# Brain Tumors Classification and Segmentation

**Computer Science Program**

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- Problem definition
- Objectives
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- System architecture
- Functions and features
- Algorithms and techniques
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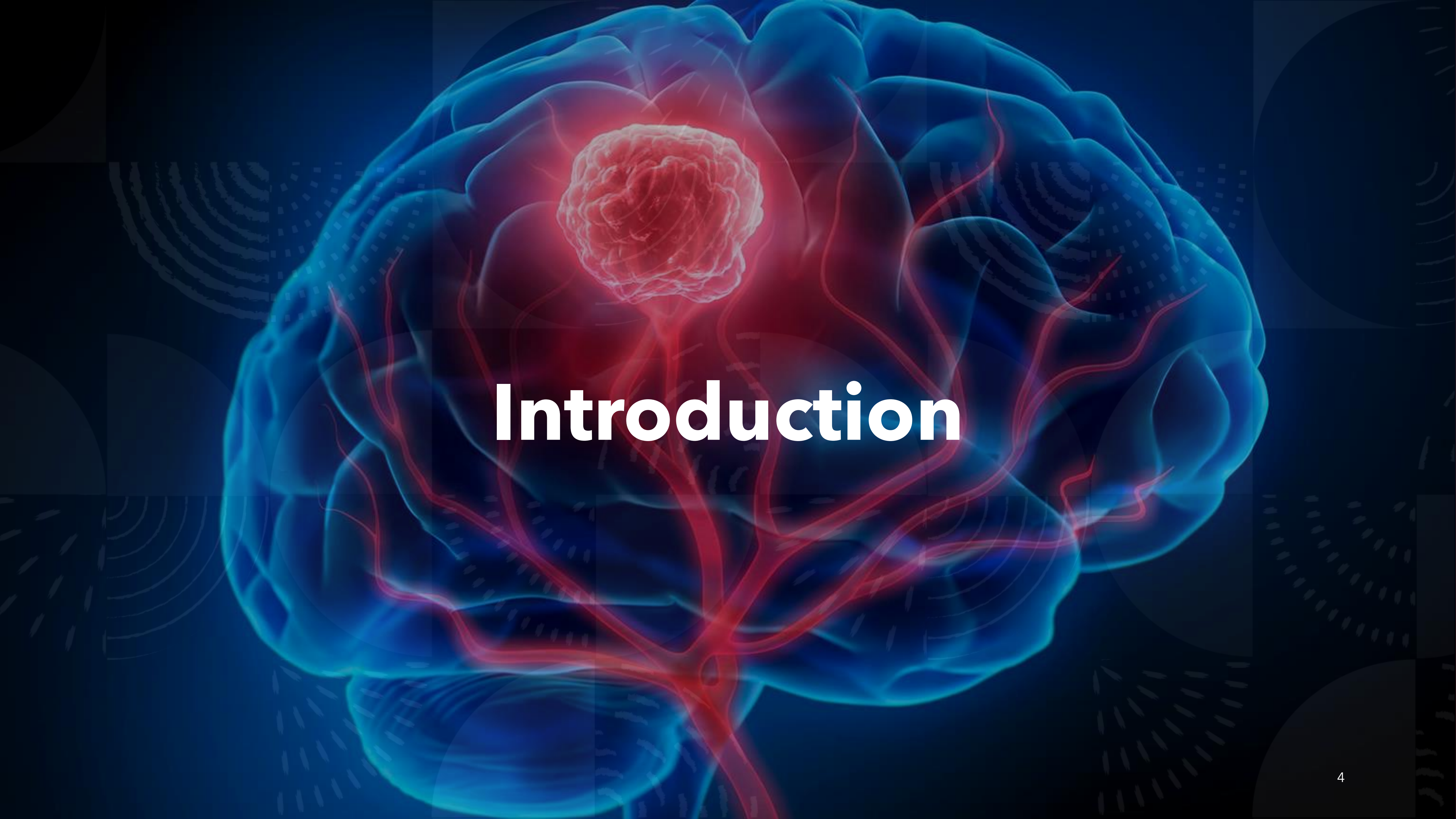
# Introduction



- Brain tumors are abnormal cell growths in the brain, classified as benign or malignant.
- Early detection and accurate diagnosis are vital for better treatment.
- Brain tumors impact physical, cognitive, and emotional well being

# Distribution of Brain Tumor Types

| Tumor Type | Approximate Prevalence (%) |
|---|---|
| Meningioma | 30-40% |
| Glioblastoma (GBM) | 15% |
| Other Gliomas | 10-20% |
| Pituitary Tumors | 10-15% |
| Schwannomas | 8-10% |
| Medulloblastomas | 1-2% |
| CNS Lymphomas | 1-2% |
| Craniopharyngiomas | 1-2% |

All statistics are based on data from the Central Brain Tumor Registry of the United States **(CBTRUS)**.

# Problem Definition

- Identifying tumor types, locations, and extents from MRI scans is crucial but challenging.
- Manual scan interpretation is time-consuming, error-prone, and varies with radiologists' expertise.
- Delayed diagnoses and inconsistent outcomes increase pressure on medical professionals.

# Objectives

- Classify brain tumors from MRI scans.
- Identify affected regions and tumor proportion.
- Perform brain 3D reconstruction for enhanced visualization.
- Support doctors with accurate, timely insights.

