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Automatic Detection of Brain Tumor from MRI Scans Using Maxima Transform

K. Somasundaram[1] and T. Kalaiselvi[2]

Department of Computer Science and Applications,
Gandhigram Rural Institute—Deemed University,
Gandhigram–624 302, Tamil Nadu, India
E-mail: [1]ka.somasundaram@gmail.com; [2]kalaivpd@gmail.com

***ABSTRACT*—In this paper we present a technique to detect the tumor from magnetic resonance imaging brain scans. Usually tumors occupy the locations of normal tissues and their intensity characteristics differ from the surrounding normal tissues. Using this knowledge we have developed a method to locate the regions occupied by brain tumors. Initially our method extracts the brain by removing the unwanted non-brain regions like skull, scalp, fat and muscles. Then the brain is segmented into well known regions like WM, GM, CSF and background using FCM algorithm. In T2 scans the tumor intensity characteristics are similar to CSF. So the CSF class is analyzed for symmetric property along the central vertical line. If no symmetry is found then the image with CSF class is segmented further into CSF and tumor classes using extended maxima transform. This transform helps to separate the tumor region from the normal CSF region. This computer assisted tool helps the neurosurgeon to take decision during their surgical planning.**

KEYWORDS:* Brain Extraction, Fuzzy Segmentation, Symmetry Analysis, Maxima Transform, MRI Brain Scans.

I. INTRODUCTION

A brain tumor is a cluster of abnormal cells growing in the brain. Primary brain tumors are those that begin in the brain and tend to stay in the brain. Metastatic brain tumors begin as a cancer elsewhere in the body and migrate, or metastasize, to the brain. There are more than 120 different types of brain tumors; some are malignant (cancer), many are benign (non-cancerous). The cause of brain tumors is unknown. Benign or malignant, primary or metastatic, brain tumors are treatable. More knowledge about brain tumors has been gained in the last ten years than in the past hundred years due to involvement of high resolution techniques like Computed Tomography (CT), Magnetic Resonance Imaging (MRI), functional MRI (fMRI), Positron Emission Tomography (PET) and Single Photon Emission Computed Tomography (SPECT) in medical imaging. Imaging techniques to diagnose, stage, and follow patients with brain tumors are central to the clinical management. MRI is the most commonly used technique for lesion detection, definition of extent, detection of spread and in evaluation of either residual or recurrent disease.

The existing tumor detection methods broadly classified into three categories: atlas-based methods [1], [2], symmetry property-based methods [3]–[5] and feature-based methods [6]–[9]. Most of the methods are semi-automatic and require user intervention either to initiate or to refine the results.

In this paper we propose a fully automatic method to detect brain tumor. We make use of bilateral symmetry property of human brain to detect the abnormality and maxima transform to locate the tumor region. The structural arrangement of the whole brain is similar on the both side of hemisphere and is symmetrical about the vertical axis through the brain centre. Tumors appear hyper intense in T2-w scans and have intensity close to that of Cerebro Spinal Fluid (CSF). The presence of abnormal tissues in the CSF class can be detected by measuring the vertical symmetry of the CSF image [10]. Fuzzy Symmetric Measure (FSM) is used as a threshold to discriminate between normal and abnormal CSF images. Imaging intensity for tumors or lesions usually occupies the high end gray spectrum of T2-w scans [8]. In our method these high intensity tumor regions are located and separated from CSF class of abnormal scans using extended maxima transform. The role of extended maxima transform is to identify groups of pixels that are significantly higher than their immediate surrounding. Our method is tested over ten brain volumes of normal and abnormal subjects. The results are compared with existing methods and visually verified by the medical experts.

