RELM: A Machine Learning Technique for Brain Tumor Classification

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Abstract: Brain tumor is called as abnormal growth of a group of malicious or benign cells which causes a mass of unwanted cells in the central processing unit of our body, the brain. There are many existing automated techniques to detect them. The detection of these cells is a tedious task and requires great proficiency in order to provide a great deal of cure to them. In the proposed approach, we present an automated brain tumor detection system which not only detects them but also classify them into types based on the features extracted. The brain MRI images needs to be processed and normalized before the system performs the further steps. The pre-processing is key step since it directly affects the quality of classification. Advancing to the next step, the proposed approach uses Principal Component analysis with Normalized GIST (PCA-NGIST) method to extract the features from the brain MRI images. The extracted features, from the datasets are fed to a classifier algorithm for the network to be trained using these features. The training algorithm used in our case is Regularized Extreme Learning Machine (RELM). A test images from the partitioned dataset is given as an input for detection of tumor and further classification if tumor exists. By utilizing the proposed approach, the accuracy percentage of classification rate would be higher.

Keywords: Data Pre-processing; Normalized-GIST Descriptor; Principal Component Analysis; RELM; Classification of brain tumor

I. INTRODUCTION

In human body, brain is referred to as management center which is responsible for executing a large number of activities carried out in our body with a huge number of connections and neurons present in our body. A serious medical condition is caused by the abnormal growth of cells in the brain. Brain tumors of different types exist which could be either benign or malignant. The patients could have a chance of recovery and survive their life by the detection of the brain tumor in the early stages which depends on the knowledge and experience of the physician [1]. An effective tool which is an automated system for brain tumor classification could be used by the physicians in carrying out the treatment successfully. These automated system uses devices of magnetic resonance (MR) imaging to capture the images which are used to diagnose the brain images by the radiologists [2]. Many studies were proposed during the recent years for an automated system that could detect and classify the brain tumors from the MRI images. For example, a method that was proposed by Wongthanavasu and Sompong [3] for segmentation of brain tumor which is hybrid segmentation method that is using cellular automata and fuzzy c-means algorithm. This method used a similarity function along with gray level co-occurrence matrix (GLCM) which solved the problem of seed growing that was found in the existing segmentation methods and BraTS2013 dataset was evaluated for this method. An automated system was proposed by Sehgal et.al [4] for detection of brain tumors based on segmentation of images and extraction of tumor from those images. The feature circularity was utilized by the authors and the area of tumor was extracted from the brain images that were segmented. An average of 72.9% similarity was achieved when the authors compared the images of the ground truth with their images that were segmented. The authors in [5] proposed a semi- automatic segmentation technique of MRI of the brain which is based on the interaction of the humans. A feature map was generated by using this technique from MRI and an active contour model was initialized for segmenting the required region from the images. The ground truth value images results were used to compare it with the original images that are segmented manually. Multistage approach proposed by Praveen and Agrawal[6] uses a set of steps to detect brain tumor from the MRI the steps include processing the image through noise reduction, cropping, histogram equalization and scaling; GLCM and histogram techniques were used for extraction of the features; and

random forest (RF) classifier was used for classification. An accuracy of 87.62% was achieved for the classification using this approach which utilized dataset of 120 patients to test this approach. In another paper [7], features were extracted from the MRI based on the wavelet method proposed by the authors. In this method, brain MRI were segmented using Markov random field (MRF) model. To detect the brain tumors from the 3D images Abbasi et al. [8] proposed an automatic detection method. The histogram matching and bias field matching were used to segment the ROI from the image's background. Later, the brain tumor detection was done using the RF method. BraTS2013 dataset was used to evaluate this approach. Deep learning methods were also used for brain tumor classification from the Computed Tomography (CT) images such as single Convolutional Neural Network (CNN) method [11] and Multiple CNN method with discrimination method [9, 10]. In [12-14], CNN architecture was introduced by the authors to classify the brain tumors. The features were extracted from the pixels of input image of the brain in the CNN architecture, convolution and pooling were the used to perform this operation. Recently, a deep learning method that is Extreme Learning Machine Local Receptive Fields (ELMRF) was proposed by Ari and Hanbey which classified the tumor as either malignant or benign. Sixteen patient's images were collected as the dataset for this method. Among which images of nine patients were used as training dataset and the other images were used as testing dataset. Even though the classification of brain tumors were improved by the deep learning methods, there was a need for large number of datasets for training, computation cost was high and training the systems would consume a lot of time.

