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Efficient multi-class brain tumor classification from MRI images using InceptionResNetV2 bottleneck features and a lightweight dense classifier

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ABSTRACT
The precise classification of brain tumors from magnetic resonance imaging (MRI) is essential for early diagnosis and effective treatment planning. This research introduces an efficient transfer learning framework that employs the InceptionResNetV2 architecture, pre-trained on ImageNet, as a frozen deep feature extractor, and couples it with a lightweight, strongly regularized fully connected classifier for four-class brain tumor classification (glioma, meningioma, pituitary tumor, and no tumor). The approach tackles the key challenges of limited annotated medical data and high computational cost by pre-computing 1,536-dimensional bottleneck features, so that only 158,954 parameters are trained. A benchmark dataset of 7,023 MRI images was employed for evaluation, partitioned into 70% training, 15% validation, and 15% test subsets. Evaluation measures including accuracy, precision, recall, F1-score, and the normalized confusion matrix were used to verify the model. Experimental findings indicate that the proposed model attains a test accuracy of 94.58%, a weighted precision of 0.9461, a weighted recall of 0.9458, and a weighted F1-score of 0.9459, with a validation accuracy of 95.18%, while requiring only about 12 minutes of training on a CPU-only workstation. The results demonstrate the robustness and practical significance of the proposed framework, establishing it as a computationally efficient alternative to fully fine-tuned deep models for automated brain tumor classification.

Keywords: Brain tumor classification; Magnetic resonance imaging (MRI); Transfer learning; InceptionResNetV2; Deep learning; Bottleneck features

1. Introduction

Brain tumors are among the most life-threatening neurological disorders, characterized by the abnormal and uncontrolled growth of cells within the brain or the central nervous system. According to global cancer statistics, tumors of the brain and central nervous system account for a substantial share of cancer-related morbidity and mortality worldwide [1], and their incidence continues to rise [2]. Brain tumors are broadly categorized according to the World Health Organization (WHO) classification of central nervous system tumors [3], with gliomas, meningiomas, and pituitary tumors being among the most frequently diagnosed types. These tumor types differ considerably in their origin, growth behavior, malignancy, and treatment strategy; consequently, the accurate identification of the tumor type is a critical prerequisite for effective treatment planning and improved patient survival.

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Magnetic resonance imaging (MRI) is the preferred non-invasive modality for brain tumor diagnosis owing to its superior soft-tissue contrast, high spatial resolution, and absence of ionizing radiation. In routine clinical practice, MRI scans are interpreted manually by radiologists — a process that is time-consuming, expensive, and inherently subjective. The diagnostic outcome depends heavily on the experience of the examining expert, and inter-observer variability can lead to inconsistent conclusions, particularly for tumor types with overlapping visual characteristics such as meningiomas and gliomas. The growing volume of medical imaging data further increases the workload of radiologists, motivating the development of accurate and efficient computer-aided diagnosis (CAD) systems for automated brain tumor classification.

In recent years, deep learning — and in particular convolutional neural networks (CNNs) — has achieved remarkable success in medical image analysis, consistently outperforming traditional machine learning approaches that rely on handcrafted features [4]. Beginning with AlexNet [5], increasingly deep architectures such as VGG [6], ResNet [7], and Inception-ResNet [8] have pushed the state of the art in image recognition. However, training such deep networks from scratch requires very large annotated datasets, which are rarely available in the medical domain due to the cost of expert annotation and patient privacy constraints. Transfer learning (TL) [9] addresses this limitation by reusing representations learned on large-scale natural image datasets such as ImageNet [10] and adapting them to the target medical imaging task, thereby achieving strong performance with limited training data and modest computational resources.

Building upon the strengths of TL, we propose an efficient framework that combines the powerful feature extraction capabilities of a frozen, ImageNet pre-trained InceptionResNetV2 backbone [8] with a lightweight, regularized fully connected classification network, trained on pre-computed bottleneck features to discriminate among four classes: glioma, meningioma, pituitary tumor, and no tumor (healthy). The following are the Research Questions related to our study:

1. RQ1: How can transfer learning techniques be employed to enhance the identification and classification of brain tumors in MRI images?
2. RQ2: Can a completely frozen InceptionResNetV2 backbone, used as a bottleneck feature extractor, achieve accuracy competitive with fine-tuned deep models at a fraction of the computational cost?
3. RQ3: What role do regularization techniques — dropout, weight decay, and LeakyReLU activations — play in preventing overfitting of a compact classification head trained on a limited medical dataset?
4. RQ4: What are the comparative performance metrics (e.g., accuracy, precision, recall, F1-score) of the proposed model against existing brain tumor classification methods?

