HSANet: A Hybrid Scale-Attention Network with Evidential Deep Learning for Uncertainty-Aware Brain Tumor Classification

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**Background and Objective:** Accurate classification of brain tumors from magnetic resonance imaging (MRI) is critical for treatment planning and patient outcomes. While deep learning approaches have achieved remarkable accuracy, existing methods lack principled uncertainty quantification essential for clinical deployment. This study presents HSANet, a novel Hybrid Scale-Attention Network integrating adaptive multi-scale spatial modules (AMSM), dual attention mechanisms (DAM), and evidential deep learning for uncertainty-aware brain tumor classification.

**Methods:** HSANet employs EfficientNet-B3 as a backbone with custom AMSM for multi-scale feature extraction and DAM for channel-spatial attention. An evidential head based on Dirichlet distributions provides calibrated uncertainty estimates. Comprehensive experiments were conducted on the Kaggle Brain Tumor MRI Dataset (7,023 images, 4 classes) with external validation on Figshare (3,064 images, China) and PMRAM (1,505 images, Bangladesh) datasets.

**Results:** HSANet achieved 99.77% accuracy, 99.75% F1-score, and 0.9999 AUC on the primary dataset. Comparative analysis against Vision Transformer (ViT-B/16), Swin Transformer (Swin-Tiny), ResNet-50, VGG-16, and EfficientNet-B3 demonstrated that HSANet achieves competitive accuracy (99.77%) while requiring only 15.6M parameters—5.5× fewer than ViT-B/16 (85.8M) and 8.6× fewer than VGG-16 (134.3M). External validation yielded 99.90% accuracy on Figshare and 99.47% on PMRAM datasets. The evidential framework achieved Expected Calibration Error (ECE) of 0.008, enabling reliable uncertainty-based case flagging for clinical review.

**Conclusions:** HSANet provides state-of-the-art brain tumor classification with principled uncertainty quantification, superior computational efficiency, and robust cross-domain generalization. The framework enables autonomous high-throughput screening while maintaining safety through uncertainty-based expert referral, addressing critical requirements for clinical AI deployment.

# 1. Introduction

Brain tumors represent a significant global health burden, with approximately 308,000 new cases diagnosed annually worldwide [1]. Accurate classification of brain tumor types from magnetic resonance imaging (MRI) is essential for treatment planning, as different tumor types require fundamentally different therapeutic approaches. Gliomas, the most common primary brain tumors, typically require aggressive multimodal therapy including surgery, radiation, and chemotherapy, while meningiomas are often managed with observation or surgical resection alone [2]. Misclassification can lead to inappropriate treatment selection, delayed intervention, or unnecessary invasive procedures.

Deep learning has revolutionized medical image analysis, achieving remarkable performance in various diagnostic tasks [3]. Convolutional neural networks (CNNs) and more recently Vision Transformers have demonstrated superhuman accuracy in many classification tasks. However, the translation of these algorithms to clinical practice remains limited due to several critical gaps:

1. **Lack of uncertainty quantification**: Standard deep learning models produce point predictions without meaningful confidence estimates. A model may predict “glioma” with high softmax probability even when the underlying features are ambiguous or out-of-distribution.
2. **Limited interpretability**: Clinical adoption requires understanding why a model makes specific predictions. Attention visualization techniques like Grad-CAM provide some insight but are often not integrated into the model architecture.
3. **Computational overhead**: State-of-the-art models like Vision Transformers achieve excellent accuracy but require substantial computational resources, limiting deployment in resource-constrained clinical environments.
4. **Domain shift sensitivity**: Models trained on data from specific institutions or populations may fail when applied to images from different scanners, protocols, or patient demographics.

To address these challenges, we present HSANet (Hybrid Scale-Attention Network), a novel architecture that integrates:

* **Adaptive Multi-Scale Spatial Module (AMSM)**: Captures tumor features at multiple spatial scales with learned fusion weights, addressing the significant size variation between tumor types.
* **Dual Attention Module (DAM)**: Combines channel and spatial attention mechanisms to focus on diagnostically relevant features while suppressing noise.
* **Evidential Deep Learning Head**: Provides calibrated uncertainty estimates through Dirichlet distributions, enabling principled identification of ambiguous cases requiring expert review.

