A Comprehensive Framework Analysis of Cycle GAN-Based Modality Translation: Enhancing Brain Tumor Diagnostics from FLAIR to T2w

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***Abstract*—Brain tumors remain a major healthcare challenge due to their complexity, high mortality rates, and profound impact on patients' lives, making accurate diagnosis and treatment crucial. Multi-modal MRI scans, particularly FLAIR and T2-weighted (T2w) images, offer complementary information about tumor structure and progression. However, real-world clinical settings often face the challenge of missing imaging modalities, limiting comprehensive assessments. To address this issue, we propose a CycleGAN-based framework for translating between FLAIR and T2w MRI scans using the BraTS dataset from the Medical Decathlon Challenge. This dataset includes 3D MRI scans with segmentation masks outlining key tumor regions such as edema, non-enhancing tumor, and enhancing tumor. Our framework uses U-Net-based generators and PatchGAN discriminators, optimized with multiple loss functions, including adversarial, cycle consistency, structural similarity index (SSIM), and pixel-wise losses. These ensure that the generated images are both anatomically accurate and visually realistic. We apply preprocessing steps like intensity normalization, background removal, and data augmentation to maintain structural details and enhance training stability. Our quantitative evaluation shows promising results, achieving SSIM scores of 0.8226 for T2w and 0.7767 for FLAIR. Qualitative analysis further highlights improved tumor visibility and clearer anatomical structures, particularly around tumor boundaries. By addressing the challenge of incomplete imaging datasets, our method not only enhances data availability for tasks like tumor segmentation but also supports more comprehensive diagnostic workflows. This approach represents a step forward in advancing precision medicine for brain tumor analysis through multi-modal MRI synthesis.**

***Index Terms*—Brain Tumor, Multi-modal MRI, CycleGAN, Image-to-Image Translation, Medical Imaging Enhancement**

I. Introduction

BRAIN tumors are among the most prevalent and deadly forms of cancer, with the World Health Organization (WHO) estimating that over 700,000 new cases of primary brain and central nervous system (CNS) tumors are diagnosed annually worldwide [1]. Brain tumor detection and analysis are crucial in medical imaging as they can significantly influence diagnosis, treatment, and prognosis. Neuroimaging techniques, such as MRI scans, are the gold standard for visualizing brain tumors due to their non-invasive nature and high resolution [2]. However, the complexity of brain tumor characteristics—such as their varying shapes, sizes, and locations—makes manual tumor segmentation both time-consuming and error-prone [3]. Thus, automation in brain tumor analysis is becoming increasingly important [4]. This research addresses the challenges of traditional methods for detecting brain tumors, particularly the issues with accuracy and efficiency in manual segmentation. Manual methods often struggle to distinguish between tumor types like gliomas, meningiomas, and metastases, and are prone to errors due to operator variability [5]. Automated systems also face difficulties with different MRI sequences, such as FLAIR and T2-weighted images, which vary in contrast and resolution, leading to inconsistent results. This highlights the need for more advanced automated systems that can provide faster, more accurate, and consistent tumor segmentation [6]. The proposed approach uses a dual-task Generative Adversarial Network (GAN) with CycleGANs to translate images between FLAIR and T2-weighted MRI scans, based on a UNet architecture. CycleGANs are ideal as they work with unpaired datasets, common in medical imaging. The framework includes two generators: one to convert FLAIR to T2-weighted images and the other to do the reverse. Cycle-consistency loss ensures important tumor features are preserved, improving segmentation accuracy. Using both MRI modalities enhances tumor boundary detection and segmentation, employing perceptual losses like SSIM and

pixel-wise loss to refine the model's performance. Specifically, the framework will learn to generate synthetic T2-weighted images from FLAIR images and vice versa, thus improving the reliability and accuracy of brain tumor segmentation. The expected outcomes include improved segmentation accuracy, better generalization to new MRI scans, and more effective tumor detection using both FLAIR and T2-weighted MRI data. By integrating SSIM and pixel-wise loss, the model will enhance both perceptual and pixel-level accuracy.

