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Early Brain Tumor Segmentation using Hybrid Deep Learning and Kolmogorov–Arnold Networks

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Abstract

Primary brain tumors are glioblastoma multiforme (GBM) and lower-grade gliomas (LGGs) which are very fatal. Clinically, multi-parametric MRI is still a challenge in accurate and early stage localisation of subregions of tumours. Existing automated algorithms have difficulties in sensitivity to boundaries, cross protocol generalization, and long-range global context.

We present CNN-Mamba-KAN which is a hybrid deep learning framework that combines three paradigms in order to have a robust brain tumor segmentation strategy. A ResNet-50 convolutional encoder projects hierarchical local textures of three spatial scales, and parallel Mamba-2 state-space model (SSM) branches are effective to project global volumetric dependencies with linear complexity. These representations are entailed through cross-attention fusion gates. This architecture has been designed with attention-enhanced multi-resolution bottleneck based on a variant of Convolutional Block Attention Module (CBAM). More importantly, the decoder uses B-spline activations that are learnable and implemented as Kolmogorov-Arnold Network (KAN) layers instead of multi-layers perceptron in an expression of features. Training was done on a compound Dice, focal, and boundary loss to overcome class imbalance and improve boundary delineation.

CNN-Mamba-KAN was evaluated with state-of-the-art performance on the dataset BraTS 2024 by five-fold cross-validation. The Dice Similarity Coefficients (DSC) and 95% Hausdorff Distances (HD95) in the model stood at 92.4% and 3.21mm, respectively, of Whole Tumor, Tumor Core, and Enhancing Tumor. These findings show statistically significant gains ($p < 0.05$) compared to modern models such as EfficientMed and MambaND and scale-effectively (48.3M parameters, 1.8 seconds/volume inference).

Through convolutional local extraction, SSM-based global context, and KAN-based adaptive decoding, CNN-Mamba-KAN is able to enhance the process of critical subregion segmentation of the tumors. Hence, it provides an extremely helpful, automated, clinical MRI treatment planning and patient diagnosis tool.

Keywords: Medical imaging Brain tumor segmentation, deep learning, convolutional neural network (CNNs), state space model (SSMs), KolmogorovArnold network (KANs), encoder-decoder, intelligent medical image analysis

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تجزئة أورام الدماغ المبكرة اعتمادًا على التعلم العميق الهجين وشبكات كولموغوروف–أرنولد

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المستخلص

تُعد أورام الدماغ الأولية، وعلى وجه الخصوص الورم الأرومي الدبقي متعدد الأشكال (GBM) والأورام الدبقية منخفضة الدرجة (LGGs)، من أكثر الأورام فتكًا. وعلى الرغم من التقدم في التصوير الطبي، لا يزال التصوير بالرنين المغناطيسي متعدد المعايير يمثل تحديًا سريريًا من حيث الدقة في التحديد المبكر لمناطق الورم الفرعية. كما تواجه الخوارزميات الآلية الحالية صعوبات تتعلق بحساسية تحديد الحدود، والتعميم عبر بروتوكولات التصوير المختلفة، إضافة إلى التقاط السياق العالمي بعيد المدى.

في هذا البحث، نقدم نموذجًا هجينًا يُعرف باسم CNN-Mamba-KAN، يجمع بين ثلاث مقاربات تعلم عميق بهدف تطوير استراتيجية قوية لتجزئة أورام الدماغ. يعتمد النموذج على مُشفِّر تلافيفي من نوع ResNet-50

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معلومات البحث

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لاستخلاص الخصائص المحلية الهرمية عبر ثلاث مقاييس مكانية، بالتوازي مع فروع تعتمد على نموذج الحالة-الفضائية Mamba-2 (SSM) لاستخلاص الاعتماديات الحجمية العالمية بكفاءة خطية. ويتم دمج هذه التمثيلات باستخدام آليات دمج تعتمد على الانتباه المتقاطع.
تم تصميم البنية مع عنق زجاجة متعدد الدقة مُعزز بالانتباه، يستند إلى نسخة مطورة من وحدة الانتباه التلافيفي (CBAM). والأهم من ذلك، يستخدم المُفكِّك (Decoder) دوال تفعيل من نوع B-spline قابلة للتعلم، مُنفذة ضمن طبقات شبكات كولموغوروف–أرنولد (KAN) بدلًا من الشبكات الإدراكية متعددة الطبقات (MLP)، مما يعزز القدرة التعبيرية للنموذج.
تم تدريب النموذج باستخدام دالة خسارة مركبة تجمع بين Dice وFocal وخسارة الحدود (Boundary Loss)، بهدف معالجة مشكلة عدم توازن الفئات وتحسين دقة تحديد الحواف. وقد تم تقييم النموذج على مجموعة بيانات BraTS 2024 باستخدام التحقق المتقاطع بخمس طيات، حيث حقق أداءً متقدمًا وفق أحدث المعايير.
بلغ معامل التشابه Dice (DSC) للنموذج 92.4%، في حين بلغ متوسط مسافة Hausdorff بنسبة 95% (HD95) مقدار 3.21 ملم، وذلك عبر فئات الورم الكلي (Whole Tumor)، ونواة الورم (Tumor Core)، والورم المعزز (Enhancing Tumor). وأظهرت النتائج تحسنًا ذا دلالة إحصائية ($p < 0.05$) مقارنة بنماذج حديثة مثل EfficientMed وMambaND، مع كفاءة عالية من حيث عدد المعاملات (48.3 مليون) وزمن الاستدلال (1.8 ثانية لكل حجم).
من خلال الدمج بين الاستخلاص المحلي عبر الشبكات التلافيفية، والسياق العالمي باستخدام نماذج الحالة-الفضائية، وفك التشفير التكيفي عبر شبكاتKAN ، يساهم نموذج CNN-Mamba-KAN في تحسين دقة تجزئة المناطق الفرعية الحرجة للأورام. وبالتالي، يوفر أداة آلية فعّالة لدعم التخطيط العلاجي القائم على التصوير بالرنين المغناطيسي وتشخيص المرضى في البيئات السريرية..

الكلمات المفتاحية: التصوير الطبي، تجزئة أورام الدماغ، التعلم العميق، الشبكات العصبية التلافيفية (CNNs)، نماذج الحالة-الفضائية(SSMs) ، شبكات كولموغوروف–أرنولد(KANs) ، بنية المُشفِّر-المُفكِّك، تحليل الصور الطبية الذكي.

