BRAIN TUMOR DETECTION USING FUUZY CO-CLUSTERING FOR IMAGES ALGORITHM

MAJOR PROJECT SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF DEGREE OF

Master of Technology

In

Information Systems

Submitted By:

HEENA HOODA

(2K11/ISY/07)

Under the Guidance of

Dr. O. P. Verma

(HOD, Department of IT)

DEPARTMENT OF INFORMATION TECHNOLOGY
DELHI TECHNOLOGICAL UNIVERSITY
(2011-2013)

CERTIFICATE

This is to certify that **Heena Hooda (2K11/ISY/07)** has carried out the major project titled **"Brain Tumor Detection using Fuzzy Co-Clustering for Images Algorithm"** in partial fulfillment of the requirements for the award of Master of Technology degree in Information Systems by **Delhi Technological University**.

The major project is a bonafide piece of work carried out and completed under my supervision and guidance during the academic session **2011-2013**. To the best of my knowledge, the matter embodied in the thesis has not been submitted to any other University / Institute for the award of any Degree or Diploma.

Dr. O. P. Verma
Head of Department
Department of Information Technology
Delhi Technological University
Delhi-110042

ACKNOWLEDGEMENT

I take the opportunity to express my sincere gratitude to my project mentor Dr. O.P. Verma, Head of Department, Department of Information Technology, Delhi Technological University, Delhi for providing valuable guidance and constant encouragement throughout the project .It is my pleasure to record my sincere thanks to him for his constructive criticism and insight without which the project would not have shaped as it has.

I humbly extend my words of gratitude to other faculty members of this department for providing their valuable help and time whenever it was required.

Heena Hooda

Roll No. 2K11/ISY/07

M.Tech (Information Systems)

E-mail: heenahooda@gmail.com

ABSTRACT

Medical image processing is currently the most emerging and challenging area of research in the field of image processing. Magnetic Resonance Imaging (MRI) is one of the most widely used imaging technique for the diagnosis and planning the treatment of brain tumor patients. The mapping of tumor in MRI images is done manually in the clinical environment by the radiologist depending on their visual interpretation. This mapping is very time consuming and tedious task and error prone due to human dependency. To overcome the shortcomings of mapping the tumor manually, the researchers are keen to develop automatic tumor segmentation system. Automatic tumor segmentation system involves contouring the tumor part in the image and using various measures for its quantification. This study presents a fully automatic technique to detect brain tumor from sample MRI images. The proposed strategy makes use of fuzzy co-clustering for images (FCCI) algorithm for initial segmentation of MRI images. The result of the proposed approach corresponds well to the ground truth in tracking the total area of the tumor. The real time database is taken from Rajiv Gandhi Cancer Institute & Research Centre, Delhi, India (RGCI&RC) and results are validated by the radiologist.

Table of Contents

Figures and Tables

Chapter 1

INTRODUCTION

1.1 Background

Medical image segmentation has received significant attention, due to the many practical applications of segmentation results. An impressively large amount of research effort has even focused on specific areas of the body or specific modalities, such as the segmentation of images of the brain in MRI images. Automatic detection and segmentation of brain tumor from brain MR images offer a mechanism for overcoming the effort involved in the manual segmentation of large datasets. It also promises reproducibility which is affected by inter and intra observer variability. But automated systems have significant problems to achieve these objectives. The major problems are, pixel intensities violate the independent and identically distributed assumption within and between images due to the nature of brain MRI images, and presence of a significant amount of artifacts and intensity inhomogeneity in MRI images [1, 2]. Therefore, automated method should take into account these problems to achieve reproducible segmentation results and developing clinically accepted automated methods remains an active research area.

Many techniques have been proposed to automate the brain tumor detection and segmentation in recent years. These techniques are based on morphological operations, edge detection, fuzzy sets theory, classification, region growing, neural networks and clustering and other image segmentation methods. Kiran Thapaliya et al have proposed an effective algorithm to detect brain tumor using morphological gradient and morphological operations [3]. Vidhya S. Dessai et al

have designed a multithreaded framework using k-means clustering and morphological operations in parallel to segment multiple MRI images [4]. Ishita Maiti et al have presented a color based brain tumor segmentation method based on combination of watershed method and edge detection algorithm [5]. H. B. Kekre et al have developed a vector quantization segmentation method along with morphological operations to find out cancerous mass from MRI images [6]. Sudipta Roy et al have presented a fully automatic algorithm for detection of brain tumor using symmetric analysis and watershed segmentation [7]. Dr. M. Karnan et al have made use of ant colony optimization along with fuzzy c-means algorithm for brain MRI image segmentation [8]. Rajendran et al have proposed a region based fuzzy c- means clustering for brain tumor segmentation in [9]. The method uses the tumor class output of fuzzy clustering to initialize the region based algorithm, the region based moves towards the final tumor boundary. M.A. Jaffar et al have proposed an automatic brain MR image segmentation method using curvelet transform for noise removal and FCM for the automatic segmentation of brain MR images in [10]. Ming–Ni Wu et al have proposed a color based segmentation algorithm using k-means clustering and histogram clustering to segment the position of tumor from other objects from input MRI images [11]. R. B. Dubey et al have explored the comparison of level set method; modified watershed approach and modified region growing method for extraction of tumor from brain MRI images [12]. N.Nandha Gopal et al have presented an intelligent system to diagnose brain tumor using Fuzzy C means along with optimization techniques [13].

Thresholding based tumor detection and segmentation methods [14, 15] which integrated with watershed and histogram analysis have been proposed. Kadam D. B. et al [16] have used eight textural features to train the MLP network in segmenting brain tumor. Automated brain tumor segmentation with two phases is proposed by Khontalou et al in [17]. In first phase tumor is detected

and segmented by combination of histogram analysis with symmetry analysis using morphological operations. Then tumor is detected by applying fuzzy classification method or symmetry analysis and some morphological operations. A supervised hybrid fuzzy ANN based for tumor detection is proposed in [18] by Pradhan et al. A comparative study of adaptive network based fuzzy inference system (ANFIS), k-nearest neighbors (KNN) and fuzzy c-means (FCM) for brain tumor segmentation is conducted in [19] by Khalid et al. Various methods have already been proposed for brain tumor segmentation [20-22], but still there is a scope to develop significant segmentation technique.

1.2 Motivation

There are diverse motivations for the development of methods for automatic medical image segmentation. Accurate segmentations are needed in clinical and scientific applications, but the need for manual intervention is both time consuming and subject to manual variation. Another motivation for pursuing automatic tumor segmentation methods is alleviating the manual work and reducing the variability associated with defining radiation therapy target areas. This is especially important with respect to new technologies such as radio surgery and intensity-modulated radiation therapy that allow more precise treatment options than traditional technology.

Although manual segmentation by qualified professionals remains superior in quality to automatic methods, it has two drawbacks. The first drawback is that producing manual segmentations is extremely time consuming, with higher accuracies on more finely detailed volumes demanding increased time from medical experts. The second problem with manual segmentations is that the segmentation is subject to variations both between observers and within the same observer. Accurate automatic methods would be advantageous since they are not subject to this variation and thus the significance of changes in volumes could be more easily assessed.

The study of automatic brain tumor segmentation represents an interesting research problem in Machine Learning and Pattern Recognition, since it represents a problem that humans can learn to do effectively, but developing highly accurate automatic methods remains a challenging problem. This is easily explained by the fact that humans must use high-level visual processing, and must incorporate specialized domain knowledge to perform this task [23], which makes developing fully automatic methods extremely challenging.

1.3 Present Work

A fully automatic image segmentation system is presented in the thesis for detection of brain tumor from MRI images. Image Segmentation is carried out with the help of fuzzy co-clustering for images (FCCI) algorithm and the parameters used in FCCI are optimized using bacterial foraging optimization algorithm. The segmented image along with the intracranial mask extracted from sample MRI images is used to detect and extract brain tumor and calculate the area of tumor from sample MRI scan images of the brain. The result of the proposed system matches up well with the ground truth in mapping tumor on the MRI images and quantifying the area of tumor. This work is being carried out in collaboration with Rajiv Gandhi Cancer Institute and Research Centre, Delhi. It is a retrospective analysis of about 50 patients diagnosed with brain tumor. For this purpose the real time MRI image database is taken along with their reports. The effectiveness of the proposed technique is validated with the opinion of the radiologist from RGCI & RC, Delhi, India.

1.4 Thesis Organization

The remainder of the thesis is organized as follows: chapter two is a detailed discussion of the medical background required to understand the process of brain tumor detection. This chapter

includes the anatomy of brain, Medical Resonance Imaging (MRI), and brain tumor. The chapter three gives a brief introduction about segmentation, techniques based on segmentation and its application in medical field. The fourth chapter presents the Bacterial Foraging Optimization Algorithm (BFOA) used to optimize the parameters involved in our system along with the algorithm. Similarly, chapter five provides a detailed discussion of the Fuzzy Co-Clustering for images (FCCI) algorithm and its advantages over other clustering techniques. Chapter six presents the proposed tumor detection and segmentation framework. This chapter includes a brief discussion on the first two modules, preprocessing and segmentation using FCCI, of the proposed frame work. Chapter seven presents the results and validates the output of the proposed tumor detection and segmentation system against ground truth. Also it presents some sample results for qualitative evaluation and discussion on the results. Finally, chapter eight concludes the thesis and presents ideas for future work.

Chapter 2

MEDICAL BACKGROUND

2.1 Brain Anatomy

Brain is extremely focused organ of the human body which helps us to cope with the environment. Human brain serves as the manager for all the functions performed by the body such as words, actions, thoughts, and feelings that are centered in the brain. In this section we describe the brain tissue structure and its anatomical parts.

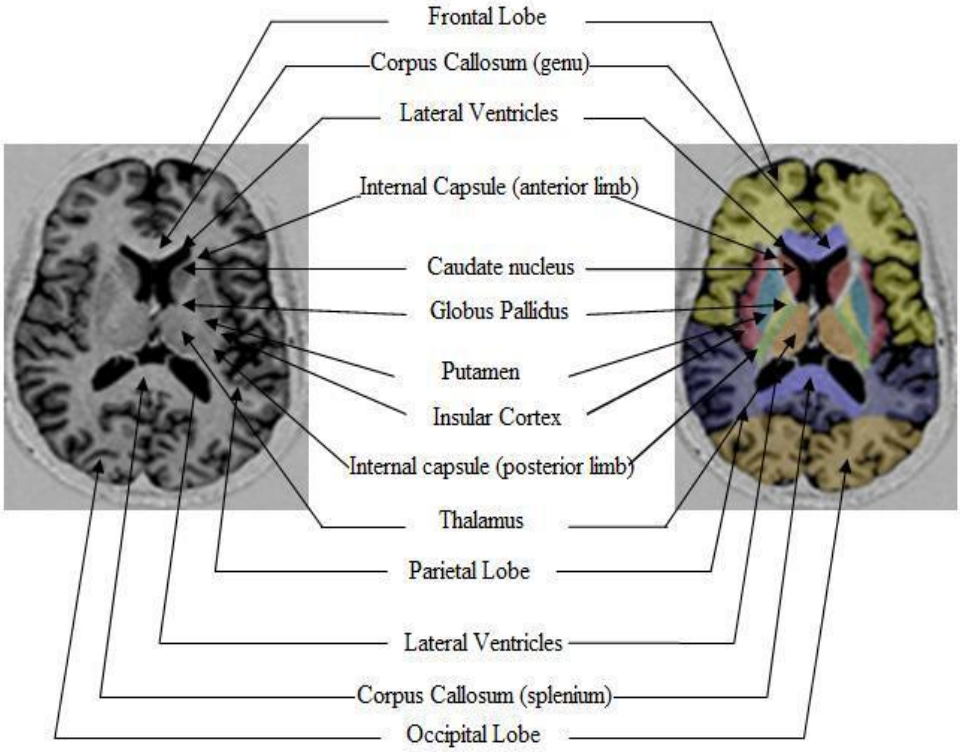


Figure 2.1 Overview of Human Brain Structure in MRI

The brain mainly comprises of two types of tissue as shown in figure 2.1: gray matter (GM) and white matter (WM). Gray matter consists of neuronal and glial cells, also known as neuroglia or glia and the basal nuclei. The former controls brain activity and the later are the gray matter nuclei located deep within the white matter. The basal nuclei are made of caudate nucleus, putamen, pallidum and claustrum. White matter fibers are myelinated axons which connect the cerebral cortex with other brain parts. The corpus callosum, a thick band of white matter fibers, joins the left and right hemispheres of the brain [24].

The brain also contains cerebrospinal fluid (CSF) that consists of glucose, salts, enzymes, and white blood cells. This fluid circulates through ventricles around the brain and the spinal cord to protect them from injury. There is also another tissue called meninges used as membrane for covering the brain and spinal cord [24].

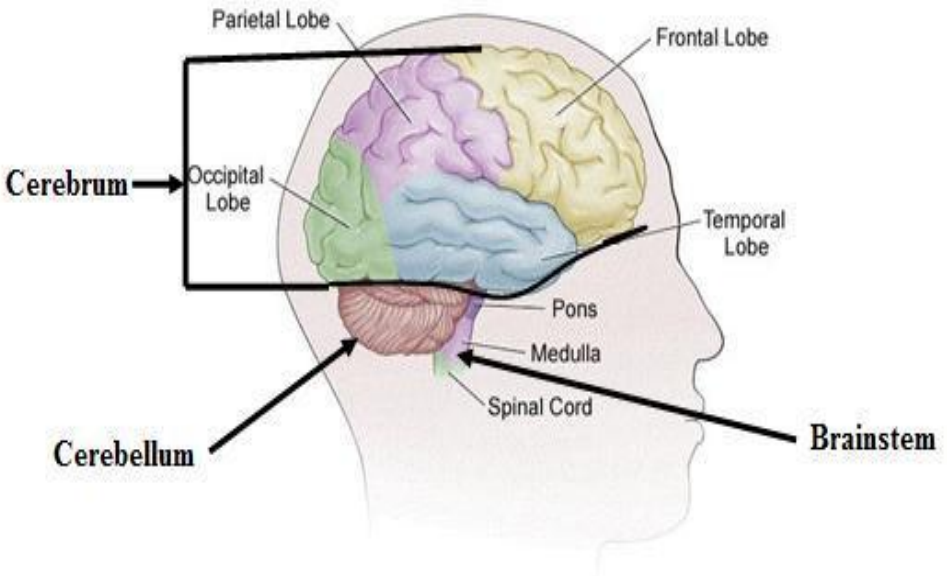


Figure 2.2 Anatomy of human brain

Anatomically the brain is composed of the cerebrum, the cerebellum and the brain stem as shown in figure 2.2. The largest part of the brain is the Cerebrum which helps in controlling conscious thought, movement and sensation of human body. It comprises of two halves, the right and left cerebral hemispheres, each managing the opposite part of the body. Each hemisphere is divided into four lobes: the frontal, temporal, parietal, and occipital lobes. The second largest part of the brain is the cerebellum which helps in controlling motor functions such as walking, balance, posture, and coordination of movement of human body. It is situated at the back of the brain and is connected to brain stems. Both cerebrum and cerebellum have a thin outer cortex of gray matter, internal white matter and deeply situated masses of gray matter. The brainstem is located at the bottom of the brain and connected to spinal cord. It controls many vital functions including motor and sensory pathways, cardiac and repository functions, and reflexes. It has three structures: the midbrain, pons and medulla oblongata [24].

2.2 Magnetic Resonance Imaging

A variety of imaging techniques are used to study parts of human body, including computed tomography (CT), magnetic resonance (MR) imaging, and single photon emission computed tomographic (SPECT) imaging, positron emission tomographic (PET) scanning, and cerebral angiography. At this moment, CT and MR imaging are the most widely used techniques, because of their widespread availability and their ability to produce high resolution images of normal anatomic structures and pathological tissues. CT is the fastest modality, making it the preferred examination for imaging critically ill or medically unstable patients. SPECT and PET imaging serve smaller roles, although their ability to provide information on tissue biology and physiology can be greatly helpful. PET scanning is also used to evaluate tumor grade.

Magnetic Resonance Imaging (MRI) is a powerful visualization tool that permits to acquire images of internal anatomy of human body to be acquired in a secure and non-invasive manner. It is based on the principles of Nuclear Magnetic Resonance (NMR), and allows a vast array of different types of visualizations to be performed. This imaging medium has been of particular relevance for producing images of the brain, due to the ability of MRI to record signals that can distinguish between different 'soft' tissues (such as gray matter and white matter) [26].

In brain imaging, two of the most commonly used MRI visualizations are T1-weighted and T2-weighted images. These weightings refer to the dominant signal (whether it be the T1 time or the T2 time) measured to produce the contrast observed in the image [26]. Since areas with high fat content have a short T1 time relative to water, T1-weighted images can be thought of as visualizing locations of fat. In contrast, since areas with high water content have a short T2 time relative to areas of high fat content, T2-weighted images can be thought of as visualizing locations of water.

