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Region Merging Implementation on MRI Images using LabVIEW and VHDL

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Abstract

In today's world accuracy of medical analysis, particularly of the brain to diagnose various tumours or its effect on other parts of the body became prominent. The use of region merging algorithm to reduce edge space and merge common parts together gives more accurate results of MRI. The implementation of this technique enables a better and fast treatment to the diseased. Reduction of access time is one of the major advantages compared to other approaches used till now. This paper discusses merging algorithm implemented in LabVIEW and VHDL and the results are compared. The technique makes use of adjacency graph which is implemented using its regions and edges. The merging algorithm performs the transformation of the L partitions into T partitions where $L < T$ represents H segments of the final transform.

Keywords: Lab VIEW, Merging Algorithm, MR Images

1. Introduction to the Work

The need for brain image segmentation is to get a better analysis on the structure and lobes of it, which in turn are essential for the estimation of the tumours and the spatial variation which affects the other parts in the body. The brain is the most essential part of the human living system where each and every part of the body works in association with it.

Needless to say, the human body stops functioning with even a minor changes in brains spatial orientations. So, there is a need to develop an efficient technique to analyse each and every part or lobe of the brain for its spatial orientations. The brain mainly is classified as the white and gray matter along with the cerebral fluid of the spine. It consists of number of overlapping layers which have to be analysed as non overlapping layers for best possible analysis of its structure for various diagnosis and its treatment.

The segmentation process of edge detection in brain using Region merging technique gives us best possible ways to contour the edges which in turn gives a major separation of change in even a minute pixel values. The similarity and dis-similarity between the pixels in same brain image or when compared to other standard values gives the range of tumours or mal functioning of the parts of body. Along with merging the implementation of watershed technique which can easily find the edges as compared with the catchment basins of river where water is allowed to fall in two basins and the water falling on edge is collected in either of basins.

The work is well implemented in LabVIEW and VHDL where implementation in LabVIEW takes the direct images of brain with real image segmentation shown on its front panel. The coding is best implemented in VHDL for watershed and merging techniques. The main advantage of this proposed work is reduction of the access time for tumours detection and spatial resolution which can be taken as pixel value.

2. Existing Systems

There is no much research done in this field, except for the multi fuzzy clustering which gave a clear image of the MR image for small lobe synthesis. The technique involves medium accuracy but the access time is a bit high, which gives a slow result in critical scans. Another method is the tissue network optimization where the lower regions are not segmented properly and gives insufficient data. Random vector field transformation involves partial loss of the critical data and hence not merely suited for the diagnosis.

3. NILabVIEW

NI LabVIEW is one of the best software that one can use in image analysis as the image can be directly called, without storage of any addresses. It gives the pictorial representation of the image directly for the eye analysis of the specialists. It takes the input directly from the system and its block diagram consists levels of abstraction of required data. The font panel on the run of the code gives the diagrammatic representation with the detection of tumours shown or spotted.

4. Region Merging Algorithm

More often merging of similar regions identified as similar pixels can be merged together to even get more valuable information about lobes and its spatial orientations. The merging results in homogenous information placed together from all visuals and likewise give its accurate values. Moreover edge detection gives the region separation of dis-similar lobes and thus can attain accurate values for each region for diagnosis. Initially we partition L images using watershed technique and the merging algorithm performs the transformation of the L partitions into T partitions where L < T represents H segments of the final transform. It can be considered as the H partition taken reduces the time function *Tc*.

Dis-similarity Functions in the Region

The main implication of access time used in this system can be considered as to reduce the mean error.

Consider $D_m = \{D_1, D_2 \dots\dots D_m\}$ be the M partitions and $T_r = \{S_1, S_2 \dots\dots S_r\}$ represent the pixels of the regions or lobes in brain. $D_m$can be taken as the first transform given after the watershed technique, then we have L-1 partitions generated by adjacent region pairs, in which the edges detected will be having a minimum time function *Tc*.

$$Tc = \frac{Ti * Tj}{Ti + Tj}[M(Di) - M(Dj)]^2$$

Where *T* represents size of the region, $M(D_i)$ represents region mean and *Tc* gives minimum optimal regions. If the value goes beyond certain threshold value, then merging technique terminates.

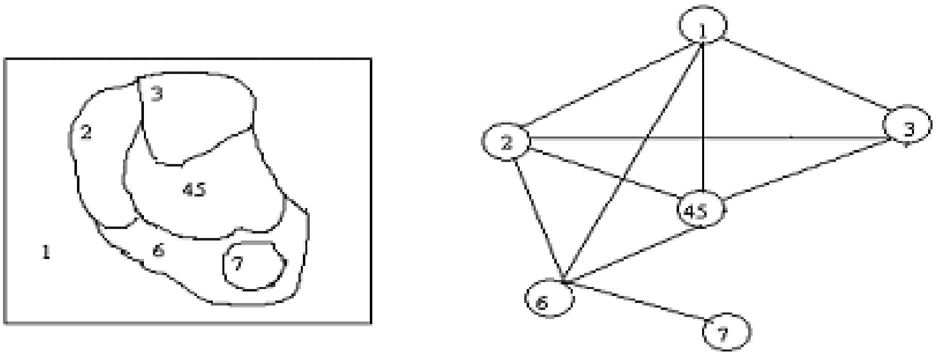

Figure 1: Region Adjacency Graph before merging and after merging

5. Proposed Architecture

The merging algorithm explained in earlier parts of paper is a good contour extractor and will be a slow result when implemented in software. The extraction of regions based on dis-similarity and pixels of lobes is a highly difficult task.

