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A NEW HYBRID METHOD FOR MEDICAL IMAGE SEGMENTATION

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ABSTRACT

The present work is an attempt to measure the efficiency of a region method in segmenting a Medical imaging. To accomplish our study, we conceive a new hybrid clustering method which combines a neural network and a genetic training, in order to realize a fuzzy learning, and adapt a new tool for clustering called ACE (Alternating Cluster Estimation). The ACE is a new clustering model constituted of two update equations which, in contrast to classical models, are user specified and are not necessary relating to an objective function. The used neural network is composed of five layers each one, except the first, corresponds to a step of the fuzzy learning. The values optimised by the genetic training algorithm are the weights which represent the centres of membership functions characterizing linguistic terms. System input and output will be respectively, colorimetric components and cluster centres. Image data segmentation using colors space can be a valuable tool to visually assess and quantify the loss of neural. The HSV color space is used in order to, partly, get rid of the RGB space correlation. The experimental results obtained using the proposed method are encouraging.

Keywords: *Fuzzy, clustering, ACE, Neural networks, Genetic training, The HSV color space,Medical image segmentation.*

1. INTRODUCTION

Image segmentation is the partition of an image into several regions of interest such that the contents of each region have similar characteristics.

The complexity of human brain structure mandates the use of computerized approaches derived from computer vision, image analysis, and applied mathematics fields to extract brain data. Successful numerical algorithms in segmenting anatomic structures in neuroimages can help researchers, physicians, and neurosurgeons to investigate and diagnose the structure and function of the brain in both health and disease. However, extracting the ventricle, the brain, and brain tumors in magnetic resonance (MR) images is often highly challenging due to the convoluted shape, blurred boundaries, inhomogeneous intensity distribution, background noise, and low intensity contrast between adjacent brain tissues. In general, the interest tissues in the brain are white matter (WM), gray matter (GM) and cerebral spinal fluid (CSF) [14]. In the analysis of MRI images, image segmentation techniques play a key role [11]. Magnetic resonance imaging (MRI) is an important diagnostic imaging technique to obtain high quality brain images in both clinical and research areas because it is virtually noninvasive and it possesses a high spatial resolution and an excellent contrast of soft tissues [10, 13].

Cheng [1] classifies color image segmentation into: histogram thresholding, feature space clustering, region based approaches, edge detection, fuzzy techniques, physics based approaches and neural networks approach.In this contribution and according to the classification presented above, we are interested in each of the space feature clustering, the fuzzy techniques and the neural network approaches.

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Generally, clustering is to be seen as a tool for the exploration of data. Its main purpose is to group objects into clusters on the basis of similarity between them [2]. Many of clustering algorithms are adapted for image segmentation. FCM (Fuzzy C-Means) for example is one of the most common and the more used algorithm in this domain. Other examples exist alike, among which we cite: PCM (Probabilistic C-Means), K-nearest neighbour, and K-means.

On the level of image segmentation, clustering is used for partitioning an image into homogeneous regions such that each region is a set of pixels having the same characteristics and grouped around a centre. One way to describe the existing relationship between the set of pixels and the centre is the use of the clustering models which seem to be the most suitable for this task. The majority of these clustering models define good clusters as extrema of objective functions. Their membership functions are restricted to particular shapes which are determined by the update equations derived from the models' objective functions. Nevertheless, the user might be interested in choosing membership function shapes that are considered more useful for its application. Thus, the use of a more generalized clustering model seems to be interesting.

Neural networks are a learning device widely applied for pattern recognition. Their extended parallel processing capability and non linear characteristics are used for classification and clustering [1]. However, the problem of this tool is the convergence to a local minimum. This limitation, generally, prevents them to attain the desired optimal solution.

Genetic algorithms are an optimisation tool. Their fundamental utility consists on the exploration of a large potential solutions space in a parallel way, until obtaining the best solution. Recently, they proved their efficiency in neural networks training [7].

The exact research question is to construct a new hybrid method of fuzzy clustering based on models, in the goal, to segment a medical color image into some homogeneous regions.

In the present paper, we attempt to define a flexible clustering method for color image segmentation. This is obtained by adapting a more general clustering model called ACE (Alternating Cluster Estimation) which liberates the user from the objective function constraint and by using a neuro-fuzzy network with a genetic training. By the use of Neuro-fuzzy systems we combine the learning capabilities of neural networks with the interpretability of fuzzy systems. On the other hand the utilization of a genetic training comes of its rapidity of prototyping and ability to reach an optimal model. However, these two features are obtained only by defining good parameters and choosing initial potential solutions near to the desired one. The image pixels will be classified according to the obtained model.

We think that of this manner, we will benefit contributions of the theory of the fuzzy wholes, neural networks and the genetic algorithms, to give back our more effective proposed method.

The first section introduces the ACE paradigm. The second and the third define respectively, the fuzzy modelling and the neural networks. The fourth presents, within three parts, an exhaustive description of the suggested method and the last exposes the experimental results and discussion.

2. ACE DESCRIOTION

ACE (Alternating Cluster Estimation) is a more general model defined by alternating iteration architecture and can be customized by user defined membership and prototype functions [3]. It is composed of two equations one to update the partition matrix that contains the degrees to which objects belong to different clusters and the other to update clusters prototypes. The two equations may or not optimise a particular objective function, since that using equations corresponding to a specific model objective functions will be no more compulsory. In this model clusters and cluster centres are estimated by alternatingly updating partitions and prototypes. This is the reason behind its appellation: 'Alternating Cluster Estimation' [3].

The user of the ACE interface can imagine that he has a membership function tool bar and a prototype function one at his disposal. So he has only to choose one function from each, better than that he can even choose different functions for the same implementation. The main particularity of the ACE is that it can be seen as a frame work since it allows the generation of new clustering algorithms.

3. FUZZY MODELLING

Fuzzy c-means is an unsupervised technique that has been successfully applied to feature analysis, clustering, and classifier designs in fields such as astronomy, geology, medical imaging, target recognition, and image segmentation [12]-,[15],[16],[17].

Fuzzy modelling is designed to mimic how the human brain tends to classify some information or data imprecisely. In fuzzy models, information is processed in terms of fuzzy sets characterized by an associated membership functions. The specific fuzzy inference is then processed by the fuzzy set, defining the inputs, combined with a collection of fuzzy rules to produce an output that can be compared with the actual values observed in the real world [4]. Fuzzy modelling is typically classified into two categories which differ in their capacity to represent different kinds of information: Mamdani-Assilian model based on human experience and Takagi-Sugeno model which is more appropriate for a data based approach [5].

