SoBT-RFW: Rough-Fuzzy Computing and Wavelet Analysis Based Automatic Brain Tumor Detection Method from MR Images

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Abstract. One of the important problems in medical diagnosis is the segmentation and detection of brain tumor in MR images. The accurate estimation of brain tumor size is important for treatment planning and therapy evaluation. In this regard, this paper presents a new method, termed as SoBT-RFW, for segmentation of brain tumor from MR images. It integrates judiciously the merits of rough-fuzzy computing and multiresolution image analysis technique. The proposed method starts with a simple skull stripping algorithm to remove non-cerebral tissues such as skull, scalp, and dura from brain MR images. To extract the scale-space feature vector for each pixel of brain region, the dyadic wavelet analysis is used, while an unsupervised feature selection method, based on maximum relevance-maximum significance criterion, is used to select relevant and significant textural features for brain tumor segmentation. To address the uncertainty problem of brain MR image segmentation, the proposed SoBT-RFW method uses the robust rough-fuzzy c-means algorithm. After the segmentation process, asymmetricity is analyzed by using the Zernike moments of each of the tissues segmented in the brain to identify the tumor. Finally, the location of the tumor is searched by a region growing algorithm based on the concept of rough sets. The performance of the proposed SoBT-RFW method, along with a comparison with related approaches, is demonstrated on a set of synthetic and real brain MR images using standard validity indices.

Keywords: Brain tumor detection, segmentation, clustering, fuzzy set, rough sets, wavelets.
1. Introduction

Automatic segmentation of healthy and pathologic brain tissues from MR images plays an important role in brain tumor detection application. Early and accurate tumor segmentation from brain MR images is a difficult task in cancer research that involves various disciplines covering pathology, MRI physics, radiologist’s perception, and image analysis based on intensity and shape. Conventionally, the brain tumor from MR images is interpreted visually and qualitatively by radiologists. Advanced research requires quantitative information such as the size of the brain tumor. There are many issues and challenges associated with brain tumor segmentation. Brain tumors may be of any size, may have a variety of shapes, may appear at any location, and may appear in different image intensities. Some tumors also deform other structures and appear together with edema that changes intensity properties of the nearby region. Edema appears around tumor mainly in the white matter regions and may also contain infiltrative tumor cells. For many human experts, manual segmentation is a difficult and time consuming task, which makes an automated brain tumor segmentation method desirable. There are many possible applications of an automated brain tumor segmentation method. It can be used for surgical planning, treatment planning, monitoring of therapy, examining efficacy of radiation and drug treatments, vascular analysis, and studying the differences of healthy subjects and subjects with tumor.

The challenges associated with automatic brain tumor segmentation have given rise to many different approaches [5, 8, 13, 18, 19, 35, 40, 41, 51]. Sung et al. [46] used local thresholding based approach, where threshold values are estimated by computing partial volume information of each region on PD- and T2-weighted MR images, whereas Stadlbauer et al. [45] calculated threshold values by using the Gaussian distribution of data values in healthy brain T2-weighted images. However, the brain MR image exhibiting tumor is difficult to segment by thresholding the image intensities due to the fact that the T1-weighted MR image with contrast enhancement, typically using a gadolinium agent, is the standard modality for identifying tumors. This modality results in active tumor tissue appearing with bright intensity. Unfortunately, blood vessels also appear bright while parts of tumor that are necrotic do not have higher levels of intensity. Therefore, the information provided by the intensities in this modality is not always consistent, and it is generally impossible to segment the tumor by thresholding the intensities in this image modality [23].

Classification based tumor detection algorithms are widely used in brain tumor detection applications, since multi-modal data sets can easily be handled using these methods. These methods are constrained to the supervised [34, 39] or unsupervised [10, 50]. Menze et al. [34] combined a healthy brain atlas with a tumorous brain atlas to segment brain tumors using a generative probabilistic model and spatial regularization. In [40], the abnormal regions are first detected using a registered brain atlas as a model for healthy brains. Then, the intensity properties of the different tissue types are determined by using the robust estimates of the location and dispersion of the normal brain tissue intensity clusters. In the next stage, it is determined from the T2 image intensities whether edema appears together with tumor in the abnormal regions. Finally, geometric and spatial constraints are applied to the detected tumor and edema regions. Bauer et al. [2, 3, 39] combined support vector machine classification using multispectral intensities and textures with subsequent hierarchical regularization based on conditional random fields. This method requires four modalities, namely, T1-weighted, T1-weighted with contrast agent, T2-weighted, and FLAIR to classify the tumor region. Other methods are based on statistical pattern recognition techniques, for example, the method proposed by Kaus et al. [20]. This method combines the information from a registered atlas template and user input to supervise training of a clas-
sifier, demonstrating the strength of combining voxel-intensity with geometric brain atlas information. This method was validated against meningiomas and low-grade gliomas. Gering et al. [12] proposed a method that detects deviation from normal brains using a multi-layer Markov random field framework. The information layers include voxel intensities, structural coherence, spatial locations, and user input. Cuadra et al. [9] presented high-dimensional warping to study deformation of brain tissue due to tumor growth. This technique relies on a prior definition of the tumor boundary.

To automatically segment and label tumors in the MR images of the human brain, a system has been proposed in [8] that integrates knowledge-based techniques with multispectral analysis. An unsupervised clustering algorithm is used for initial segmentation. The segmented image, along with cluster centers for each class is provided to a rule-based expert system, which extracts the intracranial region. Multispectral histogram analysis separates suspected tumor from the rest of the intracranial region, with region analysis used in performing the final tumor labelling. Fletcher-Heath et al. [10] combined fuzzy clustering and integrated domain knowledge to improve the tumor segmentation applied on T1-, T2-, and PD-weighted images. Veloz et al. [50] incorporated the intricate nature of the tumor in MR images into fuzzy c-means and formulated a fuzzy region growing with an automatic initialization of the seed points. In [36], an algorithm is proposed based on spatial accuracy-weighted hidden Markov random field and expectation maximization approach for both automated tumor and enhanced-tumor segmentation. It incorporates the spatial interpolation accuracy of low-resolution images into the optimization procedure of the hidden Markov random field to segment tumor using multi-channel MR images with different resolutions, for example, high-resolution T1-weighted and low-resolution T2-weighted images. A semi-automated method has been developed in [52] for brain tumor and edema segmentation and volume measurement using the MR image. A hybrid level set segmentation method is exploited driven by region and boundary information simultaneously, where region information serves as a propagation force and boundary information serves as a stopping functional.

Texture is a fundamental characteristic of an image and plays an important role in the human visual system for recognition and interpretation of images. The analysis of image texture content is extremely important in medical image analysis. It requires the understanding of how humans discriminate between different texture types. In a medical image, texture can be considered to be the visual impression of coarseness or smoothness caused by the variability or uniformity of image tone. The textural properties of a brain MR image are likely to provide valuable information for classification or segmentation, where different object regions are treated as different texture classes. The segmentation of these images is necessary in order to identify different meaningful regions. Also, there is a change in appearance of most textures when viewed at different resolutions, and during the empirical division from macro to micro textures. Texture can also be defined as a local statistical distribution of pixel pattern (micro region) in observer’s domain [7, 17, 47]. Psychovisual studies reveal that the human visual system processes images in multiple scales. The visual cortex has separate cells that decomposes images into filtered images of various band of frequencies and orientation; thus capable of preserving both local and global information. Hence, the methods for texture analysis, based on the concept of multiscale processing of the human visual system, are superior over the more traditional ones. Texture is especially suited for this type of multiresolution analysis, using both frequency and spatial information due to its inherent characteristics.

