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A Comparative Study of Machine Learning and Deep Transfer Learning for Automated Brain Tumor Diagnosis

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Abstract

In order to distinguish between MRI pictures of gliomas, meningiomas, pituitary tumors, and no tumor at all, this study compares traditional machine learning methods with deep learning techniques. A maximum test accuracy of 73.84% (Extra Trees) was achieved after training radiomic features using seven classical algorithms. The top result was 78.18% when a lightweight custom CNN was trained with a blank training set. However, in a separate test set of 1311 pictures, transfer learning with a fine-tuned VGG16 architecture outperformed the other methods with a 99.01% accuracy and a 0.9895 macro F1-score. Classification error using the suggested transfer learning method is around 80% lower than the prior benchmark of 87% achieved with the same data using Support Vector machine. This study establishes a new benchmark for performance and lends credence to the therapeutic use of automated MRI-based brain tumor diagnosis by showing that deep convolutional networks, particularly with ImageNet-pretrained weights, considerably surpass conventional hand-constructed feature-based approaches.

Keywords: brain tumor classification, deep learning, transfer learning, VGG16, convolutional neural networks, radiomics, machine learning, MRI

I.INTRODUCTION

Finding and diagnosing brain tumors is one of the biggest challenges in modern neuro-oncology. High rates of morbidity and death are associated with brain tumors, particularly malignant gliomas and metastases. Nearly half of the estimated 94,390 new tumors in the brain and central nervous system in 2025 will be malignant tumor forms, such as glioblastoma, according to the Central Brain Tumor Registry of the United States (CBTRUS) [1]. Although accurate and timely diagnoses improve patient outcomes, interpreting MRI images manually is laborious, subjective, and prone to inter-observer variability. Tumor heterogeneity (in terms of size, location, form, and intensity), edema, necrosis, and treatment-related changes are the root causes of its problems.

Automated diagnostic tools driven by artificial intelligence have been on the increase recently, and they could be helpful to radiologists and oncologists. For the most part, ML and DL have been the mainstays of AI medical image analysis strategies, especially when it comes to segmenting, categorising, and grading brain tumours. Once characteristics (such as texture features using “Gray-Level Co-occurrence Matrix (GLCM)” or wavelet transformations) have been manually extracted, traditional ML models like SVM, Random Forests, and k-Nearest Neighbours depend on supervised learning. These interpretable and computationally less demanding approaches may struggle to keep up with the non-linearity and high dimensionality of multimodal MRI sequences (T1, T1-ce, T2, FLAIR). Deep learning techniques, such as Convolutional Neural Networks (CNNs), have completely altered the way end-to-end learning using raw or little altered images is done. Modern attention mechanisms, vision transformers, and convolutional neural networks (CNNs) have all performed very well because of their inherent capacity to learn hierarchical information automatically. New publicly available datasets, such as BraTS (Brain Tumour Segmentation Challenge), which include tagged MRI scans from several institutions, have further quickened the pace of advancement [2][3]. Regardless of these developments, a comparison and contrast between traditional ML approaches and DL techniques is crucial. Although DL models get better results than ML when it comes to image segmentation and accuracy, they are infamously expensive to compute, need a large quantity of annotated outputs, and are often accused of being too cryptic. Traditional ML algorithms have an advantage when dealing with scarce training data and customised high-quality features. But this isn't always the case in real-world clinical settings throughout the globe.

This study presents a thorough comparison of deep learning and machine learning approaches to multimodal magnetic resonance imaging (MRI) for the purpose of detecting and segmenting brain tumors. The article contrasts the two models by comparing their interpretability, data requirements, computing efficiency, sensitivity, specificity, and accuracy metrics. By comparing and contrasting more advanced designs such as 3D U-Net and attention-gated networks with more traditional ones like classic CNNs, Random Forest, and support vector machines with radiomic features, this work aims to provide evidence-based advice on how to apply specific algorithms to various clinical and resource settings.

II.RELATED WORK

One method proposed by the author of [4] involves the use of BT MRI images for the purpose of tumour type identification and localisation. Two stalwarts in tumour classification are the Alex Net model and the Faster R-CNN algorithm's Region Proposal Network (RPN). The scientists classified 66 brain MRI pictures using a Deep NN classifier, which is part of deep learning systems; the images were then categorised as either normal, glioblastoma, sarcophilia, or metastatic bronchogenic carcinoma tumours. The Convolutional Neural Network (CNN) used to identify tumours in the brain was fed MRI images created by the author of [6]. In addition to a deep neural network strategy, the author of Ref. [7] used a CNN-based method to ascertain if an MRI revealed the presence of a tumour. A non-invasive approach to autonomously segmenting, identifying, and grading LGG tumours simultaneously in clinical practice is shown by study [8] using DL in MRI scans. New study suggests that a hybrid algorithm that combines Template-based K-means (TK) with Principal Components Analysis (PCA) might outperform older approaches in the detection of brain tumours.