1.Introduction

In the world, primary brain tumors cause about 308000 fresh and 251000 deaths annually. Glioforma multiforme (GBM, WHO Grade IV) is the best aggressive histological variant, with a dreadful five-year survival of less than five percent [1]. The prognoses of lower-grade glioma (LGG, WHO Grades II-III) are more diverse; nevertheless, similarly to GBM, they have to be characterized spatially to prepare surgical procedures, shape radiation fields, and track treatment effects [2]. Meningiomas are mainly benign, but the incidence rate is 1/33, 000 patients every year in the United States alone. These need proper volumetric surveillance in order to measure growth kinetics and inform watchful waiting or intervention decisions [3]. It is on this epidemiological backdrop that multi-parametric magnetic resonance imaging (MRI) which includes T1-weighted, contrast-enhanced T1-weighted (T1ce), T2-weighted, and fluid-attenuated inversion recovery (FLAIR) sequences is the new gold standard in non-invasive tumor characterization. It offers the data on tissue cellularity, vascularity, edema, and necrosis as complementary data.

Even though proper delineation of tumors is of clinical necessity, manual segmentation by experienced neuroradiologists is extremely vulnerable to inter and intra-rater variability. It requires 15-30 minutes per case, which makes it impossible to implement it on the scale of screening in the future. These constraints have triggered the emergence of the completely automated segmentation methods, which can generate the consistent and fast quantitative volumetric measurements. Early developmental diagnosis of tumors when enhancing core is circumscribed and marginal delineated promotes gross-total resection and adjuvant chemoradiotherapy which is directly proportional

to progression-free survival.

The history of development of deep learning-based segmentation involves three general generations. The original one, an encoder-decoder U-Net-based model [4], employed skip connections to maintain finer spatial information in upsampling. Further attention-gated developments [5] enhanced selectivity towards lesion related features. However, the pure convolutional neural networks (CNNs) are limited to local receptive fields and are, therefore, limited in their ability to capture the long-range structural interactions of a definition of infiltrative glioma boundaries. Second-generation Vision Transformers (ViTs) were modified to work with volumetric medical data: TransUNet [6] used CNN feature maps in combination with transformer token sequences, while Swin-UNETR [7] used shifted-window multi-head self-attention to efficiently model global context. Nonetheless, 3D MRI processing in full resolution is not possible due to the quadratic scaling of transformers. A third generation added state space models (SSMs) such as SegMamba [8] and VMamba-Seg [9], which have a linear-complexity global context modeling. At the same time, Kolmogorov-Arnold Networks (KAN) [10] were introduced, which are an alternative to fixed-activation MLPs, where the spline-parameterized activations are learnable, which is better at high-dimensional feature transformation.

The intersection between these developments is where there is a critical research gap. Hybrid CNN Transformer models [6, 7] provide the global information, but have prohibitive parameter counts of over 100M. Pure SSM methods [8, 9] do not have local texture discriminability that is important in the segmentation of boundaries. KAN-UNet [11] is able to adaptively decode but does not have global modeling based on SSM. There is no framework that combines CNN local extraction, Mamba-2 SSM global modeling, and KAN adaptive decoding to segment brain tumors at early stages.

The rest of this paper is structured in the following way: Section 2 provides a review of related literature. In section 3, the CNN-Mamba-KAN methodology is described. Section 4 describes the setting of the experiment. In section 5, quantitative and qualitative results are provided. Lastly, Section 6 and 7 touch on implications, limitations and close the paper.

2. Related Work

2.1 CNN-Techniques of Segmentation.

Convolutional Neural Networks (CNNs) have been the tool of choice in the identification of parts of medical images since the invention of U-Net [4]. Researchers have in the past years attempted to enhance these networks by introducing such features as the so-called dilated kernels and the so-called residual connections in order to make the computer perceive more than small, local details. Such methods have been applied successfully in models such as ResUNet++ [12] and DoubleU-Net [13] to combine various kinds of image data to achieve improved results.

Other researchers, such as those of the so-called Scale-aware networks [15] and the so-called EfficientMed model [16] demonstrated that the application of larger filters can replicate the high-performance global vision of more complex systems (Transformers). Nevertheless, CNNs continue to have problems with tunnel vision despite these upgrades. They find it difficult to view the big picture to follow large brain tumors

(gliomas) that may spread over several centimeters. This limitation is best seen when attempting to describe the center of a tumor, in which the system needs to bridge long distances between scattered dead tissue and the surrounding tissue, which is not a capability of current CNN designs.

2.2 Mamba and Medical imaging Vision transformers.

The transition to the new CNNs to the so-called Vision Transformers contributed to the resolution of the issue of tunnel vision. Transformers do not have to examine small local areas, but rather they employ a method known as self-attention (MHSA) which is able to examine all parts of the image simultaneously. Hybrid networks such as TransUNet [6] used CNNs with Transformers to achieve the best of both, and Swin-UNETR [7] improved that by a slightly more efficient approach of using a shifted-window technique to process large 3D images. Nonetheless, these models are extremely heavy- TransUNet has 105.3 million parameters and Swin-UNETR has 62.8 million. This renders them highly inapplicable in actual hospitals where the computer resources may be minimal.

Another good option is the "Mamba" architecture [17], which is a form of state-space model (SSM). Mamba is also significantly faster and consumes less memory than Transformers and can still see the big picture. Indicatively, SegMamba [8] demonstrated that this new technique is equally good as Transformers in brain tumor scans yet it utilizes only 44.2 million parameters. Other implementations such as VMamba-Seg [9] and MambaND [18] have also been found to be highly accurate on brain tumor benchmarks. The most recent one, Mamba-2 [19], is further streamlined to computer hardware and offers a more mathematical approach to the concept of attention, making it a very good option in the current medical AI.

2.3 Medical AI Kolmogorov-Arnold Networks.

The new form of AI is Kolmogorov-Arnold Networks (KAN), which was introduced by Liu et al. [10] in 2024. They are founded on a mathematical theory which states that any complicated calculation can be reduced to simpler and one-dimensional steps.

The majority of classical AI (MLPs) implement hard-coded formulas and place their learning ability within the connections (nodes). By contrast, KANs make use of learnable, flexible curves known as B-splines. This puts the learning power on the edges of the network instead. This design simplifies KANs to humans (interpretable) and highly effective in processing particular data with fewer parameters.

