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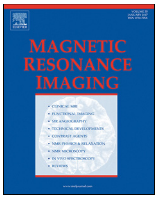

Review Article

A review on brain tumor diagnosis from MRI images: Practical implications, key achievements, and lessons learned

Mahmoud Khaled Abd-Ellah[a], Ali Ismail Awad[b,c,*], Ashraf A.M. Khalaf[d], Hesham F.A. Hamed[d]

[a] Electronics and Communications Department, Al-Madina Higher Institute for Engineering and Technology, Giza, Egypt
[b] Department of Computer Science, Electrical and Space Engineering, Luleå University of Technology, Luleå 97187, Sweden
[c] Faculty of Engineering, Al-Azhar University, P.O. Box 83513, Qena, Egypt
[d] Electronics and Communications Department, Faculty of Engineering, Minia University, Minia, Egypt

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ABSTRACT

The successful early diagnosis of brain tumors plays a major role in improving the treatment outcomes and thus improving patient survival. Manually evaluating the numerous magnetic resonance imaging (MRI) images produced routinely in the clinic is a difficult process. Thus, there is a crucial need for computer-aided methods with better accuracy for early tumor diagnosis. Computer-aided brain tumor diagnosis from MRI images consists of tumor detection, segmentation, and classification processes. Over the past few years, many studies have focused on traditional or classical machine learning techniques for brain tumor diagnosis. Recently, interest has developed in using deep learning techniques for diagnosing brain tumors with better accuracy and robustness. This study presents a comprehensive review of traditional machine learning techniques and evolving deep learning techniques for brain tumor diagnosis. This review paper identifies the key achievements reflected in the performance measurement metrics of the applied algorithms in the three diagnosis processes. In addition, this study discusses the key findings and draws attention to the lessons learned as a roadmap for future research.

1. Introduction

Brain tumors consist of abnormally growing tissue resulting from the uncontrolled multiplication of cells, and this tissue has no physiological function inside the brain. Tumors not only increase the size of and pressure in the brain but also cause swelling, all of which cause abnormal neurological symptoms. According to the National Brain Tumor Foundation (NBTF), the number of people in developed countries who die as a result of brain tumors has increased by 300% [1, 2]. Brain tumors are classified as either metastatic or primary brain tumors. In primary tumors, the cells are originally brain cells, but in metastatic tumors, the cancer cells have spread into the brain from another infected area of the body. Gliomas are the main type of tumor currently attracting the interest of brain tumor researchers. The term glioma describes different types of gliomas, ranging from high-grade (HG) tumors, called glioblastoma multiforme (GBM), to low-grade (LG) tumors, such as oligodendrogliomas or astrocytomas. Chemotherapy, radiotherapy, and surgery may be applied to treat gliomas [3].

The main goal of computerized brain tumor diagnosis is to obtain important clinical information regarding the tumor presence, location, and type. The information obtained through clinical imaging can guide and control any future interventions and thus leads to the correct diagnosis and treatment of the tumor. These automatic brain tumor diagnosis methods include different techniques that can be organized in a pyramid. At each stage of the pyramid, distinct techniques are needed to prepare, select, label, and describe the data, as indicated in [4].

Early tumor diagnosis plays a significant role in enhancing treatment possibilities. Brain imaging techniques, such as positron emission tomography (PET), single-photon emission computed tomography (SPECT), computed tomography (CT), magnetic resonance imaging (MRI), and magnetic resonance spectroscopy (MRS), are used to provide information about the location, size, shape, and type of brain tumor to assist in the diagnosis. MRI provides rich information about the anatomy of human tissues, and due to its widespread availability and soft tissue contrast, it is considered to be a standard technique. MRI uses radio frequency signals with a powerful magnetic field to produce images of human tissues [5, 6].

Brain tumor diagnosis consists of tumor detection, segmentation, and classification processes. Brain tumor detection techniques are mainly used to identify MRI images of tumors from a database, which is

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[*] Corresponding author.

E-mail addresses: mahmoudkhaled@ieee.org (M.K. Abd-Ellah), ali.awad@ltu.se (A.I. Awad), ashkhalaf@yahoo.com (A.A.M. Khalaf), hfah66@yahoo.com (H.F.A. Hamed).

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considered a basic and obvious process. However, brain tumor segmentation techniques are used for localizing and isolating different tumor tissues inside MRI images. Furthermore, brain tumor classification techniques are used to classify abnormal images as malignant or benign tumors. These three hybrid methods and techniques present useful information to radiologists and aid in the understanding of MRI information required for diagnosis.

Significant work in the field of brain tumor diagnosis has been conducted by many researchers over the past several decades. Both tumor segmentation and classification methods have been proposed. The clinical acceptance of diagnosis methods has depended on the degree of user supervision and the simplicity of computation [4]. However, the clinical applications are still limited, and although an extensive amount of work has been performed, clinicians still depend on the manual projection of the tumor, probably because of the lack of a connection between clinicians and researchers.

This study presents a review of the most important existing brain tumor diagnosis methods. The survey focuses on MRI brain tumor diagnosis with traditional machine learning and deep learning techniques. Although several reviews are available in the literature, a specific focus is typically placed on one particular process, such as segmentation in [4-9], classification in [10], or diagnosis in [3, 11-13]. This article offers a comprehensive overview of the whole brain tumor diagnosis system in terms of tumor detection, segmentation, and classification. In addition, the study covers the applications of traditional machine learning and deep learning approaches in each phase or process of the system.

The contributions of this study span multiple dimensions. First, the study takes the entire brain tumor diagnosis system using MRI images into account and considers the current conventional machine learning and deep learning approaches for brain tumor diagnosis. Second, a complete picture of the differences between and similarities of several techniques is provided in terms of their performance in three brain tumor diagnosis processes. Furthermore, the study introduces the available MRI image databases that are used in evaluating the performance of the reported techniques. Third, an extended discussion of the current research findings and possible future improvements and trends is provided. Fourth, a potential trial of integrating the three diagnosis processes is outlined for future research using a single automated system or model.

The remainder of this review is structured as follows. Section 2 presents necessary information on the brain tumor diagnosis framework, the benefits of machine learning and deep learning techniques for radiologists and clinicians, brain MRI images and available databases, and the deep learning paradigm. Section 3 is dedicated to an in-depth discussion of brain tumor diagnosis, which consists of tumor detection, segmentation, and classification. This section introduces the key achievements that have emerged from using classical machine learning and trending deep learning techniques and related comparisons. Section 4 is dedicated to discussing the research findings, the limitations, and the lessons learned. Finally, conclusions are provided in Section 5. A concise representation of the flow of this survey is shown in Fig. 1.

2. Preliminaries

The general framework of a computer-aided diagnosis (CAD) system for brain tumor diagnosis using MRI images, as summarized in Fig. 2, consists of data collection, preprocessing, segmentation, feature extraction, feature selection, feature reduction, classification, performance evaluation and diagnosis. Data collection is the process of obtaining the brain images required for diagnosis that will be fed through the diagnosis techniques. Brief explanations of the image types and the databases are provided in Sections 2.2 and 2.3, respectively. The preprocessing stage is a simple but necessary stage of brain image analysis. Preprocessing is commonly used to improve the resolution and contrast and to reduce the noise in the images. Several preprocessing approaches can be used, such as unsharp masking, median filters and Wiener filters. Median filters are most commonly used in the preprocessing stage to preserve image edges [3].

Several segmentation methods are used to perform the segmentation task. One of these methodologies is the multilayer artificial neural network (MANN). Many researchers have used the MANN and maintain a similar structure and learning algorithm but mention it in different ways, such as the feedforward backpropagation neural network (FFBPNN), the backpropagation neural network (BPNN), and the multilayer perceptron (MLP). Other segmentation methodologies and techniques include edge-based algorithms, region-based techniques, and clustering algorithms (e.g., k-means, mean shift, fuzzy c-means (FCM), and expectation maximization), and high performance can be achieved by deep learning algorithms. There are different methods for feature extraction, e.g., wavelet transform, texture features, Gabor features, principal component analysis (PCA), decision boundary feature extraction, and spectral mixture analysis. Many different approaches have been developed for medical image segmentation and analysis, as described in [14].

An increase in the feature vector dimension considerably decreases the accuracy of the system. Hence, feature selection techniques are applied to select the most important features. The popular feature selection algorithms used in the literature are sequential backward selection (SBS), genetic algorithm (GA), particle swarm optimization (PSO), and sequential forward selection (SFS), while independent component analysis (ICA), PCA, and kernel PCA are used for feature dimensionality reduction [10].

Several classifiers are used in the detection and classification stages, and they are reported here as they are mentioned in the published papers, such as support vector machine (SVM), kernel SVM (KSVM), feedforward backpropagation neural network (FFBPNN), self-organizing mapping neural network (SOMNN), backpropagation neural network (BPNN), probabilistic neural network (PNN), artificial neural network (ANN), probabilistic neural network-radial basis function (PNN-RBF), normalized cross-correlation (NCC), PSO, sequential minimal optimization (SMO), learning vector quantization (LVQ), multilayer perceptron (MLP), k-nearest neighbor (KNN), hybrid of genetic algorithm and support vector machine (GA-SVM), spectral clustering independent component analysis (SC-ICA), least-squares feature transformation (LSFT), fuzzy Hopfield neural network algorithm (FHNN), sparse representation classification (SRC), unsupervised linear discriminant analysis (ULDA), FCM and convolutional neural network (CNN). Most of these tools are used efficiently; however, the highest performances are achieved by deep learning algorithms.

2.1. Machine learning: a clinical perspective

From a clinical perspective, the goal of brain tumor diagnosis is to accurately detect and localize tumor tissues from MRI images using well-established clinical information and diagnostic features. The correct clinical diagnosis should lead to timely and appropriate disease treatment. To achieve this goal, it is important to obtain clinical knowledge and a database representing the information at a high level from which a decision and diagnosis can be made [4]. Manual brain tumor diagnosis is time consuming and less accurate due to the variety of tumor shapes and types, as there are more than 120 known types of brain tumors.

Machine learning has received considerable interest in modern computing, and the medical field is one of the areas of interest. The brain tumor diagnosis field has adopted different modern machine learning techniques. For instance, advanced algorithms such as image denoising [15, 16], image reconstruction [17-19], skull stripping, and registration [20] have been applied to simplify the use of brain images and to enhance the obtained information. Therefore, machine learning has created opportunities for collaboration among clinicians, engineers

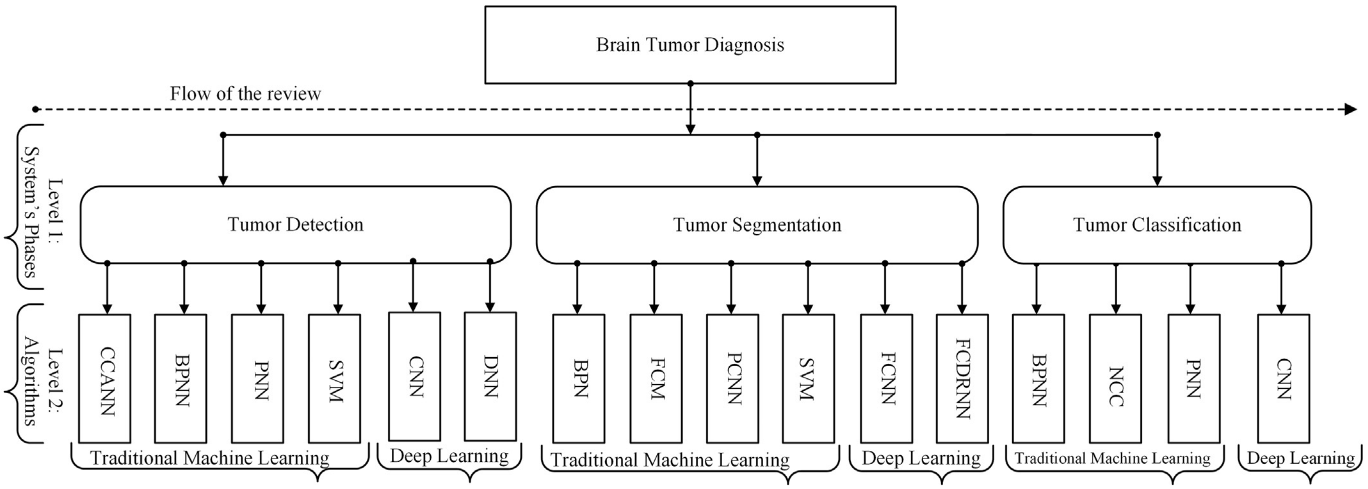

Fig. 1. The flow of the article with respect to the tumor detection, segmentation, and classification processes, with two levels of information. Level 1 is used for representing the main brain tumor diagnosis operations, while level 2 shows the identified traditional machine and deep learning techniques.

and computer scientists to develop semiautomatic, and later, fully automatic, tumor diagnosis tools with enhanced accuracy and reduced processing time.

