

Generative Creation of Synthetic 3D Tumors in MRI Head Scans

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October 2024

1. Abstract

The goal of this project was to develop a process for creating brain MRI datasets by adding synthetic tumors, aimed at improving the accuracy of tumor detection models. By generating synthetic tumors and embedding them into healthy brain MRI scans, the project creates a more diverse dataset. Unique images are produced by slicing the scans from various angles, providing different perspectives of the synthetic tumors. Using the DenseNet model, we evaluated the impact of these augmented datasets on tumor detection accuracy. The results indicated improvement in model accuracy and recall, underscoring the effectiveness of synthetic data augmentation. The developed tool offers a valuable contribution to medical research by generating diverse, synthetic data without the need for additional labeling. This expanded dataset can enhance tumor identification in 3d MRI head scans, providing researchers with enriched resources for developing more accurate diagnostic models and thereby improving early diagnosis and supporting clinicians in more accurate and efficient medical diagnostics.

2. Introduction

In head and brain medicine, the doctors work with CT and MRI scans to diagnose medical problems. These medical imaging techniques are essential tools in the diagnosis of various conditions, including the detection of tumors. However, the interpretation of these scans is largely manual, relying on the expertise of radiologists to identify abnormalities. Despite their experience, human error can occur, and subtle signs of early-stage tumors or other suspicious findings might be missed. The complexity and volume of medical images, combined with the long hours and fatigue that radiologists often face, further increase the likelihood of diagnostic errors. This is particularly concerning in cases where early detection is critical for successful treatment.

In addition, doctors manually examine patients' scans by checking different sections, directions, and depths in order to reach the specific area of interest. Since this is a manual process, the doctor may not always direct the viewing angle of the scan in a way that is optimal for diagnosing the problem. Furthermore, the diagnostic systems that radiologists rely on typically display the images along the X, Y, and Z axes. This approach segments the scan into specific planes or slices, which can sometimes limit visibility, particularly when it comes to detecting small or early-stage tumors. These subtle abnormalities may not be easily noticeable in one particular plane and could be missed entirely if they don't stand out in the slice being examined. This creates an additional challenge, as the process does not always allow for a comprehensive view of the entire area in three dimensions. As a result, some findings can be overlooked, and early detection, which is critical for improving treatment outcomes, may not be achieved. This increases the need for more

advanced diagnostic techniques beyond traditional sectional imaging to ensure that even the smallest anomalies are detected. Inaccurate or delayed diagnosis can directly impact the patient's future health, making the accuracy and thoroughness of this process vitally important.

Given the limitations of manual diagnosis, there is a growing need to incorporate automated tools, particularly artificial intelligence (AI), into the process of analyzing medical scans. AI systems have the potential to significantly enhance diagnostic accuracy by identifying patterns and anomalies that might not be visible to the human eye, especially in the early stages of disease. By leveraging machine learning models, AI can analyze vast amounts of scan data quickly and comprehensively, providing an additional layer of precision that complements the work of radiologists.

However, for AI-based systems to be truly effective, the quality and quantity of data used to train these models are crucial. High-quality datasets that include a wide range of medical scans, particularly those featuring diverse types and stages of tumors, are essential for creating models that can accurately identify abnormalities. The more extensive and varied the dataset, the better the AI recognizes subtle signs of tumors across different patients and scan conditions. This is particularly important for early detection, where tumors may be small or difficult to distinguish from surrounding tissue.

Training AI models requires not just a large volume of data but also properly annotated scans that indicate the exact location, size, and characteristics of tumors. This data enables the model to learn what to look for, improving its ability to flag suspicious areas in new, unseen scans. As a result, AI has the potential to not only increase the accuracy of diagnoses but also to reduce the time it takes to interpret scans, allowing for faster interventions and better outcomes for patients.

