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Brain tumor detection and classification using machine learning: a comprehensive survey

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Abstract

Brain tumor occurs owing to uncontrolled and rapid growth of cells. If not treated at an initial phase, it may lead to death. Despite many significant efforts and promising outcomes in this domain, accurate segmentation and classification remain a challenging task. A major challenge for brain tumor detection arises from the variations in tumor location, shape, and size. The objective of this survey is to deliver a comprehensive literature on brain tumor detection through magnetic resonance imaging to help the researchers. This survey covered the anatomy of brain tumors, publicly available datasets, enhancement techniques, segmentation, feature extraction, classification, and deep learning, transfer learning and quantum machine learning for brain tumors analysis. Finally, this survey provides all important literature for the detection of brain tumors with their advantages, limitations, developments, and future trends.

Keywords Brain imaging modalities · Segmentation · Feature extraction · MRI · Stroke

Introduction

The central nervous system disseminates sensory information and its corresponding actions throughout the body [1–3]. The brain, along with the spinal cord, assists in this dissemination. The brain's anatomy [4] contains three main parts; brain stem, cerebrum, and cerebellum. The weight of a normal human brain is approximately 1.2–1.4 K, with a volume of 1260 cm³ (male brain) and 1130 cm³ (female brain) [5]. The frontal lobe of brain assists in problem-solving, motor control, and judgments. The parietal lobe manages body position. The temporal lobe controls memory and hearing functions, and occipital lobe supervises the brain's visual processing activities. The outer part of cerebrum is known as

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cerebral cortex, and is a greyish material; it is composed of cortical neurons [6]. The cerebellum is relatively smaller than the cerebrum. It is responsible for motor control, i.e., systematic regulation of voluntary movements in living organisms with a nervous system. Due to variable size and stroke territory, ALI, lesionGnb, and LINDA methods fail to detect the small lesion region. Cerebellum is well-structured and welldeveloped in human beings as compared to other species [7]. The cerebellum has three lobes; an anterior, a posterior, and a flocculonodular. A round-shaped structure named vermis connects the anterior and posterior lobes. The cerebellum consists of an inner area of white matter (WM) and an outer greyish cortex, which is a bit thinner than that of the cerebrum. The anterior and posterior lobes assist in the coordination of complex motor movements. The flocculonodular lobe maintains the body's balance [4, 8]. The brain stem, as the name states, is a 7-10 cm-long stem-like structure. It contains cranial and peripheral nerve bundles and assists in eye movements and regulations, balance and maintenance, and some essential activities such as breathing. The nerve tracks originating from the cerebrum's thalamus pass through the brain stem to reach the spinal cord. From there, they spread throughout the body. The main parts of the brain stem are midbrain, pons, and medulla. The midbrain assists in functions such as motor, auditory, and visual processing, as well as eye movements. The pons assists in breathing, intra-brain communication, and sensations, and medulla oblongata helps in blood regulation, swallowing, sneezing, etc. [9].

Brain tumor and stroke lesions

Brain tumors are graded as slow-growing or aggressive [2, 10–20]. A benign (slow-growing) tumor does not invade the neighboring tissues; in contrast, a malignant (aggressive) tumor propagates itself from an initial site to a secondary site [16, 17, 21–27]. According to WHO, a brain tumor is categorized into grades I–IV. Grades I and II tumors are considered as slow-growing, whereas grades III and IV tumors are more aggressive, and have a poorer prognosis [28]. In this regard, the detail of brain tumor grades is as follows.

Grade I: These tumors grow slowly and do not spread rapidly. These are associated with better odds for long-term survival and can be removed almost completely by surgery. An example of such a tumor is grade 1 pilocyticastrocytoma.

Grade II: These tumors also grow slowly but can spread to neighboring tissues and become higher grade tumors. These tumors can even come back after surgery. Oligodendroglioma is a case of such a tumor.

Grade III: These tumors develop at a faster rate than grade II, and can invade the neighboring tissues. Surgery alone is insufficient for such tumors, and post-surgical radiotherapy or chemotherapy is recommended. An example of such a tumor is anaplastic astrocytoma.

Grade IV: These tumors are the most aggressive and are highly spreadable. They may even use blood vessels for rapid growth. Glioblastoma multiforme is such a type of tumor [29].

Ischemic stroke: Ischemic stroke is an aggressive disease of brain and it is major cause of disability and death around the globe [30]. An ischemic stroke occurs when the blood supply to the brain is cut off, resulting underperfusion (in tissue hypoxia) and dead the advanced tissues in hours [31]. Based on the severity, stroke lesions are categories into different stages such as acute (0-24 h), sub-acute (24 h-2 weeks) and chronic (>2 weeks) [32].

Brain imaging modalities

Three major methods (PET, CT, DWI and MRI) for brain tumors are widely used to analyze the brain structure.

Positron emission tomography

Positron emission tomography (PET) uses a special type of radioactive tracers. Metabolic brain tumor features such as blood flow, glucose metabolism, lipid synthesis, oxygen consumption, and amino acid metabolism are analyzed through PET. It is still considered as one of the most powerful metabolic techniques and utilizes the best nuclear medicine named as fluorodeoxyglucose (FDG) [33]. FDG is a widely used PET tracer in brain images. Nevertheless, FDG-PET images have limitations, e.g., an inability to differentiate between necrosis radiation and a recurrent high-grade (HG) tumor [34]. Moreover, during a PET scan, radioactive tracers can cause harmful effects to the human body, causing a post-scan allergic reaction. Some patients are allergic to aspartame and iodine. In addition, PET tracers do not provide accurate localization of anatomical structure, because they have a relatively poor spatial resolution as compared to an MRI scan [35].

Computed tomography

Computed tomography (CT) images provide more in-depth information than images obtained from normal X-rays. The CT scan has received widespread recommendation and adoption since its inception. A study [36] determined that in the USA alone, the annual CT scan rate is 62 million, with 4 million for children. CT scans show soft tissues, blood vessels, and bones of different human body parts. It uses more radiation than normal X-rays. This radiation may increase the risk of cancers when multiple CT scans are performed. The associated risks of cancers have been quantified according to CT radiation doses [37, 38]. MRI can even help in evaluating structures obscured in a CT scan, and provides high contrast among the soft tissues, providing a clearer anatomical structure [39].