The motivation for the proposed work is driven by the critical need for accurate, early identification of brain tumors to enhance patient outcomes. The challenges of limited annotated datasets, the high computational cost of fine-tuning large backbones, and the absence of a healthy (no-tumor) class in many existing studies underscore the need for efficient and clinically realistic solutions. The main contributions of this work are summarized as follows:

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- A transfer learning pipeline based on frozen InceptionResNetV2 bottleneck features is developed for four-class brain tumor MRI classification, eliminating the need for costly end-to-end training of deep convolutional layers.
- A compact classification head with only 158,954 trainable parameters is designed, combining LeakyReLU activations, dropout regularization, and weight decay to control overfitting.
- The proposed model achieves a test accuracy of 94.58% and a weighted F1-score of 0.9459 on a dataset of 7,023 MRI images, while requiring only about 12 minutes of training on a CPU-only workstation.
- A comprehensive evaluation is provided, including per-class precision, recall, and F1-score, a normalized confusion matrix, an analysis of the training and convergence behavior, and a comparison with existing work.

The remainder of this paper is organized as follows. Section 2 reviews related work on brain tumor classification. Section 3 describes the materials and methods, including the dataset, preprocessing, and the pre-trained backbone. Section 4 presents the proposed methodology. Section 5 reports the experimentation, results, and analysis. Finally, Section 6 concludes the paper and outlines directions for future work.

2. Literature review

2.1. Classical machine learning approaches

Automated brain tumor classification has been an active research area for more than a decade. Early approaches relied on classical machine learning pipelines in which handcrafted features — such as intensity histograms, texture descriptors, wavelet coefficients, and shape measures — were extracted from MRI images and fed into conventional classifiers. Zacharaki et al. [11] combined texture and shape features with support vector machines (SVMs) to classify brain tumor type and grade. El-Dahshan et al. [12] proposed a hybrid scheme based on the discrete wavelet transform, principal component analysis, and neural network / k-nearest neighbor classifiers. Cheng et al. [13] improved the classification of gliomas, meningiomas, and pituitary tumors by augmenting the tumor region and partitioning it into subregions before feature extraction, reporting an accuracy of 91.28% on the widely used Figshare dataset. Bahadure et al. [14] employed Berkeley wavelet transform features with an SVM for tumor detection, while Ismael and Abdel-Qader [15] combined two-dimensional discrete wavelet and Gabor statistical features with a back-propagation neural network. More recent handcrafted pipelines include the hybrid PCA–NGIST descriptor with a regularized extreme learning machine by Gumaei et al. [16], which reached 94.23% accuracy, and the modified local binary pattern variants of Kaplan et al. [17]. While these methods demonstrated the feasibility of computer-aided tumor classification, their performance is fundamentally limited by the discriminative power of manually engineered features and their sensitivity to segmentation quality.

2.2. Deep learning with custom CNN architectures

The advent of deep learning shifted the field toward automatically learned representations. Pereira et al. [18] demonstrated the effectiveness of CNNs with small convolutional kernels for brain tumor analysis in MRI, establishing deep networks as a powerful tool for neuro-imaging tasks. Paul et al. [19] were among the first to apply CNNs directly to axial MRI slices for three-class tumor classification, and Abiwinanda et

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al. [20] trained a relatively shallow CNN from scratch on the Figshare dataset, achieving a validation accuracy of 84.19% and illustrating both the promise and the limitation of training small networks on limited medical data. Mohsen et al. [21] combined discrete wavelet transform features with a deep neural network classifier, while Anaraki et al. [22] optimized CNN hyperparameters with genetic algorithms to improve classification of tumor types and glioma grades. Seetha and Raja [23] reported 97.5% accuracy with a compact CNN, and Badža and Barjaktarović [24] designed a simple 22-layer CNN that attained 96.56% accuracy under record-wise ten-fold cross-validation. Irmak [25] proposed fully optimized CNN frameworks for multiple brain tumor classification tasks, and Díaz-Pernas et al. [26] introduced a multiscale CNN inspired by the human visual system that achieved 97.3% accuracy for joint classification and segmentation. Ayadi et al. [27] further confirmed the competitiveness of carefully regularized custom CNNs across several MRI datasets.

2.3. Capsule networks and advanced architectures

To address the limited ability of CNNs to model spatial hierarchies between features, Afshar et al. [28] explored capsule networks (CapsNets) for brain tumor type classification, reporting an accuracy of approximately 86.56%, and subsequently improved performance to 90.89% by providing coarse tumor boundaries as an additional input [29]. Sultan et al. [30] proposed a deeper CNN architecture and reported an overall accuracy of 96.13% for the three-class Figshare problem, demonstrating that carefully designed deep models can achieve high performance without transfer learning.

