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Brain Tumor Detection Using Deep Learning and Machine Learning

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Dedications

All praises and much gratitude to almighty Allah, the most compassionate and magnificent, who gave us the power, the courage to work hard and persistence to complete this modest work

We would like to thank our supervisor, **Dr. Hakima Zouaoui**, for allowing us to conduct our research. Also, her generosity, compassion, and the time she spent with us.

Finally, to our dear parents, to all our families, to all those dear to us, to all our friends, we dedicate the culmination of our 22 years of study.

Abstract

Brain tumors, particularly gliomas, are among the most prevalent and aggressive types of brain tumors. Accurate diagnosis and classification of gliomas are crucial for effective treatment planning and patient management.

In this thesis we are focusing on the development of a hybrid model capable of detecting brain tumors and classifying them from MRI images. The model is designed to perform two main tasks : tumor segmentation and tumor grade classification. leveraging the BraTS2020 dataset, which provides a comprehensive collection of MRI scans with annotated tumor regions and corresponding grades. The model integrates a U-Net architecture for precise segmentation of tumor regions in MRI scans and a Support Vector Machine (SVM) classifier for determining tumor grades as High-Grade or Low-Grade Gliomas. The U-Net model is trained to accurately segment the tumor regions from the surrounding healthy brain tissue, while the SVM classifier is trained to classify the segmented tumors into their respective grades based on features extracted from the segmented images.

Keywords : Brain Tumor, Glioma, U-Net, SVM, MRI, BraTS, Tumor Segmentation, Grade Classification.

Résumé

Les tumeurs cérébrales, en particulier les gliomes, comptent parmi les types de tumeurs cérébrales les plus répandus et les plus agressifs. Un diagnostic précis et une classification des gliomes sont essentiels pour une planification efficace du traitement et une gestion optimale des patients.

Dans cette thèse, nous nous concentrons sur le développement d'un modèle hybride capable de détecter les tumeurs cérébrales et de les classifier à partir d'images IRM. Le modèle est conçu pour effectuer deux tâches principales : la segmentation des tumeurs et la classification de leur grade. En s'appuyant sur la base de données BraTS2020, qui fournit une collection complète d'IRM avec des régions tumorales annotées et leurs grades correspondants, le modèle intègre une architecture U-Net pour une segmentation précise des régions tumorales dans les IRM et un classificateur SVM (Support Vector Machine) pour déterminer les grades des tumeurs en gliomes de haut grade ou de bas grade. Le modèle U-Net est entraîné pour segmenter avec précision les régions tumorales du tissu cérébral sain environnant, tandis que le classificateur SVM est entraîné pour classifier les tumeurs segmentées en fonction des caractéristiques extraites des images segmentées.

Mots-clés : Tumeur cérébrale, Gliome, U-Net, SVM, IRM, BraTS, Segmentation des tumeurs, Classification des grades.

ملخص

تُعد أورام الدماغ، وخصوصاً الأورام الدبقية، من بين أكثر أنواع أورام الدماغ انتشاراً وعدوانية. يُعتبر التشخيص الدقيق وتصنيف الأورام الدبقية أمراً بالغ الأهمية للتخطيط العلاجي الفعّال وإدارة حالة المرضى.

في هذه الأطروحة، نركز على تطوير نموذج هجين قادر على اكتشاف أورام الدماغ وتصنيفها من صور التصوير بالرنين المغناطيسي. تم تصميم النموذج لتنفيذ مهمتين رئيسيتين: تقسيم الأورام وتصنيف درجاتها. يعتمد النموذج على مجموعة بيانات BraTS2020، التي توفر مجموعة شاملة من صور الرنين المغناطيسي مع مناطق الأورام المشروحة والدرجات المقابلة لها. يدمج النموذج بين بنية U-Net لتقسيم دقيق لمناطق الأورام في صور الرنين المغناطيسي ومصنف آلة ناقلات الدعم SVM لتحديد درجات الأورام كأورام دبقية عالية الدرجة أو منخفضة الدرجة. يتم تدريب نموذج U-Net على تقسيم مناطق الورم بدقة عن الأنسجة السليمة المحيطة في الدماغ، بينما يتم تدريب مصنف SVM على تصنيف الأورام المقسمة إلى درجاتها بناءً على الخصائص المستخرجة من الصور المقسمة.

الكلمات المفتاحية: أورام الدماغ، الأورام الدبقية، SVM ،U-Net، التصوير بالرنين المغناطيسي، BraTS، تقسيم الأورام، تصنيف الدرجات.

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List of abbreviations

AI Artificial Intelligence.

BraTS Brain Tumor Segmentation dataset.

DL Deep Learning.

HGG High-Grade Glioma.

LGG Low-Grade Glioma.

ML Machine Learning.

MRI Magnetic Resonance Imaging.

SVM Support Vector Machine.

U-Net U-Net Convolutional Neural Network.

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Chapitre 1

General Introduciton

1.1   Introduction

Traditionally, radiologists rely on MRI scans to detect brain tumors, While this method is effective, it also has limitations analyzing hundreds of scans manually is time consuming and prone to human error. That is where technology comes in. With recent advances in artificial intelligence, especially deep learning, we now have powerful tools that can learn from medical images and help with faster and more accurate diagnosis.

