BRAIN TUMOUR DETECTION FROM MRI IMAGES USING HYBRID GENETIC FCM

Deepa
Student, CSE&IT Department
The NorthCap University, Gurgaon, India

Akansha Singh
CSE&IT Department
The NorthCap University, Gurgaon, India

Krishna Kant Singh
EEE Department
Dronacharya College of Engineering, Gurgaon, India

Abstract— **Brain Tumour is a type of illness. Brain tumour emerges when unusual mass grows in the brain. Brain tumour affects the normal functionality of the brain. Symptoms of brain tumour include problem in eyesight, distribution in the mind and vomiting. It can be dangerous for human life. With the advancement in computer aided techniques the diagnosis of brain tumour from MRI images has become an interesting area for researchers. The imaging methods like CT scan, MRI capture brain images that can be used for diagnosis purpose. MRI technique is mostly used for brain tumour as it gives more detail structure of the brain. The aim of this paper is, to propose a method for detection of tumour from MRI images. Hybrid genetic fuzzy method is used to detect the brain tumour from MRI images.**

Keywords— Brain Tumor, FCM, Genetic Algorithm

I. INTRODUCTION

Main organ in human nervous system is the human brain it is located in human head and covered by skull. The function of the human brain is to control the overall parts of the human body. It is a one kind of organ that allows human to adapt and endure varying environmental condition. The human brain enables human to execute action and share thoughts and feeling. Fig 1. shows the basic structure of brain.

When abnormal cells grow in the brain some functionalities of the brain are disrupted. This problem is called brain tumor .Brain tumor are of two types, primary brain tumor and secondary brain tumor [1]. Primary brain tumor can be cancerous or non-cancerous but secondary brain tumor is always malignant (cancerous). Primary brain tumor originates in the brain itself. Secondary brain tumor can originate in other parts of the body like lungs cancer, kidney cancer, bladder cancer etc. Many people die due to this disease. If the tumor is detected correctly at an early stage then a large number of lives can be saved.
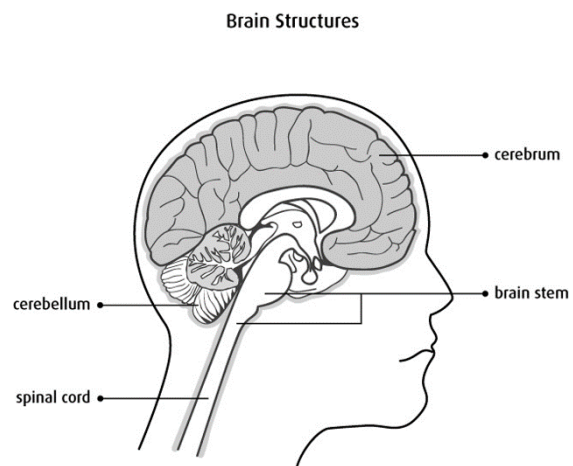

Fig. 1. The major part of human brain

In many cases, the physician gives the treatment for the hit rather than the treatment for the tumor. So, the proper tumor detection is the necessary task for the treatment of the brain tumor. The life of a person can be saved who is affected by brain tumor by detecting the tumor early [2] and correctly. Image segmentation methods can be used for detection of brain tumor from MRI images.

Image segmentation is a process of partitioning a digital image into multiple regions. The main motive of the segmentation is to change the representation of an image in to more meaningful and make it easy to analyze. Image segmentation is used to locate objects and boundaries of an image. In medical field image segmentation [3] play significant role for the diagnosis. Medical image have noise [4], poor contrast and missing boundaries, so medical image segmentation can be consider as a difficult problem. The brain image can be scanned by Magnetic Resonance scanner or can be scanned by computer tomography scanner. For the diagnosis Magnetic Resonance can be more comfortable than the computer tomography scanner because it does not use radiation [5] and thus it does not affect the human body.

Image segmentation basically works on two fundamental properties of intensity value, i.e., discontinuity and similarity [6]. In formal way, the first one image segmentation approach is based on partitioning of image into edges and corners on the basis of changing in the intensity value of pixel. The second image segmentation approach is based on segment an image into regions. It is based on the similarity criteria. There are many segmentation techniques are used such as, artificial intelligence based segmentation method, histogram based method, and region based method, physical based method, network based method and clustering method as Fuzzy c means clustering, K mean clustering and Exception Maximization, Mean shift clustering [7-9].

