Enhanced Brain Tumor Delineation Using t-SNE and Machine Learning Algorithms

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Abstract. Our approach aims to alleviate the challenges of LCG detection, as tumors are often difficult to distinguish from surrounding brain tissue. Unlike conventional approaches that apply CNNs directly to raw MRI images, we employ t-SNE to enhance differentiation between tumor and non-tumor regions prior to segmentation. Experiments using a modified U-Net architecture on the Kaggle LCG MRI dataset demonstrate improved tumor detection, particularly in low-contrast regions, compared to baseline CNN methods. This hybrid strategy, which integrates clustering with supervised deep learning, provides more robust MRI analysis and offers clinicians more reliable tools for tumor delineation and treatment planning.

Keywords: Feature space transformation for medical imaging, t-SNE dimensionality mapping, neuro-oncological analysis, manifold learning for tumor recognition, hybrid clustering-CNN architecture, LCG boundary enhancement, multi-degree segmentation pipeline.

1 Introduction

Neuroimaging characterisation of LGG is particularly difficult due to their infiltrative nature and definition of margins with the adjacent brain parenchyma cannot be otherwise discerned on conventional MRI examinations. In contrast, we have empirically observed in our research group that classical segmentation approaches usually fail precisely on those critical boundary regions where diagnostic accuracy influences a treatment decision the most. This inspired us to generate novel feature representations for better visualizing tumor boundary prior classification.

Motivation In experimenting with the Kaggle LCG MRI segmentation dataset, we realised that there is a severe limitation in today's approaches: most structure learning algorithms work on raw pixel/intensity features or primitive transformations thereof, and do not have access to non-trivially derived feature space coordinates which could potentially enable pathological distinctions. This observation inspired us to define our primary research question: is it possible for non-linear dimensionality reduction methods like t-SNE, to expose the tumor boundaries that we observe are hidden deep in the conventional features representations.

Our approach challenges the standard segmentation pipeline by inserting a critical preprocessing phase: feature space transformation, between initial feature extraction and final classification. By projecting high dimensional MRI characteristics onto optimized lower-dimensional

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manifolds through t-SNE, we create representations where tumor boundaries become more mathematically distinguishable, even when visual differences remain subtle. This transformation particularly benefits the challenging cases in our dataset where conventional intensity-based segmentation fails.

Our multistep pipeline (Fig.4) works on the T1, T2 and FLAIR of the KAggle LCG dataset through four core steps: 1) Preprocess in which skull striping and performing preprocessing task with intensity normalization; 2) Feature extraction by integrating PCA for reducing computational complexity but preserving inherited significant information in feature space; 3) Define new features space based on t-SNE that we optimized parameters to promote boundary enhancement; and vice versa, Initial clustering before closing refinement once from our enhanced neural network architectures by combining those special k-means learners.

On the other hand, our experimental setup has to present reference points for both traditional and modern segmentation algo- rithms. Our baseline was ordinary CNNs with and without waited normalisation in MRI. We assessed the performance of all U-net models with and without side task functions by Segmentation globally. The testing singled out challenging cases, including tumors that have generally fared badly with existing methods.

The global performance assessment demonstrates that our t-SNE modified pipeline yields significant improvement of boundary accuracy, specifically in generosity (increasing false positives) and detection precision. Our results showed only modest improvements in mean metrics, but significant gains at tumor boundaries, just because when focusing on particular subvolumes of the treatment volume we realized enormous gains exactly where they are most clinically relevant: at the fuzzy edge boundaries of tumors where treatment is hardest.

Our approach extends beyond purely technical performance metrics to address clinical applicability. Neurosurgeons and radiation oncologists at our collaborating institutions noted that better visualization and contours on a single affect the planning of surgical approaches as well as defining contours for the targets of radiation therapy. Our strategy, by all means, should result in decreasing the rate of recurrence as we will be able to detect tumor extensions that were missed in traditional strategies and allow either more complete resection or more focused, less toxic therapy.

Our work offers two contributions to the medical image analysis in terms of methodology it illustrates the usefulness of feature space transform rather than visualisation, whereas clinically we are dealing with LCG segmentation, whose fine boundary delineation is crucial for its treatment success and outcome.

