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An improved Gabor wavelet transform and rough K-means clustering algorithm for MRI brain tumor image segmentation

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Abstract
Image processing is significant in the medical field which provides detailed information about medical images and image segmentation is an essential part of medical image processing. In the medical field, various modalities have been utilized such as X-ray, CT scan and MRI, etc. MRI provides accurate results than other techniques. Our proposed technique is highly focused on tumor identification using MRI image segmentation. The proposed methodology consists of five stages namely, pre-processing, feature extraction, feature selection, classification, and segmentation. Initially, input MRI images are given to the preprocessing stage to fit the images for further processing. In this preprocessing phase, the input images are converted into a transform domain with the aid of Improved Gabor Wavelet Transform (IGWT). Then, GLCM related features are extracted and important features are selected with the help of the Oppositional fruit fly algorithm (OFFA). Then, the selected features are given to the support vector machine (SVM) classifier to classify an image as normal or abnormal. After the classification process, the abnormal images are selected and given to the segmentation process. For segmentation, in this paper, we utilized an effective rough k-means algorithm. The performance of the proposed methodology is evaluated in terms of Sensitivity, Specificity, and Accuracy. The experimental results show that our proposed method attained better results compared to existing work.

Keywords Image segmentation · Preprocessing · Feature extraction · Gabor wavelet transform · Oppositional fruit fly algorithm · Rough K-means

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1 Introduction

Image processing and its segmentation is one of the interesting areas of medical science. In medical image technology, both MRI and CT scan (Computerized Tomography) used to create the pictures of the inside of the body, from that MRI provides accurate visualization of anatomical structures of tissues. When compared to a CT scan, MRI is better because it does not affect the human body [29]. The human body is made up of several types of cells. The brain is a highly specialized and sensitive organ of the human body. The brain tumor is a very harmful disease for human beings [5].In medical science, MRI (magnetic resonance imaging) is a tool that can produce detailed pictures of parts of the body and also to detect the Brian tumor and its segmentation from an image [8]. A brain tumor is a disease in which cells are increased uncontrollably in the brain. Brain tumor has two types one is a malignant tumor and the other is a benign tumor. A malignant tumor is typically known as brain cancer that can spread outside the brain. A benign tumor is incapable of spreading beyond the brain itself and their growth is self-limited, sometimes they cause problems because of their surgery and location [4].

In this case, some operations are needed to detect the brain tumor from MRI image, for this reason, we use the wavelet transform it deals with discrete data in medical image processing. These are decomposing functions in the frequency domain for preserving the spatial domain [30]. In many research areas such as texture analysis and image segmentation Gabor wavelets are widely used and to capture the local structure corresponding to spatial frequency, spatial localization, and orientation selectivity [24, 32]. Gabor wavelet analysis is useful in extracting texture features of magnetic resonance and it has tunable center frequencies to optimally achieve joint resolution in spatial frequency domains [3, 9, 17, 19, 21, 22]. A lot of feature selection approaches are available namely, principal component analysis (PCA), wavelet transform, Gabor filters, Linear discrimination analysis (LDA), and optimization algorithms. Some of the feature extraction approaches are given in [10–13, 16, 18, 20]. Similarly, dimension reduction approaches [14, 15] mainly used. To reduce the computation complexity dimension reduction approach is used.

MR Image segmentation is done via clustering. Clustering is a process of grouping a set of patterns into several clusters. In the clustering analysis, several unsupervised learning techniques are used to solve the clustering problems. There are several unsupervised learning techniques such as k means algorithm, fuzzy c means algorithm, etc. From that k means is one of the simplest unsupervised techniques that solve the well-known clustering problem [25]. The K means clustering is used to group the objects and it depends on the attributes/ features into k number of groups. In this, the grouping is based on Euclidean distance between the data and the corresponding cluster centroid [6]. Fuzzy c means clustering is one of the unsupervised learning techniques these are applied in real-time problems such as astronomy, geology, medical imaging, and target recognition, and image segmentation. The clustering techniques are very essential because the medial images are limited spatial resolution, poor contrast, noise, and non- uniform variation [23, 33]. The edges of different tissues in MRI brain images are unclear. So, clustering techniques are widely used for brain tumor detection and segmentation purpose [35].

The main objective of the proposed methodology is to effectively segment the abnormal portion of the MRI brain image. Here, for the segmentation process, a rough K-means algorithm is utilized. The introduced rough k-means algorithm is a novel algorithm that is a hybridization of the roughest theory and k-means algorithm. The proposed method overcomes the drawbacks present in the individual rough set theory and k-means algorithm. The contribution of the proposed methodology is listed below;

- To increases the segmentation accuracy, in the pre-processing stage, the input image is converted into a transform domain with the aid of IGWT.
- For the feature extraction process, different types of texture features are extracted. Twenty-six features are extracted,
- To minimize the time complexity, important features are selected with the help of OFFA,
- For the segmentation process, a novel rough k-means algorithm is developed.
- The performance of the proposed methodology is analyzed in terms of different metrics.

