'National Conference on Recent Advances of Computational Intelligence Techniques in Science, Engineering and Technology'
International Journal of Scientific Research in Computer Science, Engineering and Information Technology | ISSN : 2456-3307 (www.ijsrcseit.com)

Implementation of Image Based Classification and Early Screening System for The Classification of Neurodegenerative Diseases

Neha Gopal N*, Dr. Manimozhi I
Department of Computer Science and Engineering, East Point College of Engineering and Technology, Bengaluru, Karnataka, India

ABSTRACT
Neurodegenerative Disease (ND) mainly arises due to the death of nerve cells particularly in the myelin envelops of the neurons which are present in brain, spinal cord, and peripheral nerves. This causes problems in mental functioning or problems associated with movement of the body. There are different types of ND diseases, but the current work is focused on well known, Alzheimer's disease. ND disease covers a wide variety of mental symptoms whose detection is not possible by the visual examination made by the radiologists. This project presents a fully automatic image analysis method that will classify the given dataset as Alzheimer's disease (AD) subjects or as normal subjects. In this work Visual Saliency (VS) model is used to calculate the saliency of images which includes features like intensity and edges. Saliency maps are fused into a solitary map to obtain a master saliency map, and are fed to Support Vector Machine (SVM) that classifies subjects into AD or normal subjects.

Keywords: AD, SVM, VBM, Visual saliency, MRI

I. INTRODUCTION

Neurodegenerative diseases are a debilitating condition where progressive degeneration or death of nerve cells takes place which causes problems in mental functioning, or with movement. It basically affects neurons of human body, neurons are the building blocks of nervous system that includes brain, spinal cord, peripheral nerves. Neurons neither reproduce nor replace themselves so once when they are damaged or die, they cannot be replaced by human body. Neurodegenerative diseases comprise variety of mental symptoms which cannot be evolved by the visual analysis made by radiologists. Worldwide it is estimated that approximately 20-30 million people suffer from neurodegenerative diseases. Many researchers have suggested that neuroimaging may become one of the valuable tools in the early detection and diagnosis of neurodegenerative diseases. Biochemical, clinical, neuropsychological analysis against neuroimaging remains to be demonstrated for large population, but still there exists sufficient evidence of patients suffering with different states of neurodegenerative diseases. The main aim of analysing structural brain MR images is to find anatomical changes, either local or global, that is related to functional disturbances. In particular radiologists examine

images by looking at unique regions and compare them by searching differences [1].In existing method the morphometric brain analysis method consists of a set of strategies which is aimed to extract and quantify anatomical differences between groups of subjects. Voxel-based Morphometry (VBM) [2] and Deformation-based Morphometry (DBM) [3] are the most used techniques to compare populations.

In this work we propose an automatic image analysis method inspired by the radiologist visual perception. The method is built on a visual saliency model and is extended to involve a learning process that imitates the adaption of a radiologist visual perception.

II. METHODS AND MATERIAL

In this project we take the set of normal and abnormal MR images of the patients and compare them. The entire dataset is trained in traning phase; this dataset will Calculate the saliency information from the patients MR images, the selected features include edges, intensity, orientation. Support Vector Machine is one of the most popular technique that is used in this work which will classify individuals with several neurological disorders. By using neuroimaging data [7] (MR brain images) a complete review and comparison of SVM based approaches for classifying neurological and psychiatric diseases can be made. Features like binary tissue [5] segmentation, cortical thickness estimations, intensity [2], textural information [3],[4] is fed to SVM classifier. The computational time, the presence of unwanted, irrelevant and noisy features is reduced by using dimensionality reduction technique.