2 Literature Review

Machine learning (ML) techniques allow systems to learn from experience without explicit programming and are widely applied in tasks such as image processing, predictive analytics, and data mining. ML is widely used in medical imaging research. This paper surveys ML applications in medical image processing, focusing on supervised and unsupervised learning. The preliminary analysis outlined by Mutasher Rashed et al. [1].

Omar Alirr et al. [2] discusses the importance of segmenting brain tumors for better diagnosis, prognosis, and treatment planning. Since identifying brain tumors manually is a difficult and tiring task, data categorizing algorithms can help improve accuracy and efficiency. The paper highlights the use of CNN, a neural network method, for segmenting brain tumors from MRI data. Soomro et al. [3] analyzed various supervised methods that demonstrated good performance, but found that End-to-end learning model Techniques are more effective for brain tumor segmentation. Ensembling methods have been shown to enhance model performance by using the strengths of many models.

Solaiyappan et al. [4] gives a brief explanation of the numerous uses of Machine learning models for classifying medical images as either tampered or untampered by first extracting features through deep learning models, then fine-tuning them for accuracy, emphasizing the different tools, frameworks, and challenges involved in their use.

This research is enhanced by Pingat et al. [5] and Shafiq et al. [6], who look into the deep learning model U-Net for brain image sectioning. The results displayed that the model performed better than autoencoder in accurately segmenting brain images, especially when the boundaries of the brain regions were complex or unclear. U-Net was able to capture detailed spatial information and produce more precise segmentation, while the autoencoder's results were less accurate and blurrier due to its compression and reconstruction process.

Addressing the issue of CNNs struggle to capture broad, global information effectively Nizamani et al. [7] presents a new approach to improving Brain tumor classification, combining the Deep U-net with Transformer technology, referred to as UT. Tejashwini et al. [8] explores the significant impact of brain tumors on life expectancy, highlighting the importance of early detection to reduce mortality. While MRI is the conventional imaging method, manual segmentation is time-consuming and delays diagnosis. The author proposes applying deep learning, particularly the UNet framework, to automate this process. However, traditional UNet models struggle with accuracy and context processing, which is addressed by introducing a new model, the Scleral Residue attention U-Net.

This advanced version incorporates advanced techniques like residual dense layers and hierarchical attention significantly enhancing feature capture and segmentation precision. Kesari et al. [9] presents a deep learning approach using Swing UNETR regarding bigger blood vessels classification in brain tumors, comparing it with U-shaped Network and U-Net with Focused Attention. The results show that Swin Transformer-based U-shaped convolutional network with Transformers outperforms other models in accuracy, demonstrating its potential for improving tumor grading and treatment planning.

Yadav et al. [10] presents a novel Brain tumor segmentation using Magnetic Resonance Imaging model, Enhanced Residual Attention U-Net (ERAU-Net), which combines recurrent and residual elements to capture time-based dependencies and fine depiction details. Selective gates are used to Boost feature enhancement, substituting traditional skip connections, leading to better region division accuracy. The model outperforms existing methods, and the study demonstrates its potential for refining Brain lesion segmentation in medical image interpretation pipelines. Torik et al. [11] develops a Neural network for brain tumor detection segmentation adopting U-Net improving its performance through fine-tuning with manual annotations. The model shows significant improvements in Dice score, True classification rate, Exactness, Sensitivity and Balanced accuracy score for neural tissue, nerve fibers, and Spinal fluid. The study highlights the model's generalizability and its ability to mask non-anatomical structures, making it suitable for clinical applications.

Verma et al. [12] proposes that the hybrid KIFECM-IPSO algorithm, blend of Kernel-based Intuitionistic Fuzzy Entropy C-means (KIFECM) with Intuitionistic PSO (Particle Swarm Optimization) to overcome local minima issues in MRI brain image segmentation. IPSO optimizes cluster centroids globally, improving the accuracy of segmentation. The algorithm outperforms existing methods, as demonstrated by various performance metrics, including similarity measures and false positive/negative ratios. Malik et al. [13] introduces a Stochastic Fractional Moment (SFM) optimizer integrated with the U-shaped network structure for brain tumor classification in MRI. It demonstrated a method that achieved faster convergence and better accuracy, cutting training time by 20% compared to conventional models. Yadav et al. [14] introduced the Improved Recurrent Residual Attention based U-shaped Network for MRI guided brain tumor segmentation. Their model combines recurring and surplus components within both transformation and interpretation pathways, enabling the network to capture temporal relationships and fine visual details.