Brain MR images may contain information over a large range of scales and the spatial frequency structure also changes over different regions, that is, non-periodic signal. In medical imaging perspective, the resolution of the imagery may be different in many cases, and so it is important to understand how
information changes over different scales of imagery. The wavelet based multiresolution analysis is most effective for this purpose [11, 22, 31]. Moreover, wavelet theory is well suited in this area of study where signals are complex and non-periodic. Furthermore, wavelets are particularly good in describing a scene in terms of the scale of the textures in it [48, 49]. During the past two decades, wavelet analysis has become an important paradigm for multiresolution analysis, and has found important applications in image analysis [1, 48, 49]. However, the existing automatic brain tumor segmentation methods from MR images reported in [5, 6, 8, 9, 10, 12, 13, 18, 19, 20, 35, 36, 40, 41, 51, 52] have not used multiresolution techniques to extract features. Also, it has not been paid much attention earlier.

The process of automatically extracting tumors from MR images is a challenging process due to the gradual transition between tumor, edema, and surrounding brain tissue. This results in the ambiguity of the structural boundaries. Hence, one of the main problems in tumor segmentation from brain MR images is uncertainty. Some of the sources of this uncertainty include imprecision in computations and vagueness in class definitions. In this background, the rough-fuzzy computing provides a mathematical framework to capture uncertainties associated with human cognition process [26, 37]. It is an efficient hybrid technique based on judicious integration of the principles of rough sets [38] and fuzzy sets [53]. The basic concept and characterizing features of rough set theory and its integration with fuzzy set theory, have been provided in [37] for developing an efficient soft computing strategy of machine learning. In pattern recognition and image processing, while the membership functions of fuzzy sets enable efficient handling of overlapping classes, the concept of lower and upper approximations of rough sets deals with uncertainty, vagueness, and incompleteness in class definitions. Since the rough-fuzzy approach has the capability of providing a stronger paradigm for uncertainty handling, it has greater promise in application domains of pattern recognition and image processing, where fuzzy sets and/or rough sets are being effectively used and proved to be successful [26, 37].

In this regard, the paper presents a texture-based brain tumor detection method, termed as SoBT-RFW, judiciously integrating the merits of multiresolution image analysis and rough-fuzzy computing. The multiresolution wavelet analysis is used to extract scale-space feature vector for each pixel of the given brain MR image. Since the boundary between brain and skull is relatively strong on T1 scan, a new skull stripping algorithm is introduced to extract the brain tissues and remove non-cerebral tissues like skull. The skull stripped feature vectors are considered for more accurate segmentation. However, the use of wavelet decomposition may give rise to some irrelevant and insignificant features. Hence, the selection of appropriate features using some feature selection algorithms is required. In this background, an unsupervised feature selection method, reported in [30], is used to reduce the dimensionality of feature space by maximizing both relevance and significance of the selected features. Next, the robust rough-fuzzy c-means algorithm [28, 29] is used for the segmentation of tumor from given brain MR image. It integrates judiciously the merits of rough sets, and probabilistic and possibilistic memberships of fuzzy sets. While the integration of both membership functions of fuzzy sets enables efficient handling of overlapping classes in noisy environment, the concept of lower and upper approximations of rough sets deals with uncertainty, vagueness, and incompleteness in class definition. In effect, it groups similar textured tissue classes contained in the image. After the segmentation process, asymmetry is analyzed by using the Zernike moments of each of the tissues segmented in the brain to identify the tumor class. Once the tumor class is extracted by rough-fuzzy clustering algorithm, the result is further improved by a sequence of post-processing steps. The tumor class extracted by the clustering algorithm may include some non-tumorous brain tissues, which can be removed by a new post-processing method. The proposed post-processing technique includes different morphological operations and a simple region
growing approach based on the concept of rough sets. The performance of the proposed approach, along with a comparison with related methods, is demonstrated on a set of synthetic and real brain MR images both qualitatively and quantitatively.

The structure of the rest of this paper is as follows. Section 2 briefly introduces the necessary notions of rough sets and wavelet analysis. In Section 3, the proposed SoBT-RFW algorithm is presented based on the theory of rough-fuzzy computing and multiresolution image analysis. A few case studies and a comparison with other methods are presented in Section 4. Concluding remarks are given in Section 5.

2. Basics of rough sets and wavelet analysis

This section presents the basic notions in the theories of rough sets and wavelet analysis.

2.1. Rough Sets

The theory of rough sets begins with the notion of an approximation space, which is a pair \( < U, R > \), where \( U \) be a non-empty set, the universe of discourse, and \( R \) an equivalence relation on \( U \), that is, \( R \) is reflexive, symmetric, and transitive. The relation \( R \) decomposes the set \( U \) into disjoint classes in such a way that two elements \( x \) and \( y \) are in the same class iff \((x, y) \in R\). Let denote by \( U/R \) the quotient set of \( U \) by the relation \( R \) and \( U/R = \{ X_1, \cdots, X_i, \cdots, X_m \} \), where \( X_i \) is an equivalence class of \( R \), \( i = 1, 2, \cdots, m \). If two elements \( x \) and \( y \) in \( U \) belong to the same equivalence class \( X_i \in U/R \), we say that \( x \) and \( y \) are indistinguishable. The equivalence classes of \( R \) and the empty set \( \emptyset \) are the elementary sets in the approximation space \( < U, R > \). Given an arbitrary set \( X \in 2^U \), in general, it may not be possible to describe \( X \) precisely in \( < U, R > \). One may characterize \( X \) by a pair of lower and upper approximations defined as [38]:

\[
\underline{R}(X) = \bigcup_{X_i \subseteq X} X_i \quad \text{and} \quad \overline{R}(X) = \bigcup_{X_i \cap X \neq \emptyset} X_i. \tag{1}
\]

Hence, the lower approximation \( \underline{R}(X) \) is the union of all the elementary sets which are subsets of \( X \), and the upper approximation \( \overline{R}(X) \) is the union of all the elementary sets which have a non-empty intersection with \( X \). The interval \( < \underline{R}(X), \overline{R}(X) > \) is the representation of an ordinary set \( X \) in the approximation space \( < U, R > \) or simply called the rough set of \( X \). The lower (respectively, upper) approximation \( \underline{R}(X) \) (respectively, \( \overline{R}(X) \)) is interpreted as the collection of those elements of \( U \) that definitely (respectively, possibly) belong to \( X \). Further, a set \( X \) is said to be definable or exact in \( < U, R > \) iff \( \underline{R}(X) = \overline{R}(X) \).

In [38], Pawlak discussed two numerical characterizations of imprecision of a subset \( X \) in the approximation space \( < U, R > \): accuracy and roughness. Accuracy of \( X \), denoted by \( \alpha_R(X) \), is the ratio of the number of objects in its lower approximation to that in its upper approximation; namely

\[
\alpha_R(X) = \frac{|\underline{R}(X)|}{|\overline{R}(X)|}. \tag{2}
\]

The roughness of \( X \), denoted by \( \rho_R(X) \), is defined as \( \rho_R(X) = 1 - \alpha_R(X) \). Note that the lower the roughness of a subset, the better is its approximation. Further,
1. As $\mathcal{R}(X) \subseteq X \subseteq \mathcal{R}(X)$, $0 \leq \rho_R(X) \leq 1$.

2. By convention, when $X = \emptyset$, $\mathcal{R}(X) = \mathcal{R}(X) = \emptyset$ and $\rho_R(X) = 0$.

3. $\rho_R(X) = 0$ if and only if $X$ is definable in $\langle U, R \rangle$.

