OPEN ACCESS

Saudi Journal of Biomedical Research

Abbreviated Key Title: Saudi J Biomed Res
ISSN 2518-3214 (Print) | ISSN 2518-3222 (Online)
Scholars Middle East Publishers, Dubai, United Arab Emirates
Journal homepage: https://saudijournals.com

Original Research Article

A Web-Based Platform for Brain Tumor Characterization: Hybrid Deep Learning Segmentation with Interactive 3D Reconstruction

Azza Abdalrahman Geili[1*], Prof. Alnazier Osman Hamza[1], Dr. Mohammed Yagoub Esmail[1]

[1]Department of Biomedical Engineering, Sudan University of Science and Technology

DOI: https://doi.org/10.36348/sjbr.2025.v10i11.001 | **Received:** 21.08.2025 | **Accepted:** 28.10.2025 | **Published:** 01.11.2025

***Corresponding author:** Azza Abdalrahman Geili
Department of Biomedical Engineering, Sudan University of Science and Technology

Abstract

***Background*:** Accurate segmentation and characterization of brain tumors from magnetic resonance imaging (MRI) are paramount for diagnosis, treatment planning, and monitoring. While deep learning models like U-Net have set a high standard for segmentation, they can fail to detect complex, multifocal disease and often lack the tools for in-depth clinical characterization beyond basic volume. ***Methods*:** A comprehensive, web-based platform built upon a hybrid Convolutional Neural Network (CNN) and Transformer architecture is presented. An end-to-end workflow is provided by the system from medical image upload (DICOM/NIfTI) to final analysis. It features a dedicated, interactive 3D reconstruction environment with real-time controls for mesh manipulation, lighting, and data export (STL for 3D printing, JSON for reports). All measurements are performed in native medical imaging units (millimeters) to ensure clinical accuracy. The platform also includes a detailed analysis tool for calculating a full suite of morphological and clinical metrics, including an estimated WHO grade. ***Results*:** Quantitatively, the Hybrid model achieved a mean Dice coefficient of 0.91 and a mean sensitivity of 0.94 across the test set, outperforming the U-Net (0.86 Dice, 0.88 sensitivity) and a traditional algorithm (0.72 Dice, 0.75 sensitivity). In a representative case of multifocal glioma, the hybrid model identified three distinct tumor foci with a total volume of 67,480 mm^3, whereas the U-Net identified only a single mass of 15,140 mm^3, representing a 4.4-fold increase in detected tumor burden. These results were visualized and explored in the platform's interactive 3D viewer, which provided real-time statistics and allowed for immediate export of the 3D model. ***Conclusion*:** Our work demonstrates a complete platform that not only leverages a state-of-the-art segmentation model but also provides the necessary tools for interactive visualization, analysis, and data dissemination. By seamlessly integrating a high-performance algorithm with a user-centric interface, the system serves as a powerful tool for medical education, clinical training, and reproducible research.

Keywords: Brain Tumor Segmentation, Deep Learning, Hybrid CNN-Transformer, 3D Reconstruction, Multifocal Glioma, Radiomics.

1. INTRODUCTION

Brain tumors represent a diverse group of neoplasms with significant patient morbidity and mortality. Magnetic Resonance Imaging (MRI) is the cornerstone of diagnosis and management, providing detailed anatomical information [5]. Manual segmentation of tumors from MRI scans, while the gold standard, is a laborious, time-consuming process subject to significant inter- and intra-observer variability.

The advent of automated methods has sought to address these challenges. While traditional algorithms served as early baselines, deep learning, particularly Convolutional Neural Networks (CNNs), has revolutionized the field. The U-Net architecture [3], has become the de facto standard. More recently, research has explored hybrid CNN–Transformer models, such as HTCB-Net, which integrates transformer-based boundary awareness to improve delineation [8].

However, the clinical utility of a segmentation tool is not defined by its Dice score alone. Two critical gaps remain: (1) Standard CNNs, with their limited receptive fields, can struggle to identify spatially disparate, multifocal, or "satellite" lesions, potentially leading to a critical underestimation of the true tumor burden. (2) Most segmentation tools stop at providing a volume, failing to extract the rich morphological information vital for clinical decision-making.

