

## ● *Technical Innovations and Notes*

# THREE-DIMENSIONAL STYLIZATION OF STRUCTURES OF INTEREST FROM COMPUTED TOMOGRAPHY IMAGES APPLIED TO RADIOTHERAPY PLANNING

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**Purpose:** Techniques to detect structures of interest and model them as simple geometric shapes to enhance their visualization are presented.

**Methods and Materials:** Three-dimensional visualization techniques can be used to enhance the detection of critical structures by enclosing them in a readily perceived bounding volume. This article describes stylization techniques that define three-dimensional shapes that conform to the real shape of the structures in the case of the spinal cord and the eyeballs. The term stylization can, thus, be defined as a combination of segmentation and the production of a tight bounding volume. The stylization techniques attempt to minimize the region that belongs to the solid produced and does not belong to the real structure, but they also attempt to ensure that the solid produced is a bounding volume to the real structure.

**Results:** The results produced by these techniques proved to be efficient and, thus, provide a means of easily visualizing the critical regions.

**Conclusion:** The stylization technique can be seen as an adaptive volumetric contour. With potential use in clinical practice, it also provides a platform for further investigations of the geometric stylization concept.

Computer graphics, Image processing, Scientific visualization, Medical imaging, Stylization of structures.

## INTRODUCTION

Applying volume visualization techniques to computed tomography is potentially a powerful aid to a clinician attempting to perceive three-dimensional structures from two-dimensional tomograms. It is a technique, which although mostly confined to computer graphics research laboratories, is beginning to be used clinically (12).

Computed tomography is routinely used in radiation therapy planning. However, perceiving 3D relationships between structures from tomograms is a very demanding and time-consuming task. It is also difficult, using computed tomography (CT), to verify whether a radiation beam intersects a critical structure in the planning process or not.

It is, thus, necessary to extract these critical structures so that they can be more easily visualized. However, critical structures may exhibit low contrast against surrounding tissue. In this article we look at techniques in which such structures are automatically detected and en-

closed in a (visually emphasized) bounding volume. We call this process stylization of critical structures.

In this article, two kinds of critical structures are dealt with: the spinal cord, which is a very long structure that normally extends for many slices within the CT data set; the eyeballs, which are in a difficult position when a region in the upper part of the brain must be irradiated.

In radiation therapy planning, data is normally acquired through CT as a series of two-dimensional images. This series of images is the basis for treatment planning. Other imaging modalities provide better contrast between soft tissues, but CT is the best modality for radiotherapy planning because it provides anatomic information in terms of electron density ratios, required for dose calculation (13).

In CT studies of a head, typical critical structures that must be protected against high dosage of radiation are the spinal cord and the eyeballs. The spinal cord is more likely to be intersected by a radiation beam, because it is a very long structure. A radiotherapy planning system should, thus, provide a means of reassuring the oncolo-

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gist that the spinal cord is not reached by an oblique radiation beam (2). The design of oblique beams, which should encompass the target volume while excluding the spinal cord, is, thus, a very difficult task in radiotherapy planning.

The identification of anatomical structures, however, and also of the target volume, are very time consuming in conventional radiotherapy planning systems (8). Although medical images have been greatly improved over the past few years, identification of anatomical structures has not yet been brought to a reasonable level of development.

In conventional systems, anatomical features are identified by means of manual or semiautomatic techniques. This task must be performed, or at least monitored, by the physician. A typical CT study contains 50 to 100 axial images, which must be examined separately, so that anatomical structures can be contoured and the extent of the disease and surrounding healthy organs can be delineated (3). These conventional techniques require extensive interaction of the user in clinical practice, and thus, are very demanding.

## RELATED WORK

In most contexts in medical imagery, the critical operation is segmentation of data to select structures of interest. Segmentation is, except in simple cases, a difficult operation to perform. It is not always the case that the data possesses a distinguishing attribute that will enable voxels to be grouped into a structure of interest that defines the segmentation operation. The simple operation of thresholding, based on the value of individual data samples only, functions in imagery where there is a high contrast between the structure of interest and other structures. Thus, thresholding is used with CT data to distinguish bony structure from soft tissue (6, 7).

