Automatic Axis Extraction from "Tubular" Structures In CT Images- An Application in Virtual Colonoscopy

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ABSTRACT

This paper presents a new method for axis extraction from "tubular" structures in CT images. The axis is important in virtual colonoscopy systems because it offers more efficient measurement features and better interactive visualization possibilities.

The proposed method is based on the "pseudo-tubular" structure of the Colon. To find a good estimation of the Colon axis, the method is organized in two steps: In the first step, the voxels are organized in sequential clusters along the structure using a region-growing strategy and a cylindricity criterion. Each cluster has a distinct point (which is a good candidate to be part of the axis, identified by the cylindricity criterion), and an internal partial ordering of the cluster's voxels. This information structure allows us, in the second step, to propose three instances (one per principal coordinate axis) of an estimation problem to be solved with the Takagi-Sugeno-Kang Method (TSK). Based in the resulting solutions it is possible to build a piece-wise linear estimation of the colon axis.

This method has produced good results. It is robust in face of the "pseudo-tubular" shape of the colon. It has been tested on a set of Colon CT images from previously prepared patients. The results are illustrated with animations of virtual colonoscopy and a set of measurements and visualizations. Medical practitioners had a good perception of the method's potential in the field of virtual colonoscopy applications.

Keywords
Virtual colonoscopy, axis extraction, 3D Image processing, Medical Imaging

1 INTRODUCTION

Virtual colonoscopy is an alternative to diminish invasive practices in colonoscopy procedures used in colorectal cancer detection. A 3D model of the patient's colon is created from CT images. Using this geometrical model, the expert can perform visual examination and polyp detection. [1].

The main steps in virtual colonoscopy, from a computational point of view are:

- Image acquisition from the patient's colon region
- Segmentation of the colon in the image
- Axis (or central line) computation
- Interactive visualization (guided by the axis)
- Measurement, polyp detection and localization tools

This technique, although less invasive than the optical colonoscopy, requires quite a demanding preparation on the patient´s side. Nevertheless, this practice has had an important impact in the reduction of mortality due to colon cancer.

Research initiatives meant to improve virtual colonoscopy systems [1],[2] focus on the reduction of the invasive aspects of patient preparation with new methods of colon segmentation [3], and the improvement of visualization and measurement tools to be able to identify and locate polyps and other pathologies [4].

This paper presents a new axis extraction approach starting from a segmented 3D Image of the colon. The results obtained allow us to expect a "good behavior" in tubular structures that, like the colon, have complex shapes and characteristics such as local diameter variations and big curvatures. Other interesting tools for virtual colonoscopy based on axis computation are also presented: interactive navigation, measurement, and section height visualization.

2 AXIS EXTRACTION – GENERAL CONCEPTS

The extraction of the axis of a "tubular" structure such as the colon, involves finding a line whose points fulfill a series of characteristics [4]:

- **Centricity:** The points should be situated as far as possible from the surface or walls of the structure. Each point of the axis defines a section in the perpendicular plane to the axis at that point. In that section, the point of the axis should maximize the minimum distance to the border.

- **Connexity**: The points of the axis must, of course, be connected, and the line must have a "smooth" behavior (no discontinuities in its second derivative)
- **Singularity:** The axis must be one voxel in width.
- **Efficiency:** Computation time should be short.
- **Automation**: The method should not have to require human intervention.

The task may be approached in different ways. We may classify them in the following categories:

- **Manual extraction**: Based on human expert interactive work on the 2D images of the CT. Manually, the expert points out a pixel as part of the central axis of the segmented volume [4].
  Advantages: We will always have exactly one point per slice of the CT image.
  Disadvantages: The extracted line may or may not be precisely located on the center line. Human expert work is based on the CT slices, not on perpendicular sections of the segmented 3D images. Moreover, connectivity criteria are not guaranteed and, obviously, the procedure is not automatic.
- **Thinning**: Based on the successive elimination of border voxels from the segmented volume, in order to keep the "resulting" center. [5], [6].
  Advantages: The axis points determined are (by construction) connected and far from the borders of the segmented volume.
  Disadvantages: High sensitivity to "local pathologies" of the segmented structure (curvature, diameter) and to limitations of the initial segmentation.
- **Distances Map:** Based on the computation of the distance from each voxel to the nearest border in the segmented volume. Each voxel is labeled with the negative of this distance. The proposed axis is the traversal minimal cost path [7], [8], [9], [10], [11].
  Advantages: Based on the end points, this is an automatic process. The proposed axis is continuous and is located far from the borders of the segmented volume. In vascular structures, these methods present a very good behavior.

