Harish Sharma
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Communication and Intelligent Systems

Proceedings of ICCIS 2023, Volume 1

Springer

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Volume 967

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Ashish Kumar Tripathi · Lipo Wang
Editors

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Preface

This book contains outstanding research papers as the proceedings of the 5th International Conference on Communication and Intelligent Systems (ICCIS 2023), which was held on 16–17 December 2023 at Malaviya National Institute of Technology Jaipur, India, under the technical sponsorship of the Soft Computing Research Society, India. The conference is conceived as a platform for disseminating and exchanging ideas, concepts, and results of researchers from academia and industry to develop a comprehensive understanding of the challenges of intelligence advancements in computational viewpoints. This book will help in strengthening congenial networking between academia and industry. This book presents novel contributions to communication and intelligent systems and is a reference material for advanced research. The topics covered are intelligent systems: algorithms and applications, smart data analytics and computing, informatics, and applications, and communication and control systems.

ICCIS 2023 received many technical contributed articles from distinguished participants from home and abroad. ICCIS 2023 received 750 research submissions. After a very stringent peer-reviewing process, only 102 high-quality papers were finally accepted for the presentation and publication.

This book presents the first volume of 34 research papers related to Communication and Intelligent Systems and serves as a reference material for advanced research.

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Dr. Vivek Shrivastava has approximately 20 years of diversified experience of scholarship of teaching and learning, accreditation, research, industrial, and academic leadership in India, China, and USA. Presently he is holding the position of Dean Research and Consultancy at National Institute of Technology Delhi. Prior to his academic assignments he has worked as System Reliability Engineer at SanDisk Semiconductors Shanghai China and USA. Dr. Shrivastava has significant industrial experience of collaborating with industry and Government organizations at SanDisk Semiconductors. He has made significant contribution to the design development of memory products. He has contributed to the development and delivery of Five-Year Integrated B.Tech.-M.Tech. Program (Electrical Engineering) and master's program (Power Systems) at Gautam Buddha University Greater Noida. He has extensive experience in academic administration in various capacities of Dean (Research and

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A Comparative Study of DL and ML Models for Brain Tumor Detection

Gurpreet Singh, Amit Chhabra, and Ajay Mittal

Abstract Brain tumor detection is a critical component of modern health care, with early and accurate diagnosis significantly impacting patient outcomes. Brain tumors are often detected and diagnosed using imaging techniques including CT scans, radiography, and MRI. In this study, we investigate the effectiveness of various state-of-the-art deep learning models, including VGG16, AlexNet, and CNN as well as machine learning models, including RF, SVM, and KNN in the perspective of brain tumor detection. Datasets used for the study, namely Brain Tumor Image Segmentation Benchmark and glioma, are exploited to test them with respect to major parameters: accuracy, precision, and recall. VGG16 and AlexNet are effective in capturing complex image attributes and thus considered in this work for analyzing and classifying brain tumor images, and the Convolutional Neural Network algorithm is employed as a reference. The comparative analysis quantifies and exhibits the efficiency and limitations of these algorithms. VGG16 achieved remarkable results with a precision of 93.27%, recall of 93.72%, accuracy of 95.23%, and an F1-score of 94.22%.

Keywords Brain tumor · CNN · VGG16 · AlexNet

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1 Introduction

1.1 *Background*

In recent times, digital medical images have played a crucial role in the detection of various illnesses, while also serving as valuable resources for training and research purposes. To streamline the creation of medical reports and advance medical image research, there is a pressing need for a precise and efficient computer-assisted diagnostic system [1]. The existing method to compute clinical imaging scans has utilized much time, has not diagnosed the brain tumor (BT) accurately, and attained many errors. Brain tumor becomes a major health issue and attains 10th rank for causing life loss in contrast to other medicinal circumstances. To recognize BT, MRI is an extensive method. This technique consists of non-hostile and effective components to capture thorough pictures of soft tissue. Hence, the details regarding the outline, place, and size of such tumors are obtained and the necessity of taking extreme ionizing radiation is eliminated among patients. Presently, more attention is provided to diagnosing BTs automatically and several extensive solutions have taken place [2]. These advancements are done in the healthcare domain with the rapid growth of ML and image processing.