II. METHOD OVERVIEW

Sometimes, tumors have similar intensity characteristics of non-brain tissues like fat, muscles and background clutters. Hence the brain portion should be extracted first to eliminate

these overlapping intensity artefacts. Our method then checks whether any abnormality is present within the slice and separate the abnormal slices from normal ones. For normal slices, CSF is symmetrical about the vertical central line. So the presence of abnormal tissues in the CSF class can be detected by measuring the vertical symmetry of the CSF image. Hence a fuzzy segmentation is done to generate a CSF image from extracted brain portion and a fuzzy symmetric measure (FSM) is calculated for CSF image to discriminate between normal and abnormal scans. In CSF region tumor appears as increased MR image intensity which possesses local maxima. Hence an extended maxima transform is used to extract the region with maximum intensity from the CSF class and treat them as region of tumors.

Fig. 1 illustrates the pipeline that we use for extracting the tumor region from MRI brain scans. It mainly contains three steps: 1) Brain portion extraction, 2) Abnormality detection and 3) Tumor segmentation. As an illustration, the results for two sample slices obtained at different stages are shown in Fig. 2.

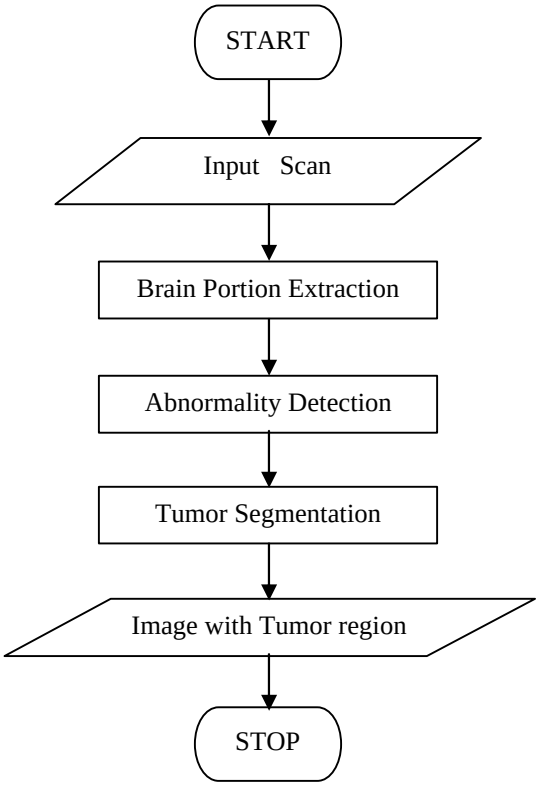

Fig. 1: Flowchart of Proposed Method

The detailed description of the procedure is as follows.

A. Brain Portion Extraction

Numerous Brain Extraction Algorithms (BEA) are available in literature. Our T2-BEA [11] makes use of anisotropic diffusion process [12], optimal thresholding and morphological processes [13] to separate the brain from non-brain portions. The diffusion process is used to highlight the brain from T2 head scan. Then an intensity threshold is computed using which a rough binary brain portion is generated. The morphological operations, erosion and dilation, and connected component analysis are then performed on the rough brain portion to produce the brain mask. Finally the brain mask is used to extract the brain from T2 scans. In Fig. 2, the extracted brain portions are shown in column 2.

B. Abnormality Detection

The extracted brain is segmented into four major classes WM, GM, CSF and background using fuzzy c-means (FCM) algorithm. FCM uses the fuzzy theory and is suitable for the anisotropic nature of volumes that are affected by PVE. This method is frequently used in pattern recognition and never misses a region [14], [15]. The aim of using FCM is to find cluster centres that minimize a dissimilarity (objective) function given by,

$$J_m = \sum_{i=1}^{n}\sum_{j=1}^{c} u_{ij}^{m} d_{ij}, \quad \ldots (1)$$

where $m \in [1,\infty]$ is a weighting exponent, $u_{ij} \in [1,0]$ is the degree of membership x_i in the cluster j, x_i is the i^{th} element of d-dimensional measure data, c_j is the d-dimensional center of the cluster and d_{ij} is the Euclidean distance between i^{th} data point (x_i) and j^{th} centroid (c_j).