This project focused on inserting synthetic tumors into 3D brain scans. The primary goal is to aid medical professionals by contributing to the field of AI in healthcare. Specifically, we aim to expand the dataset of 3D medical imaging, which is critical for training AI models to identify and diagnose tumors more accurately. By enriching the database with various 3D scans containing different tumor sizes and locations, we can improve the model's ability to detect smaller tumors that might be missed during manual diagnosis. "A very exigent task for radiologists is early brain tumor detection. Brain tumor raises very fast, its average size doubles in just twenty-five days" Amin et al. (2020). Additionally, training AI with scans that feature tumors from different angles and sections allows the models to better adapt to real-world variations in medical imaging. As the field of medicine increasingly incorporates automated decision-making and AI-driven diagnostics, having a well-trained model capable of identifying subtle abnormalities is essential for improving patient outcomes and supporting clinicians in their work.

3. Related Work

The article "Brain Tumor Segmentation Using Synthetic MR Images - A Comparison of GANs and Diffusion Models" Usman Akbar et al. (2024) evaluates the use of synthetic medical images for brain tumor segmentation, comparing the performance of four Generative Adversarial Networks (GANs) and a diffusion model. The authors demonstrate that training segmentation networks (U-Net and Swin transformer) on synthetic images results in performance that is 80-90% of what can be achieved with real data. While GANs perform reasonably well, diffusion models show a risk of memorizing training images, which could complicate image sharing. The study emphasizes the potential of synthetic medical images to overcome privacy barriers in medical data sharing but calls for further work to ensure their validity.

"Label-Free Liver Tumor Segmentation" Hu et al. (2023) presents an innovative approach to liver tumor segmentation using synthetic tumors generated from CT scans, thereby eliminating the need for manual annotation. They developed a synthetic tumor generation strategy that produces tumors indistinguishable from real ones in terms of shape and texture, which even experienced medical professionals occasionally misidentify during visual examinations. The researchers' key contributions include embedding clinical knowledge into the tumor synthesis process, enabling the generation of tumors that align closely with medical imaging characteristics. The AI models trained on these synthetic tumors achieved a Dice Similarity Coefficient (DSC) of 59.81% in segmenting real liver tumors, which surpasses the performance of existing methods that rely solely on real tumors. This groundbreaking finding suggests a paradigm shift from traditional label-intensive approaches to more efficient label-free AI development for tumor segmentation. The synthetic tumors not only enrich training datasets, allowing for the creation of various tumor sizes and types but also enhance the detection rates of small tumors, crucial for early cancer diagnosis. Furthermore, the authors conducted a Visual Turing Test with radiologists to validate the realism of the generated tumors, which successfully confused both junior and senior professionals, underscoring the effectiveness of their approach. Overall, this research provides compelling evidence for the potential of synthetic data in medical imaging, paving the way for advancements in automated tumor detection and improving the efficiency of training AI models without the extensive costs associated with manual annotations.

The article "TuMore: Generation of Synthetic Brain Tumor MRI Data for Deep Learning Based Segmentation Approaches" Lindner et al. (2018) presents a method for creating synthetic brain tumors within MRI images of healthy subjects to generate large datasets for training deep learning models in tumor segmentation. The authors develop a technique that deforms an icosahedron to simulate realistic glioblastoma shapes and insert them into MRI scans, also simulating

the tumor mass effect by applying a displacement field. This approach allows for the automatic generation of precise ground truth annotations without the need for manual segmentation, addressing the scarcity of annotated medical data and facilitating the development of accurate and robust automated segmentation methods.

The article "3D Slicer as an Image Computing Platform for the Quantitative Imaging Network" Fedorov et al. (2012) discusses the open-source software platform 3D Slicer, which has become a central tool in medical imaging research. It highlights 3D Slicer's capabilities in image analysis, visualization, and segmentation, specifically in the context of the Quantitative Imaging Network (QIN), a National Cancer Institute initiative. The platform supports a wide range of medical imaging formats and offers tools for preclinical and clinical research, enabling reproducible workflows. Key features include support for multi-modal imaging data, quantitative analysis, and the ability to integrate custom algorithms and modules. The platform has a significant role in oncology, helping researchers analyze tumor data, evaluate therapy response, and support radiomics research. It fosters collaboration through its extensibility, allowing integration of plugins and advanced processing methods.

