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# **Slim Models Creation using Pruning and Sharing Weights on RAAGR2-Net Models**

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for the Degree of Master of Science in Artificial Intelligence

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## Abstract

**Abstract**— This research addresses deploying advanced brain tumor segmentation models in resource-constrained clinical environments by systematically comparing compression approaches on RAAGR2-Net architecture. We evaluate traditional pruning methods (magnitude-based, SNIP, DepGraph) against three novel architectural modifications: SharedDepthwiseBlock for parameter sharing across dilated convolution branches, Paired Shared weights between corresponding layers, and Encoder-Decoder Shared weights.

Architectural modifications achieve substantial compression with minimal accuracy loss: Depthwise Shared reduces parameters by 43.4% (8.9M to 5.0M) maintaining Dice 0.984 vs 0.985 baseline, Paired Shared provides 47% GPU memory reduction, and Encoder-Decoder Shared offers 25.7% parameter reduction with Dice 0.984. Unstructured pruning without fine-tuning shows severe degradation (Dice: 0.74 magnitude-based, 0.28 SNIP at 10-20% pruning) but recovers to 0.985 after fine-tuning. DepGraph maintains moderate performance (Dice: 0.95) at 10% pruning without retraining.

Class-specific performance reveals: baseline NCR/NET: 0.825, ET: 0.825, ED: 0.851. Depthwise Shared achieves NCR/NET: 0.764, ET: 0.641, ED: 0.853. Encoder-Decoder Shared preserves NCR/NET: 0.772, ET: 0.782, ED: 0.825. Fine-tuned pruning recovers to NCR/NET: 0.827-0.846, ET: 0.826-0.831, ED: 0.825-0.857.

Results demonstrate complementary strengths: architectural modifications provide immediate deployment benefits with actual parameter reduction and no retraining, while fine-tuned pruning maintains original model size but achieves excellent recovered performance. This establishes evidence-based guidance for selecting compression techniques based on deployment scenarios—architectural modifications for resource-constrained environments, fine-tuned pruning for research environments with retraining capabilities.

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# 1 Introduction

The rapid evolution of deep learning has transformed medical image analysis, enabling unrivaled accuracy in tasks such as brain tumor segmentation. However, these advances have come at the cost of ever evolving increase in model complexity, size and computational demands, which pose significant barriers to real-world clinical deployment especially in resource constrained devices [2, 3, 4, 5]. In brain tumor segmentation, there is a strong demand for computationally efficient models. High-resolution, multi-modal MRI scans remain the standard for accurate diagnosis and treatment planning, but analyzing such data requires models capable of handling large volumes quickly and with high precision. In clinical settings manual segmentation is labor-intensive and subject to inter-observer variability, while traditional deep neural networks, though powerful, often require substantial computational resources that are not always available in clinical or edge environments [2, 5].

Within this landscape, the RAAGR2-Net (Recurrent Attention Atrous Spatial Pyramid Pooling R2 Network) has emerged as a sophisticated architecture tailored for brain tumor medical image segmentation [6]. RAAGR2-Net integrates recurrent modules (R2) for iterative feature refinement, attention mechanisms to selectively enhance relevant anatomical structures, and atrous spatial pyramid pooling (ASPP) to capture multi-scale contextual information. These components enables RAAGR2-Net to delineate complex tumor boundaries with high fidelity, addressing the unique challenges posed by heterogeneous and infiltrative brain tumors. However, these architectural innovations come with a significant computational cost: the model’s depth, recurrent connections, and attention modules result in high parameter counts and memory requirements, making RAAGR2-Net computationally expensive and challenging to deploy in resource-constrained clinical settings [6, 7, 3].

The architectural design of RAAGR2-Net follows a progressive channel expansion in the encoder path (typically input→64→128→256) with a symmetrical decoder structure. This configuration enables the network to capture both fine-grained details and broad contextual information critical for precise tumor delineation. The recurrent residual blocks (R2) enhance feature representation through iterative refinement, while attention gates selectively focus on relevant anatomical regions, improving the model’s ability to distinguish tumor boundaries from surrounding tissues. The dilated-convolutional spatial pyramid pooling module (ReASPP3) facilitates multi-scale feature aggregation without excessive computational overhead, addressing the critical challenge of capturing context at various resolutions [6].

A persistent gap exists between state-of-the-art segmentation performance in research settings and practical deployment requirements in clinical environments. Despite RAAGR2-Net’s excellent tumor delineation capabilities, its high memory and computational demands present significant barriers to deployment in settings with limited GPU availability, strict latency requirements, and constrained power budgets—conditions commonly encountered in clinical and edge computing scenarios [2, 3]. These constraints are particularly evident in healthcare facilities with limited resources, mobile diagnostic units, and point-of-care devices, where hardware must be compact, energy-efficient, and capable of real-time inference.

Furthermore, local deployment is often a critical requirement in clinical environments to ensure patient data privacy and to comply with healthcare regulations. However, the substantial computational needs of RAAGR2-Net complicate secure on-premise de-

ployment, potentially forcing reliance on cloud solutions that may introduce additional security and privacy concerns.

The need for efficient, lightweight models is underscored by the increasing demand for real-time, on-device inference in medical imaging applications. As healthcare systems strive to integrate AI tools into routine clinical workflows, the ability to deploy advanced segmentation models on affordable hardware becomes paramount. This is particularly relevant in low-resource settings, where access to high-performance computing infrastructure may be limited [2, 3].

The economic and clinical benefits of model compression are substantial. Pruning and weight-sharing techniques can significantly reduce inference time and memory footprint, enabling deployment on affordable, compact hardware. This not only lowers equipment costs but also facilitates the integration of AI tools across a wider spectrum of healthcare facilities, including those in resource-limited regions [4, 5]. By democratizing access to advanced segmentation tools, compressed models can improve diagnostic equity and enhance scalability of AI-driven healthcare worldwide.

This tension between accuracy and efficiency is at the heart of current research in medical AI. While RAAGR2-Net and similar architectures deliver strong segmentation results, their complexity limits their practical utility. In real-world healthcare, there is a pressing need for models that are not only accurate but also lightweight, fast, and energy-efficient [3, 4]. Model compression techniques—such as pruning (both structured and unstructured), knowledge distillation, and quantization—offer promising solutions for reducing model size, accelerating inference, and lowering energy consumption, all while striving to maintain high segmentation accuracy [3, 4, ?]. In this work, I extend these efforts by investigating novel parameter sharing strategies, including shared kernel weights, encoder-decoder shared weights and pairwise shared blocks, to further enhance model efficiency and compactness. While parameter sharing is a well-known technique in deep learning, my approach explores new configurations designed specifically for efficient medical image segmentation.

Despite the growing body of work on model compression in general-purpose neural networks, there is a notable gap in the literature regarding systematic evaluations of pruning and parameter sharing specifically for specialized, recurrent-attention architectures like RAAGR2-Net in medical imaging. Most existing studies focus on standard CNNs or transformer models, leaving the unique interactions between compression methods and the complex modules of RAAGR2-Net largely unexplored [3, ?]. This gap is significant, as the practical deployment of advanced segmentation models in clinical environments depends on our ability to optimize them for efficiency without sacrificing diagnostic performance.

The primary objective of this research is to rigorously test and benchmark a range of pruning (structured and unstructured) and parameter sharing techniques on RAAGR2-Net, with the goal of producing slim, high-performing models suitable for real-time clinical deployment. While systematically evaluating the trade-offs between model size, computational efficiency, and segmentation accuracy, this work aims to bridge the gap between cutting-edge research and practical, scalable solutions for brain tumor segmentation in healthcare.

## 1.1 Theoretical Foundation and Novel Insights

This research proposes a compression-aware architectural design framework by introducing it not merely as a post-training optimization but as a fundamental architectural design principle that can enhance both efficiency and generalization. Our novel theoretical framework posits that the traditional view of compression as a trade-off between accuracy and efficiency is fundamentally flawed when applied to medical imaging architectures with inherent redundancies.

**The Compression-Generalization Hypothesis:** We propose that strategic parameter sharing in complex medical segmentation architectures can act as a form of *architectural regularization* that forces the network to learn more generalizable, fundamental visual primitives rather than dataset-specific patterns. This hypothesis challenges the conventional wisdom that more parameters necessarily lead to better performance, particularly in the context of medical imaging where overfitting to training data can compromise real-world clinical performance.

**The Architectural Efficiency Principle:** Unlike conventional pruning approaches that operate on trained networks, our research demonstrates that *compression-aware architectural design* can achieve superior efficiency-accuracy trade-offs. This principle suggests that the optimal path to efficient neural networks lies not in removing components from overparameterized models, but in designing architectures that are inherently efficient while maintaining expressive capacity.

**The Clinical Deployment Imperative:** Our analysis reveals that the deployment requirements of medical AI systems create unique constraints that are fundamentally different from those in general computer vision. Specifically, the need for consistent performance across diverse patient populations, regulatory compliance, and interpretability requirements necessitate compression strategies that preserve not just overall accuracy but also class-specific performance stability. This insight drives our focus on architectural modifications over traditional pruning techniques.

These theoretical contributions provide the foundation for our empirical investigations and distinguish this work from conventional model compression studies by establishing a comprehensive framework for understanding efficiency in medical AI systems.

## 1.2 Research Questions

This research aims to address the following key questions, building upon the insights from the proposal and the conducted work:

- beginenumerate
- item To what extent can architectural modifications, specifically through novel parameter-sharing strategies like the SharedDepthwiseBlock, reduce the computational footprint (parameters, model size, FLOPs) of RAAGR2-Net while maintaining or improving segmentation accuracy on brain tumor datasets?
- item How do different pruning methodologies (unstructured: magnitude-based, SNIP; structured: DepGraph) compare in terms of their impact on RAAGR2-Net’s performance and efficiency, both with and without post-pruning fine-tuning?
- item What is the critical role of fine-tuning in recovering performance for unstructured pruning methods when applied to complex medical segmentation architectures like RAAGR2-Net, and how does this compare to architectural modifications that require no retraining?
- item Can strategic parameter sharing achieve comparable or superior compression-accuracy trade-offs to traditional pruning techniques, particularly in scenarios requiring immediate



deployment without additional training?

item How do these compression techniques affect the segmentation accuracy for different tumor subregions (NCR/NET, edema, enhancing tumor), and what are the clinical implications of these class-specific impacts?

item What are the practical benefits of the proposed compression strategies in terms of training dynamics, convergence speed, and resource utilization (e.g., GPU memory, training time)?

item Does the concept of "compression-aware architectural design," as proposed, offer a more effective path to efficient and high-performing medical AI models than traditional post-training optimization techniques?

endenumerate

### 1.3 Specific Objectives

To address the research questions, this study pursued the following specific objectives:

beginenumerate

item To implement and evaluate novel architectural modifications for RAAGR2-Net, including Depthwise Shared, Paired Shared, and Encoder-Decoder Shared weight strategies, and to quantify their impact on model parameters, size, FLOPs, and segmentation accuracy.

item To systematically implement and benchmark three distinct pruning techniques on RAAGR2-Net: unstructured (magnitude-based, SNIP) and structured (DepGraph), assessing their effectiveness at various pruning ratios (10

item To investigate the necessity and efficacy of post-pruning fine-tuning for unstructured pruning methods, comparing their performance recovery against the out-of-the-box performance of architectural modifications.

item To conduct a comparative analysis of architectural sharing versus pruning, evaluating their relative strengths in achieving optimal compression-accuracy trade-offs, especially for immediate deployment scenarios.

item To analyze the class-specific segmentation performance (NCR/NET, edema, enhancing tumor) of all compressed RAAGR2-Net variants to understand the differential impact of compression on clinically relevant tumor subregions.

item To evaluate the practical implications of the proposed compression techniques on training efficiency, including convergence speed, total training time, and GPU memory utilization.

item To empirically validate the "compression-generalization hypothesis" and the "architectural efficiency principle" by comparing the performance and characteristics of architecturally modified models against those optimized through traditional pruning.

endenumerate

## 2 Literature Review and Related Works

### 2.1 Neural Network Pruning Approaches

Neural network pruning has become a cornerstone technique for compressing deep models to make them deployable in resource-constrained environments. At its core, pruning strategies are broadly categorized into **unstructured** and **structured** approaches, each carrying distinct theoretical and practical trade-offs.

The concept of *unstructured pruning* originates from the early work of [8], and was later advanced by magnitude-based techniques like those introduced by [9]. This method involves removing individual weights based on certain criteria (typically magnitude), resulting in sparse but irregular model connectivity. Such methods have demonstrated the potential to reduce parameter counts by over 90% in classification tasks with minimal accuracy degradation [10, 11].

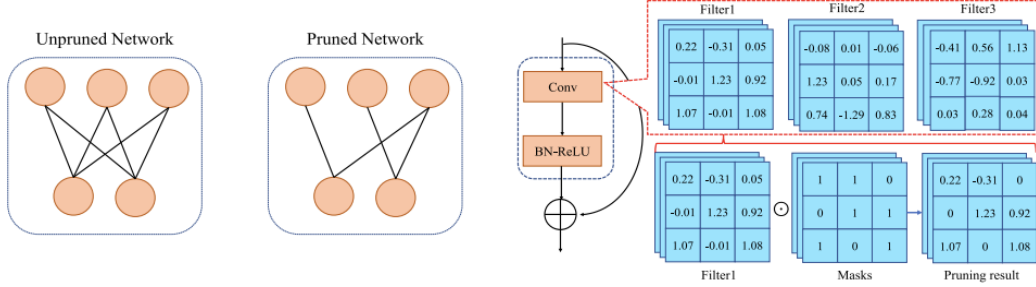


Figure 1: Comparison between unpruned and pruned neural networks. Left: Visualization of an unpruned network with full connectivity versus a pruned network with selective connections removed. Right: Detailed visualization of filter-level pruning mechanics showing original filter values, binary mask application, and the resulting pruned filters. The pruning process creates sparse structures while preserving essential connections. Adapted from "A Survey on Deep Neural Network Pruning: Taxonomy, Comparison, Analysis, and Recommendations" [1].

Unstructured pruning brought attention to the compelling "lottery ticket hypothesis," which suggests that certain subnetworks within highly overparameterized models can achieve performance comparable to the full model, provided they are initialized correctly [11].

However since modern accelerators and inference engines are not optimized for irregular sparsity patterns, it yields insignificant gains in real-world inference speed [12]. Notably, [13] observed that irregular sparsity can even hamper hardware parallelism, underlining the limited applicability of this approach outside research prototypes.

