TumorLytix: Unsupervised Brain Tumor Detection and Segmentation

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***Abstract*—This report introduces an unsupervised approach for brain tumor detection and segmentation by integrating CycleGAN-based image translation with conditional diffusion models. This method addresses the challenge of limited labeled data in medical imaging through a two-step process. First, CycleGANs are utilized to generate pseudo-paired healthy and tumor-infected image pairs from unpaired datasets, enabling robust anomaly detection. Second, conditional diffusion models refine tumor boundary segmentation through iterative denoising, ensuring precise and accurate delineation of pathological regions. Extensive experiments on the BraTS 2022 dataset, comprising MRI scans from n patients across four modalities (T1w, T1ce, T2w, and Flair), demonstrate that the implemented method achieves enhanced segmentation performance compared to conventional generative frameworks. These results highlight the potential of this approach for advancing unsupervised medical image analysis.**

I. Introduction

The detection and segmentation of brain tumors in medical imaging remain significant challenges due to the reliance on large, annotated datasets. Traditional approaches either frame the problem as a two-class classification task, identifying the presence or absence of tumors, or employ segmentation models such as U-Net and Transformers that require precise ground-truth masks. These methods are effective but impractical in real-world clinical environments, where manual annotation is both time-intensive and resource-prohibitive. Radiologists often spend hours annotating individual scans, making it unrealistic to scale these efforts across large patient populations. Moreover, publicly available datasets like BraTS, while valuable, fail to encompass the full variability of tumor types, sizes, and imaging conditions encountered in diverse clinical settings.

A recent survey on "Deep Learning for Brain Tumor Segmentation" [5] emphasizes that the challenges of supervised methods go beyond their reliance on annotated data. Their scalability is limited by the need for retraining and re-annotation when addressing new tumor types or imaging modalities. Additionally, resource-constrained clinics struggle with the high computational demands and specialized expertise required to deploy these methods effectively. These limitations highlight the urgent need for innovative, adaptable solutions that minimize dependency on annotated data while maintaining high performance. To address these challenges, unsupervised methods have emerged as promising alternatives, leveraging smaller datasets and synthetic augmentation to reduce dependency on manual annotation. Building on these advancements, this report presents a scalable, efficient, and accurate deep-learning framework for brain tumor detection and segmentation.

A. Research Contributions

By eliminating the need for large annotated datasets, this approach aims to deliver a robust solution capable of :

- Minimize reliance on large annotated datasets for accurate tumor detection and segmentation.
- Develop a precise method for segmenting tumor regions with high accuracy.
- Create a scalable and adaptable solution capable of addressing tumor variability in segmentation across diverse clinical settings.

This paper addresses the challenge of accurately segmenting brain tumors in medical images, where traditional CycleGAN methods often struggle due to the introduction of artifacts and distortions. To overcome these limitations, we implement a method that combines the strengths of CycleGAN with diffusion models. While CycleGAN facilitates image domain adaptation, the diffusion model enhances tumor region segmentation by iteratively refining details and preserving anatomical accuracy.

By leveraging the generative capabilities of diffusion models, we make an effort to ensure high segmentation accuracy with fewer errors. Furthermore, the framework's adaptability allows it to generalize across diverse medical settings and tumor variations, making it a robust solution for real-world clinical applications.

II. Related Work

Brain tumor segmentation has traditionally relied on supervised learning methods, which require large amounts of annotated data. However, due to the limited availability of labeled medical datasets, unsupervised and semi-supervised approaches have gained popularity. CycleGAN has shown effectiveness in medical image segmentation, particularly for domain adaptation, as demonstrated in the *CycleGAN-medical-image-segmentation* repository [1]. Despite its advantages, CycleGAN struggles with maintaining structural consistency and can introduce artifacts that degrade segmentation accuracy. Similarly, f-AnoGAN [2] offers a fast, unsupervised method for anomaly detection using GANs, but it primarily focuses on anomaly detection rather than segmentation.

Recently, diffusion models have gained attention for their ability to generate and segment images in an unsupervised manner, producing high-quality results with fewer artifacts. The work *Fast Unsupervised Brain Anomaly Detection and Segmentation with Diffusion Models* [3] presents a probabilistic framework utilizing denoising diffusion processes for enhanced anomaly detection and segmentation. However, these models can be computationally intensive. The combination of CycleGAN and diffusion models, as seen in *Cycle-Diffusion*

[4], demonstrates the potential to merge domain adaptation with detailed generative capabilities for improved segmentation, minimizing the reliance on labeled data. This report builds upon these advancements by proposing a unified pipeline that integrates both CycleGAN and diffusion models, enhancing segmentation accuracy while tackling issues related to training stability and artifact reduction.

