International Journal of Basic and Applied Sciences, 14 (3) (2025) 143-149

International Journal of Basic and Applied Sciences

Website: www.sciencepubco.com/index.php/IJBAS
https://doi.org/10.14419/2d97nf77
Research paper

Analysis of DL-Algorithms for Segmentation of Tumor

Sarita , Rajeshwar Dass *

Department of ECE, DCRUST, Murthal, Sonipat(Haryana), India
**Corresponding author E-mail: rajeshwardass.ece@dcrustm.org*

Received: June 26, 2025, Accepted: July 2, 2025, Published: July 18, 2025

Abstract

Precisely identifying brain tumors in MRI images is essential for medical image analysis, as it significantly aids in diagnosis, therapy planning, and tracking disease progression. Despite the rapid advancement of Deep learning methods, especially neural networks, which have added prominence for their effectiveness in image-related tasks, a systematic comparative analysis of leading DL architectures using the Figshare BTMR dataset is still lacking. This study addresses this gap by experimentally evaluating six prominent DL models—VGG16, VGG19, ResNet18, ResNet50, MobileNet, and Xception—used as backbone encoders for brain tumor segmentation. Each model's performance is objectively measured using"metrics such as Mean Intersection over Union (mIoU) and Mean Dice Similarity Coefficient"(mDSC). The findings provide valuable insights into the balance between segmentation accuracy and efficiency, assisting in the selection of suitable models for real-time and clinical implementation. This work serves as a benchmark reference, guiding future efforts in selecting effective DL-based architectures for brain tumor segmentation tasks.

Keywords: *Brain; Tumor; MRI; Segmentation.*

1. Introduction

Tumors are among the most dangerous and grave conditions that can harm the central nervous system. Such cases are life-threatening if the issues are not detected early and treated in the right way. On top of that, if such abnormalities are in the brain, neurological functions may be severely affected, thus resulting in a drastic decrease in the quality of life or even death, if timely identification is not provided. Thus, the first stage of brain tumor detection and identification, carried out with high accuracy, is the key to making sound clinical choices, planning more effective therapy, and possibly extending the life span of patients(1). Among the different imaging techniques, MRI is considered the most reliable method for diagnosing a brain tumor. The major advantage of this technique is soft tissue resolution, which leads to the anatomical structures being seen in high detail, and is non-invasive, so it is safe to use several times for both diagnosis and follow-up(2). On the other hand, manual delineation of tumor tissues from MRI images is still a hard and time-consuming job, and it is prone to errors. Generally, this work requires the skills of a specialist, and the interpretation may be inconsistent due to differences in observer expertise and judgment.

In this connection, several works focus on the automation of brain tumor detection and localization. AI-operated segmentation is the backbone of contemporary medical image analysis, and it is a powerful tool that can eliminate dependency on human staff and increase the reproducibility and accuracy of outcomes. Despite all this, this job remains stubbornly complex because of the heterogeneity of a tumor's appearance, mentioned in the variety of its form, size, microstructure, and location, and due to the presence of noises, intensity inhomogeneity, and other artifacts in MRI images.

The problem has been historically addressed with traditional image processing approaches such as thresholding, region growing, and clustering techniques. These classical techniques, on one hand, provide simplicity and interpretability, but, on the other hand, generally lack robustness and adaptability when dealing with large, heterogeneous datasets or atypical tumor presentations. So, in the end, the performance of these methods in real clinical settings is often below par.

Deep learning, especially CNNs, has impactfully changed the medical image segmentation scene, which was traditionally dominated by handcrafted feature extraction methods. CNNs have the potential to self-learn hierarchical and discriminative characteristics from the raw image data; thus, they are the perfect choice for complex pattern recognition tasks such as brain tumor segmentation. The models herein effectively capture both spatial and contextual information over multiple layers, thus resulting in a highly accurate localisation of tumor regions. Furthermore, the adaptive learning capability of CNNs allows them to be configured for specific segmentation tasks, resulting in their dominance in recent medical image analysis research (3).Benchmarking results from modern studies indicate that CNN-based methodologies are more accurate, reliable, and capable of generalizing than traditional segmentation techniques across various datasets (4,5).

