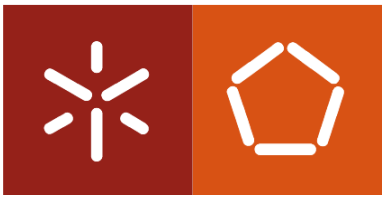

Analysis of the effects of the radiation therapy in cancer treatment by medical image processing

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Thesis report

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Resumo

Esta dissertação inicia-se com uma breve introdução, onde se pode ler o principal objectivo, realizar uma segmentação de um órgão/estrutura em sub-segmentos e realizar uma análise da radiação após um tratamento de radioterapia. De seguida, há uma pequena introdução ao que é o cancro, bem como alguns dos de maior relevância para esta dissertação. Seguidamente, a implementação das várias interfaces criadas, quer para identificação dos contornos das estruturas, quer para o objectivo final. Por fim os resultados obtidos dessas interfaces, onde se pode observar o cumprimento dos objectivos propostos. Por fim as conclusões obtidas, juntamente com a validação pelo Doutor da área em questão e propostas para trabalho futuro, nomeadamente a segmentação de estruturas mais complexas, como o recto e o sigma-cólon.

Abstract

This dissertation begins with a brief introduction, where the main objective, segmentation of an organ/structure into sub-segments and performing a radiation analysis after a radiotherapy treatment. Then, there is a short introduction to what cancer is, as well as some of the most relevant to this dissertation. After, the implementation of the various interfaces created, for the identification of the contours of the structures and for the final objective. Finally, the results obtained from these interfaces, where its possible to observe the fulfillment of the proposed objectives. Finally the conclusions obtained and the validation by a Doctor of the field, and proposals for future work, namely the segmentation of more complex structures, such as rectum and sigma-colon.

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Chapter 1

Introduction

1.1 Motivation

Nowadays, the effects of radiotherapy to treat cancer patients are a significant medical concern [6]. The analysis of these effects is done by experts in the field, through the analysis of medical images of the organs. This type of analysis is time-consuming because it is a manual analysis, and some tasks without support of equipment or computerized techniques. A fast and accurate segmentation of organs at risk, such as the bladder would be of benefit for the planning of radiotherapy. This planning includes the amount of radiation that the adjacent organs are getting. The division of the structure in straight sections can lead to a better identification of the amount and location of the radiation. The automatic segmentation of the sigma-colon is a novel topic, only some references from a medical point of view by manual anatomic analysis can be found, as in [2]. This project was proposed by a research group, the UITTFM "'Unidad de Investigación y Transferencia Tecnológica Física-Médica"'.

1.2 Objectives

The objective of this work is to divide structures in sub-segments, allowing a better analysis of the radiation in the treatment of cancer. To do that, a

better understanding of the dificulties of getting the contour of those structures is needed. Thus, the creation of an interface that allows the contouring of structures and its application in the isolation of tumors is the first stept. Finaly, the creation of an interface that will help in the division of structures in sub-segments, starting with the bladder, and then the rectum and sigma-colon.

1.3 Thesis Structure

This dissertation is organized as follows. The present Chapter summarizes the motivation and objectives. The Biological and Technical Context is presented in Chapter 2, followed by the Algorithms and Implementation procedures in Chapter 3. Chapter 4 discusses the challenges when implementing and the results. Finally, conclusions are presented in Chapter 5, with the description of achieved objectives and presentation of ideas for future research.

Chapter 2

Biological and Technical Context

2.1 Cancer

A term for diseases in which some of the body's cells begin to divide without control. These extra cells may form growths called tumors [15].
According to some studies, most of the cancers are related to heritable factors, and a few cases are related to environmental exposures such as, substances and radiation, for example, the chemicals in tobacco smoke or ultraviolet rays from the sun [9].
The genetic changes that contribute to cancer tend to affect three main types of genes: proto-oncogenes, tumor suppressor genes, and DNA repair genes.
Proto-oncogenes and Tumor suppressor genes are involved in normal cell growth and division. When these genes are altered in certain ways or are more active than normal, they allow cells to grow or survive when they should not. DNA repair genes are involved in fixing damaged DNA. Cells with mutations in these genes tend to develop additional mutations in other genes, causing the cells to become cancerous.
A cancer that has spread from the part of the body where it started to other parts of the body is called Metastatic cancer. When cancer cells break away from a tumor, they can travel to other areas of the body. The cancer cells

can spread through the lymph system or the bloodstream. If the cells travel through the lymph system, they may end up in nearby lymph nodes or they may spread to other organs, if the cells travel through the bloodstream, they can go to any part of the body. However, many of these cells die, but some may settle in a new area, begin to grow, and form new tumors. This spread of cancer to a new part of the body is called metastasis [27].
There are a A to Z List of Cancer Types, however in this thesis, will be focused on three: the Endometrial Cancer, the Colorectal Cancer and the Glioblastoma.

2.1.1 Endometrial Cancer

The uterus is a muscular organ where a fetus grows. According to where the cancer starts, if it starts in the endometrium, the inner lining of the uterus, its an Endometrial cancer, if it stats in the muscle and tissue that support the uterus its an Uterine sarcoma. Some of the factors that leads to have this types of cancer are: Obesity, taking estrogen alone, without progesterone, radiation therapy to the pelvis, taking tamoxifen for breast cancer, etc. The most common sign of endometrial cancer is unusual vaginal bleeding and usually be cured. Uterine sarcoma is harder to cure [13].

2.1.2 Colorectal Cancer

Colorectal Cancer or Bowel Cancer is a cancer that forms in tissues of the large intestine. Depending on what part it can be separated in Colon Cancer or Rectal Cancer, depending on where is formed, in the tissues of the colon or in the tissues of the rectum, however, is the same type of cancer [23]. The World Health Organization in the World Cancer Report 2014 says that globally, in 2012 the most common cancers diagnosed were those of the lung (1.8 million cases, 13.0% of the total), breast (1.7 million, 11.9%), and large bowel (1.4 million, 9.7%) [24], shown in Figure 2.1 [10].

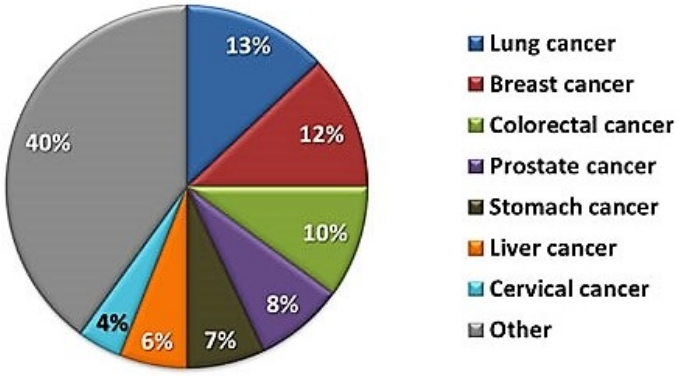

Figure 2.1: Worldwide Cancer Cases

2.1.3 Cancer Stages

Usually, colon cancer or rectal cancer starts with a polyp. A polyp is an abnormal growth of epithelial tissue in the wall of the large intestine. Not all of the polyps become in cancer, they can be removed before it. When they don't are removed, they grow as cancer and the cancer cells can spread to surrounding tissues and create metastasis [18].

To increase the prediction of survival of patients, cancer staging systems where created. The tumor, node, metastasis (TNM) staging system of the American Joint Committee on Cancer (AJCC) [8] and the International Union Against Cancer (UICC) [25] is now the standard for endometrial and colorectal cancer staging [7].

In Figure 2.2 [7], we can see how the system is evaluated according to the cancer characteristics.

Category		Definition
Primary tumor (T)	TX	Primary tumor cannot be assessed
	TO	No evidence of primary tumor
	Tis	Carcinoma in situ (intraepithelial or intramucosal carcinoma)
	T1	Tumor invades the submucosa
	T2	Tumor invades the muscularis propria
	T3	Tumor invades through the muscularis propria into the subserosa or into the nonperitonealized pericolic or perirectal tissues
		Optional expansions of T3:†
		pT3a-minimal invasion: <1 mm beyond the border of the muscularis propria
		pT3b-slight invasion: 1–5 mm beyond the border of the muscularis propria
		pT3c-moderate invasion: >5–15 mm beyond the border of the muscularis propria
		pT3d-extensive invasion: >15 mm beyond the border of the muscularis propria
	T4	Tumor directly invades other organs or structures (T4a) or perforates the visceral peritoneum (T4b)
Regional lymph nodes (N)	NX	Regional lymph nodes cannot be assessed
	N0	No regional lymph nodes metastasis
	N1	Metastasis in one to three lymph nodes
	N2	Metastasis in four or more lymph nodes
Distant metastasis (M)	MX	Presence of distant metastasis cannot be assessed
	M0	No distant metastasis
	M1	Distant metastasis

Figure 2.2: TNM System

In Figure 2.3 [7], the stages of cancer are created, and in order to visually understand them, we can see in Figure 2.4 [5] a representation in the Colon.

TNM			
Stage 0	Tis	N0	M0
Stage I	T1	N0	M0
	T2	N0	M0
Stage IIA	T3	N0	M0
Stage IIB	T4	N0	M0
Stage IIIA	T1,T2	N1	M0
Stage IIIB	T3,T4	N1	M0
Stage IIIC	Any T	N2	M0
Stage IV	Any T	Any N	M1

Figure 2.3: Stages of Cancer According to TNM System

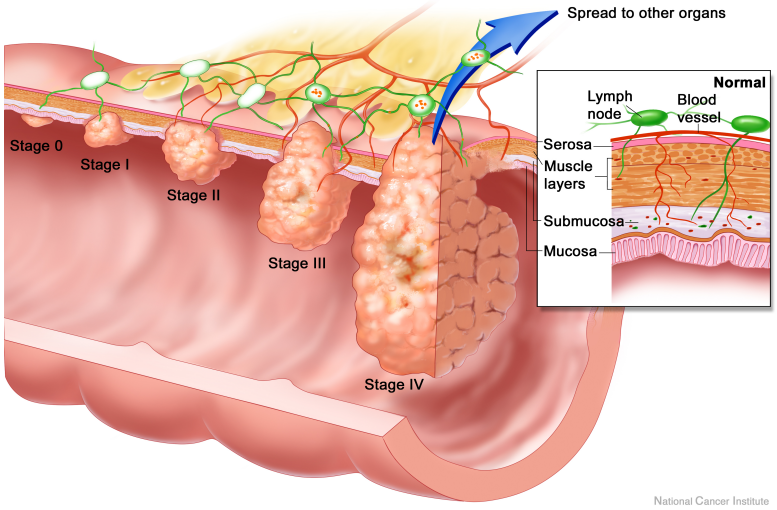

Figure 2.4: Different Stages of Colon Cancer

In the past decades, advances in the prognosis of the disease have resulted in a raise of five-year survival from 33% in 1970s to 55.3% in 1990s. It shows the importance of a good prognosis, not only to increase the five-year survival, but also, to help the development of new therapeutic modalities and a reliable preoperative stratification of high and low risk patients [11].

2.1.4 Treatment

The treatment for endometrial cancer is mostly surgery, hysterectomy, removal of both ovaries and both fallopian tubes, and sampling or removal of

surrounding lymph nodes, then radiation therapy [14]. For colon cancer are highly based on the stage, and for each one, different approaches can be used.

In Stages 0 and I, the cancer has not spread, so to remove it, two types of surgery can be made. Doing a polypectomy, the removal of the polyp or local excision through a colonoscope as shown in Figure 2.5 [28], or doing a partial colectomy, the removal of part of the colon, if the tumor is too big to be removed by local excision, in Figure 2.6 [29].

