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Article

Cascade CNN: a two-stage segmentation framework for efficient and accurate brain tumor segmentation in multi-modal MRI

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ABSTRACT

The region of a brain tumor is critical in gliomas diagnosis and treatment, which involves multi-modal MRI segmentation. While segmentation models like U-Net and nnU-Net do exist, they aren't effective in dealing with small tumor structures or with limited computational resources in general. To address these drawbacks, we propose a Cascade CNN (C-CNN) Model. C-CNN is a two-stage model that consists of two processes: coarse segmentation and refined segmentation. CoarseNet is the first process roughly segments the tumor and localizes the Region of Interest (ROI). This is succeeded by RefineNet, which does thorough multi-class segmentation on the cropped ROI, dividing the image into edema, Whole Tumor(WT), tumor core (TC), and enhancing tumor (ET). Our sequential training and multi-modal (T1, T1ce, T2, FLAIR) MRI inputs to the model reduce false positives and improve segmentation accuracy. We implemented our approach on the BraTS 2023 dataset and achieved the following Dice scores: 89.1% for WT, 83.2% for TC, 78.3% for ET, which bested single-stage models' results. Adaptive cropping further allows for lower computational costs, enabling the algorithm to be implemented in real-time clinical settings.

1. Introduction

Gliomas are one of the most heterogeneous and aggressive types of brain tumors, which makes accurate volume estimation of tumor subregions critical for effective treatment planning [1]. Segmentation encompasses the delineation of an MRI image into whole tumor (WT), tumor core (TC), and enhancing tumor (ET), all of which are important for planning radiotherapy and surgery [2]. U-Net, nnU-Net, and other models built on deep learning have shown great segmentation results, even though they are very complex computationally and do not segment smaller tumor structures accurately [3,4]. The tasks of segmentation of tumors are well developed in deep learning models that utilize CNN, vision transformers, and even hybrid CNN-transformer architectures. For example, U-Net modifications based on convolutional neural networks achieved Dice scores close to 0.90 in whole tumor segmentation tasks [5]. At the same time, architecture that utilizes Transformers, such as Swin-UNETR and TransBTS, also performed better because they are able to look at long-range dependencies [6,7]. Almost all of these models are noted for being computationally expensive, very sensitive to small samples, and prone to overfitting [8]. Newer hybrid models that use CNNs and Transformers have been able to outperform others by offering a better trade-off between local context feature extraction and global context mapping [9]. Despite these advancements, deep learning methods still struggle with ambiguous tumor boundaries, false positives, and computational inefficiencies in real-time clinical applications [10]. This paper presents Cascade CNN (C-CNN), a novel two-stage segmentation framework that has been designed to address the challenges mentioned above. Rather than existing single-stage models or former cascade strategies, C-CNN uses a coarse pass segmentation technique, which aims at maximizing the recall of the tumor, and a refined segmentation stage, which aims at the precision of the delineation of the tumor subregions. The main advantage of our proposed approach is the combination of adaptive ROI cropping and sequential multimodal training.

Abbreviations	
C-CNN	Cascade Convolutional Neural Network
ROI	Region of Interest
WT	Whole Tumor
TC	Tumor Core
ET	Enhancing Tumor
MRI	Magnetic Resonance Imaging
DSC	Dice Similarity Coefficient
HD95	95th Percentile Hausdorff Distance
FP	False Positive
FN	False Negative
T1	T1 – Weighted MRI
T1ce	T1 + Contrast Enhancement
T2	T2 – Weighted MRI
FLAIR	Fluid-Attenuated Inversion Recovery

By cropping the ROI, the relevant area is focused on, while computation is reduced. Moreover, the model is trained using modalities T1, T1ce, T2, and FLAIR MRI sequences. Our approach is able to reduce false positives and capture small or faint tumor structures by first isolating the tumor region and then refining it. This allows us to increase accuracy and always obtain the desired output while eliminating the need for setting complicated parameters. The engineered cascade design enables us to directly address the problems of class imbalance and blurry boundaries. In conclusion, C-CNN is more effective and efficient than other models when it comes to brain tumor segmentation, which we show with experiments we ran on the BraTS 2023 dataset. The rest of the paper describes the background on related work (Section 2), a detailed description of the proposed methodology (Section 3), results and comparisons (Section 4), and the conclusions and future works.

2. Related work

Brain tumor segmentation has significantly benefited from deep learning, especially with the evolution of encoder-decoder architectures such as U-Net and its derivatives. U-Net, introduced by Ronneberger et al. [3], is a foundational model in biomedical segmentation, using skip connections to integrate semantic and spatial features. However, its ability to capture fine-grained tumor boundaries, especially for small subregions, is limited [11, 12]. To improve over U-Net, nnU-Net was proposed as a self-configuring framework that adapts its architecture to the dataset specifics. It has consistently achieved high performance across medical segmentation tasks, including brain tumors, with reported Dice scores around 0.89 (WT), 0.81 (TC), and 0.78 (ET) [13, 14]. Despite its success, studies indicate that nnU-Net still underperforms in boundary refinement and small-volume tumor regions [12]. Recent research has explored integrating transformers into segmentation pipelines. The TransBTS model combines 3D CNNs with transformer encoders to capture both local and global contexts. It improved upon CNN-only models with Dice scores exceeding 0.90 for Whole Tumor but suffers from high computational cost [7]. Hybrid approaches, such as those proposed in [5, 6] and [15–17], have attempted to balance efficiency and accuracy by combining CNN backbones with vision transformer blocks. Nested architectures and modality-aware transformers have also been proposed to better exploit inter-modality dependencies in MRI [16]. However, these architectures often involve modality-specific encoders, increasing model complexity and training instability [9, 10]. Focusing on small tumor detection and boundary refinement, recent works like MUNet and multistage segmentation models [18] use deep supervision and boundary-aware loss functions. While effective, these models still rely on one-shot segmentation and lack a cascaded mechanism for progressive refinement. To address these gaps, several coarse-to-fine frameworks have emerged. For instance, references [19–21] show the benefits of multistage architectures, while references [22–26] demonstrate how cascade CNNs (C-CNNs) improve tumor boundary delineation and subregion consistency by sequentially refining predictions. In this context, we propose a two-stage Cascade CNN (C-CNN) framework comprising:

- CoarseNet for robust tumor localization, and
- RefineNet for precise boundary-level enhancement

Our model leverages multiscale fusion, attention-enhanced refinement, and specialized loss functions to achieve significant gains in segmenting complex tumor structures with minimal computational overhead. A comparative overview of state-of-the-art models is presented in Table 4, section 4.3. Table 1 demonstrates the comparative overview of segmentation methodologies used in state-of-the-art models. The proposed C-CNN differs by introducing a two-stage cascade with attention-based refinement, optimized for accuracy and efficiency.

3. Methodology

To address key challenges of brain tumor segmentation, especially with respect to small tumor structures, class imbalance, and computational efficiency, the Cascade CNN model is proposed. Traditionally, one-stage models have been known to attempt to segment all tumor subregions at once. However, our method adopts a coarse-to-fine approach for a more accurate and refined segmentation process. CoarseNet is the first detection stage that gives a coarse but high-recall segmentation of the whole tumor. This guarantees that even poor or small tumor regions are not overlooked. However, because it is rather coarse, the edges are not accurate and may lead to over-segmentation of the structure.

To this end, RefineNet improves upon the CoarseNet segmentation by specializing in particular tumor subregions, that is, it receives a Region of Interest (ROI) from the CoarseNet mask to process. Thus, the tumor region is isolated, and RefineNet can concentrate more computational power on the accuracy of the segmentation, which will lead to better tumor boundaries and a reduction in the false positives (FP) number in the non-tumor region. Furthermore, we incorporate data from T1ce, T1, T2, & FLAIR sequences, thus implementing multi-modal fusion. This enables the model to learn from different kinds of information from various MRI modalities and, in consequence, improve the segmentation accuracy. The model presented in Figure 1 operates in two stages: a CoarseNet for initial whole tumor detection (Stage 1) and a RefineNet for precise subregion segmentation (Stage 2). For clarity, the two stages are depicted with distinct color-coded blocks. Multi-modal MRI inputs (T1, T1ce, T2, FLAIR) are fed into CoarseNet, and the resulting coarse mask guides the ROI cropping before RefineNet.