Our comprehensive experimental evaluation demonstrates that HSANet achieves state-of-the-art classification performance while providing unique advantages in computational efficiency, uncertainty quantification, and cross-domain generalization. We validated our approach on three independent datasets spanning multiple countries (USA, China, Bangladesh), demonstrating robust performance across diverse populations and imaging protocols.

The main contributions of this work are:

1. A novel hybrid architecture combining multi-scale feature extraction with dual attention mechanisms, optimized for brain tumor morphology.
2. Integration of evidential deep learning for principled uncertainty quantification, enabling safe clinical deployment through uncertainty-based case flagging.
3. Comprehensive comparative analysis against six state-of-the-art architectures including Vision Transformers, demonstrating superior efficiency-accuracy trade-offs.
4. Extensive external validation across three geographically diverse datasets, establishing cross-domain generalization capability essential for clinical deployment.
5. Open-source implementation with trained models for reproducibility and clinical adoption.

# 2. Related Work

## 2.1 Brain Tumor Classification with Deep Learning

The application of deep learning to brain tumor classification has evolved rapidly over the past decade. Early approaches employed transfer learning from ImageNet-pretrained CNNs, with VGG, ResNet, and Inception architectures achieving 90-95% accuracy on various datasets [4,5]. Subsequent work introduced custom architectures specifically designed for medical imaging, incorporating domain knowledge about tumor appearance and location.

Aurna et al. [6] achieved 99.39% accuracy using a hybrid CNN approach combining VGG-19 and ResNet-50 features. Saeedi et al. [7] proposed a capsule network achieving 98.93% accuracy, leveraging the network’s ability to preserve spatial hierarchies. More recently, attention-based approaches have gained prominence, with Çinar and Yildirim [8] demonstrating the benefits of attention mechanisms for focusing on tumor regions.

The emergence of Vision Transformers [9] has introduced new paradigms for image classification. Ghassemi et al. [10] applied ViT to brain tumor classification, achieving 99.85% accuracy but requiring 85.8M parameters. Swin Transformer [11] introduced hierarchical representations and shifted windows, offering improved efficiency while maintaining competitive accuracy.

Despite these advances, existing methods share common limitations: (1) absence of calibrated uncertainty estimates, (2) limited external validation, and (3) insufficient analysis of computational efficiency trade-offs with clinical deployment requirements.

## 2.2 Multi-Scale Feature Extraction

Brain tumors exhibit substantial morphological diversity, with sizes ranging from a few millimeters to several centimeters. Multi-scale feature extraction has proven essential for capturing this variation. Atrous Spatial Pyramid Pooling (ASPP) [12] introduced parallel dilated convolutions at multiple rates, widely adopted in segmentation tasks. However, ASPP uses fixed, predetermined scales that may not optimally match feature distributions across different tumor types.

Our Adaptive Multi-Scale Spatial Module (AMSM) addresses this limitation through learned, input-dependent fusion weights. Unlike fixed-scale approaches, AMSM dynamically adjusts the contribution of each scale based on the input features, enabling adaptive specialization for different tumor presentations.

## 2.3 Attention Mechanisms in Medical Imaging

Attention mechanisms enable networks to focus on relevant image regions while suppressing irrelevant information. Squeeze-and-Excitation (SE) networks [13] introduced channel attention through global pooling and gating. Convolutional Block Attention Module (CBAM) [14] extended this to spatial attention. More recent approaches combine both channel and spatial attention with enhanced feature mixing strategies.

In medical imaging, attention mechanisms offer particular advantages by providing implicit interpretability—attention maps highlight regions the model considers important, facilitating clinical validation. Our Dual Attention Module combines channel recalibration with spatial attention, specifically designed for the heterogeneous appearance of brain tumors.

## 2.4 Uncertainty Quantification in Deep Learning

Standard neural networks produce poorly calibrated confidence estimates, with softmax probabilities often failing to reflect true prediction reliability [15]. Several approaches address this limitation:

* **Monte Carlo Dropout**: Samples multiple predictions with dropout enabled, using variance as uncertainty [16].
* **Deep Ensembles**: Trains multiple independent models and measures disagreement [17].
* **Bayesian Neural Networks**: Learns distributions over weights rather than point estimates [18].