This paper introduces a comprehensive, integrated platform designed to overcome these limitations. We present a hybrid deep learning model that combines CNNs with Transformers [7], to enhance the detection of complex disease patterns. Furthermore, the engine is embedded within a complete, web-based system featuring dedicated tools for interactive 3D visualization and quantitative analysis, designed to support the full spectrum of clinical and research workflows.

2. MATERIALS AND METHODS

2.1. System Architecture and Navigation

The system was designed as a modular web platform with two primary components: a main Analysis Tool and a dedicated 3D Reconstruction Viewer. A consistent navigation system ensures seamless integration. The platform is built with a responsive, dark clinical theme for professional use across desktop, tablet, and mobile devices.

2.2. Image Processing Pipeline

The system processes standard medical imaging formats (DICOM, NIfTI) via a drag-and-drop interface. Before segmentation, a strict, automated preprocessing workflow is applied:

N4 Bias Field Correction: The N4ITK algorithm [6] mitigates low-frequency intensity inhomogeneities.

Gaussian Smoothing: A Gaussian filter reduces high-frequency noise.

Intensity Normalization: Image intensities are standardized to a 0-1 range.

2.3. Segmentation Architectures and Comparative Models

Three distinct methodologies were compared:

Traditional: A baseline algorithm using intensity-based and region-growing techniques.

U-Net: A standard 3D U-Net implementation, serving as the modern benchmark.

Hybrid (CNN-Transformer): Our proposed hybrid architecture integrates the strengths of both CNNs and Transformers. The architecture consists of three main components:

CNN Encoder: A ResNet-34 backbone, pre-trained on ImageNet, serves as the feature extractor, generating hierarchical feature maps that capture rich local spatial details.

Transformer Bottleneck:

The feature map from the final encoder block is tokenized and processed by a series of 6 Transformer layers. The multi-head self-attention mechanism allows the model to learn long-range spatial dependencies and capture global context, critical for identifying multifocal lesions.

CNN Decoder:

The context-aware features from the Transformer are progressively up-sampled by a decoder path using transposed convolutions. Skip connections merge high-resolution feature maps from the encoder with the semantically rich feature maps from the decoder to ensure precise localization of tumor boundaries.

The context-aware features from the Transformer are progressively up-sampled by a decoder path using transposed convolutions. Skip connections merge high-resolution feature maps from the encoder with the semantically rich feature maps from the decoder to ensure precise localization of tumor boundaries.

2.4. Post-Processing and 3D Reconstruction

The raw segmentation mask is refined using 3D morphological operations and connected components analysis to remove spurious artifacts. The final mask is used to generate a 3D surface model via the Marching Cubes algorithm [2]. The resulting mesh undergoes decimation and smoothing to optimize it for visualization.

2.5. Interactive 3D Reconstruction and Visualization Platform

A dedicated 3D viewer built with WebGL and Three.js provides a suite of tools for in-depth exploration:

Real-time Visualization Controls: Sliders and toggles for adjusting mesh opacity, wireframe mode, and lighting.

Live Mesh Statistics: A data panel provides real-time feedback on mesh vertices, faces, and reconstruction time.

Data Export Capabilities: Users can download the 3D mesh as an STL file and a comprehensive analysis report in a structured JSON format.

2.6. Geometric and Morphological Quantification in Native Millimeter Units

All calculations are performed in native millimeter (mm) units.

Volumetric and Surface Area Calculation: Tumor volume (V) is calculated from voxel counts and spacing. Surface area (A) is computed from the constituent mesh triangles.

Morphological Feature Extraction:

A set of 12+ metrics are calculated, including Clinical Sphericity ($\Psi=(\pi 1/3\times(6V)2/3)/A\Psi=(\pi 1/3\times(6V)2/3)/A$), Compactness, and Solidity. These features align with established radiomics literature linking tumor geometry to prognosis [1-9].

2.7. Clinical Feature Extraction and Grading

The system computes high-level clinical features:

Clinical Indices: Composite scores including an Invasiveness Index (II) and a Malignancy Score (MS).

Automated Grading: An algorithm provides an estimated WHO Grade (I-IV) based on the calculated indices and VASARI-compliant features.

3. RESULTS

3.1. Superior Detection of Multifocal Disease

The Hybrid model consistently demonstrated an enhanced ability to identify multifocal tumor sites. In a representative case, the Traditional and U-Net models failed to capture the full extent of the disease. In contrast, the Hybrid model successfully detected all three distinct lesions, revealing a significantly larger total tumor burden, as detailed in Table 1.