The segmentation [10] can be achieved by the clustering. Clustering can be performed one of two different ways, either by the grouping [11] of the pixels or either by the partitioning of the pixels. In the grouping, the pixels are collected together on the basis of some condition. Whereas in portioning the image are divided into regions based on some criteria. There are many clustering algorithms used to perform the segmentation. *Abdel-Maksoud et al* authors proposed hybrid clustering techniques. Authors integrate the fuzzy c-means [12] algorithm with k-means algorithm. To follow the thresholding and image segmentation stage authors provide accurate brain tumor detection. Authors take the benefits of both techniques, k-means clustering algorithm takes the minimal computation time for image segmentation and FCM clustering algorithm provides the accuracy for "image segmentation". Results of proposed algorithms authors evaluated it by comparing it with pervious developed algorithm and performance also checks by the processing time and accuracy of the algorithm [13].

Melegy et al proposed a segmentation method for "normal" and "pathological" brain MRI images with the help of fuzzy approaches. In the present paper authors developed an "automatic segmentation" method. The method names are given by the authors for this method is PIGFCM. With the help of this method brain tissues are separated with "grey" matter, "white" matter "cerebrospinal" fluid. This separation done by the prior information. Pathological brain has no of more class's like's necrosis and edema abnormal tissues classes' .This method applied on the both images like real and simulated images [14].

Huang et al. worked on the classification problem. Author proposed segmentation method by using classification. We know that promiscuous brain segmentation is a very difficult task because we find the "diversity" and "ambiguity" in brain boundaries. Author proposed an automatic segmentation method, it is novel method for solving these problem. The method name is LIPC, it is based on classification. With the help of proposed LIPC method authors classify all voxel into different-different classes. With the help of LIPC authors divide all data into classes, these classes are belongs into

different-different class's model. Author checks the proposed method by using synthetic and online available data [15].

Makropoulos et al proposed a method for the segmentation a neonatal brain it is very challenges task. In this paper author used EM ("Expectation maximization") algorithm. Author use the brain images of 24 weeks neonatal. Apply the method is more than 24 weeks neonatal brain image is the future work of the paper.

Hamamci et al worked on the T1 weighted image of the brain. Author used the "Cellular automata" based method.
This method work on the bases of shortest path, authors used it for the segmentation. After the segmentation author work on the "heterogeneous" brain segmentation. Author used the segmentation techniques as a "Tumor -cut" for divide the tumor tissues into many parts.

II. PROPOSED ALGORITHM

The present work contains a proposed method for the Brain tumor detection taking MRI images as input. The method proposed is based on two algorithms:

- Genetic Algorithms

- FCM Clustering Algorithm

The figure 2 shows the flowchart explaining the working of the proposed method. There are four main parts which are followed in order to obtain the desired results.
Step 1. Input Brain MRI images.
Step 2. Apply Pre-processing for remove the noise or De-noising
Step 3. Perform Clustering using hybrid techniques (Genetic and fuzzy c-means techniques)
Step 4. Detecting the tumor from the above processes images

1. Pre- Processing
This phase is the first phase of the implementation. In this phase removes the noise from the images and improves the images quality. Brain images should have minimum noise and maximum quality because these are more sensitive in comparison to the other medical images.
The Magnetic Resonance Images are corrupted by the Poisson and Gaussian noise [18]. There are many algorithms to de-noising the Magnetic Resonance Images. These algorithms are designed to elimination the Gaussian and Poisson noise from the Magnetic Resonance brain images. In there, we used the median filter for de-noising the image I1. Median filter is an effective and nonlinear method for elimination of noise. . It is low pass filter to reduce the noise. It can do excellent job of rejecting certain type of noise. Median filter woks on moving pixel to pixel of the images. The median value for each pixel is calculated and each pixel value is replaced by its neighboring pixel value. Median filter has the pattern of the

