"BRAIN TUMOR PERCEPTION USING DEEP LEARNING"

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ABSTRACT: *The human brain serves as the central component of the human body, orchestrating its functionality. Brain tumors emerge from abnormal cell growth and division within the brain, potentially leading to the development of brain cancer. Computer vision plays a pivotal role in healthcare by alleviating the burden of making precise decisions. Among imaging modalities like magnetic resonance imaging (MRI), computed tomography (CT) scans, and X-rays, MRI scans stand out as one of the most prevalent and safest methods for obtaining detailed images, capable of detecting minute abnormalities. Our research endeavors to explore the diverse applications of brain MRI in detecting brain cancer. In this study, we employed the bilateral filter (BF) to eliminate noise from MR images before processing. Subsequently, the tumor region was delineated using binary thresholding and Convolutional Neural Network (CNN) segmentation techniques. The datasets were divided into training, testing, and validation subsets, enabling our machine to discern the presence of brain tumors in subjects. Various performance metrics including accuracy, sensitivity, and specificity were utilized to evaluate the outcomes. Dense layers within the CNN architecture efficiently extract features from brain MRI images, enhancing diagnostic accuracy. The experiment was conducted primarily on MRI data due to its ability to provide comprehensive insights into cellular structure and function. It is anticipated that our proposed methodology will outperform existing approaches in brain tumor detection.*

INTRODUCTION: The brain, being the paramount organ in the human body, is susceptible to abnormalities in cell growth, known as brain tumors. These tumors typically

I. INTRODUCTION:

Medical imaging serves as a crucial tool in clinical practice, providing visual representations of the body's internal structures for diagnostic and therapeutic purposes, along with insights into organ and tissue functionality. Its primary objective is to aid healthcare professionals in diagnosing and treating patients by visualizing hidden anatomical features beneath the skin and skeleton. Additionally, medical imaging contributes to the establishment of a comprehensive database of normal anatomy and physiology, facilitating the identification of abnormalities. The term "medical imaging processing" pertains to the manipulation of images using computer technology, encompassing various techniques such as image acquisition, presentation, storage, and communication. This process is integral to identifying and managing medical disorders, establishing a standard reference for normal organ anatomy and function, which aids in the detection of abnormalities. A wide array of techniques is utilized in medical imaging, including electromagnetic energy modalities like X-rays and gamma rays, organic imaging, radiological imaging solography, magnetic scoping, thermal imaging, and isotope imaging. These technologies provide diverse capabilities for documenting the structure and function of the human body, each with its own strengths and limitations when compared to image-generating generators.

One method of image processing involves the utilization of a computer to modify digital images, offering numerous benefits such as flexibility, adaptability, and efficient data storage and communication. With the advancement of various image scaling algorithms, images can be stored in a more space-efficient manner. This technique employs multiple sets of rules to concurrently execute operations on images, enabling processing of both 2D and 3D images across various dimensions. Brain tumors represent one of the most prevalent and deadliest brain disorders globally, posing significant threats to countless lives. Characterized by the rapid proliferation of cancerous cells within the brain, brain cancer presents a formidable challenge to healthcare systems worldwide. According to recent cancer studies, over a hundred thousand individuals worldwide receive diagnoses of brain tumors annually, underscoring the magnitude of the issue. Despite ongoing efforts to address the challenges associated with brain tumors, patient outcomes remain largely unfavorable. In response to this pressing health concern, researchers are increasingly turning to computer vision technologies to enhance understanding of the early stages of tumor development and to explore innovative treatment modalities aimed at combating brain tumors effectively. Standard diagnostic procedures for brain disorders often involve magnetic resonance imaging (MRI) and computed tomography (CT) scans, which aid in detecting the presence and location of brain tumors, crucial for treatment planning. The ability of these scans to generate high-definition images of diseased tissues surpasses their continued popularity. Various treatment options for tumors, including surgery, radiation therapy, chemotherapy, and others, are available, with factors such as tumor size, type, and grade observed on MR imaging influencing treatment decisions. Additionally, these imaging modalities serve to identify metastasis, the spread of cancer to other body regions. Accurate diagnosis of specific brain conditions is paramount for effective treatment and to mitigate the risk of misdiagnosis. While computer-aided diagnostic (CAD) technologies are commonly used, they may lack precision. The primary objective of computer vision is to produce more reliable outputs, typically assisting physicians in their visual interpretation of images and reducing interpretation time. Despite advancements enhancing the trustworthiness and accuracy of medical diagnoses, segmenting MR images of tumors and their surroundings remains challenging. Particularly, tumors located in specific brain regions with indistinct image intensities further complicate computerized detection and segmentation of brain tumors.