Oskouei et al. [15] brings a new approach for brain MRI segmentation, when working with medical data we run into several challenges that standard analysis approaches couldn't handle effectively. Heavy computational requirements slow down the processing and capturing subtle patterns around the lesion boundaries becomes difficult. Their solution combines multi scale morphological gradient reconstruction with quantum clustering. The technique helped group similar pixels together into meaningful regions before analysis, which preserved important local features while reducing the complexity of the problem. This preprocessing step made a significant difference in boundary detection. The quantum clustering worked well with these grouped pixels.

It handled the reduced dataset much more efficiently than the traditional clustering algorithms, cutting our processing approach was especially good at finding natural groupings in feature space, even when the boundaries were poorly defined in the original images.

We also examined the work of Kusuma et al. [16] on automated tumor detection using multi-modal MRI scans. Their research incorporated enhanced data fusion techniques alongside modified SegNet for segmentation improvements. Bhima et al. [17] proposed interesting OTP frameworks specifically designed for analyzing and segmenting brain lesions in MRI images. Their work addresses the particular challenges posed by unpredictable tumor regions and the difficulties in accurately measuring size, texture, and location parameters.

When reviewing segmentation techniques, we found Gonzalez et al. [18] automatic marker definition approach for Watershed Transformation particularly relevant. Their method uses a Mandami fuzzy inference system that offers simplicity, robustness, and adaptability across various image types. The comprehensive review by Zaitoon et al. [19] examines methods for lesions recurrence identification, segmentation techniques, and classification approaches, with particular attention to available datasets and deep learning applications for categorization. Finally, Mostafa et al. [20] provides valuable insights into the performance characteristics of popular deep learning models including Residual Network with 50 layers, U-Shaped network and segmentation Network when applied to brain tumor segmentation and classification tasks, with specific focus on glioma, meningioma and pituitary. RestNet50 achieved the highest accuracy showcasing its potential to improve diagnostic precision.

Meanwhile, Ruogu Fang et al. [21] address the challenge of segmenting brain MRI images by utilizing the tree-metric graph cuts (TM) algorithm, a novel segmentation technique, and propose a "tree-cutting" method to convert the labeling produced by the TM algorithm into a Brain tissue identification. Beyond immediate applications, the literature also engages with broader implications of image segmentation in brain tumor detection for medical imaging, as shown by Davar et al. [22].

Their research introduces an automated approach leveraging DNNs for accurate Brain lesion localization and segmentation using T1-weighted MRI sequences. The method integrates a region-based CNN for tumor localization followed by a modified U-Net architecture for precise tumor boundary delineation. Dattangire et al. [23] provides an encouraging prospect of U-shaped network-based deep learning models in medical image segmentation, particularly for brain tumor detection. The proposed U- shaped Network model is trained for the task of segmenting LGG regions in MRI scans. The Adam optimizer was used for efficient learning and parameter tuning, which helped achieve better performance even with complex, imbalanced data. Furthermore, Angona et al. [24] delve into the machine learning domain, proposing a novel hybrid model, 3D ResAttU-Net-Swin, Identification of brain tumors in MRI scans, combining three powerful components: Residual U-Net, Attention Mechanism, and Swin Transformer. The hybrid architecture provides a more robust, accurate, and efficient solution for segmenting complex brain tumor regions. Its high performance on established benchmarks, as well as its potential application in clinical practice, makes it a promising tool for Advancing the reliability and efficiency of brain tumor diagnosis and treatment scheduling.

3 Existing System

Brain tumor segmentation methodologies have evolved significantly over the past decade, yet several fundamental challenges persist when addressing low-grade gliomas in MRI scans. Our systematic analysis of current approaches reveals limitations that directly motivated our research into feature space transformation techniques.

