

DCNN and ResNet50-based Novel AI Framework for Automated Segmentation of Accurate Brain Tumor Diagnosis and Classification using Deep Convolutional Neural Networks

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ABSTRACT

The brain is the most important regulating system of the human body, and the abnormal growth of cells in the brain may result in brain tumors, which can cause serious health and life problems. Timely diagnosis and correct categorization are crucial to plan treatment and enhance prognosis in patients with these tumours. Modern diagnostic methods, including biopsies, imaging such as CT, PET, and MRI, are still very common, but they have drawbacks such as being invasive, subjective, and interpreted differently by different people. In response to these challenges, machine learning (ML) and deep learning (DL) systems for automated tumor detection, classification and segmentation in medical imaging have emerged as

promising solutions. In this review, the authors emphasize recent developments of ML and DL techniques focusing on MRI-based tumor analysis. It compares traditional ML models like Support Vector Machines (SVM), K-Nearest Neighbors (KNN), Random Forest, and Extreme Learning Machines, with the latest DL architectures, such as CNN, ResNet50, a 50-layer deep Convolutional Neural Network (CNN) architecture used for brain tumor detection by analyzing MRI scans to identify tumors with high accuracy, and transformer-based models. The work also covers frequently used datasets, evaluation metrics and segmentation methods, including simple thresholding and clustering, to more sophisticated deep learning frameworks. In addition, it highlights the need for further research and the need for increased attention to 3D modeling and attention mechanisms in enhancing diagnostic accuracy. The results show that deep learning models, especially DCNN-based, outperform traditional ML models in terms of accuracy, efficiency, and clinical reliability, making them suitable for brain tumor diagnosis.

Keywords: Brain Tumor Classification, CNN, Deep Learning, Brain Tumors, Healthcare, Brain Tumor Detection

Introduction:

The human brain is the primary control unit in the human body, which controls various physiological processes and allows humans to adjust to the different environments they live in [1]. It also facilitates vital activities like thinking, communicating, and expressing feelings. The brain is made up of three kinds of tissue: white matter, gray matter, and cerebrospinal fluid. One of the most important traits of the gray matter is the presence of neurons and glial cells that process information and help maintain the proper functioning of the brain. It is important in controlling general brain activity. Myelinated axons, which allow communication between different brain regions by neural pathways, make up white matter. The corpus callosum is one of the most important parts of white matter, providing a bridge between the two hemispheres of the brain, allowing for the synchronized working of the hemispheres [2, 3]. Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0, x)$. $P(i, j) = \max(m, n)$ and $R X(i+m, j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_i x_i + b$ and $\sigma(x) = 1 / (1 + e^{-x})$ whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta (\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ Brain tumors are abnormal and uncontrolled growth of brain cells. This abnormal growth may cause pressure on surrounding tissues, disrupting the normal functions of the brain, due to the rigidity of the skull. In a few instances, tumors can metastasize to other areas of the body, which decreases vital biological functions [4, 5]. The early diagnosis of brain tumors is critical for good treatment planning and survival rates of the patients [6, 7]. As the disease progresses or metastasizes, the chances of successful treatment reduce significantly. Thus, high-quality and available diagnostic tools are essential in saving lives through early detection. There are two broad methods for the diagnosis of brain tumour: invasive and non-invasive. Biopsy methods are invasive techniques, surgical removal of a tissue sample for microscopic analysis by

pathologists, to look for cancer cells. While a biopsy is the most accurate way to diagnose cancer, it also has some drawbacks, including a higher risk for surgical complications and recovery time. Non-invasive techniques such as physical exams and medical imaging are safer and more frequently used. Imaging techniques like Computed Tomography (CT) scan and Magnetic Resonance Imaging (MRI) are not only fast but also accurate in detecting any abnormalities and tracking the course of the disease [8-11]. The fundamental reaction–diffusion formulation is expressed as: $\partial c / \partial t = D \nabla^2 c + \rho c(1 - c/K)$ where the diffusion term controls the migration of tumor cells through healthy tissues and is defined as: $\nabla^2 c = \partial^2 c / \partial x^2 + \partial^2 c / \partial y^2 + \partial^2 c / \partial z^2$. Exponential growth assumes unrestricted cell multiplication: $N(t) = N_0 e^{rt}$ and $N(t) = K / (1 + A e^{-rt})$. The tumor volume and surface area are mathematically represented by: $V = (4/3)\pi r^3$ and $A = 4\pi r^2$. The tumor growth is further calculated through logarithmic progression models: $r = (1/t) \ln(V_t/V_0)$. the Dice Similarity Coefficient (DSC): $DSC = 2|X \cap Y| / (|X| + |Y|)$ and while classification-based approaches the sigmoid activation function used in convolutional neural networks is given by: $\sigma(x) = 1 / (1 + e^{-x})$ and the binary cross-entropy loss function is expressed as: $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ to gradient descent equations: $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$. But the diagnostic interpretations of these scans can differ, depending on the experience and expertise of the radiologist performing the scan, which can impact diagnostic consistency [12]. $S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(i-m,j-n)K(m,n)$ Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0,x)$. $P(i,j) = \max(m,n)$ and $R = X(i+m,j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_i x_i + b$ and $\sigma(x) = 1 / (1 + e^{-x})$ whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$. Finally, the performance of CNN-based tumor segmentation and classification models is evaluated using similarity and accuracy metrics such as the Dice Similarity Coefficient (DSC), given by: $DSC = 2|X \cap Y| / (|X| + |Y|)$ To overcome these disadvantages, Computer-Aided Diagnosis (CAD) has been introduced to assist radiological analysis by providing automated help for diagnosis, and to enhance the reliability and efficiency of diagnosis. Medical imaging is becoming a field of increasing AI applications, such as using machine learning and deep learning for the detection and analysis of brain tumors [13-17]. Image segmentation is one of the key challenges in this area, where the goal is to identify the region of interest to detect abnormalities. Segmentation of MRI data for brain tumor segmentation, however, is difficult because of the presence of image noise, low contrast, blurred boundary, intensity variation and complicated tissues. An accurate identification and classification of tumors, which are frequently irregular in shape and size, thus requires sophisticated computational methods [18, 19].

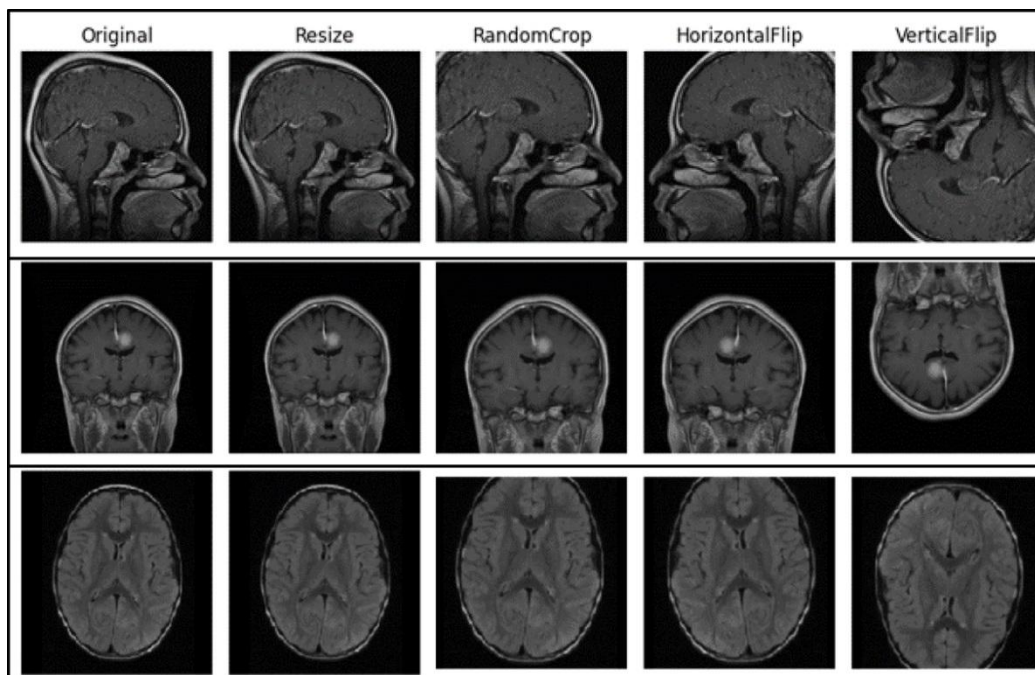


Figure 1.1: Anatomical Structure of the Human Brain MRI images in this figure were obtained from the publicly available Brain Tumor MRI Dataset on Kaggle [20]

Medical imaging has seen the emergence of AI-powered automatic and semi-automatic segmentation tools that are proving increasingly useful. For the purposes of beginning treatment, including surgery, chemotherapy, or radiotherapy, your doctor must first precisely establish the size and location of your tumour. In the field of medical diagnosis, AI algorithms are valuable tools for detecting and segmenting brain tumors, particularly due to their ability to provide a high degree of reliability [21-24]. Brain tumors are growths of brain tissue that are abnormal and growing in an uncontrolled way. The abnormal growth has formed a tumor in the brain and is compressing and disrupting the normal function of the brain. These tumours can be broadly divided into two categories: Benign (non-cancerous) and Malignant (cancerous). Malignant brain tumors can rapidly expand and destroy normal adjacent tissues, and can also invade other parts of the body [25, 26]. Based on their behavior and level of aggressiveness, brain tumors are further categorized into four grades:

- i. Grade 1: These tumors are slow-growing and do not normally spread. They are usually located in an area of good prognosis and often can be completely removed through surgery.
- ii. Grade 2: These tumors grow slowly and can invade surrounding tissues or can become more severe over time. They can be treated, but tend to come back. An example includes oligodendroglioma.
- iii. Grade 3: These tumors are more aggressive than Grade 2 tumors and more likely to spread to the surrounding tissues. It is often not enough to treat the patient with surgery, and other forms of treatment, such as chemotherapy or radiotherapy, may be necessary. For example, anaplastic Astrocytoma is a cancer.

iv. Grade 4: They are the most aggressive and most malignant; they grow quickly and are very invasive and they can penetrate blood vessels and move rapidly. An example is glioblastoma multiform [27-30]. Early detection and proper diagnosis are critical to successful treatment planning and increased survival rates in patients with brain tumors. The detection of brain tumors, however, is a difficult task because of the differences in shape, size, location of the tumor, imaging modalities, and scanning parameters [31, 32]. The fundamental reaction–diffusion formulation is expressed as: $\partial c / \partial t = D \nabla^2 c + \rho c(1 - c/K)$ where the diffusion term controls the migration of tumor cells through healthy tissues and is defined as: $\nabla^2 c = \partial^2 c / \partial x^2 + \partial^2 c / \partial y^2 + \partial^2 c / \partial z^2$. Exponential growth assumes unrestricted cell multiplication: $N(t) = N_0 e^{rt}$ and $N(t) = K / (1 + A e^{-rt})$. The tumor volume and surface area are mathematically represented by: $V = (4/3)\pi r^3$ and $A = 4\pi r^2$. The tumor growth is further calculated through logarithmic progression models: $r = (1/t) \ln(V_t/V_0)$. the Dice Similarity Coefficient (DSC): $DSC = 2|X \cap Y| / (|X| + |Y|)$ and while classification-based approaches the sigmoid activation function used in convolutional neural networks is given by: $\sigma(x) = 1 / (1 + e^{-x})$ and the binary cross-entropy loss function is expressed as: $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ to gradient descent equations: $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$. But the diagnostic interpretations of these scans can differ, depending on the experience and expertise of the radiologist performing the scan, which can impact diagnostic consistency. $S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(i-m,j-n)K(m,n)$ Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0,x)$. $P(i,j) = \max(m,n)$ and $R X(i+m,j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_i x_i + b$ and $\sigma(x) = 1 / (1 + e^{-x})$ whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$. Finally, the performance of CNN-based tumor segmentation and classification models is evaluated using similarity and accuracy metrics such as the Dice Similarity Coefficient (DSC), given by: $DSC = 2|X \cap Y| / (|X| + |Y|)$. To overcome these difficulties, the traditional and advanced intelligent methods have been developed. Traditional methods like Leksell Gamma Knife and radiation therapies help with treatment, but require a high degree of skill and take time to administer [33]. Brain tumor detection can be done using a variety of medical imaging techniques, such as Computed Tomography (CT), Magnetic Resonance Imaging (MRI), and Positron Emission Tomography (PET). Of these, one of the most common is MRI, which employs magnetic fields and radiofrequency pulses to generate detailed images of internal brain structures, and is a non-invasive technique. By using advanced MRI techniques like Chemical Exchange Saturation Transfer (CEST), it is possible to image the low-concentration substances that are not visible in standard MRI or even Magnetic Resonance Spectroscopy [35, 36]. Brain tumor diagnosis typically involves several different types of MR scans, such as Fluid Attenuated Inversion Recovery (FLAIR), T1-weighted, and T2-weighted. But it is still a complex problem to accurately localize areas of tumors in MRI images [37, 38]. Due to the complexity of the data, changes in the MRI are often hard to detect by the human visual system. To overcome this limitation, Computer-Aided Diagnosis (CAD) systems have been developed that aid radiologists and make diagnostic decisions more accurate [39, 40]. Nevertheless, issues like brain necrosis and imaging

ambiguities remain a problem, and there is a need for enhanced machine learning solutions.