In this project, we focus on building a hybrid system to detect brain tumors and determine whether they are low-grade or high-grade. We use a U-Net model for segmenting the tumor regions in MRI images. After identifying these regions, we extract important features and feed them into a Support Vector Machine (SVM) classifier to make the final prediction.

We use the BraTS2020 dataset, focusing on T2-weighted FLAIR images, to train and test our system. Our goal is to create a pipeline that is not only technically sound but also practical and helpful for medical professionals in real-world settings.

1.2   What is a Brain Tumor ?

A **brain tumor** is an abnormal mass of tissue in which cells grow and multiply uncontrollably, without the mechanisms that regulate normal cell behavior. Brain tumors can be broadly categorized into *benign* (non-cancerous) and *malignant* (cancerous) forms, each with varying

levels of severity and progression [1].

Brain tumors are generally divided into two main categories :

- **Primary brain tumors :** These originate in the brain and include common types such as :
  — *Gliomas* – tumors arising from glial cells, which provide support and insulation to neurons [2].
  — *Meningiomas* – tumors that form in the membranes surrounding the brain and spinal cord [3].
  — *Pituitary adenomas* – tumors that develop in the pituitary gland [3].
  — *Medulloblastomas* – fast-growing tumors more commonly seen in children [1].
- **Secondary (metastatic) brain tumors :** These originate from cancers elsewhere in the body (such as the lungs or breast) and spread to the brain [1].

Among gliomas, two major clinical subtypes are often considered for diagnostic and prognostic purposes [2] :

- **Low-Grade Gliomas (LGG) :** Slow-growing tumors that often have a better prognosis.
- **High-Grade Gliomas (HGG) :** Aggressive tumors with rapid progression and poor prognosis.

Accurate detection and classification of these tumor types are essential for clinical decision-making, which has led to the integration of artificial intelligence (AI) and deep learning (DL) methods into medical imaging workflows.

1.3   Problem Statement

Despite the advancements in medical imaging, the accurate identification and classification processes of the brain tumors in MRI scans remains a challenging task. Also the manual segmentation is time-consuming, not forgetting the human error, and the need fo expert knowledge. Existing automated methods often struggle with inconsistent tumor boundaries and data imbalance, especially when distinguishing between low-grade and high-grade gliomas.

There is a clear need for a robust and efficient system that can both segment brain tumors

accurately and classify their grade reliably. This project aims to address that gap by combining DL for tumor segmentation with classical ML for tumor grade classification providing a practical hybrid solution that balances performance and .

1.4   Objectives

1.4.1   General Objective

To develop an automated system for brain tumor detection, segmentation, and classification using DL and ML techniques on MRI scans.

1.4.2   Specific Objectives

1. Explore and preprocess the BraTS dataset, focusing on T2-weighted MRI images.
2. Train a U-Net model for precise segmentation of brain structures, including tumor regions.
3. Extract tumor regions from the segmentation masks and classify them as low-grade or high-grade gliomas using an SVM classifier.
4. Evaluate the performance of the segmentation and classification models using appropriate metrics.
5. Build a simple application that integrates both models for real-time inference and visualization.

1.5   Motivation

The potential of using DL and ML in brain tumor detection and classification is truly remarkable. It can help reduce the time required for diagnosis, which is life saving on early intervention. Moreover, it offers the promise of improved accuracy and consistency in medical decisions by minimizing the subjectivity and fatigue that can affect human experts.

Through this project, we aimed to contribute to that goal by building an automated system that segments brain tumors from MRI scans and classifies them into Low-Grade Glioma (LGG) or High-Grade Glioma (HGG). We used a U-Net architecture for precise segmentation of tumor

regions, followed by a SVM classifier to determine the tumor type. This combination ensures both spatial understanding of the tumor and a robust classification mechanism.

Our motivation stems from the desire to support the medical community with practical AI tools that can speed up diagnosis and reduce the burden on healthcare professionals, especially in regions where access to experienced radiologists may be limited.

1.6   Contributions

This thesis presents a complete pipeline that combines DL and ML techniques for brain tumor detection and classification using MRI scans. The primary goal was to build an accurate and practical system that can assist in identifying and distinguishing between Low-Grade Gliomas (LGG) and High-Grade Gliomas (HGG).

The key contributions of this work are as follows :

- **Tumor Segmentation with U-Net** : We trained a U-Net model to segment brain tumors from T2-weighted MRI images. This architecture was chosen for its proven effectiveness in biomedical image segmentation, allowing us to extract precise tumor regions. [4]

- **Tumor Classification using SVM** : After segmentation, we extracted features from the segmented tumor areas and used them to train a SVM classifier. This model classifies the tumor as either LGG or HGG, offering a straightforward yet powerful method for diagnosis.

- **Dataset Utilization and Visualization** : We utilized the BraTS dataset [5], specifically T2 modality images, and developed custom visualizations to help evaluate model predictions. These visualizations include overlays and individual class masks to clearly demonstrate the model's performance.

