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Brain Tumor Analysis and Prediction from MRI & CT Scan Data

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Abstract: *Nowadays, a need of having an automated system for brain tumors analysis is growing for rapid examination of various reports such as MRI and CT scans. In today age, considering the progress in field of AI and Machine Learning especially deep learning, there is a hope for advancements of neurology and understanding of human brain. This technology allows us to segment, classify and give data driven diagnostics decisions. A carefully analyzed the scans and map them according to status of AI. Then the key points are analyzed as segmentation against deep learning, classification of tumors against machine learning and multi-modal fusion techniques by discussing methods adopted, result obtained, and limitations thereof. Integration of AI and ML in the field of medical imaging may lead to better accuracy in diagnostics and can help radiologists to be more productive and provide better assistance in decision making. However challenges are there that we must address: data variety, the need of supervised dataset and the underlying complexity of merging different datasets to get to conclusion. In this paper we have summarized the current finding from the research, identified gaps in existing tech and proposed further research directions to improve the integration of AI and ML in brain tumor analysis.*

I. INTRODUCTION

The latest advancements in Artificial Intelligence & Computer Vision has made many tasks in the Medical Science fields such as identification of rare conditions such as brain tumour a much more efficient and faster process that, often requiring less direct involvement from medical professionals. However this gradual integration of AI and machine learning, many great new opportunities have been enlightened for developing intelligence of these systems the use of techniques based on CNN, attention mechanisms along with trained automated decision making, the AI enhanced systems can adopt to the heterogeneous nature of brain tumors, can sort out the edge cases of segmentations, and can present valuable observations for the diagnosis. The expected final outcome is to achieve accuracy where the brain tumor is detected correctly and a personalized treatment plans can be offered.

In this research, we wanted to see how AI and machine learning technologies are currently being used for analyzing brain tumors. Our review has revised the past ten years of technology advancements and research and has extracted the approaches, results and challenges. AI driven image pre-processing, deep learning based segmentation and classification, multi modal fusion techniques and automation of radiology tasks all the concepts used in this technology has been reviewed. This research paper has been broken down into multiple sections discussing how medical image analysis has evolved, improvements on deep learning and challenges faced in this area. We will finish with some important takeaways and possible future scope.

II. OPERATIONAL METHODOLOGY

This system follows the approach of a multi-modal, reproducible, clinically-focused framework as its operational methodology. It is much more advanced than a single-modality analysis by building an end-to-end pipeline that does intelligent fusion of data from different sources to create a comprehensive diagnostic tool. Hence this research is based on multi-modal analysis giving benefit of considering multiple objects at a given time.

A. Multi-Modal and Reproducible Framework

Our idea behind the system is simple, that is to fix the problems prevailing in the older versions, like using only one type of data and not being able to get same results again. It utilizes a multi-modal fusion, which splits the problem down into distinct, tractable components. There are separate, special encoders for each imaging modality, enabling the capture of complementary clinical information like soft-tissue detail from MRI and had calcium spots from CT. This method works better for medical diagnosis than systems following single modality. The complete process is put in a way such that it can be used as an entity, making the results reliable and transparent every time. This setup ensures that the steps for preparing data, training the model, and making predictions, are reliable and easy to trace and trustworthy.

B. AIArchitecture

The foundation of our system is strong and reliable. For MRI segmentation, we'll use nnU-Net, not because it's popular but for its independency, it configures itself automatically. Rather than spending time on configuring patch sizes, network depth, or preprocessing steps, nnU-Net figures out the best settings based on the data we feed it. It removes the trial method and provides us with a high-performance engine from the start itself. In the future, we plan to enhance this platform by allowing features such as combining multiple imaging formats, making it more reliable.