II. LITERATURE SURVEY:

A technique has been developed for utilizing MRI to detect tumors. Image processing technologies, particularly through machine learning, play a vital role in aiding radiologists and computers in monitoring tumor regions during diagnosis and treatment. A novel system called SR-FCM-CNN, combining fuzzy C-means with super-resolution and convolutional neural networks along with extreme learning machine algorithms, has been introduced for identifying brain tumors. The Fuzzy Clustering Algorithm (FCM) is a commonly used fuzzy partition clustering technique. Zhang's super-resolution (SR) method enables the enhancement of low-resolution (LR) MRI images to high-resolution (HR) levels. DICOM-formatted MRI scans are utilized for the analysis. Tumor segmentation from HR MRI images is conducted using the FCM method and various image processing techniques. The newly developed FCMSR segmentation method, tailored for this study, proves to be more effective than SR segmentation for MRI image segmentation. The SqueezeNet architecture has been implemented as a feature extractor to enhance the portability of the proposed method across different platforms. After segmentation, images are processed through the SqueezeNet framework to extract their features. These features are then fed into an ELM classifier to determine the nature of the tumor (benign or malignant). In various academic works (references [28-30]), CNN architectures are commonly utilized for tasks such as image classification, object recognition, and detection, lauded for their high accuracy. The Extended SqueezeNet Architecture (ESA) is a comprehensive data collection structure inspired by artificial neural networks. CNNs are adept at handling large datasets due to their extensive memory and well-structured models. The SqueezeNet framework, one of the latest CNN architectures, is employed in this study.

In the realm of brain tumor diagnosis and treatment, a range of image-processing tools and methodologies are being developed [2]. The initial step in image processing techniques, known as segmentation, involves isolating affected areas of brain tissue from MRI scans. Various semi-automatic and fully automatic segmentation methods are employed for analyzing tumors. MRI properties like image textures, local histograms, and structural tensor eigenvalues are utilized in brain tumor segmentation studies [7]. Advancements in medical technology empower clinical professionals to offer more efficient e-healthcare solutions, benefiting numerous medical fields. Biomedical imaging applications leveraging computer vision are gaining traction as they equip radiologists with crucial information for optimizing treatment approaches. X-ray, MRI, ultrasound, and CT scans are among the various medical imaging techniques revolutionizing the diagnosis and treatment landscape for doctors and patients. A plethora of image-processing methods and techniques are employed in the realm of brain tumor diagnosis and treatment. The initial phase of image processing involves segregating infected areas of the brain from healthy ones in MRIs, a process termed "segmentation" [1]. Tumor segmentation holds paramount importance in the diagnosis, treatment, and assessment of cancer treatment efficacy. Several automatic and semi-automatic segmentation methods are utilized for tumor analysis [8]. Brain tumors are categorized as abnormal cell growths, which may be either cancerous or benign [3]. Gliomas, the most prevalent type of brain tumor, originate from glial cells (Ferlay et al., 2010). Gliomas are further classified into glioblastoma (GBM) and high-grade glioma (HGG) subtypes based on pathological evaluations (LGG). Glioblastoma stands out as one of the most aggressive and challenging-to-treat forms of brain tumors in humans (Bleeker et al., 2012). Various histologically distinct components constitute a glioma, including peritumoral edema, a necrotic core, an elevating and non-enhancing tumor core, and an enhancing tumor core. Multimodal MRI scans, encompassing T1-weighted, gradient-enhanced T1-weighted (T1Gd), and Fluid Attenuation Inversion Recovery (FLAIR) images, offer complementary profiles for different glioma subregions.