Chapitre 2

State of the Art

2.1   Medical Imaging in Brain Tumor Diagnosis

Magnetic Resonance Imaging (MRI) has emerged as the gold standard for brain tumor diagnosis due to its superior soft tissue contrast, high spatial resolution, and non-invasive nature [6]. Unlike other imaging modalities such as CT scans, MRI provides detailed structural information without exposing patients to ionizing radiation, making it particularly valuable for serial monitoring and treatment planning [7].

The multimodal nature of MRI is especially useful in brain tumor assessment, with each sequence highlighting different aspects of the tumor [8] :

- **T1-weighted (T1)** : Provides excellent anatomical detail and clearly delineates boundaries between gray and white matter. Tumors typically appear hypointense (darker) compared to surrounding tissue.
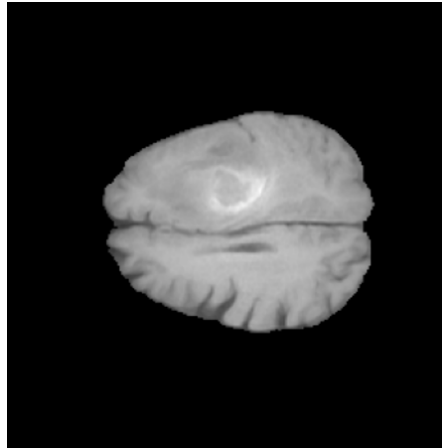
FIGURE 2.1 – Example of T1-weighted MRI sequence.

- **T1 with contrast enhancement (T1ce)** : After gadolinium administration, areas with disrupted blood-brain barrier (characteristic of high-grade tumors) enhance, appearing hyperintense and revealing the active tumor core.
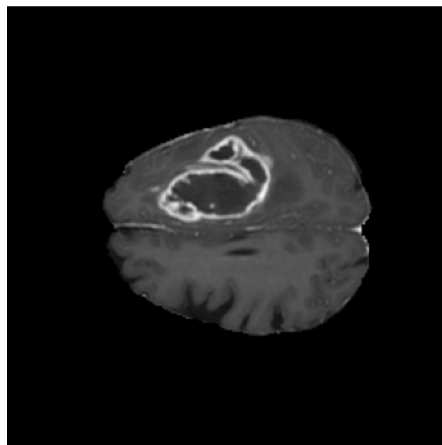

FIGURE 2.2 – Example of T1-weighted contrast-enhanced MRI sequence.

- **T2-weighted (T2)** : Highlights areas with increased water content, making it valuable for identifying edema and infiltrative tumor components. Tumors and surrounding edema appear hyperintense.
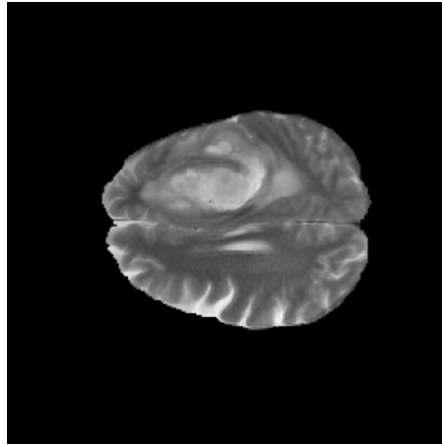
FIGURE 2.3 – Example of T2-weighted MRI sequence.

- **Fluid-Attenuated Inversion Recovery (FLAIR)** : Suppresses cerebrospinal fluid signals, enhancing the visibility of periventricular lesions and edema associated with tumors.
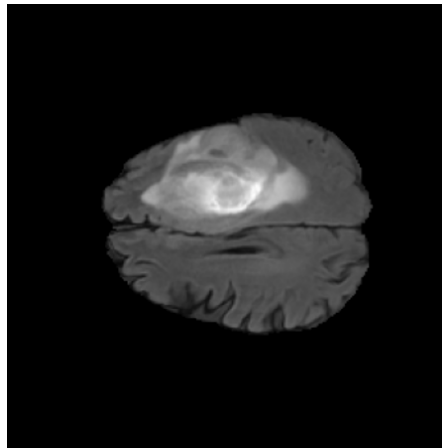
FIGURE 2.4 – Example of FLAIR MRI sequence.

Traditionally, neuroradiologists diagnose brain tumors by visually inspecting these multiple MRI sequences, mentally integrating information across modalities to determine tumor boundaries, assess grade, and identify critical structures [9]. This process is inherently subjective, time-consuming, and susceptible to inter-observer variability, with studies reporting considerable disagreement even among experienced radiologists These limitations have driven significant interest in developing computational approaches for automated and semi-automated tumor analysis.

2.2 The BraTS Dataset

The Brain Tumor Segmentation (BraTS) challenge and dataset represent a landmark initiative in standardizing the evaluation of brain tumor segmentation algorithms [7, 8]. Since its inception in 2012, BraTS has evolved into the most widely adopted benchmark for algorithm development and performance assessment in this domain [10].