Brain Tumor Classification

The human brain consists of 3 main parts: the cerebrum, cerebellum, and brain stem [41, 42]. The second largest structure in the brain, the cerebellum, controls motor activities like balance, posture, walking and overall coordination. Situated at the back of the brain and is in close association with the brain stem. The cerebrum and cerebellum can be divided into an outer cortex of grey matter, a middle layer of white matter and an inner layer of grey matter [43]. The brain stem is located at the bottom of the brain and connects the brain to the spinal cord. It is crucial for regulating important life functions, such as motor control, sensory processing, heart rate, breathing, and reflexes. The brain stem is composed of three distinct parts in terms of structure: midbrain, pons and medulla oblongata [44]. Brain tumors are a mass of abnormal and uncontrolled cells, brain cells [45, 46]. In terms of etiology, they are primary or secondary tumors and in terms of location, they are located in the brain, and in terms of pathological features, they are benign or malignant [47]. Over 120 types of brain tumors have been identified by the World Health Organization (WHO) based on the type of cells from which the tumor originated and the way the tumor behaves. They vary from slow-growing and low-grade to more aggressive. Tumors are graded from I (the least aggressive) up to IV (the most malignant and fastest growing). The type of tumor determines the classification, but grading is especially a reflection of the growth rate and aggressiveness of the tumor [48, 49].

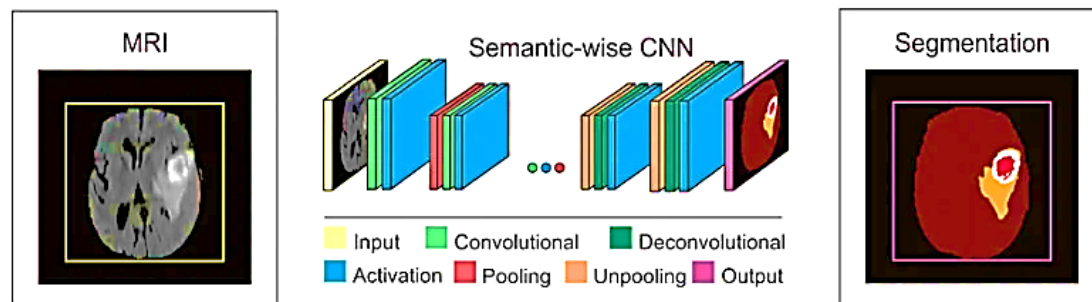


Figure 1.2: Semantic-wise CNN architecture for brain tumor segmentation task [50]

Gliomas are a very prevalent type of brain tumor in adults. There are 2 types of gliomas – S_h low-grade gliomas (LGG) variations at $m_x = \beta_r$, *if* $m_x = \beta_1$ and *if* $m_x = \beta_2$ and high-grade gliomas (HGG) In case $m_x = \beta_g$ and $m_x = \beta_r$ and $m_x = \beta_b$ at $S_h = 60^\circ$. The World Health Organization (WHO) classifies LGGs as Grade I or Grade II and HGGs as Grade III or Grade IV. The right kind of tumor diagnosis is crucial for effective treatment planning and to prevent medical mistakes [51]. Table 1 shows an overview of the different types of brain tumors and summarizes the most common types of brain tumors.

$$S_h = 60^\circ \begin{cases} 0 + \frac{(\beta_g - \beta_b)}{(m_x - m_n)}, & \text{if } m_x = \beta_r \\ 2 + \frac{(\beta_b - \beta_r)}{(m_x - m_n)}, & \text{if } m_x = \beta_g \\ 4 + \frac{(\beta_r - \beta_g)}{(m_x - m_n)}, & \text{if } m_x = \beta_b \end{cases} \quad \text{Eq (1)}$$

Table 1: Brain Tumor Grading and Classification

Tumor Type	Description	Ref
Benign	Less aggressive with slow growth	[52]
Malignant	Extremely dangerous, and grows rapidly and uncontrollably.	[53]
		[54]
Primary Tumor	Appears in the body of the brain itself.	[55]
Secondary Tumor	Begins in some other organ (lungs or breast) and spreads to the brain.	[56]
Grade 1	It is typically well structured with slow development.	[57]
Grade 2	Abnormal cell patterns, but it grows slowly.	[58]
Grade 3	Displays greater proliferation when compared to Grade II tumors.	[59]
Grade 4	Exhibit rapid growth and high malignancy	[60]
Stage 0	Malignant but non-invasive to adjacent cells	[61]
Stage 1–3	Progressive stages of malignancy	[62]
Stage 4	Highly malignant and rapidly spreading, invading surrounding tissues	[63]

Imaging Modalities

Over the years, medical imaging techniques have been extensively used for brain structure abnormalities detection, and they are generally classified into structural and functional modalities [64]. In case $m_x = \beta_g$ and $m_x = \beta_r$ and $m_x = \beta_b$ at $S_h = 60^\circ$

S_s shows the CT, the main applications of structural imaging are for the detection of tumors, injuries, and other neurological disorders [65], while $m_x - m_n$ shows functional imaging that is used to provide a detailed assessment of metabolic processes, lesions, and brain activity.

$$S_s = \left(\frac{m_x - m_n}{m_n} \right) \quad \text{Eq (2)}$$

Some of the common imaging modalities used for the localization of brain tumors are Computed Tomography (CT), Magnetic Resonance Imaging (MRI), Single-Photon Emission Computed Tomography (SPECT), Positron Emission Tomography (PET), functional magnetic resonance imaging (fMRI), and ultrasound (US). These imaging techniques help to define important tumor

features like size, location, and shape [66]. binary cross-entropy loss function is expressed as: $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ to gradient descent equations: $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$. But the diagnostic interpretations of these scans can differ, depending on the experience and expertise of the radiologist performing the scan, which can impact diagnostic consistency. $S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(i-m, j-n) K(m,n)$ Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0, x)$. $P(i,j) = \max(m,n)$ and $R \times X(i+m, j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_i x_i + b$ and $\sigma(x) = 1 / (1 + e^{-x})$ whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$. MRI is the most common method because it does not involve any harmful ionizing radiation and is non-invasive. Rather, it forms high-resolution 3D images of internal body structures using a powerful magnetic field and radiofrequency (RF) pulses [67]. Normally, the protons of water molecules are oriented in a random direction. Without an external magnetic field, they are randomly oriented, but when they are presented with an external magnetic field, they align themselves with that field. When a high-energy RF pulse is applied, this orientation is disrupted temporarily, and the protons change the direction of their spin. When the pulse is switched off, the protons realign themselves and emit RF signals. The signals emitted are captured by the scanner and transformed into detailed images [68, 69].

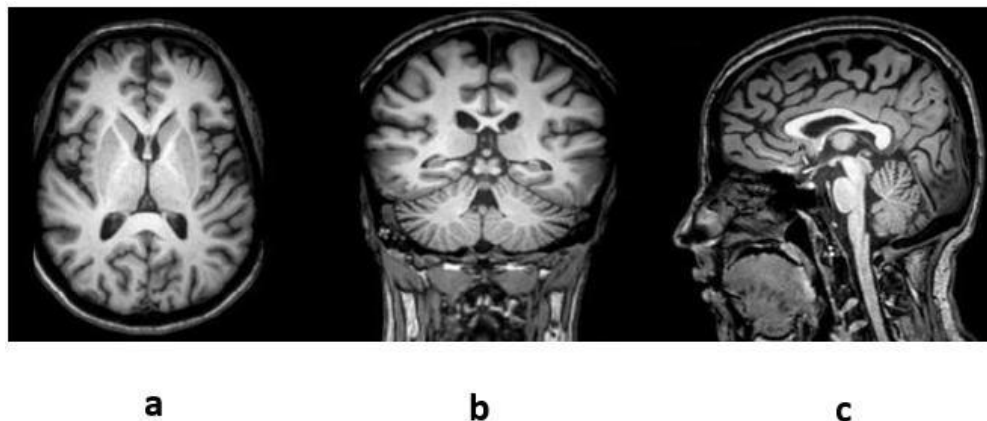


Figure 1.3: Fundamental planes of MRI: (a) Image of axial (b) Image of coronal and (c) Image of sagittal [70]

The variations seen on MRI images are primarily differences in the amount of RF energy absorbed or emitted by the different regions of the brain. For example, white matter (WM) is about 70% water, gray matter (GM) about 80% and cerebrospinal fluid (CSF) nearly 100% water. These variations give different MRI-signals as shown in Figure 1.3. MRI imaging can be done in 3 different planes: coronal, sagittal, and axial. Commonly used sequences for brain imaging are T1-weighted, T2-weighted, and Fluid-Attenuated Inversion

Recovery (FLAIR). For In case $m_x = \beta_g$ and $m_x = \beta_r$ and $m_x = \beta_b$ at $S_h = 70^\circ$ T1 images are useful for determining the difference between gray and white matter, and T2 images will make tumors more visible because water-rich areas show up [71]. FLAIR sequences are more useful for separating pathological abnormalities from cerebrospinal fluid (CSF) [72], [73]. Low to intermediate intensity areas are usually visible in the T1-weighted images, whereas they are visible as brighter areas in the T2-weighted or FLAIR images and will help to detect them [74]. Blood oxygenation can be used to estimate neural activity by using the functional MRI (fMRI) technique, with the potential to map regions that are active through linking blood flow and cognitive function [75, 76]. Computed tomography (CT) imaging, however, requires rotating X-rays and detectors around the body to generate cross-sectional images of the body. They are created with advanced algorithms and provide a unique picture of the bones and tissues; and are often filled with contrast agents to detect abnormalities. Benefits of CT scan include the following: useful when patients cannot have MRI, they are faster imaging modalities, and they have relatively low radiation exposure and increased availability [77, 78]. Brain tumors are one of the top cancer killers in the world. In recent years, radiology and pathological images have increasingly been utilized for processing by computer-aided detection and diagnosis (CAD) systems, which are increasingly using machine learning (ML), deep learning (DL) and computer vision techniques. The purpose of these systems is to assist radiologists in the detection of diseases in different organs, especially in the brain [79, 80]. AI classification and segmentation, such as ML and DL models, have been studied and found to be achieving great results in the automation of tumour detection tasks [81].

Classification Approaches:

Classification is the arrangement of data into categories or groups with similar attributes. Classifier: A predictive model that classifies input data based on the features that it has, using predefined classes [82]. The primary purpose of classification models is to correctly classify data samples into the appropriate groups. Classification is an important task in medical image analysis that is implemented using machine learning and deep learning methods, and there is a difference in the way the features are extracted during this process [83].

$$y = \arg \max \left\{ p(y = C_k) \prod p(x|y = C_k) \right\} \quad \text{Eq (3)}$$

Machine Learning:

Machine Learning is a subset of Artificial Intelligence in which systems learn from data without any explicit programming. It is used in medical imaging for processing and analysis of images for extracting and classifying features of interest. In general, there are two types of machine learning algorithms, namely supervised learning and unsupervised learning [84, 85]. While supervised learning trains models on labelled

data sets, unsupervised learning is concerned with finding hidden patterns and structures in unlabeled data sets. The analysis of brain tumors has been a favorite area of research using ML approaches. The general architecture of a classification pipeline using an ML consists of several components, including image pre-processing, image feature extraction, feature selection and classification [86].

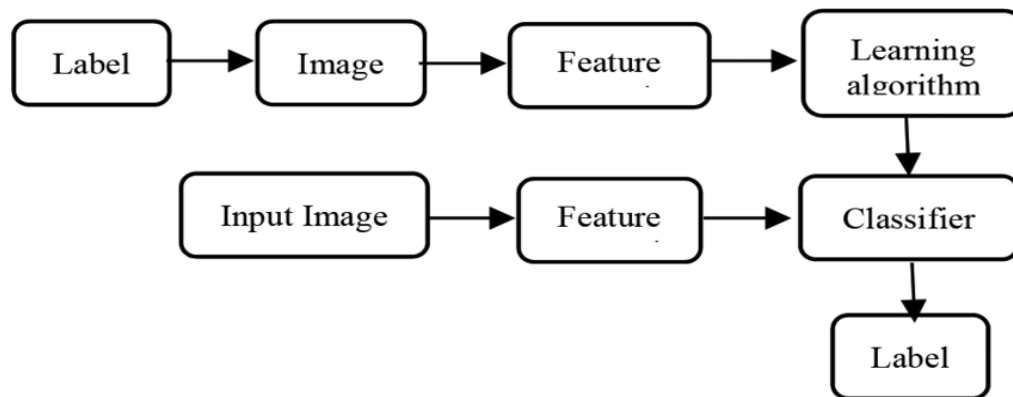


Figure 1.4: ML block diagram.