II. Literature Review

Gupta et al. [7] Gupta et al. (2021) explore using CycleGANs for brain tumor detection and classification with MRI scans, combining them with InceptionResNetV2 for classification. Their approach uses CycleGANs to generate synthetic MRI images for data augmentation and image translation between different MRI modalities, improving classification accuracy. While this method shows promise, it focuses mainly on data augmentation and relies on pre-trained models. In contrast, our research integrates CycleGANs for FLAIR to T2-weighted MRI translation followed by UNet-based segmentation, directly enhancing tumor segmentation and boundary delineation. This makes our approach more versatile and focused on improving segmentation across multiple tumor types and MRI modalities.

Mohammadi Azni et al. [8] focus on improving brain tumor segmentation by integrating CycleGANs with deep learning models for multi-channel MRI images. Their two-step approach first uses CycleGAN to generate synthetic features from different MRI modalities, which are then used by segmentation networks. Transfer learning further enhances feature extraction, improving segmentation accuracy. While their study uses CycleGANs for feature extraction and segmentation, our research integrates CycleGANs for FLAIR to T2-weighted MRI translation followed by a UNet-based segmentation network in a single pipeline. This enables more precise tumor boundary delineation and improves model generalization across multiple modalities and datasets, addressing challenges like data scarcity and modality variability.

Wang et al. [9] propose a Two-Stage Generative Model (TSGM) combining CycleGANs with Variance Exploding stochastic differential equations (VE-JP) for brain tumor detection. The first stage generates synthetic abnormal MRI images using CycleGANs, and the second stage reconstructs healthy regions, highlighting tumor abnormalities. This model incorporates multi-modal MRI data to improve segmentation accuracy. While Wang et al. (2022) use a two-stage framework, our approach integrates CycleGANs for MRI modality translation (e.g., FLAIR to T2-weighted) and tumor segmentation within a single UNet-based pipeline. This unified model directly improves tumor boundary delineation and addresses challenges like data scarcity and modality variability.

Xue et al. [10] reviews deep learning methods for multi-modal tumor segmentation, highlighting the importance of combining data from various MRI modalities (T1, T2, FLAIR) for more accurate segmentation. The authors discuss architectures like CNNs, U-Net, and CycleGANs, emphasizing the challenges of handling modality variability and the need for large annotated datasets. Despite advancements, they point out issues with generalization across diverse datasets and imaging protocols.While Xue et al. focus on the general benefits of multi-modal segmentation, my research integrates CycleGANs for FLAIR to T2-weighted image translation, followed by UNet-based segmentation in a unified pipeline. This approach directly improves tumor boundary delineation, optimizing both translation and segmentation in one model. Unlike their work, which uses separate models for each task, my research also focuses on enhancing model generalization across various MRI modalities, addressing challenges like data scarcity and modality-specific variability.

Veit et al. [11] explore using CycleGANs for data augmentation in CT image segmentation, specifically transforming contrast-enhanced CT images into non-contrast images to augment the training dataset. They show that using synthetic data generated by CycleGANs significantly improves the segmentation performance of a U-Net model, especially in out-of-distribution scenarios, enhancing model generalization. While Veit et al. (2019) focus on CycleGAN-based data augmentation for CT segmentation, my research applies CycleGANs for multi-modal MRI translation (FLAIR to T2-weighted images), followed by UNet-based segmentation in a unified pipeline. This approach directly targets tumor segmentation, improving both image translation and segmentation accuracy, unlike their separate augmentation and segmentation process.