2.2.1 Pros and Cons of MRI

MRI is the most frequently used neuroimaging technique for the evaluation and follow up review of patients with brain tumors for many reasons. It does not use ionizing radiation like CT, SPECT, and PET studies. Its contrast resolution is higher than the other techniques, making it preferable for detecting small lesions and isodense lesions on unenhanced CT. Also, it is more sensitive than CT to detect lesion enhancement. The ability of MRI devices to generate images in the sagittal, axial and coronal planes provides better localization of a lesion in the 3D space of the brain and allows structures involved by the tumor to be more clearly delineated. Finally, MR imaging eliminates the beam-hardening artifact produced by the skull base on CT, making it better for evaluating lesions in the posterior fossa and in the inferior frontal and temporal lobes. The

acquisition of both functional and anatomical information about the tumor during the same scan may be the most important benefit of MR imaging [27].

Despite of several advantages there are some limitations to MRI that must be acknowledged. The most important being the lack of specificity. Although, enhancement does not always correspond to histologic tumor grade, in general, higher grade tumors will frequently show enhancement on MR imaging. However, an exception can be seen in a very slow-growing tumor which will frequently show contrast enhancement regions within the tumor. Similarly, some higher grade tumors will not enhance [28]. Hence, although MR features of a lesion can be helpful, but sometimes histologic verification is necessary to perform a diagnosis. MR imaging is also not able to distinguish the edge of a tumor, or determine the full extent of disease. Possible tumor cells are known to exist beyond the borders of abnormal contrast enhancement [28]. Hence, MRI alone cannot be applied to determine whether tumor is present or not following such a therapy. In spite of these limitations, MRI remains the standard imaging technique in human neurooncolgy.

2.3 Brain Tumor

A brain tumor is the mass of tissue that grows abnormally due to uncontrollable cell multiplication. The growth of a tumor takes place within the skull and interferes with normal brain functions. Tumor can harm brain by increasing pressure inside it, pushing against the skull, and by attacking and damaging nerves and healthy brain tissues [29].

Brain tumors are classified depending on the location of the tumor, the type of tissue, whether they are noncancerous (benign) or cancerous (malignant) and site of origin (primary or secondary) [30]. World Health Organization (WHO) classifies brain tumors into more than 120 types. According to WHO, the classification of brain tumor is done on the basis of by cell origin and

behavior of the cells from benign to malignant. Types of tumor are also assigned a grade, ranging from Grade I to IV depending on the rate of growth of malignant; though there are variations in grading systems depending on the tumor type [29].

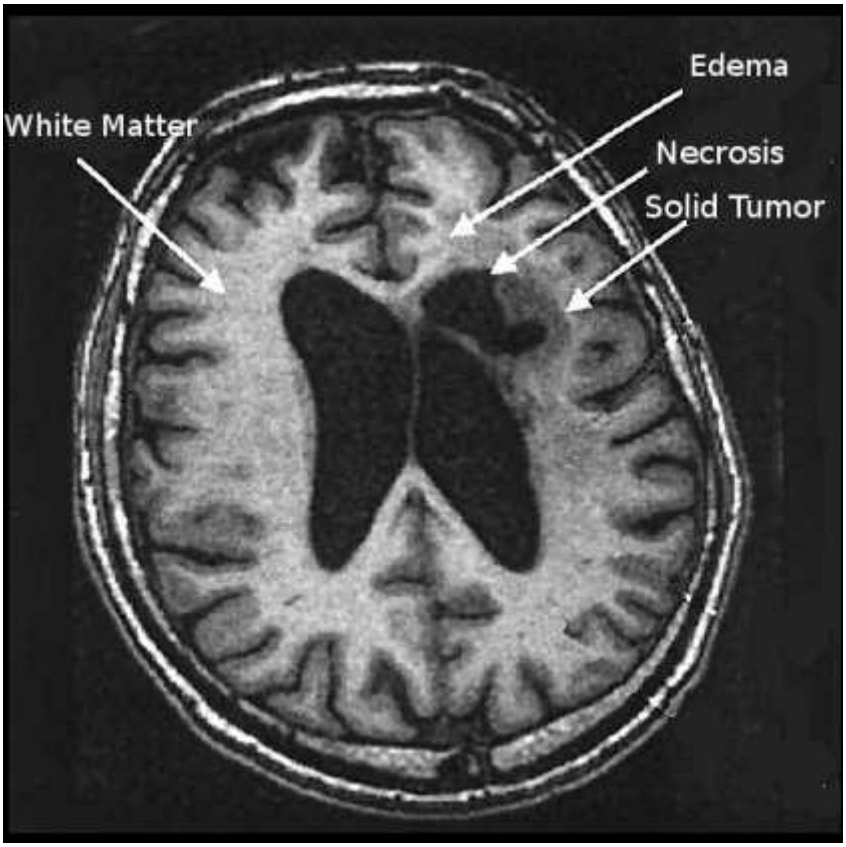


Figure 2.3 Brain MRI image showing tumor areas

The tumors that originated in the brain and are named for the cell types from which they originated are known as primary brain tumors. Benign tumors grow slowly and do not spread elsewhere or affect the surrounding tissues. However, growing in a limited space, a benign tumor can put pressure on the brain and compromise its function. On the other hand, malignant tumors grow quickly and can invade the surrounding tissues. Each of these tumors has unique clinical, radiographic and biological characteristics. Secondary brain tumors originate from another part of the body. These tumors are

actually composed of cancer cells from somewhere else in the body that have metastasized, or spread, to the brain. The secondary brain tumors are commonly caused by lung cancer, certain sarcomas, breast cancer, melanoma, bladder cancer, and testicular and germ cell tumors [29].

2.3.1 Role of MRI in Brain Tumor

Imaging plays a vital role in treatment of brain tumor patients at different stages and usually has a significant job in each of them. Several phases of management can be considered:

- detection or confirmation that a structural abnormality is present,
- localization and assessment of the extent of any abnormality,
- characterization of the abnormality,
- assessment of the nature of a tumor,
- facilitation of additional diagnosis procedures, and planning for surgery or other types of therapy,
- intraoperative control of rejection progress,
- monitoring of response to therapy.

Chapter 3

IMAGE SEGMENTATION

3.1 Introduction

Image segmentation is one of the most important tasks of image analysis. Segmentation is defined as a technique which subdivides an image into its constituent regions or objects depending on the problem being solved [31]. The process of image segmentation should stop when the object of interest is found. Every pixel in an image is allocated to one of the regions. The main objective of image segmentation is to divide an image into regions having high degree of correlation with objects of significance in the image. A good segmentation is typically one in which pixels in the same category have similar grey scale of multivariate values and form a connected region and neighboring pixels which are in different categories have dissimilar values.Segmentation can be mainly classified into complete and partial. The resultant disjoint regions of complete segmentation correspond exclusively with input image objects. While the resultant regions in partial segmentation do not correspond exclusively with input image. Image segmentation is often considered as a pattern recognition problem since classification of pixels is involved in the process of segmentation [33].

3.2 Techniques of Image Segmentation

On the basis of different properties of an image, the approaches to image segmentation can be classified into discontinuity based segmentation and similarity based segmentation [32]. In discontinuity based segmentation the image is divided on the basis of sudden change in intensity.

This includes techniques like edge detection. While in similarity based segmentation the image is divided into regions which are similar depending on a set of predefined criteria. This includes techniques like thresholding, region growing and clustering.

3.2.1 Edge Detection based Segmentation

Edge detection based segmentation attempts to resolve image segmentation by detecting the edges or pixels between different regions that have abrupt changes in intensity [32]. This results in a binary image. Edge based techniques do not require a priori information about the image content and is comparatively faster in computation. On the basis of theory edge based segmentation methods can be classified into gray histogram and gradient based method [34]. Region boundaries and edges are strongly related as there is often a sharp transition in intensity at the region boundaries. Another segmentation technique use edge detection techniques as the basis for segmentation process. The edges identified by edge detection are often disconnected. To segment an object from an image however, one needs closed region boundaries. The desired edges are the boundaries between such objects.

3.2.2 Thresholding based Segmentation

Thresholding based segmentation is easy but effective technique for segmenting images having light objects on dark background [32]. Thresholding algorithms are fast and economical in computation but require prior knowledge about image. Multilevel image is converted into a binary image by applying thresholding operation. A proper threshold T is chosen, to divide image into objects and split objects from background. Any pixel (x, y) is assigned to a region whose intensity is greater than or equal to threshold value T, else pixel is assigned to background [35]. On the basis of choosing the value of threshold, two types of thresholding techniques are global and local

Thresholding. In global thresholding T is constant whereas in local thresholding there can be multiple thresholds to compensate uneven illumination. Threshold selection is generally done manually however it is possible to choose threshold by automatic thresholding selection algorithms. Limitation of thresholding method is that it is sensitive to noise as it does not take into account spatial features of an image.

3.2.3 Region based Segmentation

Region based segmentation is relatively simple and has higher noise immunity as compared to edge detection method [34]. Region based segmentation is used to divide an image into regions that are similar according to some predefined criteria [32]. Segmentation techniques based on region mainly include following methods:

Region Growing: Region growing is a process [36] that group pixels in whole image into sub regions or larger regions based on predefined criterion [31]. Region growing can be achieved by performing the following steps:-

- Select a group of seed pixels in original image.
- Select a set of similarity criterion such as gray level intensity or color and set up a stopping rule.
- Grow regions by appending to each seed those neighbouring pixels that have predefined properties similar to seed pixels.
- Stop region growing when no more pixels met the criterion for inclusion in that region.

Region Splitting and Merging: Rather than choosing seed points, user can divide an image into a set of arbitrary unconnected regions and then merge the regions [34] in an attempt to satisfy the

conditions of reasonable image segmentation. Region splitting and merging is usually implemented with theory based on quad tree data.

Let R represent the entire image region and select a predicate Q

- We start with entire image if Q(R) = FALSE [1], we divide the image into quadrants, if Q is false for any quadrant that is, if Q (Ri) = FALSE, We subdivide the quadrants into sub quadrants and so on till no further splitting is possible.
- If only splitting is used, the final partition may contain adjacent regions with identical properties. This drawback can be remedied by allowing merging as well as splitting i.e. merge any adjacent regions Rj & R_k for which, Q (Rj U Rk) = TRUE
- Stop when no further merging is possible.

3.2.4 Clustering based segmentation

Clustering is a straight forward technique for classification and easy to implement. Clustering is an unsupervised learning algorithm, where one needs to identify a finite set of categories known as clusters to classify pixels. Clustering use no training stages rather train themselves using available data. Clustering is mainly used when classes are known in advance. A similarity criteria is defined between pixels [37], and then similar pixels are grouped together to form clusters. The grouping of pixels into clusters is based on the principle of maximizing the intra class similarity and minimizing the inter class similarity. The quality of a clustering result depends on both the similarity measure used by the method and its implementation. Clustering algorithms are classified as hard clustering and soft clustering.

3.3 Medical Applications of Image Segmentation

Medical imaging techniques are used in order to gain information on specific organs or parts of human body, physiological abnormalities such as tumors and cysts, or any other structures like bone, cartilage, and vessels. In general, analysis of medical images requires segmentation of the images. Image segmentation is methods are in practical use in field of radiology in order to assist or automate multiple procedures. Significant roles of image segmentation applications in the following areas and this can be observed from references [32].

- Anatomical research on regular body structure,
- Quantification of tissues in several metrics like distance, cross-sectional and surface area, and volume,
- Classification of several special tissues like white matter and gray matter of brain,
- Diagnostic radiology,
- Localization of abnormalities, malfunctions, and pathologies,
- Prognosis and treatment planning,
- 2D and 3D registration of imaging data acquired at various times,
- Computer-aided surgery, and
- Volume correction in functional imaging data.

Chapter 4

BACTERIAL FORAGING OPTIMIZATION ALGORITHM

4.1 Introduction

Bacterial foraging optimization algorithm (BFOA), proposed by Passino [38], has been broadly acknowledged as a global optimization algorithm. BFOA has drawn the interest of researchers from various fields of knowledge since its origin, due to its biological motivation and refined structure. The key idea of this algorithm is inspired by the social foraging behavior of *Escherichia coli* bacteria in multi-optimal function optimization.

4.2 Description

The aim of bacteria in BFOA is to maximize energy attained per unit time in search for nutrients. The locomotion of bacteria is achieved with the help of a set of tensile flagella during foraging. The tumble or swim are the two basic operation performed by the bacteria at the time of foraging. The movement of the flagella can be in the clockwise or counterclockwise direction depending upon the operation (tumble or swim) performed by the bacteria [39].

In BFOA, the bacteria like to move towards a nutrient gradient and avoid unfavorable environment, this process is known as Chemotaxis. The bacteria move for a longer duration in the favorable environment. They are enlarged if they get sufficient food whereas in the presence of suitable temperature they replicate themselves. This phenomenon motivated Passino to introduce a step of reproduction in BFOA. The chemotactic progress may be terminated due to occurrence

of abrupt environmental conditions and a group of bacteria may be traversed to a new location. This comprises the event of elimination-dispersal BFOA.

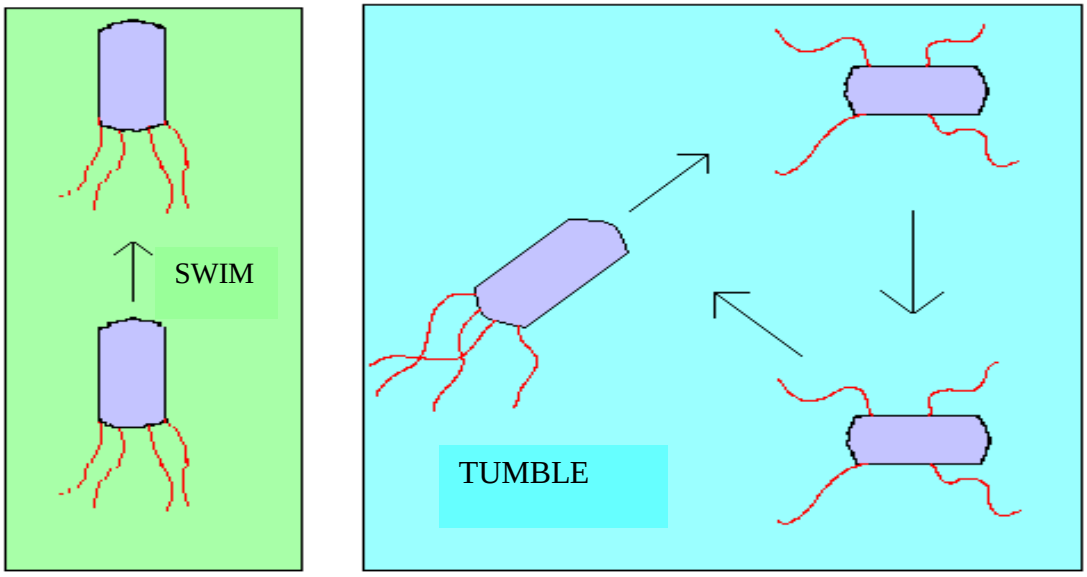


Figure 3.1 Swim and tumble of a bacterium

Hence, a bacterium goes through four phases during its entire lifetime as explained below:

Chemotaxes: The movement of the bacteria in search of nutrients is termed as chemotaxes. It consists of two modes of locomotive behavior, namely tumble and swim. The bacteria tumble when the flagella rotate clockwise. In this motion, there is least displacement and after completion the bacteria is aligned along a random direction. On the other hand, the bacteria swim in counter-clockwise rotation. In this motion bacteria move forward in a particular direction. During its lifetime the bacteria alternates between these modes of motion. In locations with high nutrient concentration the bacteria swims more often than it tumbles and vice versa in areas with less favorable conditions. Thus, by continuously swimming and tumbling the bacteria effectively conducts the foraging process [35]. The tumbling process can be mathematically represented as

$$\theta^i(j+1,k,l) = \theta^i(j,k,l) + C(i)\frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}}$$

Where θ represents *i*-th bacterium at *j*th chemotactic, *k*-th reproductive and *l*-th elimination-dispersal step, *C*(*i*) is the step size taken in the random direction specified by the tumble (run length unit) and Δ indicates a vector in the random direction whose values lie in the range [-1, 1].