The BraTS dataset is particularly valuable due to its :

- **Multimodal approach** : Each case includes four co-registered MRI sequences (T1, T1ce, T2, and FLAIR), enabling algorithms to leverage complementary information [11].
- **Standardized preprocessing** : All images undergo skull-stripping, resampling to isotropic 1mm³ voxels, and registration to a common anatomical template, reducing technical variability [8].
- **Expert annotations** : Each tumor is manually segmented by experienced neuroradiologists following a standardized protocol, with additional verification to ensure quality [7].
- **Multi-institutional data** : Images are acquired from multiple institutions using different scanners and protocols, promoting the development of robust algorithms [10].

The BraTS 2020 dataset, specifically, comprises 369 training cases and 125 validation cases, with each case including pixel-wise annotations for three tumor sub-regions [12] :

1. **Enhancing Tumor (ET)** : Areas showing hyperintensity in T1ce relative to T1
2. **Tumor Core (TC)** : Encompassing the ET, necrotic components, and non-enhancing tumor
3. **Whole Tumor (WT)** : Including all tumor tissues and surrounding edema

This hierarchical annotation structure enables the evaluation of algorithms at multiple levels of detail, from gross tumor detection to fine-grained sub-region delineation [8]. The BraTS datasets and associated challenges have catalyzed significant methodological advances, with performance metrics improving consistently year over year [13].

2.3   Traditional Machine Learning Approaches

Before the deep learning revolution, brain tumor segmentation and classification relied heavily on traditional machine learning techniques coupled with handcrafted feature extraction [14]. These approaches typically followed a pipeline of preprocessing, feature extraction, and classification using conventional machine learning algorithms.

Support Vector Machines (SVMs) were particularly popular for brain tumor classification and segmentation due to their strong theoretical foundations and effectiveness with high-dimensional data [15]. Zacharaki et al. [?] developed an SVM-based system that extracted 161 features including intensity, texture, and shape characteristics from multi-parametric MRI, achieving 85% accuracy in discriminating between different tumor types. Similarly, Reza and Iftekharuddin [?] combined texture features with fractal analysis and SVM classification to segment brain tumors, demonstrating competitive performance on earlier BraTS datasets.

Random Forest (RF) classifiers also showed promise due to their robustness to overfitting and ability to handle multi-class problems efficiently. Zikic et al. [?] employed RF with context-aware features for brain tumor segmentation, while Festa et al. [16] achieved strong results in the BraTS 2013 challenge using RF with handcrafted features. Tustison et al. [?] further refined this approach by incorporating an extensive feature set derived from multiple MRI sequences, winning the BraTS 2013 challenge.

K-Nearest Neighbors (k-NN) algorithms were explored by Simi and Joseph [?], who combined texture features with k-NN classification for tumor segmentation. Huang et al. [17] also investigated k-NN for brain tumor classification using multispectral MRI features.

Despite their success, these traditional approaches faced significant limitations :

- **Dependence on handcrafted features** : Their performance was heavily contingent on the quality of manually designed features, requiring substantial domain expertise [?].
- **Limited contextual understanding** : Most methods struggled to incorporate broader spatial context, often relying on voxel-wise or small-patch features [18].
- **Computational inefficiency** : Sequential processing of feature extraction followed by classification led to lengthy processing times impractical for clinical settings [?].
- **Suboptimal performance on heterogeneous tumors** : The high variability in tumor

appearance often challenged these methods, particularly for complex or atypical cases [7].

These limitations ultimately paved the way for the adoption of deep learning techniques, which could learn hierarchical features directly from data and better capture the complex patterns present in brain tumor images.

2.4   Deep Learning in Brain Tumor Segmentation

The advent of deep learning, particularly Convolutional Neural Networks (CNNs), has revolutionized brain tumor segmentation by enabling automatic hierarchical feature learning directly from imaging data [18]. This paradigm shift has eliminated the need for handcrafted features, dramatically improving segmentation accuracy and robustness.

Among deep learning architectures, U-Net has emerged as the cornerstone for medical image segmentation, including brain tumor analysis [?]. Its distinctive encoder-decoder structure with skip connections effectively combines localization and contextual information, preserving fine details while capturing broader tumor patterns. Urban et al. [?] were among the first to apply CNNs to brain tumor segmentation, while Pereira et al. [?] demonstrated that carefully designed CNN architectures could outperform traditional methods on the BraTS challenge.

Several U-Net variants have been developed specifically for brain tumor segmentation :

- **3D U-Net** : Çiçek et al. [19] extended the original 2D architecture to process volumetric data, better capturing the three-dimensional nature of tumors. Isensee et al. [20] further refined this approach, achieving top ranking in the BraTS 2018 challenge with a 3D U-Net variant.

- **U-Net++** : Zhou et al. [?] proposed a nested architecture with redesigned skip pathways to bridge the semantic gap between encoder and decoder features. Experimental results showed improved performance on several medical segmentation tasks, including brain tumors.

- **Attention U-Net** : Oktay et al. [?] incorporated attention gates to highlight relevant features and suppress irrelevant regions, improving segmentation accuracy particularly at tumor boundaries. Schlemper et al. [?] demonstrated the effectiveness of this approach

for multi-class tumor segmentation.