Li et al. [12] focus on the use of deep convolutional neural networks (CNNs) for brain tumor classification using multi-modal MRI data. They propose a hybrid model combining CNNs with recurrent neural networks (RNNs) to capture both spatial and temporal features in MRI scans. The model is designed to handle the inherent temporal changes in tumor growth by analyzing MRI scans taken at different time points. Their method achieves high accuracy in classifying tumors into various types and stages. In contrast, our research utilizes CycleGANs for FLAIR to T2-weighted MRI translation, followed by UNet-based segmentation, focusing on direct tumor boundary delineation rather than classification. Unlike Li et al.'s hybrid approach, which integrates temporal features for classification, our framework aims to improve segmentation accuracy and model generalization across MRI modalities.
In conclusion, the related work section compares various deep learning methods for brain tumor segmentation, with an emphasis on CycleGANs and multi-modal MRI data. Our framework advances brain tumor segmentation by addressing challenges related to data scarcity, modality variability, and model generalization.

III. Datasets

A. Data Collection & Preprocessing

The information used in this research information from the Brain Tumor Segmentation (BraTS) Dataset, which is regularly updated the TASK01_BrainTumor section from the

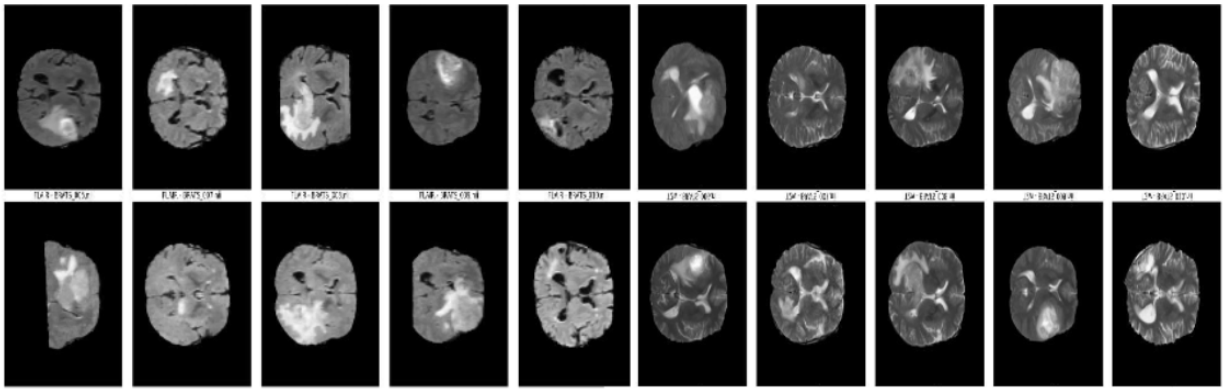

Fig. 1. Overview of Datasets

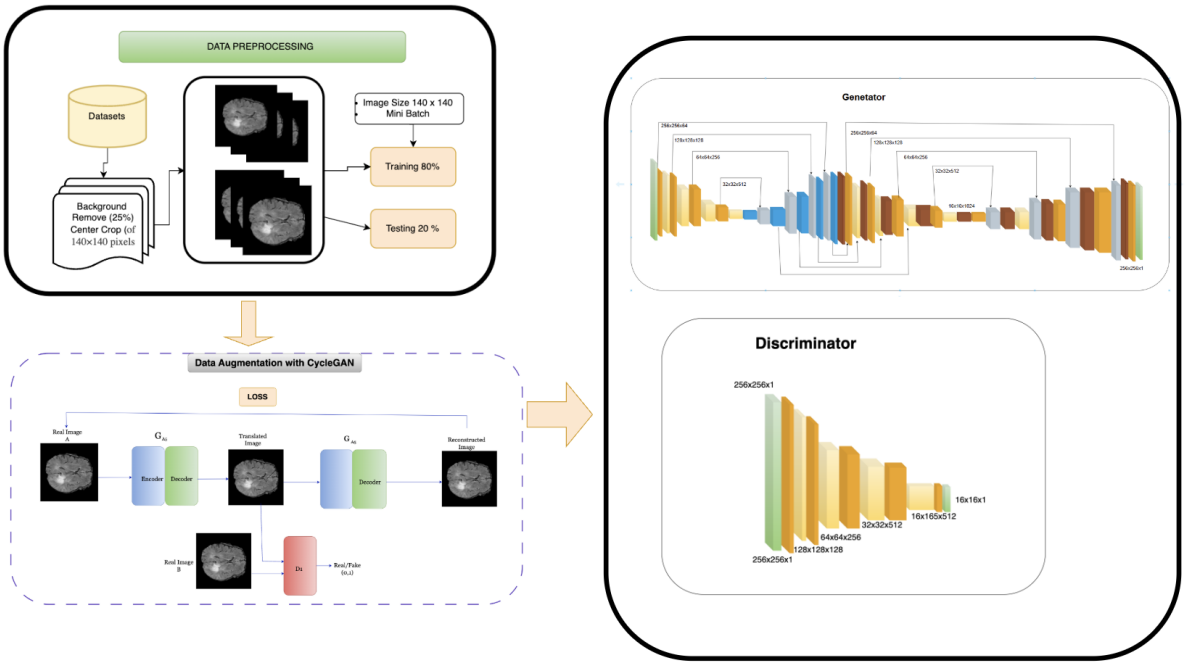

Fig. 2. Workflow Diagram of CycleGAN Architecture

Medical Decathlon Challenge is the primary dataset used in this project. It includes four MRI modalities: T1-weighted (T1), T1-weighted with contrast (T1-Gd), T2-weighted (T2), and FLAIR (Fluid-Attenuated Inversion Recovery), each offering a comprehensive view of brain structure and pathology. Tumors are labeled and categorized into regions like necrotic/non-enhancing tumor core, peritumoral edema, and enhancing tumor. Figure 1 shows the overview of the BraTS dataset includes 3D MRI volumes with a typical resolution of 240x240x155 (Height x Width x Depth), with multiple 2D slices representing cross-sectional views of the brain. Each patient has four 