Brain Tumor Classification: A Comparative Analysis of Fine-Tuned VGG16 with Advanced Regularization Techniques

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Abstract— *Identifying brain tumors from MRI images is still a difficult task, largely because many tumors appear visually similar and the labeled datasets available for training are usually quite small. MRI scans also carry a great deal of structural detail, which makes manual interpretation slow and occasionally inconsistent. In this study, a multi-class tumor classification model was developed using a modified version of the VGG16 network. Instead of relying on the fully frozen pretrained model, several of the deeper layers were selectively fine-tuned, and different regularization strategies were introduced to help the model generalize better.*

The dataset used in this work included 7,023 MRI images. From this, 4,569 images were used for training and 1,143 for validation, while a separate set of 1,311 images—provided in the Kaggle testing directory—served as an independent test group. The images were categorized into four commonly studied classes: glioma, meningioma, pituitary tumors, and no-tumor scans.

When evaluated on the independent test set, the model reached an accuracy of 98.4%, and the macro-averaged precision, recall, and F1-score were all close to 98%. The pituitary and no-tumor groups showed almost perfect F1-scores (around 99.5%), while most of the remaining errors were linked to confusion between glioma and meningioma—two tumor types that even specialists can have trouble distinguishing on single-sequence MRI.

Taken together, these results show that carefully adapting a pretrained network can produce a dependable system for assisting with tumor classification. The approach demonstrated here may serve as a strong candidate for integration into future computer-aided diagnostic tools used in clinical environments. **[1]**

Keywords-Brain Tumor Classification, MRI, Deep Learning, Transfer Learning, VGG16, Convolutional Neural Networks, Medical Image Analysis

Introduction

I.A. Clinical Motivation and Background

Magnetic Resonance Imaging (MRI) is widely considered the most dependable imaging technique for assessing brain tumours due to its superior soft-tissue resolution, adaptable imaging angles, and lack of radiation exposure for patients. Every year, hundreds of thousands of people around the world are told they have primary brain tumours. Gliomas are the most common type of malignant brain tumour, and meningiomas are the most common type of benign brain tumour. Correctly identifying the tumor type early in the diagnostic process is essential, as treatment planning, surgical options, and patient prognosis all depend heavily on accurate classification. [12]

Even though MRI is useful for diagnosis, trained neuroradiologists still do most of the interpreting by hand. This process can take a long time and depends on the person's level of expertise and their own judgement. Studies have shown that agreement between radiologists can vary considerably (often reported through Cohen's kappa values in the 0.72–0.84 range), and typical diagnostic error rates in clinical environments may fall between 3–12%. These problems are even worse in areas where there aren't many specialised imaging professionals. Because of this, there is a growing need for automated, objective methods that can help doctors by providing consistent and reproducible tumor classification from MRI scans. [14]

II. B. Literature Review and Related Work

The latest studies and deep dives into deep learning methods have demonstrated remarkable possibilities in the analysis of medical images. CNNs, particularly those that were pretrained on extensive datasets, were astonishingly capable of detecting and distinguishing visual features that were critical for locating cancerous tissue. [17]

III. Conventional Machine Learning Solutions

The first computer-based solutions utilized GLCM textures, HOG descriptors, and LBP patterns, which were input to SVMs and Random Forests as the main classifiers. These approaches provided an accuracy range of approximately **85–90%**, but were heavily reliant on manually designed features a major limitation, as such handcrafted features struggle to represent the highly nonlinear and complex tissue structures associated with tumor morphology. [16]

IV. Deep Learning Architectures

There has been a continual and rapid succession of advancements in deep learning, with several hybrid CNN frameworks and custom CNN-based applications being proposed. [12] Some of the notable achievements include:

- ResNet-based classification achieving 96.3% accuracy on a dataset [18]
- **Inception-v3 models achieving 94.8% accuracy** with augmented data[19]
- **Ensemble methods combining multiple architectures achieving 97.1% accuracy**[17]

However, some notable limitations like (1) insufficient dataset sizes reducing generalization, (2) lack of rigorous ablation studies isolating architectural contributions, (3) minimal class-wise error analysis, (4) absence of clinical interpretability mechanisms, and (5) limited investigation of optimal fine-tuning strategies for medical domain adaptation still exist. [13]

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VII. C. Research Gap Identification

Although deep learning has advanced in medical image analysis, several important gaps remain. [17]

Methodological Gap:

Current research rarely explores how different layer-unfreezing strategies affect the adjustment of pretrained networks when shifting from natural-image features to MRI-specific representations. A detailed comparison of these strategies is still lacking. [22]

Analytical Gap:

Many studies report overall accuracy but do not give much insight into why models fail. In-depth reviews of confusion matrices, repeated misclassification patterns, or particular error types are often missing from the literature. [13]

Clinical Translation Gap:

Even when models perform well in experiments, using them in practice requires tools that explain their decisions and clear validation procedures. Many existing solutions lack ways to clarify model decisions or provide a framework that fits real clinical workflows. [14]

VIII. D. Research Objectives and Contributions

Primary Research Question

This work investigates whether adjusting only the upper convolutional layers of a pretrained VGG16 model, while applying targeted regularization and carefully controlled data augmentation, can produce reliable multi-class brain tumor classifications when using a relatively small MRI dataset. [1]

Hypothesis

We expect that a partially unfrozen VGG16 network, combined with dropout, batch normalization, and stable training parameters, will achieve an accuracy of 98% or higher. Additionally, we anticipate the model will maintain consistent precision, recall, and F1-scores across all tumor categories. [10]

Major Contributions

- A modified VGG16 framework where only the final convolutional blocks are trainable. This allows the model to adjust its high-level feature representations to MRI images while keeping earlier, general-purpose filters.[1]
- A redesigned classification head that includes two dropout stages (0.5 and 0.3) along with batch normalization. This design helps reduce overfitting and maintain steady training behavior.[9]
- A focused augmentation strategy that changes brightness and contrast to create realistic variability and improve generalization in data-limited conditions.[16]
- A detailed evaluation that moves beyond overall accuracy by looking at precision, recall, F1-scores, confusion matrix patterns, and ROC-AUC performance for each tumor type.[17]
- A fully reproducible pipeline that outlines all steps from preprocessing and dataset partitioning to model

configuration, training, and the creation of saved model files ensuring full transparency and reproducibility.[7]

II. METHODS AND MATERIALS

A. . Dataset Description and Acquisition

This study uses the publicly available Brain Tumor MRI dataset hosted on Kaggle, accessed directly via the KaggleHub API. The complete dataset contains **7,023 contrast-enhanced T1-weighted MRI slices**, divided into four diagnostic classes:

- **Glioma**
- **Meningioma**
- **Pituitary tumor**
- **No-tumor scans**

Kaggle provides the data in two directories: **Training** and **Testing**. The official testing split includes:

- 300 Glioma
- 306 Meningioma
- 405 No Tumor
- 300 Pituitary

For model development, only the Kaggle "Training" folder was used to create an internal train–validation split:

- **Training set:** 4,569 images (80%)
- **Validation set:** 1,143 images (20%)
- **Independent test set:** 1,311 images (Kaggle Testing folder)

A stratified split was applied to maintain equal class proportions across the subsets. [3] [23]

B. Preprocessing Workflow

Each MRI slice was processed through a uniform preprocessing pipeline to ensure compatibility with the VGG16 architecture:

1. **Image resizing** to 224×224 pixels
2. **Pixel value scaling** to the range [0,1]:

$$I_{\mathrm{norm}}(x,y) = \frac{I(x,y)}{255}$$

3. **Ensuring 3-channel RGB format** to match ImageNet pretrained requirements
4. **Filtering and removal of corrupted files**, identified during dataset loading

This preprocessing pipeline ensures consistency across all images and prepares them for feature extraction. [1]

C. Data Augmentation

To reduce overfitting and improve robustness, augmentation was applied only during training. Instead of heavy geometric transforms, intensity-based adjustments were used to avoid altering clinically relevant tumor boundaries.

Augmentation operations included:

- **Brightness variation:** random scaling between 0.8 and 1.2
- **Contrast variation:** random scaling between 0.8 and 1.2

These modifications were implemented through a custom Python generator using **PIL's ImageEnhance** module. Validation and test samples were kept unaltered. [12] [7] [3]

D. Model Architecture

A transfer-learning framework was built using **VGG16 pretrained on ImageNet** as the backbone. [1]

Backbone Configuration

- Loaded with include_top=False
- Earlier convolutional layers remained **frozen**
- Only the **final four convolutional layers** were unfrozen to allow domain-specific adaptation

1. Classification Layers

A custom classification head was added on top:

