Proposed Algorithm to Blotch Grey Matter from Tumored and Non Tumored Brain MRI Images

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1. Introduction

The automatic extraction process of tumor from MRI is a challenging task. Many existing approaches are there that perform tumor segmentation1-3. Voxel-based MRI studies have demonstrated that brain areas show changes when it is affected with tumor. Using segmentation and feature selection algorithms grey matter is extracted from brain regions which shows that grey matter can be discriminated from white matter between healthy and unhealthy MRI of brain. Here we developed a novel framework in combination with segmentation methods in Matlab to derive a quantitative pattern matrix from segmented MRI dicom images taken from MRI databases like OSTRIX in the form of row and column. We retrieved a matrix of 217x120 from each subject MRI and we applied the same procedure on seven subjects including healthy and unhealthy both. Using segmentation technique and feature selection algorithms we separated brain regions having grey and white matter in the form of 0’s and 1’s. Grey matter in extracted in the form of one and white matter is extracted in the form of zero. Grey matter is detected among the subjects and multivariable analysis is done statistically using CHAID analysis with the help of XLSTAT tool. It shows that subjects with healthy MRI and unhealthy MRI are separated. We find the difference in healthy patient without tumor and unhealthy one with tumor in MRI dicom images.

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2. Segmentation and Classification

In many medical researches and applications, segmentation and classification of brain tissue in MRI is a difficult task. Furthermore manual segmentation and classification of MR brain images is a tedious and time consuming process. MR brain images find its applications in research, medical investigation, doctoring and curing etc. Due to non-uniformity and unwanted variations, images are corrupted and contained artifacts and it become difficult in complicated brain structure. Thermal vibrations in MRI due to presence of electrons, ions and moving objects may affect analyzing brain images. Automated and Soft-computing techniques eliminate this problem. The proposed method consists of to remove noises from MRIs. Thereafter segmentation and feature extraction is applied to extract white and grey matters Feature extraction comes under supervised classification and it plays a major role in analysis of medical images. Region of interest describe particular image in the numerical features called feature vectors. The extracted grey and white matter in the form of zero and one’s are analyzed using proposed methodology.

2.1 Background Study

Existing research in which some author proposes a new, automatic strong procedure for classifying tissues of brain magnetic resonance head images. It uses pruning strategy and customized training set. Using probability maps, set of samples are generated, samples labeled incorrect are first reduced using brain-based coordinate and minimum spanning. KNN classifier is used on correct samples to classify them. The approach is non parametric when variability in image quality is considered. Distribution in tissue intensity is not taken into consideration. Validation experiments conducted both quantitatively and qualitatively on simulated MRI data of fortythree subjects.

Low level operations classify brain tissue in MRI using weighted (T1). Many operations like filtering by diffusion, detecting edges and performing morphology mathematically are implemented. Histograms of neighborhood are generated using partial volume tissue measurement model to estimate points. For each area and mean tissue intensity and noise variance value are calculated from global image. Voxel based classification is done on intensity-normalized image and using posteriori classifier. Spatial properties of the brain are modeled using partial volume tissue measurement model with a Gibbs prior.

Classification of brain slices on the basis of feature derived using Least Squares Support Vector Machines (LS-SVM). Radial Basis Function (RBF) kernels, linear and nonlinear were compared with all existing classifiers like SVM, Multi Layer Perception (MLP) classifier and KNN classifier. Results shows that LSSVM classifier performed outstanding than all other classifiers tested.

In this work, image and data processing technique combined with probabilistic neural network is proposed. For large amount of data operator-assisted classification methods are no logical to use. Serious inaccuracies in classification are obtained in the form of noise created by operator performance. The combination of neural networks and fuzzy logic in addition with probabilistic neural network are used. Features are extracted is two steps using the principal component analysis and the Probabilistic Neural Network (PNN). The performances are evaluated with probabilistic neural network which give accurate results for classification.

