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Medical Image Segmentation Using Enhanced Hoshen-Kopelman Algorithm

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Abstract: This research present a method of 2D and 3D segmentation based on the Enhanced Hoshen-Kopelman algorithm and its extension to non-lattice structure. The main feature of this method is to combine a merging strategy of a region growing algorithm with the multiple labeling technique of the EHK algorithm for regular and non-regular lattice. An efficient reconstruction algorithm is then applied to the set of edge points for the obtained segmented regions. The latest uses 3D Delaunay weighted triangulation. The combination of these already known algorithms makes the proposed approach very fast, efficient and appropriate to volumetric segmentation and particularly the anatomical structures in MRI and CTScan images.

Key words: 2D and 3D segmentation, region growing, Delaunay triangulation

INTRODUCTION

Segmentation is an indispensable tool in medical image processing and is useful in many applications such as early pathology detection, precise tumor localization, simulation and planning of chirurgical interventions, etc. The principal aim of segmentation is the extraction of significant objects present in the image either by partitioning this image into connected semantic regions or by extracting one or many specific objects from this image.

Proposed approaches attempting to solve the segmentation problem are numerous and extremely varied. The choice of a method depends on the nature of the image, what primitives are to be extracted and what are the usage constraints (algorithm complexity, real time requirement, available memory, etc...). This variety of possible methods shows that the segmentation problem is far from being solved and there exists no single technique satisfying all the image types.

In the literature, two major classes of segmentation algorithms are present: contour approach based on the estimation of the locale discontinuities of the gray level function and region approach based on homogeneous region extraction. Among the later, a fundamental algorithm is region growing which has received considerable attention from 2D and 3D image analysts and researchers. The principle of the technique is to define some criteria, called homogeneity criteria, which allow regrouping connected image pixels into larger regions. These criteria are often based on differential surface characteristics of the 3D object and a stable segmentation in quadric pieces is achieved (Monga and Bricault, 1994).

They can also be obtained from some evaluation function (Revol and Jourlin, 1994) or by RMS-approximation of image points by simple polynomial surfaces such as planes or quadrics (Djebaili, 1998). Region growing method has also been used for 3D medical image reconstruction where the voxel gray level defines some density of the volume to reconstruct as well as a regrouping criterion.

Another approach that is fundamentally geometrical which is mathematical morphology mainly consists on comparing objects under analysis to other objects with known shapes. Morphologic operators applied to 3D images are described in Agnus *et al.* (2000) where temporal image sequences considered as 3D images are segmented. Based on mathematical morphology, three-dimensional segmentation has been applied to anatomical structures in MR images on large databases (Bueno *et al.*, 2000).

In the last two decades, a promising mathematical framework based on variational models and partial differential equations has been developed and used to solve the segmentation problem. There exist two major categories of such models: parametric models introduced in Kass *et al.* (1988) and geometric models based on curve evolution theory and level sets (Caselles *et al.*, 1993; Malladi *et al.*, 1995). They allow segmentation and object reconstruction by providing compact geometric representations where evolution laws similar to physical mechanics laws are introduced such as forces, physical constraints and friction (Cohen, 1992; Lachaud, 1998; Montagnat, 1999; Montagnat *et al.*, 2001). Procedures using deformable models have been widely used for segmentation since they are well suited for object

extraction from temporal and volumetric data from image sequences such as IRM, CT scanned, X Tomography, ARM and Echography (Cohen, 1992; Montagnat, 1999; Delingette and Montagnat, 1999). These procedures have been made more efficient by using 3D pyramid images (Lachaud and Montanvert, 1999) and such hierarchical structures allow coarse to fine type segmentation. Region and edge information has also been integrated into these models (Pardo *et al.*, 2001).