2 Related works

A lot of researchers had developed brain tumor segmentation and classification. Among them some of the works are analyzed here; Ma et al. [28] have presented a new methodology named as a combined ccRFs and mpAC approach. Their approach combines random forests and active contour model for the automated segmentation of the gliomas from multimodal volumetric MR images. Especially, they employ a feature representation learning strategy to effectively explore both local and contextual information from multimodal images for tissue segmentation by using modality-specific random forests as the feature learning kernels. A different level of the structural information was subsequently integrated into concatenated and connected random forests for gliomas structure inferring. Finally, a novel multi-scale patch driven active contour model was exploited to refine the inferred structure by taking advantage of sparse representation techniques. Results reported on public benchmarks reveal their architecture achieves competitive accuracy compared to the state-of-the-art brain tumor segmentation methods while being computationally efficient.

Angulakshmi et al. [2] have suggested that the automated brain tumor segmentation method was becoming challenging in the field of medical research as a brain tumor emerges with diverse size, shape, and intensity. In that paper, spectral clustering was used for the segmentation of brain tumor tissues from Magnetic resonance images (MRI) as it creates high-quality clusters. Spectral clustering suffered from dense similarity matrix construction for massive data. To overwhelm the drawback of spectral clustering, the proposed method performed the brain tumor segmentation by (i) identifying the tumorous region labeled as Region of Interest (ROI) using super pixel-based spectral clustering. (ii) Brain tumor tissues were then segmented by performing spectral clustering over the obtained ROI of MRI. The identification of ROI alleviates the computational burden of spectral clustering. The segmentation of ROI used the spectral clustering and produced high-quality clustering results for brain tumor segmentation. The observational results were taken out on BRATS 2012 dataset and evaluated by dice score, sensitivity, and specificity metrics. The proposed method outperformed the other clustering methods with competitive dice score values for the segmentation of edema and Tumor Core (TC) regions from MRI images.

Soltaninejad et al. [34] have described that accurate segmentation of brain tumors in magnetic resonance images (MRI) was a difficult task due to various tumor types. Using information and features from multimodal MRI including structural MRI and isotropic (p) and anisotropic (q) components derived from the diffusion tensor imaging (DTI) might result in more accurate analysis of brain images. They proposed a novel 3D super voxel-based learning method for the segmentation of tumors in multimodal MRI brain images (conventional MRI and DTI). Supervoxels were generated using the information across the multimodal MRI dataset. For each super voxel, a variety of features including histograms of text on the descriptor, calculated using a set of Gabor filters with different sizes and orientations, and first-order intensity statistical features were extracted. Those features were fed into a random forest (RF) classifier to classify each super voxel into tumor core, or healthy brain tissue.

Sauwen et al. [31] have proposed that tumor segmentation was a particularly challenging task in high-grade gliomas (HGGs), as they were amongst the most heterogeneous tumors in oncology. An accurate delineation of the lesion and it was main subcomponents contribute to optimal treatment planning, prognosis, and follow-up. Conventional MRI (MRI) was the imaging modality of choice for manual segmentation and was also considered in the vast majority of automated segmentation studies. Advanced MRI modalities such as perfusion-weighted imaging (PWI), diffusion-weighted imaging (DWI) and magnetic resonance spectroscopic imaging (MRSI) had already shown their added value in tumor tissue characterization, hence there had been recent suggestions of combining different MRI modalities into a multiparametric MRI (MP-MRI) approach for brain tumor segmentation. In that paper, they compared the performance of several unsupervised classification methods for HGG segmentation based on MP-MRI data including MRI, DWI, MRSI, and PWI. Two independent MP-MRI datasets with a different acquisition protocol were available from different hospitals. They demonstrated that a hierarchical nonnegative matrix factorization variant which was previously introduced for MP-MRI tumor segmentation provided the best performance in terms of mean Dice-scores for the pathologic tissue classes on both datasets.

Mohan et al. [26] have described a review on the recent segmentation and tumor grade classification techniques of brain Magnetic Resonance (MR) Images was the objective of that paper. The requisite for early detection of a brain tumor and its grade was the motivation for that study. In Magnetic Resonance Imaging (MRI), the tumor might appear clear but physicians need quantification of the tumor area for further treatment. That was where the digital image processing methodologies along with machine learning aid further diagnosis, treatment, prior and post-surgical procedures, synergizing between the radiologist and computer. These hybrid techniques provided a second opinion and assistance to radiologists in understanding medical images hence improved diagnostic accuracy. That article aimed to retrospect the current trends in segmentation and classification relevant to tumor infected human brain MR images with a target on gliomas which include astrocytoma. The methodologies used for extraction and grading of tumors that could be integrated into the standard clinical imaging protocols were elucidated. Lastly, a crucial assessment of the state of the art, future developments, and trends were dissertated.

Al-Dmour et al. [1] have suggested that in recent decades, a large number of segmentation methods had been introduced and applied to magnetic resonance (MR) brain image analyze was to measure and visualize the anatomical structures of interest. In that paper, an efficient fully-automatic brain tissue segmentation algorithm based on a clustering fusion technique was presented. In the training phase of this algorithm, the pixel intensity value was scaled to enhance the contrast of the image. The brain image pixels that had similar intensity were then grouped into objects using a superpixel algorithm. Further, three clustering techniques were utilized to segment each object. For each clustering technique, a neural network (NN) model was fed with features extracted from the image objects and trained to reduce the labels produced by that clustering technique. In the testing phase, the pre-processing step includes scaling and resizing the brain image was applied then the superpixel algorithm partitions the image into multiple objects (similar to the training phase). The three trained neural network models were then used to predict the respective class of each object and the obtained classes were combined using majority voting. The efficiency of the proposed method was demonstrated on various MR brain images and compared with the three base clustering techniques.

