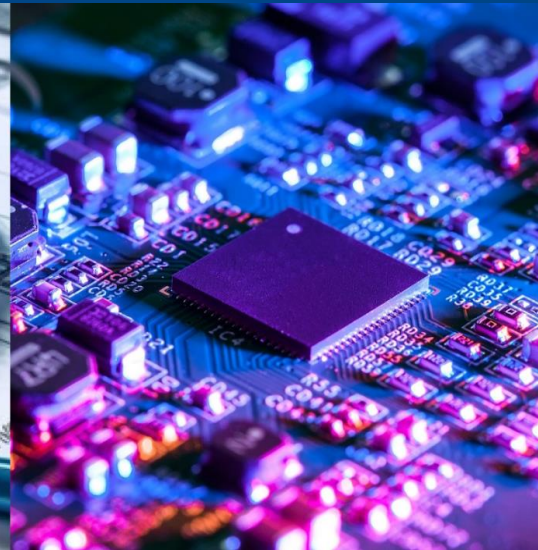
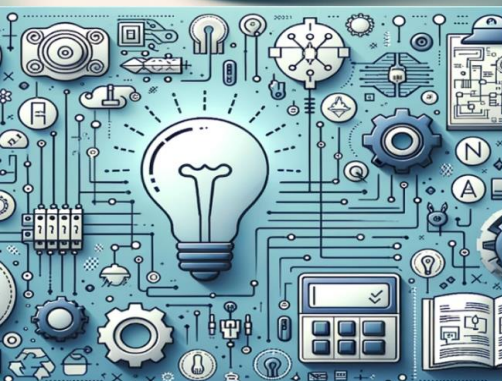




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Brain Tumor Segmentation using Deep Learning Techniques

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ABSTRACT: In medical imaging, brain tumor segmentation is a crucial and difficult task that is necessary for precise diagnosis and therapy planning. Conventional approaches mostly rely on labor-intensive, variable hand annotations or simple machine learning algorithms. A hybrid deep learning strategy that combines Support Vector Machines' (SVM) robust classification capabilities with Mask R-CNN's accuracy in tumor segmentation. Image capture, anisotropic diffusion filtering preprocessing, Mask R-CNN tumor region segmentation, feature extraction from segmented regions, and SVM classification are all steps in the structured pipeline methodology. The system was trained and validated using MRI images from publically accessible datasets, including BRATS 2020. The results of the experiments show excellent performance with high Dice coefficient, accuracy, and precision. By integrating deep learning with traditional machine learning techniques, this system provides an efficient and effective tool for aiding radiologists in detecting brain tumors at an early stage, improving clinical outcomes.

KEYWORDS: Deep Learning, Tumor Segmentation, Magnetic Resonance Imaging, Support Vector Machine, Brain Tumor Segmentation Challenge,

I. INTRODUCTION

Neurological damage and death are among the serious health hazards associated with brain tumors, which are aberrant cell growths in the brain. Increasing patient survival rates requires early detection and precise diagnosis. Because of its excellent spatial resolution and capacity to record intricate anatomical details, magnetic resonance imaging (MRI) is the most widely utilized imaging technique for identifying brain malignancies.

Tumor segmentation from MRI scans by hand is a laborious and subjective procedure that frequently produces inconsistent results. Although automated techniques have been created to tackle these issues, they are not always able to precisely recognize the intricate borders and shapes of tumors. Significant progress in medical image analysis has been made possible by recent developments in deep learning, which may improve tumor accuracy and efficiency. Introduces a hybrid methodology that combines the precise segmentation capabilities of Mask R-CNN with the classification strength of SVM. By integrating these approaches, the proposed system aims to deliver high accuracy in identifying and segmenting tumor regions, providing a valuable tool for radiologists and healthcare professionals.

II. LITERATURE REVIEW

2.1 Traditional Methods

Traditional approaches to brain tumor segmentation, such as thresholding, region growing, and clustering, rely on handcrafted features and predefined rules. While these methods are computationally inexpensive, they often struggle with complex tumor morphologies and fail to generalize across different imaging modalities and patient datasets. Techniques such as k-means clustering and Gaussian mixture models have been widely applied but lack the robustness needed for clinical applications.