In some applications, the segmentation is viewed as a pattern recognition problem. Thus, the task of delimiting regions is associated to a high level ability to classify regions in particular semantic classes. These approaches are widely used for segmenting cerebral MRI; a review is given in Bezdek *et al.* (1993). Among these, we can cite: statistical methods using Markov fields and Bayesian classification (Jaggi, 1998), the non parametric methods such K-NN algorithms introduced by Duda and Hart (1973), Parzen windows, fuzzy logic based methods (Bezdek *et al.*, 1997) and the so called Biologists methods: neural networks, genetic algorithms, etc. (Takatsuka and Jaivis, 2001; Kobashi *et al.*, 2001; Kim *et al.*, 2001).

In quest of better efficiency and precision various hybridations of these different techniques have been successfully attempted (Kapur *et al.*, 1996; Geraud, 1998; Benoit-Catlin *et al.*, 2000; Helliera and Barillot, 2001; Rey *et al.*, 2002).

In this research, a method for 2D and 3D image segmentation based on the Hoshen-Kopelman algorithm is proposed. The main feature of this method is to combine a merging strategy of a region growing algorithm with the multiple labeling technique of the EHK algorithm for regular and non-regular lattice. This procedure is very efficient and fast and may be adapted to the segmentation of anatomical structures in MRI and CTS can images which are in general quite large. An efficient reconstruction algorithm is then applied to the set of edge points for the obtained segmented regions. The latest uses 3D Delaunay weighted triangulation. The later is very efficient and fast approach makes it possible to adapt it to the segmentation of anatomical structures in MRI and CT Scan images.

THE HOSHEN-KOPELMAN ALGORITHM

Connected component analysis of grey level image divides this image into regions by labeling uniquely each pixel to a defined region. The regions discriminated by the connected component depend on the definition of neighborhood. Several definitions of neighborhood exist, however the most commonly used is the 4-connected. Basically, the algorithms for connected components

assign new labels to the first pixel of each component and attempt to propagate these labels through the neighbors. In image processing, Rosenfeld and Pfalz (1966) described an algorithm based on the classical component algorithm for graphs which is known as the classical algorithm for connected component analysis. The algorithm makes two passes through the image. The first pass assigns and propagates labels, while at the same time it creates an equivalence class table. The second pass re-assigns the labels that belong to the same class using the equivalence class table, such that all equivalence is assigned with a unique label. The final image has its connected components indexed with a unique label. While being relatively fast this algorithm requires a large amount of memory to store the equivalent class table, which depends on the image size and on the complexity of the images. The most recent algorithms, for connected component analysis, attempt to overcome the fundamental problems of either being too slow or requiring a large amount of computer memory.

In physics connected component analysis is known as cluster analysis and it is widely used for problems related to the percolation phenomena. In mid 1970s, Hoshen and Kopelman (1976) published an ingenious and efficient cluster analysis algorithm, which is known as the Hoshen-Kopelman (HK) algorithm. The time complexity of this algorithm is linear and requires small computer memory size. It remains an important breakthrough in statistical physics, since it allows the study of cluster size and the percolation problem through computer simulations. Recently, Hoshen (1998) has developed the Enhanced Hoshen-Kopelman (EHK) algorithm, which is an improvement toward cluster analysis. It is capable to yield various shape parameters and still preserves the computational time and memory space complexities of the original HK algorithm. The key idea for the efficiency of the HK algorithm, which is also essential in the EHK algorithm, lies on the concept of multiple labeling technique. The multiple labeling technique assigns different labels to pixels belonging to the same cluster. Unlike the classical connected component algorithm, which stores an equivalence class table and the equivalence are executed by a second pass over the image. The HK algorithm generates the proper label by assigning negative indexes to equivalent labels and recursively searching for the final label.

In the statistical physics terminology, an image is referred to as a lattice, the connected components are called clusters and a pixel is known as a site. The algorithm begins by scanning the lattice, pixel by pixel or site by site, from up to down and right to left direction (and back to front for 3D images).

