Pixel Size: 0.49×0.49 mm²
- Slice Thickness: 6 mm
- Slice Gap: 1 mm



1.mat

10.mat

100.mat

101.mat

102.mat

103.mat

104.mat

Significance

- 3D segmentation is significant because it eliminates the need for doctors to spend their own time segmenting and making the models themselves instead of focusing on diagnosing and treatment plans
- Automated MRI segmentation also creates more accurate 3D models because there is no human errors or variation in the models. This also allows the models to be reproduced easier.
- These 3D models would allow students and trainees to have clear models of brain anatomy and tumors which would enhance their education

Methodology

Data Preparation

- The h5py library is used to read the .mat files. From each file, two arrays are extracted; 2D array of raw pixel values(the MRI scan) and a matching binary array marking tumor locations.
- These arrays are transposed into standard row-column order and the scan values are scaled to a 0-255 range and saved as JPEG images
- The tumor arrays are converted to black and white PNG masks (.mat → JPEG + PNG.)

To facilitate quicker code run throughs, a 'MAX_SAMPLES' parameter was added to run the script with less than the total number of files in the dataset.

Image Processing with MONAI

- Once the images and masks are created, they're processed using MONAI, a medical imaging library built on PyTorch.
- Each JPEG and PNG pair is loaded and dimensioned to match PyTorch's [channels, height, width] convention.
- All data is resized to 256 by 256 pixels and scale the intensity from 0 to 1.
- These preprocessing steps are bundled into a MONAI Dataset and fed to a PyTorch DataLoader, which processes just four images at a time to conserve memory.

Methodology

The U-Net architecture - The model used is a 2D U-Net with:

- A "down path" that reduces image size while doubling feature channels, capturing both fine details and broader patterns
- An "up path" that reverses this process, returning to the original image dimensions
- Shortcut connections (skip connections) between matching layers that preserve details across the network

Training and Evaluation - The network is trained using:

1. Dice loss - measures how well the predicted tumor mask overlaps with the ground truth
2. Adam optimizer - adjusts weights based on both current and past gradients
3. Deterministic initialization (set_determinism) - ensures reproducible results

After five epochs (complete passes through the training data), the model weights are saved.

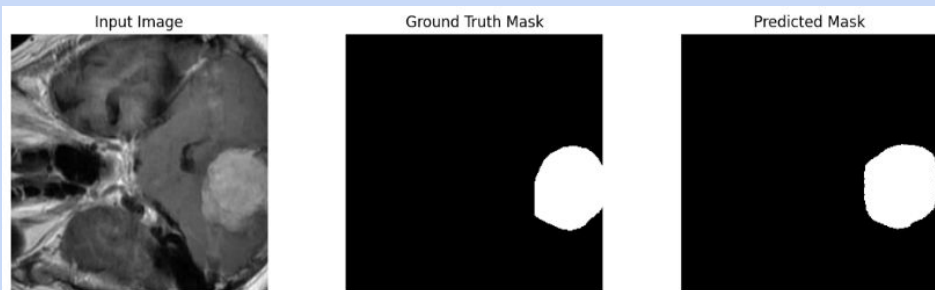
Evaluation - To evaluate performance, three random cases are selected using Python's SystemRandom. These images undergo the same preprocessing, get processed through the trained U-Net, and the results are visualized side by side:

- Original MRI scan
- Expert-drawn mask (ground truth)
- Model's predicted mask

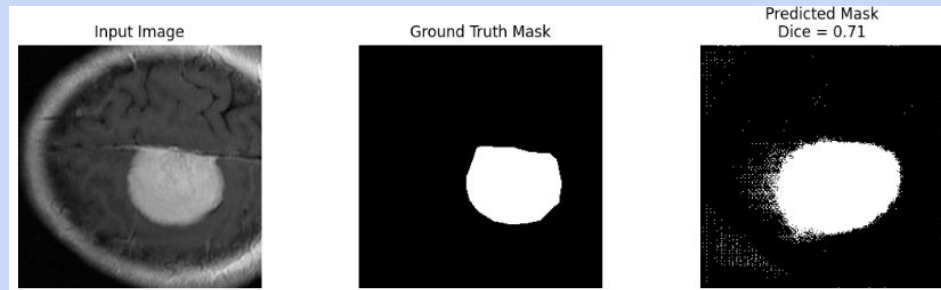
Results

Our code works as intended, mapping a discrete edge to each tumor that can assist in removal, injection, and identification. The code creates a mask delineating tumors in the assigned brain, and then our unsupervised AI model produces it's mask training on the Nanfang dataset.