Medical imaging techniques such as MRI [87], CT [88], and PET scans [89] are the most widely used methods for collecting brain cancer data and play a crucial role in detecting tissue abnormalities within the brain. Before performing analysis, image preprocessing is applied to improve image quality and reduce noise that may affect diagnostic accuracy. Common preprocessing techniques include scaling, cropping, histogram equalization, median filtering, and image enhancement. These methods help improve image clarity while preserving important regions necessary for accurate analysis [90, 91]. binary cross-entropy loss function is expressed as: $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ to gradient descent equations: $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$. But the diagnostic interpretations of these scans can differ, depending on the experience and expertise of the radiologist performing the scan, which can impact diagnostic consistency. $S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(i-m,j-n)K(m,n)$ Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0,x)$. $P(i,j) = \max(m,n)$ and $R \ X(i+m,j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1 \text{ to } n} w_{ixi} + b$ and $\sigma(x) = 1 / (1 + e^{-x})$ whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1 \text{ to } k} e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ Feature extraction is the process of transforming medical images into meaningful feature representations that capture essential characteristics while reducing redundant information [92].

$$p(C_k)p(x|C_k) = p(C_k) \prod_{i=1}^n p(x_i|C_k) \quad \text{Eq (4)}$$

This improves classification performance and minimizes the risk of overfitting. Commonly extracted features include texture, contrast, brightness, shape descriptors, Gray-Level Co-occurrence Matrix (GLCM), Gabor filters, wavelet-based features, 3D Haralick features, and Local Binary Pattern (LBP) histograms [93, 94]. After feature extraction, feature selection is performed to identify the most relevant attributes by

removing irrelevant or redundant information. Frequently used techniques in this stage include Principal Component Analysis (PCA) [95], Genetic Algorithms (GA) [96], and Independent Component Analysis (ICA) [97]. Finally, machine learning algorithms are applied to classify the processed data based on the extracted features. Common supervised learning models include k-Nearest Neighbors (KNN) [98], Artificial Neural Networks (ANN) [99], Random Forest (RF) [100], and Support Vector Machines (SVM) [101]. During training, these models are provided with labeled data, which they use to classify unseen samples. For instance, KNN classifies data based on distance measures such as Euclidean or Manhattan distance, while SVM separates classes by constructing an optimal hyperplane in a multidimensional space [102].

$$p_{\lambda}(C_k) = \frac{\sum_{i=1}^N I(y_i = C_k) + \lambda}{N + K\lambda} \quad \text{Eq (5)}$$

Extreme Learning Machine (ELM)

Extreme Learning Machine (ELM) is a modern machine learning approach that requires lower computational cost compared to traditional neural networks. It is based on a Single-Layer Feedforward Neural Network (SLFNN) [103]. In ELM, the weights between the input and hidden layers are assigned randomly, while the weights between the hidden and output layers are optimized using the Moore–Penrose inverse to achieve a least-squares solution [104]. $S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(i-m,j-n)K(m,n)$ Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0,x)$. $P(i,j) = \max(m,n)$ and $R X(i+m,j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_i x_i + b$ and $\sigma(x) = 1 / (1 + e^{-x})$ whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ This approach enhances classification accuracy while reducing model complexity, training time, and improving learning speed. An ELM network typically consists of three layers, where the connections between the input and hidden layers remain fixed after random initialization, and only the weights between the hidden and output layers are adjusted during the training process [105, 106].

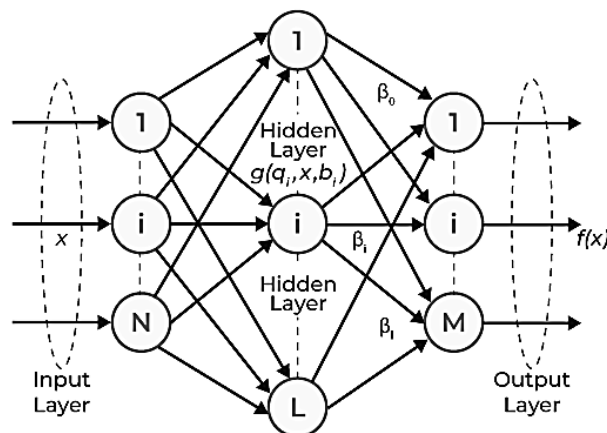


Figure 1.5: Extreme learning machine [107]

Deep Learning (DL)

A branch of machine learning known as deep learning (DL) has recently gained significant attention for developing automated, semi-automated, and hybrid frameworks capable of detecting and segmenting tumors efficiently and cost-effectively. DL models learn relevant features from large and diverse high-quality training datasets [108]. Unlike traditional machine learning approaches, deep learning integrates both feature extraction and feature selection within the training process, resulting in improved performance. Inspired by biological neural networks, DL architectures are structured in multiple layers, where each layer processes weighted outputs from the previous layer. This layered structure enables DL models to capture complex patterns and relationships with reduced reliance on manual feature engineering [109-111]. Convolutional Neural Networks (CNNs) are among the most widely used deep learning models for image classification and segmentation tasks. CNNs learn hierarchical feature representations by applying convolution operations using learned filters, which generate feature maps and help analyze spatial relationships between pixels. Binary cross-entropy loss function is expressed as: $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ to gradient descent equations: $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$. But the diagnostic interpretations of these scans can differ, depending on the experience and expertise of the radiologist performing the scan, which can impact diagnostic consistency. $S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(i-m,j-n)K(m,n)$ Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0,x)$. $P(i,j) = \max(m,n)$ and R $X(i+m,j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_i x_i + b$ and $\sigma(x) = 1 / (1 + e^{-x})$, whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ [112, 113]. These convolutional layers provide robustness against translation and distortion, thereby improving classification accuracy. Before training, preprocessing steps such as image resizing and normalization are applied to ensure that input images meet the fixed-size requirements of CNNs. Additionally, data augmentation techniques are commonly used to overcome issues related to limited and imbalanced datasets [114, 115].

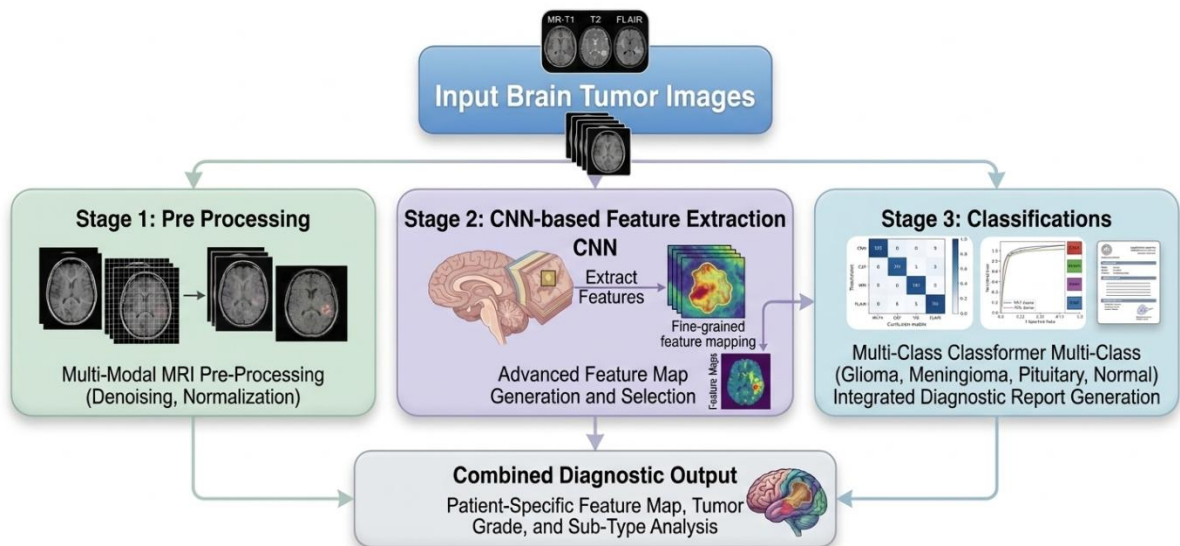


Figure 1.6: DL block diagram.

Literature Review

Initially, in medical images, simple image processing techniques such as thresholding and edge detection were used to detect brain tumors. Though these methods were the basis, they had severe problems with determining the complex boundaries of tumors correctly. These conventional methods were not so dependable due to the complex structure of the brain and the differences in the form and size of tumors [116, 117]. The emphasis moved to traditional machine learning algorithms as research progressed, such as Support Vector Machines (SVM) and Random Forests. These models obtained good results on labelled datasets in some cases. Nevertheless, they were not robust enough to deal with varying tumor morphologies and various image qualities, thus restricting their generalization capacity [118, 119]. Deep learning techniques, in particular Convolutional Neural Networks (CNNs), have become the breakthrough that has greatly advanced medical image analysis. Enhanced efficiency and accuracy have been achieved by using models like VGG, ResNet, and Inception to extract the hierarchical features in an automatic way. Nonetheless, difficulties remained particularly in managing the noise the Magnetic Resonance Imaging (MRI) scans emitted and being able to accommodate the differences between the different MRI machines and scanning guidelines [120, 121]. The efficiency of efficient Net made it an impressive solution and it was also scalable. The efficient Net proved efficient with many different datasets, and it was able to find subtle aspects in medical images by using depth, width and resolution scaling. It was highly adaptable and hence it was well-suited for use in brain tumour detection [122].

$$p_{\lambda}(x_1 = a_j | y = C_k) = \frac{\sum_{i=1}^N I(x_1 = a_j, y_i = C_k) + \lambda}{\sum_{i=1}^N I(y_i = C_k) + A\lambda} \quad \text{Eq (6)}$$

$$y_j = f \left(\sum_{i=1}^n w_{ji} x_i - \theta_j \right) \quad \text{Eq (7)}$$

This work gives special attention to the model based on the EfficientNetB2 variant, which was selected because it is able to capture complex features and improve diagnostic accuracy in general. The existing limitations in the strength, accuracy and generalizability of previous approaches will be addressed through the use of EfficientNetB2. $S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(i-m,j-n)K(m,n)$ Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0,x)$. $P(i,j) = \max(m,n)$ and $R = X(i+m,j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_i x_i + b$ and $\sigma(x) = 1 / (1 + e^{-x})$, whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ [123, 124].

$$f_t = \sigma(W_f \cdot [h_{(t-1)}, x_t] + b_f)$$

Eq (8)

Despite the success of the wide application of Efficient Net in medical imaging, its performance in the detection of brain tumors in MRI scanning is not fully explored. Hence, the research is valuable by combining EfficientNetB2 with other advanced data augmentation and preprocessing techniques to create a more efficient detection system. The methodology attempts to rectify some of the drawbacks of the above-mentioned methodologies and move on to a more valid diagnostic model [125, 126].

Classification of Machine Learning for Brain Tumors:

In this part, we discuss the use of different machine learning methods in the analysis and classification of brain tumors. The various types of ML approaches, including the more common algorithms used in tumour classification, are included in the discussion. With the improvement in diagnostic imaging, the development of these methods is now needed, as it has greatly enhanced the diagnostic accuracy and will help in the therapeutic decision-making [127, 128]. Further, this section explores the feature extraction and selection methods and their use of different ML models to get an accurate classification of tumour based on the imaging data. Based on this extensive survey, we want to pinpoint strengths, weaknesses, opportunities, and threats (SWOT) of the application of machine learning-based brain tumor classification. A Multiclass Tumor Analysis of High-Grade Malignant Brain Tumors [129, 130]. A Computer-Aided Diagnosis (CAD) system was developed for the classification of those high-grade malignant brain tumors into different classes. The proposed feature selection plan was capable of distinguishing five types of malignant brain tumors with a wide variety of features extracted from these features in six domains; this has maximized the information of the given dataset. In order to make it possible to select the features in an appropriate way, a new method was adopted, which is CVM [131, 132]. Three multiclass classifiers were trained and tested in