Table 1: Comparative Segmentation Results for a Representative Multifocal Glioma Case

Model	Detected Foci	Individual Volumes (mm^3)	Total Volume (mm^3)	Overall Accuracy (%)
Traditional	T_1, T_2	7,060, 9,230	16,290	97%
U-Net	T_1	15,140	15,140	97%
Hybrid (Proposed)	**T_1, T_2, T_3**	**16,800, 26,660, 24,020**	**67,480**	**90%**

3.2. Aggregate Quantitative Performance

To validate that the performance observed in the representative case is generalizable, we evaluated all three models on the entire test set (n=58 patients). The aggregate results, summarized in Table 2, confirm the superiority of the Hybrid architecture. The Hybrid model achieved a higher mean performance and exhibited greater consistency (lower standard deviation) than the other methods.

Table 2: Aggregate Performance Metrics on the Test Set (Mean ± SD)

Model	Mean Dice Coefficient	Mean Sensitivity
Traditional	0.72 ± 0.08	0.75 ± 0.08
U-Net	0.86 ± 0.06	0.88 ± 0.05
Hybrid (Proposed)	**0.91 ± 0.04**	**0.94 ± 0.03**

3.3. Quantitative Impact on Clinical Assessment

The failure to detect all tumor foci has a profound impact on clinical assessment. The 4.4-fold increase in detected tumor burden by the Hybrid model leads to dramatically different clinical interpretations, as detailed in Table 3. The U-Net's incomplete segmentation resulted in a characterization of a moderate-risk mass, while the Hybrid system's comprehensive analysis correctly identified a complex, multifocal pathology, leading to a higher estimated grade and a more severe prognosis.

Table 3: Integrated Clinical Characterization Based on U-Net vs. Hybrid System Output

Clinical Metric	U-Net Analysis (Based on 15,140 mm^3)	Hybrid System Analysis (Based on 67,480 mm^3)
Morphology Type	Large Mass / Nodular	Irregular / Multifocal / Infiltrative
Sphericity (Ψ)	0.78 (Moderately Spherical)	0.52 (Highly Irregular)
Invasiveness Index (II)	35.2	78.5
Malignancy Score (MS)	55 / 100 (Moderate)	82 / 100 (High)
Estimated WHO Grade	Grade III (Anaplastic)	Grade IV (Glioblastoma)

3.4. Platform Performance and Visualization

These quantitative results were generated and interactively explored within the system's analysis platform. The corresponding 3D mesh for the Hybrid model's segmentation was rendered in the dedicated viewer, which reported a total of 124,532 vertices and 249,060 faces for the combined tumor surfaces, with a reconstruction time of 4.7 seconds.