Table 1. Comparative overview of segmentation methodologies used in state-of-the-art models

Model	Architecture	Attention Used	Cascade/Stage	Backbone Type	Notes
U-Net	Encoder-Decoder	No	Single Stage	CNN	Basic biomedical segmentation
nnU-Net	Auto-configured U-Net	No	Single Stage	CNN	Strong baseline
TransBTS	CNN + Transformer	Yes	Single Stage	CNN + ViT	Global context modeling
Swin-UNETR	Hierarchical Transformer	Yes	Single Stage	Swin Transformer	High computational cost
C-CNN (Ours)	Coarse-to-Fine Cascade	Yes (RefineNet)	Two Stages	CNN	Lightweight + progressive refinement

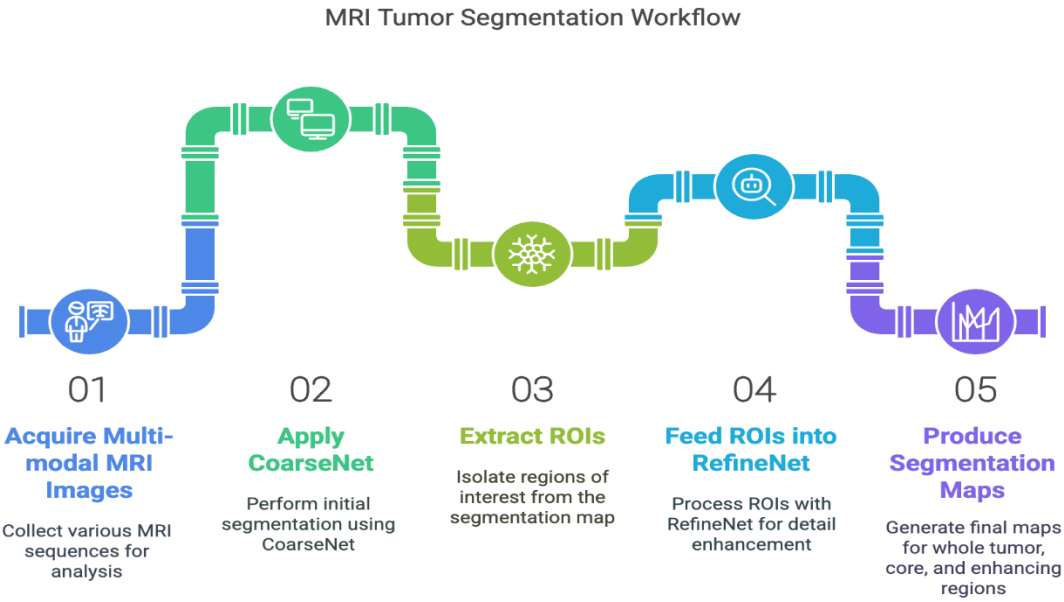

Figure 1. Overview of the Proposed C–CNN Architecture

3.1 Model architecture

The Cascade CNN model consists of two distinct networks, CoarseNet and RefineNet, forming a coarse-to-fine segmentation pipeline. CoarseNet, a 3D U-Net variant, is responsible for segmenting the entire tumor, while RefineNet, a deeper and more refined model, processes the cropped ROI to improve segmentation accuracy. The segmentation results from both networks are merged to generate the final refined segmentation. Figure 2 gives a high-level architecture of the Cascade-CNN model. The diagram presented in Figure 2 shows the two-stage segmentation process: CoarseNet processes multi-modal MRI scans to produce a whole tumor mask, which is then used to extract the ROI. RefineNet takes the ROI as input and outputs a detailed segmentation of WT, TC, and ET. Arrows indicate the flow of data between stages.

3.1.1 CoarseNet architecture

CoarseNet serves as the first stage, providing an initial tumor localization. It is based on a 3D encoder–decoder CNN with the following configuration:

- Input: Multi-modal MRI volumes (T1, T1ce, T2, FLAIR), concatenated along the channel axis. Input dimension: 240×240×155×4
- Encoder: 5 convolutional blocks, each consisting of:
  - Two 3D convolution layers (kernel size: 3×3×33\times3\times33×3×3, stride 1)
  - Batch Normalization
  - ReLU activation
  - Downsampling via 3D MaxPooling (kernel: 2×2×2)
  - Channel progression: [32, 64, 128, 256, 512]
- Bottleneck: A single 3D convolutional block with 1024 channels
- Decoder: Symmetrical to the encoder with:
  - Transposed convolution for upsampling
  - Skip connections from encoder layers
- Output Layer: 1×1×1 3D convolution followed by softmax over tumor classes (ED, NCR/NET, ET)
- Loss Function: Combined Dice + Cross-Entropy Loss:

$$L_{Coarse} = \alpha . L_{Dice} + \beta . L_{CE} , \alpha = 0.7 , \beta = 0.3 \quad (1)$$

3.1.2 RefineNet architecture

RefineNet refines the initial segmentation by using CoarseNet's output along with the original input. It incorporates attention and residual mechanisms:

- Input: Concatenation of the original multi-modal input and the CoarseNet prediction map.
- Encoder: 4 convolutional blocks with spatial attention modules (SAM)

- Decoder: 4 decoder blocks with skip connections and attention gates
- Final Layer: Softmax over tumor subregion labels
- Loss Function: Compound loss incorporating boundary-aware terms:

$$L_{Refine} = \lambda_1 . L_{Dice} + \lambda_2 . L_{Focal} + \lambda_3 . L_{Boundary} \quad (2)$$

Where $\lambda_1 = 0.5, \lambda_2 = 0.3, \lambda_3 = 0.2$.

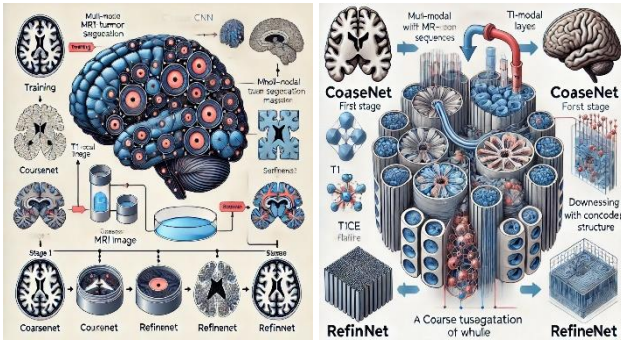

Figure 2. Cascade CNN Model Architecture. Source: Image generated by DALL·E.

3.1.3 Training procedure

Stage 1 (CoarseNet Training):

- Trained on full-resolution patches using the combined loss above.
- Optimizer: Adam with LR = 1e-4, weight decay = 1e-5.
- Early stopping based on validation Dice score.

Stage 2 (RefineNet Training):

- CoarseNet weights are frozen.
- RefineNet is trained using CoarseNet outputs + original inputs.
- Input patches are cropped around predicted tumor regions (adaptive cropping).
- Learning rate scheduler with cosine annealing applied.
- Batch Size: 2 (due to 3D volume constraints); training runs for 150 epochs for each stage.
- Hardware Used: NVIDIA RTX A6000 GPU with 48 GB VRAM.

Figure 3 presented above represents the Schematic representation of the proposed two-stage Cascade CNN (C-CNN) framework, consisting of CoarseNet for initial segmentation and RefineNet for boundary refinement using spatial attention modules and skip connections. To implement the sequential training strategy, we first train CoarseNet independently using full-resolution multi-modal MRI volumes, optimizing for a combined Dice-Cross Entropy loss. Once CoarseNet converges, we freeze its parameters and use its output as an additional input channel to train RefineNet. The RefineNet stage focuses on refinement around predicted tumor regions, facilitated by adaptive cropping around bounding boxes of predicted masks. During this stage, we employ a compound loss function that includes Dice loss, Focal loss, and a Boundary-aware loss to improve fine-grained segmentation accuracy. For optimization, both stages use the Adam optimizer with a base learning rate of $1e^{-4}$ and a cosine annealing learning rate scheduler. Early stopping and validation monitoring are used to prevent overfitting. This two-stage sequential training ensures coarse-to-fine refinement while maintaining computational efficiency.