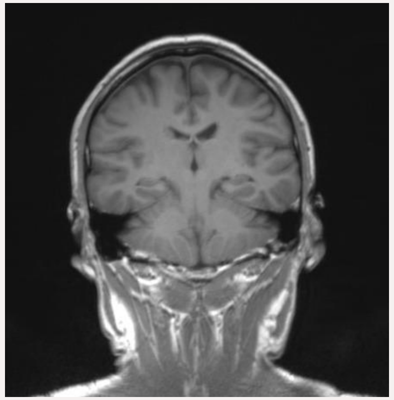
# Dataset

# Classification Dataset :

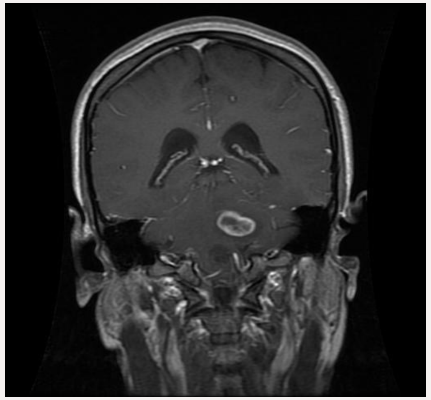
| Class | Training & Validation images | Testing images |
|---|---|---|
| Glioma | 1321 | 300 |
| Meningioma | 1339 | 306 |
| No Tumor | 1595 | 405 |
| Pituitary | 1457 | 300 |

# Segmentation Dataset :

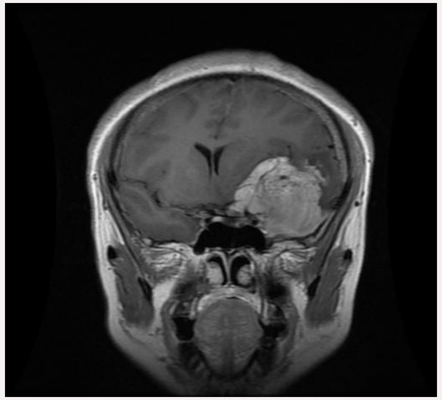
| Class Label | Number of MRI Images and Masks |
|---|---|
| Glioma | 1426 MRI images and masks |
| Meningioma | 708 MRI images and masks |
| Pituitary | 930 MRI images and masks |