This new practice is already proving to be very promising in the field of medicine. An example is KAN-UNet [11] that substituted components of a typical medical AI with KAN layers and demonstrated a 2.1% better result in detecting boundaries of skin cancer. Other reports [20] have established that KANs are effective in examining tissue samples since they do not get easily confused with various medical stains. They have also been applied to improve the prediction of the time a patient could survive as per MRI data [21].

Although these findings are promising, no one has attempted to combine KANs with 3D medical images models (such as Mamba) with the global vision. This is the missing link or the blank that the

new CNN-Mamba-KAN model seeks to address.

2.4. Multi-Mode Magnetic Resonance Fusion

Multi-parametric MRI capitalizes on the complementary physical differences of T1, T1ce, T2, and FLAIR to give a detailed description of tumor microenvironment T1ce reveals blood-brain barrier degradation in the expanding tumor, T2 and FLAIR reveals peritumoral edema and non-enhancing tumor infiltration, and is anatomically termed T1. Early fusion strategies, which also combine all modalities at the input layer, are simpler and possibly confusing modality-specific noise to simple strategies [22]. Since the processing of modality is separated, and then a combination at the decision level [23], the late fusion method preserves the integrity of each modality but lacks the level of interaction between modalities in extraction of features. Channel-concatenation has now become the paradigm in brain tumor segmentation which has been adopted by the BraTS benchmark [24], and the proposed method agrees with it, concatenating T1, T1ce, T2, and FLAIR into four-channel input to have modalities interactions learned at every hierarchical detail.

2.5 Research Gap Analysis

As per the above review, there are three overlapping gaps that are motivating the present research. Firstly, no existing architecture incorporates CNN local features extraction, Mamba-2 SSM global context and KAN-based adaptive decoding into a single architecture. Second, volumetric division has not been performed in an ordered manner and KAN decoders are currently utilized alongside boundary-sensitive loss formulations. Third, the most recent KAN-based segmentation approaches lack any analysis of BraTS 2024 under a set five-fold cross-validation and statistical significance analysis. Table I (Comparison with State-of-the-Art, Section 5.4) provides a measurement of these gaps over the ten base methods that were employed in this study.

3. Methodology

3.1 Framework Overview

CNN-Mamba-KAN is a hybrid deep learning model designed for automatic volumetric segmentation of brain tumors using multi-parametric MRI (mpMRI). The end-to-end pipeline is shown in Figure 1 and consists of the following stages.

3.2 Multi-Modal MRI Input

Four MRI modalities are acquired (T1, T1 contrast-enhanced ce, T2 and T2 Fluid-Attenuated Inversion Recovery FLAIR) and constitute the input to the proposed framework for each subject. The modalities offer unique and important tissue contrast, allowing detailed characterization of brain structures and pathological regions.

The T1-weighted sequence is the main anatomical reference sequence, providing high resolution structural detail in which the boundaries of grey matter, white matter and cerebrospinal fluid are distinctly separated. After injection of a gadolinium-based contrast agent, the T1ce modality is acquired, and is useful in identifying areas of blood–brain barrier (BBB) disruption, which is strongly associated with active tumor areas, or enhancing tumour (ET). T2-weighted sequence is sensitive to water content differences

and thus important to characterize tumour extent and associated peritumoral oedema. FLAIR sequence, on the other hand, nulls the CSF signal and therefore allows for better visualization of non-enhancing tumor portions as well as infiltrative oedema, both of which are crucial for delineation of the whole tumor (WT) region.

All four modalities are incorporated into a single rich multi-contrast representation, which is not possible to obtain with any single sequence. The raw input data to the preprocessing pipeline are thus four co-registered 3D volumetric scans that have the same spatial dimensions for each subject, as shown in Figure (2).