III. Methodology

The objective is achieved using two advanced techniques:

1) **CycleGAN for Artificial Tumor Image Generation:** CycleGAN synthesizes artificial tumor images from healthy brain scans. This approach generates pseudo-paired healthy-diseased image pairs, circumventing the reliance on real labeled data.
2) **Conditional Diffusion for Tumor Segmentation:** A conditional diffusion model is utilized to iteratively refine tumor boundary segmentation by transforming noisy inputs into clear reconstructions. This method enables the detection of subtle differences between healthy and diseased regions.

IV. Experiments

Given the limited availability of annotated data, this approach leverages an unpaired dataset consisting of healthy brain MRI scans and tumor-affected brain MRI scans. The primary challenge lies in the unpaired nature of this dataset, as the scans do not correspond to the same brain. To address this, we employ CycleGANs, a powerful generative adversarial network framework, to translate between the two domains. This enables us to exploit the structural differences between healthy and tumor-affected scans, facilitating the detection and segmentation of tumors without the need for paired or annotated data.

A. CYCLE GAN

CycleGAN is a deep learning model designed for image-to-image translation on unpaired datasets, where no direct correspondence exists between the input and output images. In this approach, the task is treated as an image reconstruction problem. Specifically, we work with two unpaired image domains: healthy and tumor-affected brain MRI scans. The objective is to learn the features of one domain and transfer them to the other. for this case, the focus is on extracting tumor textures from the tumor-affected domain and imposing them onto the healthy scan domain, effectively generating paired data.

1) Architecture: The architecture of CycleGAN 1 comprises two main components: generators and discriminators. Generator G learns to generate tumor-infected images from the healthy domain A, while generator F creates corresponding healthy brain MRI scans from the tumor domain B. Each domain is associated with a discriminator that distinguishes between real samples (from the actual dataset) and fake samples (produced by the generator). The interplay between the generators and discriminators improves the model's performance, where generators aim to fool the discriminators, and discriminators strive to identify fake images accurately.

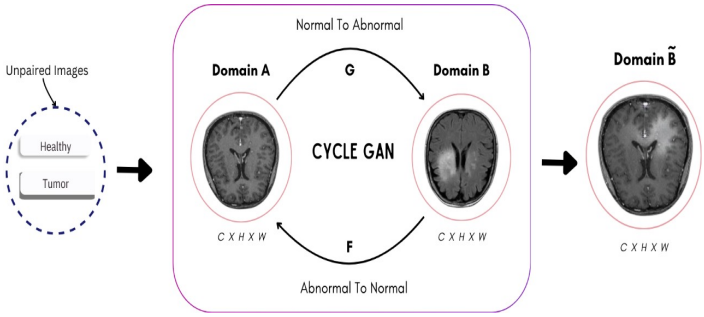

Fig. 1. CYCLE GAN Model Architecture

Each CycleGAN generator has three sections: Encoder, Transformer, and Decoder. The architecture is directly referenced from the original CycleGAN paper [13]. The details of the architecture can be found in 2. Compared to the original implementation, we used the Instance Norm in place of the Batch Norm. Instance Norm is used to normalize each image independently and reduce spatial dependencies between images in a batch to extract high-level content in each image. Additionally, we use Leaky RELU for better gradient stability as it avoids deactivating neurons with negative activation. In discriminator follows a PatchGAN discriminator. The difference between a PatchGAN and a regular GAN discriminator is that rather the regular GAN maps from a 256×256 image to a single scalar output, which signifies "real" or "fake", whereas the PatchGAN maps from 256×256 to 70×70 array of outputs X20, where each Xij signifies whether the patch is in the image is real or fake.

