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A Two-Stage Generative Model for Unsupervised Brain Tumor Detection Using Cyclegan and Diffusion Models

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Abstract- ***Brain tumor detection from MRI images is a critical task in medical image analysis, yet it remains challenging due to limited labeled data, complex tumor structures, and high annotation costs. Traditional supervised learning methods depend heavily on large annotated datasets, which are often difficult to obtain in real clinical scenarios. To address these challenges, this research proposes a two-stage unsupervised generative learning framework for brain tumor detection and segmentation. In the first stage, a CycleGAN model is employed to generate synthetic abnormal MRI images [3] from healthy MRI images, creating pseudo-paired healthy–abnormal data without manual annotation. In the second stage, a conditional diffusion-based generative model is applied [4],[5] to reconstruct healthy images from abnormal inputs by learning the joint distribution between healthy and abnormal image pairs. The difference between the reconstructed healthy image and the original abnormal image is used to localize tumor regions. The proposed system is evaluated using confusion matrix–based performance metrics including precision, recall, F1-score, accuracy, and Dice similarity coefficient. Experimental results demonstrate that the proposed framework effectively detects and segments tumor regions, achieving reliable performance without requiring labele training data. This approach provides a robust, scalable, and annotation-free solution for medical image anomaly detection and brain tumor analysis.***

Index Terms- ***Brain Tumor Detection, MRI, Cyclegan, Diffusion Model, Unsupervised Learning, Anomaly Detection, Medical Image Segmentation.***

I. INTRODUCTION

Brain tumors are among the most severe and life-threatening neurological disorders, requiring accurate and early diagnosis for effective treatment planning. Magnetic Resonance Imaging (MRI) is widely used for brain tumor analysis due to its high spatial resolution and ability to capture detailed structural information of brain tissues. However, manual tumor segmentation from MRI scans is a complex, time-consuming, and error-prone process that depends heavily on expert radiologists.

In recent years, deep learning techniques [9],[12] have shown significant success in medical image processing [1],[2],[4] tasks such as classification, detection, and segmentation. Most existing approaches are supervised learning methods that require large amounts of labeled MRI data. However, obtaining pixel-level annotations for medical images is expensive, time-consuming, and often impractical in real-world healthcare environments. This limitation reduces the scalability and real-world applicability of supervised models.

Unsupervised learning and generative modeling have emerged as promising alternatives for medical anomaly detection. These methods learn the distribution of healthy images and detect abnormalities by identifying deviations from the learned normal patterns. Models such as Variational Autoencoders (VAE) [2] and Generative Adversarial Networks (GAN) [1] have been widely explored for this purpose. However, these models often suffer from limitations such as blurry reconstructions, mode collapse, instability during training, and incomplete coverage of the data distribution.

To overcome these limitations, this research proposes a two-stage generative framework that integrates CycleGAN-based synthetic data generation with diffusion-basedconditional reconstruction. The proposed approach enables unsupervised learning of healthy and abnormal brain image distributions and

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detects tumors by analyzing reconstruction differences. This framework eliminates the dependency on labeled datasets while maintaining high detection and segmentation accuracy.

II. RELATED WORK

Several generative models have been used in unsupervised medical image anomaly detection. [1],[2],[4] Among them, Variational Autoencoders (VAE) and Generative Adversarial Networks (GAN) are the most commonly used approaches The existing system uses Variational Autoencoders (VAE) and Generative Adversarial Networks (GAN) for unsupervised brain tumor detection from MRI images. These models learn the distribution of healthy brain MRI images and identify abnormal tumor regions using reconstruction error.

In the VAE-based approach, the model is trained using healthy MRI images to learn a compressed latent representation of normal brain structures. During testing, abnormal MRI images are reconstructed using the trained VAE. Since the model has learned only healthy patterns, tumor regions are not reconstructed properly, resulting in high reconstruction error. These high-error regions are identified as tumor areas.

In the GAN-based approach, the generator learns to produce realistic MRI images while the discriminator learns to differentiate real and generated images. The GAN model learns the distribution of healthy brain images. During detection, the discriminator or reconstruction error is used to identify abnormal patterns. Regions that deviate from the learned healthy distribution are classified as tumor regions.

Although VAE and GAN approaches are effective in unsupervised learning, they suffer from limitations such as blurry reconstructions (VAE), training instability (GAN), mode collapse, and incomplete coverage of complex MRI data distributions. These limitations reduce detection accuracy, especially for small or complex tumor structures.