Nabizadeh et al. [27] have described that automated recognition of brain tumors in magnetic resonance images (MRI) was a difficult procedure owing to the variability and complexity of the location, size, shape, and texture of these lesions. Because of intensity similarities between brain lesions and normal tissues, some approaches make use of multi-spectral anatomical MRI scans. However, the time and cost restrictions for collecting multi-spectral MRI scans and some other difficulties necessitate developing an approach that could detect tumor tissues using single-spectral anatomical MRI images. In that paper, they present a fully automatic system, which was able to detect slices that include tumors and, to delineate the tumor area. The experimental results on a single contrast mechanism demonstrate the efficacy of our proposed technique in successfully segmenting brain tumor tissues with high accuracy and low computational complexity. Moreover, they include a study evaluating the efficacy of statistical features over Gabor wavelet features using several classifiers. This contribution fills the gap in the literature, as is the first to compare these sets of features for tumor segmentation applications.

Tang et al. [7] have presented a new multi-atlas segmentation (MAS) framework for MR tumor brain images. The basic idea of MAS was to register and fuse label information from multiple normal brain atlases to a new brain image for segmentation. Many MAS methods have been presented with success. However, most of them were developed for normal brain images, and tumor brain images usually pose a great challenge for them. Due to that tumors cause difficulties in the registration of normal brain atlases to the tumor brain image. To address those challenges, in the first step of our MAS framework, a new low-rank method was used to get the recovered image of the normal-looking brain from the MR tumor brain image based on the information of the normal brain atlases. Different from conventional low-rank methods that produce the recovered image with distorted normal brain regions, our low-rank method harnesses a spatial constraint to get the recovered image with preserved normal brain regions. Then in the second step, normal brain atlases can be registered to there covered image without influence from tumors. Those two steps were iteratively preceded until convergence, for obtaining the final segmentation of the tumor brain image. During the iteration, both the recovered image and the registration of normal brain atlases to the recovered image were gradually refined. Their experimental results show that their presented method can get effectively recovered images and also improves segmentation accuracy. Kermi et al. [13] have presented a new fully automated, fast, and accurate brain tumor segmentation method that automatically detects and extracts whole tumors from 3D-MRI. Their presented method was based on a hybrid approach that relies on a brain symmetry analysis method and a combining region-based and boundary-based segmentation methods. Their segmentation process consists of three main stages. In the first one, image pre-processing was applied to remove any noise and to extract the brain from the header image. In the second stage, automated tumor detection was performed. That was based essentially on the FBB method using brain symmetry. Their result constitutes the automatic initialization of a deformable model, thus removing the need of selecting the initial region of interest by the user. Finally, the third stage focuses on the application of region growing combined with a 3D deformable model based on geodesic level-set to detect the tumor boundaries containing the initial region, computed previously, regardless of that's shape and size. Their presented segmentation system has been tested and evaluated on 3D-MRIs of 285 subjects with different tumor types and shapes obtained from the BraTS'2017 dataset. Their achieved results turn out to be promising and objective as well as close to ground truth data.

3 Problem definition

Image segmentation is a classical problem in computer vision and is of utmost importance to medical imaging. In brain tumor detection several MRI segmentation methods are used. But it can some disadvantages. These are listed below.

- In the MRI segmentation k means clustering method is used. This method can segment tumors from different brain MRI images. The problem of this method is it produces a different result for the different numbers of clusters. It requires prior knowledge (number of clusters) and the inability to handle noisy data. In the k mean clustering method, the detection of edges still not robust enough.
- In the MRI segmentation, a region-based segmentation method is used, but the computation of this method is time-consuming, the noise or variation of intensity provides holes or over-segmentation and it may not distinguish the shading of the real image and it has extended computational cost and noise sensitivity.
- One of the simple image segmentation techniques is a thresholding technique, but in this case, only two classes are generated and it cannot be applied to multichannel images.
- In the medical image segmentation, the region growing technique is applied. But it requires a user interface for the selection of seed points in each region and it is a very time-consuming process.
- In image segmentation, edge detection technique is used, but this technique is sensitive to noise, inaccuracy, time consumption, etc.

These are the main drawbacks of various existing works, which motivate us to do this research on MRI segmentation. We are intended to propose a suitable method to achieve more segmentation accuracy in MRI images.

4 Proposed methodology

The primary goal of our research is to design and develop an approach for tumor identification and segmentation using a novel rough k-means algorithm. In this paper, initially, the MRI image is pre-processed to make it fit for segmentation. Then, the image is converted into a transform domain using IGWT. Then, different types of features are extracted from each image present in the database. A large number of features is a great obstacle for the classification process. So, important features are selected using OFFA. Then, the selected features are given to SVM to classify an image as normal or abnormal. After classification, abnormal images are selected and given to the rough k means clustering algorithm to segment the ROI region. Here the traditional k means clustering algorithm is modified using rough set selection, in which lower and upper approximation set can be used in k means clustering. The performance of the proposed technique is evaluated using segmentation accuracy. The suggested method is implemented in the MATLAB platform shows in Fig. 1.