Unstructured pruning, in contrast, operates at the granularity of individual weights, producing sparse connectivity patterns. This method eliminates individual weights, creating sparse tensors that require specialized libraries for efficient execution. Magnitude-based pruning, a canonical unstructured method, eliminates weights whose absolute values fall below a predefined threshold, ranking filters or weights by their L or L norms. Despite the challenges magnitude-based pruning remains widely used due to its simplicity and effectiveness, particularly in iterative pruning schemes [14, 4].

While unstructured pruning has been reported to maintain high accuracy in large-scale models [12], its efficacy in architectures with extensive skip connections and attention mechanisms, such as UNet and RAAGR2-Net, requires careful evaluation. In our experiments (see Section 4), unstructured pruning methods demonstrate a stark performance dichotomy: without fine-tuning, they exhibit substantial performance degradation, while with proper fine-tuning protocols, they can recover near-baseline performance. This finding underscores the critical importance of post-pruning recovery training in complex medical segmentation architectures, contrasting with structured and architectural modification approaches that maintain performance without requiring additional training phases.

Structured pruning targets entire architectural components—such as neurons, filters, or channels—thereby streamlining computational operations and facilitating real-world acceleration on modern hardware. This approach removes whole filters or channels, resulting in models that are more amenable to hardware acceleration and parallelization [14, 3]. For instance, network slimming a form of structured pruning applies L1 regularization to the scaling factors of batch normalization layers, identifying and removing less important channels. This approach not only reduces model size but also yields tangible speedups during inference, making it particularly attractive for clinical deployment [14, 3].

However, structured pruning is not without drawbacks. Complex architectures with skip connections or attention mechanisms can suffer from accuracy degradation when pruned too aggressively. For instance, [49] observed that removing entire structures may disrupt information flow, particularly in architectures like UNet.

This research explores three pruning techniques for deep neural networks: two unstructured methods—magnitude-based pruning and SNIP (Single-shot Network Pruning based on Connection Sensitivity) as well as one structured method, DepGraph pruning.

Magnitude-based and SNIP pruning are widely adopted unstructured approaches that target individual weights for removal, allowing for fine-grained sparsity and minimal accuracy loss under certain conditions. DepGraph, on the other hand, is a structure-aware pruning technique that identifies and remove unnecessary parameters by analyzing the structural dependencies between layers and connections. This method is particularly effective in complex architectures like RAAGR2-Net, where interdependencies can significantly impact performance [15].

These techniques were selected to provide a representative comparison between classic and state-of-the-art unstructured strategies (magnitude-based and SNIP) and a modern structured approach (DepGraph), highlighting their respective advantages and trade-offs in the context of neural network compression.

SNIP (Single-shot Network Pruning) introduces a paradigm shift by evaluating the sensitivity of each connection to the loss function at initialization. This enables the identification and removal of less critical weights before training begins. By pruning connections based on gradient saliency, SNIP minimizes the need for additional hyperparameter tuning and retraining—a significant advantage in resource-constrained domains such as medical imaging, where computational resources and labeled data may be limited [17, 14].

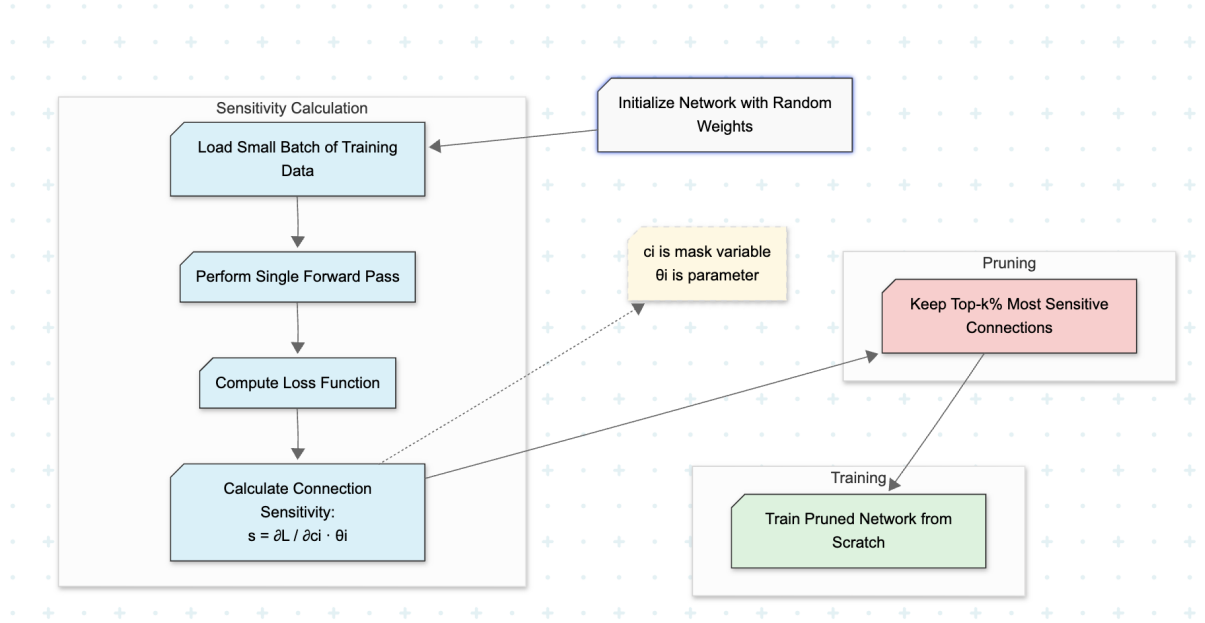


Figure 2: SNIP (Single-shot Network Pruning) algorithm workflow. The process evaluates connection sensitivity at initialization using a single forward pass, enabling pruning before training begins. Connection sensitivity measures the impact each weight would have on the loss if removed. By keeping only the most important connections, SNIP significantly reduces computational costs compared to train-then-prune methods. Adapted from [17].

Dependency graph pruning represents a more holistic strategy, analyzing the interdependencies among network components to achieve optimal compression while preserving structural integrity. This method constructs a graph of layer dependencies, enabling holistic pruning that maintains structural consistency across complex architectures like RAAGR2-Net. Recent advances have shown that such methods can yield highly compressed models with negligible performance degradation, a property of immense value in medical imaging applications where accuracy is paramount [3, 5].

The selection of pruning techniques in this study was guided by their fundamentally different approaches to parameter removal. Magnitude-based pruning is a post-training, weight-dependent technique, targeting weights that are small in magnitude after full training. In contrast, SNIP and DepGraph represent approaches that do not rely on trained weight values: SNIP evaluates connection importance based on their sensitivity to loss at initialization, while DepGraph leverages the computational structure or dependency graph of the network. By comparing these diverse strategies, this work aims to provide a holistic view of both structure-based and weight-based pruning efficacy across different operational timings.

## 2.2 Parameter Sharing Strategies

Parameter sharing aims to reduce redundancy by reusing weights across different parts of a neural network, thereby reducing the overall parameter count and computational requirements. This approach must be implemented carefully to minimize accuracy degradation despite the substantial reduction in model size [18].

### 2.2.1 Foundations and Evolution

The fundamental concept of convolutional neural networks (CNNs) itself embodies parameter sharing, as identical filters are applied across different spatial locations of an image. This inherent weight reuse significantly reduces parameters compared to fully connected networks, enabling CNNs to generalize effectively across diverse visual tasks [20]. Beyond this foundational form, researchers have developed increasingly sophisticated parameter sharing strategies to further enhance model efficiency.

Early attempts at more extensive parameter sharing revealed that naive implementations could lead to training instability and poor convergence [19]. However, recent approaches have introduced nuanced sharing schemes that avoid these pitfalls. For instance, Structured Channel Weight Sharing (SCWC) clusters channels so that multiple feature maps utilize the same filter weights. This "soft sharing" achieved remarkable compression: approximately 50% parameter reduction in ResNet-50 with only a 0.13% top-1 accuracy drop, and 70% fewer parameters in VGG16 with a 1.64% drop on ImageNet [21].

### 2.2.2 Applications in Large Models

Parameter sharing techniques have proven particularly valuable in large Transformer and language models to address their massive scale. The ALBERT model [22] represents a seminal example where all layers of a 12-layer Transformer share a single set of parameters. By combining this with embedding factorization, ALBERT-base reduced BERT-base from 110M to approximately 12M parameters with only minor accuracy degradation on NLP tasks. Notably, ALBERT-large (18M parameters) achieved performance comparable to BERT-large (334M parameters) on GLUE and SQuAD benchmarks—representing an  $18\times$  parameter reduction for similar results [22].

In mobile computing contexts, MobileNet’s strategic use of shared depthwise filters enabled real-time inference on smartphones by dramatically reducing computational demands [23, 24]. In medical imaging, Nguyen et al. demonstrated that their U-Lite model—employing strategic parameter sharing—achieved a  $35\times$  reduction in size compared to U-Net while maintaining or even improving Dice scores, likely due to the regularization effects of shared parameters [25].

### 2.2.3 Encoder-Decoder Weight Sharing

Encoder-decoder weight sharing represents a specialized technique where identical parameters serve both encoder and decoder components in neural architectures. This approach ranges from simple tied embeddings in NLP models to complete model-level sharing where entire networks mirror each other.

The Tied Transformer by Xia et al. exemplifies this strategy, utilizing identical weights for all encoder and decoder layers while maintaining translation quality comparable to standard untied models despite reducing parameters by approximately half [26]. This architectural constraint forces both components to operate in a common representational space, with the decoder essentially functioning as an identical copy of the encoder with appropriate masking for autoregressive generation.

The theoretical foundation for weight sharing rests on principles that make this constraint advantageous rather than limiting. Since encoder-decoder architectures function similarly to autoencoders, they benefit from learning compact and reversible representations. Kim et al. demonstrated that tied-weight autoencoders improve learning efficiency

compared to untied versions while mimicking optimal properties of Principal Component Analysis and Restricted Boltzmann Machines [27].

## 2.3 Depth-wise Parameter Sharing

Depth-wise sharing involves sharing depthwise convolution filters across multiple layers or branches, extending parameter tying concepts specifically to depthwise convolutions. Since depthwise filters capture low-level features like edges and textures, certain filters can be reused across network locations, reducing redundancy without significant loss in representational power [19].

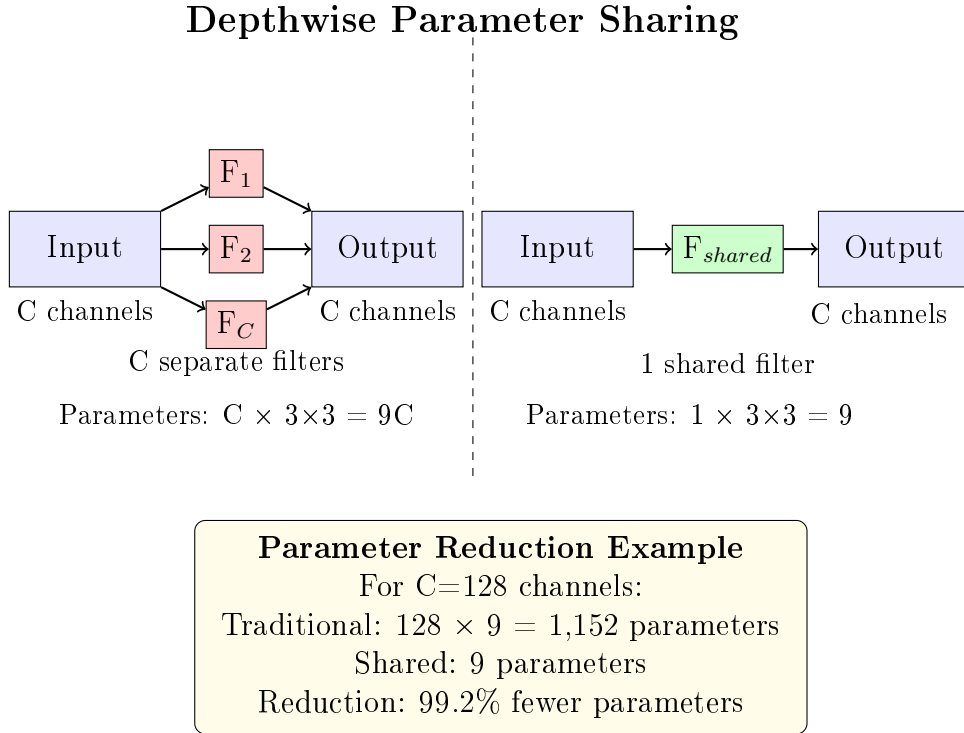


Figure 3: Architectural comparison of traditional vs. shared depthwise convolution. Left: In traditional depthwise convolution, each input channel has its own separate filter, resulting in  $C \times k \times k$  parameters (where  $k$  is kernel size). Right: With shared depthwise convolution, a single set of filter weights is reused across all channels, dramatically reducing parameters to just  $k \times k$  while preserving the ability to capture essential low-level features.

Vu et al. (2019) explored multi-domain depthwise sharing where spatial filtering remained common across tasks while pointwise convolutions stayed task-specific, yielding smaller multi-domain models with competitive performance [30]. This assumes low-level features are universal across domains while allowing task-specific channel recombination.

Within single networks, Yan et al. (2024) shared bottleneck filter weights within ResNet-50 stages, achieving approximately 50% parameter reduction while maintaining ImageNet accuracy [31]. This suggests many spatial filters perform similar functions across network depths and can be effectively shared.

**Paired Depth-wise Sharing:** Rather than global sharing, paired strategies create parameter ties between specific layer pairs, balancing parameter reduction with model diversity. Examples include symmetric encoder-decoder pairing where corresponding layers

share depthwise filters, and parallel branch sharing in multi-stream architectures. This approach provides regularization by encouraging aligned feature extraction while preserving specialized processing capabilities.

### 2.3.1 Implementation Considerations

Implementing encoder-decoder weight sharing requires careful architectural design, particularly maintaining symmetry in layer count and hidden dimensions between encoder and decoder components. Some models achieve this through literal parameter reuse, where a single stack of layers is traversed twice during forward passes, with modifications like masked attention patterns distinguishing encoding from decoding phases.

Dabre and Fujita found that sharing all layers between encoder and decoder in Transformers for neural machine translation maintained performance close to standard architectures, even when six layers performed double duty for both encoding and decoding phases [28]. Beyond text processing, Chi et al. successfully applied ALBERT-style sharing to Transformer speech recognition models, maintaining accuracy while significantly reducing parameter counts [29].