The main aim of this research is to identify the best deep learning architectures, VGG16, VGG19, ResNet18, ResNet50, MobileNet, and Xception, through a thorough investigation using the Figshare Brain Tumor MRI (BTMR) dataset. These models are compared by various performance metrics, in particular mean Intersection over Union (mIoU) and Dice Similarity Coefficient (DSC), as these are widely used

quantitative measures of the segmentation quality. This analysis outlines the model that is capable of the best balance between segmentation accuracy and resource efficiency while also allowing for the implementation of such in the clinical real-time setting.
Innovation
The principal innovations of this research are:

- Comprehensive Model Benchmarking on Figshare Dataset: The current work represents a detailed comparative evaluation of six popular deep learning models — VGG16, VGG19, ResNet18, ResNet50, MobileNet, and Xception — on the Figshare Brain Tumor MRI (BTMR) dataset by presenting a thorough review of these architectures that has not yet been done for the BTMR dataset. Prior studies mostly concentrated on a single model or a specific architecture.
- Standardized Evaluation Metrics: The authors employ significantly consistent and standardized metrics such as Mean Intersection over Union (mIoU) and Mean Dice Similarity Coefficient (mDSC), which objectively address the segmentation performance and thus clearly provide clinical deployment a better view.
- Augmentation Strategy for Limited Data: Boosting the training process from the limited data set through the appropriate application of many augmentation techniques (rotation, flipping, and translation) resulted in the improvement of the model's robustness.
- Performance-Computational Cost Trade-off Analysis: Beyond assessing segmentation accuracy, this study also points out the balance between model complexity and performance. Here, emphasis is on lightweight models (MobileNet, for instance) that are suitable for resource-limited environments and on deeper models (ResNet50 and Xception, for instance) that serve high-precision clinical tasks.
- Practical Insights for Real-World Applications: This research is not only providing deep learning models' explicit recommendations for deployment in practice but also discussing the usual cases of high-end hospital systems versus those of portable or mobile diagnostic devices, which are not common in the previous

The rest of the article is organized in this way:
Section 2 gives an account of various studies that employ MRI for the identification of brain tumors.
Section 3 amplifies the suggested approach, detailing the preprocessing, model realization, and assessment parameters.
Section 4 is concerned with the experiments and their explanation.
Section 5 sums up the paper and suggests possible research avenues that can be pursued in the field of brain tumor detection by automation.

2. Previous research work

Brain tumor segmentation using MRI is an important task in medical image analysis that can provide primary assistance in diagnosis, treatment planning, and patient monitoring. Conventional segmentation methods, like thresholding, clustering, and region growing, are not able to deal with the high variability of tumor appearance, noise, and artifacts in the image. Therefore, the DL methods, especially CNNs, are accepted as the most suitable solution due to their high accuracy, robustness, and automation capabilities.

2.1. Evolution from classical to CNN-based models

The impact of CNN-based models on brain tumor segmentation in medical images has been sweeping. U-Net by Ronneberger O et al. (6) featured an encoder-decoder configuration with skip connections that retained local information and facilitated the achievement of higher segmentation accuracy. U-Net rapidly became the standard for biomedical image segmentation tasks.

Following U-Net, nnU-Net, Isensee F et al. (7)presented a self-configuring system that customizes the preprocessing, network architecture, and training methods of a dataset automatically. nnU-Net has led several medical segmentation challenges, showing high performance of automatic configuration compared with manual tuning.

2.2. Integration of attention mechanisms

The latest innovations have proved that attention mechanisms' inclusion allows models to focus better on pertinent parts of the image without noise interference and hence, better segmentation results. For example:

- Maji D et al. (2022)(8) introduced a new Attention Res-UNet with a guided decoder that substantially improves boundary delineation and feature refinement.
- Sun J et al. (2020)(9) made a Nested Residual Attention Network that uses both residual connections and attention modules to intensify global and local feature learning.

Such networks are the best in identifying the complicated boundaries of tumors, especially in cases of irregular shapes or when tissues are overlapping.

2.3. Emergence of transformer-based models

The Transformer design, initially made famous by the language domain, has recently worked wonders for medical image segmentation experiments due to its extraordinary powers of comprehending the direct impact of far-flung elements. For instance,

- Hatamizadeh A et al. (2022)(10) unveiled Swin UNETR, which merges the Swin Transformer backbone with a U-Net-like decoder. This model is very good at local and global context and even bests the BraTS brain tumor segmentation challenge.
- Xu Y et al. (2024)(11) laid out a segmentation scheme that taps into Swin-T's deep, nuanced reasoning capability. They showed on CNNs, their approach improves accuracy and boundary precision.

Transformer-based architectures are perfect for going beyond what CNNs can do, especially when it comes to calculating the relations of distant points in an image, which is very important for segmenting large or diffuse tumor regions.