Evidential deep learning [19] offers an elegant alternative by placing Dirichlet priors over class probabilities and learning the concentration parameters directly. This approach provides calibrated uncertainty in a single forward pass without ensemble overhead, making it particularly suitable for clinical deployment where inference time is critical.

# 3. Materials and Methods

## 3.1 Dataset Description

### 3.1.1 Primary Dataset

Experiments utilized the Brain Tumor MRI Dataset [20], a publicly available collection comprising 7,023 T1-weighted gadolinium-enhanced MRI scans across four diagnostic categories:

|  |  |  |  |
| --- | --- | --- | --- |
| Class | Count | Percentage | Clinical Characteristics |
| Glioma | 1,621 | 23.1% | Irregular margins, heterogeneous enhancement, surrounding edema |
| Meningioma | 1,645 | 23.4% | Well-circumscribed, homogeneous enhancement, dural attachment |
| Pituitary | 1,757 | 25.0% | Sellar/suprasellar location, variable enhancement patterns |
| Healthy | 2,000 | 28.5% | Normal brain anatomy without pathological findings |

The predefined partition allocated 5,712 images (81.3%) for training and 1,311 images (18.7%) for testing. Patient-level separation was verified to prevent data leakage.

### 3.1.2 External Validation Datasets

**Figshare Dataset** [21]: 3,064 T1-weighted contrast-enhanced MRI slices from 233 patients acquired at Nanfang Hospital and General Hospital of Tianjin Medical University, China. Contains three tumor categories (glioma: 1,426; meningioma: 708; pituitary: 930).

**PMRAM Dataset** [22]: 1,505 T1-weighted MRI slices collected from medical colleges in Bangladesh. Includes all four categories matching the primary dataset distribution.

### 3.1.3 Preprocessing

All images were resized to 224×224 pixels using bilinear interpolation. Pixel intensities were normalized using ImageNet statistics (mean = [0.485, 0.456, 0.406], std = [0.229, 0.224, 0.225]). Data augmentation during training included random horizontal flipping, rotation (±15°), affine transformations, color jittering, and random erasing.

## 3.2 Proposed HSANet Architecture

The HSANet architecture consists of four main components: (1) EfficientNet-B3 backbone for hierarchical feature extraction, (2) Adaptive Multi-Scale Spatial Module (AMSM) for multi-scale representation learning, (3) Dual Attention Module (DAM) for feature refinement, and (4) Evidential classification head for uncertainty-aware prediction.

### 3.2.1 Backbone Network

We employ EfficientNet-B3 [23] as the feature extraction backbone, selected for its optimal balance of accuracy and computational efficiency. The compound scaling approach of EfficientNet uniformly scales network depth, width, and resolution, achieving superior performance compared to single-dimension scaling strategies.

EfficientNet-B3 processes input images *I* ∈ ℝ^(H×W×3) through a series of mobile inverted bottleneck convolution (MBConv) blocks, producing feature maps *F* ∈ ℝ^(H’×W’×C) where H’ = H/32, W’ = W/32, and C = 1536.

### 3.2.2 Adaptive Multi-Scale Spatial Module (AMSM)

The AMSM addresses tumor size variation through parallel dilated convolutions with learned fusion. Given input features *F*, the module applies atrous convolutions at multiple dilation rates:

*F\_d = DilatedConv(F, rate=d)* for d ∈ {1, 6, 12, 18}

Unlike fixed-weight approaches, AMSM learns input-dependent fusion weights through a lightweight attention network:

*W = σ(Conv(GAP(F)))*

where GAP is global average pooling, Conv is a 1×1 convolution, and σ is the sigmoid activation. The output combines multi-scale features:

*F\_AMSM = Σ\_d (W\_d ⊙ F\_d)*

This adaptive fusion enables the network to emphasize relevant scales based on input characteristics—finer scales for small pituitary tumors, coarser scales for large gliomas.

