

Final Project



Introduction to Imaging AI with Applications in Medical Imaging

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Task I



Sampling and Fourier Transform of Grayscale Images

Error-free Image Reconstruction From a Digital Image



- The theoretical maximum spatial frequencies $f_{u_{max}}$ and $f_{v_{max}}$ that can be represented without aliasing, based on the sampling rates provided.
- This can be solved using the **Nyquist-Shannon sampling theorem**, which states that the maximum representable frequency is half the sampling frequency.
- So, the sampling rate in the x-direction and y-direction respectively:

$$\Delta x = \frac{1}{20} \frac{\text{samples}}{\text{mm}}$$

$$\Delta y = \frac{1}{10} \frac{\text{samples}}{\text{mm}}$$

Error-free Image Reconstruction From a Digital Image



- Based on the Nyquist-Shannon theorem states the maximum frequency that can be represented without aliasing is:

$$f_{max} = 2\Delta$$

- Thus we get the theoretical maximum values:

$$f_{u_{max}} = 2\Delta x = \frac{1}{10} \frac{cycles}{mm} \quad \text{and} \quad f_{v_{max}} = 2\Delta y = \frac{1}{5} \frac{cycles}{mm}$$

Memory Requirement for a Color Image



- **Sampling Rate:** 20 samples/mm in the x-direction & 10 samples/mm in the y-direction.
- **Image Dimensions:** assume the image dimensions are $W \times H$ mm.
- **Color Channels:** a color image typically has three channels: Red, Green, and Blue (RGB).
- **Bit Depth:** each channel can distinguish 1024 values. Bit depth per channel = $\log_2(1024) = 10$ bits.

Memory Requirement for a Color Image



- **Number of Sampling Points** = $(20 \text{ samples/mm}) \cdot (10 \text{ samples/mm}) \cdot W \cdot H = 200 \cdot W \cdot H$ samples
- **Memory Per Sample** = $3 \cdot 10 = 30 \text{ bits} = 3.75 \text{ bytes}$
- **Minimum Memory Requirement** = $(\text{number of sampling points}) \cdot (\text{memory per sample in bytes}) = 750 \cdot W \cdot H$ bytes
- Since we are at a 10 bits RGB image case, the only known format that easily deals with this in a **lossless manner** is **TIFF** (can go to 3×16 bits for the 3-channel color image).

Number of Colors Based on Quantization



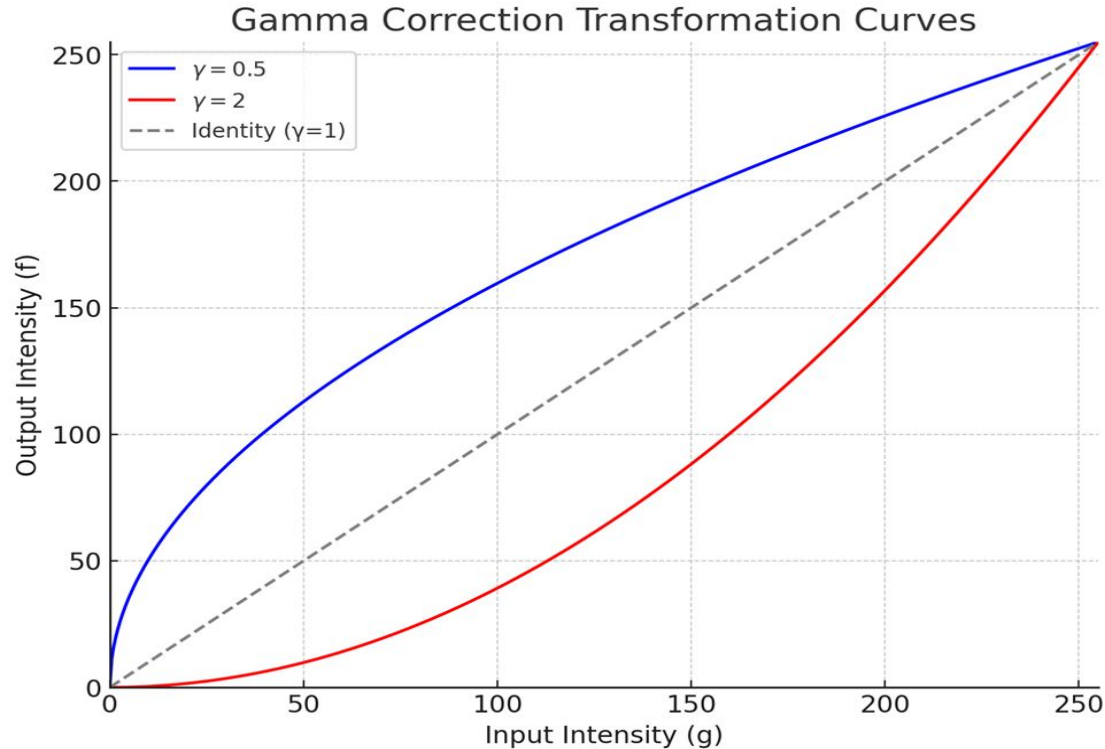
- Since there are 1024 potential values per color channel, there are as many color representations as the number of value combinations.
- So, **Number of Combinations** = $1024^3 = 1,073,741,824$ colors represented with the quantization we chose.