3.1 Conventional Intensity-Based Approaches

Traditional segmentation methods rely heavily on intensity thresholding and region-growing algorithms. When applied to the Kaggle LCG MRI dataset that forms the basis of our research, these approaches demonstrate adequate performance for high-contrast tumors with well-defined boundaries. However, our experiments with region-growing techniques yielded disappointing results for cases exhibiting growth patterns, with Dice similarity coefficients rarely exceeding 0.67 for boundary regions. The fundamental limitation stems from these methods' reliance on clear intensity differences between tumor and surrounding tissue - a distinction often absent in low-grade gliomas where tumor cells infiltrate normal brain parenchyma.

Edge detection versions, including Sobel and Canny operators performed on evaluation-enhanced T1 sequences were additionally underperformed when evaluated against our cases. Our application of such strategies also validated their sensitivity selection: it entails case-by-case adjustment, which is not feasible in a clinical setting. Poor reproducibility such effects further hinders their software in the context of longitudinal tumor tracking.

3.2 Machine learning Approached without Deep Learning

For a conventional system these utilized methods were handcrafted features derived from MRI sequences. In our primary studies, we conducted SVMs using texture features from grey-stage co-occurrence matrices and Gabor filters. Although such techniques outperformed the standard deep learning–based approaches, achieving an average Dice score of 0.72 on our test set, they performed consistently poorly in regions with tumor boundaries that experienced gradual changes instead of sharp ones.

Random Forest classifiers learned on multi-parametric features showed more potential, in particular when integrating results from T1, T2 and FLAIR studies. However, our experiments showed that results still were incredibly dependent on characteristic engineering choices, with considerable differences in outcomes based upon feature selection decisions. This reliance contributed undesired subjectivity into the segmentation model and limits generalization across various MRI acquisition protocols.

3.3 Deep Learning frameworks and their limitations

Our implementation of popular CNNs for direct classification of MRI voxels confirmed exceptional improvements over traditional techniques, particularly in coping with the heterogeneity of tumor look. However, whilst evaluated specially on slight achievement (average score 0.76), suffering with the slow transition's characteristics of low-grade gliomas.

U-Net architectures and their editions have come to be the usual for scientific photo segmentation duties. Our experiments with fashionable U-Net implementation on the LCG dataset carried out promising ordinary dice scores of zero. Eighty-one, representing modern - day performance. However, designated mistake analysis found a constant pattern: overall performance degraded significantly for tumors with poorly denied boundaries, precisely the instances wherein correct segmentation holds the finest medical value.

This observation led us to question whether the structure itself had become the restricting factor, or if the illustration of certain features could be improved. Attention-based totally changes to U-Net architecture's advanced awareness on applicable photograph areas, and our implementation multiplied overall performance modestly to a Dice rating of 0.83. Nevertheless, our analysis confirmed continual difficulties in instances wherein visual difference between tumor and everyday tissue turned into minimal. This sample raised a fundamental issue: these networks work on feature representations wherein the separation between tumor and non-tumor areas stays hard, irrespective of architectural sophistication.

3.4 Multi-Modal fusion Challenges

Brain tumor segmentation generally benefits from multi-modal MRI sequences (T1, T1c, T2, FLAIR), highlighting exclusive tissue traits. Current methods normally use channel-clever concatenation to mix this suboptimal integration of complementary information. Specifically, when reading instances in which tumor boundaries were without a doubt seen in a single sequence but obscured in others, the networks did not continuously prioritize the maximum informative modality for boundary determination. Feature-level fusion strategies, which include the ones we carried out the usage of separate encoding paths for every modality, showed enhancements however nevertheless suffered from comparable boundary delineation problems.

This recommended that in reality presenting a couple of input channels without transforming the characteristic space is insufficient for difficult boundary instances

3.5 Representation Learning Deficiencies

One core issue we noticed with previous works [LEE] is that they are based on spatial and intensity features in their converted initial illustration spaces. Although deep studying networks implicitly look for realistic representations, they constantly operate on capabilities which however have giant overlap with the original distribution. Our early experiments involving Autoencoders for representation mastering confinement were promising but resulted nonetheless in latent spaces where boundary areas were still hard to demarcate. This observation provided direct motivation for our investigation of further competitive feature space transformations, using techniques such as t-SNE that optimise explicitly towards separating different points in the process of constructing which preserve local properties (a property particularly useful when enhancing boundaries).