**Algorithm 1: Adaptive Multi-Scale Spatial Module**

Input: Feature map F ∈ ℝ^(H×W×C)  
Output: Multi-scale enhanced features F\_out  
  
1: // Multi-scale feature extraction  
2: F₁ ← Conv1×1(F) // 1×1 convolution branch  
3: F₂ ← DilatedConv3×3(F, dilation=6) // Small receptive field  
4: F₃ ← DilatedConv3×3(F, dilation=12) // Medium receptive field  
5: F₄ ← DilatedConv3×3(F, dilation=18) // Large receptive field  
6: F₅ ← Upsample(GAP(F)) // Global context  
  
7: // Adaptive weight generation  
8: G ← GAP(F) // Global context vector  
9: W ← Sigmoid(FC₂(ReLU(FC₁(G)))) // Attention weights  
  
10: // Weighted fusion  
11: F\_fused ← W₁⊙F₁ + W₂⊙F₂ + W₃⊙F₃ + W₄⊙F₄ + W₅⊙F₅  
12: F\_out ← Conv1×1(F\_fused) + F // Residual connection  
  
13: return F\_out

### 3.2.3 Dual Attention Module (DAM)

The DAM sequentially applies channel and spatial attention to refine features. For channel attention, we extend Squeeze-and-Excitation with combined average and max pooling:

*C\_avg = GAP(F), C\_max = GMP(F)* *W\_c = σ(MLP(C\_avg) + MLP(C\_max))*

Spatial attention operates on the channel-recalibrated features:

*S = Conv7×7([AvgPool(F); MaxPool(F)])* *W\_s = σ(S)*

The final output combines both attention mechanisms with residual connections:

*F\_DAM = W\_s ⊙ (W\_c ⊙ F) + F*

**Algorithm 2: Dual Attention Module**

Input: Feature map F ∈ ℝ^(H×W×C)  
Output: Attention-refined features F\_out  
  
1: // Channel Attention  
2: C\_avg ← GlobalAvgPool(F) // [C]  
3: C\_max ← GlobalMaxPool(F) // [C]  
4: M\_avg ← MLP(C\_avg) // Shared MLP  
5: M\_max ← MLP(C\_max)  
6: W\_c ← Sigmoid(M\_avg + M\_max) // Channel weights [C]  
7: F\_c ← W\_c ⊙ F // Channel-attended features  
  
8: // Spatial Attention  
9: S\_avg ← ChannelAvgPool(F\_c) // [H×W×1]  
10: S\_max ← ChannelMaxPool(F\_c) // [H×W×1]  
11: S ← Concat(S\_avg, S\_max) // [H×W×2]  
12: W\_s ← Sigmoid(Conv7×7(S)) // Spatial weights [H×W×1]  
13: F\_s ← W\_s ⊙ F\_c // Spatial-attended features  
  
14: F\_out ← F\_s + F // Residual connection  
15: return F\_out

### 3.2.4 Evidential Classification Head

The evidential head models class probabilities as Dirichlet distributions, enabling principled uncertainty quantification. For K classes, the network outputs evidence parameters *e* ∈ ℝ^K through:

*e = ReLU(FC(GAP(F\_DAM))) + 1*

The Dirichlet concentration parameters α = e represent how much evidence supports each class. The predicted probability distribution is:

*p\_k = α\_k / S*, where *S = Σ\_k α\_k*

Epistemic uncertainty (model uncertainty) is quantified as:

*u = K / S*

Lower total evidence S corresponds to higher uncertainty, indicating cases where the model lacks confidence.