Thresholding, whether it is applied to pixels in the data collection plane or to voxels in a volume data set, is a pixel-based context independent operation—it operates on each pixel independently of the results of the same operation on neighboring pixels. More elaborate approaches, although diverse, all tend to employ methods that in some way operate by considering groups of data samples. All such methods incorporate higher level processing using some kind of domain specific knowledge.

Worth *et al.* (17) describe the use of a neural net to segment magnetic resonance brain images that they claim compares with a human segmentation in separating gray from white matter. Here, the higher level processing is invested in the neural network structure that functions over groups of pixels.

Methods that go beyond point-by-point processing can currently be categorized into clinically proven methods and those that are potentially useful but which have not been fully tested in a clinical environment. For example, in the former category, Tracton *et al.* (16) combine segmentation methods in two and three dimensions. The use

of both two and three-dimensional information is a feature of the work reported in this article and is an obvious geometric approach, as in the end the features that are of interest are three-dimensional entities. Other methods in clinical use are described in (4, 11).

In the latter category, the most popular general approach is some kind of atlas-based method. This means using, in some way, *a priori* information about the organs that are the subject of segmentation. The nature of the *a priori* information and the way in which it is corresponded or compared with real data are the distinguishing features of these approaches. Many of these approaches are termed active or flexible in the sense that they are able to adapt the model data to the real data to take into account lack of exact correspondence in, for example, shape. Cootes *et al.* (5) use a shape model of the heart left ventricle that is represented by 96 key points built from 66 examples. Certain shape deformations are parametrized and the parameters are varied to fit the model to the data. Only shape deformations that are found in the 66 examples—the training set are allowed. Similar deformable model approaches are reported in (1, 10, 15).

Atlas-based techniques use *a priori* anatomical information usually with some kind of adaptive method. Segmentation techniques that are adaptive but which do not use *a priori* information are also under investigation. A method that is being actively pursued in many applications, including medical imagery, is the active contour models (or snakes) of Kass *et al.* (9). Snakes are structures of connected points that are parametrized using a physically based model. A snake adaptively fits an image feature by employing an energy minimization criterion.

The work described in this article is loosely related to atlas-based methods in that an *a priori* shape is implicitly assumed for a particular structure of interest—for example, a sphere for an eyeball. It could also be considered in that the *a priori* shape is grown, by comparison with the data, into a bounding volume.

## OVERVIEW OF STYLIZATION TECHNIQUES

Extraction of structures of interest is the term used to refer to the identification of voxels within a CT dataset that belong to these structures. Because this kind of process labels the voxels of interest within the dataset, these voxels define a binary set of volumetric data that can be rendered in the same way as the rest of the CT data, but using other parameters so that they can be clearly recognized.

Stylization of structures of interest, on the other hand, is the term used to refer to the process of producing 3D geometric solids that satisfy the following points: (a) the geometry of the stylization should relate to the geometry of the reality, that is, the shape of a 3D geometric solid created to stylize a specific structure conforms to the shape of this structure. (b) The process must guarantee that the stylization produced is a bounding volume rela-

tive to the structure. This is an important point in radiotherapy planning. No portion of a critical structure should be outside the bounding volume; otherwise, it would be susceptible to being exposed to high radiation doses delivered by radiation beams.

The features of stylization that distinguish the approach are as follows. Stylization is a combination of segmentation and the production of a tight bounding volume. The bounding volume is produced simultaneously along with the segmentation. The segmentation process and the bounding volume are one and the same thing. The bounding volume is efficient in the sense that it tightly encloses the structure of interest. The output of the process is a computer graphics solid that goes directly into a rendering process.

The process performs segmentation or detection of structures in the data collection plane and uses plane to plane coherence. It, thus, performs low-level processing in the two-dimensional data plane and moves through three-dimensional space by assuming the existence of a variation of the two-dimensional structure in adjacent planes. Because of the nature of CT data, this seemed to us to be an attractive alternative to operating directly on voxel data—particularly because the data that we worked had coarser resolution between planes. In the examples shown in this article the method was applied to a dataset of 41 slices and a dataset of just 23 planes—the resolution within each plane being 512 by 512.

The technique can be seen as an adaptive volumetric contour. A three-dimensional bounding volume grows until it encloses the structure of interest.

The stylization techniques used can be summarized as follows: (a) spinal cord stylization: techniques are presented that attempt to model a section of the spinal cord on a slice of CT data as a circle. The circles generated on each slice are then connected to form a 3D structure. (b) Eyeball stylization: techniques that stylize the eyeballs and also the lenses attempt to model these structures as spheres.