3 PROPOSED METHOD

The proposed method improves the geometric quality and robustness of the automatic solution. The main characteristic is the use of a "fuzzy" method (robustness) for piecewise curve adjustment (geometric qualities). Based on the 3D tubular characteristics of data, we propose a preprocessing stage that improves the conditions in which the Takagi-Sugeno-Kang (TSK) technique [12], [13] may be used.

The method is presented in two phases:

First Phase, **data structuring**, seeks the creation of a first rough estimation of a centerline of the tubular structure. This line is called *primitive centerline.* The primitive centerline is a polyline whose first point (in the particular case of the Colon`s images) can be computed automatically. Beginning at this point (the chosen point), and based on a growing strategy using the "Manhattan distance", and on a cylindricity criterion, we propose the next "chosen point" (the end of the axis of the biggest "cylindrical" section compliant with the cylindricity criterion). The sequence of chosen points is the primitive centerline of the tubular structure. The voxels are labeled with the Manhattan distance from the initial point (fig.1). Each vertex of the primitive center line has a "cylindrical section" of the structure associated to it (fig.3).

Once the primitive centerline has been established, voxels conforming the colon are also labeled with membership values based on their distance to each vertex of the primitive centerline. The voxels are organized in "clusters" associated to each vertex. The primitive centerline´s vertices generate a total order among clusters. The voxels within each 'cluster' are ordered considering their proximity to the neighboring 'clusters' (the previous one and the next one).

The second phase of the method, **Axis computation**, consists of a non-linear piecewise estimation of the colon's axis, by using the Takagi-Sugeno-Kang method (TSK) [14],[15],[16]. To implement this method, the ordering of voxels from the previous phase is used to generate three TSK instances in one dimension (one for each Cartesian coordinate). With the same order, the three solutions are integrated in one 3D line which is our proposal for the centerline of the tubular structure being analyzed (the colon, in our case).

Based on this centerline, an interactive navigation system can be guided inside the structure, different normalized measurements can be made on the sections (perpendicular to the axis), and then the morphological characteristics of the internal surface can be automatically estimated.
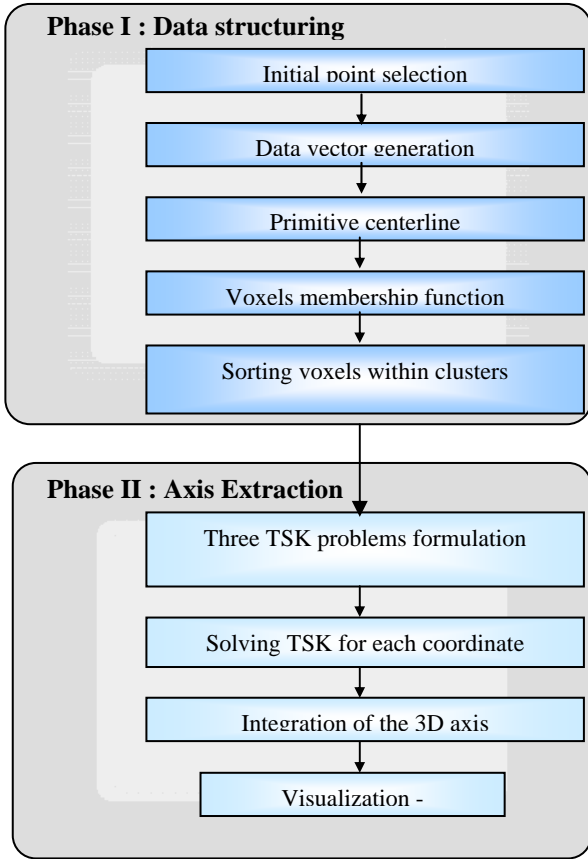
Phase I : Data structuring

- Initial point selection
- Data vector generation
- Primitive centerline
- Voxels membership function
- Sorting voxels within clusters