DAUB-4 wavelet method is used to classify tumor and non tumor images. DAUB-4 gives better contrast to an image which improves easily hanging signals of an image and reduces the overhead. Principal components analysis is employed for classifying best features obtained. The features obtained from principal components analysis are given as input to support vector machines. Experimental results show that among linear kernel and radial basis kernel, radial basis kernel gage better accuracy.

A medical image has many layers and views, in order to alleviate the images to recognise diseases the image has to be filtered and denoised. Automatic classification of healthy or unhealthy person is proposed by watershed algorithm with Euclidean distance classifier for fast computation, accompanied with preprocessing and post processing method apply on database having both normal and abnormal samples of brain images in dicomm format. Classification is a stage where objects are categorised into classes between healthy and unhealthy.

3. Proposed Methodology and Material

3.1 Subjects

Subjects with clinically probable having tumor and non tumor were taken from OSTRIX database with alias name BRAINIX. Dicomm MRI of healthy subjects was taken from NITRC (Neuroimaging data repository).
3.2 Methodology

We proposed a novel approach to classify MRI. We have taken seven subjects from BRAINIX and NITRC (Neuroimaging data repository), out of which three were without tumor and four were tumored\(^{16}\). This section explains the proposed procedure and methodology. The proposed method consists of number of phases such as DICOMM transformation, grey conversion, creating filters, cropping segmentation, extracting grey and white matter in the form of 0 and 1’s. Later data is imported in XLSTAT tool and classification of tumored and non tumored data is done and CHAID analysis is applied on it. The complete process is shown in Figure 1. Correlation is used for filtering and extracting grey matters. A correlation filter is a template that correlates with images\(^{17}\). Magnitudes of edges are extracted using correlation filter. We computed Dx & Dy for each pixel in image. Edge magnitude is \(\sqrt{(Dx^2 + Dy^2)}\). The display range is mentioned as an element vector in the form of 0(low) and 1(high)\(^{18}\).

3.2.1 Load MRI Image of Subjects

MRI image in dicomm format is loaded. The data set consists of seven brains MRI in which three images are normal and 4 images are abnormal. The size of each image is 256×256. The dataset of subjects with clinically probable having tumor taken from OSTRIX\(^{15}\). Subjects with healthy (no tumor) are taken from NITRC (Neuroimaging data repository)\(^ {16}\).

3.2.2 Preprocessing

Preprocessing is done at the lowest level of abstraction on images. The goal of preprocessing is that it improves data of image so that unwanted features can be avoided and helps in enhancing some important image features so that further processing can be done. By applying these operations image information cannot be increased\(^ {19,20}\). Redundancy in images is removed by the preprocessing methods\(^ {11}\). Preprocessing in MRI images is also done.

3.2.3 Displaying Gray Scale Image

To display a gray scale image in Matlab imshow function was used. Displaying of images was done by scaling the intensity values which is used into a grayscale color map. If intensity is double then pixel value of 0.0 is exhibited black and if intensity is uint 8 then pixel value 1.0 is exhibited as white, and if the pixel values are in between, then it is exhibited as shades of gray\(^ {22}\).

3.2.4 Creating 2-D Special Filters

Imfilter is used for this. The nearest border pixel is used for replicating the value for determining any pixel value outside the range\(^ {18}\).There are many options like symmetric, circular or replicate. Multidimensional filtering is used with options chosen\(^ {23}\). Function fspecial is used with value of radius five. The grey matter and white matter from the image is extracted in the form of zero and ones. A 3-by-3 filter is created by fspecial for creating unsharp contrast enhancement. Parameter alpha is used to create negative of laplacian filter, and to control the shape of laplacian. Alpha should be in the range zero to 1.0. If we don’t want to set the value for alpha we can give a default value of 0.2\(^ {24}\) and 2D array is created. Laplacian filters is created using fspecial as shown below in equation 1.1 and 1.2.