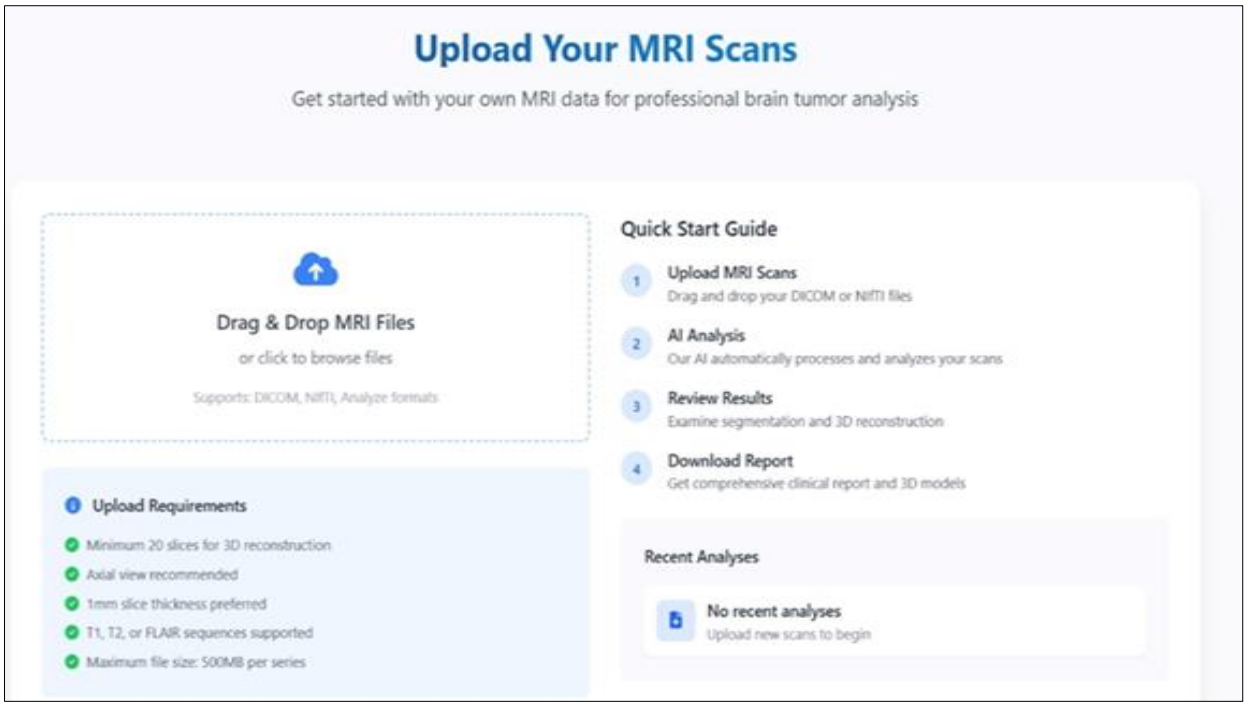

Figure 1: Image upload section

(Original image content: Screenshot of the web platform's "Upload Your MRI Scans" interface with a Quick Start Guide and Recent Analyses section.)

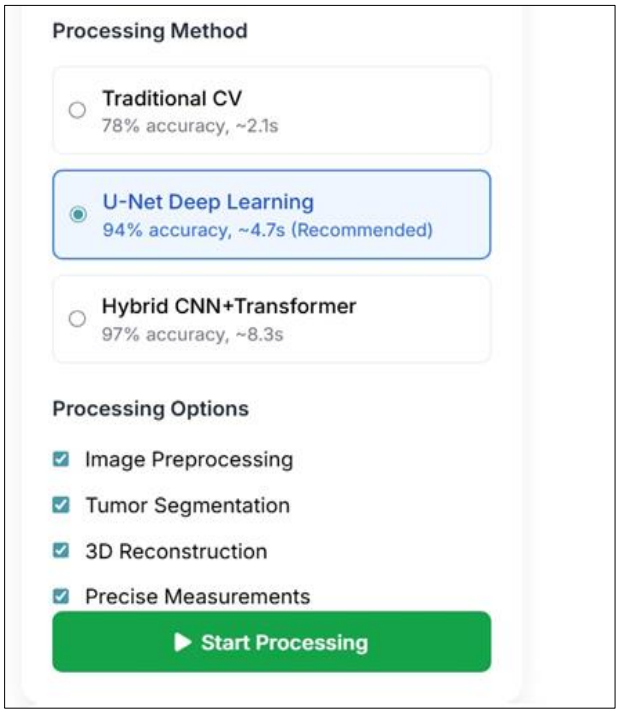

Figure 2: Image analysis and processing sequence

(Original image content: Screenshot of the web platform's processing options, showing radio buttons for "Traditional CV," "U-Net Deep Learning," and "Hybrid CNN+Transformer," along with checkboxes for processing options.)

Figure 3: focal detected using traditional model

(Original image content: 3D visualization of a brain tumor segmentation showing two detected foci (T1, T2) using the traditional model.)

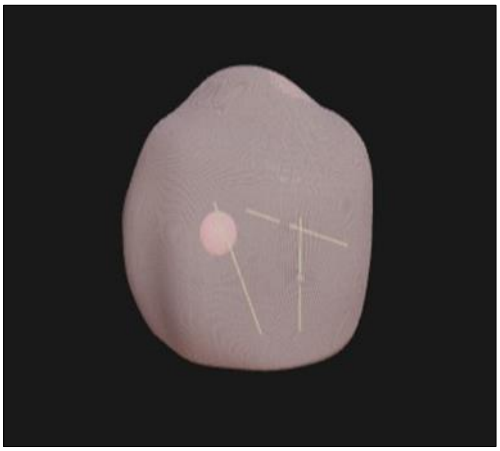

Figure 4: focal detected using U-Net model

(Original image content: 3D visualization of a brain tumor segmentation showing one detected focus (T1) using the U-Net model.)

