

Abstract

This project addresses the critical challenge of generating missing MRI sequences using a Generative Adversarial Network (GAN) model. The primary objective is to develop a cost-effective and time-efficient solution that reduces the need for multiple MRI scanning sessions, thereby minimizing patient discomfort and optimizing clinical workflows. By leveraging the BraTS 2023 dataset, which includes a balanced representation of MRI sequences (T1, T2, T1ce, and FLAIR) from 1,251 subjects and annotated by expert neuroradiologists, we ensure a comprehensive and diverse dataset for training and validation.

Our methodology involves the adaptation of a squeeze attention U-Net model, which has been specifically redesigned to operate in 2D data sequences, ensuring efficient utilization of available computational resources while maintaining model performance. This model is capable of accurately generating high-quality MRI sequences from existing ones, effectively addressing the challenge of incomplete imaging data.

Experimental results demonstrate the efficacy of our approach, showcasing significant improvements in generating missing MRI sequences, which is crucial for accurate brain tumor segmentation. This advancement not only enhances the diagnostic process but also reduces the time and cost associated with traditional MRI scanning procedures.

In addition to the practical implications, our work contributes to the field by providing a robust framework for medical image synthesis, potentially transforming clinical practices. Future work will focus on extending the model to 3D, leveraging additional datasets such as BraTS 2024 for further experimentation, and exploring real-world applications in clinical settings. Implementing our technology in a clinical environment will demonstrate its practical value, improve diagnostic workflows, and directly benefit patient care. Additionally, we acknowledge that the results could be further improved with more time and resources, addressing current limitations and enhancing overall performance.

يتناول هذا المشروع الأساسي المتمثل في توليد تسلسلات التصوير بالرنين المغناطيسي المفقودة باستخدام نموذج الشبكة التوليدية التنافسية (GAN).

الهدف الرئيسي هو تطوير حل فعال من حيث التكلفة و الوقت يقلل من الحاجة إلى جلسات تصوير بالرنين المغناطيسي متعددة، مما يقلل من انزعاج المريض و يُحسن سير العمل السريري من خلال الاستفادة من مجموعة بيانات BraTS 2023، التي تشمل تمثيلاً متوازناً لتسلسلات التصوير بالرنين المغناطيسي (FLAIR, T1, T2, T1CE) من 1,251 مريضاً و موثقة من أطباء أشعة عصبية معتمدين، و نضمن وجود مجموعة بيانات شاملة و متنوعة للتدريب و التقييم.

تتضمن منهجيتنا تعديل نموذج Squeeze Attention U-Net Model، و الذي تم إعادة تصميمه خصيصاً للعمل علي تسلسلات بيانات ثنائية الأبعاد، مما يضمن الاستخدام الفعال للموارد الحسابية المتاحة مع الحفاظ علي أداء النموذج. هذا النموذج قادر علي توليد تسلسلات التصوير بالرنين المغناطيسي عالية الجودة من تسلسلات الموجودة، مما يعالج بشكل فعال تحدي البيانا التصويرية غير المكتملة.

تظهر النتائج التجريبية فعالية نهجنا، حيث تبرز تحسينات كبيرة في توليد تسلسلات التصوير بالرنين المغناطيسي المفقودة، و هو أمر حاسم في اكتشاف أورام الدماغ بدقة. هذا التقدم لا يعزز فقط عملية التشخيص و لكنه أيضا يقلل من الوقت و التكلفة المرتبطة بإجراءات التصوير بالرنين المغناطيسي التقليدية.

بالإضافة إلي الآثار العملية، يساهم عملنا في المجال من خلال توفير إطار عمل قوي لتوليد الصور الطبية، مما قد يُحدث تحولاً في الممارسات السريرية. سيركز العمل المستقبلي علي تمديد النموذج للعمل علي البيانات ثلاثية الأبعاد، و الاستفادة من مجموعات بيانات إضافية مثل BraTS 2024 للمزيد من التجارب، و استكشاف التطبيقات العملية في البيانات السريرية. سيظهر تطبيق تقنيتنا في البيئة السريرية قيمتها العملية، يحسن سير العمل التشخيصي، و يعود بفائدة مباشرة علي رعاية المرضى. بالإضافة إلي ذلك، نقر بأنه يمكن تحسين النتائج بشكل أكبر مع المزيد من الوقت و الموارد، مما يعالج القيود الحالية و يعزز الأداء العام.

Keywords

Brain Tumor Segmentation, BraTS Dataset, Brain MRI, Generative Adversarial Network (GAN), MRI synthesis, Patch GAN, SE Attention U-Net

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Table of Contents

Table of Contents.....	iii
List of Figures	v
List of Tables	vi
List of Equations	vii
Glossary	viii
1 Introduction.....	1
1.1 Overview	1
1.2 Problem Statement.....	1
1.3 Scope and Objectives.....	2
1.4 Report Organization (Structure)	2
1.5 Work Methodology	2
1.6 Work Plan (Gantt chart)	3
2 Related Work (Literature Review).....	4
2.1 Multimodal MRI synthesis using unified generative adversarial networks [2]	4
2.1.1 Summarization and Main Modules	4
2.1.2 Advantages and Disadvantages Compared to Our Work	4
2.2 Convolutional neural network for intramodality brain MRI synthesis [4]	4
2.2.1 Summarization and Main Modules	4
2.2.2 Advantages and Disadvantages Compared to Our Work	5
2.3 A layer-wise fusion network for multimodal MR image synthesis [5]	5
2.3.1 Summarization and Main Modules	5
2.3.2 Advantages and Disadvantages Compared to Our Work	5
2.4 MRI Image Synthesis Using Switchable Cycle-Consistent GAN [6]	6
2.4.1 Summarization and Main Modules	6
2.4.2 Advantages and Disadvantages Compared to Our Work	6
2.5 MRI Cross-Modality Image-to-Image Translation [7]	6
2.5.1 Summarization and Main Modules	6
2.5.2 Advantages and Disadvantages Compared to Our Work	6
2.6 GAN to Synthesize Missing T1 and FLAIR MRI Sequences [9].....	7
2.6.1 Summarization and Main Modules	7
2.6.2 Advantages and Disadvantages Compared to Our Work	7
3 The Proposed Solution	9
3.1 Solution Methodology	9
3.2 Functional/ Non-functional Requirements	10

3.2.1	Model Libraries and Frameworks	10
3.2.2	Web Application Frameworks	10
3.2.3	Hardware Specifications	10
3.3	System Analysis & Design	10
4	Dataset & Pre-processing	11
4.1	Dataset	11
4.2	Data Pre-processing	11
4.2.1	Image Artifacts	13
5	Implementation, Experimental Setup, & Results	15
5.1	Implementation Details	15
5.2	Experimental / Simulations Setup	16
5.3	Conducted Results	18
5.4	Testing & Evaluation	18
5.4.1	T1 Losses	20
5.4.2	FLAIR Losses	20
5.4.3	T2 Losses	21
6	Discussion, Conclusions, and Future Work	22
6.1	Discussion	22
6.1.1	Results	22
6.1.2	Limitations	22
6.2	Summary & Conclusion	23
6.3	Future Work	24
6.3.1	Combining Multiple Models for Enhanced Prediction	24
6.3.2	Testing on Segmentation Models	24
6.3.3	Extending Synthesis to Other Organs	25
6.3.4	Cross-Dataset Evaluation	25
6.3.5	Real-World Synthesis Application	25
	References (or Bibliography)	27

List of Figures

Figure 1 Gantt chart	3
Figure 2 Architecture Framework.....	9
Figure 3 System Architecture	10
Figure 4 Images Pre-processing.....	12
Figure 5 Artifacts	14
Figure 6 Generator Network Architecture	15
Figure 7 Discriminator Network Architecture	15
Figure 8 GAN Model Network Architecture	17
Figure 9 Generator Loss Over Epochs for Generating T1	20
Figure 10 Generator Loss Over Epochs for Generating FLAIR	21
Figure 11 Generator Loss Over Epochs for Generating T2	21

List of Tables

Table 1 DataSets Details.....	8
Table 2 Results for Synthesized T1	18
Table 3 Results for Synthesized T2	18
Table 4 Results for Synthesized Flair	18

List of Equations

Equation 1 Mean Absolute Error	19
Equation 2 PSNR.....	19
Equation 3 Generator Loss.....	19
Equation 4 Total Loss	20

Glossary

Magnetic Resonance Imaging (MRI): A medical imaging technique used in radiology to form pictures of the anatomy and the physiological processes of the body.