The fuzzy portioning is carried out through an iterative optimization of the objective function given in equation (1), with the update of membership u_{ij} and the cluster centers c_j using:

$$u_{ij} = \frac{1}{\sum_{k=1}^{c}\left[\frac{d_{ij}}{d_{ik}}\right]^{\frac{2}{m-1}}}, \quad \ldots (2)$$

$$c_j = \frac{\sum_{i=1}^{n} u_{ij}^{m} x_i}{\sum_{i=1}^{n} u_{ij}^{m}} \quad \ldots (3)$$

This procedure will stop if the improvement of the objective function over the previous iteration is below a threshold value, $\varepsilon \in [1,0]$. By iteratively updating the cluster centers and the membership grades for each data point, FCM iteratively moves the cluster centers to the "right" location within a data set.

The FCM algorithm as proposed by Bezdek [14] is:

Step 1: Randomly initialize the membership matrix U = [u_{ij}], $U^{(0)}$ that has a constraint equation given by

$$\sum_{i=1}^{c} u_{ij} = 1, \forall j = 1,..n \quad \ldots (4)$$

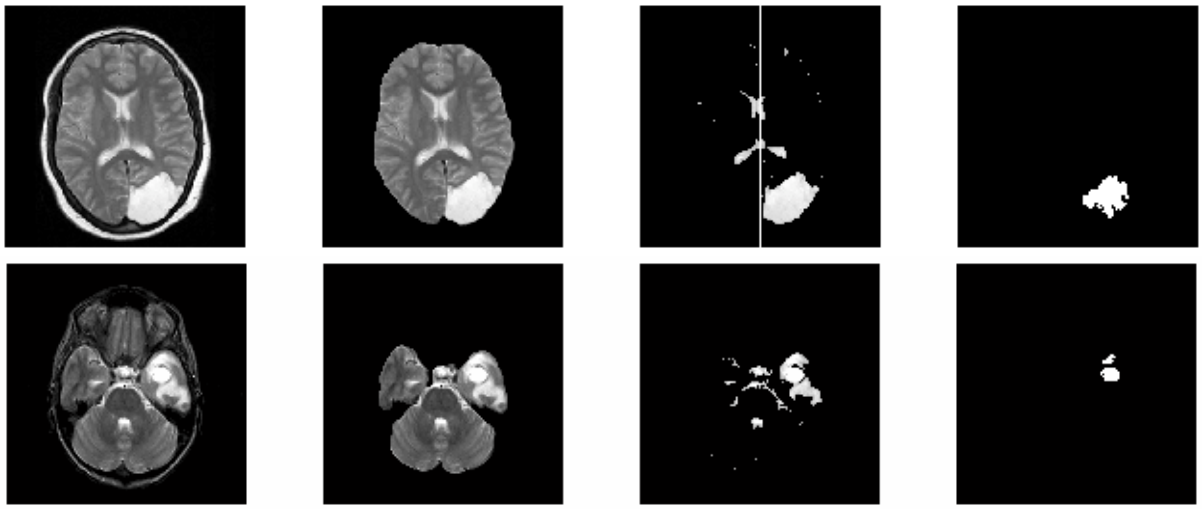

Fig. 2: Two T2-w scans with tumor in row1 and row2, Original scans are given in column 1, extracted brain portions in column 2, CSF regions with central vertical line in column 3 and extracted tumor regions by extended maxima transform are in column 4.

Step 2: At the k^{th} step, calculate the centroids and objective function by using the equations (3) and (1) respectively.
Step 3: Update $U^{(k)}$, $U^{(k+1)}$ by using the equation (2).
Step 4: If stopping criteria ($\varepsilon \leq 0.00001$) is met then stop; otherwise return to Step 2.

