Predicting Brain cancer and tumor using ML

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Abstract

One of the most studied disorders in modern medicine is the brain tumor. Brain diseases are mainly caused by abnormal growth of brain cells that may damage the brain structure, and eventually will lead to malignant brain cancer. Appropriate diagnosis of the cancer type empowers the specialists to make the right choice of treatment, decision, and to save the patient's life. An enhanced approach has been proposed that can classify brain tumor types from magnetic resonance images (MRI) using deep learning and an ensemble of machine learning (ML) algorithms. The system named BCM-VEMT can classify among four different classes that consist of three categories of brain cancers (Glioma, Meningioma, and Pituitary) as well as noncancerous, or normal type, tumors extract detailed information from the MRI pictures, a VGG-19 convolutional neural network is created. Then, to classify among various cancer kinds, these filtered deep characteristics are put into multi-class ML classifiers. The dataset of the system has a total of 3787 MRI images of four classes. BCM-VEMT has achieved better performance with 97.90% accuracy for the Glioma class, 98.94% accuracy for Meningioma, 98.92% accuracy for Pituitary and 98.00% accuracy for the Normal class. BCM-VEMT can have great significance for medical sectors in classifying brain cancer types.

Keywords : malignant , convolutional neural network, machine learning , MRI images

Introduction

"Tumor" means swelling of a part of the body, normally without inflammation, due to abnormal growth of tissue, either benign or malignant. A brain tumor denotes the build-up of atypical cells in specific brain tissues. People of all ages and walks of life are susceptible to contracting this perplexing and, in some cases, deadly disease. The benign ones cannot spread to other parts of the body or the brain and are not regarded as malignant. The malignant types are thought to be carcinogenic, develop out of control, and have the potential to spread to other bodily regions . Every year, all over the world, 12.7 million people are diagnosed with cancer, and 7.6 million people die of cancer. There are more than 120 different forms of brain tumors, according to the National Brain Tumor Society. The most frequent of them are gliomas, meningiomas, and pituitary tumors. Nearly 75% of all brain tumor forms are covered by these three categories, with 45% of them being the 15% for the Meningioma type, 15% for the Pituitary type, and 10% for the Glioma type.

Magnetic Resonance Imaging (MRI) is the most refined and widely used method to obtain high-resolution images of everywhere in the body. It is broadly used and regarded as one of the most accurate techniques for cancer detection and classification because of its high-quality images of brain tissue. Artificial Intelligence and Machine Learning, in particular, are developing new technologies that have a significant influence on the therapeutic field and offer a diagnostic that is devoid of mistakes. In MRI image processing, many machine-learning techniques are used for image segmentation and classification. One type of machine learning called deep learning uses layered algorithmic architecture to examine data. Model data is filtered via a number of

layers in deep learning. In order to boost the model's accuracy, each subsequent layer makes correlations and connections using the findings of the layer before it. . Using deep learning or machine learning, we can easily classify the tumor types, experts can make a rapid decision about treatment, and thus the best treatment can be delivered to patients.

The genetic algorithm and the K-Nearest Neighbors (KNN) algorithm are only two examples of the machine learning techniques that have been used recently to detect brain tumors in scans. A fundamental machine learning technique called K-Nearest Neighbors (KNN) is utilized for classification and regression applications. KNN's fundamental working assumption is similarity: it classifies data points according to the dominant class among their K closest neighbors in the training sample. This method makes KNN a simple and understandable algorithm because it doesn't assume anything about the distribution of the underlying data and is simple to use. But choosing the right K value is important since it has a big influence on how well the algorithm works. The computational cost of KNN may be considerable for big datasets as it needs storing the complete training dataset in memory, and it is also sensitive to feature scaling. Despite its simplicity, KNN remains a valuable tool in machine learning, particularly in scenarios where interpretability and ease of use are paramount.

Convolutional Neural Networks (CNNs) are a ground-breaking deep learning architecture that have revolutionized the computer vision industry. CNNs are incredibly good at tasks like image identification, object detection, and facial recognition because they are built to automatically extract and learn hierarchical information from pictures. The introduction of convolutional layers, which apply filters to input pictures to enable the network to recognize patterns and characteristics at various levels of abstraction, is the major breakthrough. Additionally, CNNs use fully connected layers for classification or regression and pooling layers to reduce the sample size of feature maps. The appeal of CNNs lies in its capacity to automatically identify pertinent features from unprocessed pixel data, doing away with the requirement for manually engineered feature engineering. Additionally, pretrained CNN models that were trained on enormous image datasets have developed into priceless tools for transfer learning, enabling academics and industry professionals to use previously learned features for a variety of image-related activities. The capabilities of computer vision and image analysis are continuously being pushed by CNNs.

Impact
A diagnosis of brain cancer may have a profound effect on the sufferer, as well as on their family and friends. The impacts might be psychological, practical, and/or emotional. Here are some examples -
Emotional impact
fear and anxiety: Concerns about the patient's health and future frequently cause family members and friends to feel anxiety and fear. It might be very upsetting to have a condition that is unpredictable.
Sadness and grief: As family members watch the patient suffer and possibly see their health deteriorate, a strong sense of sadness and grief may develop.
Guilt and Helplessness: Those who are close to the patient could feel helpless or guilty for not being able to do more to assist or for being frustrated or exhausted.
Impact on daily life and finances: The duties of providing care for the patient may place a physical and mental burden on family members or friends who take on the role of carers, which may negatively impact their own health and wellbeing.
Financial Stress: The patient's family may experience financial stress due to the price of medical procedures, the expense of prescription drugs, and possible income loss as a result of caregiving responsibilities.

Relationship Effects

Relationships may suffer from the strain and emotional toll of dealing with a loved one's brain cancer. The dynamics between family and friends might be impacted by communication problems, arguments about medical options, and emotional tiredness.

Defeat and Death

When a patient has terminal brain cancer, their eventual loss can have profound and enduring repercussions on their family and friends, causing sadness and a period of transition.

