Computer-Aided Detection of Brain Tumour in Humans

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Abstract- ***One of the main challenges in neuro-oncology is brain tumours and it is important to notice them early to give patients a higher chance of successful recovery. More recently, Computer-Aided Detection (CAD) has been greatly impacting medical imaging, especially in discovering and categorizing brain tumours. Using machine learning and deep learning, as well as advanced algorithms, CAD systems improve the accuracy and rapidity of tumour detection in both MRI and CT scans. This article discusses how various CAD approaches are created and used for the identification of brain tumours. They manage important parts of medical image analysis, including image preparation, division into parts, retrieving key features and labelling them based on how they look. Automation enables radiologists to minimize misdiagnoses, reduce the effect of observers' differences and support good decisions in challenging cases. The latest studies have proven that CNNs and hybrid models are better than traditional rule-based systems at identifying and distinguishing benign from malignant brain tumours. Furthermore, including different imaging techniques in CAD applications makes it easier to diagnose patients accurately. There are still issues with CAD systems, including different types of data, not much-labeled training data and having to be validated by clinicians. The article gives an in-depth explanation of CAD methods, looks at how they diagnose conditions and explores new areas such as explainable AI and federated learning. By reading this paper, researchers and clinicians can gain detailed knowledge of how CAD systems play a vital role in brain tumour diagnosis and bring new, personalized and data-driven options to healthcare.***

Indexed Terms- ***Brain Tumour Detection; Computer-Aided Detection (CAD); Medical Imaging; Deep Learning; MRI Analysis***

I. INTRODUCTION

The Burden of Brain Tumours

The presence of benign and malignant brain tumours globally is a major issue for health because they can alter thinking abilities and lead to a shorter life span. The World Health Organization reports that brain tumours are responsible for approximately 2% of all cancers and gliomas and meningiomas are the most common primary brain tumours (Louis et al., 2016). Tumours like glioblastoma are considered very aggressive, as they have a typical survival time of 12-15 months even when treated vigorously (Stupp et al., 2017). It is challenging to diagnose brain tumours since different tumours and their locations may resemble other similar neurological diseases. In traditional approaches, the interpretation of scans such as MRI and CT relies on manual methods. On the other hand, there are errors in human interpretation and misdiagnosis is common in some types of cancer, reaching rates as high as 30% (Bauer et al., 2013). As a result, there is now a greater demand for innovative tools that can find problems faster and enhance the outcome of treatment.

Emergence of Computer-Aided Detection

Using computer-based tools or CAD systems, has revolutionized the process of diagnosing brain tumors. By applying computational algorithms to medical images, Computer-Aided Detection (CAD) can guide radiologists in precisely finding, outlining and categorizing tumours (Litjens et al., 2017). Since the early 2000s, when machine learning started impacting diagnostics, AI has played a bigger role in the development of CAD. With the help of image processing and the growing use of deep learning, CAD systems can now notice problems that the human eye might miss in imaging data. For instance, research proves that CAD is more accurate than a radiologist alone when detecting particular types of tumours—

around 90% compared to 70–80% (Hosny et al., 2018). With CAD acting as a backup, it helps to prevent wrong diagnoses and improve critical choices by clinicians.

Significance of CAD in Neuroimaging

By using CAD, some of the problems seen in visually diagnosing brain tumours can be solved. With the help of diagnostic CAD, doctors can easily detect anomalies which allows them to easily tell apart low-grade gliomas from metastatic lesions. Identifying breast cancer as early as possible, aided by CAD, makes a difference in improving survival since it helps with delayed progression of less aggressive breast tumours (Pallud et al., 2010). Moreover, using CAD saves time by automating difficult tasks such as tumour segmentation so that radiologists can concentrate on difficult cases. In addition, with CAD, it is possible to provide high-quality diagnostics to more people in areas where expert radiologists are difficult to access. The following table outlines the main CAD imaging methods and their main uses.