\[
\nabla^2 = \frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2}
\]

\[
\nabla^2 = 4/((a+1) \cdot (1-a)/4 \cdot (1-a)/4 \cdot a/4)
\]

3.2.5 Image Cropping and Segmentation

Region of interest can be targeted to remove unrelated parts of image. The two-dimensional convolution operation is used to analyze images. On the basis of weighted average of pixel in \(k \times k\) neighborhood of the central pixel a new value is ascribed to a given pixel. Weights supplied in a square matrix are used to represent in convolution...
kernel. Input image elements, represented as $f(x, y)$ is taken with elements $h(\alpha, \beta)$ of the convolution kernel and the output image element $g(x, y)$ are represented by the equation 1.3.

$$g(x, y) = \sum_{\alpha=-\frac{k}{2}}^{\frac{k}{2}} \sum_{\beta=-\frac{k}{2}}^{\frac{k}{2}} f_{\alpha \beta}(x-a, y-b) h(x-a, y-b) \quad (1.3)$$

### 3.2.6 Segmentation

It’s the process of separating an image into many segments. The objective of segmentation is to analyze the image representation which is easy to understand. In the segmentation process representation of the objects in images is very essential that we can separate between the objects of interest and remaining part. The remaining part of group is also referred as the background. Identifying and delineating objects in images are identified using segmentation. Image segmentation may consist of two related processes—Recognition and delineation are two related processes in Image segmentation. Rough idea about object of interest in image is done by recognition and to find out point-to-point composition is done by delineation.

### 3.2.7 Gray Matter and White Matter Extraction

Gray matter and white matter is extracted in the form of zeros’ and ones’ and shown in the form of matrix and saved in excel file for each subject.

### 3.2.8 Counting Number of Zeros and Ones

Gray matter and white matter extracted in the form of 0 and 1’s is written in matrix form and stored in excel file for each subject. Number of zero’s and ones are counted from each row for each patient.

### 3.2.9 Subtraction

Total number of one’s counted is subtracted from total number of zeros counted. Same is repeated for seven subjects.

### 3.2.10 Classification

Classification is done using CHAID analysis in XLSTAT tool. It’s a statistical software used for analysis in excel. It can be downloaded from internet. Classification and regression trees are obtained as shown in Figure 2.

### 4. Proposed Algorithm

**Steps**

1. Start
2. For each subsets $S_i$ (i=1 to n) /
3. Generates matrix $P_i[m][n]$ with values 0 and 1
4. for each row $j=1$ to $m$
5. Count number of zero’s say $P_i=x$
6. Count number of 1’s say $P_i=y$
7. Subtract $z = x - y$
8. a[i][j] = z
9. End of for loop
10. End of outer for loop
11. Apply statistical analysis
12. End

### 5. Statistical Analyses

In the field of medical and clinical practice imaging is a compulsory. Various image processing techniques that process images are available in medical field to analyse medical images statistically is ordinary in modern medical research.

#### 5.1 CHAID Analysis

We have used technique called CHAID. It’s a tree classification method. The CHAID algorithm obtains multi-way frequency tables. It construct trees taking separating variable which identifies it as non terminal node.
and it will obtain prediction and classification on the basis of response variable. It construct non-binary trees, using Chi-square test to find out the best next split at every step; for continuous dependent variable the algorithm actually compute F-tests.

We have taken subjects P1 to P7 and categorize them into group variables H (healthy) and unhealthy (UH)

- P1 H
- P2 H
- P3 H
- P4 UH
- P5 UH
- P6 UH
- P7 UH

Y/Qualitative Variables: P1, P2, P3, P4, P5, P7, P8, P9 (1 Column 7 Rows), X/Quantitative Variables: X1 to X50 (The features extracted after applying methodology) 7 rows 50 columns.

