DA526 : IMAGE PROCESSING WITH MACHINE LEARNING PROJECT

CEREBRASCAN: BRAIN TUMOR SEGMENTATION

By -

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PROBLEM STATEMENT

Brain tumors pose significant challenges, requiring timely detection and accurate diagnosis for effective treatment. To address this, we propose the development of a deep learning-based solution capable of accurately segmenting brain tumors from MRI images. This solution aims to streamline the diagnostic process, enabling prompt medical intervention and ultimately improving patient outcomes. By leveraging advanced technology, we seek to empower healthcare professionals with a tool that enhances their ability to identify and monitor brain tumors, facilitating tailored treatment strategies and minimizing the risks associated with delayed diagnosis.

Designing an accurate and advanced software solution to detect brain tumors in MRI images aids physicians in making informed treatment choices, resulting in time and cost savings while ensuring patients receive the right care

RELATED WORK

In recent years, brain tumor segmentation has seen a rise in innovative methodologies to automate this complex task. Traditional machine learning methods have employed threshold-based, region-based, and boundary-based segmentation techniques, each with distinct advantages and drawbacks. These approaches have driven efforts towards fully automated segmentation, essential for enhancing efficiency in medical image analysis.

Ranjbarzadeh et al. proposes a preprocessing method to focus on smaller image sections, reducing computation time and overfitting. They introduce a Cascade CNN that efficiently mines local and global features. Additionally, a Distance-Wise Attention mechanism is introduced to improve segmentation accuracy by considering the tumor's center location within the brain.

Xi Guan et al. introduces AGSE-VNet, an automated brain tumor MRI data segmentation framework designed to address the challenges outlined. In this approach, each encoder incorporates a Squeeze and Excite (SE) module, enhancing useful information within each channel while suppressing irrelevant data. Additionally, each decoder integrates an Attention Guide Filter (AG) module, leveraging an attention mechanism to guide edge information and eliminate noise interference. By utilizing these modules, the framework aims to improve segmentation accuracy by emphasizing relevant features and reducing the impact of irrelevant information.

Smarta Sangui et al. employs a modified U-Net architecture within a deep learning framework for brain tumor detection and segmentation from 3D MRI images in ".nii" format. The modified U-Net involves downsampling images for feature extraction, followed by classification and upsampling to the original size. Trained on the BRATS 2020 dataset, the model achieves a remarkable test accuracy of 99.4%, outperforming other deep learning-based approaches.

Sidratul Montaha et al. proposes a fully automated approach for brain tumor segmentation using 2D U-net architecture on the BraTS2020 dataset. It employs normalization and rescaling before training the model on all MRI sequences to determine optimal performance. Training utilizes the Adam optimizer with a learning rate of 0.001 on the T1 MRI sequence, achieving an accuracy of 99.41% and a dice similarity coefficient (DSC) of 93%. Further training with different hyperparameters assesses robustness and consistency in performance.

DATASET

For this project, we plan to use the BRATS 2020 dataset. The BraTS (Brain Tumor Segmentation) dataset for 2020 is a widely used benchmark dataset in the field of medical imaging, specifically designed for brain tumor segmentation tasks. It consists of 369 multimodal MRI (Magnetic Resonance Imaging) scans acquired from patients with brain tumors, including T1-weighted, T1-weighted with contrast enhancement, T2-weighted, and FLAIR (Fluid-Attenuated Inversion Recovery) images. The dataset provides ground truth annotations for different tumor sub-regions, such as the necrotic core, edema, and enhancing tumor, allowing researchers to evaluate the performance of their segmentation algorithms. This dataset is substantial in size, comprising a large collection of MRI scans and associated annotations.