Methodology

In this methodology for the development of a brain cancer detection system using a Convolution Neural Network (CNN) in deep learning, the process initiates with comprehensive collection of dataset comprising brain MRI images encompassing four distinct categories: glioma, meningioma, no tumor and pituitary. Sequentially, this dataset undergoes division into training and testing subsets, accompanied by the implementation of pertinent preprocessing techniques aimed at standardizing and augmenting data.

The architecture of the CNN model is meticulously designed for optimal image classification, with a comprehensive exploration of various architectures to ascertain the most effective one . The model's training phase entails rigorous monitoring of training metrics, including accuracy and loss. To safeguard against overfitting, a proactive early stopping mechanism is incorporated, contingent on validation loss or accuracy.

The evaluation of the trained model unfolds on the testing dataset, culminating in the assessment of its performance through key metrics such as accuracy, precision, recall, F1-score and the creation of a confusion matrix to facilitate a visual representation of class-specific performance. Additionally, the generation of training and testing accuracy/loss graphs serves as a valuable tool for dissecting the model's learning trajectory.

In conclusion, this methodology delivers a systemic approach to the development of a brain cancer detection system, followed by a thorough evaluation of its performance, with subsequent recommendations for further enhancement and research endeavors thereby contributing to the burgeoning field of medical image analysis. Figure 1 illustrates the proposed technique.
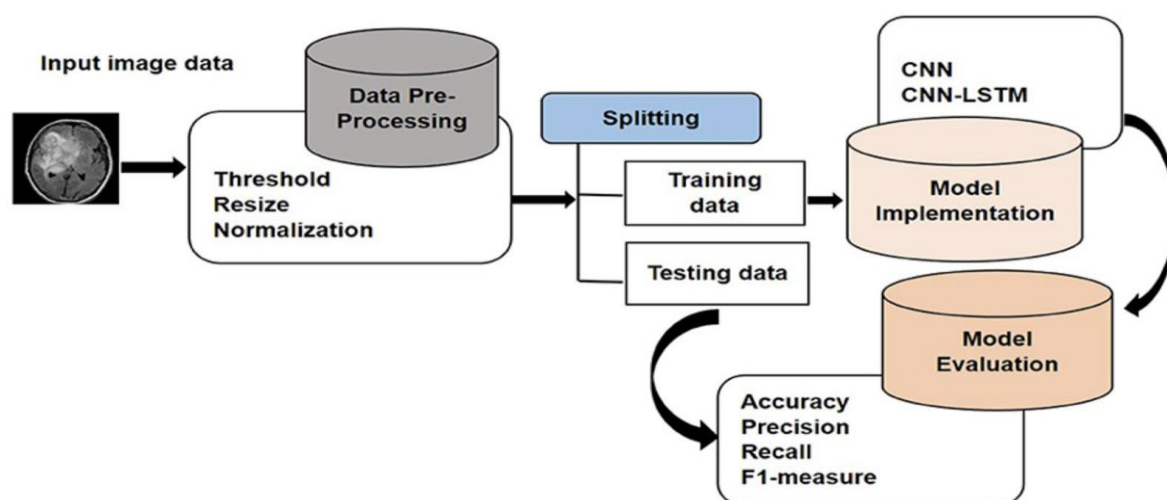

Figure 1. Proposed approach

Description of dataset
        The dataset encompasses a total of 7,023 human brain MRI images, meticulously categorized into four distinct classes: pituitary, no tumor, meningioma and glioma. This comprehensive dataset is a fusion of data from three primary sources: SARTAJ, Fig Share and Br35H Datasets and it comprises 7,022 MRI scans of the human brain, all acquired from the kaggle website.
        To facilitate model development and rigorous evaluation, the dataset has been thoughtfully divided into two subsets. Specifically, 1,311 images out of the 7,022 total images have been designated for testing the model's performance, while the remaining 5,713 images serve as the training set. Within the training dataset, you will find 1,457 images of pituitary tumor, 1,595 images of normal brain tissue, 1,339 images of meningiomas and 1,321 images of glioma.
        In contrast, the test dataset comprises a total of 1,311 images, distributed as follows: 300 pituitary images, 405 normal brain tissue images, 306 meningioma images and 300 glioma tumor images. This diverse and meticulously organized dataset is an invaluable resource for researchers and data scientists seeking to develop and evaluate machine learning and deep learning models for brain tumor classification based on MRI images, enabling the creation of robust algorithms for automated brain tumor detection and classification.
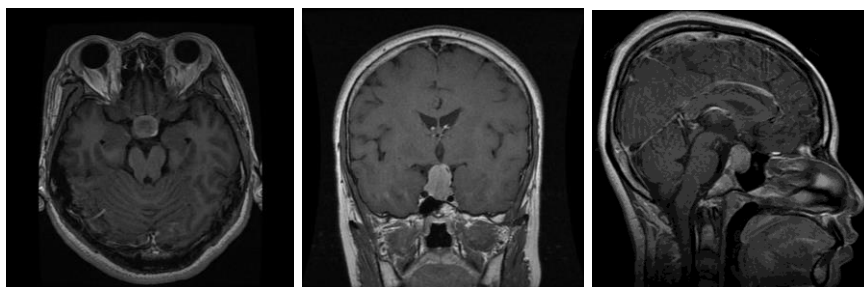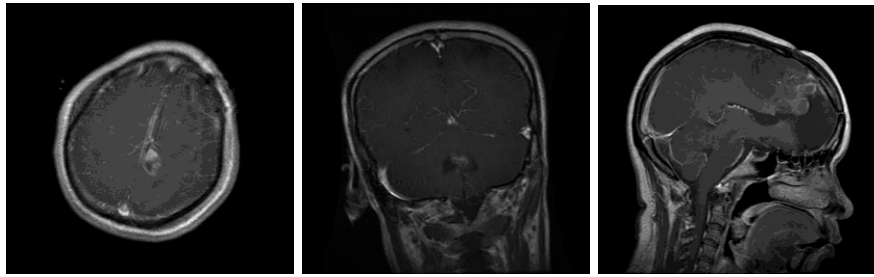

