People's Democratic Republic of Algeria
Ministry of Higher Education and Scientific Research
University Of Ferhat Abbas
Faculty of Sciences

Ferhat ABBAS University of Setif

Domain: Mathematics and Computer Sciences

Specialty: F3I

Presented by: Hiba DJARI and Malak LAMARA

Subject

Deep Learning Models for Brain Cancer Segmentation and Prognostic Analysis

The jury:

Pr. Abdelouahab MOUSSAOUI	President	UFAS1 SETIF
Dr. Skander HAMDI	Supervisor	UFAS1 SETIF
Dr. Imene ZENBOUT	Examiner	UFAS1 SETIF

Academic Year: 2024/2025

Abstract

Deep Learning (DL) has introduced transformative potential in medical diagnostics, particularly in oncology, where complex tumor structures present significant challenges for treatment planning. The accurate segmentation of brain tumors from Magnetic Resonance Imaging (MRI) is a critical first step, and recent advancements in DL have greatly enhanced the efficiency and reliability of this process. By integrating these precise segmentation outputs with clinical and genetic data, prognostic analysis can be substantially improved, paving the way for more accurate tumor prediction and robust clinical decision support.

This thesis aims to develop and evaluate a comprehensive pipeline for brain tumor analysis, from segmentation to survival prediction. It focuses on comparing advanced DL architectures for segmenting brain tumors and explores the adaptation of large-scale, general-purpose vision models for this specialized medical task. The ultimate goal is to fuse imaging features with clinical and genetic data to accurately estimate patient survival probability and stratify risk levels, thereby enhancing personalized treatment strategies.

This work offers a thorough exploration of both established and cutting-edge DL models for brain tumor segmentation and prognosis. The first contribution is a comparative analysis of segmentation models, including a standard U-Net, a DeepResUNet, and a VGG19-based U-Net, alongside foundational models like a fine-tuned Segment Anything Model (SAM) and the specialized Medical Segment Anything Model (MedSAM). The results underscored the effectiveness of MedSAM, which demonstrated superior performance . The second contrirbution introduces a prognostic analysis pipeline that leverages features extracted from the segmentation masks. This pipeline proved highly effective, with the Support Vector Machine (SVM) model showing notable success in accurately identifying high-risk patients, while the XGBoost model demonstrated strong predictive power for classifying low-risk patients.

Overall, these contributions validate a powerful, integrated approach for brain cancer analysis. The findings confirm that leveraging both CNN-based architectures and fine-tuned foundational models can yield highly accurate tumor delineations. Furthermore, the successful integration of these segmentation results into a prognostic pipeline demonstrates the critical role of automated image analysis in fostering personalized and more effective clinical management of brain tumors.

Contents