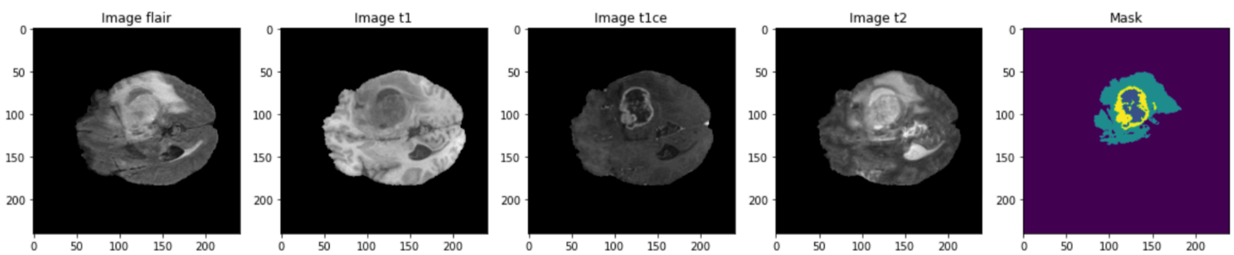

Fig 1. The 4 different modalities with the provided mask.

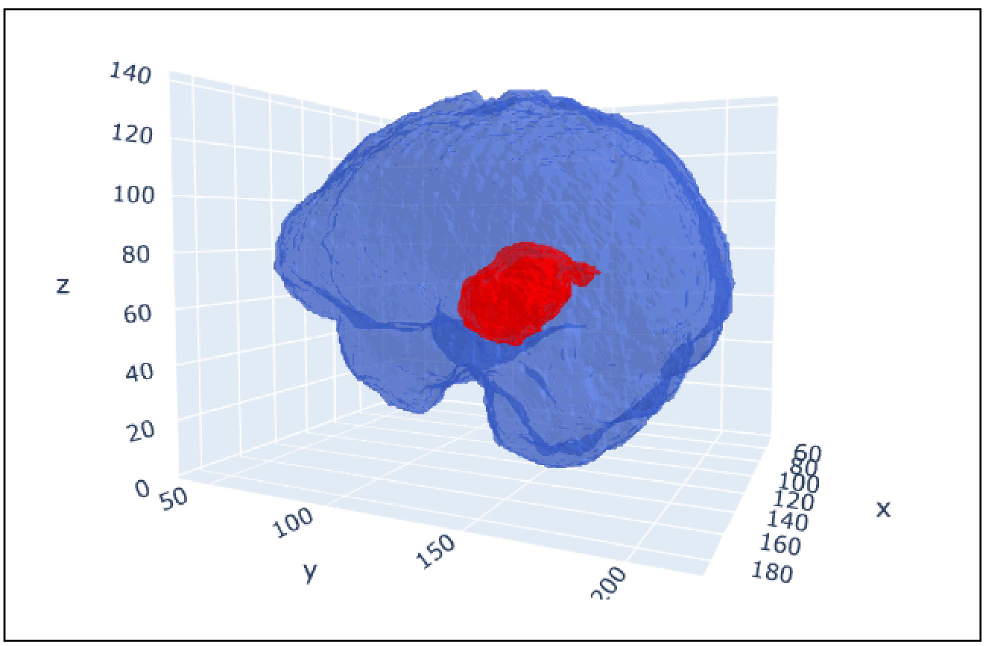

Fig 2. A 3D visualization of the brain (blue) featuring a tumor (red).