MRI is the most robust way of diagnosis in this technological era. In this, no ionized radiation is applied to the patient, and the information related to place, size, and structure of human tissues and body parts is easily acquired. The resultant scans provide clarity and accuracy. Magnetic Resonance Imaging results in enhancing the accuracy to diagnose disease because of which the requirement of hostile empirical processes is eradicated. Furthermore, a responsible resource is obtained from this technology for localizing the lesions and planning operating interferences [3]. BT Magnetic Resonance Imaging has diverse methods such as chest X-ray and 3D multi-band scanning. Particularly, three-dimensional multi-band MRI is a more feasible way to locate the lesion regions in an accurate way and offers crucial details to doctors. This progress assists this approach in capturing diverse structures in similar tissue.

In the contemporary healthcare landscape, numerous medical institutions and websites provide extensive data on a wide array of diseases. These data sources serve as valuable resources for researchers, enabling them to apply various algorithms either for diagnosing clinical conditions or evaluating the performance of newly developed algorithms [4]. MRI stands out as the widely utilized imaging practice for identifying brain tumors. MRI possesses the unique capability to furnish detailed information about the size, shape, and location of human tissues and organs without subjecting patients to high levels of ionizing radiation. The resulting MRI images are exceptionally clear and precise. MRI has substantially enhanced diagnostic capabilities, obviating the need for invasive procedures such as thoracotomies or laparotomies. Additionally, it offers a dependable means to locate lesions and plan surgical interventions [3]. Brain tumor MRI involves various techniques, including

X-ray chest scanning and three-dimensional multi-band imaging. Notably, 3D multi-band MRI, in contrast to 2D imaging, allows for the precise localization of lesion areas, providing clinicians with vital information. This underutilized advancement enables MRI to capture multiple structures within the same tissue.

Image preprocessing is a critical step in the analysis of MR images, aimed at increasing the likelihood of detecting suspicious regions. This step primarily focuses on enhancing fine image details and reducing noise in the acquired images, thus enhancing the image's overall quality. Medical MR images that are degraded by noise tend to be less reliable and accurate [5]. One common form of degradation in MR images is the presence of a smooth signal intensity variation, which is referred to as intensity non-consistency, RF inhomogeneity, or bias field. This variation can lead to a reduction in high-frequency image properties, such as edges and contours, ultimately resulting in blurry images. Several image preprocessing approaches are adopted to enhance the segmentation and feature identification methods in which MRI images are employed in input. During this preprocessing step, a variety of filtering techniques are utilized to remove noise from the images. These techniques work to suppress undesirable distortions and enhance certain image characteristics. The process of segmentation includes splitting a picture into discrete areas that are identical with regard to a selected attribute, such as hue, saturation, or texture [6]. Segmentation is to make an image's description more concise, expressive, and understandable. Some researchers have argued that physically detecting edges is superior to computer-assisted boundary detection when it comes to separating feature extraction challenges from the task of automatic lesion boundary detection. Nevertheless, it is crucial to develop automated segmentation techniques in order to build computerized systems of diagnosis for brain tumor identification. By measuring specific attributes or traits that set one input pattern apart from another, feature extraction aims to diminish the original dataset. To perform feature extraction, pixels are measured representing a fragmented object from which various features can be calculated [7]. GLCM is a statistical approach to converting image data into numerical data for texture analysis according to pixel spatial relation where the characteristics of image texture are possible to be defined by computing the co-occurrence matrix. The texture of various diseases can be obtained in the epithelial image of the skin, such as contrast, correlation, entropy, uniformity, and energy.