SEGMENTATION

Grey level segmentation may be achieved using standard region growing technique which is a merging process at various levels. Usually, two or more steps are used; the first step (step 1) operates at the pixel level which is referred as a pre-segmentation step. At this stage the lattice is regular. The further segmentation merging steps consist on whether regions obtained from step 1 may be merged or not. The first two segmentation steps may make use of uniformity predicates associated to the characteristic attributes of region say R_i are as follow:

- $P_1(R_i) = [(MAX_i - MIN_i) < Threshold_1]$ where MAX_i and MIN_i are respectively the minimum and maximum gray level in region R_i
- $P_2(R_i) = [V(R_i) < Threshold_2]$ where $V(R_i)$ is the gray level variance of points in region R_i . We have $Threshold_2 = (Threshold_1)^2$

The thresholds may be chosen in any standard manner, this issue is not discussed here. Other merging steps may make use of other predicates such as shape or texture.

In this research, we propose using a variation of the EHK algorithm for grey level image segmentation. While the main features of the algorithm are preserved, the notion of non occupied site does no longer apply here since all sites (or pixels) are labeled. The background is also a region. For step 1, the standard HK algorithm is used since at the pixel level, the lattice is regular. The clusters obtained correspond to the regions of the pre-segmentation step. After the completion of step 1, a region adjacency graph may be constructed. This graph corresponds to a non regular lattice. This latter may become quite large for very large images. In order to perform step 2 and further merging steps in an efficient manner, we propose and make use of EHK algorithm to non-lattice environments as described by Al-Futaisi and Patzek (2003).

Relative to other region growing segmentation methods which are at best $O(n \log n)$ in time complexity (n being, the number of pixels or voxels), this method is linear in $O(n)$. In Fig. 1, we have plotted the computational time in seconds for random binary 3D images of sizes ranging from 100^3 to 300^3 (a 2.6 GHz Intel Pentium IV with 2 GB DDR400 RAM PC was used).

Two more features make this method very attractive. Firstly, the memory requirement depends solely on the

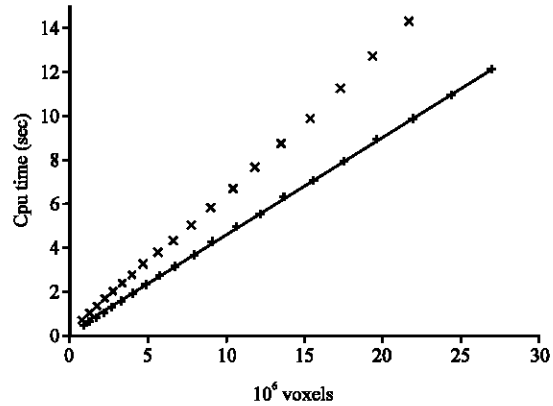


Fig. 1: Cpu times as function of 3D image size in voxels; our method (+), standard region growing method (x)

maximum number of labels needed and not on the size of the image. Secondly, this method can be highly parallelized as shown in Tiggemann's work on percolation (Tiggemann, 2001) where system sizes as high as 20000^3 were considered.

RECONSTRUCTION

Once done with previous steps, each region of the segmented 3D image is delimited with a set of edge points from which we can get the region surface using appropriate reconstruction method. In practice, even for modest regions, the number of points can be quite large (for example a 20 pixel diameter cylinder across 10 slices counts some 600 points) while large regions may require more than 100,000 points. Following (Kies *et al.*, 2005), we used efficient 3D Delaunay triangulation (3DT) algorithm. The outcome of 3DT is a set of pair wise linked edge points, in which each linked triplet forms a triangular face and each face quadruplet forms a tetrahedron. The outer surface or the crust of the region of interest is a subset of the set of all triangular faces resulting from 3DT. If the crust is convex that the solution is straightforward: it is the Convex Hull. To tackle the problem of the Concave Hull, much elaborated algorithms have been developed.