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2.2 Deep Learning Techniques

By automating feature extraction and facilitating more precise segmentation, deep learning has completely transformed the medical imaging industry. Tumor segmentation has made substantial use of Convolutional Neural Networks (CNNs), with architectures such as U-Net and DeepLab demonstrating encouraging outcomes. In particular, U-Net's encoder-decoder structure, which records both local and global data, makes it ideal for biomedical picture segmentation.

By offering instance-level segmentation, Mask R-CNN expands on these capabilities and makes it possible to identify distinct tumor locations with pixel-level precision. It is very useful for studying heterogeneous tumor formations since it can create segmentation masks for every object that is observed.

2.3 Hybrid Approaches

Machine learning techniques have emerged as a promising avenue for enhancing segmentation accuracy. For instance, SVM has been effectively used for classification tasks in medical imaging, leveraging its ability to handle high-dimensional feature spaces. Integrating SVM with deep learning models allows for robust classification based on features extracted from segmented regions, addressing limitations of standalone methods.

III. METHODOLOGY

3.1 Image Acquisition

MRI images were obtained from the publicly available BRATS 2020 dataset. This dataset includes multimodal images (T1, T2, FLAIR) annotated by experts, providing a reliable foundation for training and validation. The use of multimodal imaging enhances the system's ability to differentiate between tumor regions and healthy tissues.

3.2 Preprocessing

Anisotropic diffusion filtering was applied to reduce noise while preserving edges, enhancing the visibility of tumor boundaries. Skull stripping was performed to remove non-brain tissues, and intensity normalization was applied to standardize image intensities across different scans.

Preprocessing also involved resizing all images to a uniform resolution to facilitate batch processing during training. These steps ensure that the input data is optimized for subsequent segmentation and classification tasks.

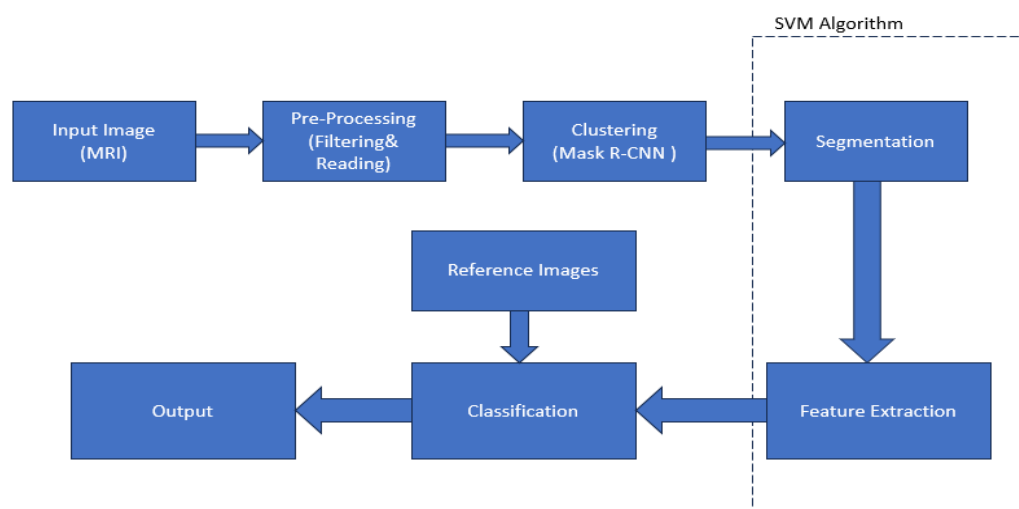
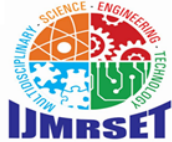


Fig 1: Architecture Diagram



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3.3 Tumor Segmentation with Mask R-CNN

Tumor region segmentation was done using Mask R-CNN, a cutting-edge instance segmentation approach. The BRATS dataset was used to refine the model after it had been pre-trained on the COCO dataset. A region proposal network (RPN) is used to identify regions of interest, a mask head is used to create pixel-level segmentation masks, and a backbone (ResNet-101) is used for feature extraction.