METHODOLOGY

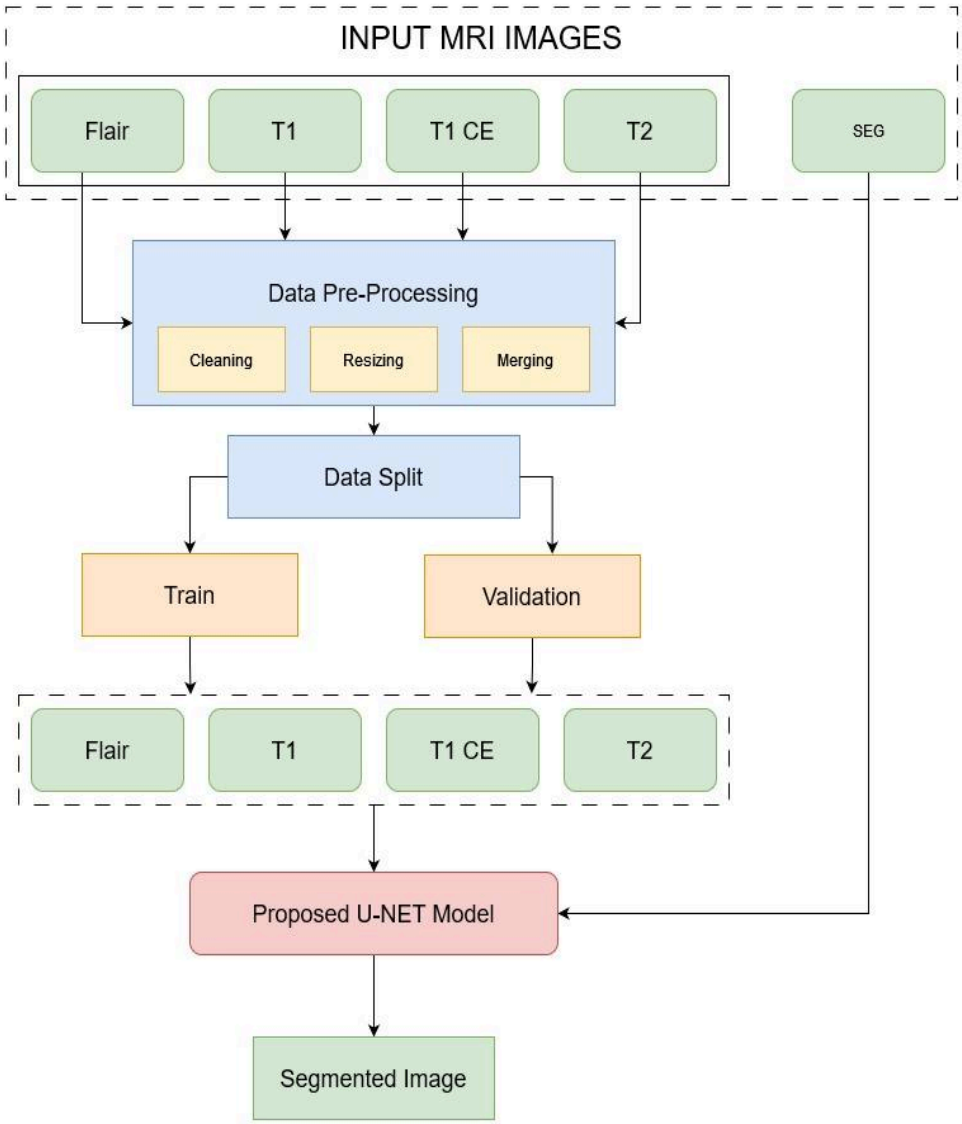

Fig 3. Methodology used for this project

The methodology we are applying for our project can be split into the following phases.

Preprocessing : Our preprocessing strategy adopts a focused approach, targeting specific regions of interest within the MRI volume. This method, termed Focused Preprocessing, allows for the extraction of key features while discarding irrelevant background information. We standardize this process across all volumes, ensuring consistency and efficiency in feature extraction. With each volume containing 155 slices, we implement slice selection criteria to identify informative slices. Through domain knowledge, we select a subset of 84 consecutive slices, starting from the 25th slice, optimizing our analysis while minimizing computational overhead.

Data Splitting : The preprocessed data is divided into training, validation, and test sets using the train_test_split function from the sci-kit-learn library. We adopt a 70-15-15 split ratio for training, validation, and testing to maintain an appropriate balance between the datasets. This partitioning scheme ensures that the model is trained on a diverse range of data while also providing adequate samples for evaluation.

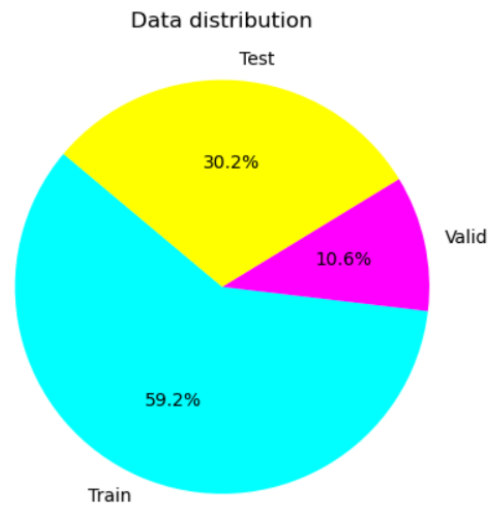

Fig 4. Distribution of Dataset Split

Model Training : The compact U-Net model is compiled using the Adam optimizer with a learning rate of 0.001 and trained for 20 epochs. During training, we employ callback functions for dynamic learning rate adjustment and logging of training metrics. By iteratively optimizing parameters through backpropagation and gradient descent optimization, the model learns to map input images to their corresponding tumor masks, enhancing its robustness and generalization capability.