terms of their accuracy in multiclass classification based on the features chosen. Experimental performance was improved with the proposed approach, which yielded approximately 2, 3 and 4 per cent improved results with KNN, mSVM and NN, respectively. The accuracy of the Neural Network classifier was the highest (95%) and also supported the effectiveness of the proposed methodology for the classification of Malignant brain tumors [133]. The second CADx system was suggested to stage stomach diseases, including gastric cancer, gastritis and gastric ulcers [134]. Combined with image augmentation techniques such as Xception CNNs (including depthwise separable convolutions), this work has overcome the lack of medical data. Class Activation Maps were applied to highlight the regions of interest in CNNs to resolve the poor feature visualization problem and the lesion areas of the abnormal images were added to the normal image to augment the dataset [135, 136]. This enhanced CNN training, along with the outcome of the training, was compared based on confusion matrices and performance metrics such as specificity, sensitivity, F1-score, and AUC. These results were found to be very effective for the augmentation of the dataset as well as in the performance of the classification as a whole with the aid of CAM techniques [137, 138]. A hybrid machine learning framework was proposed in [139], which fused feature extraction based on a MAP-Firefly Optimization Algorithm with intensity, shape-based, and texture-based features. The proposed method performed with 99.2% accuracy in the brain stroke detection and 88.3% accuracy in the brain tumor classification [140]. The system could recognize three different tumour areas and classify MRI image data of stroke and tumour into four classes. The best of the evaluated models is the Hybrid Support Vector based Random Forest Classifier (HSVFC) [141], which gives an accuracy of 0.91 with a false positive rate of 0.06 for brain tumor classification and an accuracy of 0.99 with a false positive rate of 0.0 for brain stroke classification. Moreover, HSVFC produced better mean classification accuracy than several other available models like ResNet-18 [142], SVM [143], Decision Classifier (DC) [144], KNN [145] and FFNN [146] for brain tumors (76.55%) and brain strokes (98.17%) binary cross-entropy loss function is expressed as: $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ to gradient descent equations: $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$. But the diagnostic interpretations of these scans can differ, depending on the experience and expertise of the radiologist performing the scan, which can impact diagnostic consistency. $S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(i-m,j-n)K(m,n)$ Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0,x)$. $P(i,j) = \max(m,n)$ and $R \ X(i+m,j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_i x_i + b$ and $\sigma(x) = 1 / (1 + e^{-x})$ whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$. The combination of hyperspectral imaging and the Firefly Algorithm was used in another study to improve tumour localization by optimizing the clustering process. A focus of the research was the need for detailed descriptions of the data sets, benchmarking with other localization methods, evaluation of these data sets on multiple methods, and the correct interpretation of the results. The accuracy of the proposed method was 96.47%, the sensitivity was 96.32%, and the specificity was 98.24%, which is better than the reported methods [147, 148]. Rectified Linear Unit

(ReLU), expressed as: $f(x) = \max(0, x)$. $P(i, j) = \max(m, n)$ and $R X(i+m, j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_{ixi} + b$ and $\sigma(x) = 1 / (1 + e^{-x})$ whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$. Likewise, in [149], a Brain Tumor Classification (BTc) framework was introduced based on pre-trained deep neural networks and MRI images. The framework chose the three best learned features, which were used to create an ensemble model and tested by applying some machine learning classifiers. The study was conducted using three publicly available brain MRI datasets and promising performance improvement was reported, but there are some limitations. These included a lack of comparison with medical imaging-specific specialized deep learning models, poor descriptions of the datasets, and poor interpretability and explainability of the ensemble framework. Furthermore, there were no detailed performance metrics and a full comparative study, which limits the overall assessment of the proposed methodology [150, 151].

Deep Convolutional Neural Networks DCNNs for brain Tumor

The focus of this section is to discuss the use of Convolutional Neural Networks (CNNs) in brain tumor analysis. It addresses various architectures and techniques used in CNN and their application in brain tumour classification, their development in the medical field and significance in the improvement of the diagnostic and therapeutic process. In CNNs, special emphasis is paid to the feature extraction and feature selection processes, and the role of different CNN models in the correct classification of medical imaging data of brain tumors. Besides, the pros and cons of CNN-based brain tumor classification systems are summarized and future research directions are provided in this review [152]. To overcome the problem of limited labeled datasets, the study proposed a novel method for brain MRI classification using unlabeled data for feature learning, thereby learning meaningful features without manual annotations. The framework proposed in this work was based on self-supervised learning; thus, the data augmentation method and model training approach were used to extract features and, for the supervised classification tasks, a pre-trained classifier was used as an encoder. The study also examined the effect of contrastive loss-based pretraining, data diversity and augmentation techniques on classification accuracy. The study did have some drawbacks, however, such as a lack of detail in the unlabeled dataset, the lack of discussion about augmentation strategies, the pre-training settings, and hyperparameter optimization. Experimental results showed that the contrastive loss-based pre-training not only outperforms random initialization and ImageNet-based pre-training, but also revealed that the diversity and augmentation methods of the datasets affect the classification performance significantly [153]. Multi-modal MRI data with missing modalities were used for brain tumor segmentation. The Dual Disentanglement Network combined both modality-specific information and tumor-specific information via its MD-Stage and TD-Stage modules, respectively. The method performed better on BRATS 2018 than existing methods, especially when the modalities were missing. These encouraging findings were accompanied by a lack of detailed ablation analyses, extensive comparisons with

state-of-the-art methods, and analyses under different degrees of missing data. However, it was found that the framework was reliable and effective for segmentation tasks, and was able to capture correlations between imaging modalities and tumor regions with the help of affinity-guided dense tumor-region information [154]. Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0, x)$. $P(i, j) = \max(m, n)$ and $R X(i+m, j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_{ixi} + b$ and $\sigma(x) = 1 / (1 + e^{-x})$ whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ In various studies presented in [155] three BRATS datasets were used to test a TD-CNN-LSTM network through the k-fold cross-validation approach to check the generalization capability of the tested model. The experimental results showed that the TD-CNN-LSTM model could achieve an accuracy of 98.90% on the test set, which was higher than the baseline model, the 3D-CNN model. $S(i, j) = (I * K)(i, j) = \sum_m \sum_n I(i-m, j-n)K(m, n)$ Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0, x)$. $P(i, j) = \max(m, n)$ and $R X(i+m, j+n)$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_{ixi} + b$ and $\sigma(x) = 1 / (1 + e^{-x})$, whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$ There were no comparisons made to other advanced deep learning architectures, and no analysis of the effect of alternative network designs and hyperparameter variations. Overall, the results demonstrated the ability of the TD-CNN-LSTM model to handle all four MRI images of the brain tumor simultaneously, with excellent potential for clinical applications, despite these limitations. The authors in [156] identified various deep learning architectures based on transfer learning, such as Inception ResNetV2, Xception, InceptionV3, ResNet50, and DenseNet201, to detect brain tumors. The study was aimed at finding the optimal configuration to detect tumors at an early stage by combining the performance of seven deep learning models with traditional machine learning classifiers. In [157], the authors used a fine-tuned DenseNet201 model to tackle imbalanced datasets, using deep transfer learning. Average pooling layer features were extracted and two feature selection techniques, such as EKbHFV and MGA were tested. The framework achieved over 95% accuracy on both the BRATS2018 and BRATS2019 datasets, but the study did not provide enough details about the properties and preprocessing of the datasets and the experimental configurations. Further studies were suggested to be carried out to assess the discriminative power of the feature selectors, explore the effect of changing the threshold and hyperparameters, and assess the robustness of the model in case of external datasets. The study, however, had shown that the proposed method was more efficient and effective for multi-class brain tumour classification than some of the neural network models used previously. Uncontrolled growth of tumour cells is one of the critical indicators of tumour disease and machine learning techniques were discussed for brain tumour identification in [158].

Table 2. Comparative analysis of different methods with a discussion on the advantages and disadvantages of Machine Learning, CNN, and Transformer-based Techniques [159].

Approach	Main Contributions	Advantages	Disadvantages
CNNs	Suggested a Dual Disentanglement Network to segment brain tumors from multi-modal MRI data	Delivered more precise and dependable segmentation outputs	Absence of comparative results with other approaches
Machine Learning	Proposed a new framework for multi- class categorization of malignant brain tumors	Provided high recognition rates, reaching up to 95.86%	Dependent on manually crafted features
CNNs	Explored deep transfer learning approaches for detecting brain tumors in 2D MRI images	Achieved superior accuracy and F1 performance compared to prior models	Missing thorough details about dataset specifications
Machine Learning	Hybrid system combining techniques for MRI-based detection of brain anomalies	Showed reliable classification for both tumors and strokes	Needs more comparative studies with other frameworks
CNNs	Introduced Time Distributed CNN- LSTM hybrid approach using 3D MRI data	Attained classification accuracy as high as 98.90%	Limited comparative analysis with advanced deep learning approaches
Machine Learning	Improved CADx system for gastric disorder recognition using image augmentation	Demonstrated enhanced AUC and F1-score performance	Dataset information was insufficient
Machine Learning	Enhanced clustering optimization for localizing tumors in brain scans with hyperspectral imaging	Achieved better specificity and higher accuracy	Tested on limited datasets without diverse evaluation
CNNs	Implemented self-supervised pretraining with contrastive loss for MRI classification	Reached validation and test accuracies beyond 97%	Not thoroughly compared with already established Techniques

Rectified Linear Unit (ReLU), expressed as: $f(x) = \max(0, x)$. $P(i, j) = \max(m, n)$ and $R_{X(i+m, j+n)}$ where R represents the pooling region over the extracted feature map. $z = \sum_{i=1}^n w_{xi} + b$ and $\sigma(x) = 1 / (1 + e^{-x})$ whereas multi-class tumor classification problems utilize the Softmax function: $P(y_i) = e^{z_i} / \sum_{j=1}^k e^{z_j}$. The CNN model parameters are optimized using gradient descent and backpropagation $w_{t+1} = w_t - \eta(\partial L / \partial w_t)$ and $L = -\sum [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$. The study evaluated the literature on previous studies of tumor classification based on ML and carried out experiments on the architecture ResNet5.0, along with transfer learning. While the paper did not explicitly state that it was identifying a particular gap in the research, the proposed model successfully classified meningioma, pituitary tumors and glioma with a precision of 96%. Furthermore, the model achieved superior performance compared with six other machine learning methods on the same data set, which helps to verify its performance in the tumor grading task.

Brain Tumor Segmentation Using MRI (Mathematical Morphology)

Machine learning, deep learning, thresholding, region growing and fuzzy logic techniques are discussed in the following section in the context of brain tumor segmentation. Many studies and applications have been targeted at brain tumor segmentation using fuzzy logic and clustering methods, both supervised and unsupervised. Fuzzy c-means clustering and region-based segmentation techniques were used to accurately identify the boundaries of the tumor in several methods. Furthermore, classifiers like Support Vector Machines (SVMs) were employed for the classification of tumor pixels using some features like mean intensity values and texture descriptors extracted [160]. Several other proposed methods involved introducing contrast enhancement, dimension reduction and Random Forest classifiers using frameworks to enhance segmentation accuracy. A hybrid clustering method based on K-means and fuzzy c-means was also developed to improve the performance of the tumor boundary detection and to suppress the image noise, thereby improving the segmentation performance [161]. MRI-based brain tumor segmentation has been extensively used with Convolutional Neural Networks (CNNs).

Most CNN-based methods use small convolutional kernel sizes to maintain the fine spatial detail and avoid overfitting. Moreover, segmentation and feature extraction of the image using gray-level intensity and texture properties show promising results with high Dice Similarity Coefficient (DSC) scores. To effectively capture local and global contextual information, more advanced deep-learning architectures such as two-pathway CNNs, multiscale residual attention networks, and hybrid CNN-SVM architectures have been used. Recent developments in 3D MRI data processing, transfer learning, and normalization methods have also improved the accuracy, stability, and reliability of these brain tumor segmentation systems [162].

Method and Materials

Automated brain tumor classification in MRI images using machine learning techniques has been a subject of many studies. Typically, the standard workflow consists of: pre-processing, feature extraction, feature selection, and classification.

In order to distinguish between normal and abnormal brain images, features extracted using the wavelet transform (WT) have been proposed and reduced using Principal

Component Analysis (PCA) and subsequently fed to a neural network. Ensemble classifiers consisting of different classifiers such as SVM, Artificial Neural Networks (ANN) and k-Nearest Neighbors (kNN) can achieve high accuracy in distinguishing between benign and malignant tumors by analyzing texture, shape and boundary-related features. Other methods, such as Wavelet Energy features and Biogeography-Based Optimization (BBO), are also used to improve the performance of the SVM classifiers. The other researchers combined segmentation, texture feature extraction and SVM-based classification to achieve high sensitivity and specificity in different datasets. Artificial Neural Networks (ANNs) and PCA have been widely used for multiclass brain tumor classification tasks and hybrid kernel-based SVM models with texture descriptors like Gray-Level Co-occurrence Matrices (GLCMs) have been proven to increase the accuracy of classification. Furthermore, the hybrid systems that integrated more than one ML method, such as ANN and KNN, showed good performance in both the binary and multiclass tumor detection applications.

Use of deep learning for the classification of brain tumors on MRI.