2.4. Multi-modal MRI segmentation approaches

Current research puts a lot of emphasis on the necessity of multi-modal MRI that amalgamates various MRI sequences like T1, T2, FLAIR, and T1-CE to take segmentation performance to the next level. Multi-modal input takes both normal and abnormal parts of information to a higher degree, thus enabling more accurate tumor detection. The following are significant contributions,

- Farhan A et al. (2025)(12), who had the idea of a quite an ensemble dual-modality approach, adeptly merging multiple MRI modalities to boost the segmentation robustness.
- Peivandi M et al. (2023)(13) appraised the Segment Anything Model (SAM) in brain tumor segmentation, thus proving its ability for generalization across various MRI modalities.

Multi-modal approaches excel over single-modality models, mostly in identifying tumor boundaries in the cases of the most complicated nature.

Even if major research effort has been invested in transformer-based models, attention mechanisms, as well as U-Net derivatives, it turns out that the majority of these studies are dataset-specific, especially around the BraTS dataset, and mostly deal with one architecture to define them. A few studies go as far as to provide a comprehensive benchmarking of multiple CNN-based architectures on the Figshare BTMR dataset, which indeed consists of T1-weighted contrast-enhanced MRI images of glioma, meningioma, and pituitary tumors.

So, this study is the one that fills the gap and provides a systematic comparative analysis of six popular CNN-based models (VGG16, VGG19, ResNet18, ResNet50, MobileNet, and Xception) using metrics such as mIoU and mDSC. While newer models leverage transformers and attention mechanisms, CNN-based architectures remain highly relevant for real-time clinical applications due to their lower computational requirements, ease of deployment, and well-understood behavior.

3. Methodology

The deep learning models—VGG16, VGG19, ResNet18, ResNet50, MobileNet, Xception- were implemented to segment BTMR images from the dataset (the publicly available Figshare dataset). A detailed methodology is shown in Fig.1 . A detailed dataset explanation is provided in Section 3.1.

3.1. Dataset

A publicly available data set of"3064 T1-weighted contrast-enhanced images"(14) collected in five years, i.e., 2005 to 2010" from three different kinds of tumors in the brain: Meningioma (708), Pituitary tumor (930), & Glioma (1426). out of 3064, only 3000 images have been used for this study. The dataset is divided into training and testing data as 80% and 20%, respectively.

3.2. Augmentation

The efficacy of the model is affected by the magnitude of the database. The model's efficacy increases as the dataset's size increases. Consequently, the dataset that is accessible is expanded through the implementation of augmentation techniques. The majority of researchers employ transformational techniques for augmentation, including rotation and twisting. In this work, we have used rotation (90,180), flipping (horizontally, vertically), and translation (1, -1, 2) for augmentation.

3.3. Segmentation

It is a core task in computer vision and image processing that involves dividing an image into significant segments or regions. It aims to reduce or transform the representation of an image into a more meaningful and simpler form for analysis. In medical imaging, for instance, segmentation plays an important role in detecting anatomical structures, locating tumors, calculating tissue volume, and guiding treatment planning.

Algorithm 1 outlines each step necessary for the segmentation of a tumor.

3.4. Pseudo Code

```
Algorithm 1: Tumor Segmentation using BTMR images
        Input: Path to BTMR Images
        Output: Segmented Tumor
1       Load the Dataset, split the dataset into training and testing in a 80:20 ratio
        Data Augmentation,
        - apply
2       - rotation(90 & 180),
        - flipping(Horizontaly and Vertical)
        - translation(±1, ±2 pixels)
        Preprocessing
3       -Resize images to the input size required by models
        -Normalize Pixel Value
        Model training Loop,
        initialize pre-trained model with Imagenet weights,
        Modify the final layer for the segmentation task,
        set hyperparameters,
         - Optimizer: SGDM
4       -  Learning Rate: 0.01
        -  Batch Size: 16
         - Epochs:50
         - Loss: Cross Entropy
        Train the model on the training set
        Save the trained model
        Model testing and evaluation:
5       -Predict segmentation mask on the test set,
        - computer IoU and DSC across the test set
6       Analyze performance vs complexity
7       Select the model based on the highest mIoU and the Highest mDSC
        end
```

3.5. Parameters for evaluation

The most common parameters used by the researchers for performance evaluation of brain tumor segmentation techniques is DSC and IoU(15) . The IoU calculates the intersection region of the original image and the segmented image.