Model Evaluation : We define several custom functions for evaluation metrics to assess the model's performance comprehensively across different tumor regions. These metrics include dice coefficients for each tumor class (necrotic/core, edema, enhancing), precision, sensitivity, and specificity. By evaluating these metrics, we gain insights into the segmentation accuracy and effectiveness of the model in delineating tumor regions.

THE MODEL : U-NET

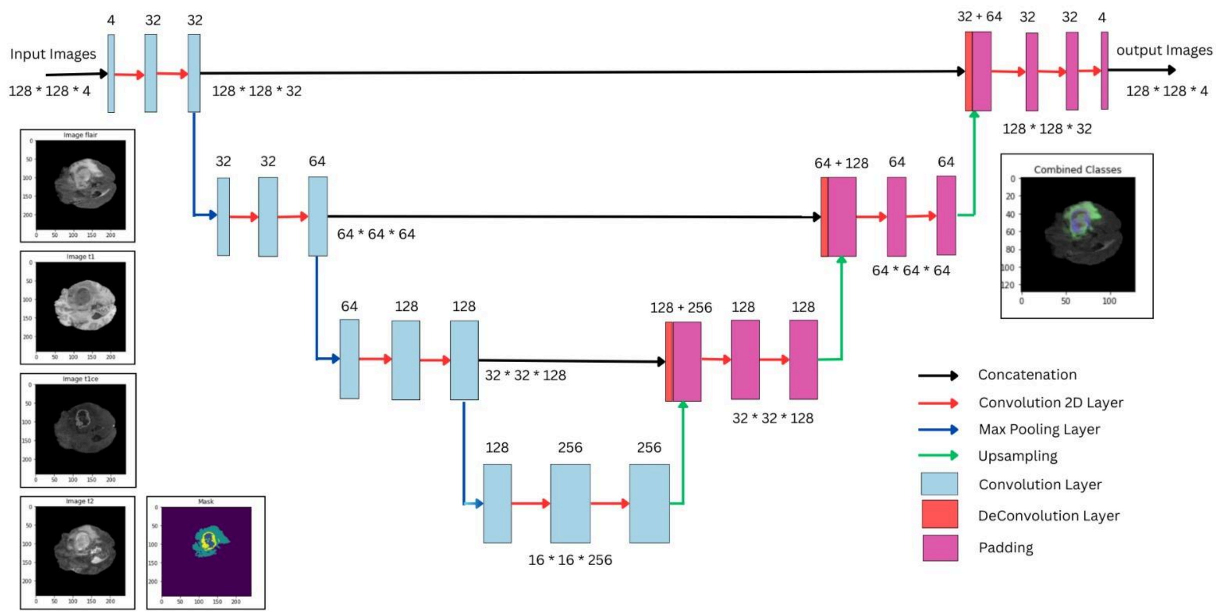

Fig 5. The U-Net Architecture

This project utilizes a U-Net based model for precise segmentation of MRI images. U-Net stands as a seminal architecture in medical image analysis, renowned for its efficacy in segmenting anatomical structures across diverse imaging modalities. Its unique U-shaped design, comprising a contracting and expansive pathway, addresses the intricate challenges of semantic segmentation tasks. The contracting pathway acts as a feature extractor, capturing contextual information through successive convolutional layers. Subsequently, the expansive pathway utilizes upsampling layers to refine segmentation boundaries, ensuring accurate delineation of target structures.

In the realm of brain tumor detection from MRI images, U-Net has emerged as a cornerstone, offering exceptional performance and adaptability. Leveraging its robust architecture, U-Net precisely identifies tumor regions amidst the complex anatomical details of the brain, facilitating early detection and intervention. Furthermore, its capacity to learn from diverse datasets enhances its utility, enabling seamless integration into clinical workflows. As the medical community continually seeks more efficient and accurate diagnostic tools, U-Net plays a pivotal role in advancing medical imaging technology, ultimately contributing to improved patient outcomes in the realm of brain tumor diagnosis and treatment.

