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SEGMENTATION OF TOMOGRAPHIC IMAGES

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ABSTRACT

The objective of this paper is to show what the current techniques in image processing, artificial intelligence, and computer graphics can do in computed tomography. More concretely, we wish to show that given the tomographic data what can be done in order to:

a) improve the spatial resolution
b) improve the visualisation of the data
c) improve the identification of anatomic structures

Thus, we shall not deal with different hardware, nor with various reconstruction algorithms. We shall assume that the data is given and ask what can be done from there on. Examples, documenting each of the above points, will be presented.

1. Introduction

In the past five years a rapid spread of CT Scanners through the medical establishment has also generated a large amount of pictorial data which in turn is begging for intelligent processing. Today we are witnessing the 3-D generation of X-ray CT Scans with improved spatial resolution, speed of scanning, flexibility of taking slices in different orientations, etc. Various head holders have been developed for a better registration of the physical image and its object [29, 6]. In addition to the X-ray CT Scans, we see more and more emission tomographic machines available [27], thus generating complementary data to the X-ray CT Scans.

In view of this overwhelming reality of the quantity and quality of image data, we in the image processing, computer graphics and artificial intelligence community are asking how our technique can be used for some improvements. In this paper we shall present some approaches that have been taken by ours and other laboratories in the effort of improving:

a) the spatial resolution, in particular in the Z coordinate
b) the visualisation of the data
c) the identification of anatomic structures.

The relevant literature is vast and in spite of honest effort to cover all the grounds we may have missed some.

What follows will be a presentation of the points a). through c)., in that order. At the end we shall venture some future efforts in these areas.

2. The Spatial Resolution

The fundamental limitation on spatial resolution stems from the trade-off between the dose of radiation (safety) and the sensitivity of detectors. The standard detectors currently are scintilation counters and as Hounsfield [14] points out, the current resolution is close to theoretical limits.

Other detectors have been considered such as Xenon [9], which do allow thinner sections, 3 mm. as opposed to the standard 12 mm. [21, 22, 31], however these detectors are not as sturdy as the scintilation counters. Chu and his colleagues have experimented with Cadmium Telluride (Cd Te) as an X-ray detector. These detectors are stable and easy to handle and have high detection efficiency. Their efficient conversion of energy to charge permits high spatial resolution. Unfortunately, due to polarization, the tailing of noise is high. There are also variable leakage currents and long 'memory'. In view of all these disadvantages, it is improbable that these detectors will be practical for CAT Scanners.

So far we have considered only collinated beams. Another way to improve the spatial resolution is to have fan-beam geometry[31], and finally cone-beam geometry. In comparison to collinated beams, the cone-beam allows a more compact experimental lay-out; in comparison to a fan-beam, requires fewer exposures and hence a lower radiation dose.[24] However, the reconstruction algorithm for a cone-beam is a challenging problem computationally. For review see [8].

A different approach to improving the spatial resolution in between the slices was taken by Glenn and his colleagues.[10] They have taken multiple, overlapped 8 mm. sections. This data was then deconvoluted and displayed 1 mm. thin sections. Of course this implies increased data collection and thereby increased dose.

We have considered this problem in our laboratory as well. There are two basic solutions for increasing the spatial resolution in between slices:

a) using interpolation in between slices
b) taking some additional measurements.

The interpolation technique is based on the assumption that geometric structure between two consecutive slices is continuous. This approach has been used by us,[4], (see Figure 1) as well as by Herman [12], and Brooks at al. [5], for reconstructing the three-dimensional anatomic structure.