2.4. Transfer learning approaches

Because annotated medical datasets are typically small, transfer learning has become the dominant paradigm in recent brain tumor classification research. Khawaldeh et al. [31] adapted a modified AlexNet for non-invasive glioma grading from MR images. Talo et al. [32] applied a pre-trained ResNet34 with fine-tuning for automated brain abnormality detection, and Lu et al. [33] combined AlexNet with transfer learning for pathological brain detection. Kaur and Gandhi [34] systematically compared several pre-trained networks for automated brain image classification and confirmed the superiority of transfer learning over training from scratch. For the multi-class tumor problem, Swati et al. [35] fine-tuned a pre-trained VGG19 network in a block-wise manner and achieved an average accuracy of 94.82% on the Figshare dataset. Deepak and Ameer [36] employed a pre-trained GoogLeNet as a feature extractor combined with classical classifiers and reported an accuracy of approximately 97.1% using five-fold cross-validation. Rehman et al. [37] compared AlexNet, GoogLeNet, and VGG16 under both freeze and fine-tune regimes, attaining up to 98.69% accuracy with a fine-tuned VGG16. Çinar and Yildirim [38] augmented a ResNet50 backbone with additional layers, and Noreen et al. [39] concatenated multi-level features from Inception-v3 and DenseNet201, reporting accuracies above 99% on the three-class problem. Kang et al. [40] ensembled deep features from multiple pre-trained networks with machine learning classifiers across three MRI datasets, and Alanazi et al. [41] developed an isolated CNN subsequently adapted by transfer learning for tumor/mass classification. Notably, Ullah et al. [42] benchmarked nine pre-trained architectures for brain tumor MRI classification and found InceptionResNetV2 to be the best-performing backbone, supporting the architectural choice made in the present work. Hybrid deep–classical schemes have also been reported

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by Senan et al. [43], who combined ResNet18 and AlexNet features with an SVM, and by Aamir et al. [44], who fused features from two parallel streams.

2.5. Feature fusion, optimization, and generative approaches

A further line of research enhances deep pipelines with augmentation, feature selection, and generative modeling. Sajjad et al. [45] combined a fine-tuned VGG19 with extensive data augmentation for multi-grade tumor classification. Khan et al. [46] fused multimodal deep features with a robust feature selection strategy, and Sharif et al. [47] proposed active deep feature selection for joint segmentation and recognition of brain tumors. Saba et al. [48] fused handcrafted shape and texture descriptors with VGG19 features. Özyurt et al. [49] integrated neutrosophic set theory with CNN features and SVM classification, while Toğaçar et al. [50] proposed BrainMRNet, which incorporates attention modules and hypercolumn features. Ghassemi et al. [51] pre-trained a network as a generative adversarial network (GAN) discriminator before fine-tuning it for tumor classification, achieving about 95.6% on the Figshare dataset. Raja [52] combined Bayesian fuzzy clustering-based segmentation with a hybrid deep autoencoder, and Mzoughi et al. [53] developed a multiscale 3D CNN for volumetric glioma grading.

2.6. Brain tumor segmentation and related tasks

Closely related to classification, brain tumor segmentation has been extensively studied, driven largely by the multimodal BraTS benchmark of Menze et al. [54] and the expert-annotated glioma collections of Bakas et al. [55]. Havaei et al. [56] proposed cascaded two-pathway CNNs for tumor segmentation, and Kamnitsas et al. [57] introduced DeepMedic, an efficient multi-scale 3D CNN with a fully connected conditional random field. Encoder–decoder architectures such as U-Net [58] have become the de facto standard for biomedical segmentation, and comprehensive reviews of deep learning-based brain tumor segmentation are provided by Işın et al. [59]. Although segmentation is not the focus of the present work, these studies underline the maturity of deep learning for neuro-oncological image analysis.

2.7. Deep learning in broader medical imaging and surveys

Beyond neuro-imaging, landmark studies have demonstrated expert-level performance of deep networks in dermatology [60], diabetic retinopathy screening [61], and chest radiograph interpretation [62], reinforcing the clinical potential of CNN-based CAD systems. Comprehensive overviews of deep learning in medical image analysis are given by Shen et al. [63] and Anwar et al. [64], while brain-tumor-specific surveys by Tandel et al. [65], Nazir et al. [66], Muhammad et al. [67], and Amin et al. [68] chart the rapid evolution of the field between 2015 and 2022 and consistently identify transfer learning as the most reliable strategy for small datasets. More recently, vision transformers [69] have emerged as an alternative to CNN backbones, although their data requirements remain a challenge for medical applications. A summary of key methods based on different attributes is outlined in Table 1.

Table 1. Summary of representative related works on brain tumor MRI classification.

Study	Year	Method	Classes	Reported Accuracy
Cheng et al. [13]	2015	Tumor region augmentation +	3	91.28%

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		handcrafted features		
Gumaei et al. [16]	2019	PCA–NGIST features + regularized ELM	3	94.23%
Abiwinanda et al. [20]	2019	Custom CNN trained from scratch	3	84.19%
Badža & Barjaktarović [24]	2020	Custom 22-layer CNN	3	96.56%
Díaz-Pernas et al. [26]	2021	Multiscale CNN	3	97.3%
Afshar et al. [28]	2018	Capsule network (CapsNet)	3	86.56%
Sultan et al. [30]	2019	Deep CNN	3	96.13%
Swati et al. [35]	2019	VGG19 with block-wise fine-tuning	3	94.82%
Deepak and Ameer [36]	2019	GoogLeNet features + classical classifiers	3	97.1%
Rehman et al. [37]	2020	Fine-tuned VGG16	3	98.69%
Noreen et al. [39]	2020	Inception-v3 / DenseNet201 feature concatenation	3	99.3%
Kang et al. [40]	2021	Ensemble of deep features + ML classifiers	4	—
Ullah et al. [42]	2022	Transfer learning (InceptionResNetV2 best of nine)	4	98.91%
Proposed method	—	Frozen InceptionResNetV2 features + dense classifier	4	94.58%