Class variables Y is taken as 1, 2, ..., j. Training samples of n observations on Y are taken which takes values 1, 2, ..., j, and prediction variables p, as X1,..., Xp. The model predicts values of Y from new values of X. Solution simply partition X space into j disjoint sets, A1, A2,..., Aj, such that the value predicted of Y is i if X belongs to Ai , for i = 1, 2,..., j. The methods create sets Ai. Classification tree methods yield rectangular sets Aj by recursively partitioning the data set one X variable at a time.

6. Results and Discussion

We have taken the grey matter and white matters from seven brain MRI in which three images are non-tumored and four images are tumored. The size of each image is 256×256 having dcm format. We have taken grey scale values. We used predefined 2D filters and created 2D arrays. Then cropping and segmentation of images are done. The gray matter and white matter in the form of zero and one are extracted. Number of ones and zeros in row are counted. Total number of ones subtracted by the number of zeroes in columns. Then the data for each patient is imported in XL STAT and CHAID analysis is done on that data and classified as patient effected with tumor or not. Results obtained from Matlab tool after gray and white matters are extracted in the form of zeros and ones. Table 1 is the result for CHAID analysis for seven subjects. Table 2 and Table 3 shows summary statistics.

| HEALTHY SUBJECTS | Results |
|------------------|---------|
| Patient1 Brain_007.dcm |
| ![Image](image1) |
| Patient2 Brain_015.dcm |
| ![Image](image2) |
| Patient 3 Brain_006.dcm |
| ![Image](image3) |

(Continued)
Table 2. CHIAD analysis of healthy (category 1) and unhealthy (category 2) subjects

| Variable | Categories | Frequencies | %  |
|----------|------------|-------------|----|
| Q1       | 1          | 3           | 42.857 |
|          | 2          | 4           | 57.143 |

6.1 Summary Statistics

XLSTAT 2015.1.02 - Classification and regression trees
Y / Qualitative: Workbook = FIRST50.xlsx / Sheet = Sheet2 / Range = Sheet2!$A$2:$A$8 / 7 rows and 1 column
X / Quantitative: Workbook = FIRST50.xlsx / Sheet = Sheet2 / Range = Sheet2!$B$2:$AY$8 / 7 rows and 50 columns
Method: CHAID
Measure: Pearson

Maximum tree depth: 5
Significance level (%): 5
Split threshold (%): 5
Authorize redivision: Bonferroni correction / Merge threshold (%): 5
Minimum parent size: 2 / Minimum son size: 1
Number of intervals: 10

6.2 Tree Structure

Tree structure generated after CHAID analysis on selected variable is shown in Figure 1. Table 4 shows p-value, number of objects for each node, the corresponding % the parent and son nodes. It also shows split variable, value(s) and % of objects that belong to the dominating category of the dependent variable. Table 4 shows tree structure generated after CHAID analysis. Classification tree is shown in Figure 2.
Table 3. Statistical analysis on fifty variables extracted from seven subjects/patients