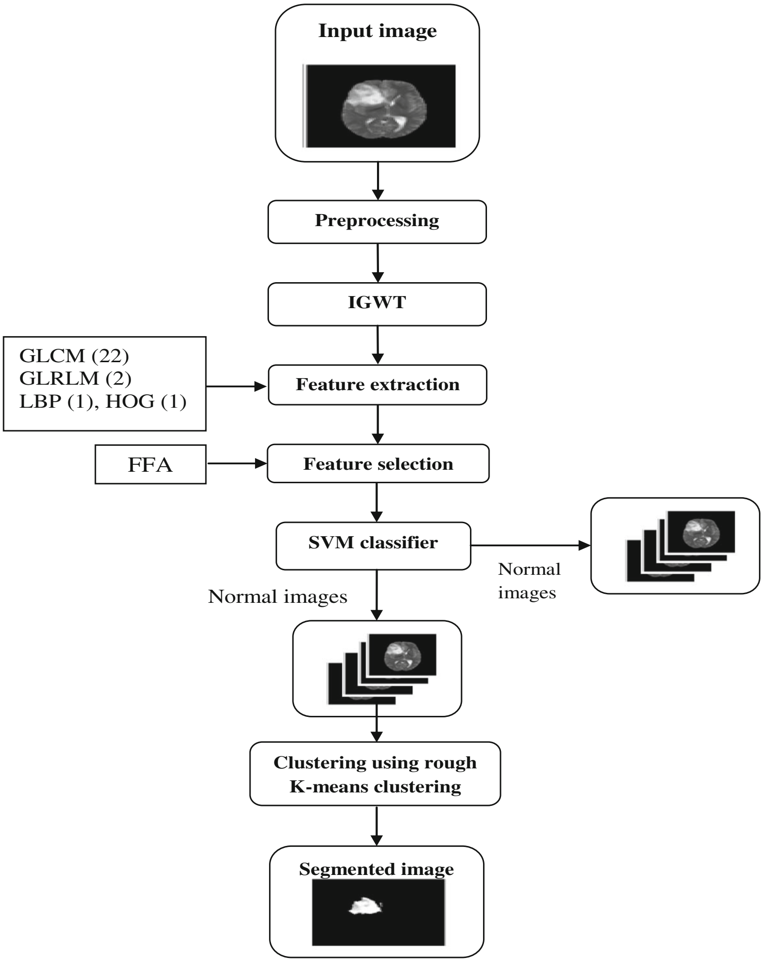


Fig. 1 Proposed Brain MRI Image Tumor Segmentation

4.1 Preprocessing

To enhance the quality of an image in this work we have executed a preprocessing work. Here, we initially process with some constrains they may damage the quality of the image. Therefore, we execute manual correction in preprocessing. Therefore, we can enhance the quality of the image to make it ready for further processing. Once this process is finished, the processed images are given to the next level to apply Improved Gabor Wavelet Transform (IGWT). Where feature extraction is executed for further processing. The suggested technique utilizes the Preprocessing of the brain MR image is the first step in our proposed technique. Preprocessing of an image is done to reduce the noise and to enhance the brain MR image for further processing. The purpose of these steps is basically to improve the image and the image quality to get more surety and ease in detecting the tumor.

4.2 Improved Gabor wavelet transform

In this section, the input image is converted into a transform domain. This will make a classification process perfect. For IGWT, the basic wavelet is

$$g(t) = \frac{1}{\sigma\sqrt{2\pi}} \exp\left(-\frac{t^2}{2\sigma^2} + j2\pi t\right), (\sigma > 0) \tag{1}$$

$$\int_{-\infty}^{\infty} |g(t)| dt = 1 \tag{2}$$

The IGW family $\{g, f, \tau\}$, is generated by scaling and translating eqa 3 and it is written as

$$g_{f,\tau}(t) = |f| g[f(t-\tau)] = \frac{|f|}{\sigma\sqrt{2\pi}} exp\left[-\frac{f^2(t-\tau)^2}{2\sigma^2} + j2\pi f(t-\tau)\right] \tag{3}$$

Where *f* is denoted as dominant factor and σ is denoted resolution factor. Compared to GWT's equation, IGWT's eq. 4 utilized f rather than *1/a* for scaling.

$$\widehat{g}_{f,0}(\gamma) = \int_{-\infty}^{\infty} g_{f,0}(t) e^{-j2\pi\gamma t} dt = exp\left[-\frac{2\pi^2\sigma^2(\gamma-f)^2}{f^2}\right] \tag{4}$$

Where $g_{f,\tau}(\gamma)$ is the Fourier transform.

4.3 Feature extraction

After the preprocessing, texture features are extracted. In this paper, four types of texture features are extracted from each image namely, GLCM, GLRLM, LBP, and HOG. Totally 26 features are extracted from each image.

4.4 Feature selection

After the feature extraction, important features are selected using OFFA. This is because a large number of features create great barriers to classification. Fruit fly algorithm is an algorithm that simulates the foraging behavior of fruit flies. The fruit fly algorithm is a novel technique for seeking global optimization. It began from the examination n on food hunting behaviors of fruit fly swarm. The fruit fly is a superfood hunter with sharp osphresis and vision. At, to begin with, it identifies food source by noticing a wide range of fragrances floating all around and flies toward the corresponding place. After reaching close towards the food, it might discover food or go to that particular place with its delicate vision. Food sources are represented by the optima and the methodology of foraging is reproduced using the iteratively seeking the optima in the OFFA. The improved form of fruit fly algorithm is said to be OFFA. It provides improved performance than the fruit fly algorithm. The step by step process of feature selection is explained below;