DICOM Viewer: A software application used to view and analyze medical images stored in the DICOM (Digital Imaging and Communications in Medicine) format.

T1, T2, FLAIR, T1ce Sequences: Different types of MRI sequences. T1 and T2 refer to relaxation times in MRI, FLAIR is a sequence that nullifies fluid signal, and T1ce is T1 with contrast enhancement.

Motion Artifacts: Distortions in medical images caused by patient movement during the imaging process.

Ringling Artifacts: Type of distortion that appears as spurious oscillations or "ringing" near sharp transitions or edges within the image.

Cropping Artifacts: Unintended truncation or cutting off parts of the image, usually at the edges. This artifact typically occurs when the field of view (FOV) is too small.

Voxel: A three-dimensional pixel representing a value on a regular grid in a three-dimensional space, used in the context of MRI imaging.

Tumor Core (TC): The part of a tumor that includes both necrosis and enhanced tumor regions.

Enhancing Tumor (ET): Includes regions of the tumor that show enhancement post-contrast.

Whole Tumor (WT): The combined region including edema, enhanced tumor, and necrosis in brain tumor imaging.

1 Introduction

1.1 Overview

When diagnosing brain-related issues, doctors typically rely on magnetic resonance. imaging (MRI). To obtain a comprehensive understanding, multiple scans, often around four sequences, are required. However, this prolonged exposure to the imaging machine can result in imaging complications such as motion artifacts and noise, among others.

Therefore, employing a Deep Learning tool to synthesize MRI images emerges as an efficient and cost-effective solution for numerous patients. To explore the latest advancements in research, we have compiled a collection of results and the corresponding accuracy achieved in synthesizing different types of radiations. We continue to stay abreast of the latest developments in the field.

1.2 Problem Statement

The cost of MRI sequences in the brain ranges from 3,500 LE to 5,000 LE, placing a financial burden on many patients. Additionally, accessing the DICOM Viewer, a crucial tool for efficient image processing, can prove challenging, particularly in rural areas with limited availability.

We have chosen to address these challenges because we firmly believe that the synthesis of MRI sequences holds great potential for improving the efficiency, cost-effectiveness, and accessibility of MRI care. By tackling these issues, we can enhance the diagnosis and treatment of various medical conditions, particularly benefiting patients in rural and remote areas.

To overcome these obstacles, we propose the development of an AI model capable of synthesizing MRI sequences from a single input sequence. This breakthrough would enable clinicians to acquire all the necessary MRI sequences for a patient, even with access to only one MRI scanner. By reducing the time and cost associated with MRI care, our solution aims to make this essential diagnostic tool more accessible for all doctors, even if they have access to only one or two types of sequences.

This advancement would empower clinicians to obtain all the required MRI sequences for a patient, even if they only have access to a limited number of sequence types. By reducing the time and cost associated with MRI care, our solution aims to make this crucial diagnostic tool more accessible to doctors, enabling them to provide comprehensive and accurate diagnoses using a streamlined process.

1.3 Scope and Objectives

Our primary objective is to synthesize Sequences for MRI, focusing on a specific type of Sequence that is being imaged. Leveraging Deep Learning, we can synthesize the remaining Sequences. These synthesized results are then displayed on a Dicom Viewer, accompanied by supporting tools, to create an integrated work environment. By harnessing the power of cloud support, doctors can access and utilize these processed images at any time and from any location, aiding them in the diagnosis process.

1.4 Report Organization (Structure)

Our project workflow begins with the doctor utilizing an imaging modality (MRI) to capture a 2D series of brain images. The doctor selects a specific type of MRI (T1, T2, Flair, or T1ce), and we subsequently synthesize the remaining types. Alternatively, if the doctor chooses two types, we synthesize the remaining ones. These images are then transmitted to the Picture Archiving and Communication System (PACS) for data archiving.

Next, the images are sent to a deep-learning model to synthesize the missing types. The resulting data, including image URLs, is stored in a database. Subsequently, the data is forwarded to the DICOM Viewer, where image processing tools such as Zoom, Pan, and others can be applied. To access the DICOM Viewer, user authentication via sign-in is required.

1.5 Work Methodology

We embarked on an extensive exploration across various fields to identify a promising idea. After careful consideration, we chose the concept of synthesizing MRI sequences and visualizing them on a DICOM Viewer, incorporating advanced imaging processing tools. To lay a strong foundation, we delved into an extensive literature review on medical images and cutting-edge techniques such as Neural Networks. With our research complete, we proceeded to apply different network architectures from the literature review to our dataset, comparing established techniques with novel approaches.

This phase involved dividing our team into two subgroups. The first group focused on implementing deep learning tasks, including network development, hyperparameter tuning, and data processing. The second group directed their efforts towards creating the DICOM Viewer, encompassing frontend and backend development, as well as database integration. Ultimately, our goal was to seamlessly integrate the developed deep learning model into the DICOM Viewer.

To ensure smooth progress, the execution of our proposed plan depended on a well-defined timeline, which we established after carefully selecting the project idea. We prioritized setting up effective risk management strategies and designing comprehensive training plans to ensure smooth progress and mitigate potential challenges. By considering these factors early on, we could lay a solid foundation for the project and effectively manage its implementation.

To maintain quality assurance, we adopted multiple strategies. We utilized a task management dashboard, such as "Trello," to assign specific tasks to team members, along with predefined deadlines. We held regular meetings with our supervisor on a weekly basis to track the project's progress and seek guidance. Additionally, as a team, we conducted periodic meetings to evaluate results, discuss achievements, and address any encountered challenges in the project.

1.6 Work Plan (Gantt chart)

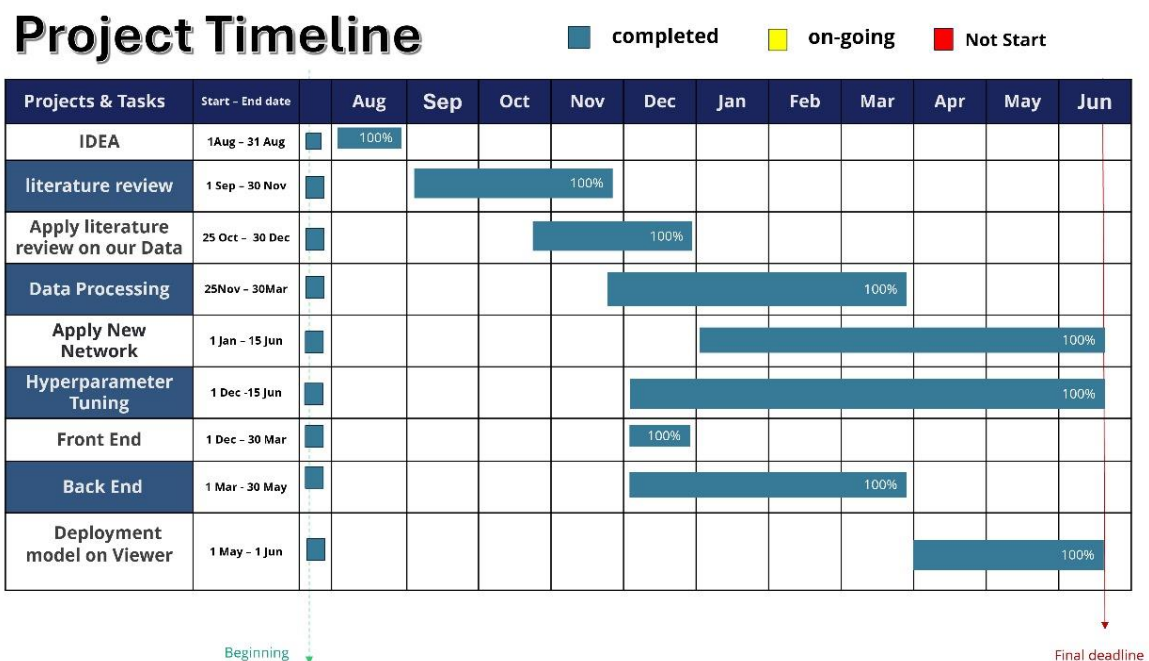


Figure 1 Gantt chart

2 Related Work (Literature Review)

Recently, the synthesis of magnetic resonance images from other sequences has become an active research topic in the medical imaging field. This approach has great potential to improve image quality, reduce imaging time, and enhance diagnostic accuracy.

