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TITLE:

**“AN APPARATUS AND A METHOD FOR VISUALIZATION OF MAGNETIC  
RESONANCE IMAGES”**

APPLICANTS:

**Shashi Bhushan Mehta, (Indian Citizen)**

residing at 3334, 6<sup>th</sup> Cross, 13<sup>th</sup> Main, HAL II Stage, Indira Nagar, Bangalore, 560 038,  
and

**Dr. Santanu Chaudhury, (Indian Citizen)**

residing at Flat No. B8, 164/78, SandHead Housing Co-op Society Ltd, Kolkata 45  
and

**Dr. Amarnath Jena, (Indian Citizen)**

residing at 47, Charakh Sadan, Vikas Puri, Delhi.

The following specification particularly describes the nature of this invention and the manner in which it is to be performed

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# AN APPARATUS AND A METHOD FOR VISUALIZATION OF MAGNETIC RESONANCE IMAGES

## Technical Field

The invention relates to an apparatus for an interactive visualization of Magnetic Resonance Images (MRI) for tissue anatomy. The present invention particularly relates to an apparatus and method for obtaining a cluster-prototype for soft-segmentation and reconstruction for soft-visualization of the boundaries of overlapping of non-homogenous and non-uniform tissue types.

## Background and prior art

Interpretation of 2D MR images of brain is important for surgical planning, treatment strategies and therapy for cases of brain tumor, multiple sclerosis lesions and other diseases like Alzheimer's disease, Dementia, etc. An image visualization tool for diagnostic use can shorten the time required for diagnosis, improve diagnostic accuracy and increase the diagnosis throughput of the doctor. Identifying different types of tissues in the MR image of brain is the most challenging problem for interpretation and diagnosis. Difficulties in the 2D MR image based identification of brain tissues are due to Partial volume averaging: more than one type of tissue can lie within finite spatial extent of an imaging system's point spread function, Tissue non-homogeneity and non-uniformity, which leads to fuzziness at the boundary regardless of the imaging system's quality, Variability in tissue types and Imaging variability.

Commonly prevalent visualization tools exploit gray value distribution in the images. These tools improve visibility of the MR images and enhance the diagnostic value of the MR images through modified histogram equalization and matching technique referred to as window width/ window level based method. Radiologists extensively use window width and window level tools for MR data visualization.

There are various methods for MR data visualization, interpretation and analysis.

US 5812691 discloses a method of 'Identifying fuzzy or blurred objects within a multidimensional scene', the said invention has two methods. The first method consists of **steps of scanning** a scene or a desired object then generating a digital image and **storing in digital** format. Determining strength of connectedness of each pixel with other pixels **in the image** and creating another scene, comprising, pixels having strengths of

connectedness with other pixels above threshold. Then finally displaying said created scene. The second method consists of detecting Multiple Sclerosis (MS) in MRI. The steps involved in the method are creating digital representation of image and storing it. The strength of each pixel element is determined along with clustering pixels having strength above threshold value, into fuzzy connected white matter, gray matter, ventricle and lesion components, which is followed by identification of fuzzy connected lesion component as MS lesion and displaying it.

US 5425368 discloses a 'Method and apparatus for estimating tissue volumes in magnetic resonance images'. The invention consists of the following steps, here the input is an MRI image, the histogram is plotted for above image, and clusters are chosen so as to represent tissues. Selection of centroid from the clusters is performed, where the selected centroid represents each tissue. The distance between each pixel to the centroid is computed then the membership value to each pixel in a cluster is computed. Further a new centroid for each cluster is computed. It is now observed if there is separation between old and new centroid. And if separation exists difference between the old and new centroid is found. The difference is compared with a threshold. If difference is greater than threshold then old is substituted by new centroid. Again the step of computing distance between each pixel to the centroid is performed till there is no difference. Then the image is reconstructed.

US 5058176 discloses 'Image Diagnosis Apparatus'. This method uses WL and WW. There are 2 ways of calculating WW and WL; either it can be done manually or automatically. The steps involved are collection of data corresponding to tissue to be examined. The collected data is converted into 2D image this is the reconstruction process. The Memory for storing 2D-image is used to store the image. The WL and WW values are manually set by the user. After setting the WL and WW values image is generated. Calculation of WL and WW for each image is done by storing calculated value. The other method of calculating WW and WL, choosing a combination of WL and WW values, WL value is by taking value between maximum and minimum value. WW value is calculated by multiplying difference between Maximum and Minimum value by a factor (said factor varies from 0.5-1 or 2 or 1-3)

US 5261050 discloses 'Apparatus for processing a digital image for window width, level and curve shape'. WW and WL processing is done on digital image and result is stored as n-bit digital windowed signal in a memory. Using curve shaped image processing means, said n-bit image transformed into m-bit image (where  $m > n$ ). Both WW and WL processing is done by using a look up table. Curve shaping uses another look-up table.

US Patent 6,584,216 on 'Method for Standardizing the MR Image Intensity Scale' provides a method for standardizing MR image intensity scales by post-processing intensity transformation techniques on routinely acquired images, without requiring specialized acquisition protocols and calibration phantom. The standardizing method offers previously unattainable consistency of intensity meaning of tissues by devising a transformation that is specific to a given MRI protocol and for any body region to provide standardized images. Essentially the histogram of a given volume image is deformed to match a 'standard' histogram for corresponding protocol and body-region. The parameters of the standard histogram are 'learnt' in a training step. This permits standardizing and fixing 'windows' by protocol, body region, and tissue regions, thereby minimizing or eliminating the human interaction required in the per-case manual window adjustments that are otherwise required in visualizing MR images at physician viewing stations.

But none of the above systems use neural network based clustering scheme to determine the possible views. This neuro-fuzzy system helps obtain better view of the tissue anatomy. In addition the prior art does not give a system that identifies different regions and distinct boundaries between them in MR images on the basis of gray level distribution and displayed intensity level. Further the prior art does not indicate how the above system facilitates detailed analysis of the diseased region by distinguishing different components.