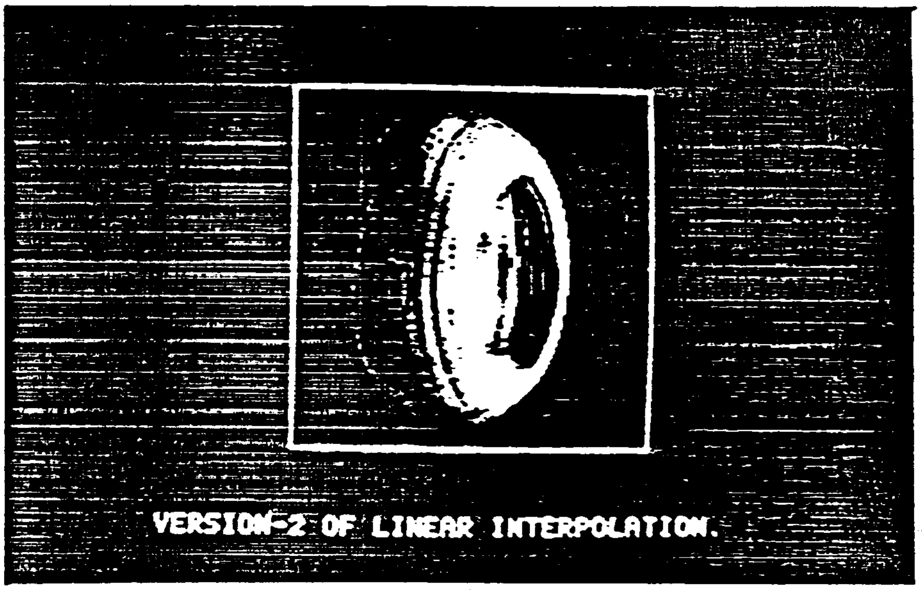

FIGURE 1

The interpolation technique could be aided by the anatomy atlas, so that certain obvious discontinuities in the structure are recorded. The disadvantage of this method is, however, that in general it is an approximation only to the reality.

The second method requires taking more measurements (X-rays) but has the advantage that the reconstruction process is more data driven than knowledge driven.

Consider the following case:

Assume that in addition to the tomographic slices we take two orthogonal X-rays (see Figure 2 a,b). Assume also that for now we are interested only in reconstructing the bone structure. Then the X-ray has (due to the film) the high spatial resolution, while the tomographic slice represents the estimate (the average) of the geometry in the volume as shown in Figure 2c.