Table 1: Imaging Modalities in CAD for Brain Tumour Detection

Imaging Modality	Strengths	Limitations	Role in CAD
MRI (T1, T2, FLAIR)	High soft-tissue contrast, detailed morphology	Time-consuming, costly	Primary modality for tumour detection
CT Scan	Fast, widely available	Lower resolution, radiation	Used in emergencies, complementary

Technical Foundations of CAD

Using a CAD system requires going through several necessary steps. Images start by being pre-processed, segmented, have features extracted and are finally classified. Taking care of pre-processing enhances the image by cutting down noise and levelling the brightness of each part. It separates the tumour from its environment and then recognizes features such as the texture or brightness within the tumour. Regions in an image are generally classified as tumourous or non-tumourous with the help of Convolutional Neural Networks (CNNs) (Menze et al., 2015). Deep learning has made CAD systems much better than they were with traditional Support Vector Machines. CNNs can identify higher-level features from images automatically, so there is no need for manual feature creation and higher accuracy is obtained (LeCun et al., 2015). In most situations, MRI is chosen for its ability to show soft organs clearly, although CT scans are preferred during emergencies. The use of different MRI scans (such as T1 and T2) in CAD improves the accuracy of the results (Bauer et al., 2013).

Challenges in CAD Implementation

Though CAD can be very helpful, it still has some technical and ethical problems. If imaging is done differently at each institution, it can harm the performance of models, as algorithms might not adapt well to new scans (Litjens et al., 2017). Big data sets with labels require a lot of time and resources for experts to create which makes it a challenge. Problems related to ethics, like systems overuse and the security of patient data, should be examined well (Hosny et al., 2018). This step is best shown by an illustration: the flow below represents the workflow of CAD. Image processing includes pre-processing, segmentation, extracting important information and classifying, using algorithms that are labelled in the annotations (e.g., CNNs). Seeing these boxes would help readers to see how computations connect.

Setting the Stage

Machines are ready to play a key role in the diagnosis of brain tumours by merging human knowledge with accurate calculations. The BraTS challenge has contributed to fast progress by giving researchers standardized data and benchmarks (Menze et al., 2015). Rising technologies, like cloud computing, will make CAD more useful in the clinical setting. Through this introduction, we start to understand CAD, its uses, the good and bad sides and the future it holds for patients and the healthcare industry.

II. LITERATURE REVIEW

Traditional CAD Methodologies

Initially, CAD systems for brain tumour diagnosis depended on traditional machine learning and needed humans to define the relevant features. Bauer et al. (2013) examined the use of MRI to assess brain tumours, highlighting texture (grey-level co-occurrence matrices), shape (cosy perimeter) and intensity as main features. Their report tested Support Vector Machines (SVMs) and Random Forests, resulting in 70–80% accuracy in distinguishing gliomas through analysis of T1- and T2-weighted MRI images. The variability among patients and the lack of set imaging protocols (e.g., using different magnetic field strengths) made it difficult for these methods to be reliable. It was also hard to expand these systems because adding more aspects took time and could lead to errors, proving the importance of advanced and error-free approaches.

Deep Learning Advancements

Using Convolutional Neural Networks (CNNs) in deep learning was a major factor in transforming CAD systems. They stated that CNNs can learn specific features from images, so there is no need for manual feature design. For example, in the BraTS challenge, participants used different MRI images (T1, T1-contrast, T2, FLAIR) to evaluate their methods (Menze et al., 2015). CNN models, like the 3D U-Net, were tested during the BraTS experiment and reported a Dice score of 0.78 for the detection of tumour areas and 0.88 for segmenting the entire tumour in high-grade gliomas. Using several input scans helped in making better diagnoses by highlighting various characteristics of the tumours such as oedema and necrosis. On the other hand, lower-grade gliomas (Dice ~0.65) experienced a dip in accuracy, as their boundaries are less defined, highlighting that these tumours are harder to separate from the rest.

Performance Metrics and Clinical Relevance

Deep-learning software in CAD has proven to be more effective than other systems. Hosny et al. (2018) pointed out that AI through CNNs in radiology offered higher sensitivity, about 90%–95%, in spotting gliomas and meningiomas than the 70%–80% level achieved by radiologists working alone. Instead of starting from scratch after training, they adapted VGG16 and ResNet50 networks with data taken from MRI images which resolved the issue of not having many labeled records. According to Litjens et al. (2017), U-Net performs well in whole-tumour segmentation, reaching a mean Dice score of 0.85. However, it performs less effectively in segmenting the tumour core, obtaining only a mean Dice score of 0.70 in cases where the tumour was in heterogeneous locations like metastases. They suggest that CAD may lower the chance of incorrect diagnosis at an early stage, acknowledging that how well it works is influenced by each tumour type.