2.1 Multimodal MRI synthesis using unified generative adversarial networks [2]

2.1.1 Summarization and Main Modules

This paper introduces a unified generative adversarial network (GAN)

framework for synthesizing multimodal MRI images. The model integrates multiple MRI modalities into a unified architecture, leveraging a GAN to generate realistic and cross-modally consistent images. The approach combines feature extraction and fusion mechanisms to ensure that the generated images preserve anatomical structures while maintaining high fidelity.

2.1.2 Advantages and Disadvantages Compared to Our Work

The advantage of this approach lies in its capability to handle multiple MRI modalities within a single framework, ensuring consistency across different imaging types. The GAN architecture enables the generation of high-quality images that are crucial for clinical applications. However, challenges such as training instability and the requirement for large datasets may limit its practical application. In contrast, our squeeze attention U-Net model is tailored for reducing MRI scan times, providing a more targeted solution for clinical efficiency.

2.2 Convolutional neural network for intramodality brain MRI synthesis [4]

2.2.1 Summarization and Main Modules

This study proposes a deep learning-based convolutional neural network (CNN) specifically designed for intramodality synthesis of brain MRI images. The model focuses on enhancing the resolution and quality of MRI scans while preserving anatomical structures. It utilizes a CNN architecture to extract and learn high-level features that are critical for improving the visual quality of synthesized images.

2.2.2 Advantages and Disadvantages Compared to Our Work

The advantage of this approach is its specialization in intramodality MRI synthesis, which allows for the generation of high-resolution images with improved anatomical detail. The CNN framework is effective for this purpose, leveraging deep learning techniques to enhance image quality. However, challenges related to the model's sensitivity to variations in image quality and the need for extensive data for training may limit its widespread application. In contrast, our squeeze attention U-Net focuses on reducing MRI scan times, offering a more direct benefit for clinical workflows.

2.3 A layer-wise fusion network for multimodal MR image synthesis [5]

2.3.1 Summarization and Main Modules

This study introduces a layer-wise fusion network that incorporates self-supervised learning to synthesize multimodal MR images. The approach consists of three main stages: feature extraction using self-supervised learning tasks, feature fusion through a channel attention mechanism, and image generation using a GAN framework. The model aims to generate high-quality MR images from available modalities, with an emphasis on retaining anatomical details and ensuring structural consistency.

2.3.2 Advantages and Disadvantages Compared to Our Work

The key advantage of this approach lies in its sophisticated fusion strategy and use of self-supervised learning, which enhances the robustness and quality of the generated images. The model's ability to leverage both 2D and 3D contextual information is particularly beneficial for maintaining anatomical fidelity. However, the complexity of the model and the need for extensive computational resources might pose challenges for implementation in resource-constrained settings. In comparison, our squeeze attention U-Net model, redesigned for 2D operations, offers a more resource-efficient solution while still achieving high-quality image synthesis. Additionally, our work focuses specifically on reducing MRI scan times, providing a clear and immediate benefit in clinical workflows.

2.4 MRI Image Synthesis Using Switchable Cycle-Consistent GAN [6]

2.4.1 Summarization and Main Modules

This paper proposes a switchable cycle-consistent GAN for synthesizing multi-contrast MRI images. The model focuses on maintaining cycle-consistency between different MRI contrasts while allowing for switchable generation between them. It aims to produce images that are not only realistic but also consistent across different MRI contrast types, thereby improving the versatility of MRI data synthesis.

2.4.2 Advantages and Disadvantages Compared to Our Work

The advantage of this approach is its capability to handle multi-contrast MRI synthesis and maintain cycle-consistency, ensuring coherent and realistic image generation. The switchable generation feature adds flexibility to the synthesis process, allowing the model to adapt to different imaging requirements. However, challenges such as training instability and the potential for reduced image fidelity due to the use of GANs may impact its performance. In contrast, our squeeze attention U-Net focuses on reducing MRI scan times, providing a more specialized solution for clinical applications.

2.5 MRI Cross-Modality Image-to-Image Translation [7]

2.5.1 Summarization and Main Modules

This study presents an image-to-image translation method for crossmodality MRI synthesis. The approach uses a deep learning framework to translate MRI images from one modality to another, enhancing the utility of MRI data across different imaging modalities. It focuses on adapting MRI images from one modality to simulate images from another modality while preserving important anatomical features.

2.5.2 Advantages and Disadvantages Compared to Our Work

The advantage of this approach lies in its ability to perform cross-modality image translation, which enhances the versatility and accessibility of MRI data. The deep learning framework allows for efficient image synthesis across modalities, providing valuable insights for clinical applications. However, challenges may arise in preserving fine anatomical details and ensuring

structural consistency across different modalities. Our squeeze attention U-Net, in contrast, focuses on improving MRI scan times directly, which provides a clear advantage for clinical workflows.

2.6 GAN to Synthesize Missing T1 and FLAIR MRI Sequences [9]

2.6.1 Summarization and Main Modules

This paper proposes the use of GANs to synthesize missing T1 and FLAIR MRI sequences for brain tumor segmentation. The model aims to improve the completeness and accuracy of brain tumor segmentation by generating missing sequences that are crucial for accurate tumor delineation. It uses a GAN architecture to generate synthetic MRI sequences that complement existing data and enhance segmentation model performance.

2.6.2 Advantages and Disadvantages Compared to Our Work

The advantage of this approach lies in its focus on synthesizing missing MRI sequences, which improves the completeness and accuracy of brain tumor segmentation models. The use of GANs ensures that the synthesized sequences are realistic and compatible with existing MRI data, thereby enhancing the clinical utility of segmentation models. However, challenges such as training instability and the requirement for large datasets for effective model training may limit its applicability. In contrast, our squeeze attention U-Net focuses on reducing MRI scan times, offering a more focused and efficient solution for clinical applications.

Table 1 DataSets Details

Paper	published	Model	Dataset	Data Used	Evaluati on model	Accuracy
Multimodal MRI synthesis using unified generative adversarial networks	2020	GAN	the Brain Tumor Segmentation Challenge (BRATS2015)	The dataset was randomly separated into five groups. One group was used for testing, while the remaining four groups were utilized to train the model.	(NMAE), (PSNR), (SSIM), (NIQE), (VIF)	T2 as the input : T1 -> 0.950 T1c -> 0.974 Flair -> 0.958 T1 as the input : T2 -> 0.969 T1c -> 0.974 Flair -> 0.959
Deep learning-based convolutional neural network for intramodality brain MRI synthesis	2022	U-Net	BRATS'2018 MRI dataset (Challenge for Brain Tumor Segmentation)	dataset of 477 patients clinically diagnosed with glioma brain cancer. It was randomly split into 64%, 16%, and 20% as training, validation, and test set, respectively.	(MSE), (MAE), (PSNR), (SSIM)	T1->T2 : 0.932 T2->T1 : 0.937 T1->FLAIR : 0.946
A-layer-wise fusion network incorporating self-supervised learning for multimodal MR image synthesis	2022	GAN	Brain Tumor Segmentation Challenge 2018 (BraTS 2018) dataset	80% of the 285 samples as the training set and the remaining 20% as the test set.	(PSNR), (MSE), (SSIM)	T1+T2->Flair : 0.9272 T2 -> Flair : 0.8772
Multi-Contrast MRI Image Synthesis Using Switchable Cycle Consistent Generative Adversarial Networks	2022	GAN	BraTs2015, lseg2017, MRBrain13, ADNI, RIRE	220 subjects, 176 subjects randomly selected for training and the rest for testing 18 subjects for training and remaining 5 subjects for testing 16 subjects for training and the remaining 4 for testing 40 subjects are randomly selected for training and the remaining 10 for testing 19 subjects, randomly chooses 16 subjects as for training and the rest for testing	(SSIM)	T1->T2 : 0.910 T2->T1 : 0.893 T1->T2-Flair : 0.873 T2->T2-Flair : 0.875
MRI Cross-Modality Image-to-Image Translation	2020	GAN	BraTs2015, lseg2017, MRBrain13, ADNI, RIRE	220 subjects, 176 subjects randomly selected for training and the rest for testing 18 subjects for training and remaining 5 subjects for testing 16 subjects for training and the remaining 4 for testing 40 subjects are randomly selected for training and the remaining 10 for testing 19 subjects, randomly chooses 16 subjects as for training and the rest for testing	(SSIM)	T1->T2 : 0.910 T2->T1 : 0.893 T1->T2-Flair : 0.873 T2->T2-Flair : 0.875
Generative Adversarial Networks to Synthesize Missing T1 and FLAIR MRI Sequences for Use in a Multisquence Brain Tumor Segmentation Model	2021	GAN	BraTs	Trained, validated, and tested using 210 glioblastomas (GBMs)	(SSIM)	T1 : Median SSI ranged from 0.82 to 0.92 FLAIR : median SSI ranged from 0.76 to 0.92

3 The Proposed Solution

3.1 Solution Methodology

After researching existing deep learning tools in the field of brain MRI synthesis, we identified that most of them work by taking one sequence as input and outputting another, such as inputting a T1 sequence and outputting a T2 sequence, and so on. However, we aim to integrate a deep learning network to cover all possibilities for the four sequences. This means that with one sequence as input, such as a T1 sequence, our system will output the remaining three sequences (T1, T2, Flair, T1ce), not just one. Similarly, if two sequences are inputted, the other two will be outputted.