Among the two models presented previously, we are interested in Mamdani's model. It is composed of five steps described as the following:

- **Inputs fuzzification**: all fuzzy statements in the antecedent are resolved to a degree of membership between 0 and 1. If there is only one part to the antecedent, this is the degree of support for the rule.
- **Application of fuzzy operators in the antecedent**: if there are multiple parts to the antecedent, fuzzy logic operators (AND,OR), implemented by drastic product, are applied with the purpose of resolving the antecedent to a single number between 0 and 1. This is the egree of support for the rule.
- **Implication from the antecedent to the consequent:** the output fuzzy set is reshaped using the degree of support for the entire rule. The implication method is implemented by drastic product (i.e. minimum).
- **Aggregation of the consequents across the rules**: the fuzzy sets that represent the outputs of each rule are combined into a single fuzzy set. The aggregation method only occurs once for each output variable. A drastic sum (i.e. maximum) is used for implementing the aggregation method.
- **Defuzzification**: the final output for each variable, which is a single number, is obtained by the application of a defuzzification method. It is up to the model designer to decide of the defuzzification method [6].This later returns a defuzzified value out, of a membership function mf positioned at associated variable value x, using one of several defuzzification strategies, according to the argument, type. The variable type can be one of the following:centroid: centroid of areabisector: bisector of areamom: mean value of maximumsom: smallest (absolute) value of maximumlom: largest (absolute) value of maximumIf type is not one of the above, it is assumed to be a user-defined function. x and mf are passed to this function to generate the defuzzified output.

4. NEURAL NETWORKS

Neural networks are structured systems composed of a simple calculation units working in parallel. Their task is determined by the structure of the network, connections solidity and the operations accomplished by the nodes.

Their main interest lies in their inherent capacity of learning and then generalizing [7][8]. Two types of neural networks are distinguished: the feed-forward network and the back-forward one.

a. Feed-forward neural network; Layers' outputs can not be propagated towards the precedent layers, thus, the actual outputs are not influenced neither by the future outputs nor by themselves. Rosenblatt, Multi Layer Perceptron (MLP), Adaline and Adaptive logical network(ALN), are examples of this type of networks.

b. Back-forward neural network; In this kind of networks, each cell is linked to all the others one and it has even a back on itself. Signals can be propagated forward or back propagated. Hopfield, Kohonen and gross berg, are examples of the back-forward networks. Defining a specific architecture for a network is not resolving a given problem. Thus, a configuration of the weights adapted to the sufficient for given problem is to be determined. This is the training process role [9]. Training is a development phase of a neural network during which the network behavior is modified by wkay of an algorithm until obtaining the desired behavior. Algorithms devoted to networks training often converge to local minima which is, unfortunately, not always the best solution. The mentioned problem can be overcome by a Genetic Training.

Genetic training, as well as classical neural network training algorithms, operates upon the network connections weights by modifying them until the stabilization of the network. It uses three fundamental "genetic" operators: selection, crossover, and mutation. To achieve the optimal solution, genetic training optimizes a specified function called adaptation function which calculates at each iteration the network error.

5. PROPOSED METHOD

The method that we propose is founded upon the adaptation of the ACE and the utilization of a neural network trained by a genetic algorithm to extract a set of valid local fuzzy models composing the global model. In order to use the ACE for color image segmentation, we define the first update equation as a membership function calculating the degrees to which pixels belong to different clusters and the second one as a prototype function which calculates the new clusters centres. With the aim of estimating the cluster and the cluster centres (the membership and prototype functions), a combined estimation scheme is defined. This later employs three symbolic training tools: Mamdani fuzzy inference, multilayers neural network and genetic algorithm to train the neural network.

In the following, we give an exhaustive description of the proposed method in the "fig. 1". Next, we elucidate the different steps which allow the estimation of the partition matrix U and the prototype vector V.

5.1. Initial model definition

In this step, we built the initial rules base describing the relationship between the input space (pixels) and the output space (clusters centres). This rules base is composed of a collection of the MA (Mamdani-Assilian) rules, each rule has the following form (1):

$$\textbf{If } \wedge_{l=1 \ldots p} \mu_{il}(x^{(l)}) \text{ Then } v_{im}(y(m)) = \mu_i(p+m)(y(m)) \qquad (1)$$
$$\forall\, m = 1, \ldots, q \;;\; i = 1, \ldots, c$$

where:

- c, is the number of clusters.
- X=(x(1)…x(p)) is the system input vector and Y= (y(l)…y(q)) is the corresponding system output vector.
- $\wedge: [0, 1]^2 \rightarrow [0, 1]$ is the T-norm.
- μ_{il}, v_{im} : IR → [0, 1]; i = 1,…,c ;l=1,…,p+q ; m=1,…,q : are membership functions.

We call the rule left part the antecedent and the right one the consequent.

To form the MA rules, two information, to be determined by the user, are required: the clusters number to determine the rules number and the values of the initial clusters centres according to which the initial model is defined.

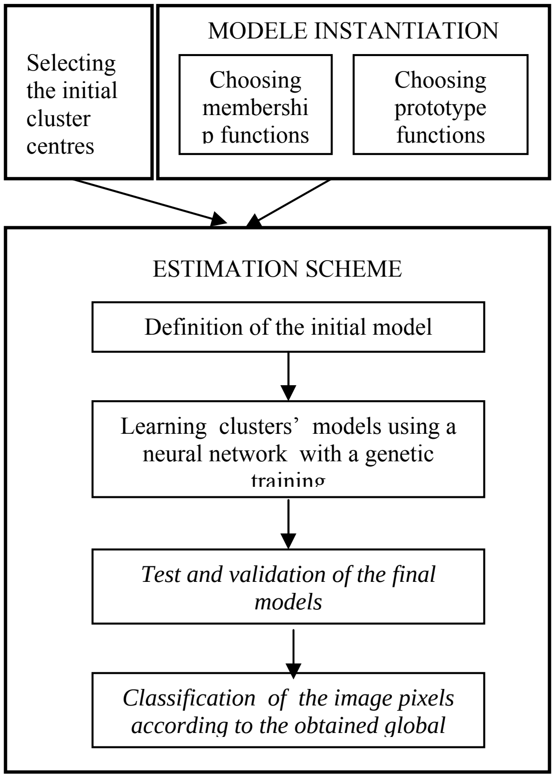


Fig. 1: Global system description

5.2. Neural network design

We implement the Mamdani-Assilian fuzzy steps on a feed-forward neural network composed of five layers, such as each layer, apart from the first, corresponds to a step of the fuzzy learning. In the following, the size, the input, the task, the output and the initialisation of each network layer are given:

- The first layer consists of three nodes and does no processing but simply buffers the system inputs: the colorimetric components of the image pixels.