Swarming: It has been noticed that several bacteria species including E.Coli form stable spatio temporal ring shaped swarms in the presence of a semi solid nutrient medium. The E.Coli cells when stimulated by a high level of succinate release an attractive called aspertate that helps them aggregate in such groups. This cell-cell attraction can be mathematically represented as [35]

$$J_{cc}(\theta, P(j,k,l)) = \sum_{i=1}^{S} J_{cc}(\theta, \theta^i(j,k,l))$$

$$= \sum_{i=1}^{S}[-d_{\text{attractant}}\exp(-w_{\text{attractant}}\sum_{m=1}^{p}(\theta_m - \theta_m^i)^2)] + \sum_{i=1}^{S}[h_{\text{repellant}}\exp(-w_{\text{repellant}}\sum_{m=1}^{p}(\theta_m - \theta_m^i)^2)]$$

where p is the dimension of search space, $J_{cc}(\theta, P(i, j,k, l))$ is the cost function that is to be added to the original cost function, $d_{attract}$, $w_{attractt}$, $h_{repellant}$, $w_{repellant}$ are the coefficients which determine the depth and width of attractant and height and width of repellant, which are to be selected properly. S is the total number of bacteria; h_{im} is the m_{th} component of i_{th} bacterium position h_i.

Reproduction: In this step, the least healthy bacteria die out. The healthiest bacteria (based on the nutrient function) then asexually split into two (without mutation and crossover) at the locations replacing the dead bacteria. This keeps the swarm size constant.

Elimination and Dispersal: Environmental factors such as running water or extreme temperatures may cause a group of bacteria to die out or get transferred to some other location. To

incorporate this in the algorithm, on the basis of a very small probability some bacteria are killed off and their replacements are placed at random points in the solution space.

4.3 Bacterial Foraging Algorithm

Parameter definition

p: the dimension of the search space

S: the number of bacteria in the population iterated by counter i

N_c: the number of chemotactic steps iterated by counter j

N_s: the number of swims after tumble iterated by the counter m

N_{re}: the number of reproductive steps iterated by counter k

N_{ed}: the number of elimination dispersal events iterated by the counter l

p_{ed}: elimination dispersal probability

C(i,k): the size of step taken in a random direction specified by tumble

The Algorithm:

[Step 1] Initialize all the parameters defined above

[Step 2] Elimination dispersal loop: l=l+1

[Step 3] Reproduction loop: k=k+1

[Step 4] Chemotaxis loop: j=j+1

1. For i=1,2...,S perform a chemotactic step for bacterium i as follows
2. Calculate fitness function J (i,j,k,l).
3. Assign J_{last} = J(i,j,k,l) to update the value of the fitness function in case of better solution
4. Tumble: generate a random vector $\Delta(i)$ with each element $\Delta_m(i)$, m=1,2,...,p. The value of $\Delta_m(i)$ is a random number in the range [-1,1].

5. Move:Let

$$\theta^i(j+1,k,l) = \theta^i(j,k,l) + C(i)\frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}}$$

Where θ^i is the chemotactic step size C(i) in the direction of the tumble for bacterium i

6. Calculate J(i,j+1,k,l)
7. Swim

   i) Let m=0 (counter for swim length)

   ii) while m<N_s (if have not climber down too long)

   – Let m=m+1

   – If J(i,j+1,k,l)<J_{last} let J_{last} = J(i,j+1,k,l) and let

$$\theta^i(j+1,k,l) = \theta^i(j,k,l) + C(i)\frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}}$$

   And use this θ^i(j+1,k,l) to calculate new J(i,j+1,k,l)

   – Else, let m=N_s.

   This is the end of the while statement.

8. Go to the next bacterium (i+1), if i is not equal to S (i.e., go to 2. to process the next bacterium)

[Step 5] if j<N_c, go to step 4 and continue chemotaxis process since the life of the bacteria has not ended.

[Step 6] Reproduction

1. For the given *k* and *l*, and for each *i* = 1,2,..., *S* , let

$$J^i_{health} = \sum_{i=1}^{N_c+1} J(i,j,k,l)$$

be the health of the bacterium *i*. Sort bacteria and chemotactic parameters *C*(*i*) in order of increasing cost J_{health}.

2. The S_r bacteria with the maximum J_{health} values die and the remaining S_r bacteria with the lowest values split by replicating themselves.

[Step 7] if $k<N_{re}$, go to step 3. The number of specified reproduction steps has not been reached, so we start the next generation of the chemotactic loop.

[Step 8] Elimination-dispersal: For i=1, 2... S with probability $P_{ed,}$ eliminate and disperse each bacterium with insufficient nutrient. To perform this task if bacterium is eliminated simply disperses another bacterium to a random location in the optimization domain. If $l<N_{ed}$, then go to step 2; otherwise end.

The flowchart of the complete algorithm is illustrated below in figure 4.1.

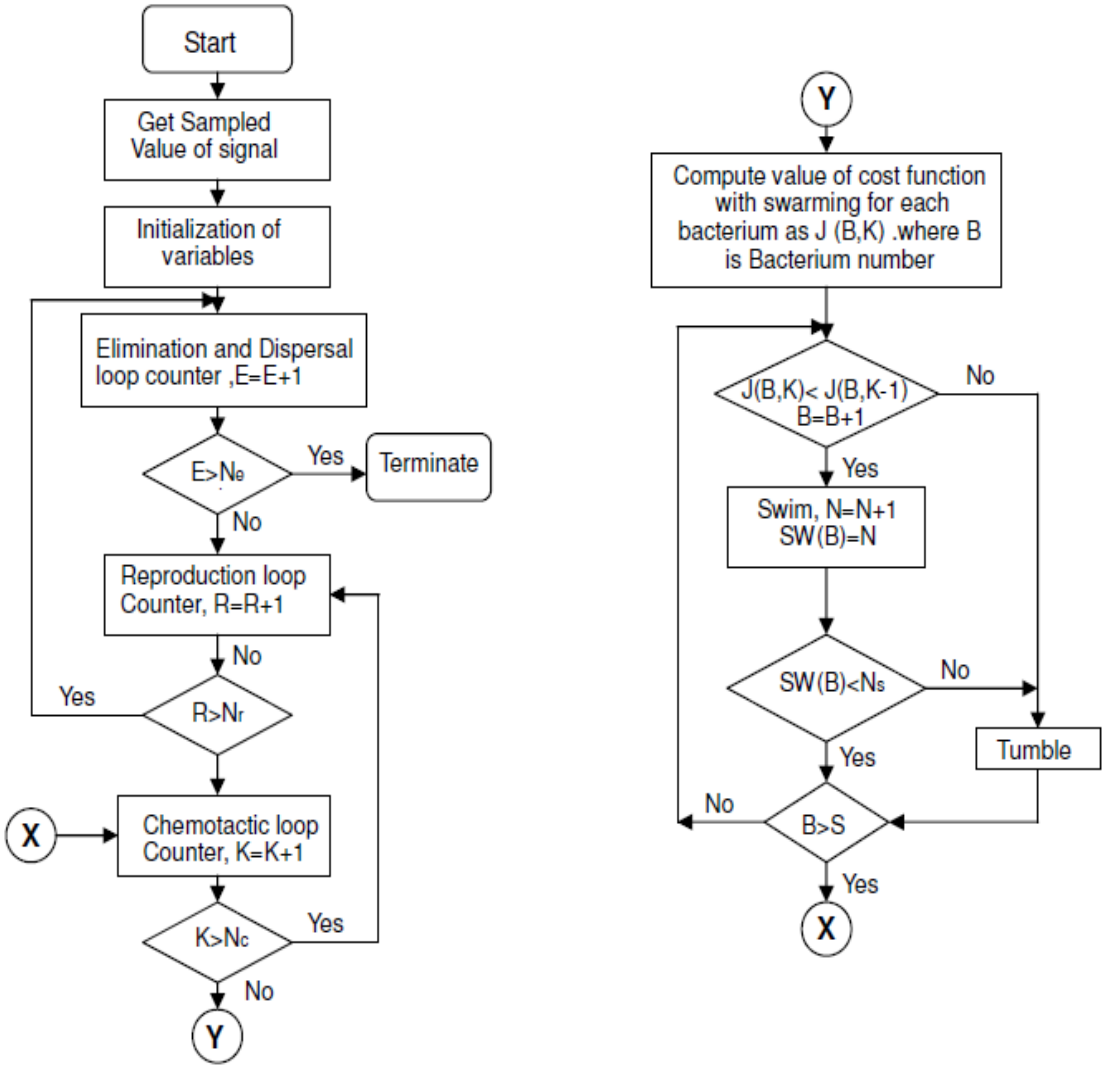


Figure 4.1 Flowchart of the Bacterial Foraging Optimization Algorithm

Chapter 5

FUZZY CO-CLUSTERING FOR IMAGES

5.1 Introduction

Fuzzy co-clustering is a color segmentation technique which assigns membership function to both the objects and the features. This approach is adapted for the segmentation of natural images. The resulting segmentation offers a good tradeoff between color differencing and human perception.

5.2 Co-Clustering

Co-clustering simultaneously clusters both objects and features together [40]. This provides two membership functions: the partition or object membership function and the ranking or the feature membership function. The latter serves to filter out the relevant features only during the computation of the object membership function and thus solves the problem of sparseness of data by reducing the dimensionality. The co-clustering algorithm is thus suited to applications with large dimensions and is found to be apt for our experiments on multi-feature color images. The problem of outliers is also minimized by using feature membership function [41]. The problem with using only the feature memberships is that it may lead to coincident/overlapping clusters therefore highlighting the need for both feature and object memberships. Further it includes the distance function of feature data points from the feature cluster centroid in the co-clustering process to create richer co-clusters than other fuzzy co-clustering algorithms. The inclusion of the distance factor in the degree of aggregation reduces the optimization problem to a minimization one. In this algorithm co-clustering is integrated with the Fuzzy approach with a view to obtaining

distinct clusters. Both the object and feature memberships in this method are fuzzy, i.e. the object membership is calculated when different clusters compete for a data point and feature memberships are defined when different features compete for a cluster. Thus it has two constraints on the two fuzzy memberships (object and feature memberships).

5.3 FCCI Algorithm

Fuzzy Co-clustering for images (FCCI) [38] algorithm incorporates the distance between each feature data point and the feature cluster centre as the dissimilarity measure and the entropies of objects and features as the regularization terms in the objective function. In FCCI, the images captured are transformed from RGB to CIELAB color space.

The advantages offered by FCCI algorithm are as follows:

- It is insensitive to initialization and form distinct clusters. (Fuzzy clustering)
- It performs well in high dimensions and provides well defined clusters. (Co-clustering)
- It minimizes the impact of outliers to improve the accuracy of co-clustering. (ranking/feature memberships)
- Its objective function integrates the distance measure of input features w.r.t. feature centroid into the entropy regularization framework.
- It is reasonably fast enough.

The objective function J_D to be minimized in the FCCI algorithm is stated below in equation (1):

$$J_D = \sum_{c=1}^{C}\sum_{i=1}^{N}\sum_{j=1}^{K}\mu_{ci}v_{cj}D_{cij} + T_U\sum_{c=1}^{C}\sum_{i=1}^{N}\mu_{ci}log\mu_{ci} + T_V\sum_{c=1}^{C}\sum_{j=1}^{K}v_{cj}logv_{cj} \quad \text{.....(1)}$$

The total memberships of all attributes in a cluster must sum to 1, hence the above equation is subjected to the constraints:

$$\sum_{c=1}^{C} \mu_{ci} = 1, \qquad \mu_{ci} \in [0,1], \quad \forall i = 1,...,N$$

$$\sum_{j=1}^{K} v_{cj} = 1, \qquad v_{cj} \in [0,1], \quad \forall c = 1,...,C$$

where, C is the number of clusters, N is the number of data points i.e., N = N1*N2(N1*N2 is the dimension of the input image), K is the number of color features, μ_{ci} is membership function of data point i to cluster c, v_{cj} is membership function of feature j to cluster c, T_U and T_V are the weighting parameters that determine the degree of fuzziness and D_{cij} is the Euclidean distance between data point X_{ij} and cluster centroid p_{cj} given as:

$$D_{cij} = d^2(X_{ij}, p_{cj}) = (X_{ij} - p_{cj})^2$$

The constrained optimization problem for FCCI algorithm is now defined as:

$$F = \sum_{c=1}^{C}\sum_{i=1}^{N}\sum_{j=1}^{K} \mu_{ci} v_{cj} D_{cij} + T_U \sum_{c=1}^{C}\sum_{i=1}^{N} \mu_{ci} log\mu_{ci} + T_V \sum_{c=1}^{C}\sum_{j=1}^{K} v_{cj} log v_{cj} + \sum_{i=1}^{N} \lambda_i \left(\sum_{c=1}^{C} \mu_{ci} - 1\right) + \sum_{c=1}^{C} \gamma_c \left(\sum_{j=1}^{K} v_{cj} - 1\right)$$

After solving the optimization problem with the help of Lagrange's multipliers λ_i and γ_c, the value of the membership functions and centroid is calculated as:

$$\mu_{ci} = \frac{\exp\left(-\sum_{j=1}^{K} \frac{v_{cj} D_{cij}}{T_U}\right)}{\sum_{c=1}^{C} \exp\left(-\sum_{j=1}^{K} \frac{v_{cj} D_{cij}}{T_U}\right)}$$

$$v_{cj} = \frac{\exp(-\sum_{i=1}^{N} \frac{\mu_{ci} D_{cij}}{T_V})}{\sum_{j=1}^{K} \exp(-\sum_{i=1}^{N} \frac{\mu_{ci} D_{cij}}{T_V})}$$

$$p_{cj} = \frac{\sum_{i=1}^{N} \mu_{ci} X_{ij}}{\sum_{i=1}^{N} \mu_{ci}}$$

The steps involved in the FCCI algorithm are stated below [42]:

[Step 1] Read the input RGB color image.

[Step 2] Convert RGB color image to CIELAB color space.

[Step 3] Define the number of color features in color space as K=2, i.e. A and B.

[Step 4] Perform the 2d to 1d transformation to generate data point X_{ij} in the j_{th} dimension, j=1, 2 for each pixel, I=1,…..,N where N is the size of the data.

[Step 5] Initialize the value of T_u and $T_{v.}$as 10 and 10^6 respectively.

[Step 6] Define the number of clusters as C=2.

[Step 7] Obtain the corresponding value of μ_{ci} for C=2.

[Step 8] Defuzzification: Convert fuzzy membership matrix to a binary image by defining the cut-off/threshold point. Our algorithm is run at a threshold point of μ_{ci} (cut-off) =0.5.

Output = 1, if $\mu \geq 0.5$

= 0, otherwise

[Step 9] Map the selected coordinates of clusters from that of original RGB image and display all clusters.

[Step 10] Reconstruct the color image, for comparison purpose, by representing each cluster with

its centroid (A, B) value and the original L value. The μ_{ci} (cut-off) =0.5 threshold is found to be generally acceptable for comparison of segmentation results.

[Step 11] Calculate the segmentation error ISE as the number of object pixels that have not been selected, and OSE as the number of non object pixels that have been selected. Calculate the average segmentation error.

The flowchart for the above steps of FCCI Algorithm is shown below in figure 5.1.

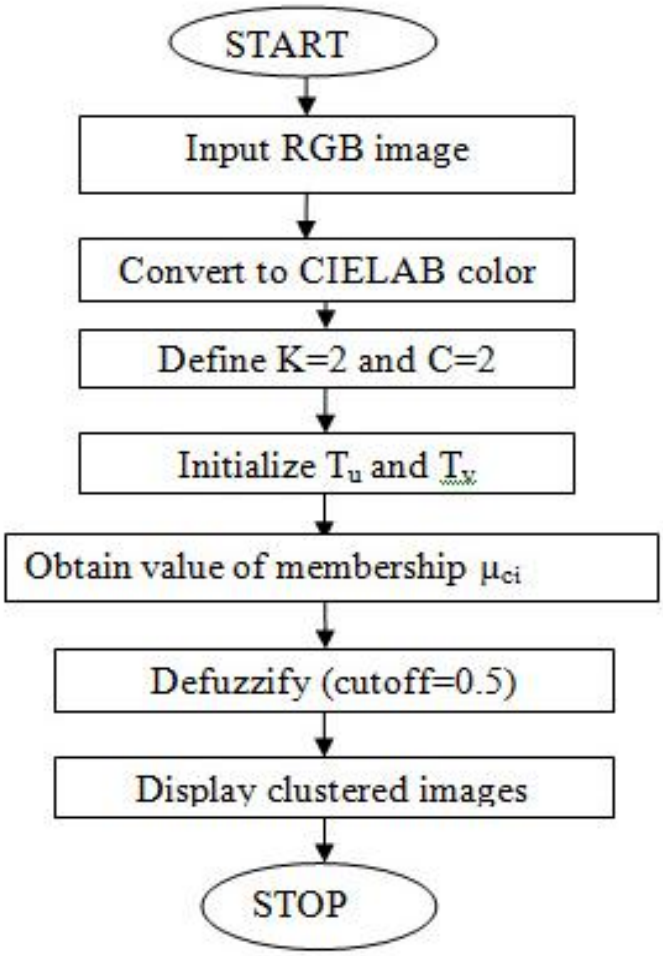


Figure 5.1 Flowchart of FCCI algorithm

Chapter 6

PROPOSED APPROACH

6.2 Introduction

In this thesis, a framework for an automatic brain tumor detection and segmentation based on fuzzy co-clustering for images algorithm is proposed. The designed system consists of two main components: preprocessing and segmentation. Initially, the MRI images are processed before being fed as an input to the system. In the real time database, there are some problems that need to be resolved before performing segmentation operation. The problems like intensity inhomogeneity correction, background noise removal are removed in the preprocessing section. The non brain tissues such as skull and fat from head MRI scans are also removed in this section. The second component of the framework is segmentation in which the tumorous slice is detected. It includes image registration, tumor extraction and tumor mapping.