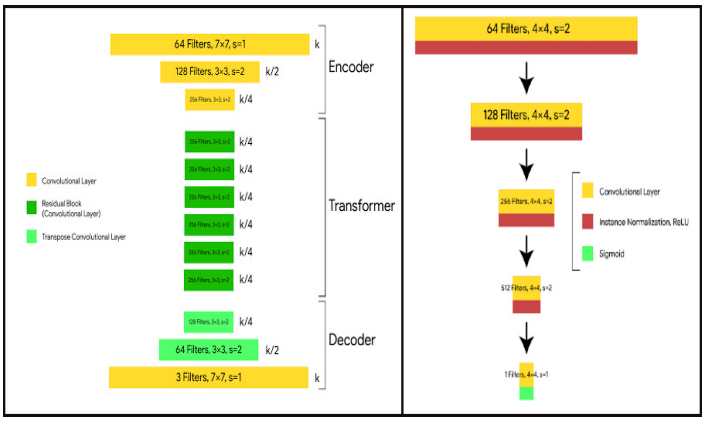

Fig. 2. (Left) - Generator, (Right) - Discriminator

2) Loss Function: The adversarial loss for generator G encourages G to produce images that are indistinguishable from the target domain Y, as determined by the discriminator D_X. Similarly, the adversarial loss for generator F encourages F to produce images that are indistinguishable from the target domain X, as determined by the discriminator D_Y. We implement this using MSE loss function.

$$\text{Loss}_{\text{advers}}(F, D_x, Y, X) = \frac{1}{m} \sum (1 - D_x(F(y)))^2$$

$$\text{Loss}_{\text{advers}}(F, D_x, Y, X) = \frac{1}{m} \sum (1 - D_x(F(y)))^2$$

The cyclic consistency loss ensures that when an image is translated from one domain to another and back, it remains similar to the original. This loss forces the generators G and F to maintain consistency in the transformation process.

$$\mathcal{L}_{cyc}(G, F, X, Y) = \frac{1}{m} \left[(F(G(x_i)) - x_i) + (G(F(y_i)) - y_i) \right]$$

The total loss combines the adversarial and cyclic consistency losses. It ensures that the generators G and F produce realistic images while also maintaining the consistency of the transformations between domains X and Y.

$$\begin{aligned}\mathcal{L}(G, F, D_g, D_f, Y, X) = &\mathcal{L}_{\text{advers}}(G, D_g, X, Y) \\ &+ \mathcal{L}_{\text{advers}}(F, D_f, Y, X) \\ &+ \mathcal{L}_{cyc}(G, F, X, Y)\end{aligned}$$

3) Training Details: For effective training, we Collected over 1500 healthy brain MRI scans and around 3500 tumor brain MRI scans as shown in 4 . On training over 75 epochs in batches of 32 images, we achieved a high accuracy of 88.2% in tumor image generation and an accuracy of 73.7% in healthy image generation as seen in 3

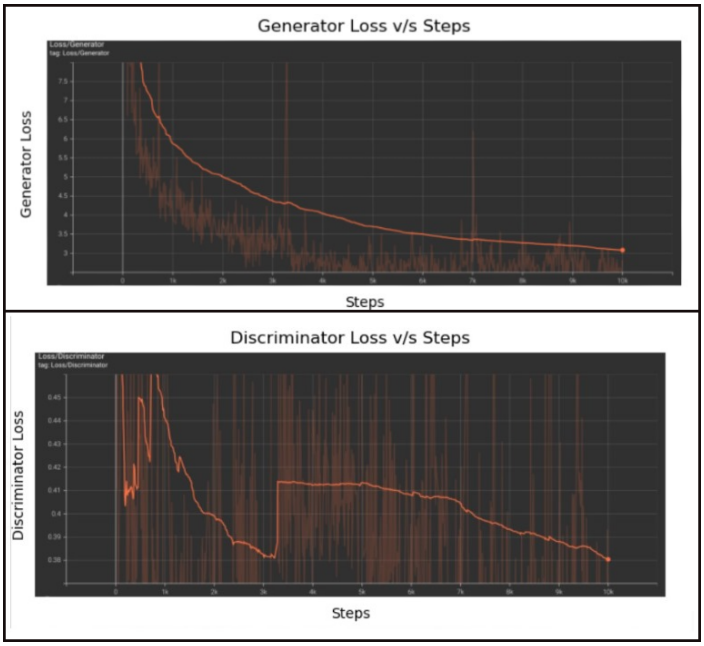

Fig. 3. Training Output - Loss curves

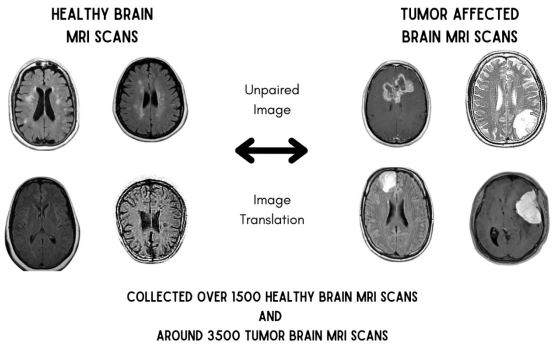

Fig. 4. Training Data Sample

4) Experimental Results: Generated paired healthy-tumor data 5.