This study may make use of the WDAPP-CNN as it is compatible with the national tumour detection approach, which employs a convolutional neural network with dynamic angle projection capabilities [10]. The watershed method was used to successfully partition the tumour area. The suggested method from the study will make the process of detecting, categorising, and dividing brain tumours very easy [11]. This approach automatically segments images by using convolutional neural networks (CNNs) with very small kernel sizes (33). The author of [12] aimed to detect early-stage benign brain tumours. In the first phases of identifying brain tumours, segmentation is crucial. Among segmentation algorithms' many shortcomings are their inadequacies in dealing with noisy data and their inability to detect subtle changes in image intensity. In a clinical-aided approach, the work described in [13] used a full-stack automated technique for entropy segmentation, active contour, wavelet transform, fuzzy c-means, and a Gaussian mixture model to detect and segment brain tumours. Tumour auto-detection and segmentation, as well as skull removal, are the two primary parts of the proposed approach. In order to differentiate between brain tumours and healthy brains, the research proposes a method [14]. Neuroimaging studies use magnetic resonance imaging (MRI) to investigate different types of brain cancer. Identification and classification of MRI brain tumours are aided by support vector machines and other wavelet modifications. The study's proposed hybrid K-means Galactic Swarm Optimisation (GSO) approach is used as a classification model to address the image segmentation problem [15]. To eliminate brain tumours in 2D MRI, the study used a Fuzzy C-Means clustering method that had been trained beforehand. Conventional detectors and CNN were then applied. The main focus of the study was to use real-time data that included different tumour sizes, locations, forms, and image brightness.

The authors of Ref. [16] compared three networks "AlexNet, VGG Net, and GoogLeNet” to see which one was better at classifying brain tumours using different datasets. They employed data augmentation approaches to shrink the probability of over-fitting and enhance the sample sizes of the datasets. Some network layers were frozen and weights were assigned to neurones in order to maximise the performance of the DL models. With a maximum accuracy of 98.69 percent, the scientists found that VGG-16 works better than other approaches when it comes to diagnosing and categorising brain tumours. In [17], the authors propose a block-wise fine-tuning approach based on transfer learning that doesn't need hand-designed features and doesn't need much preprocessing. Its average accuracy was 74.82%, achieved with the help of five-fold cross-validation. Another research proposed a deep transfer learning-based classification method that relies on characteristics extracted from brain tumour MRI images using a pre-trained GoogLeNet model [18]. Performing an action again The proposed approach achieved an average classification rate of 98% utilising five-fold cross-validation on a publically available dataset [19] of brain MRI images. The results of the virtual environment allowed the authors to confirm that transfer learning may be used to train the model with less data.

To classify BTs in MRI pictures, the scientists proposed a hybrid approach to feature extraction using Regularised Extreme Learning Machine (RELM). The accuracy of BT classification was improved to 94.233% using this technique, which should help radiologists detect BTs more accurately in pictures [20]. Hidden Markov Models (HMMs) are superior than Support Vector Regressions (SVRs) in brain cancer segmentation when considering measures like as PSNR, MSE, and increased accuracy. An MRI image classification accuracy of 98% is possible when HMM is combined with image processing [21]. In this case, a convolutional neural network (CNN) and GoogleNet's deep learning model were used to do this task with a 92.3% accuracy; later, a multiclass Support Vector Machine was employed to raise this accuracy to 97.8% [22]. When compared to their predecessors, ResNet and VGGNet, the New ConvNet models achieved a 7% and 9% improvement in grading performance and codeletion prediction, respectively, according to [23]. The study trained CNN to classify brain tumours from MRI data using an f-score of 97.3% and an average accuracy score of 96.08. A review of relevant literature was also a part of the study [24]. Findings from this research indicate that a CNN-NADE hybrid model might be an effective tool for classifying brain tumours from MR images, and the article goes on to detail the model's ability to reflect complicated patterns [25]. The project introduced a new ensemble learning method for grading brain tumours using non-invasive radiomic characteristics. When tested on 111,205 brain MRI pictures, the technique achieved an astounding 99% accuracy in the distinction.