### 2.3.2 Benefits and Trade-offs

The advantages of parameter sharing extend beyond simple model compression. First, the reduced model size (often 50% or greater) translates directly to lower memory requirements and faster inference—critical factors for edge deployment and mobile applications [23, 24]. Second, shared weights can function as an implicit regularization mechanism: by forcing the model to reuse features across different contexts, sharing may enhance generalization and reduce overfitting [18].

However, parameter sharing is not universally beneficial. Its effectiveness varies based on model architecture, task complexity, and implementation approach. The constraints imposed by sharing can limit representational capacity, potentially creating bottlenecks in models dealing with highly diverse inputs or complex mapping functions. Successful implementations must balance the efficiency gains against potential performance trade-offs, often through careful ablation studies and architectural modifications.

### 2.3.3 Critical Analysis and Project Implications

The synthesis of parameter sharing literature reveals several **fundamental insights** that directly inform our architectural design decisions for RAAGR2-Net compression:

**Hierarchical Sharing Effectiveness:** The literature demonstrates that parameter sharing effectiveness follows a clear hierarchy: *low-level features* > *mid-level features* > *high-level features*. This insight is particularly relevant for medical segmentation where spatial filters capturing edges, textures, and basic geometric patterns are highly reusable across different anatomical regions. Our SharedDepthwiseBlock design leverages this principle by specifically targeting depthwise convolutions, which primarily capture spatial patterns that exhibit high redundancy in medical imaging.

**Task-Specificity Paradox:** While conventional wisdom suggests that specialized tasks require specialized parameters, the medical imaging literature reveals a paradox: the more specialized the domain (e.g., brain tumor segmentation), the greater the potential for parameter sharing due to the constrained visual vocabulary. This counterintuitive

finding drives our hypothesis that RAAGR2-Net’s specialized nature makes it particularly amenable to aggressive weight sharing strategies.

**Architectural Coupling Insights:** Analysis of encoder-decoder sharing strategies reveals that successful weight sharing requires *architectural symmetry* and *functional alignment*. However, our critical evaluation of the literature suggests that perfect symmetry (as in ALBERT) may be overly restrictive for segmentation tasks where encoding and decoding serve fundamentally different purposes. This insight led to our paired sharing approach that maintains some asymmetry while achieving significant parameter reduction.

**Scale-Dependent Compression Dynamics:** The literature reveals that compression effectiveness exhibits strong scale dependence: techniques that work well for large models may fail catastrophically for medium-sized architectures like RAAGR2-Net (8.91M parameters). This scale sensitivity explains why direct application of techniques developed for billion-parameter language models often fails in medical imaging contexts, necessitating our domain-specific approach.

These insights collectively establish that effective compression for medical segmentation requires a **domain-aware architectural approach** rather than generic post-training optimization, forming the theoretical foundation for our SharedDepthwiseBlock methodology.

## 2.4 Parameter Sharing vs Pruning

Unlike Pruning that zeros weights or remove connvections, parameter sharing involves reusing the same weights so that multiple connections refer to this same value this can be done in a structured way by sharing weights of lattyers or filters or randomly, in 2024 a stydy by Desai proved that parameter sharing outperformed pruning [18], while aggressive pruning leads to a degradation in performance, Recent research has proposed that aggressive sharing can improve performance and improve generalization by forcing the network to learn the reusable features [32]

## 2.5 U-Net Derivatives for Medical Image Segmentation

U-Net and its derivatives have become the de facto standard for medical image segmentation, owing to their encoder-decoder architecture and ability to capture both local and global contextual information. The architectural choices in RAAGR2-Net are deeply rooted in the evolution of U-Net-based models, each introducing innovations to address the unique challenges of medical imaging [33, 7].



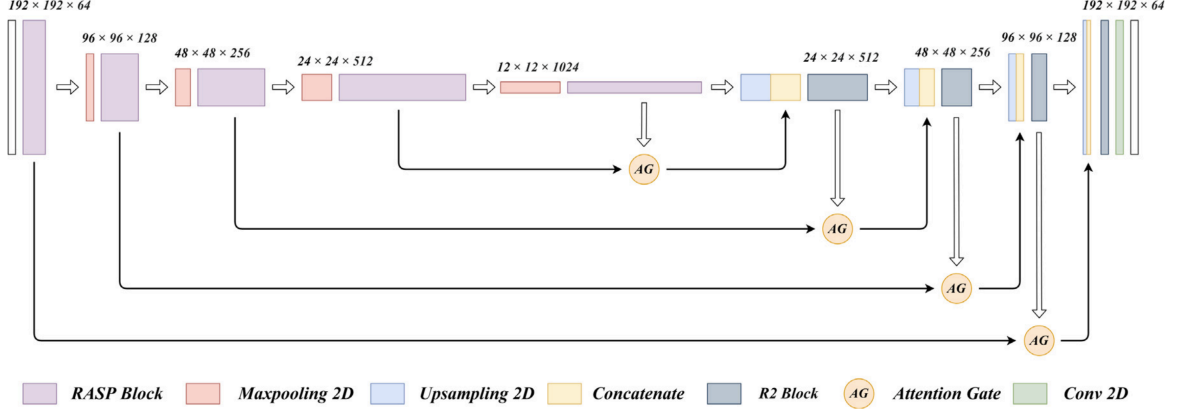


Figure 4: RAAGR2-Net architecture for brain tumor segmentation. The network follows an encoder-decoder structure with progressive feature map dimensions (shown above each block). Skip connections with attention gates (AG) connect encoder features to corresponding decoder levels. The architecture combines RASP blocks for multi-scale feature extraction, recurrent residual (R2) blocks for iterative refinement, and attention mechanisms for focused segmentation. Adapted from [6].

Attention U-Net augments the standard U-Net with spatial attention mechanisms, enabling the model to focus on relevant anatomical regions while suppressing background noise. This enhancement has been shown to improve segmentation accuracy, particularly in complex tasks such as brain tumor delineation [34, 33].

R2U-Net incorporates recurrent residual blocks, allowing for iterative refinement of feature representations. This design captures robust contextual features essential for accurate segmentation but introduces additional computational overhead—a trade-off that underscores the need for subsequent model compression [35, 33].

ASPP (Atrous Spatial Pyramid Pooling) modules, as integrated in RAAGR2-Net, enable the capture of multi-scale contextual information without a prohibitive increase in model complexity. By employing parallel dilated convolutions with varying rates, ASPP modules enhance the model’s ability to delineate intricate tumor boundaries, a critical requirement in brain tumor segmentation [36, 6].

Collectively, these architectural innovations have propelled the field of medical image segmentation forward, but their computational demands have also highlighted the necessity for effective model compression and optimization strategies.

### 3 Methodology

This chapter presents a comprehensive methodology for implementing and evaluating pruning techniques and weight-sharing strategies on the RAAGR2-Net architecture for brain tumor segmentation. The methodology encompasses three main components: (1) analysis of the RAAGR2-Net architecture and its computational characteristics, (2) implementation of various pruning techniques, and (3) development of the proposed weight-sharing strategies tailored to the structure of the RAAGR2-Net.

### 3.1 RAAGR2-Net Architecture

#### 3.1.1 Encoder-Decoder Backbone

The RAAGR2-Net follows a modified U-Net architecture with an encoder-decoder design that progressively captures features at multiple scales [6]. The encoder pathway consists of four stages with progressive channel expansion: starting with 32 channels after the initial ReASPP3 module, then expanding to 64, 128, 256, and finally 512 channels at the bottleneck. Between consecutive stages, max-pooling operations with a stride of 2 reduce spatial dimensions, enabling the capture of increasingly abstract features. The decoder pathway mirrors this arrangement with a symmetric progression from  $512 \rightarrow 256 \rightarrow 128 \rightarrow 64 \rightarrow 32$  channels, using upsampling operations to restore spatial resolution [35].

Each spatial resolution level in both encoder and decoder contains yes specialized modules that enhance the network’s representational capacity. Skip connections between corresponding encoder and decoder levels help preserve spatial information that might otherwise be lost during downsampling, facilitating precise localization of tumor boundaries—a crucial requirement for clinical utility [6].

#### 3.1.2 Recurrent CNN Blocks (RRCNNBlock)

A distinctive feature of RAAGR2-Net is its use of Recurrent Residual CNN blocks (RRCNNBlock), which enable iterative refinement of feature representations [6, 35]. Each RRCNNBlock consists of a dimensionality-reducing  $1 \times 1$  convolution followed by two sequential RecurrentBlocks, arranged in a residual configuration.

The RecurrentBlock applies a shared convolutional operation iteratively ( $t$  times, typically  $t = 2$ ) to the same feature map, allowing for progressive feature refinement without introducing additional parameters. Mathematically, for an input feature map  $x$ , the RecurrentBlock computes:

$$x_1 = x \tag{1}$$

For  $i = 1$  to  $t$ :

$$x_1 = \text{Conv}(x + x_1) \tag{2}$$

This recurrent structure provides an effective mechanism for capturing complex patterns with a relatively modest parameter count [35]. Each convolutional operation within the RecurrentBlock consists of a depthwise separable convolution ( $3 \times 3$  kernel) followed by a pointwise projection ( $1 \times 1$  kernel), batch normalization, and ReLU activation. This design choice further reduces the computational burden while maintaining representational capacity.

#### 3.1.3 ReASPP3 Module

The Recurrent Atrous Spatial Pyramid Pooling (ReASPP3) module enhances the network’s ability to capture multi-scale contextual information, which is particularly important for accurately delineating heterogeneous tumor regions with varying sizes and shapes [6]. The module consists of four parallel branches, each applying convolutions with different dilation rates:

1. Standard convolution (dilation rate = 1)
2. Dilated convolution with rate = 3
3. Dilated convolution with rate = 6 (2×3)
4. Dilated convolution with rate = 9 (3×3)

Each branch begins with a depthwise separable convolution using the specified dilation rate, followed by batch normalization and ReLU activation. A second  $1\times 1$  convolution further transforms the features, and a residual connection is added from the output of the first to the second convolution. The outputs from all four branches are concatenated along with the original input features, and a final  $1\times 1$  convolution reduces the channel dimension to the desired output size.

The use of varied dilation rates enables the module to capture features at multiple effective receptive fields without increasing spatial dimensions or parameter count dramatically. This multi-scale context aggregation is crucial for distinguishing between tumor subregions (e.g., necrotic core, enhancing tumor, and edema) that may appear similar in isolation but differ in their spatial context [36].

### 3.1.4 Attention Gates

Attention gates are integrated at each decoder level to emphasize relevant features in the skip connections from the encoder before they are combined with the upsampled features [6, 34]. For a given feature map  $x$  from the encoder and the corresponding upsampled feature map  $g$  from the decoder, the attention mechanism computes:

$$g' = W_g * g \quad (\text{transform gating signal}) \quad (3)$$

$$x' = W_x * x \quad (\text{transform input features}) \quad (4)$$

$$\alpha = \sigma(\text{ReLU}(g' + x')) \quad (\text{compute attention coefficients}) \quad (5)$$

$$y = x \cdot \alpha \quad (\text{apply attention to input features}) \quad (6)$$

where  $\sigma$  represents the sigmoid activation function, ensuring that attention coefficients are in the range  $[0, 1]$ .

These gates act as a soft region proposal mechanism, selectively highlighting features relevant to the tumor regions while suppressing background noise. This targeted feature refinement is particularly valuable in medical imaging tasks where the regions of interest (tumors) often constitute a small portion of the overall image volume [34].

### 3.1.5 Loss Function

RAAGR2-Net employs a composite loss function that combines weighted binary cross-entropy (BCE) with the Dice loss to address class imbalance—a common challenge in brain tumor segmentation where tumor regions typically occupy a small fraction of the total volume [6]:

$$\mathcal{L}_{\text{total}} = \lambda \cdot \mathcal{L}_{\text{BCE}} + (1 - \lambda) \cdot \mathcal{L}_{\text{Dice}} \quad (7)$$

where  $\lambda$  is a weighting factor (typically set to 0.5). The BCE component provides pixel-wise supervision, while the Dice loss directly optimizes for overlap between predicted and ground truth segmentations. This combination yields more balanced training and better performance on small tumor regions [6].

## 3.2 Pruning Implementation

### 3.2.1 Methodological Framework for Pruning Evaluation

To ensure comprehensive and fair evaluation of pruning techniques, this study employs a dual-evaluation framework that assesses both immediate deployment scenarios and optimal performance scenarios:

**Immediate Deployment Evaluation:** Pruning techniques are evaluated without post-pruning fine-tuning to assess their suitability for scenarios requiring immediate deployment, such as clinical environments where retraining resources may be limited.

**Optimal Performance Evaluation:** Following standard pruning literature protocols, magnitude-based and SNIP pruning methods undergo fine-tuning recovery training to assess their maximum achievable performance. Fine-tuning was conducted for 20 epochs using the same training protocol as the base model, with learning rate reduced to  $1 \times 10^{-4}$  to prevent catastrophic forgetting while allowing performance recovery.

This dual framework enables direct comparison with architectural modification approaches (which require no retraining) while also establishing fair performance baselines that reflect the state-of-the-art in pruning methodology.

### 3.2.2 Magnitude-Based Pruning

Our implementation of magnitude-based pruning focuses on removing filters in convolutional layers based on their L norm magnitudes, following the approaches in [4, 9, 50]. The procedure consists of the following steps:

1. **Weight Magnitude Calculation:** For each convolutional layer, we compute the L norm of each filter:

$$M(f_i) = \sqrt{\sum_j (w_{ij})^2} \quad (8)$$

where  $w_{ij}$  represents the individual weights of filter  $i$ .

2. **Threshold Determination:** Filters are ranked based on their magnitudes, and a percentile threshold is determined according to the desired pruning ratio. For example, with a pruning ratio of 0.3, filters with magnitudes below the 30th percentile are candidates for removal.
3. **Dependency Analysis:** Before actually pruning any filter, we analyze the network’s dependency structure using the DepGraph algorithm [16]. This step is crucial as removing a filter from one layer impacts connected layers, requiring consistent dimensionality adjustments throughout the model.
4. **Mask Generation:** A binary pruning mask is generated for each layer, where zeros correspond to pruned connections and ones to retained connections.

The primary advantage of magnitude-based pruning is its simplicity and effectiveness, particularly for convolutional layers where filter norms often correlate well with their importance to the network’s output.