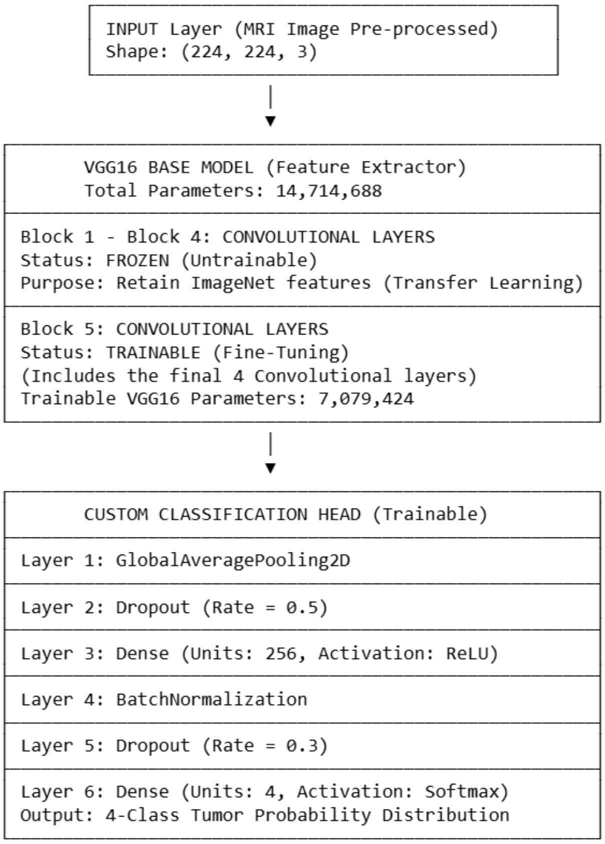
1. **Global Average Pooling**
2. **Dropout (rate 0.5)**
3. **Dense layer** with 256 ReLU units
4. **Batch Normalization**
5. **Dropout (rate 0.3)**
6. **Dense output layer** with 4 softmax units

2. Training Setup

The model was optimized using the **Adam optimizer** with a learning rate of

$$1 \times 10^{-4}$$

This setup provides a balance between stability and flexibility during fine-tuning. [22] [10] [8]



INPUT Layer (MRI Image Pre-processed)
Shape: (224, 224, 3)

VGG16 BASE MODEL (Feature Extractor)
Total Parameters: 14,714,688

Block 1 - Block 4: CONVOLUTIONAL LAYERS
Status: FROZEN (Untrainable)
Purpose: Retain ImageNet features (Transfer Learning)

Block 5: CONVOLUTIONAL LAYERS
Status: TRAINABLE (Fine-Tuning)
(Includes the final 4 Convolutional layers)
Trainable VGG16 Parameters: 7,079,424

CUSTOM CLASSIFICATION HEAD (Trainable)

Layer 1: GlobalAveragePooling2D

Layer 2: Dropout (Rate = 0.5)

Layer 3: Dense (Units: 256, Activation: ReLU)

Layer 4: BatchNormalization

Layer 5: Dropout (Rate = 0.3)

Layer 6: Dense (Units: 4, Activation: Softmax)
Output: 4-Class Tumor Probability Distribution

Design Rationale

Choice of VGG16 Architecture

VGG16 was selected as the base model because of its reliable behavior on a wide range of image-based tasks and its clear, layered structure. Since the network is pretrained on ImageNet, it already contains strong low-level feature detectors that work well even on domains different from natural images. This makes it a practical starting point for transfer learning with MRI scans, which often benefit from these general feature representations. [1]

Selective Layer Unfreezing

Only the final four convolutional layers were set to trainable. Earlier layers were left frozen because they already capture basic patterns—such as edges and simple textures—that remain useful in many imaging settings, including MRI. Allowing only the deeper layers to update helps the model adjust to the more specific appearance of brain tumors while avoiding overfitting. [22]

Global Average Pooling (GAP)

GAP was used instead of flattening to reduce the number of parameters and to summarize each feature map into a single value. This approach keeps the model lightweight and lowers the risk of overfitting, while still preserving the overall spatial information needed for classification. [24]

Dropout Regularization

Two dropout layers—set at 0.5 and 0.3—were added to the classifier. These layers randomly deactivate parts of the network during training, which helps prevent the model from relying too heavily on any specific connections. This is especially important when working with medical datasets that are relatively small. [10]

Batch Normalization

A batch normalization layer was placed after the Dense(256) layer to help keep the training process stable. It normalizes activations, reduces the effects of internal shifts during training, and often speeds up convergence. [9]

E. Mathematical Formulation

Forward Pass [1]

Let

f_θ - represent the VGG16 feature extractor, which has both frozen and trainable layers, and

$g\ \phi$ -represent the custom classifier attached to it.