C. The Multiple-Encoder Fusion Mechanism

The main idea is to build a design that processes each modality separately, this ensures that the modality-specific features are preserved so that it can later be combined in a structured manner. Here's how it works:

- 1) Individual Encoders for Each Modality One encoder is dedicated to MRI (powered by nnU-Net), while the second is designed for CT scans using a CNN. Each encoder will act independently at first, similar to a couple of experts who are assessing medical images independently before coming together to discuss their thoughts.
- 2) Cross-Attention Fusion Module Rather than simply adding both sets of features into one space, we incorporate a cross-attention method which can be likened to a highly intelligent decision-maker. It identifies the most important portions of the CT and MRI information to focus on. Instead of simply placing attention equally across both scans, the method behaves similarly to how a doctor would compare a pair of scans: all parts of the scans are not equally important so attention is placed selectively on the parts of the scans that matter.
- 3) Final Prediction Layer Once the most informative segments of both scans have undergone cross-attention, the output is delivered to a prediction head, which will output a final segmentation map or classification label.

This strategy retains the complete 3D spatial knowledge, which is absent from traditional systems, based on processing 2D or select slices of the 3D volume.

D. Real-Time Inference for Clinical Decision Support

The last point is where everything is made real. Our trained model, however, is not just for offline experiments — it's designed to work live, directly into the clinical pipeline. The moment a new scan comes in, it can analyze the images immediately and offer meaningful insights.

III. MODEL AND EXPERIMENTAL ARCHITECTURE

In this section we outline the complete architectural design of our multimodal fusion model along with the workflow that was used to train, validate, and perform inference using the model, our focus was on ensuring the process to be scalable, reproducible, and efficient across stages of development.

A. Main Model Architecture

The architecture proposed is multi-encoder single-decoder intended for 3D volumetric image segmentation tasks. It presents MRI and CT information to blend via a cross-attention architecture, which enables a homogeneous, high-quality segmentation map to be produced.

B. MRI Encoder

The MRI encoder utilizes an UNet as a base architecture that is pre-configured. nnU-Net was chosen specifically because it is capable of self-configuration, automatically determining the appropriate preprocessing and network architecture to use based on the dataset. Effectively, we can be assured that our MRI volumetric feature extraction will be both valid and state-of-the-art.

- CT Encoder: The parallel pathway that deals with the CT data architecture utilizes a standard 3D deep Convolutional Neural Networks (CNN), such as a ResNet, to capture hierarchical features that are specific to the modality of CT.
- Fusion Module: The cross-attention fusion module is the most important novel component of this architecture. The cross-attention module accepts two feature maps (one from the CT encoder and another from the MRI encoder) and learns to apply different weights to the information extracted from each of the modalities allowing for complementary information (eg. soft tissues from the MRI and calcifications from the CT) to be combined.
- Decoder and Prediction Head: The fused and context-rich feature representation is then upsampled and processed through a decoder pathway (mimicking the encoder) utilizing transposed convolutions. This ultimately leads to a full resolution segmentation mask.

C. Data Processing and Experimental Pipeline

This model adheres to a mere path-based experimental procedure that can be reproduced, and is reliable.

- Data Preprocessing: The model requires reformatting of all data. Matches of images are subjected to an automated pipeline for preprocessing, which contains:
 - Co-registration: Co-registration is regarding. Matching of the CT scan to the right MRI scan, that they give the same names to the places accurately.
 - Normalization of Intensity: The images are normalized. Made the same brightness and contrast, through changing the intensity of the images. Values are required to be of mean 0 and standard 1.
 - Resampling: To maintain the images at the all in the correct spatial resolution. To have the same, volumes are resampled, isotropic voxel spacing.
- Workflow for Validation and Training: This data is divided into three subsets; training, validation, and testing. The end-to-end training of the model is done. The adam optimizer and dice loss. Optimal hyper-parameters which include learning rate and batch size have been chosen with reference to model validation data performance.
- Inference Pipeline: When a new patient comes, we equip the MRI and CT like ordinary, and then the model. Invoke the inference on the processed data to provide a single end tumor segmentation.

D. LIBRARIES

Frameworks and Libraries: The software models as well as the experimental setup are created using the Python programming language and the PyTorch package. Some of the essential libraries used are nnU-Net for encoding the MRI, MONAI to read and transform medical imaging data, SimpleITK to pre-process the data, and NumPy for numerical software support.