The performance of these deep learning models on BraTS challenges has improved consistently over time. In BraTS 2018, Myronenko [21] achieved exceptional results with an encoder-decoder architecture incorporating variational components. McKinley et al. [22] further advanced the field with an ensemble of 3D U-Nets, achieving Dice scores of 0.91, 0.83, and 0.78 for whole tumor, tumor core, and enhancing tumor, respectively. The BraTS 2020 challenge saw even more impressive results, with top-performing methods consistently achieving Dice scores above 0.90 for whole tumor segmentation [13].

The success of deep learning approaches for brain tumor segmentation can be attributed to several factors :

- **End-to-end training** : These models learn optimal features directly from data rather than relying on predetermined feature extractors [18].
- **Hierarchical feature representation** : The multiple convolutional layers capture features at various scales, from fine textures to global tumor shape [23].
- **Data augmentation techniques** : Strategies like random rotations, flipping, and elastic deformations effectively expand the training data, improving generalization [**?**].
- **Ensemble approaches** : Combining multiple models or architectures has proven particularly effective, mitigating individual model weaknesses [**?**].

Despite these advancements, challenges remain in achieving clinically acceptable performance across diverse patient populations and imaging protocols, driving continuous innovation in the field.

2.5 Tumor Classification Using Deep Features

While segmentation delineates tumor boundaries, classification determines tumor type and characteristics—a critical aspect of diagnosis and treatment planning. Modern approaches increasingly leverage deep features, either independently or in conjunction with traditional machine learning classifiers like Support Vector Machines (SVMs).

Pretrained Convolutional Neural Networks (CNNs) have proven extremely effective as feature extractors for brain tumor classification. Afshar et al. [24] employed a modified ResNet

architecture to extract deep features from brain MRI, achieving 93.68% accuracy in classifying tumors into different grades. Similarly, Deepak and Ameer [25] utilized DenseNet for feature extraction followed by SVM classification, reporting improved performance compared to traditional methods. Sajjad et al. [?] extended this approach by fine-tuning VGG-19 on brain tumor images, extracting features from intermediate layers for subsequent classification.

The integration of SVMs with deep features represents a particularly successful hybrid approach. Talo et al. [?] extracted features from ResNet-50 and classified them using SVMs with different kernel functions, achieving 97.2% accuracy in discriminating between tumor types. Cheng et al. [26] combined hand-crafted and deep features with SVM classification, demonstrating superior performance over either feature type alone. Kumar et al. [27] further refined this methodology by incorporating feature selection techniques before SVM classification, reducing dimensionality while maintaining discriminative power.

Convolutional Autoencoders (CAEs) offer an alternative approach to feature learning, particularly valuable when labeled data is scarce. Nalepa et al. [28] employed a CAE to learn unsupervised representations from brain MRI, using these features with an SVM classifier for tumor grading. Khawaldeh et al. [29] similarly used CAEs for feature extraction followed by a non-linear SVM, achieving 91.2% classification accuracy. Sun et al. [?] combined CAE-derived features with a random forest classifier, demonstrating robust performance even with limited training examples.

Feature fusion techniques have emerged as a powerful strategy to combine complementary information. Amin et al. [30] developed a multi-modal fusion approach combining features from different MRI sequences, improving classification accuracy by 4-6% compared to single-modality methods. Zhou et al. [?] proposed a hierarchical feature fusion framework integrating both low-level and high-level features from multiple CNN layers, achieving 96.7% accuracy in glioma grading. Yang et al. [?] introduced a multi-stream architecture extracting and fusing features from different MRI modalities, demonstrating superior performance over single-stream networks.

The success of these deep feature-based approaches stems from their ability to :
- Capture complex, high-level tumor characteristics not easily described by handcrafted features [24]

- Leverage transfer learning from models pre-trained on large datasets [?]
- Combine the representational power of deep learning with the strong theoretical foundations of classical classifiers like SVM [?]

The integration of deep features with traditional classifiers represents a bridge between conventional and modern approaches, often yielding superior performance compared to either method used in isolation.

2.6 Multiclass Tumor Region Segmentation

Accurate delineation of different tumor sub-regions represents one of the most challenging aspects of brain tumor analysis, requiring discrimination between biologically distinct components that may appear visually similar [8]. The BraTS challenge specifically evaluates algorithms on their ability to segment three tumor sub-components : Enhancing Tumor (ET), Tumor Core (TC), and Whole Tumor (WT).

Multi-class tumor segmentation approaches have evolved significantly in recent years. Zhao et al. [?] proposed a multi-scale CNN architecture specifically designed to address the hierarchical nature of tumor sub-regions, achieving meaningful improvements in enhancing tumor segmentation. Wang et al. [?] developed a cascaded approach where initial whole tumor segmentation guided subsequent sub-region delineation, reducing false positives in non-tumor regions. Kamnitsas et al. [23] introduced DeepMedic, a dual-pathway 3D CNN architecture that simultaneously processed input at different resolutions, effectively capturing both fine details and broader contextual information.