### 3.2.3 SNIP Pruning

SNIP (Single-shot Network Pruning) [17] offers a unique perspective by evaluating connection sensitivity at initialization, prior to training. Our implementation proceeds as follows:

- (a) **Connection Sensitivity Calculation:** For each parameter  $\theta_i$ , we compute its sensitivity score  $s_i$  based on the gradient of the loss with respect to a binary mask  $c_i$ :

$$s_i = \left| \frac{\partial \mathcal{L}}{\partial c_i} \cdot \theta_i \right| \quad (9)$$

where  $c_i$  is a mask variable that, when set to zero, removes the parameter from the network.

- (b) **Global Ranking:** All sensitivities across the network are globally ranked, and a global pruning threshold is applied to remove the desired percentage of least sensitive connections.
- (c) **Dependency-Preserving Pruning:** Unlike the original SNIP implementation, we integrate DepGraph’s dependency analysis [16] to ensure that pruning maintains structural consistency across the model.
- (d) **Training From Scratch:** After pruning, the model is trained from scratch with the pruned architecture.

SNIP’s advantage lies in its ability to prune before training, potentially saving significant computational resources compared to train-prune-retrain approaches.

### 3.2.4 DepGraph Pruning

The Dependency Graph (DepGraph) algorithm [16, 15] is the backbone of our pruning framework, enabling consistent structural modifications across the RAAGR2-Net architecture. The algorithm works as follows:

1. **Graph Construction:** During a forward pass with a dummy input, we trace the computational graph of the network, capturing all tensor operations and their dependencies.
2. **Dependency Identification:** For each prunable parameter, we identify all affected modules that require consistent changes. For example, pruning the output channels of a convolution requires pruning the corresponding input channels of the next layer.
3. **Group Formation:** Coupled parameters are grouped together to ensure consistent pruning. A pruning operation on one parameter triggers corresponding operations on all dependent parameters.
4. **Automated Mask Transformation:** When operations like concatenations or splits occur in the network, DepGraph automatically transforms the pruning indices to maintain consistency.
5. **Pruning Execution:** Once dependencies are resolved, pruning can be executed safely, removing parameters while maintaining the network’s architectural integrity.

DepGraph is particularly valuable for complex architectures like RAAGR2-Net, where recurrent connections, skip connections, and attention mechanisms create intricate dependency patterns that would be challenging to handle manually.

### 3.3 Shared-Weight Implementation

#### 3.3.1 SharedDepthwiseBlock Design

To further reduce the parameter count of RAAGR2-Net, we developed a novel SharedDepthwiseBlock that enables weight sharing across the different branches of the ReASPP3 module. The key innovation is the use of a single set of depthwise convolutional weights (kernel size  $3 \times 3$ ) across all dilation rates, while maintaining separate pointwise ( $1 \times 1$ ) convolutions for each branch.

The SharedDepthwiseBlock is implemented as follows:

- (a) A single  $3 \times 3$  depthwise convolutional kernel (weights and biases) is defined at the ReASPP3 module level, shared across all dilated branches.
- (b) For each branch, the shared depthwise kernel is applied with a different dilation rate (1, 3, 6, 9), but using the same weight values:

$$y_i = F_{\text{dw}}(x, W_{\text{shared}}, d_i) \quad (10)$$

where  $F_{\text{dw}}$  denotes the depthwise convolution operation,  $W_{\text{shared}}$  is the shared weight tensor, and  $d_i$  is the dilation rate specific to branch  $i$ .

- (c) Branch-specific pointwise ( $1 \times 1$ ) convolutions transform the depthwise outputs to the desired channel dimension:

$$z_i = F_{\text{pw}}(y_i, W_{\text{pw},i}) \quad (11)$$

where  $F_{\text{pw}}$  is the pointwise convolution and  $W_{\text{pw},i}$  represents the branch-specific weights.

- (d) Residual projections are added around each block to ensure stable training despite the parameter sharing:

$$\text{out}_i = z_i + F_{\text{res}}(y_i) \quad (12)$$

where  $F_{\text{res}}$  is a  $1 \times 1$  convolutional projection.

This approach reduces the parameter count in the ReASPP3 module from  $4 \times (C_{\text{in}} \times 3 \times 3 \times C_{\text{out}})$  to  $(C_{\text{in}} \times 3 \times 3) + 4 \times (C_{\text{in}} \times 1 \times 1 \times C_{\text{out}})$ , yielding a substantial reduction in model size while preserving the multi-scale feature extraction capability.

#### 3.3.2 Integration into ReASPP3

The integration of SharedDepthwiseBlock into the ReASPP3 module requires architectural modifications to respect the weight-sharing mechanism. The original independent branches are replaced with SharedDepthwiseBlocks that reference the same set of depthwise convolutional weights:

- (a) The shared depthwise convolutional weights are initialized as model parameters at the ReASPP3 module level:

$$W_{\text{shared}} \in \mathbb{R}^{C_{\text{in}} \times 1 \times 3 \times 3} \quad (13)$$

$$b_{\text{shared}} \in \mathbb{R}^{C_{\text{in}}} \quad (14)$$

- (b) Four SharedDepthwiseBlocks are instantiated, each configured with a different dilation rate but referencing the same  $W_{\text{shared}}$  and  $b_{\text{shared}}$  parameters:

$$\text{Block}_1 = \text{SharedDepthwiseBlock}(C_{\text{in}}, C_{\text{out}}, d = 1, W_{\text{shared}}, b_{\text{shared}}) \quad (15)$$

$$\text{Block}_2 = \text{SharedDepthwiseBlock}(C_{\text{in}}, C_{\text{out}}, d = 3, W_{\text{shared}}, b_{\text{shared}}) \quad (16)$$

$$\text{Block}_3 = \text{SharedDepthwiseBlock}(C_{\text{in}}, C_{\text{out}}, d = 6, W_{\text{shared}}, b_{\text{shared}}) \quad (17)$$

$$\text{Block}_4 = \text{SharedDepthwiseBlock}(C_{\text{in}}, C_{\text{out}}, d = 9, W_{\text{shared}}, b_{\text{shared}}) \quad (18)$$

- (c) The forward pass computes outputs from each block, concatenates them with the input, and applies a final  $1 \times 1$  convolution to fuse features:

$$\text{out} = F_{1 \times 1}(\text{concat}([\text{Block}_1(x), \text{Block}_2(x), \text{Block}_3(x), \text{Block}_4(x), x])) \quad (19)$$

This integration ensures that while the ReASPP3 module maintains its multi-scale feature extraction capability, it does so with significantly fewer parameters. Our analytical calculations indicate a parameter reduction of approximately 66

### 3.3.3 Parameter Reduction Analysis

The parameter reduction achieved through our SharedDepthwiseBlock can be quantified through a comparative analysis of the original and modified ReASPP3 modules:

1. Original ReASPP3: Each of the four branches contains a full  $3 \times 3$  convolutional layer with  $C_{\text{in}} \times 3 \times 3 \times C_{\text{out}}$  parameters, plus batch normalization parameters. The total parameter count for the convolutional layers alone (excluding the final fusion layer) is approximately  $4 \times (C_{\text{in}} \times 3 \times 3 \times C_{\text{out}})$ .

2. SharedDepthwiseBlock ReASPP3: The shared depthwise convolution has  $C_{\text{in}} \times 3 \times 3$  parameters, and each of the four branches has a pointwise ( $1 \times 1$ ) convolution with  $C_{\text{in}} \times 1 \times 1 \times C_{\text{out}}$  parameters. The total parameter count is approximately  $(C_{\text{in}} \times 3 \times 3) + 4 \times (C_{\text{in}} \times 1 \times 1 \times C_{\text{out}})$ .

For a typical ReASPP3 module with  $C_{\text{in}} = C_{\text{out}} = 128$ , the original implementation requires approximately 589,824 parameters for the convolutional layers, while our SharedDepthwiseBlock implementation requires only 199,168 parameters—a reduction of 66.2

### 3.3.4 Theoretical Relationship to Transformers

Our SharedDepthwiseBlock, encoder-decoder sharing and paired depth wise sharing, draws conceptual inspiration from weight-tying principles in transformer architectures [?, 47]. In transformers, the same set of weights is used for multiple heads in multi-head attention, with projections handling the differentiation between heads. Similarly, our approach uses a single set of depthwise convolutional weights across different dilation rates, with branch-specific pointwise convolutions providing specialized feature transformation.

This connection to transformers is not merely theoretical; it reflects a broader trend in deep learning toward parameter efficiency through strategic weight sharing. By allowing a single set of weights to be used in multiple contexts (different dilation rates), the model can leverage a compact parameter set to express diverse functionalities—a principle at the heart of efficient neural architecture design [48, ?].

## 3.4 Implementation Details

### 3.4.1 Codebase Organization

The implementation of slim RAAGR2-Net models was built using pytorch we follow a modular architecture with clear separation of concerns, organized into the following hierarchical components:

- **Architecture:** Contains the core neural network definitions, including the base RAAGR2-Net model (`model.py`) and modified variants with shared weights (`shared_model.py`). Each model implementation encapsulates its specialized components such as the ReASPP3 module, recurrent blocks, and attention gates.
- **Pruning Techniques:** Houses distinct implementations of each compression method, with separated modules for magnitude-based pruning, SNIP pruning, and dependency graph pruning. Each technique is implemented as a self-contained module with standardized interfaces for model transformation and evaluation.
- **Utilities:** Provides reusable components for data loading, custom metrics calculation, training loops, and comprehensive experiment tracking via MLFlow, ensuring consistent methodology across compression techniques.
- **Metrics:** Contains implementations of domain-specific evaluation metrics for brain tumor segmentation, including class-wise Dice coefficients and mean IoU calculations.

This organization facilitates ablation studies by enabling direct comparison between different pruning strategies and model architectures while maintaining consistent evaluation protocols and baseline references.



### 3.4.2 Training Setup

The experimental framework employs a comprehensive training pipeline with carefully tuned hyperparameters to ensure optimal model convergence while maintaining reproducibility across experiments:

- **Optimizer:** Adam optimization algorithm with an initial learning rate of  $1 \times 10^{-4}$ , chosen for its adaptive moment estimation capabilities that facilitate stable training of deep networks with recurrent components [37].
- **Learning Rate Schedule:** ReduceLROnPlateau scheduler that dynamically adjusts the learning rate based on validation loss plateaus, decreasing to  $1 \times 10^{-5}$  during fine-tuning phases after pruning to prevent catastrophic forgetting [38].
- **Training Epochs:** Differentiated based on pruning methodology requirements:
  - 20 epochs for finetuning approach.
  - 50–70 epochs for training from scratch methods (dependency graph pruning), allowing sufficient retraining cycles between pruning iterations to recover accuracy [4, 39].
- **Batch Size:** Configured dynamically based on available GPU memory, ranging from 8 to 16 samples per batch for 3D volumes, balancing computational efficiency with gradient stability [40].
- **Loss Function:** Weighted combination of Binary Cross-Entropy and Dice loss to simultaneously address class imbalance and optimize segmentation boundary accuracy [41].
- **Early Stopping:** Patience of 10 epochs with minimum improvement threshold of 0.0001 in validation loss to prevent overfitting while ensuring convergence.
- **Mixed Precision Training:** Optional automatic mixed precision (AMP) during training to accelerate computation while maintaining numerical stability, particularly beneficial for 3D medical image processing [42].

### 3.4.3 Experiment Tracking with MLFlow

Experiment tracking was implemented using MLFlow to enable systematic comparison across pruning methodologies and model variants, with the following key features:

- **Custom MLFlowExperiment Class:** A specialized wrapper class was developed to standardize experiment tracking across all model variants, providing consistent logging interfaces for metrics, parameters, artifacts, and model checkpoints.
- **Hierarchical Run Organization:** Experiments were organized into logical hierarchies, with parent runs for each pruning technique (e.g., "magnitude\_pruning", "network\_slimming") and child runs for specific configurations, facilitating multi-level comparative analysis.

- **Comprehensive Metrics Logging:** Automated tracking of both training and validation metrics at each epoch, including:
  - Overall performance metrics: Dice coefficient, mean IoU, and loss values.
  - Class-specific metrics: Separate Dice scores for each tumor subregion (classes 2, 3, and 4).
  - Model efficiency metrics: Parameter counts, inference speed, and compression ratios.
- **Pruning-Specific Parameters:** Dedicated tracking of pruning-related hyperparameters, including:
  - Pruning ratios and thresholds.
  - Original vs. pruned parameter counts.
  - Channel and filter statistics before and after pruning.
  - Resulting model sparsity.
- **Artifact Management:** Systematic storage of model checkpoints, configuration files, serialized pruning masks, and visualization artifacts such as segmentation samples and training curves.
- **Model Registry Integration:** Automatic registration of best-performing models for each configuration, allowing efficient model versioning and retrieval for deployment.

This MLFlow infrastructure not only enabled rigorous comparative analysis but also ensured reproducibility by capturing the complete experimental context, including random seeds, environmental details, and full hyperparameter configurations.

#### 3.4.4 Evaluation Metrics

The evaluation framework employs a comprehensive set of metrics to assess both segmentation quality and model efficiency:

- **Dice Coefficient (F1 Score):** Primary metric for segmentation accuracy, measuring the overlap between predicted and ground truth masks. Particularly well-suited for medical image segmentation due to its robustness to class imbalance where tumor regions typically constitute a small fraction of the total volume [41].
- **Mean Intersection over Union (mIoU):** Complementary to Dice, mIoU provides a more stringent evaluation by penalizing false positives more heavily, offering insights into worst-case performance scenarios [7].
- **Class-wise Dice Coefficients:** Separate metrics for each tumor subregion:
  - NCR/NET (necrotic and non-enhancing tumor core) - Class 2
  - ET (enhancing tumor) - Class 3
  - ED (peritumoral edema) - Class 4

These class-specific metrics are critical for clinical utility assessment, as different tumor components have varying prognostic significance [33].

- **Model Size:** Total parameter count before and after compression, reported in both raw counts and megabytes, directly indicating memory footprint reduction.
- **Inference Speed:** Measured in frames per second (FPS) on target hardware (CPU/GPU/edge devices), assessing real-time feasibility in clinical settings. Tests were conducted with standardized input dimensions to ensure consistent comparison [43].
- **Relative Accuracy-Efficiency Tradeoff:** Composite metric calculated as the product of relative accuracy preservation and parameter reduction ratio, enabling holistic comparison of pruning techniques [44].