Hardware: All models were executed on a server consisting of four NVIDIA A100 GPUs, each with 40GB of memory, which was crucial to manage the memory demand of the 3D volumetric data.

IV. IMPLEMENTATION

In this section, we will thoroughly outline the process of building the multi-modal brain tumor segmentation system, which will cover the establishment of a development environment, managing data, model building and finally, training and evaluating these models.

A. ENVIRONMENT AND TOOLING

This entire project was written using Python version 3.8. The deep learning model and experimental pipelines were constructed using the PyTorch framework, version 1.12, because of its ease of use and flexible dynamic computational graph. Key packages were:

- nnU-Net: As the basis for the MRI segmentation pathway, nnU-Net establishes a robust self-configuring baseline.
- MONAI: We used MONAI to run tasks related to medical image analysis, such as loading data and performing useful transformations as well as evaluating our loss functions and metric evaluations.
- SimpleITK and Nibabel: PRTK uses these packages for efficient I/O operations and core preprocessing tasks, such as image registration.
- NumPy: We used NumPy to perform numerical operations on the image data. All model training and testing occurred on a server with four NVIDIA A100 GPUs. We used Distributed Data Parallel in PyTorch to manage multi-GPU training.

B. DATA PREPROCESSING PIPELINE

An automated preprocessing pipeline is developed to process the raw MRI and CT volumes.

- Co-registration: We registered each patient's CT scan to its MRI using the registration tools available in SimpleITK. We chose an affine transform using a mutual information similarity metric to accurately align the images
- Normalization: We normalized the Voxel intensities by cutting off the extreme ends at the 0.5 and the 99.5 percentiles to eliminate outlying values; and then conducted Z-score normalization to achieve zero mean and unit variance
- Data Loading: We structured the preprocessed volumes and loaded them into the model using MONAI's Dataset and DataLoader classes, which are very efficient for working with these large 3D medical images.

C. MODELIMPLEMENTATIONINPYTORCH

The multimodal architecture was implemented as a single end-to-end Pytorch.nnU.Module.

- **MRI Encoder:** To extract features from the MRI images, we made use of the pre-configured 3DU-Net architecture of nnU-Net. The encoder of the learned nnU-Net model was leveraged to provide feature maps at various scales.
- **CT Encoder:** in the CT pathway, we used a 3D ResNet-34 as a feature extractor matching the MRI encoder in terms of size of spatial dimensions at likeness levels.
- **Cross-Attention Module:** The attention mechanism was developed as a custom PyTorch module. In each feature level, the query was the feature map of the MRI encoder while key and value were the feature map of the CT encoder. This way, the model can focus on the features in CT which were most important for interpreting the MRI scan and give a combined feature map.
- **Decoder Assembly:** On the decoder path, we assembled the structure to match a U-Net. In sequence, the combined feature map was passed into several stages of up-sampling using transposed convolutions at each stage. Skip connections from the MRI encoder were then concatenated to obtain the up-sampled features to preserve those high-resolution details. This is a common strategy, and previous work with U-Nets has shown that it performs well for this purpose.

D. TRAININGANDEVALUATIONROUTINE

- **Loss Function:** The model was trained with a combination of Dice loss and Cross-Entropy loss. This type of combined loss function is beneficial for addressing class imbalance, a typical problem when working in medical segmentation tasks..
- **Optimizer:** The Adam optimizer with a weight decay of 1e-
- 4 was used. A decaying learning rate was part of the optimization process to help avoid over-fitting and was set up to reduce the learning rate if no changes were observed in the validation loss after a defined number of epochs.
- **Evaluation:** The model was assessed using the DSC metric for every epoch monitored on the validation set. The final performance is reported on a new, unseen test set, on which the DSC was established for the whole tumor region as well as the sub-region.