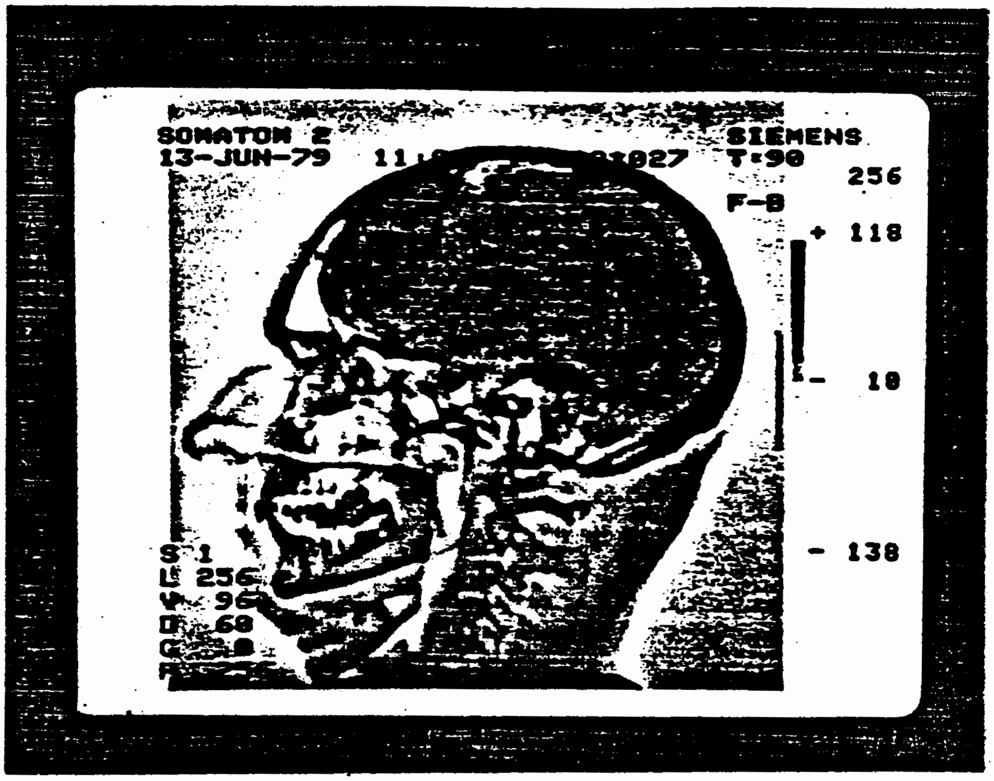

FIGURE 2a

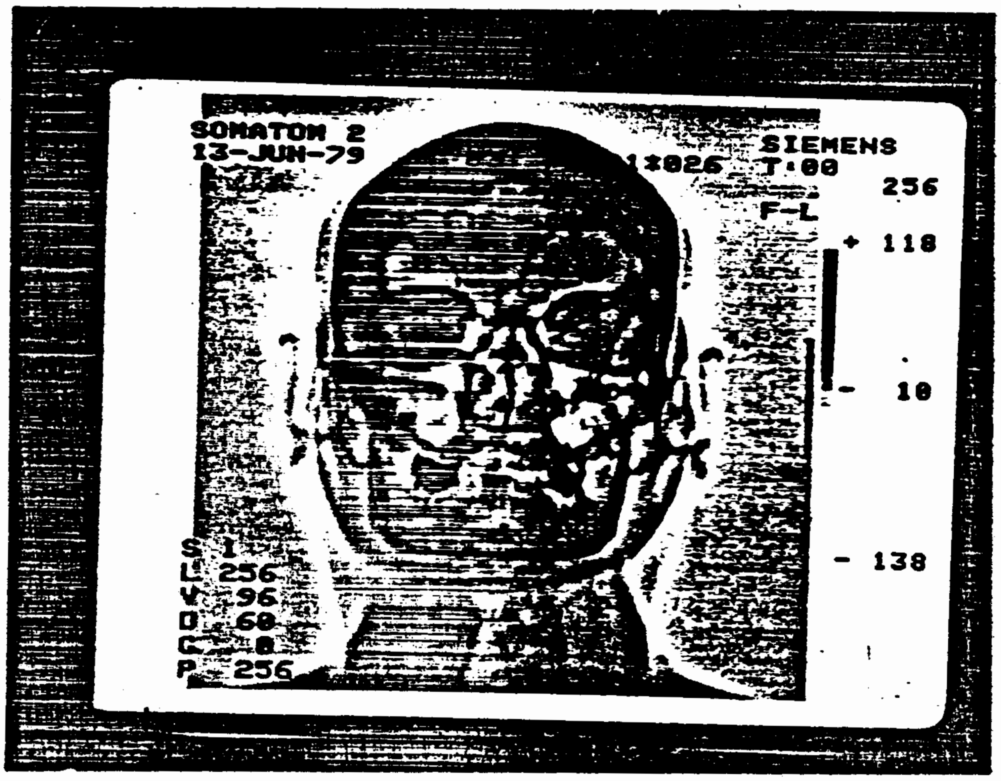

FIGURE 2b

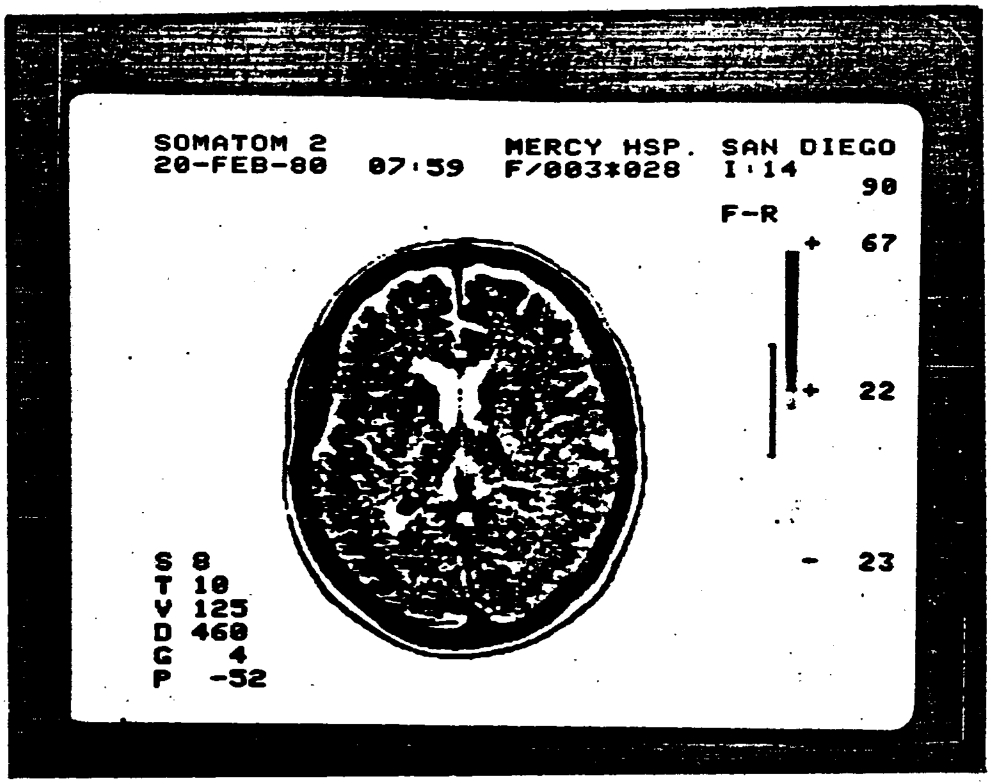

FIGURE 2c

The process of reconstructing goes as follows:

1) find the continuous structures in both X-rays

2) project them onto the tomographic volume, thereby creating boxes of continuous structures

3) within each box we can proceed two ways:

3a) interpolate using the tomographic slice and checking for each row or column with the two X-rays

3b) apply the reconstruction algorithm [23] on the two X-rays and if ambiguity occurs check for continuity principle with the tomographic slice.