### 2.2. Multiresolution Analysis Using Wavelets

Wavelets mean small waves, that is, short duration finite energy functions. The multiresolution analysis is designed to provide good time resolution and poor frequency resolution at high frequencies and good frequency resolution and poor time resolution at low frequencies [31, 48, 49]. In multiresolution analysis, a scaling function is used to create a series of approximations of a function or image, each differing by a factor of 2 from its nearest neighboring approximation. Additional functions, called wavelets, are then used to encode the difference in information between adjacent approximations. Scaling function $\phi(t)$ and wavelet function $\psi(t)$ are defined as follows:

$$\phi_{j,k}(t) = 2^{j/2}\phi(2^j t - k); \quad \psi_{j,k}(t) = 2^{j/2}\psi(2^j t - k);$$

for all $j, k \in \mathbb{Z}$. Here $k$ determines the position along $x$-axis; and $j$ determines function’s width, that is, how broad or narrow it is along $x$-axis. The scaling function $\phi(t)$ and wavelet function $\psi(t)$ are chosen appropriately to satisfy the orthonormality condition. The wavelet subspaces $W_j$s form an orthogonal decomposition of $L^2(\mathbb{R})$ function space and hence they are related to nested subspaces $V_j$s as follows:

$$V_{j-1} = V_{j-2} + W_{j-2}; \quad V_j = V_{j-1} + W_{j-1} = V_{j-2} + W_{j-2} + W_{j-1};$$

where $V_j$ is the function space spanned by $\phi_{j,k}(t)$ over $k$ and $W_j$ is the function space spanned by $\psi_{j,k}(t)$.

If a function $f(t) \in L^2(\mathbb{R})$, its wavelet transform is

$$W_\phi(j_0, k) = \langle f(t)\phi_{j_0,k}(t) \rangle = \frac{1}{\sqrt{N}} \sum_t f(t)\phi_{j_0,k}(t);$$

$$W_\psi(j, k) = \langle f(t)\psi_{j,k}(t) \rangle = \frac{1}{\sqrt{N}} \sum_t f(t)\psi_{j,k}(t);$$

where $j_0$ is an arbitrary starting scale and $N$ is the number of samples taken from the signal. The $W_\phi(j_0, k)$’s are called approximation or scaling coefficients and $W_\psi(j, k)$’s are referred to as detail or wavelet coefficients. In fast wavelet transform, at scale $j$, the approximation and detail coefficients, $W_\phi(j, k)$ and $W_\psi(j, k)$, respectively, can be computed by convolving the scale $j + 1$ approximation coefficients, $W_\phi(j + 1, k)$, with the time-reversed scaling and wavelet vectors, $h_\phi(-n)$ and $h_\psi(-n)$, respectively, and subsampling the results.

Like one dimensional wavelet transform, the two dimensional wavelet transform can be implemented using the separable two dimensional scaling and wavelet functions. It is done by taking one dimensional wavelet transform of the rows of two dimensional function or image, followed by one dimensional wavelet transform of the resulting columns. Hence, it generates four subbands at each level, namely, approximation, horizontal, vertical, and diagonal subbands. The approximation part is iteratively decomposed as the decomposition level is increased in case of standard wavelet transform. Hence, if an input image is decomposed upto $l$th level, total $d = 3l + 1$ number of subbands is generated.
3. SoBT-RFW: Proposed brain tumor segmentation methodology

This section presents the proposed SoBT-RFW method for segmentation of brain tumor from MR image in detail. It consists of mainly five steps as mentioned in Fig. 1 and described below:

1. Generation of mask from the input MR image for identification of brain region;
2. Decomposition of the MR image using wavelet and selection of relevant and significant features for clustering;

![Figure 1](image-url)
3. Rough-fuzzy clustering to generate segmented image;
4. Asymmetricity analysis using the Zernike moments of each of the tissues segmented in the brain to identify the tumor; and
5. Post-processing to separate brain tumor from non-tumorous brain tissues.

Fig. 1 presents the block diagram of the proposed brain tumor identification method considering the brain MR image as an example. It also shows all the intermediate images obtained through the proposed technique. The subbands generated using wavelet decomposition are named as to reveal their orientation information. The approximation, horizontal, vertical, and diagonal subbands are denoted by LL, LH, HL, and HH, respectively, while these are followed by a number indicating the wavelet decomposition level. A prefix 'M' is used with subband name to denote the masked subband.

Let the input brain MR image be $I$ with size $M \times N$. Hence, the total number of pixels is $n_{tot} = MN$. Let $\hat{X} = \{x_1, \ldots, x_i, \ldots, x_{n_{tot}}\}$ be the set of pixels of the input image $I$. To identify brain region, a mask is generated from input brain MR image using a new skull stripping algorithm, termed as S3. The algorithm is based on the thresholding method and mathematical morphology. After generating the mask, the input brain MR image is decomposed up to $l$th level using dyadic wavelets resulting into $d = 3l + 1$ number of subbands. Hence, each pixel $x_i \in \hat{X}$ of the input brain MR image is represented by $d$ features. The mask is then applied to each of the subbands to generate the feature vectors for only brain region. In effect, a reduced set $X \subset \hat{X}$ is generated considering only brain region, where $X = \{x_1, \ldots, x_i, \ldots, x_n\}$, $n < n_{tot}$ is the number of pixels within the brain region. An unsupervised feature selection algorithm [30], based on maximum relevance-maximum significance criterion, is used to select $m$ number of relevant and significant features from the whole set of $d$ features for clustering. Next, the rough-fuzzy clustering algorithm is used to segment the brain region into several tissue classes, while asymmetricity analysis is performed on each segmented tissue class to identify the tumor. However, the extracted tumor region may include some non-tumorous healthy brain tissues, which may decrease the overall performance of the proposed algorithm. Hence, a post-processing method is introduced, which uses mathematical morphology and rough set based region growing approach, to isolate brain tumor and healthy brain tissues. Each step of the proposed brain tumor detection method is elaborated next one by one.

### 3.1 S3: Proposed Skull Stripping Method for Identification of Brain Region

The skull stripping is the process of removal of non-brain tissues such as skull, scalp, dura, and eyes from brain MR images. It is used as an important pre-processing step in many brain MR image processing applications. This method of identifying brain matter plays a vital role in segmentation of brain tissues, pathology detection, multi-modality brain image registration, and so forth. For example, during segmentation of brain tissues, the skull stripping algorithm is incorporated to identify the region of interest. As a result, it reduces the misclassification of brain tissues during segmentation which, in turn, improves the segmentation accuracy as well as minimizes the execution time of segmentation algorithm by eliminating the objects of non-cerebral tissues.

In this regard, a new skull stripping algorithm, termed as S3, is proposed for identification of brain region from MR images. The basic assumption of the S3 method is that white matter is surrounded by darker gray matter and even darker cerebrospinal fluid (CSF) in T1-weighted brain MR images. The membrane at brain surface that borders the brain matter has darker intensity values than that of skull and
CSF. It is also assumed that the brain region is larger than the skull portion. The S3 algorithm consists of a sequence of steps. Before applying the binary mathematical morphology operations, this method initially segments the image into brain and non-brain regions using the threshold value computed adaptively from image intensities. Hence, the selection of a threshold value is crucial to generate the initial mask for brain tissues. The goal of achieving binarization of input image is to locate the region of membrane at brain surface and thus approximate the threshold value. This membrane identification includes removal of the background pixels from the input brain MR image and calculation of mean intensity value within this identified region. Based on the initial mean value of the entire image, the skull starting locations are approximated and final mean value is calculated for this identified region, which contains less number of background pixels.