neighbor, it is called the window. Windows are sliding window that slide from one pixel to another pixel over the whole image.
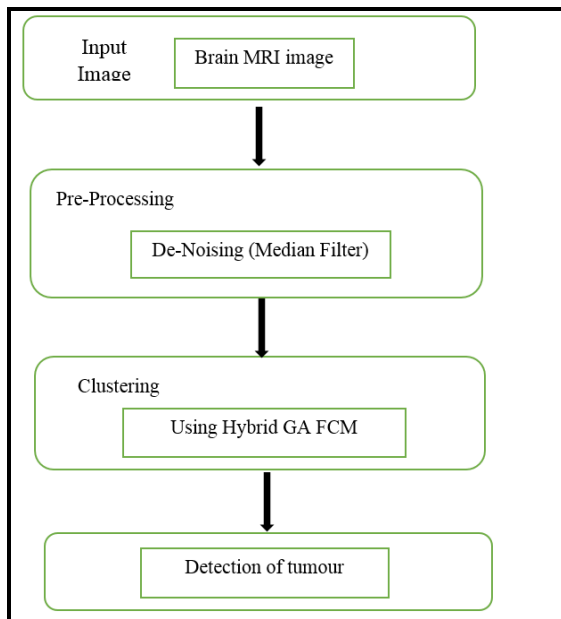

Figure 2. Flowchart of the proposed method

2. *Clustering through the Hybrid GA FCM*

Clustering marks the third step in the method proposed. Pre-Processing was followed by the clustering of the image I2 for tumor detection. To detect the tumor from the MRI brain image I2, we use FCM clustering optimization by GA. The FCM algorithm is determined by the choices of initial cluster centers, so its effect goes to the clustering results. To overcome this effect and get better results for detecting the tumor from Magnetic Resonance brain images, we proposed hybrid Genetic Fuzzy C – means method. A clustering technique based on GA suggested by Maulik et al. [19], minimizes the objective function of Fuzzy C – means by using Genetic algorithm. In proposed work Genetic algorithm used to minimize the DB index.
Figure 2 shows the flowchart containing the Hybrid structure of Genetic FCM algorithm.

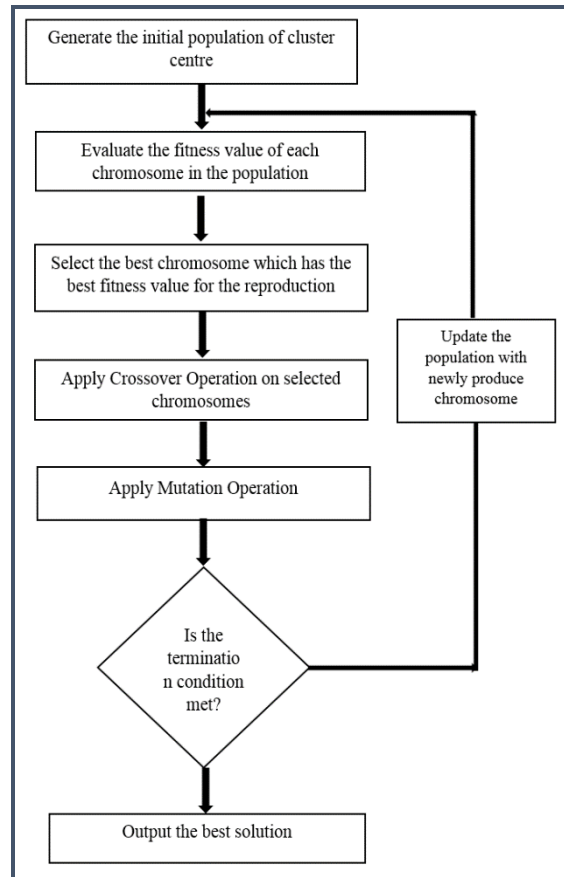The steps are explained in detail below:

Figure 3 Hybrid Structured Genetic FCM Flow chart.

Step 1. *Population initialization*
In starting we select the random values of the centers, and in starting we have k number of cluster as C_1 , C_2 , C_3……..,C_k. , and each cluster has its own center like$\{q_1$,q_2 , q_3……$q_k\}$. The T number of chromosomes initialized randomly for each of the centers. So the population size is T*k.

Step 2. *Calculate the fitness value*
In this, we have a fittest function which is used for the evaluation of the fitness value for the each of the T chromosomes. This fitness function is constructed from the Fuzzy C – means algorithms [20]. From this function we evaluate or update the value of the cluster center of image I2.
This step divides into two phases. These are following.
Phase I. Find the cluster of images I2 by using one iteration of the Fuzzy C – means.
Phase II. Compute the DB index [21] value of the fined above cluster.
Phase I Clustering
In phase I, we used an operator called the one iteration Fuzzy C – means. In Tumor detection from the MRI brain image we need two clusters; these clusters represent the Tumor and Non Tumor area. So, we assigned the value 2 for k. For each of the

population of image I2, it is decrypted to obtained cluster centers. The cluster centers are then updated using the scheme below.