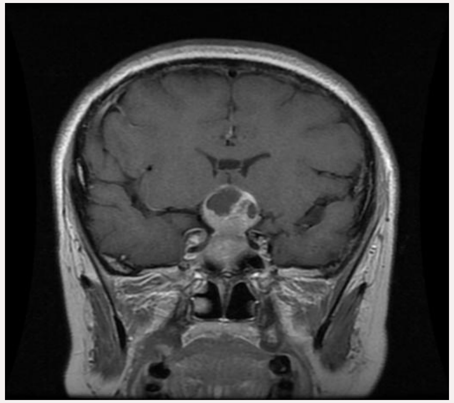
No tumor category



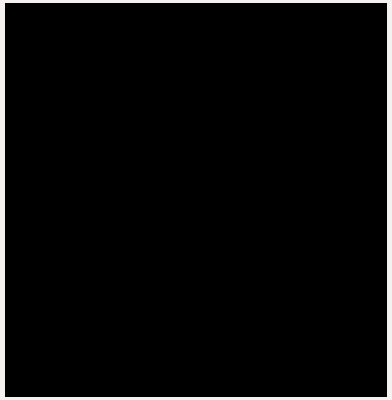
Glioma tumor category



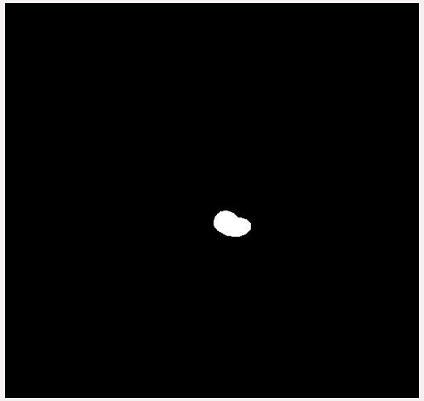
Meningioma tumor category



Pituitary tumor category



No tumor mask

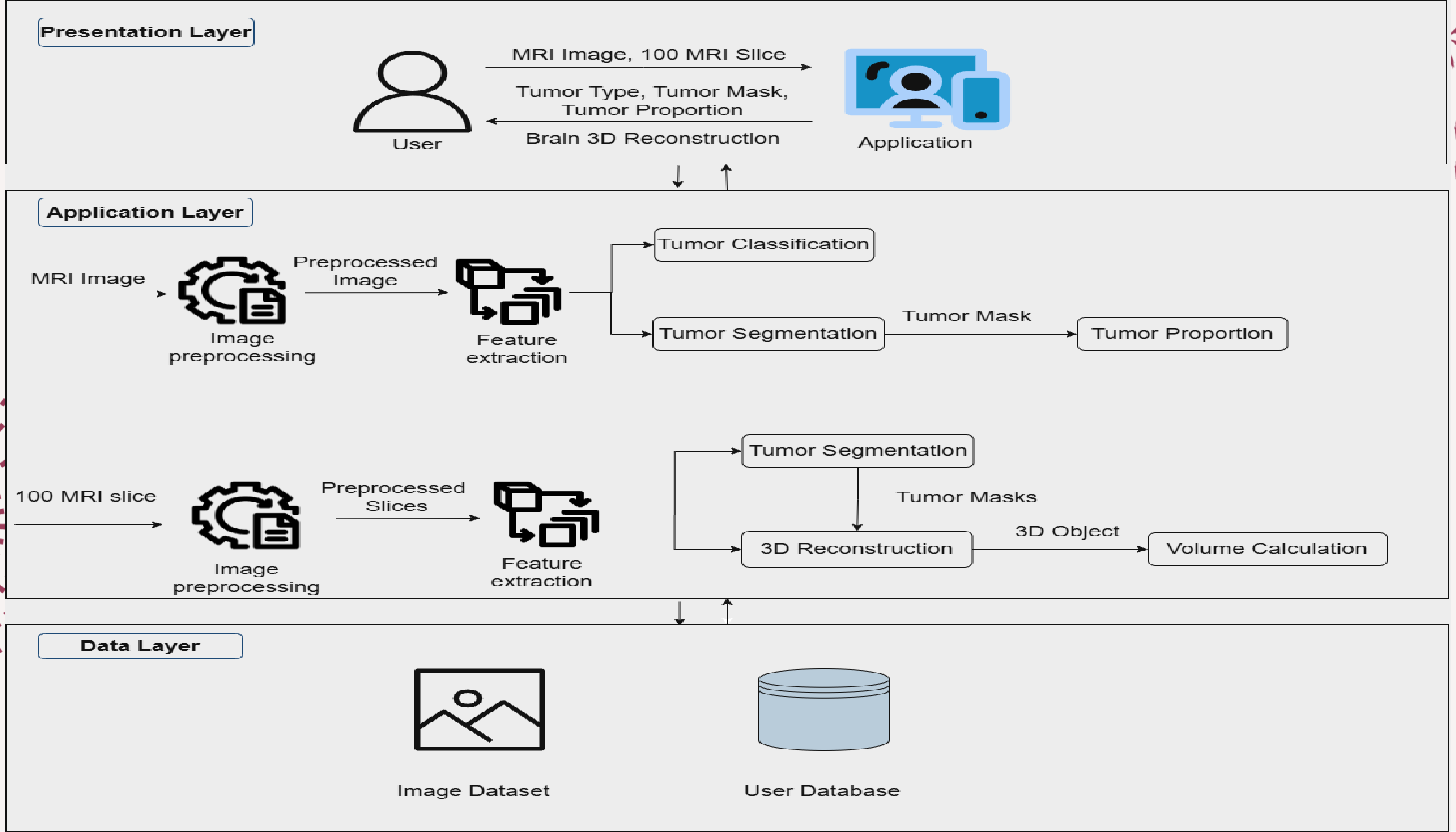


Glioma tumor mask

Meningioma tumor mask

Pituitary tumor mask

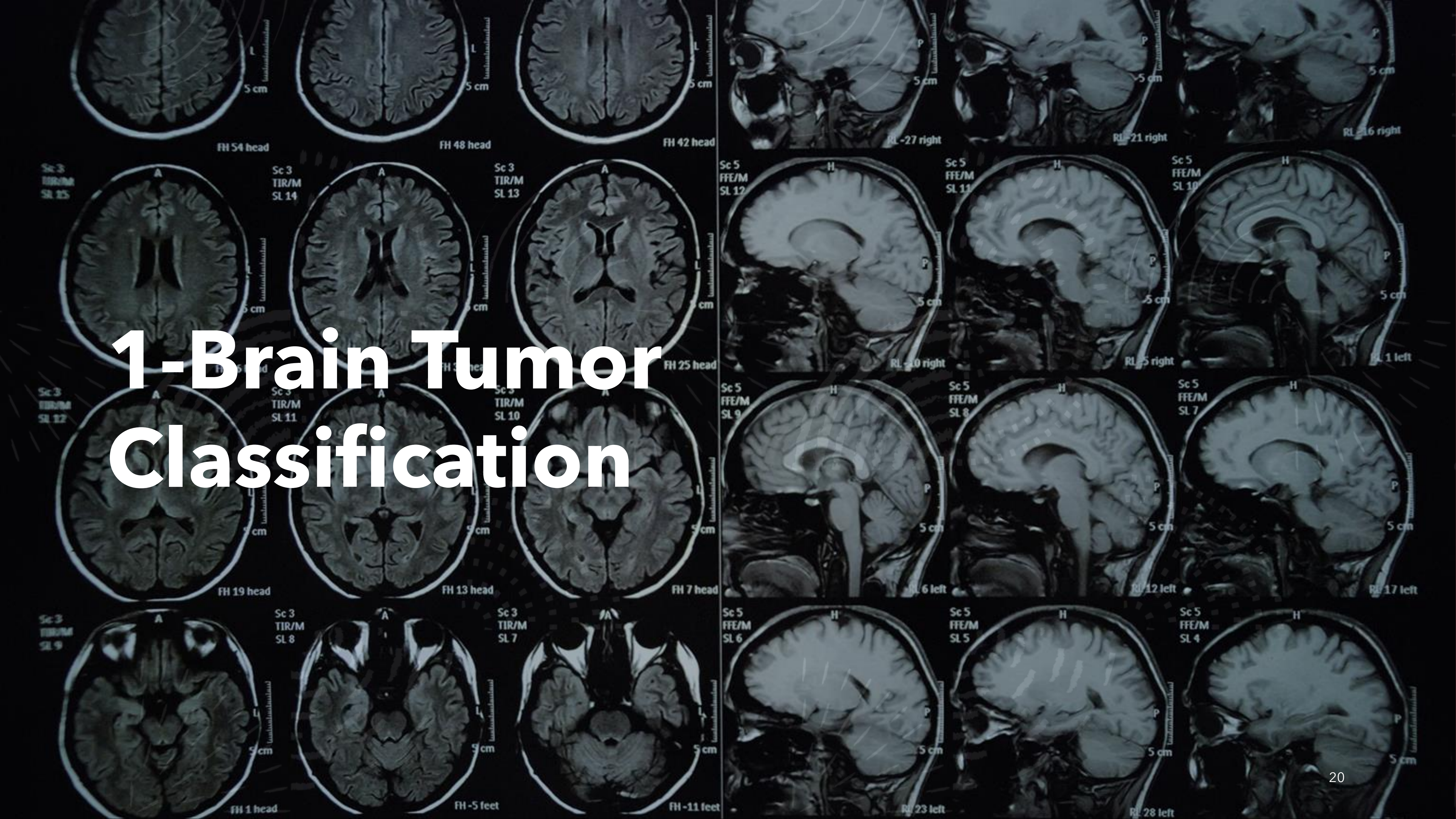
# System Architecture


Presentation Layer
MRI Image, 100 MRI Slice
Tumor Type, Tumor Mask, Tumor Proportion
Brain 3D Reconstruction
User
Application
Application Layer
MRI Image
Image preprocessing
Preprocessed Image
Feature extraction
Tumor Classification
Tumor Segmentation
Tumor Mask
Tumor Proportion
100 MRI slice
Image preprocessing
Preprocessed Slices
Feature extraction
Tumor Segmentation
Tumor Masks
3D Reconstruction
3D Object
Volume Calculation
Data Layer
Image Dataset
User Database