The membrane of the brain is localized as the region, where the intensity, starting from initially approximated skull boundary, attains below the final mean value to the immediate exterior intensity of where intensity value, moving inwards, reaches above the final mean value. After identifying the membrane roughly, the threshold value is computed from the intensity values of pixels located within the membrane region.

If the slices of a brain MR volume have discontinuity along cerebral border line due to partial volume effects at skull boundary, the thresholding method cannot separate the brain region from the non-brain area. Hence, opening morphology filtering is applied to completely disjoint the brain and non-brain regions. Then, the brain portion is extracted as the largest connected component. There might be some holes within and along the periphery of the brain surface since the intensity values of CSF may be lower than the computed threshold value in some brain MR slices. Hence, closing morphology operation is embedded in the proposed methodology to produce the smoothed border and accurate skull-stripped brain MR images. Both of these morphology operations use an octagonal shaped structuring elements with different dimensions. The proposed methodology uses median filtering as denoising step prior to the calculation of threshold value as well as the application of morphological operations. Each of these steps of the proposed skull stripping methodology is enumerated below:

1. Apply median filtering with a window of size $3 \times 3$ to the input image.
2. Compute the initial mean intensity value $T_i$ of the image.
3. Identify the top, bottom, left, and right pixel locations, from where brain skull starts in the image, considering gray values of the skull are greater than $T_i$. 

![Figure 2. Block diagram of the S3 algorithm for brain extraction](image-url)
4. Form a rectangle using the top, bottom, left, and right pixel locations.
5. Compute the final mean value $T_f$ of the brain using the pixels located within the rectangle.
6. Approximate the region of brain membrane or meninges that envelop the brain, based on the assumption that the intensity of skull is more than $T_f$ and that of membrane is less than $T_f$.
7. Set the average intensity value of membrane as the threshold value $T$.
8. Convert the given input image into binary image using the threshold $T$.
9. Apply a $13 \times 13$ opening morphological operation to the binary image in order to separate the skull from the brain completely.
10. Find the largest connected component and consider it as brain.
11. Finally, apply a $21 \times 21$ closing morphological operation to fill the gaps within and along the periphery of the intracranial region.

A preliminary version of the S3 algorithm is also presented in [42]. The graphical representation of the S3 algorithm is shown in Fig. 2 for both synthetic (BrainWeb) and real (IBSR) brain MR images.

### 3.2. Feature Selection Using Multiresolution Wavelet Analysis

The classical wavelet transform includes downsampling operations by a factor that causes wavelet expansions to be shift-variant. But, overcomplete representation of wavelets overcomes the shift-varying nature of classical wavelet expansion. Additionally, the overcomplete wavelet transform is convenient over the subsampled methods as downsampling decreases the size of the subbands at each increasing level of decomposition and thus may bias the decomposition at higher levels. Hence, the proposed methodology includes feature-extraction scheme that uses multiresolution dyadic wavelet filtering without downsampling. After generating $d$ subbands or features for a given image $I$, the mask is applied to each subband to generate the feature vectors for the brain region only. Hence, a reduced set $X = \{x_1, \cdots, x_i, \cdots, x_n\}$ is generated from $\hat{X}$ consisting of pixels within the brain region. Each pixel or object $x_i \in X$ is represented by $d$-dimensions, each dimension corresponding to each subband generated from wavelet decomposition. However, in wavelet-based image segmentation method, a number of insignificant and irrelevant features may be generated. The presence of such features may lead to a reduction in the valuable information for segmentation.

In this background, an unsupervised feature selection algorithm [30] is used in the proposed brain tumor segmentation method to select $m$ relevant and significant subbands or features from the whole set of $d$ features for efficient segmentation. The energy measure is used to compute both relevance and significance of a feature set, which is defined as follows:

$$E(S) = \frac{1}{n|S|} \sum_{i=1}^{n} \sum_{j=1}^{|S|} (x_{ij}^2 - \overline{x}^2)$$

where $n$ is the number of objects and $S$ is the feature set. The $\overline{x}$ is the mean of feature vectors of all objects and is given by

$$\overline{x} = \frac{1}{n|S|} \sum_{i=1}^{n} \sum_{j=1}^{|S|} x_{ij}.$$
Hence, the energy content provides higher values for the features having high variance, indicating that these features contain more information. On the other hand, the energy content measure yields low energy values for the smoothed subbands indicating textural uniformity [30].

Let \( C = \{A_1, \ldots, A_i, \ldots, A_j, \ldots, A_d\} \) be the set of \( d \) features and \( S \) is the set of selected features. The relevance \( \gamma_{A_i} \) of the feature \( A_i \) is defined as

\[
\gamma_{A_i} = E(\{A_i\}),
\]

while the significance \( \sigma_{A_j}(\{A_i, A_j\}) \) of the feature \( A_j \) with respect to the feature set \( \{A_i, A_j\} \) defines the extent to which the feature \( A_j \) is contributing in the energy estimation computed using (7). The change in energy estimation when a feature is removed from the feature set, is the measure of the significance of the feature, and is given as [30]

\[
\sigma_{A_j}(\{A_i, A_j\}) = \gamma_{\{A_i, A_j\}} - \gamma_{A_i}.
\]

The higher the change in energy estimation, the more significant the feature is. If the significance is 0, then the feature is dispensable. Therefore, the problem of selecting a set \( S \) of relevant and significant features from the whole set \( C \) of \( d \) features is equivalent to maximize both the total relevance of all selected features and the total significance among the selected features. To solve the above problem satisfying maximum relevance-maximum significance criterion [27], the relevance \( \gamma_{A_i} \) of each feature \( A_i \in C \) is first calculated. The feature \( A_i \) is selected as the most relevant feature that has the highest relevance value \( \gamma_{A_i} \). In effect, \( S \leftarrow S \cup \{A_i\} \) and \( C \leftarrow C \setminus \{A_i\} \). The significance of each of the remaining features of \( C \) is calculated with respect to the already selected features of \( S \) and it is removed from \( C \) if it has zero significance value with respect to any one of the selected features. From the remaining features of \( C \), feature \( A_j \) is selected that maximizes the following condition:

\[
\gamma_{A_j} + \frac{1}{|S|} \sum_{A_i \in S} \sigma_{A_j}(\{A_i, A_j\}).
\]

As a result of that, \( S \leftarrow S \cup \{A_j\} \) and \( C \leftarrow C \setminus A_j \). The above steps are repeated until the desired number of features \( m \) is selected. In practice, the value of \( m \) is set as \( \lfloor \sqrt{d} \rfloor \), where \( d \) represents the total number of features or subbands corresponding to the given image [30].

### 3.3. Robust Rough-fuzzy C-means Algorithm for Segmentation

In the proposed method, the robust rough-fuzzy c-means (rRFCM) [28, 29] algorithm is used for segmentation of brain MR images. The rRFCM adds the concepts of fuzzy memberships, both probabilistic and possibilistic, of fuzzy sets, and lower and upper approximations of rough sets into \( c \)-means algorithm. While the integration of both probabilistic and possibilistic memberships of fuzzy sets enables efficient handling of overlapping clusters in noisy environment, the rough sets deal with uncertainty, vagueness, and incompleteness in cluster definition.