Several specific challenges complicate multi-class tumor segmentation :

- **Data imbalance** : Tumor sub-regions occupy a small fraction of the brain volume, creating severe class imbalance. Myronenko [21] addressed this through a combination of weighted loss functions and focal loss, specifically targeting challenging boundary regions. Isensee et al. [20] employed a region-based training strategy that oversampled patches containing tumor sub-regions, achieving more balanced training.
- **Overlapping regions** : The hierarchical nature of tumor sub-regions (ET $\subset$ TC $\subset$ WT) creates inherent overlap that can confuse classification systems. McKinley et al. [22] tackled this through a cascaded architecture with hierarchical loss functions that explicitly

modeled these relationships. Jiang et al. [31] proposed a multi-task learning framework where auxiliary tasks helped distinguish overlapping regions.

- **Variable appearance** : Tumor sub-regions show considerable variability across patients and can mimic other pathologies. Zhou et al. [**?**] employed attention mechanisms to focus on discriminative features for each sub-region, while Wang et al. [**?**] leveraged ensemble techniques to improve robustness to appearance variations.

- **Need for multi-modal integration** : Different tumor sub-regions are best visualized in specific MRI sequences (e.g., enhancing tumor in T1ce, edema in FLAIR). Shen et al. [**?**] developed multi-encoder architectures that extracted sequence-specific features before fusion, while Chen et al. [32] employed attention-based fusion to weight the contribution of each modality dynamically.

Performance metrics for multi-class segmentation vary considerably across sub-regions. While whole tumor segmentation typically achieves Dice scores around 0.90 in recent BraTS challenges, enhancing tumor segmentation remains more challenging with top performances around 0.80-0.85 [12]. This performance gap reflects the smaller size and more variable appearance of enhancing components compared to the whole tumor region.

Recent work has increasingly focused on uncertainty estimation in multi-class segmentation. Mehta et al. [33] incorporated Bayesian neural networks to provide uncertainty maps alongside segmentations, highlighting regions where the model lacked confidence. Eaton-Rosen et al. [34] similarly demonstrated the value of uncertainty quantification for clinical decision support, particularly for ambiguous tumor boundaries.

The continued advancement of multi-class tumor segmentation approaches promises to improve diagnostic accuracy and treatment planning by providing more detailed characterization of tumor heterogeneity.

2.7   Challenges in the Field

Despite significant progress, several persistent challenges continue to impact the development and clinical translation of automated brain tumor analysis systems.

Class imbalance remains a fundamental issue in both segmentation and classification tasks.

Brain tumors typically occupy less than 1% of the total brain volume, creating extreme imbalance that can bias models toward the majority (healthy tissue) class [**?**]. While techniques such as patch-based training [18], specialized loss functions [20], and data augmentation [**?**] have partially addressed this issue, performance on smaller tumor sub-regions (particularly enhancing tumor) continues to lag behind whole tumor segmentation.

The **interpretability of deep models** presents another significant hurdle, particularly for clinical adoption. The "black box" nature of deep learning approaches creates reluctance among clinicians to trust automated segmentations without understanding the underlying decision process [35]. Recent work by Natekar et al. [36] has explored visualization techniques to highlight features influencing segmentation decisions, while Lucieri et al. [37] demonstrated the value of attention maps for explaining tumor classification outcomes. Despite these efforts, creating truly interpretable deep learning systems remains an open challenge.

Generalization across different MRI scanners and patients continues to limit clinical applicability. Models trained on specific datasets often experience performance degradation when applied to images acquired with different hardware, field strengths, or acquisition parameters [7]. Zech et al. [**?**] documented this domain shift problem in medical imaging, while Kamnitsas et al. [23] proposed domain adaptation techniques to mitigate its effects. More recently, Shaw et al. [**?**] explored adversarial domain adaptation specifically for brain tumor segmentation, showing promising results in cross-scanner generalization.

The **lack of labeled data** remains a fundamental limitation, particularly for rare tumor types or unusual presentations. While the BraTS dataset has grown substantially, it still represents a fraction of the true biological variability of brain tumors [10]. Semi-supervised approaches by Sedai et al. [**?**] leverage unlabeled data to improve generalization, while Zhao et al. [**?**] demonstrated promising results with data-efficient few-shot learning techniques. Transfer learning approaches by Ghafoorian et al. [38] have also shown potential in adapting pre-trained models to limited target datasets.

Additional challenges include :

- **Computational efficiency** : 3D deep learning models often require substantial computational resources beyond what's available in many clinical settings [23].
- **Longitudinal analysis** : Most current approaches treat each time point independently,

missing the opportunity to leverage temporal information in patient monitoring [**?**].

- **Integration with other data types** : Combining imaging with clinical, genomic, and pathological data remains challenging despite its potential to improve diagnostic accuracy [10].

- **Clinically relevant evaluation metrics** : Standard technical metrics like Dice coefficients may not directly translate to clinical utility, creating a disconnect between research advances and clinical impact [39].