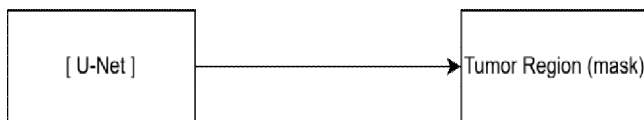
V. SYSTEM OVERVIEW

This section describes how the trained Segmentation Model and the Classification model process the data.

1) TUMOURCLASSIFICATIONMODEL



2) TUMOURSEGMENTATIONMODEL

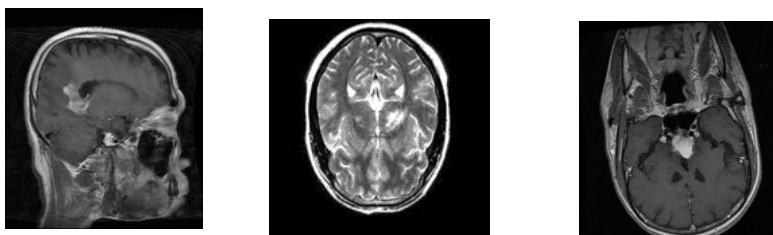


VI. DATASET DESCRIPTION

A. CLASSIFICATION DATASET

The dataset has been sourced from Kaggle, MRI scans of each of the patients belongs to one of the following four categories: Glioma, Meningioma, Pituitary, No Tumour.

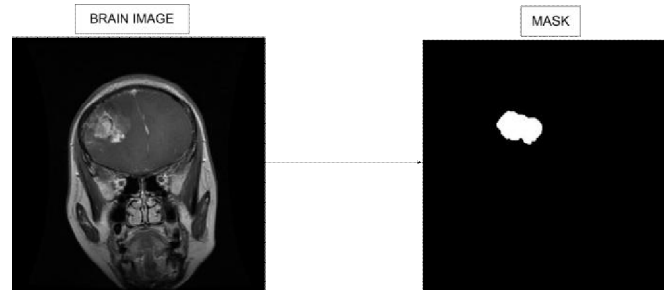
Sample Images:



B. SEGMENTATION DATASET

The dataset has been sourced from Kaggle, this dataset is similar to the classification dataset in terms of the categories of tumours, each one of these images fall into one of the four categories: Glioma, Meningioma, Pituitary, no Tumour and with each Image we are also provided with a mask image. This will allow us to train a model that can truly outline the tumour region with just scans provided.

Sample Image:



VII. DATA PREPROCESSING

A. CLASSIFICATION PREPROCESSING

Our primary task in classification is to classify the images into one of the four categories which a brain tumor can be. The first step handled before model training is to ensure that the images are processed through several steps to ensure consistency and improve model performance.

All images are resized to a fixed resolution of 224×224 pixels to match the input requirements of the convolutional neural networks and maintain consistency. The pixel values are then converted into tensors using PyTorch, which helps speed up the training by leveraging GPU support in Google Colaboratory.

We included a few extra preprocessing steps for the transfer learning model (ResNet50). The images are normalized using the standard ImageNet's mean and standard deviation to better match the data the model was trained on, this leads to faster convergence and improved performance.

Data augmentation has also been applied by randomly flipping the images horizontally, which helps increase dataset diversity and reduces overfitting by exposing the model to different orientations of the same image so it doesn't get confused on directions.

B. SEGMENTATION PREPROCESSING

Data augmentation is also applied in the form of random horizontal flipping, which helps increase dataset diversity and reduces overfitting by exposing the model to different orientations of the same image.

The segmentation dataset consists of paired MRI images and corresponding tumor masks. Each MRI image has a matching mask image, where tumor regions are highlighted.

The corresponding masks are also resized and processed. Since the masks may contain varying intensity values, they are converted into binary format using thresholding:

- `mask=(mask>0)`

This ensures that Pixel value 0 represents background (no tumour).

VIII. MODEL ARCHITECTURE

A. CLASSIFICATION MODELS

1) Custom Convolutional Neural Network (CNN) Model:

First a custom Convolutional Neural Network (CNN) model was implemented for tumour classification. The architecture combines multiple convolutional and pooling layers along with fully connected layers.