The membership of the sample (point of image I2) s_j to cluster centre q_i.

$$u_{ij} = \left(\sum_{l=1}^{k} \left(\frac{\|q_i - s_j\|}{\|q_l - s_j\|} \right)^{2/(\mu-1)} \right)^{-1} \quad (1)$$

The value for i ranges from 1 to k and that of j ranges from 1 to T, where k is the no cluster and μ ($1 < \mu \le \infty$) is the fitness index. And u_{ij} is the membership to the cluster center of each point of the image I2.

By this eq. 2 the cluster centre is updated.

$$q_i = \frac{\sum_{j=1}^{n} u_{ij}^{\mu} s_j}{\sum_{j=1}^{n} u_{ij}^{\mu}} \quad (2)$$

q_i Are the updated Centres.
Phase II: Validity Index of cluster.

$$I_{i,z} = \left(\frac{1}{N_i} \sum_{j=1}^{N_i} \| s_j - q_i \|^z \right)^{1/z} \quad (3)$$

Where q_i is the centre of the C_i cluster of ith position.

$$ds_{ij,t} = \| q_i - q_j \| \quad (4)$$

$ds_{ij,t}$ represents "Minkowski" distance that characterizes the clusters C_i and C_j with centroids q_i and q_j of order t in image I2.
Next $V_{ij,t}$ is defined below.

$$V_{ij,t} = \max_{i,j \ne i} \left\{ \frac{I_{i,z} + I_{j,z}}{ds_{ij,t}} \right\} \quad (5)$$

DB Index can be interpreted as,

$$DB = \frac{1}{K} \sum_{i=1}^{k} V_{ij,t} \quad (6)$$

In order to obtain appropriate number of clusters DB index is minimized.

Step 3. *Selection*
Chromosomes selected in this way, the fittest chromosomes have fittest value (chromosomes that minimize the DB Index value are chosen) for the reproduction.

Step 4. *Crossover*
A single-point crossover is used having a fixed crossover rate of k_c. If the crossover is not used there will be high similarity between the reproduced chromosomes and the parent chromosomes.

Step 5. *Mutation*
Mutation is another operator of genetic. Mutation process takes place by replacement of the genes of chromosomes randomly at different positions with a new value. Mutation rate is k_m each chromosomes is mutated with this rate.

Step 6. *Termination criterion*
1. If the number of iteration is reached.

2. If we get the minimum improvement between consecutive iterations and it is below the threshold value then the whole procedure is terminated and the output obtained is the best solution.

Otherwise, some of the chromosomes belonging to older population are updated and steps 2 through 5 are repeated for newly produced chromosomes.

4. Detection of tumor
The resulting RM matrix is H× W, where H represents the number of rows, W represents the number of column, this matrix consisting of ones and zeros pixel values, these values are indicating "Tumor" and "Non-Tumor" pixels respectively. Each cluster C_1 and C_2 has an associate cluster center q_1 and q_2 respectively; these are obtaining from Hybrid Genetic Fuzzy C mean. C_1 and C_2 are clusters these have Tumor and Non-Tumor pixels respectively in Image I2.

$$RM(m,n) = \begin{cases} 1 & \| S(m,n) - q_1 \|^2 \le \| S(m,n) - q_2 \|^2 \\ 0 & otherwise \end{cases}$$

$\| S(m,n) - q_1 \|^2$ Denotes Euclidean distance between the cluster center and points representing the input image

III. EXPERIMENT AND RESULT

To check the execution and results of the proposed method, we work on three data sets. First is DICOM [22]. DICOM data set contains the 22 MRI images of brain tumor. All DICOM data set files have ".DCM" extension. All files are encoded into the JPEG format. DICOM has no basic fact images for implied images. Next is BW data set [23]. The files extension of this dataset has ".MNC". BW data set is the phony data base. It contains three sequence of images T1, T2 and proton density images. This data set consist 152 brain MRI images. The last data set used BRATS [24] data set. The BRATS data set consists 30 glioma patients image along with "edama" and "active tumor". BRATS data set has the ground truth picture for evaluate the result of the introduced method. BRATS' data set consists the 81 brain MRI images.
The table 1 shows the real images that are used in this paper. The ground truth detection of tumor obtained by manual analysis and by ground truth images. This work implemented using MATLAB R2015a. We run our experiment on Intel Core i5-5200U CPU 2.20 GHz 4 GB RAM. The value of the

various parameter of proposed Genetic FCM method are k_m = 0.001, k_c =0.5, μ = 2 the maximum number of iteration are used is equal to 100. The quality result shown in Table 1. The results obtains from the three deferent data sets MRI brain Images.