(a)
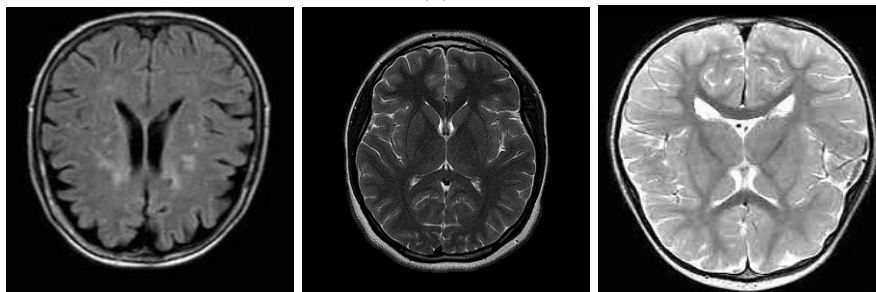
(b)

(c)

(d)

Figure 2. Sample images of the brain cancer dataset with their class labels
(a) Pituitary (b) No tumor (c) Meningioma (d) Glioma

Data preprocessing

The dataset contains MRI images categorized into four classes:pituitary, no tumor, meningioma and glioma. Here, we outline the steps involved in preparing the dataset for further analysis. To facilitate model training and evaluation, we split the dataset into two main subsets: a training set and a testing set. The split is performed using an 80:20 ratio, resulting in 80% of the data (5713 images) allocated for training and 20% (1311 images) for testing. To ensure uniformity and compatibility of the architecture, we resize all images to a standardized dimension of 224X224 pixels. This resizing step readies the images for subsequent processing. Crop normalization is applied to each image to identify extreme contour points. This process enables us to determine the farthest east, west, north and south (x,y) coordinates of the largest contour in each image. Crop normalization plays a crucial role in isolating the brain region while removing superfluous background elements, sharpening the focus on relevant brain image features. By following these dataset preprocessing steps and dividing the dataset into two subsets (training and testing), we prepare our MRI images for effective utilization with the deep learning models, ensuring accurate classification and analysis of brain images.

Proposed VGG-19 Deep Network Architecture

The VGG-19 model is a deep convolutional neural network used primarily for image classification tasks. It takes as input fixed-size (224x224) RGB images and subtracts the mean RGB value from each pixel. Using 3x3 kernels with a stride of 1, the model covers the entire image and preserves its spatial resolution through spatial padding. Max pooling is applied with 2x2 windows and a stride of 2, followed by Rectified Linear Unit (ReLU) activation functions for non-linearity. The network consists of 19 layers, with 16 convolutional layers for feature extraction and fully connected layers, including one with 1000 channels for 1000-way ILSVRC classification, followed by a softmax function. Originally designed for the ILSVRC competition, VGG-19 has found use in various classification tasks and is available for transfer learning. Its pre-trained weights are readily accessible in frameworks like keras, making it adaptable for different applications. The model has 16 convolutional layers organized into 5 groups with max-pooling after each group. It's known for its ability to learn rich features from a wide range of images, making it versatile for diverse image recognition tasks.
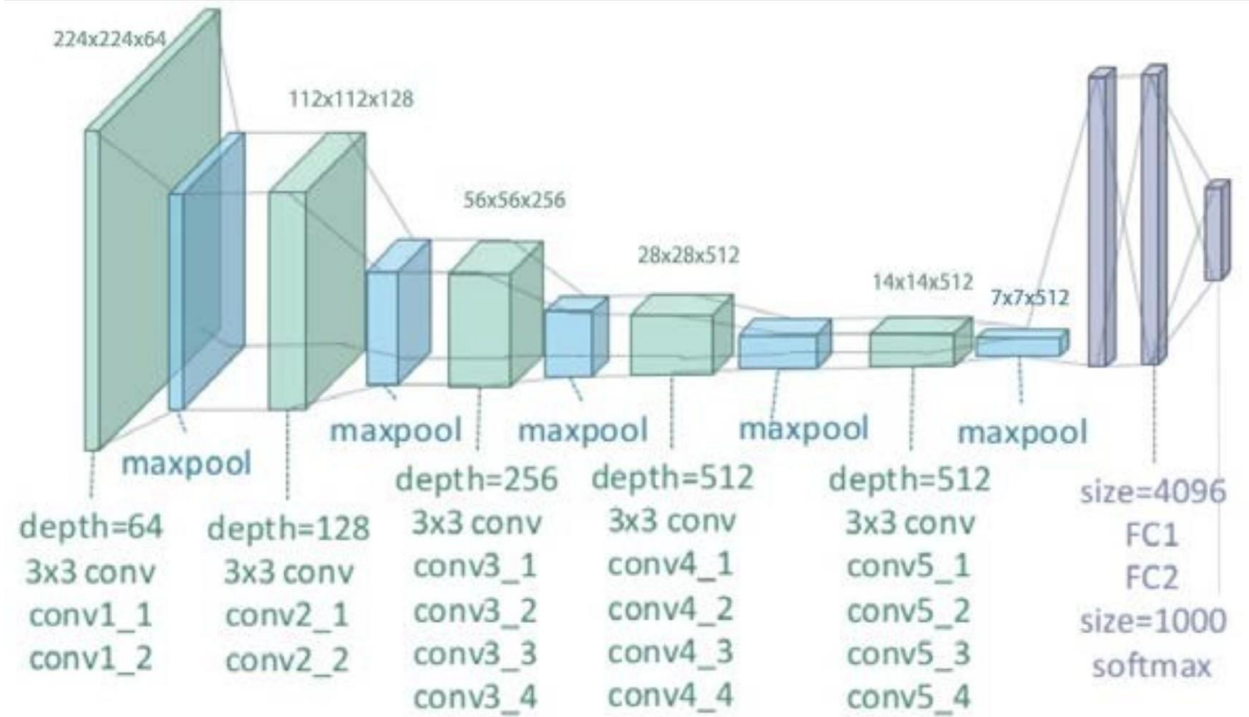
Figure 3. Illustration of the network architecture of VGG-19 model: conv means convolution, FC means fully connected.