Task II



Image Enhancement Using Gamma Correction

Gamma Correction Transformation Curves



How to Determine the Coefficient C



- The constant c is a scaling constant that ensures our outputs remain in the $[0,255]$ range.
- Therefore, c determined as:

$$c = 255^{1-\gamma} \quad \text{if } g, f \in [0,255]$$

Gamma Values on Image Enhancement



- For γ_1 , T_G increases the brightness of the image. Specifically, the transformation maps lower input values to higher output values, enhancing shadow details.
- For γ_2 , T_G decreases the brightness of the image. For $\gamma > 1$, the transformation maps higher input values to lower output values, enhancing contrast in bright regions.

Minimum Slope of Transform Function



In general:

- For $\gamma > 1$ (compression): The slope decreases as $g \rightarrow 0$. Minimum slope occurs near $g = 0$.
- For $\gamma < 1$ (spread): The slope increases as $g \rightarrow 0$. Minimum slope occurs near $g = 255$.

Minimum Slope for Gamma < 1



- Minimum slope for grey value **spread** ($\gamma < 1$):

$$\frac{df}{dg} = 255 \cdot 0.5 \cdot \left(\frac{g}{255} \right)^{-0.5}$$

- The slope decreases as $g \rightarrow 255$ and the **minimum slope occurs at $g=255$** :

$$\frac{df}{dg}_{g=255} = 255 \cdot 0.5 \cdot (1)^{-0.5} = 127.5$$

Minimum Slope for Gamma > 1



- Minimum slope for grey value **compression** ($\gamma > 1$):

$$\frac{df}{dg} = 255 \cdot 2 \cdot \left(\frac{g}{255} \right)^1$$

- The slope decreases as $g \rightarrow 0$, and the **minimum slope occurs at $g=0$** . However, near $g=0$, the slope asymptotically approaches zero.
- To avoid extreme compression in practical applications, a small positive threshold g (e.g., $g=1$) is typically used. At $g=1$:

$$\frac{df}{dg}_{g=1} = 255 \cdot 2 \cdot \left(\frac{1}{255} \right)^1 \sim 2$$

Task III



Threshold-based Image Analysis

Task Overview



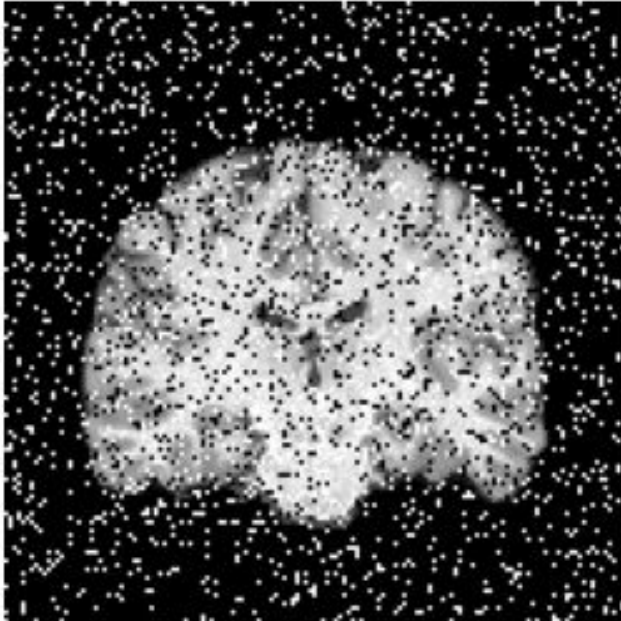
Objective: perform threshold-based segmentation on a brain image to distinguish between background, grey matter, and white matter.

Methods:

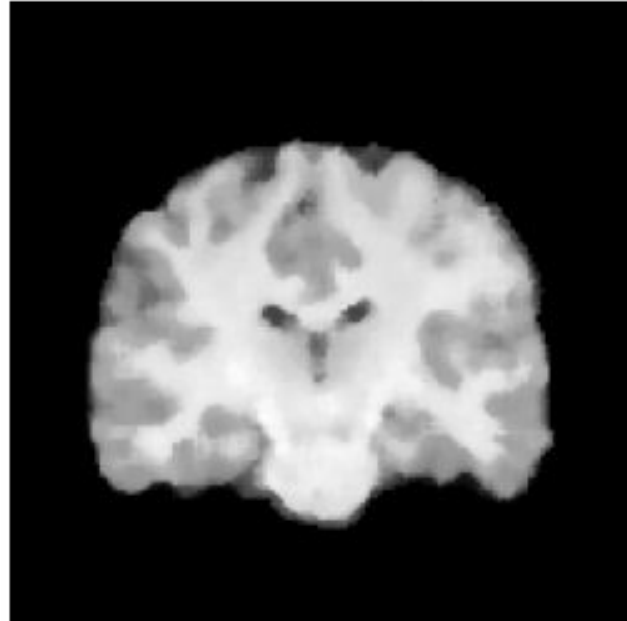
- Use of a median filter to remove noise.
- Otsu thresholding for segmentation.
- Bilinear and nearest neighbor interpolation for up-sampling

Median Filter to Denoise the Image

Original Image (Noisy)



Filtered Image



Otsu Thresholding for Segmentation



```
# perform multi-Otsu thresholding
thresholds = threshold_multiotsu(filtered_image, classes=3)
background_threshold, gray_matter_threshold = thresholds

# create binary masks
background_mask = filtered_image <= background_threshold
gray_matter_mask = (filtered_image > background_threshold) & (
    filtered_image <= gray_matter_threshold
)
white_matter_mask = filtered_image > gray_matter_threshold
```