For instance, areas exhibiting higher intensity on a T1Gd scan compared to a T1 scan serve as diagnostic indicators for the enhancing tumor sub-region. Glioma segmentation in pre-operative MRI images facilitates the quantitative morphological characterization and assessment of glioma sub-regions. Predicting survival outcomes hinges on this segmentation as crucial factors stem from the tumor's location, ascertainable only through surgical means. This quantitative approach holds promise for glioma grade assessment and treatment planning, thus offering significant diagnostic and research prospects [15]. Automatic segmentation offers advantages such as speed, consistency in accuracy, and resilience to fatigue. However, this task poses challenges due to the substantial variability in appearance and shape, ambiguous boundaries, and imaging artifacts (Sharma and Aggarwal, 2010). Indeed, one of the most daunting tasks in medical image processing lies in the automated segmentation of brain tumors using multimodal MRI data. Detection and classification of brain tumors in MR images can be facilitated through techniques involving the extraction of tumor regions, subsequent extraction of textural features using a grey level co-occurrence matrix (GLCM), and tumor classification [4]. Shasidhar proposed employing a fuzzy c-means (FCM) technique with specific adjustments for brain tumor detection via MRI. Texture characteristics are initially extracted from brain MR images, followed by the utilization of a modified feature correspondence mapping (FCM) algorithm for tumor detection. This modified FCM method has demonstrated average speed enhancements of approximately 80 times compared to standard FCM approaches [12]. Rajesh and Malar introduced a classification method for brain MR images employing a combination of crude set theory and a feed-forward neural network classifier. The application of rough set theory aids in feature extraction from magnetic resonance (MR) images.

A feed-forward neural network classifier is supplied with specific features, reliably distinguishing between a healthy brain and one with a condition at a confidence level of 90%. Ramteke and Monali demonstrated the automatic classification of brain MR images into two categories—normal and abnormal—utilizing image attributes and automated abnormality identification [9]. The KNN classifier is employed to assign images to predetermined categories based on statistical texture data extracted from both normal and aberrant images, achieving an 80% classification accuracy. Othman devised a neural network classification method for brain tumor diagnosis based on probabilistic models. This method utilizes a probabilistic neural network for classification following feature extraction via principal component analysis (PCA) (PNN). Jafari and Shafaghi proposed a hybrid approach for brain tumor detection in MRI images, employing support vector machines (SVM) and utilizing texture and intensity features. This system demonstrates improved resilience and achieves an accuracy rate of approximately 83.22%.

III. METHODOLOGY:

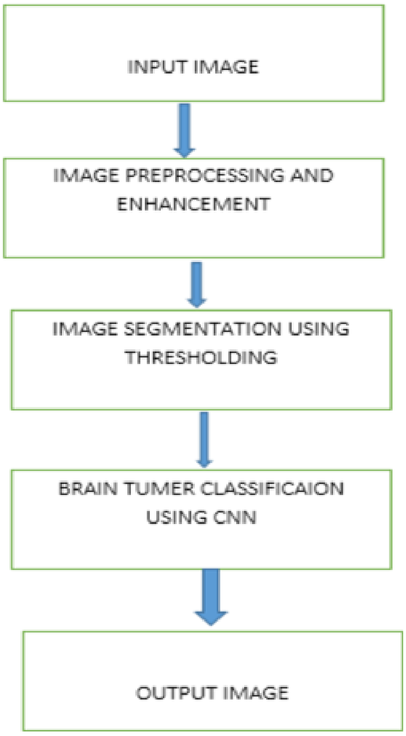

Figure 3.1: Overall Architecture

The CNN takes the brain tumor image through several stage in its methodology: preprocessing, enhancement, ar segmentation, culminating in tumor detection and resu display. This entire architecture is illustrated in Figure 3.1.