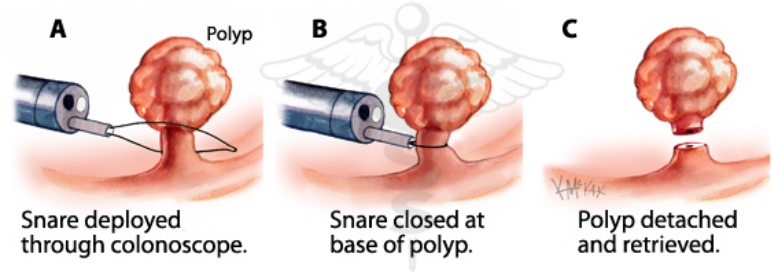

Figure 2.5: Polypectomy

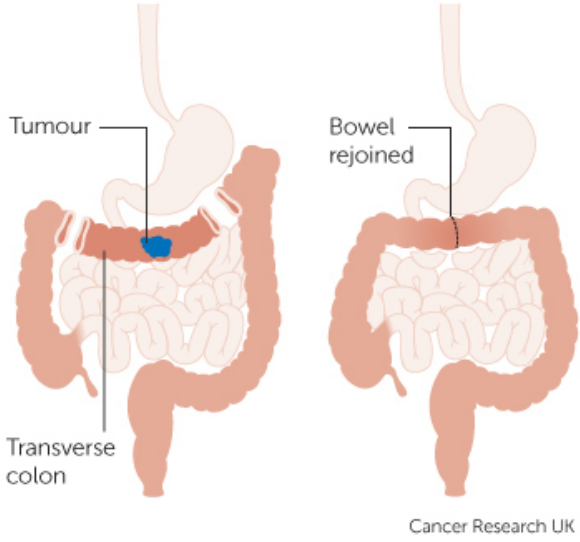

Figure 2.6: Partial Colectomy

Like in Stages 0 and I, many Stage II colon cancers have not yet spread to the lymph nodes, so a partial colectomy may be the only treatment needed.

However, in some cases may be used chemotherapy after surgery, if the cancer has a higher risk of coming back. It depends of certain factors: cancer looks very abnormal, it has grown into nearby blood or lymph vessels, the surgeon did not remove at least 12 lymph nodes, it was found in or near the edge of the surgical specimen, meaning that some cancer may have been left behind, it had blocked off obstructed the colon and it caused a perforation in the wall of the colon. In extreme cases, if the surgeon is not sure that all of the cancer was removed because it was growing into other tissues, radiation therapy may be used to try to kill any remaining cancer cells in the area where the cancer was growing.

In Stage III, the cancer has spread to nearby lymph nodes. Partial colectomy surgery to remove the section of the colon with the cancer along with nearby lymph nodes followed by adjuvant chemo is the standard treatment. In some cases, may also be used radiation therapy, to kill some cancer cells that might have been left behind after surgery.

In the last stage, Stage IV, the cancer has spread from the colon to distant organs and tissues. In most cases surgery is unlikely to be the solution. However, if there are only a few small areas of cancer spread, a partial colectomy to remove the cancer along with nearby lymph nodes, plus surgery to remove the areas of cancer spread, may help the patient to live longer or even cure him. Chemo can be given as well, before and/or after surgery. If the metastases cannot be removed, chemo may be given before any surgery. Then, if the tumors shrink, surgery to remove them may be tried. Chemo would then be given again after surgery. The interstitial brachytherapy, an internal radiation that uses a radioactive source that is put inside the body in or near the tumor [26], has been used on different kind of cancer, as tongue cancer [1], prostate cancer [12], gynecological malignancies [16], etc.

2.1.5 Glioblastomas

Glioblastomas are highly malignant tumors that arise from astrocytes, the star-shaped cells in the brain and spinal cord, or supportive tissue of the brain, that reproduce quickly and are supported by a large network of blood

vessels. Are generally found in the cerebral hemispheres of the brain, but can be found anywhere in the brain or spinal cord. Usually contains a mix of cell types and they are nourished by an ample blood supply and can be difficult to treat because of that. Dead cells may also be seen, especially toward the center of the tumor. Because these tumors come from normal brain cells, it is easy for them to invade and live within normal brain tissue. However, glioblastoma rarely spreads elsewhere in the body. Because glioblastomas can grow rapidly, the most common symptoms are usually caused by increased pressure in the brain and it represents about 15.4% of all primary brain tumors and about 60-75% of all astrocytomas. The first step of treatment is a procedure to make a diagnosis, relieve pressure on the brain, and safely remove as much tumor as possible through surgery. Because gliblastomas have finger-like tentacles, they are very difficult to completely remove. Radiation and chemotherapy may be used to slow the growth of tumors that cannot be removed with surgery. Chemotherapy may also be used to delay the need for radiation in young children [4].

2.2 Medical Images

Medical imaging is a rapidly expanding field. It started with X-rays, a type of radiation called electromagnetic waves. X-ray imaging creates pictures of the inside of the body, in different shades of black and white [21]. The next modality that appeared was ultrasonography, the visualization of deep structures of the body by recording the reflections or echoes of ultrasonic pulses directed into the tissues [22]. Since then, three-dimensional imaging of anatomical structures was made possible with Computed topography (CT) scan, a type of imaging that uses special x-ray equipment to make cross-sectional pictures of the body [19], and Magnetic Resonance Imaging (MRI) scan, uses a large magnet and radio waves to look at organs and structures inside the body [20].

2.2.1 Medical Images Analysis

Accurate segmentation of medical images is a key step in contouring during radiotherapy planning. CT and MRI are the most widely used radiographic techniques in diagnosis, clinical studies and treatment planning. Those images, are often stored in Digital Imaging and Communications in Medicine (DICOM) formats, a standard for handling, storing, printing, and transmitting information in medical imaging. It includes a file format definition and a network communications protocol [17].

Snakes Segmentation

Snakes are possibly the most popular curve evolution algorithm. A model that iteratively solve a partial differential equation (PDE), and make the curve or snake deforms its shape, to minimize internal and external energies. The internal component keeps the curve smooth, while the external component attaches the curve to image structures, such as edges, lines, etc. The SNAKE algorithm presented on [3], will be used in this work to identify the contour of structures.

Chapter 3

Algorithms and Implementation

To achieve the final goal of analyze the effects of radiotherapy, two sub tasks has to be complete, Figure 3.1. The first task: understand the difficulty of identify the boundary of each organ irradiated. Therefore, the first interface in Matlab, called "Interface Contour", was made. This interface allows the user to load a various number of CT or MRI scans and with a semi automatic tool identify the contour of a structure. Then, the implementation of the previous interface to a real case, identification and isolation of the glioblastoma, "Interface Glioblastoma". Finally, the second task: get the sub-segments of structures. The implementation of the interface "Segmentation of Bladder" and the adaptation to complex structures, like rectum and sigma-colon, in the interface "Segmentation of Rectum and Sigma-Colon".

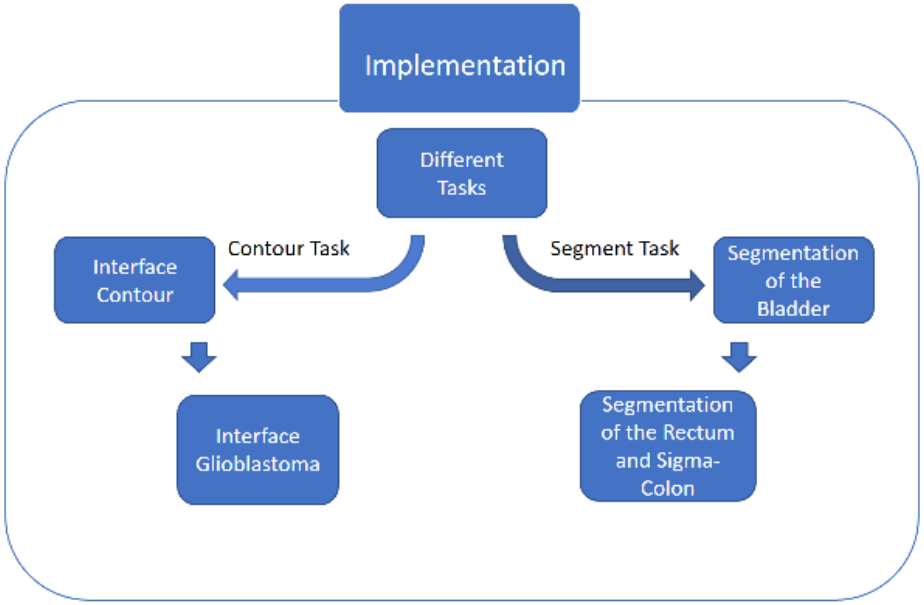

Figure 3.1: Pipeline

3.1 Interface Contour

This interface can be separated in three sections: reading and interpretation of DICOM files, execution of the SNAKE algorithm and results analysis.

3.1.1 Reading and Interpretation of DICOM files

The first section, as shown in Figure 3.2, contains two different tools, load the DICOM files and freely choose what image to see and work on. The "load" tool, search all DICOM files in the correspondent directory, as shown in the first block of code.

After that, a few transformations in the images, contained in those files, are made to make possible the visualization of them. This transformations are needed because of the plot limits of Matlab.

```
for i=1:numel(files)
 name=files(i).name;
 data_file=dicominfo(name);
 data_n=data_file.InstanceNumber;
 data_files{data_n}=data_file;
end
...
X = uint8(255 * mat2gray(img,[700 2500]));
Y=imadjust(X);
rgbImage = cat(3, Y, Y, Y);
```

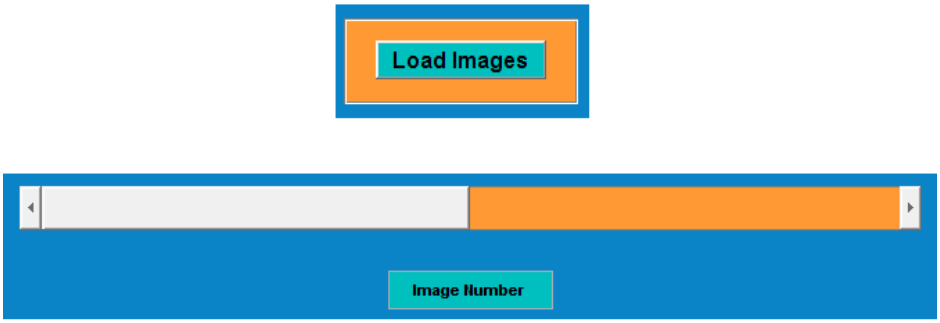

Figure 3.2: Load and Slider buttons and code

After that, the first image is represented, as shown in Figure 3.3, and the user can start contour the structure in the current image, and go forward or backward in the "slider" button.

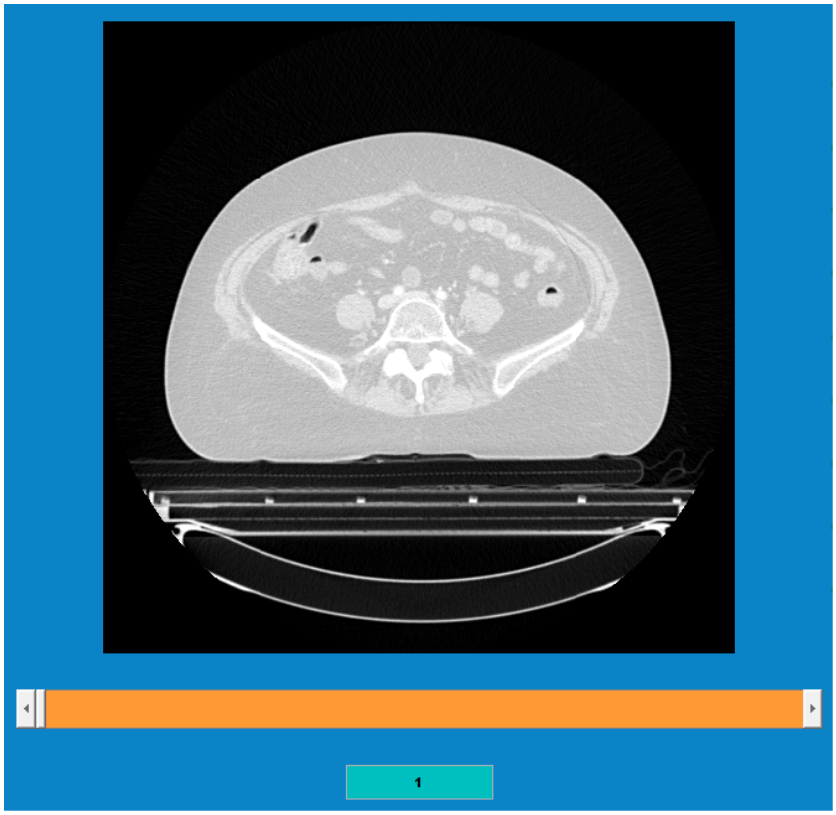

Figure 3.3: First Image

3.1.2 Execution of the SNAKE Algorithm and Results Analysis

In the Execution section, the user has to choose some points of the contour of the structure, as shown in the Figure 3.4 and Figure 3.5.