Result (Images) - Otsu Thresholding



brain-bg



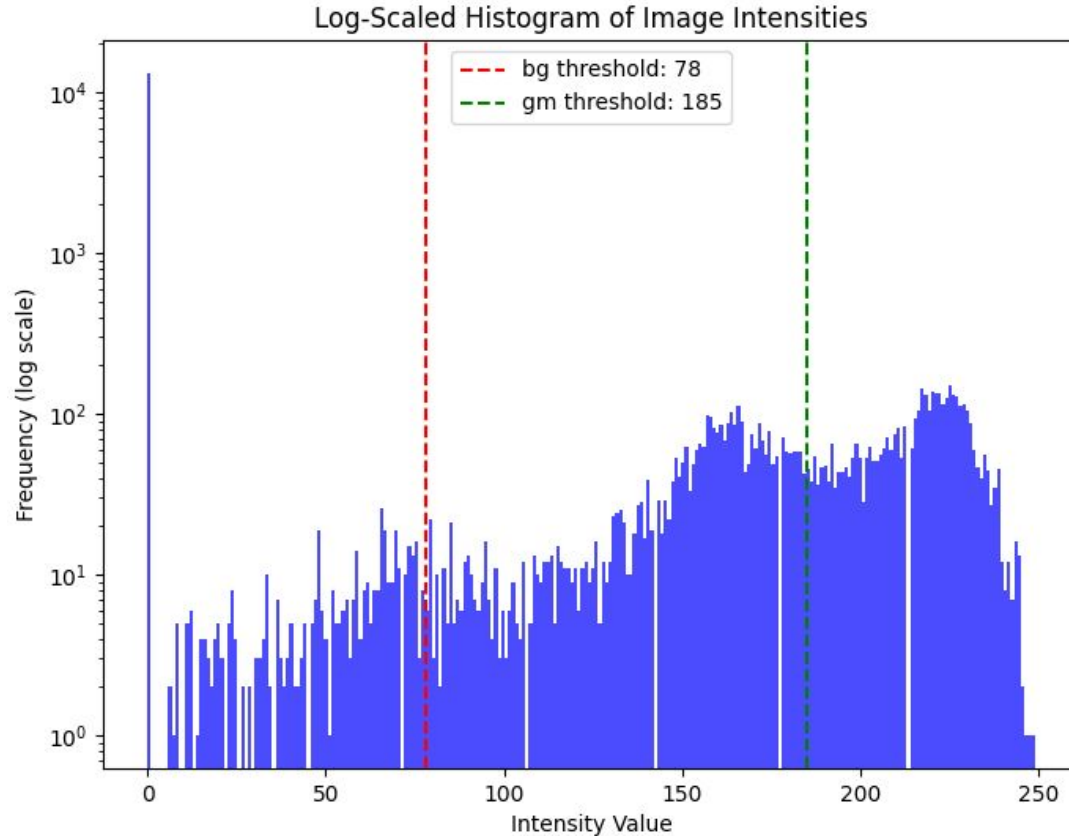
brain-gm



brain-wm



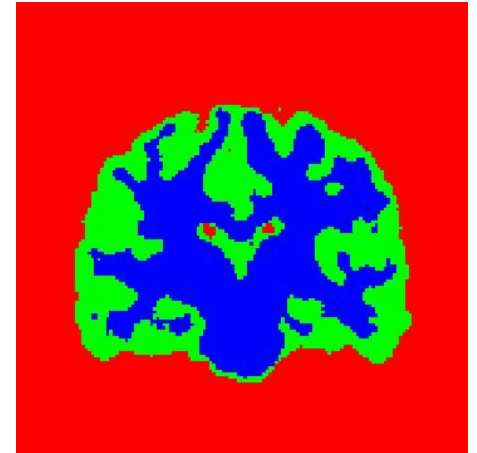
Result (Histogram + Intensities) - Otsu Thresholding



Three Masks Into a Single Image - Otsu Thresholding

```
# combine masks into a single color image
# background: red, grey matter: green, white matter: blue
colored_image = np.zeros((*filtered_image.shape, 3), dtype=np.uint8)
colored_image[background_mask] = [0, 0, 255] # red for background
colored_image[gray_matter_mask] = [0, 255, 0] # green for gray matter
colored_image[white_matter_mask] = [255, 0, 0] # blue for white matter
```

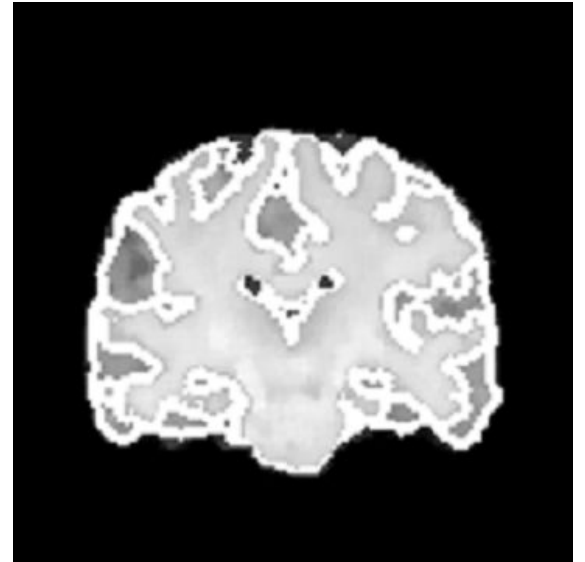
- Background in red, gray matter in green, and white matter in blue.