Phase II : Axis Extraction

- Three TSK problems formulation
- Solving TSK for each coordinate
- Integration of the 3D axis
- Visualization -

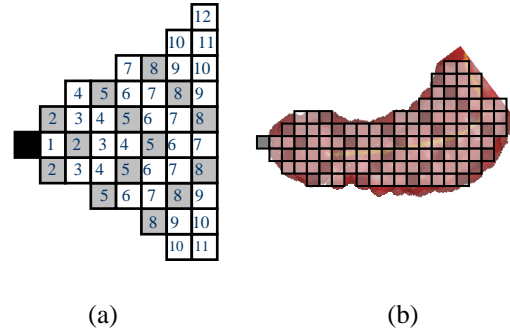**Diagram of the proposed method**

(a)   (b)

Fig. 1. (a) Layer generation from the manhattan distance, (b) P_0 Layers and manhattan distance inside the colon's human model from the P_0 point

b) Distance to the nearest border

Let us define a "border voxel" as a voxel in the structure for which at least one of its 6-neighbors doesn't belong to the structure. For each voxel of the structure we compute the distance to the closest "border voxel" in one of the 6 main directions.

3) The sequence of points for the primitive centerline

The primitive centerline is a polyline through the tubular structure. Its segments define sections which also have a tubular shape according to a cylindrical criterion.

a) Criteria for the tubular sections

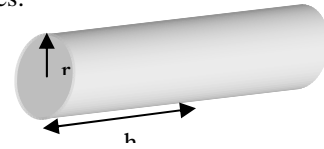The colon is supposed to be divided in sections of uniform tubes.

Fig. 2. R and H Parameters of a tubular section

Each section of the tube, as an approximation to the original structure, must have a height **h** greater or equal to two times its **r radius.** This way its main axis is in a direction close to the true axis of the structure.
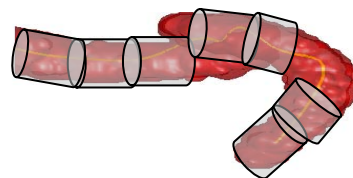

Fig. 3. Tubular sections throughout the colon

In order to build the cylindrical segments we can use two parameters: volume V and height h.

Volume (V) is estimated by the number of voxels present in the section.

In this section, each one of the phases of the proposed method is introduced in detail.

Information structuring

The method assumes that it has a 3D segmented image of the tubular structure i.e. the colon. The output of this phase is: a sequence of points which are the first point of the axis of "clusters" with pseudo-cylindrical shape (the primitive centerline) and the clusters with an order defined among its voxels. This phase has the following steps:

1) Selection of an initial point P_0 in one of the ends of the tubular structure:

In the case of the colon, the initial point chosen is the voxel in the lowest level of the z axis. (We can assume that it is the beginning of the rectum).

2) Data vector generation of each voxel

a) Manhattan distance to P_0

The Voxel P_0 is labeled with zero value (the initial voxel). Remaining voxels are labeled with the value of their Manhattan distance to P_0. In this context, the set of voxels with the same label value (the Manhattan distance to P_0) will be called "layer" (fig.1.a).

Height (h) is estimated by the number of layers present in the section. (The layers were generated using the Manhattan distance)

Based in the volume formula for a cylinder ($V = \pi r^2 h$) and the proposed relation ($h > 2r$), we have a criteria for an acceptable cylindrical shape:

$$h^3 > \frac{4V}{\pi} \qquad (1)$$

Where h, the length of the section, is estimated by the number of layers, and V, the volume of the section, is estimated by the number of voxels in the section.

b) The primitive centerline algorithm

i. P_0 is defined as the original point (layer 0). P_0 is taken as new "chosen point" P_i. A new section (future tubular section) is initialized with P_i as member.

ii. With P_i as the starting point, we include in the current section the voxels of the next "layer", in increasing order of layers, until condition (1) is true or there are no more layers to include.

iii. From the voxels in the last layer included in the current section, we choose the voxel with the greatest border distance. This is the new "chosen point" P_{i+1}. A new section (future tubular section) is initialized with P_{i+1} as member. Increment **i** and return to (ii)