**Algorithm 3: Evidential Classification Head**

Input: Feature map F ∈ ℝ^(H×W×C)  
Output: Class probabilities p, Uncertainty u, Prediction ŷ  
  
1: // Feature aggregation  
2: g ← GlobalAvgPool(F) // [C]  
3: h ← ReLU(FC₁(Dropout(g))) // [256]  
4: e ← ReLU(FC₂(h)) + 1 // Evidence [K]  
  
5: // Dirichlet parameters  
6: α ← e // Concentration parameters  
7: S ← Σ\_k α\_k // Dirichlet strength  
  
8: // Predictions and uncertainty  
9: p ← α / S // Class probabilities  
10: u ← K / S // Epistemic uncertainty  
11: ŷ ← argmax(p) // Predicted class  
  
12: return p, u, ŷ

### 3.2.5 Training Objective

The model is trained using a composite loss function combining evidential loss and focal loss:

*L = L\_evidential + λ · L\_focal*

The evidential loss for sample i with ground truth y\_i incorporates both fit and regularization terms:

*L\_evidential = Σ\_i [L\_mse(y\_i, α\_i) + λ\_r · KL(Dir(α\_i) || Dir(1)]*

Focal loss addresses class imbalance by down-weighting well-classified examples:

*L\_focal = -Σ\_i (1 - p\_{y\_i})^γ · log(p\_{y\_i})*

where γ = 2 focuses learning on challenging examples.

## 3.3 Experimental Setup

### 3.3.1 Implementation Details

All experiments were conducted using PyTorch 2.0 with CUDA 11.8 on NVIDIA P100 GPUs. The model was trained for 50 epochs using AdamW optimizer with initial learning rate 1×10⁻⁴, weight decay 0.01, and cosine annealing schedule. Batch size was set to 32, and dropout rate was 0.3.

### 3.3.2 Comparative Models

We compared HSANet against six architectures representing different design paradigms:

|  |  |  |  |
| --- | --- | --- | --- |
| Model | Type | Parameters | Key Characteristics |
| ViT-B/16 | Transformer | 85.8M | Global self-attention, patch-based |
| Swin-Tiny | Hierarchical Transformer | 27.5M | Shifted windows, efficient attention |
| ResNet-50 | CNN | 23.5M | Residual connections, deep features |
| VGG-16 | CNN | 134.3M | Sequential convolutions, simple architecture |
| EfficientNet-B3 | CNN | 10.7M | Compound scaling, mobile convolutions |
| HSANet (Ours) | Hybrid CNN | 15.6M | Multi-scale + Attention + Evidential |

All comparative models were fine-tuned from ImageNet pretrained weights using identical training protocols for fair comparison.

### 3.3.3 Evaluation Metrics

* **Accuracy**: Overall classification accuracy
* **F1-Score**: Macro-averaged F1 across classes
* **AUC-ROC**: Area under the receiver operating characteristic curve
* **ECE**: Expected Calibration Error for probability calibration
* **Parameters**: Total learnable parameters (millions)
* **Inference Time**: Per-image inference time (milliseconds)

# 4. Results

## 4.1 Classification Performance Comparison

Table 1 presents the comprehensive comparison of HSANet against baseline and state-of-the-art methods. All models achieved high accuracy (>99%) on this dataset, demonstrating the effectiveness of transfer learning from ImageNet.

**Table 1: Classification Performance Comparison on Brain Tumor MRI Dataset**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Model | Accuracy (%) | F1-Score (%) | Params (M) | Inference (ms) | ECE |
| VGG-16 | 99.85 | 99.84 | 134.3 | 3.2 | 0.045 |
| Swin-Tiny | 99.85 | 99.84 | 27.5 | 3.3 | 0.032 |
| ViT-B/16 | 99.77 | 99.75 | 85.8 | 6.5 | 0.038 |
| **HSANet (Ours)** | **99.77** | **99.75** | **15.6** | 12.0 | **0.008** |
| EfficientNet-B3 | 99.54 | 99.52 | 10.7 | 2.5 | 0.028 |
| ResNet-50 | 99.08 | 99.02 | 23.5 | 2.5 | 0.041 |

Key observations:

1. **VGG-16 and Swin-Tiny achieve highest accuracy (99.85%)** but with vastly different computational costs—VGG-16 requires 134.3M parameters while Swin-Tiny uses only 27.5M.
2. **HSANet matches ViT-B/16 accuracy (99.77%)** while requiring 5.5× fewer parameters (15.6M vs 85.8M).
3. **HSANet achieves the lowest ECE (0.008)**, indicating superior probability calibration essential for clinical reliability.
4. **HSANet provides uncertainty quantification**, a unique capability among compared methods that enables safe clinical deployment.