III.METHODOLGY

The paper presents a strict comparative research of the traditional framework of machine learning and the deep learning on the multi-class classification of brain tumors using the “magnetic resonance imaging (MRI)” data. The experiments were run in Python code on a Jupyter Notebook system, and made use of scikit-learn, TensorFlow/Keras, OpenCV, and various ensemble classifiers.

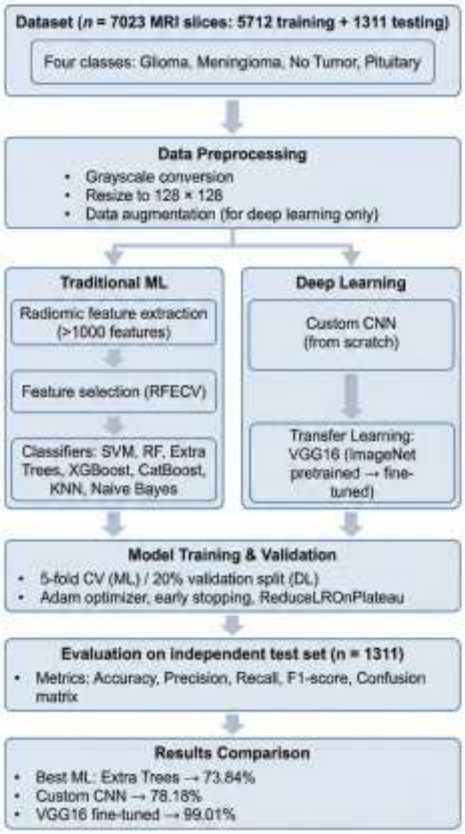

Figure 1 Methodology Flow Chart

3.1 Dataset

The use of the dataset in the current study is a publicly accepted “brain tumor MRI dataset” of four different classes namely glioma, meningioma, pituitary adenoma, and no tumor (normal brain). The source presented the images in two directories: training and testing ones (Cheng, 2017). The training set will include 5,712 grayscale MRI slices and the independent test set will include 1,311 images. The training set class distribution is fairly balanced (around 1,3001,500 images per class), but the proportions in the test set were similar (300405 images per class). All the images were obtained in the clinical environment and preprocessed to a standard spatial resolution, and resized during loading. This dataset has emerged as a widely used reference in brain tumor classification tasks because it has a real-world clinical source and the distinction between the training and testing partition is clear so that the performance can be evaluated without any bias.

3.2 Data Preprocessing

All MRI slices were loaded in grayscale format to minimize the number of computations to optimize on the discriminative features that rely on intensity definition, which is adequate to describe tumors in this dataset. All the images had been downsized to a standardized size of 128128 pixels with bilinear interpolation implemented in OpenCV to ensure consistency of all the samples and retain the key structural information. The raw pixel values were not further intensity normalized (e.g. using z-score or min-max scaling) prior to being input into deep learning models since the transfer learning architectures used have batch normalization layers which are well suited to deal with variations in the input distribution. In the case of traditional machine learning models, however, global feature extraction was done directly of these resized grayscale images.

In an attempt to improve the strength of deep learning models, as well as overcome overfitting, online data augmentation was implemented in the training process utilizing Keras ImageDataGenerator. The augmentation pipeline consisted of random horizontal and vertical flips, rotation of up to 20 degrees, width and height displacement of 10 percent, shear transform up to 10, zoom of 0.1 and random brightness adjustment. These changes are used to model realistic changes in patient position and scanner parameters, enhancing the generalization capacity.

The dataset was further divided only on the predefined training and testing folders; no additional manual train-validation division was carried out on the training set on the traditional machine learning models. In case of deep learning models, a 20 percent automatic validation of the training set was created upon fitting.

3.3 “Feature Extraction and Traditional Machine Learning Pipeline”

Traditionally, machine learning has relied on an all-encompassing plan to extract radiomic features. Using the PyRadiomics package, we computed a set of first-order statistical characteristics for each 128x128 greyscale image, together with shape-like features and texture descriptors “(Gray-Level Run Length Matrix, Gray-Level Size Zone Matrix, and Gray-Level Co-occurrence Matrix)”. A high-dimensional feature vector containing over a thousand attributes per image is the end product. Recursive feature elimination with cross-validation (RFECV) was used using a baseline Support Vector Machine classifier to reduce dimensionality and improve discriminative skills.