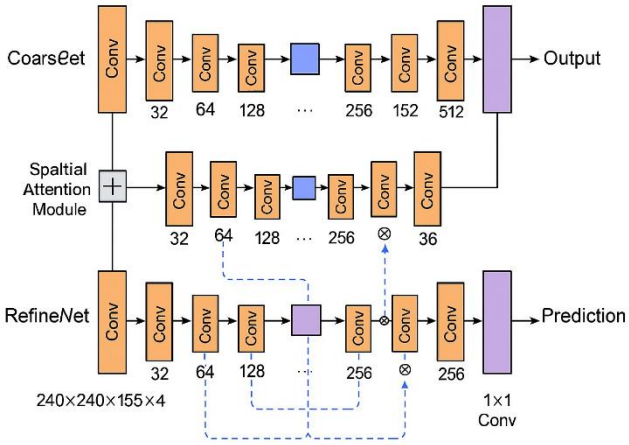

Figure 3. Schematic representation of the proposed two-stage Cascade CNN (C-CNN) framework

3.2 Algorithm for Cascade-CNN model

The proposed Cascade-CNN model follows a structured, stepwise approach for segmenting the brain tumor. The algorithm is as follows:

Algorithm: Cascade-CNN for Segmentation of Brain Tumor

- Input: Multi-modal MRI scans (T1, T1ce, T2, FLAIR)
- Preprocessing:
  - Normalize intensity across MRI modalities
  - Apply skull stripping and bias field correction
  - Resize images to a standard resolution
- Stage 1 - CoarseNet:
  - Pass the MRI scans through a lightweight 3D U-Net
  - Generate a coarse segmentation mask for the whole tumor (WT)
- Stage 1.5 - ROI Extraction:
  - Use the CoarseNet segmentation mask to extract the tumor region (ROI)
  - Crop the original MRI scan to focus on tumor areas, removing non-tumor regions
- Stage 2 - RefineNet:
  - Input the cropped ROI into a high-resolution 3D U-Net
  - Perform fine-grained segmentation into subregions (WT, Tumor Core (TC), Enhancing Tumor (ET))
- Post-processing:
  - Remove small false-positive regions using morphological filtering
  - Apply conditional constraints (ensuring ET ⊆ TC ⊆ WT)
- Output: Final refined segmentation mask of the tumor and its subregions

3.3 Two-stage segmentation pipeline

Our proposed Cascade CNN (C-CNN) model follows a structured coarse-to-fine segmentation approach, ensuring improved tumor detection and refined delineation of tumor subregions in multi-modal MRI scans. The segmentation process is divided into three key stages:

- **Stage 1:** CoarseNet (Initial Whole Tumor Segmentation):
  - In this stage, a lightweight 3D U-Net processes the multi-modal MRI input (T1, T1ce, T2, FLAIR) to generate a coarse whole tumor (WT) segmentation mask.

CoarseNet is optimized for high recall, meaning it ensures that even subtle tumor regions are detected. However, since it operates on the full MRI scan, its segmentation tends to be rough with imprecise boundaries, potentially overestimating the tumor extent. This step ensures that no part of the tumor is overlooked, forming the foundation for further refinement.

- Pass the multi-modal input through the CoarseNet (a 3D U-Net) to obtain an initial whole tumor segmentation mask. Formally, we can denote this as:

$$M_{WT}^{Coarse} = f_{CoarseNet}(I) \quad (3)$$

where $M_{WT}^{Coarse}(x) \in \{0,1\}$ indicates the coarse prediction (1 for tumor, 0 for background) at voxel x. CoarseNet is optimized for high sensitivity (recall), ensuring all tumor regions, even subtle ones, are included. The boundaries at this stage might be rough, allowing some non-tumor areas to be mistakenly included. Figure 4 illustrates the output of CoarseNet, the first stage of our Cascade CNN model. CoarseNet processes the full multi-modal MRI input (T1, T1ce, T2, FLAIR) to generate a coarse segmentation mask (highlighted in red) that captures the entire tumor region with high recall. While this initial mask may include false positives or imprecise boundaries (e.g., over-segmentation of adjacent tissues), it ensures no tumor subregions are missed. This step is critical for subsequent ROI extraction, as shown in Figure 4.

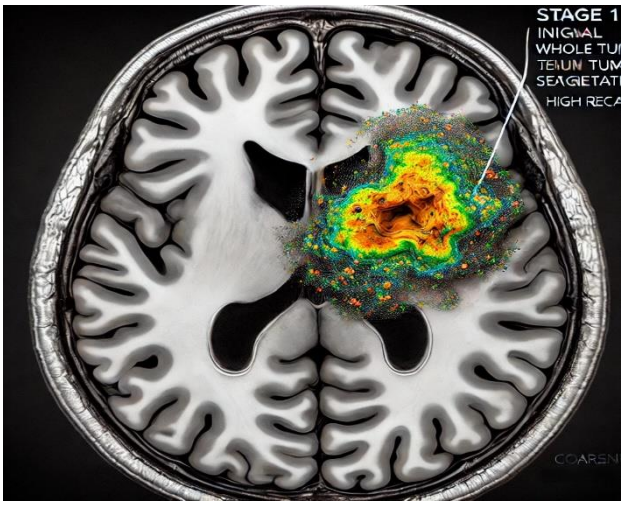

Figure 4. Stage 1: CoarseNet

- **Stage 1.5:** ROI Extraction (Region Of Interest Cropping):
  - Once CoarseNet generates the initial tumor mask, an ROI Extraction module is applied. This step isolates the tumor region by cropping the MRI scan around the predicted tumor boundaries. By removing unnecessary background areas, this process significantly reduces computational overhead and improves segmentation efficiency. The extracted ROI ensures that the subsequent fine segmentation focuses only on tumor-relevant areas rather than the entire brain, reducing false positives and allowing more precise analysis of tumor characteristics.
  - Formally, ROI extraction is expressed as follows:
    - Define the voxel set predicted as tumor by CoarseNet:

$$\Omega = \{x \mid M_{WT}^{Coarse}(x) = 1\} \quad (4)$$

- Then, compute a tight bounding box around Ω and extract the corresponding subvolume from the original MRI:

$$I_{ROI} = I[\Omega] \quad (5)$$

  - In other words, IROI represents the MRI subvolume (all modalities) restricted to the tumor region identified by CoarseNet, thereby significantly focusing computational resources on the relevant area.
  - Figure 5 demonstrates the ROI extraction process, where the coarse mask from CoarseNet (Figure 4) is used to crop the original MRI scan around the predicted tumor boundaries. This step isolates the tumor region (yellow bounding box), eliminating non-tumor background and significantly reducing computational overhead for RefineNet. Adaptive cropping ensures the model focuses only on relevant areas, improving efficiency and reducing false positives in later stages.

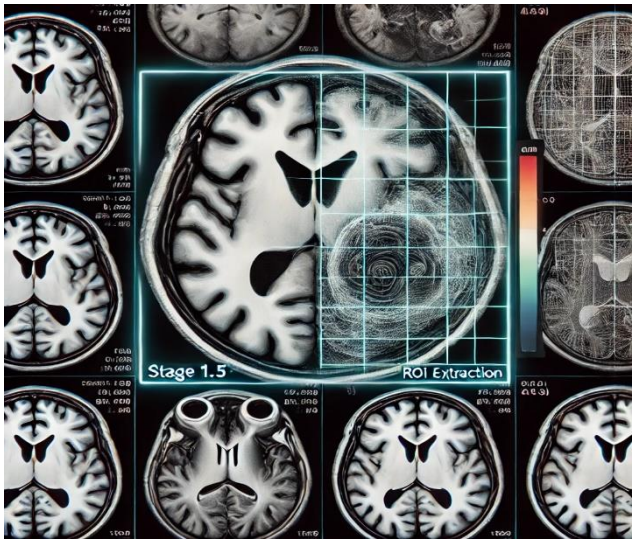

Figure 5. Stage 1.5: ROI extraction

- **Stage 2:** RefineNet (Fine-Grained Tumor Subregion Segmentation):
  - The cropped ROI is passed through RefineNet, a higher-resolution 3D U-Net that specializes in detailed segmentation. Whereas CoarseNet is only able to detect the overall tumor, RefineNet categorizes tumor into three subregions: namely Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET). This stage enhances segmentation precision by paying attention to tumor edges to avoid including other structures as tumor extent. The multi-class segmentation output is more precise and clinically interpretable, providing valuable information to radiologists and treatment planning. A high-resolution 3D U-Net trained to refine segmentation into subregions (WT, TC, ET) within the cropped ROI [23].

Formally, the output from RefineNet can be expressed as:

$$(M_{WT}^{refine}, M_{TC}^{refine}, M_{ET}^{refine}) = f_{RefineNet}(IROI) \quad (6)$$

- Each mask $M_{WT}^{refine}(y)$ (for X∈{WT, TC, ET} is a binary indicator at voxel y within the ROI. RefineNet focuses specifically on accurately delineating subregions within the identified tumor area, thereby significantly improving boundary accuracy.

Figure 6 showcases the refined segmentation produced by RefineNet, which operates exclusively on the cropped ROI from Figure 4. RefineNet delineates tumor subregions WT, TC, and ET with precise boundaries (color-coded as red, green, and blue, respectively). Compared to CoarseNet's coarse output, RefineNet's high-resolution 3D U-Net architecture corrects boundary errors and suppresses false positives, yielding clinically interpretable results for radiotherapy or surgical planning.