Deep learning techniques for brain tumor categorization are widely available in the literature; however, several technological obstacles remain. First, most existing studies address the three-class problem (glioma, meningioma, pituitary tumor) and do not include a healthy (no-tumor) class, whereas a clinically deployable system must also distinguish tumorous from non-tumorous scans; the present study therefore targets the more general four-class problem. Second, many high-performing approaches rely on full fine-tuning of large backbones [35], [37], [39], which is computationally expensive and prone to

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overfitting on small datasets. Third, although InceptionResNetV2 has been identified as one of the strongest backbones for this task [42], comparatively few works have examined it as a completely frozen feature extractor coupled with a compact, strongly regularized classification head. Filling these deficiencies may lead to more efficient, objective, and practically applicable early brain tumor diagnostic methods, which is the aim of the present work.

3. Materials and methods

3.1. Dataset

The effectiveness of the proposed model depends on a legitimate and suitable dataset being available. The research in question makes use of the following dataset.

3.1.1. Brain tumor MRI dataset

The experiments were conducted on a publicly available brain tumor MRI dataset [70] comprising 7,023 images belonging to four classes: Glioma, Meningioma, Pituitary Tumor, and No Tumor (healthy). The collection contains T1-weighted contrast-enhanced MRI slices gathered from multiple public sources and is widely employed for the development and assessment of machine-learning algorithms for the automated categorization of brain tumors. The dataset is crucial because it offers an invaluable resource for developing and testing computer vision algorithms that classify brain tumors and help doctors identify and diagnose brain diseases early on. Unlike the frequently used three-class Figshare collection, this dataset additionally contains a healthy (no-tumor) category, enabling the more clinically realistic four-class classification problem addressed in this work.

3.1.2. Data partitioning

The dataset was randomly partitioned at the class level into training, validation, and test subsets using a 70:15:15 split ratio. For each class, the image files were shuffled prior to splitting to ensure an unbiased distribution across the three subsets. The resulting partition contained 4,914 training images, 1,057 validation images, and 1,052 test images. Table 2 summarizes the dataset partitioning. The class-wise composition of the test set was as follows: Glioma (243 images), Meningioma (246 images), No Tumor (300 images), and Pituitary Tumor (263 images).

Table 2. Dataset partitioning across training, validation, and test subsets.

Subset	Number of Images	Percentage
Training	4,914	70%
Validation	1,057	15%
Test	1,052	15%
Total	7,023	100%

3.1.3. Preprocessing and normalization

All MRI images were resized to a uniform spatial resolution of 224 × 224 pixels with three color channels (RGB) to match the input requirements of the InceptionResNetV2 architecture. Pixel intensities were normalized to the range [0, 1] by rescaling each pixel value by a factor of 1/255. This normalization stabilizes gradient-based optimization and accelerates convergence during training. Images were loaded and processed in mini-batches of 32 using the Keras ImageDataGenerator utility, with categorical (one-hot) encoding applied to the class labels.

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3.2. Pre-trained InceptionResNetV2 backbone

InceptionResNetV2 [8] is a member of the Inception architectural family that integrates the multi-scale feature extraction capability of Inception modules with the residual connections introduced by ResNet [7]. When the number of layers rises in very deep networks, a vanishing/exploding gradient issue arises; residual "skip connections" address this difficulty by letting the network learn residual mappings rather than simply learning the intended output, allowing certain connections to be bypassed and the output to be linked directly. The network comprises a stem block followed by repeated Inception-ResNet-A, Inception-ResNet-B, and Inception-ResNet-C modules interleaved with reduction blocks, totaling more than 50 million parameters when trained on ImageNet [10].

In this work, InceptionResNetV2 pre-trained on the ImageNet dataset was employed as a fixed feature extractor (bottleneck feature approach). The fully connected classification layers of the original network were removed (include_top = False), and a global average pooling layer was applied to the final convolutional feature maps, yielding a compact 1,536-dimensional feature vector for each input image. The convolutional weights of the backbone were kept frozen; no fine-tuning of the pre-trained layers was performed. Bottleneck features were computed once for the training, validation, and test subsets in a single forward pass over each subset and stored as NumPy arrays. This strategy substantially reduces the computational cost of training, since the expensive convolutional stages are executed only once, and only the lightweight classification head is optimized.