- The second one (fuzzification layer) consists of a number of nodes equal to the number of linguistic terms. The input of each neurone is a value computed from a numerical value over the discourse universe and the connection weight. Each neurone calculates the fuzzy membership function. The output is the input membership degree to a linguistic term of the appropriate linguistic variable. Connection weights are the linguistic terms centres.

- The third one (conjunction layer) consists of a number of nodes equal to the number of rules. The input of each neurone is the membership degree. In this layer the logic operator AND is applied.

The output is the antecedent degree. Layer weights are initialised at one.

- The nodes of the fourth layer (implication layer) realize the fuzzy implication via the minimum function. The input of each neurone is the antecedent degree; the output is a fuzzy degree. Layer weights are initialised by the initial clusters centre membership.

- The last one (aggregation and defuzzification layer) is composed of one node. It aggregates the rules outputs then calculates the numeric value of the cluster centre using a specific prototype function. Layer weights are initialised at one.

“Fig. 2” illustrates the neural network architecture upon which some weights values examples are inscribed.

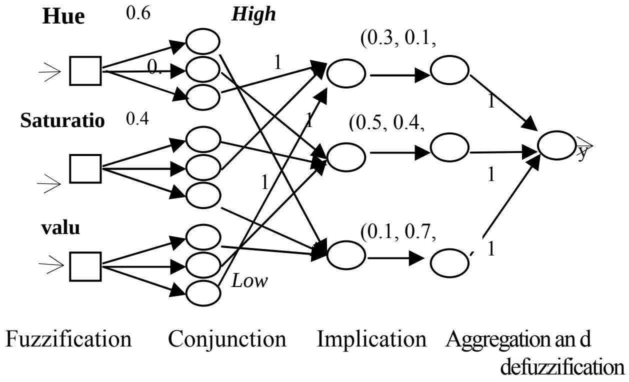
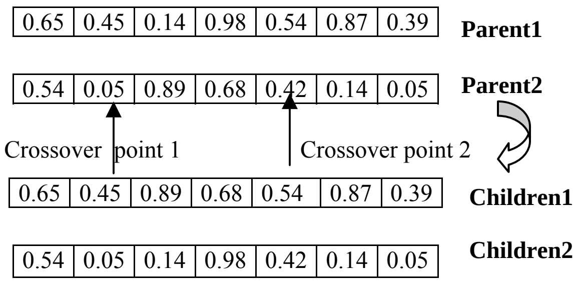


Fig. 2 : Neural network architecture

5.3 Genetic Training

In this step, we use a genetic training which inherits all genetic algorithm concepts and principles.



0.65	0.45	0.14	0.98	0.54	0.87	0.39	**Parent1**
0.54	0.05	0.89	0.68	0.42	0.14	0.05	**Parent2**
0.65	0.45	0.89	0.68	0.54	0.87	0.39	**Children1**
0.54	0.05	0.14	0.98	0.42	0.14	0.05	**Children2**

Fig.4: *Two point crossover*

As any training algorithm, the genetic algorithm has the task to up date the network weights, its particularity is that it updates only the weights of the first layer in view of the fact that the neural network is a Feed-Forward one. The other connections weights will be automatically updated as a result of the first layer weights modified by the training algorithm. As they represent the first layer weights, the centres of membership functions characterizing linguistic terms are the values optimised by the genetic training.

All the basic elements of the genetic training are carefully chosen to fit best the segmentation process needs. In what follows, a description of the different elements is given:

- Gene; it is one of the weights of the first layer connection.

Chromosome; it is composed of a set of genes, in other terms it contains the linguistic terms centres of the fuzzification layer weights.

- Population; is the collection of the defined chromosomes, where each chromosome represents an eventual initialisation of the fuzzification layer weights.

Fitness function; it evaluates the difference between the desired output of the network and the calculated one, accordingly the fitness of each chromosome is determined as (2):

$$f_i = Y - Y^{(t)} \qquad (2)$$

such Y is the desired network output and $Y^{(t)}$ is the network calculated output.

The genetic training algorithm that we propose follows in its functioning the basic GA (*Genetic algorithm*) methodology :

It starts with an encoding of the potential solutions as a vector strings (chromosomes). In this method a real coding is used. "Fig. 3" presents an example of the encoding of the fuzzification layer weights ：

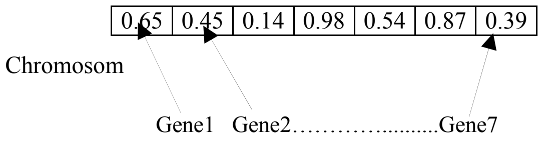


Fig. 3 : *Real coding*

Next, a particular selection of an initial population of solutions is done via the 'Roulette Well Selection' method. Then fitness is calculated for each solution. Afterwards, a selection and breeding (Crossover and mutation) of parents occurs to create new solutions (children). In this paper a crossover and a mutation in two and multiple points, respectively, are utilized. The "fig. 4" shows an example of a crossover process :
A mutation of existing solutions takes place occasionally. It improves the chances to find the optimal solution by widening the solutions' space.

"Fig. 5" explains the mutation operation :

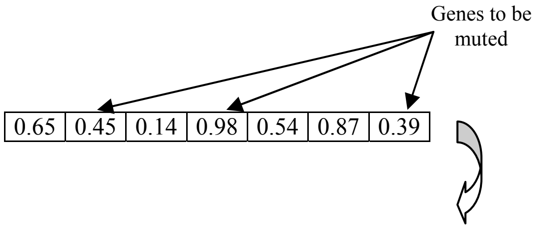


Fig. 5: Mutation in multiple points

By analogy with the biological genetic system where mutations are rare, a higher probability (0.6) is given to the crossover process than to the mutation process (0.01).

Likewise to any training algorithm, all genetic training steps proceed in an iterative manner, that is to say in generations. The number of iterations is fixed to 20. The algorithm runs until the search converges or the number of iterations is achieved.

6. CONCLUSION

In this work, we attempted to define a new clustering method to be used for a medical segmenting image. The goal of brain image segmentation is to accurately identify the principal tissue structures in these image volumes. Our principal objectives are achieved via the obtaining good results of the segmentation of the different medical image and the fixation of best parameters of the proposed method based on visual analysis and the index for performance evaluation proposed by Jaccard similarity.

The proposed method brings out two fundamental advantages: the flexibility, in the sense where it allows the generation of the more adequate algorithm to segment a given image and the generalization since it embodies many well-known clustering models. Moreover, the method defines good clusters, that means the extracted image regions are well delimited. This fact comes of the utilization of a neurofuzzy network and a genetic training.

Our perspectives aim the improvement of the adaptation function, the increase of the number of population and to modify some operators of the genetic training algorithm.

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APPENDIX

EXPERIMENTAL RESULTS AND DISCUSSION

In this section, we present the results obtained by applying the new method upon a medical image.