2. 1 Variational Autoencoders (VAE):

VAEs [2] learn a probabilistic latent representation of input images and reconstruct them through a decoder network. In anomaly detection, VAEs are trained on healthy images so that abnormal regions are not well reconstructed, and reconstruction error is used for detection. However, VAEs often produce blurred reconstructions due to their Gaussian latent space assumptions, which reduces the precision of anomaly localization and segmentation.

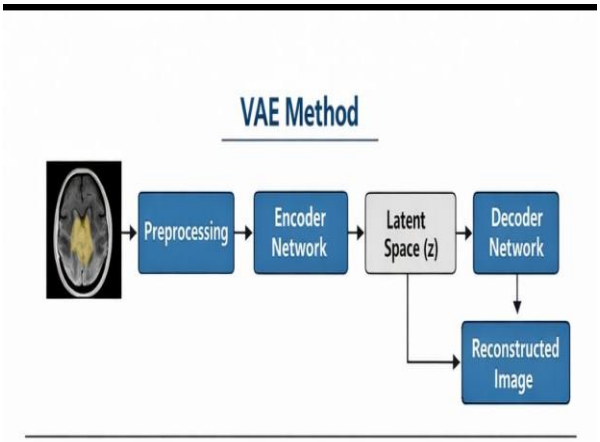

Fig-1VAE flow diagram

Algorithm 1: VAE-Based Brain Tumor Detection

Input: MRI Images
Output: Tumor Detection Mask

1. Load MRI dataset
2. Preprocess images
   - Noise removal
   - Intensity normalization
   - Resize to fixed dimensions
3. Initialize VAE model parameters
4. Encode input image using encoder network
5. Compute latent mean (μ) and variance (σ)
6. Sample latent vector

$$z = \mu + \sigma \cdot \epsilon$$

7. Decode latent vector to reconstruct image
8. Compute loss function
   - Reconstruction loss
   - KL divergence loss
   - Total loss = Reconstruction + KL loss
9. Compute reconstruction error map
10. If reconstruction error > threshold → Tumor region
11. Else → Normal region
12. Generate tumor segmentation mask

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2. 2 Generative Adversarial Networks (GAN)

GANs consist of a generator and a discriminator trained in an adversarial manner.[1] GAN-based anomaly detection methods learn the distribution of healthy images and reconstruct input images to identify abnormal regions. Although GANs generate visually realistic images, they suffer from training instability, mode collapse, and difficulty in covering the full data distribution. These issues limit their reliability in medical applications.3. Proposed Method

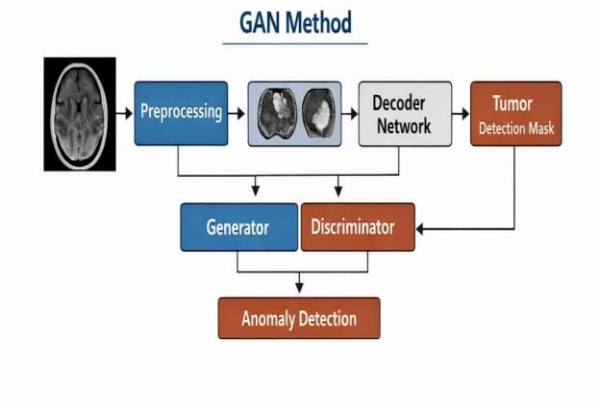

Fig-2 GAN flow diagram

Algorithm 2: GAN-Based Brain Tumor Detection

Input: MRI Images

Output: Tumor Detection Mask

1. Load MRI dataset
2. Preprocess images
3. Initialize Generator (G) and Discriminator (D)
4. Train Discriminator:
   - Sample real MRI images
   - Generate fake images:

   $$x_{fake} = G(z)$$

   - Compute discriminator loss
   - Update discriminator weights
5. Train Generator:
   - Generate fake images
   - Pass to discriminator
   - Compute generator loss
   - Update generator weights
6. Repeat steps 4–5 until convergence
7. Detection phase:
   - Input MRI image into discriminator/reconstruction model
   - If output indicates abnormal → Tumor present
   - Else → Normal brain
8. Generate tumor mask

