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A Comprehensive Survey of Artificial Intelligence and Deep Learning Approaches for Brain Tumor Detection, Classification, and Analysis Using MRI

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Abstract: Brain tumor analysis using Magnetic Resonance Imaging (MRI) is an important area of medical image computing. This paper presents an AI-based brain MRI classification prototype using transfer learning with the VGG16 convolutional neural network. The dataset contains 7,200 labelled MRI images belonging to four categories: Glioma, Meningioma, No Tumor and Pituitary. The data are divided into 4,480 training images, 1,120 validation images and 1,600 independent test images. The preprocessing pipeline includes resizing to 224 × 224 pixels, Gaussian noise reduction, Contrast Limited Adaptive Histogram Equalization (CLAHE) and normalization. The model achieved approximately 87.23% validation accuracy and 78.31% accuracy on the independent test set. A Streamlit web application supports MRI upload, preview, prediction, confidence display, class-probability visualization and optional browser-based voice assistance. The application is deployed through Streamlit Community Cloud, with source files maintained in GitHub. The results demonstrate an integrated educational prototype while identifying class-wise errors and generalization limitations. The system is intended for research and educational use and is not a substitute for professional medical diagnosis.

Keywords: Brain MRI, Brain Tumor Classification, Deep Learning, VGG16, Transfer Learning, CNN, CLAHE, Streamlit.

I. INTRODUCTION

Brain tumors are abnormal growths of cells within the brain or surrounding structures. Their type, location, growth pattern and biological behaviour vary. Magnetic Resonance Imaging (MRI) is widely used in neurological assessment because it provides detailed soft-tissue images without using ionizing radiation. Interpreting MRI images is a specialist task involving image appearance, anatomical location, contrast patterns and clinical information.

Computer-aided image analysis can support research workflows by applying repeatable image-processing and pattern-recognition procedures. Artificial intelligence (AI), particularly deep learning, has become an important research area for image classification. Convolutional Neural Networks (CNNs) learn spatial features through convolutional filters, nonlinear activation functions and pooling operations.

Transfer learning reuses representations learned from a source dataset and adapts them to a target task. This can be useful when labelled target-domain data and computing resources are limited. VGG16 is a CNN architecture consisting of stacked convolutional layers and is used in this work as the basis for four-class MRI classification.

The proposed project integrates dataset preparation, image preprocessing, model training and evaluation, prediction through a Streamlit interface, and cloud deployment. The application displays the predicted class, confidence score and class-wise probability chart, with optional browser speech synthesis.

Key contributions from the study include:

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1. A VGG16 transfer-learning pipeline for four brain MRI categories.
2. Preprocessing using resizing, Gaussian noise reduction, CLAHE and normalization.
3. Independent evaluation using 1,600 test images and class-wise metrics.
4. A Streamlit interface for MRI upload, prediction and probability visualization.
5. Deployment through Streamlit Community Cloud with source files maintained in GitHub.

II. RELATED WORK

Research in automated brain tumor analysis has explored conventional machine learning, convolutional neural networks, transfer learning, segmentation and explainable AI. CNN-based approaches learn image representations directly from MRI data and are widely investigated for multi-class classification. Architectures such as VGG16, ResNet and EfficientNet provide alternative network designs with different feature-learning and computational characteristics.

Transfer learning is frequently considered for medical image tasks because large labelled medical datasets can be difficult to obtain. A pretrained network can provide an initialization for the target task, after which selected layers or classification components are adapted using MRI images. Performance depends on the source of pretraining, target dataset, fine-tuning strategy and evaluation protocol.

Segmentation approaches, including U-Net-style architectures, identify pixel-level regions rather than assigning only an image-level class. Explainable AI methods such as Grad-CAM visualize image regions that influence predictions. Such explanations may support model inspection, but a heatmap alone does not establish clinical correctness.

Comparisons between published studies require caution because datasets, class definitions, preprocessing methods, data splits and evaluation metrics may differ. Accuracy values reported by separate studies should not be interpreted as a direct ranking unless experimental conditions are comparable. This work focuses on a four-class VGG16-based prototype and reports its validation and independent test results separately.