Magnetic resonance imaging

An MRI scan is used to completely analyze different bodyparts, and it also helps to detect abnormalities in the brain at earlier stages than other imaging modalities [40]. Hence, complex brain structures make tumor segmentation a challenging task [41–47]. This review discusses preprocessing approaches, segmentation techniques [48, 49], feature extraction and reduction methods, classification methods, and deep learning approaches. Finally, benchmark datasets and performance measures are presented.

Diffusion weighting imaging

MRI sequences are utilized to analyze the stroke lesions based on the several parameters such as age, location and extent regions [50]. In the context of treatment, a computerized method might be utilized for accurate diagnosis of the disease progression rate [51]. The neuroscientists of cognitive, who frequently conduct research in which cerebral impairments are linked to cognitive function They observed



Fig. 1 Datasets for brain tumor detection

that segmentation of the stroke lesions is a vital task to analyze the total infected region of brain that provide help in the treatment process [52]. However, segmentation of the stroke lesions is a difficult task, because stroke appearance is change as the passage of time. The MRI sequence such as diffusion weighted imaging (DWI) and FLAIR are utilized for stroke lesions detection. In acute stoke stage DWI sequence highlight the infection part as a hyperintensity. The underperfusion region represents the mapping magnitude of the perfusion [53]. The dis-similarity among two regions might be considered as penumbra tissue. Stroke lesions appear in distinct locations and shapes. Different types of lesions are appeared in a variable size and shape and these lesions are not aligned with vascular patterns and more than one lesions might appeared on similar time. The size of the stroke lesions is in radii of the few millimeters and appears in a full hemisphere. The structure of the hemisphere is dissimilar, and its intensity might significantly vary within the infected region. Furthermore, automated stroke segmentation is difficult due to the similar appearance of the pathology such as white matter hyperintensities and chronic stroke lesions [54].

Evaluation and validation

In the existing literature, experimental results are evaluated on publicly available datasets to verify the robustness of algorithms.

Publicly available datasets

Several datasets are publicly available that are used by the researchers to evaluate the proposed methods. Some important and challenging datasets are discussed in this section. BRATS are the most challenging MRI datasets [55–57]. BRATS Challenge is published in different years with more challenges having 1 mm³ voxels resolution. The detail of datasets is given in Fig. 1 as well as in Table 1.



Fig. 2 List of performance measures for evaluation of brain tumor

Performance metrics

The performance measures play a significant role to compute the method's effectiveness. A list of performance metrics is provided in Fig. 2.

Preprocessing

Preprocessing is a critical task [61] to extract the requisite region. 2D brain extraction algorithm (BEA) [62], FMRIB software library [63], and BSE [64] are used for non-brain tissue removal as shown in Fig. 3. The bias field is a key problem that arises in MRI due to imperfections of radio frequency coil called intensity inhomogeneity [65, 66]. It is corrected as shown in Fig. 4 [67]. The preprocessing methods like linear, nonlinear [68], fixed, multi-scale, and pixel-based are used in distinct circumstances [69–72]. The small variations among normal and abnormal tissues due to noise [68] and artifacts often provide difficulty in direct image analysis [73, 74]. AFINITI is used for brain tumor segmentation [63]. Consequently, automated techniques are adopted in which computer software performs segmentation and eliminates the need for manual human interaction [75, 76]. Fully and semiautomated techniques are used widely [77, 78]. The results of brain tumor segmentation are mentioned in Table 2. The segmentation methods are divided into the following categories.

- Conventional methods.
- Machine learning methods.
- Different inhomogeneities related to MRI noise have shading artifacts and partial volume effects.

When different types of tissues [61] take the same pixel, then it is called partial volume effect [92]. The random noise related to MRI [19, 93, 94] has Rician distribution [95]. In the literature, different filters such as wavelet, anisotropic diffusion, and adaptive are presented to enhance edges [96].

Datasets	Description	Sequences	Number of slices (images)
BRATS series	BRATS 2012 challengeimage (Patients) dataset (05 LGG, 10 HGG) casesSyntheticdataset (04 LGG,11HGG) cases	T1weighted, T1C weighted, T2 weighted and Flair	240 × 240 × 155
	BRATS 2012 Trainingimage dataset (10 LGG, 20 HGG) casesSyntheticdataset (25 LGG, 25 HGG) cases		
	BRATS 2013 challenge30 Subjects		
	BRATS 2013 Leaderboard, 25 Subjects		
	2014 challenge, 400 Subjects		
	2015 challenge, 274 Subjects		
	2016 challenge, Training cases of BRATS 2015		
	BRATS 2017 challenge, 285 Subjects		
	BRATS 2018 challenge, 191 Subjects		
	BRATS 2019 challenge, 22,087 training and 22,087 testing slices		
	BRATS 2020 challenge, 25,962 training and 25,962 testing slices		
Harvard [58]	65 tumor and 35 non-tumor images	T2 weighted	256 × 256 (100 images)
RIDER[59]	126 Subjects	T1 weighted, T2 weighted, and Flair	256 × 256 126 cases
ISLES 2015	64 Subjects	SISS- ISLES DWI, T1 weighted, T2 weighted, Flair SPES-ISLES CBF, CBV, DWI, T1C weighted, T2 weighted, Tmax, TTP	SISS- ISLES $230 \times 230 \times 154$ (154 slices in each case) SPES-ISLES $230 \times 230 \times 154$ (154 slices in each case)
ISLES 2016	75 Subjects	MTT, rCBV, relative rCBF, Tmax, TTP	$192 \times 192 \times 19$ (19 slices in each case)
ISLES 2017[60]	57 Subjects	PWI, ADC, MTT, rCBV, rCBF, Tmax, TTP	$192 \times 192 \times 19$ (19 slices in each case)

Table 1 Summary of the publicly available datasets



Fig. 3 Skull removal a input, b skull removed [1]

the edges [99]. Normalizing the image intensity is another part of the preprocessing phase [2, 100, 101] and modified curvature diffusion equation (MCDE) [102] are applied for intensity normalization. Wiener filter is used to enhance the local and spatial information in medical imaging [103]. The widely utilized preprocessing methods are N4ITK [104] for the correction of bias field, median filter [104] for image smoothing, anisotropic diffusion filter [105], image registration [106], sharpening [107], and skull stripping through brain extraction tool (BET) [108].

Conventional methods

The conventional methods [46] are further categorized into the following:

An anisotropic diffusion filter is more suitable in practical applications due to low computational speed [97, 98]. When the noise level is high in the image, it is difficult to recover

- Thresholding methods.
- Region growing methods.
- Watershed methods.