Then a binary image of CSF is created by removing the other regions like WM and GM. In that CSF image the foreground indicates the region of CSF and background is in black color as shown in column 3 of Fig. 2.

Abnormal tissues in the CSF class can be detected by measuring the symmetry of the CSF image. Here the symmetry is computed by the fuzzy symmetric measure (FSM) [16] given by:

$$\text{FSM}(\text{csf}_s) = \frac{1}{1+\left(\frac{n_L - n_R}{100}\right)^2} \quad \ldots (5)$$

where n_L and n_R are the number of foreground (white) pixels in the left and right half of the CSF image present at either side of the central vertical line (Y axis) of slice *s*. The symmetry values calculated from normal CSF classes are generally much larger than 0.1, and the values for abnormal CSF classes are much smaller than 0.1 [10]. We fix 0.05 as a threshold value to FSM. If FSM (csf_s) < 0.05 then the slice *s* is abnormal otherwise it is a normal slice. The threshold value 0.05 was obtained after doing several experiments on both normal and abnormal scans.

When an MRI is acquired, the head position sometimes may not coincide with the world co-ordinate of the image acquisition system. There may be a tilt in the acquired image. To perform the symmetry test for the CSF in MRI, the tilt has to be corrected. For this a slice transformation is done. An intelligent system is used [17] to detect the edges of the interhemisphere fissure (IHF) present in the extracted brain. IHF is a deep cleft and a longitudinal fissure between the cerebral hemisphere (CH) and is filled by CSF. The bilateral symmetry checking is done about the boundary line separating the CHs. Liang *et al.* [18] defined that the boundary between the CHs must lie within the IHF In each 2D axial slice, edge1 is marked at the nadir of the upper portion of cleft and edge2 is fixed at the zenith of the lower portion of cleft. Then a line is drawn by joining these two edges that corresponds to the boundary line passing through IHF. The detected boundary line is used to transform the MRI scans to the ideal world co-ordinate, here the Cartesian co-ordinates system. This alignment is done by composite transformation of translation followed by rotation. The transformation of the image shown in Fig. 3(a) to world co-ordinate with a translation distance d and rotation angle ? is shown in Fig. 3(b).

C. Tumor Segmentation

Tumor segmentation is the main contribution of our work. Here we make use of extended maxima transform to detect the tumor locations. It is the regional maxima of the H-maxima transform [19]. It finds the peaks which are *n* intensity values higher than the background in regions. It is a robust peak finder, depends only on contrast. It performs first H-maxima transform followed by recognition of regional maxima.

H-maxima transform is based on morphological reconstruction, repeated dilations of image followed by masking. The H-maxima transform is given by Koh *et al.* [20]:

$$HMAX_h(f) = R_f(f-h) \quad \ldots (6)$$

where $R_f(f-h)$ is the morphological reconstruction by dilation of image f with respect to $(f-h)$. This morphological operation suppresses all points whose value