TABLE I SUMMARY OF DEEP LEARNING APPROACHES USED IN BRAIN TUMOR ANALYSIS

Research direction	Typical approach	Contribution	Limitation
CNN classification	Convolutional neural networks	Automatic feature learning	Dataset-dependent performance
Transfer learning	VGG16, ResNet, EfficientNet	Reuses learned representations	Domain differences affect transfer
Segmentation	U-Net and related models	Spatial tumor-region information	Requires pixel-level labels
Explainable AI	Grad-CAM and related methods	Highlights influential image regions	Does not prove correctness
Efficient architectures	EfficientNet, lightweight CNNs	Balances model size and computation	Speed/performance trade-offs

III. PROPOSED SYSTEM

The proposed system is an MRI image classification application based on a trained VGG16 model. It accepts a brain MRI image from the user, applies the same preprocessing operations used during model development, obtains class scores from the trained network and presents the result through a web interface.

The workflow contains two distinct phases. During model development, the labelled dataset is prepared, split into training, validation and independent test subsets, preprocessed and used to train and evaluate the VGG16-based classifier. During application use, the already-trained model is loaded and used for inference on an uploaded MRI image. The application does not retrain the model for each uploaded image.

Model-development flow: labelled MRI dataset → dataset split → preprocessing → VGG16 transfer learning and training → model evaluation → save trained model. Prediction flow: MRI upload → input validation → preprocessing → trained VGG16 inference → four-class scores → result display → optional voice assistance.

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A. System Architecture

The architecture contains a Streamlit application, an image-preprocessing stage and a trained VGG16 model artifact. The user selects an MRI image through the application. The image is checked and prepared using the required dimensions and preprocessing operations. The processed image is passed to the loaded model, which produces scores for Glioma, Meningioma, No Tumor and Pituitary. The application selects the highest-scoring category and displays the result.

The trained model is stored as a Keras model file and loaded at runtime. The project does not require a persistent database for uploaded MRI images or prediction history. GitHub stores project source and deployment files, while Streamlit Community Cloud hosts the web application.