We address the specific segmentation task of extracting the important tissue from different type of the brain image. The magnetic resonance images.(MRI) is an advanced medical imaging technique providing rich information about the human soft tissue anatomy.

Our principal aim is showing that the choice of number of the cluster ,membership and prototype functions, in the same way, their parameters influences widely the quality of the segmentation. So, choosing the more adequate functions and parameters implies acquiring a good segmentation.

In this paper, Jaccard similarity is employed as the index for performance evaluation. The formula of Jaccard similarity is given:

$$J(S_1, S_2) = \frac{|S_1 \cap S_2|}{|S_1 \cup S_2|} \quad (3)$$

Where S1 is the golden standard; S2 is the segmented area; ∩ is intersection operator; ∪ is union operator [18].

"Fig. 6"shows horizontal Cut of the brain Image

"Fig. 6.a" ,"fig. 6.b", Fig. 6.c" and "fig. 6.d" present the different results of the brain image segmentation , the first one is obtained by applying the triangular membership function with the parameters equals to 2,5 for Alpha ,1 for sigma and 3 for number of clusters. The second is got by applying the exponential membership function and the same parameters as the precedent figure. We observe an improvement of the detection of the gray matter and cleanness of the contour of every component of the brain in the second figure so the triangular membership function gives better results than the exponential function.

"Fig 6.c" shows the segmented image with the following parameters: 4 clusters, alpha = 2 and sigma = 0, 7. we have a good detection of the

ray matter, the white matter and the LCR, also, parts, oiled and bony, are visualized , we notice

that the choice of the number of the clusters influences also the result of the segmentation.

"Fig. 6.d" and Fig. 6.e" are obtained by using the exponential membership function with the same number of clusters which is fixed to 5, regarding the structure of the human brain. In order to fix the better parameters of alpha and sigma, different values of parameters were used.

This comparison shows that the values 2 and 0,7 for Alpha and sigma respectively gives a better segmentation.

"Fig. 7" shows the IRM image representing a tumor untra cranial and more precisely a Tumor of the posterior pit at a patient of 51 years

"Fig. 7.a", "Fig. 7.b", "Fig. 7.c", Fig. 7.d" and "7.e" present the different results for segmentation of the same image.

When the number of clusters is three, we note an invading white matter, while the gray matter is almost absent. The cerebral spinal fluid (CSF), represented in white color, perfectly distinguishes itself of the structure remainder. We also notice a stain, of dark color, nearly situated to the middle of the white matter.

The interpretation of components is improved completely when the number of cluster is five. A good detection of the gray matter, the white matter and the CSF, the tumor is nearly distinguishable by the color, clear gray, to the center of the brain

Seen the previous obtained results, It is clear that the exponential membership function provides a good result.

On the followings, we are going to work using only exponential membership function with the parameters (2 for alpha and 0, 7 for sigma).

"Fig. 8" is SPECT cerebral image presenting a pathology to the level of the left temporal region displacing the third ventricle slightly toward the right, can evoke a tumor or a vascular accident

The segmentation of this SPECT image helped us to detect the surrounding liquid, CSF, in addition to that, we note:

a dark zone in the left temporal region, of irregular shape in occipital right, surrounded by an influx liquid perished lessoned hyper active, of defence.

“Fig. 8.a” is obtained by the application of the proposed methods with the Mom (mean of maximum method) prototype function for both components: Hue and Saturation, the Som (smallest of maximum method) one is applied for the Intensity.

By the variation of the prototype function, we obtain the result mentioned in the figures “Fig. 8.b”, “Fig. 8.c”, Fig. 8.d”. According to the application of Jaccard similarity used to evaluate the best segmentation, Mom, Mom, Som prototype functions is proved to be the adequate combination.

From the figure 9 until the figure 20, We are going to segment every image with the best noted parameters, that are fixed by:

Exponential membership function-

Parameters: alpha=2,5, sigma=1

Mom, Mom, Som prototype functions

To the level of each figure , the segmentation will be presented with two different numbers of clusters, by calculating every time their evaluation.

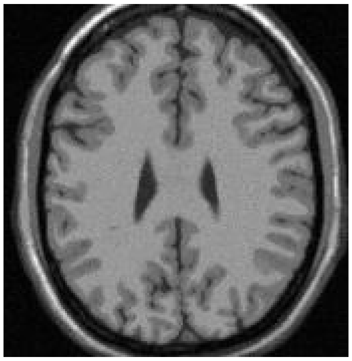

Fig. 6- brain image

(horizontal Cut of the brain)

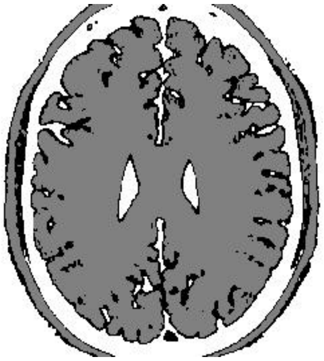

Fig.6a
Triangular membership function
Parameters : alpha=2,5, sigma=1
Nbr_clust=3; Evaluation = 0;567

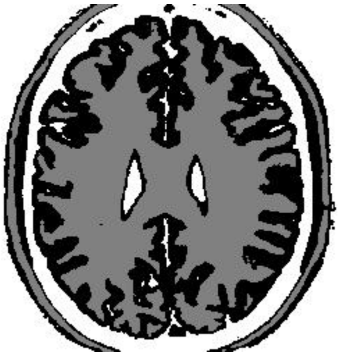

Fig.6b
Exponential membership Function
Parameters : alpha=2,5, sigma=1
Nbr_clust=3 ; Evaluation = 0,542

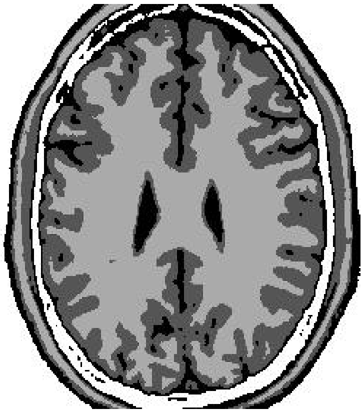

Fig.6c

Exponential membership function-
Parameters : alpha=2, sigma=0.7
Nbr_clust=4; Evaluation = 0,456

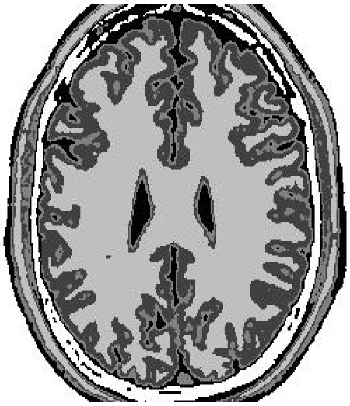

Fig.6d
Exponential membership function-
Parameters : alpha=2,5, sigma=1
Nbr_clust=5; Evaluation ==0,245

