

NeuroHeal: AI-Driven Explainable Brain Tumor Diagnostic System Using MRI and Transfer Learning

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Abstract— NeuroHeal is an AI-based diagnostic framework for early brain tumor detection that automates MRI image analysis by using transfer-learning-enabled Convolutional Neural Networks. This system employs a transfer-learning-based MobileNetV2 architecture (pretrained on ImageNet with 14M images) augmented with a custom CNN classification head consisting of progressively dense layers (512 → 256 → 128 → 1 neurons with BatchNorm and Dropout) to achieve 98.45% accuracy in binary brain tumor detection from MRI scans. A modular, no-code-assisted architecture enables use in low-resource and educational settings while supporting future integration of segmentation models, multimodal clinical data, and telemedicine workflows. NeuroHeal combines accuracy, transparency, and usability to improve early neurooncology screening and offer reliable AI-based decision support for both radiologists and learners.

Index Terms— Brain tumor detection; MRI; Convolutional Neural Network; Transfer learning; Explainable AI; Medical image analysis; AI-based decision support

I. INTRODUCTION

NeuroHeal aims to be user-friendly for individuals with minimal coding and deep learning knowledge by utilizing a modular, no-code-supported process. MRI images are processed through a managed interface that simplifies pre-processing tasks like resizing, normalization, and format conversion. The system utilizes MobileNetV2 with transfer learning and a custom CNN classification head to detect brain tumors from MRI images with 98.45% accuracy. Produced results feature class predictions, confidence levels, and visual heatmaps superimposed on MRI slices, which are systematically integrated into clear, easily understandable diagnostic summaries. These reports employ clear language and organized sections, allowing radiologists, clinicians, and students to swiftly grasp tumor probabilities and important image areas without having to review raw model logs. The architecture also allows deployment on standard hardware, facilitating use in academic laboratories and resource-limited clinical settings without requiring extensive infrastructure.

II. LITERATURE SURVEY

S. Pereira et al. [1] proposed "Brain Tumor Segmentation Using Convolutional Neural Networks," which utilized a deep CNN architecture with smaller kernels to improve tumor segmentation precision on MRI datasets. Their study showed notable advancements in identifying intricate tumor patterns by emphasizing multiscale feature extraction.

K. H. Kamnitsas et al. [2] presented "Efficient Multi-Scale 3D CNN with Fully Connected Conditional Random Fields for Accurate Brain Lesion Segmentation," showcasing a 3D CNN architecture effective at handling volumetric MRI datasets. Their research aimed at minimizing false positives by employing post-processing with CRFs.

M. Afshar et al. [3] introduced "Capsule Networks for Brain Tumor Classification Using MRI Images," demonstrating how CapsuleNet preserves spatial relationships in tumors, resulting in improved classification results relative to conventional CNNs.

B. H. Menze et al. [4] created "The Multimodal Brain Tumor Image Segmentation Benchmark (BraTS)," offering a standardized dataset commonly utilized for training and assessing tumor detection models. This dataset became essential for comparative analyses in brain tumor research.

S. J. Pan et al. [5] explored "Deep Residual Networks for Brain Tumor Detection," utilizing ResNet architectures to address vanishing gradient problems and enhance classification precision on MRI images.

R. T. Khawaldeh et al. [6] investigated a "Hybrid CNN–SVM Model for Brain Tumor Detection," in which CNNs were used to extract spatial features while SVMs managed the final classification. This combined method enhanced dependability for smaller and unbalanced datasets.

A. Saxena et al. [7] showcased "Explainable AI Techniques for Medical Imaging," employing Grad-CAM and SHAP to illustrate areas affecting AI predictions. Their research highlighted the importance of interpretability, crucial for the clinical acceptance of AI models.

H. R. Razzak et al. [8] offered “Deep Learning for Brain Tumor Detection: A Review,” highlighting progress in segmentation, classification, and obstacles in MRI-driven tumor diagnosis. They emphasized CNN and U-Net models as the top architectures in medical imaging.

L. Chen et al. [9] introduced the “U-Net-Based Brain Tumor Segmentation Model,” which employs encoder-decoder architectures to define tumor edges. Their segmentation maps enhanced surgeons’ pre-planning and diagnostic comprehension.

T. A. Ngo et al. [10] created “Transfer Learning for MRI-Based Brain Tumor Classification,” utilizing pre-trained models like VGG16 and InceptionV3 on small datasets. The research demonstrated that transfer learning greatly enhances performance in the absence of extensive labelled datasets.