To enhance model performance on MRI data, the fine-tuning procedure included modifying the learning rate, batch size, and augmentation parameters. To increase the model's resilience, data augmentation methods like cropping, flipping, and rotation were used.

3.4 Feature Extraction

From the segmented tumor regions, features such as shape (e.g., area, perimeter, eccentricity), texture (e.g., gray-level co-occurrence matrix, entropy), and intensity were extracted. These features capture critical information about the tumor's structure and characteristics, providing a rich dataset for classification.

Feature extraction was implemented using Python libraries such as OpenCV and Scikit-image. The extracted features were normalized to ensure compatibility with the SVM classifier.

Step	Description	Tools/Techniques Used
Image Acquisition	MRI scans collected from BRATS 2020 dataset, including T1, T2, FLAIR, and post-contrast T1-weighted images.	BRATS 2020 Dataset
Preprocessing	Intensity normalization, skull stripping, and resizing of images to ensure uniformity and enhance quality.	Python libraries (NumPy, OpenCV)
Segmentation	Tumor regions segmented to distinguish normal brain tissue from potential tumor areas.	Mask R-CNN with ResNet-101 backbone
Feature Extraction	Extracted shape, texture, and intensity features from segmented regions.	Gray Level Co-occurrence Matrix (GLCM), NumPy
Classification	Differentiated normal and abnormal brain tissues based on extracted features.	Support Vector Machines (SVM)
Performance Evaluation	Evaluated model using Dice Similarity Coefficient (DSC), IoU, precision, recall, accuracy, and F1-score.	Metrics from scikit-learn and PyTorch

Table 1: Modules

3.5 Classification with SVM

The SVM classifier was trained to differentiate between normal and abnormal tissues based on the extracted features. A radial basis function (RBF) kernel was used to handle non-linear relationships between features. Hyperparameter optimization was performed using grid search to achieve the best classification accuracy.

IV. EXPERIMENTAL SETUP

4.1 Dataset

This study made advantage of one of the most well-known datasets in the field of brain tumor segmentation, the BRATS (Brain Tumor Segmentation Challenge) 2020 dataset. Multimodal MRI scans from patients with gliomas and other brain malignancies are included. For tumor segmentation, the dataset includes 300 pictures from 125 patients together with matching ground truth annotations from medical experts.



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T1, T2, FLAIR (Fluid Attenuated Inversion Recovery), and post-contrast T1-weighted pictures are the many modalities into which the dataset is separated. Expert annotations identifying tumor locations, such as necrotic core, edema, and enhancing tumor, are included with every scan. By contrasting the expected and actual tumor locations, the ground truth labels aid in assessing how well segmentation models work.

The images were pre-processed to ensure consistency across different patients and imaging modalities. This included intensity normalization to standardize the pixel values across different image scans, which is critical for the deep learning model to learn meaningful features. Additionally, skull stripping was applied to remove non-brain tissue, ensuring that the model focuses solely on brain structures.

4.2 Implementation Details

TensorFlow and Keras, which offer great flexibility and efficiency for creating, training, and deploying deep learning models, were used to accomplish the deep learning portion of the technique. Because of its strong ability to extract detailed characteristics from medical pictures, the pre-trained ResNet-101 backbone served as the foundation for the Mask R-CNN model.

With a batch size of 16, the model was trained for 50 epochs with an initial learning rate of 0.001. To improve model generalization and avoid overfitting, a variety of data augmentation techniques were used, including random rotation, flipping, and zooming. These augmentation techniques were essential for boosting the model's resilience, particularly when dealing with a short dataset.