4. Proposed methodology

The proposed framework combines the spatial feature extraction capabilities of the frozen InceptionResNetV2 backbone with a compact, regularized dense classification network, ensuring both high accuracy and computational efficiency for early and accurate brain tumor diagnosis. The flow diagram shown in Fig. 1 depicts the proposed work and illustrates the sequential process, which is also explained in Algorithm 1.

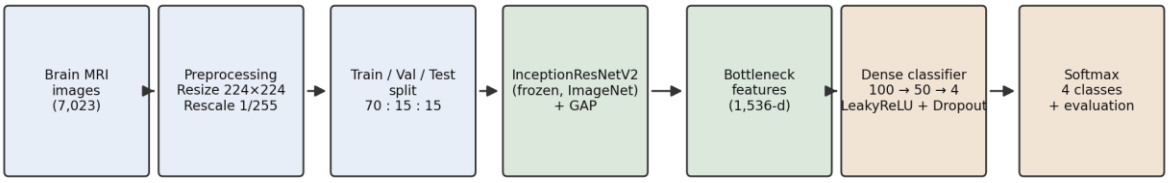


Fig. 1. Proposed architectural flow.

4.1. Proposed model

The proposed model efficiently extracts and classifies features from 224 × 224 × 3 input images. The frozen InceptionResNetV2 backbone reduces each input image to a 1,536-dimensional bottleneck feature vector via global average pooling. The classification head consists of a flatten layer followed by two hidden dense layers with 100 and 50 neurons, respectively, each activated by the Leaky Rectified Linear Unit (LeakyReLU) function [73] with a negative slope coefficient of $\alpha = 0.3$. LeakyReLU was selected over the standard ReLU to avoid the “dying neuron” problem by allowing a small, non-zero

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gradient for negative inputs. To reduce overfitting, dropout regularization [72] was applied after the first and second hidden layers with dropout rates of 0.5 and 0.3, respectively. The model classifies brain MRI images using class probabilities from a four-neuron softmax output layer. Spatial feature extraction and classification are balanced in this design for good diagnostic performance. Table 3 shows the architectural details of the proposed model, and a detailed description is given in Algorithm 2.

Table 3. Architectural details of the proposed classification head.

Layer	Output Shape	Activation	Parameters
Flatten (input: bottleneck features)	1536	—	0
Dense (100 units)	100	LeakyReLU (α = 0.3)	153,700
Dropout (rate = 0.5)	100	—	0
Dense (50 units)	50	LeakyReLU (α = 0.3)	5,050
Dropout (rate = 0.3)	50	—	0
Dense (4 units, output)	4	Softmax	204

The classification head contains a total of 158,954 trainable parameters, which is negligible compared with the tens of millions of parameters in the full InceptionResNetV2 network, making the proposed approach computationally efficient.

Algorithm 1. Brain tumor detection and classification.

Input:
- Brain Tumor MRI dataset (7,023 images, 4 classes)

Output:
- Classification results indicating Glioma, Meningioma, Pituitary Tumor, or No Tumor

Step 1. Prepare the Data:
- Load the brain tumor MRI dataset.
- Shuffle images class-wise and split into train/validation/test (70:15:15).
- Resize all images to 224 × 224 × 3 and rescale pixel values by 1/255.
- One-hot encode the class labels.

Step 2. Extract Bottleneck Features:
- Load InceptionResNetV2 (ImageNet weights, include_top = False, global average pooling).
- Freeze all convolutional weights.
- Forward-pass each subset once; store 1,536-d feature vectors as NumPy arrays.

Step 3. Train the Classification Head:
- Train the dense classifier (Algorithm 2) on the training features.
- Monitor validation accuracy and loss after every epoch.

Step 4. Evaluate:
- Compute accuracy, precision, recall, F1-score and the confusion matrix on the test set.

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Algorithm 2. Brain tumor classification using the proposed dense classification head.

Input:
- Bottleneck feature vectors (1,536-d) extracted by InceptionResNetV2

Output:
- Classification results (Glioma / Meningioma / No Tumor / Pituitary Tumor)

Procedure:

Step 1: Define the Architecture
- Flatten layer (input: 1,536-d features)
- Dense layer: 100 units, LeakyReLU ($\alpha = 0.3$); Dropout (0.5)
- Dense layer: 50 units, LeakyReLU ($\alpha = 0.3$); Dropout (0.3)
- Output layer: 4 units (softmax function)

Step 2: Compile
- Loss: categorical cross-entropy
- Optimizer: Adam (learning rate 1e-4, weight decay 0.001)

Step 3: Train
- 500 epochs, batch size 32, validation monitoring per epoch

Step 4: Output
- Obtain class probabilities and predicted tumor category for each image

5. Experimentation, results and analysis

5.1. Experiment setup

The proposed model was created utilizing Python, TensorFlow/Keras, NumPy, and scikit-learn for deep learning and evaluation, with Matplotlib employed for visualization. All experiments were executed on a standard CPU-only Windows workstation, demonstrating that the approach does not require GPU acceleration. The dataset was partitioned into training, validation, and testing subsets as described in Section 3.1.2. The model was trained with the Adam optimizer [71] using the categorical cross-entropy loss over 500 epochs with a batch size of 32; owing to the pre-computed bottleneck features, the complete training required approximately 12 minutes and 18 seconds. Table 4 represents the hyperparameters used to train the proposed model.