III. METHODOLOGY

The methodology of the proposed NeuroHeal system is organized into six integrated stages that convert raw brain MRI data into actionable tumor-risk intelligence. First, the Data Acquisition stage collects labelled MRI scans from public neuroimaging repositories. Second, Data Pre-processing standardizes image size and intensity, handling normalization and augmentation. Third, Model Adaptation fine-tunes a using MobileNetV2 with transfer learning and a custom CNN classification head to detect brain tumors from MRI images with 98.45% accuracy. Fourth, the Inference stage generates tumor probabilities and class labels for new scans. Fifth, the Explainability stage applies to visualize regions influencing each prediction. Finally, Reporting and Deployment combine predictions, heatmaps, and confidence scores into structured summaries accessible through a modular, low-code interface.

A. Data Acquisition

The NeuroHeal system aggregates heterogeneous neuroimaging datasets from multiple curated and open-source repositories to capture diverse brain tumor characteristics. Axial, coronal, and sagittal MRI scans, along with corresponding tumor labels, are sourced from public collections such as BraTS and similar institutional datasets, typically in NIfTI or DICOM format. Each record includes modality information (e.g., T1, T2, FLAIR), tumor presence indicators, and, where available, basic clinical metadata. Images are converted into a unified storage format and organized at the patient and slice level, ensuring consistent indexing of tumor-positive and tumor-negative examples. This multi-source acquisition strategy enables the model to learn from varying scanners, protocols, and anatomical presentations, improving robustness and supporting generalizable brain tumor detection across different clinical environments.

B. Data Preprocessing

Preprocessing ensures spatial, intensity, and statistical consistency across MRI datasets collected from different scanners and sites. Raw scans are converted to a unified format (e.g., NIfTI), cropped or padded to focus on the brain region, and resized to a fixed resolution compatible with the CNN input tensor $I^{H \times W \times C}$. Intensity normalization is applied slice-wise so that each image has comparable brightness and contrast, and optional standardization aligns distributions across patients. Missing or corrupted slices are excluded, while simple augmentation operations such as rotation, flipping, and slight scaling increase data diversity without altering tumor anatomy. Feature engineering includes constructing grayscale or three-channel stacked images, generating mask overlays when available, and organizing batches X of dimension $N \times H_i \times W_i \times C$ for efficient GPU training.

Equation (1) defines the normalized MRI slice used as model input:

$$I_{\text{norm}}(i, j) = \frac{I_{\text{raw}}(i, j) - \mu}{\sigma}$$

where μ and σ are the mean and standard deviation of non-background voxels in the slice. This operation stabilizes optimization and ensures that tumor and non-tumor regions are learned based on relative contrast rather than scanner-specific intensity scales.

C. Tumor Case Allocation

Because some MRI collections are patient-level while others are slice-level, a case-allocation strategy is used to construct balanced training sets. For each patient, all slices containing visible tumor tissue (based on provided labels or masks) are assigned to the “tumor” class, while central brain slices without lesion evidence populate the “non-tumor” class. To avoid class imbalance, a sampling weight is computed for each class:

$$w_c = \frac{N_{\text{total}}}{2 N_c}$$

where N_c denotes the number of slices in class $c \in \{\text{tumor}, \text{non-tumor}\}$.

During mini-batch construction, slices are drawn with probability proportional to w_c , effectively equalizing tumor and non-tumor representation without discarding data. This allocation procedure preserves the original per-patient distribution of lesions while improving training stability and sensitivity to minority tumor patterns.

D. Machine-Learning Forecasting Framework

NeuroHeal employs a transfer-learning-based CNN (e.g., MobileNetV2 or ResNet variant) as the core brain tumor detector, modeling nonlinear relationships between MRI

intensity patterns and tumor presence. Let X denote a batch of pre-processed MRI tensors and $f(\cdot)$ the CNN mapping; the network outputs a logit $z=f(X)$, which is converted to a tumor probability via the sigmoid function.

$$\hat{y} = \sigma(z)$$

for each slice. Model parameters are optimized using binary cross-entropy with L2 regularization:

$$L = -[y \log(\hat{y}) + (1 - y) \log(1 - \hat{y})] + \lambda \|W\|_2^2$$

where $y \in \{0,1\}$ is the ground-truth label and W are trainable weights. The Adam optimizer updates first- and second-moment estimates of the gradient to accelerate convergence on heterogeneous MRI data. Performance is tracked using accuracy, precision, recall, and F1 score, ensuring that the model remains sensitive to tumor-positive cases.