This approach aims to enhance the quality of the images extracted from the neural network, facilitating diagnosis, speeding up examinations, reducing the patient's time inside the MRI machine, and lowering costs as only one second is needed for an MRI scan. Additionally, we plan to increase accuracy by synthesizing MRI images using 3D technology to create a full volume, rather than just 2D slices.

Moreover, our tool will integrate seamlessly with DICOM Viewer and include processing tools such as zoom, pan, and annotations to assist doctors in diagnosis and decision-making. This system will be added to the cloud, making it easily accessible at any time and from anywhere.

Our primary goal is to develop a DICOM Viewer capable of synthesizing MRI sequences of the brain to assist doctors in making diagnoses regardless of location or time. Additionally, we aim to streamline the imaging process for patients and achieve the highest imaging quality in the shortest time and at the lowest cost possible.

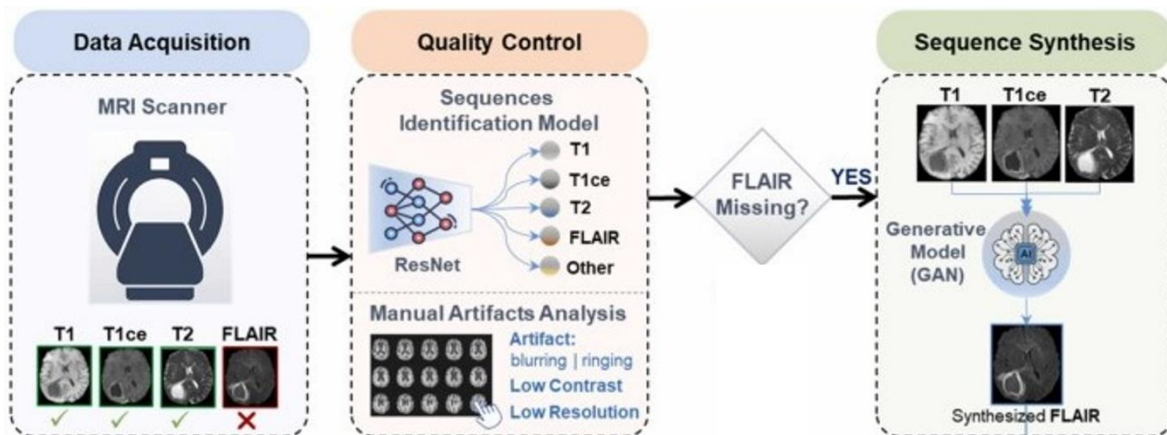


Figure 2 Architecture Framework

3.2 Functional/ Non-functional Requirements

3.2.1 Model Libraries and Frameworks

- NumPy
- TensorFlow
- Keras
- CV2
- Matplotlib

3.2.2 Web Application Frameworks

- React Native
- FastApi

3.2.3 Hardware Specifications

- GPU Info: {'GPU Name': 'Tesla K80', 'Total Memory (GB)': 11.9}
- CPU Info: {'Logical CPUs': 16, 'Physical Cores': 16, 'Max Frequency (MHz)': 2400.0, 'Min Frequency (MHz)': 1200.0}
- RAM Info: {'Total Memory (GB)': 125.37}

3.3 System Analysis & Design

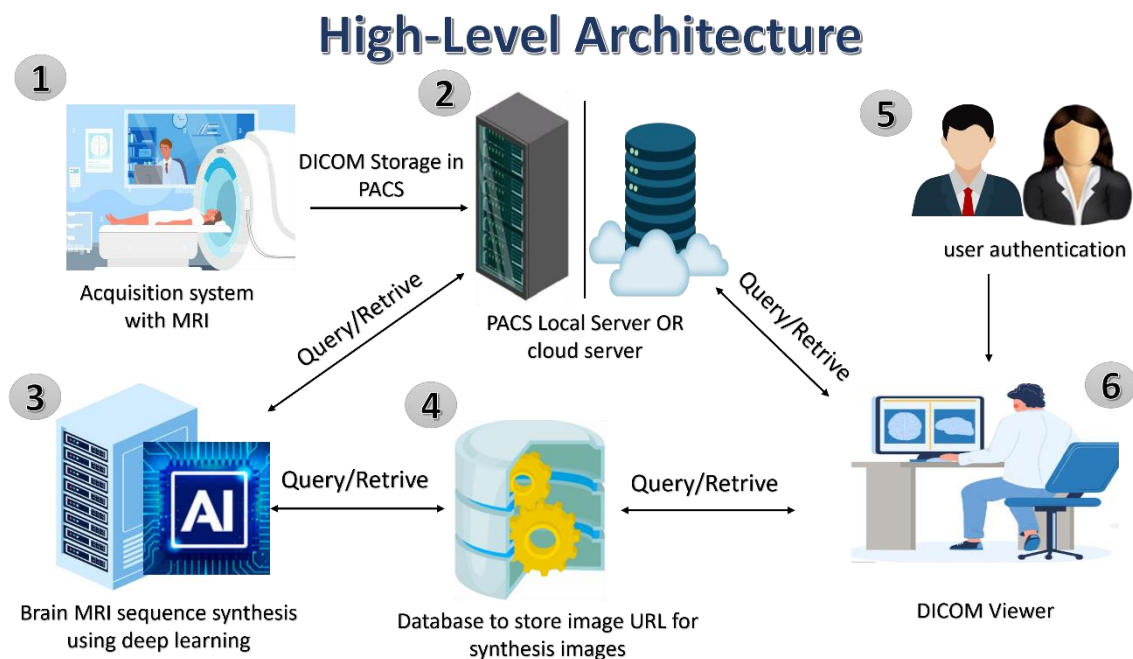


Figure 3 System Architecture

4 Dataset & Pre-processing

4.1 Dataset

We employed the widely recognized brain tumor segmentation dataset, BraTS2023, which includes data from multiple institutions and incorporates various clinical protocols. This dataset, renowned for its robustness and comprehensive nature, was obtained from a wide array of sources, ensuring a high degree of diversity and a broad representation of different patient demographics and tumor characteristics. The dataset comprises several MRI sequences, including T1-weighted, T2-weighted, T1-weighted contrast-enhanced (T1ce), and Fluid-Attenuated Inversion Recovery (FLAIR) images, which are essential for the accurate identification and segmentation of different brain tumor structures. The dimensions of the brain MR images were standardized to $240 \times 240 \times 155$ voxels, providing a uniform framework for analysis and ensuring consistency across the dataset.

In total, the dataset contains imaging data from 1,251 subjects. Each subject's data is accompanied by meticulously curated segmentation annotations of brain tumors, which include different tumor subregions such as peritumoral edema, contrast-enhancing tumor, and non-enhancing necrotic core. The non-enhancing necrotic core and the contrast-enhancing tumor together are referred to as the tumor core (TC), while the combination of these regions along with peritumoral edema constitutes what is known as the whole tumor (WT). The segmentation annotations in BraTS2023 are of high quality, as they are performed by expert board-certified neuroradiologists, ensuring the reliability and accuracy of the labels. This meticulous annotation process is crucial for developing and validating advanced segmentation algorithms that can assist in clinical decision-making and treatment planning.

4.2 Data Pre-processing

To enhance the image synthesis task and ensure the stable training of Generative Adversarial Networks (GANs), a comprehensive and meticulous data preprocessing approach was undertaken. This involved several critical steps to prepare the data for optimal model performance. First, normalization of all data was performed to standardize the intensity values across different images, ensuring consistency and aiding in the convergence of the GANs during training. Additionally, background slices, defined as those without any brain tissue, were meticulously removed to eliminate irrelevant information that could confuse the model. Furthermore, the black background was carefully cropped from all slices used in the training

process, which served to reduce unnecessary computational overhead and allowed the model to focus more precisely on the regions containing brain tissue and tumors. By concentrating on these specific areas, the GANs were better able to learn the intricate details necessary for accurate image synthesis, ultimately contributing to more effective and reliable model performance in the challenging task of image synthesising.