In this article, the direction that is normal to the tomogram slices is referred to as z direction, and the directions within slices x and y.

### *Stylization of the spinal cord*

In CT images, soft-tissue segmentation is much more difficult than bony segmentation simply because of the nature of this image modality, which is mostly used for the study of bony structures. Different types of soft-tissue structures cannot be distinguished easily. One could use thresholding to extract the spinal canal, because it is surrounded by bone. However, the spinal cord, which is

contained in the spinal canal, is much smaller than the spinal canal. In addition, the spinal canal is not entirely enclosed by bone in many transverse CT slices.

Therefore, thresholding, which is a commonly used technique for bone segmentation, is not suitable for soft-tissue segmentation in this context. An alternative technique, which is described next, attempts to stylize the spinal cord rather than to extract it.

### *Overview of the spinal cord delineation process*

Spinal cord stylization comprises detection in all slices followed by connection in three dimensions, defining a 3D object that efficiently comprises the spinal cord. The most complex part in this process, however, is to locate the spinal cord, and thus, to define the region of interest on each slice.

A 2D algorithm to analyze the spinal cord should take into account the following points: (a) the spinal cord is surrounded by soft tissue of a lower Hounsfield value range; (b) the vertebrae form an anatomically complex bony structure that surrounds the spinal cord.

Because the cross-section of the spinal cord has an approximate shape of a circle, the most efficient geometric object to stylize the spinal cord is a series of cylinders, or to be more precise, a series of truncated cones, which may also be oblique.

The approach that stylizes the structure of interest geometrically<sup>1</sup> has the following advantages over an approach that extracts the structure of interest volumetrically:<sup>2</sup> (a) a geometric structure composed of several circles would occupy little memory, whereas a volumetric structure would have to have all voxels belonging to its bounding box stored, in a binary volume format. (b) The shape of the structure itself is much simpler in the geometric case, and it is fairly simple to render geometric structures using both surface and cloud representation.

However, it is difficult to predict the exact location and radius of a circle (cross-section of a truncated cone) that would contain the cross-section of the spinal cord on a specific slice of CT data.

The first reason is that CT does not exhibit a sufficiently high contrast between different types of soft tissue, as mentioned before. The second reason is that thresholding the data to identify different types of soft tissue would have to be performed on each slice separately, because the threshold values selected for one slice may not be the right values for the neighboring slice.

### *Methods for spinal cord localization on slices based on its relationship with the vertebrae*

The easiest visual clue about the location of the spinal cord is its spatial relationship with the vertebral bony

<sup>1</sup> What is meant by geometric stylization is that the solid representing the structure of interest is defined by geometric primitives within the volumetric data rather than by labeling voxels as belonging to not to the structure of interest.

<sup>2</sup> What is meant by volumetric extraction is that all voxels inside the region considered to belong to the structure of interest are labeled differently from the rest of the data.

structure surrounding it. Therefore, most techniques so far developed for the delineation of the spinal canal take this as a starting point. For example, Cornelius and Fellingham (6) developed a system to aid the interpretation of CT slices of the spine, locating the spinal cord and automatically computing anatomical measurements. Their method takes advantage of knowledge of symmetry, shapes, and spatial relationships of vertebrae to locate the spinal cord and also major components of vertebral bone.

In general, the first step in the process for the outline of the spine consists of determining its position on each slice. Among the slices of a CT dataset that intersect the spine, some show the spinal canal completely surrounded by bony structure, assuming a roughly circular shape, and others show bony structure that do not form a closed connection around the spinal cord, because of the presence of the foramina, which give passage for the nerve roots. These two classes of slices are referred to as closed and open intersections, respectively. Figure 1a shows an example of a closed intersection, and Fig. 1b illustrates the open intersection. Because the interslice resolution in a typical CT study is low, the connectivity between the bones that compose the vertebrae varies greatly from slice to slice.

Cornelius and Fellingham use closed intersections to make measurements of the spinal canal. To locate the spinal cord within the spinal canal, the center of mass is found from all soft tissue pixels within the canal and also the minimum and the maximum diameters for hypothetical circular regions defined from that point.