In order to create a diagnosis for the input image, the diagnostic system's classification phase must make inferences about the data acquired in the earlier steps. Two methods are used to classify images: The first merely considers the categorical dissimilarity between the two classes (melanoma and benign) and assigns the data item a class label of 0 or 1 [8]. The next strategy involves trying to model $P(y|x)$. In addition to giving the data item a class label, this also opens up the option of a class subscription. Image classification is performed using machine learning models.

Support Vector Machine (SVM) is an effective machine learning (ML) model, and Vapnik developed this model in 1992 for tackling the complicated physics problems involving higher nonlinearity. The SVM algorithm is useful for handling the data with higher dimensionality and nonlinear associations amid the input variables and the output class labels [9]. To achieve this, kernel functions are implemented.

These functions are assisted in converting the input data into a space of high dimensionality, at which a linear separation is carried out. This algorithm works flexibly and robustly to supervised learning (SL) that becomes popular in numerous applications, including such as to classify images, detecting objects, bioinformatics, and NLP. The major purpose is that a feature space is mapped onto another feature space at higher latitudes with nonlinear transformation with the objective of acquiring a precise linear delimitation hyperplane (LDH) [10]. SVM is capable of computing the distance among dissimilar data points in the extended feature framework in a direct manner, for which the kernel functions are processed. Based on distinct mapping approaches, the partition of kernel functions is done into diverse classes: linear kernel (LK), polynomial kernel (PK), and radial basis kernel (RBK) functions.

Decision tree (DT) is extensively utilized by machine learning (ML) algorithms in a variety of applications such as for classifying the data, handling multi-output issues, and tackling values and outliers. This algorithm is visually simple, and its generation can be done fast due to the exception of the preceding hypothesis related to the data. The decision tree (DT) algorithm performs more efficiently as compared to the conventional methods [11]. It is a method for structuring a set of training data in the form of trees, with root nodes and leaves. The root is utilized to define the initial point to build this algorithm and its initial event, the central construct to describe the study or chief attribute of the dataset. The probabilities considered in such a path are similar to branches which are generated via root and associated with nodes and further associate those nodes with others. Every internal node is used to illustrate a decision related to an attribute which verifies the way to split the data into its child node. Furthermore, splitting, subtree or branch, and pruning are diverse terms which are included in this algorithm. These terms are deployed for defining that some particular specific nodes are removed [12].

Random Forest (RF) is a kind of supervised machine learning (ML) method which is helpful for tackling the issue related to classifying the data. While classifying the data, this algorithm emphasizes dealing with the categorical data. To perform regression tasks, Random Forest (RF) aims to handle the continuous data. This algorithm is planned on the basis of an enormous amount of decision trees (DT), in which every DT is employed for predicting a class, and the class having a supreme number of predictions is considered the predictive class of this algorithm [13]. This algorithm is developed in some particular stages in which every DT of this algorithm consists of a tree-like sequence related to decision nodes.

Artificial Neural Network (ANN) is a robust algorithm of supervised machine learning (ML). Several collections of interrelated artificial neurons are contained in this algorithm to perform computation. For this, a connectionist method is adopted. This algorithm is implemented in various application domains such as to recognize speech, detect autism genes, classify the data and in natural language processing (NLP). There are three kinds of nodes included in the standard algorithm, namely input, hidden, and output [14]. The initial ones have the explanatory metrics, and the variation is found in the level of features from model to model. The output nodes are composed of dependent variables and their amount is selected according to the chosen possibilities. The links and signals propagated in a forward direction are considered

to associate the nodes. The data regarding every link are utilized to measure diverse numerical weights. Every node focuses on multiplying the input value of the previous node with the weight and performing its addition [15]. An activation function (AF) is exploited for propagating the signal into the subsequent layer. Some extensive AFs are known as SoftMax, tan-sigmoid, and purlin. The sigmoid activation function (SAF) is considered the most effective one. Moreover, this algorithm is also composed of diverse components: weight initialization, feedforward (FF), backpropagation (BP) for error, updating weights, and bias [16, 17].