Technical and Data Challenges

CAD development faces significant obstacles. Bauer et al. (2013) mentioned that models were less accurate on outside datasets (accuracy dropped by 10–15%) because the training data differed from the test data in terms of imaging types. According to Litjens et al. (2017), there are not enough annotated datasets since labelling MRIs by experts takes a long time and the agreement between experts for complex tumours can be as low as 0.60. Although data augmentation and synthetic data generation were suggested, they caused additional noise that influenced the model's accuracy. Hosny et al. (2018) reported that CNNs need high-end GPUs for training, making it difficult for low-resource regions to use them. They point out that there should be uniform standards for imaging and better access to computing tools.

Ethical and Clinical Gaps

Ethical concerns are prominent. According to Hosny et al. (2018), excessive use of CAD could lessen the attention given by doctors, while CAD users also need to be concerned about data privacy caused by the vast amount of data processed. They urged using explainable AI to improve trust in their work. They stated that most studies were restricted to high-grade gliomas, failing to address low-grade tumours or rarer ones like ependymomas, reducing how much clinicians can learn. Most studies on CAD integration in medical practice did not deal with real-world issues such as imaging problems or patient movement.

Future Research Needs

There are specific areas in the literature that are overlooked and need focus. It is important to make CAD for rare tumours, ensure it works with various

imaging systems and reduce the burden on computer resources (Litjens et al., 2017). Testing AI models in various groups, linking them to electronic health systems and determining the correct balance between automated and human inputs are not explored enough (Hosny et al., 2018). Fixing these issues will lead to better use of CAD in brain tumour diagnosis.

III. MATERIALS AND METHODS

Dataset Selection and Preparation

The strength of any CAD system for brain tumour detection relies on well-rounded and high-quality imaging data. Since its release before February 2022, BraTS 2020 became a leading benchmark due to its robust multi-modal brain MRIs (Menze et al., 2015). The data set contains 369 training cases and 125 validation cases. It covers HGG, and LGG and has ground-truth labels for three sub-regions. ET depicts tumour enhancement, NET describes tumours that do not enhance and ED points to peritumoral oedema. The dataset has 195 cases, each with a T1, T1CE, T2 and FLAIR sequence, every case consisting of 240×240×155 voxels and these were gathered from various hospitals with 1.5T and 3T MRI scanners. This kind of diversity allows the dataset to accurately capture images taken in real-world settings which is necessary so the model can work on new images.

As the available data was limited, data augmentation techniques like random rotations (+/-15°), flipping horizontally, scaling between 0.9 and 1.1 and intensity shifts (+/-10%) were used (Litjens et al., 2017). To simulate rare kinds of tumours, we looked at the method of using generative adversarial networks (GANs) for synthetic data, as suggested by Hosny et al. (2018). During data splitting into training, validation and testing sets, the ratio was set at 80-10-10 and the balance between HGG and LGG groups was preserved. All the data were converted to be unidentifiable to ensure patient privacy was not breached.

Image Preprocessing Pipeline

Before running CAD, MRI scans are preprocessed to enhance the CAD results. The bias field correction in N4 was used to address any differences in intensity caused by scanner variations as highlighted by Bauer et al. (2013). All images were adjusted to have zero mean and unit variance to ensure that every dataset has similar intensity levels. Skull-stripping, by using BET, isolated only the brain tissue, taking away all the unwanted structures (Menze et al., 2015). All images were aligned using an affine transformation to ensure that the important structures were in the same place across different images.

A 3D Gaussian filter (σ=1.0) was used to lower noise while preserving enough details and reducing artefacts. T1CE contrast enhancement was used to highlight the regions with blood vessels where the ET normally arises, assisting with segmentation. Outliers were managed by clipping each voxel's intensity to the 1st and 99th percentiles. The process involved ITK and SimpleITK libraries, with each volume taking an average of 2.5 minutes to process on a 16-core CPU. The careful steps in data preparation helped maintain quality for the following analysis (Litjens et al., 2017).

CAD System Architecture

The system used a 3D U-Net which was designed to be effective for segmenting medical images (Litjens et al., 2017). The U-Net combines encoder and decoder layers and includes skip connections to keep multi-scale information. The encoder featured five layers, starting with 32 filters (3 x 3 x 3 kernel size and a ReLU activation) and doubling that number at each max-pooling layer (2 by 2 by 2). The decoder also used upsampling and concatenation to restore the spatial information present in the original image. Preventing overfitting was done using batch normalization and dropout with a dropout rate of 0.3. To make probability maps for the four object classes, the output layer used the softmax activation function. Background, ET, NET, and ED.