Bourne [4] has shown that if the difference between two slices is unambiguous, than one can reconstruct the slice from the two projections. Basically, his algorithm employs the assumption about coherency of objects under reconstruction, which measured from slice to slice. Currently we are investigating [28] what the constraints are which can be detected from the individual X-rays, (continuous structures), which in turn will reduce the ambiguity. Examples of some reconstructed slices based on the above idea are presented in Figure 3.

The advantage of this method is that from an additional two X-rays one can improve the spatial resolution in between slices at best with the resolution of the X-ray, at worst with the resolution of detectable discontinuities on the X-rays.

This technique is very attractive in view of the Siemens machine which will provide automatically the topographic maps, which are nothing more than just two orthogonal X-ray projections, as shown in Figures 2 a,b.

3. Visualisation of the Data

The essence of computerized tomography is non-invasive visualisation of the internal

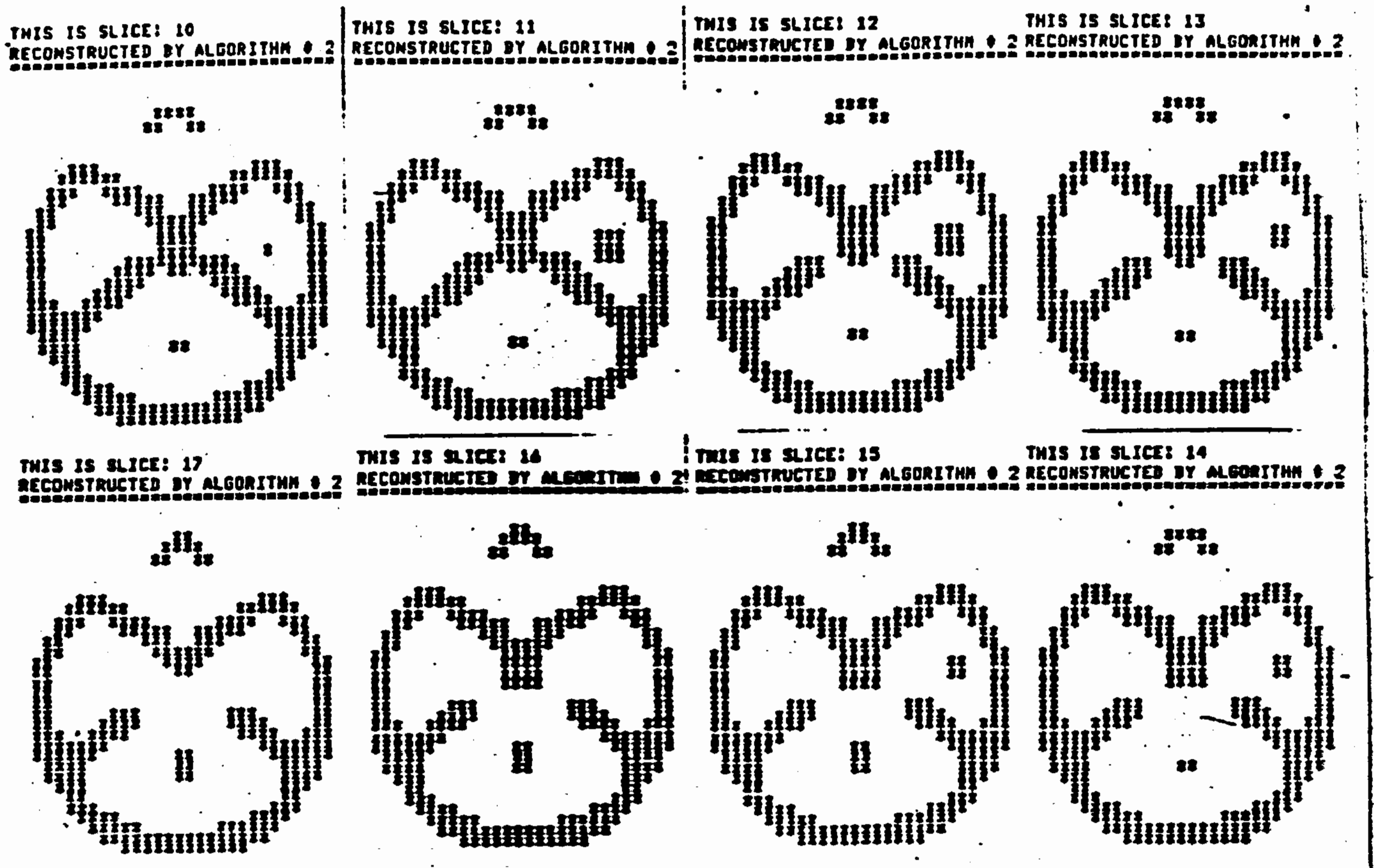

FIGURE 3

structures of the human body. Thus the application of the computer graphics technique is just a natural thing to do with this data. Hounsfield already in 1976 was concerned with the picture quality of the CT Scans. The first thing that comes to mind is an interactive graphics-image processing system which enables the user to selectively enhance various structures using different gray values or focussing on spatially distant structures, and to perform various computation on them such as area average and standard deviation, and perhaps others. Such systems have been developed in various tomographic centers. Just to mention a few: Glenn et al. [11], Philipson [25], Anderson et al. [1], etc. As a sample of what these standard graphic image processing systems provide we cite Huang et al. [15], the system called CTIP - an on-line image-processing software package.