6.2 Preprocessing

The input of preprocessing block is MRI brain image. In preprocessing part of the system the image is first processed in order to remove noise and inhomogeneity and then intracranial mask of image is extracted to process further. The major sources of degradation of images in MRI are the sensitivity inhomogeneity of the receiver coils, coil tuning, gradient eddy currents, RF standing wave effects, and RF penetration effects. A common problem that arises due to these sources is intensity inhomogeneity (bias field), image corruption with a slowly varying multiplicative spatial field across the images. Intensity inhomogeneity is not always visible to human observer, but it causes significant tissue misclassification problems when intensity based segmentation is used.

Therefore, it is required to correct intensity inhomogeneity in the brain MR image prior to tumor detection and segmentation. The noise is reduced by passing the images through median filter. Median filter is more effective when one wants to reduce noise and preserve edges simultaneously. The intention of doing pre processing is to ensure that we can identify the exact shape of the tumor without any loss of information.

The next step in the preprocessing stage is to isolate the intracranial mask from the entire image. The extra cranial region consists of bones which do not contain the tumor and hence its inclusion is insignificant in the detection of tumor. There is significant difference in the intensity of intracranial and extra cranial region. This difference can be used as a measure to remove the extra cranial mask from the MRI images. In this we have used automatic threshold value selection using Otsu's algorithm to automatically choose threshold value. Then, mathematical morphology operations on a binarized image are applied stage by stage to get the intracranial mask from input MRI image.

6.3 Segmentation

The second section of our framework is the segmentation. The input consists of the preprocessed images (reduced noise, registered and segmented brain) and some information on the tumor provided by the preprocessing section. The automated segmentation method that we have developed is composed of two phases: tumor detection and mapping. In detection of tumor FCCI algorithm is applied to the image obtained from section 6.2 and then morphological operation are applied to get the exact shape of the tumor. The tumorous region is mapped on the input MRI image and area is calculated for quantification. The values of the parameters T_u and T_v used in the FCCI algorithm are optimized using the BFOA (explained in section 4) with the following initialization:

1. The number of bacteria S = 50
2. The swimming length of bacteria N_s= 4
3. The number of iteration in the chemotactic step N_c=100
4. The number of reproduction steps N_{re}= 2.
5. The number of elimination and dispersal events N_{ed}=2
6. The probability of elimination/dispersal of bacteria P_{ed}= 0.25.

Chapter 7

RESULTS & DISCUSSIONS

The following system configuration has been used while conducting the experiments:

Processor: Intel Core 2 Duo

Clock Speed: 2.4 GHz

Main Memory: 4 GB

Hard Disk Capacity: 512 GB

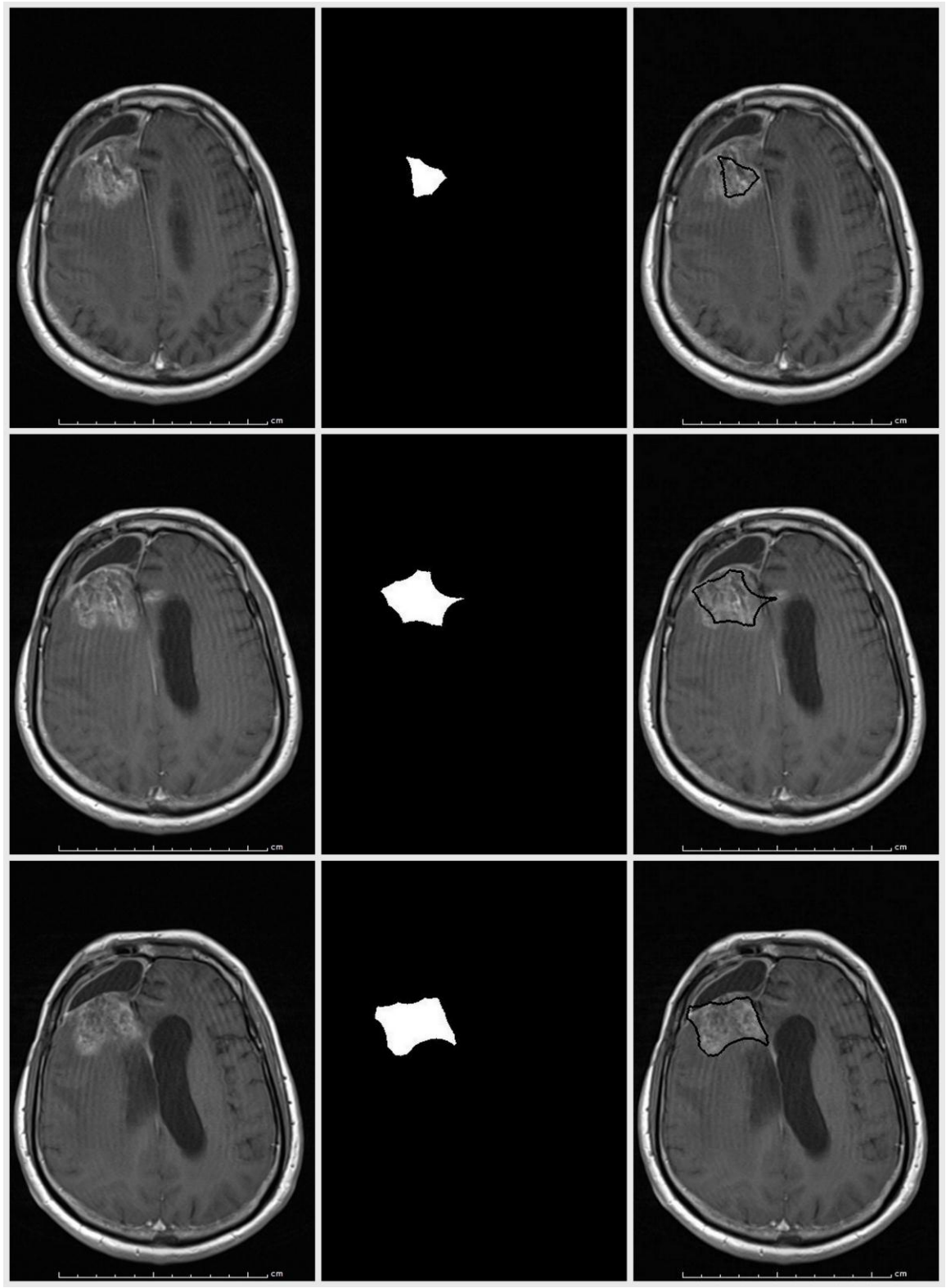
Software Used: MATLAB 7.9.0 (2009b)

The retrospective analysis is carried out on 50 MRI image real time database taken from RGCI&RC, Delhi. On this MRI image database we have applied proposed scheme as explained in section 6 to detect brain tumor. The 50 input MRI images of brain tumor detection are illustrated in figure 7.1 with extracted tumor area along with their mapping on input images. The results of the proposed scheme are validated by the radiologist from RGCI&RC. The quantitative analysis of MRI images is shown in table 7.1 with the help of ground truth, true positive, false positive and false negative. Ground truth is the tumor area manually mapped by the radiologist. The area accurately measured by the system is termed as “True Positive” whereas the error encountered is termed as “False Positive” and “False Negative”. False Positive is the area of tumor detected by the system which does not belong to the ground truth and False Negative is the area of tumor left by the system which belongs to the ground truth. It can be seen from the table that the true positive pixels of tumor corresponds well with the ground truth.

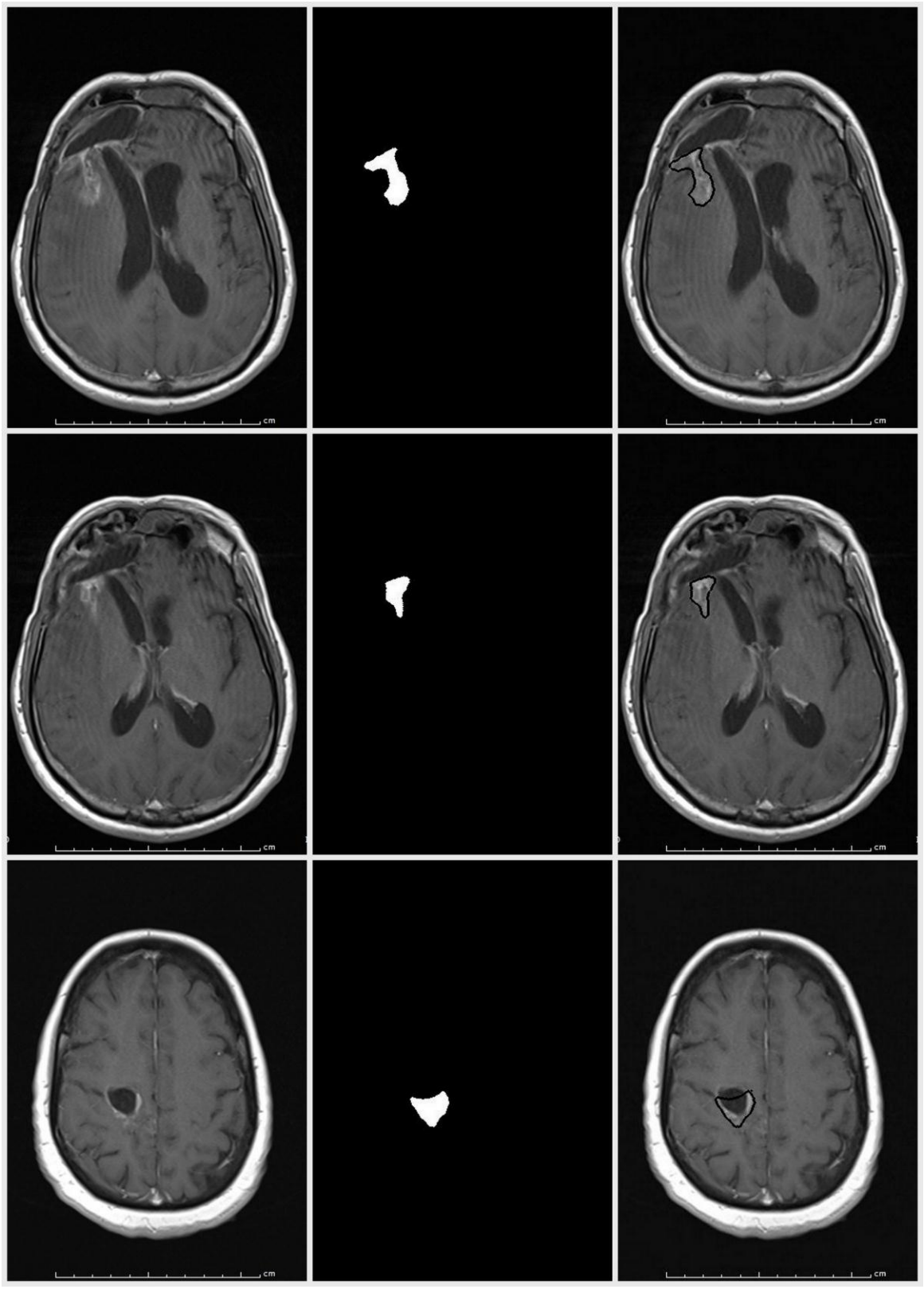
S. No.	Patient No.	Ground Truth	True Positive	False Negative	False Positive
1	1	1928	1590	338	0
2	1	4360	4142	218	0
3	1	4916	4767	149	0
4	1	2056	2056	0	0
5	1	1150	1050	100	0
6	2	1651	1420	231	48
7	2	1884	1846	38	0
8	2	2324	2301	23	157
9	2	514	514	0	0
10	3	8265	5751	2514	102
11	3	10102	7880	2222	481
12	4	744	707	37	0
13	4	1498	1498	0	0
14	5	5212	4170	1042	521
15	5	5680	5312	768	0
16	5	4794	4794	0	0
17	6	13422	13422	0	0
18	6	11022	10912	110	3306
19	6	9164	8973	191	2749
20	7	1983	1884	99	0
21	7	1802	1442	360	0
22	7	1686	1686	0	33
23	7	2704	2569	135	0
24	7	3845	3845	0	0
25	7	2705	2705	0	1082
26	8	5500	4510	990	0
27	8	6705	5834	871	335
28	8	6171	4937	1234	0
29	8	7412	5930	1482	1482
30	9	1315	1202	113	0

31	9	1968	1575	393	0
32	10	6748	6681	67	0
33	10	5758	5471	287	0
34	10	3495	3461	34	0
35	11	4295	4081	214	0
36	11	4434	4434	0	0
37	11	4360	4360	0	0
38	11	2903	2323	580	0
39	12	2362	2339	23	0
40	13	1889	1771	118	0
41	13	2891	2313	578	0
42	14	6288	5031	1257	0
43	15	5028	4526	502	0
44	15	4824	4342	482	0
45	15	2918	2918	0	0
46	16	1496	1378	118	0
47	16	4913	4451	462	0
48	16	5295	5182	113	0
49	16	4106	3833	273	0
50	16	1754	1611	143	38

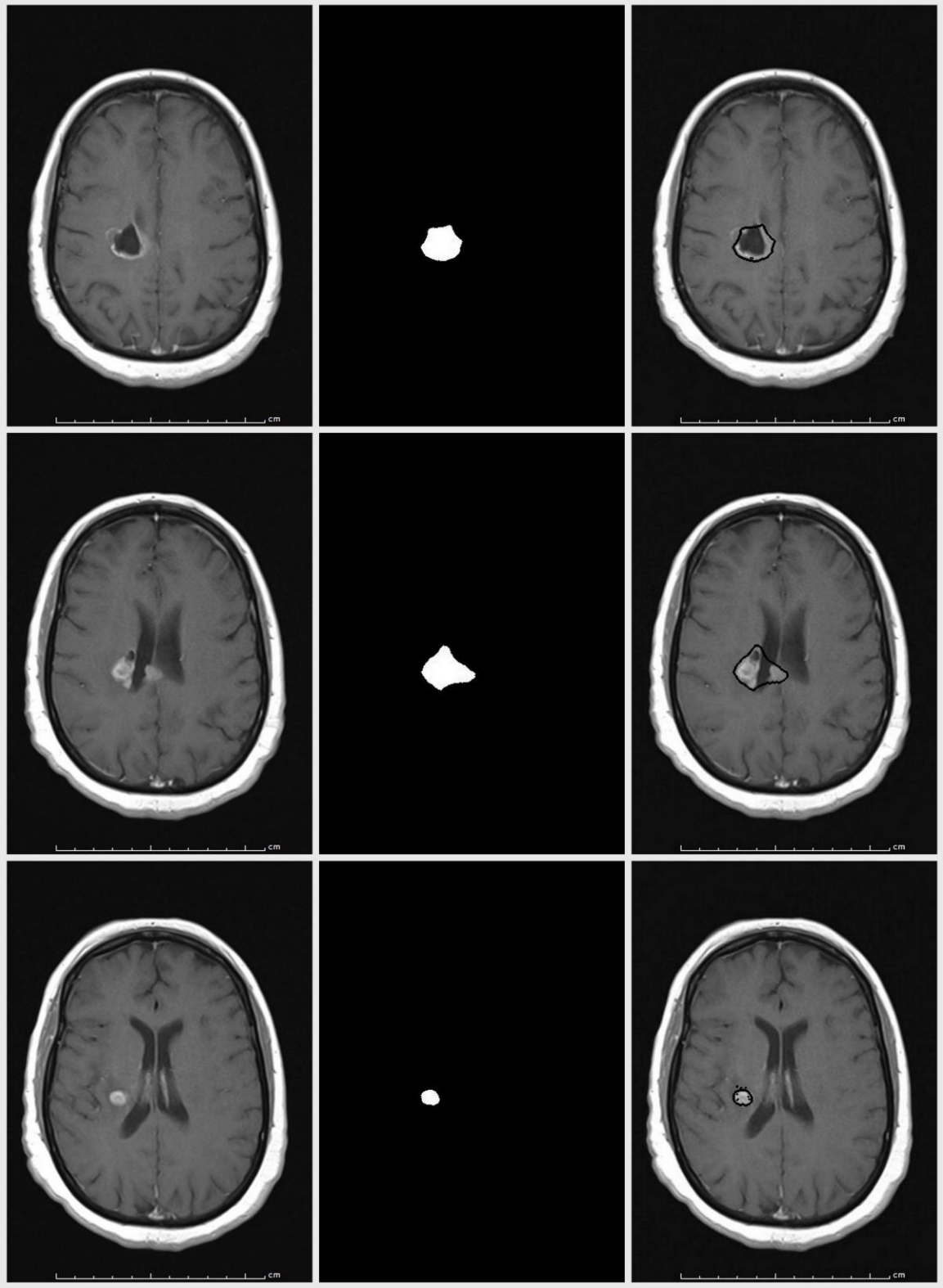
Table 7.1 Quantitative Analysis of MRI image database



