



A survey on brain tumor detection techniques for MR images

Prabhjot Kaur Chahal¹ · Shreelekha Pandey¹ · Shivani Goel²

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Abstract

One of the most crucial tasks in any brain tumor detection system is the isolation of abnormal tissues from normal brain tissues. Interestingly, domain of brain tumor analysis has effectively utilized the concepts of medical image processing, particularly on MR images, to automate the core steps, i.e. extraction, segmentation, classification for proximate detection of tumor. Research is more inclined towards MR for its non-invasive imaging properties. Computer aided diagnosis or detection systems are becoming challenging and are still an open problem due to variability in shapes, areas, and sizes of tumor. The past works of many researchers under medical image processing and soft computing have made noteworthy review analysis on automatic brain tumor detection techniques focusing segmentation as well as classification and their combinations. In the manuscript, various brain tumor detection techniques for MR images are reviewed along with the strengths and difficulties encountered in each to detect various brain tumor types. The current segmentation, classification and detection techniques are also conferred emphasizing on the pros and cons of the medical imaging approaches in each modality. The survey presented here aims to help the researchers to derive the essential characteristics of brain tumor types and identifies various segmentation/classification techniques which are successful for detection of a range of brain diseases. The manuscript covers most relevant strategies, methods, their working rules, preferences, constraints, and their future snags on MR image brain tumor detection. An attempt to summarize the current state-of-art with respect to different tumor types would help researchers in exploring future directions.

✉ Prabhjot Kaur Chahal
prabhjot_kaur@thapar.edu

Shreelekha Pandey
shreelekha.pandey@thapar.edu

Shivani Goel
shivani.goel@bennett.edu.in

¹ Computer Science & Engineering Department, Thapar Institute of Engineering & Technology, Patiala, India

² Department of Computer Science & Engineering Department, School of Engineering & Applied Sciences, Bennett University, Greater Noida, India

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1 Introduction

Brain tumor¹ and its analysis is of great interest due to the growing technology in medical image processing. According to the survey conducted by National Brain Tumor Foundation (NBTF), the development of brain tumor amongst masses and the death rate due to brain tumor is succeeding previous year's statistics across the globe [52, 95]. Also in past few decades several works have proposed frameworks or approaches to highlight the brain tumor area which may or may not be followed by phases like classification, treatment planning and outcome predictions. Brain tumor segmentation in medical images is critical and is generally governed by factors like poor contrast, noise, and missing boundaries [27]. For effective control of these factors, diagnosing processes like magnetic resonance (MR) imaging, positron emission tomography (PET) and compute tomography (CT) scan, are employed. These imaging processes are helpful in detecting different types of diseases. Usage of harmless magnetic fields and radio waves makes MR images very popular in successfully diagnosing and treating brain tumors [57].

Accurate detection and precise localization of abnormal tissues are crucial for diagnosis. This fact is fully supported by the existence of effective approaches employing segmentation or classification or their combination for brain characterization both quantitatively as well as qualitatively. Based on human interactivity, MR images can be processed using manual [46, 98, 170], semi-automatic [19, 35, 164], and fully automatic techniques [48, 58, 61, 155, 160]. In medical image processing, segmentation/classification should be accurate which is thus commonly performed by experts manually and hence time consuming. On the same hand, designing a fully automatic and efficient segmentation approach is yet far from reality. Moreover, such systems always demand for a second opinion as the main object here is human life [56]. Also in the absence of experts, the performance of automatic techniques depends solely on the knowledge bases. Researchers have proposed several methods to improve such knowledge bases and thus the capability of tumor detection systems. The clinical and pathological acceptance of any techniques solely rely on the computation ease and the degree of user supervision [166]. The manual methods requires complete user supervision so an urge for better solutions rises. The existing semi-automatic or interactive methods definitely dominate in practice currently as well as in coming time. Semi-automatic methods are popularly adapted in clinical applications by radiologist to replace time consuming and challenging tasks of manual process [107, 114]. User initialization is required in almost

¹Life threatening brain tumor compresses/displaces brain tissues to make room for the growing mass. Tumor can occur in any body part hampering the normal working of the system but is fatal when arise in brain. Different types of brain tumors exist varying in shapes, sizes, and/or positions which have to be dealt accordingly [63]. The abnormal tumors can be clubbed as primary and secondary brain tumors that, based on their characteristics even get streamlined further. Primary tumors are formed when cancer tissues initiates and stays at the same place as well as position. The secondary (or metastatic) tumors are those which spread to other body parts from where it is emerged. As per the terminology of radiologists, primary tumors is either benign (slow growing, less aggressive, and noncancerous) or malignant (rapid growing, life threatening, and cancerous). In addition to these primary information, the treatment planning depends on grade and tissue cell information which is usually collected during a process called biopsy. Tissue cell type identifies those cells that had given rise to the tumor and tumor grade estimates its aggressiveness. Tumors often have different grades at various stages of their growth [15, 96].

all semi-automatic methods and to assure accuracy repeated user interaction is mandatory. Under such circumstances, this manuscript is an attempt to visualize the acceptance and growth of such automatic/semi-automatic systems in medical as well as research domain for various tumor types.

The prospective here is to have a comprehensive review of traditional as well as current approaches in the field of medical image processing, especially brain tumors, highlighting their pros, cons, and future challenges/trends [21, 44]. Emerging machine learning and soft computing approaches have created a remarkable impact in medical imaging too [72, 79]. As highlighted in one of the recent reviews, deep learning based brain tumor segmentation is in trend [7]. Thus, the manuscript attempts to summarize as well as discuss recent studies that have explored deep learning architecture, its mechanism, performance and quickness from the perspective of their quantitative utility in MR image based tumor identification systems. Along with a detailed assessment of current scenario, highlights to future directions are also provided. Review is structured in a worthwhile way to remain useful not only for an expert but for a novice too who has abstract knowledge in the field of CAD systems for brain tumor. The manuscript is also guiding with a view for researchers to get an open gate for those works that would handle brain tumor variability. Complete coverage of all categories of tumor detection techniques has been done to understand performance differences in any category of technique. The manifold contributions of this manuscript are summarized as below:

- 1) The review is more targeted for budding researchers, therefore manuscript focuses more on completeness and attempts to analyze existing traditional techniques as well as the emerging ones. The depth and width of survey done helps not only the beginners but experts and radiologists too by providing wider options.
- 2) Effective brain tumor segmentation and classification result in better detection but analysis too. These phases however depend on background knowledge related to the type of MR image modality, tumor type, and data source used in preparing the system. The review is conducted to include studies covering each of the said aspect with respect to a variety of tumor types rather focusing on a few ones.
- 3) Classification is driven by segmentation and there are many works that target on efficient segmentation which may or may not be followed by classification. Thus, the manuscript discusses approaches individually from both the phases and their combinations too, i.e. hybrid systems.
- 4) Statistical analysis of MR image modalities, data sources, as well as current scenario in each of the considered detection technique is also presented. Utilization of the best modality based on the ease of availability is summarized considering the articles covered in this review as well.

The rest of the manuscript is arranged in five more sections. Section 2 discusses commonly used MR image types and the importance of contrast parameters. Section 3 briefly presents an overall process followed generally in brain tumor detection systems. In addition, it focuses the popular datasets used in this domain. Section 4 discusses current trends in the brain tumor detection techniques especially for MR images. Section 5 summarizes as well as highlights the observations made while preparing the survey. It also evaluates all the considered detection techniques from the perspective of certain identified parameters. Lastly, the best works for some of the popular tumor types from each detection category is presented in this section. Finally, Section 6 deliberately recapitulate the techniques and future challenges.

2 MR image and contrast

Segmentation/classification of MR images needs to be very efficient for proper analysis of brain tumor. A range of works have utilized the capabilities of image segmentation techniques to extract the meaningful content from medical images (i.e., tumor) which thus helps in proper analysis of brain tumor. But, the variability of tumor shapes and the presence of cerebrospinal fluid (CSF) particularly make a difficult brain tumor detection task more complex.

Irrespective of the superiority of segmentation technique employed, quality of segmentation depends greatly on contrast of medical images, amount of noise, and lastly incomplete boundaries. Particularly, in medical images good contrast supersedes all other basic requirements, as an abnormal structure is identified completely on the basis of certain contrast characteristics. Contrast is a function of tissue density in MR images [52, 58]. In other words, good image contrast is a native property of brain MR images and thus their generation do not need any kind of contrast enhancing agents. This fact is also responsible for the popular usage of these images in brain tumor detection. However, image contrast is influenced by intrinsic (Table 1) and extrinsic (Table 2) parameters. Proper tuning of these parameters helps to change the contrast behavior and highlight the regions of interest, i.e. differentiate tumor tissues from the normal (inner) brain tissues (fat, gray matter - GM, white matter - WM, and CSF) [15]. The visual representation of normal brain tissues is depicted in Fig. 1.

Differences in the compositions of tissue types result in varying MR image signals. Accordingly, different types of pulse sequences are used to emphasize various aspects of normal and tumor tissues. Variable sequences have different completion time and also they provide diverse valuable information. For the purpose of clarity, a few images from each of the MR image types considered in this manuscript are shown in Fig. 2. Depending upon the pulse sequence used, an MR image can be T1-weighted (T1-W) or T2-weighted (T2-W). Sometimes to get better results a special pulse sequence is employed to obtain fluid attenuated inversion recovery (FLAIR) or proton density weighted (PD-W). Apart from these some diffusion based MR images like diffusion weighted image (DWI) and apparent diffusion coefficient (ADC) are also popularly used. DWI and ADC are particularly useful in early diagnosis and longitudinal evaluations. During the study, it is observed that a variation of T1-W obtained using a contrast agent Gadolinium is also popular in the community. It is known as CE-T1W and is similar to T1-W with enhanced clarity as is shown in Fig. 2.

Table 1 Intrinsic parameters

Proton density (PD) measures relative concentration of protons in the concerned tissue to that in water at same temperature and volume.

Longitudinal relaxation time constant (T1) is defined as the time when 63% of the longitudinal magnetization has recovered. It measures the re-growth of longitudinal magnetization and is also known as *spin – lattice relaxation*.

Transverse relaxation time constant (T2) is defined as the time when 63% of the transverse magnetization has decayed. It measures the decay of transverse magnetization and is also known as *spin – spin relaxation*.

Chemical shift arises due to the differences in resonance frequencies of fat and water. This MR image artifact happens because the water and the fat structure shift with different frequencies in the organ.

Susceptibility indicates whether a tissue attracts or repels out in the magnetic field. It may also be defined as the extent to which a tissue gets magnetized when placed in an external magnetic field.

Table 2 Extrinsic parameters

Magnetic field strength (MFS) should be both strong and uniform MFS to draw proper conclusions. Its measuring unit is Tesla (T) and most of the systems work at 1.5T.

Radiofrequency (RF) is an electromagnetic wave with frequency range similar to that of radio and television transmissions. The prone tissue gets heated and highlighted by absorbing the pulses of the applied radiofrequency energy. The preferred range for RF pulses is 1 MHz -100 MHz.

Repetition time (TR) is the time that exists between succeeding pulse sequences of the same curve. It determines the longitudinal magnetization between each pulse. Image contrast properties are controlled by TR variations.

Echo time (TE) refers to the time between the radiofrequency excitation pulse and the signal peak induced in the coil.

Inversion time (TI) is the time period between the initial 180° RF pulse (to invert the magnetization) and the 90° RF pulse (to get the residual longitudinal magnetization into the transverse plane). This pulse sequence is the core component of an inversion recovery pulse sequence.

RF pulse amplitude (flip angle) is the angle that rotates the net magnetization relative to the main magnetic field direction by 120°, applying the RF excitation pulse.

b-value measures the strength and timing of the gradients applied to generate the diffusion-weighting images. It is used to control the effect of diffusion, for example, higher b-value is needed for stronger diffusion effects to sense the slow moving water molecules.

Another attempt of this study is to highlight MR image modalities that are frequently used in the research domain of brain tumor detection. The different MR modalities as shown in Fig. 2, vary from each other on the bases of various parameters, i.e. intrinsic and extrinsic. The easily available and the commonly worked MR image sequences are T1-W and T2-W. The researchers working on traditional techniques retrieve high accuracy rates with T2-W MR sequences even more than 90% but steadily this trend has changed and the demand of systems handling all types emerge. The same can be observed in Tables 6 and 7 where T1-W, T2-W, CE-T1W and FLAIR are maximum utilized. Figure 3 depicts the usage trend (in percentage) of various MR images and is prepared based on the papers reviewed in this manuscript. No doubt the proportion of DWI is very small, but based on the observations made it can be said that in coming scenario the diffusion based will be preferred due to its sensitivity to detect even minute infarcts as compared to T1-W and T2-W, which are the current winners.