While some traditional machine learning techniques have resulted in satisfactory classification accuracy, deep learning techniques have made a great contribution to brain tumor classification by significantly overcoming the need for manual feature extraction. In the field of tumour classification and grading, Convolutional Neural Networks (CNNs) have demonstrated outstanding results among these methods. Deep CNN architectures have proven to be effective for the task of glioma severity classification and grading with high accuracy rates. There have also been several CNN-based models created for categorizing MRI scans into tumor types, like glioma, meningioma, and pituitary tumors. Furthermore, transfer learning has been used with pre-trained models like VGG-16, ResNet and Inception-v3, which further enhance the performance, especially on smaller datasets. Deep CNN models, tailored to specific datasets, along with data augmentation and cross-validation techniques, have proven to achieve higher accuracy, sensitivity and specificity in comparison to several pre-trained deep CNN models. A few studies also incorporated active learning and Bayesian optimization methods to enhance the CNN training efficiency and the robustness of the model. Transfer learning and fine-tuned CNN architectures such as AlexNet, GoogleNet and EfficientNet have also been used to accurately classify tumor grade and subtypes. These models saw high validation accuracy and good generalization ability, using pre-trained weights and MRI datasets. Multiclass classification has also been proposed using hybrid CNN approaches like Gaussian-CNNs and separable convolution-based models to achieve efficient classification. When comparing the architectures, fine-tuned architectures (VGG16 and AlexNet) have been seen to perform exceptionally well in datasets based on MRI, with classification accuracies of more than 98%. In recent years, the optimization-based CNN model and hybrid deep residual network trained by an evolutionary algorithm have been introduced and demonstrated to improve the performance of segmentation and classification on benchmark datasets.

Hybrid Techniques

Hybrid methods involve using several algorithms and methods together to achieve

high accuracy and reduce the constraints of any single method. Usually, these systems start with the segmentation to identify tumor regions and then classify them using machine learning/Deep learning models. In the brain tumor detection and multiclass classification tasks, several hybrid techniques performing the combination of fuzzy c-means segmentation, SVM and ANN classifiers with high accuracy are performed. Likewise, Artificial Neural Network-based hybrid segmentation/classification systems achieved an accuracy of over 98%. Conventional image processing methods (image enhancement, morphological processing, thresholding) together with classifiers (kNN) have also yielded good results. Moreover, SVM classifiers combined with Discrete Wavelet Transform (DWT) features are shown to enhance the classification of benign and malignant tumors. The multilevel segmentation methods with CNN-based feature extraction and SVM classifiers have been proven to be effective in the detection of cancer and non-cancer tissues. The clustering approaches like fuzzy c-means, DWT, PCA, and deep neural clusters have been used in other hybrid combinations and have achieved near-perfect accuracy in multiclass classification. Furthermore, hybrid deep learning systems that combine optimization algorithms, like CNN deep networks trained with modified metaheuristic optimization algorithms, have shown classification and segmentation accuracy over 98%, which is very effective for analyzing brain tumors at a higher level.

Problem Statement

Magnetic Resonance Imaging (MRI) detection and diagnosis of brain tumors can be a complex, lengthy and time-consuming procedure. Normally, doctors review MRI images by hand to detect tumors, but this can lead to diagnosis errors and inconsistencies. This underscores the need for automated and reliable image analysis systems that can help healthcare professionals to accurately detect brain tumors. Typically, an automated brain tumor detection process comprises a number of stages, such as: Acquisition of raw MRI data or pre-processed MRI data, and the use of the pre-processing techniques to enhance the quality of the image and minimize the bias, Analysis of MRI images for the identification of regions containing tumors. Clinical examination and validation of tumor areas by visualization. Many computer-aided systems have been suggested to detect tumors, but only a few of these systems have been applied and tested in real clinical scenarios. The primary reason is that image noise, lack of contrast, superposition of gray and white matter areas, differences in MRI machines and the reliance on expert interpretation make the task difficult. These restrictions highlight the critical requirement for an accurate, robust and standardized method to detect and diagnose brain tumors from MRI scans.

Proposed Technique

This research proposes a conceptual taxonomy, called Data, Image Segmentation Processing, and View (DIV). The DIV framework is the three key elements needed for building an advanced deep learning-based brain tumor diagnostic system. The study also points to the fact that, although there are various methods of segmentation, few models have been fully validated and standardized. So, a systematic framework is needed to enhance the reliability, accuracy and comparability of medical image segmentation systems based on deep learning methods. Early and precise

identification of a brain tumor is one of the major challenges in neuro-oncology. The most commonly used imaging technique for the diagnosis of tumors is MRI, which often requires a lot of effort and a high degree of expertise. Besides, MRI scans can be interpreted differently by various radiologists. Brain tumors are especially hard to detect because they can have poorly defined margins, look like normal brain tissue and have various shapes, sizes and forms. The present computer-aided diagnostic systems have enhanced the detection of tumors, but there are still many limitations. Manual feature extraction, binary tumor detection, incompatibility with different MRI modalities, and lack of explainable decision-making processes are a few of the limitations of several systems. To solve these problems, a hybrid deep learning model based on ResNet50-based Deep Convolutional Neural Networks (DCNNs) and Vision Transformers (ViTs) is proposed here. The purpose of the proposed model is to enhance brain tumor detection, segmentation and classification in MRI images. Furthermore, the framework can automatically learn discriminative features and generate more interpretable decision-making processes, which enhances the trustworthiness and reliability of the framework for clinical applications.

Data Collection and Data Analysis.

In this section, the proposed research methodology for fine-grained brain tumor (BT) classification is presented. The method is essentially in two steps. The first is a description of the research data set employed for fine-grained brain tumor classification. Second, it describes the proposed deep learning-based framework and its architecture for detecting and classifying MRI images into three categories: meningioma, glioma and pituitary tumor. The dataset used for this classification task was the one employed in the previous study. The dataset employed in this classification task was the same as in the previous study. This section discusses the methodology used for the preparation and preprocessing of the dataset used for the fine-grained brain tumor classification. The proposed structure is to use the MRI data sets and deep learning methods to classify the meningioma, glioma and pituitary tumors accurately.

Dataset and Preprocessing

The data set used in this study was a publicly available data set of Contrast-Enhanced MRI (CE-MRI) [121]. MRI data were obtained from 233 patients with brain tumors during five years (2005-2010) at the Nanfang Hospital and General Hospital of Tianjin Medical University. In total, this dataset consists of 3062 magnetic resonance imaging (MRI) images of three brain tumor types (1426 images of gliomas, 708 images of meningiomas and 930 images of pituitary tumors) taken from three imaging views. Further description of the data is presented in Figure 3.1 and Table 6. The images obtained from the MRI are displayed as 2D volumes with a resolution of 512 x 512 pixels and a pixel spacing of 0.49 x 0.49 mm². In addition, the tumor areas in the MRI scans were manually segmented by three experienced radiologists [121]. It is available on Figshare, stored as a .mat file and has been kept with the original image resolution of 512 x 512 pixels. The suggested deep learning framework was designed to have an input image size of 224 x 224 pixels. So, the pre-processing steps were applied to make the dataset compatible with the proposed architecture. First, the MRI

images were converted into commonly used image formats, including .jpg and then the resizing operations were performed in MATLAB. The images were resized based on the deep learning model and the pre-trained architectures proposed. In particular, the image from MRI was scaled to the size of 224×224 pixels and DarkNet19-based images were resized to 256×256 pixels. The data was subsequently split into training and testing sets, in a 70:30 ratio. The experimental evaluation was performed on all 3064 MRI images. These consisted of 2146 images (495 meningioma images, 652 pituitary tumor images, and 999 glioma images) for training. Then there were 213 meningioma images, 278 pituitary tumor images and 428 glioma images that were reserved for testing.

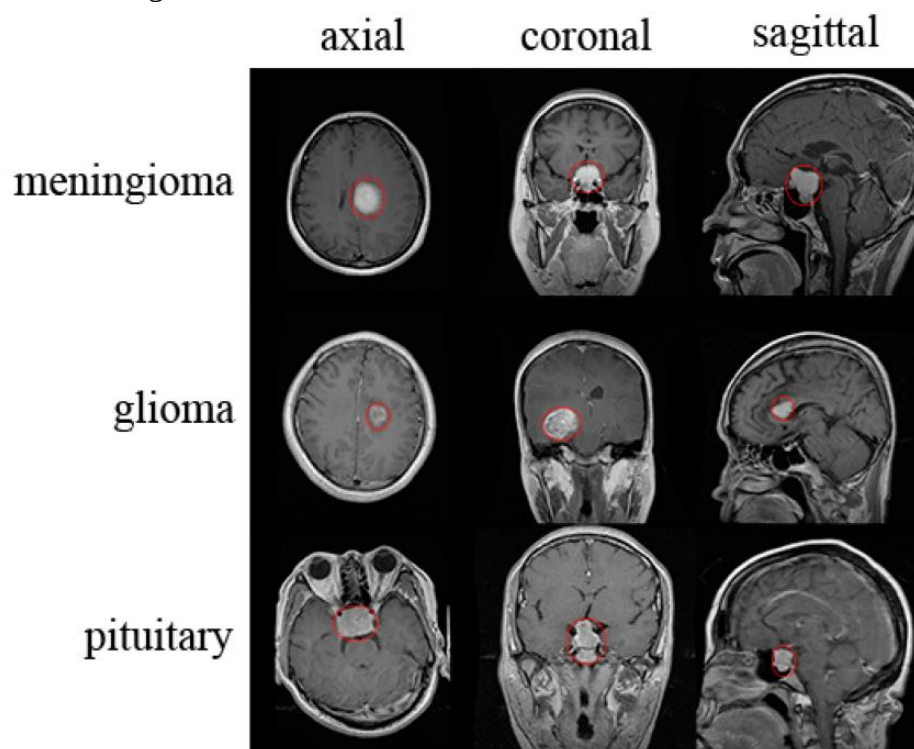


Figure 3.1. Three different tumors (meningioma, glioma, and pituitary tumor) in three different views.

Table 3. Explanation of CE-MRI dataset.

Tumor Class	Patients	Images	View of MRI.	No. of MRI. Images
Meningioma	82	708	A *	209

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			C *	268
			S *	231
			A *	291
Pituitary	62	930	C *	319
			S *	320
Glioma	89	1426	A *	494
			C *	437
			S *	495
Total	233	3064		3064

* Axial = A, * Coronal = C, and * Sagittal = S.

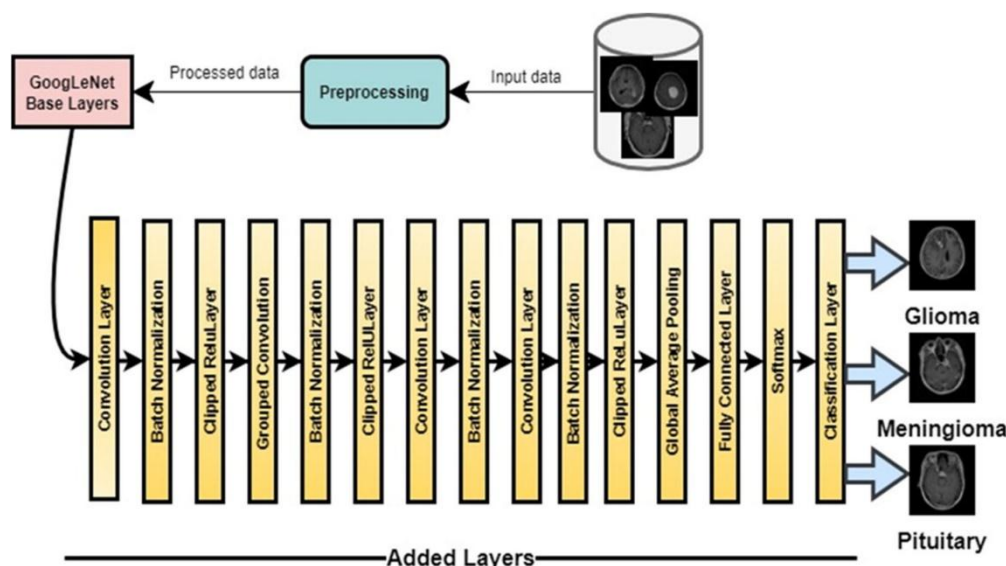


Figure 3.2. Architecture of the proposed hybrid model.

The proposed model and technique are summarized in this section.