Let \( X = \{x_1, \ldots, x_j, \ldots, x_n\} \) be the set of \( n \) objects and \( V = \{v_1, \ldots, v_i, \ldots, v_c\} \) be the set of \( c \) centroids, where \( x_j \in \mathbb{R}^m \) and \( v_i \in \mathbb{R}^m \). In the rRFCM, each of the clusters \( \beta_i \) is represented by a cluster center \( v_i \), a probabilistic lower approximation \( A(\beta_i) \) and a probabilistic boundary region \( B(\beta_i) = \{\overline{A}(\beta_i) \setminus A(\beta_i)\} \), where \( \overline{A}(\beta_i) \) denotes the upper approximation of cluster \( \beta_i \). According to
the definitions of lower approximation and boundary of rough sets [38], if an object \( x_j \in A(\beta_i) \), then \( x_j \notin A(\beta_k), \forall k \neq i \), and \( x_j \notin B(\beta_i), \forall i \). That is, the object \( x_j \) is contained in \( \beta_i \) definitely. Hence, the memberships of the objects in lower approximation of a cluster should be independent of other centroids and clusters. Also, the objects in lower approximation should have different influence on the corresponding centroid and cluster. From the standpoint of compatibility with the cluster prototype, the membership of an object in the lower approximation of a cluster should be determined solely by how far it is from the prototype of the cluster, and should not be coupled with its location with respect to other clusters. As the possibilistic membership \( \nu_{ij} \) given by (15) depends only on the distance of object \( x_j \) from cluster \( \beta_i \), it allows optimal membership solutions to lie in the entire unit hypercube rather than restricting them to the hyperplane given by (14).

On the other hand, if \( x_j \in B(\beta_i) \), then the object \( x_j \) possibly belongs to cluster \( \beta_i \) and potentially belongs to other clusters. Hence, the objects in boundary regions should have different influence on the centroids and clusters, and their memberships should depend on the positions of all cluster centroids. So, in the rRFCM, the membership values of objects in lower approximation are identical to (15) of possibilistic c-means [21], while those in boundary region are the same as (14) of fuzzy c-means [4]. If \( A(\beta_i) \neq \emptyset \) and \( B(\beta_i) \neq \emptyset \), the centroid for the rRFCM is calculated based on the weighting average of the probabilistic lower approximation and probabilistic boundary, which is as follows:

\[
v_i = \omega C_1 + (1 - \omega) D_1
\]  

(12)

where \( C_1 = \frac{\sum_{x_j \in A(\beta_i)} (\nu_{ij})^{\hat{m}_2} x_j}{\sum_{x_j \in A(\beta_i)} (\nu_{ij})^{\hat{m}_2}} \); and \( D_1 = \frac{\sum_{x_j \in B(\beta_i)} (\mu_{ij})^{\hat{m}_1} x_j}{\sum_{x_j \in B(\beta_i)} (\mu_{ij})^{\hat{m}_1}} \).  

(13)

The parameters \( \omega \) and \( (1 - \omega) \) correspond to the relative importance of lower and boundary regions, while \( \hat{m}_1 \in [1, \infty) \) and \( \hat{m}_2 \in [1, \infty) \) are the probabilistic and possibilistic fuzzifiers, respectively. The probabilistic membership \( \mu_{ij} \) and possibilistic membership \( \nu_{ij} \) are given by

\[
\mu_{ij} = \left[ \sum_{k=1}^{c} \left( \frac{|x_j - v_i|^2}{|x_j - v_k|^2} \right)^{\frac{1}{\hat{m}_1 - 1}} \right]^{-1} \quad ; \text{subject to} \quad \sum_{i=1}^{c} \mu_{ij} = 1, \forall j, \quad 0 < \sum_{j=1}^{n} \mu_{ij} < n, \forall i, \quad \text{(14)}
\]

and \( \nu_{ij} = \left[ 1 + \left( \frac{|x_j - v_i|^2}{\eta_i} \right)^{\frac{1}{\hat{m}_2 - 1}} \right]^{-1} \quad ; \text{subject to} \quad 0 < \sum_{j=1}^{n} \nu_{ij} \leq n, \forall i; \quad \text{and} \quad \max_i \nu_{ij} > 0, \forall j; \quad \text{(15)}
\]

where the scale parameter \( \eta_i \) is given by

\[
\eta_i = K \frac{\sum_{j=1}^{n} (\nu_{ij})^{\hat{m}_2} |x_j - v_i|^2}{\sum_{j=1}^{n} (\nu_{ij})^{\hat{m}_2}}
\]

(16)

which represents the zone of influence or size of the cluster \( \beta_i \). Typically, \( K \) is chosen to be 1.
The principal axis passes through centroid \((\bar{x}, \bar{y})\) of the binary or two-tone image. The moments and the principal axis are determined using this two-tone image. The pixels belonging to brain region extracted by the S3 algorithm are assigned ‘1’ value, while background region is labeled with ‘0’, resulting in the axis of brain region is first determined based on moments. The pixels on the left and right hand sides of the principal axis in the segmented image, which is given by

\[
\bar{x} = \frac{m_{10}}{m_{00}}, \quad \bar{y} = \frac{m_{01}}{m_{00}}, \quad \theta = \frac{1}{2} \tan^{-1} \frac{2m_{11}}{m_{20} - m_{02}},
\]

where \(m_{pq}\) and \(\overline{m}_{pq}\) are the \((p, q)\)th moment and \((p, q)\)th central moment of the two-tone image with respect to origin and centroid \((\bar{x}, \bar{y})\), respectively, and are as follows:

\[
m_{pq} = \sum_{x} x^p y^q; \quad \overline{m}_{pq} = \sum_{x} \sum_{y} (x - \bar{x})^p(y - \bar{y})^q.
\]

Let \(\overline{m}_{ipq}\) be the \((p, q)\)th central moment of the \(i\)th tissue and \(\overline{m}_{i00}\) represents the total number of pixels on the left and right hand sides of the principal axis in the \(i\)th tissue of the segmented image, which is given by

\[
\overline{m}_{i00} = \overline{m}_{Li00} + \overline{m}_{Ri00}
\]
where \( \overline{m}_{L_{i00}} \) and \( \overline{m}_{R_{i00}} \) represent the numbers of pixels on the left and right hand sides, respectively, of the principal axis. The weighted areas for the tissue on either side of the principal axis and the difference between them are calculated as follows:

\[
WA_{Li} = \frac{\overline{m}_{L_{i00}}}{\overline{m}_{00}}, \quad WA_{Ri} = \frac{\overline{m}_{R_{i00}}}{\overline{m}_{00}}, \quad WA_i = |WA_{Li} - WA_{Ri}|.
\]

(21)

The quantity \( WA_i \) is used to determine the tumor class. By using the moments computed for the left and right hand sides of the principal axis, Zernike polynomials [16], \( Z_{L_{i}} \) and \( Z_{R_{i}} : \forall k = 1, \ldots, 6 \), are also determined. These components are used as the elements of feature vectors to inquire the presence of asymmetry in the \( i \)th tissue of the segmented image. The functional forms of Zernike polynomials are reported in [15]. The vectors \( V_{Li} \) and \( V_{Ri} \), which represent the shape of the \( i \)th tissue on either side of the principal axis, are determined as follows:

\[
|V_{Li}| = \sqrt{\sum_{k=1}^{6} (Z_{kLi})^2}; \quad |V_{Ri}| = \sqrt{\sum_{k=1}^{6} (Z_{kRi})^2}.
\]

(22)

The Euclidean distance \( D_i \) and the normalized \( D_i \) for the \( i \)th tissue are computed as follows:

\[
D_i = \sqrt{\sum_{k=1}^{6} (Z_{kLi} - Z_{kRi})^2}; \quad ND_i = \frac{2D_i}{|V_{Li}| + |V_{Ri}|}.
\]

(23)

If the normalized \( D_i \), that is, \( ND_i \), of the \( i \)th tissue is lower than a predefined threshold value, it is indicated that the \( i \)th tissue of brain region does not contain tumor. If \( ND_i \) distance is higher than the threshold, presence of asymmetry in brain MR image is indicated. After detecting asymmetry in brain region, \( D_i \) distances are weighted as follows:

\[
WD_i = D_i \times WA_i.
\]

(24)

Next, the longest weighted distance is determined. The segmented tissue for which the longest weighted distance is obtained is consider to contain brain tumor [15].