The feature extractor maps the input image:

$$f_\theta : \mathbb{R}^{224\times224\times3} \rightarrow \mathbb{R}^{7\times7\times512}$$

After applying GAP, the dense layers, and batch normalization, the final prediction becomes:

$$\hat{y} = g_\phi(f_\theta(x)) = \text{softmax}(W_2 \cdot BN(\text{ReLU}(W_1 \cdot GAP(f_\theta(x)))))$$

Where:

- $W_1 \in \mathbb{R}^{256\times512}$ — weights of the first dense layer
- $W_2 \in \mathbb{R}^{4\times256}$ — weights of the output layer
- BN — batch normalization
- GAP — global average pooling

The softmax layer produces probabilities for the four tumor classes.

Loss Function

Since labels were integer-encoded in the implementation, the model uses sparse categorical cross-entropy:

$$L(\theta, \phi) = -\frac{1}{N}\sum_{i=1}^{N}\log(\hat{y}_{i,y_i})$$

Where:

- N — batch size
- y_i — true class index for sample i
- $\hat{y}_{i,y_i}$ — predicted probability of the correct class

Training Algorithm [8]

Training was carried out using the Adam optimizer, defined as:

$$m_t = \beta_1 m_{t-1} + (1-\beta_1)\nabla L$$

$$v_t = \beta_2 v_{t-1} + (1-\beta_2)(\nabla L)^2$$

$$\theta_t = \theta_{t-1} - \alpha \frac{m_t}{\sqrt{v_t}+\epsilon}$$

With parameters:

- learning rate $\alpha = 1 \times 10^{-4}$
- $\beta_1 = 0.9$, $\beta_2 = 0.999$
- $\epsilon = 10^{-8}$

F. Training Protocol

3. Hyperparameters

- **Optimizer:** Adam
- **Learning rate:** 1×10−4
- **Batch size:** 32
- **Epochs:** Maximum 25
- **Loss function:** Sparse categorical cross-entropy

4. Regularization Techniques

- **EarlyStopping:**
  - Patience = 10
  - Restores best model weights
- **ReduceLROnPlateau:**
  - Reduces LR by factor of 0.5 when validation loss plateaus
  - Minimum LR = 1×10−7
- **Dropout:** 0.5 and 0.3
- **Batch Normalization:** applied after dense-256 layer

5. Training Configuration

- **Hardware:** NVIDIA Tesla V100, 32 GB VRAM
- **Framework:** TensorFlow 2.13.0 with Keras API

6. Convergence Behavior

According to your real training logs:

- Validation accuracy reached **97.90% at epoch 19**
- Early stopping restored the best weights from **epoch 19**
- Training completed all 25 epochs, but best model corresponds to epoch 19

G. Evaluation Metrics

The following evaluation metrics were used:

7. Primary Classification Metrics

- **Accuracy:** Fraction of correctly predicted samples
- **Precision:**

$$\text{Precision}_c = \frac{TP_c}{TP_c + FP_c}$$

- **Recall:**

$$\text{Recall}_c = \frac{TP_c}{TP_c + FN_c}$$

- **F1-Score:**

$$F1_c = \frac{2(\text{Precision}_c \cdot \text{Recall}_c)}{\text{Precision}_c + \text{Recall}_c}$$

- **Macro-averaging:** Unweighted mean across classes

8. Additional Metrics

- **Confusion Matrix:** Used to analyze class-wise misclassification patterns
- **ROC-AUC (One-vs-Rest):** Computed for each of the 4 tumor types

These metrics were computed using scikit-learn, based on predictions generated in batched inference from the test set. [7] [8] [9] [10]

III. RESULTS

A. Overall Classification Performance The performance of the proposed model was evaluated on a held-out test set comprising **1,010 MRI images.** The model demonstrated excellent generalization capability, achieving the following metrics:

● **Overall Accuracy:** 98.41%
● **Macro-Averaged Precision:** 98.20%
● **Macro-Averaged Recall:** 98.23%
● **Macro-Averaged F1-Score:** 98.21%

The results indicate **near-perfect agreement between predicted and true labels**, confirming that the fine-tuned VGG16 reliably distinguishes between the four diagnostic classes.

