



Brain Tumor Detection Using MRI Images

Rajan.B

IES College of Engineering, Thrissur, Kerala, India

P.V.N Reddy, Indirakumar.M, Hariharan. D

Dhanalakshmi Srinivasan College of Engineering and Technology, Tamil Nadu, India

Abstract— Medical image processing is the most challenging and emerging field now a days. Processing of MRI images is one of the part of this field. In this paper, modified image processing techniques were applied on MRI scan images in order to detect brain tumor. The tumor means abnormal cell growth in a human body. In this project we are find out exact position of brain tumor by using LABVIEW software. The methodology consist of three important steps: wavelet transform, clustering, histogram. First acquire gray scale image from MRI scan image and then applying the wavelet transform to split the signals. Then we are applying c the cluster algorithm is implemented to extract the suspicious regions or tumor, histogram technique gives height of the tumor and finally applying measurement technique to find out exact location area, length and depth of the brain tumor.

Keywords—Tumor, MRI,wavelet,image processing

Introduction

The tumor is a growth of abnormal cells in the tissues of the brain. The tumors are divided in to two types. Benign tumor (non-cancerous) and Malignant tumor(cancerous) benign tumor grows very slowly, and rarely spreads. Classification of benign tumors are Adenomas, Fibromas, Haemangioma, Limomas, Myomas, Nevi Neuromas, Osteochondromas ,Papillomas and Malignant brain tumor grows firstly and it has irregular boundaries, and attack to nearby brain area. The classifications of malignant tumor are Sarcoma, Carcinoma, Leukemia Lymphoma. The CT (computer tomography) and MRI (Magnetic resonance imaging) can provide detailed information about disease and identify many pathologic conditions giving an accurate diagnosis. The medical imaging is an essential tool for improving the diagnoses to understanding and treatment of a large number of diseases. We give some efforts to develop software that could be easy to modify by other researchers and user to provide interaction capabilities to construct clinical applications. So, many software packages for visualization and analysis of medical data. The Magnetic Resonance Imaging of the brain is a powerful technique for diagnosis used by physician to detect abnormalities of human body. Some years ago, most neurologists only had images of several cross sections of a brain on a light board using their knowledge to make a diagnosis or determine the course of a therapy. With an increasing interest in the field of medical image processing and semi automatic and automatic tools have appeared to assist medical diagnosis centre. For instance brain treatment allows now not only to visualize a volume of functional cortical structures but also to quantify it.

RELATED WORK

The medical imaging modalities are a very important process for deciding right therapy at the right time. Many techniques have been proposed for classification of brain tumors in MR images, most notably, fuzzy clustering means (FCM), support vector machine (SVM), artificial neural network (ANN), knowledge-based techniques, and expectation-maximization (EM) algorithm technique which are some of the popular techniques used for region based segmentation and so to extract the important information from the medical imaging modalities. An overview and findings of some of the recent and prominent researches are presented here [1-5]. have presented a neural network based technique for brain tumor detection and classification. In this

PROPOSED SYSTEM

This paper proposes a new method for estimating the number of segments and automatic segmentation of human normal and abnormal MR brain image. It has mainly four modules: wavelet transform, threshold, histogram, particle analysis. By analyzing the particle report the length, area, and depth of the tumor is analyzed.

WORKING PRINCIPLE

Here, we are acquire an image from MRI(Magnetic Resonance Imaging) and CT(Computed Technology).We have basic concepts to detect tumor in our paper, components of the image hold the tumor generally has extra concentration. Using LABVIEW SOFTWARE we can guess the exact position of area, length and depth of the tumor

In this project we are creating a temporary memory location for an image and then reading an image file, it may be standard format (JPEG,TIFF) or a non standard format known to the user. Then, by applying denoising which is the process of reconstructing a signal from a noisy one. Noise can be random or white noise with no coherence or coherent noise introduced by the device mechanisms or processing algorithms. Next wavelet transform is applied which gives the approximate and detailed coefficients at 1D and 2D signal output such as low-low, low-high, high-low, high-high.

Next, clustering is used to split each of its individual elements. It display the output for each element in the cluster for wired. Then, histogram is applied for detecting each pixel values. As histogram is a graphical representation of tabulated frequencies shown as adjacent rectangles, over discrete intervals with an area equal to the frequency of the observation in this interval. Thresholding is applied for separating foreground and background. Certain thresholding values and the pixels which are having intensity value more than the thresholding are set as white as output and rest are set as black. So, basically it provides binarisation for an image.

DENOISING:

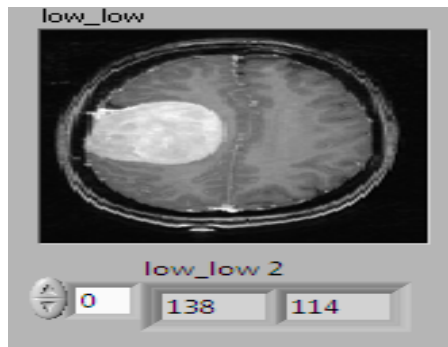
Denosing is the process with which we reconstruct a signal from a noisy one. Noise can be random or white noise with no coherence, or coherent noise introduced by the devices mechanism or processing algorithms.