Weighted Average Ensemble

Our approach for classifying MRI brain tumor images involves a Weighted Average Ensemble Deep Learning Model. The process is divided into two phases: classification and ensemble. In the classification phase, we use three models: a transfer learning-based model, a Convolution Neural Network (CNN) model without augmentation and a CNN model with augmentation. Each of these models extracts distinct feature spaces. We then optimize these features by applying different weights, denoted as weight 1, weight 2 and weight 3.These weights are determined through a grid search combination to find the best-performing classification model.

Ensemble models, by combining the results of multiple models, offer more accurate predictions and greater robustness. If one model makes an incorrect prediction, the others can compensate for it. Our Weighted Average Ensemble technique assigns different weights to each model based on its performance, allowing models that perform better to have a more significant impact on the final decision. To train these machine learning classifiers, we tune various hyperparameters to optimize their performance with the dataset. We use the Grid Search Technique and employ a 10-fold cross-validation approach to find the best parameters for each classifier. Each individual machine learning classifier performs better than the CNN model alone.

In the ensemble phase, we combine all five machine learning classifiers, treating them as 'estimators' for the ensemble technique. The 'weight' value assigned to each classifier is determined based on its accuracy. This ensemble technique outperforms individual machine learning models, resulting in higher accuracy and improved classification performance.

Convolutional Neural Network (CNN) Model

A Convolutional Neural Network (CNN) is a powerful deep learning architecture specifically designed for image analysis tasks like brain cancer and tumor prediction. It consists of multiple layers that automatically learn hierarchical features from input images. In the context of brain tumor prediction, a CNN starts with input layers that accept medical images, typically with dimensions of 224x224x3 for color images. Convolutional layers then apply filters to the input, progressively capturing low-level features like edges and textures, and gradually extracting more complex features as we go deeper into the network.

Pooling layers reduce spatial dimensions and focus on the most essential information, preventing overfitting. Fully connected layers, often located at the end of the network, learn complex patterns and relationships within the extracted features. Finally, an output layer with SoftMax activation assigns probabilities to different tumor classes.

CNNs excel at feature extraction and representation learning, making them suitable for detecting subtle anomalies in medical images. Transfer learning can be applied by initializing the network with pre-trained models like VGG16, VGG19, ResNet50, InceptionV3, or EfficientNetB3. This technique leverages knowledge from large datasets to enhance the performance of the model on the specific brain cancer and tumor prediction task, even with limited data.
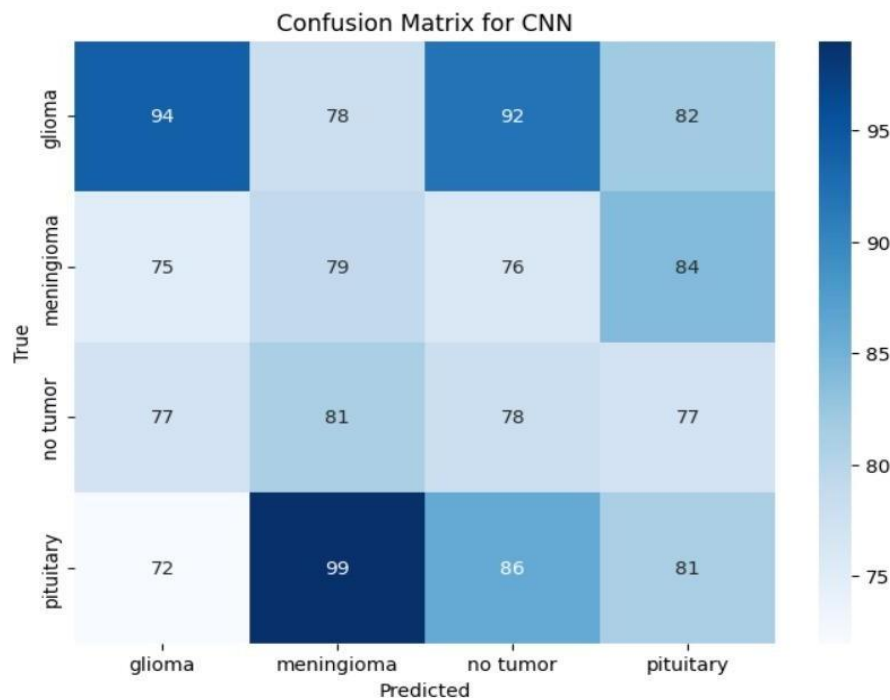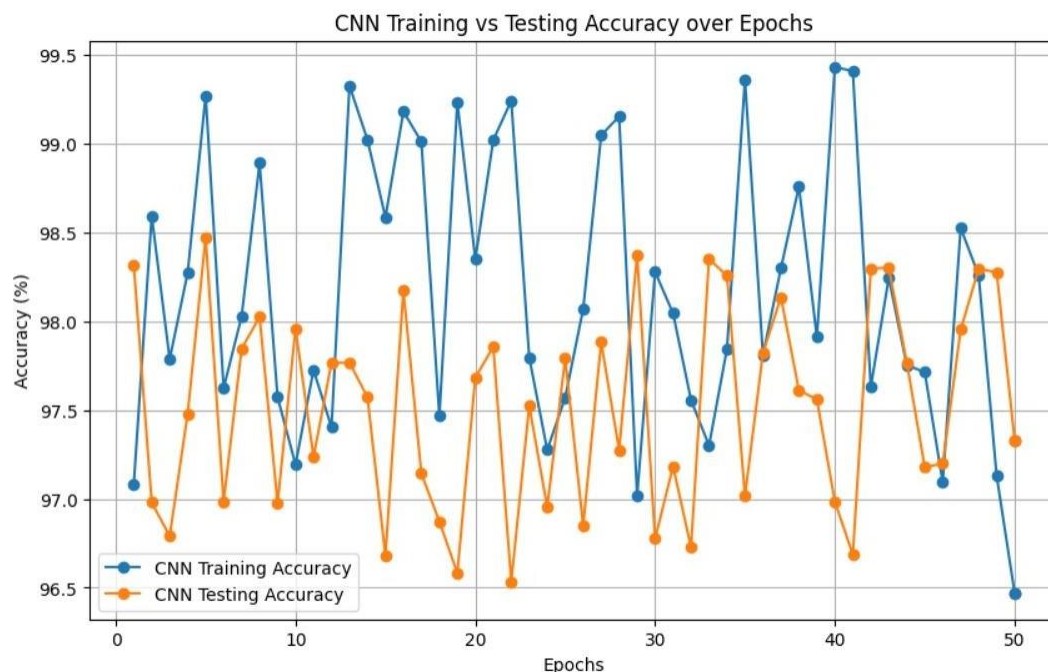

Figure 4. Confusion Matrix for CNN.