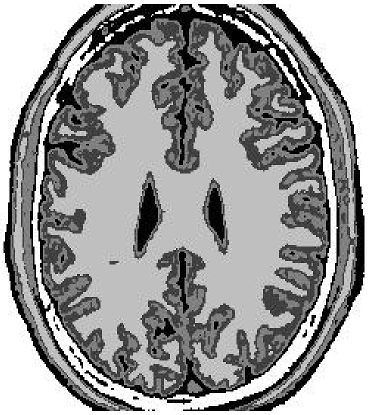

Fig.6e

Exponential membership function
Parameters : alpha=2, sigma=0.7
Nbr_clust=5; Evaluation = 0,257

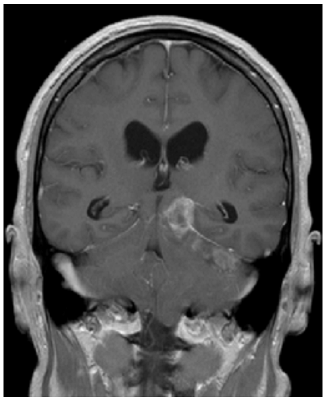

Fig. 7 - brain RM image

(representing a tumor intracrânienne)

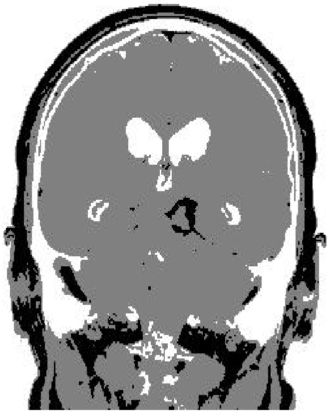

Fig. 7a

Triangular membership function-
Parameters : alpha=2, sigma=0.7
Nbr_clust=3, Evaluation = 0,499

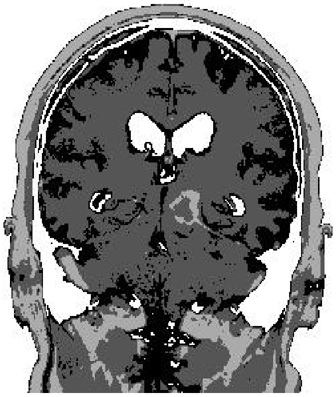

Fig.7b-

Exponential membership function-
Parameters : alpha=2, sigma=0.7
Nbr_clust=4 ; Evaluation = 0,675

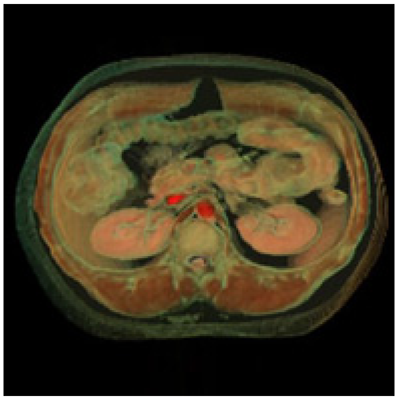

Fig. 9 Newb-3Dabed .