We can use this philosophy for the location of the spinal cord; the center of mass calculation could be performed in the closed intersections; and the circles defined in these cases would be interpolated to generate a circle on each slice, that is, circles in open intersections would be defined as the interpolation between the circles in the nearest neighboring closed intersections.

This interpolation scheme should provide an extra margin so that the process guarantees that the real structure is enclosed in the stylization produced. This is reasonable, considering the shape characteristics of the spinal cord. One possibility is to draw straight lines linking corresponding points of the two end circles, and then give

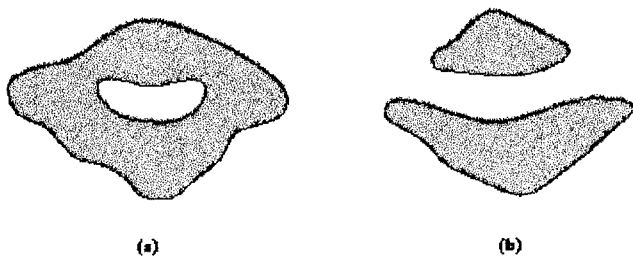


Fig. 1. Appearance of vertebrae on a slice: (a) closed intersection: spinal canal is completely surrounded by bone. (b) Open intersection: bones are not connected because of the passages for the nerve roots.

an extra margin for possible irregularities in the shape of the spinal cord.

Because this method depends on the connectivity of the vertebral structure on each slice, unsatisfactory results could be generated, especially if the resolution along the z direction is very low. Thus, it can be desirable to use information of all appropriate slices to reach a more accurate result. An alternative technique is now presented, which uses convolution to determine a concentration of high densities within a range of CT values.

#### *A method based on convolution in a soft tissue field*

The aim of the method is to model a circle on every slice (not only on closed intersections but also on open intersections) in the right location and with the right radius so as to ensure that the circle efficiently stylizes the region intersected by the spinal cord on each slice, in a prespecified region of the data.

The spinal cord has higher CT values than the remaining soft tissue within the spinal canal. Thus, taking in consideration the shape of the spinal cord, the algorithm should search, within the spinal canal, for a concentration of high CT soft tissue values defining a region with the approximate shape of a circle.

For this concentration of high CT soft tissue values to be detected, a convolution process is performed, using a kernel similar to that of a low-pass filter. The convolution is used only to determine the location of the region sought. Once the location is determined, the algorithm attempts to find a suitable value for the size of the region sought. In other words, the location determined in the first step of the process is taken as the center of a circle, and then, the algorithm attempts to find a suitable value for the radius of this circle. This circle is then taken to be the stylization of the spinal cord on that slice where the process is being carried out.

The convolution of the reconstructed data with a function kernel can be expressed as

$$V(u, v) = \iint D(u + x, v + y)K(x, y)dx dy$$

where  $V$  is the value of the convolution corresponding to the element  $(u, v)$ ,  $D$  is the resampled data, and  $K$  is the function kernel. Because we are dealing with sampled signals, we can construct a kernel from a square matrix of values. Following a sinc function, the center of the kernel has the highest value and its periphery has the lowest values, so that the gradual change in density within the region of interest in the CT slice can be highlighted, and a concentration of high CT values can be found. For best results in this convolution process, the size of the kernel should ideally conform to the size of the structure sought, that is, to the size of the spinal cord on the CT slice. If this criterion is met, the convolution will certainly

determine the center of the high CT soft tissue region. The size of this region in pixels is obviously dependent on the resolution of the data, so a suitable value must be chosen. However, with the common resolution used in CT (512 by 512), it can be assumed that the size of the region is about 15 pixels wide, so a kernel of 15 pixels wide can be chosen.

After the convolution process is performed, the voxel whose position corresponds to that of the pixel with the greatest value in the convolved image plane is taken as the center of the circle. Other criteria could be used to find the center, such as, to threshold the convolved image plane and then use a weighted average function to define the center of the circle.

Once the center of the circle has been found, it is necessary to determine the size of the region sought, that is, the thickness of the stylization of the spinal cord on the slice. One alternative is to draw circles of increasing radii around this point until the ratio between pixels intersected by the circle above a certain threshold and the total number of pixels intersected by the circle falls below a predefined minimum percentage value. The threshold value is calculated by multiplying the maximum value in the convolved image by a predefined multiplication factor, whose value lies between zero and one. When the process stops, the last value obtained for the radius is taken as the result.