Regularized Extreme Learning Machine (RELM) is a regression and classification method which has the ability to overcome the drawbacks in many applications that are linked to backpropagation. The advantages of RELM like training speed and low complexity makes it more advantageous when compared with other classifiers.

Outline of the main contributions of this work:

1. We propose an automated system for classification of the brain tumor which would help the physicians and radiologists to identify the type of tumor from the MRI.

2. We propose PCA-NGIST method which is a novel and an effective hybrid method for extracting features, significant features are extracted from the brain tumor images by using the normalized GIST descriptor with PCA. Classification of brain tumor leads to an inaccurate result because image segmentation could be affected by shadowing and illumination.

3. To reduce the problem of overfitting by its regularization property and training speed we use RELM classifier.

4. We use the grid search algorithm to optimize the parameters in our proposed approach.

5. We evaluate this approach by using the brain images of the new public dataset and the same dataset is used to compare with the other state- of-art approaches.

The organization of the paper is as follows: section I gives the introduction of the proposed approach, section II gives the proposed approach, experimental results and discussions are given in section III and finally a conclusion is summarized in section IV.

II. PROPOSED APPROACH

The proposed approach consists of mainly three steps. We need to obtain the datasets and split them into testing and training datasets. The training dataset goes through the following processes. The fundamental steps are data pre-processing, extraction of features and classification of brain tumor. We provide the brain MRI images as input and the trained model is will be the output. The consolidated architecture of the proposed system is given in the Fig. 1 below.
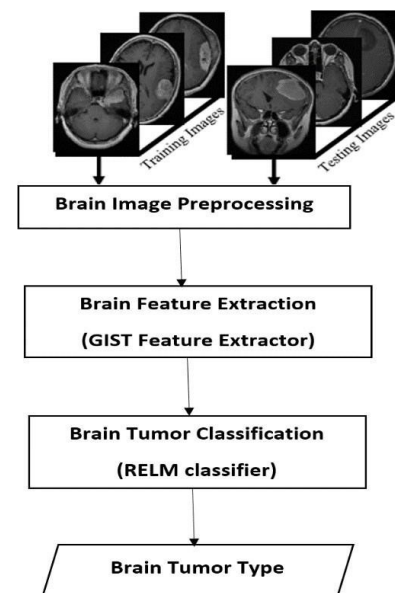

Fig 1.　Architecture of Automated Brain Tumor Detection System using RELM

A. Data Pre-processing

The data pre-processing is a very important step. The raw input image which is present in the dataset contains noise. There is a need to flush out the less significant data and enhance the salient features. After reducing the noise we need to categorize the much needed data and also convert them in a required range. The brain MRI image is converted into a range [0,1] using the normalization process. The normalization process comprises applying a function to transform the image in the desired range. In the proposed approach, we make use of the L2 norm rule which is given by (1),

$$f(x,y) = \frac{f(x,y) - V_{min}}{V_{max} - V_{min}} \qquad (1)$$

The Fig. 2 and Fig. 3 shows the transformation of the raw MRI image before and after normalization. Post the normalization process, the result is that MRI image's edges are enhanced, and region of interest is extracted.
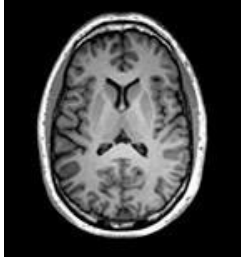

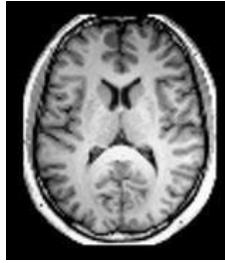Fig 2.   Before Normalization

Fig 3.   After Normalization

B. Extraction of Features.

a) GIST Feature Descriptor

The GIST Feature descriptor [18] extracts and defines the significant features from the brain MRI images. The features help to describe dominant features of an image. These features are generated by passing the normalized image through Gabor filters. After passing the images we get filtered images. We carry out the average pooling on these filtered images. We divide the images into grids 4 x 4 size and determine the average of each grid. After this step, we merge all the average values of all grids. Eventually, we will get m x n x 4 x 4 features from the MRI images.

b) Hybrid Feature Extraction method (PCA-NGIST)