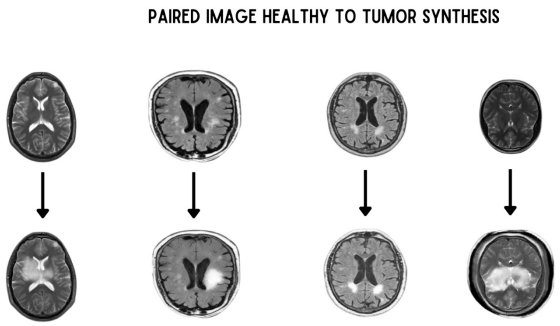

Fig. 5. Paired Data generation(Healthy to Tumor)

5) Limitations/ Research Gap: CycleGAN often struggles in reconstructing healthy images 6 from tumor-affected images due to several inherent limitations in its design and approach.

- **Mode Collapse** : CycleGAN experience mode collapse, producing limited outputs that fail to capture the diverse and irregular features of tumors. This leads to reconstruction errors, where healthy images lack fine details or exhibit repetitive patterns.
- **Unrealistic Reconstructions**: CycleGAN's adversarial loss promotes realism but lacks clinical plausibility, resulting in unrealistic reconstructions. This can lead to biologically implausible outputs, such as misinterpreting tumors as noise and erasing healthy tissues, making the reconstruction unreliable for medical diagnostics.
- **Indirect Likelihood Maximization**: CycleGAN does not optimize a likelihood-based objective like diffusion models, leading to a lack of fine-detail fidelity. This makes it struggle to capture subtle details in medical images, whereas diffusion models refine images incrementally, preserving critical details.
- **Generalization Challenges** : Tumors' variability in shape, size, location, and texture challenges CycleGAN's ability to generalize. This leads to inconsistent mappings between tumor and healthy domains, resulting in inaccurate reconstructions, such as uneven tumor removal or failure to restore healthy tissue patterns.

Without likelihood maximization, CycleGAN cannot guarantee that its generated images adhere to the true data distribution of healthy images. This is critical in medical applications where even small inaccuracies can undermine diagnostic reliability. To overcome these limitations, we encountered diffusion models as a plausible alternative. Diffusion models iteratively refine noisy inputs to generate high-resolution, detailed outputs. They optimize likelihood to model data distributions, incrementally adding details, and handle complex data better, capturing subtle features like tissue textures and tumor boundaries.

Fig. 6. CycleGAN Limitations

B. COMBINED APPROACH

1) Conditional Diffusion Models: Brain tumors significantly affect human health, necessitating accurate detection and segmentation from MRI scans for diagnosis and treatment planning. The sourced diffusion-based model 7 addresses these

challenges by offering robust reconstruction of tumor-infected images [7] [3], enabling:

- Healthy Image Reconstruction: Generating tumor-free images allows the isolation of anomalies by subtractive comparison with the input image.
- Tumor Segmentation: Precise delineation of tumor regions aids in diagnosis and therapeutic interventions.
- Noise Handling: The model is resilient to real-world noise, often present in MRI images, ensuring reliable performance.

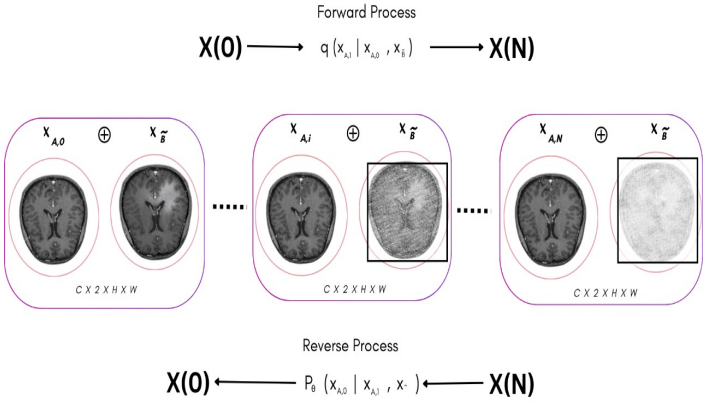

Fig. 7. Joint Probability Diffusion Model

2) U-Net Architecture: In the initial approach, we utilized a standard U-Net architecture for segmentation tasks. However, this model faced challenges in retaining spatial details and failed to deliver consistent results in detecting tumor regions. The shortcomings were primarily due to limited feature extraction capabilities and suboptimal reconstruction accuracy. To overcome these limitations, we referred to an enhanced architecture incorporating self-attentions, residual blocks and skip connections, which significantly improved spatial precision and anomaly detection performance [14] [15].