$$IoU(I_S, I_r) = \frac{|I_S \cap I_r|}{|I_S \cup I_r|} \quad (1)$$

Where I_S It is a Segmented image, $I_r$is the original image
Dice Similarity Coefficient (DSC)

$$DSC = \frac{2|I_S \cap I_r|}{|I_S|+|I_r|} \text{or} \quad DSC = \frac{1}{\frac{1}{Precision}+\frac{1}{Recall}} \quad (2)$$

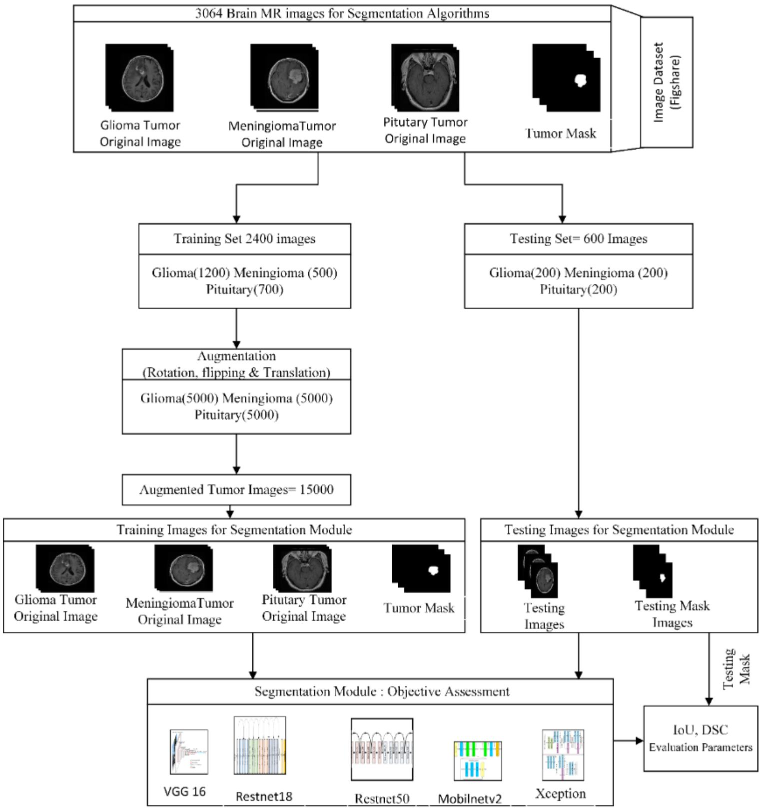


Fig. 1: Methodology Adopted for Analysis of DL-Models for Tumor Segmentaion Using BTMR Images.

4. Results

4.1. Implementation setup

The algorithm for training and testing the DL-model is developed on MATLAB 2021b, using a PC have 16 GB of memory, an Intel i5 Processor &ZOTEK 3060 12 GB graphics card. Network weights are updated using the SGDM optimizer while training, learning rate of 0.01 and a minibatch size is 16.

4.2. Performance evaluation

Six deep learning models — VGG16, VGG19, ResNet18, ResNet50, MobileNet, and Xception — were tested on the Figshare BTMR dataset. The test set included 600 images, 200 for each tumor class, which were glioma, meningioma, and pituitary tumors.
The summary of each model's performance is provided in Table 1& Fig. 2, whereas Table 2 shows the tumor-wise performance analysis.

Table 1: Comparison of DL Models for Tumor Segmentation

Segmentation Method	mIoU (%)	mDSC (%)
VGG16	88.87	71.79
VGG19	85.15	58.62
Resnet18	91	62.42
Resnet50	91.86	71.1
Mobilenet	84.45	81.6
Xception	88.2	84.66