WAVELET:

It specifies the wavelet the wavelet type of the discrete wavelet analysis. The default is db02. Wavelet must be the same type as the wavelet type you selected in the wavelet discrete wavelet transform vi to compute dwt coef. If you used the analysis filters in out of the wavelet discrete wavelet transform vi to specify wavelet, ignore this input and use the synthesis filters input of this vi to specify the synthesis filters of the wavelet

LOW-LOW:

It returns the approximation coefficients from the low pass analysis filtering on each row and each column. The low-low coefficients are a low-resolution approximation of the original 2D image.



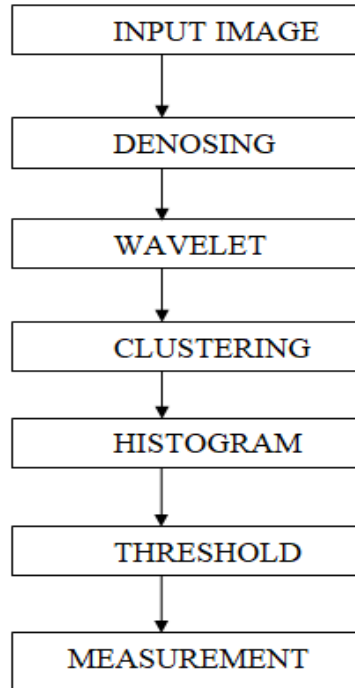


Fig 1 block diagram of brain tumor detection process

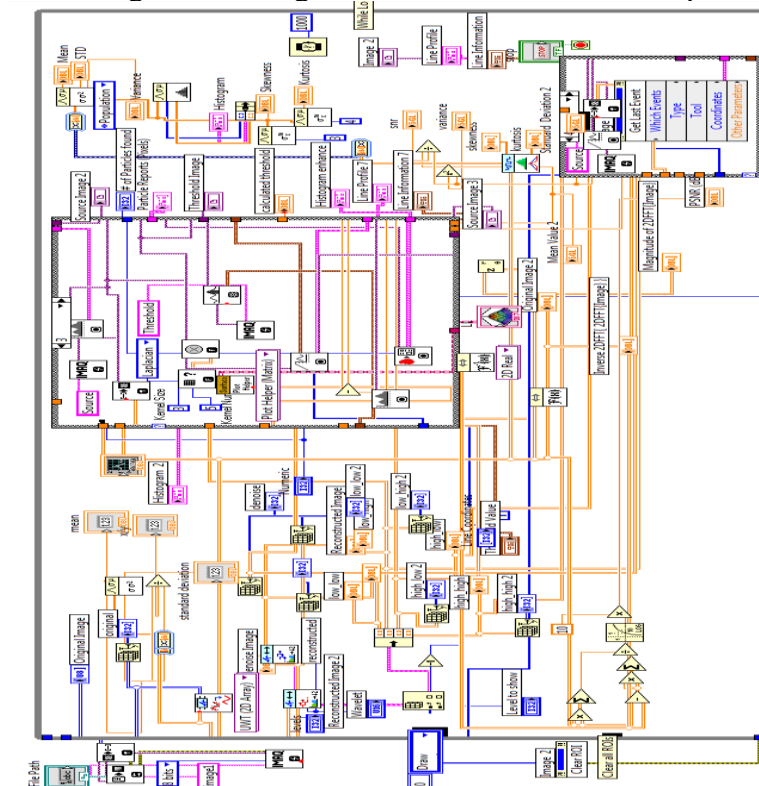


fig2 VI of block diagram of brain tumor detection process

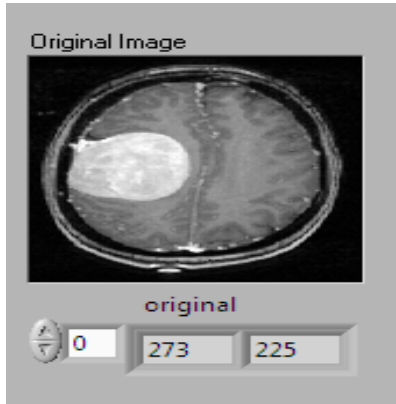


Figure2 Original image

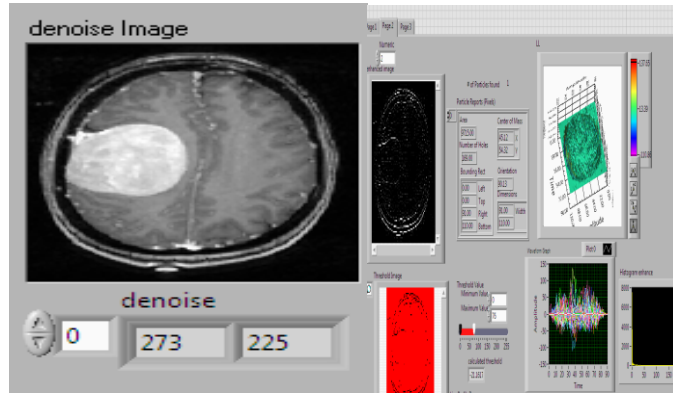


Figure 3 denoise image

LOW-HIGH:

It returns the detail coefficients from the low pass analysis filtering on each row and the high pass analysis filtering on each column. The high-frequency signal along the column direction influences the low-high coefficients.