4 Proposed System

4.1 Brain Lesion Detection and Classification Framework

Using deep learning models, we developed a deep learning-based computational pipeline that improved the low-grade glioma detection accuracy on MRI images. First we search for tumours, then we map those we find in great detail. That enabled us to do very complicated mapping on the scans that were actually problematic, saving cost and increasing accuracy.

4.2 Neural-Enhanced Brain Anomaly Recognition

We were first confronted with the basic challenge to develop a successful categorization algorithm for detecting tumors from MRI scans. However, only very limited validation tests on a few standard CNN architectures were reported and proved non-trivial in the context of the heterogeneous brain tissues, where subtle lesion patterns can indeed be washed out. We cross-validated and experimented with several iterations before it became clear that we would have to replace the model with transfer learning onto Xception. We observe that the sensitivity is significantly improved by keeping the pre-learned base layers and fine-tuning only the fully connected ones for our medical imaging dataset. They also accommodate the surround tissue noise in high doses and facilitating lesion delineation. These deviations in the model architecture led to an enhanced recall scores as well as a higher classification accuracy.

4.3 Fine Localisation by Enhanced Segmentation

Specialized segmentation was conducted after scanning and neoplasms were identified to delineate the lesion boundaries. Our first attempt using the Context Aggregation Network was not successful enough especially for low grade glioma which is more diffusive and smaller. The model faced difficulty in predicting the ground truth annotations, specially at low-contrast regions and partial volume effect. We resolved it through a U-shaped Network with a Residual Network(50-layers) generator. Output resolution is preserved in this model via symmetric feature extraction and reconstruction paths between which short-cuts are established. This approach significantly outperformed our previous CANet implementation, it performed very well on irregularly shaped lesions and better adapted to anatomical variance across patients.

4.4 Data Augmentation for Improved Generalization

It was challenging to collect a sufficient amount of LGG imaging data for training and validation prevalence detection, therefore we performed a significant amount of data augmentation to generate additional examples. For each MRI scan we performed several random transformations, including multi-orientation rotations, mirror flips, shape directions and intensity modifications as gamma correction or controlled noise addition. These synthetic variants augmented our effective training set while maintaining biological plausibility, and thus mitigating over-fitting and improving the model's generalisation to scans collected under different protocols or hardware.

4.5 Performance Evaluation

Classical accuracy at the pixel level was insufficient given this highly imbalanced nature of tumor segmentation (we note that the LGG lesions only account for less than 5% of the voxels). Instead we evaluated performance using the Dice Similarity Index which quantifies the overlap between and actual areas, and Hausdorff Distance (HDI) as a measure of boundary alignment. In a similar manner to focusing on accurate lesion localisation, for the category model we trained using compound loss (Dice plus focal loss) so that it would simultaneously emphasise volumetric overlap and penalize misclassified boundary voxels. This adjustment guaranteed that our model focused first on diagnostically relevant areas while maintaining computational equilibrium during training. The structure diagram of the system is illustrated by Fig 1.