3D volumes (one for each modality), resulting in a total of 620 2D slices per patient (155 slices for each modality). The dataset includes both High-Grade Gliomas (HGG) and Low-Grade Gliomas (LGG), which helps the model generalize better. we mainly use CycleGAN to change unpaired images with FLAIR and T2 modalities. To get the model ready for changing FLAIR images into T2-like images and the other way around, 3D volumes are handled by extracting 2D slices. The data preprocessing for the BraTS dataset begins by extracting the FLAIR (index 0) and T2-weighted (index 3) MRI modalities from the original 3D volumes sized 240×240×155. To focus on meaningful anatomical regions, slices containing more than 75% background were excluded, reducing computational overhead and ensuring the network primarily learned from slices with relevant tissue structures. Central cropping was performed to standardize the resolution, extracting 140×140 pixel slices centered on the region of interest, thereby removing extraneous areas and aligning brain structures consistently across samples. Each 3D volume was

then split along the axial axis, producing 155 two-dimensional slices per modality, resulting in a large dataset (750,000 slices) for training. This slice extraction step enhanced the dataset size and enabled the model to learn robust 2D relationships. Intensity normalization was applied using min-max scaling to normalize intensities to the [0, 1] range, mitigating variations between scans and improving the stability of training by ensuring a consistent input range. To prevent overfitting and ensure robust generalization, the slices were randomly shuffled and split into training and testing sets. Furthermore, data augmentation techniques, including horizontal/vertical flipping, small-angle rotations, and scaling, were applied to improve the model's generalization capabilities. These augmentations simulated imaging variations encountered in clinical practice, enhancing the model's resilience to differences in orientation, positioning, and contrast.

IV. Methodology

A. Model Architecture

Figure 2 shows the proposed framework leverages a CycleGAN architecture comprising two U-Net-based generators and one PatchGAN discriminator.