Table 3 summarizes values of a few contrast parameters (echo time - TE and repetition time - TR) for all the six MR image modalities and colors of normal (fat, GM, WM, and

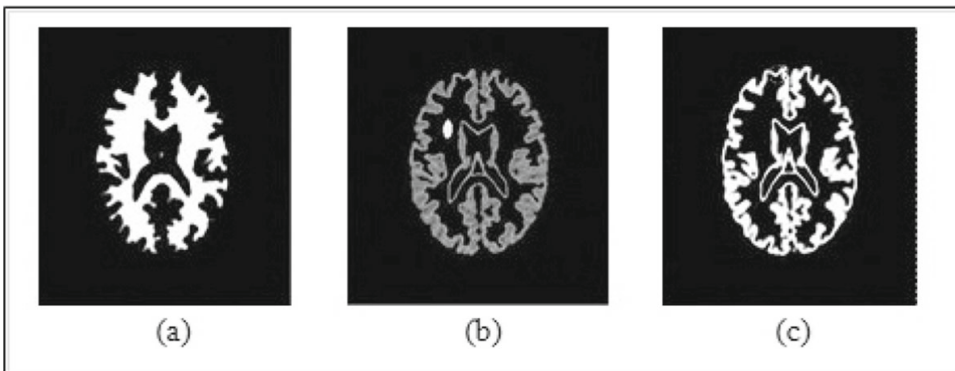


Fig. 1 Normal brain tissues after segmentation **a** White matter (WM), **b** Grey matter (GM), and **c** Cerebrospinal fluid (CSF)] [57]

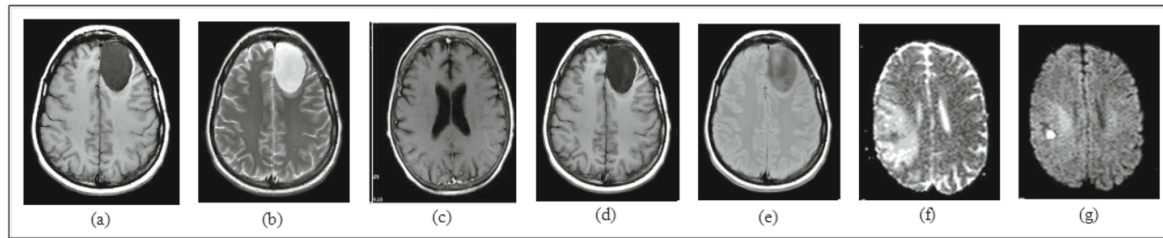


Fig. 2 The MR image types **a** T1-W, **b** T2-W, **c** CE-T1W **d** FLAIR, **e** PD-W, **f** ADC, and **g** DWI [57]

CSF) and abnormal brain tissues. Specific values of these parameters are available for all MR image types, except DWI and ADC. Instead of using single TE and TR values, most of the existing works vary these parameters within certain limits based on the protocol being followed while working with DWI and ADC MR images. The focus of any system is to effectively detect the tumor tissue by separating it from other brain tissues which are commonly differentiated based on colors. A color palette is also included to help readers in better visualization of colors associated with normal and tumor tissues in each MR image type.

3 Brain tumor detection system

The starting module is collection and acquisition of images which are to be analyzed in later phases. Standard brain tumor databases, namely BRATS [16], Harvard medical school, BrainWeb, and Internet Brain Segmentation Repository (IBSR), are commonly used by the researchers. Moreover, studies have validated their approaches on data repositories collected from various clinical and pathology labs. The pre-processing module is meant to improve image visual quality by filtering all the high noise levels. Presence of such disturbances makes abnormal/normal tissue discrimination relatively difficult and thus the precise interpretations. Next is the segmentation module that highlights region of interest and guides all the proceeding modules, especially analysis. Although segmentation is important but it may not be present sometimes when direct classification supersedes other objectives. The feature extraction module follows segmentation. A variety of standard texture features along with other information like intensity and edge, are commonly used. Robust learning models are built by picking a sub-class of relevant features and exempting the irrelevant ones. This is successfully achieved by utilizing standard dimension reduction techniques such as principle component analysis (PCA), independent component analysis (ICA), canonical correlation analysis (CCA), etc. Finally, the resultant features with reduced dimension are

Fig. 3 Usage (in percentage) of different MR image modalities in brain tumor research domain based on studies considered in the manuscript

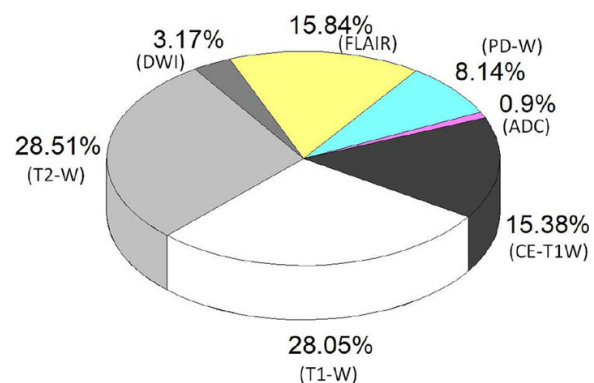



Table 3 Echo and Repetition times along with color palette of normal and abnormal brain tissues for each MR image type

						
	White	Light Grey	Medium Grey	Grey	Medium Black	Black
MR Image	T1-W	T2-W	FLAIR	PD-W	DWI	ADC
TE	< 30mm	> 80mm	> 80mm	< 30mm	User dependent	User dependent
TR	< 80mm	> 2000mm	> 3000mm	> 1000mm	User dependent	User dependent
FAT	White	Medium black	Grey	Light grey	Medium black	Medium black
White matter	Medium grey	Grey	Medium grey	Medium grey	Grey	Light grey
Grey matter	Grey	Medium grey	Light grey	Light grey	Medium grey	Medium grey
CSF	Black	White	Black	Grey	Black	White
Tumor tissue	Medium black	Medium grey	White	White	White	Black

used for classifier training to differentiate normal brain tissues from abnormal ones. After training, performance of the system is evaluated on several parameters (such as accuracy, similarity, sensitivity, dice coefficient, visual comparison, etc.). Once output is retrieved, the system is set to formulate and interpret the desired diagnosis result. To recapitulate, an expert advice is always preferred to have a second opinion for prefect diagnosis. Systems reporting improved performances, i.e. refined results assist medical specialists in making better interpretations (Fig. 4).

Though the survey is focused on tumor detection, but the scarcity of freely available medical data due to security reasons sometimes limit the important task of experimentation. Thus, based on the papers considered in this manuscript, a list of data sources having various MR images with modalities is presented in Table 4. In addition, the popularity of these data sources are also identified and the same is shown in Fig. 5. Another popular category is ‘private datasets’ which represents real data collected from clinical laboratories or pathology or hospitals. Clearly, the mostly used one is the real/private datasets followed by BRATS. The reason behind is an urge to prove the acceptability of the proposed approach in real-time scenario.

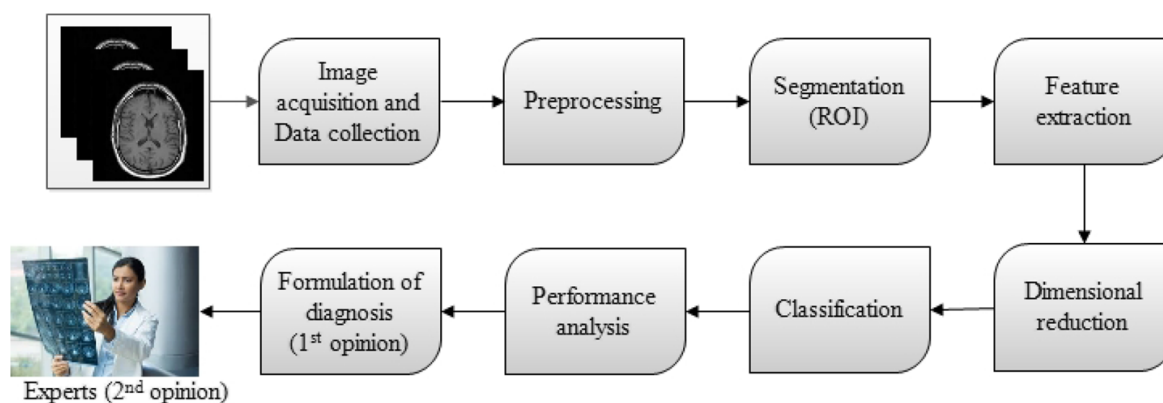
**Fig. 4** Generic process flow of brain tumor detection system

Table 4 Datasets commonly used in brain tumor detection techniques

Name	Description	Web source
BRATS	Brain Tumor Segmentation Challenge (BRATS) has the dataset available from 2012 to 2018.	https://www.smir.ch/BRATS/Start2012
BrainWeb	Simulated MR images of the human brain.	http://www.bic.mni.mcgill.ca/brainweb/
IBSR	MGH CMA Internet Brain Segmentation Repository (IBSR). Repository with raw and segmented (GM/WM/CSF) MR image volumes.	http://neuro-www.mgh.harvard.edu/cma/ibsr/
OASIS	Open Access Series of Imaging Studies. Structural MR from 416 subjects.	http://www.oasis-brains.org
Harvard medical school	Download includes the collection of electronic resources of image data, slides, presentation and software provided by NCIGT.	http://ncigt.org/downloads
NBIA	National Biomedical Imaging Archive (NBIA) is a searchable repository of vivo images providing biomedical research and academia with access to image archives.	https://imaging.nci.nih.gov/ncia/login.jsf
TCIA	The Cancer Imaging Archive provides access of public MRI/CT scan data.	https://wiki.cancerimagingarchive.net
ISLES	Ischemic Stroke Lesion segmentation is challenge of medical image. In ISLES 2016 publicly available cases includes 35 training and 40 testing.	https://www.smir.ch/ISLES/Start2016 .

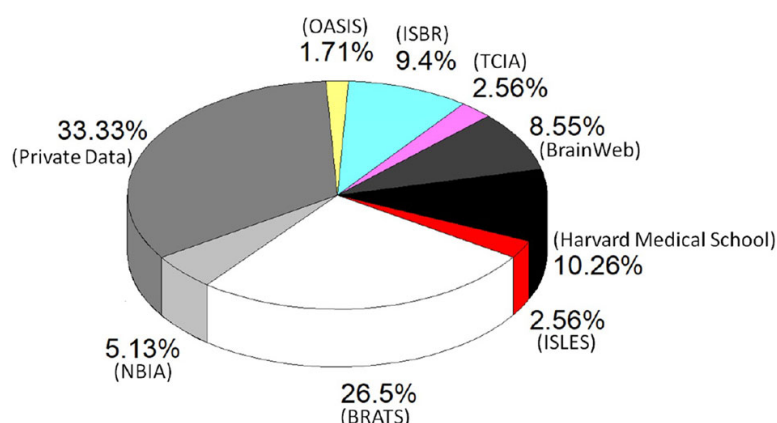


Fig. 5 Popularity (in percentage) of various data sources in brain tumor research domain based on studies considered in the manuscript

4 Traditional and emerging techniques

Among all the modules shown in Fig. 4, the manuscript focuses in reviewing brain tumor detection trends applied after data collection and image acquisition. The existing benefits of MR imaging over other diagnostic imaging techniques, as stated earlier, drives authors to focus on MR image based brain tumor detection techniques. Accordingly, range of journals (120), conference papers (40), and handbooks (8) from the last 15 years are included in this survey and each paper is categorized under one of the six categories as are shown in Fig. 6. The five standard categories considered are thresholding, region-, contour- (or shape-), statistical-, and machine-learning based. In addition to these traditional ones, the emerging categories, viz. deep learning and hybrid are also included. The following sub-sections discusses some of the prominent studies in each of these categories. Sections 4.1–4.3 focuses on segmentation approaches, Sections 4.4–4.6 targets the classification methods and lastly Section 4.7 covers on the hybrid techniques.

4.1 Thresholding based techniques

Thresholding is a simple and aged procedure for image segmentation [61, 158], based on the images with different intensities. In this method image is partitioned into different regions

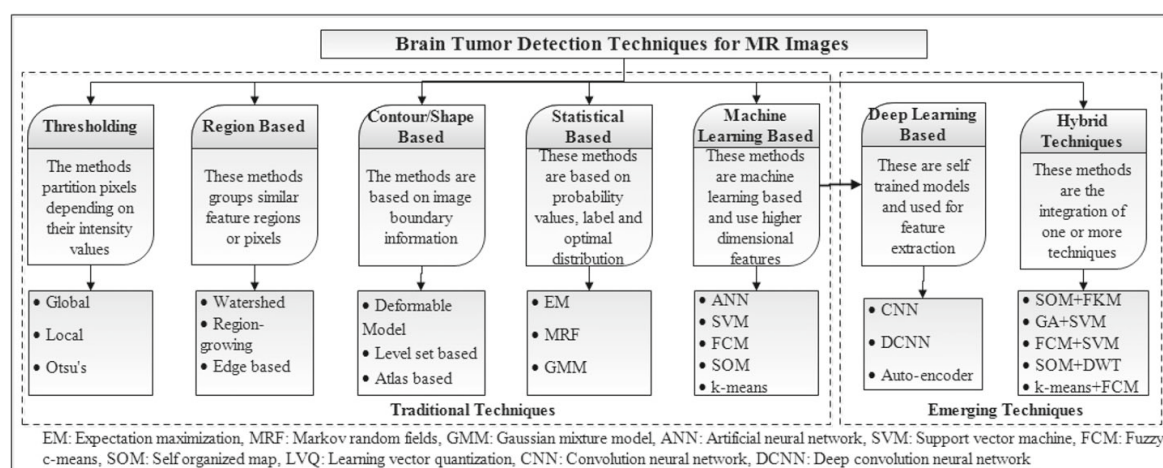


Fig. 6 Classification of brain tumor detection techniques used in MR images

by comparing their intensities with one or more predefined intensity value(s). These intensity values are known as threshold, which actually separates the image into different classes. Threshold values are generally estimated by prior knowledge related to local statistical properties like mean intensities. For example, studies efficiently computed local threshold values for T1-W images [139, 166]. There are several thresholding techniques established such as global, local, histogram, and Otsu's. Global, the simplest one, computes single threshold for entire image. It works well for images with bimodal histogram, otherwise local thresholding or histogram thresholding is preferred. Local thresholding divides image into sub-images and generates threshold of each region. It is thus computationally slower than global. On the other hand, histogram thresholding is based on the number of peaks (representing different modes or regions) in a histogram [61, 158].