The sequence $<P_o,.... P_i,... P_n>$ is a polyline which runs through the tubular structure and whose points are (at least in the main directions) as far as possible from the border. This line will be called the **primitive centerline of the structure.** It will be used to define a sequence of "clusters" of voxels throughout the structure.
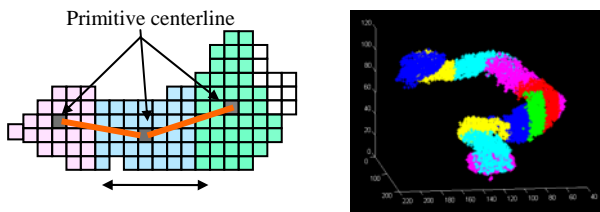

Primitive centerline

(a) (b)

Figura 4. (a) Clusters created in a section of the colon. (b) Clusters throughout the colon's structure.

c) Clusters

A cluster is a set of voxels associated to a particular vertex of the primitive centerline. We will define a fuzzy characteristic associated to each voxel called membership (how much does a voxel belong to each one of the cluster generated by the vertex of the primitive centerline).

4) Calculating the membership of each voxel to clusters

Each voxel is associated with a level of membership regarding each one of the clusters generated by each one of the vertex of the primitive centerline.

Calculation of the level of membership is determined by:

$$\mu_{ij} = (\frac{1}{D_{ij}})Dm_j$$

Where:

$\mu_{ij} =$ Membership of the i voxel to the cluster associated with the j point in the primitive centerline

D_{ij} Euclidian distance from i voxel to j point in the primitive centerline

Dm_j Minimum distance between all the voxels (not equal to j) in the structure to the j point in the primitive centerline

For each voxel in the structure, a membership value associated to each one of the vertex of the primitive centerline is computed. The voxel will belong to the cluster where the membership value is the greatest.

For voxels with two vertexes with the highest membership, the cluster assigned will be the one of the first vertex in the primitive centerline.

Each voxel will have three membership values: the value associated to its cluster, to its previous cluster (except the first one) and to the next cluster (except the last one).
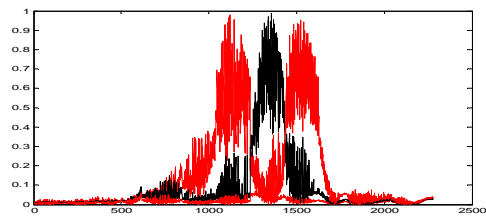

Fig. 5. Membership values of the voxels of the image. Colors illustrate the cluster to which they are assigned.

5) Ordering within each cluster

To build a total order for the voxels in a cluster (which will be used for the linear approximation later), we define a new parameter. The "relative membership" of a voxel in a cluster is the difference between its memberships to the next cluster and previous cluster.

Once the "relative membership" value is calculated, voxels are sorted using this parameter. We will find a total order inside the clusters, for the sequence of clusters, defined by the vertex in the primitive centerline.
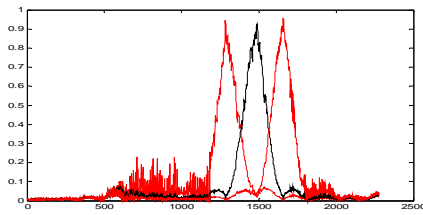

Fig. 6. Membership values of the ordered voxels.

The axis computation

Based on the structured information produced in phase one, the axis estimation for the tubular structure being analyzed is presented below:

1) *Generation of three Takagi-Sugeno-Kang (TSK) approximation instances*

The proposed method computes the axis estimation as a piecewise approximation for the set of voxels grouped in clusters. The problem statement is the estimation of three variables (the three coordinates) for each axis point based on a sequence of clusters and inside each cluster a sequence of voxels (based on the relative membership parameter). In order to reduce the complexity of the problem we propose three 1-variable problems, following a common total order of the data.

This approach allows us to compute a non-linear approximation for each coordinate and, based on these results, the final axis estimation.
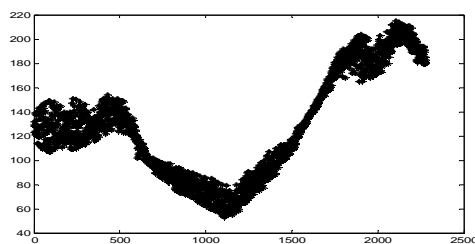

Fig. 7. Values of the x variable regarding the order parameter

2) *TSK Estimating for each component*

The next step is to find a non-linear model that can be adjusted to the information found when the coordinates of the voxels are separated according to the axes. We use the TSK (Takagi Sugeno Kang) method, well known in Fuzzy Control area (non-linear systems modeling).