A. Image Preprocessing and Image Enhancement

The dataset of Brain MRI images was obtained from Kaggl comprising approximately 1900 images encompassing norma benign, and malignant MRIs. These images serve as th primary data in the initial phase of processing. A critical aspe of preprocessing involves meticulous attention to detail. Ke steps include noise removal and image scaling. Initially, th MRI images are converted to grayscale, followed by th application of adaptive bilateral filtering to elimina distortions and clutter, thereby enhancing diagnostic ar classification accuracy. In image processing, the first step locating the image within a data repository, as processin necessitates access to an image. Images captured remai unprocessed until this stage, where the image's file path on th local device is utilized for processing. OpenCV offers over 15 color space conversion methods. For our purposes, we emplo cv2.cvtColor(input image, flag) for color spac transformations, converting the input image to black ar white.

Filters play a crucial role in image processing b attenuating high-frequency components. The median filter, nonlinear filtering technique, is effective in reducing noise b replacing each pixel's value with the median value of the window's pixels. This filter effectively suppresses speckle noise and salt-and-pepper noise. Another method for noise reduction is the bilateral filter, which calculates an average intensity from neighboring pixels and substitutes it for each pixel's original intensity based on the standard Gaussian distribution. This filter maintains smooth images while preserving edges through the nonlinear clustering of adjacent pixels. Its local operation, minimal processing time, and efficiency make it a preferred choice. Additionally, it prioritizes nearby values over distant ones in both range and domain, favoring symmetrical closeness in range and domain.

B. Image Segmentation

Image enhancement serves as a pivotal technique in augmenting the quality and clarity of images through the utilization of computational tools, incorporating both tangible and intangible improvements. This approach capitalizes on both global and local considerations, leveraging input pixel values within specific regions for localized operations. Two primary methodologies for enhancing images include spatial and transform domain techniques. Unlike the spatial approach, which operates directly on pixel values, the transform technique first employs Fourier transformation before implementing spatial enhancements. Edge detection, a fundamental aspect of image segmentation, focuses on identifying boundaries between closely related objects or regions by detecting discontinuities in pixel values, particularly notable intensity gradients. The Sobel filter is a commonly used method for edge detection, which calculates the intensity gradient at each pixel by convolving the image with horizontal and vertical kernel matrices. These derivatives are then combined to approximate the gradient magnitude, facilitating edge identification and enhancing image details, contrast, and sharpness. Despite employing a streamlined equation, $G=|Gx|+|Gy|$, Sobel filtering is utilized to address the challenges posed by noise and loss of edges during preprocessing. This method effectively computes the intensity gradient at each pixel, contributing to the prominence of edge detection in image analysis. Additionally, edge detection not only enhances image contrast and sharpness but also brings out details in shadows, thereby refining image quality and ensuring optimal visual interpretation.

Image segmentation is a technique used to partition an image into multiple sections, aimed at facilitating image analysis and interpretation while preserving image quality. This method is instrumental in delineating object edges within photographs by identifying pixels based on their intensity and properties. These segmented portions retain the original image's features, such as hue and resemblance, and find applications in various fields, including machine perception, the study of malignant diseases, anatomical and functional studies, tissue volume analysis, virtual reality visualization, anomaly detection, and object identification.Segmentation techniques enable the identification and analysis of abnormal image regions, facilitating the examination of their dimensions, volume, position, texture, and form. In medical imaging, segmentation of MR images with preserved threshold information aids in accurately localizing damaged areas. The concept of spatial proximity guiding similar characteristics is leveraged in thresholding, a rapid and straightforward technique for image segmentation.By transforming grayscale images into binary representations based on a predetermined threshold value, thresholding classifies pixels as either below or above the threshold. The cv2.threshold() method in OpenCV applies a threshold of a predetermined level to a single-channel array, producing a binary image by comparing input pixel values to the threshold. The function offers various thresholding options, and once computed, the threshold value and thresholded image are returned by the function.

1. The "src" parameter represents the Input Source Array, which should be a single-channel array containing image data encoded in 8-bit or 32-bit floating point format. It serves as the source from which the image data is extracted and should be in grayscale format.

2. The "thresh" parameter denotes the threshold value used for pixel value classification. It determines the threshold level against which pixel values are compared during the thresholding process.

3. The thresholding types "THRESH_BINARY" and "THRESH_BINARY_INV" have a maximum allowable value of 3, and they can be configured in three distinct ways. If a pixel value exceeds the threshold value, the specified thresholding type dictates whether the pixel should be assigned a particular value.