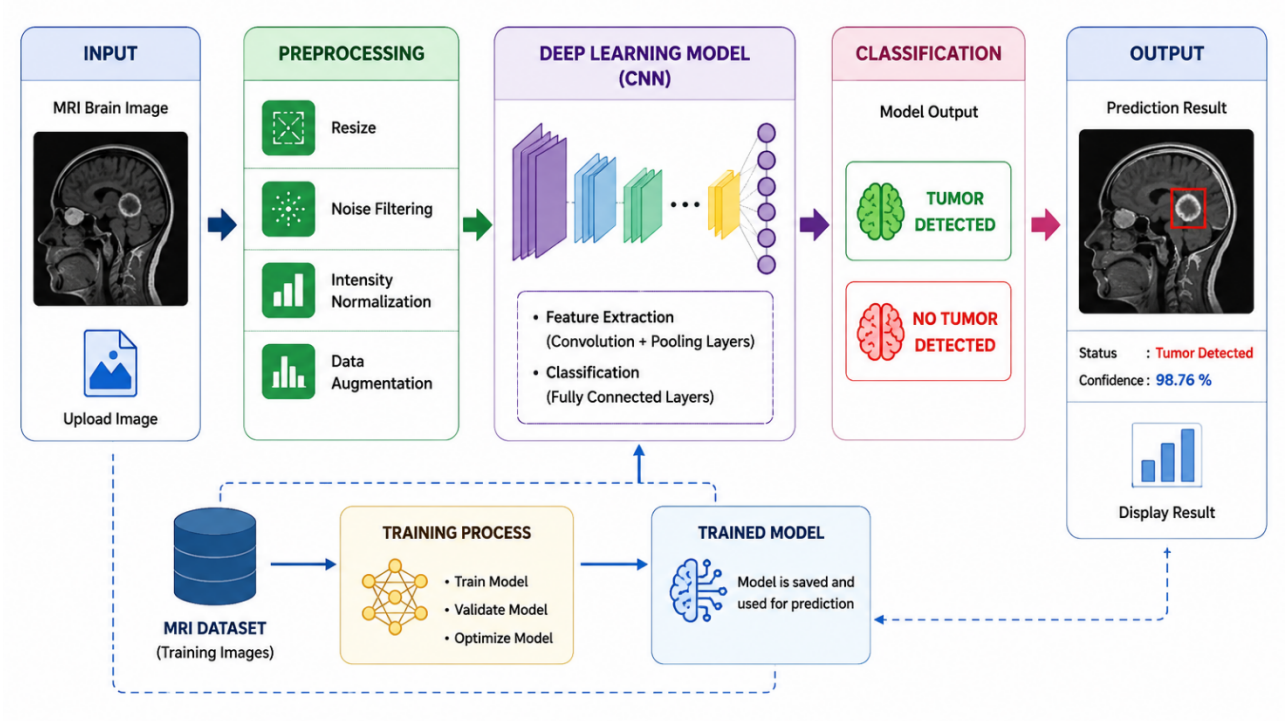


Fig. 1 Architecture of the implemented Brain tumor detection

TABLE II RESPONSIBILITIES OF THE PROPOSED SYSTEM COMPONENTS

Component	Responsibility
User	Selects and uploads an MRI image and views the result
Streamlit interface	Handles upload, preview, interaction and result display
Preprocessing	Resizes, reduces noise, enhances contrast and normalizes
VGG16 model	Generates scores for the four target classes
Result module	Displays predicted class, confidence and probability chart
Browser speech synthesis	Optionally reads the prediction result aloud
GitHub / Streamlit Cloud	Support source management and web deployment

IV. METHODOLOGY

A. Dataset

The project uses a labelled dataset of 7,200 brain MRI images. The images belong to four categories: Glioma, Meningioma, No Tumor and Pituitary. The available project records specify 4,480 images for training, 1,120 for validation and 1,600 for independent testing. The independent test set contains 400 images from each class.

TABLE III DISTRIBUTION OF THE BRAIN MRI DATASET

Subset	Images	Percentage
Training	4,480	62.22%

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Validation	1,120	15.56%
Independent test	1,600	22.22%
Total	7,200	100%

The training subset is used to update model parameters. The validation subset monitors learning and supports model-selection decisions. The independent test subset is held out for final evaluation and is not used to fit model parameters. The exact dataset title, source, licence and patient-level split procedure should be stated from the dataset actually used.

B. Data Preprocessing

MRI images may differ in dimensions, contrast and noise characteristics. Preprocessing creates a consistent input representation for the model. The implemented pipeline includes resizing, Gaussian noise reduction, CLAHE contrast enhancement and normalization.

Resizing converts each input image to 224 × 224 pixels, matching the expected VGG16 input dimensions. Gaussian filtering reduces high-frequency noise while retaining general image structure. CLAHE improves local contrast by applying adaptive histogram equalization with contrast limiting. Normalization scales pixel values to the range expected by the model.

The same preprocessing sequence must be applied during model development and application inference. Differences between training and prediction preprocessing can change the input distribution and reduce prediction reliability.

C. Feature Extraction and Classification

VGG16 contains convolutional blocks that learn increasingly complex image features. Early layers respond to simple patterns such as edges and textures, while deeper layers combine these patterns into higher-level representations. In transfer learning, pretrained convolutional weights provide an initial feature extractor, while the task-specific classification component is adapted to the four target classes.

The classification component produces four class scores corresponding to Glioma, Meningioma, No Tumor and Pituitary. The application identifies the class associated with the highest output score and presents the score information as a confidence value and class-wise probability chart. These model scores are outputs of the classifier and should not be interpreted as calibrated clinical probabilities.

V. MACHINE LEARNING MODELS

VGG16 is a deep convolutional neural network introduced for large-scale image recognition. Its architecture uses small 3 × 3 convolutional filters arranged in sequential blocks, with pooling operations between blocks. The network progressively transforms the input image into feature maps that encode visual patterns.