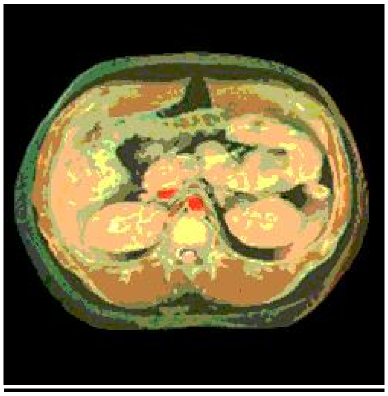

Fig. 9a

Nbr_clust=8. Evaluation = 1,687

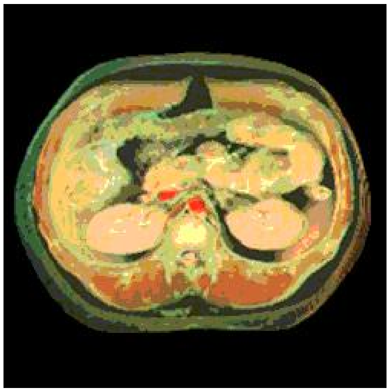

Fig. 9b

Nbr_clust= 6. Evaluation = 1,483

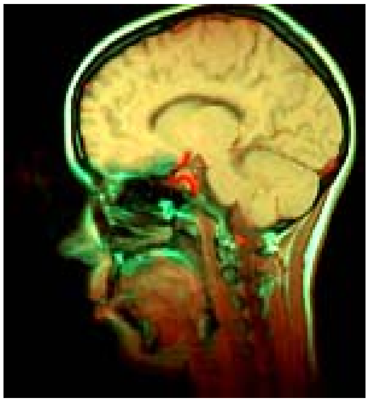

Fig. 10 Brains image

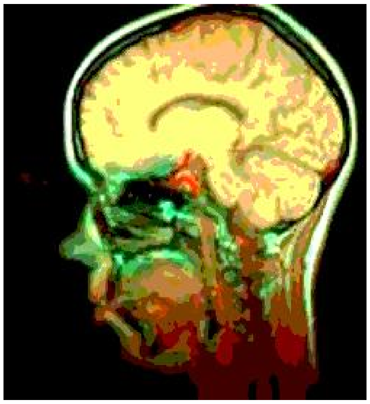

Fig. 10a

Nbr_clust=5 ; Evaluation= 1,364

Fig. 10b

Nbr_clust= 6; Evaluation = 1,483

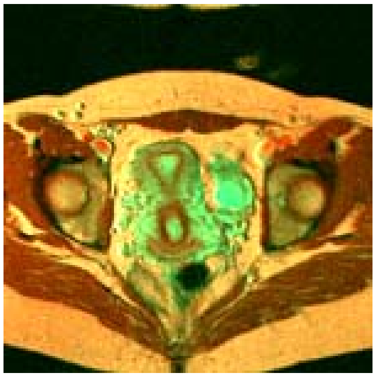

Fig. 11 Pel Image

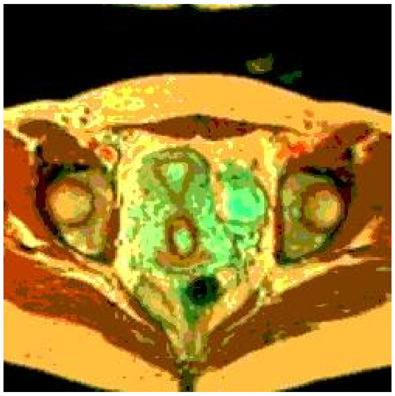

Fig. 11a

Nbr _clust= 5; Evaluation = 1,367

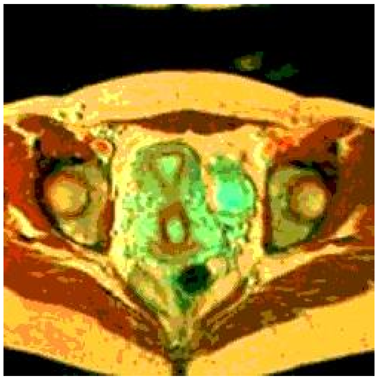

Fig. 11b

Nbr_clust= 6 ; Evaluation = 1,483

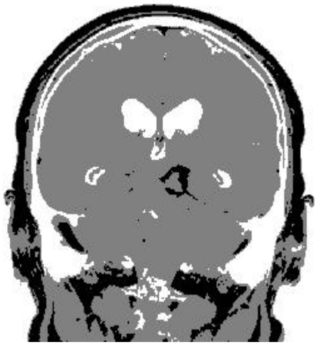

Fig.7c-

Triangular membership function
Parameters : alpha=2, sigma=0.7
Nbr_clust=4; Evaluation = 0,5

Fig.7d

Triangular membership function
Parameters : alpha=2, sigma=0.7
Nbr_clust=5; Evaluation = 0,521

Fig.7e

Exponential membership function
Parameters : alpha=2, sigma=0.7
Nbr_clust=5; Evaluation = 0,576

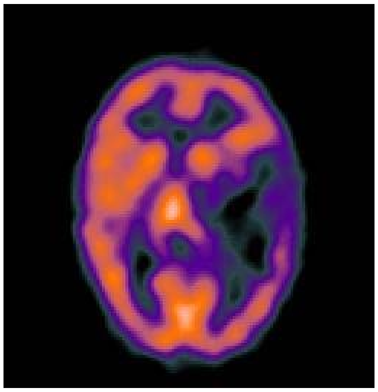

Fig. 8–Image SPECT (horizontal Cut of the brain)

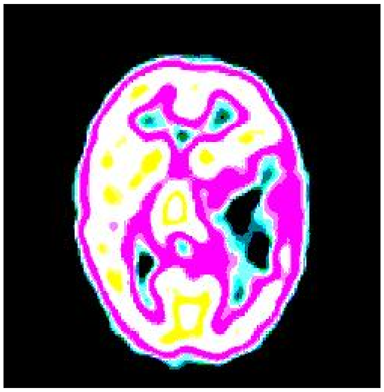

Fig. 8a
Exponential membership Function
Parameters : alpha=2, sigma=0,7
Lom, Mom, Som Prototype functions
Nbr_clust=5; Evaluation = 0,543

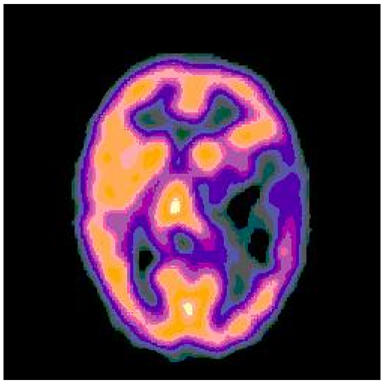

Fig. 8b
Exponential membership function
Parameters : alpha=2, sigma=0,7
Lom, Lom, Som Prototype functions
Nbr_clust=5; Evaluation = 0,337

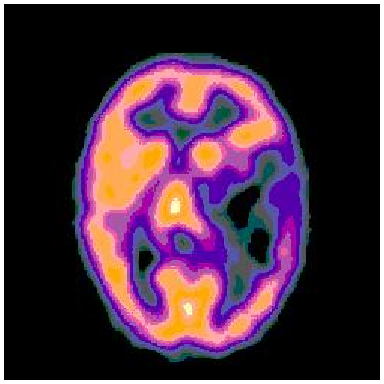

Fig. 8c-

Exponential membership function
Parameters : alpha=2, sigma=0.7
Mom, Lom, Som Prototype functions
Nbr_clust=5; Evaluation = 0,248

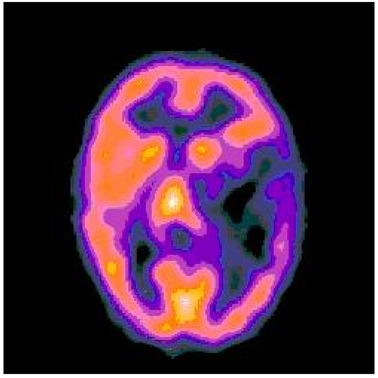

Fig. 8d-

Exponential membership function
Parameters : alpha=2, sigma=0.7
Mom, Som, Som Prototype functions;
Nbr_clust=5 ;Evaluation =0 ,289

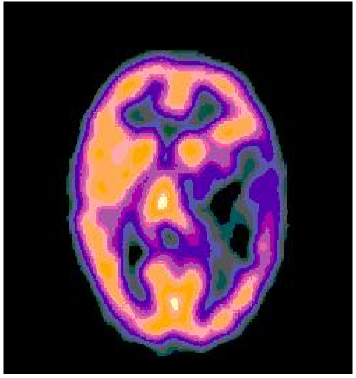

Fig. 8e-

Exponential membership function
Parameters : alpha=2, sigma=0.7
Mom, Mom, Som prototype functions
Nbr_clust=5 ; Evaluation = 0,256

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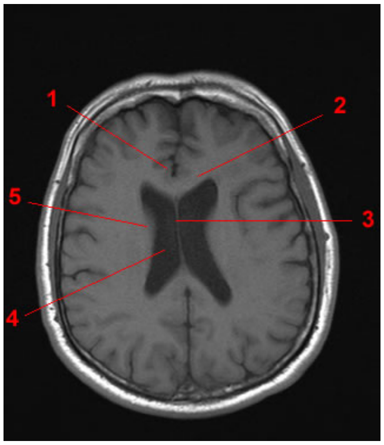