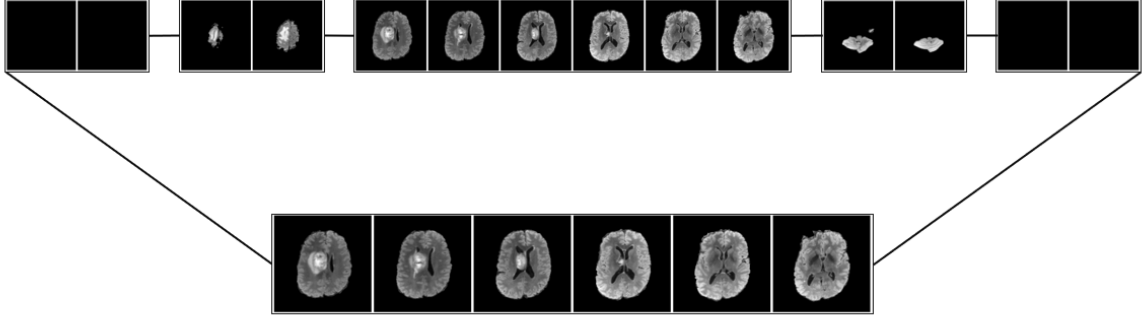


Figure 4 Images Pre-processing

Notably, this intricate process is not executed during the inference phase. Instead, at this stage, all missing sequence slices, including those representing the background, are synthesized comprehensively. This synthesis ensures that any gaps or absent portions within the sequence are accurately filled, maintaining the integrity and continuity of the data. To further ensure consistency and uniformity across the dataset, every image was meticulously resized to a standardized dimension of 256×256 pixels. This resizing step is crucial as it facilitates uniformity in processing and analysis, allowing for more reliable and comparable results. By standardizing the dimensions, we minimize variations that could potentially affect the performance and outcomes of subsequent analytical procedures.

In this study, we employ a modified two-dimensional Generative Adversarial Network (2D GAN) model to synthesize missing sequences from available magnetic resonance imaging (MRI) sequences. The purpose of this task is to enhance the completeness and quality of MRI data, facilitating more accurate medical analyses and diagnoses. To achieve this, we meticulously extracted a subset of 746 high-quality, artifact-free MRI scans from the BraTS 2023 dataset, which originally comprised a total of 1251 scans. The selection process was rigorous, ensuring that only the best scans were chosen. These selected scans included various types of MRI sequences: pre-contrast T1-weighted images, T2-weighted images, post-contrast T1-weighted images, and FLAIR (Fluid-Attenuated Inversion Recovery) images. Each of these images was carefully examined to confirm the absence of artifacts, thereby providing a robust

dataset for our GAN model to work with. By leveraging this comprehensive dataset, our modified 2D GAN model aims to accurately generate missing MRI sequences, potentially revolutionizing the way MRI data is utilized in clinical settings.

The dataset used for this study comprises 746 BraTS scans, which were carefully and randomly divided into two distinct groups to facilitate robust model training and validation. Specifically, 701 of these scans were allocated for the training phase, providing a substantial amount of data to optimize the model's learning capabilities. This training subset yielded a total of 14,025 2D images per sequence, ensuring a diverse and comprehensive range of images for the model to learn from.

For the validation phase, the remaining 45 scans were set aside. This separate validation subset plays a crucial role in evaluating the model's performance and generalization ability on unseen data. From these 45 scans, a total of 895 2D images per sequence were generated. These validation images are instrumental in assessing how well the model can predict and perform in real-world scenarios, providing insights into its accuracy and potential areas for improvement.

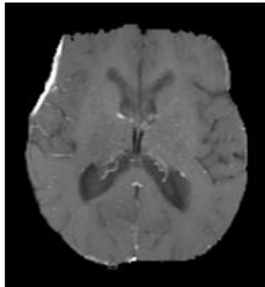
By structuring the dataset in this manner, with a clear distinction between training and validation sets, we aim to ensure the reliability and effectiveness of our model in medical imaging tasks.

4.2.1 Image Artifacts

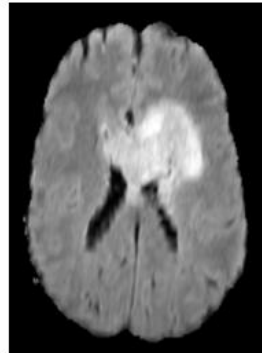
MRI is a valuable diagnostic tool for the detection and characterization of brain tumors. However, the presence of artifacts can reduce the quality of the acquired images. Artifacts can be caused by various factors, such as patient motion, magnetic field inhomogeneities, gradient nonlinearity, and radiofrequency interference.

Before delving into the core of the study, preliminary steps were taken to inspect and analyze the dataset at hand. During the inspection of the dataset entries, five MRI artifacts were conspicuous: ringing artifacts, motion artifacts (also known as blurring or ghosting), susceptibility artifacts, low contrast, and low-resolution. The degree of artifact severity was assigned to each volume as follows: "1" indicating no artifact, "2" for moderate artifact, and "3" indicating cases with severe artifact. The significance of this investigation and scoring is to avoid the inclusion of cases with severe artifacts during data preparation for the synthesis task.

**Low Resolution &
Cropping**



**Motion blur
(Ghosting)**



**Gradient nonlinearity
(Ringing)**

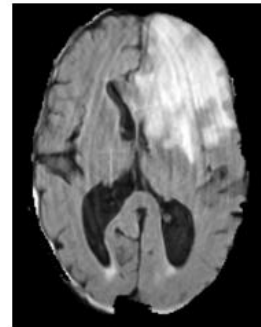


Figure 5 Artifacts

5 Implementation, Experimental Setup, & Results

5.1 Implementation Details

To enhance the performance and overall effectiveness of the GAN framework, we introduced additional modules, namely, squeeze-and-excitation attention and PatchGAN (Fig). Detailed explanations of these modules, including their key features and functionalities, are provided below.

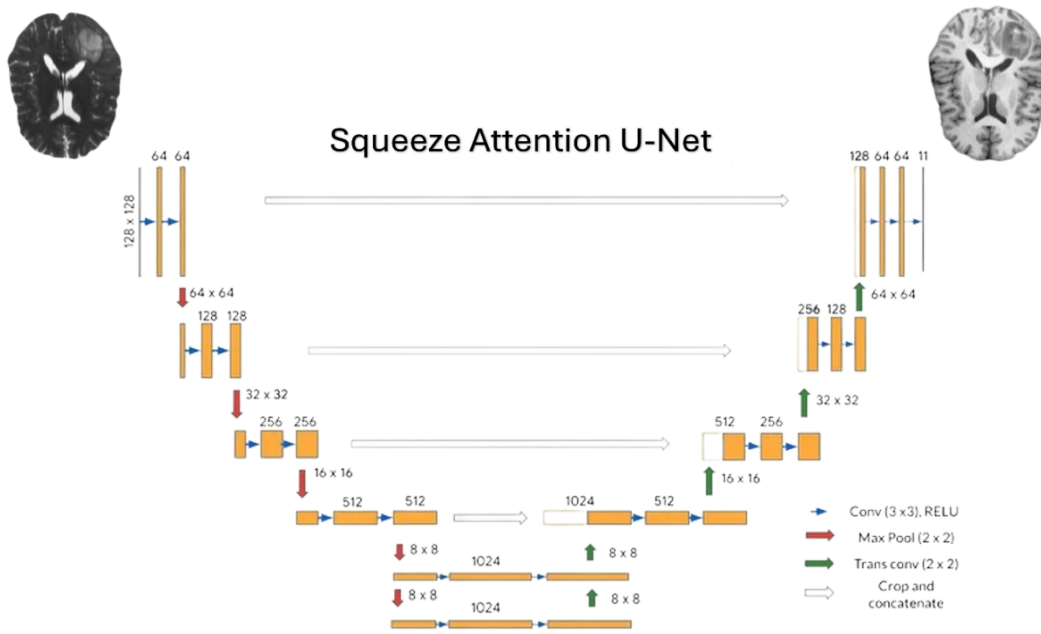


Figure 6 Generator Network Architecture

Fig. The architecture of GANs model that used for synthesizing missing MRI. Comprising two pivotal components: a dual-model generator incorporating Squeeze-Attention-UNET, and a discriminator leveraging PatchGAN for enhanced synthesis capabilities.