Step1. Solution initialization: Solution initialization is an important process. The sample selected features are considered as input. The main parameters of the FOA are the total evolution number and the low variance blocks position. In our suggested technique fruit fly represent the low variance sblock position. Initialize random location of low variance blocks position *(PX_axis, PY_axis).*

Step2. Opposite solution generation: To modify the traditional fruit fly algorithm, the oppositional method is introduced. According to opposition based learning (OBL) introduced by Tizhoosh in the current agent and its opposite agent are considered simultaneously to get a better approximation for the current agent solution. It is given that an opposite agent solution has a better chance to be closer to the global optimal solution than a random agent solution. The opposite variance blocks positions are completely defined by components.

$$OP_m = \left[op_m^1, op_m^2, \ldots\ldots op_m^d\right] \tag{5}$$

Where $OP_m = Low_m + Up_m - P_m$ with $OP_m \in [Low_m, Up_m]$ is the position of *m-th* low variance blocks OP_min the d-th dimension of oppositional blocks.

Step3. Updation using FFA: Exploration using the arbitrary path and low variance block selection. Here, P_m is the *m-th* location of low variance blocks.

$$P_m(x, y) = (PX_m, PY_m)^T \tag{6}$$

$$\mathrm{PX}_m = PX\_axis + RandomValue \tag{7}$$

$$\mathrm{PY}_m = PY\_axis + RandomValue \tag{8}$$

Step4. Position Evaluation of the suggested technique,

$$\mathrm{BP_m} = EC \tag{9}$$

Step5. Substitute position of low variance blocks into the fitness function

$$best \quad block = function(MinBP_m) \tag{10}$$

Step6. Detect the most excellent positions of low variance blocks.

$$[Excellent\ block\ Excellent\ selection] = minerror \tag{11}$$

Step7. Retains the best position of low variance block value and x, y coordinate, the fruit fly swarm will utilize visualization to flutter in that direction.

$$selected \quad block = minerror \tag{12}$$

$$\mathrm{PX}\_axis = PX(Excellentindex) \tag{13}$$

$$\mathrm{PY}\_axis = PY(Excellentindex) \tag{14}$$

Step8. Termination criteria: Enter successive optimization to replicate the execution of stages 3–6, then decide if the fitness of selected feature is better than the past selected features, if yes, execute task 7. After selecting the features the feature values are fed to the SVM for classification.

4.5 SVM based classification

After the feature selection process, the selected features are given to the SVM classifier to classify images as normal or abnormal. SVM is a nonprobabilistic calculation that is dividing data into non- linearly and linearly using hyperplanes. The main aim of the SVM procedure is to locate the hyperplane ideally. The Segregation of two classes by a hyperplane is the aim of a maximum margin such that for linearly separable data, the distance among the support vectors is increased to the full extent. Optimal Separating Hyperplane (OSH) is another recognizable form of the hyperplane. In this stage, the images are classified as normal or abnormal. The attained abnormal images are given to the segmentation process.

Consider the training data set$T = \{a_i \ , b_i\}_{i=1}^{m}$, where $a_i \in R^n$is the i^{th}input feature vectors,$y_i \in \{+1, -1\}$ is the class label ofa_i, m is the total number of training data. The classification function of SVM is calculated as follows;

$$F(a) = w^T \varphi(a) + x$$

Where;

$\varphi(a)$ Non-linear mapping function which.
x Bias.
w Weight vector.

Here, $\varphi(a)$ is used to map the input feature vector into a higher dimensional feature space,***xand***w which is used to determine the position of the separating hyper-plane. The linear decision function based SVM classification can be written as follows;

$$F(x) = Sgn\left[\sum_{i=1}^{n} \alpha_i b_i \left(\varphi(a_i).\varphi\left(a_j\right)\right) + x\right]$$

The above function only used for linear decisions. To apply the SVM classifier to non-linear decision function, a kernel function is included. In this paper, multi-kernel is used for classification function. In this manner, we can map the input data into a high dimensional feature space. The proposed non-linear decision function can be written as follows;

$$F(x) = Sgn\left[\sum_{i=1}^{n} \alpha_i K\left(a_i, a_j\right) + x\right]$$

Here, $K(a, a_i)$ represent the kernel function. In this paper, a multi-kernel is utilized and the hyper-plane separation is performed based on the multi-kernel functions. In this paper, linear kernel and quadratic kernels are used.

4.6 Rough K-means clustering

In this stage, we utilize a rough k-means clustering algorithm for executing an effective clustering process. It has the feature of both rough set and k-means clustering therefore this can provide better performance than other techniques. The Rough K-means algorithm is one of the techniques to handle the vagueness of information. The notions of lower and upper approximation of rough sets are the vital ones for rough k-means clustering algorithms. Calculations of the centroids of clusters need to be modified to include the effects of lower as well as upper bounds. In this case, rough k-means differ from the conventional k-means clustering algorithm. To understand this process, we have explained all the variables and their meanings. V is denoted as a finite ordinary set ($V = \{obj_n | \; n = 1, \ldots, N\}$), V_i denoted as i^{th} cluster, and its center is denoted as $cen_{i,}$ $i = 1, 2, \ldots, k$. A_V_i is a lower approximation and AV_i is an upper approximation. The number of objects in the rough boundary area is denoted as $|AV_i - A\_V_i|$. obj_n is denoted as each object. l_{in} be the distance between obj_n and the center cen_i of cluster V_i. Here, we explained a step by step procedure of rough k-means below.