The histogram of a digital image is a plot of the gray level values on the x-axis to the number of pixels for each gray level value on the y-axis. In the histogram of the MR image data the gray values vary from 0 to 4095. The histogram plays a key role in most of the image processing operations. The shapes of the histogram of MR images for normal patients are similar and are distinct from diseased cases. The intensity map or

histogram varies from image to image and depends on various factors (like tissue anatomy, pulse sequence, MR physics, image artifacts and many more). The shape of histogram varies due to many reasons like pulse sequence (Spin Echo, Fast Spin Echo, Multi Echo etc.), MR system (0.5T, 1T, 1.5, 3T etc.), MR system imperfection, type of receiving RF coils etc.

In MR brain images, the intensity variation at boundaries in normal cases (between White Matter (WM) or Gray Matter (GM) or Cerebellum Spinal Fluid (CSF) is gradual and not sharp. Similarly in diseased cases, there are intensity variations within the diseased area because pixels can belong to edema, necrosis, tumor and healthy tissues.

Traditional clustering algorithms require a priori knowledge about the number of clusters, nature of the data, clustering criterion etc. This is a serious limitation, since reliable estimate of the number of clusters in the MR image, in particular, for diseased cases, may not be available a priori.

### **Objects of the invention**

The primary object of the present invention is to provide an apparatus for obtaining a cluster-prototype for soft-segmentation and reconstruction to further provide a soft-visualization of the overlapping diseased and healthy tissues of an MR image of a diseased tissue.

An object of the present invention is to provide an apparatus to allow a user to manipulate and view the MR images by providing a clear demarcation of boundaries of various tissues, especially between diseased and healthy tissues.

Another object of the present invention is to provide a method for obtaining a cluster-prototype for soft-segmentation and reconstruction to obtain a soft-visualization of overlapping of healthy and diseased tissues of MR images.

Yet another object of the present invention is to provide a method to provide a clear view of a diseased tissue anatomy when there is no availability of number of clusters in the MR image of the diseased tissue. (p priori information)

Still another object of the present invention is to provide a method for selecting any cluster segment in an image such that only a desired area of the image is highlighted.

### **Summary of the invention**

The present invention relates to an apparatus and a method for interactive visualization of Magnetic Resonance Image (MRI) of a diseased tissue, wherein an input member provided to receive pixelized image data of MRI image as histogram data in the form of cells, a processor is disposed to apply pre-determined weights to the highest cell values to obtain plurality of cluster prototypes and an user interface is provided for selecting two cluster prototypes with intervening cells. The processor determines the distances between the intervening cells and the cluster prototypes and computes membership values based on the distance. User interface provided to select two alpha values between the selected cluster prototypes and thereafter belongingness of cells to corresponding prototype is determined using alpha values. A display unit is provided to display the reconstructed image to user with distinct and overlapping areas between diseased and normal tissues using pseudo shades.

Now the invention will be described with reference to the accompanying drawings, in which

**Fig 1** depicts a schematic representation of the apparatus of the present invention.

**Fig 2(a)** shows a conventional brain MR image of a tumor patient.

**Fig 2(b)** is a conventional histogram depicting a flat region in the diseased area.

**Fig 3** depicts a neural network of the present invention to determine prototypes in a given histogram.

**Fig 4** shows brain images as obtained from the neural network of **(a)** Normal patient **(b)** image at different slice position, **(c)** T2 weighted image of a tumor case.

**Fig 5** is corresponding histograms of brain images as shown in Fig 4 as obtained from the neural network.

**Fig 6** is a graphical representation of selection of prototypes from the histogram of **Fig 5** and a selection of threshold to detect membership values of prototypes.

**Fig 7** illustrates the process of segmentation

**Fig 8** is a graphical representation of triangular Gray level separation membership values showing Alpha Cuts.

**Fig 9** shows exemplified images of reconstructed by the method of the present invention, wherein the area designated as [X] shows segment cluster prototype at 74 and [Z] at 102. The [Y] pixel shows the overlapping regions where the fuzzy membership value is same.

**Fig 10** - The cluster boundaries of prototype. [X] shows segment cluster prototype at 113 and [Z] at 142. The [Y] pixel shows the overlapping regions where the fuzzy membership value is same.

**Fig 11 (a)** is a weighted image of tumor case. The area affected by tumor, edema, and necrosis is labeled; **(b)** is an image of same patient at same slice position after contrast is injected. Here the actual tumor is better delineated by white boundary is shown.

**Fig 12** depicts images of tumor cases **(a)** segmented at 149, and 181 alpha cuts at 9, **(b)** segment 149, and 181 alpha cuts at 88, **(c)** segment 9, and 12 alpha cuts at 86.

### **Detailed description of the invention**

The present invention provides an apparatus for obtaining a cluster-prototype for soft-segmentation and reconstruction to provide a soft-visualization of the tissue anatomy.

In the accompanied diagrams, the segmentation of different tissues are represented in the following shades, viz, mid gray, white and dark gray. For the sake of convenience these shades are referred to as follows; [X] representing the mid gray shade, [Y] representing the white shade and [Z] representing the dark gray shade. These representations are used in all places wherever these shades are referred in the description in conjunction with the corresponding diagrams.

The schematic representation of the apparatus of the present invention is depicted in **Fig 1**. **Fig 1** shows an MRI imaging apparatus which has a magnet section which is configured so that a static magnetic field coil (1) and a gradient magnetic field coil (2) (made up of coils for the individual x-, y-, and z- axes) are disposed in place. The static magnetic field coil (1) is energized by a static magnetic field coil driving section (3) with the gradient magnetic field coil (2) by a gradient magnetic field so that in the inside space of the magnet there are created a static magnetic field being uniform in the z-axis direction and gradient magnetic fields oriented in the same direction as that of the static magnetic field but each having a linear gradient in each direction of the x, y and z axis. An exciting coil (5) and a detecting coil (6) are disposed in the magnetic field of the

magnet section while keeping a rotational angle of 90° therebetween about the z-axis, the former coil being excited by an exciting coil driving section (7) to apply high-frequency electromagnetic wave pulses to a subject (not shown) placed in the inside space of the magnet with the later coil detecting an MRI signal coming from a desired spot of the subject and applying it to an analog to digital converting section (8). This analog to digital converting section (8) converts the detection signal into a digital signal and applies it to a processor (10), which is a micro-processor generally used for image oriented applications. The processor (10) controls the static magnetic field coil driving section (3), gradient magnetic field coil driving section (4), exciting coil driving section (7) and A/D converting section (8) to collect the MRI signal of the subject, and stores the obtained MRI signal in the memory (9). The memory (9) may comprise magnetic storage media and volatile or non-volatile semiconductor memory. The storage media may be magnetic media including tape, disc or drum, semiconductor media such as semiconductor read only memory, optoelectronic media such as a CD ROM, mechanical storage media such as punch cards, or any other information storage media which is capable of storing a program of instructions that may be executed to perform the methods of the present invention.