DeepTumorNet

The proposed hybrid DeepTumorNet structure is based on the basic structure of Deep Convolutional Neural Networks (CNNs). It is very difficult and time-consuming to train a deep CNN from scratch, as it can take months of computing and optimization. For this reason, it was decided to use a pretrained deep learning architecture to enhance efficiency and performance rather than creating a novel model. In this context, GoogLeNet was chosen as the backbone model since its performance in the ImageNet competition (ILSVRC 2014) was outstanding. GoogLeNet has a total of 144 layers, with 22 layers that are learnable and 2 convolutional layers, 4 max-pooling layers, 1 average pooling layer, 2 normalization layers, 1 fully connected layer, and 9 inception modules. There's one max-pooling layer and six convolutional layers per inception module. GoogLeNet was slightly modified to accept an input size

of $224 \times 224 \times 1$. The first model used for the GoogLeNet was the Rectified Linear Unit (ReLU) activation function. But ReLU flattens all negative values to 0. To overcome this drawback, the proposed framework used Leaky ReLU activation function to enhance feature learning by enabling minor nonzero output for negative inputs, which minimizes the dying ReLU problem, thereby improving the expressiveness of the model. The added layers are the last five layers of GoogLeNet, which were replaced by new layers. Further to this, the ReLU activation function used in the feature mapping layers was modified to Leaky ReLU, without any changes to the CNN architecture. The result of these changes is that there are now 154 layers instead of 144. The first convolutional layer used a filter size of 7×7 , thus drastically cutting down the size of the image, in terms of spatial dimensions, from the first layer. The second convolutional layer used two layers of convolution and one layer of convolution block to reduce dimensionality. Moreover, the inception modules in GoogLeNet employ various convolution kernel sizes such as 1×1 , 3×3 , 5×5 , providing feature extraction at different scales from fine-grained features to high-level abstract features. The larger the convolution kernel, the more spatial information it captures; the 1×1 kernel captures less spatial information, but has lower computational requirements and can preserve significant details of features. Another interesting addition was the “modified DeepTumorNet” architecture, which added four convolutional layers with smaller filters of size 1×1 . The more convolutional layers the network contained, the more detailed, accurate and robust feature representations the network learned. The deeper convolutional layers added in this study led to the extraction of high-level and more complex features, which helped to enhance the overall classification performance of the proposed framework over the previous convolutional layers.

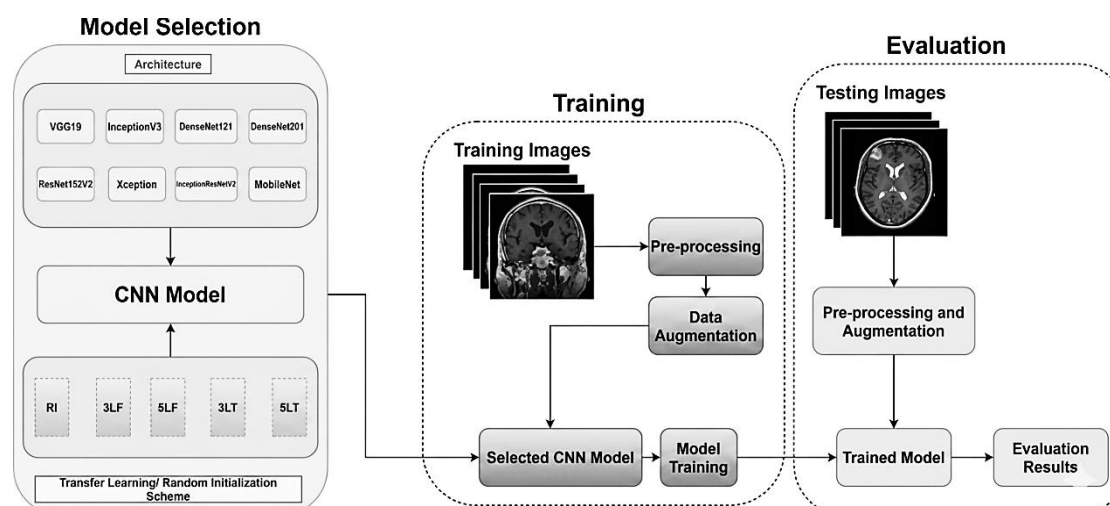


Figure 3.3: Proposed brain tumor classification system

Moreover, the global average pooling layer increased the accuracy at the network's end. Furthermore, the ReLU activation function in the feature map layer was changed to the Leaky ReLU activation function to increase the proposed model's expressiveness and overcome the dying ReLU problem. Thus, the proposed hybrid model excelled in terms of classification performance due to the added layer of the

proposed model, thereby learning more detailed, discriminative and deep features as compared to the aforementioned state-of-the-art pretrained deep learning models. The structure of the proposed hybrid DeepTumorNet approach is shown in Figure 3.3. The elaboration of the name, the type of the filter, its number, its size and its added layer epsilon is given in Table 4. Below, we discuss each layer of the proposed hybrid DeepTumorNet model in detail.

Table 4. Characteristics of added layers in the proposed hybrid model.

Layer Name	Type	No of Filter	Filter Size	Epsilon
block_16_expand	Conv	960	1×1	-
block_16_expand_BN	Batch Norm	-	-	0.001
block_16_expand_relu	Clipped ReLU Layer	-	-	-
block_16_depthwise	Grouped Conv	960	3×3	-
block_16_depthwise_BN	Batch Norm	-	-	0.001
block_16_depthwise_relu	Clipped ReLU Layer	-	-	0.001
block_16_project	Conv	320	1×1	
block_16_project_BN	Batch Norm			0.001
Conv_1	Conv	1280	1×1	
Conv_1_bn	Batch Norm			0.001
out_relu	Clipped ReLU Layer	-	-	-
global_average_pooling2d_1	Global Average Pooling	-	-	-
Logits	Fully Connected	-	-	-
Logits_softmax	Softmax	-	-	-
ClassificationLayer_Logits	Classification Layer	-	-	-

Image Input Layer

The proposed DeepTumorNet architecture starts with an input image layer, which provides the size of input MRI images. The image size in this study was $224 \times 224 \times 1$ (width $\times$ height $\times$ number of channels in the image). Grayscale images have one channel and colour images have three. The MRI image is preloaded into this input layer and then passed on for additional processing in the network.

Convolutional Layer

The convolutional layer is designed for extracting deep features from the input MRI

images and creating feature maps. Convolution is a mathematical operation applied to the image matrix and convolutional filters, the size of the filter being the size of the kernels in terms of height and width. In the convolutional layer, the model proposed here uses 7×7 , 5×5 and 1×1 size convolutional filters, while 3×3 size filters are used in the max-pooling layers. The “Padding” parameter is also used for padding the operations to maintain spatial information in the feature maps.

In the case of one-dimensional discrete convolution, it can be mathematically expressed as shown in Equation (9),

$$s(t) = (x * w)(t) = \sum_{a=-\infty}^{\infty} x(a)w(t - a) \quad \text{Eq (9)}$$

W stands for the kernel filter, x stands for the input signal, t stands for time and s is the output signal. The convolution process with two-dimensional input data is described by Equation (10).

$$S(i, j) = (I * K)(i, j) = \sum_m a \sum_n I(i, j) * K(i - m, j - n) \quad \text{Eq (10)}$$

The variables iii and jjj are the spatial position in the output matrix following the convolution operation. In this process, the center of the filter is matched with the corresponding image area, so as to achieve the best feature extraction effect. Moreover, the proposed framework uses the cross-entropy loss as the optimization objective, which is shown in Equation (11).

$$S(i, j) = (I * K)(i, j) = \sum_m a \sum_n I(i + m, j + n) * K(m, n) \quad \text{Eq (11)}$$

Activation Function

Activation functions are crucial for deep learning models because they provide the nonlinearity that is necessary. Popularly adopted activation functions are Sigmoid, Tanh, and the Rectified Linear Unit (ReLU). But any negative values on the input to ReLU get set to zero, and can cause the dying ReLU problem, where a neuron remains disabled forever. To address this problem, the DeepTumorNet model is proposed to change the ReLU activation function to the Leaky ReLU activation function in the feature mapping layers [119]. Leaky ReLU does not set negative inputs to 0 as ReLU does, but instead returns a small, nonzero number. In particular, any negative input is scaled by a small number, say 0.01, to ensure that the neurons are not turned off. In addition, the last 15 layers added to the network used a clipped ReLU activation function. This activation function acts as a threshold function by setting the output of the activation to zero if the input is below zero and limiting the output of the activation if the input is greater than a fixed ceiling value to the ceiling value. The mathematical representations of these activation functions are given in (12)–(16).

ReLU

$$f(x) = \begin{cases} 0, & x < 0 \\ x, & x \geq 0 \end{cases}, f'(x) = \begin{cases} 0, & x < 0 \\ 1, & x \geq 0 \end{cases} \quad \text{Eq (12)}$$

Sigmoid

$$f(x) = \frac{1}{1+e^{-x}}, f'(x) = f(x)(1 - f(x)) \quad \text{Eq (13)}$$

Tanh:

$$\tanh(x) = \frac{e^{2x} - 1}{e^{2x} + 1}, f'(x) = 1 - f(x)^2 \quad \text{Eq (14)}$$

Clipped ReLU:

$$f(x) = \begin{cases} 0, & x < 0 \\ x & 0 \leq x < \text{ceiling} \\ \text{ceiling}, & \geq \text{ceiling} \end{cases} \quad \text{Eq (15)}$$

Leaky ReLU:

$$f(x) = \begin{cases} 0, & x < 0 \\ \text{scale} * x, & x \geq 0 \end{cases} \quad \text{Eq (16)}$$

Leaky ReLU will give a value of 0.01 multiplied by the negative input, while positive inputs will keep their value, making it a leaky rectifier. Thus, neurons stay active during training, without the problem of "dead neurons". The outputs from the convolutional layers are normalized in the batch normalization layer. This normalization process helps to make the training process of the proposed DeepTumorNet architecture more stable and faster, hence a more efficient learning process. The batch normalization procedure is mathematically indicated in equations 17-19:

$$Y_i = \frac{X_i - \mu\beta}{\sqrt{2\sigma^2\beta + \epsilon}} \quad \text{Eq (17)}$$

$$\sigma\beta = \frac{1}{M} (X_i - \mu\beta)^2 \quad \text{Eq (18)}$$

$$\mu\beta = \frac{1}{M} + \sum_{t=1}^M X_i \quad \text{Eq (19)}$$

M is the number of all input samples, X_i are the input values, $\mu\beta$ is the mean value of the batch, $\sigma\beta$ is the standard deviation of the batch, and Y_i are the normalized values of the output after the normalization operation.

Pooling Layer

The pooling layer is used after the convolutional layer to make the feature maps that it produces smaller and eliminate redundant information. This is a down-sampling operation, which not only reduces the computational complexity, but also keeps the most significant features extracted from the input images. Average pooling and max pooling are the two most used methods for pooling. In the proposed DeepTumorNet framework, the global average pooling was applied in the last 15 layers of the framework. A pooling layer is not a learnable layer like a convolutional layer, but rather a layer that extracts features. Filters used for the pooling operation were 3×3 . The mathematical description of the pooling process is presented in equations (20) – (23).

$$S = w_2 \times h_2 \times d_2 \quad \text{Eq (20)}$$

$$w_2 = \frac{(w_1 - f)}{A + 1} \quad \text{Eq (21)}$$

$$h_2 = \frac{(h_1 - f)}{A + 1} \quad \text{Eq (22)}$$

$$d_2 = d_1 \quad \text{Eq (23)}$$

where w_1 is the width of the MRI image, h_1 is the height of the MRI image, d_1 is the thickness of the MRI image, f is the size of the filter, A is the stride or step size and S is the size of the output image.

Fully Connected Layer

The proposed architecture consists of a convolutional layer, followed by a pooling layer, followed by a fully connected (FC) layer. The role of this layer is to fuse all the features learnt from the previous layers and to find the most discriminative features that are needed for the image classification. The number of output units in the last fully connected layer was 3, which represent the three tumor classes taken into consideration in this research: meningioma, glioma and pituitary tumors. As a result, the FC layer generates three output values that are related to the target classes..

Classification Layer

The classification layer is the layer that produces the final Result of the Prediction from the Features extracted from the data.

$$U_i^l = \sum_j w_{ji}^{l-1} y_j^{l-1} \quad \text{Eq (24)}$$

$$U_i^l = f(u_i^l) + b^{(l)} \quad \text{Eq (25)}$$

The mathematical model has l layers and i and j are neurons. i represents the output produced by the classification layer, w_{ji} represents the weights of the hidden layer, y_j represents the values of input neurons, u_i represents the values of output neurons, b(l) is the bias term.

3.3.9 Softmax Layer

The fully connected layer is followed by the Softmax layer, which transforms the output variables to probability distributions for each target class. The purpose of this layer is to transform the output of the network to positive probabilities, with the total of probabilities equal to 1. The Softmax function is mathematically described in Equation (26) with the activation values represented by the symbols A, s, W, and bbb, which refer to the score vectors, weight vectors and bias parameters, respectively.

$$P(y = j | x_i, W, b) = \frac{\exp^{x_i^T W_j}}{\sum_{j=0}^n \exp^{x_i^T W_j}} \quad \text{Eq (26)}$$

In this case, A, s, W and b are weight vectors. The classification layer is the final layer of the proposed DeepTumorNet framework that generates the final output predictions for each MRI image. The Softmax activation function can be used to obtain the probabilities of the three classes of tumors, which can be used to correctly classify brain tumors as a multiclass classification.