A novel framework utilizing global thresholding to enhance binary image followed by morphological operations for tumor segmentation is presented [130]. Similarly, another work considered partial volumes of every region in PD-W and T2-W MR images to compute thresholds for segmentation. The segmented volumes of brain tissues (GM, WM, and CSF) are measured with an aim to determine the existence of neurodegenerative diseases (Alzheimer's and cerebral palsy) [149]. Furthermore, thresholding based segmentation in either case, local or global, is commonly observed as an initial phase in segmentation process because it minimally deteriorates the information provided by MR images. Working on same line, a semi-automatic fast approach calculates tumorous area from post CE-T1W MR tumorous image volumes by combining the concept of intensity threshold with morphological segmentation [59]. Thresholding is applied to selected region of interest manually. Visual results comparing set of patient data suffering from intracerebral glioma with traditional data thresholding method are presented and found to be similar. The technique is also popular in current scenario and sometimes used in combinations with other techniques to uplift the accuracy rate.

An automatic pathological area extraction approach using multi-resolution symmetry analysis and Otsu's threshold technique is also designed [50]. The approach is evaluated on T2-W and FLAIR images from BRATS dataset with axial (357) and coronal (443) images. The approach is evaluated in two phases based on accuracy values, detection (91.15%) and extraction (95%). Although the system is proposed for 2D MR, it is suitable for tumor detection in 3D as well. In recent works an effective combination of rough entropy based threshold and random forest (RF) to identify, extract, and classify four different tumor types (Glioblastoma multiforme - GBM, metastasis - MET, meningioma - MG, and granuloma - GN) is developed [84]. The study adopted thresholding to appropriately delineate tumor area in CE-T1W images, followed by morphological post processing, and lastly the RF classification. Experimental results prove that the proposed approach effectively improves diagnostic power of computer assisstive system.

An efficient threshold based segmentation approach which is easier to implement than existing threshold methods is designed [73]. The study computes threshold considering summation of unique pixel values, omitting black pixels, and then dividing by the count of unique pixels. Using the obtained threshold, gray scale image gets converted to a binary image. Experimental results are obtained on 100 MR images from TCIA (The Cancer Imaging Archive, 2017). Overall efficiency in terms of accuracy, sensitivity and specificity is reported as 96%, 94.28%, and 100%, respectively. In comparison Otsu's method results in 84.72% accuracy [147].

4.2 Region and contour based techniques

Region based methods search for group of pixels having similar features to get connected regions [161]. These methods are simple and also resistant to noise. An effective seed pixel based region-growing segmentation uses similarity criteria to verify and add neighboring pixels to a region [81, 86, 133, 134]. The process iterates till no further pixel satisfies the criteria. On the other hand, seed-based segmentation considers a set of seeds denoting the objects to be segmented. A pixel is assigned to a region whose mean is the closest to pixel's intensity. Systematic watershed segmentation is eminent in identifying background and foreground of an image. The seed point selection is really difficult in such methods but several iterations lead to the attainment of minimum values for foreground and background locations.

Edge based segmentation (EBS) methods observe hasty intensity changes near edges and thus are suitable for simple noise free images. EBS works in two-folds to balance between accuracy and noise immunity. If accuracy is higher, then noise can make image irrational; similarly higher degree of noise results in undetected image portions and incorrect object positions. Gradient based methods take difference of neighboring pixel intensities and works well for little noisy images with rapidly changing near edge intensity. Canny edge detection (CED) first filters noise, separates edge pixels, and then calculates image threshold. Sobel edge detection aids image smoothening and emphasizes high spatial frequency regions using a two dimensional spatial gradient measurements. Contour based segmentation uses a collection of control points and traces object's boundaries by evolving curves. The linear interpolation gives a piecewise linear curve. The active contour model is an effective way of segmentation, in which the object's boundaries are noticed by evolving curves. This method is capable of detecting sharp image edges. Watershed approaches have also been extensively used in brain tumor segmentation. One study proposes a watershed based segmentation algorithm for tumor detection both in 2D and 3D brain modalities [124]. Highlight is the block method employed to divide image into regions, which is then analyzed on multiple parametric values namely, edges, gray values, and local contrast of pixels. Focusing on the fact that proper parameter tuning is the key to success for watershed segmentation methods, a study explores several versions of watershed [54]. Working on the same lines, another work uses markers and floods to design marker-controlled watershed segmentation (MCWS) [116]. In place of regional minima, markers are adopted at the start of image gradient. Experiments show better accuracy values for MCWS than other segmentation methods. Moving ahead the over segmentation problem in an efficient watershed algorithm is resolved by developing a marker based watershed algorithm [25]. Internal and external markers are detected by applying atlas based approach utilizing prior image information. The algorithm uses different feature combinations such as color, edge, orientation, and texture to extract tumor region from MR images. Experiments are performed on 45 brain tumor axial orientation DWI provided by Medical College hospital. It is evident from results that color and orientation features cannot be considered for watershed segmentation. The concept of traditional watershed segmentation is effectively combined with Scale-Invariant Feature Transform (SIFT) to design a novel watershed matching approach [66]. Images are preprocessed with median and bilateral filters for artifacts removal and hence an improved segmentation quality. Watershed followed by SIFT matching between segmented and original image is done to compute tumor region. Experimental results report an accuracy of 98.5% operating on 100 T1-W images from Montreal neurological institute. In addition, other studies have worked on issues of over segmentation by means of

pre- and post-processing to eliminate noise or by merging watershed with other concepts to report better results. Researchers used region and Fuzzy c-means clustering to eradicate this above stated disadvantage [23, 68, 136]. The study of existing literature clearly states that the popularity of watershed is still prevalent due its advantages over other conventional methods.

Sobel, Prewitt and Roberts are commonly covered under edge detection to enhance image areas containing edges or significant transitions. Performance comparison of three edge-based detection techniques based on these operators is presented using a dataset of 13 patients among which 8 having tumor [129]. The aim is to retrieve tumor as well as brain structure edge pattern. Sobel is observed to report the smallest standard deviation and thus the most suitable operator in detecting brain tumor for the considered dataset. Limitations like discontinuity in detected edges, improper edge detection, false or thick edges, no edge detection in noisy images etc. usually occur with traditional edge based methods. Thus, combination of such approaches with other well known approaches is explored by many researches to effectively deal with these drawbacks. Like a combination with cellular automata (CA) is proposed [45]. Similarly, an improved Sobel edge detection algorithm utilizing the concept of image dependent thresholding is designed [17]. It first identifies closed contours with lesser false edges and then uses their intensity information for tumor extraction. Experiments are conducted on seven case studies, each with 20 – 30 images and are compared with conventional algorithms based on gray level uniformity measure, relative ultimate measurement accuracy, and Q-parameter. Improved Sobel algorithm effectively extracts tumor in all the cases. The algorithm can further be improved by decreasing boundary lines thickness and thus increasing region area. Edge detection sometimes fails to achieve the desired results, a study is introduced which combines Fuzzy inference system with edge detection to design an improved segmentation approach [101]. Initially k-means approach is applied to form clustering groups which act as an input to Mamdani fuzzy inference system to generate various threshold parameters. The classical sobel edge detector is used to feed these parameters to exactly locate the tumor position. A modified version of contour based method termed as content-based active contour (CBAC) is presented [131]. The study combines intensity and texture information within active contour to overcome issues that prevail due to the presence of diffused and false edges in input images. Efficacy of CBAC is tested on two real datasets containing more than 600 images of pre- and post-contrast T1-W and T2-W MR image modalities. Experimental results show remarkable performance in segmenting different types of homogeneous, heterogeneous, and diffused tumors as well as synthetic images.

Unlike the discussed segmentation techniques, deformable model based segmentation builds a connected model using object's prior knowledge and information like shape, texture, orientation, location etc. [102]. A few incorporates statistical information drawn from the group of training datasets too [166]. The internal and external influence weighted forces parametrically defines curves/surfaces that makes deformable models smooth. Existing deformable models are categorized as geometric and parametric model [94]. Parametric deformable models can significantly match and track anatomic structures of images over time [103]. Out of all the region based segmentation methods, deformable model based ones are the most extensively explored in addition to level set segmentation methods. Level-set segmentation segments curves or surfaces while dealing properly with issues of corner and breaking curve.

Such models are extensively incorporated in brain tumor detection system. Like a modified deformable region model is presented using 2D MR image modalities to extract and

retrieve the boundary of the brain tumor [89]. It effectively utilizes point sampling to lower the count of boundary points to be processed. The corresponding effect in the form of reduced extraction time of tumor boundary is observed when compared with traditional active contour models. However, the model is not a general one and performs poorly in some applications. It requires manual input to set the ideal boundary limits for acceptable results in those applications. A framework to segment internal brain structures is proposed by integrating spatial relations into deformable model based on initial tumor segmentation [83]. Segmentation and recognition of surrounding brain structures are based on prior knowledge of their spatial arrangement. The approach is validated on 20 cases of CE-T1W MR image. Experimental results report sensitivity of 84%. Further, a novel, accurate, and robust pipeline of region-based fuzzy clustering method called Enhanced Possibilistic Fuzzy C-Means (EPFCM), which is used for the initial segmentation of the tumor, is combined with one of the contour-based methods called parametric deformable model with gradient vector field (GVF), is introduced [123]. EPFCM output provides initial contour for deformable models to deal with the issues of initialization and poor boundary capturing. Tumor segmentation results are presented on a dataset having 10 CE-T1W and 5 FLAIR MR images. The reported average similarity and Jaccard index are 95.3% and 82.1%, respectively.

Geometric deformable model, also known as level set method helps to overcome problems like corner fabrication and curve breaking. Segmentation of 3D volumetric images are commonly done using this model as it automatically handles topological changes during splitting and merging of contours. A variational level set approach based on existing well-known method [92] is introduced for automatic bias correction and segmentation of images altered by intensity variations [33]. The presented region-based active contour model is flexible in initialization and ensures smoothness of the computed bias field by the data term while variational formulation. It uses a local intensity fitting term that attracts contour towards object boundaries and preserves regularization term to ensure accuracy. Results are compared based on coefficient of variance for two simulated images (one corrupted with bias field without noise and another with both bias and noise) from BrainWeb. The obtained lower variance values indicate that images bias corrected with the presented approach are more homogeneous. Similar form of variational methods are presented by other researchers where knowledge is preserved in the form of template guide outlines and atlases of normal brain structures [37, 119]. For accurate tumor matching, an improved semi-automatic version of level-set segmentation employing a constraint termed as PICE (prior information constrained evolution) is presented [164]. It combines image gradient and intensity information in level-set formulation. PICE is evaluated and compared with traditional level set segmentation using dataset of T1-W MR images and has reported an outstanding accuracy (nearly 98%) which is 10% more than the existing approaches. Level-set segmentation is explored in combination with region and boundary driven methods known as hybrid level set (HLS) to achieve an accurate performance [163]. The idea is to employ region method for propagation and boundary as a stopping function so as to assist user in better region of interest (ROI) selection. Experiments are performed on 246 axial tumor slices of 10 different patients. So far, semi-automatic detection methods are considered the best as human interactivity is required to initialize the segmentation process [91]. A semi-automatic level set method is used to initialize the tumor region for segmentation. A repeated segmentation process occurs by tuning the parameters of level-set. Moreover, to handle the issue of slow computing of 3D medical images, a tool that depends on level-set models is proposed.

Segmentation of images with unclear pixels – region's intensities relationship is commonly done using atlas based segmentation which allows transfer of labels as well as

segmentation. It is prominently employed to detect object's shape and patient's group morphologically in CAD. It's generic aspects are detailed beautifully that helps to set the forum for brain tumor segmentation [126]. An expectation-maximization based automated system is introduced aiming to segment brain tumor as accurately as manually [120]. In addition, it segments normal brain tissue classes, namely WM, GM, and CSF along with edema. Spatial probabilistic atlas containing expert prior knowledge of brain structures guides the whole process. Contrast enhancement based atlas is computed for each subject under consideration for better results. Experimental results obtained for T1-W, T2-W, and CE-T1W MR images proof applicability of the system. Similarly, a tool based on mesh-free method is designed to segment brain tissues (WM, GM, CSF, fats, edema, and tumor) [23]. Study aims on improvement in the registration accuracy by manually seeding atlas with the prior knowledge of tumor position and mass effect. The initial source of work is presented in [136] and is further validated on synthetic cases using a finite element method (FEM) based deformation. Experimentation results show good segmentation performance. Another mesh free based, non-parametric, automatic system is introduced to fragment brain tissues from volumetric tumor images. The tumor development model contrive as a mesh-free Markov Random Field energy minimization issue that guarantees correspondence among atlas and patient's image, preceding to registration phase. Experiments are conducted on T1-W MR images of four patient cases from ContraCancrum project and results are compared using DSC. For real patient cases DSC values of WM, GM and, CSF ranges from 70 – 82%.