PCA-NGIST is a normalized feature extractor [19,20]. It is a compound method to define and reduce the dimensionality of the image. The GIST features are initially normalized using the L2 norm mentioned in previous step and then used with the Principal Component Analysis (PCA) for feature extraction. This method prepares or consolidates the features which were a result of filtering and definition of m x n x 4 x 4 features from the GIST descriptor. The PCA is used to cut-down the dimensionality from large amount of features, which may be correlated, which is produced from GIST method. PCA method will drill down or decrease the number of features so that only the independent features which does not deteriorate the quality of classification step is retained. Using the PCA method, overfitting problem can be solved so that our trained model is not constricted when used with very less number of datasets images. The use of this compound method saves the process from segmentation. The brain MRI image is refrained from the shadowing and illumination effects which would have had a bad effect in recognition or detection of region of interest, which is the brain tumor. The PCA method generates Eigen vectors of the features defined from the NGIST method. Features with the highest Eigen values are considered for the generation of Eigen vectors. $f(x,y)$ for the Gabor filter, computed at m x n scales and orientations respectively is shown in (2),

$$f(x,y) = \left(\frac{1}{2\pi\sigma_x\sigma_y}\right) exp\left|-\frac{1}{2}\left(\frac{x^2}{\sigma_{x^2}} + \frac{x^2}{\sigma_{y^2}}\right) + 2\pi\omega x\right| \quad (2)$$

where ω is radial frequency, j is complex number of value $\sqrt{-1}$, and σ_x, σ_y are complete, non- orthogonal basis of Gabor filter [21].

The Fourier Transformation $F(u,v)$ by using the Gabor filter function $f(x,y)$ is given in (3),

$$F(u,v) = exp\left\{-\frac{1}{2}\left(\frac{(u-w)^2}{\sigma_{u^2}} + \frac{v^2}{\sigma_{v^2}}\right)\right\} \quad (3)$$

where in σ_u, σ_v will be calculated using (4),

$$\sigma_u = \frac{1}{2}\pi\sigma_x \text{ and } \sigma_v = \frac{1}{2}\pi\sigma_y \quad (4)$$

Taking the function $f(x,y)$ as the main function of Gabor wavelet transform, the Gabor filter is derived by setting the parameters such as orientation (θ) and scaling factors (α), given in (5).

$$f_{mn}(x,y) = \delta^{-m}f(x',y') \quad (5)$$

where n, m are the integer values, α > 1, and x' is calculated using (6) and (7),

$$x' = \delta^{-m}(xcos\theta + ysin\theta) \quad (6)$$

$$y' = \delta^{-m}(-xcos\theta + ysin\theta) \quad (7)$$

We know that o is the number of orientations and we calculate the value of θ using the formula, $\theta = \frac{n\pi}{o}$. Further the scale, δ^{-m} in the equations is brought up so that the energy would be more independent. When we apply the four orientations and eight scales of Gabor filter to extract brain features, we eventually get 32 brain images. These images are further divided so that they form a grid size of 4 x 4. After we apply average pooling, we would get an average intensity value of each grid which we further use to compute the GIST features vector (G) and this contains totally 8x4x4x4=512 features [18-20]. To avoid the effects of shadowing and illumination we will perform normalization of the MRI images using the formula in (8),

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$$G_{i \times 512} = \frac{G_{i \times 512}}{\sqrt{\sum_{j=1}^{512} |G_{i \times j}|^2}} \qquad (8)$$

In order to reduce the redundancy from the matrix T, which is a matrix containing a set of GIST brain features (G_i), we apply the PCA method to derive a matrix which consists of the most important and independent vectors of which the Eigen vectors are computed (V_{512*K}). The projected Eigen vectors will form a new set of compact matrix, Y_{N*K} [22] using (9).

$$Y_{N*K} = T_{N*512} \cdot V_{512*K} \qquad (9)$$

The procedure to generate the matrix, V_{512*K} we follow certain steps,

To obtain a scatter matrix given that L is different number of classes in training dataset (T) consisting of N GIST vectors $\{G_{1*512}, G_{2*512}, \ldots G_{N*512}\}$, where in G_{i*512} is a real number; and each of the training vectors belong to any one class which may be in range $j \in \{1,2,\ldots L\}$ we make use of the following calculation shown in Equation (10).