The SkullStripper module, discussed in the article on 3D Slicer, is a tool used for the removal of non-brain tissues, such as the skull, scalp, and dura, from neuroimaging data. This is a critical step in brain imaging analysis, as it helps in isolating brain structures for more precise analysis, including tasks like segmentation and registration. In medical imaging, skull stripping is essential in pre-processing MRI data, particularly for brain studies, to focus on brain tissue and eliminate distractions from surrounding structures. The SkullStripper in 3D Slicer uses algorithms to automate this process, making it faster and more reliable than manual methods.

In our project, we used 3D Slicer software for analyzing and learning the medical media domain. specifically, 3D Slicer's robust capabilities allowed us to validate our results by visualizing the segmented brain structures. We used its 3D MRI visualization tools to ensure that the segmentation and synthetic tumor additions matched expected anatomical features. We also use and integrate the SkullStripper module in 3D Slicer to segment only the brain from head MRI scans, ensuring that we focus solely on the brain region without interference from other cranial structures. This tool was essential for extracting the brain from full head scans, which improved the accuracy of our tumor insertion processes.

In "MONAI: An open-source framework for deep learning in healthcare" Cardoso et al. (2022) is about MONAI, an open-source deep learning framework specifically designed for healthcare, focusing on medical imaging. MONAI extends the PyTorch library by incorporating domain-specific features, like 3D imaging and data augmentation tools, tailored to the medical field's

unique requirements. Its goal is to simplify and accelerate the development of AI models for clinical use while ensuring robust, reproducible results that adhere to the strict standards of medical data. MONAI's strength lies in its ability to integrate seamlessly with existing PyTorch ecosystems while offering tools for training, validating, and deploying AI models, particularly in image segmentation and classification.

The paper emphasizes MONAI's modularity, allowing users to opt-in to features incrementally, thus reducing complexity and lowering the barrier to entry. Furthermore, MONAI offers various utilities for transforming and augmenting data, which are key for improving model generalization and reducing overfitting. The framework also includes engines for handling training loops, loss functions, and performance metrics, supporting distributed training on GPUs to optimize model performance. Users can incorporate third-party libraries and extend their functionality for specific medical applications. Through community-driven development and open-source licensing, MONAI has become a robust platform widely used by researchers and clinicians worldwide, accelerating progress in AI-driven healthcare solutions.

4. Algorithm

In this section, we will describe the workflow for Synthetic Tumor Insertion in 3D Head MRI Scans which we developed in this project.

The objective of our project was to insert a synthetic brain tumor into a 3D head MRI scan. This process required identifying a relevant location in the scan, generating a realistic tumor that integrates smoothly into the brain, embedding the tumor into the 3D MRI data, and producing 2D slices from the modified 3D scan to create a dataset suitable for training deep learning models.

For the process, we used healthy head MRI scans of different people, with high resolution in NRRD format. The scans were taken from different datasets from kaggle.com and 3D Slicer Fedorov et al. (2012).

We will outline the process in four key stages, detailing each one.

Stage 1: Locating the Tumor's Insertion Area

The first step involves selecting an appropriate area within the 3D head MRI scan to insert the synthetic tumor. Specifically, we need to identify a central point in the brain where the tumor will be placed. To achieve this, we used the SkullStripper module from 3D Slicer, which was integrated into our pipeline. This tool effectively isolates the brain by providing a 3D coordinate matrix that maps the brain's location within the head scan. Once the brain is segmented, the exact tumor location can either be manually selected within a specific region or determined randomly within the brain volume.



(a) The segmented brain in the front view.

(b) The segmented brain in the side view.

Figure 1

Stage 2: Creating the Synthetic Tumor

The second stage involves generating the synthetic tumor. The function responsible for this accepts parameters such as the 3D head MRI scan, tumor radius, growth level, shape deformation, and roughness level. Using these inputs, the function creates a tumor as a deformed sphere, adjusting its size and shape based on the specified parameters. The tumor's intensity values are matched to those present in the original MRI scan to ensure a consistent appearance with the surrounding brain tissue. The tumor is colored in such a way that the center of the tumor is lighter and the edges are darker by how real tumors are characterized.