4.3 Statistical based techniques

Statistical based segmentation is simpler to implement and further, the associated statistical probabilities make acceptance of such methods in medical image processing quite natural [61]. These methods work with parameters like mean, median, standard deviation, probability distribution, and amplitudes to statistically describe an image. They are mainly classified into three, namely Markov random field (MRF), Gaussian mixture model (GMM) and expectation maximization (EM). MRF is non-deterministic and considers spatial information via dependency concepts of neighbors and cliques. One can embed prior knowledge into MRF through clique possibilities. GMM in comparison has effortless implementation and requires few parameters. Lastly, EM uses other methods, like k-means for initialization of matrices such as mean and covariance. Each iteration recomputes these matrices based on changing membership of training information till the convergence criteria is reached. In general, an effective statistical simple segmentation model is designed and progressively extended for the multi-scale environment.

A novel 3D segmentation algorithm combining concept of simulated annealing (SA) with an iterated conditional version of Markov random field (MRF) is designed [68]. The algorithm segments entire 3D MR volume and all MR images acquired with MR sequence automatically, just after the training of typical echo intensities and MRF parameter setting as per the expected irregularity. It unites nonparametric intensity distributions, neighborhood correlations, and irregularities effectively. As a result, the algorithm is accurate as well as robust against noise, irregularities, and structure thickness. Also, SA improves the performance as compared to iterated conditional modes (ICM) but reports longer execution times. A novel two stage fully automated approach is proposed to separate tumorous and non-tumorous region (inclusive of edema) from multi spectral MR images [145]. The integration of Bayesian classification of Gabor decomposition with MRF classification is performed. Bayesian extracts texture features of tumor/edema which are further refined by MRF. The performance evaluation depicts DSC of 0.668 and 0.56 for tumor and edema, respectively.

The work is further extended to propose an iterative MRF framework based on pixel- as well as region-information to classify brain tumor image [146]. The main objective of applying iterative model is to overcome the issue of over segmentation and mis-characterization of the tissue types. Previously the aim is to compute the tumor area with high probability, neglecting the sub classification of different tissue types. An automatic, non-parametric, simple, fast, and mesh free method to segment brain tissues from volumetric MR image brain tumor images is presented [22]. It combines non-rigid registration of an average atlas with biomechanically justified tumor growth model to simulate soft-tissue deformations caused by tumor mass-effect. The tumor growth model is formulated as a mesh-free MRF energy minimization problem that ensures correspondence between atlas and patient image, prior to registration step. MRF efficiently computes finite differences in the neighborhood of each voxel. In addition to tumor induced deformation, it can model soft-tissue deformations and is thus clinically-oriented. Experiments are conducted on T1-W MR images of four patients database from ContraCancrum project and results are compared using DSC. For real patient cases DSC values of WM, GM, and CSF ranges from 70% – 82%. The segmentation results maintain similar accuracy as that of the existing methods.

Combining the concept of GMM and fuzzy clustering, a segmentation model termed as AS-FLGMM (adaptive scale fuzzy local GMM) is designed for accurate and robust tumor detection [76]. A novel way to adaptively determine variance in every distribution is employed based on local scale assessment technique assuming that local information within image area pursue GMM. It completely overlooks distinction of variance among Gaussian segments. Working on the same assumptions, another work proposes FLGMM (fuzzy local GMM) to automate brain tumor MR image segmentation approach [77]. Summation of weighted GMM energy function is defined as the objective function covering the whole image. The computational evaluation is performed using 40 T1-W images taken from BrainWeb and IBSR datasets which proves efficacy of the combination. Similarly, a framework based on the fusion of multiple number of Gaussians is used to apprehend spatial features of complex tissues [62]. The proposed constrained GMM (CGMM) is composed of four-dimensional Gaussians, where three represent spatial features and one is the intensity attribute per region. Satisfactory experimental results are conducted using 36 T1W real MR images derived from IBSR dataset. A study introduces a generative asymmetric Gaussian mixture model with spatial constraint (SCGAGMM) to overcome drawbacks, such as robustness and over-smoothness, of existing EM based segmentation models [75]. SCGAGMM successfully reduces the drawbacks and has flexibility to cover different tumor shapes. Segmentation performance of SCGAGMM is compared with four state-of-the-art algorithms namely, spatially constrained generative model and EM (SCGM-EM), fast and robust spatially constrained GMM (FRSCGMM), Bayesian bounded asymmetric mixture model (BAMM), and bounded generalized GMM (BGGMM). Experimental datasets consists of T1-W, T2-W', and PD MR images collected from BrainWeb and IBSR. In addition, results are obtained with synthetic as well as natural color images. In all the cases, SCGAGMM reports the best DSC values. DSC of 86.91%, 86.78%, and 67.84% is respectively attained for GM, WM, and CSF tissue classes. However, presented algorithm lacks in automatically determining the number of classes/components for different applications.

Aiming to segment brain tumor very close to manual procedure, an expectation-maximization (EM) scheme based automated system is introduced [120]. In addition to tumor, tissue classes namely WM, GM, and CSF are segmented along with edema. Segmentation is guided by spatial probabilistic atlas containing expert prior knowledge of brain structures. To achieve better results contrast enhancement based atlas is computed for each

subject under consideration. Experimental results are generated for T1-W, T2-W, and CE-T1W MR images using jaccard similarity measure. Five cases each with different tumor types are considered to compare results with manual and semi-automated methods. Compared to manual results, this system yields surface distances of approximately 1 – 4 mm. However, semi-automated method supersedes in all the considered cases evaluating jaccard similarity between 49% - 71%. Segmentation algorithm, termed as SHE, is developed by effectively combining EM with the concept of spatial accuracy weighted hidden Markov random field [112]. SHE focuses on improved segmentation quality in clinical applications where low-resolution sequences (T2-W, FLAIR) are used together with high resolution T1-W images. Experiments are performed on a dataset of 15 patients and are compared with original hidden MRF (HMRF) with EM using sensitivity and specificity parameters. Improved tissue segmentation is reported by SHE, especially for all the normal tissues (WM, GM, and CSF). Comparison is done on multiple channels of MR images as well. For axial and coronal channels, the respective sensitivity and specificity values are 76.4% and 87.5%. SHE reports the corresponding improvements of 5.3% and 1.9% when all the three channels are utilized. Another work explores spatial relationships between pixels to estimate finite mixture model parameters with Gaussian distribution assumption and introduced a simple modified EM algorithm, termed as ETM [47]. The acceptance is proved by conducting experiments on a real dataset of 32 malignant T1-W MR images (with contrast agent gadolinium). Comparison with baseline approaches is performed using Gold Standard (GS) of the image dataset, a parameter provided by Carlos Van Buren Hospital of Valparaíso-Chile. Baseline approaches compared are EM, Neighborhood EM (NEM), Hybrid EM (HEM), Fuzzy C-Means (FCM), Modified Fuzzy C-Means (FCMM), region growing (RG), and Genetic Algorithms (GA) with 4 regions or classes defined a priori (tissues types in the image) [13, 69, 165]. ETM reports the best segmentation results obtaining 95.13% accuracy on 32 T1-W MR images. Another combination utilized Hidden MRF (HMRF) with EM to efficiently segment tumor from other brain tissues [137]. It minimizes energy function during each iteration. Experiments are presented on 30 images of high grade glioma T1-W, T2-W, CE-T1W and FLAIR modalities from BRATS 2012 dataset. A comparative analysis with existing FCM algorithm proves applicability of the integration.

4.4 Machine learning techniques

Applicability of machine learning techniques in the domain of automatic brain tumor detection is extensively explored to efficiently proceed with analysis and diagnosis phases. It is observed that the introduction of such learning techniques eases work at the end of radiologists as well as experts in medical practice [28, 49]. These techniques understand relationship depth of patterns and complex data more accurately. They are broadly categorized as supervised (classification) and unsupervised (clustering) [105]. A few studies that have utilized learning for brain tumor identification are fuzzy c-means (FCM) [29, 60, 150], self-organized maps (SOM) [40, 104, 158], k-means [78, 113], support vector machine (SVM) [127, 128, 152], learning vector quantization (LVQ) [20, 42], artificial neural networks (ANN) [36, 125] etc. Subsequent sections detail utilization of such approaches. Supervised techniques derive functional relationship between features and labels during training by utilizing the labeled information. Then in testing, labels are generated for unlabeled information based on the estimated feature [26]. A range of well-known classifiers is used in several studies for the identification of brain tumor. A distance and voting function based k-nearest neighbor (KNN) is the simplest of all the classification techniques. It is known to achieve higher accuracy and stability for MR image data but is observed to

take large running time. Artificial neural network (ANN) maps an image to network of neurons which are considered as pixels. ANN considers detection as an energy minimization problem and tries to establish not only the connection but weights between nodes too while training. Weights are modified by means of an error factor computed by comparing observed and desired output for the given input. One can extract features as well using ANN. Next is support vector machine (SVM) which uses the concept of hyper planes to train itself in appropriately selecting margins and thus distinguishing between or among classes. SVM helps in overcoming issues related to local minima and neurons overhead as compared to ANN [38, 156].

Clarke is one of the first researchers who introduces an automatic segmentation system for MR images using ANN [36]. The presented classification approach segments and labels glioblastoma-multiforme (GBM) tumors using T1-W, T2-W and PD-W MR images. Later several studies exploring various classifiers come into existence. A user friendly SVM based novel segmentation approach embedded with region analysis is presented to optimally extract flexible decision boundary across tumor [169]. The approach automatically learns parameters from non-linear distribution of image data without any additional prior knowledge. Final results are obtained after region analysis. Comparative results with fuzzy clustering on a five patient dataset having 24 pairs of T1-W and CE-T1W images prove efficiency of the approach. A novel version of probabilistic neural network (PNN) integrating least squares features transformation (LSFT) of non-linear type is designed to differentiate metastatic and primary tumors [58]. The system is trained with 66 texture features of 67 T1-W post-contrast MR images. The system achieves a classification accuracy of 95.24% to distinguish metastatic and primary tumors whereas 93.48% accuracy to classify between gliomas and meningiomas. An automated diagnosis method combining an improved version of orthogonal DWT, i.e. Slantlet transform with intensity histograms is presented [100]. The main focus is to classify two-dimensional MR image as either a normal brain or one suffering from Alzheimer's disease. Feature vector is created using a two step process: intensity histogram computation followed by Slantlet transform (magnitudes of outputs corresponding to six spatial positions are used). Experiments are performed on a dataset consisting of 75 T2-W images (normal brain – 39 and Alzheimer's disease – 36) collected from Harvard Medical School. Results report excellent classification accuracy of 100% and an improvement in time localization too.

An automatic seed point selection based system termed as adaptive neuro fuzzy interface system (ANFIS) is presented for detection and diagnosis of brain tumor [138]. The system effectively combines the concepts of neural networks and anisotropic diffused filtering with fuzzy logic. ANFIS classifier is trained using three different texture features, viz. gray level co-occurrence features (contrast and energy), Haar wavelet transform, and law's energy features. Experimental results are generated using dataset consisting of 120 (80 abnormal + 40 normal) training and 80 (30 normal + 50 abnormal) testing images. Comparison with several conventional processes using parameters like accuracy, sensitivity, similarity index, extra fraction, overlap fraction, and positive prediction value proves applicability of the presented system. The respective reported values are 87%, 81%, 81.7%, 18.2%, 81.7%, and 81.7%. A study analyzing the affect of three dimension reduction techniques on classification accuracy of SVM for glioma grade is presented [171]. It suggests that careful selection of features reduces number of features by up to 98% while maintaining desired classification accuracies comparable to those reported in literature. Also feature compactness helps in more streamlined workflow with minimal computational needs. Predictive power of feature reduction techniques is valued on a dataset of 101 untreated glioma patients using

T2-W and CE-T1W MR images. Experimental results report PCA as the best candidate that uses the smallest feature set in achieving equal classification accuracy. Specifically, PCA reports 85% classification accuracy with 89% sensitivity and 84% specificity for three principal components. In comparison, the respective values for Pearson's correlation coefficients (PCC) are 82%, 89%, and 77% with two principal components; similarly for ICA they are 79%, 87%, and 75% with nine principal components.

Detection of brain tissues in the presence of unlabeled image information is commonly done via clustering. These techniques submit complete arrangement of pixel vectors to cluster examination plot then find relevant groups algorithmically. Similar objects share same cluster and dissimilar ones are placed among different clusters. Clustering identifies brain tissues as regions sharing same label [26]. A few of the popular clustering approaches in tumor detection through MR images are k-means, self-organized map (SOM), fuzzy c-means, pulse-coupled neural network (PCNN), and feedback pulse-coupled neural network (FPCNN).