The processor (10) is used for converting digitized pixels obtained from the Analog to Digital Converter (8) into histogram data and storing the same in the memory (9). The processor (10) further processes the histogram data to generate cluster prototypes by passing pixel values into an input layer, comparing neighbouring pixel values and selecting the highest pixel values in a neighbourhood, increasing the highest pixel value by suppressing the neighbouring pixel values and adding weights to the highest pixel value and storing the highest pixel values as cluster-prototypes. An user interface (11) for interfacing with a user with the help of input device (12) (a typical key board, a mouse or any compatible input devices) to select desired cluster prototypes and a threshold value. Working through the user interface (11) the user can observe data transmitted to the display (13) like a SVGA monitor.

The processor (10) assigns fuzzy values based on distance (besides this other attributes can be implemented) from prototype then select any two prototypes to display different interpretation of MR Image by applying different alpha cuts on fuzzy

membership values. The processor (10) also processes the segmented cells to display the reconstructed images of tissues of the selected section by differentiating normal, diseased and overlapping tissues utilizing pseudo shades. The output thus generated is given to the display unit (13) and also to the memory (9) for storage.

The present invention provides a method for obtaining a cluster-prototype from MR image for soft-segmentation using connectionist (dynamic prototype selection network) based approach and reconstruction to provide a soft-visualization of the tissue anatomy.

The histograms for normal images have usually varying peaks and crests. The conventional histogram of a tumor case is shown in Fig 2. Diseased areas (16) (Tumor, edema, Necrosis, or healthy pixels) of the histogram is flat over the diseased area with no distinct peak. Therefore, identification of different regions and distinct boundary between them in MR images, on the basis of gray level distribution and the displayed intensity level is extremely difficult in diseased cases.

Histograms generated conventionally are plots of gray scale value to the number of pixels, each plot on the histogram is called a cell. These histograms are used for cluster-prototyping, wherein the cells of the histogram are grouped on the basis of perceived similarities in the gray scale values. These clustered cells provide natural partitions of the pixels corresponding to different regions in the selected image.

Now by Referring to Fig 3, a connectionist network (dynamic prototype selection network) is adopted, wherein said network which is used to generate cluster-prototypes is called prototype selection network. The network iteratively smoothens the histogram by progressively increasing neighbourhoods around each cell. The input from the histogram is in the form of cell value (19 or  $H_j$ ). The prototype selection network has two layers of neurons, one visible (17) and the other hidden (18). Each cell in the histogram is represented by these two neurons. The visible layer (17) which has one neuron corresponding to each cell of the histogram receives the frequency count (number of pixels) of the corresponding histogram of MR images.

In every iteration of each cell of the histogram, selected on the gray scale for the image, each neuron collects activations in the form of pre-determined weights (21), (22), (23) and (24) having corresponding pre-determined values  $w_d= 0.0282$ ,  $w_a= 0.99$ ,  $w_{da}= -$

0.81938 and  $w_{aa} = 0.000255$  from its neighbors, the point of the highest activation value will shift toward previously stored higher value cell. By referring to **Fig 3**, the weights  $w_a$ ,  $w_d$ ,  $w_{da}$  and  $w_{aa}$  etc., are predetermined on experimental basis and hold true for all MRI images. These weights are used to strengthen a possible prototype so that cell becomes a prototype and these also inhibit the remaining cells so as to establish the supremacy of one particular cell so that all other neighbouring ones are suppressed. Thus we get one prototype. This is repeated till a number of prototypes are generated at intervals.

When a cell gains sufficient activations from its neighbours, the point of highest activation is accepted as a prototype in the form of an output (20). The value of each cell is passed into the input terminals of a network one by one. A comparator compares the values of the neighbouring cells and outputs the value that is higher. This higher value is stored in an accumulator, and this accumulator content is compared with the value of the subsequent cell and the accumulator is overwritten with the higher value. After a series of comparisons the accumulator contains the value that is highest among the cluster of cells, this value is further strengthened and all the neighbouring cells are weakened. Consequently, the asymmetry of the frequency distribution with respect to the peak is reflected in the prototype selected. At any time, the activation of the neurons in the visible layer (17) represents the chances of the corresponding cell being a prototype. Therefore, a necessity is felt to suppress the neighbouring cells having values less than the highest cell value.

Hidden layer (18) triggers an inhibitory process in the neighbourhood of the prototype. Then the strengthened value of the highest value cell is given a high activation "1" and all other neighbouring cells are given a low activation "0". Thus the high activation cell stands out and is now called the prototype.

Similarly, all other clusters are treated and their corresponding prototype is derived. Thus the histogram after applying clustering methods is made up of the normal histogram embedded with a series of prototypes at regular intervals from each other. This inhibitory process also spreads over increasing neighbourhoods over a period of time.