Sometimes the method is not able to generate an acceptable result because the level of contrast on the slice falls much below normal. When this occurs, the resulting circle is rejected and a new circle is defined based on the resulting circles of neighboring slices.

The parameter used to identify an unacceptable circle and also to define a new circle takes into consideration the shape and the disposition of the spinal cord within the body. The spine is a long and thin structure oriented roughly in a vertical direction (*z* direction). Thus, the displacement between the *x* and *y* coordinates of two adjacent circles cannot exceed a maximum limit.

### *Stylization of the eyeballs*

The eyeballs constitute another type of critical structure that must be protected against large amounts of radiation when treatment beams are cast to the target volume. The most important part within the eyeball itself is the lens, which is very sensitive to radiation.

Because the eyeballs are soft tissue structures, their gray scale contrast in relation to the surrounding structures is very low, and, thus, they are very difficult to be segmented.

The eyeballs are connected to the brain through the optic nerves and other muscles, and all these structures fall on the same range of CT numbers. Thus, it is impossible to separate the eyeballs from the other structures using thresholding. If a naive technique based on thresholding were applied to outline the eyeballs, the optic nerves, all

other muscles connected to them, and the brain would also be selected.

Because the eyeballs have a rough spherical shape, it would be advantageous to stylize them geometrically as a pair of spheres. Another reason in favor of the geometrical stylization of the eyeballs is that they are fairly small structures, and, again, because of the lower resolution along the *z* direction in CT images, defining a volumetric structure in a 3D grid can be inaccurate.

A technique for the delineation of the eyeballs and their stylization as a pair of spheres is described here. This technique attempts to find the most probable location of the center of the spheres that efficiently comprise the eyeballs as well as the most probable value of the radii of such spheres. The method involves thresholding and makes use of the scan line circle generation algorithm developed by Bresenham (14). It works in two dimensions in the first stage, defining a circle on a slice. In a later stage, the third dimension is processed to produce the coordinates of a sphere that must efficiently stylize the eyeball. The process of the third dimension in a later stage is due to the limitation of one of the dimensions having a much lower resolution.

A similar technique to the one used to determine circles to represent cross-sections of the spinal cord could be used in the case of the eyeballs, because both stylization techniques have the same philosophy, namely, to model circles on slices and then produce a 3D geometric structure from the circles. The results, however, could be affected by the neighboring structures. Considering this, an alternative technique has been investigated.

On the other hand, the technique developed for the eyeballs is not suitable for the case of the spinal cord. In the spinal cord stylization technique described in the previous section, a concentration of high density soft tissue is located, without the need to apply any threshold values within the soft tissue range (CT values within the spinal canal vary between slices, and the criterion used here to determine the location of the spinal cord is to locate a concentration of high soft tissue CT values, and not to determine a region of interest by applying thresholding). The eyeballs, on the other hand, can be distinguished from the surrounding tissue by applying a threshold value, and thus, the algorithm is based on thresholding.

### *Moving circles method*

This method makes use of Bresenham's scan line circle generation algorithm. The algorithm takes a voxel (provided by the user) known to lie inside the eyeball and draws a circle around it. The radius of the circle is set to a predefined minimum value. A maximum value for the radii is also specified for termination condition, in case no circle is found within the range of typical radii for the eyeballs. These minimum and maximum values can be suitably chosen by considering the minimum and maxi-

imum size of a typical eyeball in practice. Figure 2 illustrates the initial part of the process.

Once the circle has been drawn, it is analyzed according to the number of pixels on its edge that fall within the threshold value, and depending on the result of this analysis, one of three actions is taken. If the circle is considered to be overall inside the thresholded area, the radius of the circle is incremented. If part of it is considered outside the thresholded area, the center is moved in the opposite direction of the arc, which falls outside the thresholded area. The third action is the termination of the process, which occurs if the center is moved and the new center has already been processed.

For the special case when the whole circle falls outside the thresholded area, the vector indicating the direction to which the center of the circle should move has magnitude zero, and thus, the coordinates of the new center coincide with the ones of the previous center, that is, the center does not move at all. Because this very center has already been processed once, the process is terminated, and the coordinates of the center are taken as result.

To decide whether a circle is completely inside the thresholded area, or whether an arc of it is outside, or even whether the whole circle is outside the thresholded area, some characteristics of the eyeballs and their typical CT values, as well as the CT values of the region around it, have to be taken into account.