Training Parameters

We used a trial-and-error-based approach to perform experiments with the parameters shown in Table 8. We constantly monitored the improvement of the training validation accuracy and error to find the optimal convergence of each CNN. The training was automatically stopped if there was no validation accuracy or an increase in accuracy or an error. For the proposed DeepTumorNet model, we trained it using stochastic gradient descent (SGD) with an initial learning rate of 0.01, final learning rate of 0.01 and a minibatch size of 10 images. The proposed DeepTumorNet model was trained on 120 epochs for brain tumor classification to obtain the optimum results. After a comprehensive analysis of different conventional and modern approaches used for brain image segmentation with Magnetic Resonance Imaging technology (MRI), the Data, Image Segmentation Processing, and View (DIV)

taxonomy was established. It is also based on what they have learnt from experience, and have lived through in designing, improving and optimizing Medical Image Segmentation (MIS) based systems using deep neural networks for accurate and efficient diagnosis of brain tumours.

Table 5. Parameter values used in training networks

Name	SGDM
MiniBatchSize	10
Number of Epochs	120
Initial Learning Rate	0.01
Shuffle	every epoch
Validation Frequency	50

The proposed taxonomy was carefully developed with reference to the most important and pertinent factors affecting the development, validation and evaluation of MIS systems. It features expertise gained from practitioners and researchers in medical image segmentation using deep learning architectures in their research. In addition, the taxonomy was further refined by analyzing 30 high-quality research papers published in credible and well-indexed (Q1-Q3) journals, providing a credible and aligned structure with the latest research in medical imaging. By complementing the results of this review and their existing knowledge of MRI image segmentation, the study concludes that medical practitioners must be furnished with contemporary and automatic methods to help them distinguish between healthy and impacted brain tissues. This can be vital in the early diagnosis and correct categorisation of brain tumours to guide diagnostic decision-making.

1. The study highlights three key factors that will be used as a basis for developing the proposed system: the nature and type of MRI data to be captured for effective analysis; the implementation of the proposed system; and its limitations.
2. Segmentation process, clustering techniques and post-processing procedures to improve the accuracy of tumour detection.
3. The way in which the final diagnostic results are visualised (or displayed) to the physician for interpretation. Therefore, the MIS framework is classified into three main components, Data, Image Segmentation Processing, and View (DIV), corresponding to the three major stages in the brain tumour analysis in MRI. The Data component is the first level of the DIV taxonomy and consists of raw and processed medical imaging data along with patient-specific data. The component takes into account the dimensionality, format, and data type of MRI data, which are all vital when interpreting and analyzing the results of MRI imaging. It also takes into account the source and nature of the data, such as whether it is acquired pre-operatively or intra-operatively, and whether it is original, reconstructed, or synthetically generated. These are necessary to obtain a proper interpretation of MRI data and to prepare it for additional processing in the MRI processing workflow. The Image Segmentation Processing component's main emphasis is on converting raw or preprocessed MRI data to meaningful and interpretable visual representations. In this stage, it's the time when a range of image processing methods and computational techniques are utilized to effectively analyze MRI scans. Various techniques can be used and combined to

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get the best segmentation and further enhancement can be done to increase image clarity and accuracy. The main purpose of this stage is to accurately localize tumor areas and clearly point them out, which helps physicians to make informed diagnostic decisions.

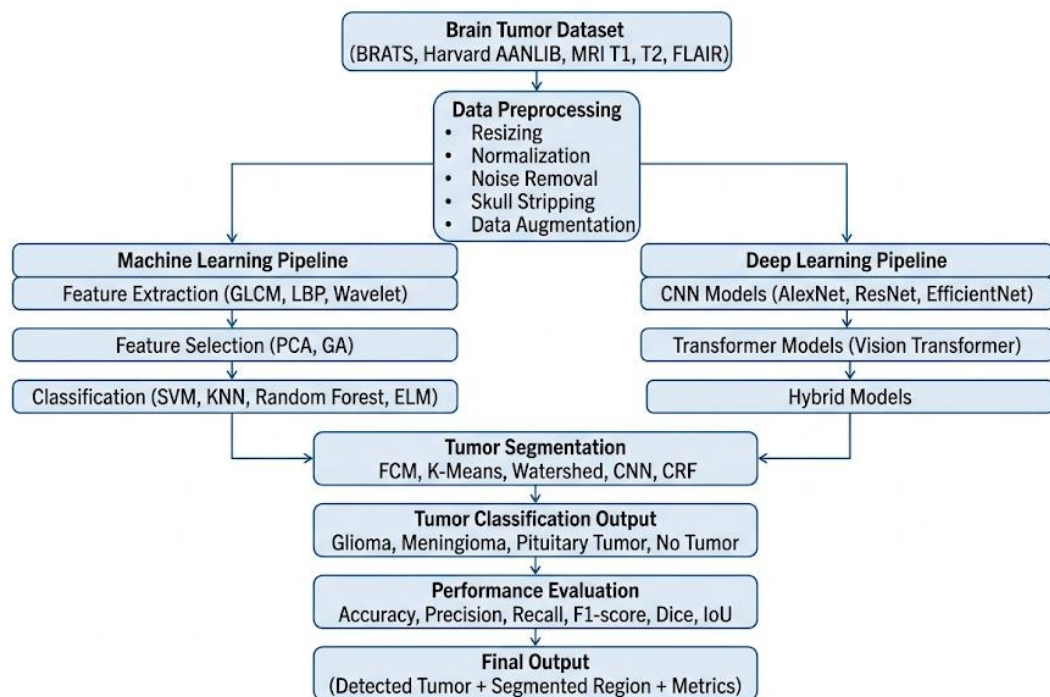


Figure 3.4: High-Resolution MRI Scans of Brain Tumors and Healthy Brain Tissues for Dataset Visualization Image Segmentation Processing Component

View Component

The View component is the last in the DIV framework and is used for the visualization of processed results to be interpreted clinically. Here, doctors examine the images they produced as a result of the MRI data, like looking through a window to diagnose the person's health problems. Factors taken into account in this phase are ease of interaction, display quality and visualization tools. This stage is where the computation-based results and medical knowledge merge—though it could be influenced by external factors that can impact diagnosis. Therefore, it is important to convey MRI data in a clear and reliable way to ensure the data is interpreted correctly. This combination of the three components, Data, Image Segmentation Processing and View, allows the DIV framework to offer a unified and structured approach to the development, evaluation and standardization of deep learning-based medical image segmentation systems. Whereas most of the existing taxonomies are only concerned with data acquisition and segmentation, the DIV taxonomy also includes the View component as it plays a key role in making data usable, interpretable, and clinically relevant. This extensive scheme provides a common ground for evaluating and assessing various medical image segmentation methods. Given its structured design,

MRI-based brain tumor diagnosis systems are more consistent, reliable, and accurate, which ultimately helps in the successful integration of deep learning solutions in real-world medical applications.

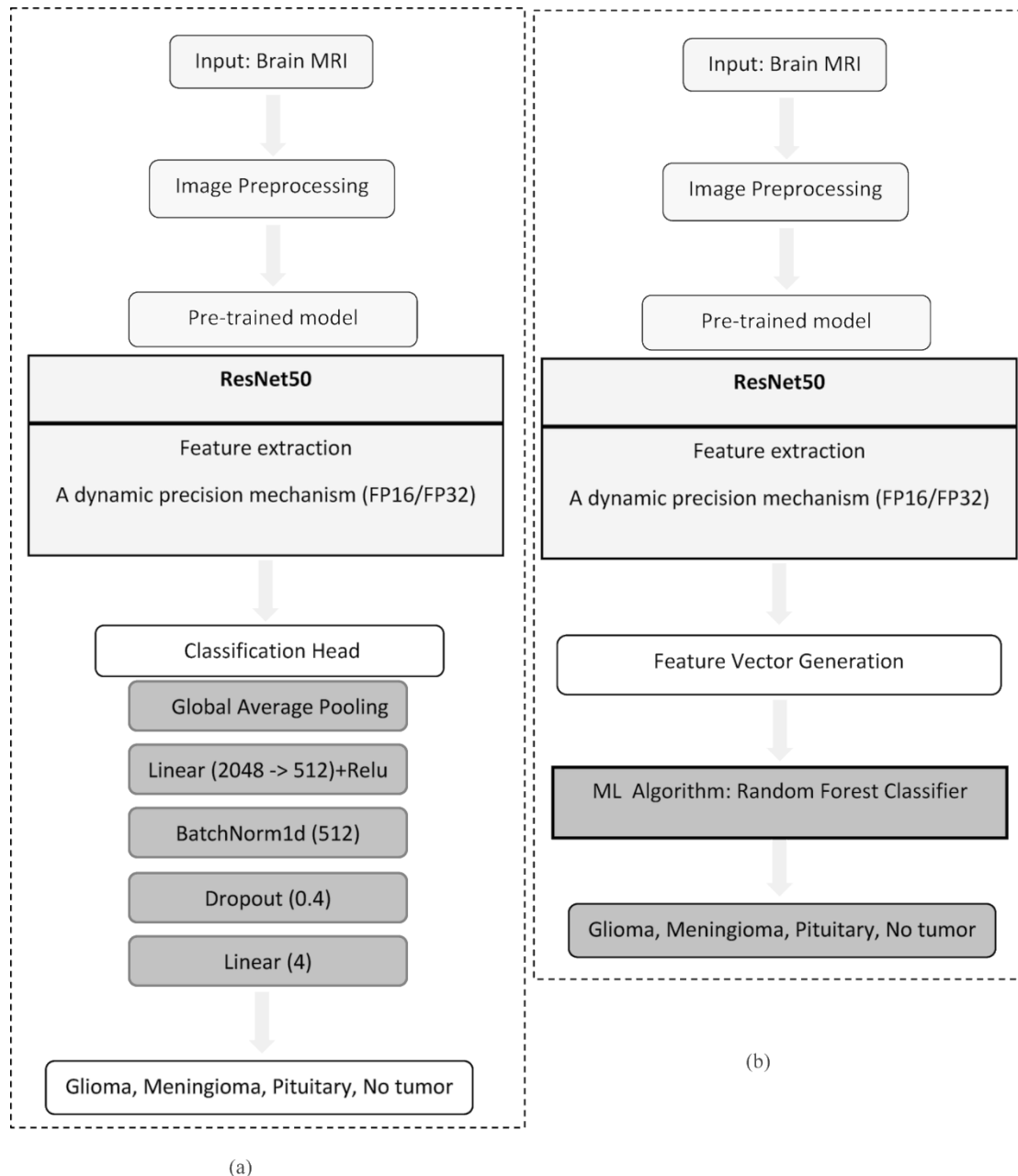


Figure 3.5: (a). the end-to-end optimized ResNet50 pipeline, (b). illustrates the hybrid ResNet50–RF framework.

Proposed Algorithm

This research work deals with various computational algorithms and methodologies to enhance the medical image segmentation for the accurate diagnosis of brain tumour by using Magnetic Resonance Imaging (MRI) data. The main target is to improve the

accuracy of brain MRI segmentation by adding deep learning techniques and clustering algorithms in the DIV framework. To overcome the problems like image noise, low contrast and segmentation error in MRI-based tumor detection systems, researchers have devised several advanced algorithms and hybrid models over the years. This study employs the main algorithms and methods described below.

Modified Fuzzy C-Means (MFCM) Algorithm

The limitations of the traditional clustering methods are the need to obtain accurate segmentation results that are widely used in detecting and segmenting brain tumors. To address these limitations, the Modified Fuzzy C-Means (MFCM) algorithm was developed, which leads to more accurate segmentation results. It can be used to do iterative clustering of MRI images, making the tumor tissue easily distinguished from non-tumor tissue, thereby improving the localization of the tumor and minimizing the bias. In this way, each pixel or data point is given a membership value representing how much it belongs to each of the clusters. This yields a more precise and sophisticated segmentation result. The algorithm is integrated with the Contrast Limited Adaptive Histogram Equalization (CLAHE) and further enhances the clustering and contrast of the image. Furthermore, even in the event of lost information due to segmentation, the re-clustering process after segmentation can retrieve such information so that the output obtained is still clear, accurate, and suitable for clinical diagnosis.

Bacteria Foraging Optimization (BFO) Algorithm

Optimal threshold values are found using the Bacteria Foraging Optimization (BFO) algorithm and an improved overall segmentation accuracy. It is based on the natural foraging mechanism of bacteria, which look for food. This optimization technique is used to determine the optimum parameter values for image segmentation, to reduce noise and enhance image quality, and finally to create more accurate and reliable segmentation boundaries.

1. The BFO algorithm is applied to optimize and fine-tune segmentation boundaries.
2. It guarantees the stability, consistency and reliability of the clustering.
3. It can be effectively used for determining the optimal segmentation parameters.

Conditional Random Fields (CRF)

To improve the sharpness of tumor boundaries in MRI images, Conditional Random Fields (CRFs) are incorporated with Convolutional Neural Networks (FCNNs). The CRFs contribute to spatial uniformity and preserve the details at the edges, leading to better tumor margin localization.

1. CRFs improve the clarity of the regions around the tumor.
2. They maintain the spatial consistency and fine edge information.
3. They enhance the post-processing part of segmentation.