Conclusion

The existing unsupervised approaches based on Variational Autoencoders (VAE) and Generative Adversarial Networks (GAN) provide a foundational framework for brain tumor detection using MRI images without requiring labeled data. These methods learn the distribution of healthy brain images and identify abnormal regions using reconstruction errors and anomaly detection mechanisms. However, VAE-based models often produce blurred reconstructions due to their probabilistic latent representations, which reduces the precision of tumor localization. Similarly, GAN-based models suffer from training instability, mode collapse, and incomplete learning of complex MRI data distributions, leading to unreliable detection results. As a result, both methods struggle to accurately reconstruct healthy anatomical structures and precisely segment tumor regions, especially in cases involving complex tumor shapes and multi-modality MRI data. These limitations highlight the need for a more stable, robust, and accurate generative framework for unsupervised brain tumor detection, which motivates the development of the proposed two-stage generative model.

III. PROPOSED METHOD

The proposed method introduces a two-stage unsupervised generative framework for accurate brain tumor detection and segmentation from MRI images. [4],[5] In the first stage, a CycleGAN model is employed to learn the transformation between healthy and abnormal brain MRI images using unpaired data. This stage generates synthetic abnormal MRI images from healthy images while preserving essential anatomical structures through cycle-consistency constraints, thereby creating pseudo-paired healthy–abnormal datasets without manual annotation. In the second stage, a joint

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diffusion-based generative model is applied to reconstruct healthy images from abnormal inputs by learning the joint probability distribution between paired images. The diffusion process gradually removes noise while being conditionally guided by the synthetic abnormal images, ensuring that only tumor regions are altered while normal brain tissues remain intact. Tumor regions are localized by computing the residual difference between the reconstructed healthy image and the original abnormal image. Additionally, a multi-modality MRI ensemble strategy is used to combine information from different MRI sequences, improving detection accuracy and segmentation reliability. This two-stage framework enables stable unsupervised learning, robust tumor localization, and high-quality segmentation without requiring labeled training data.

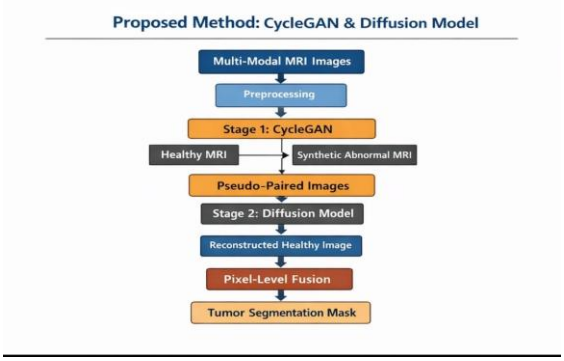

Fig-3.1 Flow Diagram of Proposed Method

Stage 1: Synthetic Data Generation using CycleGAN
In the first stage, a CycleGAN model is trained using unpaired healthy and abnormal MRI images.[3] The model learns bidirectional mappings between healthy and abnormal image domains. This allows the system to generate synthetic abnormal images from healthy images, forming pseudo-paired healthy–abnormal data without manual annotation. This stage solves the problem of unavailable paired medical datasets.

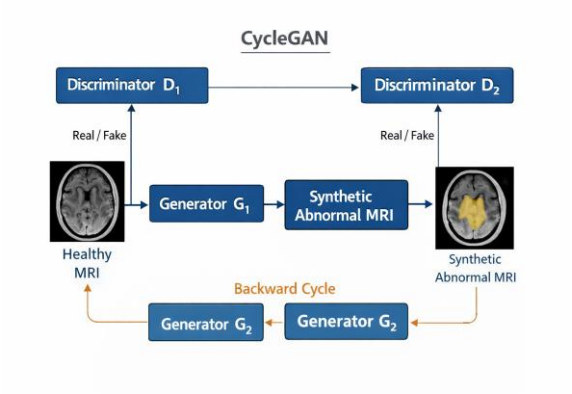

Fig-3.2 Flow diagram of CycleGAN

Algorithm 1: Stage-1 CycleGAN for Paired MRI Image Generation

Input:

- Unpaired healthy MRI images A
- Unpaired abnormal MRI images B

Output:

- Pseudo-paired images $(x_A, \tilde{x}_B)$

Steps:

1. Initialize generators
    1. $G: A \rightarrow B$(Healthy → Abnormal)
    2. $F: B \rightarrow A$(Abnormal → Healthy)
2. Initialize discriminators
    1. $D_B$for domain B
    2. $D_A$for domain A
3. Repeat until convergence:
    1. Sample healthy image $a \sim A$
    2. Generate abnormal image $\tilde{b} = G(a)$
    3. Reconstruct healthy image $\hat{a} = F(\tilde{b})$
    4. Sample abnormal image $b \sim B$
    5. Generate healthy image $\tilde{a} = F(b)$
    6. Reconstruct abnormal image $\hat{b} = G(\tilde{a})$
    4. Compute Adversarial Loss:

$$L_{GAN}(G, D_B) + L_{GAN}(F, D_A)$$

    5. Compute Cycle Consistency Loss:

$$L_{cyc} = \| \hat{a} - a \|_1 + \| \hat{b} - b \|_1$$

6. Optimize total loss:

$$L = L_{GAN} + \lambda L_{cyc}$$

7. Save generated pseudo-paired images: $(x_A, \tilde{x}_B)$

Stage 2: Joint Diffusion-Based Healthy Reconstruction

A joint diffusion model is applied to reconstruct healthy images from abnormal inputs. [4],[5] The diffusion process gradually removes noise while being guided by the synthetic abnormal image. This ensures that only tumor regions are modified, while healthy structures remain unchanged. This solves the ill-posed abnormal-to-healthy mapping problem.

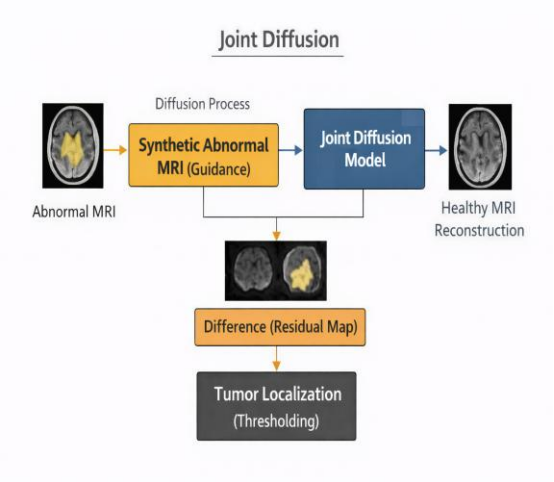

Fig-3.2 flow diagram of joint diffusion

Algorithm 2: Stage-2 Joint Diffusion Model (VE-JP)

Input:

- Healthy image x_A
- Synthetic abnormal image $\tilde{x}_B$(from Stage-1)

Output:

- Reconstructed healthy image $\hat{x}_A$

Training Phase

1. Concatenate inputs:

$$X_0 = x_A \oplus \tilde{x}_B$$

2.Sample time step $i \sim U(1, N)$

3.Sample Gaussian noise $z \sim \mathcal{N}(0, I)$

4.Apply Variance Exploding (VE) Forward Diffusion:

$$X_{i+1} = X_i + \sqrt{\sigma_i^2 - \sigma_{i-1}^2}\, z$$

5.Train score network $s_\theta$using:

$$\min_\theta \quad \mathbb{E}[\| s_\theta(X_{i+1}, i) + z \|^2]$$

6.Repeat for all diffusion steps $i = 1$to N

Sampling (Reverse Diffusion)

1.Initialize noisy sample:

$$X_N \sim \mathcal{N}(0, \sigma_{max}^2 I)$$

2. For $i = N \rightarrow 1$:

Predictor step (reverse SDE)

Corrector step (Langevin dynamics)

3.Extract reconstructed healthy image $\hat{x}_A$

4.Compute anomaly map:

$$A = | x_A - \hat{x}_A |$$

Tumor Localization and Segmentation

The tumor region is detected by calculating the difference between the reconstructed healthy image and the original abnormal image. This difference highlights pathological regions, which are thresholded to produce a tumor segmentation mask.

Multi-Modality MRI Ensemble

Multiple MRI modalities (T1w, T1ce, T2w, Flair) are combined using weighted pixel-level fusion. Each modality contributes complementary tumor information. This ensemble strategy improves detection accuracy and reduces false detections.