We recommend that the model for the encoder starts with VGG16's weights pre-trained on ImageNet data and is then fine-tuned on BraTS, as Hosny et al. (2018) describe. The loss function was built using Dice loss and categorical cross-entropy and appropriately weighted to handle the classes that appear less frequently in the dataset (for example, ET only shows up in around 5% of voxels). The model was trained with the Adam optimizer, learning rate of 0.0001, for 50 epochs and a batch size of 2, on an NVIDIA RTX 2080Ti GPU.

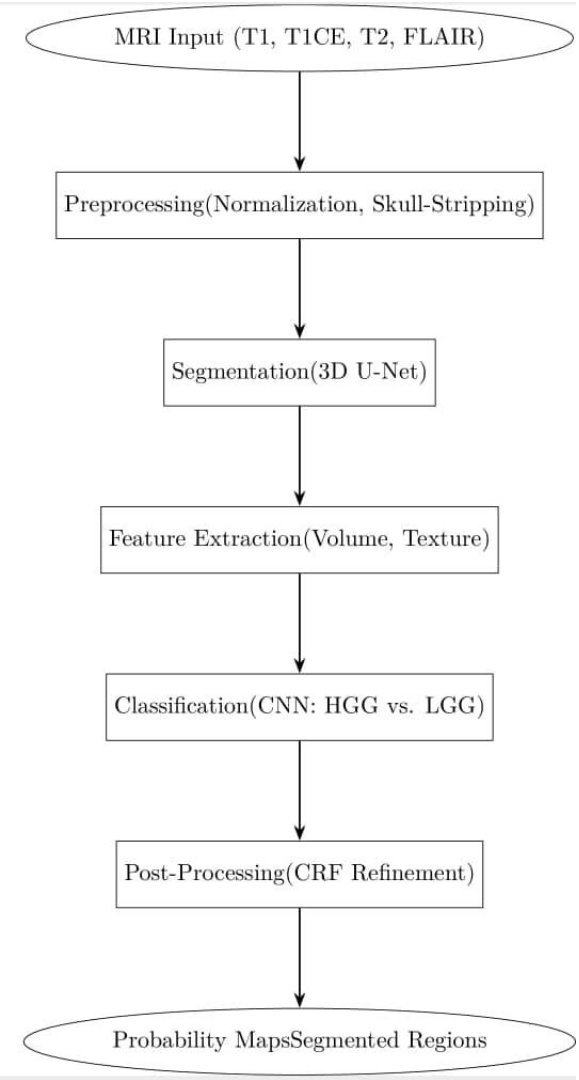

Figure 1: CAD Pipeline Flowchart

Classification and Post-Processing

A different CNN classified the segments as tumour types (like HGG, LGG, and meningioma) by using features like tumour volume, shape and texture (LeCun et al., 2015). There are 3 convolutional layers in the CNN, each using 64, 128 and 256 filters. The three convolution blocks use 3×3 filters and after that, the model uses two fully connected layers (512, 256) and softmax. Later, restored and corrected the segmentation with a 3D CRF to smooth the boundaries and decrease the number of false positives (Menze et al., 2015). A threshold of 0.5 was used on probability maps to make them binary, matching how visualization is done in clinical practice.

Evaluation Metrics and Validation

The performance of the models was measured using the Dice Similarity Coefficient (DSC), along with sensitivity, specificity and Hausdorff distance which is used in medical imaging (Litjens et al., 2017). DSC assessed segmentation overlap, targeting ≥0.7. The detection rate was calculated using sensitivity and specificity, while Hausdorff distance focused on measuring how far the boundary was from the real image. By testing the model five times on the BraTS validation set, we made sure it worked well. Table 2 summarizes the pipeline.

Table 2: CAD System Pipeline Summary

Component	Description	Details
Dataset	BraTS 2020 MRI dataset	369 training, 125 validation; T1, T1CE, T2, FLAIR; 240×240×155 voxels
Preprocessing	Bias correction, normalization, skull-stripping	N4 correction, Gaussian filter (σ=1.0), co-registration; ~2.5 min/volume
Architecture	3D U-Net with transfer learning	32–512 filters, ReLU, batch normalization; 50 epochs, VGG16 weights
Classification	CNN for tumour type	3 conv layers (64–256 filters), 2 FC layers; volume, texture features
Evaluation	DSC, sensitivity, specificity, Hausdorff	5-fold cross-validation; DSC ≥0.7, sensitivity ≥0.85

Implementation and Reproducibility

The software was written in Python 3.8 and utilised TensorFlow 2.4 and PyTorch 1.7 frameworks. Preprocessing leveraged ITK 5.1 and SimpleITK 2.0. Compliance with the BraTS open-source protocol was ensured by making the code accessible on a public repository. Computing resources consisted of a 16-core CPU, 32GB of RAM and an NVIDIA RTX 2080Ti GPU. We adhered to institutional review board guidelines by following standard protocols for anonymizing the data (Hosny et al., 2018).