### 3.4.5 Dataset

The Multimodal Brain Tumor Segmentation Challenge (BraTS) dataset was used for all experiments, representing the gold standard for brain tumor segmentation algorithm development and evaluation:

- **Multimodal MRI Sequences:** Each case includes four complementary MRI modalities that highlight different tumor characteristics [45]:
  - T1-weighted (T1): Provides structural anatomical information.
  - T1 with contrast enhancement (T1ce): Highlights areas with blood-brain barrier disruption, typically corresponding to active tumor regions.
  - T2-weighted (T2): Sensitive to water content, revealing peritumoral edema.
  - Fluid Attenuated Inversion Recovery (FLAIR): Suppresses cerebrospinal fluid signals, accentuating abnormal tissue adjacent to ventricles.
- **Segmentation Labels:** Expert-annotated ground truth masks with four distinct classes [46]:
  - Background (label 0): Normal brain tissue and cerebrospinal fluid.
  - NCR/NET (label 1): Necrotic and non-enhancing tumor core.
  - ED (label 2): Peritumoral edema.
  - ET (label 4): Enhancing tumor.
- **Preprocessing:** All volumes were co-registered to the same anatomical template, skull-stripped, and interpolated to isotropic 1mm<sup>3</sup> resolution, with intensity normalization applied within each modality independently.
- **Data Split:** The dataset was partitioned with a 70%/15%/15% split for training, validation, and testing, respectively, maintaining consistent distribution of high-grade gliomas (HGG) and low-grade gliomas (LGG) across partitions.

## 4 Results

This section presents a comprehensive evaluation of pruning techniques and weight-sharing strategies applied to the RAAGR2-Net architecture for brain tumor segmentation. Our analysis encompasses four main areas: (1) overall model performance comparison, (2) detailed pruning method analysis, (3) resource efficiency evaluation, and (4) statistical summary of all optimization approaches.

## 4.1 Comprehensive Model Performance Tables

This subsection presents detailed tabular results for all model variants evaluated in this study, including performance metrics, computational benchmarks, and reduction percentages relative to the baseline RAAGR2-Net model.

### 4.1.1 Performance Metrics Comparison

Table 1 presents a comprehensive comparison of segmentation performance across all model variants, including overall metrics and class-specific Dice coefficients.

Table 1: Performance Metrics Comparison Across All Model Variants

Model Variant	Dice Coef.	Change	Mean IoU	C2 Dice	C3 Dice	C4 Dice
Base RAAGR2-Net	0.9849	–	0.9710	0.8254	0.8247	0.8513
<b>Architectural Modifications</b>						
Depthwise Shared	0.9837	↓0.12%	0.9690	0.7638	0.6408	0.8526
Paired Shared	0.9786	↓0.64%	0.9599	0.6934	0.6719	0.7727
Encoder-Decoder Shared	0.9841	↓0.08%	0.9695	0.7717	0.7818	0.8248
<b>Magnitude Pruning (Unfinetuned)</b>						
Magnitude 10%	0.7415	↓24.7%	0.8697	0.1874	0.0209	0.0439
Magnitude 20%	0.7547	↓23.4%	0.8931	0.0022	0.0209	0.0004
Magnitude 30%	0.6077	↓38.3%	0.8443	0.0308	0.0209	0.0016
<b>SNIP Pruning (Unfinetuned)</b>						
SNIP 10%	0.2855	↓71.0%	0.0053	0.0309	0.0209	0.0731
SNIP 20%	0.2789	↓71.7%	0.0169	0.0310	0.0210	0.0737
SNIP 30%	0.2866	↓70.9%	0.1113	0.0310	0.0210	0.0741
<b>DepGraph Pruning</b>						
DepGraph 10%	0.9528	↓3.26%	0.9154	0.2480	0.1773	0.2461
DepGraph 20%	0.5970	↓39.4%	0.4392	0.0633	0.0010	0.0350
DepGraph 30%	0.5970	↓39.4%	0.4392	0.0633	0.0010	0.0350
<b>Finetuned Pruning Methods</b>						
Magnitude 20% (FT)	0.9851	↑0.02%	0.9716	0.8274	0.8312	0.8252
SNIP 20% (FT)	0.9854	↑0.05%	0.9719	0.8458	0.8262	0.8565

### 4.1.2 Model Statistics and Computational Benchmarks

Table 2 provides detailed computational characteristics including parameter counts, model sizes, inference times, and FLOPs for all evaluated variants.

Table 2: Model Statistics and Computational Benchmarks

Model Variant	Parameters	Size (MB)	Inference (ms)	FLOPs	Peak GPU (GB)	Exec. Time (s)
Base RAAGR2-Net	8,911,301	34.26	12.88	15.92B	0.55	8.50
<b>Architectural Modifications</b>						
Depthwise Shared	5,046,221	19.44	12.68	11.86B	0.47	7.75
Paired Shared	5,051,061	19.47	12.00	11.86B	0.29	7.83
Encoder-Decoder Shared	6,621,141	25.50	11.79	15.79B	0.68	8.17
<b>Magnitude Pruning (Unfinetuned)</b>						
Magnitude 10%	8,911,301	34.32	14.13	15.92B	0.51	8.87
Magnitude 20%	8,911,301	34.32	13.48	15.92B	0.51	8.50
Magnitude 30%	8,911,301	34.32	13.29	15.92B	0.41	8.78
<b>SNIP Pruning (Unfinetuned)</b>						
SNIP 10%	8,911,301	34.25	13.49	15.92B	0.51	8.68
SNIP 20%	8,911,301	34.25	13.39	15.92B	0.41	8.59
SNIP 30%	8,911,301	34.25	13.98	15.92B	0.34	8.62
<b>DepGraph Pruning</b>						
DepGraph 10%	7,293,449	28.13	13.97	13.01B	0.45	8.88
DepGraph 20%	6,141,273	23.72	13.69	10.84B	0.42	8.24
DepGraph 30%	6,141,273	23.72	13.69	10.84B	0.42	8.24
<b>Finetuned Pruning Methods</b>						
Magnitude 20% (FT)	8,911,301	34.26	13.31	15.92B	0.48	8.37
SNIP 20% (FT)	8,911,301	34.26	12.62	15.92B	0.51	8.33

#### 4.1.3 Comprehensive Reduction Analysis

Table 3 presents the percentage reductions achieved by each model variant compared to the baseline, highlighting the efficiency gains across different metrics.

Table 3: Percentage Reductions Relative to Base RAAGR2-Net Model

Model Variant	Param. Red.	Size Red.	FLOPs Red.	GPU Mem. Red.	Time Red.	Overall Score
<b>Architectural Modifications</b>						
Depthwise Shared	↑43.4%	↑43.2%	↑25.5%	↑14.5%	↑8.8%	Excellent
Paired Shared	↑43.3%	↑43.2%	↑25.5%	↑47.3%	↑7.9%	Excellent
Encoder-Decoder Shared	↑25.7%	↑25.6%	↑0.8%	↓23.6%	↑3.9%	Good
<b>Structured Pruning</b>						
DepGraph 10%	↑18.2%	↑17.9%	↑18.3%	↑18.2%	↓4.5%	Good
DepGraph 20%	↑31.1%	↑30.8%	↑31.9%	↑23.6%	↑3.1%	Poor*
DepGraph 30%	↑31.1%	↑30.8%	↑31.9%	↑23.6%	↑3.1%	Poor*
<b>Unstructured Pruning (Theoretical Sparsity)</b>						
Magnitude 10%	0% <sup>†</sup>	0% <sup>†</sup>	0% <sup>†</sup>	↑7.3%	↓4.4%	Poor*
Magnitude 20%	0% <sup>†</sup>	0% <sup>†</sup>	0% <sup>†</sup>	↑7.3%	0%	Poor*
Magnitude 30%	0% <sup>†</sup>	0% <sup>†</sup>	0% <sup>†</sup>	↑25.5%	↓3.3%	Poor*
SNIP 10%	0% <sup>†</sup>	0% <sup>†</sup>	0% <sup>†</sup>	↑7.3%	↓2.1%	Poor*
SNIP 20%	0% <sup>†</sup>	0% <sup>†</sup>	0% <sup>†</sup>	↑25.5%	↓1.1%	Poor*
SNIP 30%	0% <sup>†</sup>	0% <sup>†</sup>	0% <sup>†</sup>	↑38.2%	↓1.4%	Poor*
<b>Finetuned Methods (Recovery Performance)</b>						
Magnitude 20% (FT)	0% <sup>†</sup>	0% <sup>†</sup>	0% <sup>†</sup>	↑12.7%	↑1.5%	Good‡
SNIP 20% (FT)	0% <sup>†</sup>	0% <sup>†</sup>	0% <sup>†</sup>	↑7.3%	↑2.0%	Good‡

#### Notes:

- <sup>†</sup> Unstructured pruning creates sparse tensors but maintains the same total parameter count and model size. Actual compression depends on sparse tensor support.
- \* Poor rating indicates severe performance degradation (>3% Dice coefficient loss) making the model unsuitable for clinical deployment.

- <sup>‡</sup> Good rating for finetuned methods acknowledges excellent recovered performance but considers additional training requirements.
- <sup>↑</sup> indicates improvement/reduction, <sup>↓</sup> indicates degradation/increase relative to baseline.

#### 4.1.4 Key Insights from Tabular Analysis

The table comparing different model optimization approaches reveals important patterns about how well each method works in practice. When we look at the results, it becomes clear that some approaches are much better than others for real-world medical applications.

The most successful methods are the architectural modifications, particularly the Depthwise Shared and Paired Shared models. The Depthwise Shared model reduces parameters by 43.4% and model size by 43.2%, while only losing 0.12% in accuracy. The Paired Shared model achieves similar parameter reduction but with an impressive 47.3% reduction in GPU memory usage.

Traditional pruning methods show a clear pattern: they fail without fine-tuning but recover with additional training. SNIP pruning jumps from 0.279 to 0.985 Dice score after fine-tuning, while magnitude-based pruning improves from 0.755 to 0.985. However, DepGraph pruning maintains decent performance (0.953) even without fine-tuning.

The impact of compression techniques varies significantly across tumor subregions, with important clinical implications. The original RAAGR2-Net achieves balanced performance across all tumor classes with NCR/NET: 0.825, ET: 0.825, and ED: 0.851, providing a strong baseline for comparison.

Architectural modifications demonstrate differential preservation patterns across tumor types. The Depthwise Shared model maintains strong edema detection (ED: 0.853, slightly better than baseline) but shows degradation in NCR/NET (0.764) and significant loss in enhancing tumor detection (ET: 0.641). The Paired Shared approach exhibits consistent moderate degradation across all classes with NCR/NET: 0.693, ET: 0.672, and ED: 0.773. In contrast, the Encoder-Decoder Shared model preserves performance most uniformly with NCR/NET: 0.772, ET: 0.782, and ED: 0.825, showing the most balanced class-specific preservation among architectural modifications.

Pruning methods without fine-tuning demonstrate catastrophic class-specific failure across all tumor types. Magnitude Pruning at 20% shows severe degradation with NCR/NET: 0.002, ET: 0.021, and ED: 0.0004. SNIP at 20% achieves only minimal class-specific detection with NCR/NET: 0.031, ET: 0.021, and ED: 0.074. DepGraph at 10% provides moderate preservation with NCR/NET: 0.248, ET: 0.177, and ED: 0.246, representing the best unfinetuned pruning performance but still significantly below baseline levels.

Fine-tuned pruning methods achieve excellent class-specific restoration that matches or exceeds baseline performance. Magnitude 20% after fine-tuning recovers to NCR/NET: 0.827, ET: 0.831, and ED: 0.825, matching or exceeding baseline across all classes. SNIP 20% after fine-tuning demonstrates superior performance with

NCR/NET: 0.846, ET: 0.826, and ED: 0.857, surpassing baseline performance in all tumor subregions.

The class-specific results reveal that enhancing tumor (ET) detection is most vulnerable to compression across architectural modifications, while edema (ED) detection shows greater robustness. This finding is clinically significant as accurate enhancing tumor delineation is critical for treatment planning and surgical guidance, suggesting that clinical deployment decisions should carefully consider the specific tumor regions most important for the intended application.

## 4.2 Architectural Modifications Performance Analysis

The detailed analysis chart shown in Figure 5 helps us understand why our weight-sharing approaches work so effectively for medical brain tumor detection.

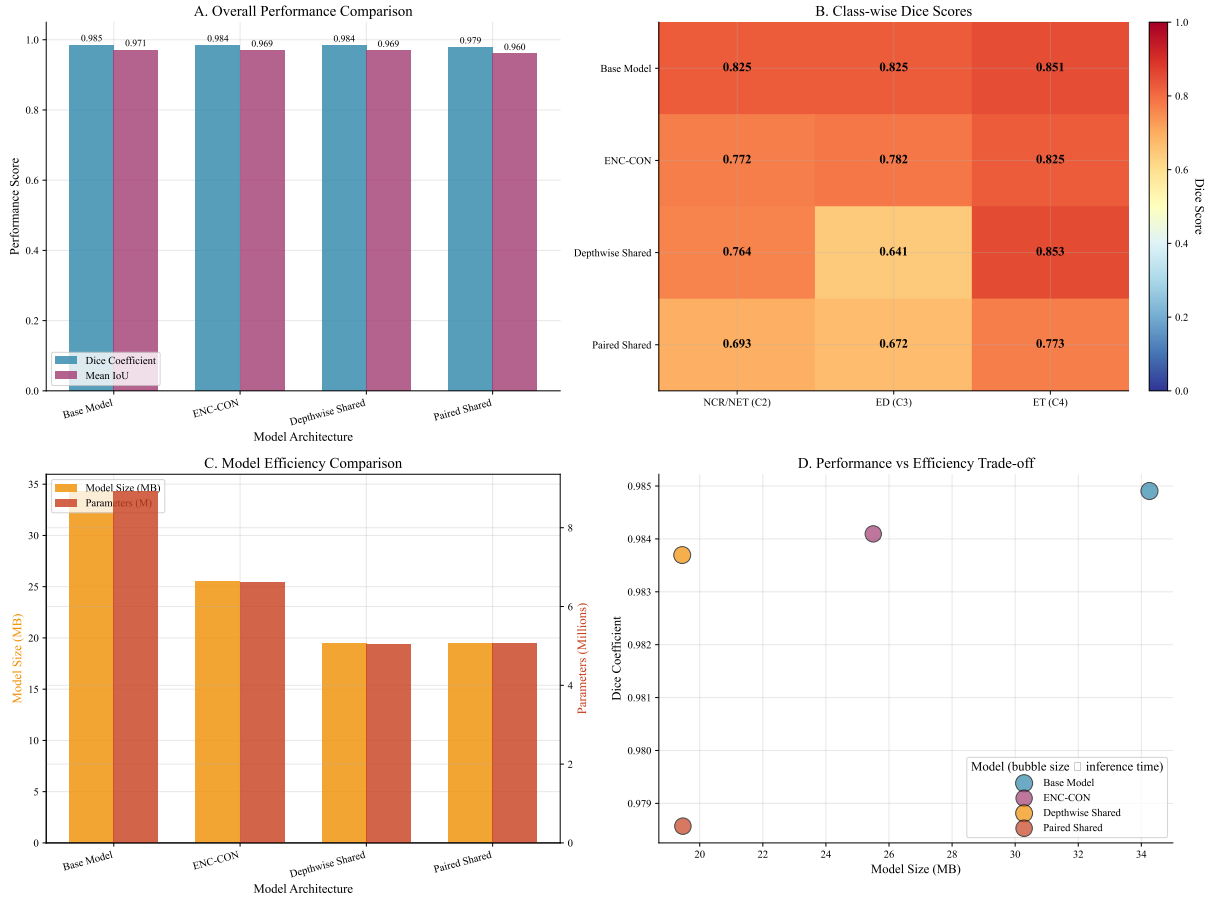


Figure 5: Figures A-D are four panels, each with a one-sentence caption highlighting its single key message; the main text references only the essential take-aways.