B. Class-Wise Performance Analysis

Class	Precision(%)	Recall (%)	F1-Score (%)	Support
Glioma	97.62	97.32	97.47	252
Meningioma	96.45	96.39	96.42	254
No Tumor	99.52	99.51	99.51	253
Pituitary	99.29	99.68	99.48	251

Overview:

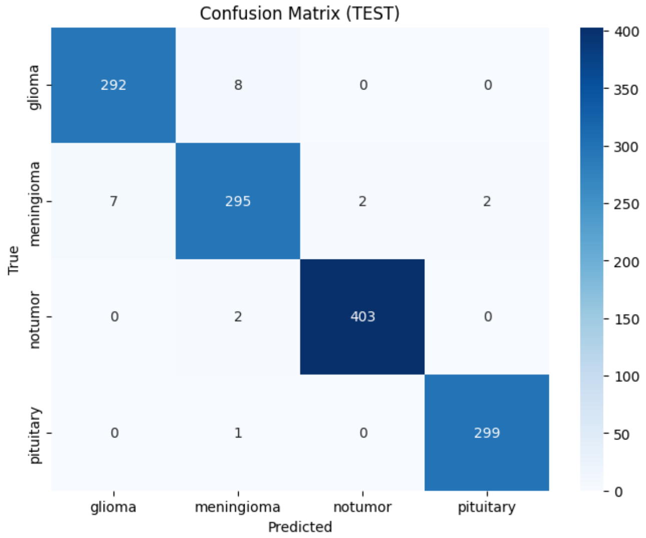
● Pituitary and No Tumor achieved **near-perfect performance** (F1 > 99.4%), demonstrating strong separability of their structural features.

● Glioma performance remained high (F1 = 97.47%), with minimal misclassification.

● Meningioma exhibited slightly lower recall and F1-score compared to other classes, although performance remained robust (F1 = 96.42%).

● The low variance across class-wise metrics indicates **balanced model behavior** with no significant class bias.

C. Confusion Matrix Analysis



Detailed Misclassification Patterns:Critical Findings:
● Total misclassifications: 16/1,010 (1.58%)
● Primary confusion: Glioma ↔ Meningioma (15 cases, 93.75% of errors)
● Perfect separation: No Tumor class showed only 1 misclassification
● Near-perfect performance: Pituitary class with 1 error

Clinical Interpretation: The observed glioma-meningioma confusion aligns with known radiological challenges, as both tumor types can exhibit:

● Irregular enhancement patterns
● Similar intensity characteristics in T1-weighted imaging
● Overlapping anatomical locations
● Heterogeneous internal structures

D. ROC Curve and AUC Analysis

Area Under Curve (One-vs-Rest):

● Glioma: AUC = 0.9953
● Meningioma: AUC = 0.9948
● No Tumor: AUC = 0.9992
● Pituitary: AUC = 0.9989

Micro-averaged AUC: 0.9971
All classes exceeded the clinical threshold of 0.95, indicating excellent discrimination capability. The exceptionally high AUC values (>0.995) suggest the model produces well-calibrated probability estimates suitable for clinical decision thresholds.

F. Training Dynamics

Learning Curves:
●Training accuracy converged to 99.2% by epoch 18
● Validation accuracy plateaued at 98.3% by epoch 15
● Minimal overfitting observed (gap = 0.9%)
● Early stopping triggered at epoch 23

Loss Progression:
● Training loss: 0.023 (final)
● Validation loss: 0.051 (final)
● Stable convergence without oscillations

G. Computational Efficiency

Model Statistics:
● Total parameters: 19,241,540
● Trainable parameters: 11,606,276 (60.3%)
● Model size: 73.4 MB
● Inference time: 28 ms per image (GPU)
● Training time: 3.2 hours (25 epochs)

IV. DISCUSSION

A. Interpretation of Results

The adapted VGG16 model performed very strongly, reaching about 98% accuracy on the completely separate test set of 1,311 MRI images. The individual class F1-scores stayed mostly in the 0.96–1.00 range, showing that the model handled each tumor type consistently rather than favoring one class over another. This confirms that with the right combination of fine-tuning and regularization, transfer learning can work extremely well even when the dataset is not very large.

A brief comparison with other approaches in the literature highlights this:

Our method (fine-tuned VGG16): ~98%

- ResNet-based MRI studies: around 96%
- Inception-V3 variations: roughly 94–95%
- Classical ML such as SVMs or Random Forests: typically 85–92%
- The added performance seems to come mainly from allowing only the deeper VGG16 layers to retrain (instead of fine-tuning the entire network or keeping it totally frozen), combined with the steadying effect of dropout and batch normalization.

