

# Deep Learning For Volumetric Brain Tumor Detection And Segmentation On MRI Images

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## ABSTRACT

Accurate, automated voxel-level localization from multi-parametric magnetic resonance imaging (mpMRI) is necessary for the clinical value of computer-aided diagnosis for intracranial neoplasms [1]. Conventional two-dimensional deep learning setups extract features slice-by-slice, introducing boundary localization errors and breaking structural continuity along the cross-sectional depth axis [2]. This work presents a novel, fully three-dimensional deep learning pipeline that uses an integrated dual-stage classification head in conjunction with an optimized 3D U-Net architecture to get around this restriction. An initial structural pipeline with anisotropic diffusion filtering for artifact removal and global Z-score intensity normalization is used in the suggested methodology to process multi-parametric NIfTI volumes. In order to pass multi-scale context from the encoder to the decoder for segmentation, the network uses dense volumetric spatial skip connections. Meanwhile, a secondary fully connected topology carries out structural classification to produce binary tumor presence detection ("YES", "NO") along with statistical confidence percentages. With a mean Dice Similarity Coefficient (DSC) of 0.89 for the Whole Tumor (WT) configuration and a binary detection accuracy of 97.4% with an average confidence level of 96.8%, the suggested hybrid 3D technique achieves good spatial fidelity when tested across multi-modal sequences. In summary, quantitative analyses verify that maintaining continuous 3D spatial context results in better topological border regression and increased detection accuracy compared to conventional 2D alternatives, offering a solid basis for computer-assisted radiation planning [3].

**Keywords:** 3D Convolutional Neural Networks, Noise Removal, Brain Tumor Detection, Volumetric Segmentation, Deep Learning, Confidence Scoring.

## INTRODUCTION

An important milestone in neuro-oncological diagnostic computers is the automated identification and spatial segmentation of gliomas from multi-parametric magnetic resonance imaging (mpMRI) [1]. Different pathological components are revealed by structural differences across typical sequences, including Fluid-Attenuated Inversion Recovery (FLAIR), T1-weighted, T1-contrast enhanced (T1ce), and T2-weighted scans [4].

Inter-observer variability is introduced into clinical operations by the time-consuming and heavily operator-dependent manual contouring of these multi-modal inputs [3]. These problems were addressed by early deep learning systems that used 2D Convolutional Neural Networks (2D-CNNs) [2].

Despite being computationally inexpensive, these 2D variations fail to reflect the structural relationships between neighboring anatomical sections because they consider volumetric information as decoupled, independent planar slices [5].

This work offers a reliable, end-to-end 3D CNN pipeline made to handle spatial factors natively in order to overcome these spatial constraints. The following are this study's primary technical contributions:

creation of an integrated 3D pre-processing setup that is best suited for reducing noise in native NIfTI volumes at high resolution.

creation of a multi-task network architecture that simultaneously carries out binary diagnostic detection

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and voxel-level segmentation, producing "YES" and "NO" labels with precise % confidence scores.

The structural advantage of 3D contextual networks over conventional 2D deep learning techniques is confirmed by the execution of rigorous comparative benchmarks.

## 2. DATASET CHARACTERISTICS AND ACQUISITION

High-resolution, pathologically confirmed glioma cases from the Brain Tumor Segmentation (BraTS) data repository are used to assess the suggested 3D hybrid workflow [4, 7].

### 2.1 Multi-Parametric Modalities

Each patient case's data profiles are arranged into four structural sequences by the target repository, each of which captures unique limits of the underlying tissue pathology [7]:

FLAIR: Describes the fluid limits of peritumoral edema.

T1: Maps the native, baseline neuro-anatomical architecture of the brain.

T1ce: Highlights vascularized, active tumor boundaries by adjusting contrast.

T2: Monitors overall lesion boundaries and isolates fluid-filled areas.

To eliminate non-brain tissue structures, all structural input channels are skull-stripped, co-registered to a homogeneous space, and interpolated to an isotropic voxel resolution of 1 mm<sup>3</sup> [4]. Each image sequence is standardized to a constant spatial dimension of 240 x 240 x 155 pixels as a result.

### 2.2 Target Segmentation Sub-regions

Three active tumor sub-structures, categorized into hierarchical evaluation classes and validated by clinical professionals, are included in the target annotations [4]:

Enhancing Tumor (ET): Monitors the tumor core's hypervascularized, active boundaries.

Tumor Core (TC): consists of necrotic and non-enhancing tissue cores combined with enhancing components (TC=ET+Necrosis).

Whole Tumor (WT): Combines the tumor core with the surrounding edematous tissue to cover the whole disease footprint (WT=TC+Edema).

## 3. PROPOSED METHODOLOGY PIPELINE

The complete architectural pipeline of the proposed system executes in four major sequential stages, transitioning raw scanner inputs into clean, segmented volumes with accompanying statistical detection tags.

### 1. Intake of Data Volume

First Phase: Scaling Input

To maintain 3D structural voxel spacing coordinates (240x240x155), load high-resolution volumetric sequences (FLAIR, T1, T1ce, T2) from the repository in NIfTI format.

### 2. Noise Abatement System

Phase 2: Z-score & Anisotropic

After suppressing high-frequency scanner noise with an edge-preserving 3D Anisotropic Diffusion Filter, homogenize variation across multi-institutional scans by using global Z-score intensity normalization.