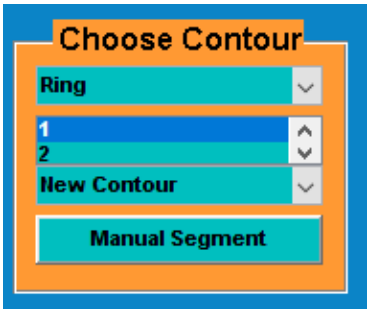

Figure 3.4: Choose Contour

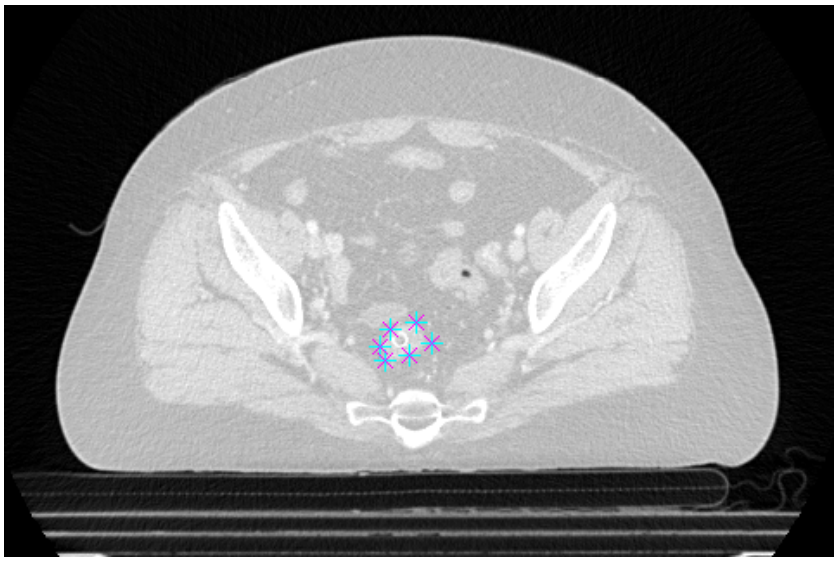

Figure 3.5: Example Points

The function implemented gets the points selected and saves them in a specific file, so the SNAKE Algorithm can find all the points of the boundary of the structure.

To do that, the user has to select the Standard, with the parameters already chosen, or the Personalized SNAKE Algorithm, and choose what value has each parameter. With this option, the user can get better results because of the variability of Medical Images, CT or MRI, and the position of the initial points selected, Figure 3.6.

```
fname0=sprintf('morphological_snake -I %s -O %s -C %s -F %s -S 1');
fname1=sprintf('-T 1 -N 200 -B -1 -E 1 -P 1');
...
instruction = [fname0,fname1];
system(instruction);
```

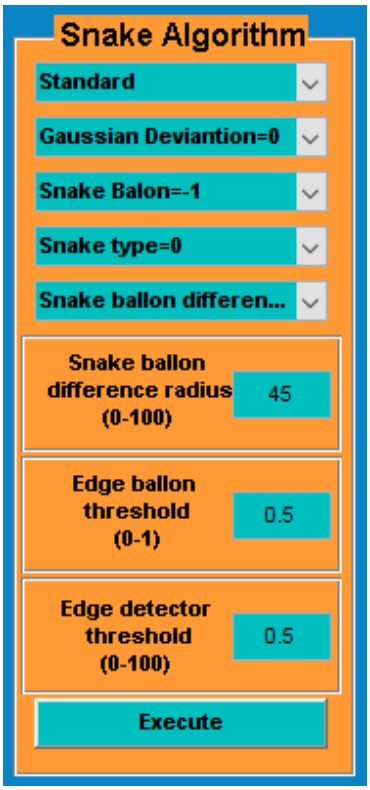

Figure 3.6: SNAKE Algorithm buttons and code

The function implemented, reads the files with the points and the image, and through solving, iteratively, partial differential equations (PDE), a smooth contour of the structure is found. The points of the new contour and the new image, with the contoured structure, are saved as shown in the code. The function, also creates a contour to be used in the next image, so the user doesn't need to choose points in every image. The analysis is done in each image and the contours are verified.

3.2 Interface Glioblastoma

With the first interface complete, a new idea and a new implementation have come. Use the contour tool in the analysis of Glioblastoma. So a new interface was made, Interface Glioblastoma. This interface is an adaptation of the first interface and can be separated in three sections too: reading and interpretation of DICOM files, execution of the SNAKE algorithm and results analysis.

3.2.1 Reading and Interpretation of DICOM files

The section of read and interpret the DICOM files is practically the same as previous interface, with some adjusts in the transformations on the images, because of type of DICOM files.

```
X = uint8(255 * mat2gray(img));
Y=imadjust(X);
```

3.2.2 Execution of the SNAKE Algorithm and Results Analysis

These too sections use the same concept as previous interface but also use an histogram classification. To do that, the user has to select in each image, three different samples, a necrosis sample, a ring sample and a external sample, as shown in Figura 3.7.

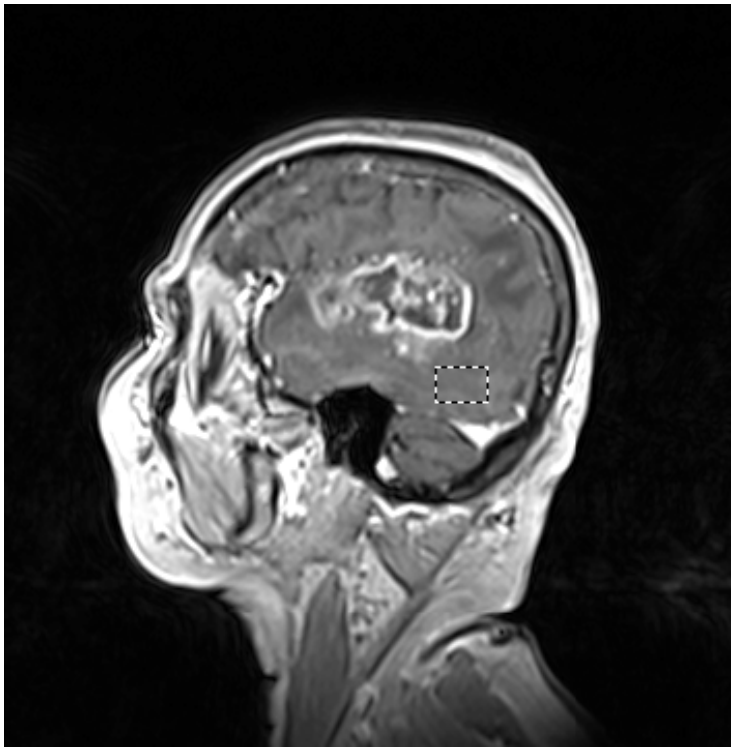

Figure 3.7: Example of External Sample

After contour every image, containing the tumor and his ring, and get multiple samples, the user has to execute two functions, "Transform Data" button, where a file with the contour in millimeters, the information if is the "ring" or the necrotic tissue and the grey value of the point. Then the function "Get Histograms", Figure 3.8, will create four histograms, one histogram of all the values inside the contours, and three containing samples of: "ring" tissue values, healthy brain values and necrotic brain values, and isolate the tumor in a new DICOM file.

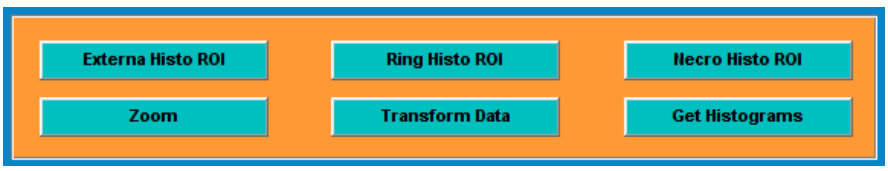

Figure 3.8: Histogram Buttons

A sub interface will open and with the help of the histograms, the user can choose values for the necrotic tissue and for the "'ring"' tissue, and for each image a classification is done. This tool, creates a new mat file, containing a matrix with the values that the user has chosen has threshold for the "ring" tissue and for the necrotic tissue.

3.3 Segmentation of the Bladder

To split in separated sections the organ, in this case, the bladder, the user as to select what organ. To do that, the first step was create a interface to get the structure from the DICOM RTSTRUCT file. This first interface is called, "Interface Get Structures".

3.3.1 Interface Get Structure

To select witch structure, first the user has to select the DICOM RTSTRUCT file, Figure 3.9. This function will read the file and interpret the values of the contours of each structure.

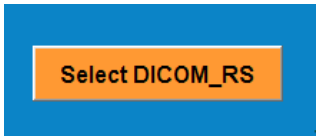

Figure 3.9: Select file button

As default, the first structure will appear. The user can change the number, and the name and contours of the correspondent structure will be represented, Figure 3.10 and Figure 3.11.

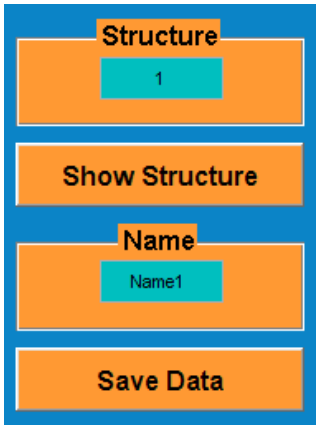

Figure 3.10: Select structure buttons - Bladder

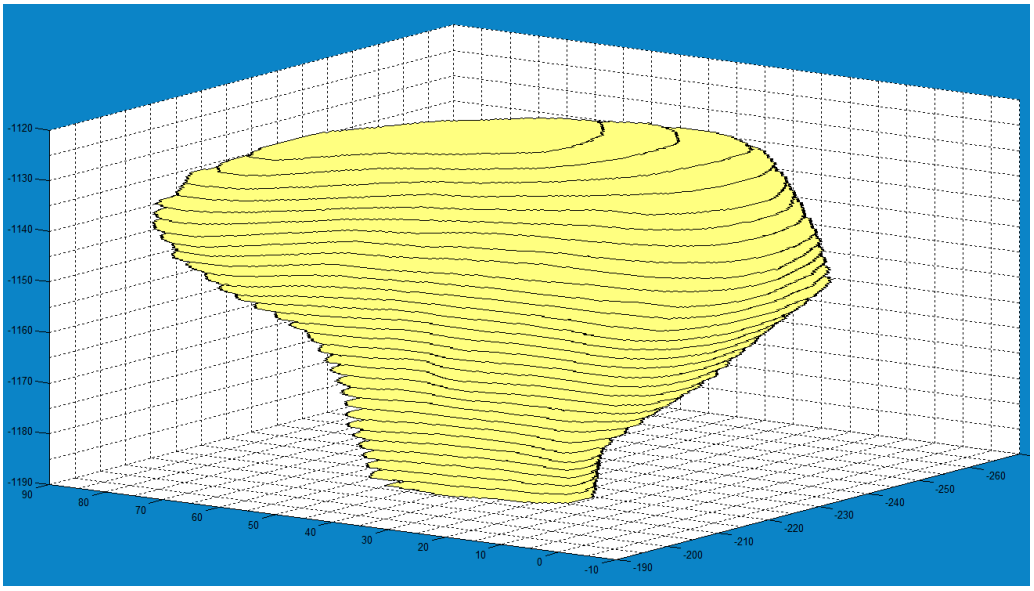

Figure 3.11: Example of Bladder structure

After find the pretended structure, the user has to save the data. This creates two mat files: one with all the points of the contours in a single matrix (n*3) and other with the contours of the structure in a cell.

Then, the user can start the segmentation of the structure by clicking in the "Segmentation Tool" button, Figure **??**. A sub interface will open, called: "Interface Segmentation", where the user will segment the structure.