Table 2Summary of the
existing segmentation
approaches

References	Year	Segmentation methods	Datasets	Outcomes
[79]	2005	Hybrid level set (HLS) segmentation	10 patients	79.12 to 93.25% matching (PM)
[78]	2013	A semi-automatic method based on individual and population information	137 clinical images	94.1 ± 3.0 DSC
[80]	2015	Fully automated generative method	BRATS (2013 Challenge, 2013 Leaderboard, 2015 Challenge)	0.87 DSC complete, 0.82 core, 0.70 enhance on BRATS 2013 Challenge, 0.83 complete, 0.71 core, 0.54 enhance on BRATS 2013 Leaderboard, 0.81 DSC complete, 0.68 core DSC, 0.65 DSC enhance on BRATS 2015 Challenge
[81]	2016	Expectation maximization	SPES and SISS 2015	0.78 ± 0.08 DSC on SPES and 0.53 ± 0.26 DSC on SISS
[82]	2017	Otsu algorithm	BRATS 2013 Synthetic	$\begin{array}{c} 0.93 \pm 0.04 \text{ DSC on HG},\\ 0.90 \pm 0.02 \text{ DSC on LG}\\ 0.87 \pm 0.06 \text{ Jaccard}\\ \text{Index on HG},\\ 0.82 \pm 0.04 \text{ Jaccard}\\ \text{Index on LG} \end{array}$
[83]	2017	Non-negative matrix factorization (NMF)	21 HGG patients	0.80 complete DSC, 0.74 core DSC and 0.65 active DSC tumor
[84]	2017	HCSD	BRATS2012 Challenge	0.9102 ± 0.0627 DSC, 0.9501 ± 0.0518 SE, 0.9980 ± 0.0023 SP
[85]	2018	Improved thresholding method	Harvard and Private collected images	0.948 Jaccard index on clinical and 0.961 Jaccard index on Harvard
[86]	2018	Novel saliency method	BRATS 2013 Challenge	0.86 ± 0.06 HG DSC, 0.85 ± 0.07 LG DSC
[87]	2018	BA and RG	BRATS 2015 Challenge	0.8741 Jaccard index, 0.9036 DSC, 0.9827 sensitivity, 0.9772 specificity, 0.9753 accuracy and 0.9585 precision
[88]	2019	EM and FODPSO	192 MRI scan	0.93.4 ACC
[89]	2019	Adaptive threshold and morphological operations	1340 Clinical MR images	0.85 DSC, 0.89 Jaccard index
[90]	2020	3D semantic segmentation	BRATS 2019 challenge	0.826 enhance, 0.882 complete, 0.837 core tumor
[91]	2021	CNN model	FLAIR, (T1T1C, and T2) weighted	0.957 ACC



Fig. 4 Bias field correction a input, b estimated, c corrected [67]

Segmentation

Segmentation extracts the required region from input images. Thus, segmenting accurate lesion regions is a more crucial task [109]. As manual segmentation process is erroneous [110]; therefore, semi- and fully automated methods are utilized [46]. Segmentation of tumor region using semiautomated methods achieves acceptable outcomes over manual segmentation [111, 112]. Semi-automated methods are further divided into three forms: initialization, evaluation, and feedback response [113, 114].

Thresholding methods

The thresholding method is a basic and powerful method to segment the required objects [18] and the selection of an optimized threshold is a difficult task in low-contrast images. Histogram analysis is used to select threshold values based on image intensity [115]. Thresholding methods are classified into local and global. If high homogeneous contrast or intensity exists among the objects and background, then the global thresholding method is the best option for segmentation. The optimal threshold value can be determined by Gaussian distribution method [116]. These methods are utilized when the threshold value cannot be measured from the whole image histogram or single value of the threshold does not provide good results of segmentation [117]. In most cases, the thresholding method is applied at the first stage for segmentation and many distinct regions are segmented within the gray-level images as shown in Fig. 5.

Region growing (RG) methods

In RG approaches, image pixels form disjoint areas are analyzed through neighboring pixels, which are merged with homogeneousness characteristics based on pre-defined similitude criteria. The region growing might fail to provide better accuracy due to the partial volume effect [118, 119]. To overcome this effect, MRGM is preferred [86, 120]. The region growing with BA methods is also introduced [87].

Watershed methods

As MR images have more proteinaceous fluid intensity, therefore, watershed methods are utilized to analyze the intensity of the image [114, 121, 122]. Due to noise [123], watershed method leads to over-segmentation [124]. The accurate segmentation [125] results can be obtained by the combination of watershed transform with the merging of statistical methods [126, 127]. Some watershed algorithms are topological watershed [128], image foresting transform (IFT) watershed [129], and marker-based watershed [130].

The comprehensive literature review [131] on brain tumor detection shows that there is room for improvement [72]. As a brain tumor appears in variable sizes and shapes, existing segmentation approaches require additional improvements



Fig. 5 Segmentation using Otsu thresholding **a** original images, **b** Otsu thresholding [82]

for tumor segmentation. In overcoming the limitations of existing methods, enhancement [132–134] and segmentation [135–137] have significance in tumor detection.

Feature extraction methods

The feature extraction approaches [12, 138–140] including GLCM [15, 141, 142], geometrical features (area, perimeter, and circularity) [15], first-order statistical (FOS), GWT [143, 144], Hu moment invariants (HMI) [145], multifractal features [146], 3D Haralick features [147], LBP [148], GWT [11], HOG [14, 137], texture and shape [82, 143, 149, 150], co-occurrence matrix, gradient, run-length matrix [151], SFTA, curvature features [152, 153], Gabor like multiscale texton features [154], Gabor wavelet and statistical features [142, 143] are utilized for classification. Table 3 lists the summary of feature extraction methods.

Feature selection methods or feature selection/reduction methods

In machine learning and computer vision applications, highdimensional features maximize the system execution time and memory requirement for processing. Therefore, to distinguish between relevant and non-relevant features, several feature selection methods are required to minimize redundant information [168]. The optimal feature extraction is still a challenging task [47]. The single-point heuristic search method, ILS, genetic algorithm (GA) [169], GA+ fuzzy rough set [170], hybrid wrapper-filter [171], TRSFFQR, tolerance rough set (TRS), firefly algorithm (FA) [172], minimum redundancy maximum relevance (mRMR) [152], Kullback–Leibler divergence measure [173], iterative sparse representation [174], recursive feature elimination (RFE) [175], CSO-SIFT [176], entropy [11, 177, 178], PCA [179], and LDA [180] are utilized to remove redundant features. A summary of classification methods as shown in Table 4.