Fig. 12 brain

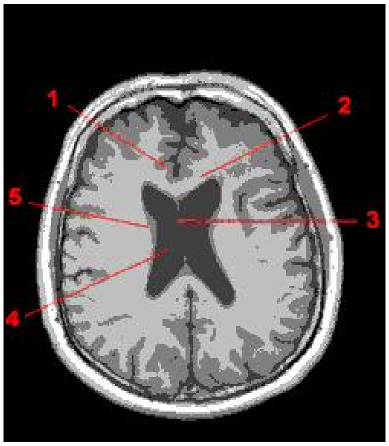

Fig. 12a

Nbr _clust= 5 ; Evaluation = 1,367

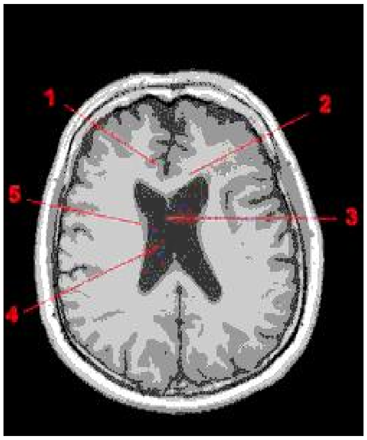

Fig. 12b

Nbr _clust= 6 ; Evaluation = 1,483

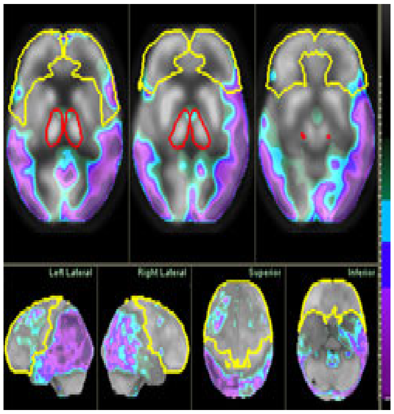

Fig. 13 Neuro_analysis_2

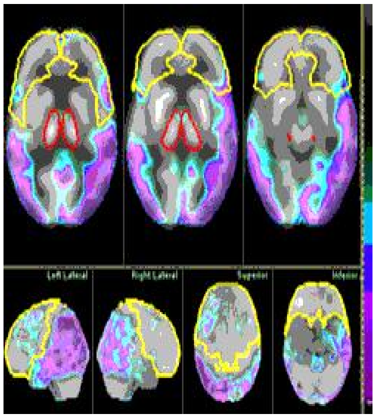

Fig. 13a

Nbr _clust= 5; Evaluation = 1,277

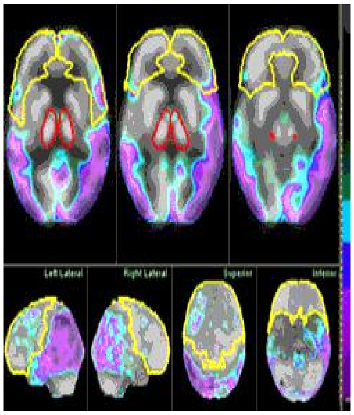

Fig. 13b

Nbr_clust=6 ; Evaluation = 1,483

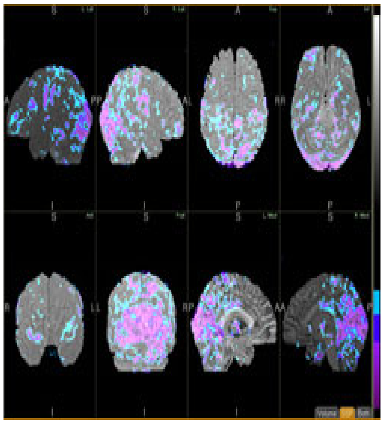

Fig. 14- Neuro_atlas_1

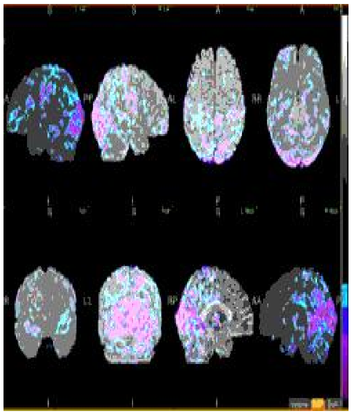

Fig. 14a

Nbr_clust=5;Evaluation=1,367

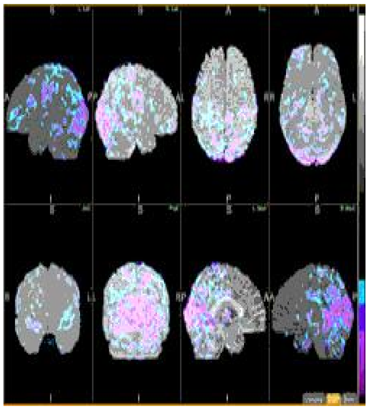

Fig. 14b

Nbr_clust=6;Evaluation=1,483

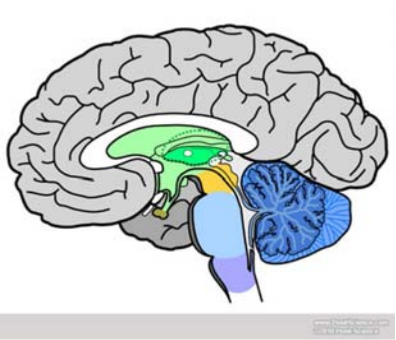

Fig. 15 brain X section

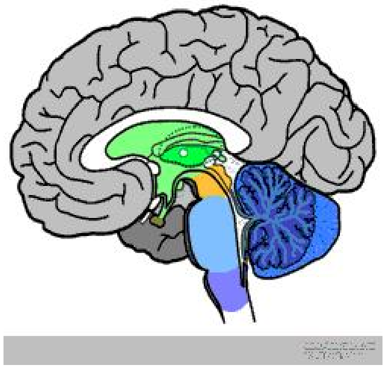

Fig 15a
Nbr_clust=5; Evaluation=1,483

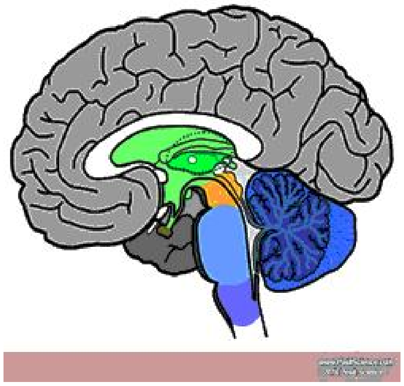

Fig 15b
Nbr_clust=6; Evaluation=1,367

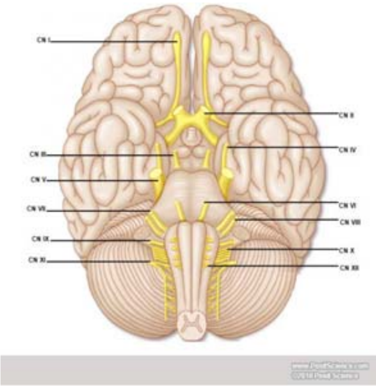

Fig. 16 cranial_nerve

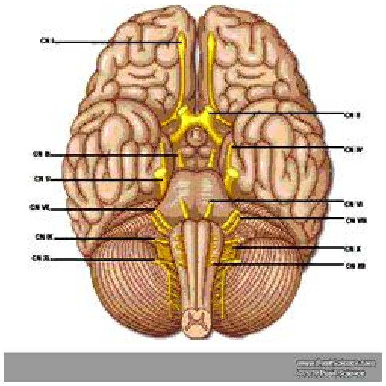