Finally, to observe and save in a DICOM RTSTRUCT file the new segments obtained, the user has to click on the "Get Segments" button, Figure 3.12, where the code bellow will check every point of the new segments and create a readable DICOM file. These functions has to read and copy the information of the original DICOM RTSTRUCT file, and for each new point, check the original point and the original information attached to it.

```
...
DICOM_RS.RTROIObservationsSequence.(sprintf('Item_%d',l+i))=
 DICOM_RS.RTROIObservationsSequence.(sprintf('Item_%d',struc_1));
DICOM_RS.RTROIObservationsSequence.(sprintf('Item_%d',l+i)).ObservationNumber=l+i-1;
DICOM_RS.RTROIObservationsSequence.(sprintf('Item_%d',l+i)).ReferencedROINumber=l+i-1;
DICOM_RS.StructureSetROISequence.(sprintf('Item_%d',l+i))=
 DICOM_RS.StructureSetROISequence.(sprintf('Item_%d',struc_1));
DICOM_RS.StructureSetROISequence.(sprintf('Item_%d',l+i)).ROINumber=l+i-1;
DICOM_RS.StructureSetROISequence.(sprintf('Item_%d',l+i)).ROIName=
 sprintf('section_%d',i);
DICOM_RS.ROIContourSequence.(sprintf('Item_%d',l+i))=
 DICOM_RS.ROIContourSequence.(sprintf('Item_%d',struc_1));
DICOM_RS.ROIContourSequence.(sprintf('Item_%d',l+i)).ReferencedROINumber=l+i-1;
DICOM_RS.ROIContourSequence.(sprintf('Item_%d',l+i)).ROIDisplayColor=color;
DICOM_RS.ROIContourSequence.(sprintf('Item_%d',l+i)).ContourSequence=0;
...

while find==0 && k<=length(fieldnames(DICOM_RS.ROIContourSequence.
 (sprintf('Item_%d',struc_1)).ContourSequence))
 if DICOM_RS.ROIContourSequence.(sprintf('Item_%d',struc_1)).
  ContourSequence.(sprintf('Item_%d',k)).ContourData(3)
   ==data_contorns{j}(1,3)
  DICOM_RS.ROIContourSequence.(sprintf('Item_%d',l+i)).ContourSequence.
   (sprintf('Item_%d',j)).
   ContourImageSequence=DICOM_RS.ROIContourSequence.
   (sprintf('Item_%d',struc_1)).
   ContourSequence.(sprintf('Item_%d',k)).ContourImageSequence;
  find=1;
 end
 k=k+1;
end
...
x=data_contorns{1,j}(:,1);
y=data_contorns{1,j}(:,2);
z=data_contorns{1,j}(1,3);
num_points=length(x);
DICOM_RS.ROIContourSequence.(sprintf('Item_%d',l+i)).ContourSequence.
 (sprintf('Item_%d',j)).ContourGeometricType=ContourGeometricType;
DICOM_RS.ROIContourSequence.(sprintf('Item_%d',l+i)).ContourSequence.
 (sprintf('Item_%d',j)).NumberOfContourPoints=num_points;
DICOM_RS.ROIContourSequence.(sprintf('Item_%d',l+i)).
 ContourSequence.(sprintf('Item_%d',j)).ContourData=[];
for k=1:num_points
 DICOM_RS.ROIContourSequence.(sprintf('Item_%d',l+i)).ContourSequence.
  (sprintf('Item_%d',j)).ContourData=[DICOM_RS.ROIContourSequence.
  (sprintf('Item_%d',l+i)).ContourSequence.
  (sprintf('Item_%d',j)).ContourData;x(k);y(k);z];
end
...
```

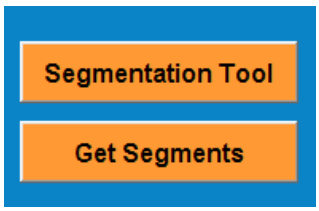

Figure 3.12: Segmentation Tool and Get Segments Buttons and code

Interface Segmentation

The sub interface allows the user the to choose the size, in millimeters, of each sub segment and where to start and end cutting. For that, all the points has to be loaded, Figure 3.13, and the user can freely move and analyze them using some plot functions of Matlab, Figure 3.14.

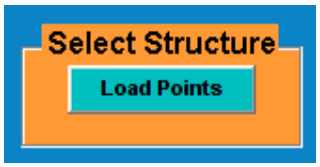

Figure 3.13: Load points button

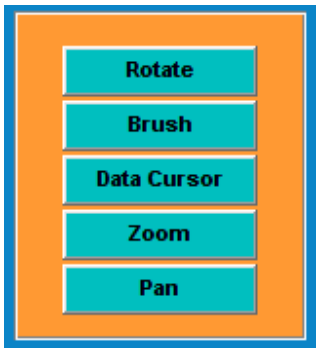

Figure 3.14: Plot Tools

As default, the cut distance is 10 mm, but it can be changed, Figure 3.15.

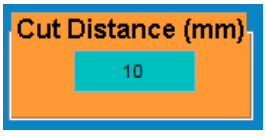

Figure 3.15: Cut Distance button

After analyze the points, the user can save the points of the structure that want to segment, choose the "start" and the "end" value in the longitudinal axis, creating a vector between the center of the contour in the "start" plane

and a mirror point in the "end" value, and then execute cutting, Figure 3.16 and Figure 3.17.

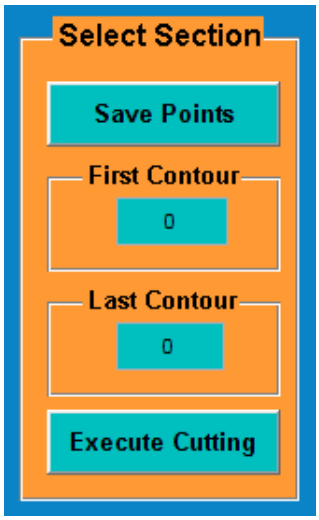

Figure 3.16: Select Section buttons - Bladder

The function is creating normal planes to the vector, with the cut distance previously chosen between them, and evaluate each points and witch planes limits them.

```
while avance<distance
 point=line(1,:,:)+unit_vector*avance;
 avance=avance+cut;
 plane_info=plane_info+check_plane(section_points,unit_vector,point);
end
info=[];
for i=1:length(section_points);
 info=[info;section_points(i,:) plane_info(i)];
end
...
plane=A*(x_p-point_x) + B*(y_p-point_y) -D + z_p;
...
```

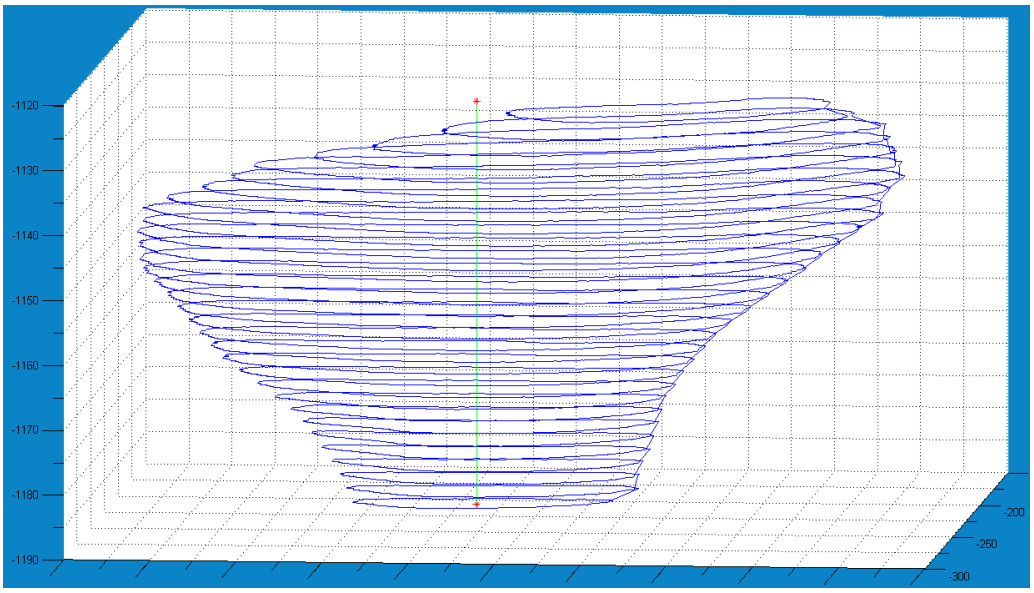

Figure 3.17: Example of points and vector - Bladder and code

Finally, the user just has to save the results, Figure 3.18. This function creates a mat file with all the points and the correspondent number of the new segment.

Figure 3.18: Save Results button

3.4 Segmentation of the Rectum and Sigma-Colon

After observe the good performance of the segmentation of the bladder, a new interface to segment the rectum and the sigma-colon was made. The complexity and mobility of this structures, make the automatic segmentation very difficult, so a semi-automatic way was made.

To split in separated sections both organs, rectum and sigma-colon, the user as to select them. To do that, the first step was create a interface to get both structure from the DICOM RTSTRUCT file. This interface is called "Interface Get Structures V2" and is an adaptation of the "Interface Get Structures" in the segmentation of the Bladder.

3.4.1 Interface Get Structures V2

Like in the "Interface Get Structures" this new interface use some of the functions, with few adaptations to work with two structures/organs instead of one. To select witch structures/organs, the user has to select the DICOM RTSTRUCT file. The function will read the file and interpret the values of the contours of each structure.

As default, the first and second structures/organs will appear. The user can change the number, and the name and contours of the correspondent structures/organs will be represented, Figure 3.19 and Figure 3.20.

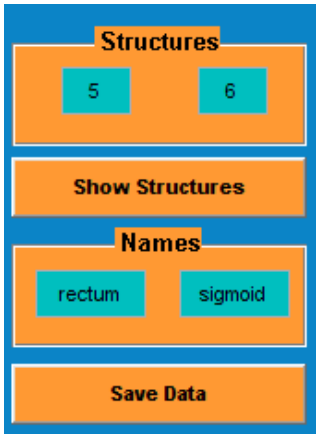

Figure 3.19: Select structure buttons - Rectum and Sigma-Colon

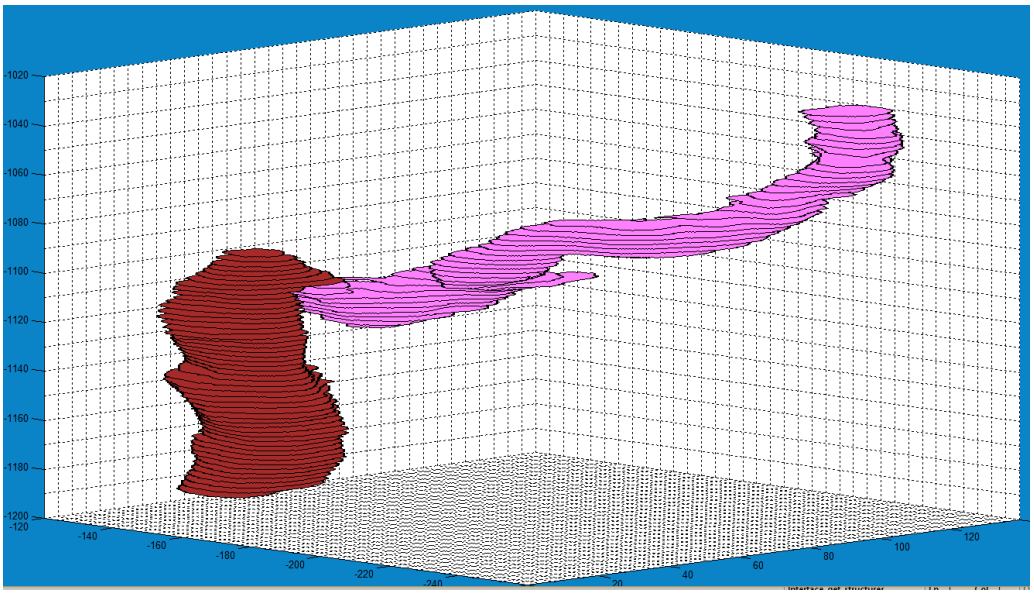

Figure 3.20: Example of Rectum and Sigma-Colon structures

After find the pretended structures/organs, the user has to save the data. This creates two mat files for each structure: one with all the points of the contours in a single matrix (n*3) and other with the contours of the structure in a cell.

To help the segmentation of complex structures like the sigma-colon, a new tool called "Interface Rendering" was created, Figure 3.21.

Figure 3.21: Rendering Tool - Rectum and Sigma-Colon

Then, the user can start the segmentation of the structure by clicking in the "Segmentation Tool" button, like in Figure **??**. A sub interface will open, called: "Interface Segmentation V2", where the user will segment both structures/organs.

Finally, to observe and save in a DICOM RTSTRUCT file the new segments obtained, the user has to click on the "Get Segments" button, like in Figure **??**, where multiple functions will check every point of the new segments and create a readable DICOM file. These functions have to read and copy the information of the original DICOM RTSTRUCT file, and for each new point, check the original point and the original information attached to it.

Interface Rendering

This new tool, tries to fill the spaces between two contours, by the creation of contours that should represent what is between the first two. With this new information and the better understanding of the structures will make possible a better segmentation. For that, the user as to load one structure at a time, Figure 3.22, and the selected structure will appear, Figure 3.23.