# Functions and Features

- Login / Sign Up For Medical Staff Only
- MRI Scan Upload
- Brain Tumor Classification
- Brain Tumor Segmentation
- Generate Tumor Mask For The Affected Area
- Tumor Proportion Estimation From a Single MRI Slice
- Brain 3D Reconstruction
- Providing Some Facts About The Tumor Like Tumor Volume
- Responsive UI

# Algorithms and Techniques



# 1-Brain Tumor Classification

# Preprocessing Techniques :

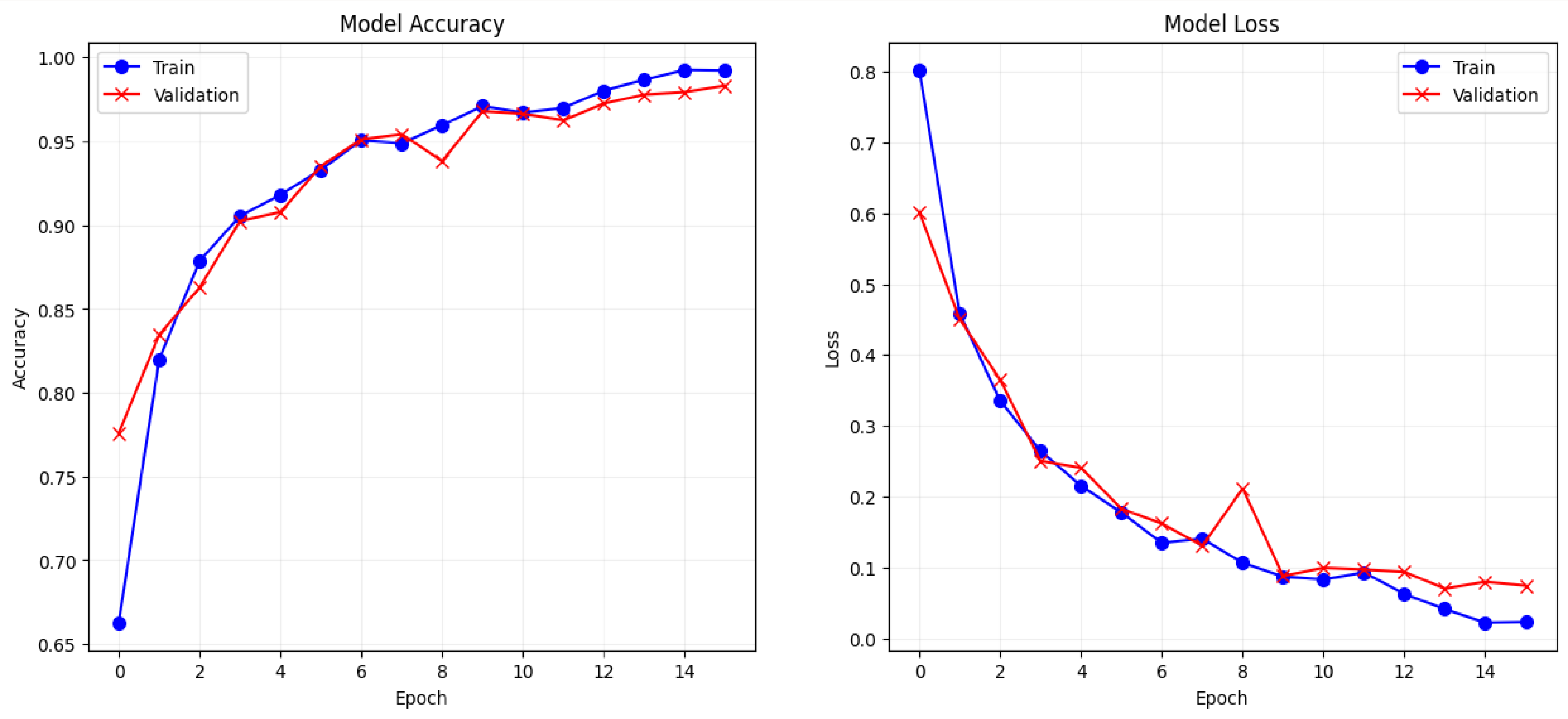
- Converting all images to PyTorch tensors
- Resizing all images to size (150,150)
- Using anti-aliasing for smoother down sampling
- Adjusting brightness within a range of 85% to 115% of the original value using color jitter
- Pixel value standardization using mean `[0.485, 0.456, 0.406]` and std `[0.229, 0.224, 0.225]`, which are common ImageNet statistics.

# Trails :

| Model Architecture | Training accuracy | Validation accuracy | Testing accuracy | Testing F1-score |
|---|---|---|---|---|
| VGG16 | 27.92 | 30.87 | 30.89 | 47 |
| MLP Mixer b16 | 91.71 | 91.23 | 91.23 | 90.75 |
| Resnet50 | 97.71 | 96.04 | 96.03 | 96 |
| Densenet 121 | 97.57 | 98.17 | 98.17 | 98.5 |

# Best Trail :

| Model | Training accuracy | Validation accuracy | Testing accuracy | Testing F1-score |
|---|---|---|---|---|
| CNN from scratch | 99.23 | 98.32 | 98.32 | 98.32 |