The system:

a) eliminates the head holder or scanning bed from the scan image

b) evaluates CT member distribution in a scan image

c) separates the region of interest in a scan picture

d) extracts the boundary of a cross section

e) computes the mass, center gravity, inertia tensor for anatomical components

f) analyses a density histogram of the region of interest in a CT Scan

So far this is processing of the 2-D data. Since the usual scans provide a series of transaxial slices through the body, it is only natural to consider all the slices in their 3-D form. The first thing that researchers attempted to do was perform orthogonal cut views, [10, 19, 22, 17, 3]. See Figure 4.

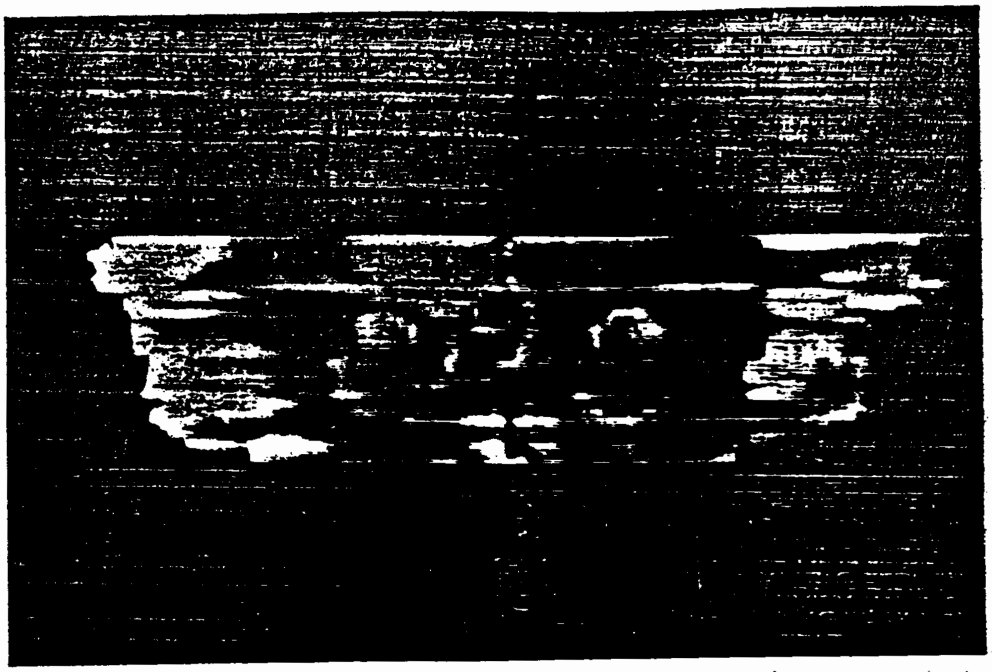

FIGURE 4

Having the 3-D data available, we can visualise it with proper shading, perspective, and hidden line elimination. There are few laboratories which have done this, [see for example, 13 and 4]. In addition to just simple display, one can manipulate the data, for example rotate, extract different anatomic structures, cut in half, etc. [see 12, 4, 18], as it is shown in Figures 5, 6, and 7.