Erosion Filter



```
# create a boundary between grey and white matter
# using erosion and overlay it on the denoised image
boundary = erosion(
    gray_matter_mask.astype(np.uint8), disk(3)
) ^ gray_matter_mask.astype(np.uint8)
overlay_image = filtered_image.copy()
overlay_image[boundary.astype(bool)] = 255 # red boundary
```



Bilinear Interpolation for Upsampling



- **Bilinear Interpolation:** which calculates pixel values by linearly interpolating between neighboring pixels, producing smoother transition

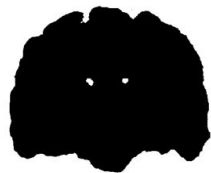
```
# bilinear interpolation
upsampled_bilinear = zoom(filtered_image, zoom=4, order=1)

bilinear_bg_mask = upsampled_bilinear < background_threshold
bilinear_gm_mask = (upsampled_bilinear >= background_threshold) & (
    | upsampled_bilinear < gray_matter_threshold
)
bilinear_wm_mask = upsampled_bilinear >= gray_matter_threshold
```

Bilinear Interpolation



im_bilinear_bg



im_bilinear_gm



im_bilinear_wm



ma_bilinear_bg



ma_bilinear_gm



ma_bilinear_wm



Nearest Neighbor Interpolation for Upsampling



- **Nearest neighbor interpolation:** When resizes an image, it assigns the values of the nearest pixel in the input image to each pixel in the output image, preserving edges but creating a more "staircase" effect.

```
# nearest neighbor interpolation
upsampled_nearest = zoom(filtered_image, zoom=4, order=0)

nearest_bg_mask = upsampled_nearest <= background_threshold
nearest_gm_mask = (
    upsampled_nearest > background_threshold
) & (
    upsampled_nearest <= gray_matter_threshold
)
nearest_wm_mask = upsampled_nearest > gray_matter_threshold
```

Nearest Neighbor Interpolation



im_nearest_bg



im_nearest_gm



im_nearest_wm



ma_nearest_bg



ma_nearest_gm



ma_nearest_wm



Task IV



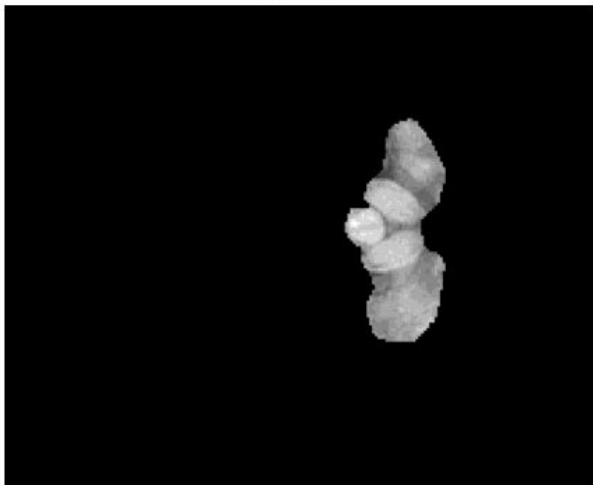
Automatic Glioma Segmentation Pipeline with U-Net Model

Data Exploration

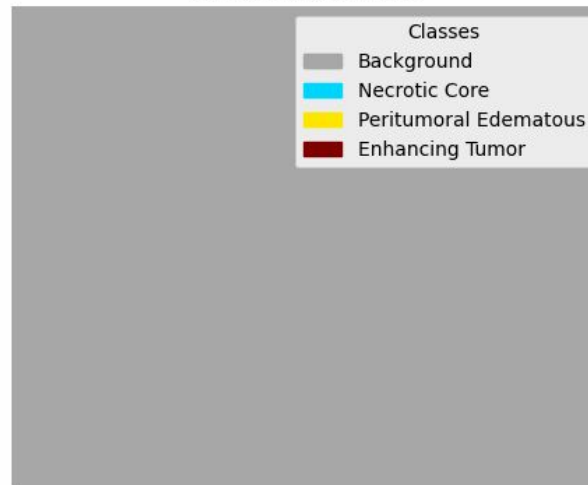


Patient ID: 00000, Modality: T1, Slice: 0

T1 Image



Segmentation Mask



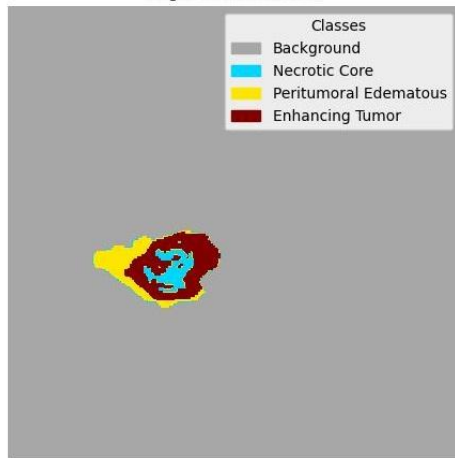
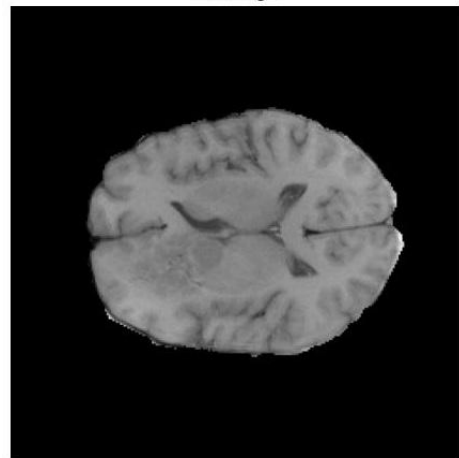
Data Cropping