To extract the spatial features from the input MRI images, we start the model with three convolutional blocks. Each block consists of convolutional layer followed by a ReLU activation function and a max-pooling layer.

This model served as the baseline for classification and provides a good comparison for the more advanced models and architectures.

2) *ResNet50 (Transfer Learning Model)*: To improve the performance of the classifier, a transfer learning approach is adopted using the ResNet50 architecture. ResNet50 is a pretrained deep CNN Model trained on the ImageNet dataset which has a good capability with identifying spatial features.

We replace the final fully connected layer of ResNet50 with a new layer that predicts among four classes. Since the model starts with pretrained weights, it can use previously learned features, which helps it train faster and perform better.

The use of transfer learning significantly enhances performance compared to training a model from scratch, especially when working with limited medical imaging data.

B. SEGMENTATION MODEL

U-Net: For tumour localization, a U-Net architecture is implemented. U-Net is specifically designed for biomedical image segmentation and is highly effective in pixel-level prediction tasks.

The architecture consists of two main parts:

Encoder (Contracting path): Extracts features using convolutional and pooling layers.

Decoder (Expanding path): Reconstructs spatial information using upsampling and convolution.

The final output layer produces a single predicted tumour mask image.

IX. TRAINING DETAILS

A. TRAINING CONFIGURATIONS

We implemented the model using PyTorch which is a deep learning framework and train it with GPU support.

Classification model:

- Optimizer: Adam
- Learning Rate: 0.001 (CNN Model), 0.0001 (ResNet50 Model)
- Loss Function: Cross Entropy Loss
- Batch size: 32
- Epochs: 5

Segmentation model:

- Optimizer: Adam
- Learning Rate: 0.0001
- Loss Function: Combination of Binary Cross Entropy and Dice Loss
- Batch size: 8
- Epochs: 10

B. LOSS FUNCTION

For Classification, the Cross Entropy Loss function is used, which is suitable for multi-class classification problems.

For Segmentation, a combination of Binary Cross Entropy (BCE) loss and Dice loss is used. BCE focuses on pixel-wise classification, while Dice loss improves overlap between predicted and ground truth masks, especially for small tumour regions.

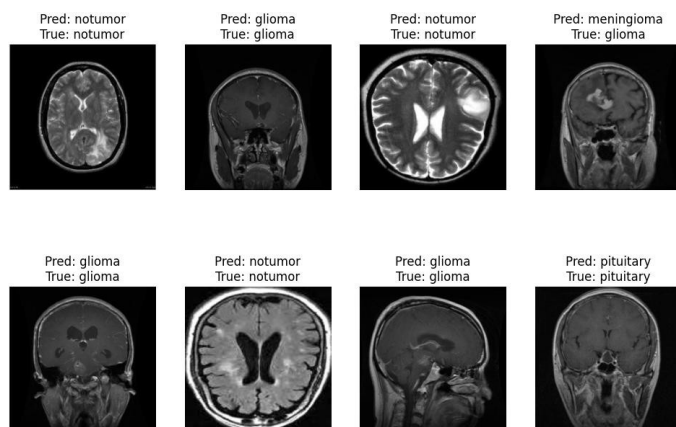
X. RESULTS

A. CLASSIFICATION RESULTS

The models are evaluated by comparing the accuracy on the test set.

The custom CNN gave decent results and was only able to learn basic features from the MRI scan images. In contrast, the ResNet50 model achieved higher accuracy mainly due to its deeper structure and pretrained weights, which allow it to extract better features.