A segmentation approach to automatically track non-enhancing growth or shrinkage of brain tumor size over time in MR images is designed [55]. Segmentation is done effectively in two phases. Starting with unsupervised fuzzy clustering, domain knowledge is subsequently integrated then the final segmentation output is generated. Experimental results generated on weighted modalities of MR images, i.e. T1-W, T2-W, and PD, are found as satisfactory. A modified Probabilistic Neural Network (PNN) combined with LVQ to classify specified ROI of tumor area is proposed [39]. Each ROI is weighted based on LVQ and then extracted ROI features are utilized to evaluate brain tumor from MRI. For experimentation 64 MR images are collected and comparison is done with conventional PNN. The results prove a classification accuracy of 100% along with that a reduction in the processing time by 79% approximately. The classification technique consisting of three stages, feature extraction, dimensionality reduction, and classification [51]. In classification stage, two classifiers have been developed, the first one is based on feed forward back propagation artificial neural network (FP-ANN) and the other on k-nearest neighbor (k-NN). These two classifier are used to identify the abnormal tissues and resulted with a success of 97% and 98% respectively. The method can be deployed for all type of MR images T1-W, T2-W and PD-W. A fully automatic and unsupervised brain tumor segmentation method along with a method to retrieve membership functions perfect MR image is designed [60]. The objective function is defined based on intensity values. Experimental results are obtained on CE-T1W MR images taken from three datasets: normal dataset (NON), glioblastoma multiforme (GBM), and meningioma (MEN). Results are better than the existing approaches. Specifically Jaccard similarity coefficient on NON is 97% whereas on GBM and MEN it is observed to be 83.61% and 76.71% respectively. A hybrid segmentation algorithm based on soft sets namely soft fuzzy rough c-means (SFRCM) is proposed to extract white matter (WM), gray matter (GM) and cerebrospinal (CSF) fluid from MR brain image with bias field correction [111]. The soft fuzzy rough sets are obtained by embedding the concept of soft sets, rough sets, and fuzzy set. The soft rough set defines the lower and upper approximations of cluster using the soft fuzzy set indicating the degree of belongingness. The approximations are defined for each pixel with fuzzified values rather than crisp values. Efficacy of the proposed algorithm SFRCM is evaluated on three brain databases: (i) simulated Brain Web database with 20 images (ii) IBSR database with 20 images and (iii) BRATS database with 10 images. T1-W, T2-W, and FLAIR MR images are used to detect high grade glioma. The visual results clearly differentiate between brain tissues and tumor. The accuracy of the tumor detection with Gaussian noise at 3% and salt and pepper at 5% turns to be 94.04% and

87.94% respectively. Combining several computational methods at each intermediate stage, an efficient as well as automatic CAD system for brain tumor diagnosis using MR images is designed [109]. The system employs FPCNN for segmentation, DWT for feature extraction followed by dimension reduction using PCA, and lastly feed forward back propagation neural network (BPNN) classifies between normal and abnormal tissues. Experimental results are obtained on 101 MR images (14 normal and 87 tumorous) taken from Harvard Medical School website. The classification accuracy on testing images is 99%, sensitivity is 100%, and specificity turns to be 92.8%. Neural network based approaches have complex architecture and demands enough training, an attempt to resolve these limitations is made by integrating SOM with unsupervised LVQ [43]. The proposed SOM based clustering module does not utilize any additional network. The generated output is further processed using concepts of thresholding and skull stripping to obtain effective segmentation. Summarization of some good works under each of the discussed traditional approaches are presented in Table 5. Basis used to choose any study are the values of performance parameters with respect to the size of experimental dataset.

4.5 Deep learning techniques

Another emerging domain of machine learning is deep learning. Its multiple layer architecture represents data with manifold layers of abstraction which helps to overcome several challenges that occur in traditional machine learning approaches. Additionally, its generalization and self-learning characteristics enable better quantitative analysis of imaging features and thus better detection of neurological disorders. As a result deep learning based segmentation/classification techniques are gaining acceptance in the field of medical imaging process [157]. CAD systems designed with deep learning techniques are frequently observed in medical image analysis ranging from breast lesions and pulmonary nodules [2, 34, 85], chest and pulmonary tuberculosis [87, 148] to brain tumors [162].

Several deep learning techniques, namely deep neural networks (DNN) [67, 162], convolutional neural networks (CNNs) [115, 117], deep convolutional neural networks (DCNNs) [14, 71], auto-encoders [110], stacked auto-encoders [46, 155], are developed for efficient brain tumor detection, segmentation, and classification using MR images. Researches in great pace continue to dig more and more deep learning approaches to achieve the best performance. Deep learning combined with other techniques is observed to enhance the classification accuracy. Working differently, one study focuses on proper treatment planning and presented a hybrid system that predicts 1p/19q status of low grade gliomas (LGG) [6]. ANTs open source software library for image registration is utilized to register multi-modal CE-T1W and T2-W images (in total 159 MR images of LGG with status non-deleted for 57 images and co-deleted for 102 images) [18], followed by tumor segmentation using semi-automatic software [8], and finally CNN classification is performed. Cross domain results reported 87.7% accuracy, 93.3% sensitivity, and 97.7% specificity.

A three-stage automatic segmentation approach, termed as WMMFCM is proposed aiming to overcome the limitations of FCM [11]. Techniques employed in respective three stages are multi-resolution wavelet (WM), morphological pyramid (M), and Fuzzy C-means (FCM) clustering. Performance is verified using two datasets: BrainWeb (152 MR images with T1-W, T2-W, and PD modalities) and BRATS (81 images from multi-modal brain tumor segmentation having glioma with T1-W, T2-W, FLAIR, CE-T1W modalities). An accuracy of 97.05% is reported for BrainWeb and with BRATS, i.e. 95.853% accuracy is achieved. In the consecutive year, another work utilized the concept of small kernels based CNN [117]. A novel way to deal with over fitting, provided fewer number of weights in the

Table 5 Summary of a few studies utilized traditional techniques for brain tumor detection

Reference	Technique	Modality	Size of dataset	Tumor type	Performance (%)
[84]	RET	T1-W, CE-T1W	100 cases	GBM, MET, MEN, Glioma	ACC: GBM: 84.6, MET: 83.5 MEN: 92.2, Glioma: 85
[73]	New thresholding method	-	100 images	-	ACC: 96, SEN: 94.28 SPEC: 100
[64]	Multi-level Otsu's thresholding	T2-W	DS-I: 1100 images DS-II: 600 images	GBM, AST, EPD, ODG	ACC: 98, SEN: 100
[81]	Statistical classification via atlas prior	T1-W, CE-T1W	20 cases	LGG, MEN	ACC: 99
[25]	Marker based watershed	DWI	45 images	-	DSC: 93.98 for the 5 features 73.93 for color & texture
[66]	Watershed matching	T1-W	200 images	-	ACC: 98.5
[47]	Modified EM	T1-W, CE-T1W	12 synthetic & 32 real	-	ACC: Synthetic: 99.96 Real: 95.13
[22]	MRF	T1-W	4 patient data(Four datasets)	-	DSC: (for tumor) DS-I: 93, DS-II: 94, DS-III: 95, DS-IV: 87

Table 5 (continued)

Reference	Technique	Modality	Size of dataset	Tumor type	Performance (%)
[75]	SCGAGMM	T1-W, T2-W, PD	100 images	-	DSC: GM: 86.91, WM: 86.78 CSF: 67.84 ACC: 100
[99]	ST	T2-W	75 images	Alzheimer's disease	ACC: intra-patient: 98.75 Inter-patient: 98
[29]	SVM	CE-T1W, T1-W, FLAIR, ADC, DWI	22 images	GBM, ODG	ACC: 87, SEN: 81 SI: 81.7
[138]	ANFIS	ADI	200 images	-	JC: Normal: 97, GBM: 83.61 MEN: 76.71
[60]	KBFC	CE-T1W	20 images	GBM, MEN	ACC: 99, SEN: 100 SPEC: 92.8
[109]	FPCNN	T2-W	101 images	GBM, MEN, Alzheimer's disease, glioma, sarcoma	ACC: 99.25
[5]	BCFCM	-	-	-	

ACC: Accuracy, ADI :Anisotropic diffused image, ANFIS: Adaptive neuro fuzzy inference system, AST: Astrocytoma, BCFCM: Bias- field corrected fuzzy c-means, CSF: Cerebrospinal, DS-I: First data source, DS-II: Second data source, DS-III: Third data source, DS-IV: Fourth data source, DSC: Dice similarity coefficient, EM: Expectation maximization, EPD: Ependymoma, GBM: Glioblastoma multiforme, GM: Grey matter, JC: Jaccard coefficient, KBFC: Knowledge based fuzzy clustering, KBFCM: K-means integrated with fuzzy c-means, LGG: Low grade gliomas, MEN: Meningioma, MET: Metastasis, MRF: Markov random field, ODG: Oligodendroglioma, RET: Rough entropy based thresholding, SCGAGMM: Spatially constrained generative asymmetric gaussian mixture model, SEN: Sensitivity, SI: Similarity index, SPEC: Specificity, ST: Slantlet transform, WM: White matter

network is presented in the paper. Starting with uncommon intensity and patch normalization, the study proved effectiveness of combination together with data augmentation. Next training with patches is done by rotating them artificially. Lastly, defined threshold is placed to impose volumetric constraints, i.e. elimination of small clusters, which are basically the erroneous ones and may be classified as small tumors. In the brain tumor experimentation phase, the accuracy rate for a baseline network turned to be 84% whereas for U-net 88% accuracy is achieved.

Focusing on the same issue of over-fitting with sparse data, an automated system based on deep convolutional neural networks (DCNN) is designed [70]. It blends DCNN with an introduction of max-out and drop-out layers. Acceptability of the approach is evaluated on BRATS 2013 dataset having T1-W, T2-W, CE-T1W, and FLAIR MR image modalities. Experiments are conducted on a system using training is to testing ratio of 80:20 based on three parameters namely, dice similarity coefficient (whole tumor - 80%, core - 67%, and enhancing - 85%), sensitivity (whole tumor - 82%, core - 63%, and enhancing - 83%), and specificity (whole tumor - 85%, core - 82%, and enhancing - 88%). Several approaches are designed to improve and outdo CNN performance in terms of hardware specifications, accuracy, and processing time especially while handling large size images [108]. The approach uses Fuzzy c-means for MR image segmentation which is followed by discrete wavelet transform (DWT) integrated with the Deep Neural Network (DNN) to classify 66 T2-W MR images into four classes: normal, glioblastoma, sarcoma, and metastatic bronchogenic carcinoma tumor. The performance of the algorithm resulted in 96.97% classification rate.

In the same year extended version of the DCNN is presented to resolve the segmentation issues [4, 115, 141]. Another popular issue studied by a large group of researchers is the occurrence of multiple tumors [108, 117]. Tumor multiplicity demands more precision and thus increases complexity; in such a scenario MR image input type and its features matter a lot. A novel multimodal supervoxel based segmentation approach integrated with random forest (RF) is introduced to work with MR as well as with diffusion tensor imaging (DTI) [143]. For each supervoxel, a variety of Gabor features are extracted to train RF classifier. It classifies each supervoxel as healthy and tumorous (core or edema) using multimodal images from BRATS and clinical dataset (30 images). Performance is reported in terms of sensitivity and dice score. The respective values for clinical dataset are 86% and 0.84. In comparison better values are reported for BRATS, 96% and 0.89 respectively. One work has proposed three different network models, namely, Interpolated Network (IntNet), Skip-Net, and SE-Net for brain tumor segmentation [74]. Experiments on BRATS 2015 MR images with four modalities (T1-W, T2-W, CE-T1W and FLAIR) prove superiority of IntNet over SE-Net and Skip-Net. IntNet achieves highest values for all the three considered parameters dice coefficient (90%), sensitivity (88%), and specificity (73%) on a complete dataset. In the current scenario, enhancement of CNN is applied to resolve extensive manual diagnosing process. An optimal automatic segmentation approach combining enhanced CNN (ECNN) with BAT algorithm is developed [153]. BAT works on the function loss whereas small kernels characteristics of ECNN allow network with less weight assignment that controls over-fitting. The performance of ECNN is found to be 3% more accurate in comparison to traditional CNN. For the segmentation of Glioblastomas (high as well as low), an end-to-end incremental DNN based model known as “EnsembleNet” is proposed [135]. It aggregates on parallel instances with incremental XCNet that generates CNNs model (2CNet and 3CNet) by using non-parametric fusion technique. The dice score turns out to be 0.88 on BRATS 2017 dataset.

4.6 Auto-encoders techniques

Auto-encoders, a fully associated neural networks able to learn effectively in an unsupervised manner, are studied extensively in the past few years so as to lessen data dimensions (encoding). The reduced representation is then processed (decoding) to reconstruct the associated input. Several works in the field of medical imaging have proved better performance of auto-encoders in comparison to PCA.