### **Processing of MR Image data from the corresponding histograms**

The visible layer (17) receives external inputs (19) and presents outputs (20) to the environment. The visible layer (17) and hidden layer (18) are also referred to as the accumulation layer and decision layer respectively. Let the  $i^{\text{th}}$  point in the histogram have a value  $H_i$ . Let  $A_i$  and  $D_i$  denote the neurons corresponding to the  $i^{\text{th}}$  point in the accumulator layer and decision layer respectively. Denote the activation of  $A_i$  by  $\alpha_i$  and that of  $D_i$  by  $\beta_i$ . The accumulator layer neuron,  $A_i$  receives as external input the scaled histogram value,  $H_i$ . In order to collect support from a neighbourhood ( $N^A_i$ ),  $A_i$  should receive inputs from nearby accumulator neurons. Further, the purpose of evidence accumulation is to gather evidence in favour of a stronger peak from its neighbourhood. So a self excitatory connection is given to  $A_i$  with a weight  $w_a$  (22) larger than the weight  $w_{aa}$  (24) assigned to lateral interconnection between two accumulator neurons. The weight  $W(A_i, A_k)$  between  $A_i$  and  $A_j$  may be specified by **Equation 1** with  $w_a > w_{aa} > 0$ .

#### Accumulator Layer weights

$$W(A_i, A_j) = \begin{cases} w_{aa} & \text{if } |i - j| = 1 \\ w_a & \text{if } i = j \\ 0 & \text{otherwise} \end{cases} \quad \longrightarrow \quad (1)$$

Since the activation of  $\alpha_i$ , of  $A_i$  is expected to provide a measure of this accumulated strength a linear function  $f_a$  saturating at +1 and -1 is employed as the activation function of accumulator neurons (**Equation 2**).

$$f_a(x) = \begin{cases} 1 & \text{if } x > 1 \\ -1 & \text{if } x < -1 \\ x & \text{otherwise} \end{cases} \quad \longrightarrow \quad (2)$$

The accumulator layer smoothes the histogram values iteratively and accumulates contextual information. The role of decision layer function  $f_d(x)$  is to accept as winner those accumulator layer neurons with high activation and to initiate a competition in the neighbourhood of the winners, whose inhibitory effect will be iteratively propagated through the network. The decision layer consists of the same number of neurons as

accumulator layer and has no lateral connections. Each neuron  $D_i$  receives as input, the output of a corresponding accumulator neuron. The decision layer is constructed so that it accepts as peak an accumulator neuron having activation more than the specified  $\phi$ . A high gain sigmoid function  $f_d$  with a threshold  $\phi$  is used as the activation function of the decision layer neuron  $D_i$  which will have a near one output when  $\alpha_i > \phi$  and near zero when  $\alpha_i < \phi$  with the transition occurring around  $\alpha_i = \phi$ . Once a neuron is identified as a winner, it has to be strengthened whereas other neurons in its neighbourhood have to be inhibited. Since the prototypes are not expected to be too close to each other, we may inhibit neurons in the larger (than that of the accumulator layer) neighbourhood of a winner. The neighbourhood of a winner  $N_i^D$  over which  $D_i$  exerts its inhibition is defined as

$$N_i^D = \{j \mid j \neq i \text{ and } |j - i| \leq r\} \text{ where } r > 1.$$

In the connectionist network for prototype detection we have used  $N^A = 20$  for the accumulator layer,  $N^D = 10$  for decision layer neurons and threshold  $\phi = 0.9$ .

For strengthening a winner and inhibiting other neurons near it, connections are established from the decision layer to the accumulator layer according to **(Equation 3)** with  $w_{da} < 0$  and  $w_d > 0$ .

$$w(D_i, A_j) = \begin{cases} w_{da} & \text{if } j \in N_i^D \\ w_d & \text{if } i = j \\ 0 & \text{Otherwise} \end{cases} \longrightarrow (3)$$

The above network is updated in a synchronous fashion. That is, in each time step all the outputs of all neurons are computed using the values generated in the previous time step. Thus each iteration consists of updating all the accumulator and decision layer neurons. Let  $\alpha_i'$  and  $\beta_i'$  denote the activation of  $A_i$  and  $D_i$  at time  $t$  respectively. The network updating equations may be written as **(Equation 4)** given below,

$$\begin{aligned}
\beta_i^0 &= \alpha_i^0 = 0 \quad \forall_i \\
\alpha_i^t &= f_d(w_a \alpha_i^{t-1} + w_{aa}(\alpha_{i-1}^{t-1} + \alpha_{i+1}^{t-1})) + H_i + w_d \beta_i^{t-1} + \sum_{j \in N_i^D} w_{da} \beta_j^{t-1} \\
\beta_i^t &= f_d(\alpha_i^t - \phi)
\end{aligned} \tag{4}$$

$$f_d(x) = \frac{1}{1 + \exp(-40x)}$$

The number of prototypes depends upon the parameters of the network; threshold value  $\Phi$ , neighborhood of accumulator  $N^A$  and neighborhood of decisions layer neuron  $N^D$ , (The number of neurons inhibited around winner) and their selection depends upon the nature of the problem and the data. By increasing  $N^D$  the number of prototypes will decrease. The network weights  $w_a$ ,  $w_{aa}$ ,  $w_d$  and  $w_{da}$ , which depend upon  $N^A$  and  $\Phi$ , are calculated using the **(Equation 5)** given below.

$$\begin{aligned}
(|N^A| - 1)w_{aa} + w_a &< 1 \\
|N^A| w_{aa} + w_a &\leq 1 \\
w_d f_d(0) &= \Phi + w_{aa} |N^A| - w_a \Phi \\
w_{da} f_d(0) &= \Phi - w_{aa} |N^A| \Phi - h - w_d f_d(0)
\end{aligned} \tag{5}$$

$N^A$  Number of neighborhood neuron for accumulator

These values have been selected after carrying out a number of careful trials for the purpose of obtaining desirable results. Other parameters used are,  $w_a = 0.99$ ,  $w_{aa} = 0.000255$ ,  $w_d = 0.0282$ ,  $w_{da} = -0.81938$ .