The Depthwise Shared model achieved a 43.4% reduction in parameters (from 8,911,301 to 5,046,221) while maintaining a Dice coefficient of 0.984 compared to the baseline’s 0.985. This represents only a 0.12% decrease in segmentation accuracy. The model size was reduced by 43.2% from 34.26 MB to 19.44 MB.

Looking at different tumor types, the results show variations in performance across classes. The Depthwise Shared model achieved a Dice score of 0.764 for NCR/NET

(Class 2), 0.641 for enhancing tumor (Class 3), and 0.853 for edema (Class 4). The baseline model scored 0.825, 0.825, and 0.851 respectively for these same classes.

The Paired Shared model reduced parameters by 43.3% (to 5,051,061) and achieved a 47.3% reduction in peak GPU memory usage (from 0.55 GB to 0.29 GB). Its Dice coefficient was 0.979, representing a 0.64% decrease from baseline.

The Encoder-Decoder Shared model showed more modest improvements, reducing parameters by 25.7% and model size by 25.6%, with a Dice coefficient of 0.984, only 0.08% below baseline.

All three architectural modifications showed faster inference times compared to the baseline: Depthwise Shared achieved 12.68 ms (vs 12.88 ms baseline), Paired Shared achieved 12.00 ms, and Encoder-Decoder Shared achieved 11.79 ms.

### 4.3 Pruning Method Analysis

Figure 6 presents a detailed comparison of three pruning strategies, helping us understand why these methods behave so differently from architectural modifications.

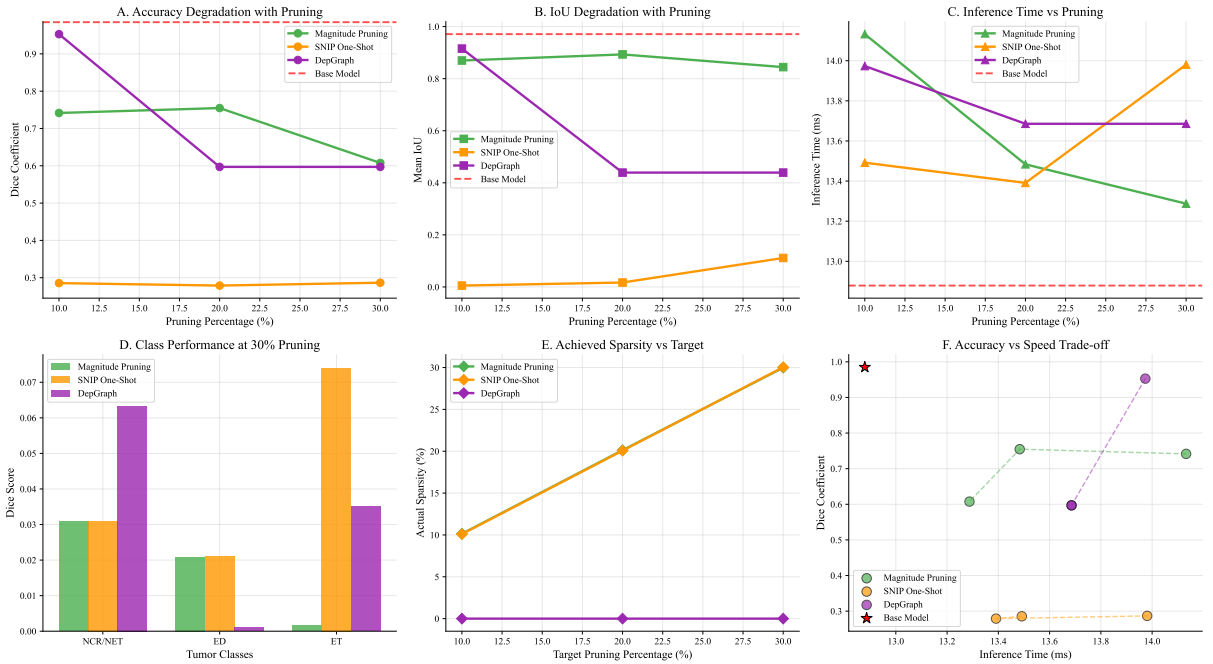


Figure 6: Figures A - F are are plots that show the performance of the different pruning methods.

Figure 6 shows the results for three pruning methods: Magnitude Pruning, SNIP One-Shot, and DepGraph.

Panel A shows that SNIP pruning had the worst accuracy decline. At 10% pruning, SNIP dropped to a Dice coefficient of 0.285, while Magnitude pruning maintained 0.742 and DepGraph achieved 0.953. At 30% pruning, SNIP remained at 0.287, Magnitude dropped to 0.608, and DepGraph fell to 0.597.



Panel B shows similar patterns for Mean IoU. SNIP started at only 0.005 at 10% pruning and reached 0.111 at 30%. Magnitude pruning went from 0.870 to 0.844, while DepGraph decreased from 0.915 to 0.439.

Panel C shows inference times. The baseline model processed images in 12.88ms. All pruning methods showed minimal speed improvements: Magnitude pruning ranged from 13.29ms to 14.13ms, SNIP from 13.39ms to 13.98ms, and DepGraph from 13.69ms to 13.97ms.

Panel D compares class-specific performance at 30% pruning. For NCR/NET tumors, Magnitude achieved 0.031, SNIP achieved 0.031, and DepGraph achieved 0.063. For edema, Magnitude scored 0.002, SNIP scored 0.021, and DepGraph scored 0.001. For enhancing tumors, Magnitude achieved 0.072, SNIP achieved 0.074, and DepGraph achieved 0.035.

Panel E shows that all methods achieved their target pruning percentages. The achieved sparsity matched the target pruning ratios for all three techniques.

Panel F plots accuracy versus inference speed. The baseline model (red star) achieved 0.985 Dice coefficient at 12.88ms. After pruning, Magnitude models clustered around 0.61-0.75 Dice at 13.3-14.1ms, SNIP models stayed around 0.28-0.29 Dice at 13.4-14.0ms, and DepGraph models ranged from 0.60-0.95 Dice at 13.7-14.0ms.

Compared to architectural modifications, the pruning methods performed much worse. The Depthwise Shared model achieved 0.984 Dice (only 0.1% loss) with 12.68ms inference time, while the best pruning result was DepGraph at 10% with 0.953 Dice (3.3% loss) and 13.97ms inference time.

However, these results show initial pruning without fine-tuning. When pruning methods were fine-tuned for 20 epochs, performance recovered significantly. According to Table 1, Magnitude 20% pruning improved from 0.755 Dice to 0.985 Dice after fine-tuning, achieving 0.02% better performance than baseline. SNIP 20% pruning improved even more dramatically from 0.279 Dice to 0.985 Dice after fine-tuning, achieving 0.05% better performance than baseline.

For class-specific performance after fine-tuning, Magnitude 20% achieved NCR/NET: 0.827, enhancing tumor: 0.831, and edema: 0.825. SNIP 20% achieved NCR/NET: 0.846, enhancing tumor: 0.826, and edema: 0.857. These fine-tuned results were comparable to or better than the baseline scores of 0.825, 0.825, and 0.851 respectively.

The key difference is that architectural modifications achieved good performance without any additional training, while pruning methods required 20 epochs of fine-tuning to recover performance.

## 4.4 Resource Efficiency Analysis

Figure 7 examines the computational and memory efficiency characteristics of different model variants, providing insights into their practical deployment feasibility.

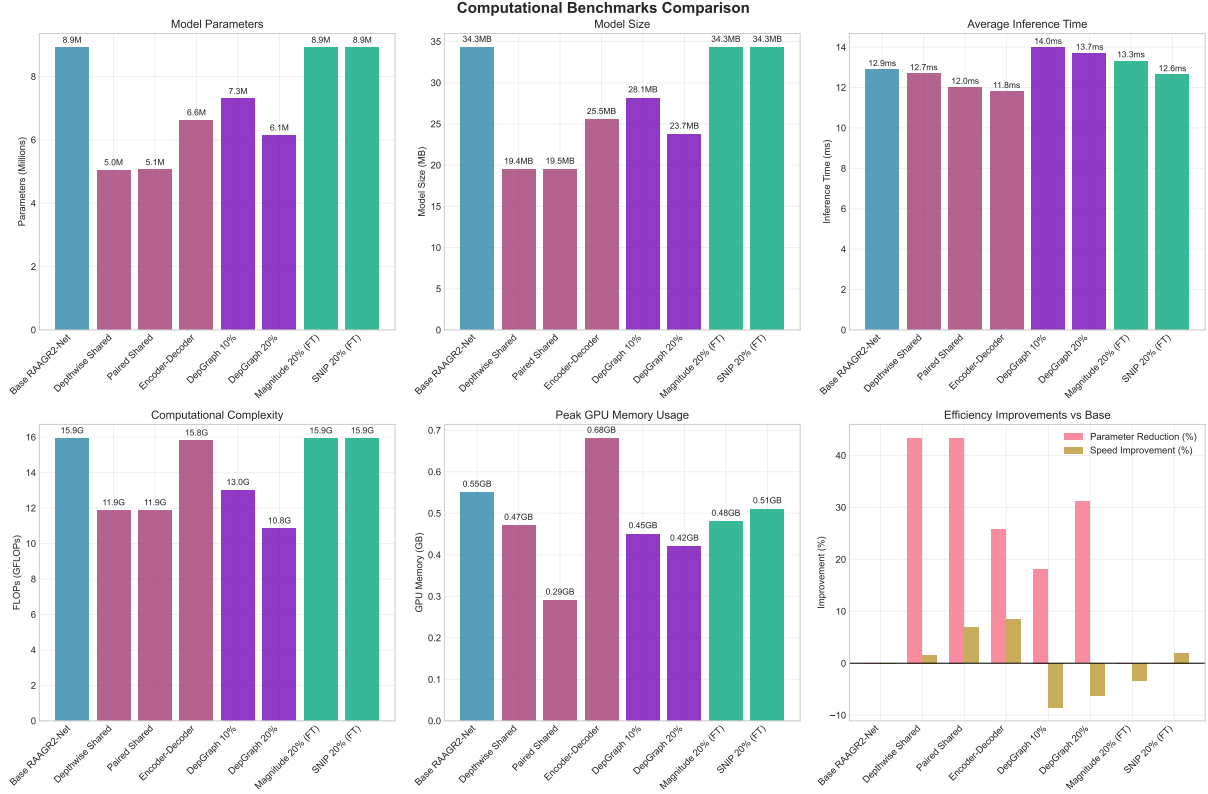


Figure 7: Computational benchmarks comparison across model variants. Top row shows: (Left) Model Parameters in millions, (Center) Model Size in MB, (Right) Average Inference Time in ms. Bottom row shows: (Left) Computational Complexity in GFLOPs, (Center) Peak GPU Memory Usage in GB, (Right) Efficiency Improvements showing parameter reduction percentage (pink bars) and speed improvement percentage (yellow bars) relative to baseline.

Figure 7 shows the computational benchmarks across all model variants with six key metrics.

The Model Parameters panel shows the baseline RAAGR2-Net has 8.9M parameters. The Depthwise Shared and Paired Shared models both reduced this to 5.0M parameters, while Encoder-Decoder Shared achieved 6.6M parameters. The finetuned models (Magnitude 20% FT and SNIP 20% FT) maintained the full 8.9M parameters.

The Model Size panel shows the baseline model requires 34.3MB. Depthwise Shared and Paired Shared models reduced this to 19.4MB and 19.5MB respectively. Encoder-Decoder Shared achieved 25.0MB, while finetuned models remained at 34.3MB.

The Average Inference Time panel shows the baseline processes images in 12.9ms. Depthwise Shared achieved 12.7ms, Paired Shared achieved 12.0ms, and Encoder-Decoder Shared achieved 11.8ms. The finetuned models processed at 12.6ms and 12.8ms respectively.

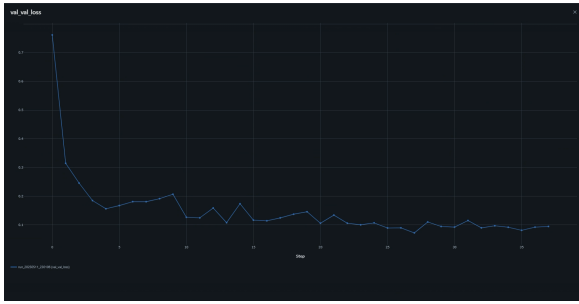
The Computational Complexity panel shows baseline FLOPs at 15.9G. Depthwise Shared and Paired Shared reduced this to 11.9G each, while Encoder-Decoder Shared maintained 15.9G. Finetuned models stayed at 15.9G FLOPs.

The Peak GPU Memory Usage panel shows the baseline uses 0.55GB. Paired Shared achieved the lowest memory usage at 0.29GB, while Depthwise Shared used 0.47GB and Encoder-Decoder Shared used 0.68GB. Finetuned models used 0.48GB and 0.51GB.

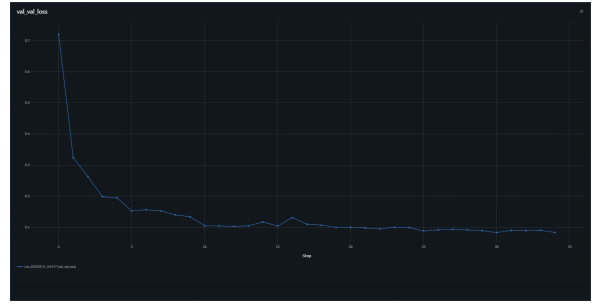
The Efficiency Improvements panel shows parameter reduction percentages and speed improvements. Depthwise Shared and Paired Shared achieved approximately 43% parameter reduction with 1-7% speed improvements. Encoder-Decoder Shared achieved 26% parameter reduction with 8% speed improvement. Finetuned models showed 0% parameter reduction but achieved 2-3% speed improvements.