Stacking denoising auto-encoders (SDAE) scheme for brainstem segmenting is found to perform well over traditional SVM [46]. Experimental results are obtained on T1-W modality using manual as well as automatic process. Shape similarity accessed via DSC ranges from 0.84 to 0.90 for four manual and three automatic annotations methods. DSC with SVM is observed as 0.88 whereas it has shown an improvement of 0.03 when SVM is embedded with the proposed scheme. Overall the proposed scheme is observed to perform better, reporting mean DSC of 0.92. Another study also utilized SDAE technique for accurate segmentation of gliomas [155]. Among several layers in the architecture three are meant for SDAE having 3000, 1000, and 500 neurons, respectively. System is trained with fixed sized 3D patches 11x11x3 of T1-W, T2-W, CE-T1W, and FLAIR MR image modalities from BRATS having 220 HGG and 54 LGG patients. Experimentation results outperform for high grade glioma as compared to low grade with DSC of 0.81 for whole tumor, 0.68 for core tumor, and 0.64 for active tumor. Another reason for the popularity of SDAE is its ability to represent complex functions finitely [162]. In comparison, existing approaches require manual interference with prior knowledge whereas in case of automatic shallow learning is involved. Utilizing this fact a novel deep learning system is proposed. The pre-processing phase extract image patches which are processed by SDAE based classification network to retrieve high level features. Finally, morphological filters are applied to fetch segmentation results. The approach has reported satisfactory performance on real patient's data collected from West China Hospital. Furthermore, other versions of denoising auto-encoders (DAEs) are also introduced for effective lesion detection and segmentation from multi sequence MR images [10]. The focus is to minimize false-positive (FP) for gliomas using a single layer DAE, which is referred as novelty detector (ND). Further the work modifies ND via cascading, i.e. cascaded ND (CND) to generate exclusive error distributions for different gliomas components. The study also demonstrates semi supervised learning by pretrained SDAEs using patches drawn from 20 patient volumes. Experiments are tested on BRATS-2013 and BRATS-2015 using T1-W, T2-W, CE-T1W, and FLAIR MR modalities. The performance is compared with previous submission [155] to BRATS 2015 challenge and resulted in an improvement of 8% in DSC considering in the tumor core for LGG volumes. Visual results are presented using ISLES 2015 challenge dataset for lesion detection of 28 patient volumes using ND and CND.

Auto-encoders are combined with other concepts too. One such study attempts to overcome several issues related to generative adversarial net (GAN) by integrating it with deep convolutional auto-encoders [24]. The system is termed as variational auto-encoder GAN (VAE-GAN) and is designed to encode complete brain MR slice context. Focus is to determine the benefits of mapping healthy anatomy to a well-structured, latent manifold with GAN. Experimental results are generated by training the system using 83 healthy cases and testing it on 49 multiple sclerosis (MS) lesions with FLAIR modality. Comparison done with deep auto-encoding models proves that the performance of spatial VAE-GAN is the best with DSC of 0.6050 ± 0.1927 . Similarly, a conditional generative network based on VAE is designed that learns input distribution by embedding label independence in latent space

[118]. Another work proposes an adaptive augmentation algorithm to train discriminative model utilizing generative models [142]. The approach helps in controlling image characteristics by tuning the latent variables properly. Results also report performance improvement over other baseline and U-net architectures. For FLAIR MR images of BRATS dataset, respective accuracies of 84% and 88% are achieved for baseline and U-net network.

Convolutional autoencoder-based inter-slice interpolation (CARISI) framework is designed for brain tumor inter-slice interpolation using convolutional auto-encoders (CAEs) [3]. The main focus is to effectively deal with the gap that occurs due to rapid changes between two consecutive image slices. Experiments performed on dataset proves the ability of CARISI in slice generation that are more accurate, refined, and helps in exhaustive 3D shape reconstruction of the brain tumor by assisting medical domain at its best. In some interpolations, it is assumed that pixels change gradually and thus experimentation satisfies with the best possible results [93]. However, the said assumption gets violated in some cases [154]. A discussion on several other common issues faced in latent consistency while investigating VAE and adversarial auto-encoders (AAE) is presented deeply in one of the research studies [32]. In addition, lesion detection in an unsupervised learning-manner with improved accuracy and latent constraint is proposed. Experiments are executed by training the model with 35 T2-W MR images extracted from Human Connectome Project (HCP) data source. Though detection performance is evaluated on T2-W images of 42 subjects taken from BRATS 2015. Accuracy is depicted through area under the curve (AUC) which turns to be 0.923 for AAE considering $\lambda=1$. A thought to replace conditional random fields (CRF) with an automatic GAN is also explored, with an aim to achieve better results compared to traditional state-of-art brain tumor segmentation methods [31]. The main reason high-order smoothing which in turn affects the performance. Experimental results generated on BRATS 2015 database outperforms CNN based approaches reporting dice coefficient of 82% and segmentation time of 10.8 seconds.

4.7 Hybrid techniques

Hybrid techniques means integrating two or more techniques es so as to attain better results compared to those reported by individual techniques. The objective of such integrations is to conquer loopholes of one technique by another technique. Based on the observations made while preparing this manuscript, the term ‘hybrid’ in respect to brain tumor detection systems has three variations, viz. segmentation-segmentation, segmentation-classification, and classification-classification. Some of the works from each of the three variations has been discussed so as to perceive their advantages as well as uses.

Integration is not new in the field of medical detection processing, hybrid techniques were popular even in back years to fulfill the increasing demands of perfection. SVM is very popular in such scenarios and is aggregated not only with traditional but with emerging techniques too. A novel technique combining wavelets individually with self-organizing maps (SOM) and SVM is presented to classify brain MR images [30]. Dataset consisting of 52 axial T2-W MR brain images (normal and abnormal, i.e. affected by Alzheimer’s disease) is utilized for performance evaluation. Effective classification results of more than 94% and 98%, reported respectively for SOM and SVM demonstrate utility of the proposed method. Another work integrates SVM with genetic algorithms (GA) and implements spatial gray level dependence method (SGLDM) to optimally extract texture features from normal and tumor regions [82]. Experiments are done on real brain dataset from Harvard Medical School website consisting of 83 images (29 - normal, 22 - malignant; suffering from low grade glioma and meningioma, and 32 - benign; suffering from bronchogenic

carcinoma, glioblastoma multiform, sarcoma, and grade IV tumors). The technique reports accuracy varying from 94.44% to 98.14% and sensitivity ranging from 91.9% to 97.3%. SVM classifier is even integrated with fuzzy c-means (FCM) clustering for tumor detection and classification [140]. Results are concluded using 120 patients bases and the performance is compared on four different datasets with ANN. Larger datasets report better performance with ANN but for smaller ones SVM is found more suitable. Overall it can be said that hybrid SVM produces satisfactory accuracy rate and lesser error rate.

FCM is another popular candidate in the hybrid category. A novel region-based fuzzy clustering method namely, enhanced possibilistic fuzzy c-means (EPFCM) is designed to overcome initialization and weak boundaries constraints in region based approaches [123]. The combination is utilized to segment tumor in 10 CE-T1W and 5 FLAIR MR images and is observed to achieve an average similarity and jaccard indices as 95.3% and 82.1%, respectively. An effective segmentation approach, KIFCM integrates k-means clustering with FCM [1]. k-means reduces execution time whereas FCM excels accuracy of brain detection. The study used three datasets, namely digital imaging and communications in medicine (DICOM) - 22 images, BrainWeb dataset - 152 images, and BRATS - 81 images. Both KIFCM and FCM report similar accuracy for these datasets but KIFCM takes lesser processing time by reducing the number of iterations. Precisely, for three datasets KIFCM respectively reports 90.5%, 100%, and 100% accuracy. Another work explores a novel combination of SOM with learning vector quantization (LVQ) to develop effective detection approach [43]. The study also proposes skull stripping algorithm. T1-W, T2-W, and FLAIR MR images of twenty patients' suffering from glial tumor is utilized to perform experiments. The skull stripping algorithm outperms other well-known algorithms on IBSR database. However, performance on BRATS 2012 dataset reports an average dice similarity indices of 91% (WM), 87% (GM), 96% (CSF), 61% (tumor), and 77% (edema) which are better than other state-of-the-art techniques.

The concept of hybrid is extended further with the idea of blending more than two techniques. FKM poorly handles issues related to large range of data. In an attempt to improve data handling capacities, FKM is integrated with SOM to design a tumor detection approach [160]. SOM assists in initial clustering and dimensionality reduction too. This combination obtains an accuracy of 96.18% and sensitivity of 87.18% for T1-W, T2-W, and FLAIR images collected from Harvard Brain Repository. It is found to perform superior in comparison to existing segmentation techniques. A hybrid, efficient, fully-automatic brain tissue segmentation framework based on clustering techniques is presented [9]. The system starts by fixing pixel intensity values in order to enhance image contrast, then super-pixel algorithm is employed to join pixels with similar intensity into objects. The objects are further processed independently using three clustering techniques (k-means, FCM, and SOM) to produce the labels corresponding to each object. Lastly, neural network (NN) is trained with extracted object features and their labels generated by clustering techniques. Results obtained on T1-W MR images collected from Internet brain segmentation repository (IBSR) are reported in terms of accuracy (98.10%), specificity (98.97%), and sensitivity (79.66%). These values are observed to outperform those achieved for other clustering approaches.

A novel algorithm, termed as SFRCM, i.e. soft fuzzy rough c-means is designed to precisely extract brain soft tissues, namely WM, GM, and CSF, with bias field correction [111]. Initially soft fuzzy rough sets are obtained by embedding the concepts of soft sets, rough sets, and fuzzy sets. They define lower and upper cluster approximations for each pixel using soft fuzzy sets indicating degree of belongingness. The efficacy of SFRCM is evaluated on simulated BrainWeb database (20 images), IBSR (20 images), BRATS (10

images) having T1-W, T2-W, and FLAIR MR images to detect high grade glioma. Visual results clearly show differences between brain tissues and tumor. Quantitatively, SFRCM achieves tumor detection accuracy of 94.04% with Gaussian noise (3%) and 87.94% with salt and pepper (5%) noise. A novel integration of an optimization technique with FKM is introduced to process MR images [159]. The bacteria foraging optimization (BFO) based modified fuzzy k-means algorithm (MFKM) is designed and is proved to take minimum computational time in handling MR image sequences. MFKM initializes segmentation process then BFO algorithm works to derive optimal threshold values. Experiments performed produce appreciable results in terms of sensitivity and specificity, which turns to be 97.14% and 93.94%, respectively.

The complete summarization of deep learning, auto-encoders, and hybrid techniques along with their relationship with MR image modalities, tumor disease, and data set affecting the performance evaluation is respectively given in Tables 6, 7, and 8. However, based on this summarization it can be said that automatic method of segmentation is mostly used with all MR image modalities whereas traditional techniques which mostly focus single modality.

5 Summary and discussions

Based on the existing literature of brain tumor detection techniques presented in this manuscript several deliberations concerning performance improvements of the developed system can be concluded. The most prominent is automatic CAD system for segmentation/classification. Firstly, the execution speed of segmentation approach can be improved by consolidating automation within it [25, 92, 159, 171]. Secondly, system adaptability can be improved by refreshing prior knowledge bases having parameters ranging from intensity to tissues, like shape, location, area, symmetry, and normal anatomic variability. Studies have worked on filtering as well as better utilization of dataset for precise results [4, 70, 141]. Another possible improvement can be done by taking care of over-segmentation and noise filtering [6, 23, 25, 66, 68, 80, 136, 155]. Furthermore, CAD systems developed using fully or semi automatic unsupervised detection approach are preferred over patient-specific trained ones. Varying benefits of existing systems as well as details of the employed technique(s) - either traditional or emerging are included in Section 4. Detection method produces open contour sometimes, and is relatively more delicate to threshold. One can think to resolve such intensity changes and threshold related issues.

The neural networks (NN) implementation and its modified versions helped researchers with great deal. The self-learning capacity of emerging deep learning techniques completely changes the scene of brain tumor detection systems. Thus, looking at the literature of past few years, usage of such techniques can be highlighted as a current trend in this domain too. Now-a-days multi-modal images are gaining interest in brain tumor segmentation as reviewed from the articles of deep learning, auto-encoders and hybrid approaches. Similarly, concepts like GA and optimization are strongly making their room. Undoubtedly, present era in the focused domain, i.e. brain tumor detection, can be characterized with huge data and high research, thus it demands for features like quickness along with accuracy. As this is somehow impossible for a single technique to fulfill, the idea of integrating two or more techniques is blindly employed. Combination may either be inter- or intra-phase. Based on the observations made, the study identifies following possibilities with respect to brain tumor detection systems. They are segmentation-segmentation,

Table 6 Summary of a few studies utilized deep learning techniques for brain tumor detection

Reference	Technique	Modality	User Interaction	Size of Dataset	Tumor Type	Performance (%)
[6]	CNN	CE-T1W, T2-W	Semi-automatic	159 images	LGG	ACC: 87.7, SEN: 93.3 SPEC: 82.22
[11]	WMMFCM	T1-W, T2-W, FLAIR, CE-T1W	Automatic	DS-I: 81 DS-II: 152	HGG, LGG, MS	ACC: DS-I: 95.853 DS-II: 97.05
[108]	DNN-DWT	T2-W	Automatic	66 images	GBM, MBC	ACC: 96.97
[143]	Supervoxel learning	T1-W, T2-W, FLAIR, CE-T1W, DTI	Automatic	30 images	HGG, LGG, edema	BRATS: SEN: 96, DSC: 89 Clinical: SEN: 86, DSC: 84 DSC: 88
[135]	EnsembleNet + Incremental (2CNet, 3CNet)	T1-W, T2-W, FLAIR, CE-T1W	Automatic	HGG: 210 LGG: 75 images	GBM	
[117]	CNN	T1-W, T2-W, FLAIR, CE-T1W	Automatic	65 images	Astrocytomas, AA, GBM, LGG, HGG	DSC: WT: 88, TC: 83 AT: 77
[70]	DCNN	T1-W, T2-W, FLAIR, CE-T1W	Manual & Automatic	30 images	LGG, HGG, Edema	DSC: WT: 80, TC: 67 AT: 85
[74]	IntNet, SkipNet, SENet	T1-W, T2-W, FLAIR, CE-T1W	Automatic	484 images	HGG, LGG, edema	Combined dataset IntNet DSC: 90, SEN: 88 SPEC: 73
[153]	ECNN	-	Automatic	-	-	ACC: 92
[168]	FC-NNs & CRFs	T1-W, T2-W, FLAIR, CE-T1W	Manual & Automatic	HGG: 220, LGG: 54 images	HGG, LGG, edema	BRATS DSC: WT: 84, TC: 73 AT: 62

