

# The detection and visualization of brain tumors on T2-weighted MRI images using multiparameter feature blocks

Phooi Yee Lau, *Student Member, IEEE*, Frank C. T. Voon, and Shinji Ozawa, *Member, IEEE*

**Abstract**—The objective of this paper is to present an analytical method to detect lesions or tumors in digitized medical images for 3D visualization. The authors developed a tumor detection method using three parameters; edge ( $E$ ), gray ( $G$ ), and contrast ( $H$ ) values. The method proposed here studied the  $EGH$  parameters in a supervised block of input images. These feature blocks were compared with standardized parameters (derived from normal template block) to detect abnormal occurrences, e.g. image block which contain lesions or tumor cells. The abnormal blocks were transformed into three-dimension space for visualization and studies of robustness. Experiments were performed on different brain disease based on single and multiple slices of the MRI dataset. The experiments results have illustrated that our proposed conceptually simple technique is able to effectively detect tumor blocks while being computationally efficient. In this paper, we present a prototype system to evaluate the performance of the proposed methods, comparing detection accuracy and robustness with 3D visualization.

## I. INTRODUCTION

IN the evolution of healthcare services, there is an increasing need for greater effective use of imaging data in medical diagnosis and individual risk assessment, treatment selection, and disease prevention. The ultimate challenge is to develop software with intelligence to combine imaging technology with a workable diagnostic system that is capable of detecting cancer in its early stages at that level of expert recognition of a cancer center specialist. We believe that diagnostic research-based patient-oriented system with the capability to distinguish the presence of tumors on medical images of healthy people and cancer patients will be one of the most pressing issues in the near future.

The analysis and study of the brain is of great interest due to its potential for studying early growth patterns and morphologic changes in the cancer process. Recent studies have demonstrated the potential of a decision support system for detecting tumors in medical images, providing radiologists with a second pair of highly trained eyes. It gives doctors access to additional information present in images that have characteristics generally accepted to be associated

with cancer, clusters of bright spots that are suggestive of lesions, patterns suggestive of tissue masses or distortions, and mark regions that have the characteristics of lesions or tumors.

Magnetic Resonance Imaging (MRI) techniques are still developing, and recent efforts have been directed primarily at improving image quality and speed of acquisition. MRI provides non-invasive, high quality images of neuro-anatomy and disease processes. Through its ability to detect contrast in the density of soft tissues, MRI is well suited to monitor and evaluate cerebral tumors as they develop and respond or, as the case may be, fail to respond to therapy [1]. There are many sequences that can be used on MRI and the different sequences often provide different contrast between tissues so the most appropriate sequence should be chosen according to disease and what the clinicians want to detect. This paper focuses on analyzing T2-weighted MRI images because medical specialists often can diagnose whether a brain tumor exists within a T2-weighted MRI images with sensitivity of 94% [2].

## II. METHODOLOGY

In considering different approaches, we studied previous methodologies that have been developed and improved upon by various authors to computationally analyze images [3],[4],[5],[6]. Vailaya (2001) analyzed low-level image features and classified input images as either indoor or outdoor images using a hierarchical classification method. Abassi (2001) studied image contours to develop a shape-based retrieval system. Epifiano (2002) proposed a global framework for texture classification based on pixel-based random closed set theory. Gering (2002) described a method that relies on the detection of abnormalities using the Expectation-Maximization technique by making use of information contained in multiple layers, e.g. voxel intensities, spatial coherence, structural relationships, and user input [7]. His methods are capable of segmenting large tumors from the surrounding brain tissue by exclusively training on normal brain images in healthy people in order to recognize deviations from normality. This requires high computational effort and disregards the presence of partial volume artifacts in images. From the available literature, we have noted that the process of analysis of the different structures present in medical images forms an essential component of every imaging application, but the computational effort and requirements are high in most of these approaches.

Manuscript received Apr 16, 2005. This work was supported in part by the VISOR Project, a Special Coordination Funds from The Ministry of Education, Culture, Sports, Science and Technology of the Japanese Government, The Keio Leading-edge Laboratory of Science and Technology, and The Iwatani Naoji Foundation.