4. The "type" parameter in the "cv2.threshold()" function indicates the type of thresholding applied, such as "THRESH_BINARY" or "THRESH_BINARY_INV". It governs the specific thresholding method used during image processing.

Morphological operations involve utilizing the structure of an input image to generate a modified version of the original, where each pixel's value in the resulting image is determined by comparing it to neighboring pixels in the input image. These operations are commonly applied in segmentation approaches, particularly on binary images, facilitating shape-based operations and various image processing tasks. This study utilizes the morphological techniques of Erosion and Dilation, which are performed simultaneously.Erosion and dilation operations encompass two primary morphological phases: opening and closing. Initially, a binary MRI image is loaded, and the opening procedure aims to connect regions that are separated by small gaps, effectively reducing them to a smaller cluster of pixels. Subsequently, the erosion is dilated to restore its original dimensions, thus bridging any gaps created during the erosion process. Once the opening procedures conclude, the closure procedure commences, wherein erosion and dilation operations address different region holes while preserving original area sizes. The fundamental morphological changes include dilation, which adds pixels to object margins, and erosion, which removes pixels. Analogous to analyzing a topographic surface, the Watershed Method evaluates an image's gradient to identify hills and valleys. This process begins by flooding isolated valleys with water of varying colors, causing water from distinct valleys to merge as the water level rises. Barriers are erected at water confluence zones to regulate water flow, and water continues to be added until all summits are submerged. The resulting segmentation is determined by artificial barriers, which dictate the segmentation outcome.

C. Cognitive Processing Neural Networks For Brain Tumor Image Classification

When erosion and dilation are applied, they undergo two primary phases: opening and closing. The initial step involves opening the binary MRI image, aiming to establish connectivity between separate objects by reducing intervening spaces to a small group of pixels. Subsequently, dilation restores the eroded regions to their original dimensions, effectively bridging any gaps formed during erosion. Further modifications to th e same structural elements in an already opened binary image have no impact on the original image. Following the completion of all opening procedures, the closure procedure is executed, where erosion and dilation address holes in different areas of the image while maintaining overall image size. The fundamental morphological operations include erosion, which removes pixels from object boundries and dilation, which adds pixels.Using an analogy to a topographic surface, the Watershed Method assesses the gradient of an image as if it were a mountain range, where steep gradients represent peaks and gentler ones represent valleys. The process begins by filling each isolated valley with water of varying colors, with rising water levels leading to the merging of water from different valleys. To control water flow, barriers are constructed at water confluence zones. Continuously adding water and erecting barriers submerges the mountains entirely, with the created barriers determining the segmentation outcome.Incorporating Keras and other essential packages for building the CNN, the Sequential package is employed to set up the neural network. The convolutional neural network for image processing is constructed using Convolution2D, with the pooling layers implemented through the MaxPooling2D layer. The flattened feature map is passed to the fully connected dense layer, which facilitates complete connection in the neural network architecture.

1) SEQUENTIAL:

An instance of such Sequential class is instantiated to launch the neural network.

identifier = Sequential classifier ()

2) CONVOLUTION:

The Convolution2D parameters are bundled together using the add method of the classifier object, which inserts the convolution layer. The number of feature detectors required is specified by the feature detectors parameter in the first argument. Two additional parameters determine the size of the matrix used by the feature detector. In CNNs, 256 detectors are commonly used to identify features. The second parameter is "input shape," which represents the actual shape of the processed image. These specifications will be used during initial processing to resize the images to the specified dimensions. Images with grayscale tones will be converted into a 2D array, while those with color will be transformed into a 3D array. In this scenario, assuming color visibility is adequate, the input shape is provided as a tuple indicating the total number of channels (three for a color image) and the dimensions of the 2D array for each channel. It is recommended to use reduced dimensions if a graphics processing unit is unavailable. The activation function is the final adjustment. Image classification requires nonlinear thinking, so the rectifier function is used to avoid dealing with negative pixel values, achieving nonlinearity.

classifier.add(Convolution2D(256,3,3), input_shape=(256, 256, 3), activation='relu', output_shape=(256, 256, 3))