Algorithm 3: Multi-Modality MRI Ensemble

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Input:

- Modalities $v \in \{T, 1, w, T1ceT2wFlair\}$
- Original image x_A^v
- Reconstructed image $\hat{x}_A^v$
- Modality weights w_v

Output:

- Final anomaly heatmap and segmentation mask

Steps:

1.For each modality v:

Compute residual:

$$R_v = | x_A^v - \hat{x}_A^v |$$

2.Apply weighted fusion:

$$I_{ensemble} = \sum_{v=1}^{m} w_v \cdot R_v$$

3.Subject to:

$$\sum_{v=1}^{m} w_v = 1$$

4.Apply thresholding on $I_{ensemble}$to obtain: Tumor segmentation mask

IV. RESULT AND DISCUSSION

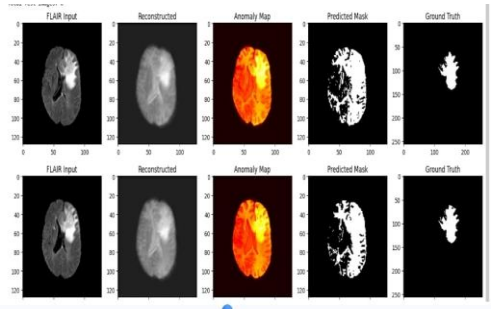

Fig:4.1

Figure illustrates the qualitative results of the proposed brain tumor detection framework using FLAIR MRI images. The first column represents the original FLAIR input image, which contains visible tumor regions within the brain tissue. The second column shows the reconstructed healthy image generated by the diffusion-based reconstruction model. Since the model is trained to learn the distribution of healthy brain structures, the reconstructed image suppresses abnormal tumor regions while preserving normal anatomical details. The third column presents the anomaly map, which highlights the difference between the original input and the reconstructed image. In this map, brighter regions indicate higher reconstruction errors corresponding to potential tumor areas. The fourth column displays the predicted tumor mask, obtained by applying thresholding on the anomaly map to segment abnormal regions. Finally, the last column shows the ground truth segmentation, which represents the actual tumor region annotated in the dataset. By comparing the predicted mask with the ground truth, it can be observed that the proposed method effectively localizes tumor regions with high spatial similarity. These results demonstrate the capability of the model to accurately reconstruct healthy brain images and identify abnormal tumor regions through residual analysis.

Loss Values: TABLE I

Epoch	1	2	3
Cycle GAN	0.23	0.19	0.25
VEJP	0.039	0.035	0.031

The training performance of the proposed two-stage generative framework is evaluated using Cycle Loss and VEJP Loss values during the optimization process. The Cycle Loss values obtained during training are 0.2364, 0.1949, and 0.2526, which indicate the effectiveness of the CycleGAN model in learning consistent mappings between healthy and abnormal MRI domains. A relatively low cycle-consistency loss suggests that the generated images preserve important anatomical structures while translating between image domains. Although minor variations in the cycle loss values are observed across iterations, the overall magnitude remains low, demonstrating stable training behavior and successful

preservation of structural information in reconstructed images. Additionally, the VEJP Loss values recorded during the diffusion-based reconstruction stage are 0.0394, 0.0356, and 0.0318, showing a gradual decrease during training. This reduction in loss indicates that the joint diffusion model progressively improves its ability to reconstruct healthy brain images from abnormal inputs by effectively modeling the underlying data distribution. The decreasing trend in VEJP loss also reflects improved denoising and reconstruction capability of the diffusion process. Overall, the combination of relatively low Cycle Loss and steadily decreasing VEJP Loss demonstrates that the proposed model achieves stable training, effective domain translation, and accurate healthy image reconstruction, which ultimately contributes to reliable tumor localization and segmentation.

V. EVALUATION METRICS

The performance of the proposed brain tumor detection and segmentation system is evaluated using a confusion matrix–based analysis, [7],[8] which provides a quantitative assessment of classification and segmentation accuracy. A confusion matrix summarizes the prediction results by comparing the model outputs with the ground truth labels and consists of four fundamental components: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN).

True Positive (TP) represents the number of tumor pixels or regions that are correctly identified as tumor by the model. True Negative (TN) refers to normal brain pixels or regions that are correctly classified as non-tumor. False Positive (FP) indicates normal brain regions that are incorrectly classified as tumor, leading to false alarms. False Negative (FN) represents tumor regions that are incorrectly classified as normal, resulting in missed detections. These four components form the basis for calculating multiple performance metrics that evaluate different aspects of model behavior.

Precision measures the reliability of positive predictions and indicates how many of the detected tumor regions are actually tumors. It is defined as:

$$\text{Precision} = \frac{TP}{TP + FP}$$

High precision implies a low false-positive rate, meaning the model produces fewer incorrect tumor detections.