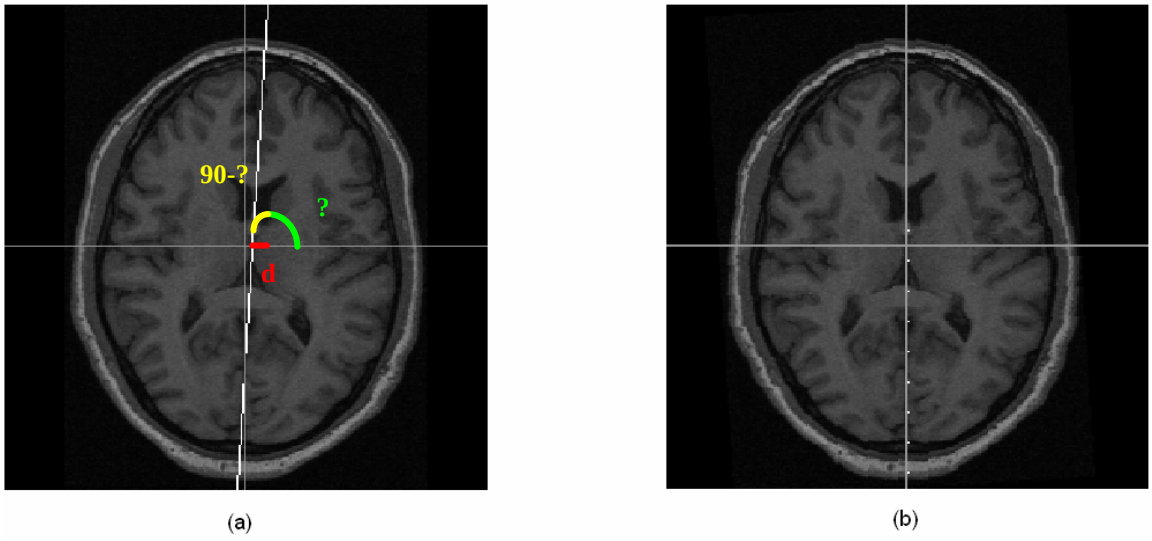

Fig. 3: (a) MR scan with detected boundary (in dotted white color) and Cartesian coordinate system with centre as origin (in light gray color) (b) Transformed image with coordinates ? and d

with respect to their neighbors is smaller than a threshold level *h*. This H-maxima transform belongs to the class of connected operators. The transform is then followed by an extended maxima operation to identify all regional maxima. Regional maxima are connected components of pixels with a constant intensity value, and whose external boundary pixels all have a lower value. The extended maxima operation is defined by:

$$EMAX_h(f) = RMAX[HMAX_h(f)] \quad \ldots (7)$$

It removes local peaks which are lower than *h* intensity values from the background. Based on the analysis done during our experiments, h is set to 10. The tumor regions extracted by using extended maxima transform is given in column 4 of Fig.2.

III. Materials Used

Ten datasets of normal and abnormal subjects were used in our experiments. The details of the datasets are given in Table 1.

The first eight datasets (v01–v08) consisting of 2 normal volumes and 8 abnormal volumes with brain tumor (Neoplastic disease) were taken from the website 'The Whole Brain Atlas' maintained by the Department of Radiology and Neurology at Brigham and Women's Hospital, Harvard Medical School. The remaining two datasets (v09–v10) were collected from KGS Advanced MR & CT Scan, Madurai, Tamilnadu, India, which were acquired from 1.5T Siemens machine for 2 normal subjects. The dimension of each slice in volumes v01–v08 is 256 × 256 pixels and slice thickness varying from 2–5 mm with 260 mm field of view. So the pixel dimension is fitted to 1 × 1 mm. The slices taken from 1.5T Siemens machines have a dimension of 448 × 512 pixels and 5 mm thickness with 40–50% inter-slice gap. The field of view is fixed to 210 × 240 mm and hence the pixel dimension is set to 0.47 × 0.47 mm.

Table 1: Details of Datasets used

No.	*Volume Identity*	*Gender*	*Age*	*Clinical*	*Total slices*
1.	v01	Female	81	Normal	54
2.	v02	Female	76	Normal	43
3.	v03	Female	51	Anaplastic Astrocytoma	56
4.	v04	Male	35	Astrocytoma	29
5.	v05	Male	62	Metastatic adeno carcinoma	24
6.	v06	Female	42	Metastatic bronchogenic carcinoma	24
7.	v07	Male	75	Meningioma	27
8.	v08	Male	22	Sarcoma	24
9.	v09	Male	43	Normal	19
10.	v10	Female	40	Normal	19

IV. Results and Discussions

Both qualitative and quantitative validations were used for the performance evaluation. The quantitative analysis parameters like false alarm (FA) and missed alarm (MA) were used to check the results of abnormality detection procedure. False alarm is an indication when the input scan which does not have a tumor is marked as abnormal during analysis [8]. Missed alarm is an indication when an abnormal image is not marked so during the analysis. Three successive versions of existing method predictive cognitive system for brain images (PCB), v.1, v.2 and v.3 [6–8] were used to compare our results as shown in Table 2. None of the alarm