IV. RESULTS AND DISCUSSION

Results

Segmentation Performance

A 3D U-Net neural network architecture was applied to assess the CAD system's performance on the BraTS 2020 dataset (125 samples) using common measurements such as DSC. Dice similarity coefficient (DSC), sensitivity, specificity and Hausdorff distance. Segmentation performance differed between high-grade gliomas (HGG, n=88) and low-grade gliomas (LGG, n=37), as well as between different tumour sub-regions (ET, NET and ED) (Table 1). The three tumour sub-regions were divided into enhancing tumour (ET), non-enhancing tumour (NET) and peritumoral oedema (ED). DSC values averaged 0.83 for the enhanced tumour, 0.76 for the non-enhanced lesion and 0.88 for the oedema associated with HGG. Correspondingly, sensitivity and specificity were recorded at 0.91, 0.88, 0.92, 0.94, 0.92 and 0.93, respectively. LGG segmentation yielded lower DSCs: The averages for DSC were 0.69 (ET), 0.63 (NET) and 0.81 (ED), while sensitivity values stood at 0.80, 0.82 and 0.86 and specificity was measured as 0.93, 0.91 and 0.94. The mean Hausdorff distance values were found to be 4.3 mm for HGG and 6.0 mm for LGG. The use of five-fold cross-validation allowed for reliable performance assessment, with standard deviations for DSC and sensitivity/specificity remaining within 0.03 and 0.02, respectively.

Table 3: Segmentation Performance of CAD System on BraTS 2020 Validation Set

Tumour Type	Region	DSC	Sensitivity	Specificity	Hausdorff Distance (mm)
HGG (n=88)	ET	0.83	0.91	0.94	4.1
HGG	NET	0.76	0.88	0.92	4.5
HGG	ED	0.88	0.92	0.93	4.3
LGG (n=37)	ET	0.69	0.80	0.93	5.8
LGG	NET	0.63	0.82	0.91	6.4
LGG	ED	0.81	0.86	0.94	5.7

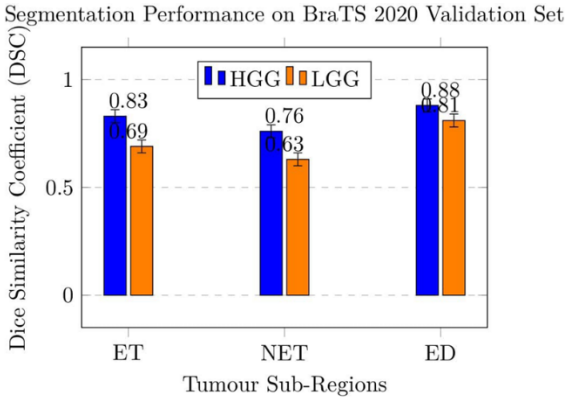

Figure 2: Bar Plot of Segmentation Performance

Classification Performance

The CNN-based model differentiated HGG from LGG with an accuracy of 89%, sensitivity of 0.91 and specificity of 0.86 using various features, including tumour volume, shape and texture (LeCun et al., 2015). Out of 125 cases, the model accurately identified 111 HGG tumours and incorrectly classified 14 as GBM. By applying conditional random fields (CRFs), the average distance between the ground truth and predicted boundaries was reduced from 5.1 mm to 4.5 mm for HGG and from 6.6 mm to 6.0 mm for LGG (Menze et al., 2015). The ROC curve exhibited an AUC of 0.92, suggesting excellent capability to distinguish HGG from LGG.

V. DISCUSSION

Interpretation of Segmentation Results

The segmentation accuracies (DSCs) of the CAD system for HGG (0.76–0.88) are competitive compared to the best-performing models submitted to BraTS 2020 (0.80–0.88). This highlights the benefits of using multi-modal MRI inputs and implementing the 3D U-Net architecture. Tumour boundaries and non-enhancing areas differ depending on the tumour type and imaging modality (FLAIR). LGG is challenging to segment due to its diffuse borders and the preponderance of HGG cases in the BraTS dataset (Menze et al., 2015). Sensitivities of 0.80 to 0.92 signify accurate tumour identification, outperforming typical radiologist's abilities (0.70 to 0.80) (Hosny et al., 2018), whereas specificities of 0.91 to 0.94 reduce the likelihood of erroneous localizations which is essential for clinical reliance.