In a semiautomatic brain tumor diagnosis, intervention from radiologists and clinicians is often required to initialize the technique, to review the result, or to manually correct errors in the process outcomes. However, in a fully automatic brain tumor diagnosis, computerized tools, which incorporate prior knowledge and human intelligence, are used for conducting the tumor diagnosis processes without a need for human interaction.

To investigate the accuracy and the required processing time that machine learning can achieve in tumor diagnosis, a brain tumor diagnosis competition was conducted on 225 cases to determine the accuracies of manual diagnosis and machine diagnosis by the Artificial Intelligence Research Centre for Neurological Disorders and a research team from the Capital Medical University. On the one hand, it was found that machine diagnosis (Biomind system) provided 195 correct diagnoses with a ratio of 87% in 15 min. On the other hand, the manual diagnosis provided 148 correctly diagnosed cases with a ratio of 66% in 30 min by a team of 15 radiologists [21]. These results demonstrate the superiority of machine learning diagnosis over manual diagnosis in terms of accuracy, processing time and the efforts of radiologists. To

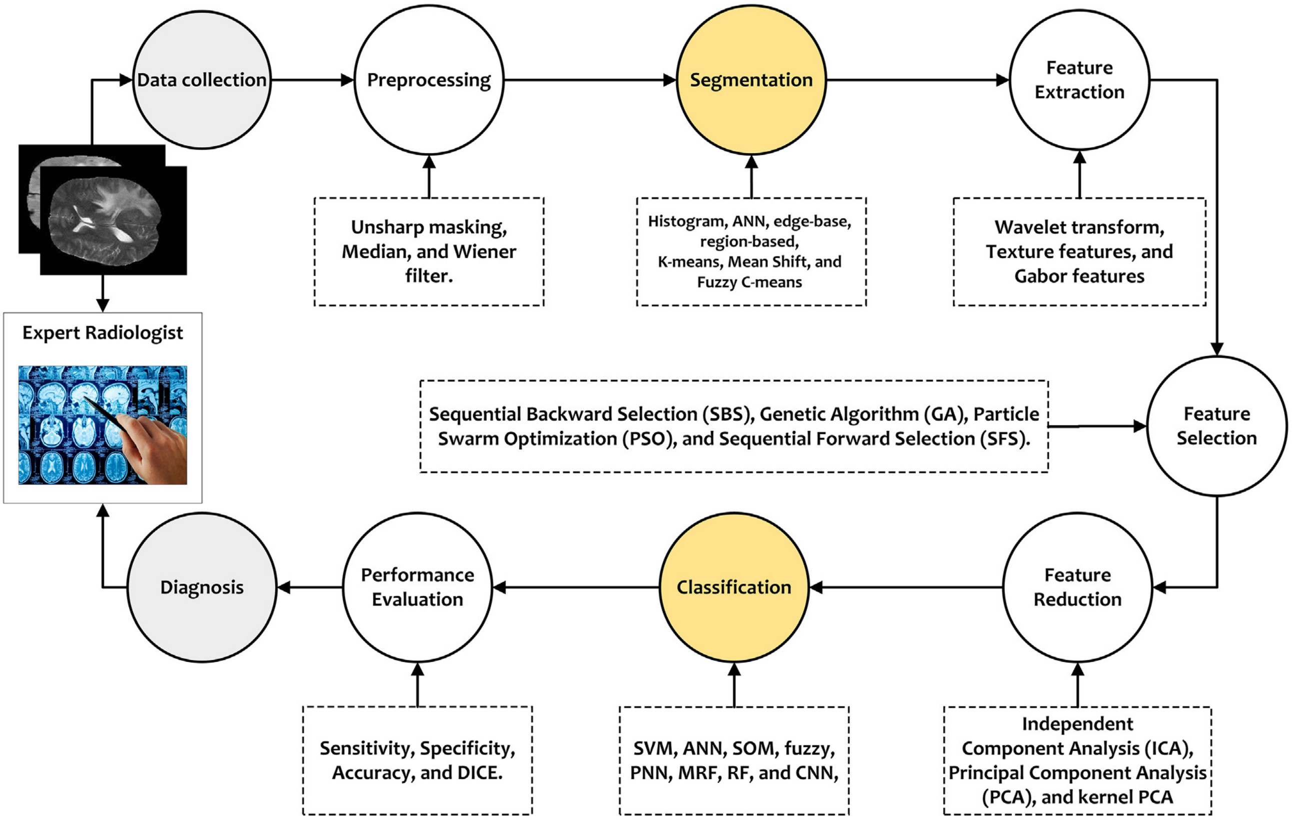

Fig. 2. A flowchart of a generic computer-aided diagnosis (CAD) system for diagnosing brain tumors. This flowchart shows all stages of a complete CAD system; it is necessary to have all the stages combined in one system. The tumor detection stage does not appear because the CAD system assumes that the tumor is present in the collected data.

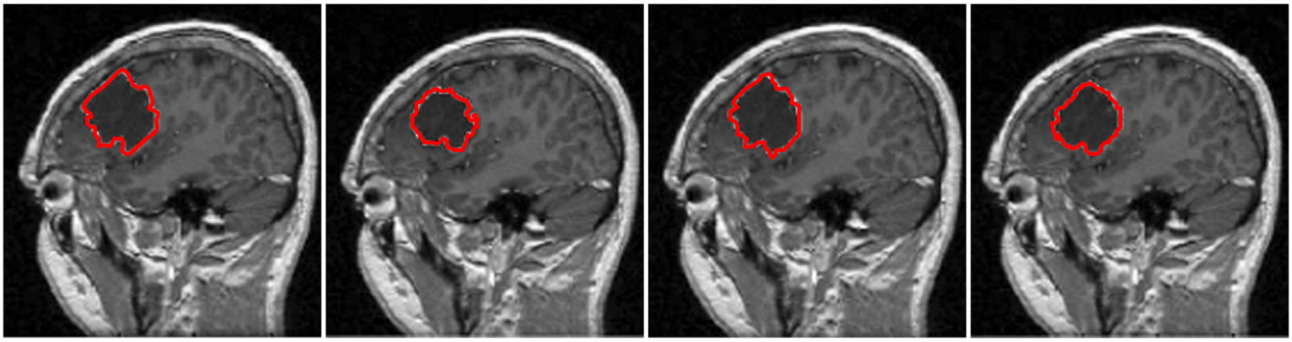

Fig. 3. Examples of the manual segmentation of glioma on the same MRI by four different experts.

further illustrate this superiority, Fig. 3 shows an example of the manual segmentation of a brain tumor on the same MRI and same patient by four different experts.

Although semiautomatic and fully automatic diagnosis techniques present superior results over manual diagnosis, manual diagnosis is still used in clinical trials, especially to distinguish tumor tissues. This review study is considered to be a further step to support the collaboration among radiologists, engineers and computer scientists to develop accurate and efficient brain tumor diagnosis tools based on machine or deep learning techniques.

2.2. Brain magnetic resonance imaging

The brain can be imaged using different modalities. These modalities are MRI, CT, SPECT and PET. At present, MRI, which was invented in 1970, is the most important imaging modality for medical brain imaging in use; it has several advantages over other imaging modalities, including being safer and providing rich information, as indicated in [22] and [2]. Fig. 4 shows examples of the four MRI modalities extracted from the BRATS 2013 database.

MRI is well known for its many advantages, which enable doctors to detect physical abnormalities in the brain. However, it is expensive and not suitable for individuals with claustrophobia [23]. During MRI image acquisition, a group of 2D images can represent a 3D brain volume. Each MRI modality plays a different role in diagnosis. Edematous regions are delineated in T2 images. Healthy tissues can be distinguished in T1 images. T1-Gd images are used for distinguishing the tumor border. Edematous regions can be distinguished from cerebrospinal fluid (CSF) in fluid-attenuated inversion recovery (FLAIR) images. The differences among the images produced by these MRI modalities can be used to create various types of contrast images. Four standard MRI modalities are applied for diagnosis: FLAIR, T2-weighted MRI (T2), T1-weighted MRI (T1), and T1-weighted MRI with gadolinium contrast enhancement (T1-Gd), as shown in Fig. 4.

2.3. Available MRI databases

Every technique needs to be validated by comparing a quantitative index with a truth model to measure the efficiency. Typically, a truth model is created by experts. New methods can also be evaluated by expert radiologists and physicians or using synthetic images [22]. A comparison of different databases is shown in Table 1.

BrainWeb was developed by the McConnell Brain Imaging Centre; an MRI simulator provides anatomical models of normal and abnormal brains. BrainWeb has an assortment of intensity nonuniformity (“RF”) levels (0, 20 and 40), and for each level, the slice thicknesses are 1 mm, 3 mm, 5 mm, 7 mm, and 9 mm with different noise levels (0%, 1%, 3%, 5%, 7%, and 9%). The Internet Brain Segmentation Repository (IBSR) was developed by The Center for Morphometric Analysis (CMA). The brain MRI database contains files formatted as 256 × 256 images with 16-bit integers.

The AANLIB database available from Harvard Medical School contains six main sections: a neuroimaging primer and sections on normal anatomy, cerebrovascular disease, neoplastic disease, degenerative disease, and inflammatory disease. The Section for Biomedical Image Analysis (SBIA) of the Center of Biomedical Image Computing and Analytics (CBICA) at the University of Pennsylvania is used for developing computer-based image analysis methods for diagnosing brain diseases, such as Alzheimer's disease, schizophrenia, autism, and traumatic brain injury (TBI). These databases were used for the Medical Image Computing and Computer Assisted Intervention (MICCAI) challenges. The Reference Image Database to Evaluate Therapy Response (RIDER) was developed by The Cancer Imaging Archive (TCIA) and contains imaging data obtained from 19 patients. Alzheimer's disease neuroimaging initiative (ADNI1) contains two types of Alzheimer's disease and contains imaging data obtained from 400 patients. Allen brain atlas provides a normal images dataset that contains imaging data obtained from 20 patients. Moreover, “ Brain-development.org” provides a dataset for normal patients collected from 3 hospitals.