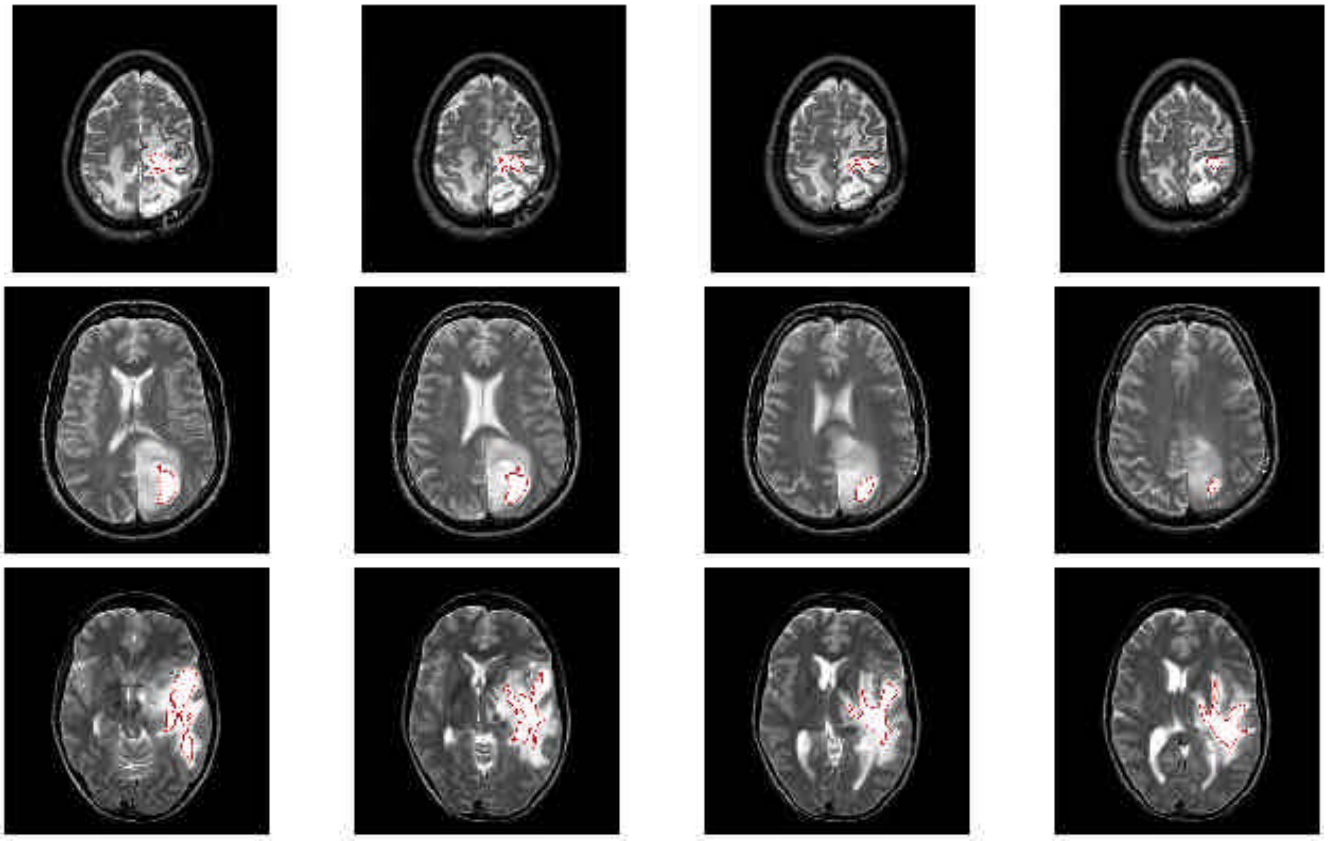

Fig. 4: Perimeter of tumor regions of abnormal slices marked by dotted lines (red color). Slices 41–44 from v03 are given in row1, slices 16–19 from v04 in row 2 and slices 9–12 from v06 in row 3