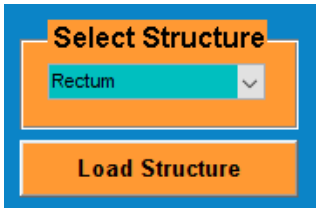

Figure 3.22: Select structure Button - Interface Rendering

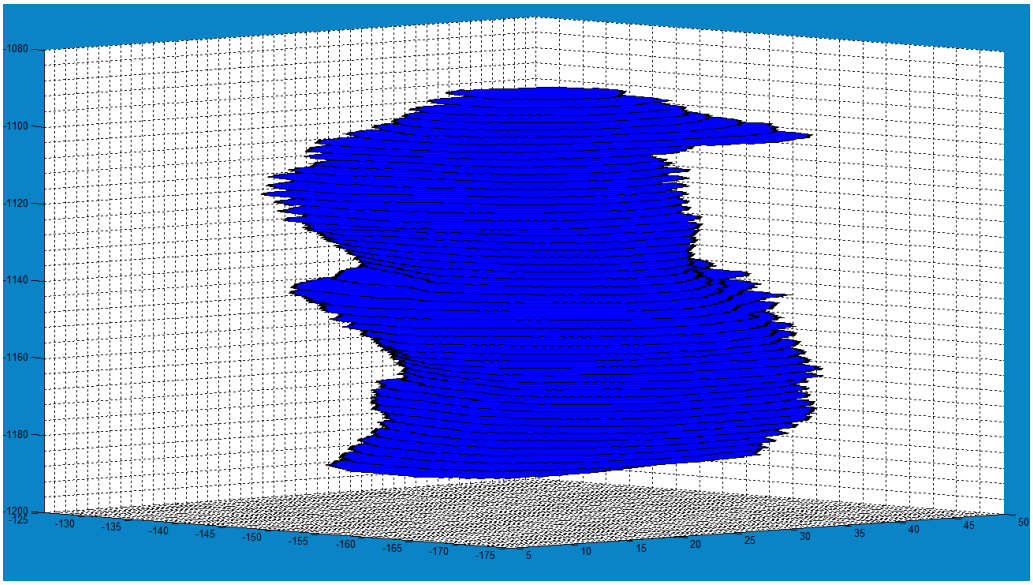

Figure 3.23: Structure Example - Interface Rendering

Then, the user has to analyze if in the same layer, same z value, has more then one contours. If has only one contour, the user use the "Normal Rendering", if not, use the "Multi Rendering", Figure 3.24.

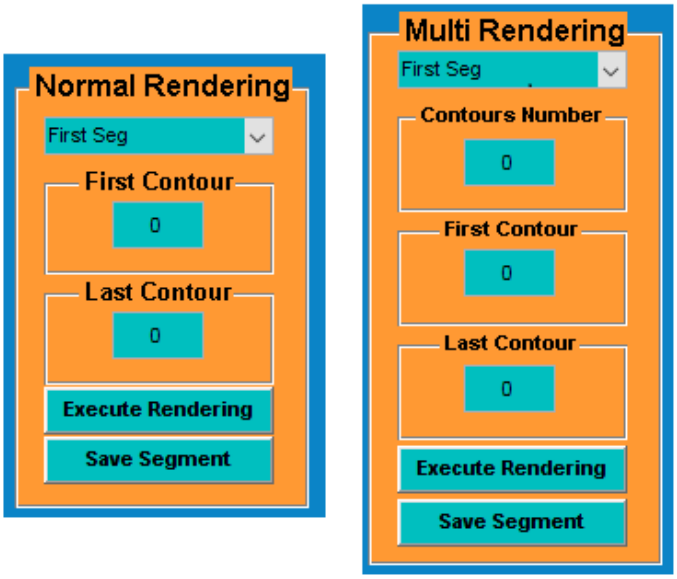

Figure 3.24: Normal and Multi Rendering Buttons - Interface Rendering

Using the equation (3.1), where the α is growing in each new contour, the algorithm creates new contours between two original contours, making the first closer and more similar to one of them and the last to the other.

$$x(j) = (1 - \alpha) * data_1(j, 1) + \alpha * data_2(j, 1); \tag{3.1}$$

In the "Normal Rendering", the algorithm starts in the beginning of the structure and between two existing contours, creates new ones, Figure 3.25.

```
for i=1:(length(new_data)-1)
 rend=normal_rendering(new_data,number_figures,i,i+1);
  ...
end
...
for i = 1: number_figures
  ...
  for j = 1: max_length
   x(j) = (1 - alpha)*data_1(j,1) + alpha*data_2(j,1);
   y(j) = (1 - alpha)*data_1(j,2) + alpha*data_2(j,2);
...
```

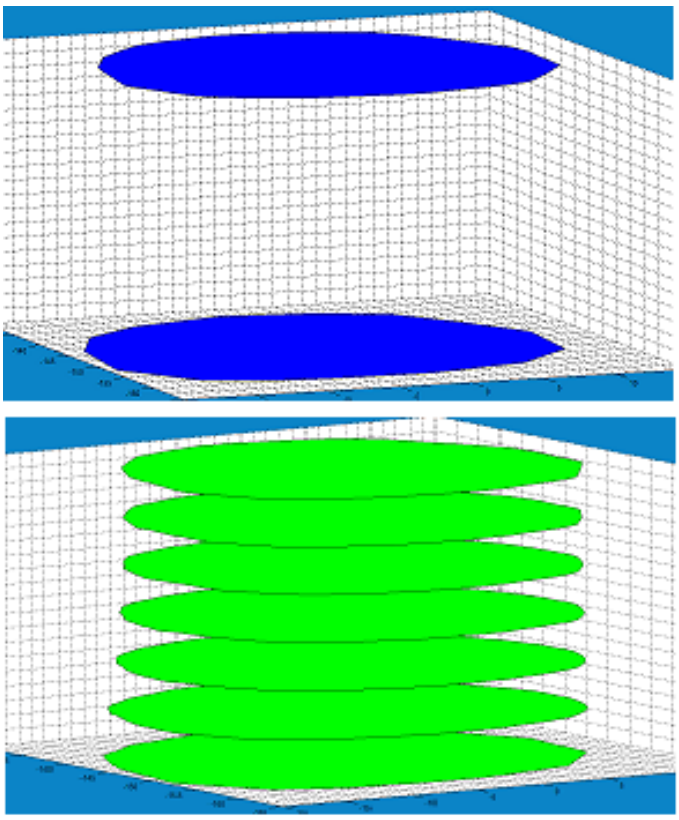

Figure 3.25: Normal Rendering Example - Interface Rendering and code

In the "Multi Rendering", the algorithm do the same thing, but for the multiples contours in the same z, it checks if the center of mass is inside the previous and next contour, creating the new contours only if this is valid, Figure 3.26.

```
if start_in_mult>1
 for i=1:number_multi
  if CDM(i,1)>min(data{start_in_mult-1}{1}) && CDM(i,1)<max(data{start_in_mult-1}{1})
   k=k+5;
   prov_data{1}=data{start_in_mult-1};
   prov_data{2}=new_data{i};
   rend=normal_rendering(prov_data,number_figures,1,2);
  end
...
while n_contorns_left>number_multi
 if check==0
  for p=number_multi:number_multi*2-1
   if CDM(i+p,1)>min(new_data{i}{1}) && CDM(i+p,1)<max(new_data{i}{1})
    k=k+1;
    rend_data{k}=new_data{i};
    prov_data{1}=new_data{i};
    prov_data{2}=new_data{i+p};
    rend=normal_rendering(prov_data,number_figures,1,2);
    ...
   end
  end
  check=1;
 else
  if number_multi-check>0
   for p=number_multi-check:number_multi*2-1-check
    if CDM(i+p,1)>min(new_data{i}{1}) && CDM(i+p,1)<max(new_data{i}{1})
     k=k+1;
     rend_data{k}=new_data{i};
     prov_data{1}=new_data{i};
     prov_data{2}=new_data{i+p};
     rend=normal_rendering(prov_data,number_figures,1,2);
     rend_data=[rend_data rend];
     k=k+6;
     rend_data{k}=new_data{i+p};
    end
   end
   check=check+1;
  end
 end
 i=i+1;
 n_contorns_left=n_contorns_left-1;
end
...
if end_in_mult<length(data)
 for i=0:number_multi-1
  if CDM(limit-i,1)>min(data{end_in_mult+1}{1}) && CDM(limit-i,1)<max(data{end_in_mult+1}{1})
   prov_data{1}=new_data{limit-i};
   prov_data{2}=data{end_in_mult+1};
   rend=normal_rendering(prov_data,number_figures,1,2);
   rend_data=[rend_data rend];
   if last_add==0;
    rend_data{k}=data{end_in_mult+1};
    last_add=1;
...
```

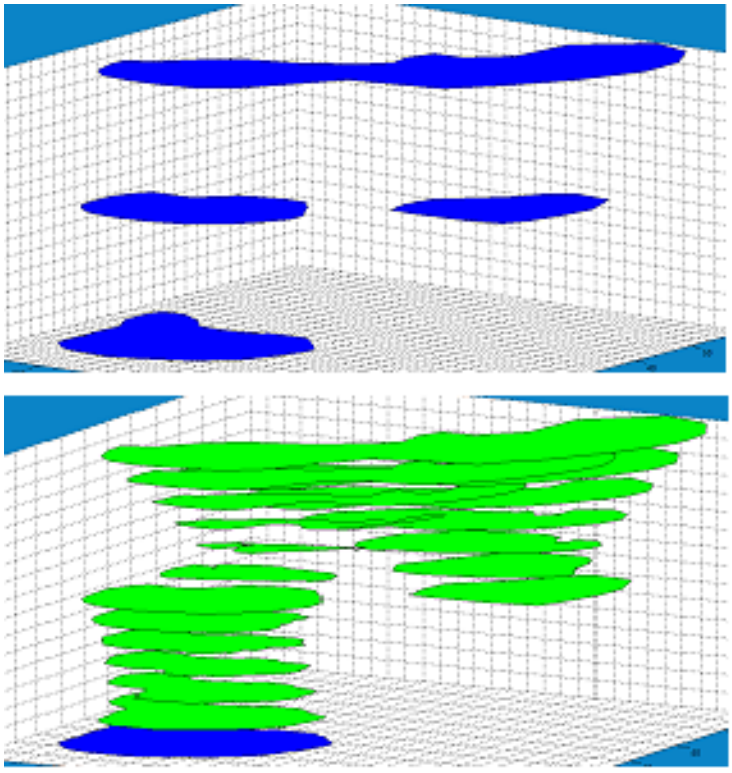

Figure 3.26: Multi Rendering Example - Interface Rendering and code

Interface Segmentation V2

To load the points like in the "Interface Segmentation", the user just has to press the "Load Points" button, like in Figure 3.13, but in this case, this function will load all the points of two different structures and get the center of mass of all the counters obtained in the "Interface Rendering". Also, the user can freely move and analyze them using some plot functions of Matlab, like in Figure 3.14.

As default, the cut distance is 10 mm, but it can be changed, like in Figure 3.15.

Because of the complexity that this structures can have, two ways of segment were created. For normal sections, where the structure only "grows" in the vertical, the user do the same thing that in the "Interface Segmentation" and choose if wants to use previous cut distance, Figure 3.27. The previous cut distance works to be sure that all the segments have approximately the same size. For example, if the last segment of a section has only two millimeters, the first segment of the next section will be joined.