POOLING: The pooling layer is responsible for reducing the size of the convolved feature. Dimensionality reduction is applied to save processing time and energy, while also aiding in model training by isolating dominant features that are rotationally and positionally invariant. There are two types of pooling: Maximum Pooling and Average Pooling. Maximum Pooling selects the highest value from the kernel-processed region of the image, while Average Pooling returns the average value of all pixels in that region. Max Pooling is commonly used. At this stage, the feature map is reduced in size. Typically, a 2 by 2 maximum pool size is established, allowing for the reduction of the feature map's size without discarding valuable image information.

classifier.add(MaxPooling2D(pool_size=(2,2)))

3) FLATTENING:

Here, all the feature maps pooled were concatenated into a single vector for further layer input. All feature maps are collapsed into a single column by the Flatten function.

classifier. add (Flatten ())

4) FULLY CONNECTION:

Using the Dense function in Keras, we will then employ the vector obtained in the previous stage as the input to the neural network. The number of hidden layer nodes is determined by the first parameter. This number can be optimized through trial and error. Models with higher dimensions require more computational resources for fitting. It is common practice to choose the number of nodes in powers of two.

classifier.add(Dense(units=64))

Next, the output layer must be added. Since we anticipate a binary outcome, we will use the sigmoid activation function in this case. If we expected more than two outcomes, SoftMax would be used. Since we only anticipate the projected probability of the classes, the output is set to 1.

classifier.add(Dense(units=1, activation='sigmoid'))

IV. RESULTS AND DISCUSSION

By utilizing Brain Web's real-time dataset, the proposed method has been practically implemented with images of sizes 256 × 256 and 512 x 512. Additionally, other metrics, such as True Positive and True Negative, have been employed to evaluate the algorithm's performance. True Positive denotes the frequency at which the proposed algorithm correctly identifies a damaged region as such, while True Negative represents the frequency at which it accurately predicts a non-damaged region as such. False Positive (FP) and False Negative (FN) metrics respectively indicate the number of times the proposed algorithm incorrectly identifies a damaged region and the number of times it erroneously classifies non-damaged regions as damaged.The sensitivity and specificity of the suggested algorithm are governed by the parameters TP, TN, FP, and FN. Comparative tests revealed that the proposed method outperformed the Convolutional Neural Network (CNN). It was observed that the proposed approach exhibited superior performance compared to other picture datasets tested. Notably, the Convolutional Neural Network (CNN)-based solution suggested for 128 * 128 images demonstrated notably enhanced output quality when compared to images of other sizes as depicted in the table and charts.

TABLE 4.1: Typical results of the suggested method for several image collections, including positive, negative, false positive, and false negative values.

Different set of Images	True Positive (%)	True Negative (%)	False Positive (%)	False Negative (%)
128 * 128 Images	82.734	83.546	15.367	14.543
256 * 256 Images	81.445	85.167	16.633	16.932
512 * 512 Images	81.144	84.778	16.954	17.312

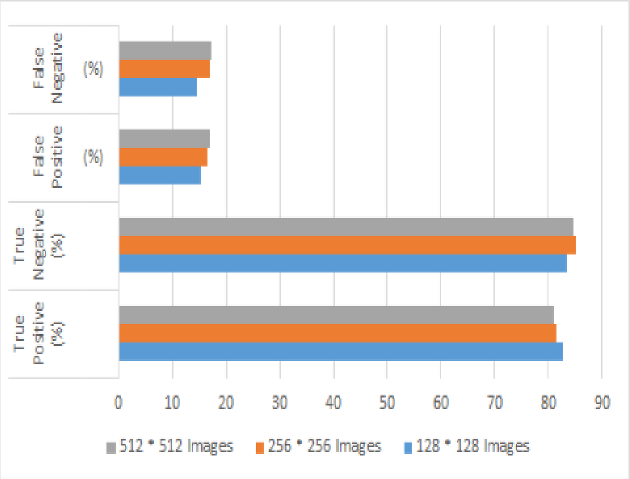

Fig. 4.1. Represents the performance analysis of CNN

According to Table 4.1, it displays the proposed methods for a few images based on positive and negative values. On the other hand, Fig 4.1 illustrates the performance analysis of CNN based on the image values.