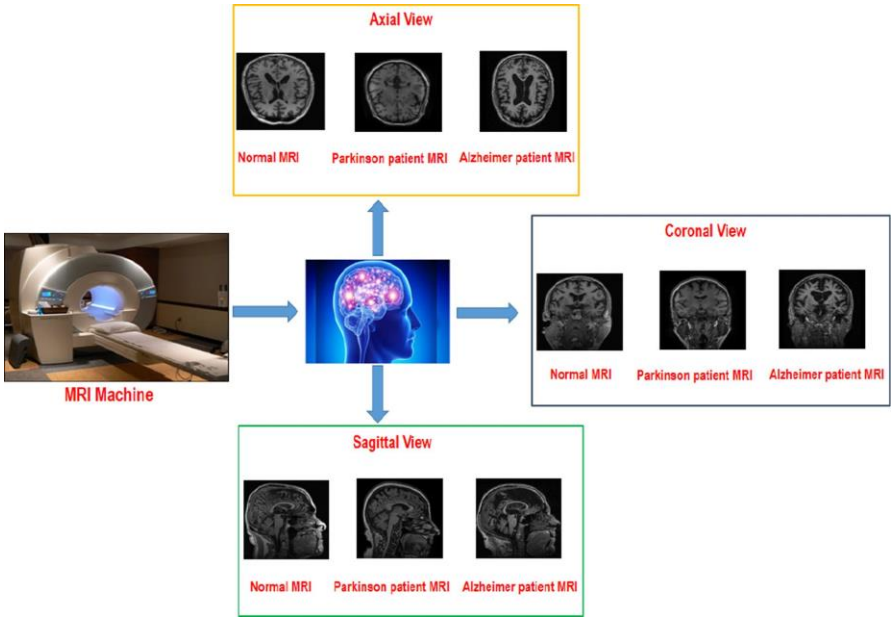

Figure. 1 General Procedure to acquire the MRI sequences from the patients suffering from Alzheimer and Parkinson diseases

The required information for classification is extracted either from specific regions of interest (ROI) [6] or from whole brain volume. Analysis which is performed on known diseases locations leads to more significant and stronger conclusions.

In this work a fusion strategy is used that will together bottom-up and top-down information flows. Bottom up stage includes a multiscale analysis of different image features, top-down flow includes learning and fusion strategies which are formulated as max-margin multiple kernel optimization problem.

The project detailed information is provided in architecture of the proposed system presented in fig.2

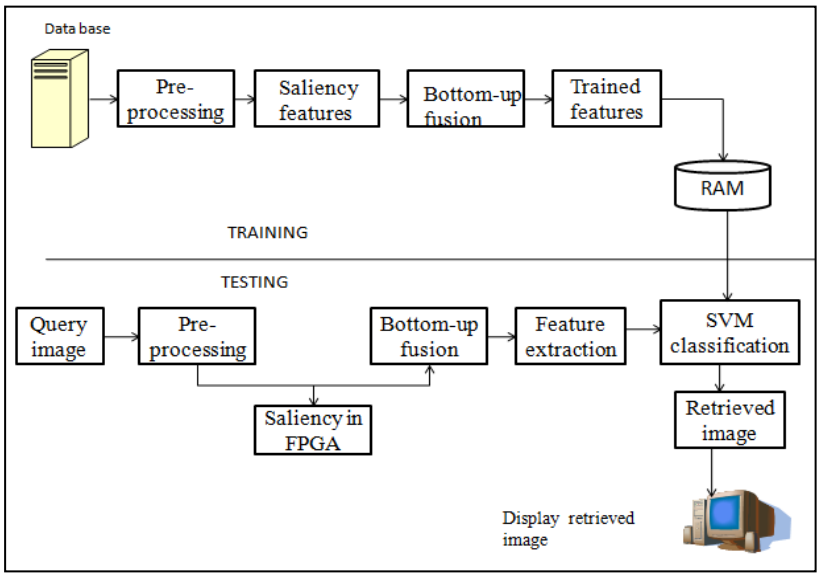

Figure 2: Architecture of the proposed approach.

MIRIAD Database

MIRIAD is a database of volumetric Magnetic Resonance Imaging (MRI) brain scans of AD sufferers. Each participant's numerous scans were collected at intervals ranging from 2 weeks to 2 years. The study was intended to investigate the viability of using MRI, as a result measure for the clinical trials of Alzheimer's treatments.

Features of MIRIAD dataset:

- back-to-back scanning at three time points.
- all scans are taken on the same scanner at the same time
- a scanning agenda is designed to provide wide range of inter-scan interval from two weeks to two years.
- multiple serial scans can be taken for both AD subjects and for normal subjects[14].

The scans are publicly available, to assist researchers in developing new techniques for the analysis of serially acquired MRI.

The images are stored in NIfTI (Neuroimaging Informatics Technology Initiative) format (.nii format). NIfTI is a file format to save volumetric MRI data. It consists of header and image data, saved in *.nii or *.hdr and an *.img file.

- *.hdr finds out whether the images are in int8, unsigned int8, int16, float or char.
- *.img extracts all the pixels in the image.