Step1. Initialization

All the parameters to be initialized the number of clusters k, the parameters $w_{l.approx}$ and $w_{b.approx}$ ($w_{l.approx}$ *and* $w_{b.approx}$ represent the relative importance of the lower approximation and boundary respectively) and the threshold Δ. Assign the objects randomly to the lower approximations of the clusters.

Step2. Computing new Centroids

Computing the new center for each cluster V_i using below given equation

$$cen_i = \begin{cases} w_{l.approx} \times \dfrac{\sum_{obj_n \in \underline{A}V_i} obj_j}{|\underline{A}V_i|} + w_{b.approx} \times \dfrac{\sum_{obj_n}\left(\overline{A}V_i - \underline{A}V_i\right)^{obj_n}}{\left|\overline{A}V_i - \underline{A}V_i\right|} & if\left(\overline{A}V_i - \underline{A}V_i\right) \neq \phi \\ w_{i.approx} \times \dfrac{\sum_{obj_n \in \underline{A}V_i} obj_n}{|\underline{A}V_i|} & otherwise \end{cases}$$

Step3. Object Assigning

Assigning the objects to the approximations for each object obj_n, calculate its nearest center cen_i and computing the differences l_{in}-l_{jn}, $1 \leq i, j \leq k$ where used to determine the membership of obj_n.

For the given threshold, if $l_{in} - l_{jn} \leq \Delta$, for any cluster pairs (V_i, V_j), then $obj_n \in AV_i$ and $obj_n \in AV_{j,}$ and obj_n cannot be a member of any lower approximation. Otherwise, $obj_n \in A\_V_i$ and $obj_n \in AV_i$ such is the minimum for $1 \leq i \leq k$. Finally, assign each object to the corresponding lower or upper approximations.

Step4. Process repeats till reaching the destination

Repeat first and second Steps until convergence, in other words, there are no more new assignments of objects. Here modified rough k means clustering algorithm is utilized for segmentation. Here the traditional k means clustering algorithm is modified using rough set selection, in which lower and upper approximation set can be used in k means clustering.

5 Result and discussion

The input Brain MRI image segmentation to be performed with the aid of modified rough k-means clustering technique and the effectiveness of the segmentation is analyzed by the measures as True positive, True negative, False positive, False negative, Sensitivity, Specificity and Accuracy.

5.1 Dataset description

To get access to the BraTS 2018 data, you can follow the instructions given at the "Data Request" page. The datasets used in this year's challenge have been updated, since BraTS'16, with more routine clinically-acquired 3 T multimodal MRI scans and all the ground truth labels have been manually-revised by expert board-certified neuroradiologists. Ample multi-institutional routine clinically-acquired pre-operative multimodal MRI scans of glioblastoma (GBM/HGG) and lower-grade glioma (LGG), with pathologically confirmed diagnosis and available OS, will be provided as the training, validation and testing data for this year's BraTS challenge. Validation data will be released on July 1, through an email pointing to the accompanying leader board. This will allow participants to obtain preliminary results in unseen data and also report it in their submitted papers, in addition to their cross-validated results on the training data. The ground truth of the validation data will not be provided to the participants, but multiple submissions to the online evaluation platform (CBICA's IPP) will be allowed. Finally, all participants will be presented with the same test data, which will be made available through email during 30 July-20 August and for a limited controlled time-window (48 h), before the participants are required to upload their final results in CBICA's IPP. The top-ranked participating teams will be invited before the end of August to prepare slides for a short oral presentation of their method during the BraTS challenge shows in Figs. 2, 3 and 4.

5.1.1 Sensitivity

The measure of the sensitivity is correctly recognizing the proportion of actual positives. It is used to recognize the positive results by the ability of the test.

$$Sensitivity = \frac{Number\ of\ true\,positives}{Number\ of\ true\,positives + Number\ of\ false\ negatives} \times 100$$

5.1.2 Specificity

The measure of the specificity is correctly measured by the proportion of negative. It is used to recognize negative results by the ability of the test.

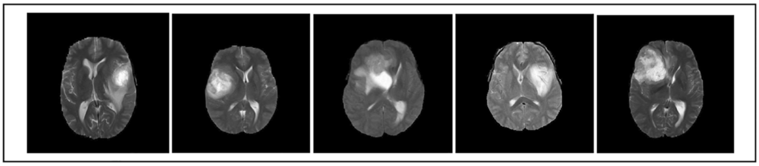


Fig. 2 Input Brain MRI Images

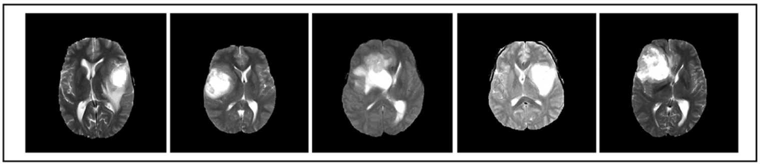


Fig. 3 Preprocessed Brain MRI Images

$$Specificity = \frac{Number\ of\ true\ negatives}{Number\ of\ true\ negatives + Number\ of\ false\ positives} \times 100$$

5.1.3 Accuracy

We can evaluate the measure of accuracy from the measure of sensitivity and specificity as given below.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \times 100$$

In the given metrics are as well appropriate for finding the efficiency of classification of the MRI image segmentation.