### 3.5 Rough Set Based Post-processing Technique for Tumor Detection

The lack of intensity or shape priors and weak contrast at boundary make unsupervised brain tumor segmentation more challenging. The clustering step may not accurately identify the brain tumor, which may include some non-tumorous tissues or may exclude some tumor region. Once the tumor class is extracted by the clustering algorithm, the result can be further improved by a sequence of post-processing steps. Hence, some post-processing technique must be embedded into brain tumor detection application to refine the final result as shown in Fig. 1. The robust rough-fuzzy \( c \)-means algorithm may result in oversegmentation or undersegmentation of brain tumor due to the ambiguities at tumor boundaries. Hence, after extracting the tumor class by the robust rough-fuzzy \( c \)-means algorithm, a new post-processing method, based on morphology and rough set based region growing operation, is used to handle efficiently these ambiguities. The brain tumor segmentation based on clustering algorithm may produce
many residual areas around the tumor region due to partial volume effect. Also, there may be small holes within the tumor class since the tumor is not homogeneous. Hence, the morphological operations, namely, closing and opening, in the order, followed by finding largest connected component, are applied to eliminate these residual areas as well as to eliminate any discontinuity within tumor mass. The closing and opening morphology use square shaped structuring element of different dimensions. Two-pass connected component labelling is embedded for finding the largest connected component. Finally, a rough set based region growing method is proposed to efficiently handle the ambiguities at anatomical tumor boundaries.

The proposed region growing technique is based on the concept of rough set theory. Let \( T \) be the tumor class. Application of various morphological operations produces the region that possibly belongs to \( T \), that is, upper approximation of the tumor class, \( \overline{A}(T) \). The lack of intensity or shape priors and weak contrast at boundary region of tumor class induce uncertainty of belongingness of boundary region pixels. Hence, it puts some non-tumorous cells into \( \overline{A}(T) \) because they are characterized as indiscernible with other actual tumorous pixels, using the available information. The accuracy of approximation of \( T \), as in (2), is defined as the ratio of the number of tumor pixels which can certainly be placed in that set to the number of tumor pixels that can possibly be placed there. In fact, it provides a measure of how closely the rough set is approximating the target set with available knowledge. Hence, the non-tumorous tissues in \( \overline{A}(T) \) are eliminated in this methodology in order to increase the accuracy of approximation. In this regard, a region growing approach based on the gradient information of input image is proposed. Hence, this region growing step concentrates on elimination of non-tumorous healthy brain tissues from pathologic region appropriately, thereby maximizing the rough set accuracy.

The centroid or center of gravity (CoG) of the tumor class is computed within \( \overline{A}(T) \) using (18). The CoG of \( \overline{A}(T) \) is assumed to certainly belong to the tumor region, and hence the CoG is assigned initially in the lower approximation of the tumor class \( A(T) \). Then, a simple region growing approach is followed with CoG as the seed point. An edge map of the input brain MR image is constructed within the region of \( \overline{A}(T) \). In this approach, Sobel’s gradient operator is used. It starts growing initially from the CoG to spread over the edge map of \( \overline{A}(T) \). The region of interest \( A(T) \) expands until a certain criterion is met, which is based on the mean gradient magnitude of input image within the region of \( \overline{A}(T) \). The region of \( A(T) \) grows until its gradient magnitude reaches a threshold value \( \Delta \). Let \( \delta(x) \) be gradient magnitude of pixel \( x \). Then \( \Delta \) is determined as:

\[
\Delta = \frac{1}{|\overline{A}(T)|} \sum_{x \in \overline{A}(T)} \delta(x), \tag{25}
\]

where \(|.|\) denotes the cardinality. Based on the value of \( \Delta \), the unassigned pixel is included in \( \overline{A}(T) \) using the pixel assignment rule for lower approximation as described below:

\[
\overline{A}(T) \leftarrow \overline{A}(T) \cup \{ x \in \overline{A}(T) | \delta(x) \leq \Delta \wedge (\exists y \in A(T) \text{ such that } x \in \mathcal{N}(y)) \}, \tag{26}
\]

where \( \mathcal{N}(p) \) represents the neighbors of the pixel \( p \) using eight-connectivity. This region growing method is repeated until no more changes occurred. After building \( \overline{A}(T) \), the boundary of \( A(T) \) is refined using the lower approximation refinement rule as presented below:

\[
A(T) \leftarrow A(T) \cup \{ x \in \overline{A}(T) | \delta(x) \geq \Delta \wedge (\exists y \in A(T) \text{ such that } x \in \mathcal{N}(y)) \}. \tag{27}
\]

This assignment rule includes the pixels that represent the boundary edge region of tumor. The block diagram of the proposed post-processing method for brain tumor detection methodology is shown in

\[\text{Diagram of the proposed post-processing method for brain tumor detection methodology is shown in...}\]
Fig. 3. Block diagram of the proposed rough set based post-processing method

Fig. 3. Fig. 4 shows an example of building the rough approximation $\overline{A}(T)$ and 2D region growing approach applied on CoG of $\overline{A}(T)$ to approximate the corresponding tumor class. As can be seen in the tumor result of Fig. 4g, there are several holes inside the brain region caused by the higher gradient magnitude values for some pixels within tumor region than the threshold $\Delta$ computed, due to the presence of noise. Also, the gradient magnitude on tumor edge boundaries may reach above the threshold value $\Delta$. These are refined using the lower approximation refinement rule of (27). Finally, the morphological closing operation is used to smooth the surface of the tumor class. The main steps of the proposed morphology and rough set based post-processing method proceed as follows:

1. Apply closing morphology with window of dimension $5 \times 5$ on the tumor class extracted by the clustering algorithm.

2. Apply opening morphology with window of size $7 \times 7$ in order to separate the tumor region from healthy brain tissues.
3. Find the largest connected component using connected component labelling and consider it as rough approximation of tumor $\bar{A}(T)$.

4. Construct an edge map from input brain MR image for region of $\bar{A}(T)$.

5. Compute the threshold value $\Delta$ using (25).

6. Compute the CoG of $\bar{A}(T)$ and consider it as seed point for region growing method.

7. Initially, $\underline{A}(T) \leftarrow \text{CoG}$.

8. The region $\underline{A}(T)$ grows by incorporating boundary region pixels by pixel assignment rule of (26).

9. Refine the boundary of lower approximation using lower approximation refinement rule of (27).

10. Assign the lower approximation of $T$, $\underline{A}(T)$, to $T$.

11. Finally, apply closing morphology with window of size $5 \times 5$ to smooth the surface of tumor class.

4. Experimental results and discussions

The performance of the proposed rough-fuzzy computing and wavelet analysis based brain tumor segmentation (SoBT-RFW) method is extensively studied on several synthetic and real brain MR images. To evaluate the performance of the proposed and different existing methods for segmentation of brain tumor from MR images, three quantitative measures, namely, Dice coefficient, sensitivity, and specificity, are used, which are described next.
4.1. Quantitative Indices

Let $A$ and $B$ be two sets representing the brain region (respectively, brain tumor) to be segmented in the ground truth or reference image and segmented brain region (respectively, brain tumor), respectively. Based on the ground truth image, the false positive (FP), false negative (FN), true positive (TP), and true negative (TN) counts can be computed for each brain region (respectively, brain tumor).