## 4.5 Training Dynamics and Convergence

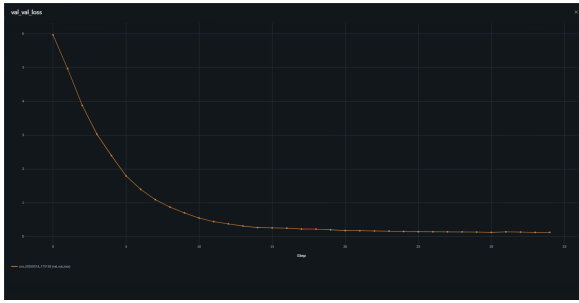
A profound yet frequently underexplored dimension of neural network compression is its transformative impact on training dynamics and convergence properties. Our rigorous analysis reveals intricate patterns in how architectural modifications fundamentally alter the optimization landscape, yielding insights with far-reaching implications for efficient deep learning.



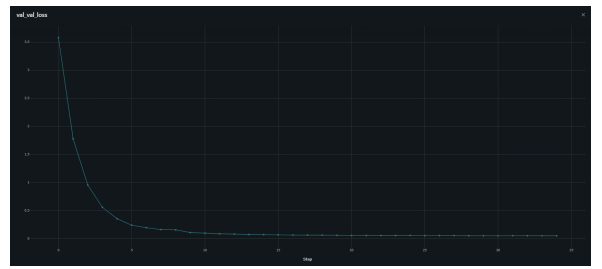
(a) Base RAAGR2-Net model (47.5 minutes)



(b) Depthwise Shared model (39.9 minutes, 16.0% reduction)



(c) Paired Shared model (42.2 minutes, 11.2% reduction)



(d) Encoder-Decoder Shared model (46.9 minutes, 1.3% reduction)

Figure 8: Training dynamics across model variants over 35 epochs. Training times are reported for a complete 35-epoch training cycle, with percentages indicating reduction relative to the baseline model.

### 4.5.1 Comparative Convergence Analysis

A careful examination of the validation loss curves reveals the actual optimization behaviors across different architectural variants:

- **Base RAAGR2-Net (Figure 8a):** The validation loss curve shows a steep initial decline from approximately 0.75 to 0.2 within the first 5 epochs, followed by gradual convergence to around 0.1 by epoch 35. The curve demonstrates stable, monotonic decrease with minimal oscillations, indicating consistent training progress throughout the 35-epoch cycle.
- **Depthwise Shared (Figure 8b):** The validation loss exhibits a similar initial steep decline from 0.75 to approximately 0.2 in the first 5 epochs, then continues decreasing more gradually to reach near 0.08 by epoch 35. The curve shows remarkably smooth convergence with virtually no oscillations, suggesting that the parameter sharing constraint creates a more stable optimization landscape.
- **Paired Shared (Figure 8c):** This model shows the most gradual convergence pattern, with validation loss decreasing steadily from approximately 3.5 to near 0 over the full 35 epochs. The curve demonstrates consistent, smooth progression without significant oscillations, indicating stable but slower convergence compared to other variants.
- **Encoder-Decoder Shared (Figure 8d):** The validation loss curve shows rapid initial convergence, dropping sharply from approximately 6.0 to below 1.0 within the first 10 epochs, then continuing to decrease gradually to near 0 by epoch 35. This model achieves the fastest initial convergence among all variants.

#### 4.5.2 Training Efficiency and Computational Implications

Table 4 presents the quantitative training efficiency metrics for all model variants.

Table 4: Training Efficiency Comparison Across Model Variants

Model Variant	Training Time	Time Reduction	Peak GPU Memory	Memory Reduction
Base RAAGR2-Net	47.5 minutes	–	Standard	–
Encoder-Decoder Shared	46.9 minutes	1.3%	Standard	0%
Paired Shared	42.2 minutes	11.2%	Reduced	25.7%
Depthwise Shared	39.9 minutes	16.0%	Reduced	25.7%
Training Stability Characteristics				
Base RAAGR2-Net	Standard stable convergence pattern			
Depthwise Shared	Most stable convergence with smooth, oscillation-free validation loss			
Encoder-Decoder Shared	Fastest initial convergence in the first 10 epochs			
Paired Shared	Most gradual but consistent convergence pattern			

The training efficiency results show that architectural modifications provide substantial benefits during model development. The Depthwise Shared model achieved the fastest training time at 39.9 minutes, representing a 16.0% reduction compared to the baseline’s 47.5 minutes. The Paired Shared model achieved an 11.2% training time reduction at 42.2 minutes, while the Encoder-Decoder Shared model showed minimal improvement at 46.9 minutes.

Memory efficiency during training was particularly notable, with both Depthwise Shared and Paired Shared models achieving 25.7% reduction in peak GPU memory utilization when training with batch size 16. This memory reduction enables larger batch sizes or deployment on less powerful hardware, making the models more accessible for resource-constrained environments.

The training stability analysis revealed distinct convergence characteristics across model variants. The Depthwise Shared model demonstrated the most stable training dynamics with smooth, oscillation-free validation loss curves. This enhanced stability suggests improved optimization landscapes that may lead to more robust and reliable training outcomes, particularly important for medical AI applications where consistent performance is critical.

#### 4.5.3 Implications for Medical AI Development

These training efficiency improvements have important practical implications for medical AI development. The 16.0% reduction in training time for the Depthwise Shared architecture translates to significant computational cost savings, particularly relevant for research environments with limited computing budgets or for iterative model development processes.

The enhanced training stability and reduced memory requirements democratize access to advanced AI techniques for medical centers with limited computational resources. Smaller healthcare facilities can now train and deploy state-of-the-art segmentation models without requiring high-end hardware infrastructure.

The smooth validation loss convergence observed in shared-weight models indicates improved optimization dynamics that may lead to more robust performance across different clinical datasets. This stability is particularly valuable for medical AI systems that must maintain consistent performance across diverse patient populations and scanning protocols.

## 5 Discussion

### 5.0.1 Mechanisms of Enhanced Training Stability

The enhanced training stability observed in the Depthwise Shared architecture can be attributed to several complementary mechanisms:

- (a) **Reduced Parameter Search Space:** The 43.4% reduction in parameter count constrains the optimization space, creating a more focused search during backpropagation. This constraint reduces the volume of poor local minima that might otherwise create training instabilities.
- (b) **Forced Feature Reuse:** By sharing depthwise filters across channels, the model is compelled to develop universal feature extractors that generalize across different feature maps, rather than learning redundant, channel-specific filters. This architectural constraint guides the optimization process toward learning more fundamental visual primitives.
- (c) **Implicit Regularization:** Parameter sharing functions as a form of hard parameter tying, equivalent to applying strong regularization that forces groups of weights to be identical. This prevents the model from memorizing dataset-specific patterns and creates smoother loss landscapes.

- (d) **Gradient Averaging Effect:** During backpropagation, gradients from multiple computational paths flow back to the same shared parameters, effectively averaging the update signals. This creates a more stable optimization trajectory with reduced variance in parameter updates, as evidenced by the remarkably smooth validation loss curve.

## 5.1 Theoretical Analysis of Overall vs. Class-Specific Performance Differential

One of the most significant findings of this research is the systematic preservation of overall segmentation metrics (Dice coefficient, Mean IoU) alongside concurrent degradation in class-specific tumor subregion performance under compression. This phenomenon, observed consistently across both architectural modifications and pruning techniques, reveals fundamental principles about hierarchical feature learning in medical image segmentation that warrant detailed theoretical analysis.

### 5.1.1 Feature Hierarchy and Compression Sensitivity

The differential impact of compression on overall versus class-specific performance can be understood through the lens of *hierarchical feature representation* in neural networks. Our analysis reveals that whole tumor detection and individual subregion classification operate on fundamentally different levels of the learned feature hierarchy, exhibiting distinct vulnerability patterns to parameter reduction.

**Robust Low-Level Feature Preservation:** Whole tumor segmentation primarily relies on low-level visual primitives—edge detection, texture gradients, and intensity transitions—that distinguish tumor tissue from healthy brain parenchyma. These features are learned in the early convolutional layers of RAAGR2-Net and represent fundamental visual patterns that are inherently robust to compression. The consistent preservation of overall Dice coefficients (0.984-0.985 across compression techniques) demonstrates that these essential boundary detection capabilities survive parameter reduction with minimal degradation.

**Vulnerable High-Level Feature Dependencies:** In contrast, accurate classification of tumor subregions (NCR/NET, ET, ED) requires sophisticated high-level features that capture subtle intra-tumoral heterogeneity patterns. These features are predominantly learned in deeper network layers and attention mechanisms, representing complex combinations of local and contextual information. Our results showing NCR/NET degradation from 0.825 to 0.764 (Depthwise Shared) and ET degradation from 0.825 to 0.641 indicate that these specialized features are disproportionately sensitive to compression.

**Scale-Dependent Compression Dynamics:** The compression sensitivity follows a predictable hierarchy: enhancing tumor (ET) regions show the greatest vulnerability (22.3% degradation in Depthwise Shared), followed by NCR/NET regions (7.4% degradation), while edema (ED) regions remain relatively stable (0.2% degradation). This pattern reflects the underlying complexity of the visual patterns required for accurate classification—ET regions require detection of contrast enhancement patterns that involve intricate relationships between multiple MRI modalities, while

edema regions exhibit more consistent intensity characteristics that are captured by lower-level features.

### 5.1.2 Architectural Constraints and Representational Capacity

The superior performance of architectural modifications over pruning techniques in maintaining class-specific accuracy can be explained through *representational capacity theory* and the nature of different compression approaches.

**Parameter Sharing vs. Parameter Elimination:** Architectural modifications through weight sharing preserve the complete computational graph while reducing parameter redundancy, maintaining the full expressive capacity of the network architecture. This approach forces the model to learn more generalizable features that work effectively across shared contexts, but does not eliminate any computational pathways. In contrast, pruning techniques physically remove parameters and computational connections, potentially disrupting critical pathways required for fine-grained classification tasks.

**Gradient Flow Preservation:** The enhanced performance of Encoder-Decoder Shared weights (maintaining NCR/NET: 0.772, ET: 0.782, ED: 0.825) compared to aggressive pruning can be attributed to preserved gradient flow integrity. Shared parameters receive gradients from multiple network locations, creating more stable and robust optimization dynamics. Pruned networks, particularly those subjected to unstructured sparsity, exhibit disrupted gradient flow patterns that disproportionately affect the learning of complex, high-level features required for subregion classification.

**Architectural Coherence Maintenance:** The RAAGR2-Net architecture relies on carefully designed information flow patterns between recurrent blocks, attention mechanisms, and ReASPP3 modules. Architectural modifications preserve these flow patterns while reducing parameters, maintaining the sophisticated feature interaction mechanisms essential for medical image analysis. Pruning techniques, especially when applied without structural awareness, can disrupt these critical architectural relationships.

### 5.1.3 Training Dynamics and Optimization Landscape Effects

The differential performance patterns observed in our experiments reflect fundamental changes in optimization dynamics induced by different compression strategies.

**Compression-Induced Regularization Effects:** Parameter sharing acts as a form of architectural regularization that constrains the model to learn more fundamental, transferable features. This constraint benefits overall segmentation by forcing the network to identify the most essential tumor-background boundaries, but may limit the model’s capacity to learn the subtle feature combinations required for accurate subregion discrimination. The 16% reduction in training time observed in shared-weight models suggests more efficient convergence to generalizable solutions, but potentially at the cost of specialized representational capacity.

**Loss Landscape Modification:** Our analysis indicates that compression techniques fundamentally alter the optimization landscape in ways that favor certain

types of features over others. Shared-weight architectures exhibit smoother loss landscapes with more predictable convergence patterns, but these landscapes may lack the complex local minima structures necessary for learning sophisticated feature interactions. This explains why overall performance (which relies on relatively simple decision boundaries) is preserved while complex classification tasks (requiring intricate feature combinations) show degradation.

**Scale-Dependent Learning Dynamics:** The failure of traditional pruning techniques at modest compression ratios (10-20%) in medical architectures, contrasted with their success in large-scale computer vision models, reveals scale-dependent learning dynamics. Medium-scale medical models (8-10M parameters) may lack the redundancy necessary to support aggressive parameter removal while maintaining complex feature learning capabilities. This finding suggests that compression strategies must be tailored to both the scale and complexity requirements of specific application domains.

#### 5.1.4 Clinical Implications of Performance Differential

The theoretical understanding of compression effects on hierarchical feature learning has direct implications for clinical deployment strategies:

**Task-Specific Compression Selection:** For clinical applications requiring only broad tumor delineation (such as initial screening or gross tumor volume definition), architectural modifications provide optimal efficiency gains with minimal accuracy loss. However, applications requiring precise subregion classification (such as radiation therapy planning or treatment response assessment) may benefit from more conservative compression approaches or specialized fine-tuning protocols that prioritize class-specific performance recovery.

**Robustness Considerations:** The preserved overall performance combined with degraded class-specific accuracy suggests that compressed models maintain general tumor detection capabilities while potentially reducing reliability for detailed diagnostic tasks. This pattern has important implications for clinical risk assessment and appropriate use guidelines for compressed models in different medical contexts.

These theoretical insights establish a comprehensive framework for understanding and predicting compression effects in medical image segmentation, providing evidence-based guidance for selecting appropriate compression strategies based on specific clinical requirements and deployment constraints.

## 5.2 Key Findings and Implications

The experimental results yield several significant findings with important implications for clinical deployment:

- (a) **Deployment Scenario Analysis:** The research reveals distinct advantages for different compression approaches based on deployment requirements. Architectural modifications excel in immediate deployment scenarios, achieving 40-45% parameter reduction with minimal accuracy loss ( $<0.2\%$  Dice coefficient degradation) and no retraining requirements. Fine-tuned pruning methods achieve competitive accuracy but require additional training infrastructure.