Figure 3 is an illustration of a cross-section of an eyeball. The cross-section represented in the figure is around the middle of the eyeball. The white region represents the area where CT numbers fall below the lower threshold value for the eyeball. The gray region represents the CT numbers that fall within both threshold values, and the dark region represents the CT numbers that fall above the upper threshold value.

The algorithm remains incrementing the radius of the circle until an arc of the circle or even the whole circle falls outside the eyeball. When it does, the radius is not incremented and the center of the circle is moved in such a way as to find the best possibility of the new circle to fall within the eyeball.

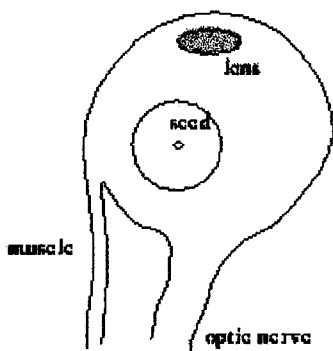


Fig. 2. Schematic diagram of eyeball after thresholding data. Given a seed, a circle is drawn around it using Bresenham's algorithm.

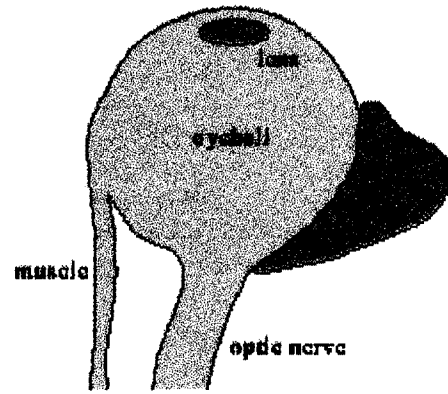


Fig. 3. Regions of CT numbers.

Figure 4a illustrates the process of how the calculation of the direction, in which the center of the circle should be moved, is performed. Vector  $\overline{JK}$  links the two intersections between the circle and the edge of the eyeball. Vector  $\overline{M}$  represents the direction along which the center must be moved. It can be easily calculated by computing the cross product between vector  $\overline{P}$ , which is defined to be perpendicular to the plane, and vector  $\overline{JK}$ . Supposing that in three dimensions the coefficients of vector  $\overline{JK}$  is  $(JK_x, JK_y, 0)$  and the coefficients of vector  $\overline{P}$  is  $(0, 0, 1)$ , then the coefficients of vector  $\overline{M}$  will be  $(JK_y, -JK_x, 0)$ . In two dimensions (*plane XY*), this can be simplified to  $(JK_y, -JK_x)$ .

Vector  $\overline{M}$  is then normalized, and the coefficients of resulting unit vector  $\hat{M}$  are rounded, so as to allow the move along one of the axes or diagonally, that is, the coefficients  $M_i$  and  $M_j$  of vector  $\overline{M}$  may assume one of three values:  $-1$ ,  $0$ , or  $1$ . This is illustrated in Fig. 4b.

For the new calculated center, a circle is drawn with the same radius as the previous one, and the process continues until a termination condition is found, which can be either of the following two: the radius value reaches the maximum value for radius or the circle is entirely outside the eyeball section. In the first case, an error is generated and in the second case, the answer will be the last circle generated.

#### Definition of a sphere from a series of circles

Once there are circles comprising the eyeballs available on a few slices, it is necessary to move from 2D to 3D, that is, to define a sphere that has these circles as cross-sections (this process is a little more difficult because of the distance between slices in CT images).

Theoretically, if there were two circles known to be cross-sections of a sphere, the determination of this sphere would be straightforward. In the case of CT images, however, there are a few factors that make the process more complex, such as the distance between slices (low resolution) and the fact that the data is not continuous but discrete, where samples are classified as belonging or not to a determined structure. Because of this, it is not advis-