In the proposed method while using LabVIEW, the image is given directly and the partitioning and lobe segmentation is done to check the original image representation and when implemented in VHDL, the use of parallel and pipelined approaches overcome the above mentioned disadvantages and give a reduced access time for fast detection of any tumours.

The proposed system includes a control unit, storage cells for the initial and partitioned image, edge detection unit, arithmetic unit.

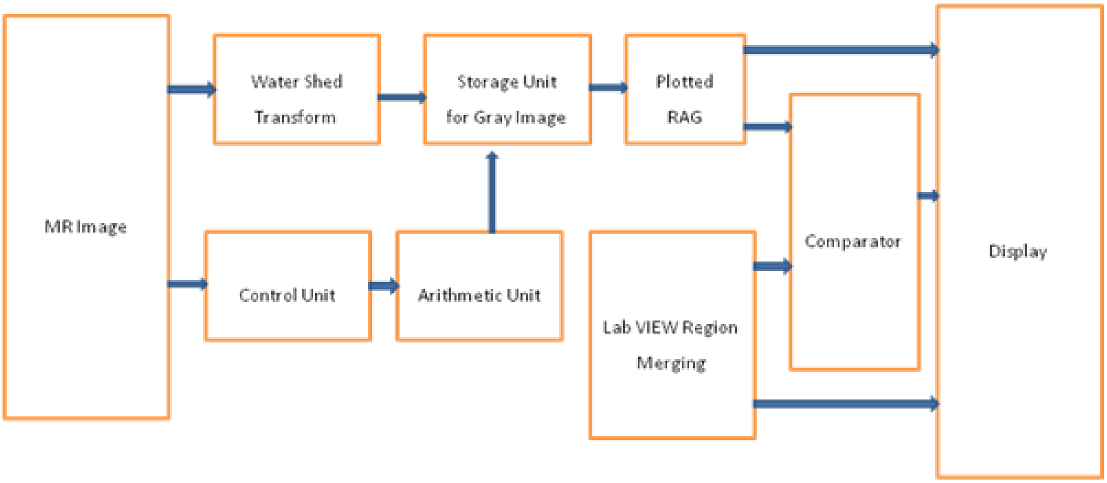

Figure 2: Block Diagram of Proposed Method

The Edge Detection

In edge detection we make use of two comparators C1 and C2, in which one is used for edge detection and other to prevent the duplication of edges. The pixel to be tested can be saved in a register for the comparison of pixels in C1. Based on clock cycles provided the edges are detected and the pixels are compared.

The control unit

The control unit considers the read, write and clock signals. It sends the signals required by the edge detection unit(EDU) and the arithmetic unit(AU). It is used in address generation techniques.

Arithmetic unit

The proposed structure to reduce time function *Tc*,which in turn increases the speed of detection. We use 16 bit multiplier and divider and 32 clock cycles can be used in division. By using pipelined structure the number of clock cycles can be reduced to 8.

6. Results

The proposed architecture gives the implementation of MR images with segmentation and merging that is associated with pixels for easy detection of tumours and highly precise medical reports, which in turn help in a better medical facility.

The techniques are well implemented in LabVIEW virtually and then coded in VHDL with pipelined techniques, which gives a ease of access time.

Table 1 Access Time for the MR Images

MR Image	Size(Pixels)	General Access Time	LabVIEW	VHDL
Image1	256×256	4.7s	20.0ms	20.0ms
Image2	256×256	3.9s	21.3ms	21.3ms
Image3	256×256	8.4s	18.7ms	18.7ms
Image4	256×256	3.9s	21.4ms	21.4ms
Image5	256×256	4.2s	19.3ms	19.3ms

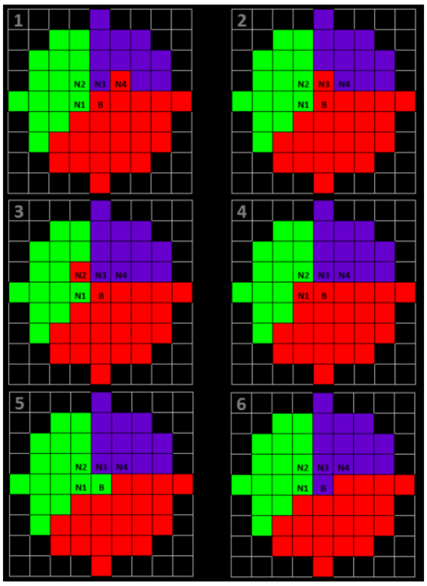

Figure3: Diagrammatic Representation of Brain Lobes

7. Conclusion

From the performance of the system and obtained results, we can conclude that the system gives a higher degree of accuracy and reduced access time which is critically used in developing medical fields.

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