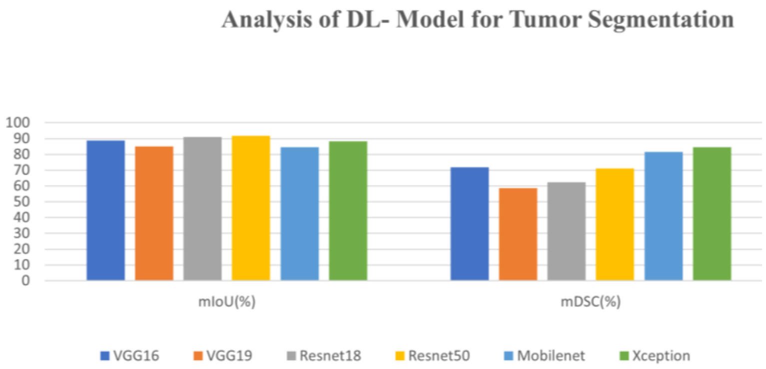
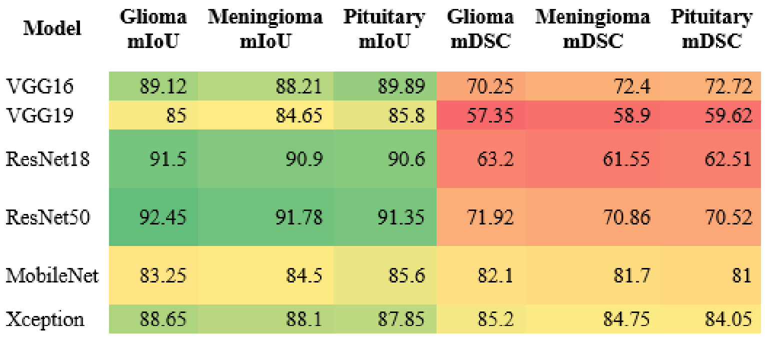


Fig. 2: Analysis of Dl-Model for Tumor Segmentation.

Table 2: Tumor-Wise Performance Analysis of DL Models

Model	Glioma(mIoU/mDSC)	Meningioma (mIoU/mDSC)	Pituitary (mIoU/mDSC)
VGG 16	89.12/70.25	88.21/72.40	89.89/72.72
VGG 19	85.00/57.35	84.65/58.90	85.80/59.62
ResNet 18	91.50/63.20	90.90/61.55	90.60/62.51
Resnet50	92.45/71.92	91.78/70.86	91.35/70.52
MobileNet	83.25/82.10	84.50/81.70	85.60/81.00
Xception	88.65/85.20	88.10/84.75	87.85/84.05



Model	Glioma mIoU	Meningioma mIoU	Pituitary mIoU	Glioma mDSC	Meningioma mDSC	Pituitary mDSC
VGG16	89.12	88.21	89.89	70.25	72.4	72.72
VGG19	85	84.65	85.8	57.35	58.9	59.62
ResNet18	91.5	90.9	90.6	63.2	61.55	62.51
ResNet50	92.45	91.78	91.35	71.92	70.86	70.52
MobileNet	83.25	84.5	85.6	82.1	81.7	81
Xception	88.65	88.1	87.85	85.2	84.75	84.05

Fig. 3: Heatmap of DL Model Tumor-Wise Performance Analysis.

The tumor-wise performance heatmap allows a comparison across the six deep learning models in terms of their segmentation accuracy over various tumor types, with mIoU and mDSC metrics shown in Figure 3. The evaluation indicates that ResNet50 invariably obtains the highest mIoU scores for all tumor types (Glioma, Meningioma, Pituitary), thus suggesting that its deep residual learning architecture enables the model to delineate tumor boundaries more accurately. On the contrary, Xception leads all models in mDSC over tumor types, hence it is the most spatially similarity-preserving model, and it produces smooth, consistent segmentation masks. It is worth noting here that MobileNet has very good mDSC values (above 81%), representing that even though it is a lightweight architecture, it has good potential for resource-constrained environments. Conversely, VGG19 has the worst performance in both mIoU and mDSC, implying that deeper plain CNN architectures without skip connections are less effective for complicated medical segmentation problems. Additionally, the fact that ResNet18, although having a high mIoU, shows a lower mDSC, points out that while it is good in detecting edges of the object, it cannot keep the hemisphere region consistent. In general, the heatmap study focuses on the compromise between segmentation accuracy, spatial accuracy, and computational efficiency, thus enabling the research of suitable models depending on specific clinical needs.

5. Discussion

The comparative study reveals considerable differences in model segmentation abilities across six different models. The details presented in this section focus on the main insights obtained from the results.

5.1. High profiles: ResNet50 and Xception

- ResNet50 led with the highest mIoU (91.86%), which shows that it was the most capable of accurately drawing the tumor boundaries with the least overlap errors. This is due to its deep structure that is supported by residual connections, which are responsible for efficient gradient flow, allowing the network to learn the complex hierarchical features that are essential for the accurate segmentation of the different tumor types.
- Xception got the highest mDSC (84.66%), which means that it was most effective at capturing spatial similarity and thus ensured that the tumor boundary predictions were coherent. The main reason for this success lies in the fact that it makes use of depthwise separable convolutions that help the process of feature extraction to be more efficient without requiring high computational power. Xception was very consistent across all the tumor types; therefore, it is highly preferable in clinical applications, where the boundary precision is necessary.