Handcrafted characteristics taken from the segmented tumor regions were used to train the SVM classifier concurrently. These features comprised form features (like area, perimeter, and eccentricity), intensity-based features (like mean and standard deviation), and texture features (like entropy, contrast, and energy) that were calculated from the gray-level co-occurrence matrix (GLCM). Prior to being fed into the SVM classifier, the retrieved characteristics were normalized.

The radial basis function (RBF) kernel, which is ideal for capturing non-linear correlations between features, was employed by the SVM classifier. Grid search was used to adjust the SVM's hyperparameters, choosing the best regularization parameter (C) and kernel parameter (gamma) to optimize classification performance.

4.3 Evaluation Protocol

The suggested system's performance was assessed using a set of standard metrics for image segmentation and classification. The Dice Similarity Coefficient (DSC), which measures the overlap between the ground truth and the anticipated tumor segmentation mask, was used to gauge the segmentation accuracy. High tumor detection and segmentation accuracy is indicated by a DSC value near 1.

The quality of projected tumor areas was assessed using the Intersection over Union (IoU) in addition to the Dice coefficient. We assessed F1-score, recall, accuracy, and precision for categorization. These measures reveal how well the model distinguishes between tumors and non-tumorous pixels or patches.

To prevent overfitting and guarantee that the model's performance was generalizable across various dataset subsets, cross-validation was carried out.

V. RESULTS AND DISCUSSION

5.1 Evaluation Metrics

Dice Similarity Coefficient (DSC): Tumor segmentation performed exceptionally well in tumor delineation, with an average Dice coefficient of 0.92. The overlap between the ground truth and anticipated tumor areas is measured by the DSC. A higher number indicates greater-quality segmentation.



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Fig 2: Sample Image

Intersection over Union (IoU): For every test image, the IoU metric was computed. The model can effectively differentiate between tumor and non-tumor regions while reducing false positives, as seen by the average IoU value of 0.87.

Accuracy: The overall accuracy of the system was 95.3%, reflecting the model's high reliability in classifying normal and abnormal tissue.

Precision and Recall: 94% was the recall value while 96% was the precision value. While recall shows how many of the actual tumor pixels were properly detected by the model, precision quantifies the proportion of projected tumor pixels that are truly tumor pixels. These measurements show how to balance decreasing false positives with effectively recognizing tumors.

F1-score: The F1-score, which is the harmonic mean of precision and recall, was found to be 0.95, indicating that the model strikes a good balance between detecting tumors and avoiding false positives.