2 Literature Survey

Rammurthy et al. (2020) projected a method recognized as WHHO-based DeepCNN in which Whale Harris Hawks optimization (WHHO) model helped to identify the brain tumor on MRI scans [18]. Afterward, the images were segmented on the basis of CA and RST. Moreover, the projected technique was employed for extracting the attributes from the segments such as tumor size and LOOP. DCNN helped in detecting the brain tumor. WHHO was a hybrid of WOA and HHO. The results revealed the supremacy of the projected method over others at 81.6% accuracy.

Dandıl et al. (2020) designed a stacked model on the basis of LSTM and Bi-LSTM for diagnosing the brain tumor [19]. The experiments were conducted on an INTERPRET database containing magnetic resonance spectroscopy signals taken from healthy and unhealthy tissues. The results confirmed that the designed model yielded an accuracy of 93.44% in classifying pseudo-brain tumors with glioblastoma, 85.56% for diffuse astrocytoma, and 88.33% for metastatic brain tissue. Moreover, the designed model proved applicable to diagnosing pseudo-brain tumors.

Shiny et al. (2021) used a hybrid of the DL-based technique to diagnose malignancies in the brain and detect pixel shifts (DCNN) [20]. There are four stages in total: input/output, segmentation, extraction of features, and classification. Decisions based on an error function may be made using the DBN + CNN combination. Maximum accuracy of 0.957 is reached, using the suggested method. Taken as a whole, the findings support the idea that the suggested DBN + CNN method can reliably categorize brain cancers and detect pixel shifts. The network's efficiency is enhanced by using the BirCat algorithms for training.

Vankdothu et al. (2022) extended another automatic technique to analyze and classify brain tumors [21]. The picture was preprocessed based on an adaptive filter to analyze the Magnetic Resonance Imaging (MRI) picture. Improved K-Means Clustering (IKMC) was presented to split the picture and the GLCM was employed for extracting the images. This technique employed a deep learning (DL) algorithm called RCNN for classifying the pictures. The presented approach was simulated on the Kaggle dataset. The simulation results depicted that the presented approach was more effective and offered an accuracy of 95.17% while diagnosing brain tumor tissues from MRI pictures.

Okashi et al. (2022) created a technique for identifying brain cancers in Magnetic Resonance Imaging (MRI) by combining numerous variables with an AdaBoost classifier [22]. The photos are preprocessed to separate the brain region as the first step in the procedure. After that, several texture characteristics are recovered from each patch of the brain picture. After this step, methods for selecting features are used to determine which of the retrieved texture characteristics are the most significant. These optimal feature vectors are provided to the AdaBoost classifier, which is trained to categorize each patch as normal or abnormal tissue. According to the results, the accuracy of detection while employing STFA, LBP, and HOG features was 46.5%, 68.96%, and 87.93%, respectively.

Senan et al. (2022) investigated several research uses a mix of deep learning and conventional machine learning to detect brain tumors [23]. Brain tumors could be classified and diagnosed using AlexNet and ResNet-18 in conjunction with the Support Vector Machine (SVM) method. The deep convolutional layers of a DL model are used to extract robust and significant deep features. Deep learning methods, such as AlexNet and ResNet-18, are used to mine features, marking the beginning of the process of merging deep and machine learning. The outcomes produced by all methods were first-rate. The greatest results are shown by a hybrid approach including AlexNet and Support Vector Machines (SVMs), which have an accuracy of 95.10%.

Raza et al. (2023) projected hybrid architecture, called dResU-Net, which amalgamates the advantages of both the U-Net model and the deep residual network to attain better segmentation results for brain tumor segmentation [24]. High-level features are extracted using the residual network as an encoder and then recovered using the U-Net decoder. The model's efficacy was measured against the BraTS 2020 dataset. The suggested model yielded encouraging outputs, with an average dice score of 0.8357, 0.8660, and 0.8004 for the tumor core (TC), whole tumor (WT), and the enhancing tumor (ET), respectively. The external cohort dice scores for TC, WT, and ET were 0.8400, 0.8601, and 0.8221, respectively, demonstrating the model's generalization capabilities [25].