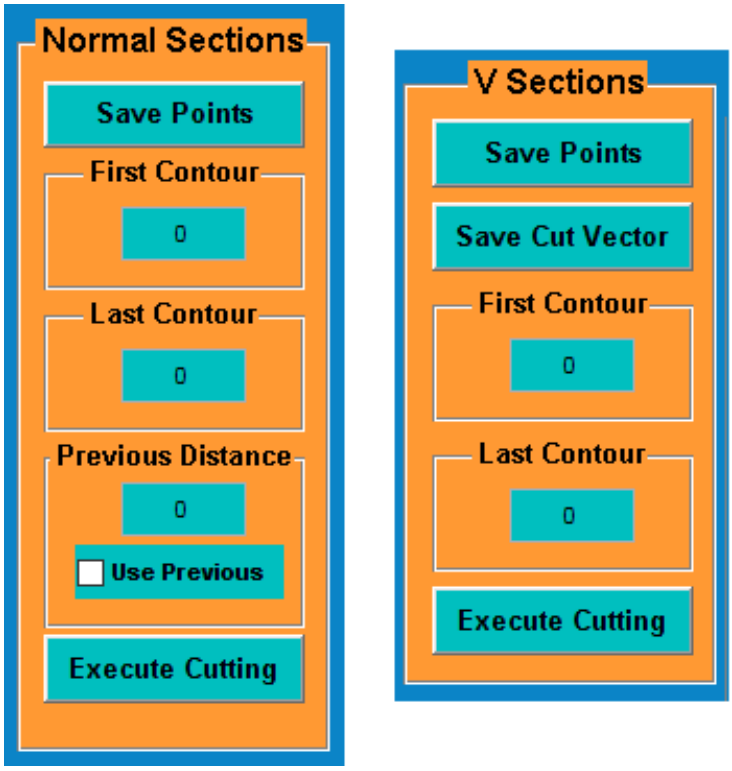

Figure 3.27: Normal and V Sections buttons - Rectum and Sigma-Colon

For the sections that change their "growth" direction, the user has to choose the "start" and the "end" value in the longitudinal axis, and select two points, that will create two vectors between the center of mass of the contour in the "end" plane and them. The function will create a plane that contains them and evaluate each point of the section, Figure 3.28

```
vector1=[line1(1,1)-line1(2,1) line1(1,2)-line1(2,2) line1(1,3)-line1(2,3)];
vector2=[line2(2,1)-line1(2,1) line2(2,2)-line2(1,2) line2(2,3)-line2(1,3)];
vector=cross(vector1,vector2);
l=length(section_points);
plane_info=zeros(l,1);
plane_info=plane_info+check_plane(section_points,vector,line1(1,:));
```

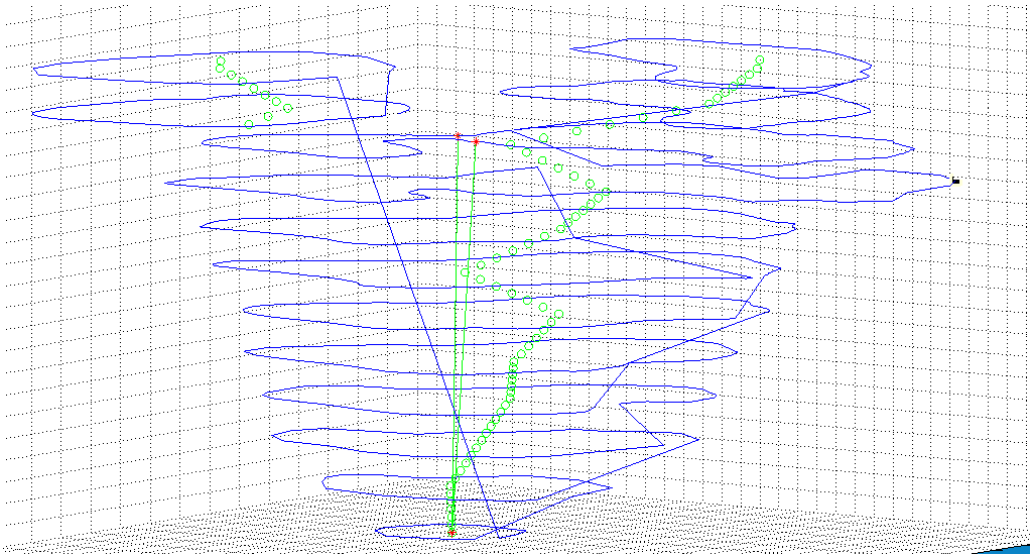

Figure 3.28: Example of points and vector - Rectum and Sigma-Colon and code

Finally, the user just has to save the results, like in Figure 3.18.

Chapter 4

Results

4.1 Problem analysis

The first problem was to understand the difficulties of identifying contours, and for this, the contours of various structures, bladder, colon, rectum, of different passions were identified. In the next section, are some of the results and relevant observations. Then, the good performance of the algorithm made possible a new experiment. Identify and isolate glioblastomas of different patients. Finally, the segmentation in sub-segments of structures, first the bladder, and then the rectum and sigma-colon of different patients are explained in the two last sections of this chapter, and an example of the analysis of the radiation of those sub-segments.

4.2 Interface Contour

The objective of this interface is a better understanding of the difficulties of identify the contour of structures and try to create a semi automatic tool to identify them. Because of the complexity of the structures in some cases its hard to get a valid contour, but this tool with few points in the edge of a structure, can indentify its contour.

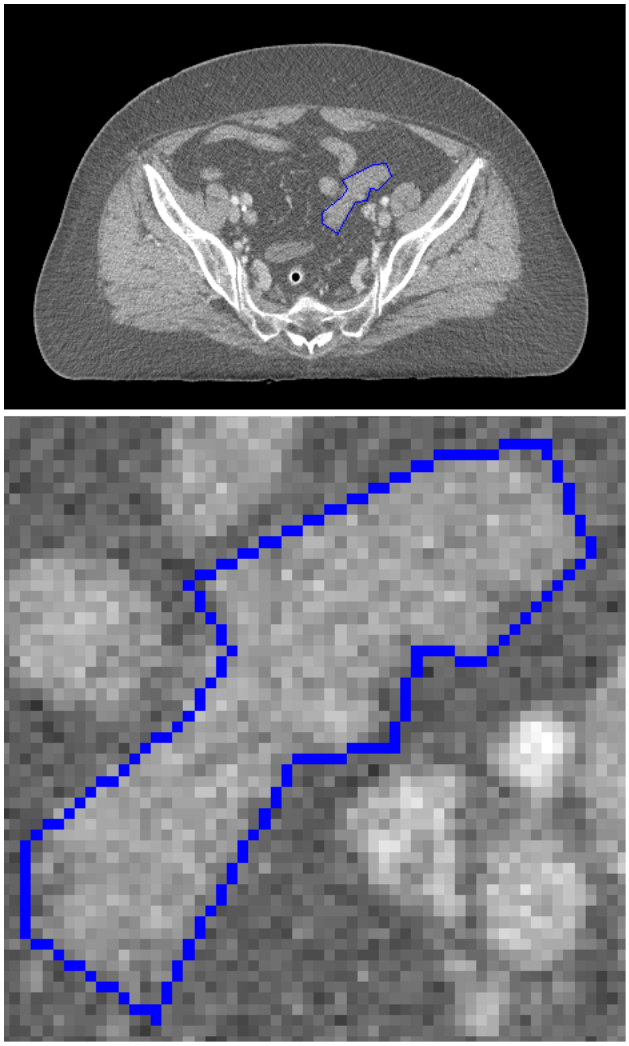

Figure 4.1: Manual Segmentation Ima. 32 - Interface Contour

In Figure 4.1, few points of a complex structure were marked, twelve in total, and with the execution of the SNAKE Algorithm, all the points of the contour were found, Figure 4.2.

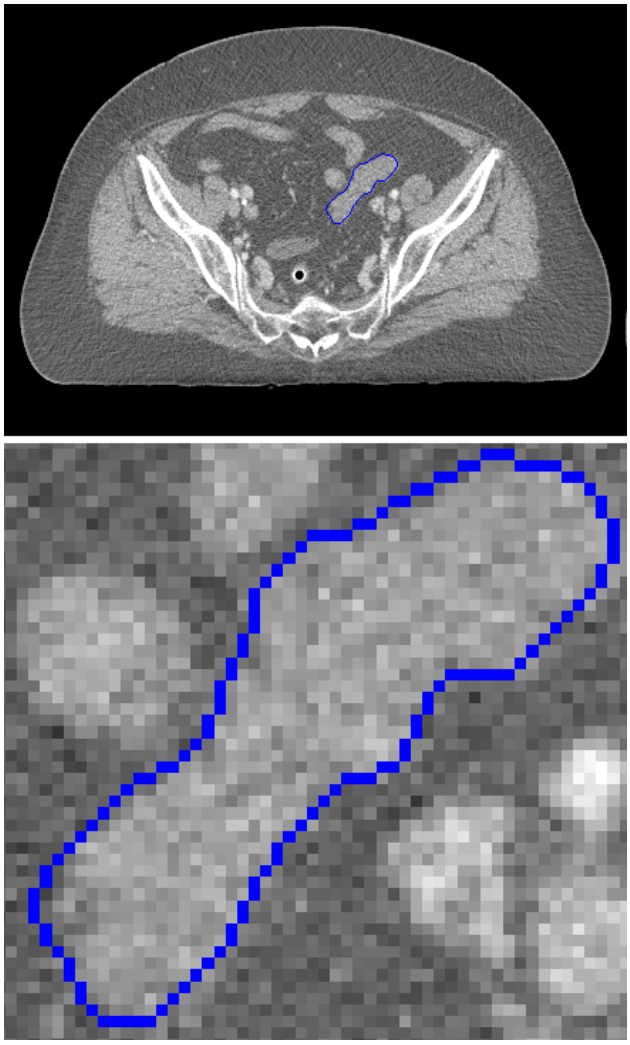

Figure 4.2: SNAKE Result Ima. 32 - Interface Contour

In some cases, using the previous SNAKE contour, Figure 4.2, does not give the best result. One of the reasons is because of the slice thickness, in this case, two millimeters between each CT images, making impossible to the algorithm found the contour, as shown in the lower left corner of the zoomed image, Figure 4.3.

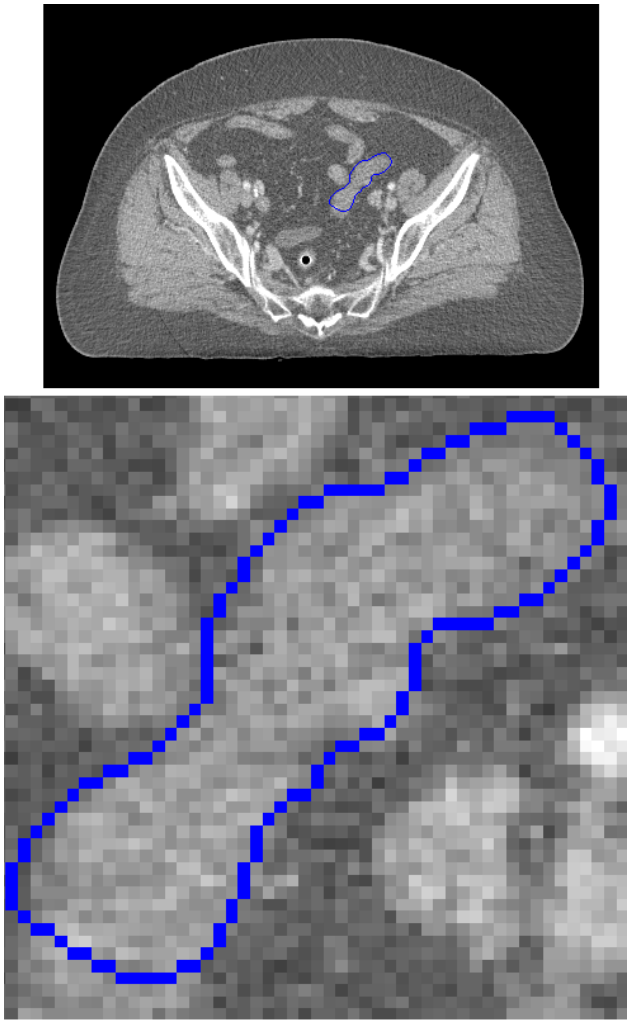

Figure 4.3: SNAKE Result Ima. 33 - Interface Contour

In those cases the user just has to do a new manual segmentation.