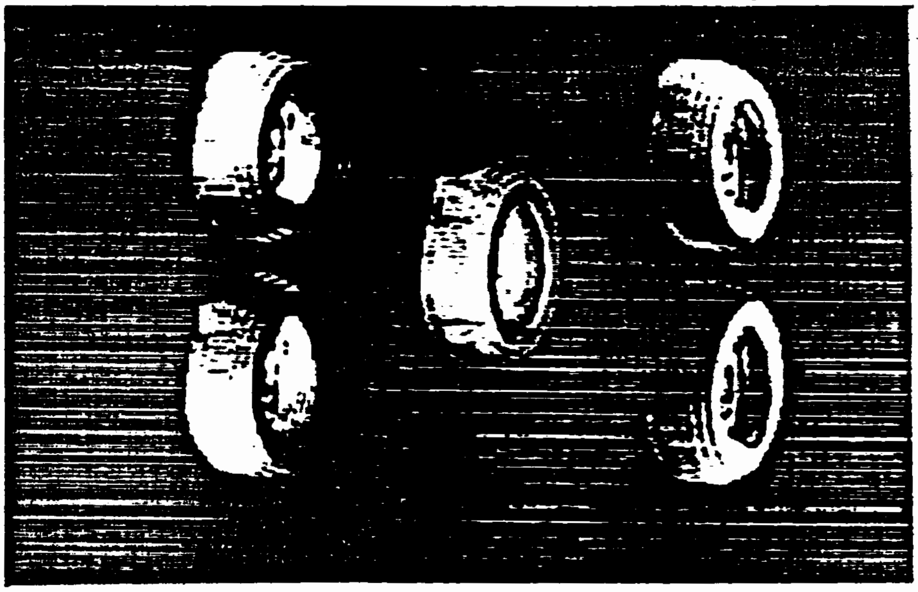

FIGURE 5

The big question remains how useful the 3-D object visualization will be for clinical usage since the current clinicians are not trained and used to viewing 3-D objects as opposed to the cross sections. Herman, [13], reports that in some special cases for surgery of a deformed spine the 3-D visualization turned out to be essential.

4. The Identification of Anatomic Structures

The tomographic images would be useless if we could not identify what we see in those

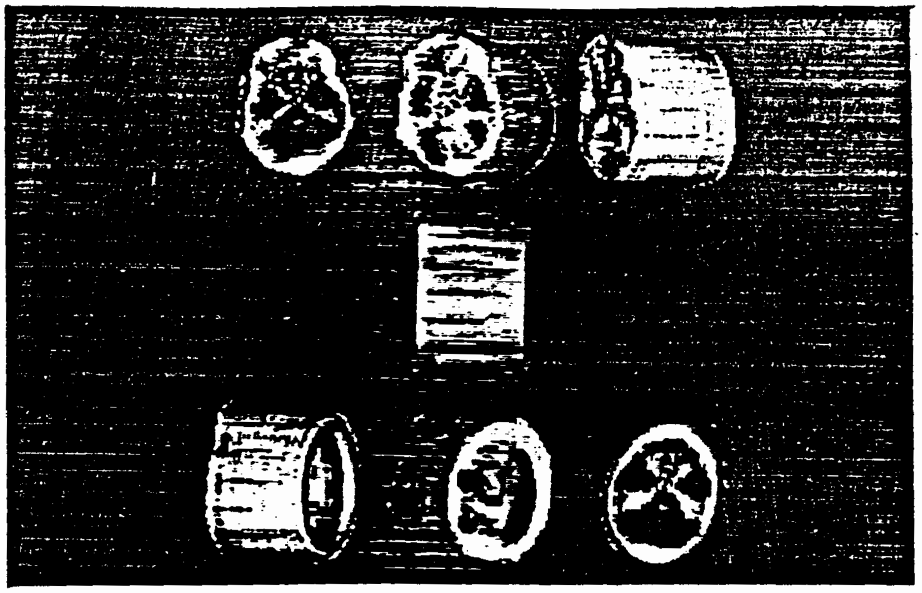

FIGURE 6

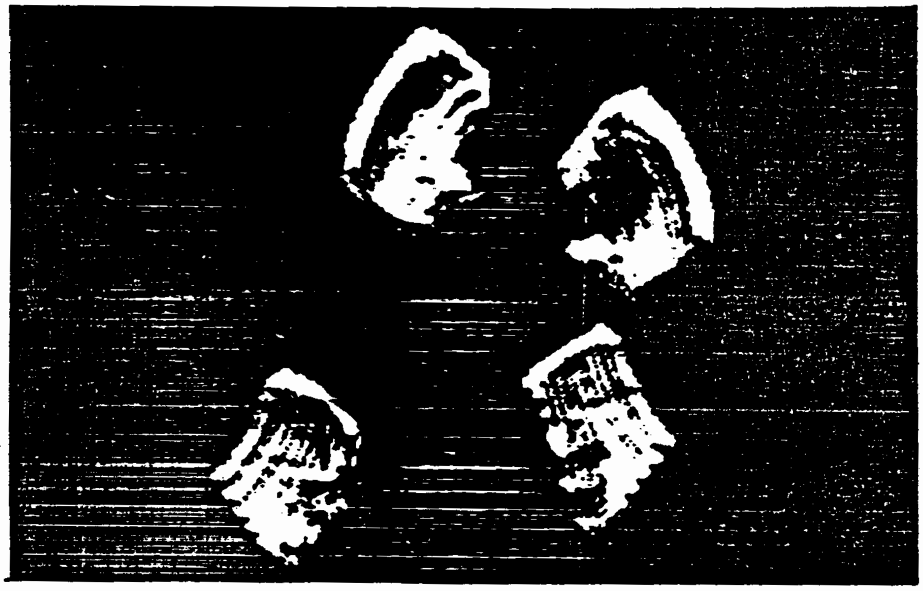

FIGURE 7

images and their meaning. Every radiologist who looks at the CT Scans identifies some anatomic structures. We observe that the radiologist doing so is using his/her knowledge of the anatomy which helps him/her to delineate the boundaries (even if they are noisy) of anatomic structures. In order to partially or fully mimic this behavior by computer one has to give the computer similar knowledge about the anatomy as the radiologist has. This fact led us to implement a computerized anatomy atlas of the brain. [16]