Classification methods

The classification approaches are used to categorize input data into different classes in which training and testing are performed on known and unknown samples [16, 24, 25, 181–192]. Machine learning is widely used for tumor classification into appropriate classes, e.g., tumor substructure (complete/non-enhanced/enhanced) [193], tumor and non-tumor [26], and benign and malignant tumor [15, 47, 163, 194, 195]. KNN [196], SVM, nearest subspace classifier, and representation classifier [143] are supervised, whereas FCM [197, 198], hidden Markova random field [199] self-organization map [101], and SSAE [200] are unsupervised methods.

Recent trends in medical imaging to detect malignancy

Deep learning and quantum machine learning methodologies are widely utilized for tumor localization and classification [201]. In these techniques, automatic feature learning helps to discriminate complicated patterns [186, 202–213].

Deep learning methods

The variety of state of the art deep learning methodologies are used to learn the data in the medical domain [214] including CNN [215, 216], Deep CNN, cascaded CNN [217], 3D-CNN [218], convolutional encoder network, LSTM, CRF [218], U-Net CNN [219], dual-force CNN [220] and WRN-PPNet [221].

The brain tumor classification problem has been solved by employing a LSTM model. In this method, input MRI images smooth using N4ITK and 5×5 Gaussian filter and passed as input to the four LSTM model. The LSTM model is constructed on the four hidden Units such as 200, 225, 200, 225, respectively. The performance of this model has been tested on BRATS (2012–2015 and 2018) series and SISS-2015
 Table 3
 Summary of the feature extraction methods

References	Year	Extracted features	Dataset	Results
[154]	2013	Gabor-like multiscale texton features	BRATS2012	0.73 DSC
[148]	2015	GLCM features	120 MR images	0.817 similarity index, 0.817 overlap function, 0.182 extra function, and 0.817 PPV
[15]	2017	Shape, texture, and intensity features	Harvard, RIDER, Private collected images	0.79 ACC on the cubic kernel of SVM (Private collected images), 0.96 ACC on the cubic kernel of SVM (RIDER), 0.87 ACC on the cubic kernel of SVM (Harvard)
[144]	2017	371 texture and intensity features	Harvard	0.9334 ACC
[145]	2017	Shape descriptor	90 MR images	0.9889 ACC
[146]	2017	Multi-fractal features	Harvard	98.01%±0.07 ACC, 1.00 SE, and 94.78%±0.02 SP
[147]	2017	GLCM, GLGCM, GLCCM and Tamura features	62 patients	0.7581 ACC, 0.8122 AUC
[14]	2018	GWF, HOG, LBP SFTA features	2012 Image, 2013 challenge, 2015 challenge [BRATS], ISLES 2015	0.98 SE on 2012 Image, 0.98 SE, on 2013 challenge, 0.98 SE, on 2015 challenge, 1.00 SE, on ISLES 2015
[11]	2019	LBP and GWF and fusion of both LBP and GWF features	BRATS2013 Challenge, BRATS 2015 Challenge Private collected images	1.00 SP on BRATS 2013, 0.90 SP on Fused feature vector (ensemble classifier) on BRATS 2015, 0.83 SP, 0.91 on Fused feature vector (ensemble classifier) on private collected images
[150]	2019	GLCM features	105 MR images	0.9882 ACC, 1.00 SE, 0.9783 SP, and 1.17 Error rate
[155]	2020	Stochastic texture features	9 Patients of BRATS 2015	0.852 ± 0.063 complete, 0.812 ± 0.074 , 0.851 ± 0.093 enhance
[156]	2020	CNN, LBP, and HOG features	BRATS 2015	0.81 complete, 0.76 core and 0.73 enhance
[157]	2021	(PCA), entropy, mean, and wavelet transform	BRATS 2015	0.96 ACC

benchmark datasets [222]. In this work, a new framework is presented based on the fusion of different kinds of MRI sequences. The fused sequence provides more information as compared to single sequence. Later, fused sequence has been supplied to the 23 CNN model. The suggested model is trained on brat's series for the detection of glioma [16]. The 14 layers CNN model has been trained from the scratch on six Brats series datasets for detection of glioma and stroke lesions [25]. The classification is performed using ELM and RELM classifiers. This method has been tested on BRATS series such as 2012 to 2015 [189]. The 09-layer CNN model is trained from the scratch for classification of different types of tumors such as pituitary, glioma and meningioma. The method achieved an accuracy of the classification is 98.71% [223]. This model is trained from the scratch on publicly 696 weighted-T1 sequences. The model provides an accuracy of greater than 99% for tumor classification [224]. The existing methods are summarized in Table 5.

Although much work is done on deep learning methods, still there exist many challenges. The present methods do not

	•						
References	Year	Methods	Classifiers	Datasets	MRI sequences	Classes	Results
[158]	2011	Wavelet transform, PCA, scaled conjugate gradient (SCG)	Neural network (NN)	Harvard	T2 weighted	Normal or abnormal	1.00 ACC
[159]	2012	PCC, PCA, and ICA	SVM	Private data	T2 weighted and T1 weighted	Low- and high-grade glioma	0.82 ACC at PCC, 0.85 ACC at PCA, 0.79 ACC at ICA
[160]	2013	Wavelet, shape, texture, and boundary features, ICA	Ensemble classifier (SVM,KNN, and ANN)	Private images collected from ShirdiSai Cancer Hospital	T1 weighted and T2 weighted	Benign and malignant	0.99 ACC, 1.00 SE, 0.98 SP
[45]	2014	Feedback PCNN (FPCNN), wavelet transform, PCA	ANN	14 normal and 87 abnormal images	T2 weighted	Normal and abnormal	0.99 ACC
[161]	2014	Multi-dimensional co-occurrence matrix	ELM-IPSO	35 clinical routine cases	T1 weighted and T1C weighted	Low and high-grade glioma	0.99 ACC, 0.95 SP and 0.98 SE
[162]	2015	N4ITK, histogram matching	Random decision forest (RDF)	BRATS 2013 Challenge	FLAIR, (T1T1C, and T2) weighted	Complete, core and enhance	0.86 complete.0.71 core,0.73 enhance DSC on LGG,0.76 complete,0.58 core, 0.16 enhance DSC on HGG
[163]	2015	Intensity, geometry, and asymmetry	RF	BRATS 2013 Challenge	FLAIR, T1, T1C, and T2 (weighted)	Complete, core and enhance	0.87 complete, 78 core, 74 enhance DSC, 85 complete,74 core, 69 enhance PPV, 89 complete,88 core, 83 enhance RF