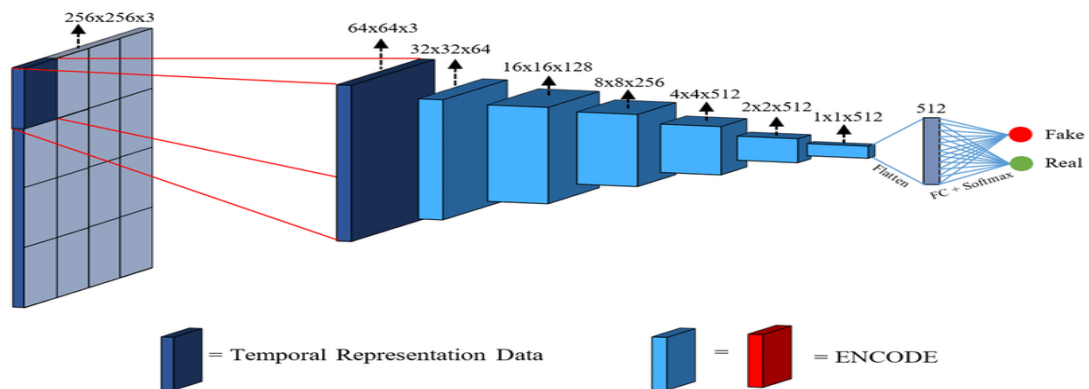


Figure 7 Discriminator Network Architecture

The SE block has been specifically developed to enhance the representational capacity of a network by emphasizing the relationships among different channels within the network. Its primary objective is to recalibrate the responses of each channel by explicitly modelling their interdependencies. Through adaptive recalibration of channel-wise feature responses, the SE block allows the network to prioritize informative channels whereas suppressing less relevant ones. This strategic approach enhances the network’s capability to discern crucial features and patterns within the data. Consequently, it enables focused attention on tumor areas, resulting in enhanced performance in tasks such as image synthesis. The adaptive recalibration process comprises two key steps: squeeze and excitation.

Our proposed generator employs squeeze attention U-Net architecture, which takes an input shape of $256 \times 256 \times 3$ and creates the input layer. The encoder blocks are applied in succession with increasing numbers of filters (64, 128, 256, and 512), and the generated features are passed to the subsequent blocks. After the last encoder block, a bottleneck block with 1024 filters is applied. The decoder blocks are then applied in reverse order, with skip connections and the bottleneck output passed through each block. Finally, a 1×1 convolutional layer with a “tanh” activation function is applied to generate the network’s output.

In our specific implementation, we use PatchGAN as a discriminator. Unlike traditional CNN architectures that make decisions based on the entire input image, PatchGAN maps the $256 \times 256 \times 3$ image to a square array of outputs. Each output prediction represents the classification of the corresponding patch as real or fake. The final decision is obtained by averaging the individual patch classifications.

5.2 Experimental / Simulations Setup

In the simulations setup for enhancing the performance of our Generative Adversarial Network (GAN) model, we have integrated specific architectural modules designed to optimize image synthesis, particularly for generating missing sections in MRI scans. The key modifications include the implementation of squeeze-and-excitation attention (SE block) within the generator and the adoption of PatchGAN in the discriminator component.

Generator Architecture: The generator in our setup utilizes a squeeze attention U-Net architecture, specifically tailored for the synthesis of high-resolution medical images. The input to this network is a $256 \times 256 \times 3$ image. The architecture follows a progressive encoding-decoding pathway where the encoder blocks increase the filter count through 64, 128, 256, and 512 as the network deepens. This is followed by a bottleneck layer equipped with 1024 filters,

which is crucial for capturing the complex features required for detailed image synthesis. The decoding path mirrors the encoding with corresponding reductions in filter counts, enhanced by skip connections that help retain spatial hierarchies between layers. The final output of the generator is formulated through a 1×1 convolution layer using a "tanh" activation function, resulting in the synthesized image (fig).

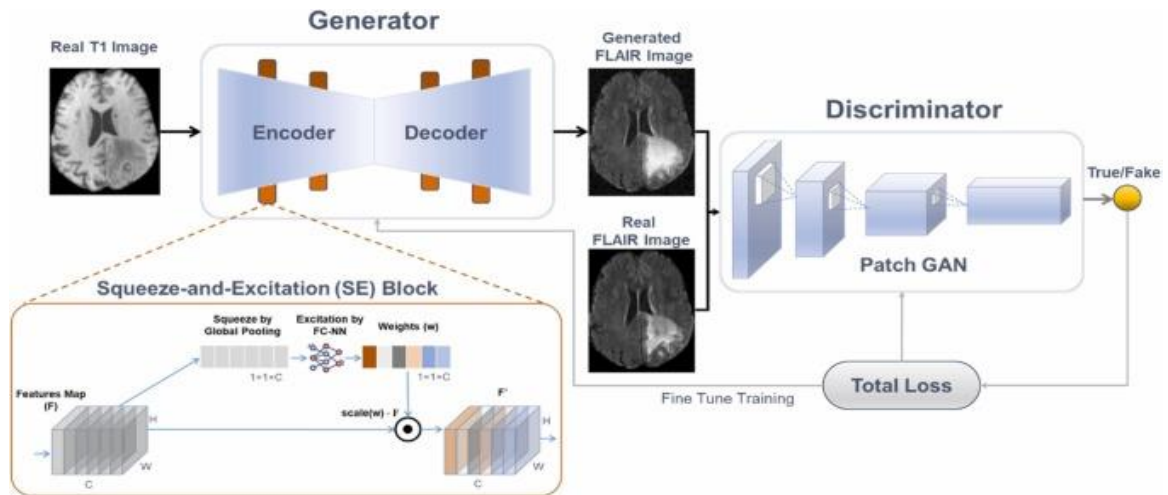


Figure 8 GAN Model Network Architecture

Squeeze-and-Excitation (SE) Block: Integrated within the generator, the SE block is designed to amplify the model's sensitivity to informative features in the input data, particularly useful for emphasizing tumor regions in MRIs. This block operates by modelling the interdependencies between different channels in the feature maps, thereby recalibrating the channel-wise responses based on their relevance to the synthesis task. This recalibration is executed in two phases: squeeze, which aggregates the global information of the channels, and excitation, which uses this information to emphasize important features and suppress the less relevant ones.

Discriminator Architecture: For the discriminator, we employ the PatchGAN model, which differs significantly from traditional full-image discriminative approaches. Instead of assessing the entire image at once, PatchGAN evaluates the authenticity of distinct 256×256 patches of the image. This method allows for finer discrimination on a local scale, enabling the discriminator to effectively assess detailed textural and structural authenticity in the synthesized images. The outputs for each patch are then averaged to derive the final decision on whether the image is real or synthetically generated (fig).

These enhancements in our GAN setup aim to significantly improve the model's ability to synthesize realistic and accurate medical images, with particular efficacy in handling complex

tasks like missing MRI reconstruction. This setup not only boosts the performance of individual model components but also harmonizes their functionalities to achieve superior synthesis quality.

5.3 Conducted Results

Table. Measurement performance for synthesizing sequences from other available sequences, with and without including full background append slices in terms of SSIM and PSNR.

Table 2 Results for Synthesized T1

	SSIM	MAE	PSNR
T2 → T1	86.77%	0.042	24.91
T1CE → T1	90.63%	0.033	26.43
FLAIR → T1	86.29%	0.043	24.42

Table 3 Results for Synthesized T2

	SSIM	MAE	PSNR
T1 → T2	90.83%	0.027	27.46
T1CE → T2	90.77%	0.022	28.42
FLAIR → T2	90.32%	0.022	28.05

Table 4 Results for Synthesized Flair

	SSIM	MAE	PSNR
T1 → FLAIR	82.03%	0.051	24.80
T1CE → FLAIR	83.68%	0.028	26.91
T2 → FLAIR	83.99%	0.030	27.12

5.4 Testing & Evaluation

As depicted in Fig. 3, the GAN employs two loss functions: one for the generator and one for the discriminator. The generator loss plays a critical role in calculating the loss components for a generator model within a GAN.