Patient ID: 00000, Modality: T1, Slice: 75

T1 Image

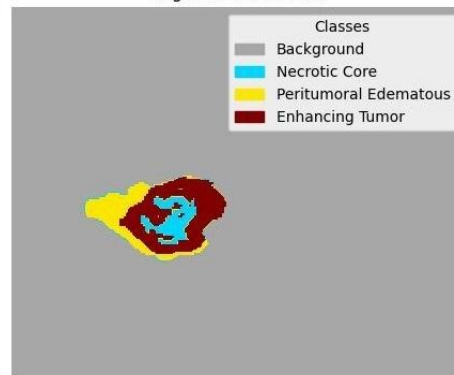
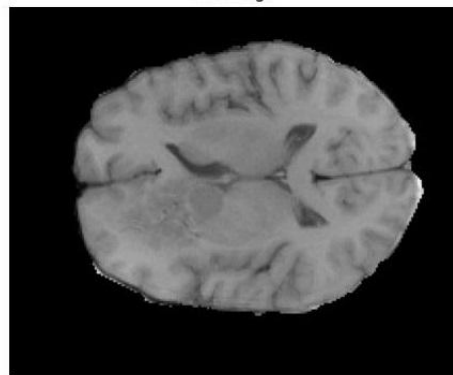
Segmentation Mask