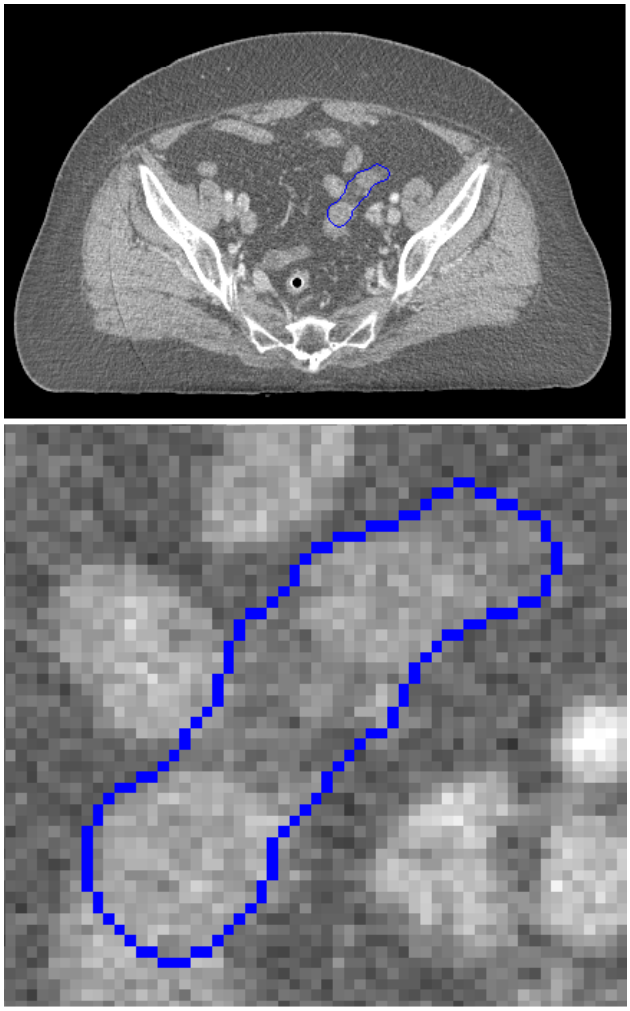

Figure 4.4: SNAKE Result Ima. 34 - Interface Contour

Other thing that can happen is that the struture has sparated parts, Figure 4.4, in those cases, the user has to do two or more manual segmentations, Figure 4.5, and the execute the SNAKE Algorithm again, Figure 4.6.

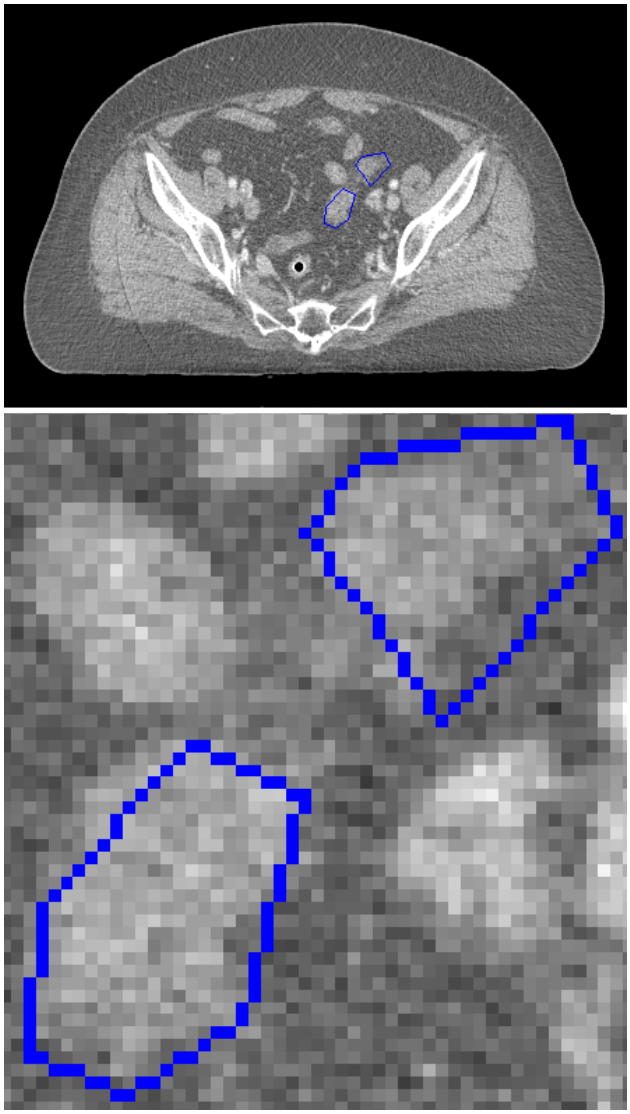

Figure 4.5: Manual Segmentation Ima. 34 - Interface Contour

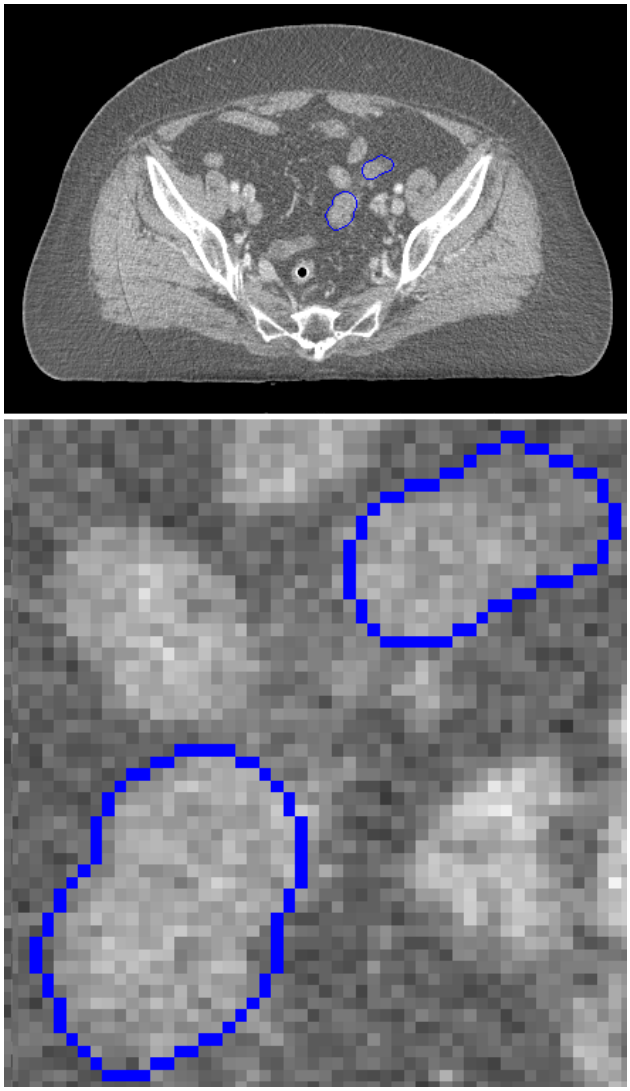

Figure 4.6: New SNAKE Result Ima. 34 - Interface Contour

4.3 Interface Glioblastoma

The purpose of this interface is to use the tools of the previous interface in a practical case, such as the isolation of a tumor, in this case a glioblastoma, had the same difficulties of the previous interface, however, the solutions to those difficulties are the same. Therefore, in Figure 4.7, an example of a successfull isolation of the tumor was made.

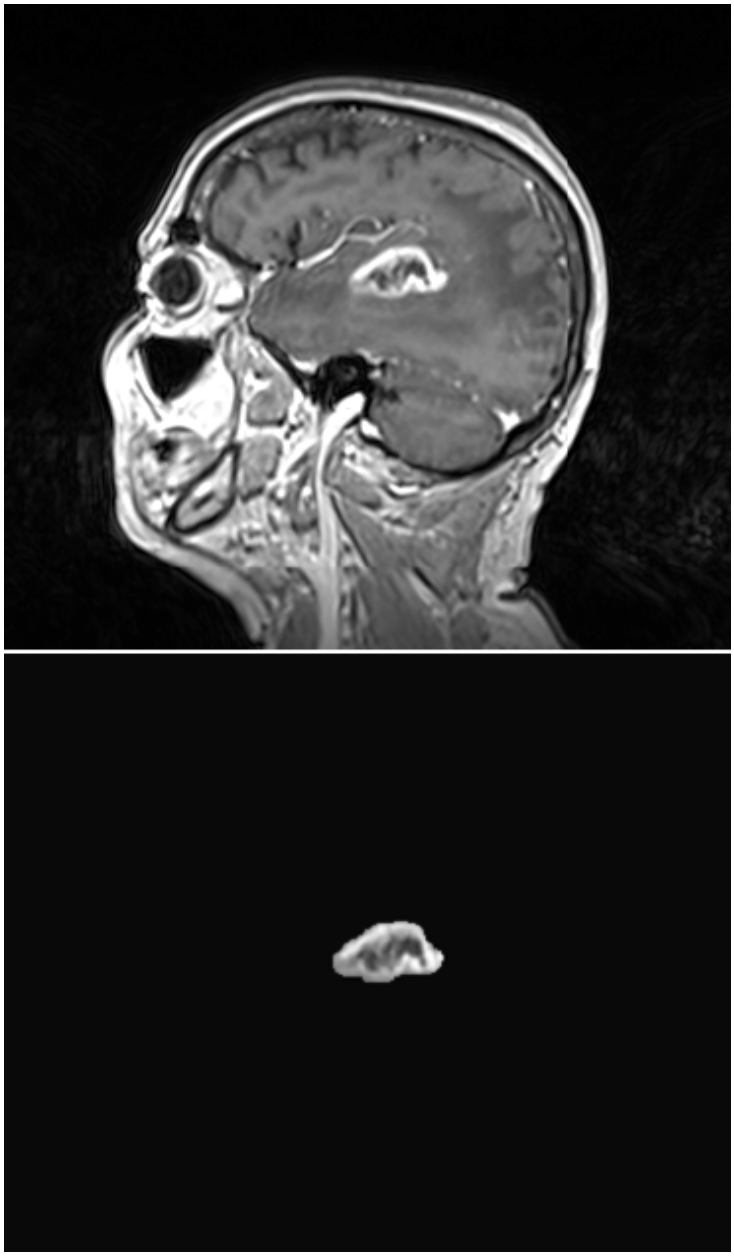

Figure 4.7: Isolated Tumor - Interface Glioblastoma

With the tumor isolated, and with samples of healthy brain, necrotic brain, and the "ring" tissue of the tumor, the information obtained in the histograms, Figure 4.8, allows the identification of the window values of each one of them.

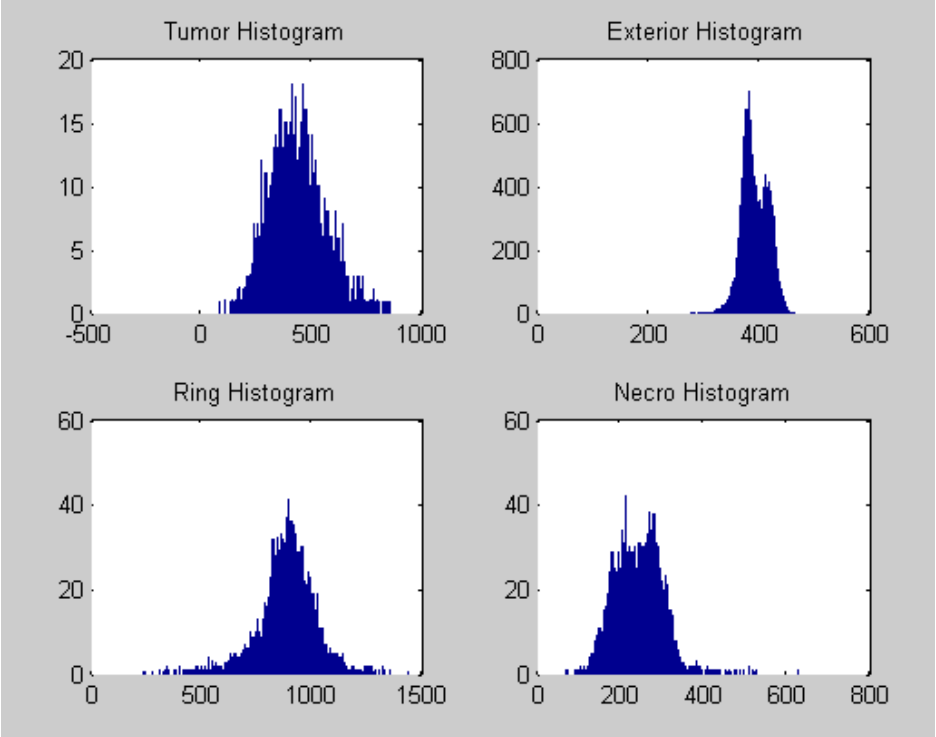

Figure 4.8: Histograms - Interface Glioblastoma

That identification will allows a more detailed study of the tumor, for example: thickness of the "ring" tissue, thickness of necrosis tissue and evaluate the evolution of the tumor.

4.4 Segmentation of the Bladder

The main objective of this interface is get a DICOM RTSTRUCT file with sub segments of a struture. The first task of the segmentation was load and select the structure and then create the new segments. This task is done to the exploration one, Figure 4.9 and then to exploration two, Figure 4.10.