The first loss component computed by the generator is the adversarial loss, which quantifies the ability of the generator to produce outputs that deceive the discriminator. It is calculated by comparing the discriminator's output for the generated output with a tensor of ones, employing a specific loss function.

Additionally, three other loss components are determined. The first is the mean absolute error (MAE), which measures the pixel-wise discrepancy between the generated and the target outputs. This loss provides a granular evaluation of the dissimilarity between the two outputs.

$$MAE = \frac{\sum_{i=1}^n |y_i - x_i|}{n} = \frac{\sum_{i=1}^n |e_i|}{n}$$

Equation 1 Mean Absolute Error

The second loss component is derived from the structural similarity index measure (SSIM), which measures the structural similarity and pixel intensities between the target and the generated outputs. SSIM loss captures the extent of structural similarity between the outputs.

The third loss component is derived from the peak signal-to-noise ratio (PSNR), which quantifies the ratio between the maximum possible power of a signal and the power of corrupting noise that affects the fidelity of its representation. PSNR loss measures the accuracy of the generated output in terms of the mean squared error (MSE) between the target and the generated images, capturing the degree of similarity in pixel intensities and overall image quality.

$$PSNR = 10 \log_{10} \left(\frac{R^2}{MSE} \right)$$

Equation 2 PSNR

To obtain a consolidated loss measure, the total loss is calculated as the average of the mean absolute error (MAE) and SSIM. This combined loss metric offers a balanced evaluation of both the pixel-wise difference and the structural similarity between the outputs.

The overall loss for the generator (Loss G) is computed by summing the adversarial loss with a weighted version of the combined loss. This weighting factor provides flexibility in adjusting the relative importance of the combined loss compared to the adversarial loss.

$$Loss_G = adversarial\ loss + 100 \times \left(\frac{SSIM + MAE}{2} \right)$$

Equation 3 Generator Loss

The discriminator loss (Loss D) is composed of two components: the loss associated with correctly classifying real samples (real loss) and the loss associated with correctly classifying generated samples as fake (generated loss). The real loss measures the discriminator's ability to recognize authentic samples, which is calculated by comparing its output for real samples with a tensor of ones. Conversely, the generated loss quantifies the discriminator's success in discerning the generated samples as fake, computed by comparing its output for the generated samples with a tensor of zeros. The total discriminator loss is the sum of these two losses, reflecting the overall performance of the discriminator in discriminating between real and generated samples during training.

$$Total\ Loss\ Computation = \arg \min_G \max_D (Loss_G, Loss_D)$$

Equation 4 Total Loss

5.4.1 T1 Losses

This plot illustrates the generator loss over epochs for generating T1 sequences from various inputs, including T2, T1ce, and FLAIR. The model's performance varies depending on the input data, with the best loss of 7.62 observed at epoch 149 for T2 inputs.

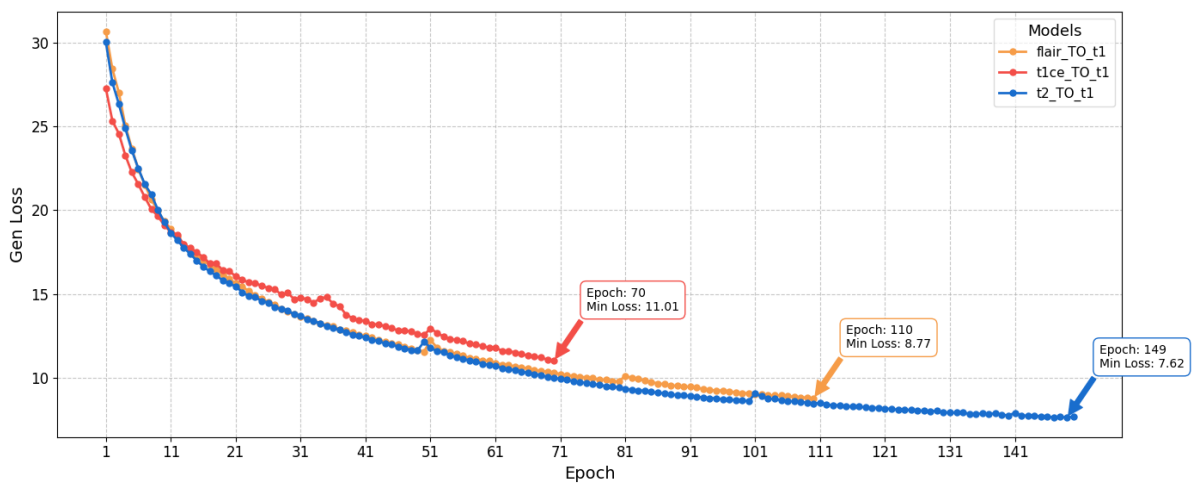


Figure 9 Generator Loss Over Epochs for Generating T1

5.4.2 FLAIR Losses

This plot illustrates the generator loss over epochs for generating FLAIR sequences from various inputs, including T1, T2, and T1ce. The model's performance varies depending on the input data, with the best loss of 11.12 observed at epoch 100 for T1 inputs.

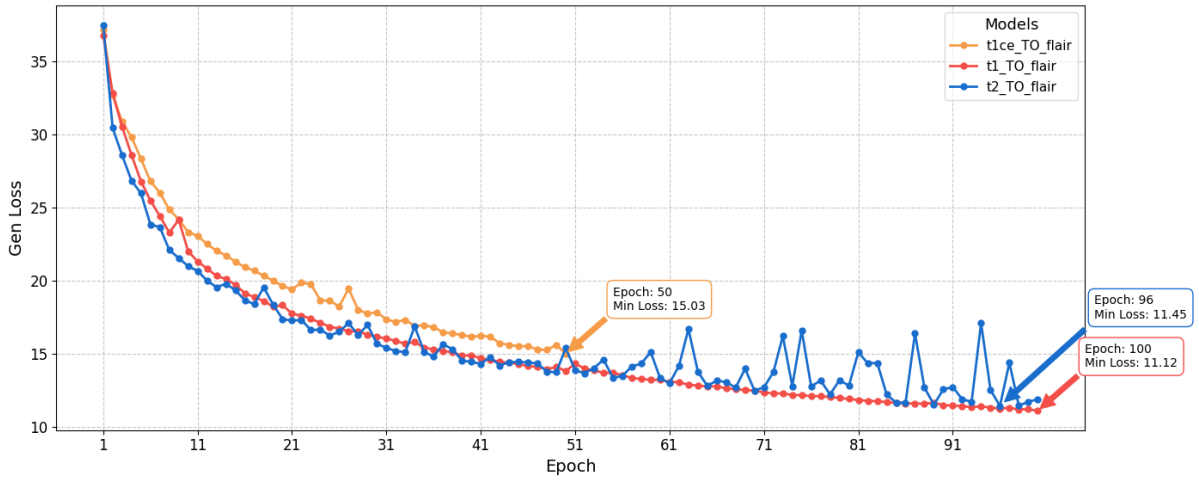


Figure 10 Generator Loss Over Epochs for Generating FLAIR

5.4.3 T2 Losses

This plot illustrates the generator loss over epochs for generating T2 sequences from various inputs, including T1, T1ce, and FLAIR. The model's performance varies depending on the input data, with the best loss of 5.77 observed at epoch 79 for T1ce inputs.

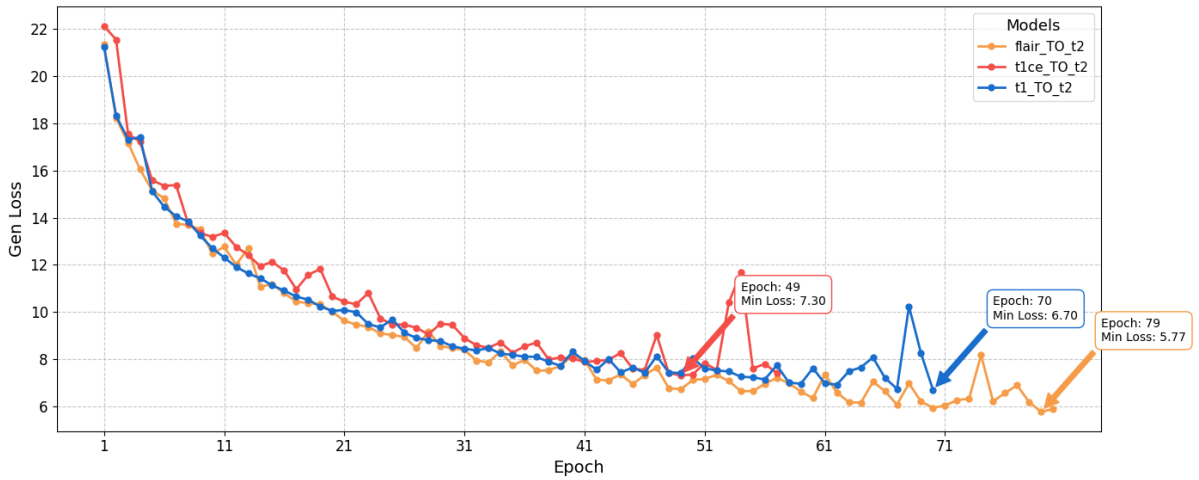


Figure 11 Generator Loss Over Epochs for Generating T2

6 Discussion, Conclusions, and Future Work

6.1 Discussion

6.1.1 Results

Deep learning techniques in brain tumor segmentation models often require multimodal MRI inputs, which may not be available in clinical practice due to several reasons. Differences in acquisition protocols across medical facilities can lead to inconsistencies, whereas image artifacts can compromise scan quality. Consequently, the absence of one or more MRI sequences during examinations poses a substantial challenge for developing brain tumor segmentation models.