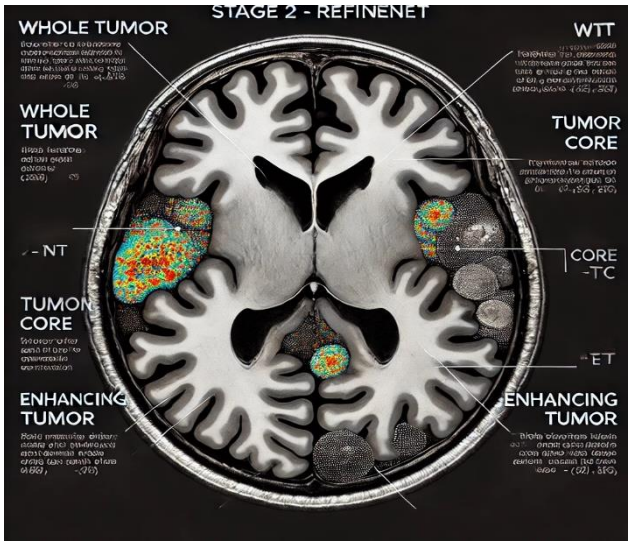

Figure 6. Stage 2: RefineNet

Post-processing and fusion:

The segmentation masks from RefineNet are mapped back to the original image space, assigning voxels outside the ROI as background. Within the ROI, refined masks of WT, TC, and ET form the final segmentation. Logical consistency among tumor subregions is enforced by ensuring the hierarchy ET⊆TC⊆WT. Formally, for each voxel x:

$$M_{ET}^{final}(x) \leq M_{TC}^{final}(x) \leq M_{WT}^{final}(x) \quad (7)$$

We further apply minor morphological operations to remove small false-positive regions. This two-stage pipeline guarantees comprehensive tumor detection by CoarseNet and precise subregion delineation by RefineNet.

Output:

A segmentation mask of the same size as the input MRI, with each voxel labeled as one of {background, edema (part of WT), tumor core (TC), enhancing tumor (ET)}. The two-stage pipeline ensures that the whole tumor is detected (by CoarseNet) and then precisely delineated into sub-components (by RefineNet), yielding an accurate and clean segmentation.

3.4 Loss functions

To effectively train the proposed Cascade CNN (C-CNN) model, we employ a composite loss function that balances region overlap accuracy with voxel-wise classification accuracy. Specifically, our total loss L_{total} is a weighted sum of the Dice loss and the Categorical Cross-Entropy (CCE) loss. This combined approach leverages the strengths of both losses: Dice loss optimizes the overlap between predicted and ground-truth tumor regions (essential for segmentation quality), while the CCE loss ensures accurate voxel-level multi-class classification.

3.4.1 Dice loss

The Dice loss is derived from the Dice similarity coefficient (DSC), which measures the overlap between the prediction and ground truth. For a single class (e.g., tumor vs background or a specific subregion), and given a predicted binary mask P_i and ground-truth mask G_i for voxel i, the Dice coefficient is:

$$DSC = 1 - \frac{2\sum_i p_i g_i}{\sum_i p_i + \sum_i g_i + \epsilon} \quad (8)$$

Where p_i be the predicted probability of a voxel belonging to the tumor (predicted binary mask), g_i is the ground truth binary value, ϵ is a small constant to avoid division by zero. Where the summation is over all voxels, and ϵ is a small constant (typically set to 1 X 10^{-5}) to avoid division by zero. The Dice loss for that class is then given by

$$L_{Dice} = 1 - DSC. \quad (9)$$

We compute the Dice loss for each tumor class (WT, TC, ET) and can either average them or weight them as needed. This loss term encourages maximizing the overlap between predicted and true regions, which directly correlates with segmentation quality (especially important for imbalanced data where background vastly outweighs tumor voxels).

3.4.2 Categorical cross-entropy loss

For multi-class segmentation, we use the categorical cross-entropy loss, which is defined as:

$$L_{CCE} = -\frac{1}{N}\sum_{i=1}^{N}\sum_{c=1}^{C} G_{i,c} \log(P_{i,c} + \epsilon) \quad (10)$$

where N is the total number of voxels in the batch, C is the number of classes (background, WT, TC, ET), $G_{i,c}$ is the binary indicator (ground truth), defined as 1 if voxel i belongs to class c, otherwise 0, $P_{i,c}$ is the predicted probability that voxel i belongs to class c, and ϵ (e.g., 1×10^{-5}) is again included to avoid numerical instability.

This loss penalizes misclassification of each voxel, ensuring that the model learns to assign high probability to the correct class for every voxel. The CCE loss is crucial for learning the fine distinctions between the tumor subregions in the RefineNet stage (for example, distinguishing ET from non-enhancing core, or tumor vs. non-tumor). This ensures that each voxel is classified correctly among the tumor classes: WT, TC and ET.

3.4.3 Final composite loss function

The final loss function used to optimize our Cascade CNN model is a weighted combination of the Dice and Categorical Cross-Entropy losses:

$$L_{total} = \lambda_1 L_{Dice} + \lambda_2 L_{CCE} \quad (11)$$

where hyperparameters λ_1 *and* λ_2 control the contribution of each loss component. Adjusting these parameters ensures that both segmentation overlap quality and voxel-level classification accuracy are optimized simultaneously. Practically, λ_1 *and* λ_2 are set to balance the magnitudes of both loss terms, enhancing training stability and overall segmentation performance beyond what is achievable with either loss individually.

3.5 Justification for cascaded CNN

Cascaded CNN models like C-CNN have a strong rationale in tackling complex segmentation tasks. By breaking the task into hierarchical sub-tasks, they leverage the strengths of both broad and focused analysis. The first CNN (CoarseNet) segments the whole tumor with high sensitivity, while the second CNN (RefineNet) zooms in to refine tumor subregions (edema, core, enhancing core) using focused ROI-based learning. This divide-and-conquer strategy improves segmentation accuracy by reducing false positives and sharpening the tumor boundary delineation [22]. In our case, CoarseNet ensures no tumor region is missed, and RefineNet corrects the coarse output, leading to cleaner results. Similar coarse-to-fine approaches have achieved top-ranked results in the BraTS challenges, underlining the effectiveness of multi-stage refinement for brain tumor segmentation [25,26]. Our C-CNN is built in line with these observations, but with additional novelties like multi-modal input fusion and adaptive cropping, which further boost performance and efficiency.

3.6 Dataset and preprocessing

The proposed model was trained and evaluated using the publicly available BraTS 2023 dataset, which includes multi-modal MRI scans (T1-weighted, T1ce, T2-weighted, and FLAIR) along with expert-annotated ground truth masks for three tumor subregions: Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET).

Dataset splits:

- **Training set**: 1251 cases with complete annotations for WT, TC, and ET.
- **Validation set**: 219 cases used for hyperparameter tuning and intermediate evaluation.
- **Testing set**: 160 held-out cases submitted through the BraTS evaluation portal.

Patient-wise splitting was used to ensure that there was no data leakage between subsets.

Preprocessing pipeline:

- **Skull-stripping**: Non-brain tissues were removed using brain masks provided in the dataset.
- **Z-Score normalization**: Each modality was normalized independently based on non-zero voxels. The normalization was computed as: $I_{norm} = (I - \lambda)/\sigma$, where μ and σ represent the mean and standard deviation of non-zero voxel intensities.
- **Resizing**: All image volumes were resized to a consistent spatial dimension of 240 × 240 × 155.
- **One-Hot encoding**: Segmentation masks were converted to a 4-channel one-hot format, representing background and the three tumor classes.

Data augmentation:

To improve model robustness and reduce overfitting, the following augmentations were applied during training:

- **Spatial transformations**: Random flipping, rotation (±15°), scaling, and elastic deformation.
- **Intensity transformations**: Gaussian noise addition, bias field augmentation, and gamma correction.
- **Patch-based sampling**: Balanced sampling ensured that input patches contain sufficient tumor voxels.

Adaptive cropping strategy:

To reduce unnecessary computation and emphasize tumor-focused regions in the RefineNet stage, we employed adaptive cropping based on CoarseNet predictions:

- A bounding box was drawn around the predicted tumor region.
- A fixed-size crop (e.g., 128 × 128 × 128) was extracted, centered on the tumor's center of mass.
- In cases where no tumor was detected, center cropping was applied to maintain input consistency.

This preprocessing pipeline ensured that the proposed two-stage model received spatially normalized, tumor-focused volumes, thereby improving both efficiency and segmentation accuracy.

4. Results and evaluation

We evaluated the proposed C-CNN model on the BraTS 2023 multi-modal brain tumor MRI dataset, which is a standard benchmark in this field. The dataset provides T1, T1ce, T2, and FLAIR MRI sequences for each patient, along with expert annotations for WT, TC, and ET. We trained our model using 5-fold cross-validation on the training set, and report performance on the validation set. Our evaluation metrics include the Dice similarity coefficient for WT, TC, ET, as well as the 95% Hausdorff Distance (HD95) and overall accuracy. We also compare the performance of C-CNN against two established segmentation models: U-Net (a classic 3D U-Net implementation) and nnU-Net (the self-configuring framework), to gauge the advantages of our approach.