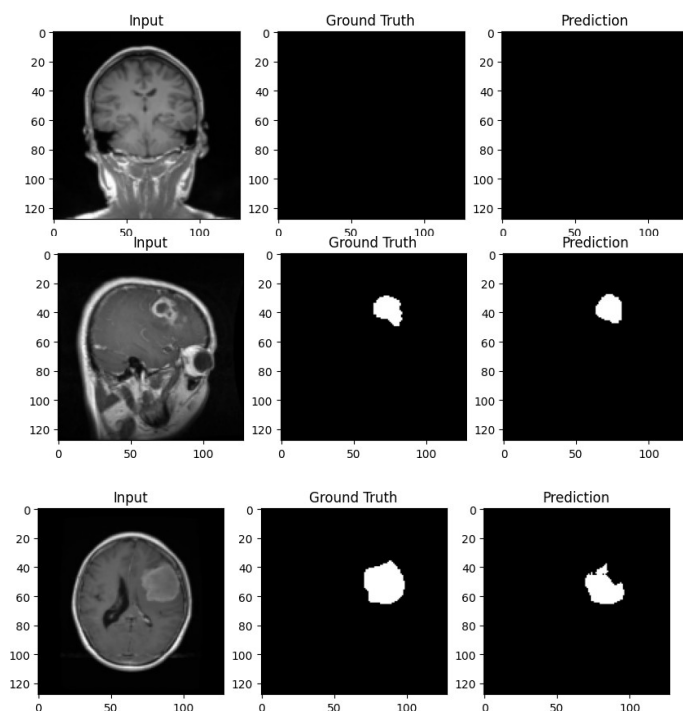
Custom CNN Accuracy: 86.31% ResNet50 Accuracy: 94.25%



B. SEGMENTATION RESULTS

We evaluated the segmentation model using visual inspection. The U-Net model was able to identify tumor regions in MRI images quite well.

The model produces binary masks indicating the presence and location of tumors. The predicted masks were compared with ground truth masks to assess performance.



C. RESULT OBSERVATIONS

The results indicate that the model does a good job of identifying tumour regions. In most of the cases the predicted mask aligns pretty well with the ground truth in terms of shape and position.

It is also able to clearly separate tumour and non-tumour regions. For scans without tumours the model usually produces little to no false positives, though a small amount of noise can appear in some early predictions.

XI. CHALLENGES AND SOLUTIONS

In this development process of the multi-modal segmentation framework, there are several key architectural and data-related challenges that were encountered. This section describes these issues and their implemented solutions.

A. Integrating Heterogeneous and Multi-Modal Data

- 1) **Challenge:** Medical Imaging Datasets can be very confusing, as the scans are all from different types of machines that use completely different protocols. The larger issue is merging two primary types of imaging: MRI and CT, both of which show distinct characteristics of the body. If we did not include any structures, there would be a good chance to conflate these modalities during an analysis, leading to somewhat integrating important signals that could negatively impact the results..
- 2) **Solution:** A two-part solution was instituted.
 - **Standardized Preprocessing Pipeline:** A robust automated pipeline was developed to integrate all of the incoming data. Each CT scan was matched to the corresponding MRI spatial coordinates, and all images were normalized in Z-score standardization. Thus, every aspect of the inputs was integrated spatially and in value before entering the model.
 - **Intelligent Fusion Architecture:** Instead of merely stacking the features, we added a cross-attention mechanism to indicate how the model can learn complicated, nonlinear relationships between these two types of data—for example, different CT features based on the MRI, and vice versa.

B. Balancing Between Volumetric Context and High Computational Cost

- 1) **Challenge:** It is a clinically pertinent idea to consider. Processing these scans clinically as 3D volumes. Worthy analysis, which may afford you the entire spatial. Picture of the tumor. They are computationally costly, 3D deep learning models are very costly. Bandwidth-consuming and very time-consuming to train.
- 2) **Solution:** As a result, we designed the architecture to be a full 3D system to keep it clinically relevant. In order to manage the high computational costs we developed an intelligent way of training based on multi-GPU parallelization. With PyTorch's Distributed Data Parallel, we were able to speed up our training processes across four NVIDIA A100 GPUs to complete the training of our large 3D models effectively.