The network architecture indicates that direct links are present between neurons lying within the neighbourhood only. These links give rise to direct interaction and those neurons falling outside the neighbourhood of a given neuron interact with it through other neurons. This indirect interaction is delayed in time. Through this interaction the frequency distribution in the histogram is smoothed using a window, which varies with the number of iterations. A threshold, which effectively decreases with the number of iterations, is maintained and whenever the smoothed value exceeds

this threshold this neuron is accepted as a winner. The accumulator layer neurons saturate only if it is a prototype (+1.0) or if it is strongly inhibited by the presence of other prototype (-1.0). It participates in the competition to become a prototype only when its activation is in the linear range of the activation function  $f(x)$ . Once a winner is detected, it exerts inhibitory influence on the neurons in the neighbourhood. This inhibition will take a number of iterations to reach neurons outside this neighbourhood. Till this inhibitory influence reaches a neuron, it performs smoothing operation as earlier and competes to become a likely prototype. Consequently, multiple prototypes can be detected in large almost uniformly distributed distributions.

Now by referring to **Fig 4**, an illustrative embodiment, wherein the MR images of T2 weighted images of a normal patient are depicted in **Fig 4 (a)** and **4 (b)**, which are T2 weighted MR images taken at different slice positions of the patient and **Fig. 4 (c)** shows a tumor case. T1 and T2 weighted images represent the two different spectral channel of the same MR image.

The above images are converted into histograms and the inputs are supplied to the connectionist-based network taking into consideration not only the peaks but also the nature of data distribution.

On application of connectionist network method as described above to said inputs of the histograms to obtain prototypes as shown in **Fig. 5(a)** and **5(b)** at gray scale values 74, 91, 102, 113, 125, 142 and 81, 92, 108, 119, 132, 143, 154, 169 respectively.

In the first image of **Fig. 5**, six cluster prototypes are identified whereas in the second slice of **Fig. 4** eight cluster prototypes are identified, since there is a change in the shape of the histogram. The second histogram has an extended plateau in the mid-range. That is why there are more cluster prototypes. The results clearly show that the activation of the neuron crossing threshold is based not only on the peaks but also on the frequency distribution in the neighbourhood. The results change adaptively with the change in the data set. Similarly, the **Fig 4 (c)** shows a T2 weighted image of a tumor patient. The number of cluster prototypes in this case as shown in **Fig. 5 (c)** is found to be fifteen at the locations 53, 64, 75, 86, 97, 110, 126, 143, 154, 166, 182, 193, 204, 217, 231. The disease-affected area around the tumor, although heterogeneous in nature

consisting of edema, necrosis, edema-tumor and normal tissue etc, has given rise to extended flat region in the histogram. However, the connectionist prototype-finding scheme has detected multiple prototypes in that region because of its unique dynamics. These prototypes can facilitate detailed analysis of the diseased region by distinguishing different components.

**Segmentation method:** The prototypes found by the connectionist scheme define partitions of pixels in the image. In order to enable construction of soft partitions so that alternative possibilities and inherent variability in the pixel values can be taken care of, a segmentation method is defined for the partitions.

Each intensity value is associated with multiple fuzzy memberships (GLS) using its distance from each prototype along the histogram as given by the **Equation 6**. If an intensity value is a prototype its membership in the partition will be obviously 1. As an example, consider the histogram of an MR image; the connectionist scheme finds six prototypes  $P_1, P_2, P_3, P_4, P_5, P_6$  spread over the intensity range (**Fig 6**). In this case each intensity value has six membership values  $(M_{1,j}, M_{2,j}, M_{3,j}, M_{4,j}, M_{5,j}, M_{6,j})$  depending upon its distance  $(d_{1,j}, d_{2,j}, d_{3,j}, d_{4,j}, d_{5,j}, d_{6,j})$  from different prototypes. The intensity values near to  $P_1$  prototype have a high membership in the partition defined by  $P_1$  as compared to its membership value and belongingness to the partitions defined by the other prototypes  $P_2, P_3, P_4, P_5, P_6$ . Using these membership functions a fuzzy segmentation of the MR image can be obtained.

$$\begin{array}{ll}
 M_{i,j} = 0 & I_{\max} < A < I_{\min} \\
 M_{i,j} = 1 - \frac{P_i - A}{P_i - I_{\min}} & 0 < A < P_i \\
 M_{i,j} = 1 - \frac{A - P_i}{I_{\max} - P_i} & P_i < A < I_{\max} \\
 M_{i,j} = 1 & A = P_i
 \end{array} \quad \Bigg| \quad \longrightarrow \quad (6)$$

where

$P_i$  Intensity value of prototypes

$M_{i,j}$  membership value  $1 \leq i \leq r$

$$1 \leq j \leq I_{\max}$$

$r$  is number of prototypes

$A$  intensity values

$I_{\max}$  Maximum Intensity

$I_{\min}$  Minimum Intensity

Each intensity value is associated with multiple membership values, which indicates its belongingness to different partitions in the image. For example, the histogram **Fig. 5(a)** of T2 weighted image (**Fig 4a**) has six prototypes at 74, 91, 102, 113, 125, and 142. The multiple membership value at the point A and B on the histogram is given in **Table 1**. It is calculated using the triangular function (**Equation 6**). As the intensity value on the histogram moves away from the prototype, the membership value decreases. A pixel can be considered to be part of more than one image partition with different degrees of belongingness as given by the membership values

Intensity value	Membership value $M_{80,1}$	Membership value $M_{80,2}$	Membership value $M_{80,3}$	Membership value $M_{80,4}$	Membership value $M_{80,5}$	Membership value $M_{80,6}$
80	0.9659	0.8854	0.7843	0.6765	0.64	0.5634
30	0.405	0.329	0.294	0.265	0.24	0.211

Table 1: Shows membership value at intensity value 80 and 30 with respect to different prototypes.

Applying different alpha cuts to the individual fuzzy sets, which are defined with respect to the prototypes; the possible segmentations of the image can be obtained. An alpha cut can be defined as crisp set  $A_\alpha$ , which contains all the elements of  $A$  with membership  $\geq \alpha$  (**Equation 7**).

$$A_\alpha = \{x \in X \mid \mu_{\tilde{A}}(x) \geq \alpha\} \quad \rightarrow (7)$$

A level fuzzy set has membership values greater than  $\alpha$  where  $\alpha$  is between 0 and 1. The segmentation method is depicted in **Fig 7**. The figure embodies two sections of an

image represented as Section 1 (25) and Section 2 (26). The Overlapping region membership value (27) is equal for both the segments and is shown.