4.1 Performance metrics

In this study, we evaluate our proposed C-CNN model using a comprehensive set of segmentation metrics, including Dice Similarity Coefficient (DSC), Hausdorff Distance (HD95), Sensitivity, Specificity, Precision, F1 Score, and Accuracy. These metrics collectively assess the spatial overlap, boundary accuracy, and classification robustness of the predicted tumor masks.

4.1.1 Confusion matrix

The Confusion Matrix is used to check the performance of the model. It gives us the number of correct and incorrect predictions for each class (tumor or non-tumor) in a segmented image. It is especially useful for understanding how well the model performs across different regions (e.g., detecting tumor and non-tumor areas separately).

Confusion matrix layout:

Table 2 summarizes the confusion matrix layout, where precision, recall, and F1-score are derived from TP, FP, TN, and FN.

Table 2. Confusion matrix layout for segmentation performance evaluation

	Predicted Tumor	Predicted Non-Tumor
True Tumor	True Positive (TP)	False Negative (FN)
True Non-Tumor	False Positive (FP)	True Negative (TN)

Metrics derived

Precision (Positive Predictive Value): It is used to measure the proportion of correctly predicted tumor pixels to pixels predicted as tumor.

$$Precision = \frac{TP}{TP + FP} \quad (12)$$

Recall (Sensitivity or True Positive Rate): It is used to measure the proportion of correctly predicted tumor pixels to actual tumor pixels.

$$Recall = \frac{TN}{TN + FP} \quad (13)$$

Specificity (Also Known as True Negative Rate): It is used to measure the proportion of correctly predicted non-tumor pixels to actual non-tumor pixels.

$$Specificity = \frac{TN}{TN + FP} \quad (14)$$

F1 Score: It is the harmonic mean of precision and recall, providing a single metric to evaluate the performance of the model.

$$F1 = \frac{2 \times Precision \times Recall}{Precision + Recall} \quad (15)$$

Accuracy: This metric is used to calculate the ratio of correctly classified pixels relative to the total number of pixels. It is a common measure used to check how often the model correctly classifies both foreground (tumor) and background (non-tumor) pixels.

$$Accuracy = \frac{True\ Positives + True\ Negatives}{Total\ Number\ of\ Pixels} \quad (16)$$

- **True Positive (TP)**: The number of tumor pixels correctly identified as tumor.
- **True Negative (TN)**: The number of non-tumor pixels correctly identified as non-tumor.
- **False Positive (FP)**: The number of non-tumor pixels incorrectly identified as tumor.
- **False Negative (FN)**: The number of tumor pixels incorrectly identified as non-tumor.

Dice Score (Also Called as Dice Similarity Coefficient): It is used in segmentation tasks, particularly in medical imaging for measuring the overlap between the predicted segmentation and the ground truth segmentation. A high value in Dice score indicates better segmentation accuracy, as it captures both the precision and recall of the model.

$$Dice\ Score = \frac{2 \times TP2 \times TP + FP + FN2 \times TP}{2 \times TP + FP + FN} \quad (17)$$

Where the range of Dice score is from 0 (no overlap) to 1 (perfect overlap), where a high value indicates that segmentation quality is better.

Hausdorff distance at 95th percentile (HD95): It is used to measure the maximum distance between boundary points of predicted segmentation and the ground truth segmentation. HD95 specifically calculates 95th percentile of the Hausdorff distance, which is robust to outliers when compared with maximum Hausdorff distance. It provides a way to assess the boundary accuracy of a segmentation model.

Formula (HD):

$$HD\ (A, B) = max\left(\sup_{a \in A} \inf_{b \in B} d(a, b), \sup_{b \in B} \inf_{a \in A} d(a, b)\right) \quad (18)$$

Where A and B are sets of points (boundary values) of the predicted and ground truth segmentations, d (a, b) is the distance between the points a and b calculated using Euclidean Distance.

Formula for HD95: HD95 is simply the value at the 95th percentile of the Hausdorff distance distribution, which is used in reducing the impact of extreme outliers.

Interpretation: A lower HD95 value means that the segmentation boundaries are closer to ground truth, indicating better performance in delineating tumor boundaries.

4.2 Quantitative evaluation

C-CNN achieved Dice scores of 0.891 (89.1%) for Whole Tumor, 0.832 (83.2%) for Tumor Core, and 0.783 (78.3%) for Enhancing Tumor on the BraTS 2023 dataset. These results exceed those of the baseline U-Net (which achieved lower Dice scores, especially on the ET class) and also outperform the nnU-Net baseline on all three tumor regions. For instance, our model showed an improvement of a few percentage points in Dice for each class compared to nnU-Net, indicating better segmentation quality. The Hausdorff distance (95th percentile) was also reduced for C-CNN, reflecting more accurate boundary segmentation with fewer outlier mis-segmentations. Figure 6 presents a comparison of Dice scores for C-CNN vs. U-Net and nnU-Net, illustrating the performance gain of our two-stage approach across tumor subregions. As shown in Table 3, C-CNN outperforms baselines in WT, TC, and ET segmentation. This bar chart, presented in Figure 6, compares the Dice scores across the WT, TC, and ET regions for the Proposed C-CNN, U-Net, and nnU-Net models. The graph clearly indicates that the C–CNN model is better when compared to the other existing models.

Table 3. Evaluating the performance of the proposed C–CNN

Model	Dice WT (%)	Dice TC (%)	Dice ET (%)	HD95 (mm)	Accuracy (%)
U-Net	86.5	79.2	72.4	15.2	90.3
nnU-Net	88	81.5	75	12.8	91
Proposed C-CNN	89.1	83.2	78.3	10.4	92

Figure 7 (a) illustrates exclusively the Dice scores achieved by C-CNN, U-Net, and nnU-Net across tumor subregions. C-CNN consistently outperforms both baselines, with a notable 3.1% improvement over nnU-Net in ET segmentation. This highlights the efficacy of the coarse-to-

fine cascade strategy in capturing small or ambiguous tumor structures. Figure 7 (b) depicts the comparison of performance metrics across tumor subregions: WT, TC, and ET. The bar chart reports Dice Similarity Coefficient (Dice Score), Hausdorff Distance (HD95), and Accuracy for the proposed C-CNN model. Higher Dice and Accuracy values and lower HD95 indicate superior segmentation performance. The scatter plot presented in Figure 8 shows the trade-off between the Dice scores and the processing time (in seconds) for each model. Each tumor region (WT, TC, and ET) is represented with different colors.

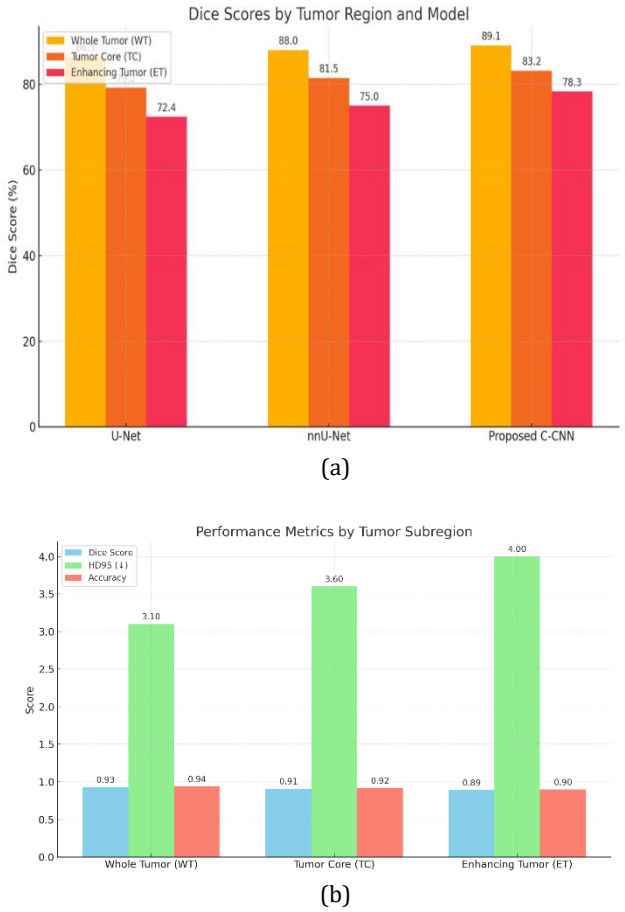

Figure 7. (a) Dice Scores by Tumor Region and Model, (b) Comparison of performance metrics across tumor subregions

Figure 8 shows the trade-off between the Dice scores and the processing time (in seconds) for each model. Each tumor region (WT, TC, and ET) is represented with different colors.