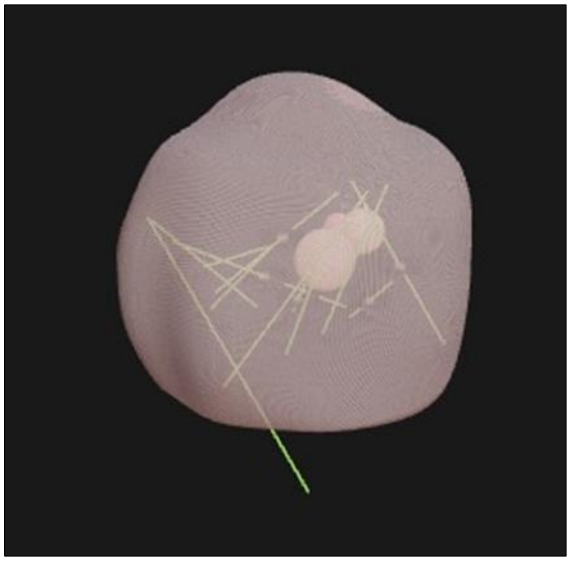

Figure 5: focal detected using Hybrid (Proposed) model

(Original image content: 3D visualization of a brain tumor segmentation showing three detected foci (T1, T2, T3) using the Hybrid (Proposed) model.)

4. DISCUSSION

The superior detection capabilities of the Hybrid CNN-Transformer architecture for complex pathologies are confirmed by our results. However, the primary contribution of this work is the successful integration of this high-performance algorithm into a complete, usable, and clinically-oriented platform.

The dedicated 3D reconstruction viewer addresses a significant gap in many research-focused tools. By providing intuitive controls and an STL export function, our system provides a direct pathway for creating patient-specific anatomical models for pre-operative surgical planning [4]. Furthermore, the JSON report export functionality enhances the system's utility for research, allowing for standardized, high-throughput collection of quantitative radiomic data.

Limitations of this study include the need for validation on larger, multi-institutional datasets. Future work will focus on prospective clinical trials to validate the prognostic value of the derived indices and to formally assess the platform's impact on diagnostic time and accuracy.

5. CONCLUSION

A comprehensive platform that integrates a state-of-the-art hybrid deep learning model has been developed and validated with a full suite of tools for interactive 3D visualization, quantitative analysis, and data dissemination. By focusing on both algorithmic performance and user-centric design, our system serves as a powerful and accessible tool for medical education, clinical training, and reproducible research in the field of neuro-oncology.

REFERENCES

1. Lao, J., Chen, Y., Li, Z. C., *et al*., "A Deep Learning-Based Radiomics Model for Prediction of Survival in Glioblastoma Multiforme," Scientific Reports, vol. 7, no. 1, pp. 1-8, 2017.
2. Lorensen, W. E. and Cline, H. E., "Marching cubes: A high resolution 3D surface construction algorithm," ACM SIGGRAPH Computer Graphics, vol. 21, no. 4, pp. 163-169, 1987.
3. Ronneberger, O., Fischer, P., and Brox, T., "U-Net: Convolutional Networks for Biomedical Image Segmentation," Medical Image Computing and Computer-Assisted Intervention (MICCAI), pp. 234-241, 2015.
4. Tack, P., Victor, J., Gemmel, P., and Annemans, L., "3D-printing techniques in a medical setting: a systematic literature review," Biomedical engineering online, vol. 15, no. 1, p. 115, 2016.
5. Toga, A. W. and Mazziotta, J. C., Brain Mapping: The Essentials. Academic Press, 2015.
6. Tustison, N. J., Avants, B. B., Cook, P. A., *et al*., "N4ITK: Improved N3 bias correction," IEEE Transactions on Medical Imaging, vol. 29, no. 6, pp. 1310-1320, 2010.
7. Vaswani, A., Shazeer, N., Parmar, N., *et al*., "Attention Is All You Need," Advances in Neural Information Processing Systems (NIPS), vol. 30, pp. 5998-6008, 2017.
8. Zhang, H., *et al*., "HTCB-Net: A Hybrid Transformer CNN-based Network for Medical Image Segmentation," arXiv preprint arXiv:2303.11935, 2023.
9. Zinn, P. O., Majadan, B., Sathyan, P., *et al*., "Radiogenomic mapping of edema/cellular invasion in glioblastoma," PLoS One, vol. 6, no. 10, p. e25451, 2011.