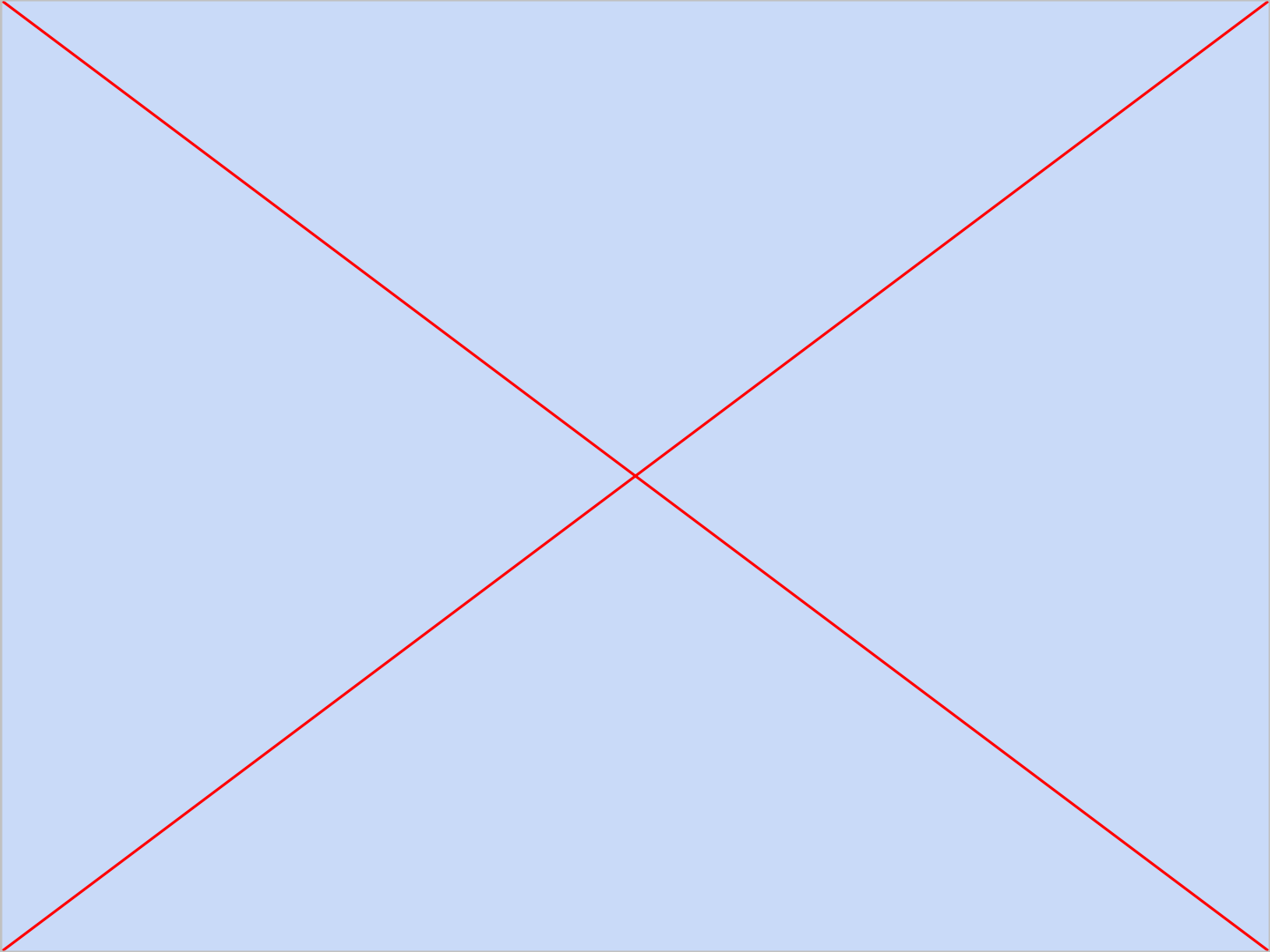
Some cases are worse than others, and any number of slice samples less than 300 will net inaccurate predicted masks.



Example from full data set



Example from 200 .mat files



Citations

[1] Veluchamy, M., Mayathevar, K., & Subramani, B. (2019). Brightness preserving optimized weighted bi-histogram equalization algorithm and its application to MR brain image segmentation. *International Journal of Imaging Systems and Technology*, 29(3), 339–352. <https://doi.org/10.1002/ima.22330>