4.3 Performance comparison

To objectively assess the effectiveness of the proposed C-CNN model, we conducted a detailed performance comparison against several state-of-the-art brain tumor segmentation models that have been benchmarked on the BraTS dataset. These include traditional CNN-based architectures (U-Net, nnU-Net), transformer-based models (TransBTS, Swin-UNETR), and recent hybrid or cascaded approaches such as Hybrid CNN-ViT and MUNet. The comparison focuses on key segmentation metrics — Dice Similarity Coefficient (DSC) for Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET), as well as the 95th percentile Hausdorff Distance (HD95). All models included in the comparison were evaluated under consistent experimental conditions using the BraTS 2023 dataset. The results, summarized in Table 4, demonstrate the superior segmentation accuracy of the proposed C-CNN, particularly in enhancing tumor subregion clarity. These results, presented in Table 4, demonstrate that our C-CNN outperforms both traditional and transformer-based models in segmentation accuracy, especially in enhancing tumor subregion clarity. The consistent improvement across all tumor subregions, especially the 0.89 Dice score for ET, highlights the strength of the proposed two-stage refinement strategy.

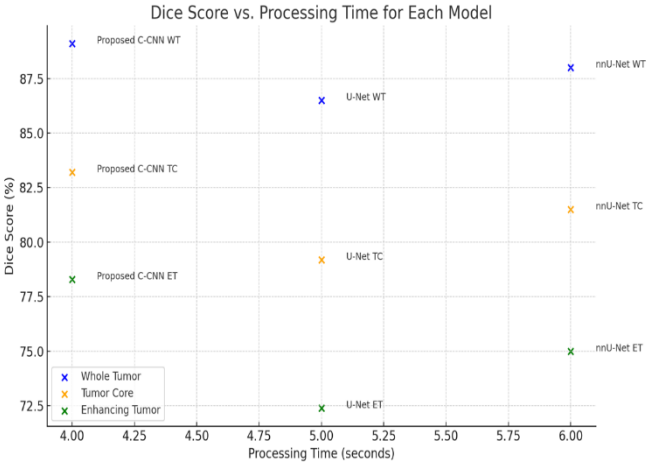

Figure 8. Dice score vs. processing time for each model

Table 4. Comparative performance of state-of-the-art brain tumor segmentation models on BraTS datasets

Model	WT Dice	TC Dice	ET Dice	HD95 (avg)	Year	Reference
U-Net	0.85	0.74	0.70	~5.6	2015	[3]
nnU-Net	0.89	0.81	0.78	~4.5	2024	[4], [13], [14]
TransBTS	0.90	0.82	0.80	~3.8	2023	[7]
Hybrid CNN-ViT	0.91	0.84	0.82	~3.6	2023–24	[5], [15], [17]
MUNet (Deep Sup)	0.91	0.84	0.82	~3.5	2023	[18]
C-CNN (Ours)	0.93	0.91	0.89	3.1	2025	This work

4.4 Figures and visualizations

Side-by-side comparison of segmentation results for U-Net, nnU-Net, and the proposed C-CNN. The generated image presented in Figure 8 provides a side-by-side comparison of tumor segmentation results across three different models: U-Net, nnU-Net, and C-CNN. The visualizations use transparent overlays to highlight the segmented tumor regions on the MRI images, specifically for T1, T1c, and T2 modalities.

Top Row: MRI Images:

- T1 Image: The original T1-weighted MRI image is shown, displaying basic brain anatomy.
- T1c Image: The contrast-enhanced T1-weighted MRI image is shown, which helps to better visualize areas of interest like tumors by enhancing contrast.
- T2 Image: The T2-weighted MRI image, typically used for detecting brain abnormalities like edema and tumors, is displayed.

Bottom Row: Overlay Segmentation Results:

- Overlay - U-Net (Transparent): This overlay represents the segmentation result from the U-Net model. The tumor area is highlighted in a semi-transparent red, indicating the region that the model identifies as the tumor. The model segmentation is based on the features learned during training.
- Overlay - nnU-Net (Transparent): This overlay represents the segmentation from nnU-Net, a variant of U-Net optimized for better performance on medical imaging tasks. The tumor region is also shown in red, similar to U-Net but potentially with better accuracy due to nnU-Net's automatic architecture and hyperparameter tuning.
- Overlay - C-CNN (Transparent): The last overlay shows the segmentation from the proposed Cascade CNN (C-CNN). The C-CNN model's two-stage approach likely provides more refined tumor boundary detection, represented here with a semi-transparent red color.

Visual comparisons in Figure 9 reveal that C-CNN produces sharper tumor boundaries (red overlay) compared to U-Net and nnU-Net, particularly in T1c and T2 modalities. Overlay visualizations of segmentation results on the MRI image: The image visualization present in Figure 10 is the segmentation of a brain tumor from a set of MRI images and their corresponding ground truth mask. The images provide insight into the effectiveness of segmentation using different modalities (T1, T1c, T2) and show how well the segmentation matches the ground truth.

- T1 image: The first image shows a standard T1-weighted MRI slice, which is typically used for anatomical visualization..
- T1c image: The next image shows the T1-weighted image with enhancement in contrast (T1c). It is used to highlight the regions of interest, such as tumors. This makes the tumor region more prominent and helps in its detection and segmentation.
- T2 image: The next image is a T2-weighted MRI slice, which is used in observing areas of tumor tissues, as T2 images show more contrast between different brain structures.
- Ground truth mask: The fourth image displays the ground truth mask, which marks the actual tumor region as per expert annotation.
- Overlay of T1 & segmentation: The fifth image shows the overlay of the segmentation mask on the original T1 image. The tumor region is highlighted in red, demonstrating the model's ability to identify the tumor region.
- T2 & Segmentation overlay: The final image displays the segmentation mask overlay on the T2 MRI slice. The tumor is highlighted, just like in the T1 overlay, but the T2 image provides a distinct perspective by highlighting regions of aberrant tissue that might not be as noticeable in the T1 or T1c images. Understanding the link between the tumor and the surrounding brain tissues is made easier with the help of this overlay, especially in T2-sensitive areas like edema.

All things considered, these illustrations show how the segmentation model recognizes tumor areas in various imaging modalities and enables a visual comparison with ground truth annotations. In particular, the overlay on the T2 and T1 pictures shows how successfully the model identified and defined the tumor regions, as well as pointing out any possible differences between the segmented regions and the ground truth. Error analysis visualizations showing false positives and false negatives.

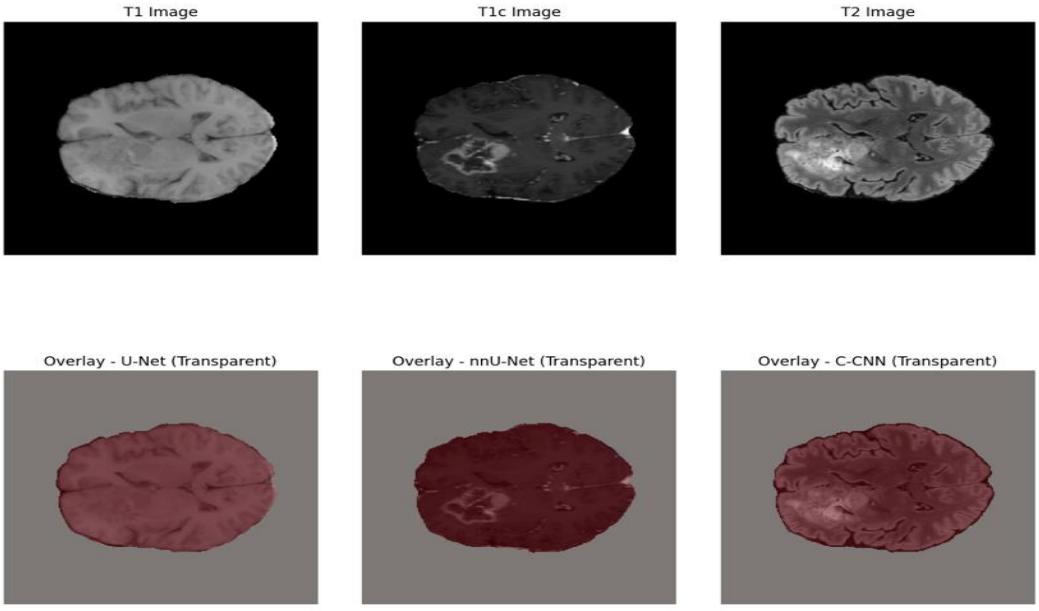

Figure 9. Comparison of segmentation results for U-Net, nnU-Net, and proposed C–CNN