Original

T1 Image

Segmentation Mask



Cropped

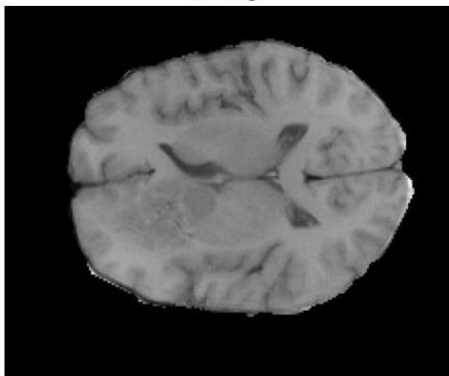
Data Augmentation



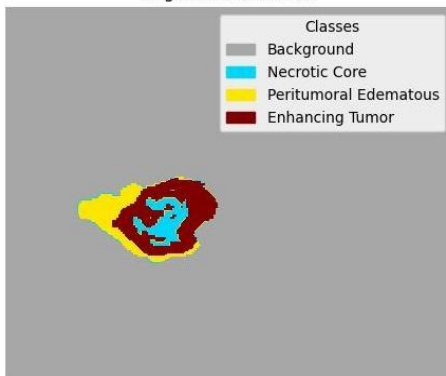
Original

Augmented

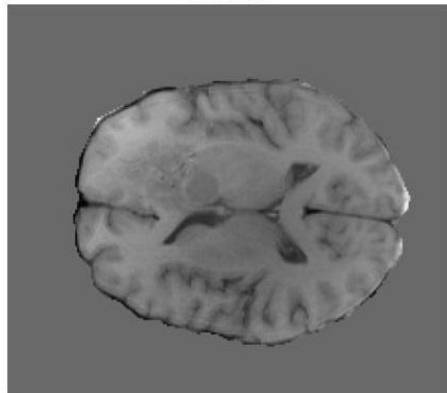
T1 Image



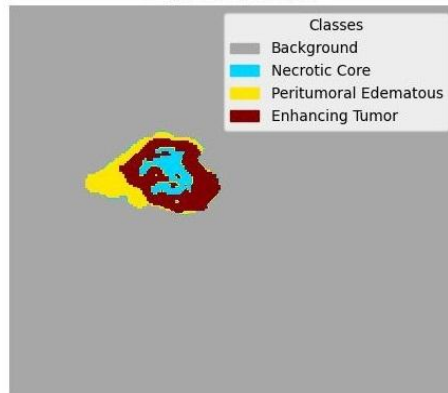
Segmentation Mask



T1 Image



Segmentation Mask

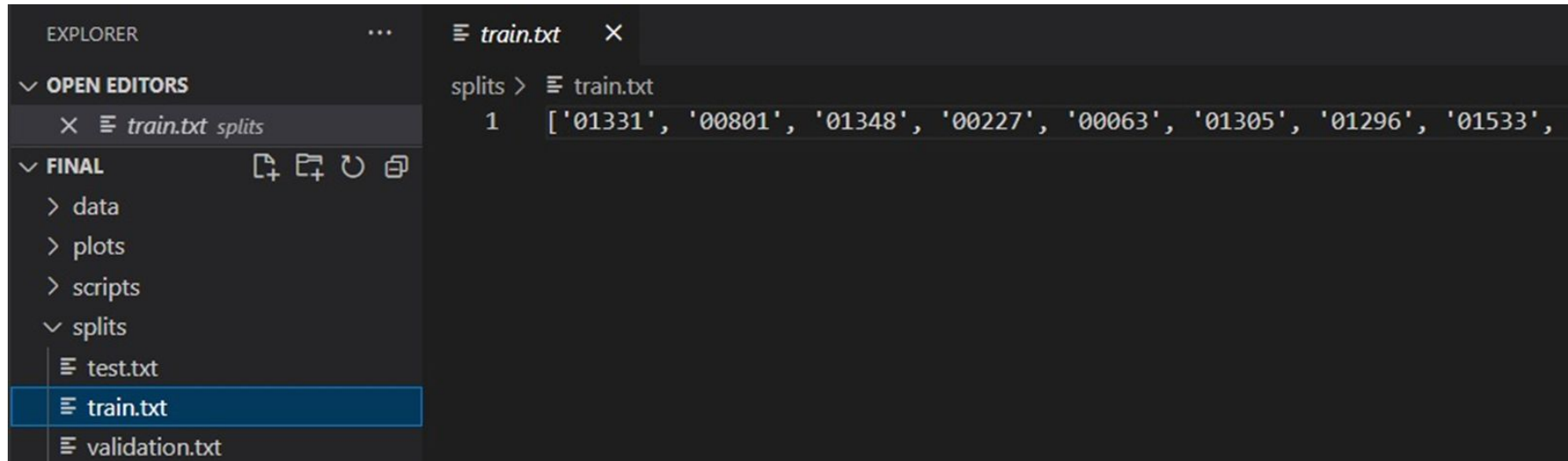


- Random flip
- Random bias field

- Random Gaussian noise
- Normalization to $[0,1]$ scale

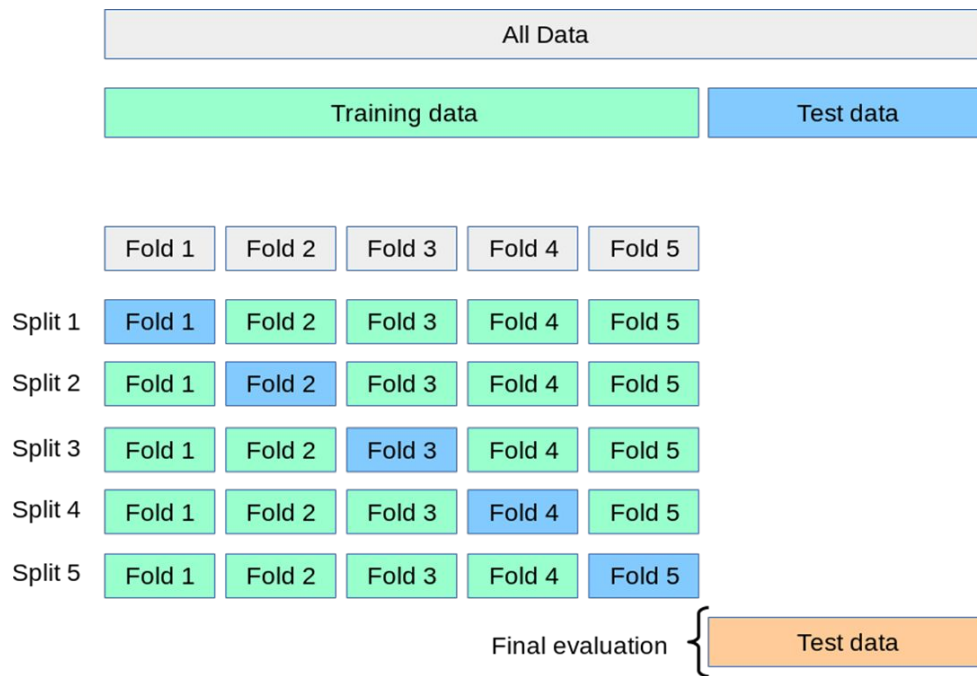
Data Splitting

- 75% of data reserved for training, 15% for validation, and 10% for testing.



Data Splitting: KFold

- 10% of data reserved for testing (same data as without cross-validation).
- 3 folds.