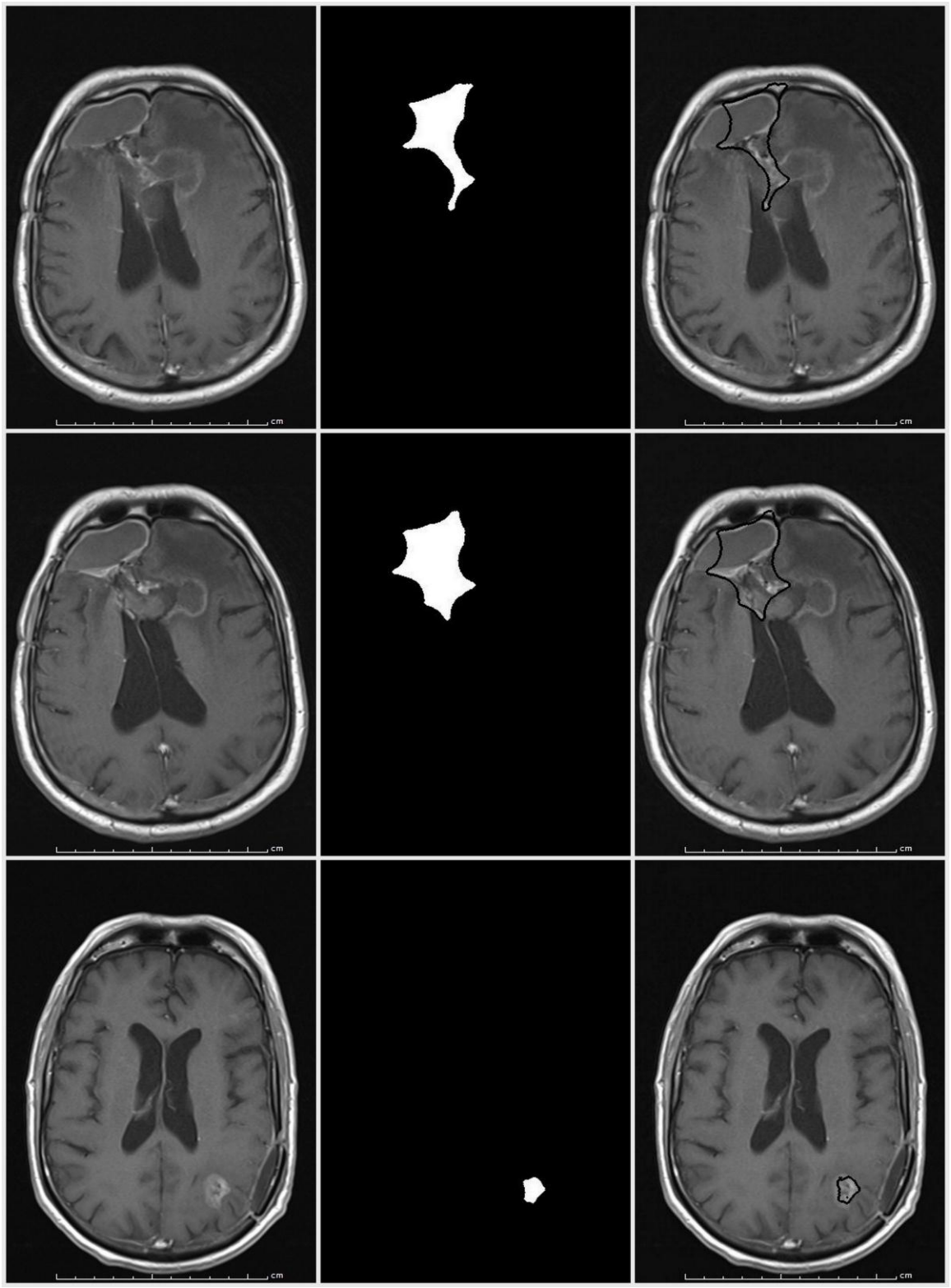
(a) **(b)** **(c)**



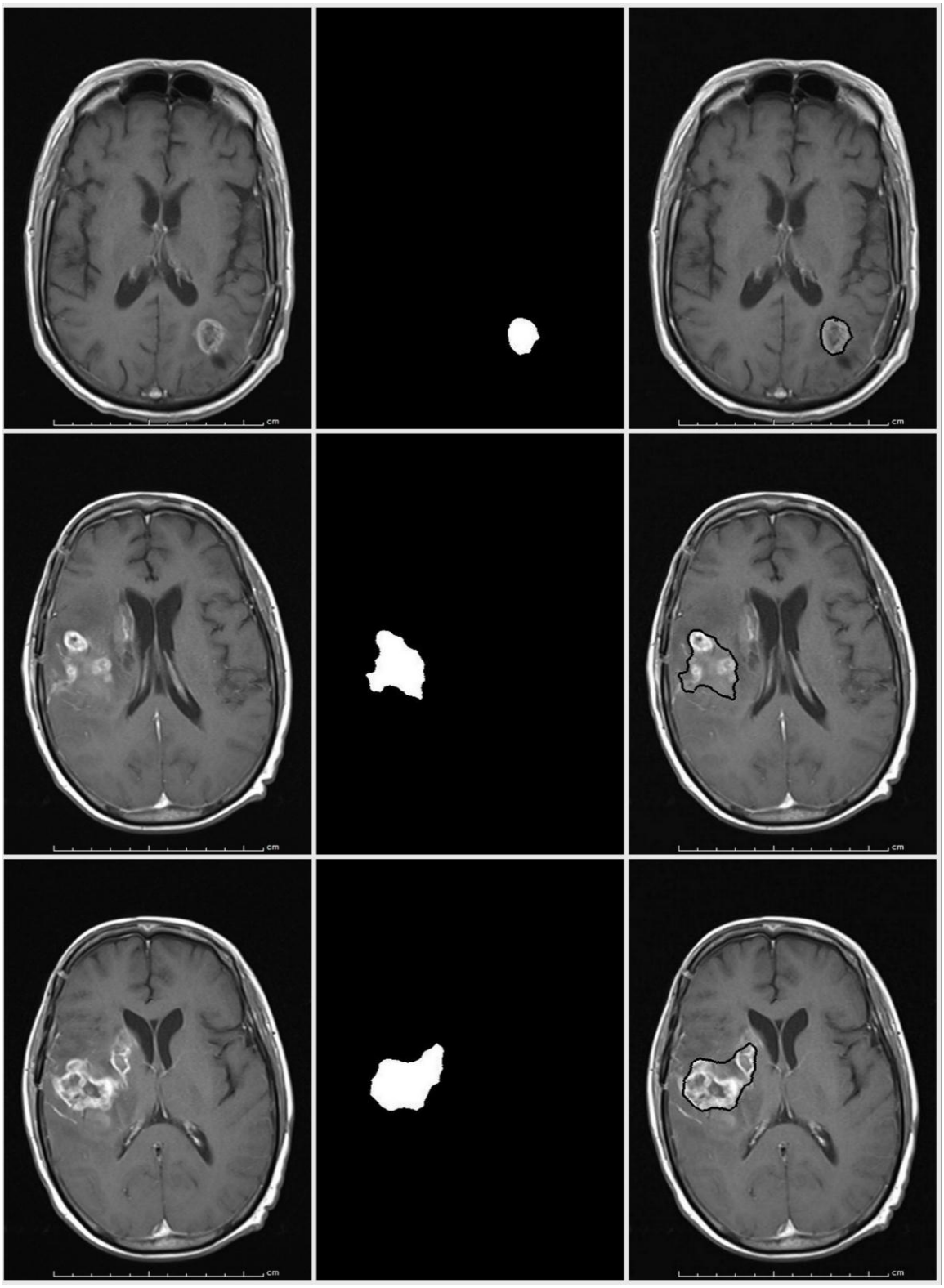
(a) **(b)** **(c)**



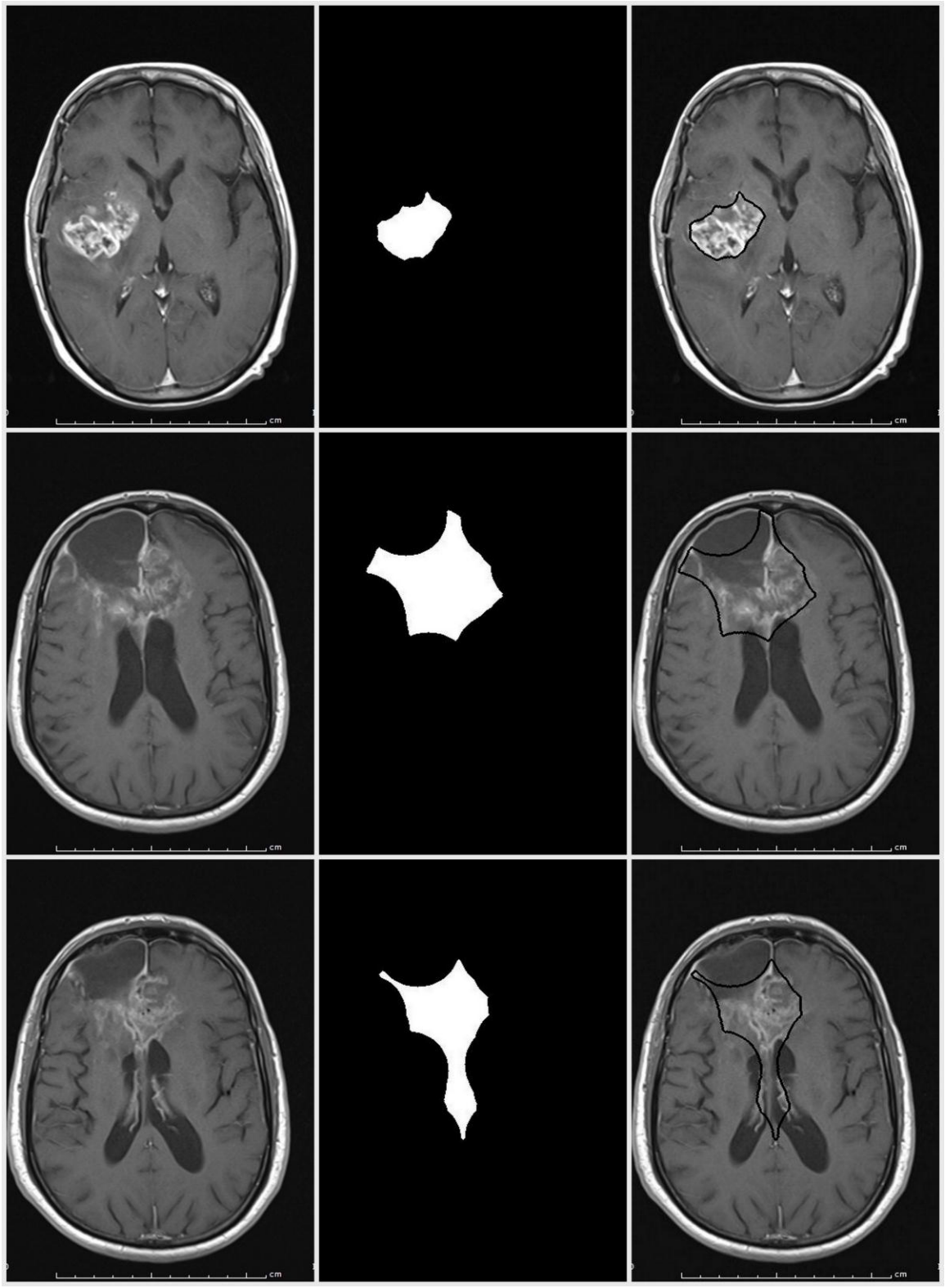
(a) **(b)** **(c)**



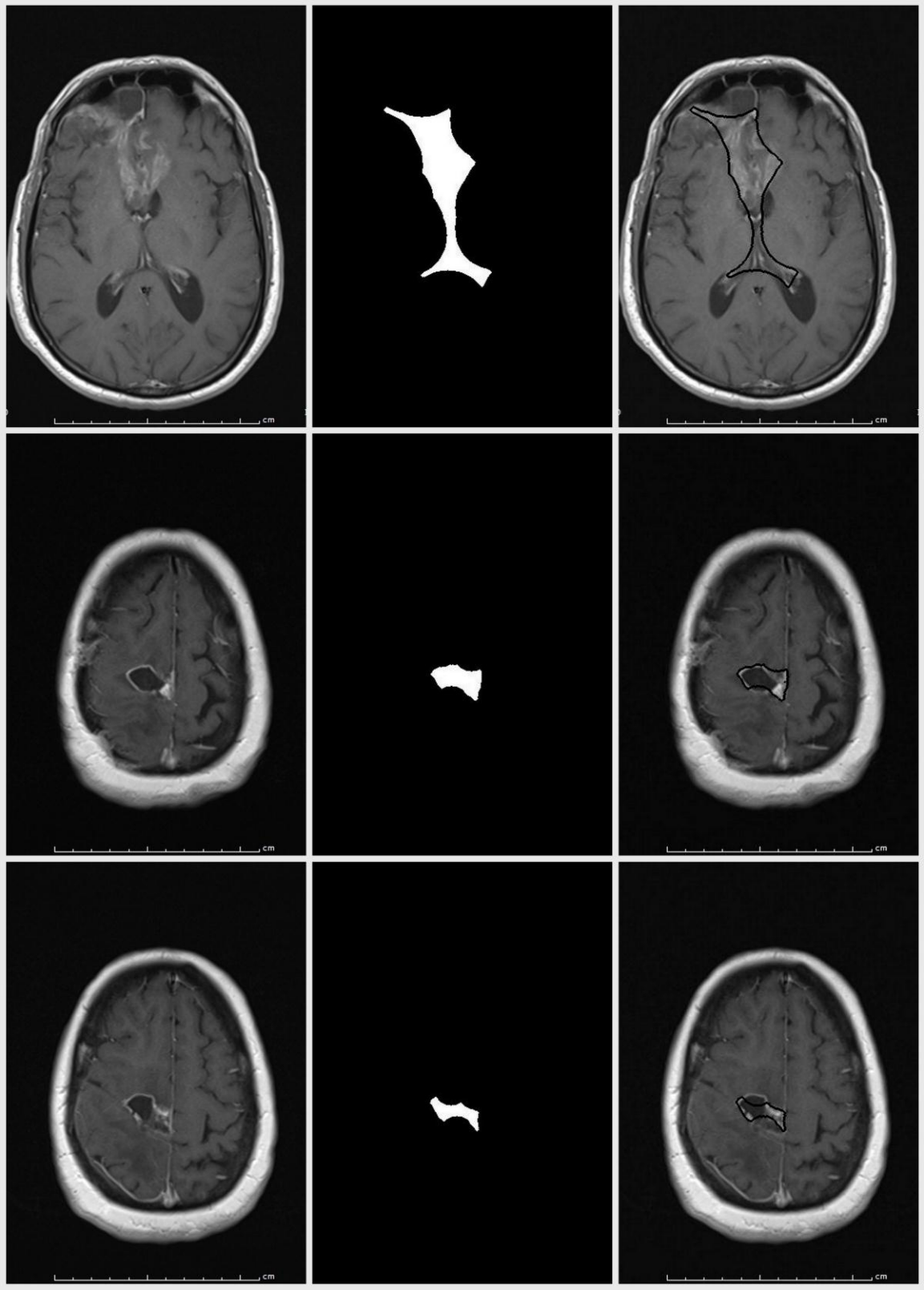
(a) **(b)** **(c)**



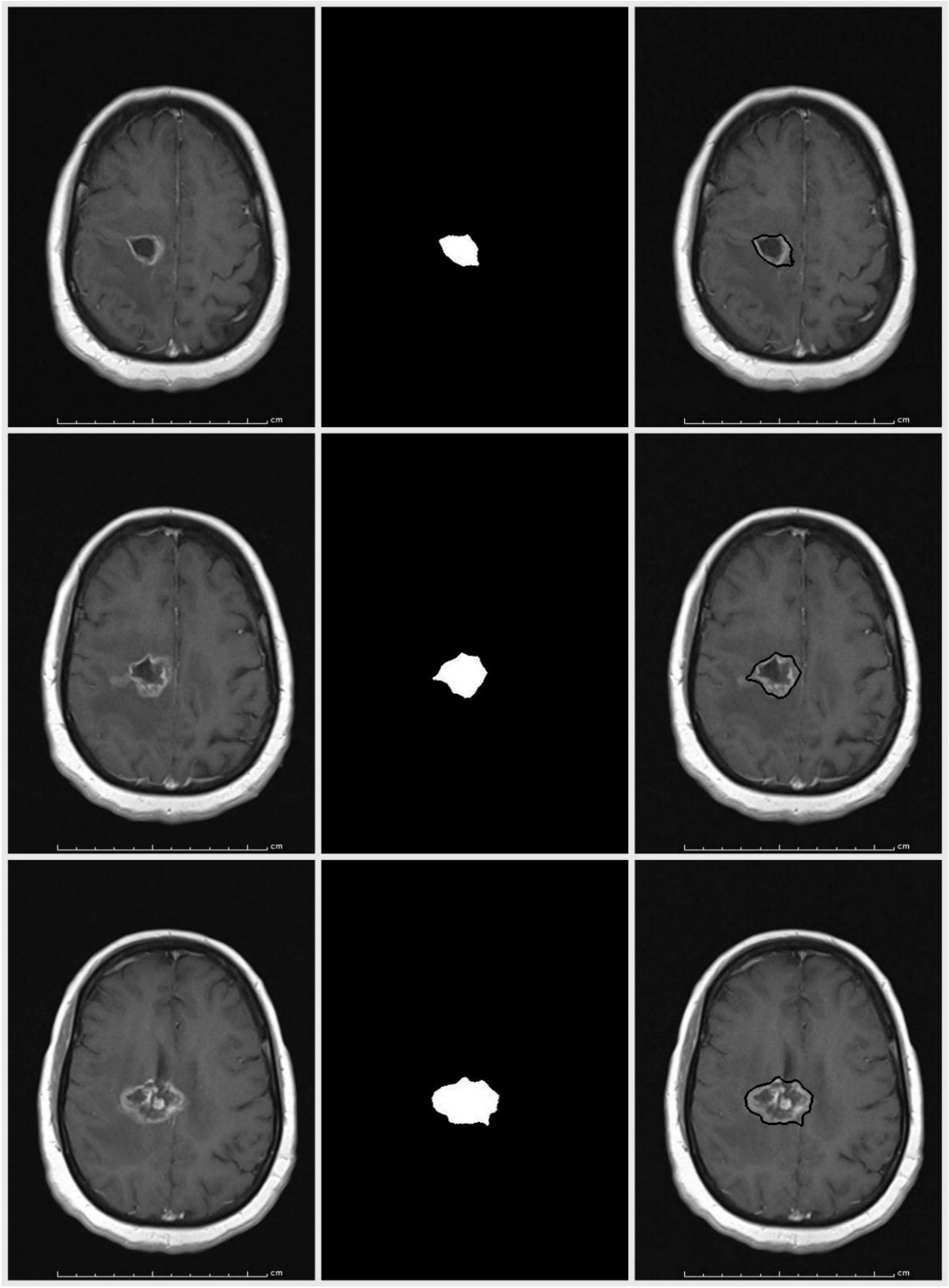
(a) **(b)** **(c)**



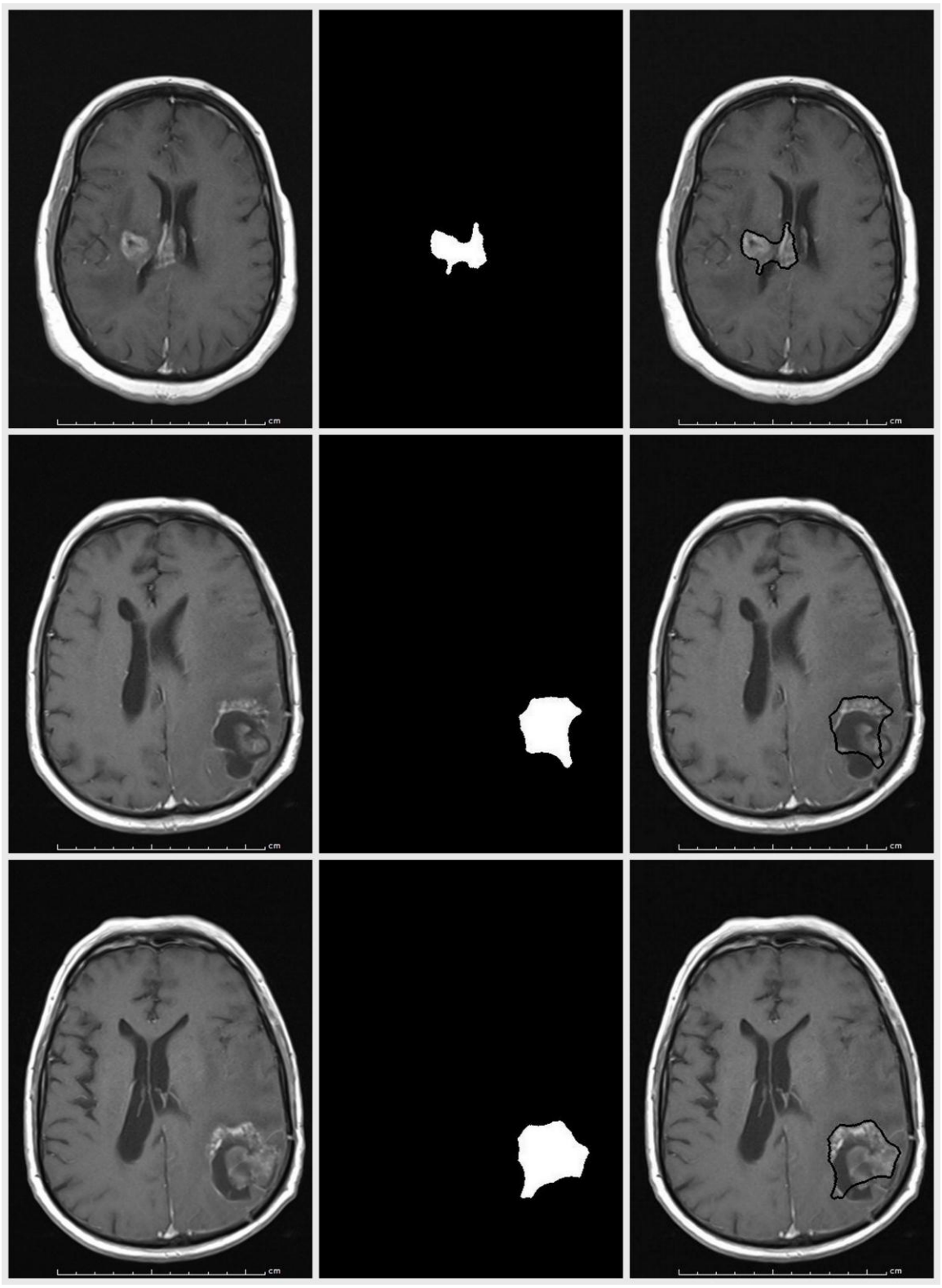
(a) **(b)** **(c)**



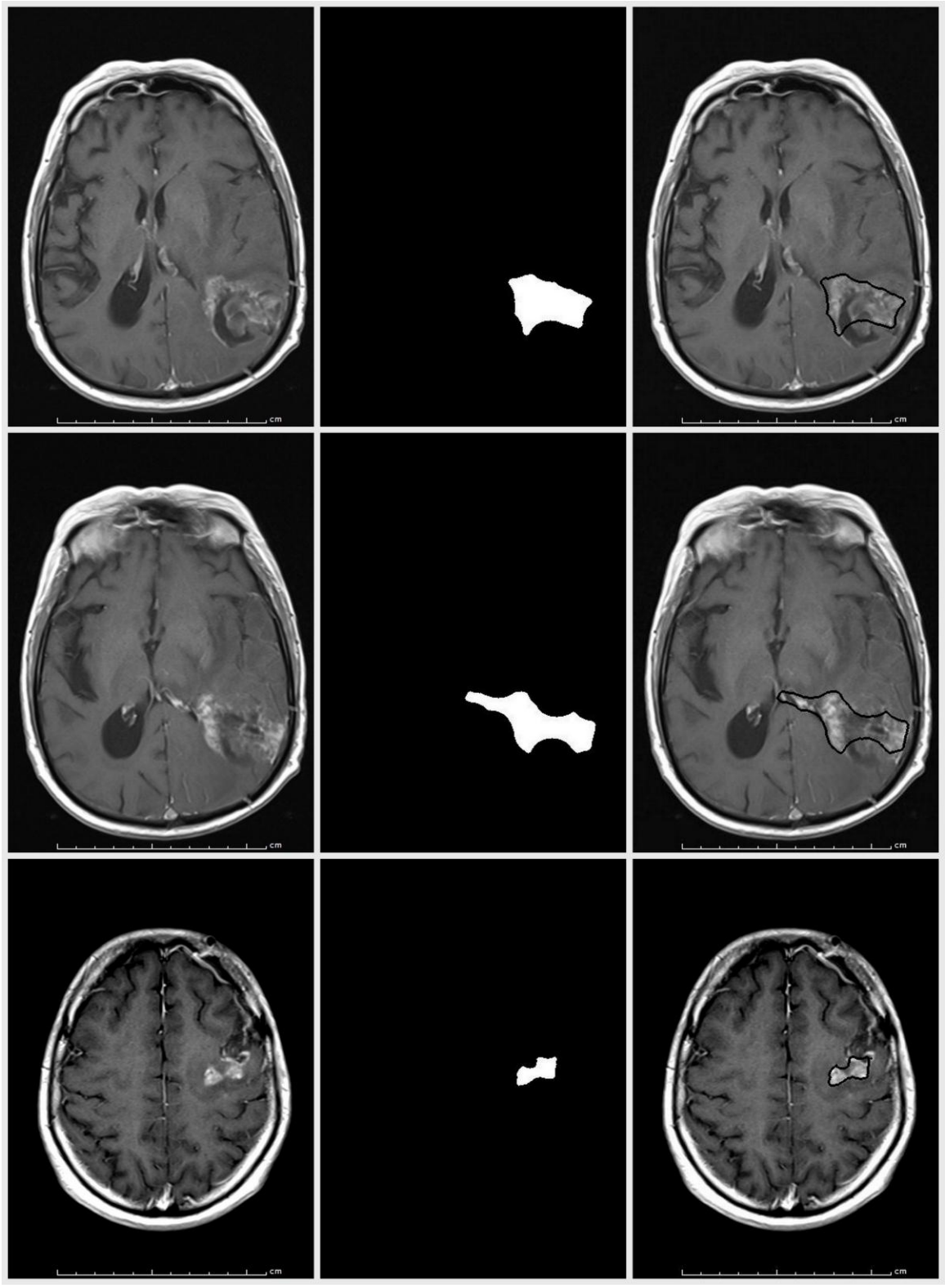
(a) **(b)** **(c)**



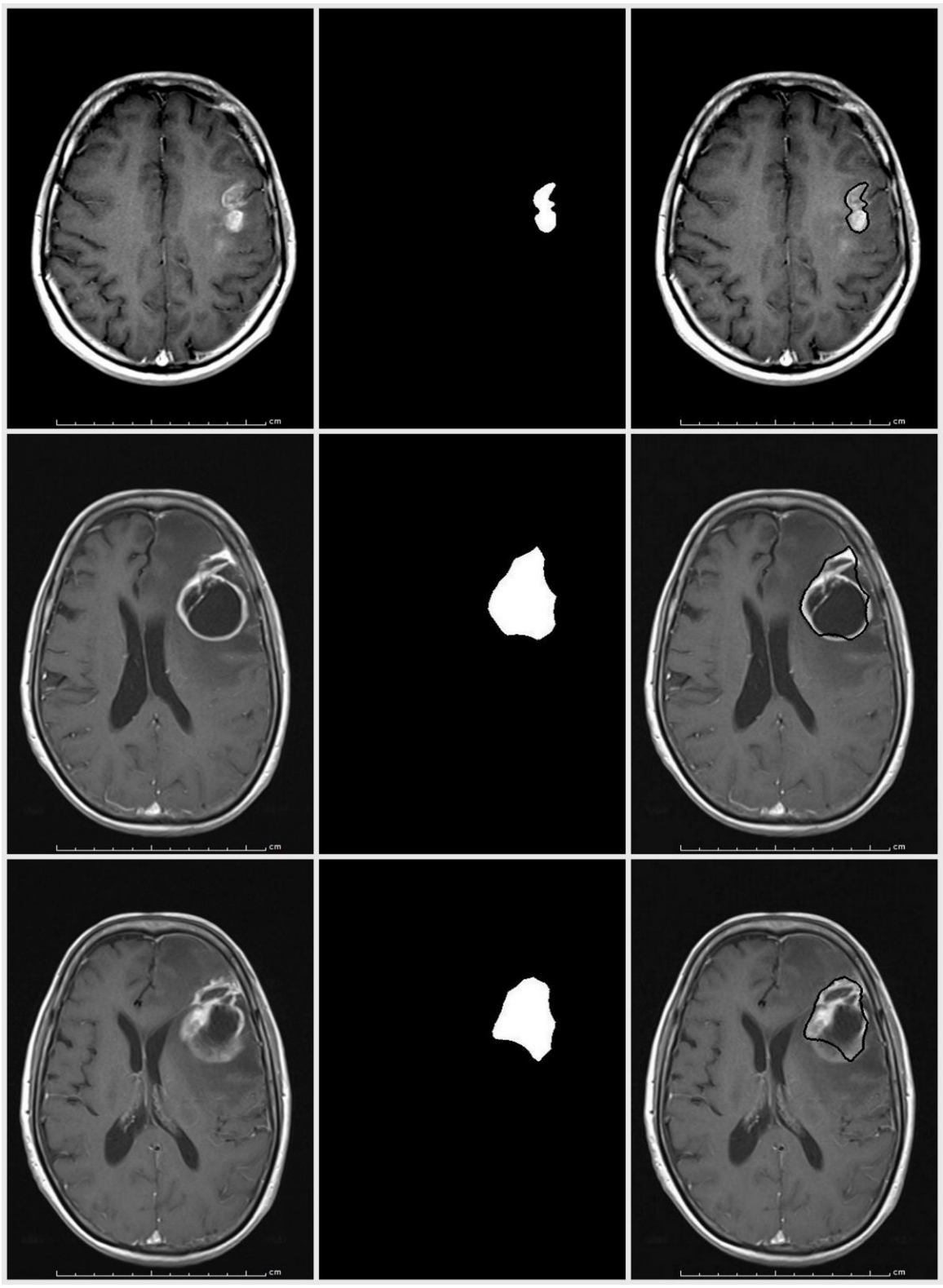
(a) **(b)** **(c)**



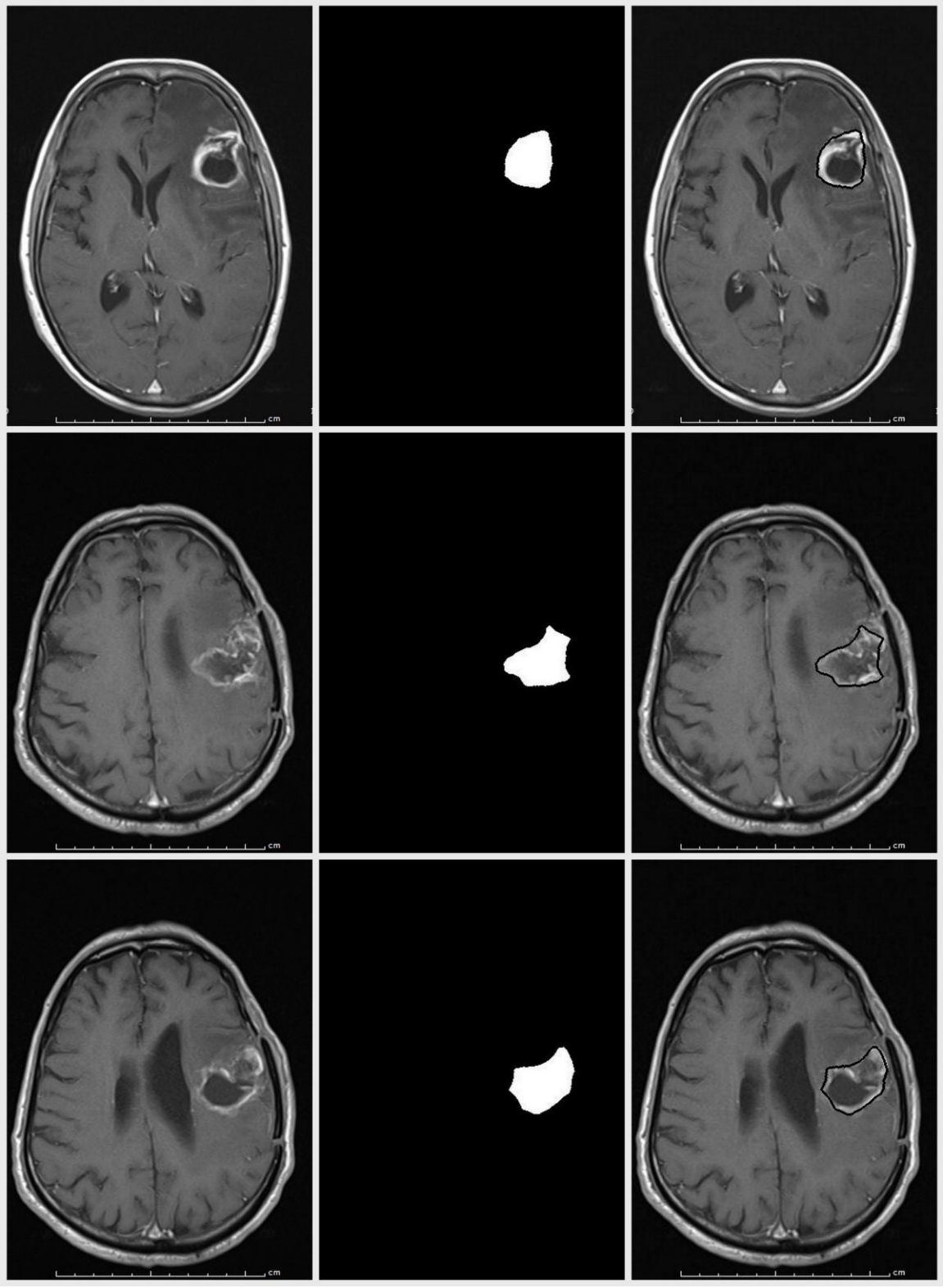
(a) **(b)** **(c)**



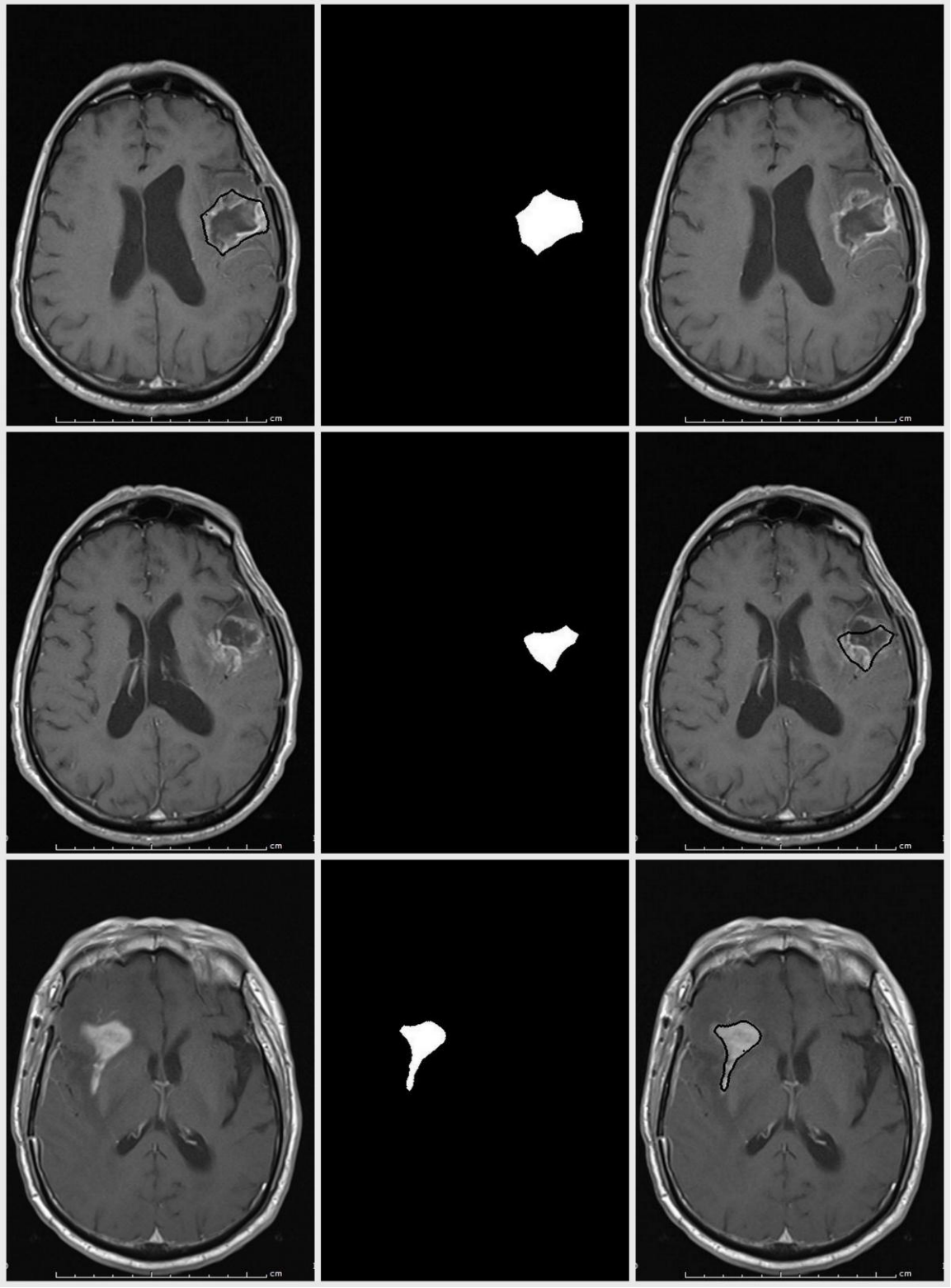
(a) **(b)** **(c)**



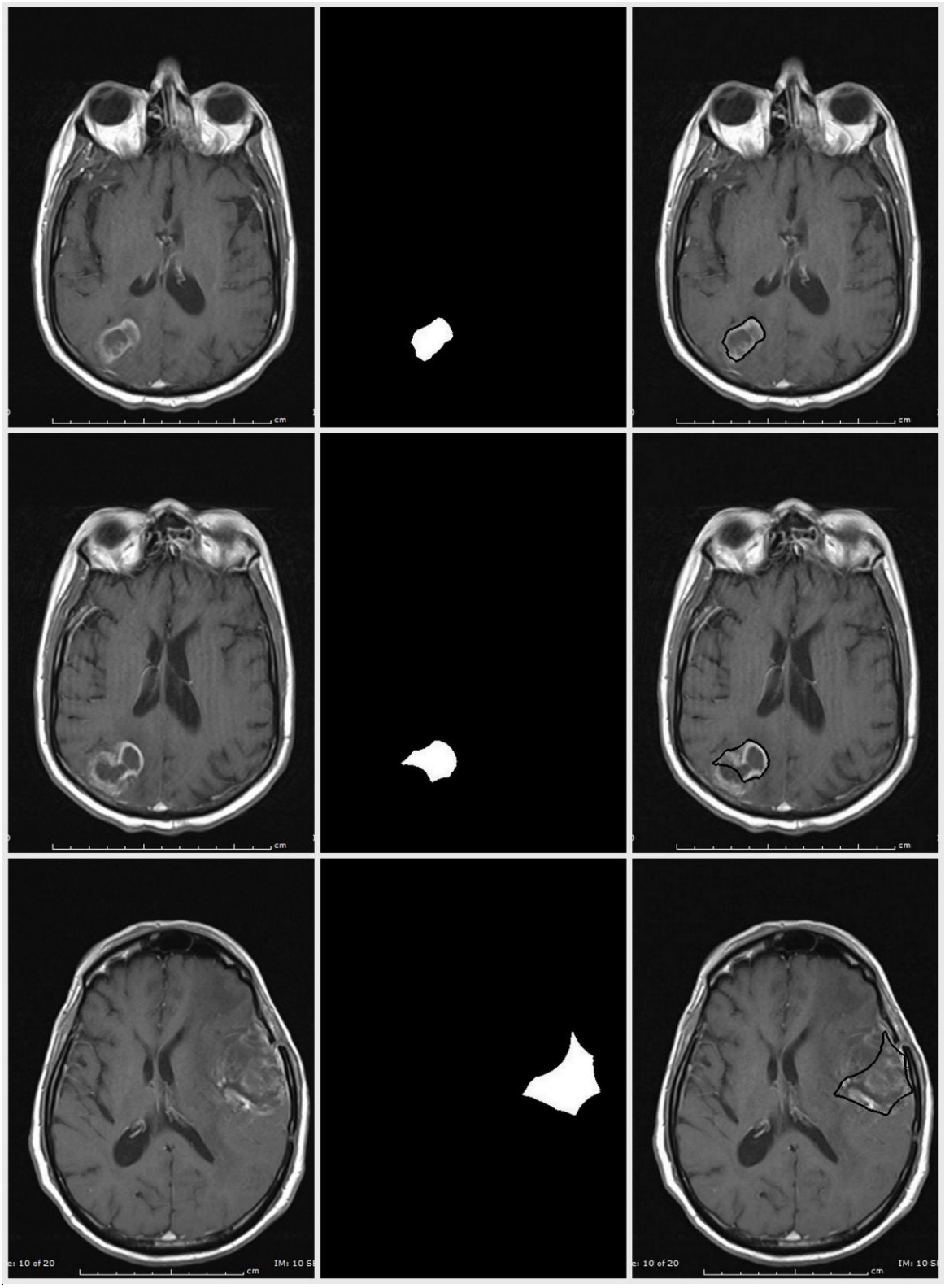
(a) **(b)** **(c)**



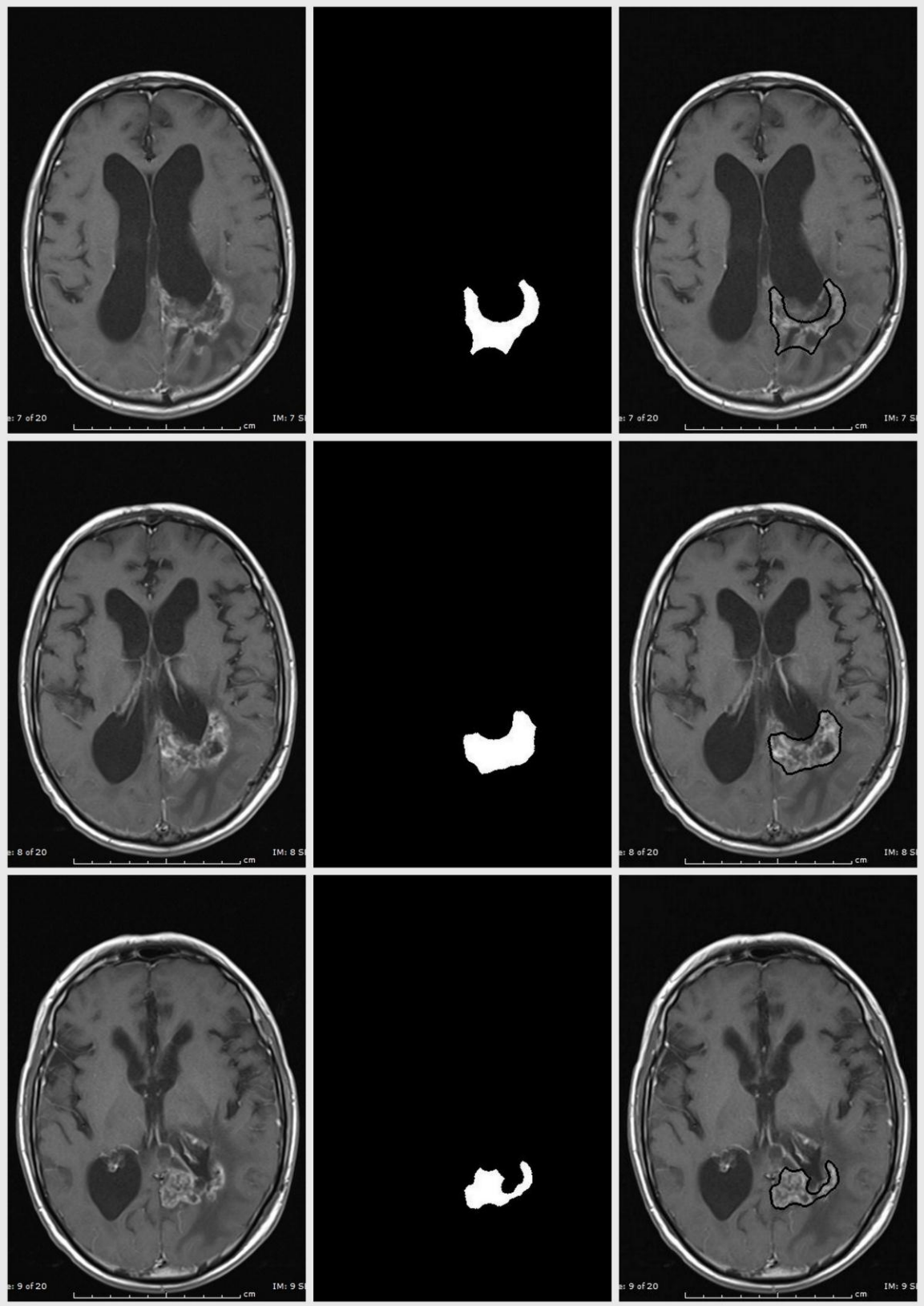
(a) **(b)** **(c)**



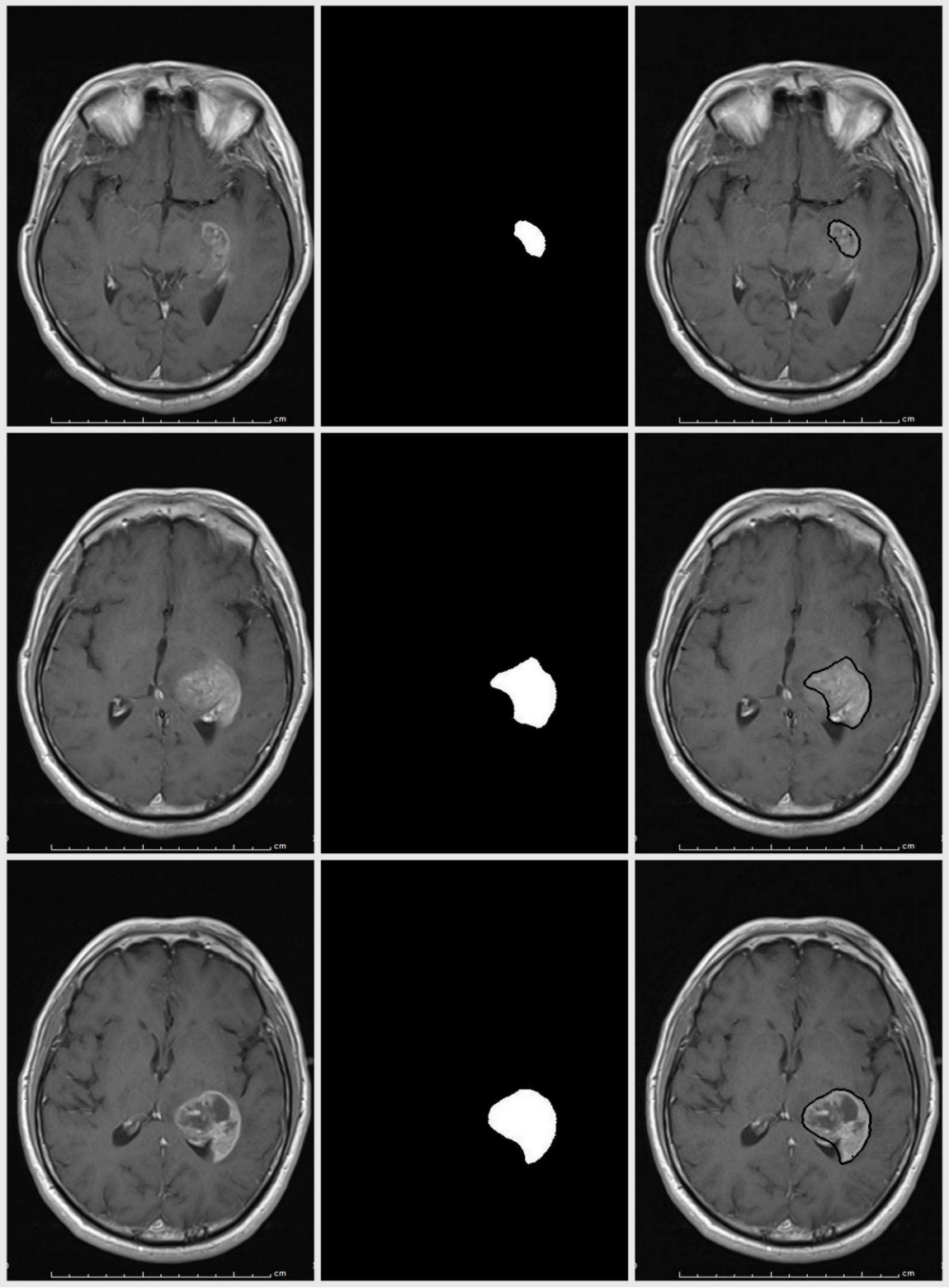
(a) **(b)** **(c)**



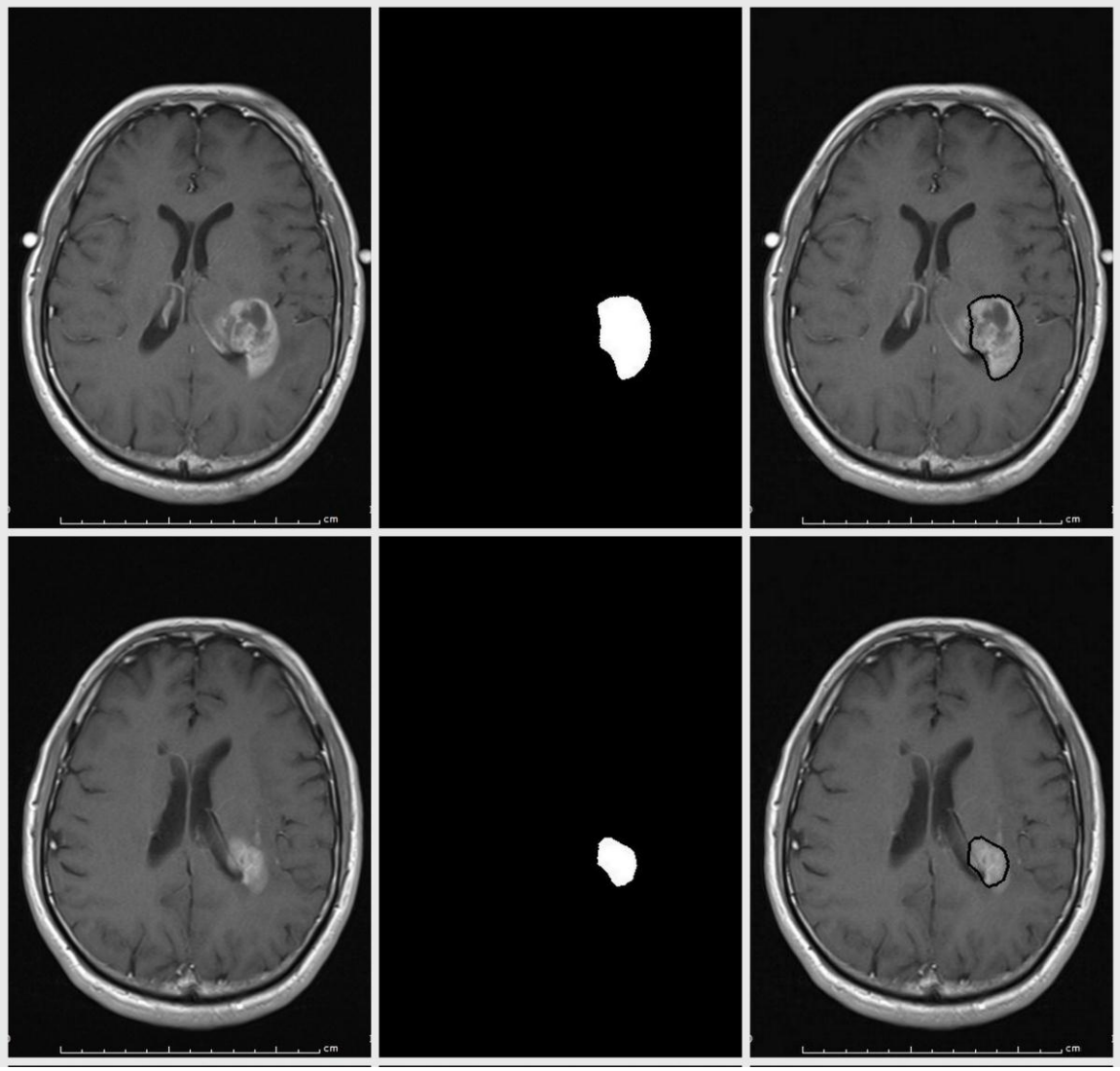
(a) **(b)** **(c)**



(a) **(b)** **(c)**



(a) **(b)** **(c)**



(a) **(b)** **(c)**

Figure 7.1 (a) Input Images (b) Images of extracted tumor from input images

(c) Tumor mapped on input images

Chapter 8

CONCLUSION

In this thesis work, a step by step methodology for automatic and unsupervised brain tumor segmentation using fuzzy co-clustering for images algorithm is presented. The tumor detection and segmentation result obtained by the proposed framework is evaluated by experienced radiologist at Rajiv Gandhi Cancer Institute and Research Centre. According to the radiologist the result of our proposed system is promising. To realize an automatic and unsupervised segmentation we implement a system composed of two modules. The first module is used to remove the skull and to reduce noise and intensity inhomogeneity from brain MR images. The second module facilitates the final segmentation of tumor region from brain MR images using fuzzy co-clustering for images algorithm. The efficiency of the system is further improved by applying bacterial foraging optimization algorithm as an optimization technique. The performance of the proposed system is evaluated on 50 real time MRI images of brain tumor patients. Quantitatively the method is validated against ground truth by calculating the true positive, false positive and false negative values. Also it presents some sample results for qualitative evaluation and discussion on the results. It can be concluded from the table that our system can efficiently detect the tumor in comparison with the ground truth. Finally, the proposed system is highly automatic in that no user intervention is required to produce tumor segmentation results in a limited time. In the future, the work of this thesis can be extended to further improve the accuracy and efficiency of the system. This can be achieved by fusion of MRI images of different modalities. Apart from calculating the tumorous region the system can also include the classification of tumor.

REFERENCES