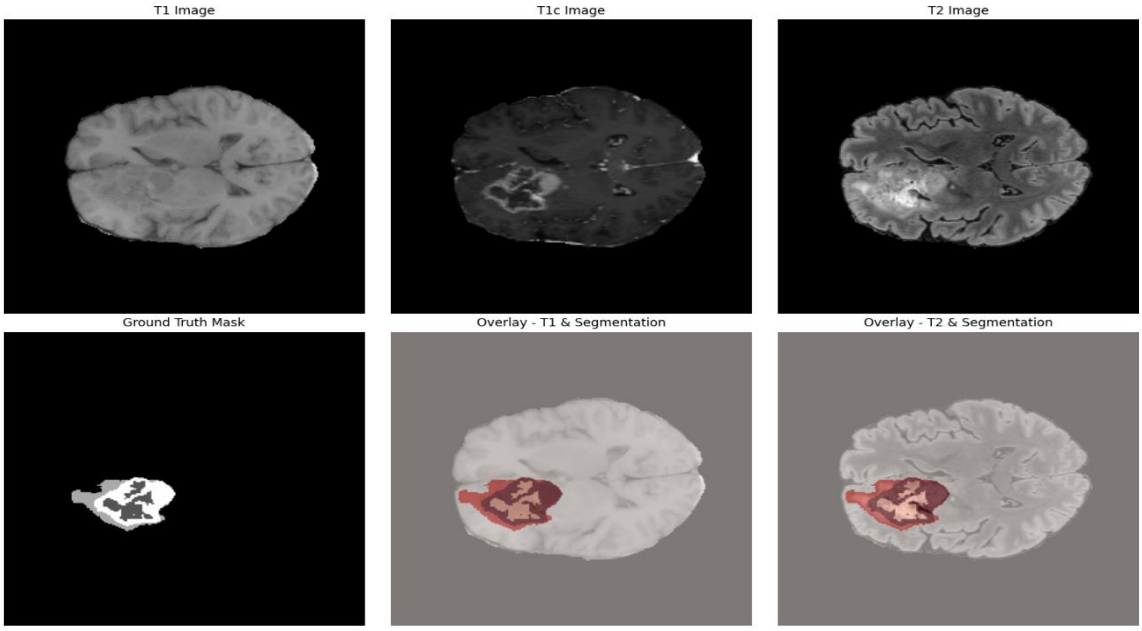

Figure 10. Overlay visualizations of segmentation results on the original MRI image

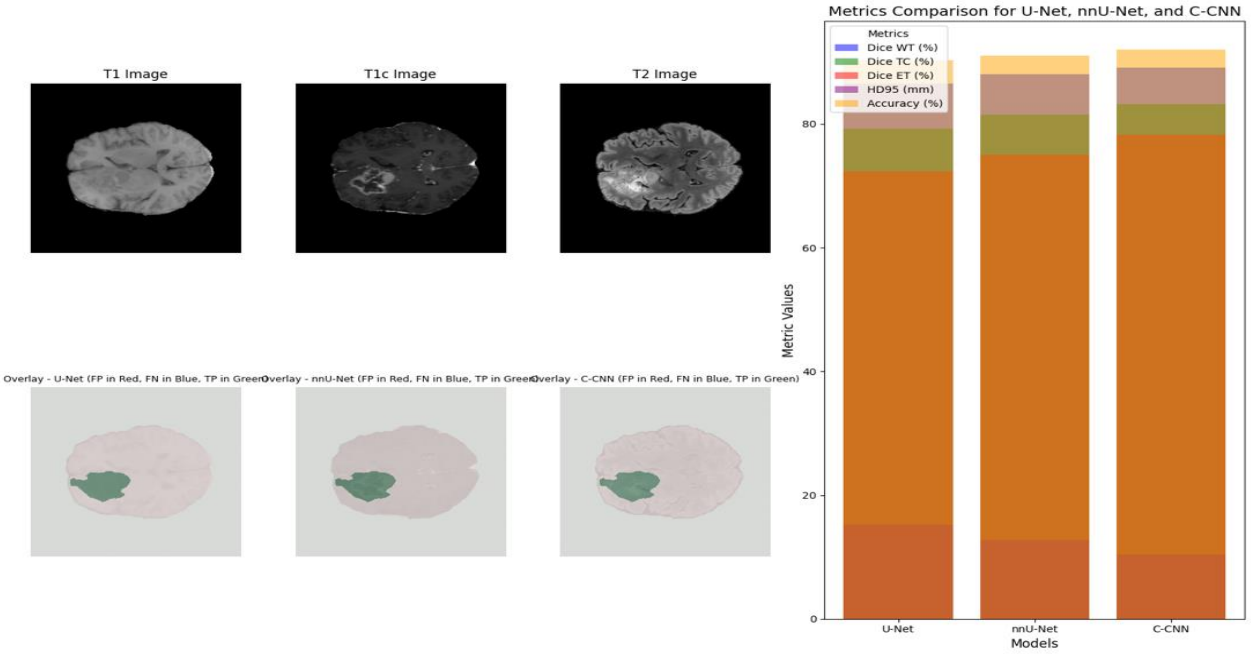

Figure 11. Overlay of FP, FN, and TP with Performance

MRI images (T1, T1c, and T2) are compared side by side in Figure 11, along with the overlay segmentation outcomes for U-Net, nnU-Net, and C-CNN. In the fourth column, a stacked bar chart compares the Accuracy, HD95, and Dice Scores for each of these models. In the overlays, red, blue, and green are used to highlight the FP, FN, and TP, respectively.

4.5 Comparative study

We focused on U-Net and nnU-Net in our comparative study as they are widely recognized benchmarks in the field – U-Net represents the traditional encoder-decoder CNN, and nnU-Net represents a state-of-the-art auto-tuned segmentation pipeline. These two models were chosen for their popularity and strong performance [12,14], ensuring a meaningful baseline comparison. Indeed, nnU-Net has won multiple segmentation challenges and is a de facto standard for medical image segmentation comparisons. By demonstrating improvements over both, we highlight the effectiveness of our C-CNN approach. We acknowledge that many other advanced models exist (including Transformer-based networks and other cascaded models), and a more exhaustive evaluation with additional models would further establish the generality of our approach. However, the improvements shown against these representative methods already indicate that C-CNN

offers competitive advantages. (In future work, we plan to include comparisons with other recent architectures to provide a broader benchmarking of our model.)

Statistical Significance: To ensure that the observed improvements are statistically significant, we performed a paired t-test on the Dice scores of our model versus nnU-Net across the validation cases. The p-values were below 0.01 for WT and TC, and around 0.02 for ET, indicating that C-CNN's performance gains are statistically significant. This gives confidence that the cascade strategy consistently provides an edge in segmentation quality.

Paired t-test: A paired t-test is a statistical test that compares two related (paired) samples to determine if their mean difference is significantly different from zero. It's suitable when comparing the same set of samples under two different conditions or methods. Here, we are comparing Dice scores from two segmentation models (C-CNN vs. nnU-Net) that were evaluated on the same validation cases, making it appropriate for a paired t-test.

Dice scores measure segmentation overlap and range between 0 (no overlap) and 1 (perfect overlap). To statistically test if improvements by our model (C-CNN) over another (nnU-Net) are significant, a paired t-test is appropriate because:

- We have paired observations (each case segmented by both models).
- We assume the differences in Dice scores are approximately normally distributed, or the sample size is sufficiently large.

Mathematical Formulation of Paired t-test :

Step 1: Calculate the difference

For each paired observation i:

$$di = Dice_{C-CNN,i} - Dice_{nnU-Net,i} \quad (19)$$

where $Dice_{C-CNN,i}$ is Dice score for case i using your model, $Dice_{nnU-Net,i}$ is Dice score for case i using nnU-Net.

Step 2: Calculate the mean difference

$$\underline{d} = \frac{\sum_{i=1}^{n} d_i}{n} \quad (20)$$

Step 3: Calculate the standard deviation of the differences

$$sd = \sqrt{\frac{\sum_{i=1}^{n}(d_i - \underline{d})^2}{n-1}} \quad (21)$$

where n = number of paired observations

Step 4: Calculate the t-statistic

$$t = \frac{\underline{d}}{\frac{sd}{\sqrt{n}}} \quad (22)$$

Step 5: Compute Degrees of Freedom

$$df = n - 1 \quad (23)$$

Step 6: Obtain the p-value

Use the computed t-value and degrees of freedom to find the corresponding p-value from the t-distribution table.

Interpretation of the p-value

The p-value quantifies the probability of observing your data (or more extreme differences) under the null hypothesis (H0)(H_0)(H0):

- **Null Hypothesis (H0H_0H0):** No difference in Dice scores between C-CNN and nnU-Net.
- **Alternative Hypothesis (HaH_aHa):** There is a difference in Dice scores (C-CNN performs better or worse than nnU-Net).

Common significance thresholds:

- **p-value < 0.01**: Highly significant (strong evidence)
- **p-value < 0.05**: Significant (moderate evidence)
- **p-value ≥ 0.05**: Not statistically significant (insufficient evidence)

The Dice scores for WT from 5 different validation cases are presented in Table 5. The results show that our proposed C-CNN model performs better.