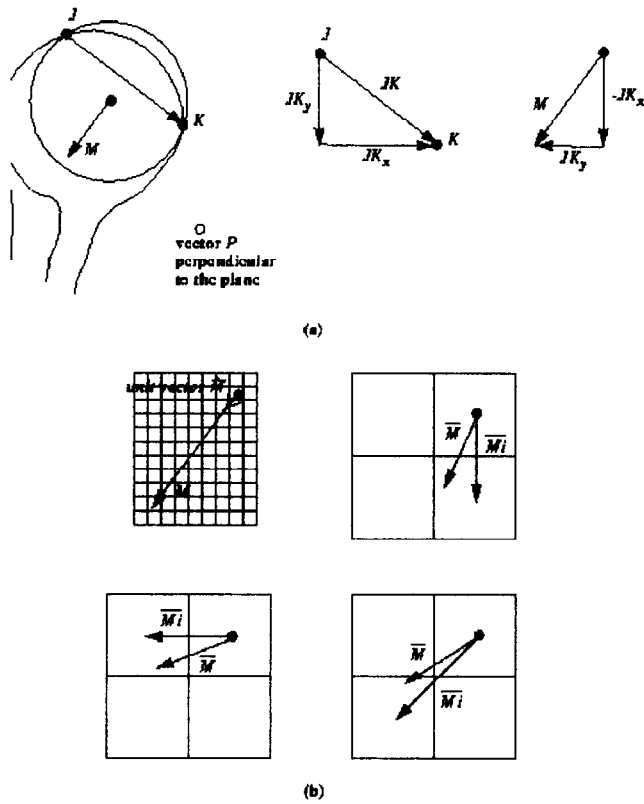


Fig. 4. Determination of direction of move: (a) determination of vector  $\vec{M}$ ; (b) determination of unit vector  $\hat{M}$  and integer vector  $\hat{M}_i$ .

able to rely upon only two circles representing cross-sections of the eyeball to derive a sphere representing the whole eyeball.

The algorithm must make sure that the generation of the sphere relies upon circles defined on slices that intersect the eyeball near its center, because these circles are defined more accurately. Even so, the low resolution along the z direction entails difficulties in calculating the z coordinate of the center of the sphere (the center of the sphere may not lie on a particular slice, and in fact, it could lie anywhere between two particular slices). For this reason, a margin of error must be considered to compensate for inaccuracies. This is thus the critical part of the process.

Once the position of the center of the sphere has been determined, it becomes very easy to determine its radius. The eyeball stylization process is then complete.

#### Practical considerations

To make the moving circles algorithm simple to work, the first thing to consider is that, when generating a circle

via Bresenham's algorithm, the circle should start being analyzed when the first voxel lying inside the eyeball is found.

The lens, which lie inside the eyeballs, have CT values higher than the threshold value. Nevertheless, it should be considered inside the eyeball, and the algorithm should account for that. Considering the typical size of the lens and the resolution of the CT dataset, a value is specified to indicate the maximum number of subsequent voxels lying above the threshold values that should still be considered as belonging to the eyeballs.

In the same way, when the circle intersects either the optic nerve or one of the muscles that connect the eyeballs to the brain, subsequent voxels lying inside the range of CT values within the threshold values should be considered as not belonging to the eyeballs.

There are a few ways to analyze each element of the circle to determine whether it lies or not within the threshold values. The most simple is to just take the value of the voxel corresponding to the coordinates of the element. A second way is to define a function that produces a value according to the voxel corresponding to the coordinates of the element and its neighbors, making, for example, a weighted average. This procedure should identify whether the element lies below, within, or above the threshold values.

The eyeball stylization method can also be used to extract the eyeballs volumetrically, as an alternative to stylizing them. There are two ways of accomplishing the extraction: (a) after a sphere has been created by the stylization method, thresholding is applied to its interior. (b) After circles have been created by the moving circles method on each slice, thresholding is applied to their interior.

The lenses are the most critical part within the eyeball. It could also be desirable to outline the lenses themselves, as well as the eyeball. The lenses are very small and thin objects, and given the typical low resolution along the z direction in CT scans, they normally appear on only one slice.<sup>3</sup> So one possibility for the outline of the lenses, although the shape of the lens on one slice looks more like an ellipse rather than a circle, is to model them as spheres, like the eyeballs, giving the extra margin necessary, because it is impossible to determine its exact position within the eyeball by just examining the data. Geometrical knowledge of the relationship between both structures, the lens and the eyeball, can play an important role in this process.

## RESULTS

The results produced with the stylization techniques described in this article show that there is great potential

<sup>3</sup> This is true in computed tomography scans that use a slice interspace of about 5 mm. When the resolution is even smaller, only a tiny portion of the lenses appear on a slice, and sometimes

the lenses do not appear at all. In these cases, a technique that makes use of spatial knowledge of such structures must be used.