The embodiment of segmentation is further explained as follows: Two prototypes of the selected image area of the histogram are chosen between which the image has to be studied. In the selected image area there can be three types of boundary areas viz., one is normal tissue area, second is diseased tissue area and third areas which could be of either a diseased or normal tissues. Different interpretations of the MR images can be generated interactively by changing alpha values within two regions normal and diseased tissue anatomy for the analyses of boundary pixels.

$$\begin{array}{l}
 \alpha_1 > n \quad \longrightarrow \quad (8) \\
 \alpha_2 < n \\
 \alpha_1 < n \quad \longrightarrow \quad (9) \\
 \alpha_2 > n \\
 \alpha_1 < n \quad \longrightarrow \quad (10) \\
 \alpha_2 < n
 \end{array}
 \quad \Bigg| \quad 1 > n > 0$$

**Alpha** cut  $n$  and membership of intensity value  $h_i$  varies from 0 to 1 (**Fig 8**). The membership of histogram intensity value (which represents the pixel intensity values) is 1 at prototype and decreases on either side of histogram. To get different interpretations of MR image the value of alpha is varied interactively from 1 towards 0. Based on the three equations (8, 9, 10) the belongingness of each pixel to prototype cluster is calculated. For the pixel if equation 8 is satisfied then pixel belongs to cluster prototype 1, if equation 9 is satisfied then pixel belongs to cluster prototype 2 and if equation 10 is satisfied then it is a boundary pixel. The pixels belonging to cluster prototype 1 are mapped [Z] pseudo shade, similarly the pixels belonging to cluster prototype 2 are mapped [X] shade. The boundary pixels satisfying equation 10 are mapped [Y].

In the accompanied diagrams the different tissues are represented in the following segments, viz, mid gray, white and dark gray. For the sake of convenience these segments are referred to as follows; [X] representing the mid gray segments, [Y] representing the white segments and [Z] representing the dark gray segments. These representations are

used in all places wherever these segments are referred in the description in conjunction with the corresponding diagrams.

**Reconstruction phase:**  $A_\alpha$  contains image pixels with a membership value higher than  $\alpha$ . By interactively choosing  $\alpha$  values (**Fig 8**), and prototypes many membership maps can be viewed for comparison. The visualization scheme implemented provides an option to the user to select any two prototypes. With the choice of prototypes user can interactively select different  $\alpha$  values for generation of virtual segments. These segments are reconstructed into images and displayed using pseudo shade. Pixels belonging to individual partitions with membership values greater than  $\alpha$  are displayed in two different shades with pixels belonging to both the partitions displayed using a third shade. Other pixels are suppressed for providing uncluttered view to the users. This scheme enables a radiologist to obtain a better interpretation of the image in terms of different tissue types.

Now referring to **Fig 4 (a) to (c)** again wherein different interpretations of a T2 weighted MR image of a normal case is depicted. This axial image shows three different tissue types: the white matter (WM), the gray matter (GM) and the cerebro spinal fluid (CSF). Here it is found that the cluster prototypes in the 1D histogram are located at 74, 91, 102, 113, 125, 142 intensity values as shown in **Fig 5**. Cluster prototypes at intensity value 74 and 102 are selected to analyze the boundaries using different segmentation (alpha cuts 0.95, 0.9, and 0.85) as shown in **Fig 9 (a) to (c)**. These two clusters belong to WM and GM respectively.

**Fig 10 (a) to (c)** belong to a set of images showing segments belonging to cluster prototypes 113 and 142, the main segments are in [Z] and [X] and the overlapping pixels which varies with different alpha (0.95, 0.9, and 0.88) values are shown in [Y]. **Fig. 9** shows different interpretations of the same T2 weighted image using window width and window level method.

The image generated by the soft visualization scheme clearly shows overlapping boundary pixels for correct delineation. **Fig. 11** shows two MR images of tumor patient; **Fig. 11 (a)** shows T2 weighted image without injecting intravenous contrast and **Fig. 11**

(b) shows T1 weighted image after injecting the contrast. The tumor area is shown as (28) and the Edema area consisting of: Tumor, Edema and Healthy tissue (edema) is shown as (29). The contrast helps to mark the tumor boundaries as shown in the image of Fig. 11 (b). But there are still chances of having tumor tissues surrounding the tumor area and infiltrating into the edema area (Not visible here). The edema area possibly has tumor (tumor-edema) and healthy tissues consisting only edema or their combination. The visualization method is applied to find possible cluster boundaries between tumor and edema. First, the cluster prototypes are marked (at 63, 76, 84, 97, 110, 122, 133, 149, 161, 181, and 191) on the histogram with the help of connectionist based approach. The prototypes 133, 149, 161, 181, 191 are located in the tumor area (which possibly pertain to tumor-edema, edema, healthy tissue region). Next, the cluster prototypes at 149 and 161 (belongs to edema and tumor region) are selected to see pixels behavior belonging to these segments and the boundary of tumor-edema area, in the edema region. The tumor boundaries are marked on the T2 weighted images based on the tumor boundaries defined in the post contrast T1 weighted images.

Three views (at alpha values 0.9, 0.88, 0.86) with selective two segments (at 149, 181) belonging to tumor edema region is shown in Fig 12 (a), (b), (c). The segments are shown in [X] and [Z] pixels belonging to prototype at 149, 181. Since the tumor infiltrates in to the edema region also, which is visible in [X] shade pixel (near the tumor area), surrounding the tumor region only. The [Y] pixels show the boundary regions. The visualization scheme helps here to see tumor-edema area in the edema region, which is confirmed by radiologist.

One of the other features of this scheme is that, any cluster segments can be selected interactively to segment the diseased area on the MR image. Here segments 76 and 110 are selected, since the said selection does not select the tumor area, the tumor area is show marked with black. The three images at different alpha values in Fig 12 shows boundary behavior of the two segments (at 76, 110) and the tumor region

In tumor cases Radiation Therapy (RT) causes changes in the white matter. This effect causes change in the geometrical shape of the white matter region, which is visible after 3-18 months of radiation therapy depending upon case to case. Normally the intensity of white matter in T2 weighted MR images is dark gray (Table 2).