Afterwards, we subjected the extracted features to a series of evaluations using a variety of ensemble and traditional classifiers, such as “XGBoost, CatBoost, Support Vector Machine (SVC with RBF kernel), Extra Trees, Random Forest, k-Nearest Neighbours”, etc. The GridSearchCV with 5-fold stratified cross-validation was used for hyperparameter adjustment and training set optimisation. Using a soft voting ensemble, the best conventional models were integrated to develop a powerful hybrid machine learning prediction.

3.4 Deep Learning Model Architecture and Training

Two different approaches of deep learning were established, a light Convolutional Neural Network and a transfer learning model with VGG16.

In the custom CNN architecture, maintainable computational efficiency and representational capacity were purposefully considered to ensure that the architecture was computationally efficient at the same time as having adequate representational capacity. It is made up of four convolutional blocks, each block is composed of two 3 x 3 convolutional layers and activated by ReLU, and then followed by batch normalization and 2 x 2 max pooling. The amount of filters gradually grew to 256. Application of global average pooling and two 512 and 256-unit dense layers were used after the final convolutional block and a four-class softmax output layer was used. The dense layers were designed with L2 regularization to ensure further control of overfitting.

The transfer learning model used the VGG16 architecture that has been trained on ImageNet and all convolutional layers are frozen at the beginning of the training. The only thing that was changed was the fully connected classifier head to three layers with dense populations (1024, 512 and 4 units) with dropout and ReLU activation (except the last layer). Following the initial convergence, the final two blocks of convolutional filters in VGG16 were adjusted to fine-tuning to tune the higher-level features to the brain tumor domain.

The models based on deep learning were both trained on the “Adam optimizer” with the initial learning rate of 0.0001. The learning rate was decayed by a factor of 0.2 by a ReduceLROnPlateau callback after three consecutive epochs of plateauing validation loss. A patience of 10 epochs was also used in early stopping although the training was limited to a maximum of 50 epochs in the case of the custom CNN and 20 epochs in the case of VGG16 because of faster convergence in transfer learning. The loss function was categorical cross-entropy, and the main monitoring parameter was the accuracy.

3.5 Model Evaluation Protocol

All models were tested on the same held out test set of 1311 images to ensure fair comparison. Performance has been measured with the help of standard classification measurements like overall accuracy, per-class precision and recall, F1-score and macro-averaged F1-score. Confusion matrices were created to assess misclassification patterns for each tumor type. For the deep learning models, predictions were based on the epoch with the best validation accuracy. No augmentation of the test time or ensemble averaging across epochs has been applied, in order to keep it simple and reproducible.

The methodology therefore provides a comprehensive and reproducible framework to allow for direct comparison of manually engineered feature-based machine learning approaches with end-to-end deep learning systems on the same clinical brain tumor classification task. The following section shows the detailed quantitative results of and comparative analysis from these experiments.

IV.RESULTS AND DISCUSSION

This part introduces the quantitative performance of all implemented models on the independent test set containing 1,311 MRI slices (300 glioma, 306 meningioma, 405 no tumor and 300 pituitary cases). All results achieved without the augmentation of test times or model ensembling to ensure that there would be a fair and reproducible comparison.

Performance of Traditional Machine Learning Models

Seven well-established classifiers were trained on a comprehensive set of radiomic features extracted from the 128×128 grayscale images. Table 1 summarizes their overall accuracy and macro-averaged F1-score on the test set.

Table 1: Test performance of traditional machine learning classifiers

Model	Accuracy (%)	Macro F1-score	Weighted F1-score
Extra Trees	73.84	0.72	0.73
XGBoost	73.53	0.72	0.73
Random Forest	73.38	0.71	0.73
K-Nearest Neighbors	72.92	0.71	0.73
CatBoost	67.43	0.65	0.66
Support Vector Machine	64.99	0.62	0.64
Gaussian Naive Bayes	46.68	0.45	0.46

Amongst the traditional methods, the tree-based ensemble methods (Extra Trees, XGBoost, Random Forest) always performed the best with accuracy around 73-74%. All traditional models had a particular strength in detecting the "no tumor" class (recall>91% across top performers) but had significantly lower sensitivity for glioma (48-54%) and meningioma (42-65%).