# CNN Model Architecture :

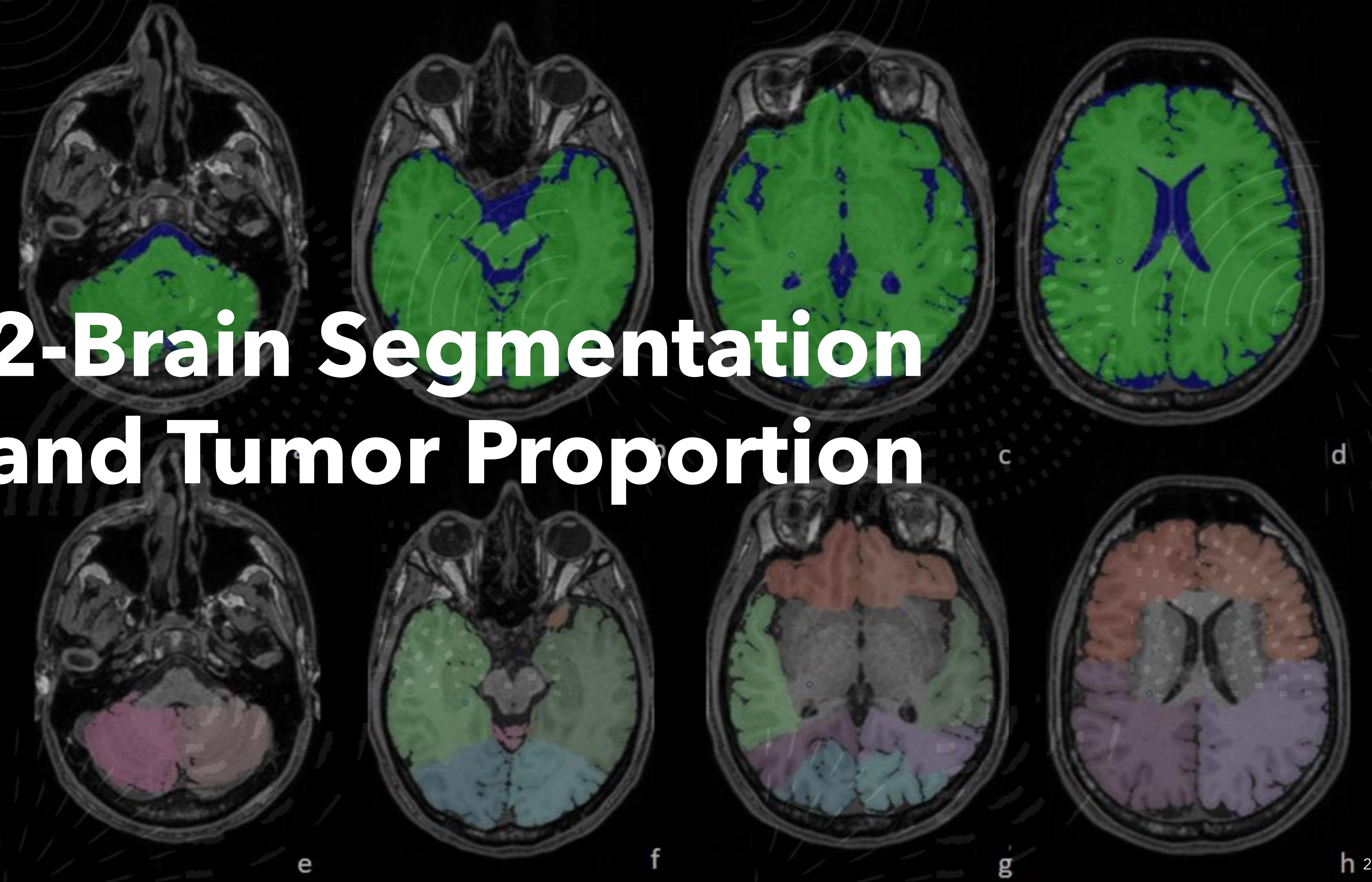
- Feature extraction block consists of 3 convolutional blocks

| | Input channels | Output channels | Kernel size | Activation | Pooling |
|---|---|---|---|---|---|
| First conv block | 3 | 32 | 4 | ReLU | 3*3 Max pooling |
| Second conv block | 32 | 64 | 4 | ReLU | 3*3 Max pooling |
| Third conv block | 64 | 128 | 4 | ReLU | 3*3 Max pooling |

- Flattening feature maps into 1D vector to be fed into fully connected layers
- Fully connected layers are as follows :

| First dense layer | Final output layer |
|---|---|
| Input is flattened features | Output equal to the number of classes |
| ReLU Activation | Cross Entropy Loss Function |
| Dropout with rate 50% | SoftMax and Adam optimizer |

# 2-Brain Segmentation and Tumor Proportion



# Preprocessing Techniques :

- Ensuring grayscale images have a channel dimension if needed
- Resizing all images and masks to size (256, 256) for consistency
- Normalizing pixel values using mean [0.0] and std [1.0] with max value 255.0
- Scaling mask pixel values to binary (0 or 1) for binary segmentation compatibility
- Converting all images and masks to PyTorch tensors using ToTensorV2
- Applying data augmentation multiple times per training image for dataset expansion
- Skipping augmentation during validation to evaluate on clean data