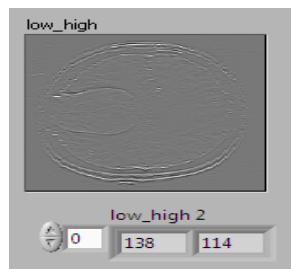
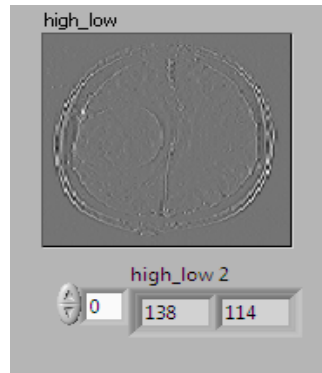


Fig 4 output

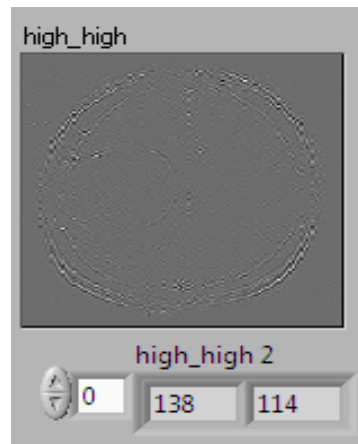
HIGH-LOW:

It returns the detail coefficients from the low pass analysis filtering on each row and the high pass analysis filtering on each column. The high-frequency signal along the row direction influences the high-low coefficients.



HIGH –HIGH:

It returns the detail coefficients from the high pass analysis filtering on each row and each column. The high-frequency signal along the diagonal direction influences the high-high coefficients



INVERSE DISCRETE WAVELET TRANSFORM:

Computes the multilevel inverse discrete wavelet transform(DWT) and returns the reconstructed signal from the approximation coefficients and the detail coefficients. An interpolator with a factor 2 and the lowpass synthesis filters and the highpass synthesis filters implement the inverse DWT at each level. Wire data to the DWT COEF input to determine the polymorphic instance to use or manually select the instance.

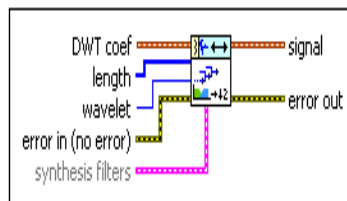


Fig 5 Inverse discrete wavelet transform

DWT COEFFICIENT:

It specifies the approximation and the detail coefficient for the multilevel inverse discrete wavelet transform(DWT). You must organize the coefficients into a waveform starting with the approximation coefficients at the largest level followed by the details coefficients at all levels in descending order.

LENGTH:

It specifies the length of the approximation coefficients, the detail coefficients and the signal. You must organize length into a 1D ARRAY starting with the length of the approximation coefficients at the largest level, the length of the detail coefficients at all levels in descending order, and the length of the signal.

PARTICLE REPORTS

It is an array that returns a set of uncalibrated pixel measurements from the detected particles. This cluster contains the following elements:

- Bounding rectangle is the smallest rectangle with sides parallel to the x-axis and y-axis that completely encloses the particle.
- Center of mass is the point representing the average position of the total mass of the particle assuming every point in the particle has a constant density. center of mass may be located outside the particle if the particle is not convex.
- Orientation is the angle of the line passing through the particle center of mass with the lowest moment of inertia.

DETERMINATION OF DEPTH FROM 3-D GRAPH

Tumour is analysed using particle analysis report. Particle analysis gives AREA, LENGTH and DEPTH of the tumour.

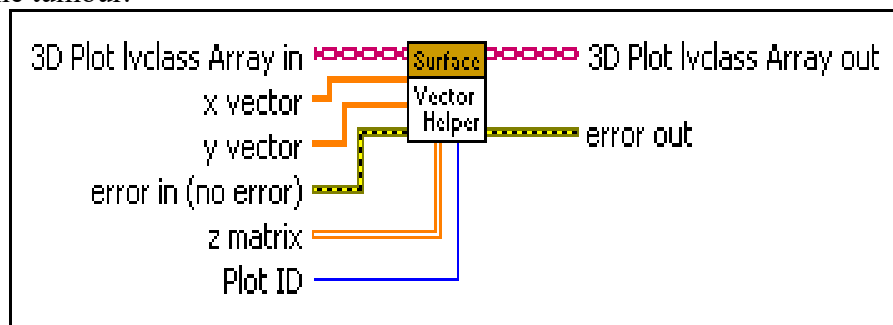


Fig 6. Depth of 3D graph

It returns the number of particle detected in a binary image and an array of reports containing the most commonly used particle measurements. It is an array that returns a set of uncalibrated pixel measurements from the detected particles. This cluster contains the following elements: area, number of holes, bounding rect, center of mass, orientation, dimension.

CONCLUSION

Finally, using particle and analysis report we can find the area, length and depth of the tumor which commonly made in the SI units and contains seven fundamental units.

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