We will follow the steps to generate a non-linear model in TSK method:

i. Create clusters from the set of information

ii. Obtain fuzzy membership functions of antecedents

iii. Obtain the consequents membership functions

iv. Calculate the system's final model.

i. Create clusters from the information set

In a regular TSK process, initial information must be exposed to a clustering process where the main objective is to find sub-groups within the data universe that have similarity or proximity. In our case, this step of the process has already been done. The structure was divided in clusters by calculating memberships (which comply with the TSK conditions).

ii. Obtain the antecedents` membership function.

Once the partition of the inputs in fuzzy sets is conducted, it is necessary to obtain the membership functions, so that it is possible to calculate the level of membership for any data belonging to a cluster, in order to obtain the appropriate model. This process is conducted through the association of a Gaussian membership function to each one of the clusters. Such function will be responsible of conducting smooth transitions between different linear pieces to be calculated later on.
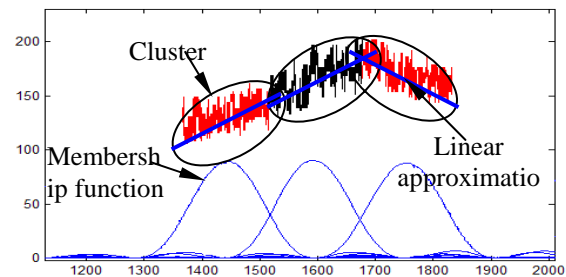

Fig. 8. Membership function and linear approximation

iii. Obtain the consequent membership function

As mentioned previously, the TSK method is based on the use of linear piece-wise approximations to generate the final non-linear approximation.

Linear approximations (straight lines) are generated for each one of the groups of information of each cluster. This straight line is named "consequent".

iv. Calculate the final model of the system.

Based on the previous steps of the process, the required data is available to compute the final model of a variable. We should multiply the membership functions with the consequents in order to obtain the final model:

$$y(x) = \sum_{i=1}^{r} \left(\left(\frac{\mu_i(x)}{\sum_{j=1}^{r} \left(\mu_j(x) \right)} \right) \bullet \left(a_i x + b_i \right) \right)$$

where :

r =   Number of clusters

$\mu =$ Membership level

$a_i x + b_i =$ Straight line approximation to the information

The result obtained from the application of the previous equation, generates the following approximation of the evolution of one coordinate along the axis.
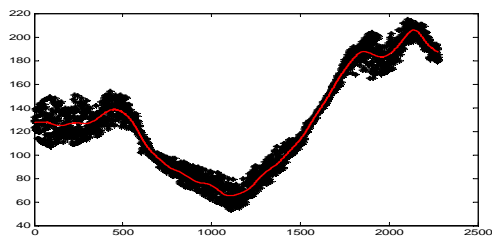

Fig. 9. Non-linear approximation of the X coordinate

The resulting model is continuous, smooth and seeks to go through the intermediate points of the data from the original system.

This process is applied to each one of the three systems that were built (one for each coordinate).
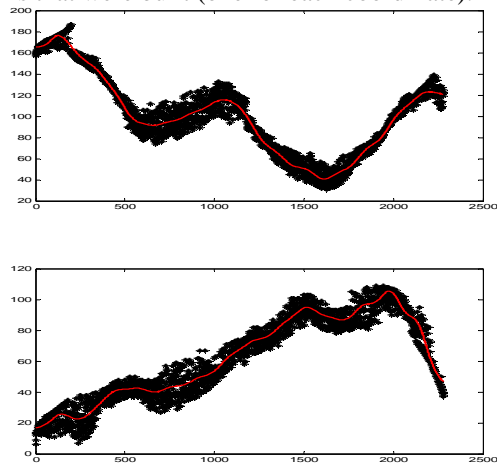

Fig. 10 Non-linear approximations of the Y and Z coordinates

3) Integration of the 3D model

The previous process produces an approximation for each one of the coordinates. We can integrate these results using the total order established in a previous step. In this way we find a 3D model of

the structure's axis. For our specific example (the colon) the 3D line is obtained in fig. 11:
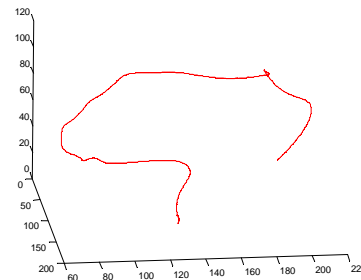

Fig. 11: Integrated solution for the axis of the tubular structure.