2CNet: Two convolutional layers, 3CNet: Three convolutional layers, AA: Anaplastic astrocytomas, ACC: Accuracy, AT: Active tumor, CNN: Convolutional neural network, CRF: Conditional random fields, DNN-DWT: Deep neural network discrete wavelet transform, DS-I: First data source, DS-II: Second data source, DSC: Dice similarity coefficient, DTI: Diffusion tensor imaging, ECNN: Enhanced convolutional neural network, EnsembleNet: End-to-end incremental deep neural networks, FC-NN: Fully convolutional neural networks, FC-ResNets: Fully convolutional residual networks, FCNs: Fully convolutional networks, GBM: Glioblastoma multiforme, HGG: High grade gliomas, IntNet: Interpolated network, LGG: Low grade gliomas, MBC: Metastatic bronchogenic carcinoma, MS: Multiple sclerosis, SENet: Squeeze-and-excitation networks, TC: Tumor core, WMMFCM: Multi-resolution wavelet morphological pyramid fuzzy c-means, WT: Whole tumor, XCNet: Number of convolutional layers

Table 7 Summary of a few studies utilized Auto-Encoders for brain tumor detection

Reference	Technique	Modality	User Interaction	Size of Dataset	Tumor Type	Performance(%)
[46]	SDAEs	T1-W	Manual & Automatic	9 patients	Brainstem cancer	DSC: 92
[155]	SDAEs	T1-W, T2-W, FLAIR, CE-T1W	Automatic	HGG: 220 images LGG: 54 images	HGG, LGG	WT HGG: 81, LGG: 72 SEN: 79, SPEC: 84 ACC: 98.04
[162]	SDAEs	-	Manual & automatic	10 images	-	DSC: 92
[10]	DAEs and SDAEs	T1-W, T2-W, FLAIR, CE-T1W, DWI	Semi- automatic	HGG: 220 images LGG: 54 images	HGG, LGG, edema	DSC: (for HGG) WT: 85, TC: 71 AT: 75
[24]	VAE-GAN	FLAIR	Automatic	Training: 83 images Testing: 49 images	MS lesion	DSC: 60.50
[118]	CVAEs	-	Automatic	Training : 3000 images Testing: 29550 images	GBM	ACC: Baseline: 84 U-net: 88
[3]	CARISI framework	-	Automatic	3064 images	Glioma, MN, PT	PNSR: 26.23
[32]	CAAE	T2-W	Automatic	Training: 35 images Testing: 42 images	Lesions	AUC: AAE with $\lambda=0.5$ is 0.906 $\lambda=1.0$ is 0.923
[31]	GAN	T1-W, T2-W, FLAIR, CE-T1W	Automatic	Training: 274 images Testing: 110 images	HGG, LGG	DSC: 82

ACC: Accuracy, AT: Active tumor, AUC: Area under the curve, CAAE: Constrained adversarial auto-encoders, CARISI: Convolutional autoencoder-based inter-slice interpolation, CVAEs: Conditional variational auto-encoder, DAEs: Denoising auto-encoders, DCNN: Deep convolutional neural networks, DSC: Dice similarity coefficient, GAN: Generative adversarial nets, HGG: High grade gliomas, LGG: Low grade gliomas, MN: Meningiomas, PSNR: Peak signal-to-noise ratio, PT: Pituitary tumors, SDAEs: Stacked denoising auto-encoders, TC: Tumor core, VAE-GAN: Variational auto-encoder-generative adversarial network, WT: Whole tumor

Table 8 Summary of a few studies utilized hybrid techniques for brain tumor detection

Reference	Technique	Modality	User interaction	Size of datasets	Tumor type	Performance (%)
[30]	DWT + SVM DWT + SVM (with radial basic function based kernel) DWT + SOM	T2-W	Automatic	52 images	Alzheimer's disease	ACC: 96
[82]	GA + SVM	T2-W	Automatic	83 images	LGG, MEN, GBM	ACC: 94.44 - 98.14 SEN: 91.4 - 97.3
[167]	DWT + PCA, ACPISO-FNN	T2-W	Automatic	160 images	Gliomas, MEN, Pick's disease, Alzheimer's disease	ACC: 98.75
[123]	EPFCM + DF	CE-T1W, FLAIR	Manual & Automatic	15 images	-	JC: 82.1, SI: 95.3
[140]	FCM + SVM	-	-	120 images	-	ACC: 91.66 (Linear) ACC=83.33 (Quadratic) ACC=87.50 (Polynomial)
[1]	K-means integrated with Fuzzy c-means	DS-II: T1-W, T2-W, PD DS-III: T1-W, T2-W, CE-T1W, FLAIR	Automatic	DS-I: 22 DS-II: 152 DS-III: 81 images	HGG, LGG	ACC: DS-I: 90.5 DS-II: 100 DS-III: 100
[43]	SOM + LVQ	T1-W, T2-W, FLAIR	Manual & automatic	20 patient data	Glial tumor	DSC: WM: 91, GM: 96 CSF: 61

Table 8 (continued)

Reference	Technique	Modality	User interaction	Size of datasets	Tumor type	Performance (%)
[160]	SOM + FKM	T1-W, T2-W, CE-T1W, FLAIR	Automatic	4 patient data	LGG, HGG, HGA, MBC	ACC: 96.18 SEN: 87.18
[132]	Semi-MriMOO, AMOSA, Multi-center encoding	T1-W, T2-W, PD	Automatic	-	Alzheimer's disease	-
[111]	SFRCM	T1-W, T2-W, FLAIR	Automatic	100 images	HGG	ACC: Gaussian (3%): 94.04 Salt & Pepper (5%): 87.94 ACC: 98.10, SEN: 79.66, SPEC: 98.97, DSC: 79.3 ACC: 98
[9]	Super-pixel algorithm + (k-means, FCM, SOM)	T1-W	Automatic	28 patient data	-	ACC: 98.10, SEN: 79.66, SPEC: 98.97, DSC: 79.3 ACC: 98
[12]	CMLS + AANN	T1-W, T2-W, CE-T1W, FLAIR	Automatic	384 images	HGG, LGG	ACC: 98
[41]	AFBNN	T2-W	Automatic	81 images	-	ACC: 99.84, SEN: 97.24 SPEN: 99.85

AANN: Adaptive artificial neural network, ACC: Accuracy, ACPSO-FNN: Adaptive chaotic particle swarm optimization forward neural network, AFBNN: Adaptive firefly backpropagation neural network, AMOSA: Archived multiObjective simulated annealing, CMLS: Cognition based modified level set, DF: Deformable model, DS-I: First data source, DS-II: Second data source, DS-III: Third data source, DSC: Dice similarity coefficient, DWT: Discrete wavelet transform, EPFCM: Enhanced possibilistic fuzzy c-means, FCM: Fuzzy c-means, FKM: Fuzzy c-means and k-means, GA: Genetic algorithm, GBM: Glioblastoma multiforme, HGA: High grade astrocytoma, JC: Jaccard coefficient, MBC: metastatic bronchogenic carcinoma, MCBE: Multi-center based encoding, MEN: Meningiomas, MOO: Multiobjective optimization, SEN: Sensitivity, SFRCM: Soft fuzzy rough c-means clustering algorithm, SI: Similarity, SPEC: Specificity

segmentation-classification, and classification-classification. It can also be segmentation-clustering and clustering-clustering. The said observation is supported by summarizing combinational techniques in Table 8. An attempt to present another perspective of the current research with respect to each tumor type is also made. Table 9 shows the best results, as far as the knowledge of authors are concerned, from each of the considered segmentation

Table 9 Summary of performances reported by techniques under each of the considered segmentation category grouped on tumor type

Tumor type	Technique	Reference	Performance Parameter				
			ACC	SEN	SPEC	JSC	DSC
GBM	Thresholding	[64]	98	100			
	Region/Contour	[164]		98			
	Statistical	[90]				72.3-82.5	
	Classifiers	[29]	98				
	Clustering	[109]	99	100	92.8	83.61	
	Hybrid	[52]	99	100	92	93	
	Deep learning	[117]	96.97			77-88	
Low grade	Thresholding	[50]					82.18-85.11
	Region/Contour	[81]	99				
	Statistical	[112]		91.7	89.4	75	
	Classifiers	[171]	85	89	84		
	Clustering	[158]		86	93		
	Hybrid	[1]	100				
	Deep learning	[11]	97.05				
High grade	Thresholding	[151]		99.89			
	Region/Contour	[83]		84			
	Statistical	[112]		91.7	89.4	75	
	Classifiers	[171]	85	89	84		
	Clustering	[158]		86	93		
	Hybrid	[111]	94.04				
	Deep learning	[11]	97.05				
Astrocytoma	Thresholding	[65]	98	100			
	Region/Contour	-					
	Statistical	[90]				76.9	
	Classifiers	[121]	85				
	Clustering	[64]	93				
	Hybrid	[160]	97.14	93.94			
	Deep learning	[117]					83
Meningioma	Thresholding	[84]	92.2				
	Region/Contour	[81]	99				
	Statistical	[120]				49-71	
	Classifiers	-					
	Clustering	[109]	99	100	92.8		

Table 9 (continued)

Tumor type	Technique	Reference	Performance Parameter				
			ACC	SEN	SPEC	JSC	DSC
Alzheimer's	Hybrid	[160]	97.14	93.94			
	Deep learning	[88]					81
	Thresholding	[122]	80				
	Region/Contour	[53]	98	96.45	99.09		
	Statistical	[106]	91				
	Classifiers	[99]	100				
	Clustering	[109]	99	100	92.8		
	Hybrid	[52]	99	100	92		
	Deep learning	[144]	100	100	100		

category grouped on tumor type. Clearly, there are still few combinations, i.e. tumor type and approach applied which can be worked on as they are either unexplored or has not yet reported acceptable accuracy.

Several attempts to automate the segmentation process have already been made and are still being made, but the analysis of existing approaches clearly proves that the level of human interference can significantly improves system's performance and thus matters a lot. Therefore, instead of either a system completely automatic or a time consuming solely manually, research will slowly reach a middle way by identifying a semi-automatic more efficient systems.

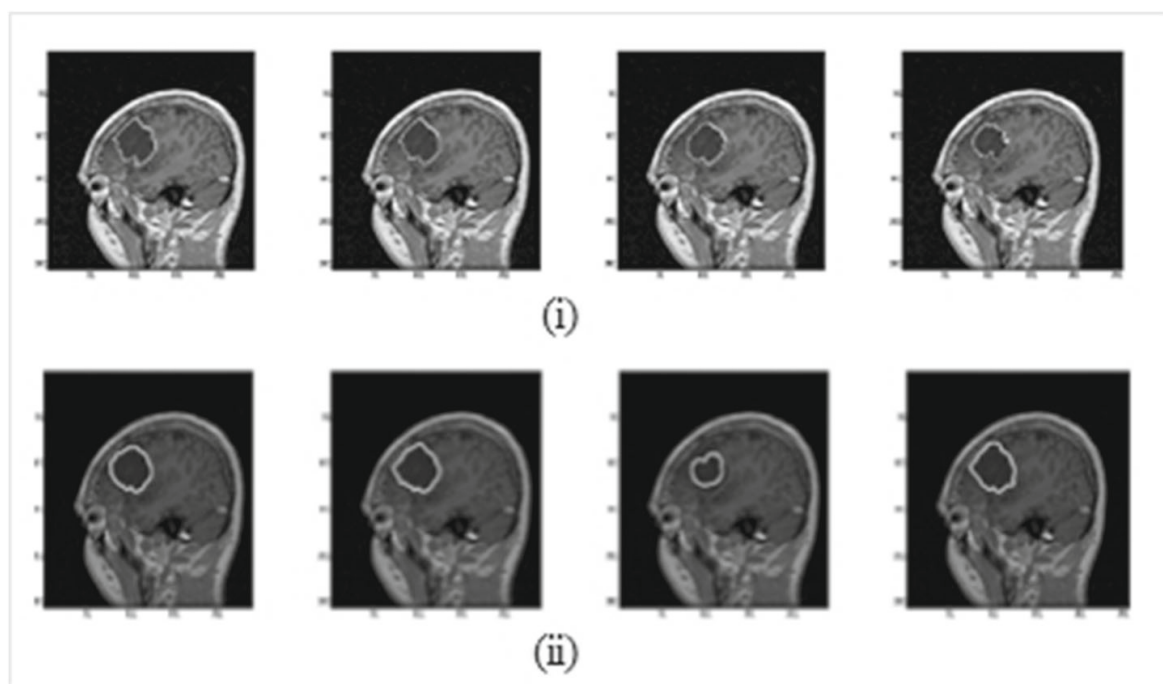


Fig. 7 (i) Manual segmentation by four different experts to detect glioma in MR image. (ii) Automatic segmentation of glioma using improved GVF snake [97]