The Dice coefficient measures set agreement. In this case, the measure is given by:

$$D(A, B) = \frac{2(A \cap B)}{|A| + |B|} = \frac{2 \cdot TP}{(FP + TP) + (FN + TP)}.$$ (28)

The Dice coefficient gives zero for non-overlapping region of interest in segmented output with that in reference image and a value of one indicating perfect agreement of segmented result with ground truth information. Higher numbers in Dice coefficients indicate that the results match with the ground truth better than results that produce lower Dice coefficients. On the other hand, the sensitivity measures the fraction of true positives that are included in a segmentation, and is as follows:

$$SN = \frac{TP}{TP + FN}.$$ (29)

A score of one of sensitivity indicates that all the points in the ground truth region of interest are included in the segmentation result. Since sensitivity does not include false positives or true negatives in its calculation, it does not indicate whether the region of interest in segmented result includes more than the corresponding ground truth region. Hence, sensitivity should generally not be used by itself to measure segmentation quality, specificity measure would be incorporated with it. The specificity measures the fraction of pixels, that do not belong to the region of interest, correctly detected, as determined by the equation

$$SP = \frac{TN}{TN + FP}.$$ (30)

4.2. Performance Analysis of Skull Stripping Method

This section presents the qualitative and quantitative performance analysis of the proposed skull stripping method (S3) on 37 T1-weighted brain MR volumes, along with a comparison with related skull stripping methods. The methods compared are BET, BSE, and ROBEX as described below:

- BET (version 2.1) [44]: brain extraction tool provided by FMRIB Software Library (version 4.1.8) executed with default fractional intensity threshold value 0.5;
- BSE (version 13a4) [43]: brain surface extractor provided by BrainSuit executed using the default parameters: diffusion iterations = 3, diffusion constant = 25, edge constant = 0.64, erosion size = 1, trim spinal cord/brain stem = true, dilate final mask = true; and
- ROBEX (version 1.2) [14]: robust brain extraction maintained by Neuroimaging Informatics Tools and Resources Clearinghouse.
Figure 5. Original, ground truth, and skull stripped images obtained using different methods on subject no. 4, 43, 44, 45, 47, 51, and 54 of BrainWeb.

The method S3 is implemented in C language and run in LINUX environment having machine configuration Intel(R) Core(TM) i7-2600 CPU @3.40GHz × 8 and 16 GB RAM. To analyze the performance of different algorithms, the experimentation is done on some benchmark simulated MR images obtained from BrainWeb: Simulated Brain Database (www.bic.mni.mcgill.ca/brainweb/) and real MR images of IBSR: Internet Brain Segmentation Repository (www.cma.mgh.harvard.edu/ibsr/). All the image volumes of BrainWeb and IBSR are of size $256 \times 256 \times 181$ and $256 \times 128 \times 256$, respectively. In this
regard, it should be noted that all the experiments are performed with no a priori knowledge about the input image. For a quantitative comparison of the performance of S3 with other skull stripping methods, the ground truth of brain matter, extracted from T1-weighted brain MR data sets of BrainWeb and IBSR available at their corresponding websites, are used. The comparative performance analysis is studied with respect to various segmentation metrics, namely, Dice coefficient, sensitivity, and specificity.

Fig. 5 and 6 present the comparative performance analysis of different methods qualitatively on few images, along with the original and ground truth images of BrainWeb and IBSR data sets, respectively, while Fig. 7 and 8 report that quantitatively on 37 brain MR images. The first, second, and third columns of Fig. 5 and 6 show the original images, corresponding ground truth images, and output skull stripped images obtained using the S3, respectively, while remaining columns present the skull stripped images produced by different existing methods. All the results reported in Fig. 5 and 6 show that over-extraction is done by the BET in slices of BrainWeb subjects numbered 4, 43, and 44 by removing some brain tissues along the cerebral border. On the other hand, under-segmentation is experienced by the BSE in slices of BrainWeb subjects numbered 45, 51, and 54, and it fails to remove the skull for most of the slices selected from IBSR data set as shown in Fig. 6, which indicates that the BSE works extremely poor on low contrast images like IBSR. The ROBEX also results in under-segmentation in slices of BrainWeb subject numbered 43 and in slices of IBSR volumes numbered 5, 15, 16, and 17.
(a) Dice Coefficient  
(b) Sensitivity  
(c) Specificity

Figure 7. Performance analysis of different mask generation algorithms on BrainWeb

(a) Dice Coefficient  
(b) Sensitivity  
(c) Specificity

Figure 8. Performance analysis of different mask generation algorithms on IBSR
From the heat maps reported in Fig. 7 and 8, it can be seen that the proposed skull stripping algorithm performs significantly better than BET, BSE, and ROBEX for segmenting the brain region. Out of 37 cases, the performance of the proposed S3 method is better than that of the BET in 29, 21, and 30 cases with respect to Dice coefficient, sensitivity, and specificity, respectively, while the S3 attains better performance compared to that of the BSE in 33, 19, and 29 cases, respectively, and also to ROBEX in 32, 9, and 36 cases, respectively, irrespective of the data sets used. Hence, the best and consistent performance is achieved by the proposed method, irrespective of the image contrast. However, the sensitivity value of the proposed method is lesser as compared to that of ROBEX in most of the cases. Since the S3 adds some boundary portion of the CSF from brain region into its background, the false negative count is increased for the brain. So, out of total 37 cases, the proposed method attains higher sensitivity values in only nine cases compared to that of ROBEX. Hence, the S3 performs better than BET, BSE, and ROBEX in 80, 81, and 77 cases, respectively, out of total 111 cases, irrespective of the quantitative indices and data sets used. The comparative performance analysis is also reported in terms of p-value computed through the sign test. For Dice coefficient and specificity, the proposed method attains p-values of 3.76E-04 and 9.55E-005 with respect to the BET, 5.42E-07 and 3.76E-04 with respect to the BSE, and 3.71E-06 and 2.76E-10 with respect to the ROBEX, respectively, which are statistically significant considering 0.05 as the level of significance. On the other hand, the ROBEX achieves significant p-value of 3.76E-04 for sensitivity only.

The S3 algorithm is purely intensity based method, which includes adaptive threshold calculation followed by morphological operations, for increased robustness. The sizes of octagonal structuring elements for opening and closing morphological operations are set experimentally. This method can be more robust by selecting the optimum values of morphology opening and closing sizes based on image characteristics. The proposed method does not require any user intervention or setting any external initial parameters to extract the brain matter and thus qualifies to be an automatic method. On the other hand, some existing methods such as BET [44] and BSE [43] require parameter adjustment to obtain satisfactory results for different data sets used. Experimental results also ensure that the proposed S3 method is suitable on both synthetic as well as real images, although they are low contrast images. It works well even for the brain volumes where BET [44], BSE [43], and ROBEX [14] fail to segment brain and non-brain regions accurately. This method is based on brain anatomy and image intensity characteristics and hence can be implemented as a part of any automatic brain image processing system [30].