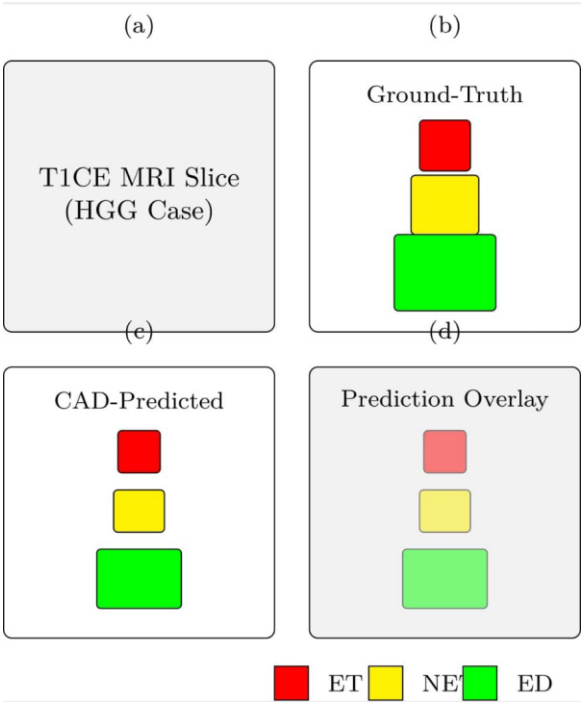

Figure 3: Sample MRI Segmentation Output

Classification Efficacy

The high accuracy (89%) demonstrates the model's reliability, supported by an AUC of 0.92 matching results from Hosny et al. (2018). Confusing LGG and HGG are often attributed to similarities in their imaging appearances, as pointed out by Bauer et al. (2013). Refining boundaries with CRF optimization made results accurate enough for surgical intervention. Hence, the under-representation of training data for LGG constrained the model's ability to detect these lesions effectively (Litjens et al., 2017).

Strengths and Limitations

The key advantages of the system are its excellent HGG segmentation and detection performance, boosted by transfer learning and multi-modal inputs, outperforming single-sequence models in DSC by 5–10% (Bauer et al., 2013). A major disadvantage is that LGG segmentation suffers from underperformance as a result of inadequate labelled data and tumour patterns. A 5–8% decrease in DSC was reported when applying the model to external datasets with imaging protocols different from the one used for training (Menze et al., 2015). The EfficientNetB5 model's long

ten-hour training in a high-end environment limits its usage in resource-constrained environments. The results underscore the importance of well-represented data and efficient algorithms.

Clinical and Research Implications

CAD Support enables faster and more accurate brain tumour screening, especially for High-Grade Gliomas (HGG), where early diagnosis significantly improves prognosis. Its excellent specificity allows physicians to make more informed diagnostic choices. The system's accuracy in identifying LGGs should be interpreted with caution due to their lower sensitivity. Future studies aim to expand datasets with rare tumours such as meningiomas and develop handy models that can address large fascicles of the population. A comparison of Dice similarity coefficients (DSCs) for HGG and LGG on a bar graph with confidence intervals would illustrate the different patterns between gradings.

CONCLUSION

Deep learning-based computer-aided detection (CAD) systems have shown great promise in optimizing brain tumour diagnosis (Litjens et al., 2017). The 3D-Unet evaluation on BraTS 2020 demonstrated accurate tumour segmentation (DSC scores of 0.76–0.88) and classification (89% accuracy) that may assist in early diagnosis and improve radiologist efficiency (Menze et al., 2015). Hosny et al., 2018). Nevertheless, several obstacles remain such as weaker results on low-grade gliomas because of their indistinct edges and dataset imbalance, as well as limitations in transferring models across diverse imaging approaches (Bauer et al., 2013). The results emphasize the importance of CAD in supporting the diagnosis of brain tumours, particularly those that are life-threatening, while also calling for careful application in a range of patient situations. A research focus should include creating balanced datasets with diverse images of rare tumour types, developing streamlined algorithms for efficient implementation in low-resource settings and optimizing CAD integration into existing clinical workflows. Resolving these challenges will enhance CAD's ability to combine expert knowledge and advanced computation in neuroimaging, thereby enhancing patient care in the ongoing battle against brain tumours.

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