Table 2: Comparison of FA and MA Obtained in our Method with that of PCB (v.1, v.2 and v.3)

No.	*Volume*	*FA (%)*				*MA (%)*			
		v.1	*v.2*	*v.3*	*Proposed*	*v.1*	*v.2*	*v.3*	*Proposed*
1.	v01	11	11	0	0	–	–	–	–
2.	v02	10	23	0	0	–	–	–	–
3.	v03	0	5	0	0	24	0	0	0
4.	v04	25	8	7	13	48	5	5	0
5.	v05	37	27	17	0	50	17	11	13
6.	v06	5	5	0	13	28	0	0	4
7.	v07	19	15	7	0	33	3	0	7
8.	v08	14	19	9	0	25	4	4	25
Average		15	14	5	3	26	4	3	6

has been noticed in our method for the normal volumes. The FA indication in our method is lower than all the versions of PCB. Out of eight data sets, our method produced FA only for 2 sets whereas PCB produced 4 or more datasets. FA for the proposed system is obtained for v04 and v06 due to the swelling edema that lead to elevated intracranial hypertension and thus affects the brain symmetrical property. However the MA in our proposed method is higher than the v.2 and v.3 and lower than v.1 of PCB. The higher value of MA in our method is due to equally scattered characteristics of tumor or hypo intense nature of tumors. So they are completely missed in datasets v05 and partially in v07 and v08.

For the qualitative validation, the perimeter of tumor regions produced by extended maxima transform is taken as a mask. By overlapping this mask on the original scans, the abnormal locations are marked. Some of the abnormal scans selected from v03, v04 and v06 with over laid tumor regions are shown in Fig .4. The selected slices from the volumes are successive slices. The extended maxima transform excellently separates the tumor from surrounding CSF volumes as shown in columns 3 and 4 of v06 (row 3). The qualitative validation of our method was done by four experts. They suggested that identifying the abnormality in MRI head scans might be useful to quicken the diagnosis and prognostic process. Further they proposed that our method would be helpful to locate the hyper intense nature of tumors or mass effect present in either of the hemisphere.

V. Conclusion

In this paper we have developed an automatic image based method to detect tumors in 2D MRI head scans. Interhemisphere fissure (IHF) and symmetrical nature of the brain are used in the tumor detection. Experimental results on 10 data sets show that the proposed method performed

well. In few cases, it performs better than the existing methods.

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REFERENCES

[1] M.B. Cuadra, C. Pollo, A. Bardera, O. Cuisenaire, J. Villemure and P. Thiran, "Atlas Based Segmentation of Pathological MR Brain Images using a Model of Lesion Growth", IEEE Trans. in Medical Imaging, vol. 23, no. 10, pp. 1301–1313, 2004.

[2] N. Moon, E. Bullitt, K.V. Leemput and G. Gerig, "Model Based Brain and Tumor Segmentation", ICPR Quebec, pp. 528–531, August 2002.

[3] H. Khotanlou, O. Colliot, J. Atif and I. Bloch, "3D Brain Tumor Segmentation in MRI using Fuzzy Classification, Symmetry Analysis and Spatially Constrained Deformable Models", Fuzzy Sets and Systems, vol. 160, pp. 1457–1473, 2009.

[4] Z. Wang, Q. Hu, K. Loe, A. Aziz and W.L.Nowinski, "Rapid and Automatic Detection of Brain Tumors in MR Images", in Proc. SPIE, Bellingham, WA, Vol., 5369, pp. 602–612, 2004.