2.4. Deep learning paradigm

Deep learning is the learning performed by a convolutional multilayer neural network, which has many hidden layers and free parameters. Unlike the commonly used multilayer neural network, each MRI input image passes through a series of convolution layers with

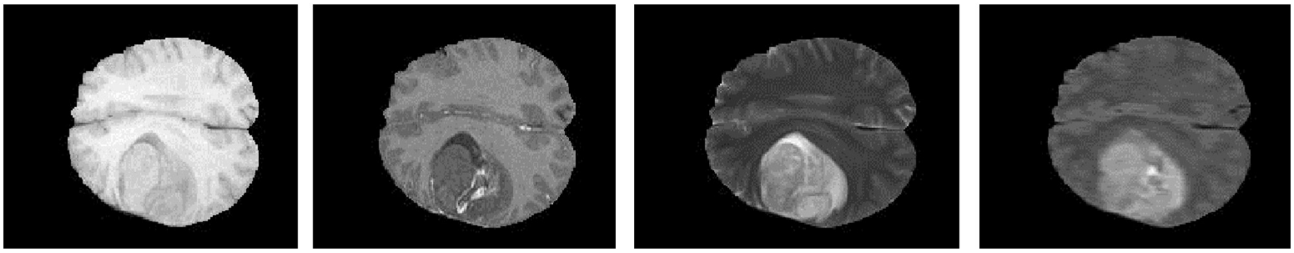

Fig. 4. Examples of different MRI modalities applied to HG glioma. The examples were extracted from the BRATS 2013 database. From left to right: T1 MRI image, T1-Gd MRI image, T2 MRI image, and FLAIR MRI image.

Table 1
An overview of available brain MRI image databases.

Name	From	Available modalities	Image type	No. of images	No. of patients	Link to the source
AANLIB	Harvard Medical School	T1- and T2-weighted MRI	Normal and tumor	-	-	http://www.med.harvard.edu/aanlib/
ADNI1	Alzheimer's disease neuroimaging initiative	T2, FLAIR, and DTI	Early AD, elderly control	200, 200	400	http://adni.loni.usc.edu/data-samples/data-types/
Allen brain atlas	Allen Institute Publications for Brain Science	T1, T2, and DTI	Normal	20	8	http://human.brain-map.org/mri_viewers/data
BrainWeb	McConnell Brain Imaging Centre	T1-, T2-, and proton-density-(PD-)weighted	Normal Multiple sclerosis (MS)	20 1	1 1	http://www.bic.mni.mcgill.ca/brainweb/
Brain-development.org	Imperial college, London	T1-, T2-, PD-weighted, MRA images, DTI images, and Diffusion-weighted images	Normal	600	3 hospitals	http://brain-development.org/ixi-dataset/
BRATS 2012	MICCAI 2012 Challenge	T1, T1-weighted (T1Gd), T2-weighted (T2), and T2 FLAIR	Glioblastoma (GBM)/HG glioma and LG glioma	45 3D	45	https://www.smir.ch/BRATS/Start2012
BRATS 2013	MICCAI 2013 Challenge	T1, T1-weighted (T1Gd), T2-weighted (T2), and T2 FLAIR	Glioblastoma (GBM)/HG glioma and LG glioma	65 3D	65	https://www.smir.ch/BRATS/Start2013
BRATS 2014	MICCAI 2014 Challenge	T1, T1-weighted (T1Gd), T2-weighted (T2), and T2 FLAIR	Glioblastoma (GBM)/HG glioma and LG glioma	50 3D	50	https://www.smir.ch/BRATS/Start2014
BRATS 2015	MICCAI 2015 Challenge	T1, T1-weighted (T1Gd), T2-weighted (T2), and T2 FLAIR	Glioblastoma (GBM)/HG glioma and LG glioma	300 3D	300	https://www.smir.ch/BRATS/Start2015
BRATS 2016	MICCAI 2016 BrainLes Workshop	T1, T1-weighted (T1Gd), T2-weighted (T2), and T2 FLAIR	Glioblastoma (GBM)/HG glioma and LG glioma	300 3D	300	https://www.smir.ch/BRATS/Start2016
BRATS 2017	MICCAI 2017	T1, T1-weighted (T1Gd), T2-weighted (T2), and T2 FLAIR	Glioblastoma (GBM)/HG glioma and LG glioma	285 3D	285	https://www.cbica.upenn.edu/sbia/Spyridon.Bakas/MICCAI_BraTS/MICCAI_BraTS17_Data_Training.zip
Cjdata	School of Biomedical Engineering, Guangzhou, China	T1-weighted contrast-enhanced	Meningioma Glioma Pituitary tumor	708 1426 930	233	https://figshare.com/articles/brain_tumor_dataset/1512427/5
RIDER	TCIA	T1, T2-weighted (T2)	Tumor	368 3D	19	https://wiki.cancerimagingarchive.net/display/Public/RIDER+NEURO+MRI
The IBSR	The CMA	T1-weighted	Normal Segmentations	21 18	21 18	https://www.nitrc.org/frs/?group_id=48

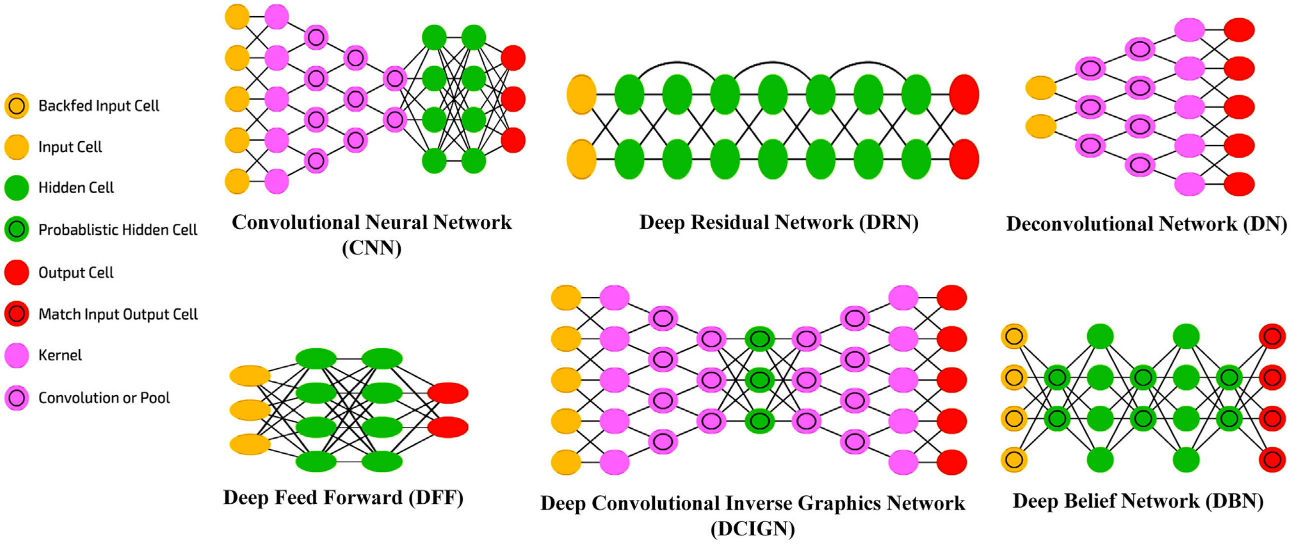

Fig. 5. A chart illustrating some common neural network types. The figure is used with copyright permission from The Asimov Institute [26].

filters (kernels), pooling layers, fully connected (FC) layers and finally, a softmax function is applied for the final decision-making task. Both classical machine learning and deep learning are artificial intelligence tools; however, deep learning has many characteristics that make it more powerful than traditional machine learning techniques. Such characteristics include a large number of free parameters, which ensures a solution for any relation; functions used in hidden layers; and complex connections between layers. Additionally, each layer can perform different tasks based on its structure and type. Despite the advantages of deep learning, common disadvantages such as the need for building a complex architecture using hidden layers, the high computational cost during training, and the large amount of data required for the training process to achieve a desired performance still remain [24]. Furthermore, these disadvantages contribute towards increasing the training time.

There are many types of and names for deep learning network structures, such as convolutional neural network (CNN), deep residual network (DRN), deep feedforward network (DFF), deep convolutional inverse graphics network (DCIGN), deep belief network (DBN), and deconvolutional network (DN), as shown in Fig. 5. The CNN architecture is the most common in the field of image processing. Its structure mainly consists of an input layer; feature extraction layers, which use convolutional layers; a rectified linear unit (ReLU) layer as an activation function; pooling layers; and classification layers [25].

The performance of deep learning methods, specifically CNN, in brain image diagnosis has increased their popularity among researchers, leading to a preference for using deep learning over traditional machine learning techniques. A CNN directly learns the representative complex features from the brain MRI images themselves, which allows the research focus to be on designing the architecture of the network rather than the extraction and reduction of the features. Patches extracted from brain MRI images are provided as inputs to the CNN, and local subsampling and trainable convolutional filters are used to extract the representative complex features [7, 10].

3. Brain tumor diagnosis

In recent years, numerous specialists in the field of medical tomography and delicate processing have made noteworthy advances in brain tumor diagnosis. Both fully automatic and semiautomatic strategies have been proposed. Clinical acknowledgment of diagnosis strategies has relied upon the simplicity of calculation and the level of supervision. As shown in Fig. 2, brain tumor diagnosis is divided into tumor detection, segmentation, and classification processes, which are discussed in-depth in this section. Performance comparisons of the reported techniques are also presented.

3.1. *Tumor detection*

Detection is the process of detecting the presence or absence of a tumor using MRI image databases. Detection is one of the most common problems in the medical field. The output of the tumor detection process is an MRI image labeled as normal or abnormal. Brain tumor detection through MRI can be performed using different techniques, such as SVM, ANN, KNN, and FFBPNN. The most commonly used techniques are summarized in Fig. 2, and different detection techniques are compared in Table 2 based on the feature type, detection methodology, and performance. Achieving the best detection method requires a large standard database as a benchmark to train the classifier and find the optimal method for feature extraction and detection.

3.1.1. *Traditional machine learning in tumor detection*

Several machine learning methods and different techniques are available for brain tumor detection through MRI. The method described by El-Dahshan et al. [27] uses DWT to obtain 1024 features and PCA to reduce them to 7. Then, the 7 features are provided to the detection stage, which uses an ANN consisting of three layers, with 7 nodes in the input layer, 4 neurons in the hidden layer, and a single neuron in the output layer. In the detection stage, two classifiers are used for the feedforward backpropagation artificial neural network (FP-ANN) and KNN. The database consists of 60 abnormal and 10 normal MRI images.

Zhang et al. [28] presented a BPNN method for identifying brain tumors in MRI images and separating normal from abnormal images. The wavelet transform is used to extract features from the images, and then PCA is applied to reduce the dimensions of the features. A 3-level decomposition with Haar wavelets has also been used to reduce the extracted features from 65,536 to 1024 and to approximate the coefficients of level 3. In total, 19 principal components are used to train the BPNN. The neural network structure is as follows: 19 nodes in the input layer, 10 neurons in the hidden layer, and one neuron in the output layer. The dataset consists of 66 images, with 48 abnormal and 18 normal images. The reduced features are sent to the BPNN classifier.

Saritha et al. [29] proposed a new method for classifying brain MRI images as normal or abnormal (pathological). Wavelet entropy-based spider web plots are applied to extract three features. A PNN is used for the detection process. The PNN has two layers: the competitive layer

Table 2
An overview of techniques for brain tumor detection by MRI. All methods in the table are machine learning methods.