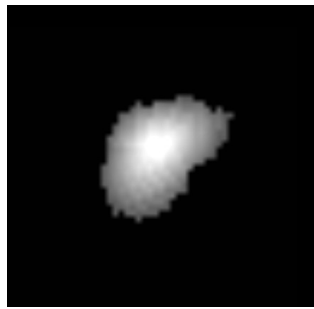


Figure 2: New synthetic tumor.

Stage 3: Embedding the Tumor in the 3D MRI Scan

The next stage is embedding the synthetic tumor into the 3D MRI scan. The function takes as input the tumor's center point, as determined in Stage 1, along with the generated tumor volume in Stage 2 and the original 3D head MRI scan. The tumor is embedded by replacing the pixel values at the tumor's location in the scan. Additionally, a blending process is applied, where the pixel intensities at the boundary between the tumor and the brain are adjusted to create a smooth transition by applying transparency. It ensures the tumor does not appear so artificial and will combine more naturally.

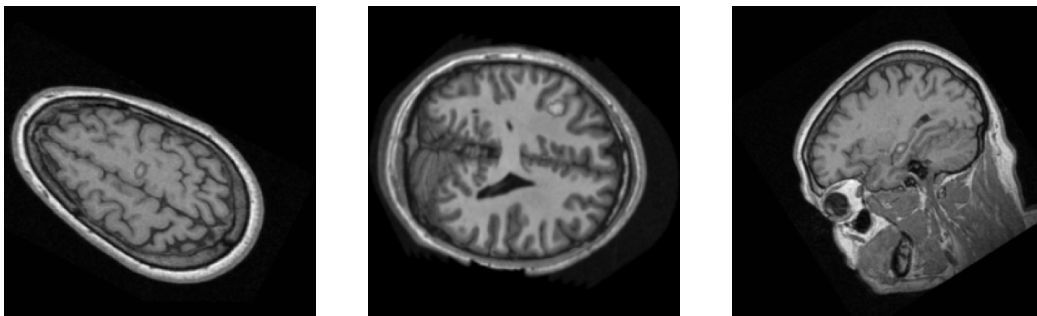


Figure 3: Examples for scans with different synthetic tumors.

Stage 4: Creating 2D Slices from the Modified 3D Scan

In the final stage, 2D slices are extracted from the modified 3D MRI scan to generate a dataset for training. The process involves defining planes that intersect the 3D volume, allowing cross-sectional views of the brain and the embedded tumor to be captured.

This stage begins by selecting three random points in the 3D space, which define a plane that cuts through the MRI volume while one of the points is near the tumor position. The points serve as references to determine the orientation and position of the plane, ensuring the captured slice reflects the desired cross-section of the tumor and brain. By computing intersections between lines and planes, the process guarantees that the slice represents a proper and well-positioned cross-section. To optimize the computation, we implemented the slicing process using NumPy, a highly efficient library for numerical computations. NumPy's ability to handle large arrays allows us to perform complex geometrical transformations and interpolation required to extract the slices quickly. The operations are vectorized, meaning calculations are applied simultaneously to the entire grid of points along the slicing plane, reducing computational time significantly. For even further optimization, we can run this code on GPU hardware using CuPy, a library that provides GPU-accelerated array operations, enabling faster processing, especially when scaling to large datasets or when generating a high volume of slices for training purposes. Once the plane is defined, a grid of points is generated along the plane to represent the pixels of the 2D slice. These points are then mapped back to the original 3D scan to retrieve corresponding intensity values. The mapping ensures a smooth and accurate representation of the tumor and brain tissue within the 2D slice. This method produces slices that accurately depict the features in the 3D volume from various perspectives.

Finally, the extracted slices are saved as 2D images. This step ensures that the slices correctly represent different angles and perspectives and that the synthetic tumor is properly integrated into the slices. The output is a diverse 2D image dataset, capturing various views of the brain and tumor, which can be used for training AI models or for further analysis.

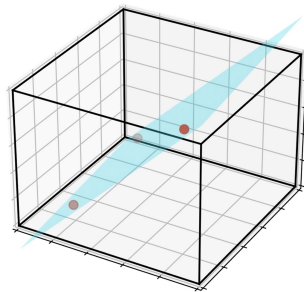


Figure 4: 3d slice.