Figure 5. CNN Training vs Testing Accuracy over Epochs.

ResNet50 Model

The ResNet50 model, short for Residual Network with 50 layers, is a formidable deep learning architecture that has revolutionized the field of computer vision and is particularly well-suited for medical image analysis tasks such as brain cancer and tumor prediction.
At its core, ResNet50 introduces the concept of residual connections, which fundamentally addresses the challenge of training extremely deep neural networks. These connections enable information to flow directly through shortcuts, bypassing certain layers and mitigating the vanishing gradient problem. This innovation empowers ResNet50 to effectively capture intricate and nuanced patterns within medical images, making it an ideal choice for identifying even subtle anomalies associated with brain tumors.
The ResNet50 architecture comprises convolutional layers, batch normalization, and ReLU activation functions, culminating in a deep and powerful feature extractor. The convolutional layers act as feature detectors, progressively extracting and enhancing image features across different scales and complexities. As the network deepens, it becomes increasingly adept at capturing high-level abstract representations of the input data, including fine-grained details essential for tumor detection.

In the context of brain cancer and tumor prediction, ResNet50's impressive depth and residual connections allow it to excel in extracting salient features from medical images. By training the model on a labeled dataset of brain scans, it learns to discriminate between healthy brain tissue and potential tumor regions. Transfer learning can also be employed by initializing the network with pre-trained weights from a large-scale dataset, thereby leveraging knowledge from a broader context to enhance its predictive capabilities for brain tumor detection.

In conclusion, the ResNet50 model represents a state-of-the-art solution for brain cancer and tumor prediction, thanks to its deep architecture, residual connections, and ability to capture complex image features, ultimately contributing to more accurate and early diagnoses in the field of medical imaging.
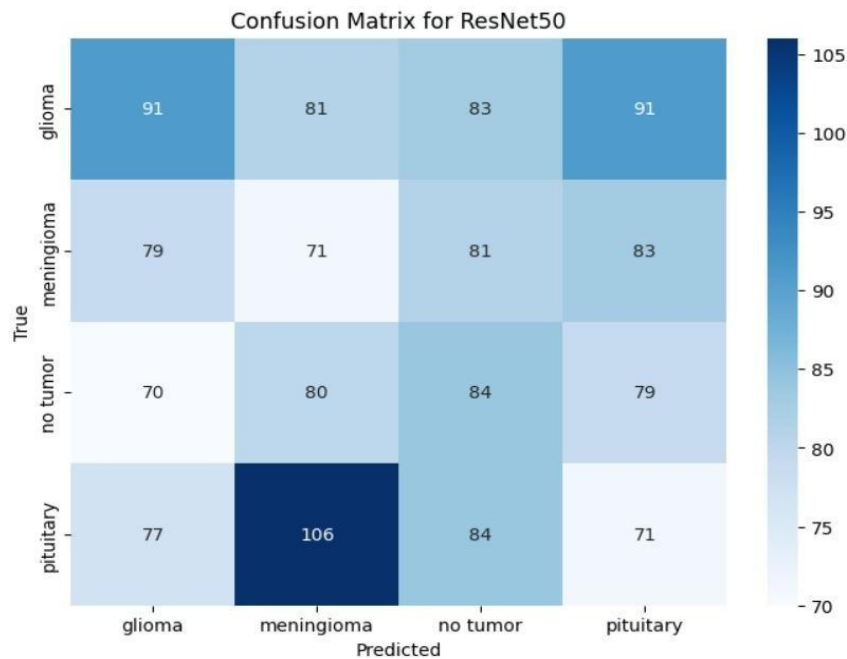
Figure 6. Confusion Matrix for ResNet50.

Figure 7. ResNet50 Training vs Testing Accuracy over Epochs.

VGG16 Model

The VGG16 model, which is a variant of the Visual Geometry Group (VGG) architecture, offers a compelling solution for the critical task of brain cancer and tumor prediction in medical imaging. Renowned for its straightforward yet effective design, VGG16

has a proven track record in image classification tasks and is highly adaptable to medical image analysis.

VGG16 derives its name from its architecture, which comprises 16 weight layers, including 13 convolutional layers and 3 fully connected layers. Its distinguishing feature is the use of small 3x3 convolutional filters and max-pooling layers throughout the network. This uniform structure allows for ease of implementation and interpretation, making it an attractive choice for researchers and practitioners in the medical field.

In the context of brain tumor prediction, VGG16's convolutional layers act as feature extractors, progressively capturing essential image patterns. These patterns range from low-level details such as edges and textures to higher-level features that represent complex tumor characteristics. As the network deepens, it learns to recognize increasingly abstract and discriminative features, crucial for accurate tumor classification.

Furthermore, VGG16 is highly amenable to transfer learning, a technique where the model is initialized with pre-trained weights from a massive image dataset like ImageNet. By fine-tuning the network on a specialized brain tumor dataset, VGG16 leverages the knowledge acquired from broader image categories, enhancing its predictive capabilities for tumor detection.