In the reconstruction process, we used principally Nina *et al.* (2001). We have also used Patrice Koehl's (2002), TETRAFOR which has very efficient 3D Delaunay Triangulation (Weighted). Once the crust faces obtained, there is one last step which consists on correctly orienting the normal of each face toward the outside of the object. The success of this last step

allows for a 3D rendering with no defects during final visualization of the results.

RESULTS

First of all and in order to validate our results, we have tested this method on various test 3D images containing various simple objects (cubes, spheres and cylinders). We have also tested random binary images of various sizes and various ratio black/white. We then segmented a 256 slices 256×256 scaled to 8 bits MRI Brain 3D image and extracted and reconstructed the brain surface as the largest region. Figure 2 shows several slices. Figure 3 represents the outer surface

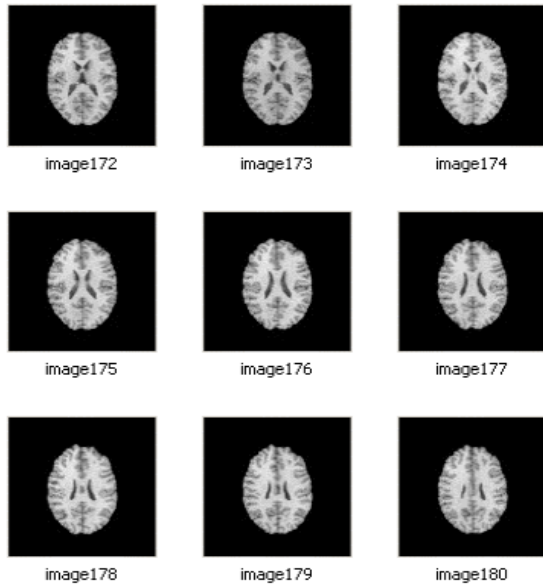


Fig. 2: A set of MRI Brain Image slices



Fig. 3: A bottom view of the whole brain reconstructed from 50% of all the edge points

reconstructed using a subset of edge points for the largest segmented region representing the whole brain.

Similar results were obtained from $256 \times 256 \times 256$ CT Scanner image of the skull of a Monkey. Figure 4 shows a sample set of slices used.

The 3D rendering after using half of all edge points as input for powercrust is shown in Fig. 5.

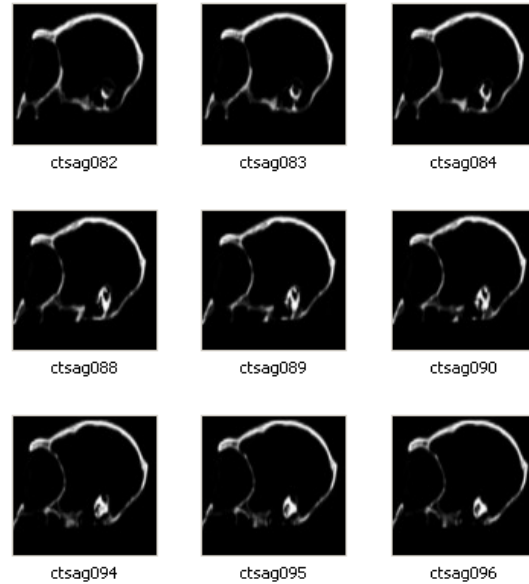


Fig. 4: A set of CT scanner image slices



Fig. 5: 3D rendering of crust obtained for the region representing the Skull of a Monkey

CONCLUSIONS

We have presented a new and very efficient method of 3D segmentation base on both the Enhanced Hoshen-Kopelman algorithm for both lattice and non-lattice environment and applied it to some test images. We have illustrated our results by reconstructing the largest region using POWERCRUST. The efficiency of the proposed segmentation approach makes it possible to tackle very large medical images with very small CPU time. An ongoing work is underway for further benchmarking. Also, an implementation of this method on parallel machines is in preparation where better performance is expected.

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