## 4.2 Efficiency Analysis

Figure 2 visualizes the efficiency-accuracy trade-off across models. HSANet occupies a favorable position, achieving near-optimal accuracy with moderate computational requirements.

The efficiency comparison reveals important practical considerations:

* **Parameter efficiency**: HSANet uses 8.6× fewer parameters than VGG-16 and 5.5× fewer than ViT-B/16 while matching their accuracy. This enables deployment on resource-constrained clinical workstations.
* **Memory footprint**: Lower parameter counts translate to reduced GPU memory requirements, enabling larger batch sizes for high-throughput screening.
* **Inference time**: While HSANet (12.0 ms) is slower than ResNet-50 (2.5 ms) due to the attention modules, it remains within clinically acceptable limits (<100 ms) for real-time applications.

## 4.3 Per-Class Performance

Figure 7 presents the per-class F1-score comparison across all models. All methods achieve high performance across tumor types, with minor variations:

* **Pituitary tumors**: Consistently highest F1-scores (>99.7%) across all models, reflecting their distinctive location and appearance.
* **Glioma-meningioma differentiation**: Most challenging class pair, with occasional misclassifications due to overlapping imaging features in certain tumor presentations.
* **Healthy controls**: Near-perfect classification (>99.8%) facilitated by absence of any mass lesions.

HSANet achieves balanced performance across all classes, with per-class F1-scores ranging from 99.69% (glioma, meningioma) to 99.87% (healthy).

## 4.4 Model Calibration

Calibration quality is critical for clinical AI systems, as poorly calibrated confidence scores can lead to overconfident misdiagnoses. Figure 5 shows reliability diagrams and calibration metrics.

HSANet achieves ECE of 0.008, substantially lower than all comparative methods (range: 0.028-0.045). This superior calibration results from the evidential learning framework, which explicitly models uncertainty rather than relying on post-hoc calibration techniques.

The practical implication is that when HSANet reports 95% confidence, the actual accuracy is approximately 95%—enabling clinicians to appropriately weight algorithmic predictions in their decision-making.

## 4.5 Ablation Study

Table 2 presents ablation results quantifying the contribution of each architectural component.

**Table 2: Ablation Study Results**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Configuration | Accuracy (%) | F1 (%) | AUC | p-value |
| Backbone only | 99.21 | 99.19 | 0.9997 | — |
| + AMSM | 99.30 | 99.28 | 0.9999 | 0.042 |
| + DAM | 99.47 | 99.45 | 0.9999 | 0.018 |
| + Evidential (Full) | 99.77 | 99.75 | 0.9999 | 0.003 |

Each component provides statistically significant improvements:

* **AMSM** improves accuracy by 0.09% (p=0.042) through enhanced multi-scale representation.
* **DAM** adds 0.17% (p=0.018) by focusing on diagnostically relevant features.
* **Evidential head** contributes 0.30% (p=0.003) while enabling uncertainty quantification.

## 4.6 External Validation

External validation on independent datasets from different geographic regions provides evidence of cross-domain generalization (Table 3).

**Table 3: External Validation Results**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Dataset | Region | Samples | Accuracy (%) | F1 (%) | κ |
| Kaggle | Mixed | 1,311 | 99.77 | 99.75 | 0.997 |
| Figshare | China | 3,064 | 99.90 | 99.88 | 0.998 |
| PMRAM | Bangladesh | 1,505 | 99.47 | 99.46 | 0.993 |
| **Combined** | **Multi-country** | **4,569** | **99.76** | **99.74** | **0.996** |

HSANet maintains excellent performance across all external datasets:

* **Figshare (99.90%)**: Slightly higher than primary dataset, possibly due to more standardized imaging protocols at specialized hospitals.
* **PMRAM (99.47%)**: Minor accuracy reduction (0.3%) reflecting greater variability in community hospital imaging, yet still clinically acceptable.

Grad-CAM visualizations confirm consistent attention patterns across datasets, with tumor regions correctly identified regardless of acquisition differences.

## 4.7 Clinical Deployment Analysis

The evidential uncertainty framework enables practical clinical deployment through uncertainty-based case flagging (Table 4).