Paper	Feature extraction	Detection methods	Data	Performance measures			Limitations
				Se (%)	Sp (%)	Ac (%)	
[27]	DWT	FP-ANN and KNN	AANLIB	100	90	97 & 98	Requires fresh training sets.
[28]	2D-DWT	BPNN	AANLIB	-	-	100	Requires fresh training sets.
[29]	2D-DWT	PNN	AANLIB	100	100	100	Fresh training set required with each change in database.
[30]	2D-DWT	SVM	AANLIB	98.12	92	97.78	The focus is on computing the wavelet-energy feature; other features are neglected.
[31]	2D DWT and GARCH	KNN and SVM	AANLIB	98.21	99.66	97.62 & 98.21	Asymmetrical; cannot model with respect to the sign of past values.
[32]	Intensity, symmetry, and texture features	AdaBoost algorithm	-	-	-	96.82	Reasons for selecting 40 features (13 intensity features, 1 symmetry feature and 26 texture features) are not mentioned.
[33]	DWT	SVM	AMDI, in Bertam, Pulau Pinang, Malaysia	-	-	65	Researchers mention that it is better to select a small set of good texture features without explaining how it can be done.
[34]	SC-ICA and ICA	ICA, SC-ICA, and SVM	MNI	76.4	99.9	98 & 96.1	Low threshold causes overclustering, which increases the cost of feature extraction.
[35]	DWT	SVM	AMDI	-	-	65	Large feature vector, which increases the classification error.
[36]	Grayscale, symmetry and texture features	SVM	Randomly selected	100	50	84	SVM trained with 46 MRI images (most of dataset used for training), which increases the accuracy.
[37]	PSO-based algorithm	PSO	Various hospitals in North India	96.24	92.76	94.42	Problematic method; some samples are misclassified.
[38]	Grayscale, symmetry and texture features	SVM, KNN, and SVM-KNN	BrainWeb	100	93.75	98	New training set required with changes in the dataset; high feature extraction complexity.
[39]	Texture feature	ANN and KNN	AANLIB	100	100	98.92 & 100	Algorithm used in feature extraction stage is not mentioned.
[40]	DWT-SGLDM	GA-SVM	AANLIB	-	-	95,6522	The system is complex, which increases computational time.
[41]	LaV	KNN and CFCM	-	95.3	100	100	Non-CSF pixels incorrectly assigned to the cluster.
[42]	-	BPNN	CIPR	-	-	96.33	Time-consuming training stage.
[43]	Texture feature	BPN and RBFN	PSG IMS	72	84	85.71	Low performance due to the small database size.
[44]	DWT	FFBPNN	AANLIB	100	92.8	99	Low specificity.
[45]	GLCM	Hybrid neuro-fuzzy system	BrainWeb AANLIB MS_MRI CHRC	98.33	97.5	98	Low specificity.
[2]	DWT	KSVM	Randomly selected	100	100	100	Selected features are not mentioned.
[46]	DT DAUB-4	SVM	AMDI, in Bertam, Pulau Pinang, Malaysia	-	-	85	Feature vectors reduced without mention of the selected features or the reason for selection.
[47]	GLRLM	SVM and FCM	Different medical centers	83.33	100	91.66	System is applied to a nonstandard database and is complex due to skull stripping stage; testing database is smaller than training dataset, which increases the accuracy.
[48]	Energy, entropy, homogeneity, contrast, correlation	Neuro-fuzzy	BrainWeb	88.9	100	95.65	Very small database.
[49]	GLCM	SMO	PSG IMS, Coimbatore	92	90	88.33	Small dataset.
[50]	Texture and GLCM	LS-SVM	BRATS 2013	-	81.33	96.63	Low number of selected features reduces the performance.
[51]	GLCM	LVQ, MLP, SOM and RBF classifiers	UKM Medical Center			93-96	Long computational time due to system complexity.
[52]	ICA	SOM neural network	Randomly selected	98.4	100	98.6	Small dataset, which may give better results.
[53]	DWT	KNN, Parzen window and ANN	AANLIB and LONI	-	-	99.2	Method can be applied to T2 images only and has classification complexity.
[54]	Gabor wavelets	CCANN	Diagnostic centers	-	-	91.8	Small database.
[55]	Intensity texture	PCNN and BPN	-	-	-	-	High system complexity due to the training and testing.
[56]	CNN	ECOC-SVM	RIDER	99.38	100	99.55	Many layers, which increases system complexity.
[57]	DWT	DNN	AANLIB	97	97	96.97	Small database.

and radial basis layer. The dataset consists of 75 MRI images: 15 normal and 60 abnormal images. A total of 52 images are used for training, and 23 images are used for testing.

In [30], Yang et al. proposed a new algorithm for early brain tumor detection by MRI. A 3-level 2D-DWT with Haar wavelets is used to extract features. Biogeography-based optimization (BBO) is utilized for optimization. A kernel-type SVM is used as a classifier with an RBF function. The dataset consists of 90 T2 MRI images with 256×256 pixels, including 5 normal and 85 abnormal images. A 3-level wavelet-energy process is used to reduce the features from 65,536 to only 10.

H. Kalbkhani et al. in [31] used 2D DWT and modeled the subband of the detail coefficients using generalized autoregressive conditional heteroskedasticity (GARCH), reducing 61,440 wavelet features to 24 features. Linear discriminant analysis (LDA) is used to extract the features, and PCA is used to reduce the feature vectors. Seven features are selected from the feature vectors with the eight-class scenario, and one feature is selected with the two-class scenario. Finally, a KNN and SVM identifier are applied for the detection process. The database contains 70 abnormal and 10 normal MRI images. The training set contains 21 abnormal and 3 normal images, while the testing set consists of 49 abnormal and 7 normal images.

Xuan and Liao [32] proposed a method for tumor detection. Three types of features are extracted from the input image, including intensity-based, symmetry-based, and texture-based features. Then, 40 features are selected, including 1 symmetry-based feature, 13 intensity-based features, and 26 texture-based features. The features are extracted from different image types, with 9 features extracted from T1 images, 12 features extracted from T2 images, and 19 features extracted from FLAIR images. An AdaBoost algorithm is then used in the detection process. The dataset contains data from 10 patients with 3 volumes of MRI images. Each volume consists of 24 slices. The dataset is divided equally into training and testing sets.

Othman et al. [33] used DWT with Daubechies wavelets to extract features from MRI images, producing 17,689 feature vectors for each image. An SVM is then applied for tumor detection with a kernel-type RBF. Sindhumol S. et al. [34] presented a technique for brain tumor detection by MRI based on spectral clustering independent component analysis (SC-ICA). Spectral distance is used to divide MRI images into different clusters, followed by the use of ICA along with an SVM. The database contains 20 abnormal and 40 normal MRI images. Later, Abdullah et al. [35] used DWT to preprocess images and extract features, producing 17,689 feature vectors for each image. An SVM is then used to identify the extracted features as normal or abnormal.

Nandpuru et al. [36] proposed a new detection technique. A median filter is used to remove noise in the preprocessing stage. Then, dilation and erosion techniques are applied to the MRI image for skull masking, and features are extracted using grayscale, symmetry and texture. PCA is used to reduce the number of features from 28 to 24 features, which are then used by an SVM in the detection stage. In total, 46 brain MRI images are used to train the SVM, and 50 MRI images are used in the testing stage.

Chandra et al. [37] proposed a new algorithm for brain tumor detection through MRI images using a clustering algorithm based on PSO. The algorithm finds the centroids of a number of clusters, finds the global best, and updates the cluster centroids based on the maximum average Euclidean distance. The database contains 110 abnormal and 62 normal MRI images.

Machhale et al. [38] designed and presented a new system for brain cancer detection. The system consists of image preprocessing, feature extraction and detection. A median filter and skull masking are applied during preprocessing. Symmetry, grayscale and texture features are extracted in the feature extraction stage, and 28 features are extracted from each MRI image. A KNN, SVM, and a hybrid (SVM-KNN) identifier are used in the detection stage. The dataset contains 96 brain MRI images, with 46 images for training and 50 for testing.

Another study by Najadat et al. [39] introduced a method for brain tumor detection. The method extracts features from brain MRI images. The ANN and KNN approaches are applied to label the brain MRI image as normal or abnormal. The database contains 615 abnormal and 95 normal MRI images. The number of features extracted from the MRI image by texture is 278.

A study by Kharrat et al. [40] also presented a new methodology, which consists of the following five stages: features are extracted by DWT and spatial gray level dependence matrix (SGLDM). Then, simulated annealing (SA) is applied for feature vector reduction, whereby 13 extracted features are reduced to 7 selected features. Stratified k-fold cross validation and the GA-SVM model are applied to optimize the parameters, which are then provided to the SVM identifier. The dataset contains 83 brain MRI images: 22 images for training (10 abnormal and 12 normal) and 61 for testing (44 abnormal and 17 normal).

Xiao et al. [41] proposed a method for estimating features from the correlation between the tumor and the lateral ventricles (LaVs) of the brain, which are then used to segment the tumor from MRI images. The approach consists of four stages: preprocessing, feature extraction, segmentation, and detection. The authors use KNN and conventional FCM (CFCM) clustering to detect abnormal images.

Ibrahim et al. [42] proposed a new technique for brain tumor detection by MRI. PCA is used for dimensionality reduction to reduce the image features to 64 features, which are provided to the detection stage. Subjects are detected as having normal or abnormal images by a BPNN with the following structure: an input layer with 64 nodes, a hidden layer with 10 neurons, and an output layer with 64 neurons.

Deepa and Devi [43] proposed a system consisting of feature extraction, detection and segmentation. Optimal texture features are extracted from the tested image using a statistical method. A BPNN and radial basis function (RBF) neural network are used in the detection and segmentation stages. The dataset contains 42 brain MRI images (25 abnormal and 17 normal), with 30 images used for training and 12 used for testing.

Mohsen et al. [44] presented a hybrid method for brain tumor detection by MRI. The image is preprocessed using a feedback pulse-coupled neural network (FPCNN). Discrete wavelet transform (DWT) and PCA are used for feature extraction and reduction. A two-level DWT decomposition is used to provide the LL subband data to the PCA as feature vectors. Then, PCA is used to select a vector of 7 features to provide to the detection stage. The FFBPNN is then used to classify the MRI image as normal or abnormal. The FFBPNN consists of 3 layers with the following structure: 7 nodes in the input layer, 5 neurons in the hidden layer, and one neuron in the output layer.

Goswami and Bhaiya [45] combined a neural network with fuzzy logic in one system, called a hybrid neuro-fuzzy system, for detecting the presence of brain tumors. The proposed system consists of image preprocessing and feature extraction using a gray-level co-occurrence matrix (GLCM). The dataset contains 100 brain MRI images (60 abnormal and 40 normal).

In [2], Abd-Ellah et al. proposed a new method for brain tumor detection by MRI. MRI images are preprocessed using a median filter, and then features are extracted by DWT. PCA is applied for feature reduction, and the detection process was accomplished using an RBF and kernel-type SVM. The dataset consists of 80 MRI images, including 10 normal and 70 abnormal images. In total, 5 normal images and 43 abnormal images are used for training the SVM, and 5 normal images and 27 abnormal images are used for testing.

Abdullah et al. [46] used Daubechies wavelets to extract features, which are then processed by PCA to reduce the feature vectors from 17,689 to 200. An SVM and kernel-type RBF are then used to detect normal and abnormal MRI images. In total, 20 normal T2 FLAIR images and 11 abnormal T2 FLAIR images with 256×256 pixels are used for training the SVM; these images were selected from a database containing images from 32 patients (22 abnormal and 10 normal images). The number of tested images and the number of images for each patient are not mentioned.

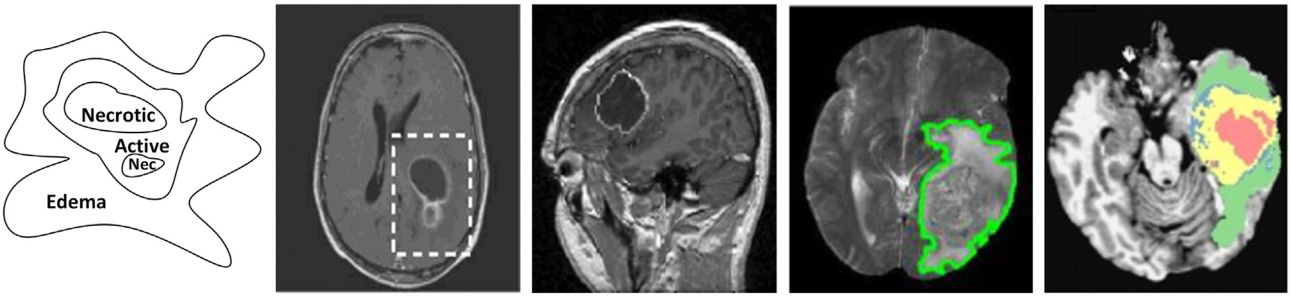

Fig. 6. Examples of different segmentation techniques applied to MRI modalities. The examples were extracted from the BRATS 2013 database.