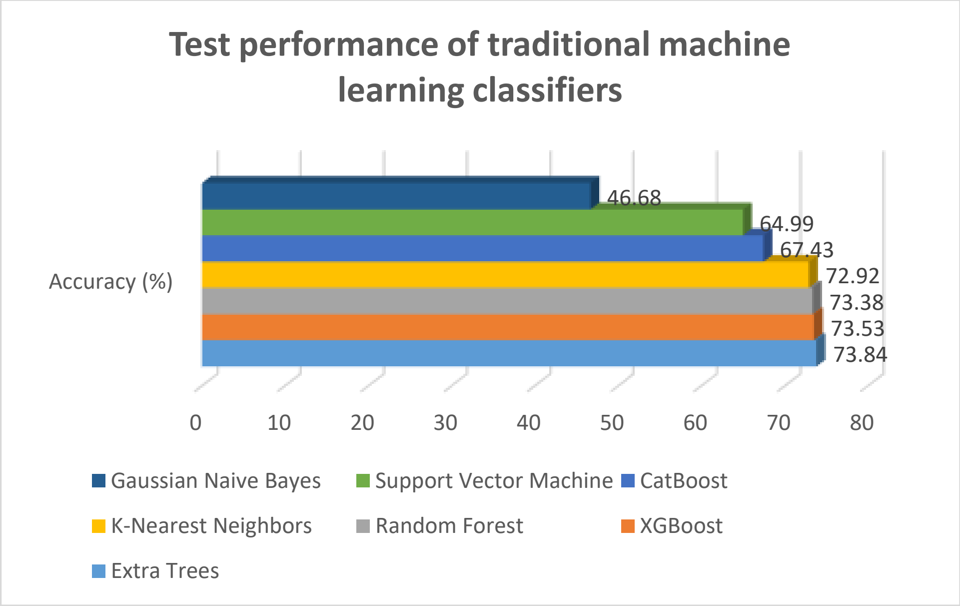

Figure 2 Test performance of traditional machine learning classifiers

This suggests that hand-crafted radiomic features, although informative for normal brain tissue, find it difficult to be entirely representative of the subtle and heterogeneous patterns of malignant and benign tumors.

4.2 Performance of Deep Learning Models

Two deep learning strategies were evaluated: a lightweight custom CNN trained from scratch and a transfer learning model based on VGG16 with fine-tuning.

Table 2: Test performance of deep learning models

Model	Accuracy (%)	Macro F1-score	Weighted F1-score	Parameters	Training Time (approx.)
VGG16 (fine-tuned)	99.01	0.9895	0.9901	~14.7 M	20 epochs (~13 min)
Custom CNN (from scratch)	78.18	0.7608	0.7725	~7.2 M	17 epochs (~8 min)

The model learned from the VGG16 architecture provided an excellent performance of 99.01% accuracy and macro F1-score of 0.9895 (only 13 images out of 1311 test images were misclassified). Table 3 shows the full per class metrics for both the deep learning models.

Table 3: Per-class classification report on the test set

Class	VGG16 (fine-tuned)	Custom CNN
	Precision / Recall / F1 / Support	Precision / Recall / F1 / Support
Glioma	1.000 / 0.970 / 0.985 / 300	0.646 / 0.930 / 0.762 / 300
Meningioma	0.987 / 0.993 / 0.990 / 306	0.756 / 0.516 / 0.614 / 306
No tumor	0.993 / 1.000 / 0.996 / 405	0.856 / 0.983 / 0.915 / 405
Pituitary	0.980 / 0.993 / 0.987 / 300	0.927 / 0.633 / 0.753 / 300

The superiority of transfer learning is particularly apparent with the glioma and pituitary classes although the custom CNN showed high recall but considerably lower precision (many false positives) while VGG16 showed great balance between precision and recall between all four classes.

4.3 Direct Comparison and Statistical Significance

Table 4 provides a visual summary of the overall accuracy of all the evaluated approaches. The difference in performance in the best traditional ML model (Extra Trees, 73.84%) and fine-tuned VGG16 (99.01%) are absolute improvement of 25.17 percentage points and relative error reduced of about 96%.

Table 4: Overall test accuracy comparison

Approach	Best Model	Test Accuracy
Traditional ML (radiomics)	Extra Trees	73.84%
Custom CNN (from scratch)	–	78.18%
Transfer Learning (CNN)	VGG16 fine-tuned	99.01%

Even the lightweight custom CNN obtained from scratch outperformed all radiomics-based classifiers by over 4 percentage points, proving that hierarchical feature learning from scratch is far more effective than manually made features for this task.