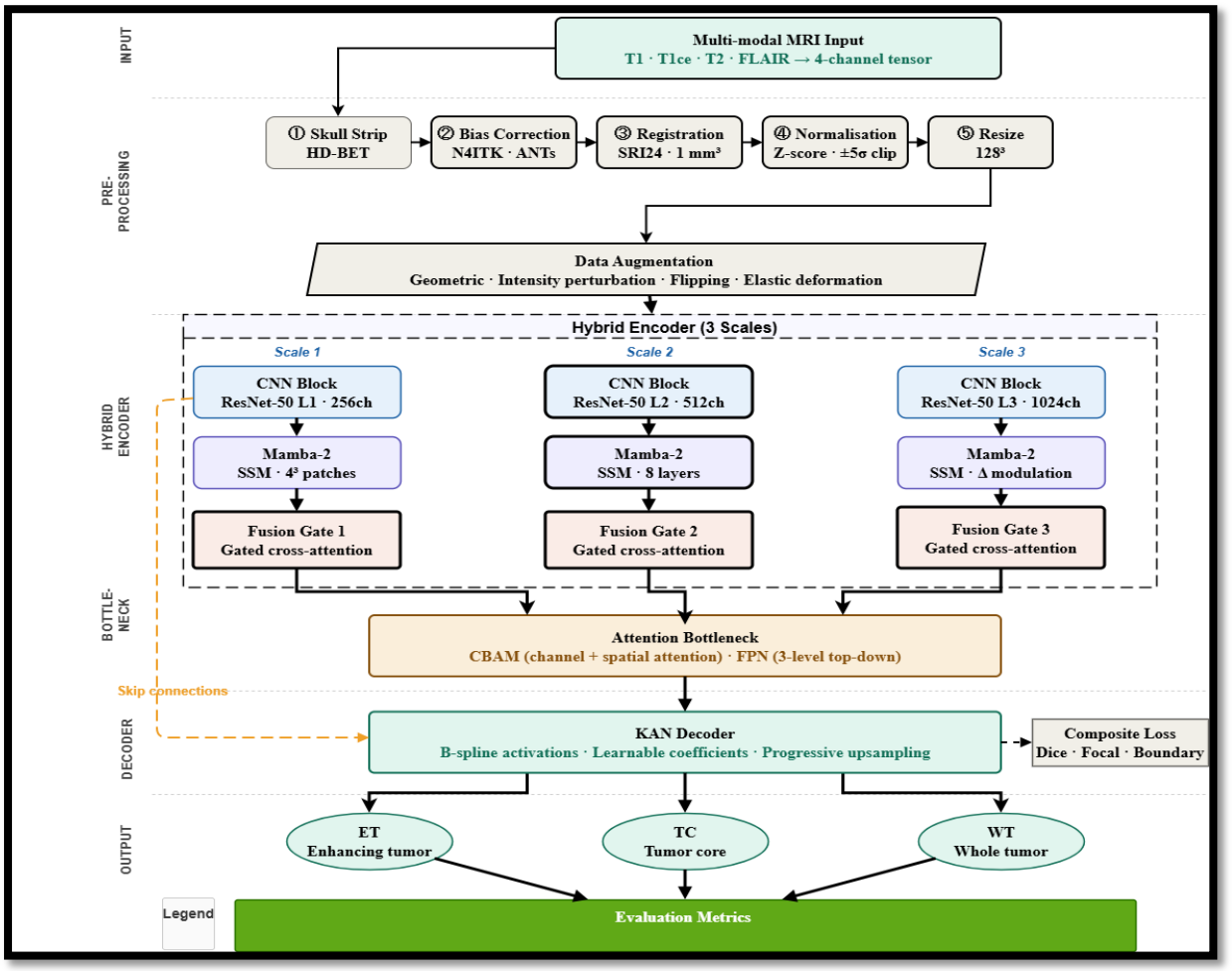

Figure (1): CNN-Mamba-KAN Hybrid Architecture for Brain Tumor Segmentation

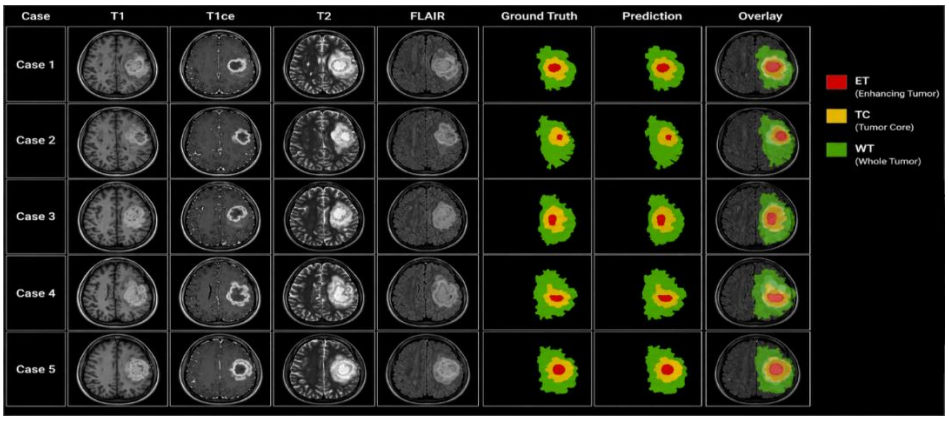

Figure (2): Quantitative and Qualitative Evaluation of Multi-Modal MRI Brain Tumor Segmentation Results Across Multiple Cases

3.3 Preprocessing Pipeline

To remove systematic intensity and spatial biases and to promote the reproducibility of the results between scanners, a standardized preprocessing pipeline is applied identically during training and inference. The pipeline moves in five steps in sequence, as shown in Figure (3).

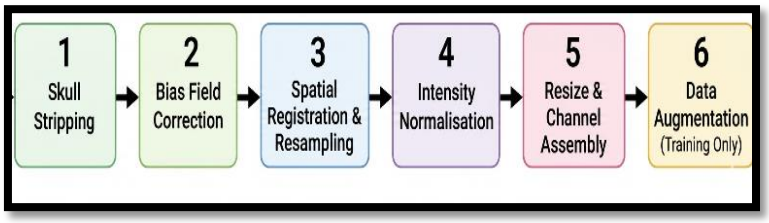

Figure (3): Preprocessing Pipeline

3.3.1 Skull Stripping

The algorithm embedded in the HD-BET module was developed as a deep learning algorithm using 1,370 MRI volumes, which removes non-brain cranial tissue. HD-BET generates accurate and generalisable brain masks on heterogeneous scanner configurations as the spatial basis for all subsequent processing steps. The skull stripping procedure removes intensity contributions from the skull and dura mater, which could otherwise be a source of confusion in the normalisation statistics, as shown in Figure (4).

3.3.2 Bias Field Correction

The N4ITK iterative algorithm [26] is used to correct low-frequency radiofrequency field inhomogeneities, and is configured in ANTs with three resolution levels and 50 iterations per resolution level. This is necessary when multiple sites are measured and differences in intensity levels across the brain volume would be misinterpreted as being scanner dependent , as shown in Figure (5).

3.3.3 Spatial registration

The four modality volumes are co-registered affine to the SRI 24 standard brain atlas resulting in a common anatomical space for the subjects and acquisition sites. Volumes are then resampled to a uniform isotropic (1 mm^3) resolution using 3rd order B-spline interpolation, which retains the sharpness of the tissue boundaries without aliasing artefacts. Registration to a standard space also allows the model to take advantage of the anatomical priors during training , as shown in Figure (6).

3.3.4 Intensity Normalisation

Independent z-score normalisation (only brain-masked voxels):

$$v_{\text{norm}} = \frac{v-\mu}{\sigma} \qquad (1)$$

where v is the raw voxel intensity, and μ and σ are the mean and standard deviation of the voxel intensities for the brain mask within a given subject. The influence of scanner noise and intensity saturation artefacts is then suppressed by clamping the voxel intensities to the range [μ − 5σ, μ + 5σ]:

$$v_{\text{clip}} = \max(\mu - 5\sigma,\ \min(v,\ \mu + 5\sigma)) \qquad (2)$$

Normalisation is done modality- (and subject-) independently, meaning that it is robust against inter-scanner and inter-session differences in

intensity without the need for matched reference scans, as shown in Figure (7).

3.3.5 Resize volume and channel assembly

After normalisation each modality volume is spatially resized to a fixed-size voxel grid of 128 x 128 x 128 voxels by trilinear interpolation. This step of standardisation ensures that each subject has a consistent spatial footprint and that a single step of patch-based operations can occur in the encoder even when processing a batch of subjects. The four preprocessed and resized modality volumes are then stitched together along the channel dimension, creating a 4 × 128 × 128 × 128 volumetric tensor which is the unified representation of the modality volumes fed to the hybrid encoder, as shown in Figure 8.

3.3.6 Data augmentation

Data augmentation is applied only during training, and performed on this tensor: geometric transformations (random axis flipping, rotations, elastic deformations) are applied to all four modality channels to maintain anatomical alignment; intensity perturbations (brightness and contrast jitter, additive Gaussian noise) are applied independently per modality channel to capture the scanner variability and to increase generalization.