Table 4. Hyperparameters used to train the proposed model.

Hyperparameter	**Value**
Input image size	224 × 224 × 3
Feature vector dimension	1,536
Loss function	Categorical cross-entropy
Optimizer	Adam
Learning rate	1×10^{-4}
Weight decay	0.001
Batch size	32
Epochs	500
Dropout rates	0.5 / 0.3
Hidden layer activation	LeakyReLU ($\alpha = 0.3$)

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Output activation	Softmax

5.2. Performance metrics

The suggested model was evaluated based on accuracy, precision, recall (sensitivity), and F1-score. The TP, TN, FP, and FN calculations were used to compute these evaluation metrics. The study characterizes true positive (TP) as tumor images of a given class accurately identified by the model, true negative (TN) as images of other classes correctly rejected, false positive (FP) as images erroneously assigned to the class (Type I error), and false negative (FN) as images of the class inaccurately assigned elsewhere (Type II error). Precision, recall, and F1-score were computed per class and aggregated using weighted averaging to account for class imbalance:

$$Accuracy = (TP + TN) / (TP + TN + FP + FN) \quad (1)$$

$$Precision = TP / (TP + FP) \quad (2)$$

$$Recall = TP / (TP + FN) \quad (3)$$

$$F1\text{-}score = 2 \times (Precision \times Recall) / (Precision + Recall) \quad (4)$$

5.2.1. Overall classification performance

The proposed model achieved an overall accuracy of 94.58% on the test set, with a corresponding test loss of 0.4261. On the validation set, the model attained an accuracy of 95.18% with a loss of 0.3674. The close agreement between the validation and test accuracies indicates that the model generalizes consistently to unseen data. The weighted-average precision, recall, and F1-score on the test set were 0.9461, 0.9458, and 0.9459, respectively. The near-identical values of these three metrics demonstrate that the model maintains a balanced trade-off between false positives and false negatives across the four classes. Table 5 summarizes the overall performance of the proposed model.

Table 5. Overall performance of the proposed model on the test set.

Metric	**Value**
Test accuracy	94.58%
Test loss	0.4261
Validation accuracy	95.18%
Validation loss	0.3674
Precision (weighted)	0.9461
Recall (weighted)	0.9458
F1-score (weighted)	0.9459
Training time	≈ 12 min 18 s (CPU)

5.2.2. Class-wise performance and confusion matrix

Table 6 reports the per-class precision, recall, and F1-score obtained on the test set. The model performed best on the No Tumor class, achieving a precision of 0.98 and a recall of 0.99 (F1-score = 0.99), which is clinically desirable since it implies that healthy scans are very rarely confused with tumorous ones. The model's high TP and low FN values for this class demonstrate accurate detection and minimize misclassification of healthy cases. The Pituitary Tumor and Glioma classes were also classified reliably, with F1-scores of 0.95 and 0.94, respectively. The Meningioma class proved to be the most challenging, with a precision of 0.89 and a recall of 0.91 (F1-score = 0.90). This is consistent with

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findings in the literature [13], [35], as meningiomas share visual characteristics such as location and intensity patterns with gliomas and pituitary tumors, making them harder to discriminate.

Table 6. Class-wise precision, recall, and F1-score on the test set.

Class	Precision	Recall	F1-score	Support
Glioma	0.95	0.93	0.94	243
Meningioma	0.89	0.91	0.90	246
No Tumor	0.98	0.99	0.99	300
Pituitary Tumor	0.95	0.95	0.95	263
Macro average	0.94	0.94	0.94	1,052
Weighted average	0.95	0.95	0.95	1,052

The normalized confusion matrix (Fig. 2) confirms these observations: the strongest diagonal response corresponds to the No Tumor class, while the majority of the residual confusion occurs between the Meningioma class and the other two tumor categories.