*1) **Overview of CycleGAN Model**:* The core implementation of the CycleGAN architecture establishes bidirectional mappings between two distinct image domains—in this case, the FLAIR and T2w MRI modalities. This is achieved using two generator networks and a shared discriminator architecture. Each generator employs a U-Net-inspired encoder-decoder structure, wherein the encoder extracts multi-scale features from input slices via a sequence of convolutional and downsampling layers. The decoder reconstructs the target domain image through transposed convolutions, supported by skip connections that retain spatially localized information critical for structural fidelity. [9] Complementing these generators, a PatchGAN discriminator evaluates the realism of synthesized images at the patch level, focusing on local features rather than the global image context to enhance fine-grained details. The training process involves alternating updates to the generator and discriminator networks. Generators are trained to minimize a composite loss function, which integrates adversarial loss to encourage realism, cycle-consistency loss to enforce bijective mappings, structural similarity (SSIM) loss to preserve perceptual quality, and pixel-wise loss to ensure low-level accuracy. In parallel, the discriminator is optimized to accurately differentiate between real and generated images at the patch scale. This adversarial interplay drives the generators to produce outputs that not only deceive the discriminator but also maintain structural and domain consistency. The training pipeline leverages PyTorch for efficient gradient computation and backpropagation. Feedback from the PatchGAN discriminator, combined with composite loss functions, guides the optimization of generator weights. This stable adversarial learning process enables high-quality, unpaired image translation between FLAIR and T2w MRI scans. The architecture ensures modality synthesis with strong structural preservation, offering a robust solution for medical imaging tasks.

*2) **Generators (U-Net-based)**:* The generators ($G_{FLAIR \to T2w}$ and $G_{T2w \to FLAIR}$) are designed using U-Net, a fully convolutional network with skip connections. This architecture efficiently captures multi-scale information, ensuring high-quality image synthesis while preserving anatomical structures. The encoder consists of sequential convolutional blocks with batch normalization and ReLU activation, progressively downsampling the input, while the decoder uses transposed convolutional layers for upsampling and incorporates skip connections to the corresponding encoder layers to retain spatial details. [13]

*3) **Discriminator (PatchGAN)**:* The PatchGAN-based discriminator distinguishes between real and generated images at the patch level, enhancing the realism of generated images by focusing on local textures. It is composed of convolutional layers with LeakyReLU activation and instance normalization. The output is a probability map where each value indicates the authenticity of a specific patch [14].

B. Loss Functions

Multiple loss functions are combined to ensure that the generated images are both realistic and structurally consistent with the original modality:

- **Adversarial Loss:** Encourages generators to produce realistic images that fool the discriminator. [15]

$$\mathcal{L}_{adv}(G, D) = \mathbb{E}_{x \sim p_{data}}[\log D(x)] + \mathbb{E}_{z \sim p_z}[\log(1 - D(G(z)))] \quad (1)$$

- **Cycle Consistency Loss:** Enforces the preservation of anatomical features by penalizing deviations when translating images back to the original modality [16].

$$\mathcal{L}_{cycle}(G_{F \to T}, G_{T \to F}) = \|G_{T \to F}(G_{F \to T}(FLAIR)) - FLAIR\| + \|G_{F \to T}(G_{T \to F}(T2w)) - T2w\| \quad (2)$$

- **Structural Similarity Index (SSIM) Loss:** Ensures the generated images retain structural and perceptual quality [15].

$$\mathcal{L}_{SSIM} = 1 - \text{SSIM}(G(x), y) \quad (3)$$

- **Pixel-wise Loss:** Reduces pixel-level differences between generated and target images using Mean Squared Error (MSE) [17].

$$\mathcal{L}_{pixel} = \|G(x) - y\|^2 \quad (4)$$

The total loss is computed as:

$$\mathcal{L}_{total} = \mathcal{L}_{adv} + \lambda_{cycle}\mathcal{L}_{cycle} + \lambda_{SSIM}\mathcal{L}_{SSIM} + \lambda_{pixel}\mathcal{L}_{pixel} \quad (5)$$

[18]