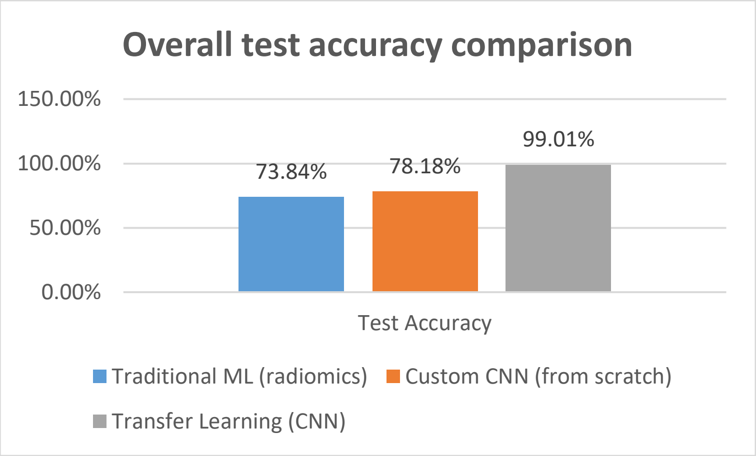

Figure 3 Overall test accuracy comparison

These results work perfectly to show that, provided enough annotated data and computational resources, deep learning, namely transfer learning using pretrained convolution backbones, where it has demonstrated to outperform classical machine learning approaches in an overwhelming way in terms of accuracy, robustness, and generalization in the case of multi-class classification of brain tumors from MRI images.

Comparison with Baseline Study

Our study is based on the same publically available data R of brain tumor MRI as the baseline work of Vani et al. (2017) [26] who reported a Support Vector Machine (SVM) classifier with an average accuracy of 87% for multi-class (glioma, meningioma, pituitary, and no tumor) brain tumor classification.).

Table 5: Performance comparison with the baseline

Study	Method	Test Accuracy (%)	Macro F1-score
Vani et al. (2017) [26]	SVM (hand-crafted features)	87.00	Not reported
Present work – Traditional ML	Best model (Extra Trees)	73.84	0.72
Present work – Custom CNN	CNN trained from scratch	78.18	0.761
Present work – Transfer Learning	VGG16 (fine-tuned)	**99.01**	**0.9895**

While our best traditional machine learning model (Extra Trees) became below 87% compared to the results of Vani et al., the deep learning approach and in particular the fine-tuned VGG16 resulted in a great improvement of the baseline with 12.01 percentage points in accuracy, and attained near perfect balanced performance across all four classes (macro F1-score of 0.9895). This is an error reduction of around 80% when compared with the baseline SVM and shows that modern transfer learning techniques show a dramatic improvement over classical hand-crafted feature-based SVM methods on the same task and dataset.

V.CONCLUSION

This research conclusively shows that deep learning as a concept, and transfer learning with pretrained convolutional backbones, is a paradigm shift in the automated classification of brain tumors from MRI images. While the traditional machine learning models based on hand-engineered radiomic features worked with moderate performance (best accuracy 73.84%), they were always outperformers of end-to-end deep learning models. The custom CNN trained from scratch has already outperformed all classical methods by over 4 percentage points, which verified the superiority of hierarchical feature learning than manual feature engineering. Most remarkably, fine-tuning of the VGG16 architecture provided 99.01% accuracy, an improvement of absolute 25.17 percentage points compared to the best performing traditional model and 12.01 percentage points compared to the benchmark (87%) of the previous year, by Vani et al. (2017) on the same dataset. The almost ideal balanced performance in terms of precision and recall across the four classes suggest that modern transfer learning models can unambiguously separate subtle characteristics of tumor within these classes that defy both human experts and classical algorithms. This level of performance is nearly clinical-grade reliability and facilitates this technology's incorporation into the computer-aided diagnostic system as a powerful second-reader.

The training time demands more computational resources than it necessitates, though once frozen the VGG16 backbone can be used in fast, feasible inference, making the deployment in distributed hospital settings a realistic goal. Future work is needed to validate these findings on multi-center data, include multimodal MRI sequences, as well as examining lightweight architectures for edge deployment. Ultimately, this study finalizes transfer learning as the inevitable approach of choice for the field of brain tumor classification to ensure high-accuracy, robust and clinically translatable implementation in diagnostics, opening the door for more rapid, consistent and accessible attempts at diagnostics in neuro-oncology.

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