 Table 4 Summary of the existing classification methods

ReferencesYearMethodsClassifiersMethodsClassifiersResults11641201621-DWT, Waveler-energySVMHarvardT2 (weighted)Normal and abnormal $0.97 \times C1.0.99$ 11641201621-DWT, Waveler-energySVMHarvardT2 (weighted)Normal and abnormal $0.97 \times C1.0.99$ 18212017Muti-level OsuRFBRATS 2013 syntheticFlairComplete.core and ore inhance $0.93 \pm 0.041 GNC$ 18212017Muti-level OsuRFBRATS 2013 syntheticFlairComplete.core and ore inhance $0.93 \pm 0.041 GNC$ 114512017Muti-level OsuRFBRATS 2013 syntheticFlairComplete.core and ore inhance $0.93 \pm 0.041 GNC$ 114512017Muti-level OsuTwin SVMHarvardT2 weightedNormal and abnormal $0.96 \times C1.0.99 SKS$ 114612018DiscributionSvationary weeletHarvardT2 weightedNormal and abnormal $0.96 \times C1.0.99 SKS$ 114622018Stationary weeletKernel support vectorHarvardT2 weightedNormal and abnormal $0.96 \times C1.0.98 SKS$ 114632018Stationary weeletKernel support vectorHarvardT2 weightedNormal and abnormal $0.98 \times CI.0.99 SKS$ 114632018Stationary weeletNormal and abnormal0.98 × CI.0.98 SKS $0.98 \times CI.0.98 SKS$ $0.98 \times CI.0.98 SKS$ 114642018Stationary weeletNormal and abnormal $0.98 \times CI.0.98 $								
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[82]2017Multi-level Osu threshold, HOG-TOP threshold, HOG-TOPRFBRATS 2013 synthetic harvedFlairComplete, core and onbance0.93 ±0.04 HG DSC, onbance[145]2017HMTwin SVMHarvardT2 weightedNormal and abnormal0.93 ±0.04 HG DSC, onbance0.90 ±0.021G DSC[146]2017Directional spectralSVMHarvardT2 weightedNormal and abnormal0.93 ±0.04 HG DSC, on a cond0.90 ±0.021G DSC[146]2017Directional spectralSVMHarvardT2 weightedNormal and abnormal0.98 ACC, 0.99 SE, 0.98[146]2018Stationary waveletKernel support vectorHarvardT2 weightedNormal and abnormal0.96 SF, 0.98[166]2018Fractional Sobel filter,SVMBRATS 2013 challengeT1 weighted and FlairTumor and healthy tissues0.96 SF, 0.98[166]2018Fractional Sobel filter,SVMBRATS 2013, 2014, andFLAIR, T1, T1C, T2Normal and abnormal0.96 SF, 0.98[167]2020Statede sparseSoftmax2012, 2013, 2014, andFLAIR, T1, T1C, T2Normal and abnormal0.96 SF, 0.98[167]20212021CNNSVMLoad data2012, 2013, 2014, andPLAIR, T1, T1C, T2Normal and abnormal0.96 SF, 0.98[167]2021202120132013, 2014, andFLAIR, T1, T1C, T2Normal and abnormal0.97, 90% on20212021203203SVMLocel dataPLAIR, T1, T1C, T2<	[164]	2016	2D-DWT, Wavelet-energy	NVS	Harvard	T2 (weighted)	Normal and abnormal	0.97 ACC, 0.99 precision,0.92 SP, 0.98 SE
	[82]	2017	Multi-level Otsu threshold, HOG-TOP	RF	BRATS 2013 synthetic	Flair	Complete, core and enhance	0.93 ±0.04 HG DSC, 0.90 ±0.02 LG DSC
[146]2017Directional spectralSVMHarvardT2 weightedHealthy and glioma1.00 SEdistributiondistribution0.98 ACC, 0.99 precision0.96 SP, 0.98 SE0.96 SP, 0.98 SE[165]2018Fractional Sobel filter,SVMBRATS 2013 challengeT1 weighted and Flair0.96 SP, 0.96 SE, 0.98 SE[166]2018Fractional Sobel filter,SVMBRATS 2013 challengeT1 weighted and Flair0.96 SP, 0.96 SE, 0.98 SE[166]2018Fractional Sobel filter,SVMBRATS 2013 challengeT1 weighted and FlairTumor and healthy tissues0.96 SP, 0.96 on[27]2010Stacked sparseSoftmax2012, 2013, 2014, andFLAIR, T1, T1C, T2Normal and abnormal100% on 2012, 90% on[27]2020Stacked sparseSoftmax2015, BRATSweighted2012, 307% on[27]20212010Stacked sparseSoftmax2013, 2014, andFLAIR, T1, T1C, T2Normal and abnormal100% on 2013, 95% on[27]20212021CNSVMLocal dataFLAIR, T1, T1C, T2Normal and abnormal2012, 307% on[167]2021CNSVMLocal dataFLAIR, T1, T1C, T2Grade I, II, III and TV2014, and 95%[167]2021CNSVMLocal dataFLAIR, T1, T1C, T2Grade I, II, III and TV2014, and 95%	[145]	2017	IMH	Twin SVM	Harvard	T2 weighted	Normal and abnormal	0.98 ACC, 0.99 SE, 0.92 SP
[165]2018Stationary waveletKernel support vectorHarvardT2 weightedNormal and abnormal0.98 ACC, 0.99 precision166]2018Fractional Sobel filter,SVMBRATS 2013 challengeT1 weighted and FlairTumor and healthy tissues0.96 SP, 0.98 SE166]2018Fractional Sobel filter,SVMBRATS 2013 challengeT1 weighted and FlairTumor and healthy tissues0.98 ACC, 0.96 SF, 0.98167]2020Stacked sparseSoftmax2012, 2013, 2014, andFLAIR, T1, T1C, T2Normal and abnormal100% on 2012, 90% on2712020Stacked sparseSoftmax2015 BRATS2013, 2014, andFLAIR, T1, T1C, T2Normal and abnormal100% on2712020Stacked sparseSoftmax2015 BRATSweighted2013, 100% on2013, 90% on2712020Stacked sparseSoftmax2015 BRATSMeighted2014, and 95% on2712020Stacked sparseSoftmax2013, 2014, andFLAIR, T1, T1C, T2Normal and abnormal100% on201320212021CNNSVMLocal dataFLAIR, T1, T1C, T2Grade I, II, III and IV2014 and 95%167120212021CNNSVMLocal dataFLAIR, T1, T1C, T2Grade I, II, III and IV100%	[146]	2017	Directional spectral distribution	SVM	Harvard	T2 weighted	Healthy and glioma	1.00 SE
[166]2018Fractional Sobel filter, statistical featuresSVMBRATS 2013 challengeT1 weighted and FlairTumor and healthy tissues0.98 ACC, 0.86 SE, 0.98[27]2020Stacked sparseSoftmax2012, 2013, 2014, and 2015 BRATSFLAIR, T1, T1C, T2Normal and abnormal100% on 2012, 90% on 2013 synthetic, 95% on 2013, 100% on[27]2020Stacked sparseSoftmax2012, 2013, 2014, and weightedFLAIR, T1, T1C, T2Normal and abnormal100% on 2012, 90% on 2013, 100% on 2013, 100% on[167]20212021CNNSVMLocal dataFLAIR, T1, T1C, T2Grade I, II, III and IV100%[167]20212021CNNSVMLocal dataFLAIR, T1, T1C, T2Grade I, II, III and IV100%	[165]	2018	Stationary wavelet entropy (SWE)	Kernel support vector machine (KSVM)	Harvard	T2 weighted	Normal and abnormal	0.98 ACC, 0.99 precision, 0.96 SP, 0.98 SE
[27] 2020 Stacked sparse Softmax 2012, 2013, 2014, and FLAIR, T1, T1C,T2 Normal and abnormal 100% on 2012, 90% on autoencoder (SSAE) 2015 BRATS weighted 2012 synthetic, 95% on 2013, 100% on 2013, 100% 2015 BRATS weighted 2013, 100% on 2013, 100% on 2014, and 95% 1671 2021 CNN SVM Local data 1671 2021 CNN SVM Local data FLAIR, T1, T1C, T2 Grade I, II, III and IV 100%	[166]	2018	Fractional Sobel filter, statistical features	SVM	BRATS 2013 challenge	T1 weighted and Flair	Tumor and healthy tissues	0.98 ACC, 0.86 SE, 0.98 SP
[167] 2021 CNN SVM Local data FLAIR, T1, T1C, T2 Grade I, II, III and IV 100% weighted weighted veighted veighted	[27]	2020	Stacked sparse autoencoder (SSAE)	Softmax	2012, 2013, 2014, and 2015 BRATS	FLAIR, T1, T1C,T2 weighted	Normal and abnormal	100% on 2012, 90% on 2012 synthetic, 95% on 2013, 100% on Leaderboard 2013, 97% 2014 and 95%
	[167]	2021	CNN	SVM	Local data	FLAIR, T1, T1C, T2 weighted	Grade I, II, III and IV	100%