Shinji Ozawa and Phooi Yee Lau are with the Department of Information and Computer Science, Keio University, Yokohama 223-8522, Japan (e-mail: [ozawa@ozawa.ics.keio.ac.jp](mailto:ozawa@ozawa.ics.keio.ac.jp); [laupy@ozawa.ics.keio.ac.jp](mailto:laupy@ozawa.ics.keio.ac.jp)). Frank C.T. Voon is with the Department of Anatomy, National University of Singapore, Singapore (email: [antvoon@nus.edu.sg](mailto:antvoon@nus.edu.sg)).

In this paper, we propose a conceptually simple supervised block-based and image-based (shape, texture, and content) technique to analyze MRI brain images with relatively lower computational requirements. Our scope is to detect a block suspected of containing malignant lesions in medical images. These are the regions that would require more thorough examination by medical experts for a second clinical evaluation. We describe the phases of this technique in two sections: the feature block section, and the multiparameter section. The first section discusses how images are divided into regions using a block-based method. The second section shows how each classified block is studied individually by calculating its multiparameter values. In this instance, the multiparameter features refer to the following three specific features: the edges ( $E$ ), gray values ( $G$ ), and local contrast ( $H$ ) of the pixels in the block being analyzed. The process flow of our proposed methodology is shown in Fig. 1.

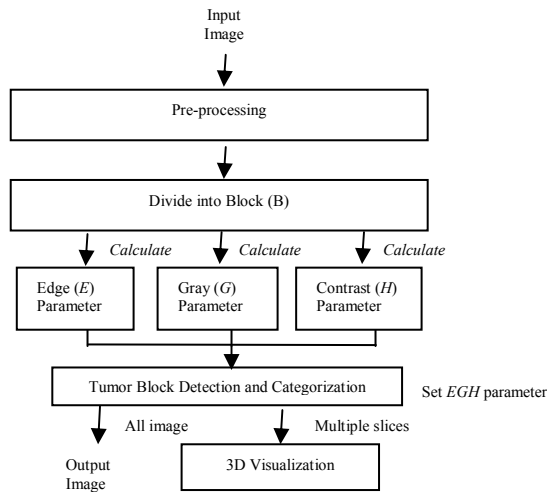


Fig. 1: Process flow of proposed methodology

### A. Feature Block

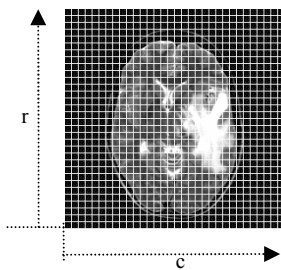


Fig. 2: Supervised block:  $ROI$  of an input image ( $256 \times 256$ ) with block size  $B$  ( $8 \times 8$  pixel)

In most medical images, the structures of interest such as tumors, lesions and arteries, occupy a percentage that is often well below 10% of the total number of pixels [8]. Conventional medical imaging involves visually comparing images side-by-side to discern differences from normal or emergence of changes with time. Detecting minute differences between two pictures however can be nearly

impossible. For the analysis of such small tissues or structures, we devised a block system that divides the region of interest ( $ROI$ ), which is highly dependent on imaging modalities, into block size ( $B$ ). A block ( $B$ ) is denoted as a part of the whole image ( $ROI$ ), divided evenly by a factor of eight, as shown in Fig. 2.

This supervised block is further divided into tumor blocks that are categorized from low-density tumor blocks to high-density tumor blocks. The different levels of the  $EGH$  value of the feature block are represented as different colors, and the color code is shown in Fig. 3.



Fig. 3: Representation of feature block value with color code

### B. Multiparameter

Recent advances in medical image analysis often include processes for an image to be segmented in terms of a few parameters and into smaller sizes or regions, to address the different aspects of analyzing images into anatomically and pathologically meaningful regions. Classifying regions using their multiparameter values makes the study of the regions of physiological and pathological interest easier and more definable. Here, multiparameter features refer to the following three specific values for the edges ( $E$ ), gray values ( $G$ ), and local contrast ( $H$ ) of the pixels.

