CHAPTER 3
DETECTION AND DIAGNOSIS OF MENINGIOMA BRAIN TUMOR USING ANFIS

This chapter briefly discussed with detection and diagnosis of meningioma brain tumor. It proposes an efficient methodology for brain tumor detection using Adaptive Neuro – Fuzzy Inference System (ANFIS). It also shows the experimental results and better performance analysis.

3.1 OVERVIEW

Tumors are formed in brain due to the uncontrolled development of cells. These tumors can be cured if it is timely detected and by proper medication. This research work proposes a computer aided automatic detection and diagnosis of Meningioma brain tumors in brain images using Adaptive Neuro Fuzzy Inference System (ANFIS) classifier. The proposed system consists of feature extraction, classification, and segmentation and diagnosis sections.

In this research work, Grey level Co-occurrence Matrix (GLCM) and Grid features are extracted from the brain image and these features are classified using ANFIS classifier into normal or abnormal. Then, morphological operations are used to segment the abnormal regions in brain image. Based on the location of these abnormal regions in brain tissues, the segmented tumor regions are diagnosed.
3.2 DETECTION AND DIAGNOSIS OF MENINGIOMA BRAIN TUMOR USING ANFIS

This research work proposes a computer aided automatic Meningioma brain tumor detection and diagnosis system using ANFIS classification approach. This method consists of Meningioma tumor segmentation methodology and its diagnosis methodology as its steps. In Meningioma tumor segmentation methodology, features are extracted from brain Magnetic Resonance Imaging (MRI) image and these extracted features are trained and classified using ANFIS classifier. Then, Meningioma tumor region is segmented using morphological operations.

In Meningioma tumor diagnosis methodology, the brain tissues are segmented into Grey matter, white matter and Cerebrospinal fluid (CSF) regions. The severity of the segmented tumor region is diagnosed into Early or advance based on the presence of tumors in brain tissues. The performance of the proposed Meningioma tumor detection and diagnosis system is analyzed in terms of sensitivity, specificity and accuracy. The flow of proposed methodology for brain tumor detection and diagnosis system is shown in Figure 3.1

3.2.1 Preprocessing

It is used to remove the noises in the brain MRI image. In this research work, median filter is applied on the brain MRI image in order to remove the noises if the source image is affected by noises.

3.2.2 Feature Extraction

In this research work, grey level and GLCM features are used to classify the brain MRI image into Meningioma tumor affected image or non-Meningioma tumor affected image. These features are explained in the following sections.
3.2.3 Grid Features

In this research work, the grid features are extracted from the preprocessed brain MRI image. This feature correlates the center pixel of 3*3 sub window with its neighboring pixels. The expressions used for computing grid features from preprocessed image are shown in Equation (3.1)-(3.4).

\[ F_1(x, y) = I_H(x, y) - \min\{I_H(s, t)\} \]  \hspace{1cm} (3.1)

\[ F_2(x, y) = \max\{I_H(s, t)\} - I_H(x, y) \]  \hspace{1cm} (3.2)

\[ F_3(x, y) = I_H(x, y) - \text{mean}\{I_H(s, t)\} \]  \hspace{1cm} (3.3)
F_4(x, y) = \text{std}\{I_H(s, t)}\} \quad (3.4)

where,

- \text{H(s,t)} is the 3*3 sub window and

- \text{I(x,y)} is the preprocessed brain MRI image.

- \text{F}_4(x, y) is the standard deviation of the brain MRI image.

### 3.2.4 GLCM Features

In this research work, GLCM matrix is constructed using the number of repeated pixels in a preprocessed image at different orientations as 0°, 45°, 90° and 135°. From GLCM matrix, the following GLCM features as Contrast, Energy, Homogeneity and Correlation are extracted.

\[
\text{Contrast} = \sum (|i - j|^2 \times p(i, j)) \\
\text{Energy} = \sum p(i, j)^2 \\
\text{Homogeneity} = \frac{\sum p(i, j)}{1 + |i - j|} \\
\text{Correlation} = \sum (i - \mu_i)(j - \mu_j) \frac{p(i, j)}{\sigma_i \sigma_j} \\
\]

where,

- \text{p(i,j)} is the elements in GLCM matrix,
- \text{\mu_i} is mean of GLCM matrix and
- \text{\sigma} is standard deviation.

### 3.2.5 Classification

In this research work, ANFIS classifier is used to classify the brain MRI image into either normal or Meningioma tumor affected image. This ANFIS classifier can be operated in two classes as supervised or unsupervised. The unsupervised ANFIS classifier works without setting of internal weights from the input features and the classification accuracy of unsupervised classifier
is low. In case of supervised classifier, the weights of the internal layer are set by
user which increases the classification accuracy. Hence, this work uses
supervised ANFIS classifier for the classification of brain MRI image into either
Meningioma tumor affected image or non-Meningioma tumor affected image.
Morphological operations as dilation followed by erosion is used to segment the
abnormal tumor region in Meningioma tumor affected image.