RESULTS

The model is evaluated on several metrics including precision, recall, sensitivity and specificity. The classification report for the various pixels shows a remarkable accuracy of 99% (99.11% Training set accuracy, 98.8% validation accuracy and 99% Test data accuracy). For the classes "NECROTIC/CORE," "EDEMA," and "ENHANCING," the recall values are 39%, 59%, and 49% respectively. These values suggest that the model can do better in correctly identifying instances of the "NECROTIC/CORE" and "ENHANCING" classes.

	precision	recall	f1-score	support
NOT tumor	1.00	1.00	1.00	150085896
NECROTIC/CORE	0.57	0.39	0.46	596551
EDEMA	0.60	0.59	0.59	1562886
ENHANCING	0.59	0.49	0.53	519083
accuracy			0.99	152764416
macro avg	0.69	0.62	0.65	152764416
weighted avg	0.99	0.99	0.99	152764416

Classification Report

We also display the Images of randomly selected patients and compare it with the ground truth to get an idea on how well the model is performing the image segmentation.

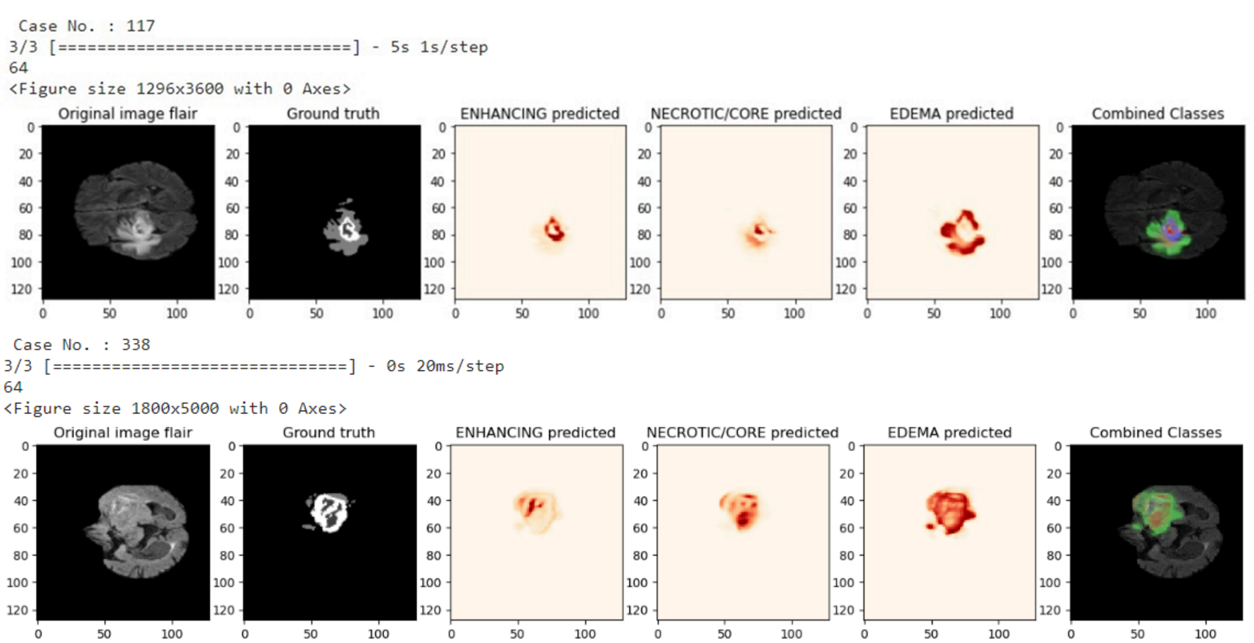

Fig 6. Predictions made by the model for random patients from test data.