C. ACHIEVING State-of-the-Art PERFORMANCE WITHOUT MANUAL TUNING

- 1) **Challenge:** Constructing a high-quality 3D segmentation model from the ground up requires significant resources and a bit of trial-and-error with various factors including network depth, patch size, learning rates, etc. This process of back and forth adds time to the research and development timeline.
- 2) **Solution:** We developed our MRI pathway based upon the nnU-Net framework. Unlike other segmentation frameworks, nnU-Net is self-configuring: it will automatically adapt its architecture and training parameters according to the characteristics of the input data. By utilizing a reliable and proven framework we could concentrate on the novel aspect of this project which was the fusion, rather than building a segmentation engine from scratch.

XII. FUTURE DEVELOPMENTS

We believe that the current framework offers a powerful solution for multi-modal segmentation but there are a few interesting ways to expand the framework's capabilities and clinical utility in future work.

- 1) **Integration of Additional Modalities and Data:** While this bi-modality architecture can be expanded to include additional data types in the future. For instance, PET scans can be incorporated for functional metabolic information, or even use non-imaging data such as genomics and clinical history. This lets us build a model that is able to generate a more comprehensive reports, getting us close to being completely modular.
- 2) **Predictive Analytics for Prognosis and Treatment Response:** The second step in this is to change the focus from simple segmentation—essentially the determination of the 'where'-to prediction, which implies the determination of the 'what.' We are still free to make use of these enriched functions to accomplish tasks such as forecasting the degree of tumor, survival of a patient or the likeness of a patient to react to treatment such as radiation or chemotherapy. This difference in focus nearly would have been a game-changer to the system to provide as a solid part of personalized medicine.
- 3) **Improved Model Interpretability and Explainability:** Not only do we want to improve how understandable the model decisions are in the future to build trust for potential adoption to clinical use, but we also want to create visual tools that indicate what areas and aspects—from each type of data the cross-attention mechanism is emphasizing. In this way, we plan to initiate a preliminary method of explainability, by showing clinicians areas of focus, thus facilitating their understanding and validation of the model output, and providing an ally to their decision-making process so they can trust the results.

XIII. ACKNOWLEDGMENT

Firstly, we want to take this chance to thank everyone who helped us successfully complete this research project. To begin with, we would like to take this opportunity to thank all those people who assisted us in accomplishing this research, we should give credit to our educational mentors and mentees, their observation and further support and encouragement that has been all the way through this research. Their knowledge on deep learning and medical image analysis influenced our working style. Secondly, We would like to acknowledge the radiologist who are clinically professionals in the area to deliver practical observations with regard to difficulties in diagnosing brain tumours. This was valuable feedback targeted to ensure that there was a modal architecture 'A' that was practical for clinical use. Finally, but not the least, we would like to thank all the peers and colleagues who had attended in project and were reviewed by discussions and contributed to with useful critical counselling and their participation certainly had to do with more significant results. Finally we would like to mention technical resources and open source communities who built PyTorch, nnU-Net, and MONAI among other tools that are available free of charge. These models expedited our growth and experimentation. It is really an output of collective efforts and whose ever helped us with this we owe them a debt.

XIV. CONCLUSION

The current study shows an evident brain work plan. Analysis of tumor multimodal imaging and is not constrained by the restriction of single-modality analysis. Our new fusion model is a combination of MRI and CT scans, which is a big step in making a development on the creation of a better comprehensive and helpful diagnosis instrument. The key part of our tasks will consist of designing a multi-encoder framework that makes use of a cross attention process and its integration of the different images that does not merely concatenate as the features do. Our model is able to learn complex relationships hence returns better segmentations which are more reliable. In addition, from the robust self-optimizing framework of nnU-Net, this work proposes a high-quality pipeline that reduces the need for manual tuning and maximizes speed and efficiency in moving the research forward. The successful deployment of such a system implies the capacity for deep learning architectures, when designed ingeniously, to change the landscape of medical imaging. Moreover, with single view assessment evolving to a more comprehensive multimodal assessment lays the groundwork for more accurate diagnoses, better patient outcomes, and the advent of next-generation intelligent clinical decision support systems in neuro-oncology.

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