Chang et al. (2023) revealed that an effective 3D segmentation model (DPAFNet) is presented [26]. To prevent network deterioration, DPAFNet uses residual connectivity and dual-path convolution to increase the network's size. Experiments comparing this research to prior work on BraTS2018, BraTS2019, and BraTS2020 show promise, with improved accuracy and Dice score. Dice scores of 79.5%, 90.0%, and 83.9% are achieved by the proposed DPAFNet for the augmenting tumor, entire tumor, and tumor core on BraTS2018, correspondingly. Dice scores of 78.2% were obtained in the enhancing tumor, 89.0% in the total tumor, and 81.2% in the tumor core on BraTS2019.

Cao et al. (2023) proposed MBANet as a multi-branch Convolutional Neural Network that could also process data in three dimensions [27]. The MBANet BU module is first constructed using the optimized shuffle unit. In the BU component, the convolution operation is carried out using group convolution after the input channel is divided, and the convolutional channels are then scrambled using the channel shuffle. The attention layer of the MBANet encoder is a new multi-branch 3D Shuffle

Attention (SA) module. Furthermore, MBANet's skip connection employs a 3D SA module to better recover the up-sampled semantic features' resolution. During tests conducted on two 2018 and 2019 BraTS datasets, it was discovered that ET, WT, and TC dice could achieve 80%, 89%, 86%, 78%, 87%, and 83%, respectively.

Tripathy et al. (2023) recommended a method for diagnosing the tumors based on EfficientNet based on transfer learning (TL) [28]. Three frameworks from the group EfficientNet-B2, EfficientNet-B3, and EfficientNet-B4 were adopted. This strategy was concentrated on improving the adequacy as well as upgrading the accuracy utilizing thresholding. The data were augmented to mitigate pictures in the dataset. The recommended method was more solid with regard to its true capacity for scaling all dimensions of profundity, width, and resolution of a picture at a constant ratio. This technique was useful to capture complex features and expand the presentation. The results showed that the recommended method provided 95% accuracy in comparison with diverse techniques.
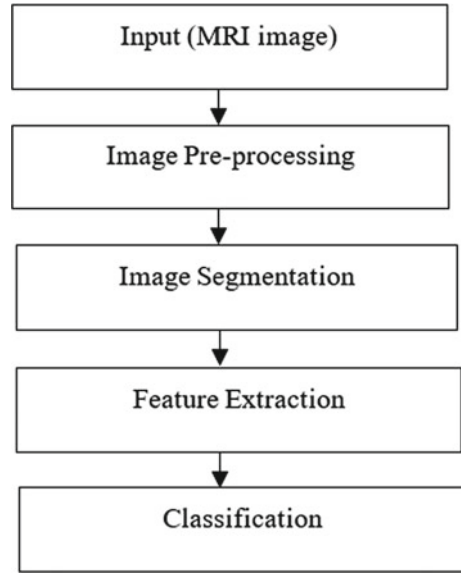
3 Research Methodology

3.1 Datasets

Separate datasets are used for testing the effectiveness of the models, i.e., BRATS and glioma. Below is the information on the datasets used for evaluation:

BRATS Dataset. BRATS (Multimodal Brain Tumor Segmentation) dataset is a pivotal store in the realm of medical imaging, specifically tailored for the demanding job of BT segmentation and classification. The dataset consists of brain MRI scans encompassing a range of modalities, including T1-weighted, T1-weighted contrast-enhanced, T2-weighted, and Fluid-Attenuated Inversion Recovery (FLAIR) images. Beyond mere imaging data, this dataset offers invaluable annotations or ground truth segmentations that delineate various brain tumor regions within the MRI scans. These annotations help researchers train and evaluate algorithms designed to precisely identify and classify different types of brain tumors, notably gliomas, which can be further categorized into distinct grades.