$$S_{N \times 512} = \frac{1}{N} \sum_{i=1}^{N} (G_{i \times 512} - \bar{G}) \cdot (G_{i \times 512} - \bar{G})^T \qquad (10)$$

where the averages of all training data vectors is $\bar{G}$ and to obtain this we use the following equation (11).

$$\bar{G} = \frac{1}{N} \sum_{i=1}^{N} G_{i \times 512} \qquad (11)$$

To filter out and obtain the optimum matrix (EV_{512*K}) we use the following Equation (12),

$$EV_{512 \times K} = \max_{argK \leq 512} |V_{512 \times N}^T \cdot S_{N \times 512} \cdot V_{512 \times N}| \qquad (12)$$

Orthogonal Eigenvectors of the Eigenvalues in matrix (S) is represented as $\{EV_{512*K} \mid k = 1,2,\ldots 512\}$.

C. Classification of Brain Tumor

Classification of brain tumor is the last step in the automated brain tumor classification system. We use a class of Extreme learning machine for this purpose. Regularized Extreme Learning Machine (RELM), is a type of Feed-forward Neural Networks (FNN). The structure of RELM consists of a network of an input layer, a hidden layer and an output layer. Initially we randomly assign the weights and biases of the input layer [23,24]. Within the hidden layer, there may be sigmoid networks, wavelet networks or other transformation functions. There is no need to tune the nodes of hidden layer. RELM uses backpropagation methods to train the network for classification purposes. The features extracted from the previous steps as fed into the classifier model.

Algorithm for Classification of Brain tumor

Input: Datasets that are split into training and testing datasets, Training class labels, parameters of weights and bias.

Output: Testing labels (l_i)

Start

1. Training phase of the network

Step 1: Initialize the weights and Biases of input layer

    1.1   select some weights (wi) and biases (bi) randomly for the nodes of input layer (xi) of RELM network.

Step 2: Computation of matrix

    2.1   Calculation of hidden layer matrix (H) using the following equation(13),

$$H = \begin{bmatrix} g(w_1 \cdot x_1 + b_1) & \cdots & g(w_M \cdot x_1 + b_M) \\ \vdots & \cdots & \vdots \\ g(w_1 \cdot x_N + b_1) & \cdots & g(w_M \cdot x_N + b_M) \end{bmatrix}_{N \times M} \qquad (13)$$

    2.2 The weight and target matrices, β and T respectively are calculated using Equation (14),

$$\beta = \begin{bmatrix} \beta_1^T \\ \vdots \\ \beta_M^T \end{bmatrix}_{M \times N} \quad and \quad T = \begin{bmatrix} T_1^T \\ \vdots \\ T_M^T \end{bmatrix}_{M \times N} \qquad (14)$$

2. Testing phase of automated brain tumor system

Step 1: Computation of matrix.

    1.1. Hidden layer matrix ($\hat{H}$) is computed using Equation (13)

    1.2 Output layer weights are generated using Equation (15).

$$\hat{\beta} = (H^T H + \lambda_I)^{-1} H^T T \qquad (15)$$

    1.3 Computation of the output matrix (Oj) using the Equation (16)

$$O_j = \hat{H}\hat{\beta} \qquad (16)$$

    1.4 Detecting the testing class label (l_i), where j belongs to L, L is the total number of the classes is given by Equation (17).

$$L_j = \genfrac{}{}{0pt}{}{arg}{j \epsilon L}\max (O_j) \qquad (17)$$

Return Test labels (l_j)

End

III. EXPERIMENTAL RESULTS AND DISCUSSIONS

A. Dataset

The dataset provided by Jun Cheng was used for this study[26,27]. the dataset contained 3064 MRI images of the brain tumor. The MRIs were taken at different planes from 233 patients which includes frontal plane, lateral plane and transverse plane. These MRIs were grouped into 3 sets: 1025 sagittal images, 994 axial images and 1045

coronal images. We have considered brain tumor images of three types for the dataset: glioma (708 images), meningioma (1426 images) and pituitary (930 images). Each image is of size 512x512 in pixels. Jun Cheng organized the MRIs of the brain, its labels and the patients' IDs, tumor mask images and coordinates of the tumor border on the of MATLAB format. Fig 4 shows the example of the dataset images.