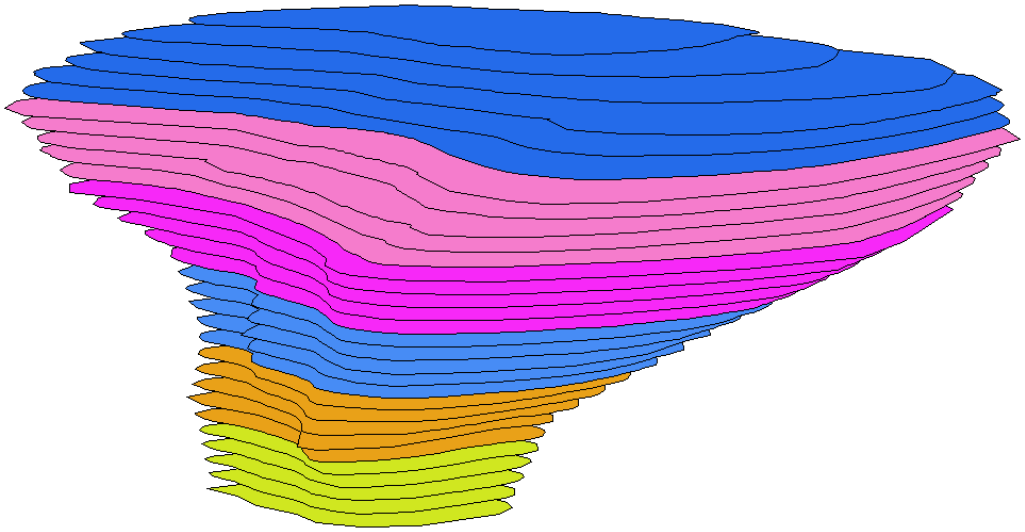

Figure 4.9: Exploration One - Interface Bladder

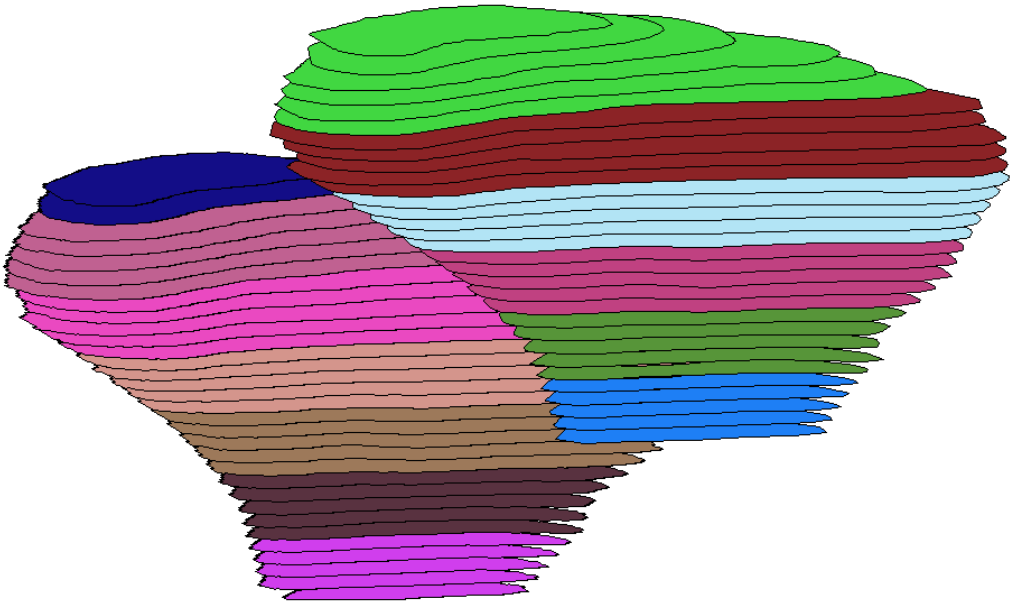

Figure 4.10: Both explorations - Interface Bladder

The comparison of both explorations is very important, because of the mobility of the structure. In this case, is possible to say that small changes

ocurred, and that the blue segment of the structure in the right, is practically the same that the lower pink segment of the structure in the left.

After import a DICOM RTSTRUCT file and analise the information on it, was possible to copy and create new DICOM RTSTRUCT, adding more information without damaging it. These task was the most important, because the final objective was reintruduce the DICOM RTSTRUCT file in the hospital platform of radiotherapy analysis (Oncentra). For that, all the information of each contour and each correspondent image had to be in the new file.

The information that Oncentra give, is the amount of radiation that each adjacent structure received. In Table 4.4 is the information in the first day of radiotherapy, where the most important is the two cubic centimeters more irradiated.

Table 4.1: Dose Volume Histograms (DVH) - Original

Structure	Dose [%]	Dose [Gy]	Volume [%]	Volume [ccm]
Bladder	108.07	7.5652	1.70	2.00
Bladder	147.52	10.3265	0.08	0.10
Bladder	14.05	0.9833	100.00	117.99
Rectum	68.03	4.7622	3.54	2.00
Rectum	91.55	6.4086	0.18	0.10
Rectum	12.05	0.8432	100.00	56.47
Sigmoid	39.55	2.7688	4.42	2.00
Sigmoid	54.67	3.8267	0.22	0.10
Sigmoid	2.00	0.1400	100.00	45.27

However, this information does not give the location of the tissues that are being more damaged, and if is a structure that changes his volume and position, in the next radiotherapy treatment, these tissues may not be at risk. That said, with the segmentation of the structure, a more detailed information can be obtained, Table 4.4.

Table 4.2: Dose volume Histograms (DVH) - New Sections

Structure	Dose [%]	Dose [Gy]	Volume [%]	Volume [ccm]
$Section_2$	58.59	4.1010	27.82	2.00
$Section_2$	82.71	5.7898	1.39	0.10
$Section_2$	26.78	1.8744	100.00	7.19
$Section_3$	77.04	5.3927	13.95	2.00
$Section_3$	115.59	8.0911	0.70	0.10
$Section_3$	20.48	1.4339	100.00	14.34
$Section_4$	89.26	6.2483	7.88	2.00
$Section_4$	139.46	9.7619	0.39	0.10
$Section_4$	14.25	0.9975	100.00	25.39
$Section_5$	82.42	5.7693	7.03	2.00
$Section_5$	135.45	9.4815	0.35	0.10
$Section_5$	14.01	0.9806	100.00	28.46
$Section_6$	53.42	3.7391	13.07	2.00
$Section_6$	82.96	5.8075	0.65	0.10
$Section_6$	14.08	0.9853	100.00	15.30

After analyse the data, the doctor can say which segments are more affected by radiation, and doing the same study for the new exploration, can predict if the same segments will be affected again or not. In this case, is possible to observe that the $Section_1$ was not detected. One of the possible reasons is the need of anonymize all the data, that might corrupt the file.

4.5 Segmentation of the Rectum and Sigma-Colon

This last interface has the objective of improve the previous one to have the ability of make sub segments of multiple structures, in this case, the Rectum and Sigma-Colon. Like in the Segmentation of the Bladder, first one exploration was segmented, Figure 4.11 and then both of them, Figure 4.12

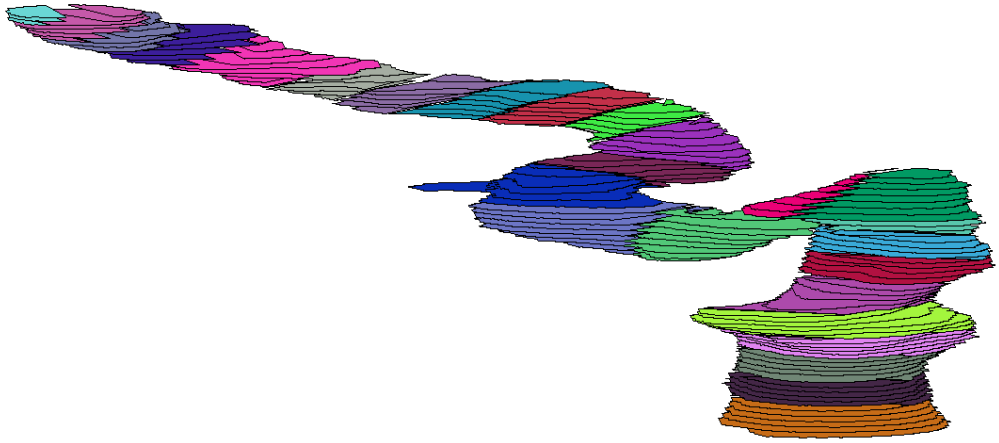

Figure 4.11: Exploration One - Interface Rectum and Sigma-Colon

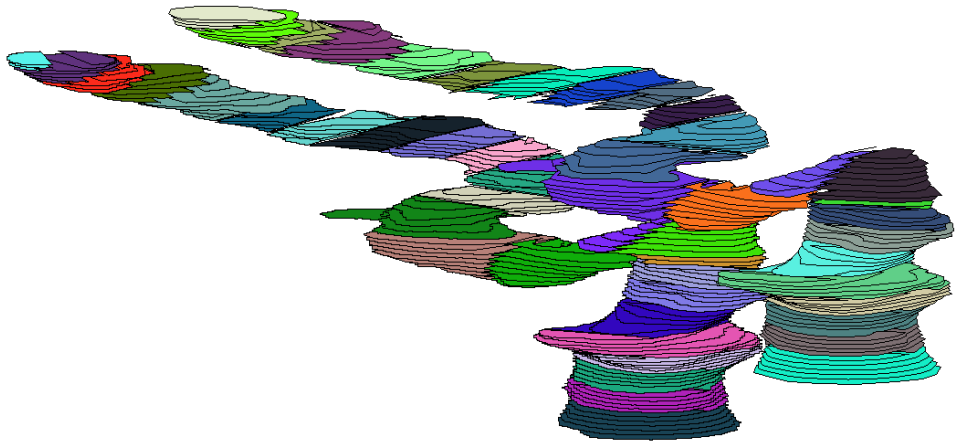

Figure 4.12: Both Explorations - Interface Rectum and Sigma-Colon

In this case, because of the complexity of the structures, the sub segments have some errors. One of the reasons is the fact that some contours of the DICOM RTSTRUCT file has only few points. As shown in Figure 4.13, the same structure, square A, can be defined by a lot of points, square B, or only for a few, square C, but in fact they are the same structure. However, this

makes the segmentation more difficult, mainly in the "V sections", Figure ??.

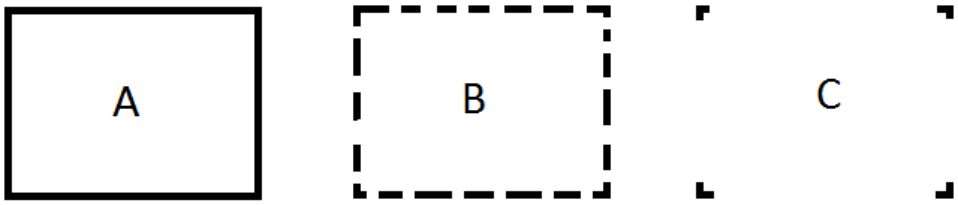

Figure 4.13: Example of contours - Interface Rectum and Sigma-Colon

Chapter 5

Conclusions

The objective of divide structures in sub-segments, allowing a better analysis of the radiation in the treatment of cancer, was fulfilled. This objective was validated by Doctors experts in the field. The medical image processing can help in time consuming tasks, such as the identification and contouring of structures, as demonstrated successfully in the Interface Contour and Interface Gliobastoma. The first step to the final goal was made with the implementation of these two interfaces and the Interface Glioblastoma can be a helpfull tool to make a more detailled study of Glioblastoma Multiform. The final goal of divide structures in sub-segments was made with the implementation of the Segmentation of the Bladder interface. This interface has the limitation that only suports simple structures like the Bladder, and because of the need to anonymize all the data, some data corruption can ocurred. Finnaly, in the trying of get the sub-segments of complex structures, like Rectum and Sigma-Colon, is possible to observe that the algorithm has some limitations and to resolve them, a new contouring has to be done.

5.1 Prospect for Future Work

The Interface Glioblastoma could be improved through multiple studies to find generic threshold values for all tumors. The Interface Contour can be used to create DICOM RTSTRUCT files with the semi automatic contours,

always with the supervising of the experts, what might be the solucion to the problem of the "'V sections"' in the Segmentation of the Rectum and Sigma-Colon and with the number of points per contour resolved, a new segmentation could be possible and the analysis of the radiation could be done.

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