5.2 Positive predictive rate

Where a “true positive” is the event that the test makes a positive prediction, and the subject has a positive result under the gold standard, and a “false positive” is the event that the test makes a positive prediction, and the subject has a negative result under the gold standard

$$PPV = \frac{Noof\,TP}{Noof\,TP + Noof\,FP} \times 100$$

5.3 Negative predictive value

Where a “true negative” is the event that the test makes a negative prediction, and the subject has a negative result under the gold standard, and a “false negative” is the event that the test makes a negative prediction, and the subject has a positive result under the gold standard.

$$NPV = \frac{Noof\,TN}{Noof\,TP + Noof\,FP} \times 100$$

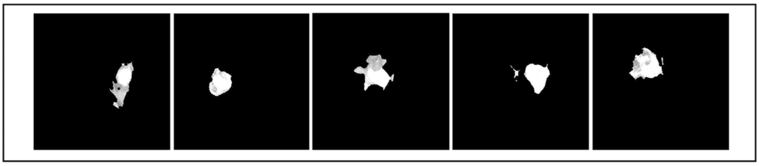


Fig. 4 Segmented Brain MRI Images

5.4 False positive rate

The false-positive rate is calculated as the ratio between the number of negative events wrongly categorized as positive (false positives) and the total number of actual negative events (regardless of classification). The false-positive rate (or "false alarm rate") usually refers to the expectancy of the false-positive ratio.

$$FPR = \frac{Noof\,FP}{Noof\,TP + Noof\,FP} \times 100$$

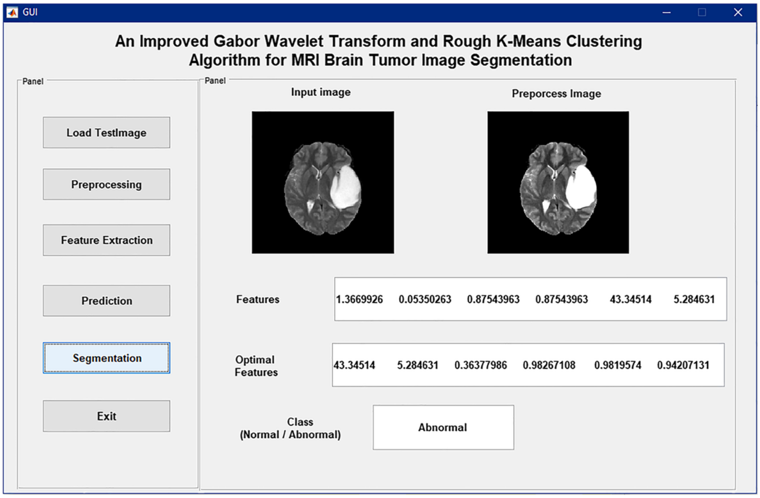
5.5 False negative rate

the false-negative rate is the proportion of positives that yield negative test outcomes with the test, i.e., the conditional probability of a negative test result given that the condition being looked for is present.

$$FNR = \frac{Noof\,FN}{Noof\,TN + Noof\,FN} \times 100$$

5.6 Comparative analysis

In our proposed improved image segmentation scheme, we highly focus to attain a very good results for effectively execute the MRI image segmentation process. Therefore, we compare our proposed technique with existing techniques to evaluate and prove efficiency and performance. However, our proposed work shows better results than the existing technique. Here, we provide the tables and graphical figures for showing the comparison of proposed and existing techniques based on results of sensitivity, specificity, and accuracy it will help to understand the better performance of our proposed work.



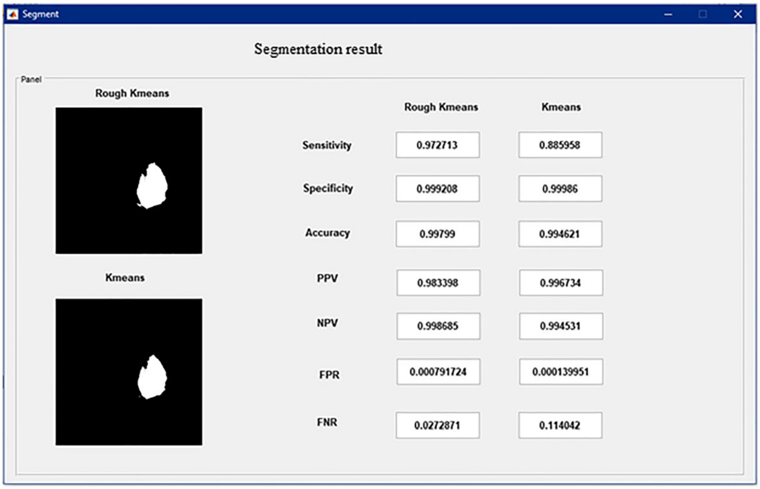
An Improved Gabor Wavelet Transform and Rough K-Means Clustering Algorithm for MRI Brain Tumor Image Segmentation

Features 1.3669926 0.05350263 0.87543963 0.87543963 43.34514 5.284631

Optimal Features 43.34514 5.284631 0.36377986 0.98267108 0.9819574 0.94207131

Class (Normal / Abnormal) Abnormal

Here feature extraction process is done by Gabor Wavelet Transform and it’s improved by the oppositional fruitfly algorithm in this above fig shows the feature value and optimal feature value.