5.2. Mobilenet: low power consumption for lightweight tasks

- Even though its architecture was designed to be lightweight for mobile and embedded systems, MobileNet still managed to get an impressive mDSC (81.6%), which indicates that it was very good in terms of segmentation performance concerning spatial consistency.

Its mIoU (84.45%), which is slightly lower than ResNet50, shows that there are some minor trade-offs in boundary precision, but it proves that the network is suitable for resource-constrained environments like portable medical devices, telemedicine, and point-of-care diagnostics.

5.3. Underperforming Models

- VGG16 performed reasonably well in mIoU (88.87%) but gave lower results in mDSC (71.79%), largely due to its shallow architecture that did not have modern design elements like residual or separable convolution layers.
- VGG19 was below expectations in all metrics and gave the lowest mDSC (58.62%). This situation shows that deeper versions of VGG do not solve segmentation problems better just because they are deeper, unless there are architectural innovations.
- ResNet18 showed better boundary accuracy (mIoU: 91%), but at the same time, it lost spatial coherence (mDSC: 62.42%), which implies that its depth is not enough to depict complex spatial relationships in tumor segmentation.

5.4. Tumor-wise analysis

Models such as ResNet50 and Xception have done well in all tumor types, thus indicating compatibility with the change in tumor morphology. While still efficient, MobileNet was more successful in glioma and meningioma cases, yet when it came to performance for pituitary tumors, there was some decline, and this drop can be explained by the smaller tumor sizes or less distinctive boundaries.

The consistently lower performance of VGG19 and ResNet18 across tumor types shows that these models have challenges in handling tumors that are harder to anatomically define.

Although they have shown their excellent capabilities, a big problem still exists in the understanding of deep learning models by clinicians. Medical practitioners are not able to trust black-box decisions without any indication of how the decision was made, thus no transparency. By using visualization techniques like Grad-CAM, it is possible to show the parts of the MRI image that are most responsible for the segmentation decision. Besides proving the model's understanding of the tumor areas, the feature can also help the clinician to be more certain. Thus, the explainability framework should be targeted to be adopted along the segmentation pipeline in the next research to allow for transparency, confidence, and to meet the regulations.

6. Conclusion

In the current research, an exhaustive experimental analysis has been performed to assess the six DL-based segmentation models for effective tumor segmentation from the original BTMR images acquired from the Figshare database. These models were chosen based on their widespread application and established effectiveness in medical image segmentation processes, especially in brain tumor analysis.

The main aim of this experimental research work is to assess and compare the robustness and segmentation accuracy of every model. For a fair and systematic comparison, every segmentation model has been evaluated with standardized and objective evaluation criteria.

Three specific parameters are used for quantitative assessment:

- Mean Intersection over Union (mIoU): This calculates the mean intersection between the segmentation map prediction and the original mask for all tumor areas. It is an accepted measure of pixel-level segmentation performance.
- Mean Dice Similarity Coefficient (mDSC): The mDSC measures the mean between precision and recall, provides a robust measure of segmentation accuracy, especially in class-imbalance datasets like small tumor areas.

Among the deep learning models assessed for tumor segmentation, ResNet50 stands out with the best performance regarding mIoU. This highlights its exceptional ability to accurately identify tumor regions with a high degree of overlap. Nonetheless, Xception attains the highest mDSC, showcasing its ability to effectively capture the spatial similarity of the segmented regions.

As a result, Xception stands out as a well-rounded model, thanks to its impressive mDSC and competitive mIoU. This makes it especially fitting for clinical applications where precise tumor boundary delineation is essential. At the same time, ResNet50 is well-suited for scenarios where the focus is on achieving high intersection accuracy.

This research highlights that beyond accuracy, interpretability plays a pivotal role in the clinical deployment of AI models. Leveraging visualization techniques like Grad-CAM can provide insights into model behavior, fostering trust and aiding validation by medical professionals

7. Future research directions

- Hybrid CNN-Transformer Models: Integrate local and global learning for improved accuracy.
- Real-World Deployment: Optimize models for inference on portable devices, consider memory footprint, computational load, and latency.
- Explainable AI: Develop frameworks ensuring model transparency, which is crucial for clinical adoption.

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