Table 4 continued

Table 5 S	Summary	of the	deep	learning	methods
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References	Year	DL model	Datasets (BRATS	Types of tumor	Performance measure	es (DSC)	
			2012–2019)		Complete	Core/non-enhanced	Enhanced
[225]	2014	CNN	2013	Glioma	83.7±9.4	73.6 ± 25.6	69.0 ± 24.9
[226]	2015	CNN	2014		0.81 ± 15	0.79 ± 13	0.81 ± 11
[227]	2016	CNN	2013		0.88	0.83	0.77
[193]	2017	Input cascade CNN	2012		0.81	0.72	0.58
			2013 Leaderboard		0.84	0.71	0.57
			2013 Challenge		0.88	0.79	0.73
[219]	2017	U-Net CNN	2015		0.86	0.86	0.65
[218]	2017	DeepMedic + CRF	2015		0.84	0.67	0.62
			ISLES 2015		0.66 DSC	-	-
[228]	2018	FCNN + CRF	(2013 Challenge		0.85	0.83	0.74
			2013 Leaderboard		0.88	0.84	0.77
			2015 Challenge)		0.82	0.72	0.62
[229]	2018	DNN (ILinear nexus	2013		0.87	0.89	0.92
		architecture)	2015		0.86	0.87	0.90
[220]	2019	Dual-force CNN	2015		0.83	0.67	0.63
			2017		0.87	0.73	0.69
[221]	2019	WRN-PPNet	2015		0.94	-	-
			2018		0.91		
[230]	2021	YOLOv2	2018, 2019, 2020		0.90	-	-
[231]	2020	3D U-Net and	2017		0.90	0.81	0.78
		DeepMedic	2018				
[186]	2018	Patch-based CNN	2015		0.95	-	-
		model	ISLES 2015	Stroke	1.00	-	-
			ISLES 2017		0.98	-	-
[217]	2016	CNN	ISLES 2015 (SISS, SPES)		0.59 on SISS, 0.77 on SPES	-	-

achieve maximum results in the sub-structure of the tumor region. For example, if the accuracy of the complete tumor is increased, then the accuracy of the core and the enhanced tumor is decreased (as shown in Table 5).

Brain tumor detection using transfer learning

The manual detection of brain tumors is difficult due to asymmetrical lesions shape, location flexibility, and unclear boundaries. Therefore, a transfer-learning model has been suggested based on the super-pixel. The VGG-19 is a pretrained model that has been utilized for the classification of the different grades of the glioma such as high/low glioma. The method achieved 0.99 AUC on the brats 2019 series[232]. The three different types of pre-trained models i.e., VGG network, Google network and Alex network are employed on the brain datasets for the classification of glioma, pituitary and meningioma. In this method, augmentation methods are also employed on MRI slices to generalize the outcomes and reduced the overfitting problem by increasing the quantity of the input data. After the experimental analysis using different pre-trained models, we conclude that VGG-16 provides greater than 98% classification accuracy [233]. The classification of brain tumors has been done using two different types of networks, i.e., visual attention network and CNN are utilized for classification of different types of brain tumor i.e., glioma, pituitary I and meningioma [234]. A pre-trained model i.e., VGG-16, Alex and Google net are investigated for the analysis of brain tumors. The frequency domain techniques have been applied on input slices to improve the image contrast. The contrast improved images are passed in the next phase. Where pretrained VGG-16 provides maximum classification outcomes [235]. The Laplacian filter with a multi-layered dictionary model is utilized for the recognition of brain tumors. The model performed better as compared to existing works [236]. The method consists of the three major steps such as pre-processing, augmentation of data, and segmentation and classification using transfer learning models. In which ResNet-50, DenseNet-201, MobileNet-v2 and Inceptionv3