4 RESULTS

An implementation of the method presented was built using the Matlab 6.5 software. The input images were obtained from a basic segmentation system for Colon axial tomography, and from a tubular geometrical model generator. The Axis extraction method was applied to these input data and the results are presented bellow.

Two Colon tomographies were used to apply the segmentation process and axis extraction.

	Dimension (Voxels)	(m.m /voxel)	Axis Length (mts)	computation time
Colon 1	256X256X130	1.4x1.4x1.4	1.54	34 Sec
Colon 2	256X256X499	1.4x1.4x1.0	2.48	52 Sec

Table 1. Dimensions of the models and axis

Table 1 shows the main images characteristics, the length of the obtained axis and the computation time of the extraction method running on Matlab in a current laptop computer.
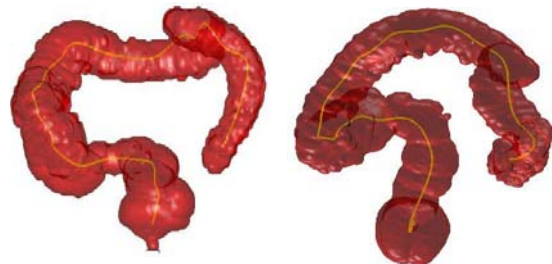

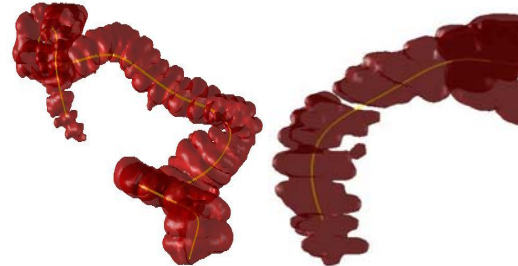Fig. 12: Frontal and upper views of the colon, with the extracted axis in yellow.

Fig. 13: Side/lateral views of the colon 2 and detail of the ascendant colon

A discontinuity of the ascendant colon can be observed in fig.13; we can observe that the algorithm outlines the axis in spite of this lack of data.

Based on the axis, we can obtain perpendicular sections along the axis and complementary measurements can be done (diameter and perimeter evolution, for example). Fig. 14(a) shows the axis and one perpendicular section with the profile generated from it -14(b).

In a similar way, we show in Fig. 15, a "terrain" view of the inside surface of the colon. It was obtained using the sections calculated along the extracted axis. This particular view can be very useful for polypus detection studies [19].
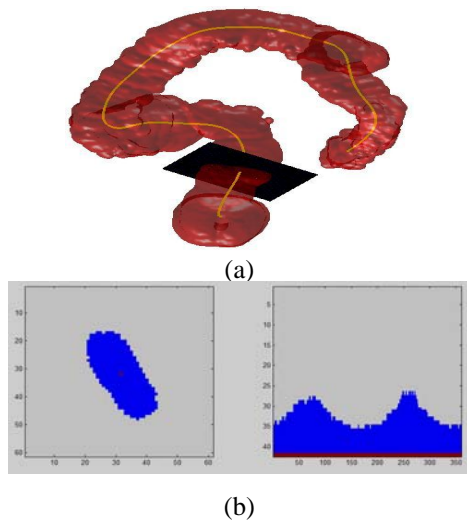

(a)

(b)

Fig. 14. (a) Perpendicular cut to the colon's human model (b) Cut's profile/section and relation of distances from the axis to the surface of the cut.
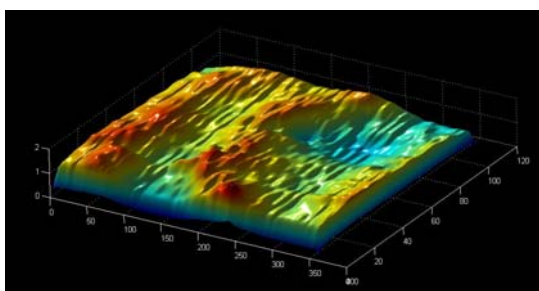