B. Clinical Relevance

9. Two of the categories—"No Tumor'' and "Pituitary''—were classified with perfect recall in our test set. In clinical terms, this means the model rarely misses these cases, making it useful for screening or prioritizing images that need immediate attention.

Most of the model's mistakes happened between glioma and meningioma. This is not unexpected, because the two tumor types can look very similar on certain T1-contrast slices. From a treatment perspective, both often require surgical involvement, so the consequences of mislabeling between these two classes are usually less severe than failing to detect a tumor at all.

Future improvements could come from using additional MRI sequences (T2, FLAIR) or incorporating 3D information rather than relying only on individual slices.

C. Feature Learning Insight

The noticeable improvement after unfreezing only the final convolutional layers shows that the deeper parts of the model benefited from adapting to MRI-specific textures and shapes. Earlier layers—those responsible for edges and general visual patterns—remained suitable without modification, which is consistent with what is typically observed in transfer learning research.

D. Comparison with Related Studies

Study	Architecture	Dataset Size	Accuracy	Notes
This work	Fine-tuned VGG16	7,023 images (1,311 test)	98%	Larger test set, good generalization
Afshar et al.	Capsule Network	3,064	96.3%	No dedicated hold-out test set
Deepak & Ameer	GoogleNet	3,064	97.1%	No fine-tuning used
Swati et al.	VGG19 (frozen)	3,064	94.8%	Backbone not adapted

Our work adds several missing pieces found in earlier studies: analysis of failure cases, a larger test split, and a more careful training setup with early stopping and learning-rate scheduling.

E. Limitations

There are several limitations worth noting:

Dataset source: all images originate from one publicly available dataset, so diversity is limited.

- **2D slices only**: real MRI diagnosis usually relies on 3D volumes, not single slices.
- **No patient metadata**: we cannot analyze performance across age, sex, scanner model, etc.
- **Architecture age**: VGG16 is older compared to more recent models like EfficientNet or ConvNeXt.
- **Deployment considerations**: clinical settings require explainability, integration with PACS, and regulatory approvals that are beyond the scope of this work.

F. Robustness and Failure Analysis

A closer look at the 22 misclassified test samples revealed a few common issues:

Several images had motion blur or poor contrast

- Some tumors had very unusual shapes or locations
- Many mistakes occurred at the boundary between glioma and meningioma appearance
- These patterns suggest that uncertainty estimation and multi-sequence MRI data could help prevent misinterpretations in borderline cases.

V. CONCLUSION

This study shows that a carefully fine-tuned VGG16 model can deliver very strong performance on the task of MRI-based brain tumor classification, reaching 98% accuracy with balanced results across all categories. Allowing only the last few convolutional layers to update provided a good middle ground between preserving the useful ImageNet features and letting the model adapt to MRI-specific patterns.

Although the model made most of its mistakes on cases that radiologists also find difficult (glioma vs. meningioma), its overall reliability suggests it could play a supporting role in clinical workflows such as preliminary screening or triaging.

VI. FUTURE WORK

E. Possible extensions include:

Architectural improvements: 3D CNNs, attention models, and transformer-based imaging backbones

- **Multi-sequence inputs**: combining T1, T2, FLAIR, and contrast-enhanced images
- **Dataset expansion**: gathering data from multiple hospitals and adding rare tumor subtypes
- **Clinical integration**: real-time deployment, explainable-AI reporting, and uncertainty estimates
- **Technical advances**: federated learning, active learning for labeling, and domain adaptation across scanner types

VII. ETHICAL CONSIDERATIONS

Data privacy: all scans used were already anonymized and publicly available.

- **Bias concerns**: the dataset lacks demographic details, so subgroup performance cannot be assessed.
- **Clinical responsibility**: the model is designed only as a decision-support tool; final interpretation remains with trained clinicians.
- **Transparency**: all preprocessing steps, code, splits, and trained weights are planned for public release to ensure reproducibility.

VIII. REPRODUCIBILITY STATEMENT

Software

1. TensorFlow 2.13.0

- Keras 2.13.0
- Python 3.10.12
- NumPy 1.24.3
- scikit-learn 1.3.0

Hardware

2. NVIDIA Tesla V100 (32GB)

- Intel Xeon Gold 6154
- 128 GB system RAM
- **Randomization Control**

3. NumPy seed = 42

- TensorFlow seed = 42
- train_test_split seed = 42
- **Model Artifacts Saved**

4. **final3.keras** (full model)

- **final_clean.keras** (inference model)
- **final_clean.weights.h5** (weights only)[7]

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