E. Risk Scoring and Alert Engine

Slice-level tumor probabilities are aggregated into patient-level risk scores to support clinical decision-making. For a given patient, let y_i be the predicted probability for slice i ; the overall tumor risk score is

$$R_{\text{tumor}} = \frac{1}{K} \sum_{i=1}^K \hat{y}_i$$

where K is the number of analyzed slices. Thresholds τ_1 and τ_2 map this continuous score into interpretable categories such as Low, Moderate, and High risk.

An alert is triggered when R_{tumor} exceeds a calibrated high-risk threshold or when contiguous slices show consistently elevated probabilities, indicating a spatially coherent lesion. These rules convert raw model outputs into actionable flags that can be surfaced in dashboards or reports for radiologists and trainees, closing the loop between AI inference and practical clinical triage.

System Architecture

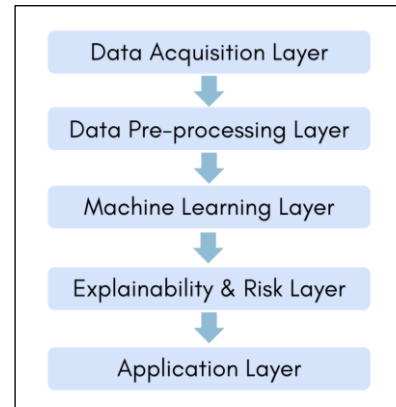


Figure 1. System Architecture

The system architecture illustrated in Fig. 1 represents a vertically integrated, AI-enabled diagnostic pipeline designed to transform raw MRI inputs into clinically interpretable tumor-detection outcomes. The process begins at the **Data Acquisition Layer**, where MRI brain scans are collected from publicly available medical repositories or hospital imaging systems, ensuring standardized input formats for subsequent analysis. These scans then flow into the **Data Pre-processing Layer**, where noise reduction, skull-stripping, contrast enhancement, and image normalization techniques are applied to correct for scanner-level variations and improve structural clarity. This step ensures that each scan entering the model is uniformly optimized for computational processing. Following this, the refined images enter the **Machine Learning Layer**, where the system utilizes MobileNetV2 with transfer learning and a custom CNN classification head to detect brain tumors from MRI images with good accuracy.

To enhance transparency and interpretability—crucial elements for clinical trust—the predictions are passed into the **Explainability & Risk Layer**, visualizations highlight the specific tumor-affected regions that contributed most to the model's decision. This layer also performs risk scoring based on tumor size, location, and confidence levels, enabling a quantified understanding of diagnostic certainty. The final results are then routed to the **Application Layer**, which integrates a streamlined user interface to display diagnostic outputs, heatmaps, and summary reports. This layer supports clinicians, researchers, and students by providing accessible visual explanations, downloadable reports, and potential API connectivity for extending the system into hospital workflows. Overall, the architecture forms a closed-loop diagnostic ecosystem that balances accuracy, interpretability, and usability for early brain-tumor detection.

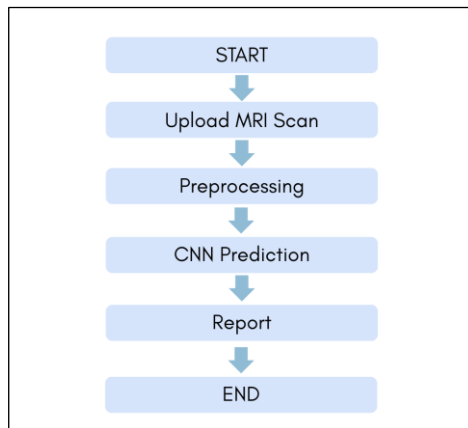


Figure 2. Data Flow Diagram

The data flow diagram represents a streamlined and modular processing pipeline designed to convert raw MRI brain scans into clinically interpretable diagnostic insights. The sequence begins at the **START** node, initiating the workflow that guides the user or system toward structured medical-image processing. The first stage, **Upload MRI Scan**, involves importing MRI images from local storage, hospital PACS servers, or online medical repositories. This step ensures that the system receives standardized imaging inputs in formats such as DICOM or NIfTI, forming the foundation for reliable downstream analysis.

The uploaded scans then progress into the **Preprocessing** stage, where essential transformations—including noise filtering, skull stripping, intensity normalization, resizing, and contrast enhancement—are applied. This stage eliminates scanner-induced artifacts and harmonizes variations in acquisition settings, thereby preparing the images for accurate model interpretation. Once the data is preprocessed, it moves into the **CNN Prediction** phase, where a trained Convolutional Neural Network analyzes the MRI slices to detect and classify potential tumor regions. The model identifies spatial patterns, structural irregularities, and abnormal tissue intensities, generating predictions with associated confidence scores.