Tissue type	T1 weighted	T2 weighted
White matter (WM)	White	Dark gray
Gray Matter (GM)	Medium Gray	Medium Gray
CSF	Dark gray	White

**Table 2:** Soft tissue contrast of pixels in T1 and T2 weighted MR images of normal tissue

After white matter changes (due to RT) the intensity of affected pixels by white matter in the T2 weighted MR image is changed to medium dark or white. This change at boundary region can be analyzed using visualization scheme. Prototypes are found at 83, 95, 106, 117, 129, 141, and 152. Two clusters are selected for analysis at 83 and 106 ([X] and [Z] in the image). The [X] region shows the white matter region. There are some [Z] pixels inside the [X] region where white matter changed. Similarly there are black region also inside the white matter where the white matter is changed. In the figure [Y] areas around the white matter shows the boundary regions. Using visualization scheme the boundary regions between the white matter and changed white matter shows better delineation for assessment verified by the clinician.

In an embodiment of the present invention, wherein an apparatus for an interactive visualization of Magnetic Resonance Image (MRI) of a diseased tissue, said apparatus comprising: an input device for receiving pixelized image and histogram data of an MRI image of the diseased tissue, a memory device coupled to said input device for storing said pixelized magnetic resonance image data, a micro processor coupled to said memory device for partitioning of images by determining cluster-prototypes from a range of gray values of histogram data, more particularly from the flat region of gray values in a dynamic prototype selection network, an input device for selecting any two cluster prototypes, said processor to generate alpha values between said selected cluster prototypes for soft segmentation, said processor to highlight the areas of images of said alpha values, display means to display the reconstructed image in distinct pseudo shades corresponding to the various overlapping areas of the images with clear demarcation of boundaries between healthy and diseased tissues.

An embodiment of the present invention, wherein the processor interactively selects different cluster-prototypes from the whole range of the histogram, more preferably in the flat gray scale region of the histogram data.

Another embodiment of the present invention, wherein alpha values are between 0 and 1 to generate various soft segmentations of MR images between selected prototypes.

Yet another embodiment of the present invention, wherein an output means coupled to processor for displaying the images with clear demarcation of boundaries between healthy and diseased tissues.

It is also an embodiment of the present invention, wherein a method for visualization of Magnetic Resonance Image (MRI) of a diseased tissue having no distinct/sharp boundaries due to tissue non-homogeneity, said method comprising: computing the histogram of a diseased tissue, processing the histogram data to generate cluster-prototypes with hidden and visible layers of pixels in a dynamic prototype selection network, iterating of the above step to arrive at plurality of prototypes, computing distance of histogram intensity values from each prototype, computing membership value of the intensity values based on the distance calculated, selecting two or more cluster prototypes, generating alpha values on the membership values, ascertaining the belongingness of each intensity values to each prototype, allocating the histogram intensity values to the selected prototypes, and reconstructing selected areas of the image and displaying the reconstructed image to the user having distinct boundaries between diseased and normal tissues.

An embodiment of the present invention, a method wherein the alpha values of the selected prototypes are between 0 and 1.

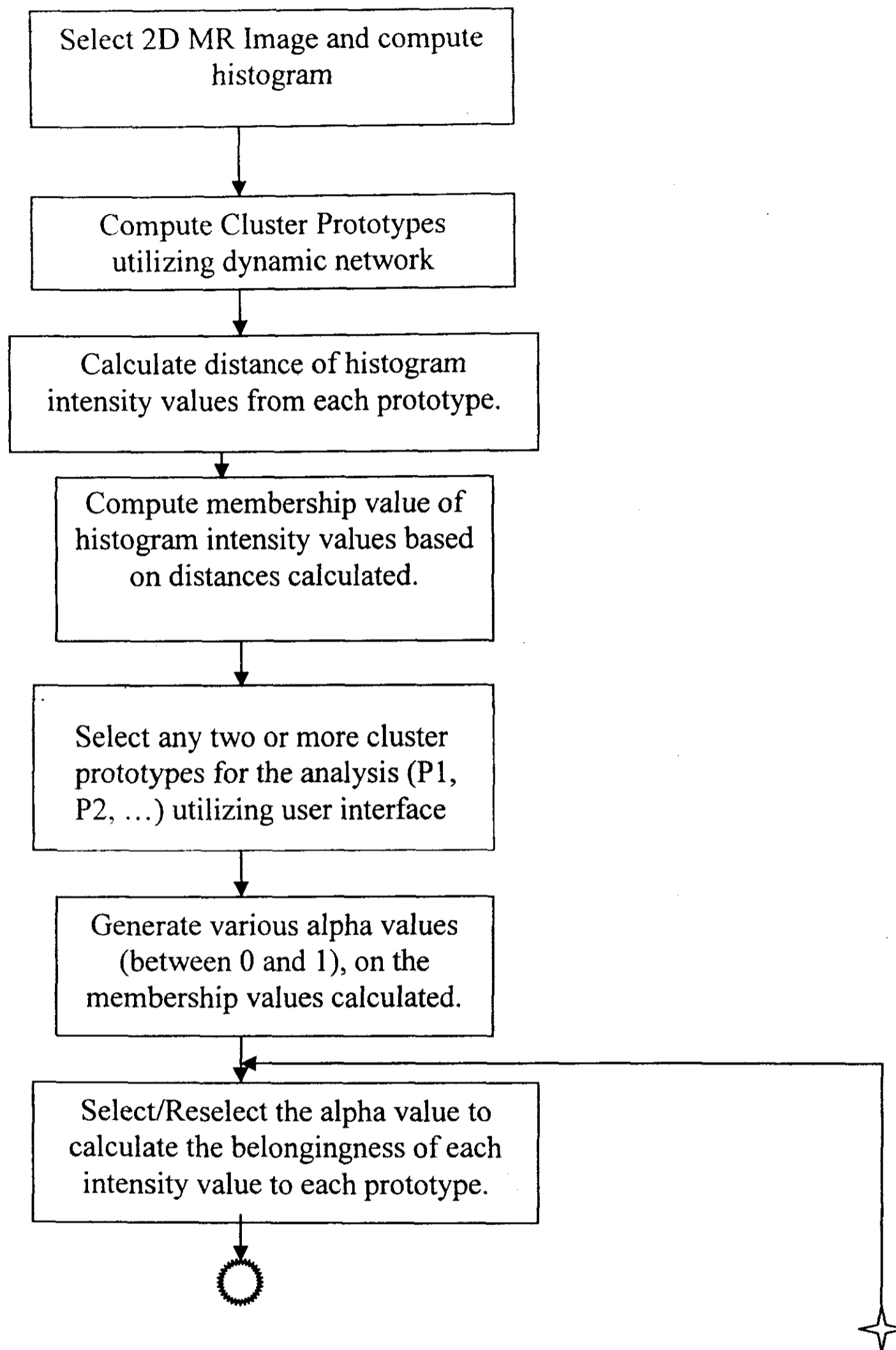
Another embodiment of the present invention, a method wherein the processor interactively selects different cluster-prototypes from the whole range of the histogram, more preferably in the flat gray scale region of the histogram data.