Image Pre-processing

The images are pre-processed to separate the information in the form of pixel content that represents the brain image and its header represents the data type of each pixel in an image. It filters the noise in the image by using Gaussian filter, and images are converted from RGB to grey. The chances of noise arrival in current MRI scans are less. It may lands due to the thermal impact.

Feature Selection and Extraction

It is a method of choosing a division of related features, for structuring powerful learning models by eliminating unwanted and unnecessary features from the image. This aides to enhance the performance of learning models by:

- Enhancing generalization capability.
- Improving model interpretability
- Speeding up learning process.

Feature Extraction

It is a unique type of dimensionality reduction. When input information to an algorithm is very vast to be computed, and if the data is unwanted (more data, with less information), then the input image will be changed into a compact depiction of set of features (known as features vector).

Obtaining the set of features by changing the input data is called feature extraction. If the features to be extracted are deliberately picked, then the feature set is expected to extract the significant information from input data, to execute the preferred function by means of reduced representation rather than the full size information [15]. In the proposed system the selected features include intensity, orientation and edges.

Visual Saliency

Visual saliency is structured into 3 stages:

- Extraction: feature vectors are extracted over the image plane
- Activation: forms an activation map using the feature vectors
- Combination: combines the map to a single map

Saliency maps with Graph Based Visual Saliency (GBVS)

After section identification on every segment of the brain MRI, the following step is to collect saliency data inside every segment. Computation of saliency maps on MR brain images is done by applying a Visual Saliency method. There are various methods to evaluate salient points and saliency maps in ordinary images. Given a specific organization and patterns of medical images, these techniques cannot be applied directly in medical environment. There are two steps in GBVS: first, form activation maps on definite feature, and second, normalizing. Saliency information depends on the relation between features of images.

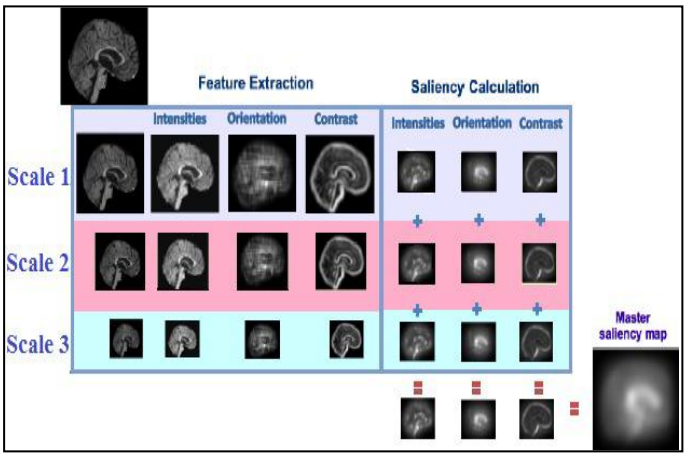

Figure 3: Saliency map Construction

Fig 3 shows the saliency map development, first the input image is deteriorated into three different scales and later features such as contrast, orientation and intensity are gathered from scaled images. The master saliency map is developed by combining all scales and components into a master saliency map.

Forming Activation Maps

Given a feature map M: $[n^2] \rightarrow$ R, calculate an activation map A : $[n^2] \rightarrow$ R, such that, intuitively, locations $(i, j) \in [n^2]$ where, as a proxy, $M(i, j)$ is strange in its vicinity and will relate to greater values of activation A. The graph vertices correspond to the image pixels while the edges stand for the regional dissimilarity between nodes. The edge weight between the nodes (i, j) and (p, q) is calculated as:

$$\omega_1((i,j),(p,q)) \triangleq d((i,j)||(p,q) \cdot F(i-p, j-q) \quad (1)$$

Where $d((i, j)||(p, q))$ encodes the dissimilarity and F $(i - p, j - q)$ represents the spatial closeness between the nodes.

Dissimilarity is calculated with

$$d((i,j)||(p,q) \triangleq \left|\log \frac{M(i,j)}{M(p,q)}\right| \quad (2)$$

The inclusion of the logarithmic metric guarantees that larger feature dissimilarities pop out easily while similar features have little impact on the edge weight. Closeness is measured with:

$$F(a,b) \triangleq exp\left(\frac{-a^2+b^2}{2\sigma^2}\right) \quad (3)$$

σ is a free parameter of GBVS Algorithm. The feature dissimilarity information is modulated by the spatial distance between nodes, thus encoding regional dissimilarity information at the graph edges. The mass of the edge from node (p, q) to node (i, j) is comparative to their variation and to their closeness in the space of M. The edge on the other way has precisely the same weight.