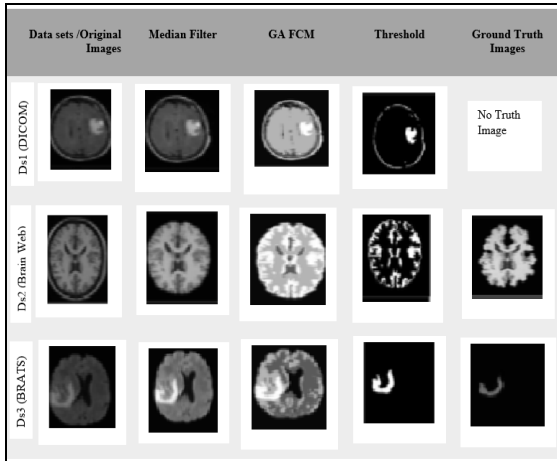Table 1 Show the result of the main stages of the proposed Method applied on three datasets,

Figure 4 Snapshot of the tumor area by using MATLAB

Table 2 Show the performance matrix of the K-means and EM methods.

Clustering Based Techniques																
K-means								Expectation Maximization								
Data sets	TP	TN	FP	FN	Accuracy	Precision	Recall	TP	TN	FP	FN	Accuracy	Precision	Recall		
Ds2	85	0	0	14	85.8	100	85	66	0	0	33	66	100	66		
Ds3	86	0	0	3	86	100	86	78	0	0	4	78	100	78		

Table 3 shows the performance matrix of the Proposed method.

Performance of Proposed method							
GAFCM							
Data sets	TP	TN	FP	FN	Accuracy	Precision	Recall
Ds2	127	13	7	5	92.1	94.77	96.2
Ds3	73	0	8	0	90.1	90.1	100

The performance proposed technique are calculated by the five techniques.
These are the following techniques.

1. TP(True Positive) = Number of image, that have tumour
2. TN(True Negative) = Number of image have not brain tumour
3.
$$FP(Flase\ Positive =$$
$$Number\ of\ images\ that\ have\ not\ tumour\ but\ detected\ as\ a\ positve\ result)$$

4. FN(Flase Negative) = Number of images have tumour but not detected
5. Recall = $\left[\dfrac{TP}{(TP+FN)}\right]$
6. Precision = $\left[\dfrac{TP}{(TP+FP)}\right]$
6. Accuracy = $\left[\dfrac{(TP+TN)}{(TP+TN+FP+FN)}\right]$

IV.   CONCLUSION

In this paper we proposed a method for detection the tumour from MRI images. We know image segmentation play important role in the medical fields. Here, two techniques integrate to detect the brain tumor from the MRI images. First one is Genetic algorithm for optimization integrate with the second one is FCM is algorithm for clustering. The accuracy and computation time of proposed method is very impressive. Tumor detection method has been successfully work on the given data sets images. The work in the implementation can be enhanced by find the type, and size of the tumor, shape and tumor location and finding changes growth present of the tumor for same patient.

V.   REFERENCE

[1] J. C. Buckner, P. D. Brown, B. P. O'Neill, F. B. Meyer, C. J. Wetmore, J. H. Uhm, "Central nervous system tumors." InMayo Clinic Proceedings, Vol. 82, No. 10, pp. 1271-1286, October 2007.

[2] K. A. Jellinger - The human nervous system: structure and function: Six Edition; European Journal of Neurology, 2009.

[3] D. N. Louis, H. Ohgaki, O. D. Wiestler, W. K. Cavenee, P. C. Burger, A.Jouvet, B.W. Scheithauer, P. Kleihues, "The 2007 WHO classification of tumors of the central

nervous system." Acta neuropathologica , Vol. 114, No. 2, pp. 97-109, August 2007.

[4] N. Tirpude, R. Welekar, "Automated detection and extraction of brain tumor from MRI images." *Int J Comput Appl*, pp. 26 - 30,Vol.77,No.4, January 2014.