Convolutional Neural Networks (CNN), 3D CNN, and DCNN

These deep learning architectures are key for feature extraction and brain image segmentation in MRIs. CNN-based models learn hierarchical representations of MRI which help reduce noise and enhance the contrast between normal and abnormal

tissues.

1. CNN-based models automatically learn meaningful MRI feature representations.
2. The volumetric MRI data is processed by a 3D CNN that extends over slices and captures spatial relations between slices.
3. Deep CNN structures improve the accuracy of tumor detection, classification, and segmentation.

LHNPSO Algorithm (Local and Hybrid Particle Swarm Optimization)

Optimisation of clustering objectives used in segmentation (LHNPSO algorithm). It enhances the delineation between normal and abnormal brain tissues, lowers segmentation errors and increases segmentation consistency.

1. Improves accuracy and precision in detection.
2. It minimizes the misclassification errors and enhances reliability.
3. It minimizes the segmentation objectives with hybrid swarm intelligence.

Kernelized Fuzzy Entropy Clustering (KFEC) and KFECSB (Modified KFEC)

These are the techniques used to segment brain tissues based on optimizing entropy values of images. They contribute to the minimization of noise, distortion, and bias of MRI images, thus improving image segmentation accuracy.

1. Effective brain tissue segmentation with KFEC and KFECSB.
2. They maximize entropy to reduce noise and distortion of the image.
3. The modified KFEC ensures robustness by optimizing the values of cluster membership.

Extremely Randomized Trees (ERT)

In brain tumor segmentation using annotated MRI data, the Extremely Randomized Trees (ERT) classifier is used. It classifies a two-stage process, which is structured and consists of training and testing.

1. ERT allows a reliable determination of tumour regions.
2. Effective two-stage learning (training and testing).
3. It has better performance than the classical tree-based approaches in terms of stability and speed.

Active Contour Models (ACM)

Active Contour Models (ACM) are evolved contours that are used to accurately define tumor boundaries by tracking the image gradients.

1. ACM improves segmentation precision and boundary detection.
2. It clearly separates the tumor core and the surrounding edema area.
3. It offers unambiguous and understandable visual outputs for clinical application.

Voxel Clustering Algorithm and VoxResNet (3D Residual Network)

VoxResNet is a 3D residual network to learn deep features from MRI data and improve its quality.

1. VoxResNet is a model that is designed to extract hierarchical spatial properties from MRI scans.
2. It is effective at enhancing image contrast and effectively eliminating noise.

3. 3D residual learning improves the accuracy of tumor segmentation.

Random Forest Classifier

The segmented MRI images are classified using Random Forest with the objective of identifying tumor-affected areas in MRI images as compared to the normal tissues.

1. Has high accuracy and strong robustness.
2. It employs several decision trees to enhance the classification.
3. It has been broadly applied for reliable image classification tasks.

Support Vector Regression (SVR) and TensorFlow Framework

Support Vector Regression (SVR) is a regression learning method that can be used together with deep learning models like CNNs. TensorFlow offers a comprehensive framework for developing and training large-scale deep learning models.

1. SVR (Support Vector Regression) can be used to model data analytically by regression.
2. TensorFlow provides an effective development environment for models.
3. It allows scaling up deep learning systems training and evaluation.

Table:6: Algorithm / Technique, Purpose / Function, Outcome

Algorithm / Technique	Purpose / Function	Outcome
Modified Fuzzy C-Means (MFCM)	Clustering and re-clustering MRI data for clearer tumour boundaries	Enhanced segmentation accuracy
Bacteria Foraging Optimization (BFO)	Threshold optimization	Improved clustering precision
CNN / DCNN / 3D CNN	Feature extraction, noise reduction, and segmentation	Improved clarity and reduced bias
Conditional Random Fields (CRF)	Boundary refinement	Accurate edge preservation
LHNPSO	Optimization of clustering objectives	Improved segmentation boundaries
Extremely Randomized Trees (ERT)	Classification of MRI images	Efficient and automated
Kernelized Fuzzy Entropy Clustering (KFEC)	Automated tissue segmentation	Reduced bias and noise

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Active Contour Model (ACM)	Tumour boundary detection	Accurate delineation
VoxResNet (3D Residual Net)	Hierarchical feature learning	Enhanced contrast

Analysis of the Proposed Block Diagram

The proposed block diagram was analyzed in this stage. In this stage, the proposed block diagram was analyzed. The proposed system aims at creating an image classification model using a Convolutional Neural Network (CNN). It is executed in a linear pipeline fashion, with each phase enhancing the performance, stability, and reliability of the model.

Dataset Collection

The first step is to collect the data, which is the basis of the entire system.

- (a) This data set consists of MRI images and labels.
- (b) It comes from the publicly available sources or custom-made data sets.
- (c) Balancing the datasets is an important step to achieve good model performance.

Image Extraction

During this phase, images are retrieved from the dataset and appropriately sorted for processing. Images are pulled and organized in a well-defined format. Efficient and automated data handling is ensured by proper organization.

Label Loading

In supervised learning, the labels are crucial since they specify the desired output for each input image. These tags can be stored as CSV, in the form of JSON, or by the folder name. Each image is labeled with the corresponding image, allowing the model to learn from labeled data meaningful patterns.

Data Preprocessing

Pre-processing of data is pivotal in preparing images for use in training models. These raw images can't be used directly, so they undergo a few pre-processing operations:

- (a) All images are scaled to a common size for uniformity.
- (b) The pixel values are scaled (e.g., between 0 and 1) to facilitate the efficiency of learning.
- (c) Noises and distortions are minimized for good image quality.
- (d) Any images not relevant to the data or images of low quality are excluded from the data set. This process helps to make sure that the data is clean, standardized, and ready to train an accurate model.

Data Integration

Images and labels are then mated into a single structured dataset after preprocessing.

This way each image is properly correlated with its label. The integrated dataset is then available for further processing, e.g. splitting and augmentation.

Data Partitioning

The dataset is split into various subsets for the correct training and evaluation of the model. Typically, the data is split as follows:

- (a) Training set: 70–80% of the data
- (b) Test set: 10–15% of the data
- (c) Testing set: 10–15% of the data

The training set is used to train the model, the validation set is used to tune the parameters of the model to avoid overfitting, and the test set is used to evaluate the performance of the final model.

Data Augmentation

When there is limited data, data augmentation can boost the diversity of the data sets and enhance the generalization of the model. These are accomplished by using transformations like:

- (a) Image rotation
- (b) 90 degree rotations
- (c) Zoom in and out
- (d) Cropping
- (e) Brightness adjustment

These are transformations that make the model more robust as it is exposed to real-world data.

Hyperparameter Setting

Pre-training important hyperparameters are set. These settings influence the learning behavior of the model and consist of:

- (a) Learning rate is the rate by which learning takes place, which is represented by.
- (b) The number of images in a batch defines the batch size, denoted by b.
- (c) Number of epochs: Number of times the dataset is used for training.
- (d) Optimizer, which optimizes weight updates in the model
- (e) Loss function, an error measure of prediction.

These parameters, which are selected through experimentation, are used to obtain optimal performance.

CNN Architecture Design

The backbone of the system is the Convolutional Neural Network (CNN), which is excellent for image processing tasks. The architecture is broken up into several elements:

- (a) Feature extraction with convolutional layers
- (b) Activation function to add non-linearity.
- (c) To stabilize training Batch normalization
- (d) Pooling layers to decrease dimensionality

There are fully connected layers at the end for making final decisions.

- (f) Softmax layer to generate probability based outputs

CNNs can capture hierarchical features like edges, textures and shapes, making them ideal for image classification.

Network Training

The training set is used to train the model architecture once it is defined. During training:

- (a) Processes input images and yields predictions on the model.
 - (b) The loss function is used to obtain the prediction error
 - (c) The model is revised to make it more accurate
 - (d) This process is repeated for several epochs
- The goal is to reduce errors and increase the accuracy of classification.

Final Model Generation

Once the training is finished, the last optimized model is achieved. This trained model is capable of making predictions on unseen MRI images. It is then stored for later use in programs like clinical systems or Web-based programs.

Performance Evaluation

The last step is to test the model with the test dataset to quantify its effectiveness. The following will be used for the evaluation:

- (a) Accuracy – overall correctness of predictions
- (b) Precision – correct prediction of positive results
- (c) Recall – percentage of correct positive answers
- (d) F1-score – gives a balance between precision and recall
- (e) Confusion matrix – shows detailed classification performance

Results & Discussions

Effectively capturing the non-linearity of the data is one of the key problems in brain tumor classification. Machine learning algorithms, especially traditional models, are not always capable of capturing complex relationships as found in medical imaging because they are linear models. This deficiency reduces their ability to differentiate the tumor characteristics accurately. This has been partially solved using Convolutional Neural Networks (CNNs), which exploit several interconnected layers to learn non-linearities. The optimization and design of CNN architectures that are capable of fully leveraging these non-linear features is however, still under active research. The other major issue is the fact that two-dimensional (2D) images are used in order to study three-dimensional (3D) structures such as brain tumors. Conventional imaging methods tend to result in 2D cuts that can be insensitive to depth-based data that are important in accurate diagnosis. This limitation can be overcome by either devising sophisticated means of deriving depth information out of 2D images or by using modalities like volumetric MRI and CT scans, which inherently give 3D representations. Another difficulty is that the current classification methods do not have multi-dimensional representations. Although 2D imaging can provide useful information, it is not able to completely represent complicating spatial, temporal, and morphological features of tumours. The addition of multidimensional insights, like time-series recordings of dynamic imaging studies or spatial differences of multi-sequence MRI scans, carries a considerable challenge in the form of the increased complexity of the data processing

and analysis. Also, the combination of attention mechanisms is an opportunity and a challenge in the classification of brain tumors. Attention modules have also been shown to help a model to focus on the most relevant parts of the input data and have been shown to improve feature extraction and classification. But they can be successfully incorporated into CNNs or Transformer-based systems only when they are carefully experimented with to find the best strategies. Moreover, it is important to consider the way the attention mechanisms can be interoperable with other parts of the classification pipeline and adapt their behavior in ways that are modifiable and useful in clinical practice. Addressing the above challenges of non-linearity, dimensionality, depth representation and use of attention mechanisms in brain tumor classification would render the methodologies more precise and reliable and eventually lead to better diagnostic results and patient care.

An Exploration of How MRI Images Are Utilized for Brain Tumor Analysis

MRI images are what the program uses to analyze brain tumors. To do this the program goes through steps to make sure it gets good information from the images:

1. Getting Kinds of Data: The program uses images in different formats, like Jpeg, Png and Tiff and in different colors.
2. Making Images the Same Size: All the images are made to be 256x256 pixels so they are all the size.
3. Making Images Work with the Program: The images are adjusted to work with the computer program using numbers for the color and how much the color changes. These numbers are $[0.485, 0.456, 0.406]$ for the color and $[0.229, 0.224, 0.225]$, for how the color changes. This helps the program understand the images.

Table: 11 Below is a summary of the dataset characteristics utilized in this exploration:

Image Name	Class	Format	Mode	Shape
Cancer(1).jpg	Tumor	Jpeg	RGB	(512,512,3)
Cancer(1).png	Tumor	Png	L	(300,240,3)
Cancer(1).tif	Tumor	Tiff	RGB	(256,256,3)
Cancer(10).jpg	Tumor	Jpeg	RGB	(512,512,3)
Cancer(10).tif	Tumor	Tiff	RGB	(256,256,3)

CONCLUSION

In this Paper, we discover in the development of brain tumor classification methods, with a focus on the shift between older methods involving machine learning to more recent deep learning models like Convolutional Neural Networks. The traditional techniques, though essential in setting the base, were usually constrained in their ability

to deal with the non-linearity and Challenge of medical imaging data. The response to some of these challenges in CNNs was automated feature extraction and hierarchical learning, and Transformers still developed the field further by proposing more contextual knowledge and the ability to capture dependencies over a long range. Comparative analysis of these methods has given an understanding that there is no universal method that is superior. They both possess their own advantages and drawbacks, and the methods should be selected based on the needs of the diagnosis and the availability of the data, as well as the clinical background. Similarly, the importance of datasets like BRATS and Harvard AANLIB has been highlighted because they are used as a benchmark to evaluate the progress and are still influencing further developments in automated tumor classification. Irrespective of these developments, issues like heterogeneity of datasets, interpretability requirements, and multimodal data integration have become urgent problems. The process for diagnosing brain tumors has changed a lot with the use of Deep Learning. In the past, doctors had to look at brain images themselves, which took a lot of time and could be different from one doctor to another. Now computers can help doctors by looking at the images and giving them results quickly. The way doctors diagnose brain tumors now uses a computer program called CNN_TUMOR. This program helps doctors find brain tumors by looking at medical images like MRI and CT scans. It turns these images into information that doctors can use to make decisions. The program was trained on a lot of images that were already labeled, so it can tell the difference between types of tumors like gliomas and meningiomas. This is very important for deciding how to treat patients.

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