- **Encoder:** The encoder extracts hierarchical features at multiple scales

  1. Residual Blocks

  $$y = \mathcal{F}(x, \{W_i\}) + x$$

  Here, $\mathcal{F}$ represents the learned residual mapping, ensuring information flow through skip connections. This prevents the loss of critical spatial details.

  2. Feature Down-sampling: Strided convolutions reduce the spatial resolution, enabling multi-scale representation.

- **Bottleneck:** Feature Compression: Bottleneck layers compress extracted features into a latent space representation:

  $$z = f_{\text{bottleneck}}(y)$$

  This latent representation captures essential information, reducing computational overhead.

- **Decoder:** The decoder reconstructs the input image:

  1. Transposed Convolutions: Perform up-sampling, reversing the compression from the bottleneck.

  2. Feature Concatenation: Skip connections concatenate encoder features with up-sampled features to preserve spatial accuracy:

  $$o_i = \text{Concat}(e_i, d_i)$$

3) Forward Process(Noise Addition): Transforms data into Gaussian noise via iterative Markov steps. the forward process systematically adds noise to an MRI image x_A turning it into a noisy version $noisy_{x_A}$

$$\text{noisy}_{x_A} = \sqrt{\alpha_t} \cdot x_A + \sqrt{1 - \alpha_t^2} \cdot \text{noise}$$

Where,

x_A: Input MRI image.
α_t: Noise schedule at time t,
noise: Random Gaussian noise added to the image.

This process creates a noisy version of x_A, helping the model learn to reconstruct it during the reverse process.

4) Reverse Process(Denoising): The reverse process is handled by the Improved U-Net, which denoises the noisy MRI scan step-by-step. The model receives:

1. The noisy image $noisy_{x_A}$
2. A paired condition image(x_B, potentially an anomaly map)

These inputs are combined as:

$$\textbf{input\_tensor} = \textbf{torch.cat}([\textbf{noisy}_{x_A}, x_B], \textbf{dim} = 1)$$

The U-Net reconstructs the original MRI (x_A) by predicting and removing the noise iteratively. Loss is calculated as:

$$\mathcal{L} = \textbf{MSE}(\textbf{reconstructed}_{x_A}, x_A)$$

5) Noise Schedule: The noise schedule is implemented using:

$$\beta_t = \textbf{linspace}(0.01, 0.999, \textbf{timesteps})$$

This linearly spaced schedule defines the variance β_t, which controls the intensity of noise at each time step.

6) Training Workflow:

- **Inputs:** Paired datasets (x_A: normal MRI, x_B: abnormal or conditional MRI).
- **Forward Pass:** Noise is added to x_A at time t, producing $noisy_{x_A}$.
- **Reconstruction:** The U-Net denoises $noisy_{x_A}$ using both the noisy image and the paired image (x_B).
- **Loss Calculation:** Mean Squared Error (MSE) is calculated between the reconstructed MRI and the original x_A:

$$\mathcal{L} = \sum_{i=1}^{n} \left(\text{reconstructed } x_A^{(i)} - x_A^{(i)} \right)^2 \tag{1}$$

- **Optimization:** The model parameters are updated using Adam optimizer to minimize the loss.

7) Training Results: The Diffusion model was trained on batches of 300 images over 50 epochs, utilizing the Adam optimizer and Mean Squared Error (MSE) as the loss function. This approach achieved a denoised or reconstructed representation of healthy images with an accuracy of 92.17% 8.