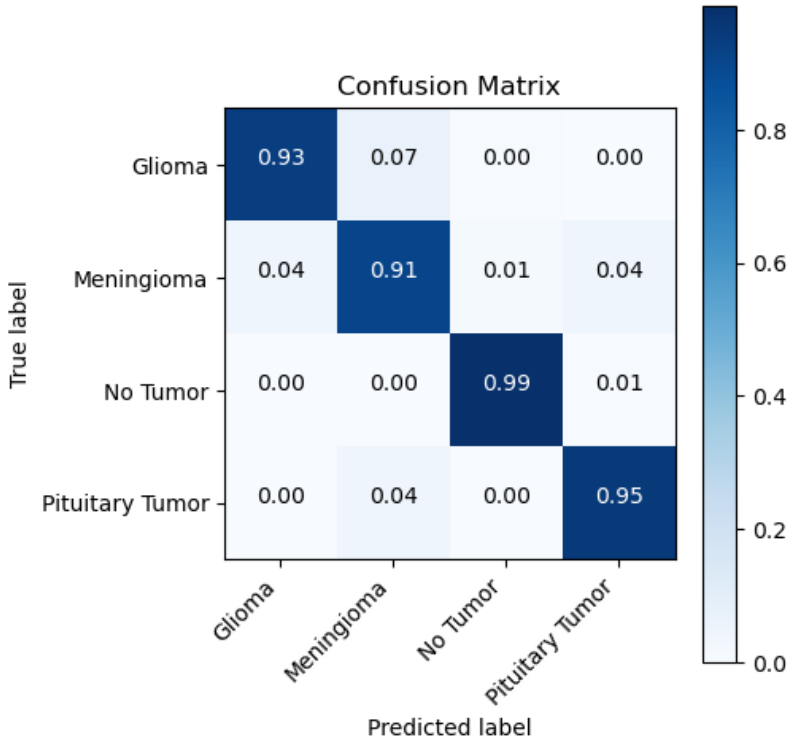


Fig. 2. Normalized confusion matrix of the proposed model on the test set.

5.2.3. Training and convergence behavior

The classification head was trained for 500 epochs on the pre-computed bottleneck features. By the final epochs, the training accuracy converged to approximately 99.1–99.4% with a training loss of about 0.015–0.021, while the validation accuracy stabilized in the range of 93.9–95.3%. The training and validation accuracy and loss curves (Figs. 3 and 4) show smooth convergence without abrupt oscillations. The moderate gap of

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roughly 4–5 percentage points between training and validation accuracy indicates a limited degree of overfitting, which was contained by the dropout regularization (rates of 0.5 and 0.3) and the weight decay applied through the Adam optimizer.

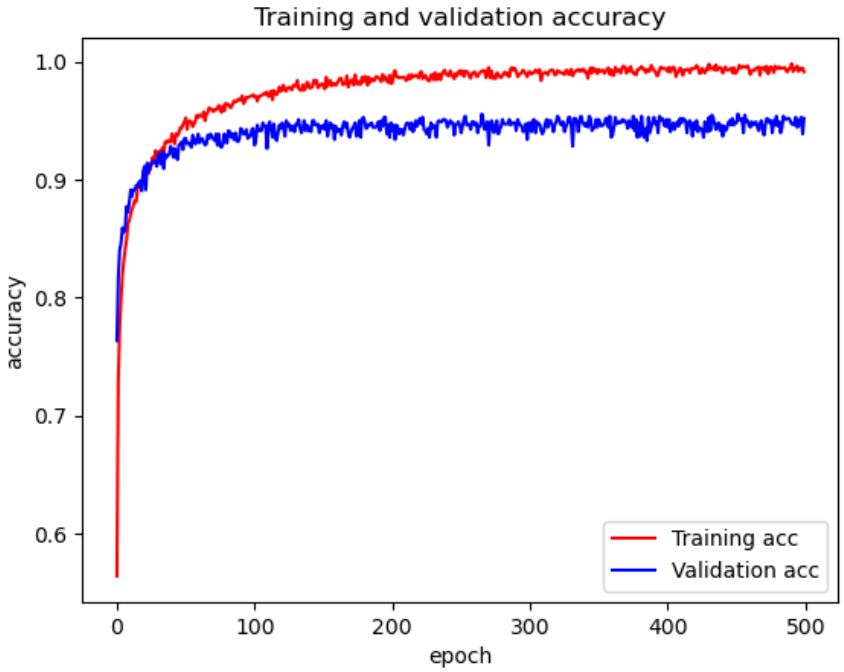


Fig. 3. Training and validation accuracy curves over 500 epochs.

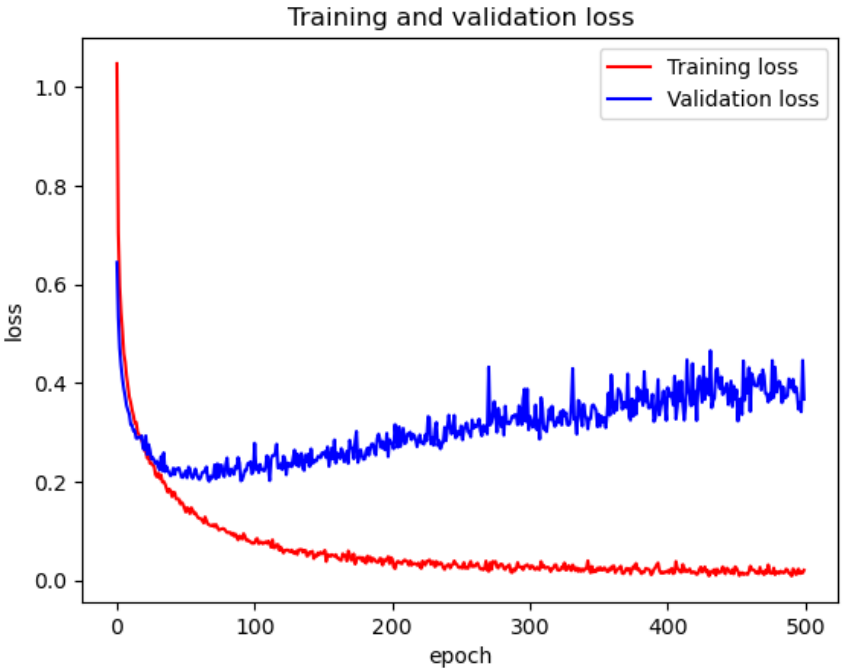


Fig. 4. Training and validation loss curves over 500 epochs.