#### A. Edge ( $E$ ) Parameter

Edge information is often used to determine the boundaries of an object. This is mainly used for analysis to derive similarity criterion for a pre-determined object. In our earlier findings, we observed that the edge pixel for a tumor image is reduced in comparison with that of a non-tumor image. The reduction of edge count for tumor images is because the brain substance has been pushed aside and compressed by the growth of the tumor within a confined space, the intracranial cavity. Symptoms occur due to the local effects of cerebral tissue compression or invasion. Thamburaj, a neurosurgeon, reports that systemic malignancy can metastasize to any location in the brain but most commonly (80%) affects the cerebral hemispheres, which accounts for the tendency of metastases to be located at the junction of the gray and white matter [9]. The incidences of cerebral compression reduce the edge counts of the cerebral hemisphere.

Given this understanding, we use the Sobel edge detection method to detect image edges ( $I_E$ ). Image  $I_1$  and  $I_2$  is obtained by filtering an input image with two convolution kernels concomitantly, one to detect changes in vertical contrast ( $h_x$ ) and the other to detect horizontal contrast ( $h_y$ ), shown in equation (1). Image output ( $I_E$ ) is obtained by calculating the gradient magnitude of each pixel, as shown in equation (2). Subsequently, the edge parameter ( $E$ ) is calculated, whereby  $E_{(r,c)}$  is increased by one each time when  $I_E(x,y) = '1'$  in a supervised block, as shown in equation (3).

$$h_x = \begin{bmatrix} -1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 1 \end{bmatrix}, h_y = \begin{bmatrix} -1 & -2 & -1 \\ 0 & 0 & 0 \\ 1 & 2 & 1 \end{bmatrix} \quad (1)$$

$$I_E(x, y) = \sqrt{I_1^2(x, y) + I_2^2(x, y)} \quad (2)$$

$$E_{(r,c)} = \sum_{(x,y) \in B} (I_{Ep} == 1) \quad (3)$$

### B. Gray (G) Parameter

In this technique, the gray parameter ( $G$ ) for each block of the brain is accumulated, and controlled by a binary image ( $I_T$ ) using the  $G_D$  value as a threshold, as shown in equation (6).  $G_D$  value is calculated using the average pixel value ( $I_{av_s}$ ) of each image slice ( $S$ ) for total image slices ( $T$ ) of an image dataset, shown in equation (4) and (5).

$$I_{av_s} = \frac{1}{65536} \sum I_p(x, y) \quad (4)$$

$$G_D = \frac{\sum_{s=0}^T I_{av_s}}{T} \quad (5)$$

$$G_{(r,c)} = \sum_{(x,y) \in B} I_p(x, y), \text{ for all } (I_T(x,y) == 1) \quad (6)$$

The assumption here is that an image can be classified using the textural features of the spatial pixel intensity values that are associated with brain tissue. Krishnan (1998) describes how each pixel from an MR image represents many tissue parameters; typically, proton density (PD), spin-lattice (T1) and spin-spin (T2) relaxation time [10]. Textural features contain information about the spatial distribution of tonal variations [11]. The concept of tone is based on the intensity of pixels within a defined region (shades of gray in a gray scale image). For this technique, we analyzed the T2-weighted MRI brain images of the Visible Human Male dataset, where the pixel ratio of the image is 1.016 mm/pixel (256 x 256 pixels within the actual human head dimensions of 260.0mm x 260.0mm). The pixels intensity for each slice was calculated to establish the threshold values and thus provide the basis for analysis of clinical MR images from patients with brain tumors.

### C. Contrast (H) Parameter

Contrast ( $H$ ) is often used to characterize the extent of variation in pixel intensity. In the present technique that we use, the computational program analyses the differences, especially in instances of strong dissimilarity, between entities or objects in an image  $I(x,y)$  using an adaptive block-based linear contrast enhancement algorithm. We adopt the minimum/maximum stretch algorithm for the 8-neighborhood connectivity, where min H and max H represent the minimum and maximum intensity values of the neighborhood pixel  $C_8(I_H)$ , as shown in equation (7). Thamburaj specifies that malignant tumor cells contain highly proteinaceous fluid [9], which is represented as high signal intensity on T2-weighted MRI images of the brain. By

studying the relational features of an image, high contrast parameter values among pixels can be filtered and studied. In our previous studies, tumor cells are often associated with higher value of contrast ( $H$ ) parameter.  $H_d$  is obtained by totaling the contrast of a supervised block, as shown in equation (8).