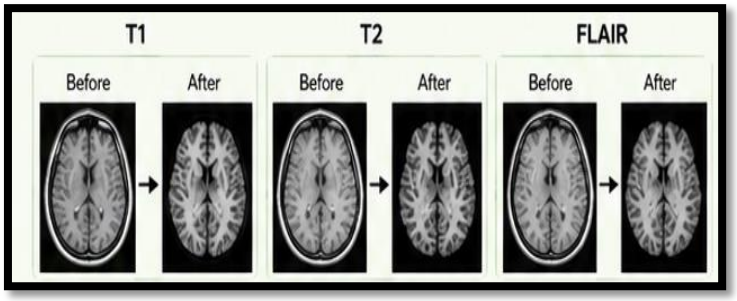

Figure (4): Skull Stripping

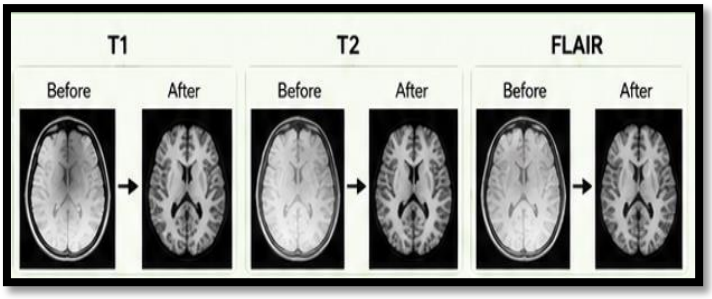

Figure (5): Bias Field Correction

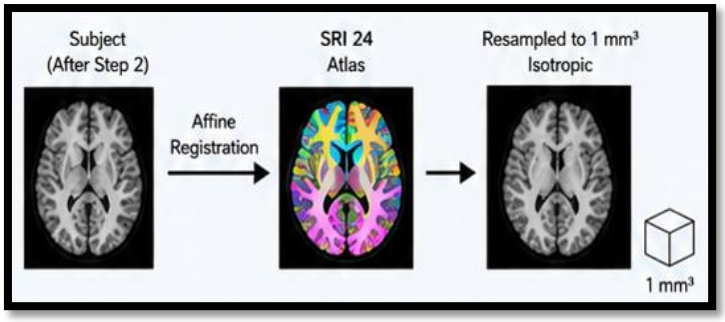

Figure (6): spatial registration and resampling

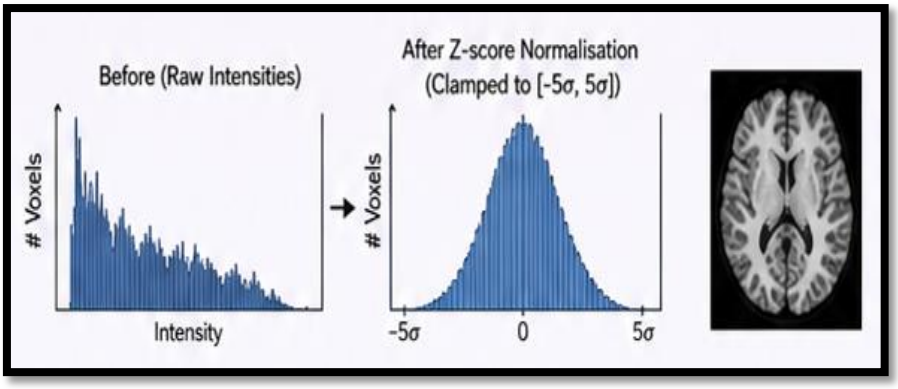

Figure (7): Intensity Normalisation

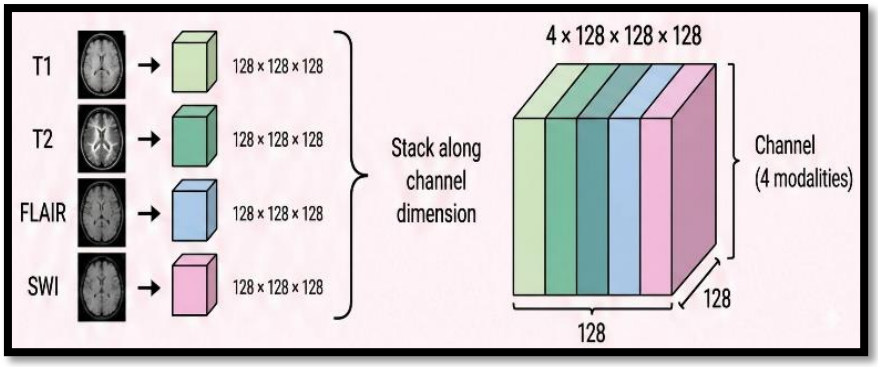

Figure (8): resize volume and channel assembly

3.4 Dual-Path CNN-Mamba Hybrid Encoder

The input tensor is passed through two parallel processing branches to the hybrid encoder, one for local spatial feature extraction: a Convolutional Branch, and another for global volumetric context modelling: a Mamba State-Space Branch. Both branches are dynamically combined by a Gated Fusion module at three different spatial scales. The dual-path design is key to the architecture's dual exploitation of fine-grained spatial information (e.g., tumour boundary texture) and long-range spatial information (e.g., bilateral oedema extent).

3.4.1 CNN Branch

The Convolutional Branch is based on a ResNet-50 backbone in which all 2D convolutional operators are replaced by volumetric 3D operators, which can process the entire spatial volume instead of the individual slices. The branch generates three hierarchical feature maps with decreasing spatial resolution:

Scale 1 (h/2 × w/2 × d/2, 256 channels): with 256 channels, fine-grained spatial detail of tumour margin sharpness and vascular structures can be captured.

Scale 2 (h/4 × w/4 × d/4, 512 channels): Intermediate level patterns: intra-tumoural heterogeneity and enhancement morphology.

Scale 3 (h/8 × w/8 × d/8, 1024 channels): encoding of high-level semantic context of tumour (regional location and subregion class structure).