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5.3. Comparison with existing work

To demonstrate the practicality of the selected method more clearly, its effectiveness was compared with other methods already in use. Table 7 lists various research studies that have examined brain tumor classification models. It should be noted that most prior studies address the simpler three-class problem without a healthy (no-tumor) category, whereas the proposed model tackles the more general four-class setting. Although some fine-tuned models report higher accuracies on the three-class problem [36], [37], [39], the proposed method achieves competitive accuracy while training only 158,954 parameters — orders of magnitude fewer than full fine-tuning approaches — and completing training in roughly 12 minutes on a CPU-only workstation, enabling the technique to run on computationally lightweight devices.

Table 7. Comparison of the proposed model with existing work.

References	Dataset	Model	Classes	Accuracy (%)
Cheng et al. [13]	Figshare	Handcrafted features + SVM	3	91.28
Abiwinanda et al. [20]	Figshare	Custom CNN	3	84.19
Afshar et al. [28]	Figshare	CapsNet	3	86.56
Sultan et al. [30]	Figshare	Deep CNN	3	96.13
Swati et al. [35]	Figshare	Fine-tuned VGG19	3	94.82
Deepak and Ameer [36]	Figshare	GoogLeNet + classical classifiers	3	97.1
Rehman et al. [37]	Figshare	Fine-tuned VGG16	3	98.69
Kang et al. [40]	Multiple (incl. 4-class)	Deep feature ensemble + ML	4	—
Ullah et al. [42]	Kaggle MRI	Fine-tuned InceptionResNetV2	4	98.91
Proposed	Kaggle MRI [70]	Frozen InceptionResNetV2 + dense head	4	94.58

5.4. Discussion

This research employs transfer learning methodologies to derive significant features from a constrained medical image dataset, utilizing the pre-trained InceptionResNetV2 network. The bottleneck feature strategy is utilized to reduce computational expenses and the time necessary for model training: the expensive convolutional stages are executed exactly once per image, and only a 158,954-parameter head is optimized. The findings demonstrate that a frozen InceptionResNetV2 backbone combined with a lightweight, regularized fully connected classifier is sufficient to achieve strong performance on four-class brain tumor MRI classification, without the need for end-to-end fine-tuning of the

deep convolutional layers, answering RQ1 and RQ2 affirmatively. The limited train–validation gap observed in Figs. 3 and 4 confirms the effectiveness of dropout, weight decay, and LeakyReLU regularization (RQ3). With respect to RQ4, the comparison in Table 7 shows that the proposed model is competitive with existing methods while addressing the more clinically realistic four-class problem at a small fraction of the computational cost. The principal source of residual error is the Meningioma class, suggesting that targeted data augmentation, fine-tuning of the upper Inception-ResNet blocks, or ensemble strategies could further improve the discrimination of meningiomas from the other tumor types.

6. Conclusion and future work

Accurate brain tumor identification at an early stage is critical. The proposed work integrated frozen InceptionResNetV2 bottleneck features with a lightweight, regularized dense classifier to improve four-class brain tumor classification from MRI images. The proposed solution's efficiency was assessed utilizing a public dataset of 7,023 MRI images spanning glioma, meningioma, pituitary tumor, and healthy categories. The model showed strong performance, with a test accuracy of 94.58%, weighted precision of 0.9461, weighted recall of 0.9458, and weighted F1-score of 0.9459, while training only 158,954 parameters in approximately 12 minutes on a CPU-only workstation. The model performed best on the No Tumor class (F1 = 0.99), meaning that healthy scans are very rarely confused with tumorous ones — an important element for clinical screening. The model's efficient feature extraction and strong regularization fill a gap left by computationally expensive fine-tuning approaches, resulting in good performance across a variety of criteria.

Future work includes fine-tuning the upper Inception-ResNet blocks and exploring ensemble strategies to improve Meningioma discrimination, applying targeted data augmentation, and integrating Explainable AI techniques such as Grad-CAM to enhance model interpretability by providing visual justifications for decisions, fostering clinician trust. Comprehensive clinical validation through extensive trials is essential to assess the model's performance across diverse patient populations and scanner conditions. Additionally, developing a user-friendly interface that combines predictions with clear explanations can streamline integration into clinical workflows and support informed decision-making by radiologists.

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