Recall (also known as sensitivity) measures the model's ability to correctly detect actual tumor regions. It is given by:

$$\text{Recall} = \frac{TP}{TP + FN}$$

High recall indicates that the model successfully identifies most of the tumor regions, minimizing missed detections.

The F1-score is the harmonic mean of precision and recall and provides a balanced evaluation of detection performance, especially in cases of class imbalance, which is common in medical imaging:

$$\text{F1-score} = \frac{2 \times (\text{Precision} \times \text{Recall})}{\text{Precision} + \text{Recall}}$$

A high F1-score indicates that the model achieves both high precision and high recall simultaneously.

Accuracy represents the overall correctness of the model by measuring the proportion of correctly classified pixels or regions (both tumor and non-tumor) among all predictions:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

Although accuracy provides a general performance measure, it can be misleading in medical imaging tasks due to the imbalance between tumor and non-tumor pixels.

The Dice Similarity Coefficient (DSC) is a widely used metric in medical image segmentation that

measures the spatial overlap between the predicted tumor region and the ground truth tumor region:

$$\text{DSC} = \frac{2TP}{2TP + FP + FN}$$

The Dice coefficient ranges from 0 to 1, where 1 indicates perfect overlap between predicted and actual tumor regions. A higher Dice score reflects better segmentation accuracy and boundary alignment.

Together, these metrics provide a comprehensive and reliable evaluation of the proposed system's performance. Precision and recall assess detection quality, F1-score provides balanced performance measurement, accuracy evaluates overall classification correctness, and Dice similarity coefficient specifically measures segmentation quality. This multi-metric evaluation framework ensures robust assessment of both tumor detection and tumor segmentation capabilities of the model.

Metrics Values: TABLE II

Mean Dice (DSC)	0.43942
Mean Precision	0.282749
Mean Recall	0.990324
Mean IoU	0.2819363
Mean HD95	32.20150
AUPRC	0.8933766

The proposed model is evaluated using several metrics such as Dice Similarity Coefficient (DSC), Precision, Recall, Intersection over Union (IoU), HD95, and AUPRC. These metrics help measure the accuracy of tumor region detection in MRI images.
The model achieved a mean Dice score of 0.439, which indicates a moderate overlap between the predicted tumor regions and the ground truth. The precision value of 0.283 shows that some non-tumor areas are incorrectly predicted as tumor regions. However, the recall value of 0.990 is very high, meaning that the model successfully detects most of the tumor regions with very few missed cases.

The mean IoU score of 0.282 also reflects the overlap between predicted and actual tumor regions. The HD95 value of 32.20 represents the boundary difference between predicted segmentation and ground truth. In addition, the model achieved a high AUPRC value of 0.893, which indicates good performance in distinguishing tumor and non-tumor regions.Overall, the results show that the proposed model is highly effective in detecting tumor regions, although some false positives slightly reduce the precision and overlap scores.

VI. DATASET

The experiments in this study were conducted using the Brain Tumor Segmentation (BraTS) dataset, [6] which is a widely used benchmark dataset for brain tumor analysis in medical imaging research. The BraTS dataset contains multi-modal MRI scans of patients diagnosed with brain tumors, including imaging modalities such as T1-weighted (T1), T1 with contrast enhancement (T1ce), T2-weighted (T2), and Fluid Attenuated Inversion Recovery (FLAIR). Each MRI scan is provided along with expert-annotated ground truth segmentation masks that identify different tumor regions. The dataset includes images that are preprocessed with skull stripping, spatial normalization, and resampling to ensure consistency across samples. In this work, the BraTS dataset is used to train and evaluate the proposed model for brain tumor detection and segmentation. The availability of multi-modal MRI images and accurate annotations makes the BraTS dataset highly suitable for developing and validating deep learning-based medical image analysis methods.

VII. CONCLUSION

This research presents a novel two-stage unsupervised generative framework for brain tumor detection and segmentation using MRI images. By integrating CycleGAN-based synthetic data generation with conditional diffusion-based reconstruction, the proposed approach eliminates the need for labeled training data while achieving reliable detection performance. The model effectively

reconstructs healthy brain structures and accurately localizes tumor regions through residual analysis. Experimental results and evaluation metrics demonstrate that the proposed framework outperforms traditional VAE and GAN-based methods in terms of reconstruction quality, stability, and segmentation accuracy. This approach offers a scalable, annotation-free, and clinically relevant solution for automated brain tumor analysis and medical image anomaly detection.

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