Fig. 5. Rendering of the stylization of the spinal cord.

of application for the stylization approach in the field of radiotherapy planning. These results, however, can be improved to provide a more accurate stylization tool. The purpose of this work was to introduce the idea of stylizing structures of interest and to provide a platform for further research, which could achieve a better degree of parameter control, so that the best results can be quickly achieved independently of the characteristics of the CT dataset.

Figure 5 shows a picture of the stylization of the spinal cord, which is the result of the process described in this section. The blocky appearance of the structure in the image is caused by the fourfold magnification process. The shading allows for the visualization of the nature of the structure, which consists of a series of oblique truncated cones. It can also be seen that the region at the top of the structure does not have enough contrast between CT values to produce an efficient result, and so the stylized region is much thicker at this location than at other locations, because an extra margin must be given to ensure that the volume does not leave any part of the spinal cord outside its boundaries.

In the case of the eyeballs, results obtained by the moving circles method are exactly the same when central seeds are taken. When a seed near the edge of the eyeball is chosen, results vary a little, but they are still correct, that is, they still comprise the eyeball efficiently.

The first part of the algorithm creates a circle around the thresholded area on one slice. This process generates very good results. The greatest limitation of the whole technique is inherent to the nature of the data, and occurs in the second part, where a sphere is created from the circles on each slice. It is obvious that the more reliable the seed is, that is, the more central to the thresholded area the seed is, the safer the result of the process will be. So seeds near or on the edge of the eyeball or seeds on peripheral slices, that is, seeds on slices where the thresholded area is small, should be avoided. This is normally the case, because the user is likely to choose a seed

as safe as possible, and the middle ones are normally selected.

It is important, however, to stress that, even if the result generated by a bad seed selection does not delineate the eyeball as desired, or if the user is not satisfied with certain results obtained, it is always possible to process the eyeball delineation again. This kind of process often runs under a tool, which shows the user one slice at a time. In such cases, the process is interactive in nature, although the task performed by the user is reduced to selecting a seed, controlling parameters, and supervising the results obtained. After the process is completed, the geometrically defined object that stylizes the eyeball is displayed in such a way that it is easy for the user to recognize the relationship between the structure itself and its stylization, and this gives the user the ability to judge whether the results are satisfactory or not. In case the results are not satisfactory, all the user must do is to select a new seed for the process to be repeated. We emphasize that unsatisfactory results have not occurred in this process in our experiments.

In practice, the time required for an eyeball delineation is negligible compared to the processing time taken by the tool that displays slices of a computed tomography dataset.

Figure 6 depicts a volume rendered image showing the skull of a live patient, the stylization of the spinal cord and the eyeballs, and three radiation beams aimed at a simulated target volume. This simulated target volume is not visible in this image because bones were rendered as completely opaque. The bottom part of one of the eyes is colored differently in the original image, appearing brighter in the black and white photograph, because it is hit by a radiation beam.

## CONCLUSION

This article describes some ideas and techniques for stylizing the spinal cord and the eyeballs from CT images for the application of radiotherapy planning. The main idea is to use simple geometric solids which conform to the shape of these structures. Some methods for defining these structures have been described that can be improved

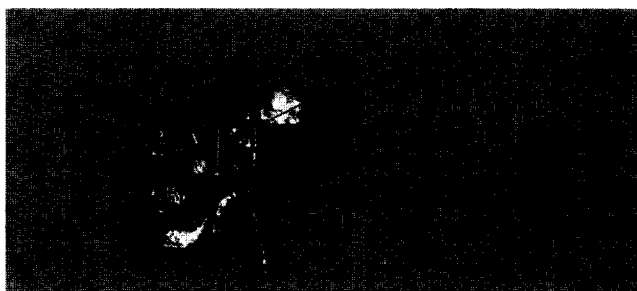


Fig. 6. Image of a radiotherapy planning process showing the stylization of the spinal cord and the eyeballs.

and also serve as a starting point for other techniques. This kind of technique can be seen as an adaptive volumetric contour, where a three-dimensional bounding volume grows until it encloses the structure of interest. The big-

gest problem involved in the stylization process is the low resolution of the third dimension ( $z$  axis), but even so, the results obtained by the techniques are good.

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