Here, we demonstrate that Generative Adversarial Networks (GANs) offer an effective solution for generating missing MRI sequences. These generated sequences can then be used as inputs in a multisequence Convolutional Neural Network (CNN) model for brain tumor segmentation. Specifically, we employ a squeeze attention U-Net in the generator and PatchGAN in the discriminator, yielding favorable results.

The synthetic sequences produced by this method play a pivotal role in accurately identifying and characterizing brain tumors. They highlight critical features such as edema and lesions, essential for precise medical diagnosis and treatment planning. By successfully synthesizing missing MRI sequences, our approach addresses a significant challenge in clinical practice, potentially improving the reliability and effectiveness of brain tumor segmentation models.

6.1.2 Limitations

The results of this graduation project on MRI missing sequence synthesis were significantly impacted by limitations stemming from GPU resource constraints and time restrictions. Limited access to high-performance GPUs extended the training times of the synthesis models, reducing the number of experiments possible within the available timeframe and restricting the complexity of models that could be utilized. Consequently, simpler and less computationally demanding models had to be employed, albeit feasible given the constraints, but did not achieve the performance levels of more advanced models in accurately synthesizing missing MRI sequences.

The prolonged training cycles also hindered effective hyperparameter tuning, as exhaustive exploration of the hyperparameter space was not feasible, potentially resulting in suboptimal model configurations. Additionally, the fixed timeline of the project imposed further constraints, limiting the scope of experiments and the extent of data preprocessing and augmentation that could be performed. More extensive preprocessing and augmentation could have enhanced the quality and diversity of the training data, thereby improving the accuracy and reliability of the synthesized MRI sequences.

Furthermore, time constraints curtailed in-depth error analysis and iterative model refinement, crucial for addressing specific weaknesses and optimizing model performance. As a result, the developed models may exhibit lower performance in terms of accuracy, precision, and consistency of the synthesized MRI sequences than what could have been achieved with more substantial resources and an extended timeframe. These constraints underscore the necessity for future research with enhanced computational resources and longer project durations to fully explore and realize the potential of the methodologies proposed in this study for MRI missing sequence synthesis.

6.2 Summary & Conclusion

The "MRI Missing Sequence Synthesis" project addresses a critical challenge in medical imaging: the incomplete acquisition of MRI sequences, which can compromise diagnostic accuracy and patient outcomes. MRI is an essential tool for diagnosing various medical conditions, but due to factors like time constraints, patient movement, or technical issues, obtaining a full set of sequences is not always possible. This project leverages advanced deep learning techniques, specifically Generative Adversarial Networks (GANs), to develop a model capable of synthesizing missing MRI sequences from available data. The dataset used for this project includes a diverse collection of MRI scans from multiple patients, ensuring the model's robustness and generalizability. Key steps in the project included comprehensive data preprocessing, such as normalizing images and augmenting the dataset to improve the model's performance, followed by an extensive training phase focusing on optimizing the neural network architecture and fine-tuning hyperparameters. Evaluation was conducted using metrics such as the Structural Similarity Index (SSIM) and Peak Signal-to-Noise Ratio (PSNR), which confirmed the high quality and accuracy of the synthesized images.

The successful development of this model has significant implications for the medical field. It enhances the diagnostic capabilities of MRI by providing clinicians with more

comprehensive imaging data, thereby reducing the need for repeat scans and improving overall patient care. This advancement not only saves time and resources but also minimizes patient discomfort and exposure to prolonged scanning procedures. Moreover, the methodology and findings from this project pave the way for further research in the field of medical image synthesis. Future work could involve refining the model by incorporating larger and more diverse datasets, exploring different neural network architectures, and conducting extensive clinical validation to ensure the model's applicability in real-world settings. Additionally, integrating this technology into MRI machines and radiology workflows could revolutionize diagnostic imaging practices, making them more efficient, reliable, and accessible. The "MRI Missing Sequence Synthesis" project demonstrates the transformative potential of deep learning in medical imaging, opening new avenues for enhancing diagnostic precision and patient care.

6.3 Future Work

6.3.1 Combining Multiple Models for Enhanced Prediction

One of the promising directions for future work is the integration of multiple models to improve the prediction accuracy of missing MRI sequences. Whereas our current approach may rely on a single model architecture, combining the predictions from several models can provide a more comprehensive understanding of the underlying patterns in the data. By leveraging the strengths of different models, we can create an ensemble approach that reduces the risk of overfitting and captures a broader range of features. Additionally, exploring techniques like model stacking or hierarchical ensembles could further enhance the robustness and generalization capabilities of the synthesis system.

6.3.2 Testing on Segmentation Models

To evaluate the practical effectiveness of the synthesized MRI sequences, it is crucial to conduct thorough testing using segmentation models. Segmenting anatomical structures and lesions from medical images is a critical task in clinical diagnosis and treatment planning. By incorporating the synthesized sequences into segmentation models, we can assess how well the generated data aligns with the ground truth and how it impacts the segmentation accuracy. Furthermore, investigating the effects of different synthesis methods on segmentation performance, such as data augmentation techniques or domain adaptation strategies, could provide valuable insights into optimizing the synthesis process for downstream tasks.

6.3.3 Extending Synthesis to Other Organs

Whereas the current project focuses on synthesizing missing sequences for brain, there is a significant opportunity to extend the synthesis capabilities to other organs and anatomical structures. Each organ presents unique challenges and imaging characteristics, requiring tailored approaches for accurate synthesis. By adapting the existing synthesis models to accommodate the anatomical and pathological variations found in organs such as the liver, kidneys, heart, and musculoskeletal system, we can broaden the applicability of the synthesis system across a wider range of clinical scenarios. This extension would involve collecting diverse datasets representing various organs and diseases, as well as refining the synthesis algorithms to account for organ-specific features and imaging protocols.

6.3.4 Cross-Dataset Evaluation

To assess the generalizability of the synthesis models, it is essential to conduct cross-dataset evaluation across different imaging centres, scanner vendors, and patient populations. Variations in imaging protocols, hardware specifications, and patient demographics can introduce challenges that may affect the performance of the synthesis algorithms. By applying the models to multiple datasets with varying characteristics, we can evaluate their robustness and adaptability in real-world clinical settings. This evaluation would involve benchmarking the synthesis performance against ground truth annotations and comparing the results across different datasets to identify potential sources of variability and areas for improvement.

6.3.5 Real-World Synthesis Application

Ultimately, the goal is to develop a real-time synthesis system that seamlessly integrates into clinical workflows and enhances the diagnostic capabilities of healthcare professionals. This requires addressing several challenges, including optimizing the synthesis algorithms for efficient computation and minimizing latency, designing user-friendly interfaces that facilitate interaction with the synthesis system, and ensuring regulatory compliance and safety standards are met for clinical deployment. Furthermore, validating the synthesized MRI sequences in clinical studies and assessing their impact on diagnostic accuracy and patient outcomes are essential steps towards clinical adoption. By collaborating with radiologists, clinicians, and industry partners, we can bridge the gap between research and clinical practice and translate the potential of MRI synthesis into tangible benefits for patient care.

By pursuing these diverse avenues for future work, we aim to advance the field of MRI missing sequence synthesis and contribute to improved diagnostic accuracy, patient outcomes, and healthcare delivery in medical imaging.

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