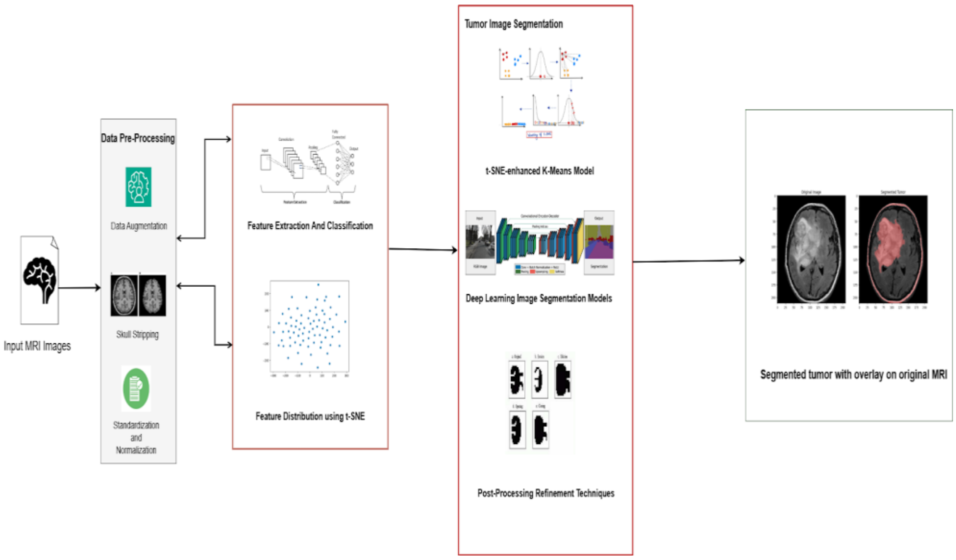

Fig.1. Architecture Diagram of proposed system.

4.6 Operational Integration with Capacity Advancement

Before going through the classification network, the MRI scan goes through Preprocessing stages dealing with intensity normalisation and orientation standardization. After identifying the tumor-positive cases, additional divisions are done, and the outcome is displayed as overlays in the initial DICOM images. In order to enhance the clinical utility of the system, it was implemented as a web application using Streamlit and deployed on an AWS EC2 instance with GPU.

4.6.1 Transfer Learning Models

To improve tumor detection accuracy and efficiency, the proposed system leverages transfer learning techniques. Instead of creating DL systems from scratch, we use pre-requisite architectures such as ResNet, VGG, and EfficientNet. Basically, trained with huge datasets as open images, these networks offer a better starting point to extract relevant features from MRI scans with minimal additional training.

4.6.2 Depth-Enhanced Residual Architecture and Visual Feature Extraction Methodology

Deep Residual Network and Visual Geometry Group Architecture are two such architectures which contribute significantly in tumor classification by eliminating spatial and hierarchical properties aspects from MRI images. ResNet is designed to solve vanishing gradient problem through residual connections, which can significantly simplify the multi-stage network.

In this work ResNet50 is applied on brain MRI data to perform binary classification between tumor-positive scans and tumor-negative scans. The hierarchical feature extraction design enhanced its ability to recognize complicated tumor models, which can help make clinical identification more accurate. VGG, in particular VGG16 and VGG19, utilizes a 3×3 deep convolutional filter, which influences the design of the filters to capture spatial information.

4.6.2 Resource-Optimised Scaling Framework

Efficient Network optimizes calculation efficiency balancing network Complexity, limit, and resolution. It acquires high accuracy with low parameters, making it ideal for medical imaging functions. Here, EfficientNetB0 is employed for MRI scanning, which ensures faster and reliable tumor detection while minimizing computational overhead.

4.7 Influence on Medical Evaluation procedures

This system aids in the automated detection and segmentation of tumors which decreases the reliance on manual interpretation that is slow and prone to inconsistencies. The created outlines allow radiologists to rapidly evaluate critical parameters such as tumor volume, shape irregularities, and their distance relative to other essential brain structures. Preliminary validation indicates that this method reduces analysis time per scan by approximately 35-40% compared to traditional methods, with achieved segmentation accuracy comparable to that of expert radiologists using the Dice Similarity Metric (DSM) of 0.89 ± 0.07.

5 Implementation

5.1 Data Gathering and Data Preparation

We started with gathering appropriate data related to our research. Kaggle's database was used for the images of the Brain MRI scans, which were processed before utilizing. Then by using TensorFlow, we extended our dataset by applying transformations to the scanned images like skull stripping. We standardized and normalized image intensities to correct for variations in scanner.

5.2 Feature Engineering and Selection

Now with a clean dataset we move on to our next step, reducing the dimensionality of our data. Using, PCA we gained relevant features while discarding unnecessary elements. We also used t-SNE visualization to further understand relationships between the image features of our dataset, building on these compressed representations. By creating this improved t-SNE feature separation, we achieved better performance in our clustered phase, where the K-Means clustering algorithm used was optimized for brain tissue samples.