[1] L. J. Erasmus, D. Hurter, M. Naude, H.G. Kritzinger and S Acho, *'A short overview of MRI artifacts',* SA Journal of Radiology, Vol. 8 ,No. 2 , August 2004, pp. 13-17.

[2] Schmidt M., Levner I., Greiner R., Murtha A. and Bistritz A., '*Segmenting Brain Tumors using Alignment-Based Feature', IEEE* 4th International Conference on Machine Learning and Applications, *ICMLA,* Dec. 2005, pp. 215-220.

[3] Kiran Thapaliya, Goo-Rak K won, '*Extraction of Brain Tumor Based on Morphological Operations',* IEEE International Conference on Computing Technology and Information Management (ICCM), vol.1, pp. 515-520, Apr. 2012.

[4] Vidhya s. Dessa, Megha P. Araker, Ram Mohana Reddy Guddeti, '*A Parallel Segmentation of Brain Tumor from Magnetic Resonance Images'*, IEEE Third International Conference on Computing Communication & Networking Technologies (ICCCNT), pp. 1-6, Jul. 2012.

[5] Ishita Maiti, Dr. Monisha Chakraborty, *'A new method for brain tumor segmentation based on watershed and edge detection algorithms in HSV colour model',* IEEE National Conference on Computing and Communication Systems (NCCCS), pp.1-5, Nov. 2012.

[6] Dr. H. B. Kekre, Dr.Tanuja Sarode, Ms.Kavita Raut, '*Detection of tumor in MRI using Vector quantization Segmentation'* IEEE International Journal of Engineering Science and Technology, Vol. 2(8), pp. 3753-3757, 2010.

[7] Sudipta Roy, Samir K. Bandyopadhyay, *'Detection and Quantification of Brain Tumor from MRI of Brain and it's Symmetric Analysis'*, IEEE International Journal of Information and Communication Technology Research, vol. 2 No. 6, pp. 477-483, Jun. 2012.

[8] Dr. M. Karnan, T.Logheshwari, *'Improved Implementation of Brain MRI image Segmentation using Ant Colony System',* IEEE International Conference on Computational Intelligence and Computing Research (ICCIC), pp.1-4, Dec.2010.

[9] A. Rajendran and R.Dhanasekaran, *'A hybrid Method Based on Fuzzy Clustering and Active Contour Using GGVF for Brain Tumor Segmentation on MRI Images'*, European Journal of Scientific Research, Vol. 61, No. 2, 2011, pp. 305-313.

[10] M. Arfan Jaffar,Quratulain,and Tae Sun Choi, '*Tumor Detection From Enhanced Magnetic Resonance Imaging Using Fuzzy Curvelet'*, Microscopy Research and Technique, Wiley Online Library, Vol. 75, No. 6, April 2012, pp. 499- 504.

[11] Ming-Ni Wu, Chia-Chen Lin,Chin-Chen Chang, *'Brain Tumor Detection Using Color-Based K-Means Clustering Segmentation',* IEEE Third International Conference on Intelligent Information Hiding and Multimedia Signal Processing(IIHMSP), vol.2, pp. 245-250, Nov.2007.

[12] R. B. Dubey, M. Hanmandlu, Shantaram Vasikarla, *'Evaluation of Three Methods for MRI Brain Tumor Segmentation',* IEEE Eighth International Conference on Information Technology, pp. 494-499, Apr.2012.