C. Training Pipeline & Implementation Details

The training pipeline involves alternating updates for the generator and discriminator to ensure effective learning. During generator training, synthetic images are generated (e.g., $G_{FLAIR \to T2w}(FLAIR)$), and the original

modality is reconstructed using cycle consistency (e.g., $G_{T2w \to FLAIR}(G_{FLAIR \to T2w}(FLAIR))$) [19]. The total generator loss is computed and backpropagated. For discriminator training, the discriminator is trained to differentiate between real and synthetic images by computing adversarial loss for both, updating its weights accordingly. The evaluation step involves assessing the quality of generated images using metrics such as Structural Similarity Index Measure (SSIM), Peak Signal-to-Noise Ratio (PSNR), and Mean Squared Error (MSE). The implementation details include training on GPUs for computational efficiency, utilizing Adam optimizers with a learning rate of 2×10^{-4}. A mini-batch size is employed to accommodate the large size of MRI data, and the models are trained for 10 epochs with periodic monitoring of loss curves and validation results [20].

V. Results

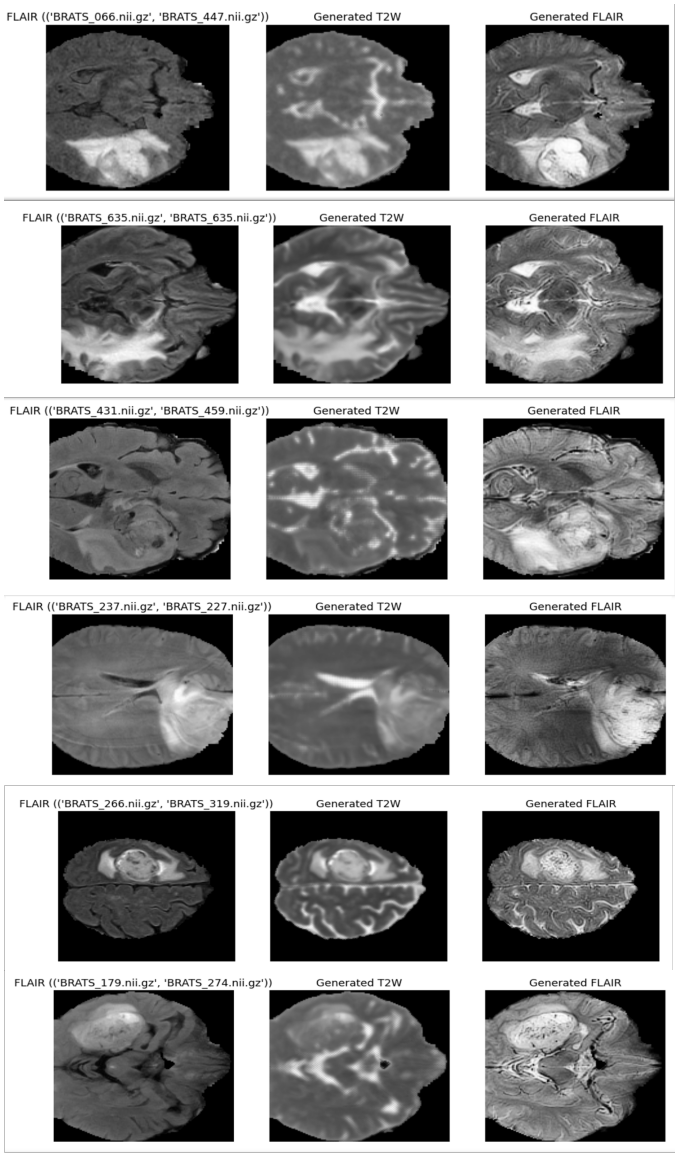

Fig. 3. Overview of Generated synthetic Images from flair to T2w

A. *Qualitative Results - Generated images*

To evaluate CycleGAN's performance, we analyzed 264 test images, with six examples shown in Figure 3. The generated T2W images preserve anatomical structures and closely resemble original T2W scans. The translated FLAIR images show improved clarity and tumor boundary contrast, enhancing diagnostic visibility. Despite minor noise, structural integrity is maintained, validating CycleGAN's effectiveness in modality translation.

Table 1 summarizes CycleGAN's performance. The model achieved an average SSIM of 0.8226 for T2W and 0.7767 for FLAIR, indicating strong structural similarity in generated images. A low test loss of 0.0391 confirms accurate and consistent modality translation. These results validate CycleGAN's effectiveness for high-quality medical image generation.