Fig. 15 'terrain' view of the internal wall of the colon throughout the axis

And, finally, when the axis is obtained, it is also possible to guide an interactive virtual colonoscopy, where a virtual camera navigates inside the colon with the support of the measurement facilities presented above.
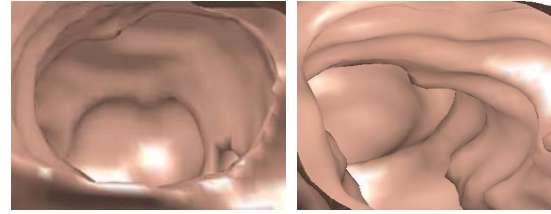

Fig.16. Virtual navigation images

In addition to the tests shown previously, the method was applied to tubular structures generated virtually for which the axis was exactly known. Four models were created for this, which are shown in fig. 17.

(a)   (b)

(c)   (d)
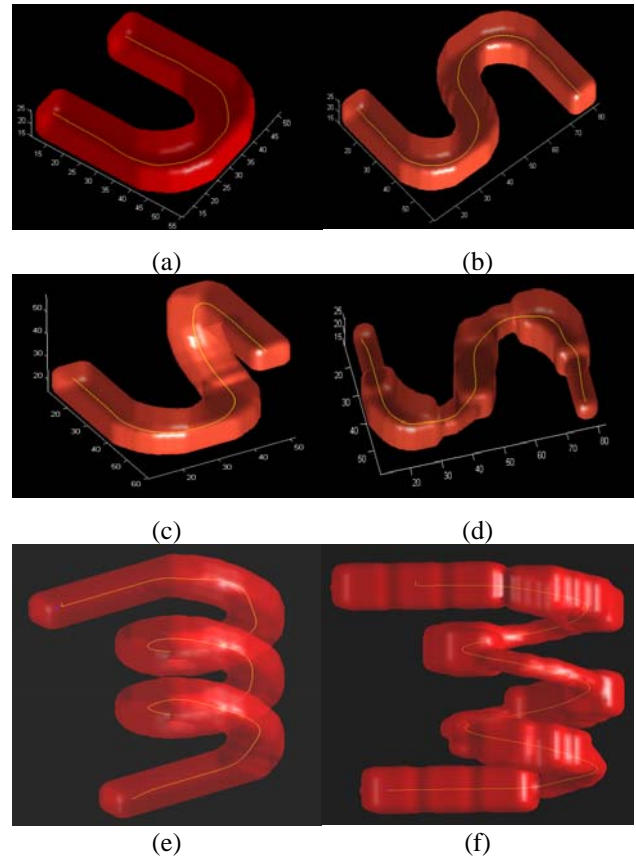

(e)   (f)

Fig. 17. (a) U shaped structure, (b) S shaped structure in the XY plane (c) S shaped structure in the XYZ plane (d) S shaped structure with changes in the radius, (e) (f) helical shape structure

Table 2 shows the error between the real axis and the automatic extracted axis using the proposed method.

Structure	Error
Model a	0.013%
Model b	0.2%
Model c	1.3%
Model d	2.1%
Modelo e	3.2%
Modelo f	4.1%

Table 2. Error in extracted axis for the generated models

5 CONCLUSIONS

An automatic method for the axis extraction of pseudo tubular structures has been presented. We have illustrated the results using an implementation oriented towards virtual colonoscopy.

 The use of criteria based on the tubular structure of a 3D image (cylindrical, layers based on Manhattan distance, axial distance to the surface), allows us to define and compute "tubular" clusters. Based on these clusters, an automatic formulation of three TSK estimation problems was done, and its results were then integrated in a robust estimation of the 3D axis of the input tubular structure.

The behavior of the presented method was illustrated with real colon images and with synthetic models. The results are interesting because of the geometric quality and the robustness of the different pseudo tubular forms and little discontinuities in the input data.

The frequency of pseudo tubular structures in biomedical problems gives this method a good potential for applications. The colon's characteristics as a pseudo tubular structure allow us to show results with a good potential impact in virtual colonoscopy applications.

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