In [58], the authors presented an automated technique for brain tumor segmentation from FLAIR MRI images. The technique uses superpixel-based extremely randomized trees, detection by SVM and an extremely randomized trees (ERTs) classifier to detect abnormal MRI images.

Parveen and Singh [47] proposed a new method for brain tumor detection by MRI. The study starts with input image enhancement and skull stripping. FCM is applied for image segmentation, and then the gray-level run-length matrix (GLRLM) is used for feature extraction. An SVM classifier is applied to identify abnormal images. The dataset contains 120 brain MRI images, with 96 images for training and 24 for testing.

Bhanumurthy and Anne [48] proposed a method that consists of three stages: feature extraction, detection, and segmentation. The extracted features, entropy, contrast, energy, homogeneity, and correlation, are provided to the detection stage, in which a neuro-fuzzy approach is used.

Deepa and Devi [49] presented an automated detection methodology. After the MRI image is preprocessed, features are extracted by applying the texture feature and GLCM. SMO is used in the detection stage. The input dataset contains 42 images: 17 normal and 25 abnormal images.

In [50], a hybrid approach for brain tumor detection by MRI is presented. The proposed method consists of three stages: preprocessing, feature extraction and detection, which use noise filtering, GLCM, and least squares support vector machine (LS-SVM), respectively. Four features are extracted: energy, correlation, homogeneity, and contrast. The dataset contains 100 brain MRI images, with 31 images for training (23 abnormal and 8 normal) and 69 for testing (52 abnormal and 17 normal).

In [51], LVQ, MLP, SOM and RBF classifiers are used in the detection stage to investigate the brain MRI dataset. Gaussian and kernel median filters are used in the preprocessing stage. Gaussian thresholding is used to extract the boundaries. Feature extraction is performed by GLCM, which provides 21 features and reduces them to 8 features via PCA. The 8 features used in the detection stage are contrast, entropy, homogeneity, correlation, moment, inverse moment, energy, and maximum probability.

Goswami and Bhaiya [52] presented a new method for identifying brain tumors by MRI based on a neural network technique. Histogram equalization, noise filtering, and edge detection are applied in the preprocessing stage. Then, features such as contrast, correlation, energy, and homogeneity are extracted by ICA and provided to the detection stage, which uses a self-organizing map (SOM) neural network.

Najafi et al. [53] proposed an automated method for brain tumor detection by MRI. The presented method consists of four processing stages: preprocessing using histogram equalization, feature extraction using DWT, dimensionality reduction using PCA, and detection. In the detection stage, three techniques are used: KNN, Parzen window and ANN. The feature vector dimension provided by DWT is 1024. Then, PCA is used to reduce the number of features to 5 for the Parzen, 6 for KNN, and 7 for ANN processes. The ANN consists of three layers, with 7 nodes in the input layer, 5 neurons in the hidden layer, and 2 neurons in the output layer. The database consists of 41 abnormal and 125 normal MRI images.

Amsaveni et al. [54] computed the features of regions of interest (ROIs) using Gabor texture features. A cascaded correlation artificial neural network (CCANN) is then used to detect the presence of a tumor. The CCANN consists of two inputs, two hidden layers, and the output layer. The dataset contains 50 brain MRI images collected from diagnostic centers. Subashini and Sahoo [55] presented a method for brain tumor detection using a BPNN and a pulse-coupled neural network (PCNN). The dataset contains 16 brain MRI images, including 8 abnormal and 8 normal images; 14 images are used for training, and 2 images are used for testing.

3.1.2. Deep learning in tumor detection

Brain tumor detection using deep learning techniques is a very recent field of research, and research papers on this subject are rare. Abd-Ellah et al. [56] used the convolutional neural network (CNN) of AlexNet as a feature extractor. Furthermore, the error-correcting output codes support vector machine (ECOC-SVM) is used in the classification stage, achieving an accuracy of 99.55%. In [57], DWT was combined with PCA for feature extraction and selection, respectively. The extracted features are classified by a seven-layer deep neural network (DNN).

3.2. Tumor segmentation

Segmentation is the process of dividing an image into ROIs to facilitate the characterization, delineation, and visualization of the data. The goal of segmentation is to change the representation of the MRI images to be more significant and easier to analyze in terms of the location and boundaries of tumors. Segmentation separates the tumor tissues, such as necrotic and edema, from normal tissues, such as white matter (WM) and gray matter (GM), as shown in Fig. 6. Additionally, tumor segmentation methods are based on similarities and discontinuities in image intensity. The intensity segmentation technique is based on dividing the MRI image using changes in the intensity, such as that at corners and edges, or similarities in the intensity by partitioning the regions based on a set of predefined criteria. The most commonly used segmentation methodologies are summarized in Fig. 2. Several methods and techniques are available for the segmentation of brain tumor MRI images, including histograms, ANN segmentation techniques, edge-based algorithms, physical model-based approaches, region-based techniques, and clustering algorithms, such as k-means, mean shift, FCM, and expectation maximization algorithms.

Different segmentation techniques and methodologies are compared in Table 3 based on the performance and limitations of the segmentation system. Mainly, prior knowledge and artificial intelligence are combined to enhance the segmentation performance. The highest performances are provided by deep learning techniques [10].

Table 3
An overview of techniques for brain tumor segmentation through MRI.

Paper	Segmentation methods	Data	Performance measures				Limitations
			Se (%)	Sp (%)	Ac (%)	Dice (%)	
[59]	outlier detection and robust estimates	3 real databases	-	-	-	80%	Large deformation cannot be handled, which causes inaccurate results.
[60]	spatially varying probabilistic atlas	-	-	-	-	60	The three Gaussians model increases the result for some cases, but the average performance is low. The Dice score is very low.
[61]	AdaBoost with PTPSA and multifractal dimension features	Siemens Medical Systems	-	-	-	48.4	The overall Dice score is low.
[62]	EMs with SPM atlas	5 different databases	-	-	-	90	It classifies the small rim around the ventricles as edema.
[63]	Thresholding and level set	DICOM	90.5	100	90.5	-	Accuracy changes with database changes.
		BrainWeb	100	100	100		
		BRATS	100	100	100		
[66]	LIPC	BRATS 2013	-	-	-	91 and 86	Patch-based features are insufficient to represent complex characteristics of the brain.
[67]	AdaBoost and graph-based segmentation	BRATS 2012	87.2	83.1	-	84.5	Time-consuming, semiautomatic method.
[68]	PCNN	Bruker BioSpin	-	-	98.1	-	Method is well suited for rodent brain feature extraction only.
[71]	ANN	PGIMER	-	-	91	-	Complexity of the system decreases the accuracy and increases the computational time.
[73]	Unsupervised SOM	29 Mayıs Hospital	53.5	95.3	-	61	Overall Dice score is low compared with other methods; features used are insufficient.
[74]	ULDA	BrainWeb	-	-	96.5	-	A verification step must be added to ensure quality.
[75]	Global thresholding	-	-	-	97	-	False segmentation occurs when tumor is adjacent to an edge.
[76]	ANN	-	-	-	90	-	Two sets of neural networks must be trained, which increases the computational time.
[77]	KNN-CRF	BRATS 2013	-	-	-	85	Performance decreases with multiple brain registration, brain atlas use, and high-dimensional feature extraction; the method is semiautomatic and requires a user.
[78]	MRF	BRATS 2013	86	86	-	85	Intra- and interintensity invariability between the training and test datasets; challenging to segment core tumor areas, which are not obvious.
[79]	Cellular automata edge detection	Publicly available sources	-	-	80	92	Method is used for tumor segmentation and does not classify tumor absence; the accuracy is not calculated, and the method is not compared with others.
[81]	FHNN	PDC and IBSR	94.8	99.1	86.78	91	Complexity of the proposed method increases the computational time.
[82]	HSOM	KMC	-	-	-	-	Performance of the enhancement was not objectively measured.
[83]	FCM and possibilistic c-means	Turbo spin echo (TSE)	94.28	95	96	-	Complexity of the system increases the computational time.
[84]	Decision tree, naive Bayes, SVM, ANN, KNN, and SVMPSO	AANLIB	-	-	100	-	The method is divided in two programs, one for preprocessing and segmentation, and the other for classification; segmented ROIs need to be stored and fed to the second program, which increases system complexity.
[85]	Modified KSVM	Government medical college	100	80	93	-	Method flowchart does not show system correctly in segmentation stage; very high system complexity, which decreases the accuracy and increases the computational time.
[86]	BPNN	-	-	-	89.9	-	Very small dataset; only 40 images used.
[87]	Cellular neural network	-	-	-	93	-	Method tested with only 3 brain images.
[88]	FFBNN	Various medical diagnosis centers	-	-	94.2	-	Classification is evaluated with 5 images, which does not yield accurate results.
[89]	Otsu, thresholding, k-means, and FCM	Online repository	-	-	90.57	-	Preprocessing technique needs some modification to increase the accuracy.
[90]	SOM neural network	BrainWeb	-	-	-	-	Low performance and high computational time.
[91]	HSOM and ANN	KMC	-	-	97	-	Different accuracy achieved for each tumor type, indicating that the method detects but incorrectly classifies tumors.
[92]	SRC	-	-	-	-	90.8	Long computational time.
[93]	BPNN	Different samples	-	-	75	-	Many simulations are needed for accurate classification, which increases the computational time.
[94]	DNN	BRATS 2013	87	89	-	88	Results change with database changes; long computational time.
[95]	FCDRNN	BRATS 2016	-	-	-	89	Many layers.
[96]	3D CNN architectures	BRATS 2015	83.08	84.60	99	84	Many layers; failure to predict the tumor region with its single resolution.
[97]	FCNN and CRF	BRATS 2013	83	92	-	87	Many layers; long computational time; does not work with T1 MRI images.
[98]	FCN	BRATS 2013	92	80	-	85	Many layers, which increases system complexity.
[99]	DNN	BRATS 2015	89	88	-	83	Low Dice score for LG glioma.
[100]	2D and 3D CNN	MICCAI 2012	-	-	-	72.5	Trained networks overfit the training data.
[101]	CNN	WCH	-	-	96	-	Very small dataset.
[102]	DNN	BRATS 2015	-	-	-	87	Poor U-net performance for core and enhanced regions.
[103]	3D CNN	BRATS 2015	89.7	91.1	-	89.8	Unsatisfying Hausdorff distance achieved.
[104]	3D Fully connected CRF	BRATS 2015	87.6	85	-	84.7	Reduced performance when using ISLES dataset.
[56]	R-CNN	BRATS 2013	95.44	81.80	99.55	87	Does not work with T1 MRI images.

3.2.1. Traditional machine learning in tumor segmentation

Several machine learning methods and techniques are available for brain tumor segmentation through MRI images. Prastawa et al. [59] described an automatic brain tumor segmentation technique using outlier detection. In this technique, a registered brain atlas is used to detect abnormal regions; then, the robust estimates are used. Geometric and spatial constraints are applied to the detected tumor. The method is applied to 3 different databases. In [60], Menze et al. proposed a probabilistic model for brain tumor segmentation using a spatially varying probabilistic atlas. The employed dataset contains brain MRI data from 25 subjects for four modalities: T1, T2, FLAIR, and post-Gadolinium T1. An explicit statistical model is built for all images. The model parameters are estimated by the maximum likelihood parameter estimation (MLPE) approach. Then, a Markov random field (MRF) is used for a spatial regularization.