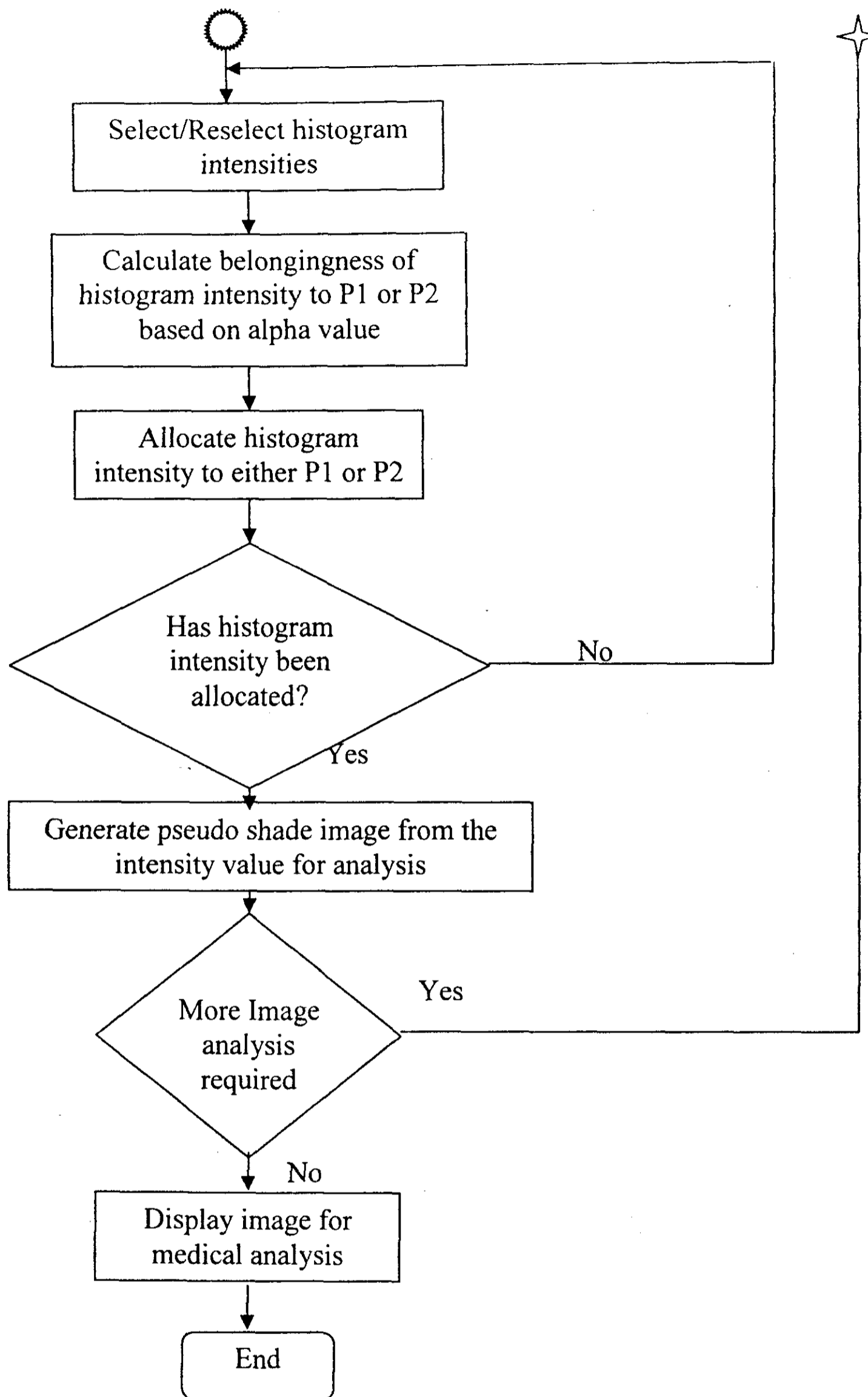
Still another embodiment of the present invention, a method wherein the dynamic prototype selection network is used to select the desired prototypes of the selected histogram.

It is also an embodiment of the present invention, a method wherein the processor selects the prototype by selecting the highest pixel values in a neighbourhood, increasing

the highest pixel value by suppressing the neighbouring histogram values and adding weights to the highest pixel value, storing the highest values as cluster-prototypes and inhibiting neighbouring cell values.

The working method of the Apparatus of the present invention is provided in the form of following flow chart:





## **Advantages**

1. The time taken for diagnosis is much lesser compared to standard methods.
2. The diagnostic accuracy is more using this neuro-fuzzy visualization tool.
3. The present invention provides a low cost PC based visualization tool.
4. The visualization tool provides the user with choice to select different virtual segments, to procure different views.
5. The image generated using this soft visualization scheme clearly shows overlapping boundary pixels for correct delineation.