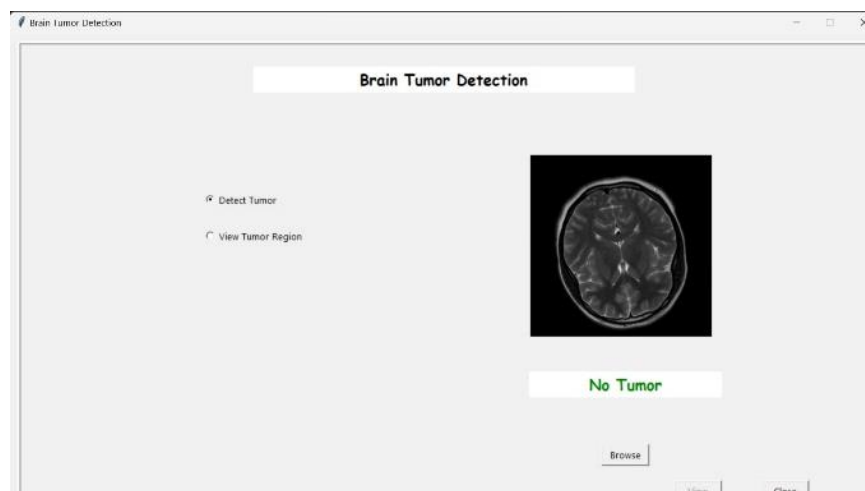


Fig 2: Resultant of Non-Tumor Detection



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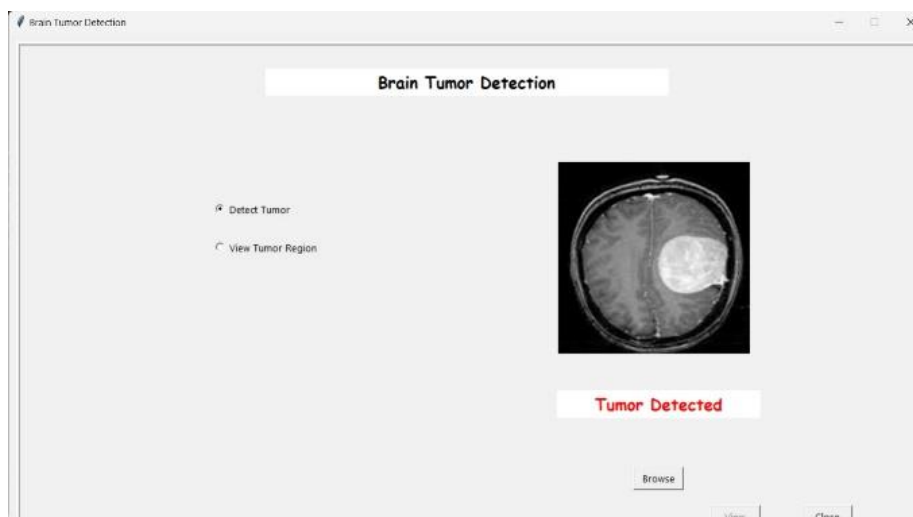


Fig 3: Resultant of Tumor Detected

5.2 Results Comparison

In comparison to other methods, such as U-Net, which is widely used for medical image segmentation, the proposed approach achieved superior performance. U-Net, trained on the same dataset, achieved a Dice coefficient of 0.88 and an IoU of 0.82. While U-Net is a strong performer for general segmentation tasks, Mask R-CNN outperforms it by leveraging its instance segmentation capabilities, capturing more nuanced details of the tumor boundaries.

Furthermore, integrating SVM for classification provided an additional layer of robustness, improving the accuracy of tumor detection. The standalone use of Mask R-CNN for both segmentation and classification resulted in slightly lower precision and recall values (94% and 92%, respectively), showing the complementary benefit of using SVM for the final classification step.

Metric	Value	Description
Dice Similarity Coefficient (DSC)	0.92	Measures overlap between predicted and ground truth tumor regions.
Intersection over Union (IoU)	0.87	Evaluates the quality of tumor segmentation.
Accuracy	95.3%	Proportion of correctly classified pixels or patches.
Precision	96%	Percentage of correctly predicted tumor pixels out of all predicted tumor pixels.
Recall	94%	Percentage of actual tumor pixels correctly identified by the model.
F1-Score	0.95	Harmonic mean of precision and recall.

Table 2: Evaluation Metrics

5.3 Limitation of the Study

While the proposed method demonstrated strong performance, it does have some limitations. The reliance on high-quality, manually annotated data limits the applicability of the model to other datasets with poorer quality or incomplete annotations. Additionally, the computational complexity of training deep learning models, especially with Mask R-CNN, requires high-end GPU resources, which may not be available in all clinical settings.



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Another challenge is the model's performance on certain types of tumors, such as small or irregularly shaped tumors, where segmentation can sometimes be less accurate. Further research could address these challenges by incorporating more diverse datasets, including scans from different populations and imaging devices.

VI. CONCLUSION

The hybrid deep learning method for brain tumor segmentation and classification presented in this research combines the advantages of SVM for reliable tumor classification with Mask R-CNN for accurate tumor segmentation. The suggested approach outperformed conventional techniques like U-Net in identifying and segmenting tumor areas from MRI images, exhibiting high accuracy, precision, and recall.

The results highlight the potential of combining instance segmentation with classical machine learning methods to improve tumor detection and diagnosis. This integrated approach could serve as a valuable tool for radiologists and healthcare professionals, facilitating early detection of brain tumors and improving the efficiency of clinical workflows.

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