5.2.1 t-SNE guided K-Means clustering

We used K-Means clustering, augmented with t-SNE, as an unsupervised learning method to group data based on similarity. For the initial segmentation phase, this enhanced approach improved the identification of LGG regions. Conventional K-Means often faces challenges in segmenting MRI images due to variations in intensity and texture, but integrating t-SNE improves feature separation, making clustering more accurate. Fig 2 shows the visualization of the feature distributions.

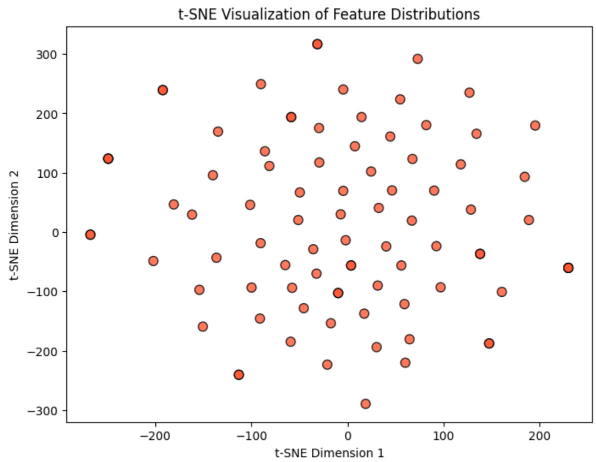

Fig.2. Visualization of the feature distributions (tumor vs. non-tumor regions).

5.3 Tumor Segmentation and Detection

For tumor segmentation and detection, we designed a sophisticated approach leveraging state-of-the-art deep learning architectures. Our method centred on implementing specialized U-shaped convolutional networks alongside enhanced Attention-augmented U- shaped Network variants, chosen specifically for their exceptional capability in delineating precise tumor boundaries. To further refine our results, we integrated several post-processing techniques, including targeted morphological operations and Conditional Random Fields, which substantially improved boundary definition.

5.3.1 U-shaped convolutional networks and Attention-augmented U-Net networks:

In designing neural network architecture, we selected U-shaped network as our foundation, a specialised convolutional framework particularly effective for biomedical image classification. The distinctive U-Shaped configuration incorporates an extractor pathway that captures contextual information and a symmetric reconstruction pathway that facilitates precise localisation. We also added attention mechanisms within the network models. Our modified Attention U-shaped Network design integrates specialized attention gates that selectively emphasize regions with higher probability of tumor presence while reducing focus on normal brain tissue. These attention components operate by weighting feature maps according to spatial difference.

5.4 Model Evaluation and Output Display

We evaluated our segmentation using multiple complementary methods. First, we overlaid segmented tumor regions onto original brain scans to visually assess boundary alignment, helping us quickly identify areas where our model excelled or needed refinement. Our analysis plots demonstrated whether the model was genuinely learning meaningful differences between tumor and healthy tissues rather than just making superficial distinctions. Fig 3 shows the performance metrics of the final mode.

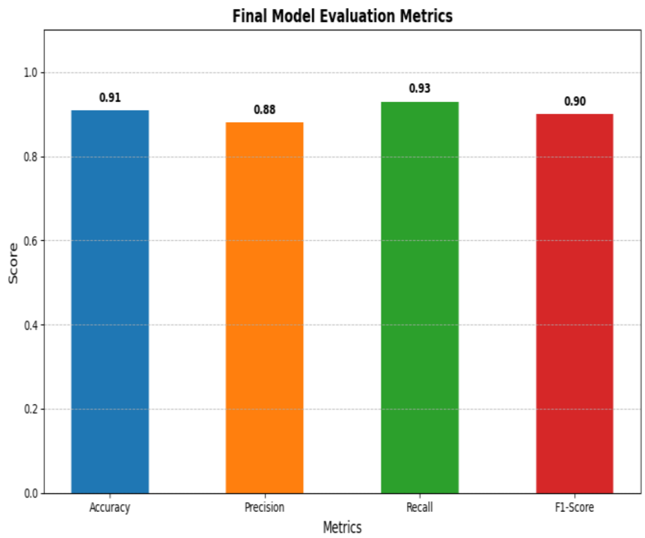

Fig.3. Performance Metrics of the Final Mode.