Method	Parameters
PCA-NGIST	Image Size = $256 \times 256 = 65{,}536$ pixels. Number of Orientations = 8 Number of Scales = 4 Block Size = $4 \times 4 = 16$ pixels. The number of Eigenvectors is: $EV \in \{50, 150, 250, 350\}$.
RELM	The number of Hidden Nodes is: $M_{RELM} \in \{1500, 1005, 1010, \dots, 2000\}$. Size of RELM grid search=21 The regularization parameter is: $(\lambda) = exp(val)$, where $val \in \{-10, -9.8, -9.6, \dots, 9.8, 10\}$ The activation function is a TANH function, $tanh(x) = \left(\frac{2}{1+e^{-2x}} - 1\right)$.

Table 1. Parameter settings

	Meningioma	Glioma	Pituitary
Meningioma	167	20	13
Glioma	28	403	2
Pituitary	5	4	277
Accuracy		92.165%	

(a)

	Meningioma	Glioma	Pituitary
Meningioma	176	17	7
Glioma	26	406	1
Pituitary	3	5	278
Accuracy		93.58%	

(b)

	Meningioma	Glioma	Pituitary
Meningioma	178	16	6
Glioma	26	407	0
Pituitary	4	6	276
Accuracy		93.689%	

(c)

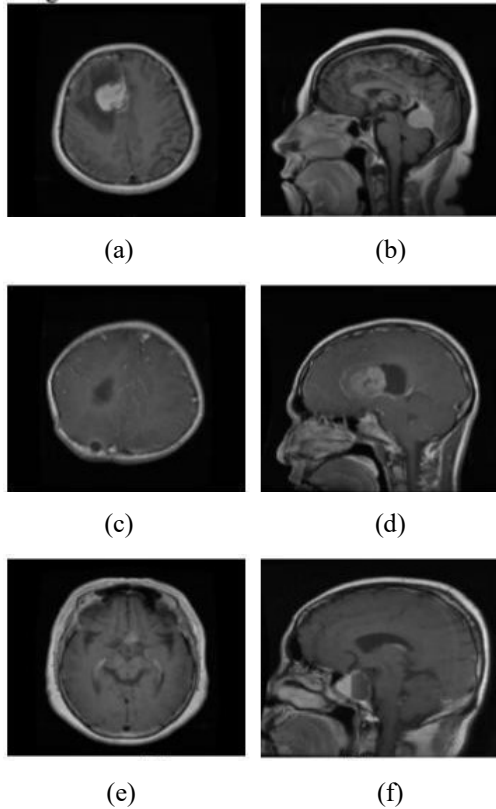|	Meningioma	Glioma	Pituitary
Meningioma	177	16	7
Glioma	20	413	0
Pituitary	6	4	276
Accuracy		94.233%	

(d)

Fig 4. Examples of the brain tumor images from the dataset; (a)-(b) Meningioma brain tumor; (c)-(d) Glioma brain tumor; (e)-(f) Pituitary brain tumor.

B. Parameters Settings

The proposed approach contains some parameters that needs to be initialized. Grid search algorithm was used to select the parameter values and our knowledge in machine learning and image processing fields. The parameter values used in our experiments are shown in Table 1. some of the parameter values are chosen empirically for our approach. For example, different Eigen values and hidden nodes of RELM were used to run the experiments and the number of selected eigen vectors that produces an optimal features and the number of hidden nodes in RELM achieves high accuracy.

Fig 5. Results of confusion matrices; (a) A confusion matrix of PCA-NGIST with RELM (EVS=50), (b) A confusion matrix of PCA- NGIST with RELM (EVS=150), (c) A confusion matrix of PCA-NGIST with RELM(EVS=250), (d) A confusion matrix of PCA-NGIST with RELM (EVS=350)

C. Experimental Results

Based on the 5-fold and holdout techniques a number of experiments were conducted. Dataset was divided in to 2 sets in hold technique: the testing dataset and the training

dataset. The training dataset is almost 70% of the dataset and the remaining 30% is the testing dataset. And in the 5-fold techniques the dataset is divide into 7 sets where 4 sets were used as training dataset and the other 3 sets were used as the testing dataset and this this was repeated for 5 times. For the evaluation, the actual and the tumor classified classes of the confusion matrices were computed during the testing phase. In Fig 4, the hold technique was used for different eigenvectors of PCA to obtain the confusion matrix of the brain tumor classification.