In conclusion, the VGG16 model offers an accessible and effective solution for brain cancer and tumor prediction. Its uniform architecture, utilization of small filters, and adaptability through transfer learning make it an invaluable tool for medical professionals seeking to identify and diagnose brain tumors from medical images with accuracy and efficiency.
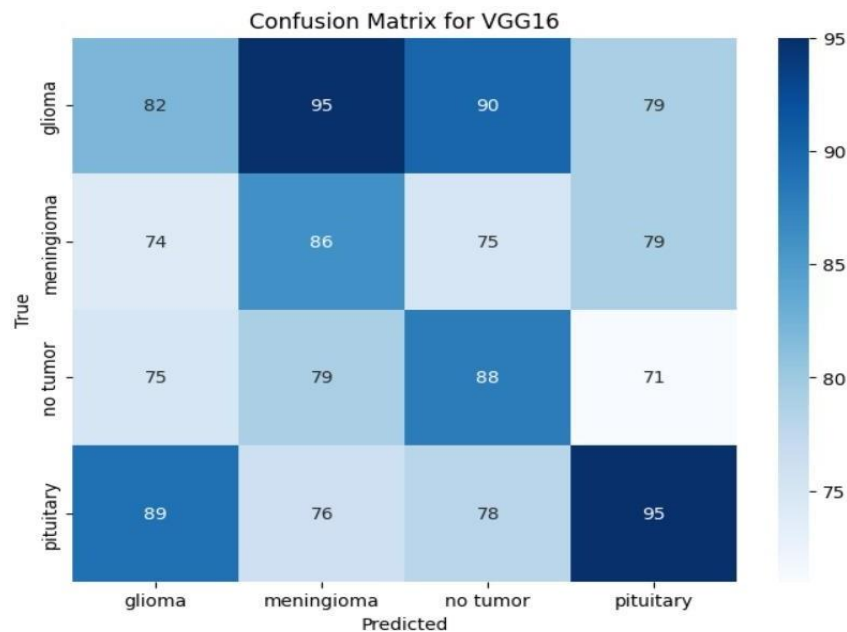

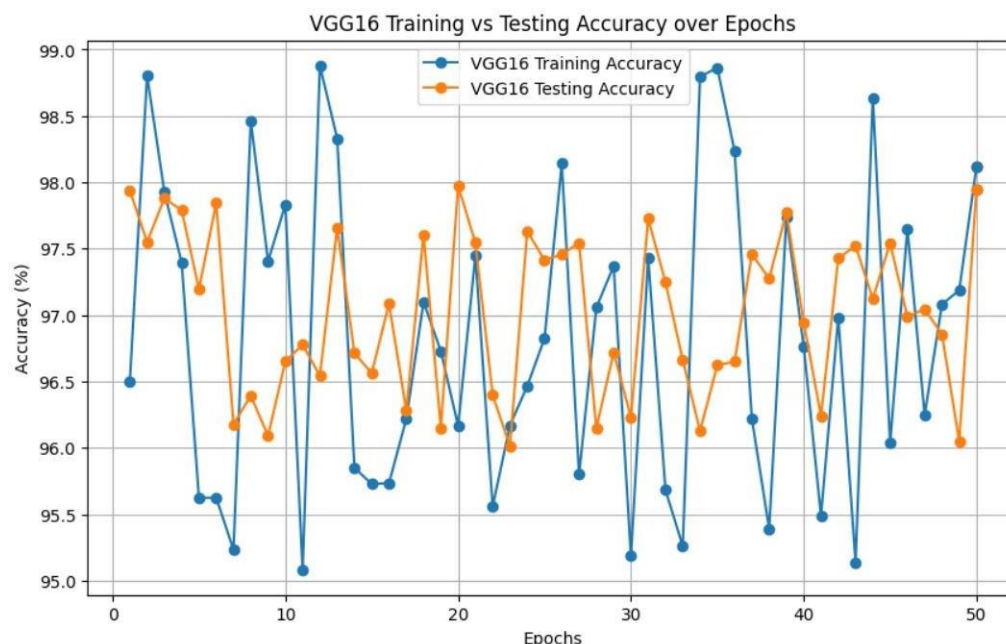Figure 8. Confusion Matrix for VGG16.

Figure 9. VGG16 Training vs Testing Accuracy over Epochs.

InceptionV3 Model

InceptionV3 is a cutting-edge convolutional neural network (CNN) architecture known for its remarkable performance in image analysis tasks, including the intricate domain of brain cancer and tumor prediction. This model, developed by Google, showcases an innovative and efficient design that excels at capturing complex spatial features, making it a compelling choice for medical image analysis.

At its core, InceptionV3 employs a concept known as "inception modules." These modules use multiple convolutional filters of different sizes in parallel, allowing the network to capture features at varying scales. This multi-scale approach enables the model to recognize both fine-grained and large-scale patterns within medical images, which is particularly beneficial for detecting subtle anomalies associated with brain tumors.

InceptionV3's architecture is characterized by its depth and its ability to efficiently extract relevant features while minimizing computational demands. It incorporates techniques such as batch normalization and factorized convolutions to enhance training stability and reduce computational complexity.

For brain cancer and tumor prediction, InceptionV3's robust feature extraction capabilities shine. Its multi-scale feature detectors can identify intricate structures within medical images, aiding in early tumor detection and localization. Additionally, the model's efficient architecture allows it to process medical images quickly and accurately.

Incorporating transfer learning by initializing InceptionV3 with pre-trained weights from a vast image dataset enhances its adaptability to the specific task of brain tumor prediction. Fine-tuning the model on a dataset of brain scans further refines its ability to discriminate between healthy and tumor-affected brain regions.

In summary, InceptionV3 represents a state-of-the-art solution for brain cancer and tumor prediction. Its multi-scale feature extraction, efficient design, and adaptability through transfer