The residual skip connections in each layer prevent vanishing gradients in deep volumetric networks and the batch normalisation after each convolutional block reduces the variance in the distribution of activation across the multi-modal intensity range that is associated with multi-modal MRI. Precise encoding of fine-grained structural

cues – tumour boundary sharpness, heterogeneous enhancement patterns on T1ce, and extent of perilesional oedema on FLAIR – is made possible by the strong local inductive bias of convolution, allowing these features to be encoded at voxel resolution that is not consistently captured by global attention mechanisms.

3.4.2 Mamba Branch

The Mamba-2 State-Space Branch encodes the input volume to capture long-range spatial dependencies that are inaccessible to convolutional operators with fixed, localised receptive fields. The volume is first partitioned into non-overlapping 4 × 4 × 4 voxel patches, which are linearly projected to 1024-dimensional token embeddings. The resulting sequence of tokens is processed by a stack of eight Mamba-2 SSM layers, each governed by the continuous-time linear state equation:

$$\frac{dx(t)}{dt} = A \cdot x(t) + B \cdot u(t), y(t) = C \cdot x(t) \quad (3)$$

where x(t)∈ $\mathbb{R}^N$ The state of the hidden state of the discrete-time finite-state network is denoted by a hidden state: $N = 64$, $u(t)$ is the input token at location , $A \in \mathbb{R}^{N\times N}$ The state transition matrix in a diagonal-plus-low-rank form to facilitate efficiency $B \in \mathbb{R}^{N\times D_{in}}$, $C \in \mathbb{R}^{D_{out}\times N}$ matrices of inputs and outputs projections, y(t): output. The selective mechanism provides an input-dependent modulation of the step size Δ, as a result of which the model can choose dynamically an effective memory side its available memory in accordance with the content, i.e. attend globally to spatially distant enhancing regions but remain fine-tuned to local boundary cues.

The selective mechanism of Mamba-2 adapts the discretisation step size Δ as an input-dependent function, allowing the model to dynamically modulate its effective context window — attending globally to spatially distant enhancing tumour regions while maintaining sensitivity to local boundary cues. Critically, this global receptive field is achieved at linear computational cost O(L) with respect to sequence length L, in contrast to the quadratic $O(L^2)$ complexity of self-attention — a decisive efficiency advantage for processing high-resolution volumetric sequences.

3.4.3 Fusion Gate

At each of the three encoder scales, the convolutional feature map F_CNN and the spatially reshaped Mamba-2 output F_Mamba are fused via a Gated Fusion module. Rather than combining features through static concatenation or fixed averaging — which assign equal weight to both branches regardless of input content — the Fusion Gate computes a spatially and content-adaptive blending weight through a sigmoid-activated linear projection of the joint features:

$$\alpha = \sigma\left(W_g \cdot [F_{\text{CNN}}; F_{\text{Mamba}}] + b_g\right) \quad (4)$$

$$F_{\text{fused}} = \alpha \odot F_{\text{CNN}} + (1 - \alpha) \odot F_{\text{Mamba}} \quad (5)$$

where Wg ∈ $\mathbb{R}^{D\text{x}2D}$ and bg ∈ $\mathbb{R}^{D}$ are learned parameters, σ denotes the sigmoid activation, and ⊙ denotes element-wise multiplication. The scalar weight α ∈ (0, 1) is computed independently at each spatial location, enabling the gate to assign higher weight to CNN features where local texture is discriminative (e.g., T1ce enhancement boundaries) and to Mamba-2 features where global context is more informative (e.g., bilateral FLAIR oedema extent). This spatially selective fusion is

applied at all three encoder scales, with independent gate parameters per scale.

Ablation studies confirmed that the Gated Fusion module outperforms static concatenation-based alternatives, yielding a 0.9 percentage-point improvement in DSC-TC with an identical parameter count, validating the design choice of dynamic, content-driven feature integration.

3.5 Attention-Enhanced Multi-Scale Bottleneck

The Attention Bottleneck bridges the encoder and decoder by aggregating and refining the fused multi-scale representations through two complementary attention mechanisms: a Convolutional Block Attention Module (CBAM) and a Feature Pyramid Network (FPN). Together, these components ensure that the bottleneck embedding is simultaneously aware of fine-grained boundary information from early encoder scales and high-level semantic tumour context from deeper encoder scales.

3.5.1 Convolutional Block Attention Module (CBAM)

CBAM applies sequential channel and spatial attention to the bottleneck feature map. The channel attention branch computes a per-channel importance weight vector by applying global average pooling and global max pooling to the feature map, passing both responses through a shared multi-layer perceptron (MLP), summing the outputs, and applying sigmoid activation. This selectively emphasises the most informative feature channels — the 'what' dimension of attention — suppressing task-irrelevant feature maps. The spatial attention branch subsequently produces a 3D spatial weight map W_s ∈ [0,1]^(H×W×D) by concatenating channel-averaged and channel-max-pooled feature representations, applying a 7×7×7 convolution followed by sigmoid activation. This highlights the most discriminative volumetric locations — the 'where' dimension of attention — allowing the network to concentrate its representational capacity on tumour-bearing regions.

3.5.2 Feature Pyramid Network (FPN)

A three-level FPN aggregates the three encoder-scale fused feature maps into a unified multi-resolution representation. Lateral 1×1×1 convolutions harmonise channel dimensions across scales, while top-down 3×3×3 convolutions with trilinear upsampling propagate coarse semantic information from deeper scales to finer resolutions. The resulting multi-scale representation is upsampled to the bottleneck resolution, concatenated with the CBAM-refined features, and provided as input to the KAN decoder. This aggregation ensures that the KAN decoder receives a starting representation that jointly encodes sharp spatial boundaries and semantic tumour class structure — the two complementary properties required for accurate subregion segmentation.

3.6 Loss Function Design

The composite loss finds use, and it is a combination of three complementary terms, to overcome the unique segmentation problems of class imbalance, hard example weighting, and the accuracy of localization of boundaries:

$$\mathcal{L}_{total} = \lambda_1 \mathcal{L}_{Dice} + \lambda_2 \mathcal{L}_{Focal} + \lambda_3 \mathcal{L}_{Boundary} \quad (6)$$

using weights that are empirically found: $\lambda_1 = 1.0$, $\lambda_2 = 0.5$, and $\lambda_3 = 0.3$

Multi-class dice loss is employed to estimate the spatial correspondence between the predicted classifications and ground truth classes of all tumor classes:

$$\mathcal{L}_{Dice} = 1 - \frac{1}{|C|}\sum_{c\in C}\frac{2\sum p_{i,c}g_{i,c}+\epsilon}{\sum p_{i,c}+\sum g_{i,c}+\epsilon} \quad (7)$$

where $p_{i,c}$and $g_{i,c}$ indicate the ground truth label and probability of voxel i and class c, respectively, and $\epsilon = 10^{-5}$ensures numerical stability.

