Contour Profiling of Brain Tumor Areas by Using Image Correlation and Peak Detection Techniques

Baki Koyuncu,[†] and Alper Pahsa[††],

Computer Engineering Dept, Ankara University, Turkey

Summary

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In this study, peak detection technique was used to generate the contour lines of the tumor area in the image of a brain slice. The tumor area was scanned and correlated with a reference image. The resultant cross correlation was plotted with respect to spatial coordinates. The peak values in this graphs represented the normal and tumor tissue transitions and they were plotted in contour form to define the outlines of the tumor area .

Key words:
Intensity Correlation, Peak Detection, Contour Mapping

Introduction

Medical diagnosis had a big role on medical treatments. It was the reflection of the patient's status and a key path for the right treatment. The main objective in diagnosis was the discrimination of malignant tumors from the healthy tissues .[1] One of the methods that was commonly used in brain tumor detection was the image processing techniques. [2].

Brain slice image was correlated with a reference image corresponding to healthy brain slice image from the same patient through a sampling area. A sampling area was generated with software and it was moved horizontally across the image. The resultant correlation image contained peaks corresponding to the dissimilar image points. These points represented the border points between tumor and healthy tissues.

The peaks were generated for every horizontal scan line across the image. These peaks were later joined to produce a contour of tumor area . This would help the surgeon to decide where to start from to remove the tumor efficiently.

Theory

To determine the malignant tumors in healthy brain structures, image processing technique was used.
This technique included a cross correlation method. It compared a template of the image (the image correlation kernel such as a mask) with the actual camera image of an object and generated a new correlation image which stated where the template matched the camera image.

A sampling mask area, MxM pixel matrix across the image, was generated by the software and the same size reference mask area of healthy brain tissue was used for cross correlation purposes . The sampling mask was moved horizontally across the object image and at every location cross correlated with the reference mask area. [2] This cross correlation technique was defined by the following formula[3].

$$f(x,y)*h(x,y)=1/(M*N)\sum\sum f*(m,n)h(x+m,\ y+n)$$

The above equation defined the two dimensional discrete cross correlation algorithms where f(x,y) and h(x,y) represented the image sampling mask and the reference mask .

The resultant correlation coefficient values were plotted against the scan positions across the image. From the theory, the cross correlation of dissimilar points gave maximum peaks and similar points gave minimum peaks.

Hence the generated maximum peaks represented the dissimilarities between the healthy and tumor areas. They showed the border lines where the healthy tissues ended and where the tumor started.

Procedure

A menu driven visual software was developed with Borland C++ Builder V6.0 application developer [4]. A sample mask to traverse the image and a reference mask (cropped region from the image) have been created with varied pixel sizes (2x2, and 5x5). Local intensity distribution was extracted from the image as intensity amplitudes between 0 and 255. These amplitudes were used in image cross correlation process of the sample mask with the reference mask. Finally the correlation coefficients across the correlation matrix were averaged to generate the peak variations for the contour mapping.

Results & Discussion

Brain slice image was generated by using tomography and computer scanning techniques. The image contained 256x256 intensity values varying between 0 and 255 . This image was identified as the local intensity distribution of the brain slice image. The tumor area was made apparent in the image by using chemical techniques. This way the tumor area on the film became a visible image area as shown in **figure 2** for the image processing operations.

 A software was written for the cross correlation method used in this study . This software generated a correlation matrix by cross correlating the sample and the reference mask matrixes . The peaks in the cross correlation matrix were plotted for every horizontal scan line across the image .

To test this software [5], the image in **figure 1** was used to see the peaks in correlation matrix. 2x2 sample mask was moved across an horizontal line and cross correlated with the reference mask at every sampling location . Reference mask was chosen from the dark region on the image. When the sample mask moved across the dark region, the cross correlation with the reference mask gave a minimum correlation coefficient amplitude and when it moved from dark to bright region the correlation gave a peak coefficient amplitude for the transition.

The peaks were generated for every transition from dark to bright and bright to dark region across every horizontal scan line. This was shown in **figure 1.** Many scans were made across the test image and the peaks for every scan were obtained representing the transition between the dark and bright regions which also represented the contour points in return.
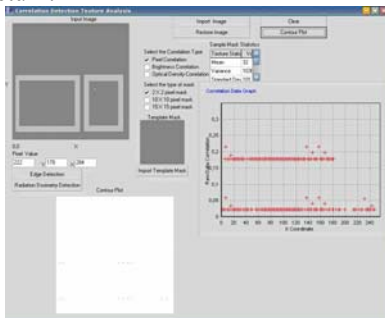

Figure-1 Software for Test image + its detected pixel correlation peaks + Contour map for 2 scans (white graph)

The above software was used on the brain slice image to see the correlation coefficient peaks . The similar scanning of sample mask and the correlation with the reference mask across the image generated coefficient peaks on every scan line. Many horizontal scan lines produced peaks for every transition from healthy to tumor areas.

These peaks were later joined to display contour map in image plane. **See figure 2**.
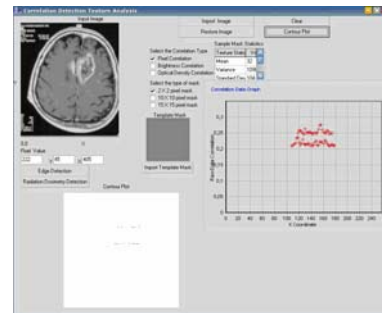

Figure-2 Software for Brain slice image + its detected pixel correlation peaks + contour map for 2 scans (white graph)

Conclusion

The results showed that the correlation algorithm developed in this study gave a clear representation of tumor contours compare to other pattern extraction and identification algorithms. Image correlation method was an efficient way to recognize the dissimilarities in the image. Correlation coefficients were peaked at the intensity transitions and this corresponded directly to the differences in the image areas .

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Prof. Dr. Baki Koyuncu
He graduated from the Electronic Engineering Department at Birmingham University, UK in 1973. He obtained his MSc from Information and Systems Engineering at Birmingham University at UK in 1975. He received his Phd. degree from Electronic/Computer Engineering Department at Loughborough University at UK. He is currently chairman of Computer Engineering Department at Ankara University in Ankara, Turkey.

Alper Pahsa
graduated from Computer Engineering at Atılım University in 2003. He also holds a minor major degree in Business Management from ATILIM University. He is currently MSc student in Ankara University Computer Engineering Department and works as a Software Test Engineer in Mission Computing Software Test Team of Peace Eagle Project in HAVELSAN AŞ