# Segmentation Trails

| Model | Val Dice | Val IOU | Test Dice | Test IOU | Augmentation |
|---|---|---|---|---|---|
| Timm-effnet-b8 | 85.72 | 75.17 | 85.91 | 78.25 | 1. Rotate and Resize<br>2. Vertical flip and normalize<br>3. Gaussian noise<br>4. Bright contrast |
| Resnet 152 | 83.62 | 72.06 | 82.47 | 74.09 | 1. Rotate and Resize<br>2. Vertical flip and Normalize<br>3. Gaussian noise<br>4. Bright contrast |
| Timm-effnet-b8 | 85.74 | 75.2 | 83.42 | 75.3 | 1. Gaussian noise<br>2. Bright contrast<br>3. Resize<br>4. Normalize |
| Resnet 152 | 83.61 | 72.09 | 83.31 | 75.06 | 1. Gaussian noise<br>2. Bright contrast<br>3. Resize<br>4. Normalize |
| Segformer1 | 83.32 | 73.59 | 84.05 | 74.08 | None |
| Effnet-b3 | 83.95 | 72.43 | 82.06 | 73.52 | None |

| Model | Val Dice | Val IOU | Test Dice | Test IOU | Augmentation |
| --- | --- | --- | --- | --- | --- |
| Dyn U-Net | 87.54 | 77.95 | 86.53 | 78.93 | 1. Rotate and Resize<br>2. Vertical flip<br>3. Horizontal flip<br>4. Normalization |
| Attention U-Net (1M Parameter ) | 85.7 | 75.13 | 85.9 | 74.21 | 1. Rotate and resize<br>2. Vertical and horizontal flip<br>3. Gaussian noise<br>4. Bright contrast and normalize<br>5. Random scale |
| Deeplab v3_Resnet 101 | 82.73 | 70.83 | 83.4 | 71.38 | 1. Rotate and Resize<br>2. Vertical flip<br>3. Gaussian noise<br>4. Bright contrast and normalize |
| U-Net with Efficient net L2 | 83.88 | 72.75 | 84.31 | 72.13 | 1. Rotate and Resize<br>2. Vertical flip<br>3. Gaussian noise<br>4. Bright contrast and normalize |
| Attention U-Net (1M Parameter ) | 86.36 | 76.9 | 86.98 | 75.67 | 1. Rotate and Resize<br>2. Vertical and horizontal flip<br>3. Gaussian noise<br>4. Random Brightness & normalize<br>5. Random scale<br>6. Elastic Transform<br>7.Grid distortion<br>8. Optical distortion<br>9.Coarse dropout |

# Best Trail :

| Model | Val Dice | Val IOU | Test Dice | Test IOU | Augmentation |
|---|---|---|---|---|---|
| Attention U-Net (1M Parameter ) | 86.47 | 76.34 | 86.95 | 79.47 | 1. Rotate and Resize<br>2. Vertical flip<br>3. Normalization<br>4. Bright contrast<br>5. Gaussian noise |

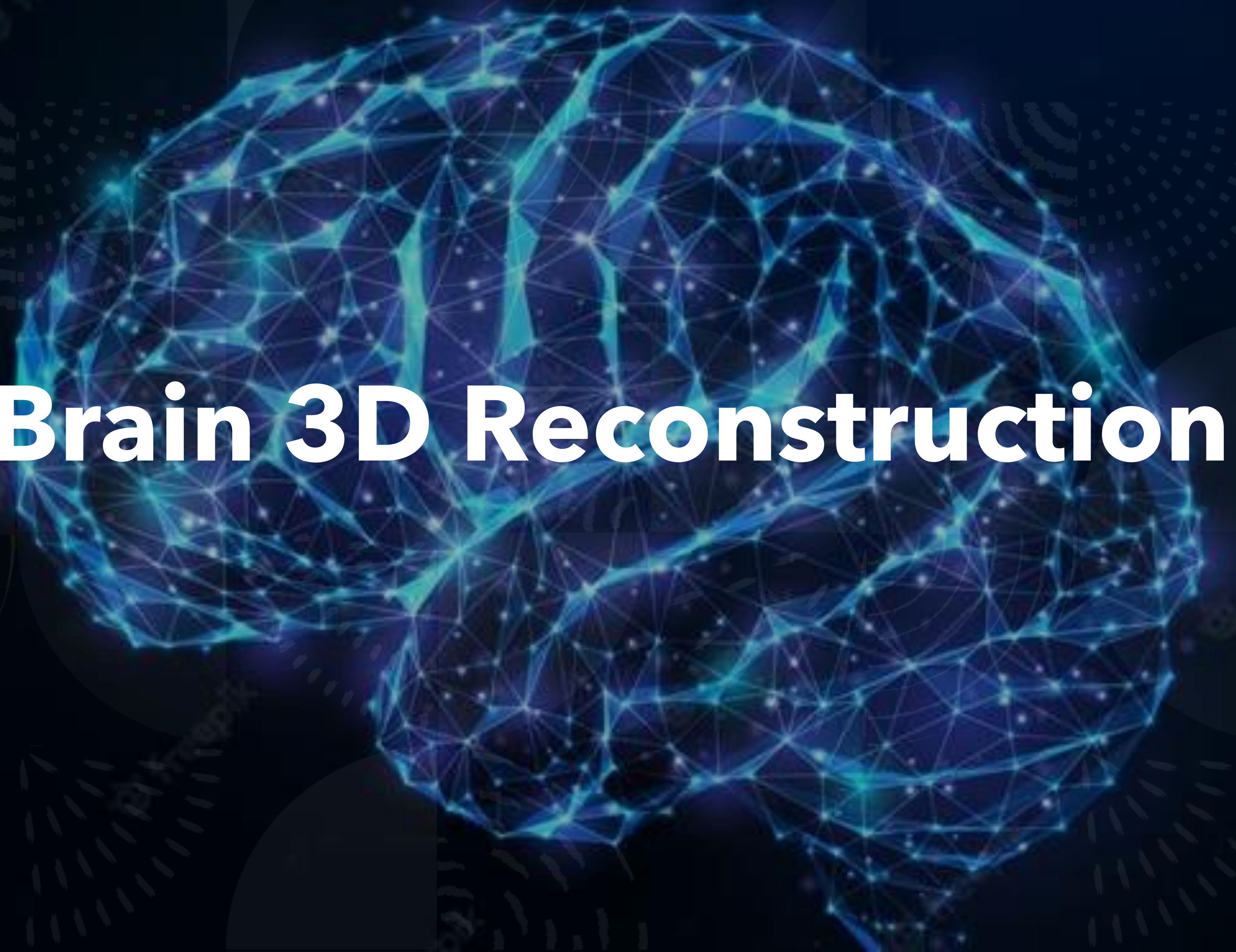
# Model architecture

- 2D Convolutional Network
- Input Channels: 1
- Output Channels: 1
- Encoder-Decoder Structure with Attention Gates
- Number of Filters per Stage: [16, 32, 64, 128, 256]
- Down sampling Strides: [2, 2, 2, 2]
- Attention Mechanism: Applied to skip connections to enhance focus on tumor-relevant regions
- Binary Cross Entropy (BCE) Loss and Adam optimizer