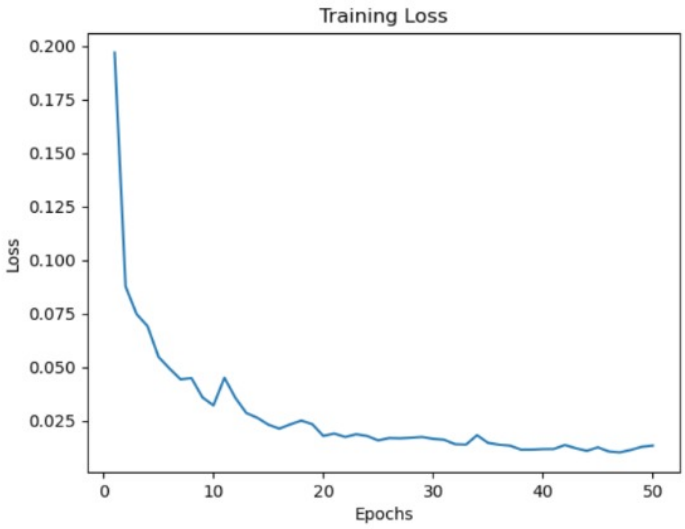

Fig. 8. Training Output: Loss Curve

C. Segmentation Mask

The segmentation process focuses on detecting and isolating tumor regions in medical images by leveraging differences between the original tumor image and its reconstructed healthy counterpart, created by the diffusion model. The methodology 9 involves the following steps:

- **Original Tumor Image:** Represents the input image from the dataset, showing the brain with visible tumor regions. Acts as the primary data for tumor detection.
- **Reconstructed Healthy Image:** Generated by the diffusion model, simulating how the brain would appear without any abnormalities. Provides a baseline for comparing and detecting anomalies.
- **Anomaly Map:** Calculated as the pixel-wise absolute difference between the tumor image and the reconstructed healthy image. Highlights areas of significant difference, which correspond to tumor regions.
- **Segmentation Mask:** Created by applying a threshold to the anomaly map to distinguish tumor areas. Refined using morphological operations to remove noise and ensure accurate delineation of tumor boundaries.
- **Overlay Image:** Combines the segmentation mask with the original tumor image for intuitive visualization. Highlights the tumor in a distinguishable color (e.g., red or yellow) over the grayscale tumor image.

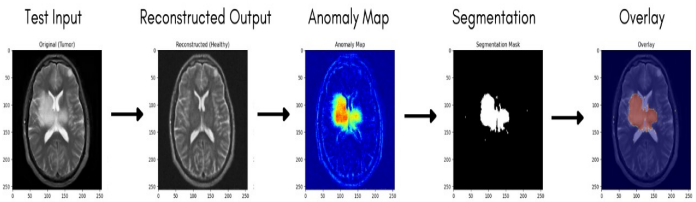

Fig. 9. Segmentation Process Flow: From Test Input to Overlay

1) Results for CycleGANs: 10 Segmentation with CycleGANs shows potential for anomaly detection but suffers from reconstruction inconsistencies and artifacts, which reduce the reliability of the results. Diffusion models, on the other hand, provide more accurate healthy reconstructions and cleaner segmentation masks, making them a better option for medical imaging tasks.

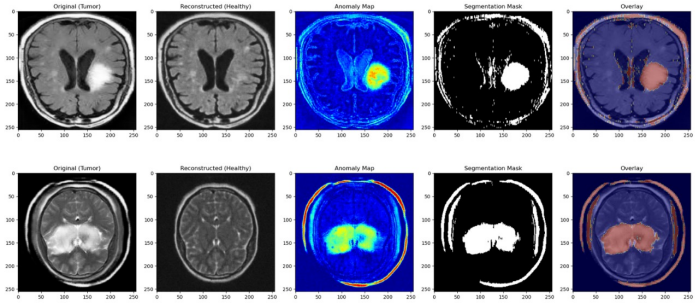

Fig. 10. Segmentation Process applied on CycleGAN

2) Results for Combined Approach: 11 The combined approach of CycleGANs and diffusion models improves tumor reconstruction and segmentation by leveraging diffusion models' accurate healthy image reconstructions. This leads to more refined segmentation masks, better tumor localization, and reduced artifacts, enhancing medical imaging diagnostics.