3.2.6 Brain Tissue Segmentation

In this research work, Multilevel Linear Clustering Algorithm (MLCA) is used to segment the classified brain MRI image into Grey matter,
White matter and CSF regions. This brain tissue segmentation algorithm is
explained in the following steps.

**Algorithm: MLCA clustering**

**Input:** Classified abnormal brain MRI image
**Output:** Segmented brain tissues

**Step 1:** Initialize the centroid of the cluster regions. In this work, the numbers of
centroid are assumed to be 3 due to the segmentation of three brain tissue
regions.

**Step 2:** Apply linear partitioning technique on cluster regions.

**Step 3:** Allocate histogram of pixels in different cluster regions and assign
individual labels to each cluster regions.

**Step 4:** The cluster regions are grouped based on the intensity variations of the
pixels.
3.3 EXPERIMENTAL RESULTS AND PERFORMANCE ANALYSIS

3.3.1 Datasets

Multimodal Brain Tumor Segmentation Challenge- BRATS 2016 dataset is used in this work to evaluate the performance of the proposed methodology. This dataset contains 120 brain MRI images in which 75 images are normal (does not contain any abnormal tissues) and 45 images are abnormal (contain abnormal tissues). This dataset also contains ground truth images which are obtained from expert radiologist.

3.3.2 Experimental Results

In this research work, Meningioma tumor is segmented and diagnosis using the brain MRI images which are obtained from open access dataset. This proposed methodology is applied on the 120 brain MRI images in which 75 images are normal (does not contain any abnormal tissues) and 45 images are abnormal (contain abnormal tissues). The proposed system classifies 74 images as normal and 44 images as abnormal. Hence, this proposed method achieves 98.66% for the case of normal images and also it achieves 97.77% for the case of abnormal images.

Figure 3.2(a) shows the source brain MRI image, Figure.3.2 (b) shows the ground truth Grey matter, Figure3.2 (c) shows the ground truth White matter and Figure. 3.2(d) shows the ground truth CSF. These ground truth brain tissue segmentation images are obtained from expert radiologist.

Figure3.3 (a) shows the proposed segmentation of Grey matter tissue, Figure3.3 (b) shows the proposed segmentation of White matter tissue and Figure3.3 (c) shows the proposed segmentation of CSF tissue.
Figure 3.2  (a) Source brain MRI image (b) Ground truth Grey matter (c) Ground truth White matter (d) Ground truth CSF

Figure 3.3  Proposed segmentation results (a) Grey matter (b) White matter (c) CSF

The extracted GLCM features for Meningioma tumor affected image and non- Meningioma tumor affected image is shown in Table 3.1
The segmented tumor region and brain tissues are used to diagnose the severity of the brain tumors. In this research work, the tumor is diagnosed into ‘Early’ or ‘Advance’ stage with respect to clinical diagnosis. The presence of segmented tumor in brain tissues is analyzed for determining the tumor stages. ‘Early’ stage is determined if the presence of segmented tumor region is in GM and WM. ‘Advance’ stage is determined if the presence of segmented tumor region is in CSF.

### 3.3.3 Performance Analysis

The following equations are used to analyze the performance of the proposed brain tumor detection and segmentation system.

\[
\text{Sensitivity} = \frac{TP}{TP + FN} \quad (3.9)
\]

\[
\text{Specificity} = \frac{TN}{TN + FP} \quad (3.10)
\]

\[
\text{Accuracy} = \frac{(TP + TN)}{(TP + FP + TN + FN)} \quad (3.11)
\]

where,

TP is True Positive,
FP is False Positive,
TN is True Negative and
FN is False Negative.
The values of these performance evaluation parameters range between 0 and 100. The performance of the proposed system is low if the value is low and the performance of the proposed system is high when the value of these parameters is high.

**Table 3.2 Performance analysis of proposed methodology**

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Experimental Results (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sensitivity</td>
<td>98.86</td>
</tr>
<tr>
<td>Specificity</td>
<td>98.95</td>
</tr>
<tr>
<td>Accuracy</td>
<td>99.01</td>
</tr>
</tbody>
</table>

Table 3.2 shows the performance analysis of proposed Meningioma tumor segmentation methodology. This proposed system achieves 98.86% of sensitivity, 98.95% of specificity and 99.01% of accuracy.

**Table 3.3 Performance comparisons of proposed methodology**

<table>
<thead>
<tr>
<th>Methodology</th>
<th>Performance Evaluation Parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Sensitivity (%)</td>
</tr>
<tr>
<td>Proposed work</td>
<td>98.86</td>
</tr>
<tr>
<td>Nilesh Bhaskarrao</td>
<td>97.72</td>
</tr>
<tr>
<td>Bahadure et al. (2017)</td>
<td></td>
</tr>
<tr>
<td>Alfonse et al. (2016)</td>
<td>96.37</td>
</tr>
</tbody>
</table>

Table 3.3 shows the performance comparisons of the proposed methodology with conventional methodologies with respect to sensitivity, specificity and accuracy.