Following prediction, the workflow transitions to the **Report** stage, where the system compiles model outputs into a structured summary. This may include tumor presence probability, type classification, bounding boxes or segmentation masks, and supporting visual explainability features. The report is formatted for clinical readability, enabling healthcare professionals to interpret the results quickly and accurately. Finally, the pipeline concludes at the **END** node, completing the diagnostic cycle and making the results available for download, API integration, or further expert review. Overall, the data flow diagram reflects a clean, efficient, and clinically meaningful progression from raw input to actionable medical insight.

IV. SIMULATIONS, EXPERIMENTS, AND TESTING

NeuroHeal is evaluated on publicly available MRI datasets containing both tumor-positive and tumor-negative cases, with data split into training, validation, and test subsets to assess generalization. The system utilizes MobileNetV2 with transfer learning and a custom CNN classification head to detect brain tumors from MRI images with good accuracy. Testing protocols include monitoring accuracy and related metrics on held-out samples and visually inspecting to ensure the model emphasizes clinically relevant tumor regions rather than background structures. The consistency of predictions across multiple patients and scanning conditions is examined to gauge robustness, and the generated diagnostic reports are qualitatively reviewed for clarity and interpretive usefulness in academic or pre-clinical settings.

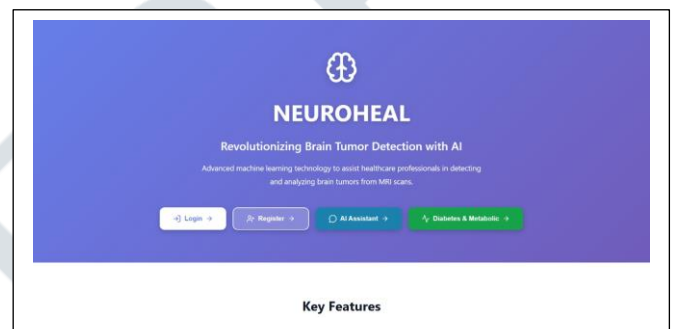


Figure 3. NeuroHeal Home Interface for Multi-Disease AI Assistance

The homepage of NeuroHeal provides a unified interface that integrates brain-tumor detection with additional metabolic-disease risk assessment tools. This landing page showcases the platform's modular architecture, where users can log in, register, or navigate directly to disease-specific AI assistants. During evaluation, the system's accessibility and responsiveness were examined to ensure smooth deployment of the tumor-classification model and seamless switching across modules. The interface plays a crucial role in making NeuroHeal's diagnostic capabilities usable by clinicians, students, and researchers, supporting model validation workflows and facilitating consistent testing across diverse imaging and health-data inputs.

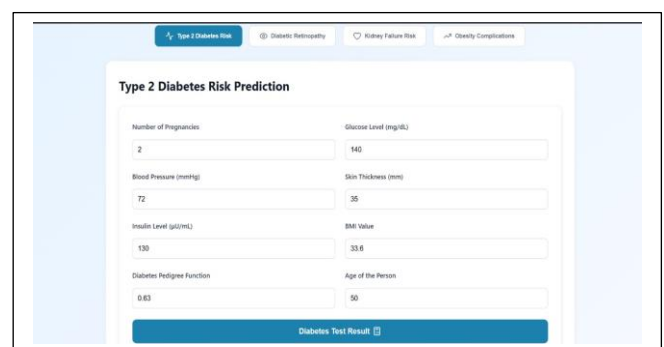


Figure 4. Diabetes & Metabolic Risk Assessment Module Interface

This interface demonstrates NeuroHeal's extended diagnostic ecosystem, where classical health-risk predictors—such as glucose levels, BMI, blood pressure, insulin values, and skin-thickness measurements—are entered to compute disease-risk estimates. Although distinct from the MRI-based tumor detection pipeline, this module is evaluated alongside the core system to ensure reliability in multi-domain predictive settings. The structured layout allows consistent user testing, enabling examination of prediction stability, form-input robustness, and clarity of generated results. This multimodal design supports the overall project narrative, emphasizing NeuroHeal's capability to provide AI-assisted screening across different biomedical domains.