From these confusion matrices, the accuracy results are calculated as:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \qquad (18)$$

Here TP is the true positive value and FP is the false positive values; FN denotes false negative value and TN denotes the true negative values.

Fig 6 describes the accuracy of the classification of brain tumors at different number of eigen vectors and RELMs hidden nodes. The best results are shown when the eigen values are equal to 350. So this is fixed and is used to represent the significant features extracted from the brain images.
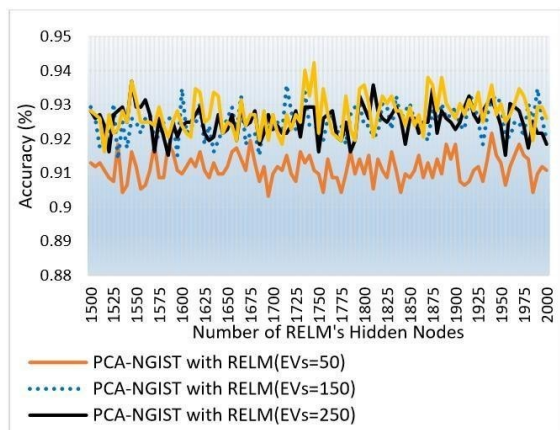

Fig 6. Accuracy of the classification of brain tumors at different number of eigen vectors and RELMs hidden nodes.

In Fig 7, the performance results of PCA- NGIST with RELM classifier is compared with the other state-of-art approaches. We can also notice that the performance of the classification using NGIST descriptor is better when compared to the classification of GIST accuracy.
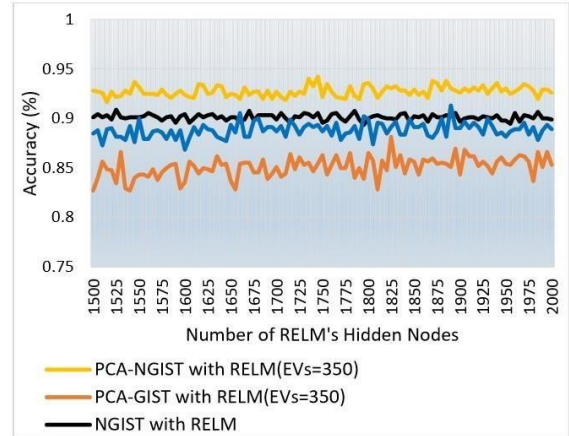

Fig 7. The performance results of PCA- NGIST with RELM classifier

The Fig 8 shows the confusion matrix which is validated using the 5-fold cross technique. The 5 different datasets classification accuracy was ranging from 91.667% to 94.935% which resulted in an average accuracy of 92.6144%. the maximum classification accuracy is shown in Fig 8.

	Meningioma	Glioma	Pituitary
Meningioma	113	15	4
Glioma	5	283	0
Pituitary	3	4	185
Accuracy	94.935%		

Fig 8. Confusion matrix of the dataset.

The proposed approach's accuracy of the classification is compared with the other state of art approaches the accuracies of the approaches are listed and compared in Table 2.

Reference	Approach	Image Size	Accuracy (%)
[13]	CNN	256 x 256	91.43
[13]	RF	256 x 256	90
[14]	CNN	64 x 64	84.19
This Study	SVM-RBF	256 x 256	91.51
	DT	256 x 256	84.33
	NB Naïve	256 x 256	66.92
	Proposed PCA-NGIST with RELM	256 x 256	**94.233**

Table 2. Comparison of brain tumor classification accuracy using the proposed approach against using the state of the arts.

We can notice that the accuracy of the classification using our proposed approach is better than the accuracy of using the state-of-the-arts techniques (e.g., CNN, SVM-RBF, and NB). The reason for this improvement in classification accuracy is due to the ability of extracting the

influential features in decrementing the type of brain tumors using the novel hybrid feature extraction method.

IV. CONCLUSION

This paper introduces a brain tumor classification approach. In the first stage images of brain are transformed into intensity values by applying step called pre-processing. Then features are extracted using hybrid feature extraction method. Finally using regularized extreme learning machine classifier, we classified brain tumor. In the proposed system, we compared a new dataset of brain tumor images and evaluated to get a classification accuracy which contained 3064 brain MRI images. The required features are extracted using PCA-NGIST. Later based on the region of interest tumor sites are identified.

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