Islam et al. [61] combined piecewise triangular prism surface area (PTPSA) and multifractal dimension features for brain tumor segmentation. A standard preprocessing method is applied to the MRI image; then, fractal, texton, and intensity features are extracted in the feature extraction stage. The extracted features are directly fed to an AdaBoost classifier. The employed dataset contains 309 brain MRI images: 99 astrocytoma images and 210 medulloblastoma images. The volumes are unwrapped into slices and realigned for every patient. Then, the slices are co-registered using the SPM8 toolbox to correct the bias field. The image is divided into 8 × 8 nonoverlapping subimages using Daubechies wavelet. The number of extracted features is 48. The performance is measured on BRATS 2012, obtaining a Dice score of 48.4%.

Nathan et al. [62] combined a probabilistic geometric model with statistical classification to segment brain tissue and tumors in MRI images. The expectation maximization (EM) is improved by using a statistical parametric mapping (SPM) atlas that provides spatial probability information. A soft threshold, a mixture model, and two Gaussian distributions are also used. Five different datasets are used to evaluate the algorithm performance.

Maksoud et al. [63] presented a segmentation method using k-means clustering combined with FCM clustering. Then, level set segmentation and thresholding stages are applied to improve the segmentation process. The technique is tested with three different databases, providing an accuracy of 90.5% for the first dataset, consisting of 22 images; 100% for the second dataset, consisting of 152 images; and 100% for the last dataset, consisting of 81 images. The images are preprocessed by a median filter for noise removal, and the brain surface extractor (BSE) algorithm is used for skull stripping.

In [64], the authors presented a method for brain tumor segmentation by MRI based on random-forest-derived probabilities and the generation of probability maps for refining MRFs. Gaussian mixture modeling (GMM) is used to model different tumor tissues. The employed dataset contains 520 brain MRI data from 30 subjects for four modalities: T1, T2, FLAIR, and T1C. The database includes 20 HG gliomas and 10 LG gliomas.

Nabizadeh and Kubat [65] presented a fully automatic technique for brain tumor segmentation based on Gabor wavelet features and statistical features with multiple classifiers. In total, 20 GLRLM features, 80 histogram of oriented gradient (HOG) features, 112 GLCM features, and 256 linear binary pattern (LBP) features yield a 475-dimension statistical feature vector. Statistical features are extracted, and PCA is used to reduce and select the important features. In total, 20 features are selected by PCA in the feature dimensionality reduction stage. The dataset contains T1 and FLAIR brain MRI data from 25 subjects.

Huang et al. [66] proposed an automatic brain tumor segmentation method for MRI images using the local independent projection-based classification (LIPC) technique. The employed dataset contains data from 120 brain MRI tumors, including 76 HG tumors and 44 LG tumors. The training database consists of 45 HG tumors and 35 LG tumors, while the testing database consists of 31 HG tumors and 9 LG tumors. Mathematical morphology and the connected component algorithm are applied in the postprocessing stage.

Jiang et al. [67] introduced a method for brain tumor segmentation that uses population- and patient-specific feature sets to construct a graph through a learning process. Then, a graph cut is used to achieve the final segmentation. The employed dataset contains 80 brain MRI images: 45 of HG tumors and 35 of LG tumors. Image modality features and Gabor features are used in the feature extraction stage. The disadvantages of this method are that the method is semiautomatic and the training is time consuming. Chou et al. [68] used 3D PCNNs to automatically extract features of rodent brain images. Morphological erosion is applied as a morphological operation after the PCNN. A spherical shape is selected to provide the smoothest mask. To restore the brain mask, a morphological dilation is applied at a later stage.

Van Leemput et al. [69] proposed a fully automated method for multiple sclerosis (MS) lesion segmentation by MRI based on MRFs that adds contextual information to the last segmentation stage. Manually labeled images are used to estimate MRF parameters. The dataset consists of 20 MS patients, and it contains T1-, T2- and PD-weighted images with 24 axial 256 × 256 slices. Khayati et al. [70] proposed an automatic method for detecting MS lesions in brain FLAIR MRI images based on an MRF model and adaptive mixture method (AMM) by applying an optimal threshold.

In [71], Sachdeva et al. developed a system for segmenting and classifying brain tumors through MRI images. A content-based active contour model (CBAC) is used to segment tumor regions. Laplacian of Gaussian (LoG), GLCM, rotation-invariant local binary patterns (RILBPs), intensity-based features (IBFs), directional Gabor texture features (DGTFs), and rotation-invariant circular Gabor features (RICGFs) are applied for feature extraction. PCA is used to reduce the number of features provided to the ANN in the final stage. A dataset for experimental work is obtained from the Department of Radiodiagnosis of the Postgraduate Institute of Medical Education and Research (PGIMER). The dataset contains 428 T1 images, providing 856 segmented regions of interest (SROIs) consisting of 118 astrocytoma (AS) regions, 59 glioblastoma multiforme (GBM) regions, 97 pediatric medulloblastoma (MED) regions, 88 meningioma (MEN) regions, 66 secondary tumor/metastatic (MET) regions, and 428 normal regions (NRs). In [72], Wu et al. presented a method for brain tumor detection and segmentation by MRI using multilevel Gabor wavelet filters, an SVM, and an affinity metric model.

In [73], a new brain tumor segmentation algorithm was presented; the algorithm segments brain tumor, white matter (WM), edematous regions, CSF, and gray matter (GM). An anisotropic diffusion filter is used in the preprocessing stage. Stationary wavelet transform (SWT) is used to extract the target features. An unsupervised SOM network is applied in the following tumor segmentation stage.

Lin et al. [74] introduced a method for the precise, accurate and efficient quantification of brain tumors by MRI. An MRI image is standardized and then segmented to compute the volume of edema. All segmented region volumes are then computed by ULDA, which consists of LDA and target generation process (TGP).

Akram and Usman [75] proposed an automatic brain tumor segmentation technique using global threshold segmentation and morphological operations, and they achieved an average accuracy of 97%. Morphological erosion and dilation are applied with a binary masked tumor window to the segmented image in the postprocessing stage. The testing database contains 100 MRI images from different patients.

In [76], Canny edge detection and adaptive thresholding are combined and applied as an image segmentation algorithm. The dataset contains 102 brain MRI images, consisting of 70 normal MRI images, 20 images of secondary tumors, and 12 images of primary tumors. The dataset is divided into 54 images for training and 48 for testing. The test set contains 16 images of tumors, with 10 malignant and 6 benign tumors. The performance is high due to the large number of MRI images used.

Havaei et al. [77] presented a semiautomatic method for brain tumor segmentation by MRI based on a KNN approach providing the simplest feature vector combined with conditional random fields (CRFs). The dataset consists of 40 brain MRI images (30 HG and 10 LG tumors). The training database contains data from 20 subjects with an HG tumor and 10 subjects with an LG tumor. However, the testing dataset contains data from only 10 subjects with HG tumors, and the segmentation methodology was tested with only images of HG tumors.

Li et al. [78] combined Markov random fields (MRFs) and sparse representation to develop a fully automatic brain tumor segmentation algorithm. The dataset consists of 64 MRI brain images, with 50 of HG tumors and 14 of LG tumors. The training database contains 20 images of HG tumors and 10 images of LG tumors, and the testing database contains 30 images of HG tumors and 4 images of LG tumors.

In [79], Charutha and Jayashree presented a new technique for brain tumor segmentation using MRI images. A preprocessing stage is applied before incorporating modified, texture-based region growing and cellular automata edge detection to enhance the efficiency of brain tumor segmentation. A median filter is used to reduce the effects of edge blurring and remove the noise present in the preprocessing stage. The disadvantages of modified, texture-based region growing are as follows: oversegmentation can occur due to the presence of noise, the accuracy depends on the image quality, and image shading cannot be distinguished.

Pinto et al. [80] proposed a brain tumor segmentation method using appearance- and context-based features with an extremely randomized forest (extra-trees). The employed dataset contains brain MRI data from 30 subjects for four modalities, T1, T2, FLAIR, and T1C, and the data include 20 HG gliomas and 10 LG gliomas.

Megersa and Alemu [81] employed mathematical morphology operations to achieve good skull stripping. FCM and a Hopfield neural network are used to propose a new hybrid method for tumor segmentation and visualization. The technique is tested with two different databases. The first dataset contains 98 MRI brain images, consisting of 55 abnormal and 43 normal MRI images. The second dataset contains 630 MRI brain images, consisting of 317 abnormal and 243 normal MRI images.

Logeswari and Karnan [82] described a segmentation method for brain MRI images. The tested image is preprocessed for noise removal and then segmented by a hierarchical self-organizing map (HSOM). A median filter is used to remove the high-frequency component in the preprocessing stage.

Rajendran Dhanasekaran [83] developed a new algorithm for brain MRI image segmentation called the enhanced possibilistic fuzzy c-means algorithm (EPFCM), which performs the segmentation process by combining possibilistic c-means and FCM.

In [84], the authors presented a CAD system consisting of four stages: preprocessing, segmentation, feature analysis, and classification. Histogram equalization is applied at the preprocessing stage, and dilation and erosion techniques are used in the segmentation stage. Six algorithms are tested, namely, decision trees, naive Bayes, SVM, ANN, KNN, and PSO. The dataset contains 125 brain MRI images from 11 people: 3 with normal images and 8 with abnormal images. The segmentation process provides 350 ROIs: 86 positive ROIs and 264 negative ROIs. The SVM-PSO and KNN algorithms achieved an accuracy of 100%.

Jayachandran and Dhanasekaran [85] developed a tumor segmentation method with tumor detection to define the presence and absence of the tumor. The method applies preprocessing and segmentation processes before extracting features using a multitexton structure descriptor (MTSD)-based technique. A modified kernel SVM is applied for image detection. Skull stripping is performed via binarization, morphological operations, and tumor region identification in the segmentation stage. The dataset contains 100 MRI brain images, including 80 abnormal and 20 normal MRI images. The dataset is divided into 90 images for training and 10 images for testing.

Amsaveni et al. [86] proposed an algorithm that incorporates preprocessing, feature extraction, and classification using a median filter, a Gabor filter, and a BPNN, respectively. The network consists of three layers, with 24 neurons in the input layer, 100 neurons in the hidden layer, and a single neuron in the output layer. Tumor segmentation is performed by using the trained features with the same selected combinations in the trained neural network. The dataset contains 40 brain MRI images, with 24 images used for training and 16 used for testing.

In [87], Duraisamy and Jane presented a cellular neural network as a segmentation tool. Hussain et al. [88] presented a method for brain MRI image segmentation by extracting features with 2D wavelets and classifying them with neural networks. The region growing method (RGM) and a thresholding process are used to segment the edematous tissue and the tumor. The dataset contains 10 brain MRI images, including 5 abnormal and 5 normal MRI images.

In [89], brain tumor segmentation using MRI based on Otsu, k-means, FCM, and thresholding methods is presented. The highest accuracy was 90.57%.

Tian and Fan [90] presented a hybrid model for brain MRI image segmentation. The model couples an SOM neural network and wavelet transform. A 2D normalized vector is extracted as a feature vector and is used as input for the wavelet transform. This approach improves the performance of neural network segmentation.

Rathi and Plant [91] proposed a hybrid segmentation technique that starts with image preprocessing and is followed by DWT for feature extraction. By extracting statistical parameters, i.e., the variance, maximum, and mean, from the DWT coefficients, a total of 24 features are extracted: 8 variance, 8 maximum, and 8 mean features. HSOM is applied in the segmentation stage, and an ANN technique is used to classify the tumor spectra into 3 types: glioma, oligodendroglioma, and astrocytoma.