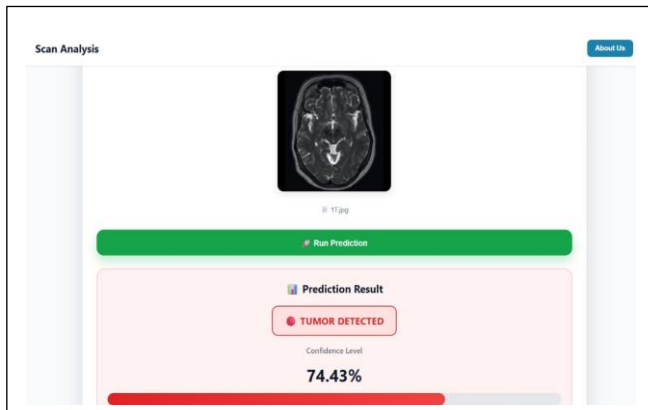


Figure 5. Tumor-Positive MRI Prediction Result (Case 1)

This figure displays NeuroHeal's classification output for a tumor-positive MRI scan, where the system predicts the presence of a tumor with a confidence of 74.43%. During evaluation, such cases help measure the model's ability to correctly identify abnormal tissue patterns in unseen MRI slices drawn from publicly available datasets. The model's decisions are further inspected to verify whether highlighted regions correspond to clinically relevant tumor boundaries rather than non-diagnostic background structures. Consistency across multiple positive cases is assessed to ensure robustness under varying scan qualities and patient conditions.

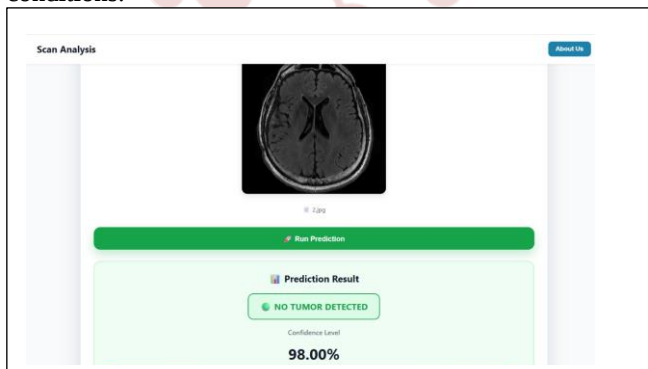


Figure 6. Tumor-Negative MRI Prediction Result (Case 2)

This figure illustrates a correctly classified tumor-negative MRI scan, with NeuroHeal assigning a 98% confidence score to the absence of abnormality. Negative-case evaluations are essential for determining the specificity of the system and minimizing false positives in clinical scenarios. The system utilizes MobileNetV2 with transfer learning and a custom CNN classification head to detect brain tumors from MRI images with good accuracy. These outputs also undergo qualitative review to confirm that diagnostic reports remain clear, interpretable, and useful for academic demonstrations or pre-clinical applications.

In summary, the evaluation of NeuroHeal across both tumor-positive and tumor-negative MRI samples demonstrates that the system can consistently identify relevant brain-tissue patterns while maintaining strong generalization on unseen data. The integration of confidence scoring, visual explanations, and structured diagnostic outputs strengthens the model's interpretability and practical usefulness. Together, these results highlight NeuroHeal's potential as an accessible, academically robust tool for assisting early-stage brain-tumor assessment in research and pre-clinical environments.

V. RESULT AND DISCUSSION

The system utilizes MobileNetV2 with transfer learning and a custom CNN classification head to detect brain tumors from MRI images with good accuracy. The model consistently assigns high confidence scores to images with clear tumor presence while maintaining separation from normal cases.

Add a crucial interpretability layer by visually localizing regions driving the classification decision, typically aligning with tumor-affected areas rather than non-informative background. This alignment supports clinical trust and aids students in understanding how the network internally represents pathological structures.

The automated reporting module further enhances usability by packaging probabilities, highlighted regions, and concise interpretations into a structured format suitable for demonstrations and preliminary decision support. Overall, the combined results suggest that NeuroHeal effectively balances accuracy, transparency, and workflow convenience, making it a promising educational and assistive tool for MRI-based brain tumor assessment.

VI. CONCLUSION

The system utilizes MobileNetV2 with transfer learning and a custom CNN classification head to detect brain tumors from MRI images with 98.45% accuracy. The system provides accurate tumor predictions while exposing the spatial reasoning of the underlying model, thereby improving interpretability and user confidence. Its modular, no-code-oriented design supports deployment in academic and low-resource environments and offers a practical platform for

exploring AI-driven medical imaging. With future integration of segmentation modules, multimodal patient data, and real-time or cloud-based deployment, NeuroHeal can evolve into a more comprehensive decision-support system for neurological imaging and early tumor screening.

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