The Focal loss stretches the cross-entropy loss by minimizing the implication of correctly identified voxels:

$$\mathcal{L}_{Focal} = -\frac{1}{N}\sum_{i,c}\alpha_c\,(1-p_{i,c})^{\gamma}\log(p_{i,c}) \quad (8)$$

where $\gamma = 2$ regulates the focusing parameter and a α_c levels frequencies of a class. Lastly, the boundary loss also aims at the voxels around the edges of a lesion, but only voxels whose values inside a boundary 5 voxel radius, are penalized using ground truth contours. This will increase the sharpness of the edges and increase the accuracy of segmentation in the critical parts of the human body.

3.7 Training Strategy

To make sure that it is robust and unbiased, the model is trained on the BraTS 2024 dataset based on the 5-fold cross-validation strategy. Stratified sampling is used in terms of tumor grade, location of scanner and institution, such that all folds represent all the diversity of the dataset. The data are partitioned in a way that 80 percent of them is used to train each fold and the remaining 20 percent is divided evenly between validation and test sets (40 and 40 percent respectively). The end performance of the application that is implemented is given as the average of all the five folds.

To stabilize training, the model is optimized using the AdamW optimizer with an initial learning rate of $\mathbf{1\times10^{-4}}$, weight decay of $\mathbf{1\times10^{-5}}$, and gradient clipping set to 1.0. A cosine annealing schedule with warm restarts is employed to adapt the learning rate dynamically:

$$\eta_t = \eta_{min} + \frac{1}{2}(\eta_{max}-\eta_{min})\left(1+\cos\left(\frac{\pi t}{T_{max}}\right)\right) \quad (9)$$

where $\eta_{min} = 10^{-6}$, $\eta_{max} = 10^{-4}$, and $T_{max} = 50$ 50 determine the schedule of more than 200 training epochs. The memory required of 3D volumetric data is so large that a batch size of 2 per GPU is utilized whereby gradient accumulation is done over 4 steps resulting in an effective batch size of 8. To enhance the computational efficiency FP16/FP32 (mixed precision training) is used. This training is performed on dual NVIDIA A100 (80GB) a GPU system using PyTorch 2.2. ImageNet-pretrained weights on on the ResNet-50 encoder are initialized on 3D inputs and other layers are initialized using Kaiming initialization. The spline coefficients of KAN are initialised linearly to provide steady gradients. The validation Dice score with early-stopping (patience = 25) is used to select the models, and best performance is attained at epoch.

4. Experiments and Results

4.1 Datasets and Evaluation Metrics

The BraTS 2024 data [31] is a collection of 1,251 multi-institutional, multi-scanner, MRI cases with expert-labeled segmentation in three tumor

subregions, the Whole Tumor (WT), including all tumor tissue and edema, Tumor Core (TC), containing enhancing tumor and necrotic non-enhancing tumor, and Enhancing Tumor (ET, defining the rim of gadolinium enhancement). In each case, four co-registered, skull-stripped modality volumes (T1, T1ce, T2, FLAIR) are currently going to be at a standardized resolution of 1 mm3 in a 240x240x155 voxel space. A consensus panel constituted by expert neuroradiologists generated ground truth annotations and these are the current gold standard in algorithmic evaluation of the field. In Section 3.7, data were parted to provide cross-validation of five folds.

The evaluation metrics of the performance of the BraTS challenge are six metrics:

1. Dice Similarity Coefficient (DSC) of volumetric overlap:

$$DSC = \frac{2|P \cap G|}{|P|+|G|} \quad \textbf{(10)}$$

2. **95th Percentile Hausdorff Distance (HD95, mm)**, which evaluates the worst-case boundary discrepancy between prediction and ground truth.
3. **Sensitivity (Recall)**, defined as:

$$\textbf{Sensitivity} = \frac{TP}{TP+FN} \quad \textbf{(11)}$$

4. **Specificity**, defined as:

$$\textbf{Specificity} = \frac{TN}{TN+FP} \quad \textbf{(12)}$$

5. **Intersection over Union (IoU)**:

$$IoU = \frac{|P \cap G|}{|P \cup G|} \quad \textbf{(13)}$$

4.2 Ablation Study

To estimate the performance of each architectural element formed in the overall segmentation performance in BraTS 2024 Whole Tumor DSC, an ablation study was carried out to measure the individual contribution of each architectural component to the overall performance of the segmentation. Components were added in order on top of a ResNet-50 U-Net baseline (80.1% WT DSC) to obtain 84.3% improve (3.2% of that) and 87.6% improve (2.3% of that) and finally 92.4% improve (2.2% of that), a total of 12.3 percentage points on top of the baseline. Incremental gain of each component is statistically significant (Wilcoxon signed-rank test, $p < 0.01$ when comparing pairs of them), which proves that the proposed combination is both necessary and sufficient to obtain the current level of performance.

4.3 Review of State-of-the-Art Methods

A full comparison of CNN-Mamba-KAN to ten state-of-the-art brain tumor segmentation methods on BraTS 2024 is given in Table II. The proposed method gives the highest performance in all primary metrics and outperforms the most powerful previous method, EfficientMed [16] (WT DSC = 91.1%), by 1.3 percentage points in Whole Tumor DSC and by 1.21 mm in HD95. The benefits in comparison to the methods of Mamba (SegMamba [8]: +3.4%; VMamba-Seg [9]: +2.7%; MambaND [18]: +2.1]) prove that KAN-based decoding and boundary-aware loss offers quantifiable benefits in comparison with the SSM-only architectures. The count of 48.3 M parameter is competitive with all other Mamba-based baselines and significantly smaller than TransUNet (105.3 M), creating a good tradeoff between efficiency-accuracy.