Segmentation result

	Rough Kmeans	Kmeans
Sensitivity	0.972713	0.885958
Specificity	0.999208	0.99986
Accuracy	0.99799	0.994621
PPV	0.983398	0.996734
NPV	0.998685	0.994531
FPR	0.000791724	0.000139951
FNR	0.0272871	0.114042

The above fig shows a proposed Rough K-means and existing K-means segmentation result attained value to prove our proposed technique will give better results shows in Figs. 5 and 6.

In this Table 1, we have compared a comparison of proposed and existing evaluation measures To prove the efficiency and performance of our proposed technique we have utilized some evaluation metrics. Fortunately, our proposed technique’s result shows better results than the existing technique.

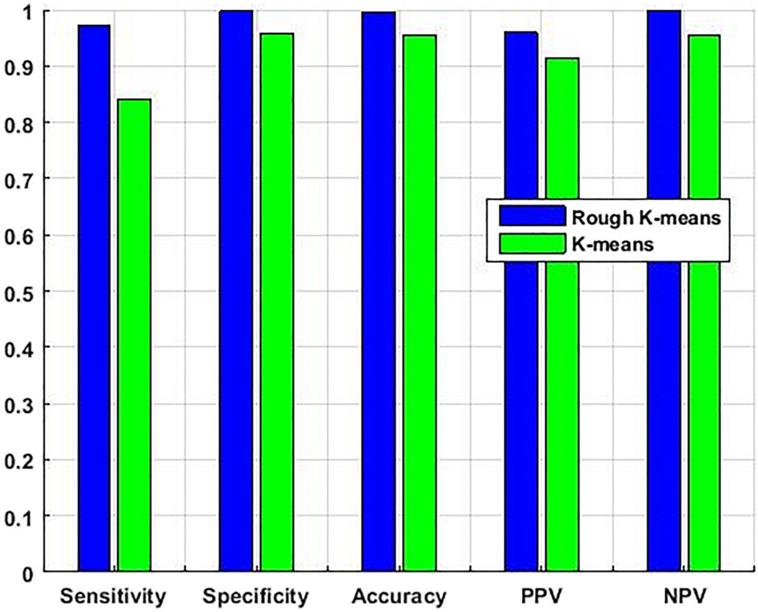


Fig. 5 Graphical representation of proposed and existing Evaluation measures

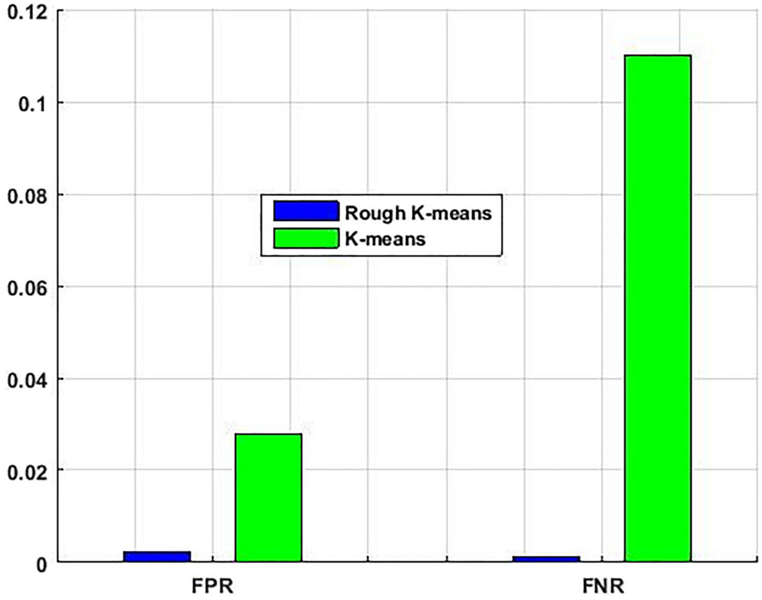


Fig. 6 Graphical representation of proposed and existing FPR and FNR Evaluation measures

6 Conclusion

Medical image processing is a significant process in the field of medical science with the help of this technology patients' disease can be easily identified and take a further step to cure the disease. The physicians get detailed information from medical images and segmentation is an essential part of it. Therefore; they require effective image processing techniques some common modalities have been utilized for medical processing such as X-ray, CT Scan and MRI, etc. MRI is considered as an effective technique to provide an accurate result than other techniques. In this technique, we decided to develop a novel technique for effective tumor identification using the MRI image segmentation process. Therefore, we can provide the improved MRI image segmentation using an improved Gabor Wavelet Transform with modified Rough k-means. Here, tradition Gabor Wavelet Transform is modified by optimization technique, and Gabor filter efficiency is also improved by the oppositional fruit fly algorithm. After the feature selection process is finished the feature values are applied to the clustering process for executing the segmentation process. Here, a rough k-means algorithm is

Table 1 Comparison of proposed and existing evaluation metrics

MRI Images	True Positive	True Negative	False Positive	False Negative	Positive Predictive Value	Negative Predictive Value	False Positive Rate	False Negative Rate
Rough K--Means	8378.076	250,384.0769	3074.7692	307.0769	0.899918	0.999859	0.00534	0.00290
K-means	3797.230	252,793.1538	665.69230	4887.923077	0.946038	0.97684	0.00139	0.49108

utilized for segmentation purposes. To prove the efficiency and performance of our proposed technique we have utilized some evaluation metrics. Fortunately, our proposed technique's result shows better results than the existing technique. We also decide to improve its efficiency and performance in future our work for obtaining better results than current work. In the future, we will be given priority on deep neural network-based segmentation.

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