[5] Y. Lu, J. Jiang, W. Yang Wei, Q. Feng and W. Chen "Multimodal Brain-Tumor Segmentation Based on Dirichlet Process Mixture Model with Anisotropic Diffusion and Markov Random Field Prior." *Computational and mathematical methods in medicine,* September 2014.

[6] J. C. Buckner, P. D. Brown, B. P. O'Neill, F. B. Meyer , C. J. Wetmore, J. H Uhm. "Central nervous system tumors." In*Mayo Clinic Proceedings*, Vol. 82, No. 10, pp. 1271-1286, October 2007.

[7] R. A. Novellines, M. D. - Squire's fundamentals of radiology; Six Edition; UPR, 2004.

[8] K.K.Singh and A. Singh, "A Study of Image Segmentation Algorithms for Different Types of Images",*International Journal of Computer Applications,* Vol.7, No.5, pp.414-417, 2010.

[9] C. Xiaohao, R. Chan, T. Zeng, "A two-stage image segmentation method using a convex variant of the Mumford--Shah Model and thresholding." Vol. 6, No. 1, pp. 368 - 390, February 2003.

[10] K.K.Singh, A. Mehrotra, M.J.Nigam, K.Pal, "A novel edge preserving filter for impulse noise removal", 2011 International Conference on Multimedia, Signal Processing and Communication Technologies (IMPACT), pp. 103-106, 2011.

[11] Janani, P. Meena. "Image segmentation for tumor detection using fuzzy inference system." *Int J Comput Sci Mobile Comput (IJCSMC)*, Vol. 2, No. 5, pp. 244 - 248, May 2013.

[12] J. Selvakumar, A. Lakshmi, T. Arivoli. "Brain tumor segmentation and its area calculation in brain MR images using K-mean clustering and Fuzzy C-mean algorithm." *Advances in Engineering, Science and Management (ICAESM), 2012 International Conference,* Vol. 7, No. 7, pp. 186 – 190, October 2015

[13] E. A. Maksoud, M. Elmogy, R. Al-Awadi "Brain tumor segmentation based on a hybrid clustering technique." *Egyptian Informatics Journal* Vol. 16, No. 1, pp. 71 – 81, March 2015.

[14] M. T. El-Melegy, H. M. Mokhtar, "Tumor segmentation in brain MRI using a fuzzy approach with class center priors." *EURASIP Journal on Image and Video Processing*, January 2014.

[15] M. Huang, W. Yang, Y. Wu, J. Jiang and W. Chen "Brain Tumor Segmentation Based on Local Independent Projection-Based Classification." *IEEE Transactions on Biomedical Engineering*, Vol. 61, No. 10, pp. 2633 – 2645, October 2014 .

[16] A. Makropoulos, I. S. Gousias, C. Ledig, P. Aljabar, A. Serag and J. V. Hajnal, A. D. Edwards, S. J. Counsell, D. Rueckert. "Automatic whole brain MRI segmentation of the developing neonatal brain." *Medical Imaging, IEEE Transactions,* Vol. 33, No. 9, pp. 1818 – 1831, September 2014.

[17] A. Hamamci, N. Kucuk, K. Karaman, K. Engin and G. Unal, "Tumor-cut: segmentation of brain tumors on contrast enhanced MR images for radiosurgery applications." *Medical Imaging, IEEE Transactions,* Vol. 31, No. 3, pp. 790 – 804, March 2012.

[18] Parker, Jim R. *Algorithms for image processing and computer vision*. John Wiley & Sons, 2010.

[19] Maulik, Ujjwal, and Sanghamitra Bandyopadhyay. "Genetic algorithm-based clustering technique." *Pattern recognition* 33, no. 9 (2000): 1455-1465.

[20] F. Höppner, F. Klawonn, and R. Kruse, Fuzzy Cluster Analysis: Methodsfor Classification, Data Analysis, and Image Recognition. New York:Wiley, 1999.

[21] D. L. Davies and D. W. Bouldin, "A cluster separation measure," IEEE Trans. Pattern Anal. Mach. Intell., vol. 1, no. 2, pp. 224–227, Apr. 1979.

[22] DICOM Samples Image Sets. <http://www.osirix-viewer.com/ datasets/>; [accessed 29.12.13].

[23] Brain Web: Simulated Brain Database. <http://brainweb.bic. mni.mcgill.ca/brainweb/>; [accessed 30.12.13].

[24] MICCA Nice 2012. <http://www2.imm.dtu.dk/projects/ BRATS2012/data.html>; [accessed 12.01.14].