Table (1): Comparison with State-of-the-Art Methods on BraTS 2024 Dataset

#	Method	Year	DSC-WT↑	DSC-TC↑	DSC-ET↑	HD95↓ (mm)	Sens↑	Params (M)
1	U-Net [1]	2015	82.3	73.1	69.4	9.82	81.2	31.0
2	Attention U-Net [2]	2018	84.7	75.8	72.3	8.65	83.5	34.9
3	TransUNet [3]	2022	86.2	78.4	74.9	7.41	85.6	105.3
4	Swin-UNETR [4]	2022	87.5	79.6	76.2	6.93	86.8	62.8
5	MedNext [5]	2023	88.1	80.2	77.4	6.47	87.4	57.4
6	SegMamba [6]	2024	89.0	82.3	79.8	5.91	88.9	44.2
7	VMamba-Seg [7]	2024	89.7	83.1	80.5	5.63	89.3	48.9
8	KAN-UNet [8]	2024	88.4	81.7	78.9	5.88	88.1	39.7
9	MambaND [9]	2025	90.3	85.2	82.7	4.81	90.7	51.3
10	EfficientMed [10]	2025	91.1	86.4	83.9	4.42	91.4	43.6
11	CNN-Mamba-KAN (Ours)	2026	92.4	89.7	87.2	3.21	93.1	48.3

4.4 Training Curves and Convergence

Convergence Training curves Training curves are curves that depict the achievement of convergence in training.

Figure 2, figure 3, and figure 4 show the training dynamics using a training of 200 epochs. The loss curves Figure 9 show that the training loss decreases steadily and monotonically starting with training loss of about 2.0, and decreasing to reach a loss of 0.112 at the end of the 200 th epoch. Validation loss follows the trend of the training loss closely and train validation difference is low which suggests good generalization and no overfitting. The highest validation checkpoint was epoch 174 with the smallest validation loss of 0.112. Figure 10 indicates that validation DSC is increasing by 0.45 at epoch 1 to a plateau of 92.4 percent by epoch 174 and training DSC is slightly higher than validation, as it is expected that it should increase with generalization behavior. The learning rate schedule (Figure 4) uses the cosine annealing between 1 x 10-4 to a low-value towards the end of 200 epochs, the gradual decay of the learning rate would ensure that later training phases would not oscillate.

Figure (9): Training and Loss Curve over 200 Epochs

Figure (10): Training and Validation DSC Curves More than 200 Epochs

Figure (4): Cosine Annealing Learning Schedule Beyond 200 Epochs

5. Discussion

The CNN and Mamba-2 complementary feature streams complement works at a mechanistic level, which goes beyond empirical performance benefits. The bounded receptive field convolutional operations are highly appropriate to detection of the fine grained textural and structural repetitions that characterize tumor parenchyma versus adjacent normal tissue - contrast enhancement gradients in T1ce, signal

heterogeneity in necrotic cores, and perilesional edema extent in FLAIR. The Mamba-2 SSM, which applies the selective state propagation method to the complete volumetric sequence of the cells, makes the tumor sub-regions of neural tissue that can be separated by non-lesion cells in any two-dimensional cut, but makes continuous structures in three-dimensional space. It is through the gated fusion mechanism that the network can be able to decide for every given spatial location whether it is the local representation or global representation that is the more diagnostically informative and this determination depends systematically on the type of tumor sub-region and the imaging sequence.

The fact that KAN activations outperform MLP activations at boundaries between tumors is a significant property of the spline as an approximation of functions with highly localized high-frequency information that cannot be represented at all by the global polynomials (or some alternate form of global activation) used by global neural network approximations. One such locally complex function is the enhancing tumor sub-region, which is sharply defined at the boundary in T1ce with sharp transitions on the order of millimetres, and the 4.1-point gain of DSC-ET with KAN introduction (Table I) is the practical expression of this approximation-theoretic benefit.

There are a number of failure modes left. Cases which contain enhancing tumor sub-regions with less than 100 voxels have disproportionately poor ET segmentation (DSC-ET below 70 percent) consisting presumably of the insufficient gradient signal when the target region occupies less than 100 voxels in the 1283 training patch. Unstable volumes (high motion artifact) - the impact of which on the BraTS 2024 is about 3 percent - are volumes that result in fragmented predictions, which saturate HD95 scores of the subjects most severely impacted. Such kinds of failures inspire further research on explicit motion correction pre-processing and location-dependent weight loss.

The 48.3 M parameter count used in the current study is a weakness because it is too large to fit on a typical software-based gradient checkpointing system (16 GB) with a full patch resolution of 128 basic at current level. The clinically acceptable per-volume inference time of 1.8 seconds does not allow the real-time integration of the intraoperative application. Interpretation to non-BraTS anacquisition protocols is still awaited to be determined; single-dataset validation is a weakness that federated learning among multi-site cohorts would solve. Future prospects are extension to four dimensional perfusion MRI to measure time dependent tumor heterogeneity, combination with radiogenomic prediction computing, and compression through knowledge distillation to run on resource limited edge devices.

6. Conclusion

This paper introduced CNN-Mamba-KAN, a new multi-modal MRI-based architecture of the hybrid deep-learning, which focuses on early-stage brain tumor segmentation, making use of three complementary paradigms: ResNet-50 convolutional encoding to extract local features, Mamba-2 state space model branches to efficient global context modelling, and Kolmogorov-Arnold Network decoding to expressive feature reconstruction. To boost the efficacy of the Fusion gate, a cross-attention fusion gate merges local and global encoder representations, a attention-enhanced CBAM+FPN bottleneck consolidates multi scale features and a composite boundary-aware loss function expressly attempts to optimize

tumor margin delineation. CNN-Mamba-KAN performs at a state-of-the-art level under five-fold cross-validation using rigorous statistical validation on BraTS 2024: Whole Tumor DSC = 92.4% (HD95 = 3.21 mm) Tumor Core DSC = 89.7% (HD95 = 4.05 mm) and Enhancing Tumor DSC = 87.2% (HD95 = 5.18 mm) and is significantly better than all ten competing methods The ablation experiment attests to the fact that every architectural element such as Mamba-2 SSM global context, KAN decoder, attention bottleneck, and boundary-aware loss had a unique, measurable and statistically significant increase in performance, which together with other elements led to a 12.3 percentage point improvement over the ResNet-50 U-Net baseline. This finding indicates that the discussion of heterogeneous architectural integration under the guidance of complementary representational capabilities of convolutional, state space, and KolmogorovArnold paradigm is a fruitful and principled avenue of knowledge to take medical image segmentation beyond the performance limit of any individual architectural family. Our hope is that CNN-Mamba-KAN framework and its design principles will inspire a wider category of future volumetric medical image analysis systems, which will result in better clinical outcomes of brain tumor patients due to more accurate, reproducible, and timely automated segmentation.

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