$$I_H(x, y) = \left( \frac{I(x, y) - \min H}{\max H - \min H} \right) \times \max H | H \in C_8(I_H) \quad (7)$$

$$H_d(r, c) = \sum_{(x,y) \in B} I_H(x, y) \quad (8)$$

## III. MATERIALS

The computational analysis is implemented on a Dell Dimension 8400 Pentium IV 3.20GHz computer with 1 GB RAM. The support analysis software used in this paper is MATLAB. The core software is PCB, which has been developed in the Ozawa Laboratory at Keio University using Visual C++ programming language. PCB is a diagnostic research-oriented system with the capability to detect tumor images on bitmapped medical images, and to make correlations between a disease and its properties with its clinical management. The system current version of the system is 3.0. In order to evaluate the performance of our proposed algorithms and methodology, the experiments were conducted on The Whole Brain Atlas v.1.0 (Case 1, Case 28 and Case 32).

## IV. EXPERIMENTAL RESULTS

### A. Detection results on single slice

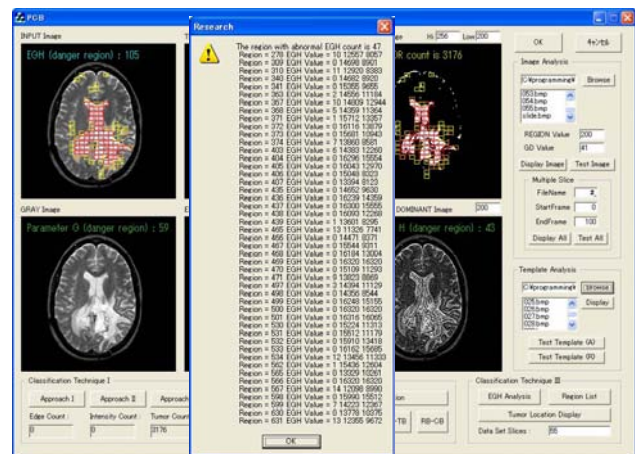


Fig. 4: The PCB system output for single slice in an MRI image

Experimental results shown in Figures 4 and 5 depict a strong value representation in using the  $EGH$  parameters for differentiating the various tumor properties and for predicting the occurrence of a tumor or lesions in T2-weighted MRI brain images. A higher  $EGH$  value depicts a greater extent of brain tissue damage and is depicted here using the color-code system shown in Fig. 3.

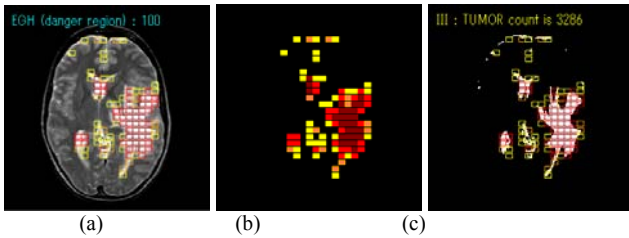


Fig. 5: Detection result: (a) Input image after calculating the danger block (b) Danger block (c) Danger block on threshold image

### B. Detection results on multiple slices

In the second set of experiments, the proposed technique was tested on a series of T2-weighted MRI brain images taken of patients with brain tumors. Experimental results show that the detected tumor blocks were marked accurately enough to produce a 3D visualization for linking and differentiating different tumor blocks with different brain illnesses using a brain model that was able to enhance the detection and interpretations. Overall, we conclude that the *EGH* parameters show comparable performances, both in their accuracy in depicting the initial prediction of the tumors in all input images, and in clearly corresponding to the clinical and pathological findings of the cases. Figures 6 (a) & 7 show the results of visualizing the tumor block found in 3D. We also compare our detection method with a single grayscale threshold technique, shown in Fig. 6 (b).