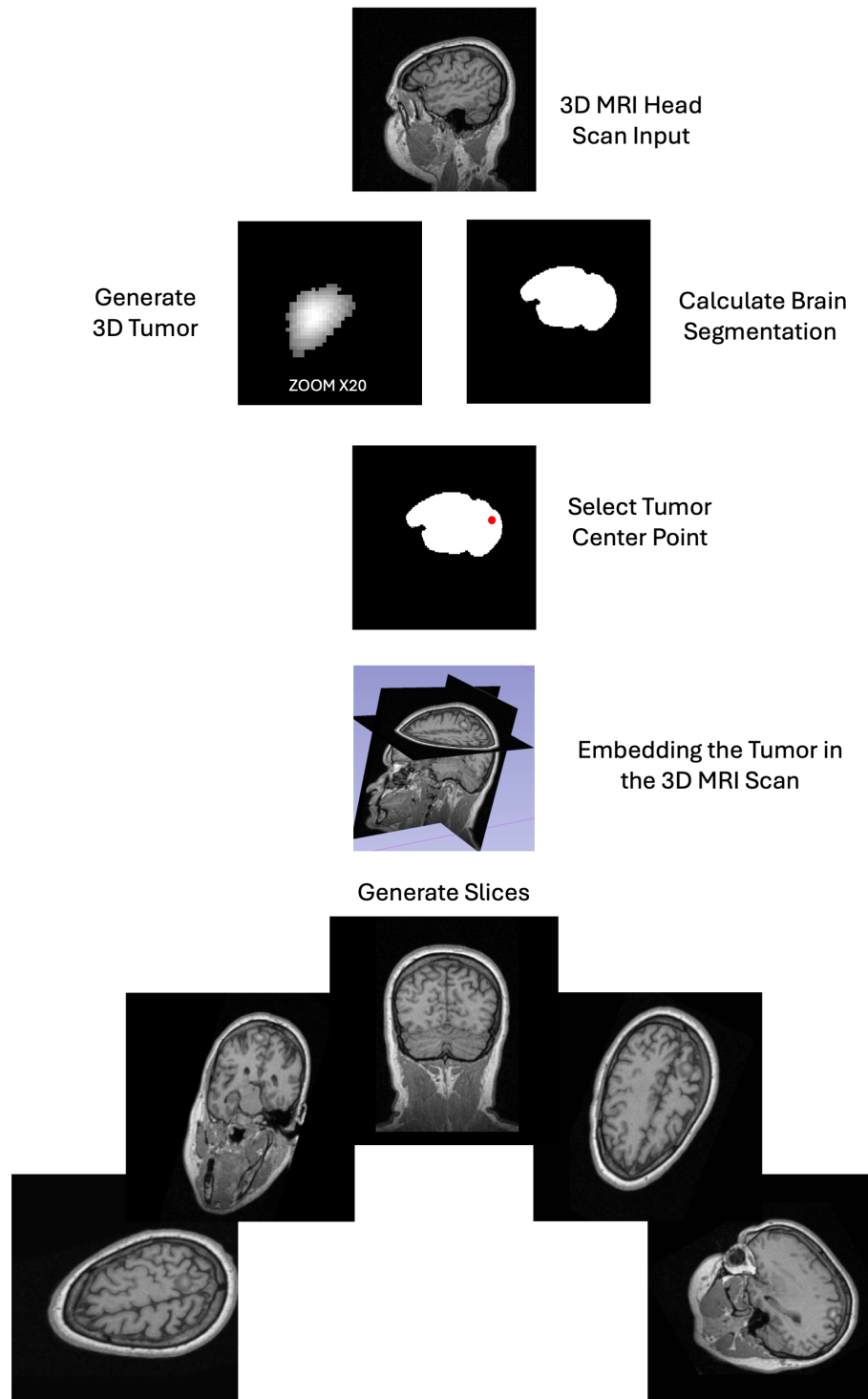


Figure 5: Diagram of the algorithm.