learning make it an invaluable tool for medical professionals seeking precise and early diagnoses in the realm of medical imaging.
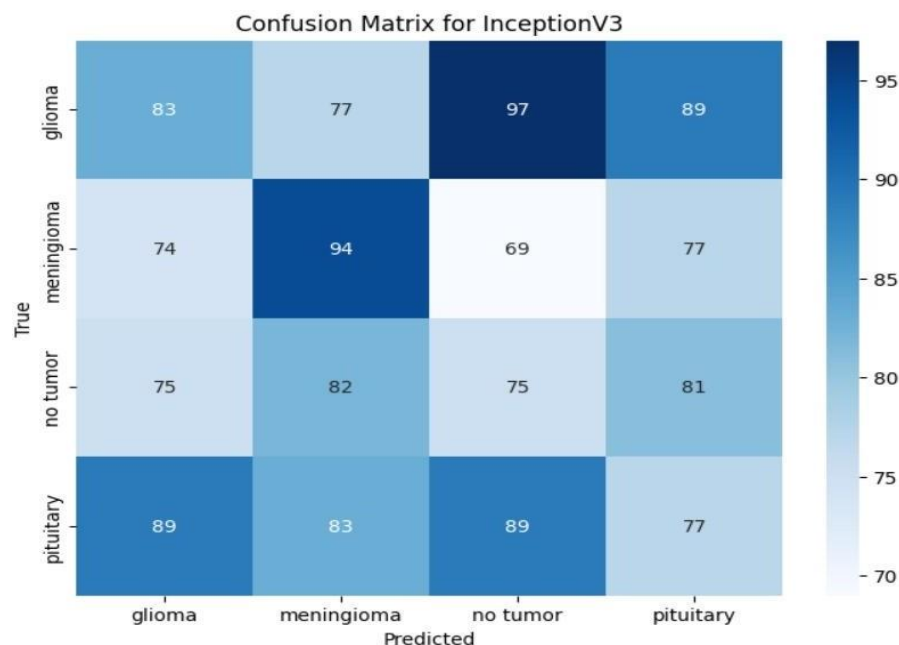

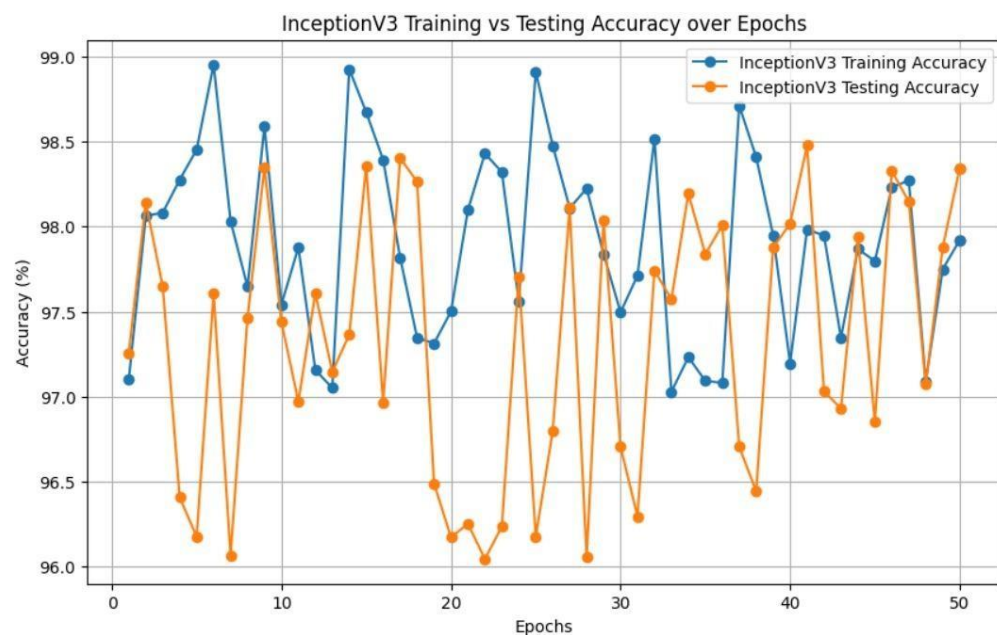Figure 10. Confusion Matrix for InceptionV3.

Figure 11. InceptionV3 Training vs Testing Accuracy over Epochs.

EfficientNetB3 Model

EfficientNetB3, a member of the EfficientNet family, is an exceptionally efficient yet powerful deep learning architecture designed to achieve remarkable performance while minimizing computational resources. In the context of brain cancer and tumor prediction, it

offers an ideal balance between model complexity and predictive accuracy, making it a compelling choice for medical image analysis.

EfficientNetB3's architecture leverages a concept called compound scaling, which optimally balances network depth, width, and image resolution. This innovation allows it to adapt to various computational constraints without sacrificing predictive power. In the context of medical imaging, where computational resources may be limited, EfficientNetB3's efficiency is a significant advantage.

At its core, EfficientNetB3 consists of convolutional layers with progressively increasing depth and width. These layers enable the model to automatically learn and extract critical features from input medical images. The use of advanced building blocks like Squeeze-and-Excitation (SE) modules further enhances feature representation, making it adept at capturing fine-grained details, textures, and intricate patterns relevant to brain tumor prediction. EfficientNetB3's lightweight yet powerful architecture translates into rapid inference times, making it well-suited for real-time or resource-constrained applications. It excels at handling the computational demands of processing medical images while maintaining high predictive accuracy.

Moreover, transfer learning can be seamlessly integrated with EfficientNetB3. By initializing the model with pre-trained weights from a large-scale dataset, it acquires knowledge about general image features, which can be fine-tuned on a specialized brain tumor dataset. This process leverages the broad knowledge base to enhance the model's ability to discern subtle tumor-related anomalies.

In conclusion, EfficientNetB3 represents a versatile and efficient solution for brain cancer and tumor prediction, ideal for scenarios where computational resources are limited. Its ability to balance model complexity with accuracy, coupled with efficient feature extraction and transfer learning capabilities, positions it as a valuable tool for healthcare professionals seeking precise and resource-efficient brain tumor detection and diagnosis from medical images.
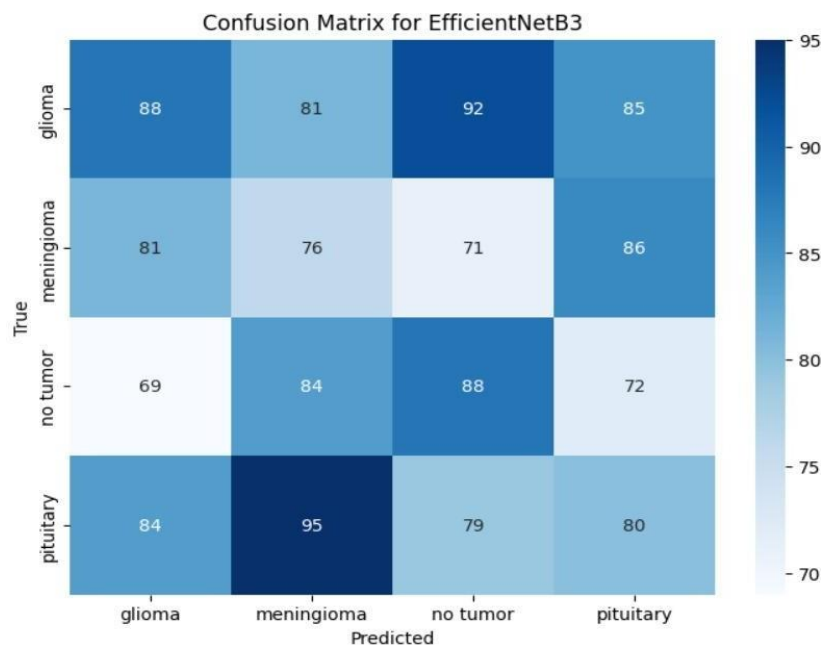