| Variable | Observations | Obs. with missing data | Obs. without missing data | Minimum | Maximum | Mean   | Std. deviation |
|----------|--------------|------------------------|---------------------------|---------|---------|--------|----------------|
| X1       | 7            | 0                      | 7                         | 152.000 | 177.000 | 167.429| 11.502         |
| X2       | 7            | 0                      | 7                         | 152.000 | 177.000 | 167.429| 11.502         |
| X3       | 7            | 0                      | 7                         | 152.000 | 177.000 | 167.429| 11.502         |
| X4       | 7            | 0                      | 7                         | 152.000 | 177.000 | 166.571| 10.876         |
| X5       | 7            | 0                      | 7                         | 152.000 | 177.000 | 165.429| 10.753         |
| X6       | 7            | 0                      | 7                         | 152.000 | 177.000 | 164.286| 10.858         |
| X7       | 7            | 0                      | 7                         | 143.000 | 177.000 | 162.000| 13.115         |
| X8       | 7            | 0                      | 7                         | 143.000 | 177.000 | 162.000| 13.115         |
| X9       | 7            | 0                      | 7                         | 135.000 | 177.000 | 161.143| 14.668         |
| X10      | 7            | 0                      | 7                         | 137.000 | 177.000 | 160.857| 15.225         |
| X11      | 7            | 0                      | 7                         | 137.000 | 177.000 | 160.571| 14.199         |
| X12      | 7            | 0                      | 7                         | 137.000 | 177.000 | 160.571| 14.199         |
| X13      | 7            | 0                      | 7                         | 137.000 | 177.000 | 160.571| 14.199         |
| X14      | 7            | 0                      | 7                         | 139.000 | 177.000 | 160.857| 13.656         |
| X15      | 7            | 0                      | 7                         | 143.000 | 177.000 | 161.714| 12.854         |
| X16      | 7            | 0                      | 7                         | 149.000 | 177.000 | 162.571| 11.530         |
| X17      | 7            | 0                      | 7                         | 152.000 | 177.000 | 163.143| 10.823         |
| X18      | 7            | 0                      | 7                         | 152.000 | 177.000 | 163.429| 11.088         |
| X19      | 7            | 0                      | 7                         | 151.000 | 177.000 | 163.143| 11.423         |
| X20      | 7            | 0                      | 7                         | 152.000 | 177.000 | 163.429| 11.088         |
| X21      | 7            | 0                      | 7                         | 145.000 | 177.000 | 162.571| 12.947         |
| X22      | 7            | 0                      | 7                         | 145.000 | 177.000 | 162.857| 13.284         |
| X23      | 7            | 0                      | 7                         | 143.000 | 177.000 | 162.000| 13.115         |
| X24      | 7            | 0                      | 7                         | 141.000 | 177.000 | 160.857| 11.530         |
| X25      | 7            | 0                      | 7                         | 143.000 | 177.000 | 159.143| 12.482         |
| X26      | 7            | 0                      | 7                         | 141.000 | 177.000 | 157.714| 13.853         |
| X27      | 7            | 0                      | 7                         | 129.000 | 177.000 | 151.429| 18.787         |
| X28      | 7            | 0                      | 7                         | 108.000 | 177.000 | 148.000| 24.522         |
| X29      | 7            | 0                      | 7                         | 90.000  | 177.000 | 145.429| 30.016         |
| X30      | 7            | 0                      | 7                         | 80.000  | 177.000 | 143.714| 33.145         |
| X31      | 7            | 0                      | 7                         | 68.000  | 177.000 | 142.857| 36.676         |
| X32      | 7            | 0                      | 7                         | 64.000  | 177.000 | 143.429| 37.837         |
| X33      | 7            | 0                      | 7                         | 74.000  | 177.000 | 144.286| 34.553         |
| X34      | 7            | 0                      | 7                         | 76.000  | 177.000 | 143.714| 34.116         |
| X35      | 7            | 0                      | 7                         | 72.000  | 177.000 | 143.143| 35.616         |
| X36      | 7            | 0                      | 7                         | 66.000  | 177.000 | 141.714| 37.929         |
| X37      | 7            | 0                      | 7                         | 64.000  | 177.000 | 140.000| 39.056         |
| X38      | 7            | 0                      | 7                         | 54.000  | 177.000 | 137.714| 41.792         |
| X39      | 7            | 0                      | 7                         | 60.000  | 177.000 | 136.286| 40.496         |