TABLE I
Results of the Model Performance Metrics

Metric	Value
Average SSIM (T2w)	0.8226488021878994
Average SSIM (FLAIR)	0.7767238470762636
Average Test Loss	0.03911158226507443

B. *Training and testing loss trends*

In Figure 4, we present the training and testing loss curves, both calculated using SSIM loss, where the testing SSIM loss is defined as

$$\begin{aligned}\text{SSIM Testing Loss} = 1 - \text{SSIM\_loss}(\text{fake\_T2w}, \text{T2w}) \\ + \text{SSIM\_loss}(\text{cycle\_FLAIR}, \text{FLAIR})\end{aligned} \tag{6}$$

a) Training loss: The training loss starts high but decreases rapidly, then stabilizes, indicating that the model effectively learns modality translation by minimizing reconstruction and SSIM-based losses. This trend reflects successful optimization during training.

b) Testing loss: The testing loss remains consistently higher than the training loss but shows stable behavior with low fluctuation, suggesting that the model generalizes well to unseen data and avoids overfitting, maintaining robust performance throughout.

c) Convergence analysis: Convergence analysis shows that both training and testing losses gradually converge—training loss stabilizes near 1.0 and testing loss around 1.1. This convergence confirms that the CycleGAN maintains a strong balance between fitting the training data and performing well on test data. The stable loss curves further validate the model's reliability in generating high-quality cross-modality images.

VI. Discussions

This study addresses the challenge of translating between unpaired FLAIR and T2W MRI scans, offering a practical solution when certain modalities are unavailable. Quantitative results show strong structural preservation with SSIM scores

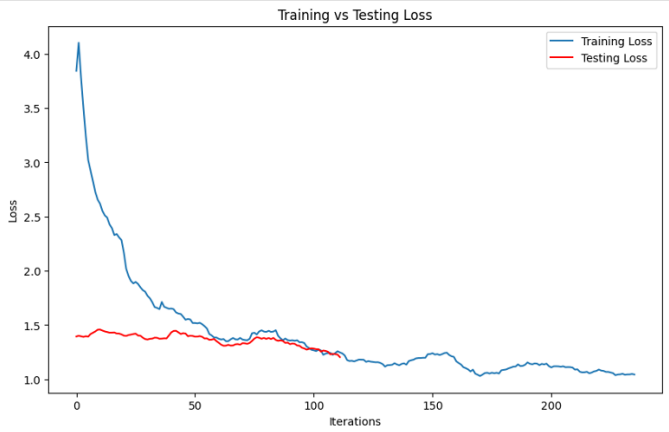

Fig. 4. Loss curve

of 0.8226 (T2W) and 0.7767 (FLAIR), and a low test loss of 0.0391, indicating high-quality, consistent outputs. Qualitative results further confirm improved clarity and tumor boundary visibility, especially in generated FLAIR images, supporting downstream tasks like segmentation. [21]. The model is robust across diverse MRI datasets, though mild blurring can occur with low-quality inputs. Future enhancements like advanced normalization or perceptual loss may address these issues. Its ability to work with unpaired data and maintain local structural accuracy makes the framework highly valuable for clinical applications, aiding in multimodal image completion and analysis.

VII. Conclusion and Future Work

Our CycleGAN-based framework for unpaired image-to-image translation between FLAIR and T2W MRI scans demonstrates strong structural fidelity, with SSIM scores of 0.8226 (T2W) and 0.7767 (FLAIR). The generated images enhance tumor visibility and structural clarity, showing potential to improve diagnostic accuracy and streamline medical imaging workflows. This approach effectively addresses incomplete datasets by generating missing modalities, supports clinical decision-making, and enhances data diversity for machine learning tasks like segmentation. Future work will focus on clinical validation, 3D volumetric translation, and improved visual quality through larger datasets and advanced loss functions. This framework marks a step forward in precision medicine and accessible diagnostic support.

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