Addressing these challenges will require multidisciplinary collaboration between computer scientists, medical imaging experts, and clinicians to develop solutions that are not only technically sophisticated but also clinically relevant and practically deployable.

Chapitre 3

Le format

Chapitre 4

Figures, tableaux et références

Chapitre 5

Conclusion générale (2 pages max)

Références

[1] National Cancer Institute, "Brain tumors," https://www.cancer.gov/types/brain, 2024, accessed : 2025-04-15.

[2] D. N. Louis, A. Perry, G. Reifenberger *et al.*, "The 2016 world health organization classification of tumors of the central nervous system : a summary," *Acta neuropathologica*, vol. 131, no. 6, pp. 803–820, 2016.

[3] Mayo Clinic, "Brain tumor overview," https://www.mayoclinic.org/diseases-conditions/brain-tumor, 2024, accessed : 2025-04-15.

[4] O. Ronneberger, P. Fischer, and T. Brox, "U-net : Convolutional networks for biomedical image segmentation," in *International Conference on Medical image computing and computer-assisted intervention*. Springer, 2015, pp. 234–241.

[5] U. Baid, S. Ghodasara, S. Mohan, M. Bilello, E. Calabrese, E. Colak, K. Farahani, J. Kalpathy-Cramer, F. Kitamura, S. Pati, S. Pereira, P. Preetha, S. Reza, C. Sako, A. Sharma, C. Silva, J. Solomon, P. Vu, C. Yogananda, A. Flanders, C. Davatzikos, R. Colen, and S. Bakas, "The multimodal brain tumor image segmentation benchmark (brats) 2020 : Validating image segmentation and outcome prediction algorithms," in *International MICCAI Brainlesion Workshop*. Springer, 2021, pp. 133–145.

[6] S. Bauer, R. Wiest, L. P. Nolte, and M. Reyes, "A survey of MRI-based medical image analysis for brain tumor studies," *Physics in Medicine & Biology*, vol. 58, no. 13, p. R97, 2013.

[7] B. H. Menze, A. Jakab, S. Bauer, J. Kalpathy-Cramer, K. Farahani, J. Kirby *et al.*, "The multimodal brain tumor image segmentation benchmark (BRATS)," *IEEE Transactions on Medical Imaging*, vol. 34, no. 10, pp. 1993–2024, 2015.

[8] S. Bakas, M. Reyes, A. Jakab, S. Bauer, M. Rempfler, A. Crimi *et al.*, "Identifying the best machine learning algorithms for brain tumor segmentation, progression assessment, and overall survival prediction in the BRATS challenge," *arXiv preprint arXiv :1811.02629*, 2018.

[9] L. M. DeAngelis, "Brain tumors," *New England Journal of Medicine*, vol. 344, no. 2, pp. 114–123, 2001.

[10] S. Bakas, H. Akbari, A. Sotiras, M. Bilello, M. Rozycki, J. Kirby *et al.*, "Segmentation labels and radiomic features for the pre-operative scans of the TCGA-GBM collection," The Cancer Imaging Archive, 2019.

[11] ——, "Advancing the cancer genome atlas glioma MRI collections with expert segmentation labels and radiomic features," *Scientific Data*, vol. 4, p. 170117, 2017.

[12] S. Bakas *et al.*, "The multimodal brain tumor image segmentation benchmark (BRATS)," *IEEE Transactions on Medical Imaging*, vol. 39, no. 12, pp. 3934–3947, 2020.

[13] F. Isensee, P. F. Jaeger, S. A. Kohl, J. Petersen, and K. H. Maier-Hein, "nnU-Net : A self-configuring method for deep learning-based biomedical image segmentation," *Nature Methods*, vol. 18, no. 2, pp. 203–211, 2021.

[14] N. Gordillo, E. Montseny, and P. Sobrevilla, "State of the art survey on MRI brain tumor segmentation," *Magnetic Resonance Imaging*, vol. 31, no. 8, pp. 1426–1438, 2013.

[15] S. Bauer, L. P. Nolte, and M. Reyes, "Fully automatic segmentation of brain tumor images using support vector machine classification in combination with hierarchical conditional random field regularization," in *International Conference on Medical Image Computing and Computer-Assisted Intervention*, 2011, pp. 354–361.

[16] J. Festa, S. Pereira, J. A. Mariz, N. Sousa, and C. A. Silva, "Automatic brain tumor segmentation of multi-sequence MR images using random decision forests," in *Proceedings of NCI-MICCAI BRATS*, 2013, pp. 23–26.

[17] M. Huang, W. Yang, Y. Wu, J. Jiang, W. Chen, and Q. Feng, "Brain tumor segmentation based on local independent projection-based classification," *IEEE Transactions on Biomedical Engineering*, vol. 61, no. 10, pp. 2633–2645, 2014.

[18] M. Havaei, A. Davy, D. Warde-Farley, A. Biard, A. Courville, Y. Bengio *et al.*, "Brain tumor segmentation with deep neural networks," *Medical Image Analysis*, vol. 35, pp. 18–31, 2017.