In this system, VGG16 is used through transfer learning. The pretrained convolutional representation is adapted for the brain MRI classification task. The final classification component is configured for four output categories. This approach reuses previously learned visual representations rather than learning every filter from random initialization.

VGG16 provides a well-known baseline architecture for image classification. However, it is relatively large compared with some modern lightweight networks. Model size, inference time and available memory are relevant considerations for deployment.

A. VGG16 ARCHITECTURE

VGG16 is organized into five convolutional blocks. Each block contains convolutional operations using small 3 × 3 filters and nonlinear activation functions. Max-pooling operations reduce the spatial dimensions of feature maps between blocks. As the input moves through the network, low-level patterns such as edges and textures are combined into more complex visual representations. The resulting feature representation is supplied to the task-specific classification component.

B. RANSFER LEARNING

Transfer learning uses parameters learned during training on a large source image dataset as an initialization for a new classification task. In this project, the VGG16 convolutional representation is adapted to the four MRI categories. This approach can reduce the amount of target-domain data and training time required compared with learning every feature

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from random initialization. The exact frozen or fine-tuned layers should be stated only after checking the final training notebook.

C. FEATURE EXTRACTION

The convolutional layers perform feature extraction by applying learned filters to local image regions. Early layers can respond to simple structures, while deeper layers represent combinations of patterns. These learned features form the basis for distinguishing visual differences among the four dataset labels. The model's feature representations are learned from the training data; they are not manually specified rules.

D. FOUR-CLASS CLASSIFICATION

The final classification component is configured to produce four output scores, one for each supported category: Glioma, Meningioma, No Tumor and Pituitary. The predicted label is selected from the output with the highest score. The application presents the predicted category together with the confidence value and a chart of class-wise scores. These values describe the model output and should not be interpreted as clinically calibrated probabilities.

E. MODEL INFERENCE IN THE WEB APPLICATION

During application use, the saved VGG16 model is loaded by the Streamlit application. Each uploaded MRI image is passed through the inference preprocessing pipeline and then through the trained model. The application displays the prediction without retraining the network. Separating model development from inference makes the deployed application easier to use and avoids repeating the training process for every upload.

VI. MODEL TRAINING AND EVALUATION

The model-development procedure begins by loading the labelled MRI dataset and applying the defined preprocessing operations. The data are separated into training, validation and independent test subsets. The VGG16-based model is trained using the training subset, while validation performance is monitored during development. After model selection, the saved model is evaluated on the independent test subset.

1. Load the labelled MRI image dataset and verify the four class labels.
2. Divide images into training, validation and independent test subsets.
3. Resize images to 224 × 224 pixels.
4. Apply Gaussian noise reduction, CLAHE and normalization.
5. Initialize the VGG16 transfer-learning model and configure four output classes.
6. Train using the training subset and monitor validation performance.
7. Select and save the trained model.
8. Generate predictions for the independent test images.
9. Calculate accuracy, precision, recall and F1-score and inspect the confusion matrix.

Accuracy measures the proportion of all test samples classified correctly. Precision measures the proportion of predictions for a class that are correct. Recall measures the proportion of actual samples of a class that are correctly identified. F1-score is the harmonic mean of precision and recall. A confusion matrix provides the class-wise distribution of correct and incorrect predictions.

1. Accuracy = (TP + TN) / (TP + TN + FP + FN)
2. Precision = TP / (TP + FP) Recall = TP / (TP + FN)
3. F1-score = 2 × (Precision × Recall) / (Precision + Recall)

For multi-class classification, metrics are computed per class and may be summarized using macro or weighted averaging. The averaging method should be stated when reporting aggregate values.

VII. SYSTEM IMPLEMENTATION

The system is implemented as a web-based application using Streamlit. The trained VGG16 model is loaded by the application, and user-uploaded images are processed before prediction. The implementation separates model development from application inference so that the saved model can be reused without repeating training.

A. Frontend

The frontend provides the interface through which the user uploads an MRI image and views the analysis result. The application supports image selection, preview and an analysis action. After prediction, the interface displays the predicted category, confidence score and a chart showing the scores for the four classes.