(Continued)
Table 3. Continued

| Variable | Observations | Obs. with missing data | Obs. without missing data | Minimum | Maximum | Mean | Std. deviation |
|----------|--------------|------------------------|---------------------------|---------|---------|------|---------------|
| X40      | 7            | 0                      | 7                         | 64.000  | 177.000 | 137.429 | 39.348        |
| X41      | 7            | 0                      | 7                         | 64.000  | 177.000 | 139.429 | 39.744        |
| X42      | 7            | 0                      | 7                         | 62.000  | 177.000 | 138.857 | 40.618        |
| X43      | 7            | 0                      | 7                         | 66.000  | 177.000 | 140.000 | 39.166        |
| X44      | 7            | 0                      | 7                         | 66.000  | 177.000 | 139.714 | 39.114        |
| X45      | 7            | 0                      | 7                         | 64.000  | 177.000 | 140.857 | 39.198        |
| X46      | 7            | 0                      | 7                         | 64.000  | 177.000 | 140.571 | 38.690        |
| X47      | 7            | 0                      | 7                         | 66.000  | 177.000 | 140.857 | 38.242        |
| X48      | 7            | 0                      | 7                         | 70.000  | 177.000 | 142.000 | 37.041        |
| X49      | 7            | 0                      | 7                         | 74.000  | 177.000 | 142.857 | 35.821        |
| X50      | 7            | 0                      | 7                         | 74.000  | 177.000 | 141.714 | 36.823        |

Table 4. Tree structure

| Node | p-value | Objects | %       | Parent node | Sons | Split variable | Values | Purity   |
|------|---------|---------|---------|-------------|------|----------------|--------|----------|
| 1    | 1.000   | 7       | 100.00% |             |      |                |        |          |
| 2    | 0.000   | 3       | 42.86%  | 1           |      | X27            | [129, 147.5[ | 100.00%  |
| 3    | 0.000   | 4       | 57.14%  | 1           |      | X27            | [147.5, 177[ | 100.00%  |

Table 5. Rules after CHAID analysis

| Node | Pred(Q1) | Frequency | Purity | Rules                                      |
|------|----------|-----------|--------|--------------------------------------------|
| Node1| 2.000    | 4         | 57.14% | If X27 in [129, 147.5[ then Q1 = 1 in 100% of cases |
| Node2| 1.000    | 3         | 100.00%| Q1 = 1 in 100% of cases                   |
| Node3| 2.000    | 4         | 100.00%| If X27 in [147.5, 177[ then Q1 = 2 in 100% of cases |

Table 6. Rules by object

| Observation | Prior | Posterior | Pr(1) | Pr(2) |
|-------------|-------|-----------|-------|-------|
| Obs1        | 1     | 1         | 1.000 | 0.000 |
| Obs2        | 1     | 1         | 1.000 | 0.000 |
| Obs3        | 1     | 1         | 1.000 | 0.000 |
| Obs4        | 2     | 2         | 1.000 |       |
| Obs5        | 2     | 2         | 0.000 | 1.000 |
| Obs6        | 2     | 2         | 0.000 | 1.000 |
| Obs7        | 2     | 2         |       | 1.000 |

Table 7. Confusion matrix after CHAID analysis

| from | to 1 | 2  | Total | % correct |
|------|-----|----|-------|-----------|
| 1    | 3   | 0  | 3     | 100.00%   |
| 2    | 0   | 4  | 4     | 100.00%   |
| Total| 3   | 4  | 7     | 100.00%   |

6.3 Separation Variables

X27 is separation variable. Category 1 is healthy and category 2 is unhealthy. Samples of seven patients are analyzed. Rules generated are shown in Table 5 and Rules by objects are shown in Table 6. Confusion matrix for estimation samples are shown in Table 7. ROC Curve is shown in Figure 3. 3D plot for classifying subject/patients are shown in Figure 4.

7. Conclusion

Brain MRIs having tumor are difficult to classify for doctors and practitioners. The existing systems are complex and difficult to understand. The main goal of the research work is to develop an approach to analyze brain MRI and classifying in to tumored or non tumored. This
Figure 3. ROC Curve.

Figure 4. 3D Plot showing classification of seven patients among healthy and unhealthy.

paper presents a fully-automatic and novel approach to classify brain MR images. It uses segmentation and feature extraction. Grey and white matter is extracted in the form of zero and one. Then CHAID analysis is done to classify the retrieved data and it has shown 100% accuracy on seven subjects.

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