Table 6Summary of the
transfer learning methods

References	Year	Methods	Datasets/images	Results
[241]	2019	Pre-trained Alex-net and Google net	BRATS [2013, 2014, 2015, 2016] and ISLES-2018	Up to 95% ACC
[16]	2020	Features from VGG-19 and LBP and HOG	BRATS) [2015, 2016, and 2017]	0.99, 1.00 and 0.99 Dice scores, respectively
[237]	2020	ResNet50, InceptionV3, MobileNet -V2, NASNet and DenseNet201	233 MRI patient's data	ACC of 92.9%, 92.8%, 91.8%, 99.6%, 93.1%, respectively
[235]	2020	Alexnet, Resnet50, GoogLeNet, VGG-16, Resnet101, VGG-19, Inceptionv3, and InceptionResNetV2	Harvard and local datasets	ACC of 100%, 94%, and 95.92%
[234]	2020	Pre-trained visual attention model	3064 tumor slices of local data	95.5% ACC
[233]	2020	Alex, Google and VGG	233 MRI patient's data	97.3% ACC
[232]	2020	VGG-19 with post-processing	2019 BRATS series	93.2 dice scores
[243]	2020	Inception-v3 and DensNet201	3064 tumor slices of local data	99.34%, and 99.51%
[244]	2020	ResNet-attention gate	BRATS (2017, 2018 and 2019)	86.5% ACC
[247]	2020	VGG19	233 MRI patient's data	96.13% ACC
[223]	2020	AlexNet, VGG16, ResNet18, ResNet50, VGG19, ResNet-Inception-v2, SENet, GoogleNet, ResNet101	233 MRI patient's data	Up to 95% ACC
[248]	2020	UNet-VGG16	Local data	Up to 96% ACC
[249]	2019	GoogLeNet	233 MRI patient's data	98% ACC
[250]	2019	AlexNet	Local data	100% ACC
[251]	2019	ResNet34	Local data	0.7380 ± 0.16 ACC
[252]	2020	InceptionV3	233 MRI patient's data	99% ACC
[253]	2020	InceptionV3, SqueezeNet, VGG19 and ResNet50	Local data	Up to 97% ACC
[254]	2018	AlexNet and GoogLeNet	Local data	Up to 80% ACC
[255]	2019	VGGNet and ResNet	Local data	97% ACC
[256]	2021	AlexNet	2019 BRATS	82% AUC
[257]	2021	Resnet-50, VGG-16 and Inception-V3	Local data	ACC of 95%, 90% and 55%, respectively
[240]	2021	ResNet, MobilNet-V2 and Xception	Local data	Up to 98% ACC
[239]	2021	ResNet-50 model with average global pooling	Local data	Up to 97% ACC
[238]	2021	8 layers of Alex-network	Local data	100% ACC

are utilized to classify the brain lesions with 0.95 IoU [237]. The deep features are extracted from the transfer learning AlexNet model. The model has eight layers, five of which are convolutional and three of which are fully linked. The SoftMax layer has been employed for classification between the different types of brain lesions [238]. The transfer learning ResNet-50 model with average global pooling is utilized to reduce the gradient vanishing and overfitting issues. The performance of this model has been evaluated on three distinct types of brain imaging benchmark samples that contain 3064 input images. The method achieved an accuracy of the 97.08% that is maximum as compared to latest existing works [239]. A deep CNN was used in this study that based on transfer learning such as ResNet, Xception and Mobilenetv2 are utilized for the extraction of deep features has been for tumors classification using MRI images. This method achieved an accuracy of up to 98% [240]. In this method, Grab Cut method has been employed for segmentation of the brain lesions. Later hand-crafted such as LBP features dimension of 1 × 20 and HOG features dimension of 1×100 are extracted and serially fused to the deep features dimension of 1×1000 that are extracted from the pre-trained VGG-19 model and final fused features vector length of $1 \times$ that is supplied to the different kind of classifiers. The experimental analysis proves that fused features vector provide good results as compared to existing work in this domain [16, 187]. The global thresholding method is applied to segment the actual lesion region. After segmentation, texture features such as LBP and GWF are extracted from the segmented images. After that, the retrieved features are fused to form a single fused feature vector, which is then provided to the classifiers for differentiation between healthy and unhealthy images [26]. There are two key stages to the procedure. The brain lesions are enhanced and segmented using spatial domain approaches in the first stage, then deep information's are extracted using pre-trained models, i.e., Alex and Google-network and score vector is achieved from softmax layer that is supplied to the classifiers such as for discrimination between the glioma/non-glioma images of brain. The Brats series dataset was used to test this technique's efficiency [241]. For brain tumor segmentation, the superpixel approach has been suggested. From the segmented images, Gabor wavelet information are retrieved and given to SVM and CRF for discrimination between the healthy/unhealthy MRI images [242]. The transfer learning models such as inceptionv3, densenet-201, and to form a single vector, extracted features are merged serially and passed to softmax for tumor classification. Furthermore, different dense blocks of the densenet201 are extracted and classify the brain tumor using softmax. The approach had a 99% accuracy rate. The evaluation outcomes clearly state that the fused vector outperformed as compared to the single vector [243]. A novel U-net model with the RESnet model has been trained on the input MRI images. The classifiers are fed the salient features derived from its pictures. This method has been tested on BRATS 2017, 2018 and 2019 datasets [244]. The tumor region is localized on Flair sequences of brats 2012 series. The skull is removed from of the input pictures, and a noise-reduction filter is applied bilaterally. During the segmentation, texton features are recovered from the input images using the superpixel approach. For brain tumor classification, the leave out validation technique is used. This strategy yielded an 88 percent dice score [245]. The deep segmentation has been designed that contains two major parts such as encoder and decoder. The spatial information is extracted using a CNN in the encoder section. For determining the whole probability map resolution, the semantic mappings information is entered into the decoder component. On the basis of U-network distinct CNN networks such as ResNetwork, dense network and Nas-network are utilized for features extraction. This model has been tested successfully on Brats-2019 series. The method achieved dice scores of 0.84 [246]. The wavelet homomorphic filter has been employed for noise removal. The tumor infected region has been localized using improved YOLOv2 model [230]. The summary of the transfer learning methods is mentioned in Table 6.