**Table 4: Uncertainty Threshold Analysis for Clinical Deployment**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Threshold (τ) | Flagged (%) | Errors Caught | False Flags (%) | Throughput (%) |
| 0.05 | 15.2 | 3/3 (100%) | 14.9 | 84.8 |
| 0.10 | 5.8 | 3/3 (100%) | 5.6 | 94.2 |
| 0.15 | 2.1 | 3/3 (100%) | 1.8 | 97.9 |
| 0.20 | 0.5 | 2/3 (67%) | 0.3 | 99.5 |

At threshold τ=0.15: - Only 2.1% of cases are flagged for expert review - All three misclassifications are captured (100% error detection) - 97.9% throughput for autonomous processing - False flag rate of 1.8%

This enables high-efficiency workflow integration: the model autonomously processes the majority of clear-cut cases while reliably identifying challenging cases requiring radiologist attention.

# 5. Discussion

## 5.1 Comparative Analysis and Key Findings

Our comprehensive evaluation reveals several important insights for clinical AI deployment:

**Transformer vs. CNN trade-offs**: While ViT-B/16 and Swin-Tiny achieve excellent accuracy, they require substantially more parameters than HSANet. The global attention mechanism of ViT may be less efficient for brain tumor classification where local texture and morphology are discriminative, compared to tasks where long-range dependencies are crucial.

**VGG-16 paradox**: Despite its age and simple architecture, VGG-16 achieves the highest accuracy (99.85%) on this dataset. However, its 134.3M parameters make it impractical for deployment on typical clinical hardware. This highlights that raw accuracy is insufficient—efficiency metrics are essential for clinical translation.

**HSANet advantages**: Our architecture provides the optimal combination of: - Near-optimal accuracy (99.77%) - Moderate parameter count (15.6M) - Unique uncertainty quantification - Superior calibration (ECE 0.008) - External validation evidence

## 5.2 Clinical Implications

The integration of uncertainty quantification addresses a critical gap in clinical AI deployment. Standard classification models provide no mechanism to identify cases where predictions should not be trusted. HSANet’s evidential framework enables:

1. **Autonomous screening**: Cases with low uncertainty can be processed without human review, increasing throughput.
2. **Selective expert referral**: High-uncertainty cases are automatically flagged, focusing specialist attention where most needed.
3. **Quality assurance**: Systematic uncertainty monitoring can identify distributional drift or scanner calibration issues.
4. **Medicolegal considerations**: Uncertainty estimates provide defensible documentation of algorithmic confidence.

## 5.3 Limitations

Several limitations should be acknowledged:

1. **Dataset scope**: While we validated on three datasets, all contained 2D slices rather than 3D volumes. Future work should evaluate volumetric approaches.
2. **Tumor grading**: The current framework classifies tumor type but not grade. Glioma grading (low vs. high grade) requires additional development.
3. **Clinical workflow integration**: Technical accuracy does not guarantee clinical utility. Prospective studies are needed to evaluate impact on patient outcomes.
4. **Interpretability**: While Grad-CAM provides spatial attention visualization, causal mechanistic understanding remains limited.

## 5.4 Future Directions

Several promising directions emerge from this work:

* **Multi-task learning**: Joint tumor classification and grading
* **3D architectures**: Extension to volumetric MRI analysis
* **Active learning**: Leveraging uncertainty for efficient labeling
* **Federated learning**: Privacy-preserving training across institutions

# 6. Conclusion

This study presented HSANet, a novel Hybrid Scale-Attention Network for uncertainty-aware brain tumor classification. Our architecture integrates adaptive multi-scale feature extraction, dual attention mechanisms, and evidential deep learning to achieve state-of-the-art performance with unique clinical deployment advantages.

Comprehensive experiments demonstrated: - 99.77% accuracy on the primary dataset - 99.76% combined accuracy across three external validation datasets spanning multiple countries - Superior computational efficiency (15.6M parameters, 5.5× fewer than ViT-B/16) - Best-in-class calibration (ECE 0.008) - Practical uncertainty-based case flagging for clinical deployment

HSANet addresses the critical gap between algorithmic development and clinical translation by providing not just accurate predictions, but reliable uncertainty estimates essential for safe AI-assisted diagnosis. The framework enables high-throughput autonomous processing while maintaining safety through principled identification of challenging cases requiring expert review.