Julazadeh et al. [92] introduced a new approach for brain MRI segmentation that takes advantage of the K-SVD dictionary learning algorithm and the SRC algorithm. Active contours without edges (ACWE) is used to increase the accuracy of the segmentation output. The employed dataset contains 80 T2 MRI brain images, with 50 images for training and 30 for testing.

Shen et al. [105] proposed a segmentation technique using neighborhood attraction through MRI based on neural network optimization. The technique modified the traditional FCM method by considering the neighborhood attraction. The improved FCM clustering (IFCM), which considers the neighborhood attraction, depends on two factors: feature attraction and distance attraction.

Xiao et al. [41] proposed a method for estimating features from the correlation between the tumor and LaVs of the brain, which was used to segment brain tumor MRI images. The approach consists of four stages: preprocessing, feature extraction, segmentation, and classification.

Sehgal et al. [106] presented a brain tumor segmentation method consisting of preprocessing with the anisotropic diffusion filtering technique, followed by application of the FCM technique for segmentation and tumor extraction using area and circularity.

Gupta and Sagale [93] presented a method for brain tumor segmentation through MRI images. After the MRI image is preprocessed by histogram equalization, binarization, morphological operators and region isolation are used for segmentation.

In [107], an automatic method for brain tumor lesion detection and segmentation using a single MRI modality and a histogram-based gravitational optimization algorithm (HGOA) is presented. The dataset contains 25 T1 MRI subjects with 181 slices for each subject. The images are preprocessed by applying a Gaussian filter for noise reduction.

Abdullah and Habtr [108] presented a new method for brain tumor detection by MRI. After the input MRI images are preprocessed, global threshold segmentation is applied. To enhance the segmentation results, morphological operations are used before the watershed segmentation.

Table 4
An overview of techniques for brain tumor classification by MRI.

Paper	Feature extraction	Classification methods	Data	Performance			Limitations
				Se (%)	Sp (%)	Ac (%)	
[110]	ROI histogram, co-occurrence matrices, and run-length matrices	LSFT-PNN	Hellenic Air Force Hospital	-	-	95.25 and 93.48	External cross-validation method has very low discriminatory accuracy.
[111]	Thresholding method	Approximate reasoning method	-	-	-	98.5	High computational cost, complexity and optimization.
[112]	Bootstrap sampling	Shelf classifiers	INTERPRET	-	-	95	Many issues involving different pathologies and pathological groupings.
[113]	GLCM	Neuro-fuzzy	Radiology Department of Tata Memorial	-	-	89	Dynamic change cannot be improved for whole images.
[114]	DCT	PNN	-	-	-	100	Very few images used to train and test the network.
[115]	Gabor texture features	SVM	-	83	96	87	Increased system complexity due to the usage of three methods for feature extraction.
[116]	Seven texture features	MKSVM	CHU de Caen	-	-	92.4	Feature extraction and selection are not explained.
[117]	GLCM	PNN-RBF	-	-	-	100	Using FDCT to decompose the input image increases the complexity; the very small training dataset yields high accuracy.
[118]	Grayscale, LoG and texture features	ANN	PGIMER	-	-	91.7	Dataset is nonstandard; performance is calculated in terms of individual class accuracy.
[119]	DWT	KSVM	Nonstandard database	100	100	100	Method is not applied to a standard database.
[120]	Centralized moment calculations	NCC	AANLIB	96.875	98	96.875	Few images are used.
[108]	Binary feature extraction	BPANN	Medical City Martyr Ghazi Al-hariri & MS-Free	100	95.83	96.96	FS is not explained.
[121]	-	PNN	Open-source directories	-	-	-	Proposed method only classifies brain tumors through MRI and does not segment them.
[122]	Supervised FS	SLPANN	INTERPRET	-	-	98.46	SLPs were trained with the whole dataset, which increases the accuracy.
[123]	CNN	CNN	BRATS 2014	-	-	-	Grade classification.

Bhanumurthy and Anne [48] proposed an RGM for tumor segmentation. In [50], a hybrid approach for brain tumor classification by MRI is presented. The proposed method consists of three stages, namely, preprocessing, feature extraction, and classification, which used noise filtering, GLCM, and LS-SVM, respectively. The tumor is segmented by a fast bounding box approach. Li et al. [109] presented an automatic brain tumor segmentation method that combines MRFs and sparse coding based on dictionary learning. The experimental dataset contains 66 brain MRI subjects with four image types for each subject: T1, T2, FLAIR, and T1C. The dataset uses 45 subjects for training and 21 subjects for testing.

3.2.2. Deep learning in tumor segmentation

Several deep learning methods and different techniques are available for brain tumor segmentation through MRI images. Havaei et al. [94] presented brain tumor localization based on a deep neural network (DNN) using a CNN, with a Dice score of 0.88. A two-pathway architecture is used to efficiently train a CNN using the global context and local details. Implementation of a graphics processing unit (GPU) leads to a significant reduction in the segmentation time. Recently, Pereira et al. [99] demonstrated an automatic brain tumor localization system based on a CNN and intensity normalization for preprocessing. The system achieved a Dice score of 0.88.

Kamnitsas et al. [104] presented a 3D CNN with a dual pathway and 11 layers for brain lesion segmentation. A dual-pathway architecture is used to incorporate global and local contextual information. A 3D fully connected CRF is applied to remove false positives. The average performance provides a Dice similarity coefficient of 0.898. In [100], a DNN for automatic brain image segmentation is proposed for 2D and 3D MRI patches, with a mean Dice score of 0.725. The convolutional layers consist of a 2×2 max-pooling layer and a layer with 5×5 kernels.

Zhao et al. [97] combined a fully CNN and CRFs to efficiently segment brain tumors. The network is trained in three stages with image patches and slices and achieved a Dice score of 0.87. In [103], the authors proposed an automatic technique for brain tumor segmentation based on DeepMedic with an 11-layer 3D CNN. The 3D CNN architecture consists of a CNN with two parallel pathways inspired by VGG. The obtained Dice score was 0.90.

In [95], a network with 22 layers is implemented using a fully convolutional residual neural network (FCR-NN) for brain tumor localization. The FCR-NN is combined with a fully convolutional architecture and optimization gains from residual identity mappings. The achieved Dice score was 0.87. Pereira et al. [98] presented a hierarchical study on brain tumor localization using an FCN with MRI histograms, which achieved a Dice score of 0.85. Casamitjana et al. [96] proposed a 3D CNN that combines global and local information in three different architectures, with a reported Dice score of 0.84.

Xiao et al. [101] proposed a segmentation method using deep learning network-based classification. A stacked autoencoder network extracts features from the input, and image patches are classified to map a binary image. Then, a morphological filter is used to produce the segmented tumor. Randhawa et al. [102] designed an automatic segmentation technique based on a DNN. The designed technique achieved a Dice score of 0.87. Abd-Ellah et al. [56] used a fully designed five-layer region-based convolutional neural network (R-CNN), which achieved a Dice score of 0.87.

3.3. Tumor classification

Classification is the process of assigning the input features to different classes or categories. Feature extraction and selection are very important for classification, particularly brain tumor classification, which requires many MRI scans from different cases with ground truth for training. The main goal of brain tumor classification is to classify tumors as benign or malignant or to classify the tumor grade using MRI images. Additionally, brain tumor classification methods can be performed via supervised techniques, such as KNN, SVM, and ANN, or unsupervised techniques, such as FCM and SOM. The commonly used methodologies are summarized in Fig. 2.

Many methods are available for brain tumor classification by MRI. Different classification techniques and methodologies are compared in Table 4 in terms of feature type, classification methodology and performance. Achieving the best classification depends on extracting an optimum feature set for classification, which is a challenging task and requires selection of the optimum classifier.

3.3.1. Traditional machine learning in tumor classification

Several machine learning methods and different techniques are available for brain tumor classification through MRI images. Georgiadis et al. [110] employed a software system for discriminating between metastatic and primary brain tumors in MRI images. The authors applied a modified probabilistic neural network classifier (MPNN) incorporated with a nonlinear LSFT. The input dataset contains 67 T1 MRI images, with 19 of meningiomas, 21 of metastases, and 27 of gliomas. In total, 36 features are extracted from each ROI: 4 from the ROI histograms, 22 from the co-occurrence matrices, and 10 from the run-length matrices.

Zarandi et al. [111] proposed a type II fuzzy expert system for brain tumor diagnosis. The proposed method consists of preprocessing with a fuzzy rule base and grouping by the existing filtering. The segmentation is performed by probabilistic c-means (PCM). A thresholding method is applied for feature extraction, and a type II approximate reasoning method is used to recognize the tumor grade. The input dataset contains 95 patients, with 95 images of type I tumors and 95 images of type II tumors.

Navarro et al. [112] presented a method for reducing the dimensionality of selected features and shelf classifiers for HMR modalities. An entropy-based selection algorithm is used for FS, and bootstrap sampling is used to obtain a final model.

Joshi et al. [113] proposed a system for detecting and classifying brain tumors. Histogram equalization is first applied to the image, followed by a feature extraction algorithm and neuro-fuzzy classifier.

Sridhar and Krishna [114] proposed a new method for brain tumor classification using a discrete cosine transform for feature extraction and dimensionality reduction. Sixteen features are extracted from the 4×4 brain MRI image with a sample dimension of 6, and these features are provided to the classification stage. The classification is performed with a PNN technique. The employed dataset contains 20 brain MRI images, which are divided into the following three different training and testing set combinations: 15 images for training and 5 for testing, 10 for training and 10 for testing, and 5 for training and 15 for testing.

Zacharaki et al. [115] proposed a multistep scheme for brain tumor classification. The proposed scheme consists of ROI definition, feature extraction, FS, and classification. However, manually selected ROIs, Gabor texture features, and support vector machine recursive feature elimination (SVM-RFE) are used to select features that are provided to the SVM layers for tumor classification. In total, 25 rotation-invariant texture features are selected from the extracted features. The employed dataset contains data from 98 patients for a total of 102 brain MRI images consisting of 24 metastases, 4 grade I meningiomas, 22 grade II gliomas, 17 grade III gliomas, and 35 grade IV glioblastomas.

Zhang et al. [116] applied PCA for FS, which reduced the number of features to 10 with a window size of 11×11 pixels. A multikernel SVM (MKSVM) is used to classify the tumor region. The distance and the maximum likelihood measures are applied to enhance the contour of the tumor region. The employed dataset contains 3 different image types, FLAIR, T2, and PD images, with 60 samples for each type.

Preethi and Sornagopal [117] proposed a method for brain MRI image classification using fast discrete curvelet transform (FDCT) and GLCM for feature extraction. A PNN-RBF, which consists of three layers, the input, hidden and output layers, is applied to classify MRI images as benign, malignant, or normal. The extracted features, contrast, energy, entropy, correlation, and homogeneity, are provided to the PNN-RBF. The training set contains 15 benign, malignant or normal MRI images.

Kumar et al. [118] used gradient vector flow (GVF) to extract the tumor boundaries. A 218-feature vector is extracted using GLCM, LoG, DGTFs, RICGFs, RILBPs, and IBFs. A PCA approach is used for feature reduction. The optimal number of features selected is 49, and these are provided to the classifier. Estimating the training network weights is accomplished by gradient descent backpropagation with momentum (DBPM). To prevent overtraining, 10-fold cross-validation is applied. The dataset contains 428 T1 brain MRI images, which provide 856 SROIs consisting of 118 astrocytoma (AS) regions, 59 glioblastoma multiforme (GBM) regions, 97 pediatric medulloblastoma (MED) regions, 88 meningioma (MEN) regions, 66 secondary tumor/metastatic (MET) regions, and 428 NRs.