Fig. 16a
Nbr_clust=6 ;Evaluation= 1,483

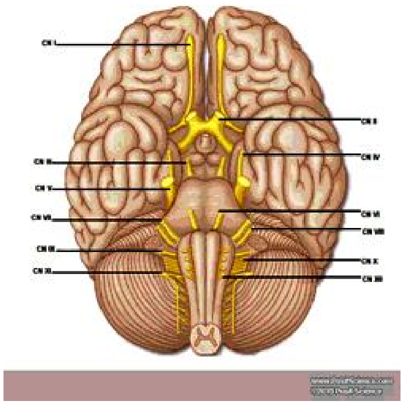

Fig. 16b
Nbr_clust=8 ; Evaluation= 1,687

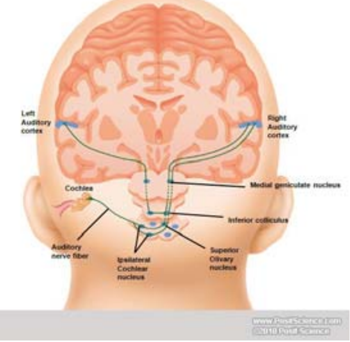

Fig. 17 auditory-pathway_0

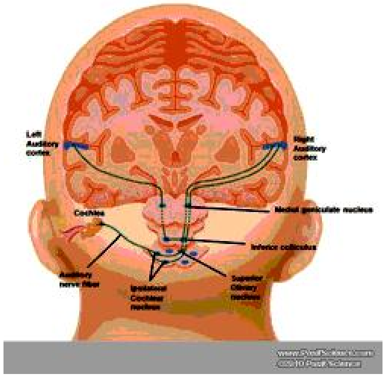

Fig. 17a

Nbr_clust=6; Evaluation =1,483

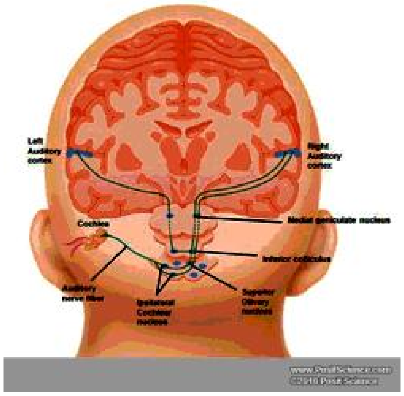

Fig. 17b

Nbr_clust=8; Evaluation =1,687

Fig. 18 meningiome-2_tmb

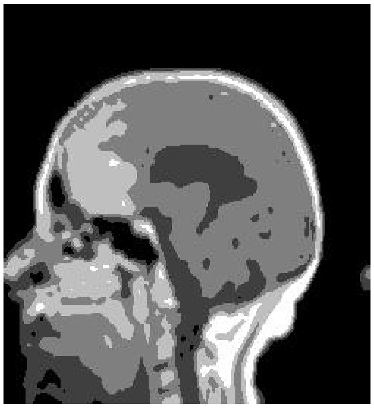

Fig 18a
Nbr_clust=5; Evaluation=1,367

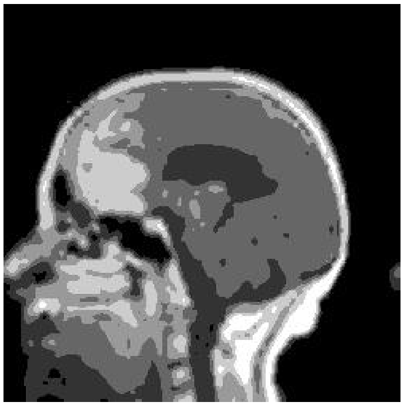

Fig 18a
Nbr_clust=6; Evaluation=1,483

Fig. 19 systeme-ventriculaire-sagittal.0002.0001_fs

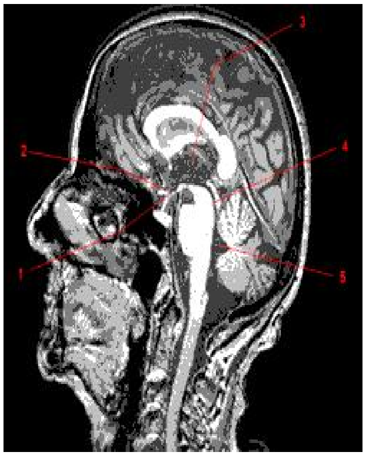

Fig. 19a
Nbr_clust=5 ;Evaluation= 1,367

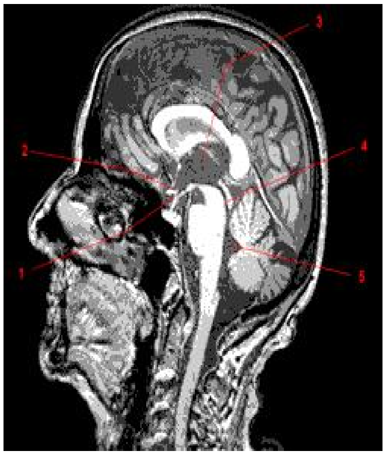

Fig. 19b
*Nbr_clust=**6** ; Evaluation= 1,**483***

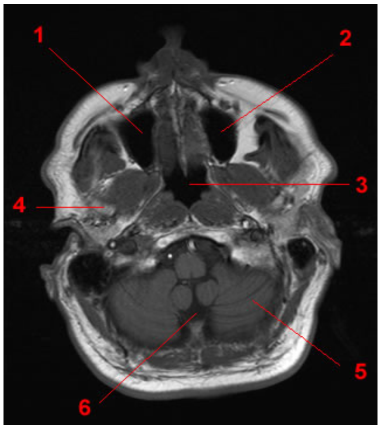

Fig. 20 IM-0003-0001_fs_fs

Fig. 20a
*Nbr_clust=**6**; Evaluation = 1,**483***

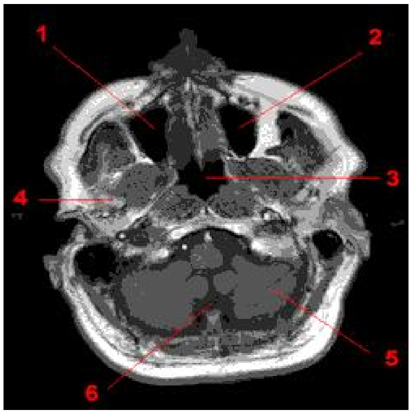

Fig. 20b
Nbr_clust=7; Evaluation=1,358