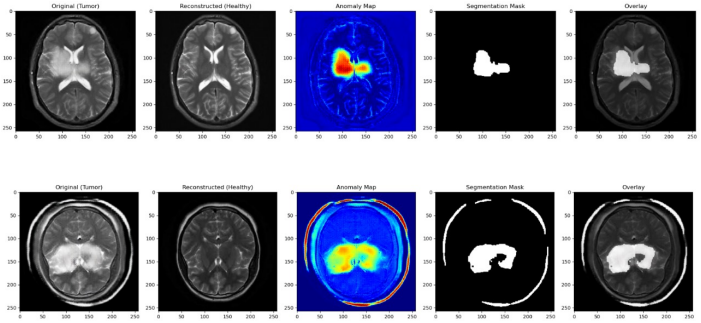

Fig. 11. Segmentation Process applied on Combined Approach

V. Evaluation

1) Ground truth: Since we lacked the necessary ground truth to assess the accuracy of the segmentation, we manually created the masks using classical image processing techniques. This enabled us to generate the required masks and obtain an accurate binary mask for evaluation. An example of the same is shown in Fig. 12.

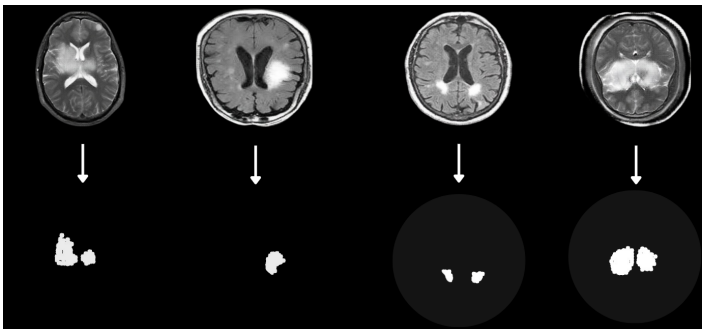

Fig. 12. Manually generated ground truth

2) Evaluation Metrics: To compare the output of two models we have used 3 evaluation metrics:

- **Recall**: Measures the model's ability to identify all relevant brain tumor regions in the segmentation task.
- **Precision**: Quantifies the accuracy of the model by evaluating the proportion of correctly identified tumor regions out of all detected regions.
- **Dice Coefficient**: Assesses the overlap between the predicted tumor segmentation and the ground truth, balancing precision and recall.

As we can see in the I our combined model has outperformed CycleGANs, in the majority of the cases hence showcase greater accuracy and completeness in predictions.

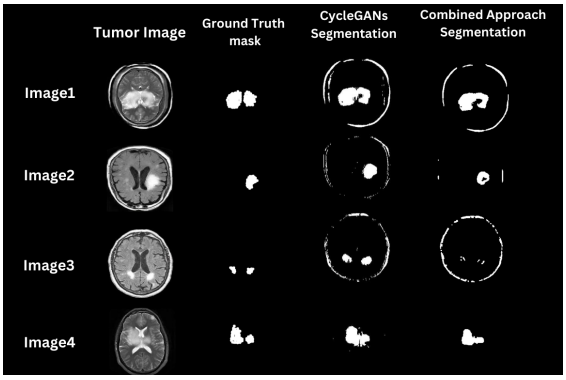

Fig. 13. Test Sample data for evaluation

File	Model	Dice Coefficient	Precision	Recall
Image1	Combined Approach	0.801097	0.866008	0.745238
Image2	Combined Approach	0.673167	0.569993	0.821946
Image3	Combined Approach	0.088042	0.057842	0.184235
Image4	Combined Approach	0.696288	0.600971	0.827540
Image1	CycleGAN	0.818890	0.743547	0.911224
Image2	CycleGAN	0.633294	0.492967	0.885300
Image3	CycleGAN	0.376559	0.240152	0.871677
Image4	CycleGAN	0.563203	0.393972	0.987299

TABLE I
EVALUATION METRICS FOR DIFFERENT MODELS

VI. CONCLUSION

We implemented a model that combines CycleGANs and diffusion models for brain tumor detection and segmentation. This model outperforms CycleGAN alone, particularly in terms of accuracy and precision in identifying tumor boundaries. By integrating these models, we improve segmentation performance and achieve more accurate tumor regions. Additionally, the unsupervised nature of the model eliminates the need for labeled datasets, enabling robust tumor localization using pseudo-paired data.

VII. FUTURE WORK

For the next step, we can integrate a CNN model to classify different brain tumor types, improving diagnostic accuracy. Using a variety of modalities, such as T1, fMRI, and FLAIR, instead of just T1C, would enhance the system's versatility. Incorporating patient-specific factors like age, genetics, and tumor grade could make the segmentation results more clinically relevant. These advancements would strengthen the model's potential for scalable and effective use in brain tumor detection and segmentation.

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