The atlas is a data base of digitized serial sections of the human brain, where every structure is labeled by its corresponding anatomic label, as it is shown in Figure 8. In addition, every structure is associated with a vector of typical values and deviations for the X-ray absorption, and the values of glucose consumption for eventual application on scans obtained from the machine PETT 5. A software package has been developed using Vector general, graphics display, and the computer PDP 11/60 for manipulating individual slices as well as the whole 3-D brain. Examples of the 3-D structures are shown in Figure 9.

FIGURE 8

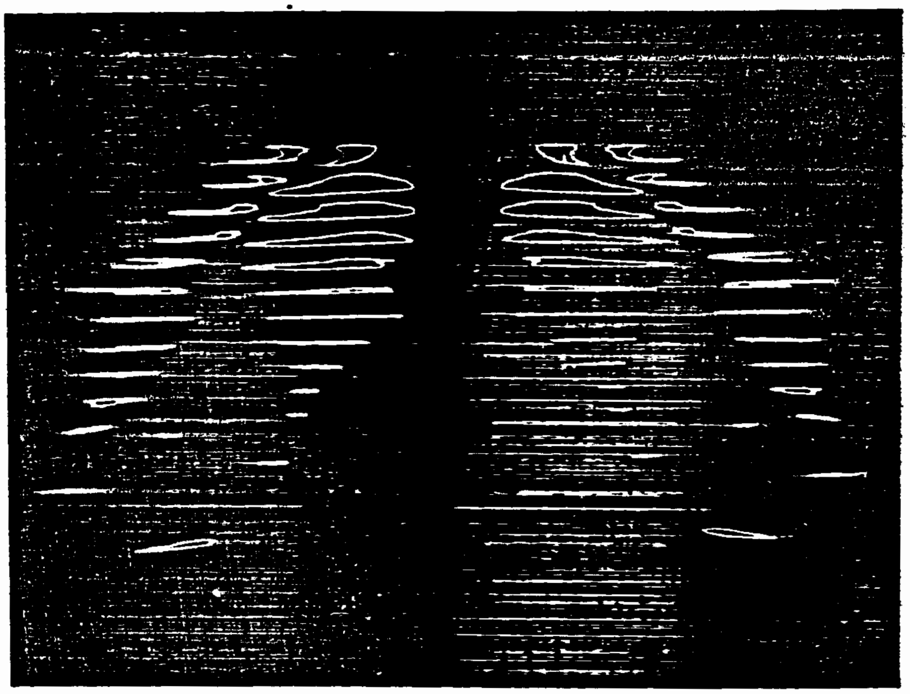

FIGURE 9

Although the computerized atlas may be justified in its own right, for example, for educational purposes,[20], our goal is to use it for guidance in the recognition of anatomic structures. Similar approaches have been taken by Ballard et al.,[2], for identification of ribcage, heart and abdominal organs. Also Selfridge et al., [26], have used a priori anatomic knowledge for boundary detection of various organs.

Our method is automation of what Gado et al.[32], has presented, that is, automatic recognition of anatomic structures found in CT Scans and overlay of them on CT Scans. What follows will be the description of our method:

Consider the input data, for example from the PETT machine as it is shown in Figure 10. The first task is segmentation. This process is composed of the following steps:

1) measurement of the histogram

2) dividing the histogram into n number of buckets, where n is an input parameter. These buckets are chosen on the basis of the largest differences between the local minimum and maximum in the histogram

3) using these buckets, threshold the picture

4) apply region growing and generate description of the region; such as:

-center of gravity
-the enclosing rectangle
-gray value and its statistics

Then the next task is to generate a similar description of the appropriate slice for the anatomy atlas, such as is shown in Figure 11.