Loss & Metric

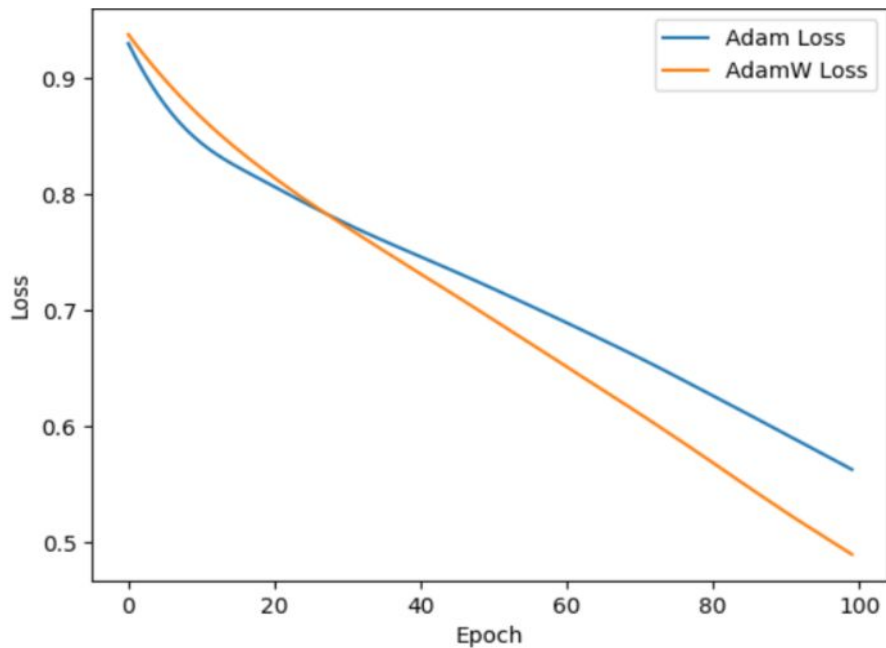


$$\text{DSC}(A,B) = (1 - \frac{2x}{\text{predicted} + \text{ground truth}})$$

Optimizer & Learning Rate Scheduler

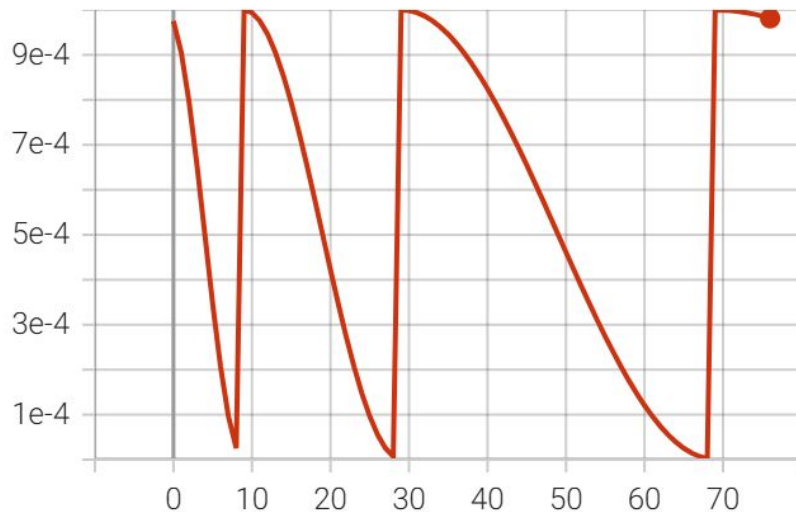


AdamW: Adam with Decoupled Weight Decay



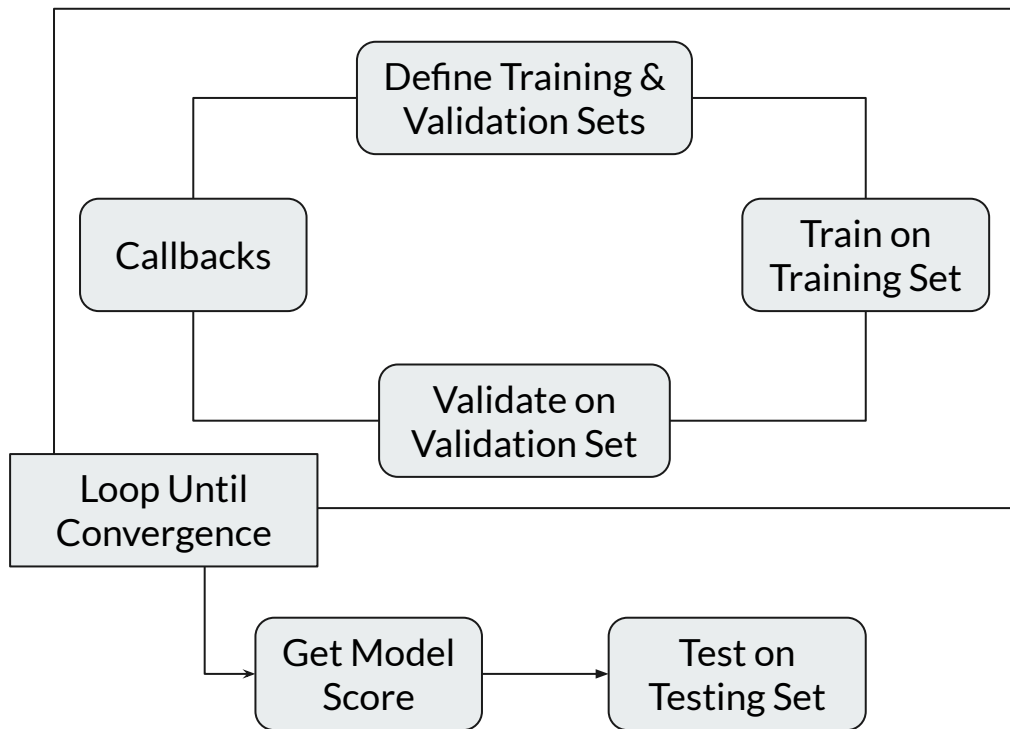
Cosine Annealing with Warm Restarts

Fold_3/LearningRate
tag: Train/Fold_3/LearningRate

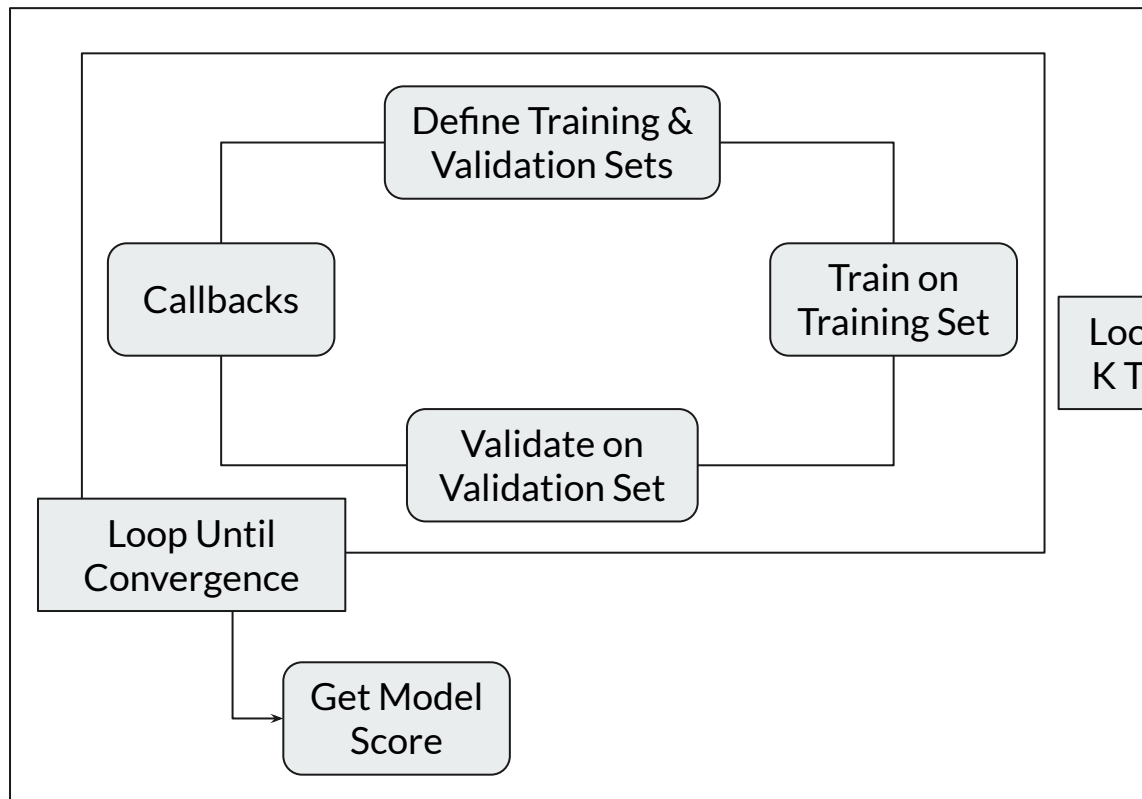


Training & Testing: Default Strategy

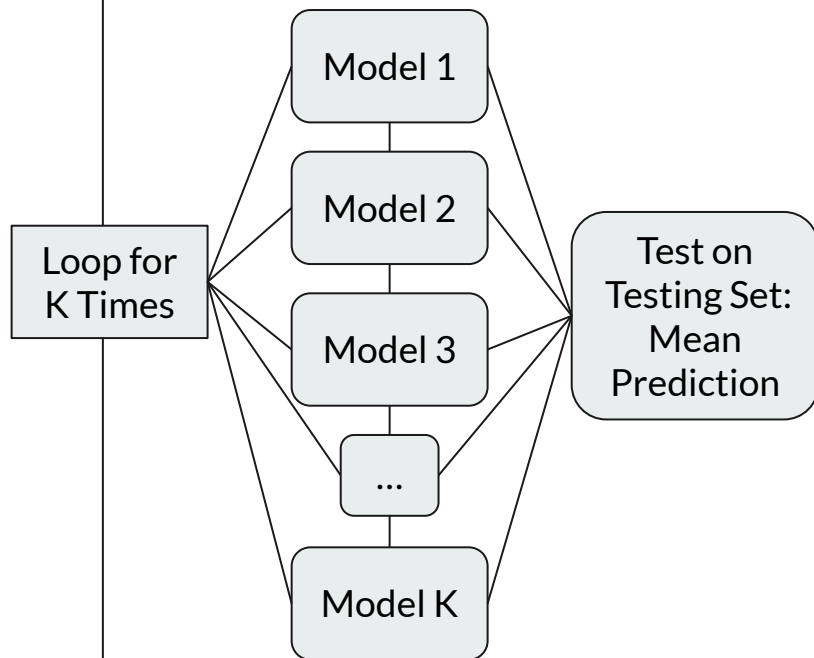
Default Training & Testing Loop



Training & Testing: KFold Cross-Validation



KFold Training & Testing Loop



Results