[13] N. Nandha Gopal, Dr. M. Karnan, *'Diagnose Brain Tumor Through MRI Using Image Processing Clustering Algorithms Such As Fuzzy C Means Along With Intelligent Optimization Techniques'* IEEE International Conference on Computational Intelligence and Computing Research (ICCIC), pp. 1-4, Dec.2010.

[14] S.Xavierarockiaraj, K.Nithya, and R.Maruni Devi, *'Brain Tumor Detection Using Modified Histogram Thresholding-Quadrant Approach'*, Journal of Computer Applications (JCA), Vol. 5, No.1, 2012, pp. 21-25.

[15] Anam Mustaqeem, Ali Javed and Tehseen Fatima, '*An Efficient Brain Tumor Detection Algorithm Using Watershed and Thresholding Based Segmentation'*, International Journal of Image, Graphics and Signal Processing **(**IJIGSP**)**, Vol. 4, No.10, 2012, pp. 34-39.

[16] Kadam D. B., Gade S. S., M. D. Uplaneand R. K. Prasad, '*Neural Network Based Brain Tumor Detection Using MR Images'*, International Journal of Computer Science and Communication (IJCSC), Vol. 2, No.2, July-Dec. 2011, pp. 325-331.

[17] Hassan Khotanlou, Olivier Colliot, Jamal Atif and Isabelle Bloch, '*3D brain tumor segmentation in MRI using fuzzy classification, symmetry analysis and spatially constrained deformable models'*, *Fuzzy Sets and Systems*, Vol. 160, Issue 10, 2009, pp.1457–1473.

[18] Nandita Pradhan and A.K. Sinha, '*Fuzzy ANN Based Detection and Analysis of Pathological and Healthy Tissues in FLAIR Magnetic Resonance Images of Brain'*, international Journal of Information Technology and Knowledge Management, Vol. 4, No. 2, July-Dec. 2011, pp. 471-476.

[19] Noor Elaiza Abdul Khalid, Shafaf Ibrahim and Mazani Manaf, '*Brain Abnormalities Segmentation Performances Contrasting: Adaptive Network-Based Fuzzy Inference System (ANFIS) vs K-Nearest Neighbors (k-NN) vs Fuzzy c-Means (FCM)'*, 15th WSEAS International Conference on Computers, Corfu Island, Greece, July 2011, pp. 285-290.

[20] Clark, M.C., Hall, L.O., Goldgof, D.B., Velthuizen, R., Reed Murtagh, F., Silbiger, M.S., *'Automatic tumor segmentation using knowledge-based techniques',* IEEE Transactions on Medical Imaging, vol. 17, pp. 187-201,1999.

[21] Prastawa, M., Bullitt, E., Ho, S., Gerig, G., *'A brain tumor segmentation framework based on outlier detection, Medical Image Analysis'*, vol. 8, pp. 275-283, 2004.

[22] A.R.Kavitha, Dr.C.Chellamuthu, Ms.Kavin Rupa, *'An Efficient Approach for Brain Tumour Detection Based on Modified Region Growing and Neural Network in MRI Images'*, IEEE International Conference on Computing, Electronics and Electrical Technologies [ICCEET], pp. 1087-1095, 2012.

[23] Prastawa, M., Bullitt, E., Moon, N., Leemput, K., and Gerig, G. (2003), '*Automatic brain tumor segmentation by subject specific modification of atlas priors*', Academic Radiology, 10(12):1341–1348.

[24] Charles R. Noback, Norman L. Strominger, Robert J. Demarest and David A. Ruggiero, *The Human Nervous System: Structure and Function*, 6th ed., Humana Press, 2005.

[25] *http://www.teamrads.com/Cases/Neuroanatomy/MRI*