Abd-Ellah et al. [119] proposed using a kernel support vector machine (KSVM) for tumor classification. The features are extracted by DWT with Daubechies wavelets. Furthermore, PCA is applied to reduce the feature vector to thirteen GLCM features. The selected features are used in the classification and training stages with the SVM. The dataset that was used consists of 120 MRI images divided into two databases. Database 1 contains 10 normal and 70 abnormal images, and database 2 contains 20 benign and 20 malignant images. In total, 5 normal, 40 abnormal, 10 benign, and 10 malignant images are used for training the SVM, and 5 normal images, 30 abnormal, 10 benign, and 10 malignant images are used for testing.

Nasir et al. [120] presented a method for classifying brain MRI images into eight different tumor types. The proposed method uses NCC in the polynomial domain as a classifier. The input dataset contains 104 T2 MRI images, with 20 normal images and 84 abnormal images and 12 images for each tumor type: glioma I, glioma III, glioma IV, meningioma, MET_Aden, MET_Bron, and sarcoma.

Abdullah and Habtr [108] presented a new tumor classification method using global and watershed segmentation for threshold segmentation and feature extraction. A feedforward BPNN is used to classify the brain tumor as benign or malignant. The network consists of one input layer with two neurons; two hidden layers with three and four neurons, respectively; and one output layer with one neuron. The dataset in the experimental work consists of 32 MRI images, with 18 normal, 10 malignant, and 4 benign images. Sixteen images are used for training the classifier, and 16 images are used for testing. Shrivastava et al. [121] presented a method for brain tumor classification based on a PNN combined with a PCA feature reduction approach.

In their work, Lisboa et al. [122] proposed two methods for tumor classification. The first method is a combination of supervised feature selection (FS) and a single-layer perceptron artificial neural network (SLPANN). The second method is a novel linear dimensionality reduction technique combined with an ANN. The dataset contains 195 patients with tumors consisting of 78 glioblastomas, 55 meningiomas, 31 metastases, 6 grade II oligoastrocytomas, 20 grade II astrocytomas, and 5 grade II oligodendrogliomas. In total, 390 features are extracted from the input images. The FS process reduces the features to 18, with 8 short-echo time (SET) and 10 long-echo time (LET) features.

Pinheiro et al. [124] proposed a hybrid method for diagnosing Alzheimer's disease that is based on verbal decision analysis (VDA). VDA is integrated with decision trees, which classify the disease as early or moderate stage. In [125], a CAD tool for diagnosing Alzheimer's disease was proposed. The method combines a learning vector quantization (LVQ) algorithm and SVM with an MRI image database.

3.3.2. Deep learning in tumor classification

Brain tumor classification using deep learning techniques is a recent field of research, and few contributions could be identified. Pan et al. [123] proposed a brain tumor classification method that uses a deep learning structure. The performance of a CNN is compared with a backpropagation neural network in terms of specificity and sensitivity. The results show an 18% improvement with use of the CNN. The employed CNN consists of 2 layers, which perform convolution and subsampling. The CNN is trained with 60,000 examples and tested with 10,000 examples. The database contains 195 patient samples, including 25 LG and 170 HG samples. In total, 600 MRI images were used for training, and 360 MRI images were used for testing.

4. Discussion and lessons learned

4.1. Research findings and limitations

Brain tumors are still a hot research topic in the medical image processing domain. This study presented a comprehensive review of the state-of-the-art techniques for brain tumor diagnosis. Tumor detection is the process of detecting the presence or absence of brain tumors through MRI images. The outcome of the detection process is that a number of images need further investigation by tumor segmentation and classification techniques. Tumor classification is the process of classifying the tumor as benign or malignant, HG or LG, or as a specific type of tumor based on the tissue analysis.

Most of the reviewed techniques focus on semiautomatic and automatic methods for tumor diagnosis. Additionally, most of them use preprocessing, feature extraction, feature reduction, segmentation, and classification methods. As most of the algorithms are sensitive to noise, the noise must be reduced. This survey indicates that these techniques for detection, classification, and segmentation mainly use KSVM, SVM, FFBPNN, SOMNN, BPNN, PNN, ANN, PNN-RBF, NCC, PSO, SMO, LVQ, MLP, SVM-KNN, GA-SVM, SC-ICA, LSFT, FHNN, SRC, ULDA, FCM, and CNN. Most of these techniques are based on tumor detection, classification, and segmentation, as well as hybrid techniques mixing these stages.

Brain MRI image detection methods can classify MRI images as normal or abnormal. Abnormal images can then be classified as benign or malignant or into grades of a malignant tumor with classification methods. Segmentation techniques can be divided into 6 major categories: region-based methods, threshold-based methods, clustering methods, statistical models, edge detection methods, ANN, and deep learning methods [10]. Selecting the best technique for a particular application is a difficult task. Therefore, different techniques can be combined together in a hybrid way to achieve the required task of detection, segmentation, or classification. Hence, using hybrid techniques may avoid the limitations of each individual method.

Feature extraction is mostly performed using DWT and GLCM. Dimensionality reduction is primarily performed using PCA and GA scores. The most commonly used methods for detection and classification are SVM, ANN, SOM, fuzzy methods, PNN, MRF, RF, and CNN, while hybrid classification methods achieved the best accuracy. SVM and CNN are the most used for tumor segmentation. CNN-based algorithms show the highest performance, especially with 2D data. The reviewed techniques can be categorized as detection, segmentation, and classification methods that use machine learning techniques (e.g., KSVM, SVM, and ANN) and deep learning techniques, such as CNNs. Deep learning techniques achieve competitive results compared to the classical machine learning techniques in brain tumor segmentation.

The main four available standard databases were explained, and the lack of resources leading to many methods being based on images collected from medical centers or hospitals was demonstrated. The MICCAI Challenge (BRATS) database is a widely used benchmark for tumor segmentation. Some researchers have attempted to solve this deficiency by combining physical and statistical modeling to generate multimodal 3D brain MRI images to simulate the major effects known to be associated with abnormal MRI images. The system synthesizes pathology in MRI and diffusion tensor imaging (DTI) to generate synthetic ground truth for MRI images with tumor tissue and edema, as in [126]. Such synthesized MRI image databases could provide a fair and unified environment for evaluating proposed brain tumor diagnosis approaches.

With respect to the performance evaluations, Table 2 shows the best results for tumor detection, achieved by Abd-Ellah et al. in [2] and Saritha et al. in [29]. The best tumor segmentation results have been achieved by Abdel-Maksoud et al. [63] and Ulku [84] using traditional machine learning techniques and by Kamnitsas et al. [103] using a deep learning approach, as shown in Table 3. The best brain tumor classification results have been achieved by Abd-Ellah et al. [119], Sridhar et al. [114] and Preethi et al. [117] with 100% classification accuracy, as shown in Table 4. It is difficult to fairly compare all of the aforementioned methods due to the lack of standard databases, especially for tumor detection and classification, as well as the lack of a unified implementation framework.

Recently, the deep learning paradigm has shown outstanding performance in medical image analysis, especially in brain tumor diagnosis. Deep learning networks have achieved higher accuracy than classical machine learning approaches. Additionally, the performance of deep learning networks increases with more data compared to traditional machine learning with complex algorithms as provided in [56]. Traditional machine learning approaches require complex feature extraction and reduction methods, which are not needed in the case of deep learning techniques. The training of deep learning techniques is a time-consuming and extremely data hungry process. Therefore, these techniques may need parallel processing tools, such as graphics processing units (GPUs), to accelerate the training process of large datasets [24]. Although deep learning has superior performance, traditional machine learning techniques still work with few advantages. The most popular advantages of traditional machine learning algorithms are that their mechanisms are easy to understand and interpret and their structures require less computational cost in terms of time and hardware components and also require less computing resources for training and testing purposes.

4.2. Lessons learned

The primary objective of this survey was to identify the key achievements to date in brain tumor diagnosis in terms of tumor detection, segmentation, and classification. The identified achievements should provide opportunities for future improvements in tumor diagnosis via understanding and improving the weaknesses. The improvements will be reflected in the performance of each method in terms of quantitative measurements, such as the sensitivity, specificity, accuracy, and Dice score. This study has identified imbalanced research efforts in tumor diagnosis processes. Most of the research has focused on tumor segmentation and classification. However, few studies have investigated tumor detection from MRI images.

Deep learning is a subcategory of the machine learning paradigm that offers more advanced capabilities over the traditional machine learning approaches. Deep learning has become an emergent and important research tool that was introduced with the objective of improving the performance of traditional machine learning methods. Deep learning allows multiple levels of representation and abstraction, which help to collect more information about MRI images and their features [127]. The present study identified a lack of deep learning deployments in tumor detection, few implementations in tumor classification, and more deep learning applications in tumor segmentation. This issue is also illustrated in Fig. 1.

This review also revealed a conspicuous lack in the precision of some researchers in describing the dataset, the type of tumor, and the algorithm's performance measures with respect to accuracy, sensitivity, and specificity, as can be deduced from the blank fields in the tables mentioned earlier in this study. More attention must be directed toward studies of brain tumors through MRI images not only for tumor detection but also for localization, segmentation and algorithm validity. Finally, all research methods should be tested via standard brain MRI databases, which allow fair comparisons and provide a unified testing environment.

Different databases are described in Table 1; some of these databases contain different image categories, such as normal and abnormal images, while others contain images of only some tumor types, such as HG and LG tumors. However, there are no databases that contain normal images and all types of tumor images with segmentation ground truth, which forces some researchers to collect images from hospitals and medical centers, as shown in Tables 1, 2, and 3. This study pinpoints the need for building a large database that contains all possible types of brain images, such as normal images, images of HG and LG glioblastomas, and images of other tumor types, which can be used as a standard benchmark for tumor diagnosis detection.

In general, the aforementioned large MRI database is required to support correct evaluations and trustworthy techniques and tools used in the different stages of brain tumor diagnosis through MRI images. A large database is also crucial for developing competition to yield better tools and generalized techniques that fulfill their tasks using a sufficient number of MRI images. Having standard databases feeds the expectation of the performance improvements and applicability of CAD methods emerging from fair comparisons and a unified deployment environment.

Although this study described several contributions that individually focus on the three main tumor diagnosis phases, it did not identify any complete diagnosis systems consisting of all three diagnosis phases. The lack of a complete diagnosis system in one package imposes two emergent problems, namely, a lack of a fully automated process, as some processes must be performed manually, and a shortage of integration among the three processes. Developing a complete and automatic system should ease the brain tumor diagnosis process for clinicians and radiologists and shift the diagnosis algorithms from research to real-world applications.

5. Conclusions

Brain tumor detection, segmentation, and classification are three processes that can be used to produce computer-aided methods for tumor diagnosis from MRI images. These methods offer enhanced accuracy, reduced noise, and improved speed compared to manual methods. Thus, these methods have been intensively researched with respect to the applications of traditional machine learning and deep learning approaches. This study reviewed various diagnosis techniques for brain MRI images. In addition, a comparative study of traditional machine learning and deep learning was provided in terms of limitations and performance metrics. The study identified an imbalance in the use of databases and benchmarks in the three processes. Standard databases are used for tumor segmentation and classification; however, no standard databases are available for tumor detection. All techniques used for tumor detection are currently traditional machine learning methods; however, promising results are expected from the use of deep learning techniques in these processes. Several traditional machine learning techniques have been applied to segmentation and achieved a maximum accuracy of 100%, and deep learning techniques have achieved a maximum Dice score of 89.8%. It is still very early to judge deep learning methods by the Dice score alone. Traditional machine learning and deep learning techniques have been applied to tumor classification, and an accuracy of 100% has been achieved by both learning categories. However, the advantages and disadvantages of each method, such as the complexity and network size, must be considered to save computation time. Overall, there is a precedence of machine learning deployments over deep learning deployments. Although there are aspirations to increase the deep learning deployments in tumor detection and classification, there is a need for standard databases for tumor detection and classification. Furthermore, there is a need to compile the three processes into one fully automated system for brain tumor diagnosis that is more clinically useful.

Declaration of Competing Interest

None

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