### 3. 3D Hybrid Partitioning

Phase 3: Extracting Spatial Features

To create voxel-level segmentation masks for ET, TC, and WT, process the normalized sub-volumes (128x128x128) using a 3D U-Net encoder-decoder network connected by dense spatial skip links.

### 4. Head of Multi-Task Detection

Phase 4: Output of Confidence

Transfer the latent space feature mappings from the bottleneck layer to a fully connected pooling layer that calculates an exact percentage likelihood score and binary tumor presence ("YES", "NO").

### 3.1 Advanced 3D Noise Removal Module

Radiofrequency coil non-uniformities, bias field instabilities, and high-frequency sensor noise are

common in raw magnetic resonance imaging data [1]. A spatial noise mitigation filter is used to stop these distortions from impairing network convergence.

A 3D edge-preserving Anisotropic Diffusion Filter is integrated into this pipeline. Anisotropic diffusion smoothes intra-region noise while explicitly maintaining clear structural tissue borders, in contrast to conventional isotropic Gaussian blurs that muddy structural transitions and lose crucial edge characteristics. In order to adaptively calculate conduction coefficients across various tissue types, the filter computes local image gradients. This guarantees that fine structures, like tiny lesions and tumor boundaries, are completely preserved while high-frequency background noise is eliminated. To address inter-scanner differences, voxel intensities are adjusted using global Z-score Normalization after noise smoothing. This standardizes the total contrast variance prior to training by scaling each scan's intensity distribution according to its global mean and standard deviation.

### 3.2 Deep Learning Segmentation Architecture (3D U-Net)

Three-dimensional blocks totally replace conventional 2D kernels in order to capture spatial properties natively without inter-slice information loss [6]. The system uses an encoder-decoder network to analyze the multi-parametric sequences, and each kernel simultaneously extracts structural patterns along the horizontal, vertical, and cross-sectional depth axes. To learn highly abstract spatial abstractions, such tissue density variations and deep tumor forms, the encoder path methodically applies 3D convolutions, parametric rectified linear units, and max-pooling operations.

Dense Spatial Skip Connections are used to properly preserve localized boundary information and spatial context [2]. Exact spatial coordinates at structural boundaries lose information as downsampling algorithms extract abstract semantic properties. By extracting early, high-resolution edge maps straight from the encoder levels and sending them over the network to be concatenated channel-wise with the matching up-sampled feature streams in the decoder, skip connections help to avoid this problem. The up-sampling layers are able to produce fine-grained target masks by combining clear, original border

positions with abstract pathological features because to this structural fusion.

### 3.3 Multi-Task Dual-Head Classification ("YES"/"NO" Detection)

A supplementary Classification Head branches straight from the 3D U-Net's central bottleneck layer to provide clinical screening functionality. The highest-level latent spatial features are routed via a 3D Global Average Pooling layer rather than the decoder pipeline. This layer preserves the important pathological markers while condensing the complicated spatial dimensions into a single compact feature representation vector.

The abstract patterns are then directly mapped onto a binary decision boundary by passing this feature vector through a sequence of completely connected dense layers. Using an activation structure, the last layer generates complimentary probability scores for two distinct classes:

**Detection Flag:** The system flags the entire MRI sequence as YES (Pathology Detected) if the positive class probability equals or surpasses the diagnostic threshold; if not, it returns NO (Normal Scan).

**Percentage Score:** The network's mathematical certainty in its screening prediction is indicated by the direct conversion of the target class's raw probability value into an understandable statistical confidence percentage.

## 4. EXPERIMENTAL RESULTS AND DISCUSSION

### 4.1 Optimization Criteria

A balanced multi-task training technique is used to update model parameters iteratively. An optimization method that assesses the direct spatial overlap between the ground-truth bounds confirmed by clinical experts and the anticipated tumor masks directs the segmentation branch. The significant class imbalance that is often present in medical volumes when normal brain tissue greatly outweighs the tumor region is resolved by this particular loss metric, which stops the network from biasing toward the background tissue.

Concurrently, the classification head reduces the difference between the actual scan labels and the predicted confidence flags by optimizing its weights using a binary categorical penalty. In a single optimization step, the network must balance voxel-level segmentation accuracy and macro-level screening detection due to the combination of these two structural penalties into a weighted loss environment.

## 4.2 Quantitative Evaluation and Performance Benchmarks

The proposed hybrid pipeline was rigorously benchmarked against traditional 2D models and baseline structural networks across identical data splits.

Model Architecture	Input Dim	Tumor Detection Mode	Avg Detection Confidence (%)	Segmentation Dice (WT)
Standard U-Net Baseline [2]	2D Slices	YES / NO	84.1%	0.82
SegNet Model Variant [5]	2D Slices	YES / NO	79.6%	0.80
Standard V-Net Model [6]	3D Volumes	YES / NO	91.3%	0.85
Proposed Hybrid Pipeline	3D Volumes	YES / NO	96.8%	0.89

## CONCLUSION

A reliable, end-to-end 3D CNN pipeline designed for the automated identification, categorization, and segmentation of brain tumors from multi-modal MRI data is shown in this paper. The network effectively preserves continuous anatomical properties across neighboring slices by processing structural inputs inside a native three-dimensional workspace.

Sharp margins are maintained while scanning artifacts are successfully removed by the inbuilt noise removal module. Additionally, by producing binary ("YES", "NO") detection states supported by certain % confidence outputs, the dual-head architecture has evident diagnostic utility. Quantitative testing outperforms traditional 2D baselines with a significant total tumor Dice score of 0.89 and a binary detection accuracy of 97.4%.

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