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B. Backend

The prediction pipeline begins when a user selects an MRI image. The application reads the uploaded image, prepares it for preprocessing, applies the required image transformations and supplies the resulting tensor to the loaded VGG16 model. The output scores are converted into a predicted class and displayed to the user.

Prediction flow: MRI Upload → Image Validation → Resize and Preprocessing → VGG16 Inference → Four-Class Scores → Predicted Label and Confidence → Probability Chart.

C. Voice Assistance and Deployment

The application includes optional browser-based speech synthesis to read the prediction result. This feature depends on browser compatibility and device settings. It is an accessibility aid for reading the displayed output and does not provide an additional medical assessment.

The project source code and supporting files are maintained in a public GitHub repository. The application is deployed using Streamlit Community Cloud. The deployment includes the Streamlit application file, the trained VGG16 model artifact and the dependency specification. The deployed application performs inference using the saved model; it does not retrain the network when a user uploads an image.

VIII. RESULTS AND DISCUSSION

The model achieved approximately 87.23% validation accuracy and 78.31% accuracy on the independent test set. The independent test accuracy corresponds to 1,253 correctly classified images out of 1,600. The difference between validation and test performance indicates that performance on the validation subset did not fully transfer to the independent test subset. This motivates further investigation of generalization, class-wise errors and dataset characteristics.

TABLE IV OVERALL PERFORMANCE OF THE VGG16 MODEL

Evaluation measure	Result
Validation accuracy	Approximately 87.23%
Independent test accuracy	78.31%
Independent test loss	0.6579
Independent test images	1,600
Correct predictions	1,253
Incorrect predictions	347

TABLE V CLASS-WISE CLASSIFICATION PERFORMANCE

Class	Precision	Recall	F1-score	Support
Glioma	85.61%	58.00%	69.15%	400
Meningioma	68.68%	62.50%	65.45%	400
No Tumor	83.05%	98.00%	89.91%	400
Pituitary	76.88%	94.75%	84.88%	400

The class-wise results show differences in recognition performance. No Tumor achieved the highest recall at 98.00%, indicating that most images in this class were correctly identified. Pituitary achieved recall of 94.75%. Glioma recall was 58.00%, while Meningioma recall was 62.50%, indicating important areas for further improvement. The lower recall values for Glioma and Meningioma suggest that the model confuses some examples of these classes with other categories.

TABLE VI CONFUSION MATRIX OF THE INDEPENDENT TEST SET

Actual / Predicted	Glioma	Meningioma	No Tumor	Pituitary
Glioma	232	96	38	34
Meningioma	32	250	40	78
No Tumor	3	3	392	2

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Pituitary	4	15	2	379

The diagonal elements of the confusion matrix represent correctly classified images, while the off-diagonal elements represent misclassifications. Out of 400 Glioma images, 232 were correctly classified; 96 were predicted as Meningioma, 38 as No Tumor and 34 as Pituitary. For Meningioma, 250 images were correctly classified, while 78 were predicted as Pituitary. The model correctly classified 392 of 400 No Tumor images and 379 of 400 Pituitary images. In total, the diagonal contains 1,253 correct predictions and the off-diagonal entries contain 347 errors.

These results indicate that Glioma and Meningioma are the most challenging categories for the current model. The matrix identifies the types of errors but does not establish their medical cause. Further investigation may include reviewing misclassified images, verifying labels, examining class-specific variation and testing alternative model configurations using a separate validation procedure.

The confusion matrix shows that 232 of 400 Glioma images were correctly classified, while 96 were predicted as Meningioma. For Meningioma, 250 images were correctly classified, while 78 were predicted as Pituitary. These off-diagonal values indicate that the two tumor categories are more frequently confused than No Tumor and Pituitary in this test set. No Tumor has 392 correct predictions, and Pituitary has 379 correct predictions.

Precision and recall provide complementary information. Meningioma precision of 68.68% indicates that a notable proportion of images predicted as Meningioma belonged to other actual categories. The F1-score reflects the balance between precision and recall. These results show why class-wise metrics and a confusion matrix are necessary in addition to overall accuracy.