When applied to MR images for analyzing the denoised image's shape and size, the segmentation technique proposed yields results similar to those depicted in Table 2 (below). The employment of a Convolutional Neural Network (CNN) for segmentation demonstrates satisfactory outcomes in terms of accuracy, sensitivity, and computational time.

TABLE 4.2: Symbolizes the Precision, Recall, and False Negative Rate of the proposed method over a range of image types.

Images	Accuracy (%)	Sensitivity (%)	Specificity (%)
128 * 128 Images	83.112	83.445	82.832
256 * 256 Images	85.323	82.456	84.743
512 * 512 Images	84.945	84.365	84.456

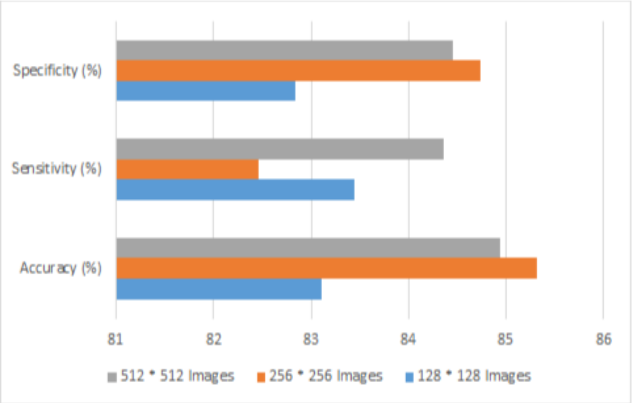

Fig. 4.2 Represents the performance of proposed CNN

According to Table 4.2, it illustrates the percentages of accuracy, sensitivity, and specificity of the images. Meanwhile, Fig 4.2 depicts the performance proposed by CNN based on the image percentage values.

In practical application, the suggested method accurately identifies the tumor area and can detect its expansion with minimal deviation from ground truth. This observation holds true for both 256 × 256 and 512 × 512 size MR images, with the smaller size image appearing to benefit more from the proposed method. In Table 4, not only the tumor's actual core but also its full extent, including partially affected tissues based on texture values, are observed, showcasing an improved state from the previous examination in the last column.

COMPARITIVE ANALYSIS

Table 4.3: Comparative Analysis Performance of Various Algorithm

Methods	Accuracy	Precision	Sensitivity	Specificity	F1-Score
KNN	86.77	81.05	84.14	82.15	77.15
Ensemble Model	95.23	93.05	94.65	86.55	81.12
SVM	91.02	78.15	92.25	78.5	83.15
Random Forest	95.76	68.15	90.15	81.15	82.45
Logistic Model	84.76	55.15	88.85	72.15	73.75
Proposed Model	96.01	94.51	96.56	87.66	85.88

Fig 4.3: Comparative Analysis Performance of Various Algorithm

Derived from the examination of the preceding two tables an graphs, Table 4.3 and Fig 4.3 are formulated to illustrate th comparative performance of the algorithm. With this dat tumor detection in the brain can be readily accomplished.

V. CONCLUSION AND FUTURE SCOPE

We proposed a computerized method for segmenting an identifying brain tumors using Convolutional Neural Networ (CNN). By accessing MR images from the provided file pat on the local device, the images are read and converted t grayscale. These images then undergo adaptive bilater filtering, a preprocessing technique used to remove noise fro the original image. After denoising the MR images, a binar threshold is applied to the resulting image, followed b segmentation of the tumor using a Convolutional Neur Network. The proposed model achieves an impressiv accuracy of 84% and demonstrates promising results whi requiring significantly less computational time an effort.Testing indicates that the proposed method benefits fro a substantial training set; however, gathering such a dataset often time-consuming and, in some cases, impractical in th field of medical image processing. The proposed approac needs to be sufficiently reliable to identify tumor areas in M scans in all scenarios mentioned above. To further improve th proposed method, weakly trained algorithms capable detecting anomalies with limited training data can be combine with self-learning algorithms to enhance accuracy and reduc computing time.

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