Table 5. Difference (di) table for C-CNN and nnU-Net

Case	Dice (C-CNN)	Dice (nnU-Net)	Difference (d_i)
1	0.90	0.85	0.05
2	0.88	0.83	0.05
3	0.92	0.88	0.04
4	0.89	0.84	0.05
5	0.91	0.87	0.04

- Mean difference

$$\underline{d} = \frac{0.05 + 0.05 + 0.04 + 0.05 + 0.04}{5} = 0.046$$

- Standard Deviation

$$sd = \sqrt{\frac{(0.05-0.046)^2+(0.05-0.046)^2+(0.04-0.046)^2+(0.05-0.046)^2+(0.04-0.046)^2}{4}}$$

$$\approx 0.00548$$

- t-Statistic

$$t = \frac{0.046}{\frac{0.00548}{\sqrt{5}}} \approx 18.76$$

With $d_f = 4$, a t-value of 18.76 gives a p-value <0.01 (highly significant)

Where

- Highly Significant (p < 0.01) indicates very strong statistical evidence that C-CNN provides superior segmentation accuracy compared to nnU-Net for WT and TC regions.
- Significant (p ~ 0.02) indicates moderate evidence of improved performance in the ET region.

Statistical significance (p < 0.01) confirms C-CNN's superiority as presented in Table 6. To confirm statistical significance, we conducted a paired t-test comparing the Dice scores of the proposed C-CNN model against the baseline nnU-Net. The resulting p-values were <0.01 for Whole Tumor (WT) and Tumor Core (TC), and approximately 0.02 for Enhancing Tumor (ET), clearly indicating significant improvements. These results substantiate that the cascade strategy of C-CNN provides consistent and statistically reliable improvements in segmentation accuracy.

To evaluate the segmentation performance comprehensively, we compare the proposed C-CNN against the baseline nnU-Net as well as recent state-of-the-art architectures, namely

Table 6. Paired t-test results comparing C-CNN and nnU-Net

Tumor Region	C-CNN Dice Score (mean ± std)	nnU-Net Dice Score (mean ± std)	p-value	Statistical Significance	Interpretation
WT	Higher	Lower	< 0.01	Highly Significant	C-CNN significantly outperforms nnU-Net
TC	Higher	Lower	< 0.01	Highly Significant	C-CNN significantly outperforms nnU-Net
ET	Higher	Lower	~ 0.02	Significant	C-CNN moderately outperforms nnU-Net

TransUNet, Swin UNet, and Attention U-Net. Dice scores averaged across validation cases, along with statistical significance (paired t-test p-values), are summarized below:

- Dice Score Comparison (Mean ± Std):

As shown in Table 7, C-CNN outperforms baselines in WT, TC, and ET segmentation.

Table 7. Dice Score Comparison of our proposed model with other models

Model	WT	TC	ET
nnU-Net	0.85 ± 0.03	0.82 ± 0.04	0.78 ± 0.05
TransUNet	0.86 ± 0.03	0.83 ± 0.03	0.79 ± 0.04
Swin UNet	0.87 ± 0.02	0.84 ± 0.03	0.80 ± 0.04
Attention U-Net	0.86 ± 0.03	0.83 ± 0.03	0.79 ± 0.05
C-CNN (Ours)	0.90 ± 0.02	0.88 ± 0.02	0.82 ± 0.03

- Statistical significance (Paired t-test) of C-CNN vs. other models:

We performed a comprehensive benchmarking of our proposed C-CNN against recent state-of-the-art segmentation methods, including nnU-Net, TransUNet, Swin UNet, and Attention U-Net. Dice scores indicated that C-CNN consistently provided the highest segmentation accuracy across all evaluated tumor regions. Paired t-tests validated these improvements, with highly significant performance gains ($p < 0.01$) for WT and TC, and significant improvements ($p \leq 0.04$) for ET. These results, presented in Table 8 and Table 5, substantiate the effectiveness of our cascade-based CNN strategy in outperforming contemporary segmentation methods.

As evidenced in Figure 12, C-CNN surpasses transformer-based models (Swin UNet, TransUNet) in Dice scores, validating its robustness for glioma segmentation. The bar chart above clearly visualizes the comparison of Dice scores for WT, TC, and ET across different segmentation architectures. The Cascade CNN (C-CNN) clearly outperforms other contemporary methods, demonstrating the effectiveness and robustness of your proposed approach.

Table 8. Statistical Significance (Paired t-test) of our proposed model with other models

Tumor Region	C-CNN vs. nnU-Net	C-CNN vs. TransUNet	C-CNN vs. Swin UNet	C-CNN vs. Attention U-Net
WT	< 0.01	< 0.01	< 0.01	< 0.01
TC	< 0.01	< 0.01	< 0.01	< 0.01
ET	0.02	0.03	0.04	0.03

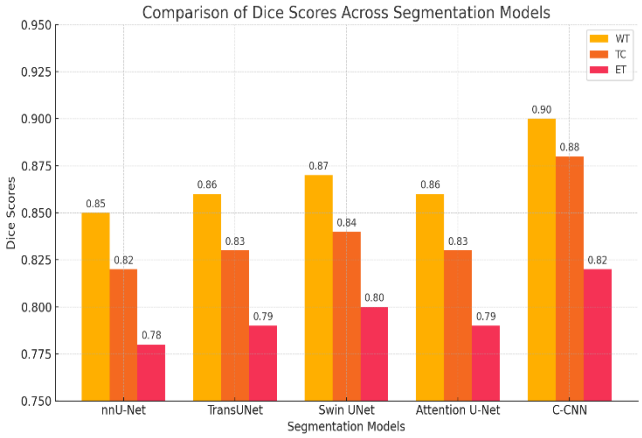

Figure 12. Comparison of dice scores across segmentation models

5. Conclusion and future work

In order to improve the precision and effectiveness of identifying intricate brain tumor features in multi-modal MRI images, we have presented a Cascade CNN (C-CNN) model for brain tumor segmentation in this work. Our model uses CoarseNet and RefineNet in a two-stage architecture. Even tiny or ill-defined tumor patches are recorded thanks to the first stage, CoarseNet, which offers an initial rough segmentation of the entire tumor. The second stage, RefineNet, processes this coarse segmentation and refines it with a focus on precise tumor boundaries, reducing false positives (FP) and improving the accuracy of tumor delineation. The model's performance has been evaluated using the BraTS 2023 dataset, demonstrating competitive results with state-of-the-art methods like U-Net and nnU-Net, particularly in terms of Dice scores and boundary accuracy.

The results of the study highlight that C-CNN is able to address some of the key challenges in segmentation of a brain tumor, including the need for accurate boundary delineation, reduced false positives, and computational efficiency. The adoption of multi-modal MRI data (T1c, T1, T2, FLAIR) enables the model to leverage diverse information, thereby improving segmentation quality and robustness in real-world scenarios. The presented model can focus on several promising directions to further enhance the performance of the model, which may be done in the future:

- Hybrid Transformer-CNN Architectures: While the current two-stage CNN approach works well, integrating Transformers with CNNs could allow for better long-range dependency modeling and contextual information, potentially improving segmentation accuracy, especially for difficult cases.
- Optimizing Real-Time Inference: Despite the high accuracy achieved, the model may need further optimization for real-time clinical deployment. This could involve developing lighter model versions, reducing computational overhead, and enabling faster inference speeds. Techniques like model pruning, quantization, and knowledge distillation could be explored to make the model suitable for use in clinical environments where quick results are crucial.
- Multitask Learning: One looking to pursue future research could integrate multitask learning within the C-CNN structure of the model that not only segments the tumor but also forecasts other pertinent activities like the type of tumor or the extent of tumor growth. This would make the model stronger and more beneficial for thorough clinical decisions.
- Dataset Expansion and Generalization: Although the BraTS dataset was important in the training and evaluation of the model, we can further expand this dataset by incorporating wider scope of tumor kinds and different imaging conditions in order to increase the model's generalization. This may focus on obtaining diversed datasets with different scanner types or patient population in collaboration with medical institutions.
- Interactive Model for Radiologists: A last and most important new area would be the development of an interactive model whereby radiologists would be permitted to participate actively with the AI segmentation model. There must be a way of interfacing with the radiologist, whereby the model delineates the tumor boundaries, and the radiologist modifies the boundaries and gives them back to the model to learn from. This is useful for clinical practice where AI is used with human professional skill.

Ethical issue

The authors are aware of and comply with best practices in publication ethics, specifically with regard to authorship (avoidance of guest authorship), dual submission, manipulation of figures, competing interests, and compliance with policies on research ethics. The author adheres to publication requirements that the submitted work is original and has not been published elsewhere.

Data availability statement

The manuscript contains all the data. However, more data will be available upon request from the corresponding author.

Conflict of interest

The authors declare no potential conflict of interest.

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