Once activation maps are computed, a normalization step is required to assure that these maps concentrate on activation (saliency).

Normalization

MRI images are standardized to grey values from 0 to 1 and features are extracted from the normalized images.

Bottom-up fusion

Features of all the three image planes are fused together to get single tumour region. The computational Visual Saliency models use different strategies to fuse information from saliency corresponding to different visual features. A common strategy is to weight the maps and then sum them up to calculate an overall saliency map.

$$S^*(x) = \sum_{\sigma,\emptyset} w_{\sigma,\emptyset} S_\sigma^\emptyset(x) \quad (4)$$

The features are stored in feature.doc, further the features are trained and are temporarily stored in RAM.

Local Binary Pattern

LBP is a straightforward and well-organized TO (texture operator). It labels the pixels of image by thresholding the surrounding of every pixel and the final result is considered in binary number. It is a unifying method to the conventionally opposing structural and statistical models of TO.

The basic idea of using the LBP is, 2-D exterior compositions is depicted by two corresponding measures: (i) neighborhood spatial examples and (ii) gray scale contrast. The LBP operator will first threshold the 3 x 3 neighborhood of every pixel with the middle value and then forms the labels for the image pixel. The histogram of these 28 = 256 distinct labels are utilized as a texture descriptor. Pixel neighborhoods are represented by the notation (P, R) where P is the neighbor pixel and R is the radius of the circle. Binary pattern having at most two bitwise transitions from 1 to 0 is said to be uniform LBP else it is known non-uniform. For instance, the patterns 00000000 has 0 transitions and 00011100 has 2 transitions, so they are uniform patterns, whereas, the patterns 00110010 has 4 transitions and 101001010 has 6 transitions and are non-uniform. In the calculation of the LBP labels, uniform patterns are utilized so that there is a different label for every uniform pattern and all the non-uniform patterns are labeled with a particular label. For example, in a (8, R) neighborhood, there are a sum of 256 patterns (58 are uniform, in total yields 59 unique labels).

The LBP feature vector is formed in the subsequent method: The analyzed window is divided the into cells. Every pixel in a cell is compared to eight other neighboring pixels. Track the pixels along a circle. If the middle pixel value is higher than the neighbor value, then it is set to "1". Otherwise "0". This gives an 8-digit binary number. Histogram is computed, over the cell of the occurrence of each number taking place, then the histogram is normalized and concatenated, this gives the feature vector for the window. The estimation of LBP of each pixel (Xc , Yc) is given by

$$LBP_{P,R} = \sum_{P=0}^{P-1} s\left(g_p - g_c\right) 2^p \qquad s(x) = \begin{cases} 1, & if\ x \geq 0; \\ 0, & otherwise \end{cases} \qquad (5)$$

where gc refers to the gray value of the center pixel gp refers to the gray value of number of pixels on a circle of radius R which forms a circular symmetric neighbor set. Each sign $(gp - gc)$ is assigned with a binomial factor $2p$.Fig 3.3 illustrates LBP thresholding. If a neighbor to a center pixel value is equal or high then it is set to 1 else it is set to 0. In anticlockwise manner, every neighbor is multiplied by powers of two and summed as given in equation (5).

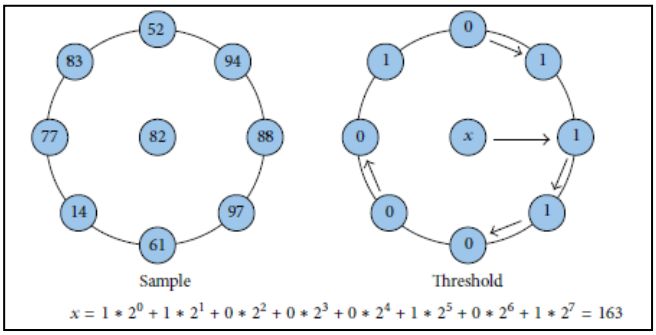

Figure 4: LBP Thresholding.