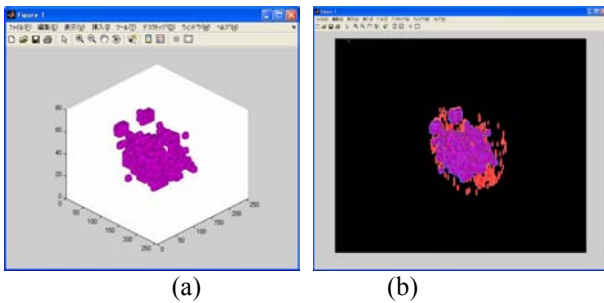


Fig. 6: (a) 3D visualization of tumor block found with lighting (b) Tumor block visualization over a threshold image (a single grayscale threshold)

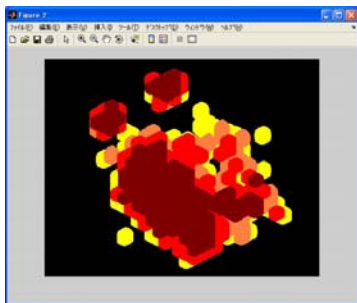


Fig 7: 3D visualization of tumor block found using color code for Case 28

## V. CONCLUSION

In this paper, we introduced a conceptually simple classification method using multiparameter features on supervised block to computationally classify brain images.

Our conclusion is that the proposed method is effectively capable of identifying tumor areas in T2-weighted medical brain images taken under different clinical circumstances and technical conditions, which were able to show a high deviations that clearly indicated an abnormalities in areas with brain disease. The response time for processing system is 176 milliseconds for each image analysis. Currently we are working towards improving the brain model to include more cases. We expect that the PCB system will become a valuable tool for the study of MRI brain images. All future efforts will focus on extending this capability to include other types of imaging modalities, e.g. PET/CT (Positron Emission Tomography/Computed Tomography) or PET, into the PCB system through a user-friendly and practical system that will be usable in medical clinics by specialists and medical practitioners.

## REFERENCES

- [1] Haney, SM, Thompson, PM, Cloughesy, TF, Alger, JR, and Toga AW, "Tracking Tumor Growth Rates in Patients with Malignant Gliomas: A Test of Two Algorithms," *AJNR Am J Neuroradiology*, vol. 22, pp. 73-82, January 2001.
- [2] Baillet, JW, Abemayor, E, Jabour, BA, Hawkins, RA, Hoh, CK, Ward, PH, "Positron emission tomography: A new precise modality for detection of primary head and neck tumors and assessment of cervical adenopathy," *Laryngoscope*, vol. 102, pp.281-288, 1992.
- [3] Vailaya, A, Figueiredo, MAT, Jain, AK, and Zhang H-J, "Image Classification for Content-Based Indexing," *IEEE Trans. Image Processing*, vol. 10, no. 1, pp.117-130, 2001.
- [4] Abbasi, S and Mokhtarian, F, "Affine-Similar Shape Retrieval: Application to Multiview 3-D Object Recognition," *IEEE Trans. Image Processing*, vol. 10, no. 1, pp.131-139, 2001.
- [5] Deng, Y, Manjunath, BS, Kenney, C, Moore, MS, Shin, H, "An Efficient Color Representation for Image Retrieval," *IEEE Trans. Image Processing*, vol. 10, no. 1, pp.140-147, 2001.
- [6] Epifanio, I, and Ayala, G, "A Random Set View of Texture Classification," *IEEE Trans. Image Processing*, vol. 11, no. 8, pp.859-867, 2002.
- [7] Gering, D, Eric, W, Grimson, L, Kikinis, R, "Recognizing Deviations from Normalcy for Brain Tumor Segmentation," *Medical Image Computing and Computer-Assisted Intervention (MICCAI)*, Tokyo Japan, pp. 388-395, Sept 2002.
- [8] Hinz, M, Pohle, R, Shin, H, Tonnie, KD, "Region-based interactive 3D image analysis of structures in medical data by hybrid rendering," *Proc. SPIE in Visualization, Image-Guided Procedures, and Display*, vol. 4681, pp. 388-395, 2002.
- [9] Thamburaj, AV, "Neurology & systemic malignancy", Apollo Hospitals, Chennai, India [http://www.thamburaj.com/cns\\_systemic\\_malignancy.htm](http://www.thamburaj.com/cns_systemic_malignancy.htm).
- [10] Krishnan, K, and Atkins, MS, "Segmentation of multiple sclerosis lesions in MRI - an image analysis approach", *Proc of the SPIE Medical Imaging 1998*, vol. 3338, pp.1106-1116, February 1998.
- [11] Gupta, R, and Undrill, P, "The use of texture analysis to delineate suspicious masses in mammography," *Physics in Medicine and Biology*, vol. 40, pp.835-855, 1995.