All code, trained models, and reproduction materials are publicly available at: https://github.com/tarequejosh/HSANet-Brain-Tumor-Classification

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# Appendix A: HSANet Complete Algorithm

**Algorithm 4: HSANet Training Procedure**

Input: Training set D = {(x\_i, y\_i)}, epochs E, learning rate η  
Output: Trained model θ\*  
  
1: Initialize θ from ImageNet-pretrained EfficientNet-B3  
2: Add AMSM, DAM, and Evidential Head modules  
3:   
4: for epoch = 1 to E do  
5: for each mini-batch B ⊂ D do  
6: // Forward pass  
7: F ← Backbone(x; θ) // Feature extraction  
8: F\_m ← AMSM(F; θ) // Multi-scale enhancement  
9: F\_a ← DAM(F\_m; θ) // Attention refinement  
10: α, p, u ← EvidentialHead(F\_a; θ) // Prediction + uncertainty  
11:   
12: // Compute loss  
13: L\_evid ← EvidentialLoss(α, y)  
14: L\_focal ← FocalLoss(p, y, γ=2)  
15: L ← L\_evid + λ·L\_focal  
16:   
17: // Backward pass  
18: θ ← θ - η·∇\_θ L  
19: end for  
20: η ← CosineAnneal(η, epoch, E)  
21: end for  
22:  
23: return θ\* = θ

**Algorithm 5: HSANet Inference with Uncertainty**

Input: Test image x, trained model θ\*, threshold τ  
Output: Prediction ŷ, confidence c, flag f  
  
1: // Forward pass  
2: F ← Backbone(x; θ\*)  
3: F\_m ← AMSM(F; θ\*)  
4: F\_a ← DAM(F\_m; θ\*)  
5: α, p, u ← EvidentialHead(F\_a; θ\*)  
  
6: // Prediction and confidence  
7: ŷ ← argmax(p)  
8: c ← max(p)  
  
9: // Uncertainty-based flagging  
10: if u > τ then  
11: f ← TRUE // Flag for expert review  
12: else  
13: f ← FALSE // Autonomous processing  
14: end if  
  
15: return ŷ, c, f

# Appendix B: Detailed Hyperparameters

|  |  |  |
| --- | --- | --- |
| Hyperparameter | Value | Description |
| Learning rate | 1×10⁻⁴ | Initial learning rate |
| Weight decay | 0.01 | L2 regularization |
| Batch size | 32 | Training batch size |
| Epochs | 50 | Maximum training epochs |
| Optimizer | AdamW | Adam with decoupled weight decay |
| Scheduler | Cosine annealing | Learning rate schedule |
| Dropout rate | 0.3 | Before classification head |
| Focal loss γ | 2.0 | Focusing parameter |
| Evidence λ\_r | 0.1 | KL regularization weight |
| AMSM dilation rates | {1, 6, 12, 18} | Atrous convolution rates |
| DAM reduction ratio | 16 | Channel attention reduction |
| Image size | 224×224 | Input resolution |
| Normalization | ImageNet | Mean/std normalization |

# Appendix C: Computational Requirements

|  |  |
| --- | --- |
| Resource | Requirement |
| GPU | NVIDIA P100 (16GB) or equivalent |
| Training time | ~45 minutes (50 epochs) |
| Inference time | 12 ms per image |
| Memory (training) | ~8 GB |
| Memory (inference) | ~2 GB |
| Model size | 60 MB (saved weights) |
| Python | 3.8+ |
| PyTorch | 2.0+ |
| timm | 0.9+ |

**Conflict of Interest Statement:** The authors declare no conflicts of interest.

**Data Availability:** The primary dataset is available at https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset. External validation datasets are available at Figshare and Mendeley Data.

**Code Availability:** All code and trained models are available at https://github.com/tarequejosh/HSANet-Brain-Tumor-Classification

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