III. RESULTS AND DISCUSSION

Fig 5a and fig 6a represents the original abnormal MRI image. Fig 5b and fig 6b shows bright region that is obtained using visual saliency technique, the high intensity regions indicates the presence of tumour. In Fig 7 shows red region which indicates the tumour region in Alzheimer's disease and also it gives information about severity of the diseases condition.

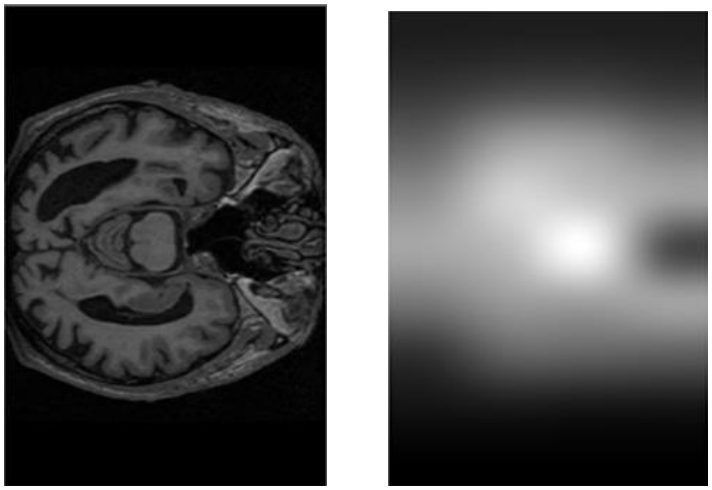

Fig 5a. Original abnormal MRI image Saliency of original image

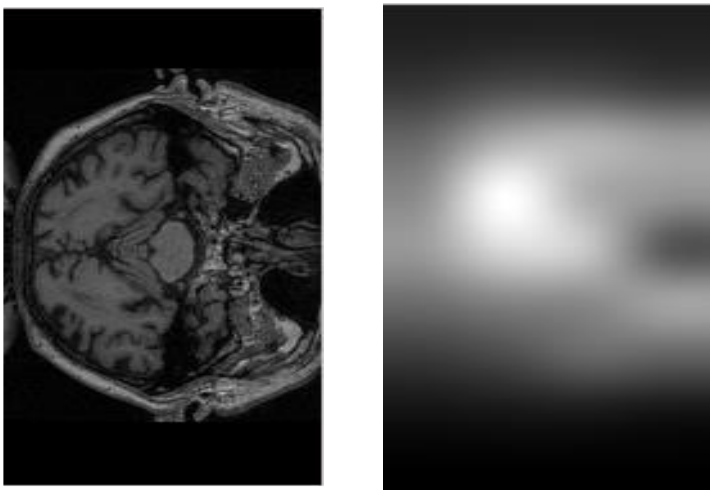

Fig 6a: Original abnormal MRI Image Saliency of original image

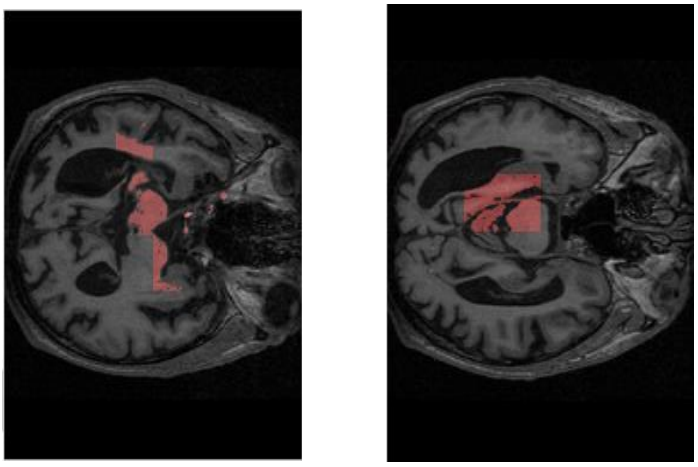

Fig 7 Represents intermediate results of the current work. The bright region obtained from using visual saliency technique in the above fig 8a and fig 8b represents the tumor region in Alzheimer's diseases and also it gives information about the size of the tumor and severity the diseases condition.

IV. CONCLUSION

This work is intended to design an automated classification system for the pathological diagnostic of the disease in its infancy stage. SVM classifier is precise and reliable in diagnosis and outcome prediction in varied clinical setting which will ultimately support Clinicians and Researchers, and patients could be treated for such disease prior to commencement of disease helping millions of people to lead their normal life.

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