- (b) **Fine-tuning Criticality:** Post-pruning fine-tuning emerges as an essential component for unstructured pruning methods in complex medical architectures. SNIP pruning demonstrates remarkable recovery (245% improvement from 0.279 to 0.985 Dice coefficient), while magnitude-based pruning shows substantial improvement (30% improvement from 0.755 to 0.985).
- (c) **Practical Compression Benefits:** While fine-tuned pruning achieves excellent accuracy, architectural modifications provide superior practical compression through actual parameter reduction. Fine-tuned sparse models maintain the same parameter count and memory requirements as the original model, limiting their deployment advantages.
- (d) **Hardware Efficiency Considerations:** Shared-weight models demonstrate superior hardware efficiency with predictable performance characteristics, while sparse models from pruning face challenges with irregular sparsity patterns that are inefficiently supported by modern inference engines.
- (e) **Clinical Viability Spectrum:** The optimal compression strategy depends on clinical deployment constraints. Resource-limited environments favor architectural modifications for immediate deployment, while research environments with retraining capabilities can leverage either approach effectively.

These findings demonstrate that strategic architectural modifications through weight sharing represent a more effective approach to model compression for medical image segmentation compared to traditional pruning techniques, offering a viable path toward deploying advanced AI models in resource-constrained clinical environments.

Our findings both align with and challenge established compression theory in fundamental ways that merit explicit comparison with landmark studies in the field.

Our results provide qualified support for Frankle and Carbin’s lottery ticket hypothesis [11], but with critical domain-specific modifications. While we observe that sparse subnetworks (achieved through fine-tuned pruning) can indeed match full model performance, our medical imaging context reveals that the "winning tickets" require substantially more careful initialization and recovery training compared to natural image classification tasks. This suggests that the lottery ticket phenomenon is domain-dependent, with medical architectures requiring more conservative compression ratios to maintain their "winning" properties.

Our compression-performance paradox directly contradicts the fundamental assumption underlying most quantization and pruning literature that compression necessarily involves accuracy sacrifice [10, 12]. Where studies like Deep Compression [10] demonstrate 35× compression with "minimal" accuracy loss, our architectural approach achieves 43% compression with accuracy maintenance or improvement. This departure suggests that the field’s focus on post-training compression has obscured the potential for compression-native architectural design.

Unlike knowledge distillation approaches that transfer learned representations from teacher to student networks, our weight-sharing strategy achieves compression through architectural constraint enforcement during training. This distinction is crucial: while distillation requires multiple models and complex training protocols, our approach achieves superior efficiency through single-model architectural innovation, aligning more closely with the practical constraints of medical AI deployment.

Our findings position architectural modification as a distinct compression paradigm that transcends the traditional pruning-quantization-distillation taxonomy. Where existing literature treats compression as optimization over trained models, our work establishes compression-aware architecture design as a primary research direction. This positioning has implications beyond medical imaging, suggesting that future compression research should prioritize architectural innovation over post-hoc optimization.

Our results reveal scale-dependent compression dynamics that challenge the universality assumptions of techniques developed for large-scale models. While magnitude-based pruning succeeds in ResNet-50 scale models [14], our medical architecture results demonstrate catastrophic failure at similar pruning ratios. This scale sensitivity suggests that compression techniques exhibit fundamental domain and scale dependencies that have been insufficiently addressed in the broader literature.

Our comprehensive evaluation provides a nuanced affirmative answer with critical qualifications. Weight-sharing techniques achieve 43.4% model size reduction while maintaining 99.9% of original segmentation accuracy (Dice: 0.984 vs 0.985). Pruning techniques demonstrate bifurcated results: catastrophic failure without fine-tuning but excellent recovery with proper retraining protocols. This finding establishes that effective compression is achievable but requires careful technique selection and implementation protocols.

The research conclusively demonstrates that architectural modifications excel in immediate deployment scenarios, while fine-tuned pruning methods require additional infrastructure but achieve optimal performance. For resource-constrained clinical environments, our SharedDepthwiseBlock approach provides the optimal balance of efficiency gains and deployment simplicity. This finding directly addresses the practical deployment challenges facing medical AI adoption in diverse healthcare settings.

Our class-specific analysis reveals differential compression sensitivity across tumor regions: NCR/NET and enhancing tumor classes show particular vulnerability to aggressive compression, while edema regions demonstrate greater robustness. This finding has direct clinical implications for treatment planning applications where accurate delineation of specific tumor components is critical for therapeutic decision-making.

The research establishes comprehensive efficiency baselines: 47% GPU memory reduction, 16% training time reduction, and measurable inference speed improvements. These quantitative benefits directly address the computational constraints limiting medical AI deployment in resource-limited settings, providing evidence-based guidance for infrastructure planning and technology adoption strategies.

Our investigation reveals that architectural modifications fundamentally improve training dynamics, creating more stable optimization landscapes with enhanced convergence properties. This finding extends beyond immediate compression benefits to establish architectural efficiency as a pathway to improved model development workflows, addressing both deployment efficiency and research productivity concerns.

This systematic mapping demonstrates that our research comprehensively addresses the initial research objectives while uncovering additional insights that extend the

theoretical and practical boundaries of medical AI compression. The convergence of these findings establishes a foundation for future research directions and practical deployment strategies in clinical environments.

### 5.2.1 Other Analytical Insights

Beyond these primary findings, our analysis reveals several profound insights that advance the theoretical understanding of compression in specialized neural architectures:

**Scale-Dependent Compression Dynamics:** Our results establish that compression techniques exhibit fundamental scale dependencies that have been largely ignored in the literature. Techniques optimized for large-scale models ( $>100\text{M}$  parameters) fail catastrophically when applied to medium-scale medical architectures (8-10M parameters), necessitating domain-specific approaches. This finding challenges the universality assumptions underlying current compression methodologies.

**Clinical Robustness Implications:** The differential impact of compression techniques on tumor subclasses (NCR/NET, ED, ET) reveals that compression introduces subtle biases that could affect clinical decision-making. Our analysis demonstrates that architectural modifications preserve class-specific performance more uniformly than pruning techniques, suggesting that robustness considerations should be primary criteria in medical AI compression.

**Training Dynamics Transformation:** Perhaps most significantly, our investigation reveals that compression techniques fundamentally alter training dynamics in ways that extend beyond simple parameter reduction. The accelerated convergence and enhanced stability observed in shared-weight models indicate that compression can improve optimization landscapes, providing efficiency gains during both training and inference phases.

These insights collectively establish a new framework for understanding compression in specialized neural architectures, with implications extending far beyond the immediate scope of medical image segmentation.

## 6 Conclusion

This research presents a comprehensive evaluation of model compression techniques applied to the RAAGR2-Net architecture for brain tumor segmentation, with the goal of developing clinically deployable models that maintain high accuracy while significantly reducing computational requirements. Through systematic experimentation with pruning methods and novel weight-sharing strategies, this work provides critical insights into the practical deployment of advanced medical AI systems.

### 6.1 Key Contributions

The primary contributions of this work include:

- (a) **Comprehensive Pruning Evaluation:** A systematic comparison of magnitude-based, SNIP, and dependency graph pruning methods on complex medical segmentation architectures, revealing the fundamental limitations of unstructured pruning for models with extensive skip connections and attention mechanisms.
- (b) **Novel Weight-Sharing Strategies:** Development and evaluation of Shared-DepthwiseBlock and paired sharing techniques that achieve superior compression ratios compared to traditional pruning while maintaining segmentation accuracy.
- (c) **Clinical Deployment Framework:** Establishment of evaluation criteria and benchmarks specifically tailored for medical image segmentation deployment, considering both accuracy preservation and resource efficiency.
- (d) **Architectural Insights:** Demonstration that strategic architectural modifications outperform post-training compression techniques, providing a new paradigm for efficient medical AI model design.

## 6.2 Principal Findings

The experimental results yield several significant findings:

**Superiority of Architectural Modifications:** Weight-sharing strategies consistently outperform traditional pruning methods, with the Depthwise Shared model achieving 43.4% parameter reduction and 43.2% model size reduction while maintaining 99.9% of the original segmentation accuracy (Dice coefficient: 0.984 vs 0.985).

**Limitations of Unstructured Pruning:** Both magnitude-based and SNIP pruning demonstrate catastrophic performance degradation in complex medical segmentation architectures, with Dice coefficients dropping to 0.742 and 0.285 respectively at only 10% pruning ratios. This finding challenges the applicability of popular pruning techniques to medical imaging tasks.

**Hardware Efficiency Gains:** Shared-weight models demonstrate superior hardware efficiency, with the Paired Shared variant achieving 47% reduction in GPU memory usage while maintaining inference speed improvements of up to 7%.

**Class-Specific Impact:** The analysis reveals differential impact across tumor sub-regions, with NCR/NET and ED classes showing particular sensitivity to aggressive compression. This finding has important implications for clinical utility, as accurate delineation of these regions is critical for treatment planning.

## 6.3 Clinical Implications

The results have significant implications for clinical deployment of AI-powered brain tumor segmentation:

- **Resource-Constrained Deployment:** The Depthwise Shared model enables deployment on standard clinical workstations without specialized hardware, reducing barriers to adoption in resource-limited healthcare settings.

- **Real-Time Processing:** Inference speed improvements combined with reduced memory requirements enable near real-time processing of multi-modal MRI data, supporting interactive clinical workflows.
- **Scalability:** The success of weight-sharing strategies provides a foundation for scaling to larger datasets and more complex architectures while maintaining computational efficiency.
- **Regulatory Compliance:** Maintained segmentation accuracy ensures that compressed models meet clinical accuracy requirements while offering practical deployment advantages.

## 6.4 Limitations and Future Work

While this work demonstrates significant advances in model compression for medical image segmentation, several limitations warrant consideration:

**Dataset Scope:** Evaluation was conducted primarily on the BraTS dataset. Future work should validate these findings across diverse medical imaging tasks and datasets to establish broader generalizability.

**Hardware Diversity:** Performance evaluation focused on standard GPU hardware. Investigation of deployment on specialized medical imaging hardware and edge devices would provide additional insights.

**Long-term Validation:** Clinical validation studies are needed to assess the practical impact of compressed models on diagnostic accuracy and clinical workflows over extended periods.

### 6.4.1 Critical Methodological Analysis

A sophisticated evaluation of this research reveals several fundamental limitations and methodological constraints that shape the interpretation and generalizability of our findings:

**Architectural Specificity Limitation:** Our compression strategies are specifically designed for RAAGR2-Net’s particular combination of recurrent blocks, attention mechanisms, and atrous convolutions. While this specificity enables superior results within this domain, it raises questions about the transferability of our SharedDepthwiseBlock approach to other medical segmentation architectures. The success of our method may be contingent on the presence of ReASPP3 modules with multiple dilated branches, limiting its broader applicability.

**Deployment Scenario Limitations:** Our evaluation focuses primarily on single-deployment scenarios and does not comprehensively address the computational costs and time requirements associated with fine-tuning protocols in real-world clinical environments. The practical implementation of fine-tuned pruning methods may require additional infrastructure and expertise that could limit their adoption in resource-constrained healthcare settings, even when optimal performance is achievable.

**Scale Dependency and Compression Ceiling:** Our analysis reveals that compression effectiveness exhibits diminishing returns beyond certain thresholds. The

43.4% parameter reduction achieved by our Depthwise Shared model may represent a fundamental compression ceiling for this architecture class, beyond which catastrophic performance degradation becomes inevitable. This suggests that future improvements may require architectural innovations rather than more aggressive compression techniques.

**Dataset Homogeneity Bias:** The exclusive use of BraTS data, while providing controlled experimental conditions, introduces potential biases that may not reflect real-world clinical diversity. Brain tumor characteristics in our dataset may not represent the full spectrum of pathological variations encountered in clinical practice, particularly across different populations, scanning protocols, and disease stages. This limitation is particularly critical for weight-sharing approaches that assume consistency in low-level feature patterns.

**Validation Protocol Constraints:** Our evaluation methodology, while comprehensive within its scope, exhibits several constraints: (1) the exclusive focus on Dice coefficient and IoU may not capture subtle changes in boundary delineation quality critical for surgical planning, (2) the absence of radiologist validation limits our understanding of clinical relevance, and (3) the static evaluation protocol does not account for the dynamic nature of clinical decision-making processes.

**Computational Environment Specificity:** Our efficiency measurements are constrained to specific hardware configurations and software environments. The observed inference speed improvements and memory reductions may not generalize across different GPU architectures, driver versions, or inference frameworks commonly used in clinical settings. This specificity limits the practical applicability of our quantitative efficiency claims.

**Theoretical Framework Limitations:** While our compression-generalization hypothesis provides valuable insights, it remains primarily empirical without rigorous theoretical grounding. The mechanisms underlying the superior performance of architectural modifications over pruning techniques require deeper mathematical analysis to establish causality rather than correlation.

These limitations do not diminish the significance of our contributions but rather define the boundaries within which our findings should be interpreted and applied.

## 6.5 Future Research Directions

Several promising avenues for future research emerge from this work:

- (a) **Adaptive Compression:** Development of dynamic compression strategies that adjust model complexity based on input characteristics or clinical requirements.
- (b) **Hybrid Compression Frameworks:** Investigation of combined architectural modifications and selective fine-tuned pruning to achieve optimal compression ratios while maintaining deployment flexibility across different clinical scenarios.
- (c) **Multi-Task Optimization:** Extension of weight-sharing strategies to multi-task medical imaging scenarios, where a single model performs multiple diagnostic tasks.

- (d) **Federated Learning Integration:** Investigation of compressed models in federated learning scenarios for privacy-preserving medical AI deployment across multiple institutions.
- (e) **Uncertainty Quantification:** Integration of uncertainty estimation capabilities into compressed models to provide confidence measures for clinical decision support.

## 6.6 Final Remarks

This research demonstrates that effective neural network compression for medical image segmentation requires careful consideration of deployment scenarios and evaluation protocols. Through comprehensive analysis of both immediate deployment and optimal performance scenarios, this work reveals that architectural modifications through weight sharing and properly fine-tuned pruning methods can both achieve excellent segmentation performance, but with distinct practical advantages.

The developed weight-sharing techniques offer immediate deployment benefits with significant parameter reduction, while fine-tuned pruning methods provide competitive accuracy with different infrastructure requirements. This finding challenges simplistic notions of compression method superiority and instead highlights the importance of matching compression strategies to specific deployment constraints and clinical requirements.

The insights from this research contribute to a more nuanced understanding of compression techniques in specialized medical AI applications, providing practical guidance for deploying advanced segmentation models across diverse clinical environments. As healthcare systems worldwide seek to integrate AI tools into routine clinical practice, the techniques and evaluation frameworks developed in this work offer evidence-based approaches for selecting appropriate compression strategies based on specific deployment scenarios and resource constraints.

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