5. Experiments & Results

The primary objective of this project was to create a tool for generating a dataset of brain MRI images containing synthetic tumors. The intention behind this was to create additional training data, particularly focusing on underrepresented tumor types, such as small and irregularly shaped tumors, which are crucial for early detection and diagnosis. To verify the impact of these synthetic images, we utilized the DenseNet (Densely Connected Convolutional Networks) model which is highly effective for image classification tasks, especially in medical imaging, including brain MRI scans. It connects layers of the network in a way that allows the model to use features from earlier layers efficiently, which helps it learn to recognize small details like tumors. DenseNet also uses fewer parameters than some other models, which means it can still achieve high accuracy without needing as much data. This makes it a good choice for our project.

To determine whether the synthetic tumor images we generated were contributing positively to model training, we followed a two-phase evaluation approach using DenseNet:

1. Baseline Evaluation (Without synthetic data):

We first trained DenseNet on an initial dataset from Kaggle.com consisting of real MRI scans, equally balanced between images with tumors and images without tumors. The goal here was to establish a baseline accuracy for tumor detection before incorporating the synthetic images.

2. Augmented Dataset Evaluation (With synthetic data including randomly angled tumor slices):

We expanded the dataset by introducing synthetic tumor images that were created with the tool we built. The dataset remained balanced, with 50% brain with tumor images and 50% brain without tumor images, ensuring that the synthetic tumors were properly represented alongside real tumors. We added to the train data from the first phase 220 new images. 110 images with synthetic tumors that were created from 20 different volumes with different tumors with random slices. And 110 images from the same volumes but without tumors.

The test dataset remained the same in both phases. This approach aimed to verify that the inclusion of synthetic images did not negatively affect the model's performance. In fact, we wanted to see whether these additional images improved the model's ability to generalize and detect tumors across various MRI scans. In the table below we detailed the results.

Table 1: Model Performance Comparison with Synthetic Data, Including Randomly Angled Tumor Slices

Dataset	Training Set (Images)	Test Set (Images)	Accuracy (%)	Recall (%)
Without Synthetic Data	485	194	90.48	85.71
With Synthetic Data	705	194	92.52	90.48

The addition of synthetic tumor images, including randomly angled slices, positively impacted the model’s performance. As shown in Table 1, the model trained with synthetic data achieved a higher accuracy (92.52%) and recall (90.48%) compared to the baseline model without synthetic data (accuracy: 90.48%, recall: 85.71%). This improvement in recall is particularly significant, as it indicates the model’s enhanced ability to correctly identify tumors, which is essential for effective medical diagnosis. Importantly, the inclusion of synthetic tumors did not diminish performance when detecting real tumors, demonstrating that synthetic data can complement real data without compromising accuracy. These results highlight the potential of synthetic data augmentation to improve tumor detection capabilities, contributing to more reliable and robust diagnostic models.

6. Conclusion & Future Work

This project demonstrated the potential of using synthetic data to enhance brain tumor detection in MRI scans. By generating synthetic tumors and embedding them in healthy brain MRI scans, we expanded our dataset and improved the model’s accuracy and recall. The inclusion of synthetic data allowed DenseNet to recognize better tumor features. As shown in the results, this approach increased the recall rate without negatively impacting the detection of real tumors, indicating that synthetic tumors effectively complement real data. In addition, the possibility of producing a synthetic dataset and relying on it for training AI models allows for saving the many resources involved in manual data labeling. The tool that adds the synthetic tumor to the image can provide information about the location, shape, and other features of the tumor in the image.

By generating and integrating synthetic tumors into existing datasets, we were able to create a more robust and diverse training set for AI models. Improving the performance of models by adding this data set allows for more accurate and earlier tumor detection, which can be essential for improving patient outcomes.

Future work can explore further optimizing tumor generation by introducing more diverse shapes and textures that mimic a wider range of tumor characteristics. Additionally, the generation process could be extended to include synthetic cases of brain hemorrhage and cancerous metastases, enhancing the dataset to address a wider variety of diagnostic challenges. Another possible direction is to develop a model trained exclusively on synthetic tumors to evaluate whether synthetic

data alone can achieve sufficient diagnostic accuracy. These extensions will continue advancing AI's role in medical diagnostics, supporting healthcare professionals in identifying complex cases with higher precision and reliability.

7. Bibliography

GitHub Link

<https://github.com/MoriahDavid/Synthetic-3D-Tumors>

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