Glioma Dataset. Glioma datasets play a crucial role as essential resources in the research of BT that begin from glial cells within the central nervous system. Among these datasets, The Cancer Genome Atlas (TCGA) Glioma Dataset stands out as a comprehensive treasure trove of molecular and clinical information from a substantial cohort of glioma patients. Researchers focus TCGA model to unravel the intricate genetic and epigenetic underpinnings of gliomas, enabling a deeper understanding of these tumors and potential avenues for targeted therapies. Additionally, the Repository for Molecular Brain Neoplasia Data (Rembrandt) dataset provides gene expression data and clinical information, further enriching the field's resources for glioma research. These datasets collectively empower medical professionals and

researchers to enhance diagnostic accuracy and treatment strategies for gliomas, ultimately advancing patient care in the realm of neuro-oncology.

3.2 Methodology

In this work, the suggested framework is based on TL in which VGG16 is integrated with Convolutional Neural Network (CNN) for BT detection. Figure 1 illustrates the process of detecting brain tumors using MRI.

The brain tumor is diagnosed in diverse phases which are discussed as:

Input MRI image and Preprocess. This phase makes the deployment of Magnetic Resonance Imaging scan as input and Gaussian filter to preprocess the images. This filter is effective for mitigating the noise and eliminating the blurriness from the images. This filter is called a smoothing operator. Moreover, it is employed to remove naturally available fine image details. The impulse response of this approach is called a Gaussian function that is implemented in highlighting the possibility of distributing the noise. The Gaussian noise is effectively eradicated using this approach. This filter is a non-uniform, linear, and low pass having a Gaussian function related to a given SD.

Segmentation. This phase deploys a snake segmentation method for segmenting the brain area from the Magnetic Resonance Imaging image. This method is planned on the basis of a raster scan. Thus, it is capable of covering the extreme edges of the picture. The SAC framework [6–8] is exploited to set a parameterized preliminary

contour curve in the image space and develop an EF for characterizing the shape of the area with respect to internal energy (IE) and external energy (EE). The features of the curve are utilized to verify the IE. According to the notion of curvature, curve length, etc., the features of a picture are assisted in explaining the latter power. The energy function is diminished, to converge the primary contour curve $C(s) = (x(s), y(s), s \in [0, 1])$ at rapid level toward the boundary of destination region, under there strains of both energies:

$$E(C) = \int_0^1 \alpha E_{\text{int}}(C(s)) + E_{\text{img}}(C(s) + \gamma E_{\text{con}}(C(s)))\mathrm{d}s. \tag{1}$$

In this, three sections are comprised in EF in which E_{int} is used to depict the IE to ensure that the curve is smooth and regular; E_{img} to depict image power that is assigned with respect to attributes of anticipated place, like edges; and E_{con} is used to denote the restricted power (curve). The major task is to verify the length and curvature. The SAC algorithm is employed due to its geometric restraints. Despite the quality of image, this algorithm emphasizes on extracting the smoother and closed boundaries. However, it has some limitations. The complex issue is of dealing with its dependence on the primary contour. The position, shape, and number of control points become capable of attaining the wanted result after choosing an applicable primary contour.

Filtering. Magnetic Resonance Imaging scans often get affected by certain kinds of noise, and to deal with such situations, the PNLM approach, which is a modification of NLM, is exploited for denoising the images. Different from the existing method, this approach attains a lower Mean Square Error value. This image consists of the weighted average of all the voxel intensities. Moreover, it is useful for computing the stored intensity value of the voxel. For a discrete noisy image, $u = \{u(i)|i \in I\}$, the computation of a predictive value of $NL[u]i$, for a pixel i, is done as a weighted average related to every pixel within the image

$$\text{NL}[u]i = \sum_{j \in I} W(i, j)u(j). \tag{2}$$

The likeness among the pixels i and j is defined as the base due to the dependence of the family of weights $\{w(i, j)\}j$, and it results in a meeting with the condition $0 \leq w(i, j) \leq 1$ and $w(i, j) = 1$. The $u(N_k)$ is employed for representing a square neighbor of set size and centered at a pixel k, whereas the likeness of the intensity gray-level vectors $u(N_i)$ and $u(N_j)$ is considered as the base to signify the likeness of 2 pixels amid i and j. For evaluating the likeness, the given equation is employed for evaluating the diminished function of ED as:

$$\left\| u(N_i) - u(N_j) \right\|_2^2, a. \tag{3}$$

In this, 'a' denotes SD related to the Gaussian kernel, and its value is 0 above. The notion of Euclidean distance leads to the development of noisy neighborhoods:

$$E\left\|u(N_i) - u(N_j)\right\|_2^2, a = \left\|u(N_i) - u(N_j)\right\|_2^2, a + 2a^2. \tag{4}$$

The ED is exploited for maintaining the order of resemblance among pixels. Moreover, this similarity leads to illustrate the sturdiness of this approach. The average of the pixels is heavily influenced by the pixels with analogous gray-level neighbors. These weights are expressed below.

$$W(i, j) = \frac{1}{z(i)} e^{\frac{-\left\|u(N_i) - u(N_j)\right\|_2^2, a}{h^2}}. \tag{5}$$

In this, $Z(i)$ represents the normalized constant.

$$Z(i) = \sum e^{\frac{-\left\|u(N_i) - u(N_j)\right\|_2^2, a}{h^2}}, \tag{6}$$

in which h is used to illustrate a degree of filtering. This metric is employed to constrict the regression of the exponential function. It is implemented to control the EF regression [22]. It results in making weights similar to a function of ED.

Classification. The classification task to classify the brain tumor category is performed using various machine learning and deep learning models, which are as follows:

1. AlexNet—developed by Alex Krizhevsky, Ilya Sutskever, and Geoffrey Hinton, it comprises eight layers, including five convolutional layers followed by max-pooling layers and three fully connected layers. What sets AlexNet apart is its use of rectified linear units (ReLUs) as activation functions and the application of dropout regularization to prevent overfitting.
2. VGG16—proposed by the Visual Graphics Group (VGG) at the University of Oxford, it consists of 16 weight layers, comprising 13 convolutional layers and three fully connected layers. VGG16 employs small 3×3 convolutional filters with a stride of 1 and max-pooling layers of 2×2 size, maintaining a simple and uniform architecture. The network's depth and use of small filters aim to capture intricate patterns in images, enabling it to learn rich representations of visual data.
3. CNN—structured with layers that automatically learn and extract hierarchical representations of the input data through convolutions, pooling, and activation functions. The core components include convolutional layers that apply filters to detect features, pooling layers that downsample the information, and fully connected layers that classify the learned features.

4. Random Forest—operates by constructing multiple decision trees during training and outputs the mode of the classes for classification or the average prediction for regression from individual trees.
5. SVM—works by finding the optimal hyperplane that best separates data points into different classes in a high-dimensional space. It aims to maximize the margin, the distance between the hyperplane and the nearest data points (called support vectors). SVM can handle complex datasets by mapping them into higher dimensions using kernel functions, allowing for nonlinear decision boundaries.
6. KNN—operates based on the principle of similarity, where it classifies new data points by considering the majority class or average value of their neighboring points. The algorithm assigns a class to a data point based on the most common class among its k-nearest neighbors, determined by a chosen distance metric (such as Euclidean distance).

VGG16 was the best-performing model among all the machine and deep learning models, the architecture of VGG16 is explained below, and the reason for VGG16's performance is its ability to learn the best representations when compared to all the other models.