[19] Ö. Çiçek, A. Abdulkadir, S. S. Lienkamp, T. Brox, and O. Ronneberger, "3D U-Net : Learning dense volumetric segmentation from sparse annotation," in *International Conference on Medical Image Computing and Computer-Assisted Intervention*, 2016, pp. 424–432.

[20] F. Isensee, P. Kickingereder, W. Wick, M. Bendszus, and K. H. Maier-Hein, "No new-net," in *International MICCAI Brainlesion Workshop*, 2018, pp. 234–244.

[21] A. Myronenko, "3D MRI brain tumor segmentation using autoencoder regularization," in *International MICCAI Brainlesion Workshop*, 2018, pp. 311–320.

[22] R. McKinley, R. Meier, and R. Wiest, "Ensembles of densely-connected CNNs with label-uncertainty for brain tumor segmentation," in *International MICCAI Brainlesion Workshop*, 2019, pp. 456–465.

[23] K. Kamnitsas, C. Ledig, V. F. Newcombe, J. P. Simpson, A. D. Kane, D. K. Menon *et al.*, "Efficient multi-scale 3D CNN with fully connected CRF for accurate brain lesion segmentation," *Medical Image Analysis*, vol. 36, pp. 61–78, 2017.

[24] P. Afshar, A. Mohammadi, and K. N. Plataniotis, "Brain tumor type classification via capsule networks," in *IEEE International Conference on Image Processing (ICIP)*, 2019, pp. 1570–1574.

[25] S. Deepak and P. M. Ameer, "Brain tumor classification using deep CNN features via transfer learning," *Computers in Biology and Medicine*, vol. 111, p. 103345, 2019.

[26] J. Cheng, W. Yang, M. Huang, W. Huang, J. Jiang, Y. Zhou *et al.*, "Retrieval of brain tumors by adaptive spatial pooling and fisher vector representation," *PLoS One*, vol. 10, no. 9, p. e0137023, 2015.

[27] A. Kumar, A. Ashok, and M. A. Ansari, "Brain tumor classification using hybrid model of PSO-SVM and ELM," in *International Conference on Computer Communication and Informatics*, 2019, pp. 1–6.

[28] J. Nalepa, M. Marcinkiewicz, and M. Kawulok, "Data augmentation for brain-tumor segmentation : A review," *Frontiers in Computational Neuroscience*, vol. 13, p. 83, 2019.

[29] S. Khawaldeh, U. Pervaiz, A. Rafiq, and R. S. Alkhawaldeh, "Noninvasive grading of glioma tumor using magnetic resonance imaging with convolutional neural networks," *Applied Sciences*, vol. 8, no. 1, p. 27, 2018.

[30] J. Amin, M. Sharif, M. Yasmin, and S. L. Fernandes, "A distinctive approach in brain tumor detection and classification using MRI," *Pattern Recognition Letters*, vol. 139, pp. 118–127, 2020.

[31] Z. Jiang, C. Ding, M. Liu, and D. Tao, "Two-stage cascaded U-Net : 1st place solution to BraTS challenge 2019 segmentation task," in *International MICCAI Brainlesion Workshop*, 2020, pp. 231–241.

[32] W. Chen, B. Liu, S. Peng, J. Sun, and X. Qiao, "S3D-UNet : Separable 3D U-Net for brain tumor segmentation," in *International MICCAI Brainlesion Workshop*, 2019, pp. 358–368.

[33] R. Mehta, T. Christinck, T. Nair, P. Lemaitre, D. Arnold, and T. Arbel, "Propagating uncertainty across cascaded medical imaging tasks for improved deep learning inference," in *Uncertainty for Safe Utilization of Machine Learning in Medical Imaging*, 2020, pp. 23–32.

[34] Z. Eaton-Rosen, F. Bragman, S. Ourselin, M. J. Cardoso, and M. Modat, "Improving data augmentation for medical image segmentation," in *Medical Imaging with Deep Learning Conference*, 2018.

[35] A. Holzinger, C. Biemann, C. S. Pattichis, and D. B. Kell, "What do we need to build explainable AI systems for the medical domain ?" *arXiv preprint arXiv :1712.09923*, 2017.

[36] P. Natekar, A. Kori, and G. Krishnamurthi, "Dem," 2020.

[37] A. Lucieri, M. N. Bajwa, S. A. Braun, M. I. Malik, A. Dengel, and S. Ahmed, "On interpretability of deep learning based skin lesion classifiers using concept activation vectors," in *International Joint Conference on Neural Networks*, 2020, pp. 1–10.

[38] M. Ghafoorian, A. Mehrtash, T. Kapur, N. Karssemeijer, E. Marchiori, M. Pesteie *et al.*, "Transfer learning for domain adaptation in MRI : Application in brain lesion segmentation," in *International Conference on Medical Image Computing and Computer-Assisted Intervention*, 2017, pp. 516–524.

[39] L. Maier-Hein, M. Eisenmann, A. Reinke, S. Onogur, M. Stankovic, P. Scholz *et al.*, "Why rankings of biomedical image analysis competitions should be interpreted with care," *Nature Communications*, vol. 9, no. 1, pp. 1–13, 2018.