# Tumor Proportion Estimation

- Perform brain segmentation to generate the binary mask for the MRI slice
- Convert the resulting mask into a PyTorch tensor
- Count all white (foreground) pixels in the tensor
- Compute the total number of pixels in the image (height × width)
- Divide the white-pixel count by the total pixel count
- Obtain the tumor proportion for that specific MRI slice

# Brain 3D Reconstruction



- Slice-wise Segmentation with Attention U-Net to generate binary tumor masks
- Compute brain volume by stacking MRI slices along the z-axis
- Compute tumor volume by stacking tumor masks.
- Create an overlapping volume of the brain and tumor, each in a distinct color for easy differentiation.
- Render the 3D object and estimate the tumor volume.
- Mean CNR of 55 samples is : 2.75

# Sample Run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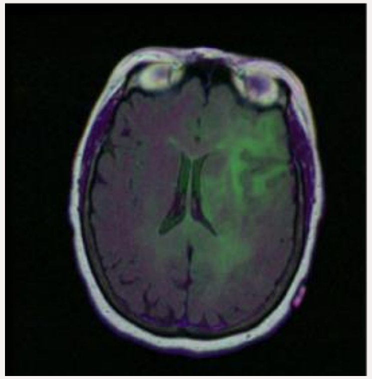
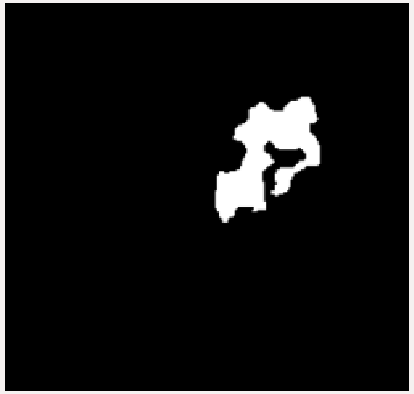
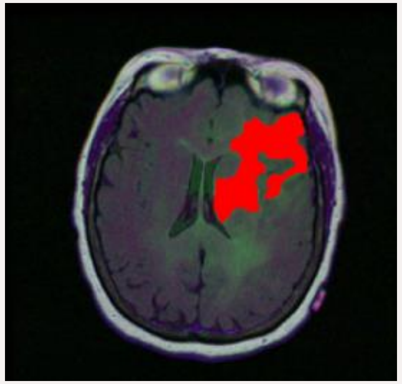
brain_tumor_cl...

# Future Work

- Optimizing the segmentation model to overlay colored tumor regions on the original MRI scan.