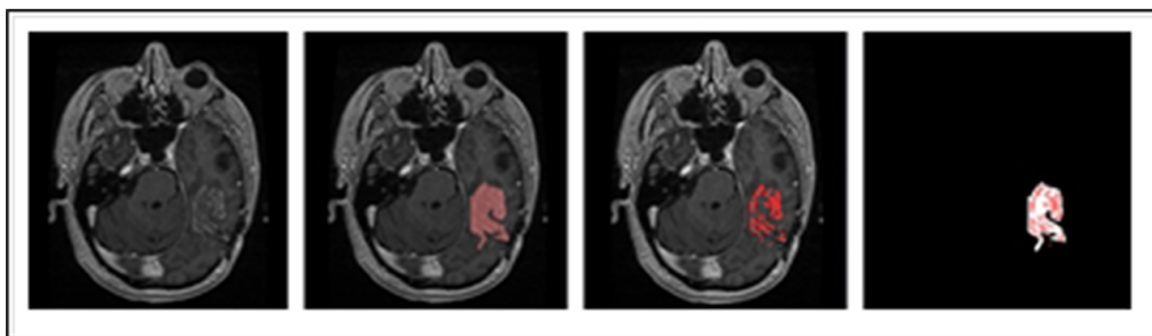


Fig. 8 Difference between manual and semi-automatic segmentations. Images in sequence are original image, manual segmentation, semi-automatic segmentation, and difference between manual segmentation [170]

Studies covered in this manuscript clearly presents depth as well as width of research in the field of brain tumor detection. One can thus easily observe that the employed techniques, MR image modalities, brain disease, data source, and number of cases definitely affect performance of the developed system. Lot many systems are handled solely as manual, semi-automatic, or fully automatic, but in some cases combination is also applied. To recapitulate automatic (without user interference) is considered the best from researcher point of view. However, the same cannot be true when applied practically on any affected patient. A second opinion is always required to assure the system's decision. References in

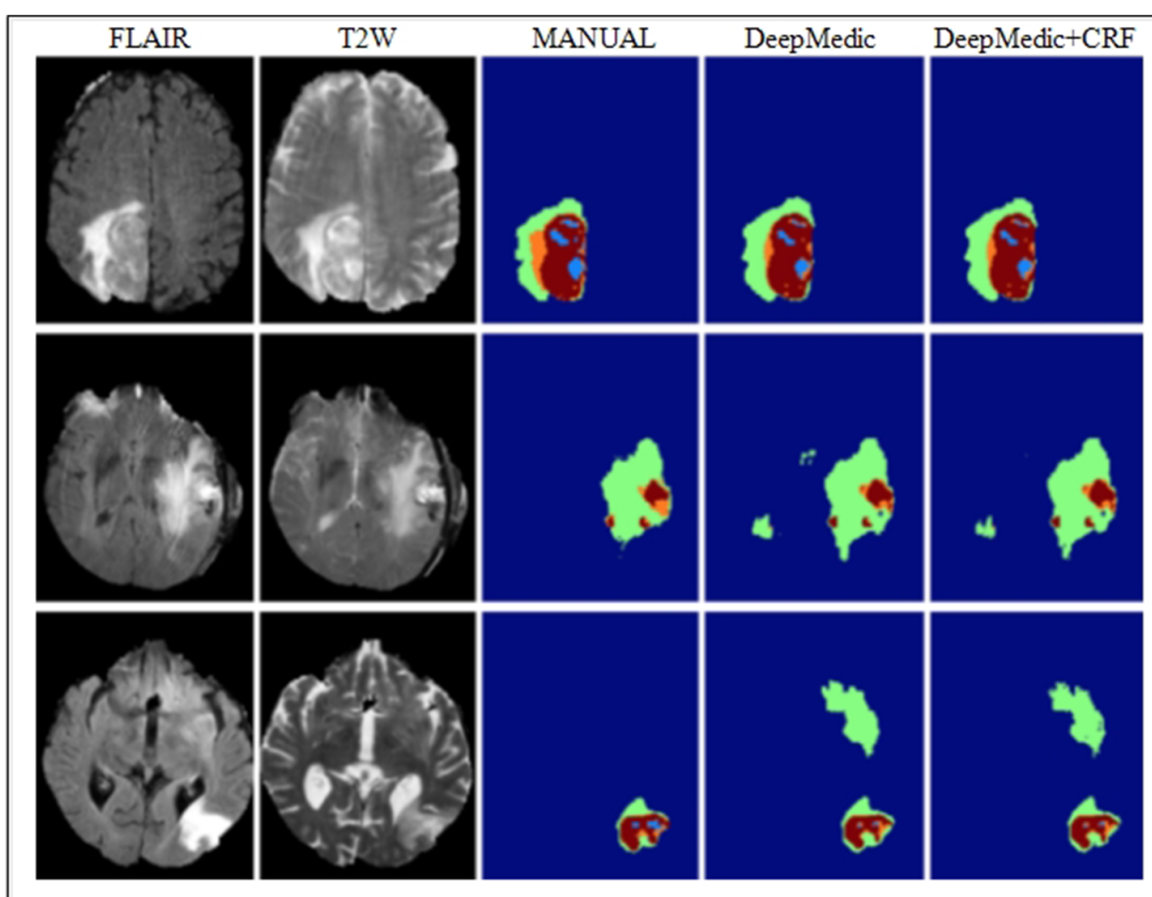


Fig. 9 Satisfying segmentation of the tumour, regardless motion artefacts (top and middle), One of the worst cases of over-segmentation observed (bottom) [80]

Table 10 Detection techniques and their values for various parameters identified during the survey

Segmentation technique	Computation time	Computational simplicity	Dataset size	Noise invariance	Support to real dataset	Spatial information
Thresholding	Slow	Low	Small	Yes	No	No
Edge based	Fast	Low	Small	Yes	No	No
Contour based	Slow	Moderate	Small	Yes	No	Yes
Region based	Slow	Low	Small	Yes	No	Yes
Atlas based	Slow	Moderate	Small	Yes	No	No
Level set	Slow	Moderate	Small	No	No	No
Deformable model	Fast	Low	Large	Yes	No	No
EM	Fast	Low	Large	Yes	No	No
MRF	Fast	Moderate	Small	No	No	No
GMM	Fast	Low	Small	No	No	No
K-NN	Fast	Low	Large	Yes	Yes	Yes
SVM	Slow	Moderate	Large	Yes	No	Yes
NN	Fast	Moderate	Small	Yes	No	Yes
LVQ	Slow	Low	Small	Yes	No	Yes
K-means	Fast	Low	Large	Yes	No	Yes
FCM	Slow	Low	Large	Yes	No	Yes
SOM	Fast	Low	Large	Yes	No	Yes
CNN	Slow	High	Small	Yes	Yes	Yes
DCNN	Slow	High	Small	Yes	Yes	Yes
Auto-encoders	Slow	High	Small	Yes	Yes	Yes

support of these observations are included in Fig. 7. Difference in observations made by four different practitioners while manually segmenting MR image to detect tumor (glioma) is clearly visible in Fig. 7(i). Similarly, Fig. 7(ii) shows automatic segmentation results generated using original as well as modified gradient vector flow snake (GVF). Again differences in locating glioma via both versions of GVF is observed, however tumor extraction is still near to accurate. From this deliberation can be concluded that automatic is not always effective. Similarly, for semi-automatic systems [170], Fig. 8 is included that displays results generated using a system assisted follow-up in neuroimaging of therapeutic intervention (AFINITI) as well as manual annotation. It is visible that the calculated tumor sizes in terms of volume are generally smaller than those marked during manual segmentation,

Though drift from traditional to emerging techniques will happen to keep various parameters (MRI sequence, tumor type, dataset etc.) synchronized. Most of studies signify need of semi-automatic as well as fully automatic systems, also proved the same with best visual results. However, there are cases where even the latest deep learning approaches fail to segment the brain MR image effectively. In Fig. 9, colors differentiate different brain tumor areas. Here manual performs better and due to over segmentation automatic segmentation lacks behind.

Lastly, an attempt to compare all the detection approaches is made based on certain parameters which are figured while surveying the existing literature in the domain. Parameters identified are computation time (time required to generate the result after an input image is provided), computational simplicity (ease with which algorithm can be implemented), dataset size (ability to handle big data), Noise invariance (capability to resist presence of noise in input image), support to real dataset (cross-domain performance), and spatial information (is the algorithm utilizing spatial image data effectively). The range of allowed values for each identified parameters is as follows: Computation time (Slow or Fast), Computational simplicity (Low, Moderate, or High), Dataset size (Small or Large), Noise invariance (Yes or No), Support to real dataset (Yes or No), Spatial information (Yes or No). Using the above information, detection approaches along with their values are presented in Table 10. Clearly, the traditional ones are better computationally but provide no support to real datasets, are not invariant to noise, and does not even utilize spatial information at the desired extent. In comparison, new participants in the domain especially the CNN, DPNN, and auto-encoders supersedes in all aspects.

6 Conclusion and future challenges

Efficient tumor identification, extraction, segmentation, and classification are some of the challenging tasks for physicians and radiologists. Automation of these modules thus occupies a major proportion of research in the domain of medical imaging. Several existing detection techniques are shown to achieve good performance on different tumor datasets. Irrespective of the accuracy percentages reported by any automatic tumor detection system using the best performing segmentation approach, a second opinion is still required for better diagnosis in any of the case. MR image contrast is a significant factor as it highly influences the process of brain tumor detection. The manuscript highlights freely available data sources to perform experimentation and guides perfect utilization of these data source with particular technique employing traditional, hybrid, deep-learning, and auto-encoders approaches. The motive of medical image processing handling tumor research is to precisely find and concentrate the tumor region to ease the operation medically.

Summarization tabulated for each of the segmentation category based on their performance helps the future researchers to a great extent. Segmentation approaches have been applied according to the behavior of MR image modality and tumor type which helps to separate abnormal tissue (edema, tumors etc.) from normal tissues (WM, GM and CSF). The real-world problems require proper addressing in the domain of medical image analysis that have been external to the domain of computer vision. Despite of various remarkable achievements done in imaging modalities and approaches, still many challenges underline the detection techniques. The computational complexity in handling multi-modal MR image modalities at a single instance is the major challenge in imaging techniques. During MR image scan for diagnosis correct tuning of parameters and motion applied to images, are the areas that can be explored in future. Exclusive difficulties emerge particularly in each imaging modality, data source, environment, pathological settings, and searching experts (for second opinion) needs to be focused in coming future to make them more cost effective.

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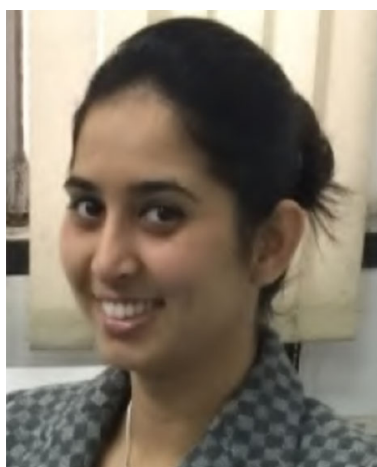
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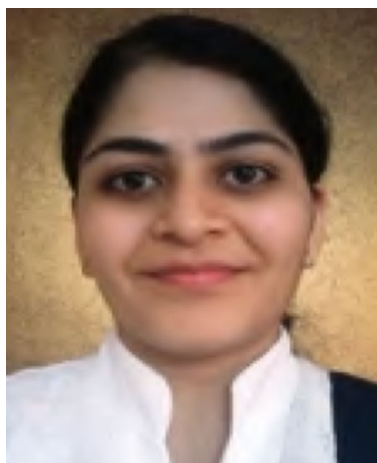
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Prabhjot Kaur Chahal received B-Tech degree (2012) from BCET, Gurdaspur and M-Tech degree (2014) from GNDU, Amritsar. She worked at Chandigarh University, Chandigarh, India as Assistant Professor (2014). She joined Thapar University, Patiala, India as a Research Scholar in CSE discipline (2015). Her research interest includes image processing mainly Medical image segmentation.



Shreelekha Pandey received BE degree (2007) from GGITS, Jabalpur and ME degree (2010) from SGSITS, Indore in computer science. She has completed PhD degree (2015) in computer science from IIITDM Jabalpur, India. She worked at Indian Institute of Information Technology, Kota, India and currently serving Thapar University, Patiala as an Assistant Professor. Her research interests include computer vision, image processing, retrieval and indexing of image data.



Shivani Goel has 18 years of teaching experience, including 15 years at the Thapar University, Patiala. Presently, she is working as Professor, Department of Computer Science Engineering, School of Engineering and Applied Sciences at Greater Noida. Her research areas include artificial intelligence, software reuse, machine learning and education technologies. She has published more than 100 papers in national/international conferences and international journals including ones with Scopus and SCI indexing. She has published two books. She is presently handling one research project on MOOCs funded by Royal Academy of Engineering, UK and FICCI.