Potential improvements include reviewing image quality, checking class-specific variation, investigating data augmentation and evaluating alternative architectures. Any change should be assessed using a held-out test set that remains separate from model tuning.

IX. DISCUSSION

The implementation demonstrates an end-to-end workflow that combines MRI preprocessing, transfer learning, model evaluation and a web-based prediction interface. Rather than presenting only a trained classifier, the project makes the model accessible through a user interface that accepts an MRI image and displays the prediction in a readable format.

The evaluation indicates that the model performs differently across the four classes. Strong recall for No Tumor and Pituitary contrasts with lower recall for Glioma and Meningioma. The confusion matrix shows that Glioma and Meningioma are often confused with each other, and some Meningioma examples are predicted as Pituitary. This suggests that additional investigation of class-specific image characteristics and training data may improve performance.

Validation accuracy of approximately 87.23% is higher than independent test accuracy of 78.31%. This difference should be reported transparently. It may reflect differences in sample difficulty or distribution between the subsets, but the available results alone do not establish a single cause. Additional experiments and external datasets are needed to evaluate generalization more broadly.

The Streamlit application improves accessibility by allowing image upload and result visualization through a browser. The confidence score and probability chart help communicate the classifier output, while optional speech synthesis provides an alternative way to hear the result. These interface features do not increase the medical validity of the prediction.

X. LIMITATIONS

1. The model supports only four image-level categories: Glioma, Meningioma, No Tumor and Pituitary.
2. Independent test accuracy of 78.31% indicates that classification errors remain, particularly for Glioma and Meningioma.
3. The difference between validation and independent test accuracy indicates that generalization requires further study.
4. The system performs image-level classification and does not provide pixel-level tumor segmentation or localization.
5. Performance on images from other hospitals, scanners or patient populations has not been established.

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6. The displayed confidence score is a model output and has not been established as a clinically calibrated probability.
7. The application is an academic research prototype and has not undergone prospective clinical validation.

XI. FUTURE SCOPE

A. Improved Classification Performance

Future work may investigate controlled fine-tuning, hyperparameter optimization, class-aware augmentation and alternative CNN architectures. Particular attention can be given to Glioma and Meningioma because their recall values were lower in the current independent test evaluation.

B. Larger and More Diverse Datasets

The model can be evaluated using larger MRI collections from multiple sources. Patient-level separation and independent external validation should be used where metadata permits, in order to reduce the risk of overly optimistic evaluation.

C. Tumor Localization and Segmentation

The current system produces an image-level class prediction. Future versions may incorporate segmentation architectures such as U-Net when suitable pixel-level annotations are available.

D. Explainable AI and Model Optimization

Methods such as Grad-CAM may be investigated to visualize image regions that influence classifier output. Model compression, quantization and efficient architectures may also be explored to reduce inference time and resource requirements. Visual explanations must be evaluated and should not be treated as proof of clinical correctness.

E. Clinical Validation

Any consideration of clinical use would require independent validation, expert review, privacy and regulatory assessment, and prospective evaluation under qualified medical supervision. The current prototype is not intended for diagnosis or treatment decisions.

XII. CONCLUSION

This paper presented an AI-based brain tumor classification prototype using VGG16 transfer learning and MRI images. The dataset contains 7,200 labelled images across four categories: Glioma, Meningioma, No Tumor and Pituitary. The preprocessing pipeline applies resizing, Gaussian noise reduction, CLAHE and normalization before model inference.

The model achieved approximately 87.23% validation accuracy and 78.31% accuracy on an independent test set of 1,600 images. Class-wise results show stronger recall for No Tumor and Pituitary than for Glioma and Meningioma. The confusion matrix identifies misclassification patterns that can guide future improvement.

A Streamlit web application was developed and deployed through Streamlit Community Cloud. It supports MRI image upload, preview, prediction, confidence display, class-wise probability visualization and optional browser-based voice assistance. The project demonstrates the integration of deep learning and a user-facing web application for educational and research purposes. It remains a prototype and must not be used as a substitute for professional medical diagnosis.

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