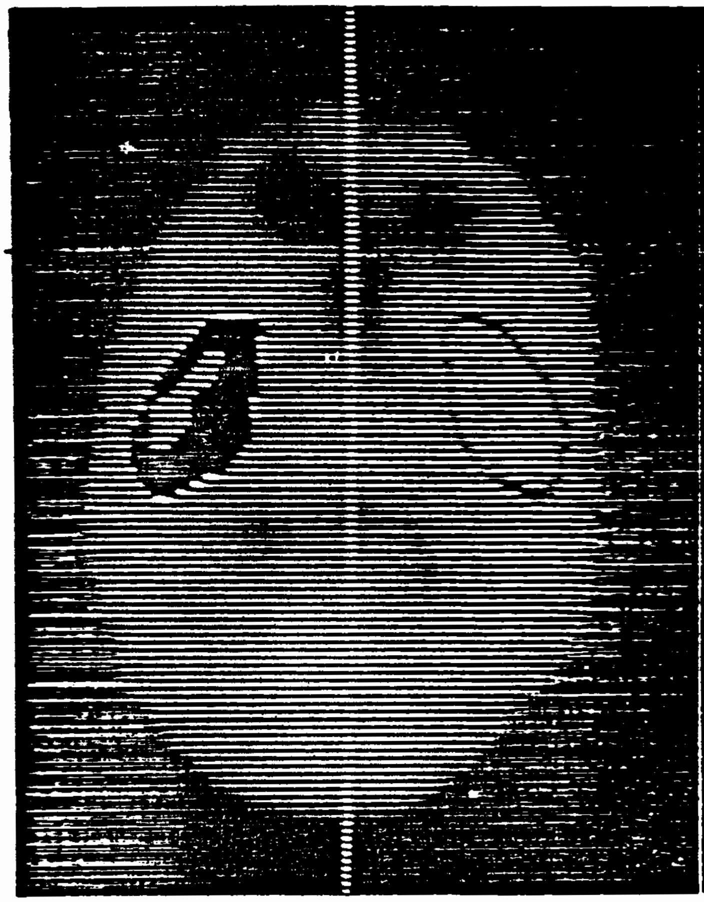

FIGURE 10

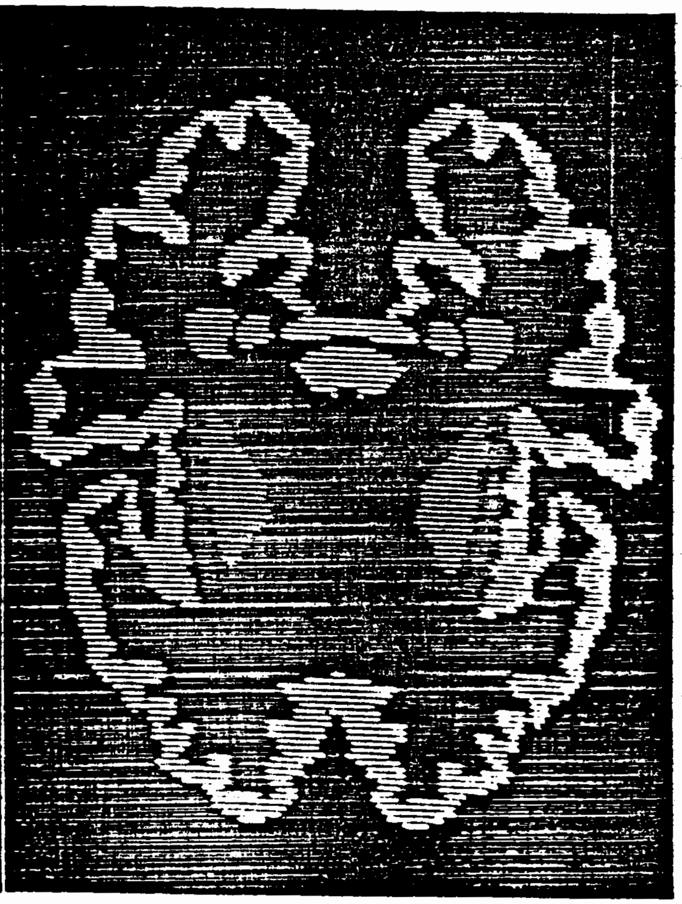

FIGURE 11

Once we have the two descriptions, we perform the matching. The matching process is currently under development.

5. Conclusion

As we have outlined in the introduction, the proposal of this paper was to analyse the quality of the data generated by the CT Scanners and see how we can improve it by the state of the art techniques from image processing, computer graphics, and the artificial intelligence resources.

We have concentrated on three issues: how to improve spatial resolution in between two consecutive slices of X-ray CT Scans, what can be done for better visualization of the 3-D data of the CT Scans, and finally how we can aid the radiologist in the recognition process of anatomic structures from the CT Scans.

We have reported some of the most exciting results in these areas in our laboratory as well as in other centers. While there is going to be continuous effort on improving the resolution of the data in the displays, we feel that the future research contribution from the computer vision community will come in finding various representational schemes of 3-D objects (parametricisation) which will enable us to compare the morphology obtained from the CT Scans in more quantitative fashion than it is so far.

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