[26] Brown, M. and Semeka, R, '*MRI: Basic Principles and Applications*. John Wiley and Sons, Inc., 3rd edition 2003.

[27] Ricci, P. E. and Dungan, D. H. (2001), *'Imaging of low- and intermediate-grade gliomas. Seminars in Radiation Oncoloy',* Vol 11, No 2 (April), 2001: pp 103-112, 11(2):103–112, 2001

[28] Kufe, D. W., Pollock, R. E., Weichselbaum, R. R., Gansler, T. S., and Bast, R. C.,editors, Holland-Frei, '*Cancer Medicine',* BC Decker Inc., 6th edition 2003.

[29] Louis D.N., Ohgaki H., Wiestler O.D, Cavenee W.K. (Eds.), '*WHO Classification of Tumors of the Central Nervous System',* International Agency for Research on Cancer (IARC), Lyon, France, 2007.

[30] Jan C. Buckner, et al., '*Central Nervous System Tumors*', Mayo Clinic Proceedings, Vol. 82, No. 10, 2007, pp. 1271-1286.

[31] R.C.Gonzalez and R.E. Wood, Digital Image Processing, Prentice-Hall, India, Second Edition, 2007.

[32] Rastgarpour M., and Shanbehzadeh J., '*Application of AI Techniques in Medical Image Segmentation and Novel Categorization of Available Methods and Tools',* Proceedings of the International MultiConference of Engineers and Computer Scientists 2011 Vol I, IMECS 2011, March 16-18, 2011, Hong Kong.

[33] Dinesh D. Patil, Sonal G. Deore, **'***Medical Image Segmentation: A Review*',International Journal of Computer Science and Mobile Computing, IJCSMC, Vol. 2, Issue. 1, January 2013, pg.22 – 27.

[34] W. X. Kang, Q. Q. Yang, R. R. Liang, *'The Comparative Research on Image Segmentation Algorithms',* IEEE Conference on ETCS, pp. 703-707, 2009.

[35] L.Aurdal, *'Image Segmentation beyond thresholding',* Norsk Regnescentral, 2006.

[36] Wahba Marian, *'An Automated Modified Region Growing Technique for Prostate*

Segmentation in Trans-Rectal Ultrasound Images', Master's Thesis, Department of Electrical and Computer Engineering, University of Waterloo, Waterloo, Ontario, Canada, 2008.

[37] V. K. Dehariya, S. K. Shrivastava, R. C. Jain, *'Clustering of Image Data Set Using K-Means and Fuzzy KMeans Algorithms'* , International conference on CICN, pp. 386- 391, 2010.

[38] K. M. Passino, '*Biomimicry of bacterial foraging for distributed optimization and control',* IEEE Control Systems 22(3), vol. 22, pp. 52-67, 2002.

[39] Swagatam Das, Arijit Biswas, Sambarta Dasgupta1, and Ajith Abraham, *"Bacterial Foraging Optimization Algorithm: Theoretical Foundations, Analysis, and Applications"*

[40] C.H.Oh, K.Honda, H.Ichihashi, '*Fuzzy clustering for categorical and multivariate data',* Proc. of IFSA/NAFIPS, July 2001, Vol. 4, pp 2154-59.

[41] W.C.Tjhi, L.Chen, '*Possibilistic fuzzy co-clustering of large document collections',* Patt. Recog. 40(2007), pp. 3452-3466.

[42] M. Hanmandlu, S. Susan, V.K. Madasu, B.C. Lovel, *'Fuzzy Co-Clustering of medical images using bacterial foraging',* 23rd International Conference on Image and Vision Computing New Zealand(IVCNZ), pp. 1-6, Nov.2008.