[5] M. Mancas, B. Gosselin and B. Macq,"Fast and Automatic Tumoral Area Localization Using Symmetry", in Proc. IEEE ICASSP Conference, Philadelphia, Pensylvania, USA, 2005.

[6] P.Y. Lau and S. Ozawa, "PCB: A Predictive System for Classifying Multimodel Brain Tumor Images in an Image-Guided Medical Diagnosis Model", in Proc. 12th International Conference on Intelligent System for Molecular Biology, Glasgow, UK, 2004.

[7] P.Y. Lau and S. Ozawa, "A Region- and Image-Based Predictive Classification System for Brain Tumor Detection", in Proc. Symposium on Biomedical Engineering, Hokkaido, Japan, pp. 72–102, 2004.

[8] P.Y. Lau and S. Ozawa, "A Multiparameter Hierarchical Representation using Region-Based Estimation Model For Detecting Tumor in T2-Weighted MRI Brain Images", Malaysian Journal Of Computer Science, Vol. 18, No. 1, pp. 1–19, 2005.

[9] R.B. Dubey, R. Ratan, M. Hanmandlu and S.K. Gupta, "Computer Assisted Segmentation of Brain Tumor", TechnoramA, A Supplement to IEI News, pp. 23–26, March 27, 2008.

[10] M.C. Clark, L.O. Hall, D.B. Goldgof, R. Velthuizen, F.R. Murtagh and M.S. Silbiger, "Automatic Tumor Segmentation using Knowledge-Based Technique", IEEE Trans. on Medical Imaging, Vol. 17, No. 2, pp. 187–201, 1998.

[11] K. Somasundaram and T. Kalaiselvi, "An Anisotropic Diffusion Based Brain Extraction Algorithm for Axial T2-Weighted Magnetic Resonance Images", Submitted after I revision to Computers in Biology and Medicine, 2009.

[12] P. Perona and J. Malik, "Scale-Space and Edge Detection using Anisotropic Diffusion", IEEE Trans. on Pattern Analysis and Machine Intelligence, Vol. 12, No. 7, pp. 629–639, 1990.

[13] M. Sonka, V. Hlavac and R. Boyle, *Image processing, Analysis and Machine Vision*, 2nd ed., Brooks / Cole Publishing Company, Pacific Grove, CA, 1999.

[14] J.C. Bezdek, *Pattern Recognition with Fuzzy Objective Function Algorithms*, Plenum Press, New York, 1981.

[15] K. Somasundaram and T. Kalaiselvi, "A Comparative Study of Segmentation Techniques Used for MR Brain Images", in Proc. International Conference on Image Processing, Computer Vision and Pattern Recognition – IPCV'09, WORLDCOMP'09, Los Vegas, Nevada, USA, vol. II, pp. 597–603, 2009.

[16] H.J., Zimmermann, *Fuzzy Set Theory and its Applications*, Kluwer Academic Publishers, 2nd ed., Boston, MA, 1991.

[17] K. Somasundaram and T. Kalaiselvi, "A Novel Technique for Finding the Boundary between the Cerebral Hemispheres from MR Axial Head Scans", in Proc. 4th Indian International Conference on Artificial Intelligence – IICAI '09, Bangalore, India, 2009.

[18] L. Liang, K. Rehm, R. Woods and D. Rottenberg, "Automatic Segmentation of Left and Right Cerebral Himispheres from MRI Brain Volumes using Graph Cut Algorithms", NeuroImage, Vol. 34, pp. 1160–1170, 2007.

[19] P. Soille, *Morphological Image Analysis: Principles and Applications*, 2nd ed., Springer Verlag, 1999.

[20] H.K. Koh, W. Shen, B. Shuter and A.A. Kassim, "Segmentation of kidney cortex in MRI studies: a constrained morphological 3D h-maxima transform approach", International Journal of Medical Engineering and Informatics, Vol. 1, No. 3, pp. 330–341, 2009.