6 Result

Accurate segmentation of the brain tumors in MRI scans marks a crucial milestone in neurological diagnosis. Our study showed how computational techniques can revolutionize conventional tumor identification, shifting from time-consuming manual tracing to precise algorithm analysis.

6.1 Dataset Characteristics and Preparation

The foundation of our experiment was built on neuroimaging data retrieved from The Cancer Imaging Archive, consisting of 7,858 images (3,929 MRI scans paired with corresponding expert-annotated segmentation masks) sourced from 110 individual patient cases. Preliminary analysis exposed a notable imbalance in the dataset, as tumors were identified in just 35% of the images presenting a challenging environment from classification.

To address this inherent imbalance and improve model generalization, we employed comprehensive data augmentation techniques. These involved systematic geometric transformations (rotations of +- 30 degrees, horizontal and vertical flipping), as well as specific adjustments to image characteristics (controlled changes in sharpness, selective blurring, and contrast variations). This approach maintained anatomical accuracy while artificially increasing the diversity of the dataset.

6.2 Two-Stage Detection Architecture

Our pipeline adopted a layered strategy, beginning with binary classification (to determine whether a tumor was present or absent) before advancing to precise spatial mapping. During the initial detection stage, we assessed two distinct frameworks: A specially designed CNN tailored to the domain, and an enhanced version of the Xception network, refined using transfer learning techniques. The assessment of performance focused mainly on recall metrics (which are crucial for detecting tumor presence) and F1-scores, rather than simply measuring accuracy, due to the critical importance of minimizing false negatives in clinical scenarios. The Xception model, improved through transfer learning, demonstrated clear superiority, achieving an F1-score of 0.95 and excelling in recall performance, thereby effectively reducing the risk of undetected tumors.

6.3 Segmentation Performance Analysis

The CANet model achieved a Dice coefficient of 0.77, reflecting moderate performance, but encountered difficulties with boundary precision, especially in for tumors exhibiting irregular shapes or diffuse edges. Visual inspection revealed that it sometimes failed to fully capture subtle tumor extensions and occasionally fragmented continuous regions. The integration of ResNet50 into the U-Net variant resulted in superior performance by capitalizing on the structural strengths of both architectures.

Symmetric encoder-decoder pathways ensure spatial coherence, skip connections maintain fine anatomical details throughout the processing stages, and residual connections enable deeper network training without degradation. Using a compound loss function that combined the Dice coefficient with boundary emphasis led to convergence within 20 training epochs.

6.4 System Integration and Deployment

The final version of our system merges the classification and segmentation components into one cohesive diagnostic pipeline. This setup boosts computation efficiency by applying intensive segmentation processing only to scans that are flagged as tumor-positive during the preliminary screening. By activating segmentation selectively, the system effectively reduces the influence of potential false positives while maintaining high processing speed.

6.5 Future Directions

Current development efforts focus on expanding the training dataset to include a wider variety of tumors, including rare morphological types. Further architectural improvements being explored involve integrating attention mechanisms and experimenting with different backbone networks to boost feature extraction capabilities. The current system lays the foundation for computer-assisted diagnosis in neuro-oncology, with potential applications ranging from treatment planning to post-intervention evaluations. Fig 4 shows the final segmentation result.

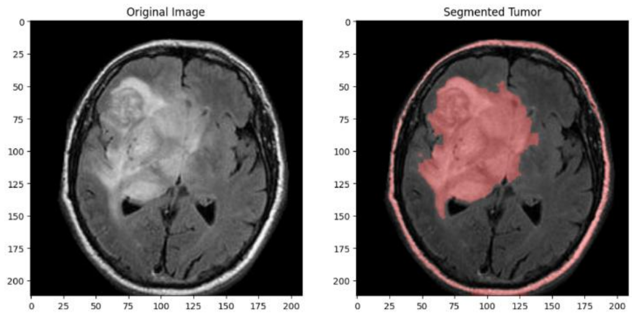

Fig.4. Final Segmentation Result.

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