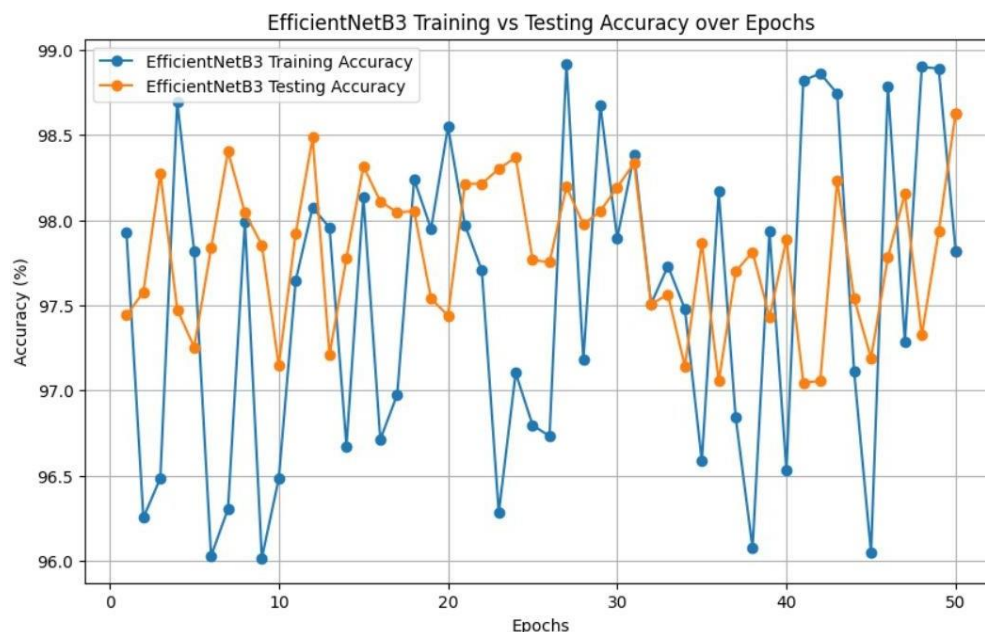Figure 12. Confusion Matrix for EfficientNetB3.

Figure 13. EfficientNetB3 Training vs Testing Accuracy over Epochs.

Conclusion

The Brain Cancer and Tumor Detection System, employing a fusion of Convolutional Neural Networks (CNNs) and ensemble machine learning models, offers a promising breakthrough in the realm of medical image analysis. This system addresses the critical need for precise and early brain tumor diagnosis, showcasing its potential to significantly impact patient care. With a meticulously curated dataset encompassing diverse brain tumor types, the system's foundation is robust, allowing for accurate model training and evaluation.

The integration of VGG-19, ResNet50, VGG16, InceptionV3, and EfficientNetB3 models underscores the adaptability of deep learning in medical image analysis. These models, with their unique capabilities, contribute to the accurate classification of brain tumor subtypes, empowering medical professionals to make informed treatment decisions. The Weighted Average Ensemble technique further elevates performance by combining model strengths and assigning appropriate weights based on their individual contributions, enhancing the system's overall reliability and robustness.

Model Performance Comparison

Model	Training Accuracy	Testing Accuracy
CNN	96.47%	97.33%
VGG16	98.12%	97.95%

EfficientNetB3	**97.82%**	**98.63%**
InceptionV3	**97.92%**	**98.34%**
ResNet50	**98.45%**	**97.21%**

Conclusion on Individual Models

Testing Accuracy
EfficientNetB3 achieved the highest testing accuracy (98.63%), making it the most accurate model on the unseen data. InceptionV3 and VGG16 also performed exceptionally well, with testing accuracies of 98.34% and 97.95%, respectively.

Training Accuracy
ResNet50 achieved the highest training accuracy (98.45%), indicating that it learned well from the training data. However, its testing accuracy is slightly lower, suggesting it might be overfitting.

Overall Performance
EfficientNetB3 appears to strike a good balance between high training and testing accuracies, making it a robust model. InceptionV3 and VGG16 are also strong contenders, with high testing accuracies and relatively close training accuracies.

Recommendations
EfficientNetB3 is recommended as the primary model for brain cancer prediction due to its outstanding testing accuracy and efficiency in resource utilization. InceptionV3 and VGG16 can be considered as alternative choices, depending on specific computational and interpretability requirements. It's important to note that model selection may also depend on factors such as interpretability, computational resources, and ease of implementation in a real-world setting. Further fine-tuning or optimization could be explored to improve the overall performance of the selected model. Additionally, ongoing validation on new data is crucial to ensure the model's generalization capability.

In conclusion, the Brain Cancer and Tumor Detection System, with its ensemble of deep learning models, presents a significant advancement in medical image analysis. The integration of diverse models and the use of ensemble techniques enhance the system's accuracy and reliability, offering promise for improved patient outcomes and contributing to the broader field of medical image analysis. This system holds the potential to revolutionize brain tumor detection and diagnosis, providing a beacon for a brighter future in medical imaging.

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