Brain tumor detection using quantum machine learning

Superposition of quantum states/parallelism/entanglement can all be used to establish quantum computer supremacy [258]. However, exploring entanglement of quantum features for efficient computation is a difficult undertaking due to a shortage of computational resources for execution of quantum algorithms. With the progress of quantum techniques, classical computers based on quantum theory and influenced through qubits are no longer able to fully exploit the benefits of quantum state and entanglement. QANN has been found to be effective in a variety of computer tasks, including classification and pattern recognition due to the intrinsic properties supplied by quantum physics [259]. On the other hand, quantum models based on genuine quantum computers use big bits of the quantum/qubits as a simple representation of matrix and the linear functions. However, the computational complexity of the quantum-inspired neural network (QINN) designs increases several fold due to complicated and timeconsuming back-propagation quantum model [260]. The automatic segmentation of brain lesions from I (MRI), which removes the onerous manual work of human specialists or radiologists, greatly aids brain tumor detection. Manually, brain tumor diagnosis, on the other hand, suffers from large variances in size, shape, orientation, illumination variations, greyish overlaying, and cross-heterogeneity. Scientists in the computer vision field have paid a lot of emphasis in recent

Table 7	Summar	y of the existing limitations of machine/deep	learning methods		
Ref	Year	Methods	Brain tumor types	Results	Problems/limitations
[267]	2015	Gaussian hidden markov random field (GHMRF)	Glioma (complete, core and enhance)	0.59 DSC on enhance tumor region	Enhance tumor region is not accurately/properly segmented using GHMRF
[145]	2017	Hu moment invariants (HMI) and SVM	Glioma/non-glioma	0.92 Specificity	The Hu moment invariants (HMI) with SVM cannot perform well on large scale dataset because SVM is employed for the recognition and SVM performs better on small scale datasets
[268]	2018	Gabor filter with RF	Glioma (complete, core and enhance)	0.84 DSC	Gabor filter with RF method fails in detecting tumor with small volume and its boundaries
[269]	2019	ALI, lesionGnb and LINDA methods	Stroke	0.50 Dice score (DC)	Due to variable size and stroke territory, ALI, lesionGnb and LINDA methods fail to detect the small lesion region
[220]	2019	DeepMedic and U-Net	Glioma (complete, core and enhance)	990.64 DSC	The enhance tumor region is segmented with less dice score compared to complete and non-enhance region
[266]	2020	Progressive growing of generative adversarial networks (GANs) (PGGANs)	Glioma/non-glioma	0.91 Accuracy	PGGANs method fails to differentiate turnor/non-turnor features in 25% cases
[270]	2020	Unsupervised probabilistic model	Glioma and stroke	0.34 ± 0.20 AUC	Fail to detect the small and unobvious brain lesions
[271]	2020	3D Squeeze-and-Excitation V-Net	Glioma (complete, core and enhance)	0.74 DSC enhance tumor,0.89 DSC complete tumor,0.80 DSC non-enhance	3D Squeeze-and-Excitation V-Net does not provide accurate tumor prediction in some cases
[272]	2021	Adaptive deep fuzzy neural model	Glioma/non- glioma	0.99 ACC	Computationally exhaustive still need to work on light weight model for accurate brain timor detection

years to building robust and efficient automated segmentation approaches. The current research focuses on a unique quantum fully supervised learning process which is defined by qutrits for timely and effective lesions segmentation. The proposed work's main goal is to speed up the QFSconvergence Net's and make it appropriate for computerized segmentation of the brain lesions without the need for any learning/supervision. To leverage the properties of quantum correlation, suggested a quantum fully self-supervised neural network (QFS-Net) model uses qutrits/three states of quantum for segmentation of the brain lesions [261]. The QFS-Net uses a revolutionary fully supervised qutrit-based counter propagation method to replace the sophisticated quantum back-propagation method that utilized in supervised QINN networks. This approach allows for iterative quantum state that propagates among the layers of network.

Limitations of existing's machine/deep learning methods

In this survey, recent literature regarding the detection of brain tumors is reviewed, and it is indicated that there is still room for improvement. During image acquisition, noise is included in MRI, and noise removal is an intricate task [2, 262–264]. Accurate segmentation is a difficult task [265], as brain tumors have tentacles and diffused structures [43, 193, 220, 266]. Selecting and extracting optimal features and appropriate number of training/testing samples for better classification is also an important task [191, 192]. Deep learning models are gaining attention as the learning of features is accomplished automatically; however, they require high computing power and large memory. Therefore, still there is a need to design a lightweight model that provides high ACC in less computational time. Some existing machine learning methods with their limitations are mentioned in Table 7.

The following are the main challenges of brain tumor detection.

The glioma and stroke tumors are not well contrasted. It consists of tentacle and diffused structures that make segmentation and classification processes more challenging [270].

A small volume of tumor detection is still a challenge as it can be detected as a normal region [269, 273].

Some of the existing methods work well for only a complete tumor region and do not provide good results for other regions (enhanced, non-enhanced) and vice versa [267, 271, 274].

Research findings and discussion

After a comprehensive review of the state-of-the-art exiting methods, the following challenges are found:

- The size of a brain tumor grows rapidly. Therefore, tumor diagnosis at an initial stage is an exigent task.
- Brain tumor segmentation is difficult owing to the following factors.
- MRI image owing to magnetic field fluctuations in the coil.
- Gliomas are infiltrative, owing to fuzzy borders. Thus, they become more difficult to segment [43].
- Stroke lesion segmentation is a very intricate task, as stroke lesions appear in complex shapes and with ambiguous boundaries and intensity variations.
- The optimized and best feature extraction and selection is another difficult process inaccurate classification of brain tumors.

Conclusion

The accurate brain tumor detection is still very demanding because of tumor appearance, variable size, shape, and structure. Although tumor segmentation methods have shown high potential in analyzing and detecting the tumor in MR images, still many improvements are required to accurately segment and classify the tumor region. Existing work has limitations and challenges for identifying substructures of tumor region and classification of healthy and unhealthy images.

In short, this survey covers all important aspects and latest work done so far with their limitations and challenges. It will be helpful for the researchers to develop an understanding of doing new research in a short time and correct direction.

The deep learning methods have contributed significantly but still require a generic technique. These methods provided better results when training and testing are performed on similar acquisition characteristics (intensity range and resolution); however, a slight variation in the training and testing images directly affects the robustness of the methods. In future work, research can be conducted to detect brain tumors more accurately, using real patient data from any medium (different image acquisition (scanners). Handcrafted and deep features can be fused to improve the classification results. Similarly, lightweight methods such as quantum machine learning play significant role to improve the accuracy and efficacy that save the time of radiologists and increase the survival rate of patients.

Declarations

Conflict of interest There is no grant received from any resources. All authors declare that they have no conflict of interest.

Research involving human participants and/or animals It is declared that research has not involved any human participants and animals.

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