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Evaluate on test data
111/111 [==============================] - 132s 1s/step - loss: 0.0243 - accuracy: 0.9911 - mean_io_u_3: 0.8298 - dice_coef:
0.5493 - precision: 0.9926 - sensitivity: 0.9889 - specificity: 0.9975 - dice_coef_necrotic: 0.4682 - dice_coef_edema: 0.6605
- dice_coef_enhancing: 0.5702
test loss, test acc: [0.02431444451212883, 0.99107825756073, 0.8297611474990845, 0.5492956638336182, 0.9925820231437683, 0.988
9145493507385, 0.9974786043167114, 0.4681934714317322, 0.6605353355407715, 0.5702260136604309]
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Model Performance on Test Data

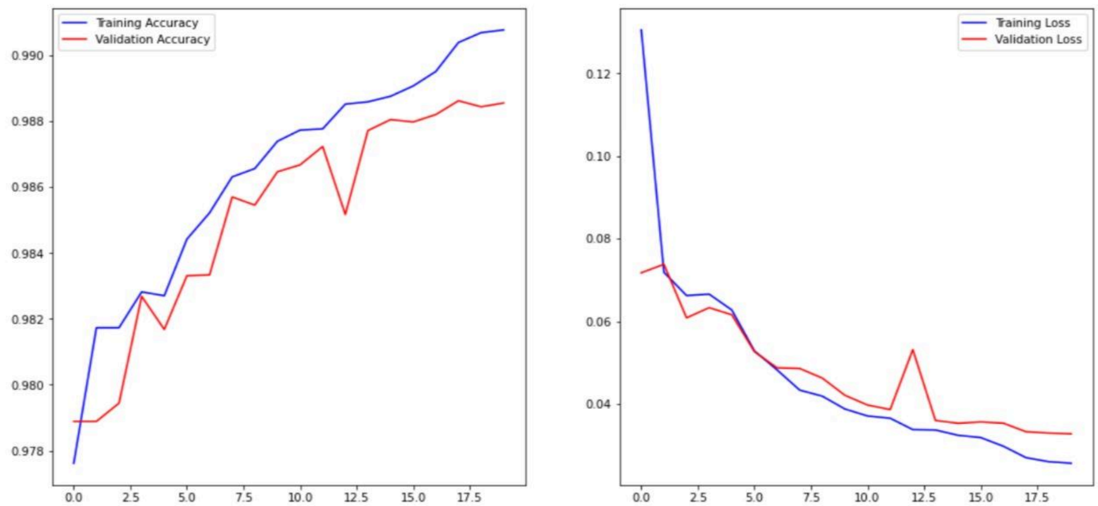

Fig 7. Training and Validation Accuracy and Loss plots

CONCLUSION

In this project, we developed a robust brain tumor segmentation algorithm using the BRATS 2020 dataset, comprising 369 MRI images with four modalities each: T1, T2, T1CE, and FLAIR. The segmentation task involved delineating four classes of tumor regions: edema, core, enhancing, and a combined class.

Utilizing a UNet architecture with 28 layers, we achieved a remarkable accuracy of 99% in segmenting brain tumors. The trained model demonstrated high sensitivity in detecting tumor regions, minimizing the risk of false negative cases and providing accurate localization of tumor boundaries. Our algorithm's performance was validated using rigorous evaluation metrics, including Dice coefficient and precision-recall curves, showcasing its reliability and effectiveness in segmenting brain tumors from multi-modal MRI scans.
Through comprehensive analysis and comparison with existing methodologies, we have shown that our approach offers significant improvements in accuracy and robustness, underscoring its potential for clinical application. The successful integration of the segmentation algorithm into existing clinical workflows can lead to enhanced diagnostic accuracy, timely treatment planning, and improved patient outcomes in the management of brain tumors.

While our project has achieved promising results, it is not without limitations. Challenges such as inter-scanner variability, data scarcity for rare tumor subtypes, and the need for real-time segmentation in clinical settings remain areas for future research and development. Furthermore, ongoing refinement and validation of the algorithm on diverse datasets and patient populations are essential to ensure its generalizability and clinical utility.
In conclusion, our brain tumor segmentation project represents a significant step towards advancing medical imaging technology for precise diagnosis and treatment of brain tumors. By harnessing the power of deep learning and multi-modal MRI data, we have laid the foundation for a scalable and accurate segmentation solution with the potential to positively impact patient care and clinical decision-making in neuro-oncology.

GitHub REPOSITORY

[CerebraScan---Brain-Tumor-Segmentation]

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