Method	Default Training Procedure, T1 Modality	Default Training Procedure, Multiple Modalities	KFold Training Procedure, Multiple Modalities
Dice Score	0.6935	0.7576	0.7616

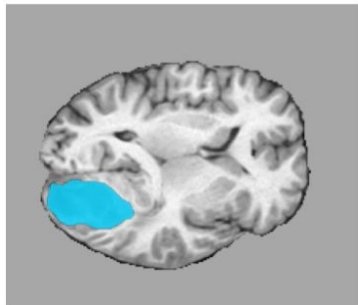
- Introducing more modalities improves model performance.
- Using KFold training and ensemble prediction technique increase prediction accuracy, although not substantially.

Results

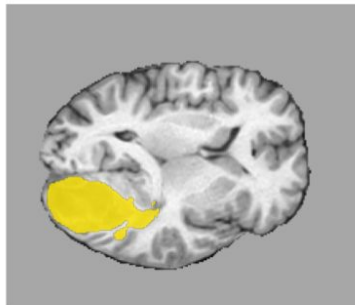


Patient ID: 00095, Slice Index: 72

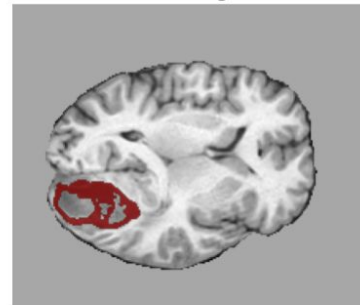
GT: Necrotic Core



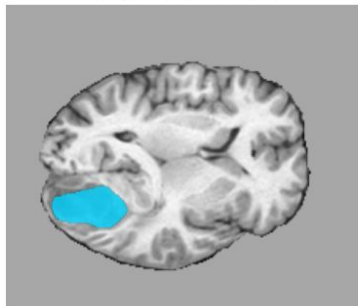
GT: Peritumoral Edematous



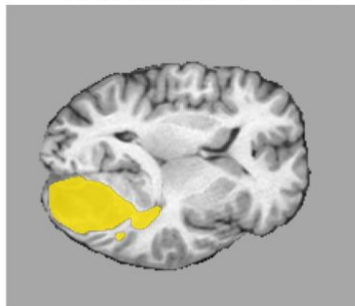
GT: Enhancing Tumor



Pred: Necrotic Core



Pred: Peritumoral Edematous



Pred: Enhancing Tumor