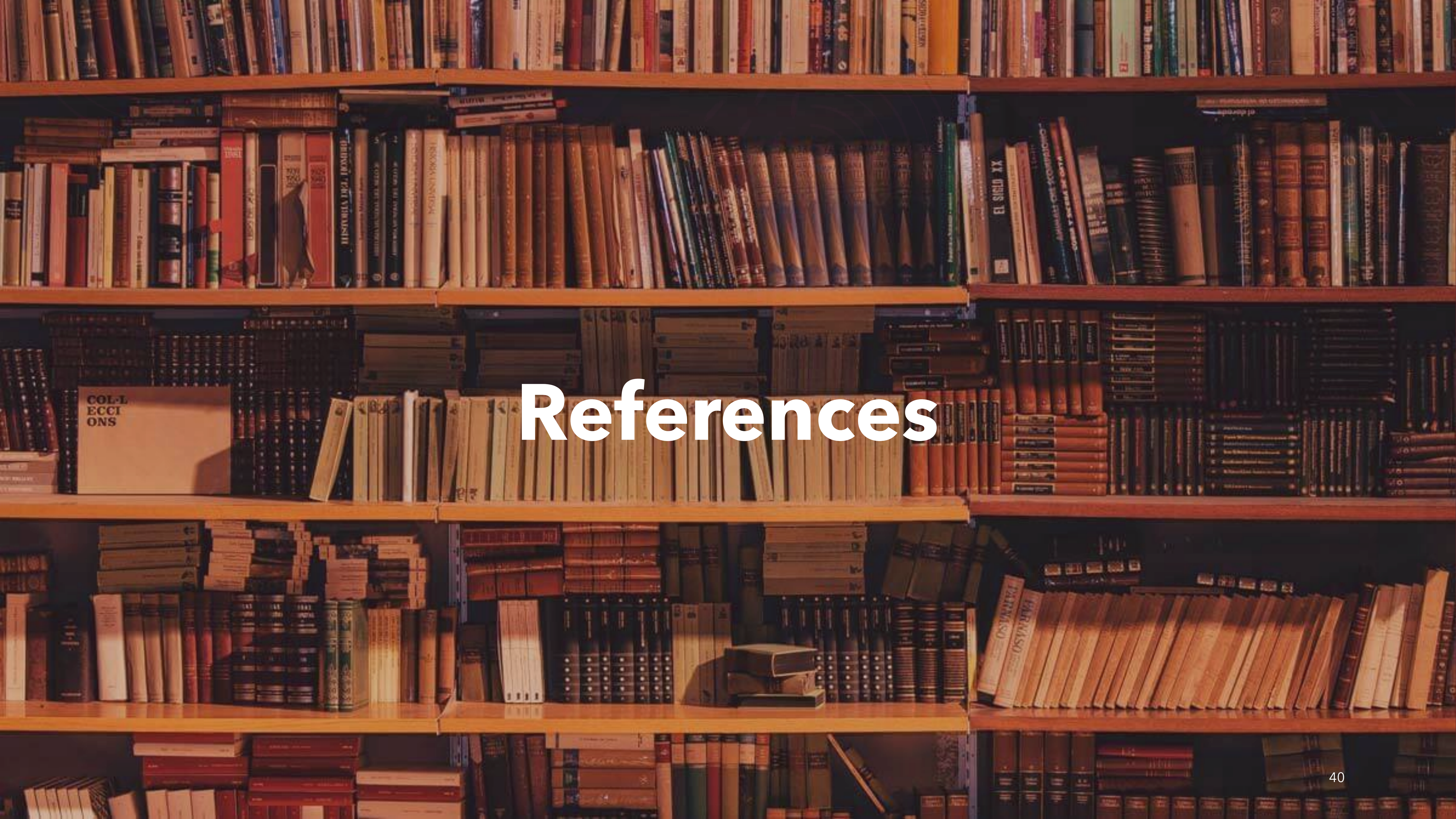
  

- Provide additional information for the medical expert, such as tumor shape, centroid, and growth rate.
- An assistant chatbot that aids medical experts in treatment planning.

# Conclusion

In conclusion, this brain tumor project demonstrates the powerful role of AI in assisting the medical field, particularly in the analysis and visualization of MRI scans. By leveraging deep learning for tumor segmentation and 3D reconstruction, we can accurately localize and measure tumor volumes, enhancing diagnostic precision. The system provides essential insights such as tumor size, shape, and location, which are critical for surgical planning and treatment. With the integration of AI, doctors are supported with faster, more consistent, and data-driven assessments. Ultimately, AI serves not to replace clinicians, but to empower them in delivering better, more informed care to patients.

# References



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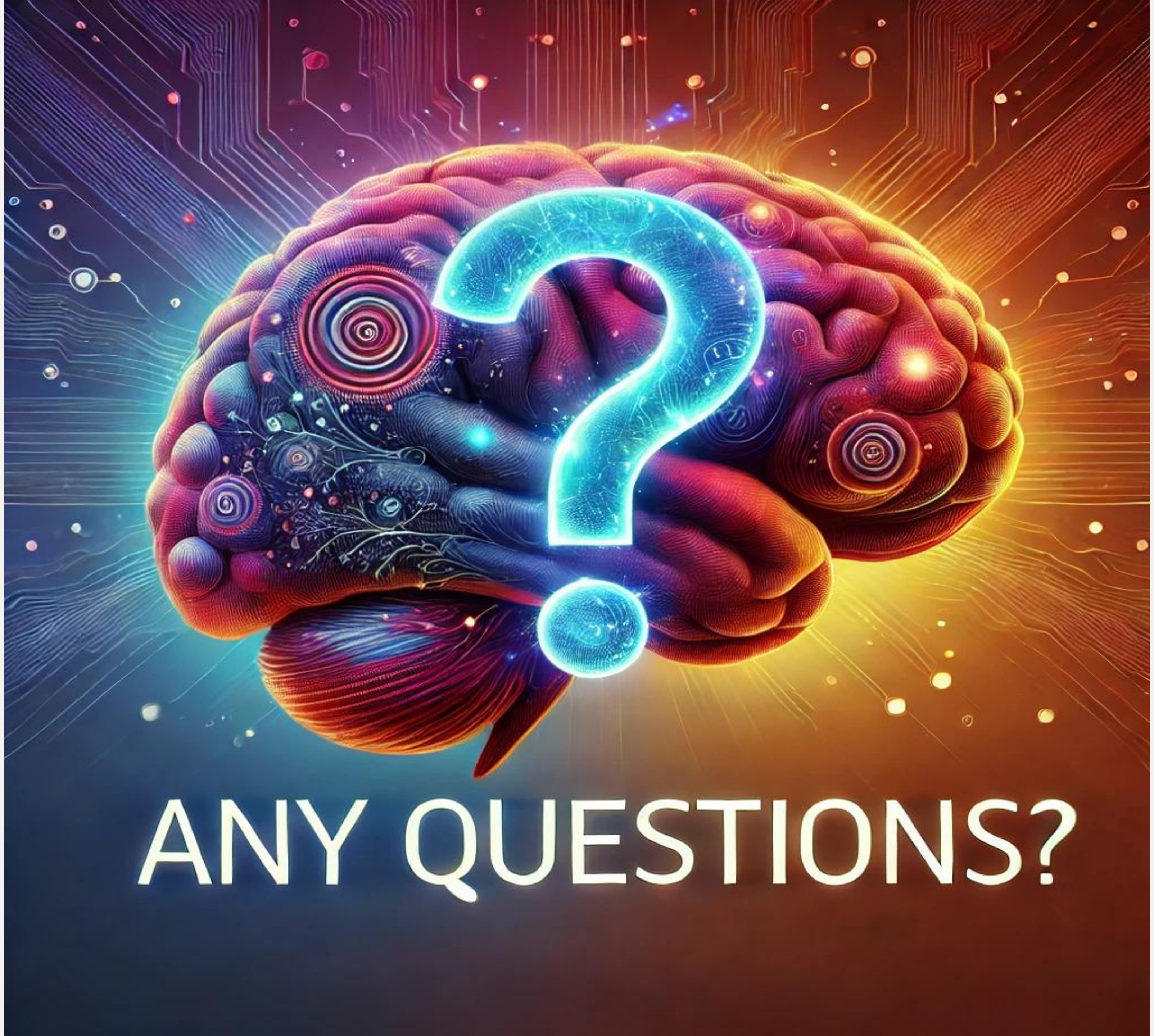
ANY QUESTIONS?


Thank you