Figure 2 illustrates VGG16 model architecture and the diverse phases of VGG16 are explained as:

1. This model contains 16 which illustrates the sixteen layers containing weights. There are 13 conv., 5 MP, and 3 dense layers that are summed up to twenty-one layers. However, only 16 weight layers such as the learnable metrics layer are employed.
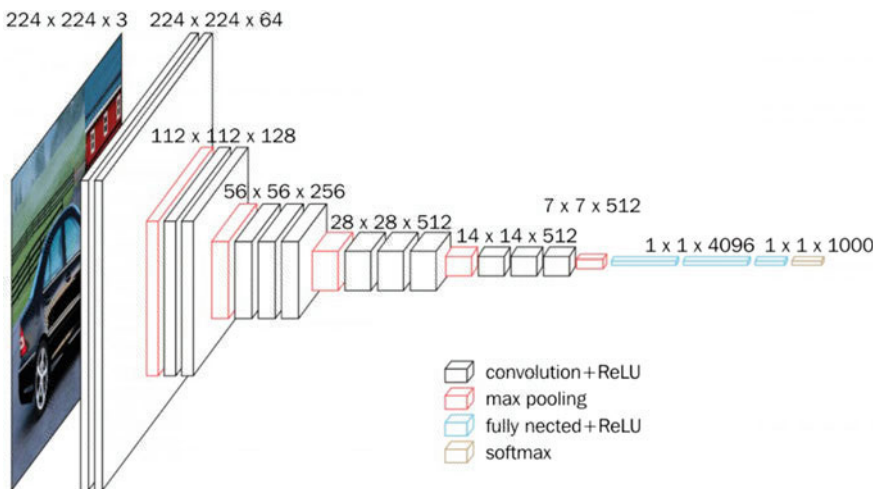2. The tensor size for input in this model is 224, 244 having three RGB channels.

Fig. 2 VGG16 model architecture

3. This model does not employ an enormous number of hyperparameters. It has only conv. layers having 3×3 a filter with stride 1 and it makes the deployment of similar padding and the MP layer has a 2×2 filter of stride.
4. The entire structure of this approach leads to arranging the conv and MP layers at a consistent level.
5. There are sixty-four filters in Conv-1 layer, 128 in Conv-2, 256 in Conv-3, and 512 in Conv-4 and Conv-5 layers.
6. A set of Conv. layers are adopted in three FCs in which the initial two employ 4096 channels each, and the last one is used to execute 1000-way ILSVRC classification. This layer consists of 1000 channels. The final layer is known as a SoftMax layer. Figure 3 illustrates the detailed visual representation of VGG16 architecture employed such as its layers, shapes, activation function, and data types.

4   Result and Discussion

The transfer learning model is applied for brain tumor detection. The presented model undergoes a comprehensive evaluation by comparing it with various other deep learning and machine learning models across several performance metrics, including accuracy, precision, recall, F1-score, and ROC. Two separate datasets (BRATS and glioma) are used to find out how well the developed models work.

As depicted in Fig. 4, sample images from the glioma dataset are provided, showcasing its four distinct classes. These four classes are meningioma, glioma, no tumor, and pituitary and the percentage share of each of these classes is shown in Fig. 5.

The following table, Table 1, presents a comprehensive overview of the model performance metrics on the glioma dataset for various machine learning models, such as AlexNet, VGG16, CNN, Random Forest, Support Vector Machine, and KNN.

Figure 6 shows the graphical representation of performance of various deep learning and machine learning models on the glioma dataset for brain tumor detection. Each model's evaluation includes precision, recall, accuracy, and F1-score metrics. These metrics play a crucial role in assessing the models' abilities to classify brain tumor cases accurately. AlexNet model achieved a precision of 92.25%, indicating that it correctly identified a significant portion of true positive cases among its positive predictions, with a recall of 93.25%, meaning it effectively captured a large portion of actual positive cases. This resulted in an impressive accuracy of 93.57% and an F1-score of 91.35%, demonstrating a balanced trade-off between precision and recall. VGG16 algorithm is deployed and it works effectively at 0.932 precision and 0.937 recall. Moreover, the accuracy is augmented to 0.952 and F1-score to 0.9422 which depicts the applicability of this algorithm to categorize infected images. In the meantime, the Convolutional Neural Network and RF algorithm performed well and offered 0.91 accuracy. Though there is a variation in their precision and recall, the SVM is also proved effective to provide 77% precision and recall and 78% accuracy. This approach is capable of handling the task of categorizing tumors in an efficient