### 4.3. Performance Analysis of SoBT-RFW Algorithm

This section presents the performance of the proposed brain tumor detection algorithm, along with a comparison with related methods. The proposed method uses robust rough-fuzzy c-means (rRFCM) [28, 29] for segmentation of brain MR images. The methods compared are $\mathcal{M}_1$, $\mathcal{M}_2$, $\mathcal{M}_3$, and BrainTumIA [39]. The methods $\mathcal{M}_1$, $\mathcal{M}_2$, and $\mathcal{M}_3$ use hard c-means (HCM) [32], fuzzy c-means (FCM) [4], and rough-fuzzy c-means (RFCM) [24, 25], respectively, while mask generation, feature extraction and selection, and post-processing steps are same as those of the proposed method. All the methods are implemented in C language and run in LINUX environment having machine configuration Intel(R) Core(TM) i7-2600 CPU @ 3.40GHz × 8 and 16 GB RAM. The source code of the proposed SoBT-RFW method, written in C language, is available at www.isical.ac.in/~bibl/results/sobt-rfw/sobt-rfw.html.

To analyze the performance of different algorithms, the experimentation is done on simulated and real brain MR images. Brain tumor image data used in this work were obtained from the MICCAI 2012
Figure 9. Segmented images for simulated high grade brain tumor images obtained using different methods: input image, ground truth, proposed, $M_1$, $M_2$, $M_3$, and BraTumIA (from top to bottom).

Challenge on Multimodal Brain Tumor Segmentation (http://www.imm.dtu.dk/projects/BRATS2012) organized by B. Menze, A. Jakab, S. Bauer, M. Reyes, M. Prastawa, and K. Van Leemput. The challenge database contains fully anonymized images from the following institutions: ETH Zurich, University of Bern, University of Debrecen, and University of Utah. For a quantitative comparison of the performance of the proposed method with other methods, the ground truth of brain tumor for this data set is obtained from its corresponding website. In this regard, it should be noted that all the experiments are performed with no a priori knowledge about the input image. The comparative performance analysis is studied with respect to various segmentation metrics, namely, Dice coefficient, sensitivity, and specificity. The metrics are calculated for tumor class only. The value of fuzzifier is 2.00, while that of weight parameter for
rough-fuzzy clustering algorithms, which represents relative importance of lower and boundary region, is set to 0.51. The final cluster prototypes of HCM are used as the initial centroids of other clustering algorithms, while Daubechies 6-tap filter is used to extract features using wavelet decomposition. Fig. 9, 10, and 11 present the effectiveness of the proposed brain tumor segmentation algorithm on few images, while heat maps of Fig. 12, 13, and 14 depict brain tumor segmentation results for fifty images quantitatively. In 3rd to 7th columns of Fig. 9, 10, and 11, the TP, FP, and FN regions are represented in red, yellow, and blue color, respectively, while red color at 2nd column represents region of interest to be segmented.
Figure 11. Segmented images for real brain tumor images obtained using different methods: input image, ground truth, proposed, $M_1$, $M_2$, $M_3$, and BraTumIA (from top to bottom).

4.3.1. Importance of Robust Rough-Fuzzy C-Means

The performance of the proposed method is extensively compared with that of the methods $M_1$, $M_2$, and $M_3$. The only difference among these methods is the clustering algorithm used. While the proposed method uses rRFCM [28, 29] algorithm, other methods, namely, $M_1$, $M_2$, and $M_3$, use HCM [32], FCM [4], and RFCM [24, 25], respectively.

The qualitative results reported in 3rd to 6th rows of Fig. 9, 10, and 11 compare the performance of the proposed method with that of the methods $M_1$, $M_2$, and $M_3$, while Fig. 12, 13, and 14 compare it quantitatively with respect to three quantitative indices, namely, Dice coefficient, sensitivity, and speci-
Figure 12. Comparative performance analysis of different algorithms on simulated high grade brain tumor

Figure 13. Comparative performance analysis of different algorithms on simulated low grade brain tumor

...respectively, on fifty brain tumor images. The proposed method attains better performance than M_1 method in 35, 20, and 32 cases, out of 50 cases each, with respect to Dice coefficient, sensitivity,
and specificity, respectively, while it provides better performance than the method $M_2$ in 33, 41, and 20 cases, respectively. Moreover, the proposed SoBT-RFW method achieves better results compared to the method $M_3$ in 32, 30, and 27 cases, respectively. The proposed method achieves significantly lower $p$-values, computed through the sign test, of $3.30 \times 10^{-3}$, $1.64 \times 10^{-2}$, and $3.25 \times 10^{-2}$ for Dice coefficient with respect to the methods $M_1$, $M_2$, and $M_3$, respectively. Also, it attains significantly lower $p$-values of $2.81 \times 10^{-6}$ for sensitivity and $3.25 \times 10^{-2}$ for specificity with respect to the methods $M_2$ and $M_1$, respectively. Hence, all the results reported in Fig. 9, 10, 11, 12, 13, and 14 establish the fact that there is a significant improvement in the segmentation results of brain tumor obtained using the rRFCM algorithm as compared to other clustering algorithms.

From all the segmented images reported in Fig. 9, 10, and 11, it can also be concluded that the proposed post-processing method works well irrespective of clustering algorithms used. But, the clustering result actually forms the base for post-processing. So, more efficient is the clustering technique, more accurate the tumor segmentation. The best performance of the proposed method using the rRFCM clustering algorithm is achieved due to the fact that the probabilistic membership function of the rRFCM handles efficiently overlapping partitions, while the possibilistic membership function of lower approximation of a cluster helps to discover arbitrary shaped cluster. In effect, good segmented regions are obtained using the proposed brain tumor segmentation algorithm.

### 4.3.2. Comparative Performance Analysis of SoBT-RFW and BraTumIA

Finally, the performance of the proposed SoBT-RFW method is compared with that of BraTumIA. The third and seventh rows of Fig. 9, 10, and 11 represent the comparative performance analysis between proposed segmentation algorithm and the existing BraTumIA software tool qualitatively, while Fig. 12,
13, and 14 depict that quantitatively with respect to Dice coefficient, specificity, and sensitivity. The proposed SoBT-RFW method provides better accuracy than the existing BraTumIA software tool in segmenting brain tumor in 42, 30, and 37 cases, out of 50 cases each, with respect to Dice coefficient, sensitivity, and specificity, respectively. The proposed SoBT-RFW method achieves significantly lower p-values of 5.82E-07 and 4.68E-04 for Dice coefficient and specificity, respectively, with respect to BraTumIA. However, it attains p-value of 1.01E-01 for sensitivity, which is lower but not significant.

5. Conclusion

The contribution of the paper lies in developing a methodology for tumor segmentation from brain MR images. It integrates judiciously a skull stripping method, dyadic wavelet analysis, unsupervised feature selection algorithm, rough-fuzzy clustering algorithm, asymmetricity analysis, and rough-set based post-processing technique. This formulation is geared towards maximizing the utility of rough-fuzzy clustering and multiresolution wavelet analysis with respect to brain tumor segmentation task from MR image. In this regard, it should be mentioned that a judicious integration of rough sets and wavelets for classification was made in [33]. The proposed post-processing method combines the merits of morphological operations and the notion of rough set theory embedded into region growing technique. It improves the performance of the brain tumor segmentation method. Formulation of the post-processing method using rough sets enables efficient handling of ambiguities at anatomical pathologic boundaries. The proposed post-processing method works significantly well, irrespective of clustering algorithms. Several quantitative measures are used to evaluate the performance of the proposed brain tumor segmentation method. Finally, the effectiveness of the proposed method is demonstrated both qualitatively and quantitatively, along with a comparison with other related algorithms, on a set of synthetic and real brain MR images.

References


