

Comparison of Software for Medical Segmentation

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Abstract—Modern medicine cannot do without the use of computer technology. For the processing of image data in medicine, multiple procedures and one of them are medical data segmentation. In this paper, we focus on an overview of individual medical image processing techniques, and the application of image processing algorithms in tools used in medicine.

Keywords—segmentation, medical data, software tool, 3d models

I. INTRODUCTION

More and more industries see a better future with more computing. They are also fully aware of this fact in the field of medicine. Medical software is increasingly helping doctors work. It is an effective tool for teaching new doctors, but also for diagnosis. It also helps in training heavy interventions on the human body. Because the human body is very sensitive, and misconduct might have fatal consequences, emphasis is placed on displaying 3D models of the human body as closely as possible. At present, there are tools that can create 3D models with millimeter accuracy. However, getting this model is not easy.

Creating a 3D model is preceded by getting data. The most common apparatus for obtaining images are CT, MRI, X-ray and PET instruments. These tools provide 2D images in various file formats. Various algorithms for image data segmentation are used to obtain the 3D model. In the work, we present a few basic principles of segmentation.

The principles are further implemented and concrete implementations of segmentation algorithms are created. These are implemented in multiple successful medical tools that are freely available to the general user, so we will not focus on implementing them, but comparing the resulting 3D models.

To evaluate 3D models, we will set up an evaluation methodology that will focus on evaluating the tools we will work with and the visual results of segmentation algorithms.

II. 3D SEGMENTATION OF MEDICAL DATA

Nowadays, with high-quality data processing technologies, various methods for 3D tissue reconstruction are widely used in the medical field. One of the essential parts of treatment is not only diagnosis but also the determination of targeted therapy. On this basis, increasing emphasis is now being placed on planning treatment using accurate navigation of the therapeutic tool, or by setting the patient's position directly based on reconstructed CT or MRI data. At the same time, care is taken to minimize and optimize damage to healthy tissues in the patient.

The process of creating a 3D model requires not only CT data but also depth information. Various tools such as depth cameras and laser are used to obtain this information. This information can then create a depth map. Thus, the depth map is a set that content the spatial position of individual points in a three-dimensional scene. The complexity of 3D tissue reconstruction is mainly due to the complexity of the human body, which consists of different

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structures with irregular shapes and sizes. The problem also arises when the human body contains foreign bodies that appear in images. These are, for example, implants or metal plates. For 3D data reconstruction, one of the following methods can be used:

1. Surface reconstruction
2. Bulk reconstruction

A. Surface Reconstruction

The density threshold is selected by the physician itself (e.g., selects the density that corresponds to the bone density). Thus, we can create multiple 3D models in which we display bodies based on different thresholds, i.e. Each type of tissue displays different color because bone, muscle or even cartilage have different density. The 3D data then searches for edges and points of the surface. Of these, the surface is interpolated by two-dimensional patches.

B. Bulk Reconstruction

Compared to the surface, the volume reconstruction is not limited by the display of the surfaces themselves. With this kind of reconstruction, the transparency and colors are used to illustrate the better volume in the images. This allows e.g. the pelvic bone appears as semi-transparent or even at an oblique angle.

In the first step, 3D reconstructions of medical data are looking for points that are uniquely identifiable between multiple input data (multiple images). Subsequently, the key points are paired within each segment. This includes calculating 3D coordinates of points from found correspondences. The next step is to create a 3D model and edit it (clean holes). The creation process can be seen in Fig. 1 [1].

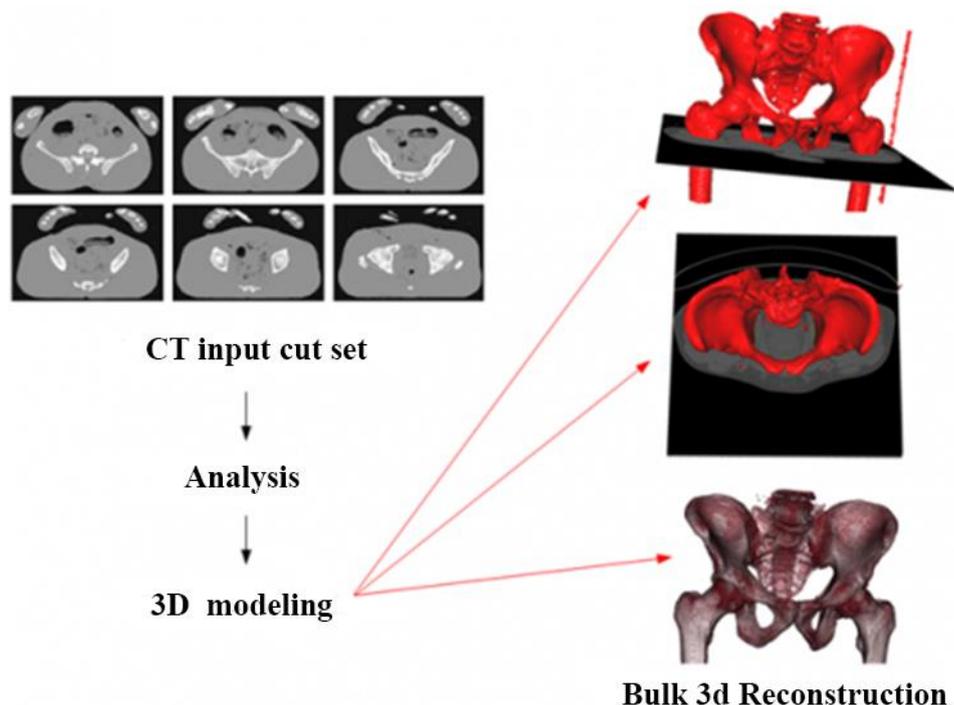


Fig. 1 The procedure for 3D data reconstruction [1]

III. DATA RETRIEVAL APPARATUS

The first step in creating a 3D model of a human body from medical image data is to obtain it. Various medical devices exist to create these data. In this section we will describe some of the basic devices for these purposes.

Nowadays, the processing of medical data has more and more possibilities due to rapid technology development as well as the advancement of digitalization of information in the world.

In medicine, the worldwide DICOM standard is used for data storage [2]. There are currently several devices that can display image information from the human body.

The most common are X-ray machines, computer tomography, ultrasound devices, as well as magnetic resonance imaging. X-ray machines produce images that are flat and cannot be seen on either the front, the middle, or the back. This problem of spatial imaging has been improved by computer tomography. The human body will be taken from different distances in a row, and thus we can determine the arrangement of individual organs in space. As a result, the human body can be seen from the side, from the front and from the top downwards [3].

A. *Techniques for obtaining flat images*

Among the best-known X-ray techniques that enable a flat image to be obtained are Skiaskopia and Skiagrafia. Skiaskopy is a radiological examination method that uses X-rays to record a three-dimensional object in a two-dimensional image. Created images are projected in real time, which means that it works as a camera that uses X-rays to display it. The main drawback of this imaging method is a higher radiation load. It is mainly used in the investigation of the gastrointestinal tract, but has significantly decreased its importance by the onset of computed tomography and magnetic resonance.

Skiagraphy or even imaging is a basic radiological imaging method that uses X-rays to photograph parts of the human body. Compared to fluoroscopy, it has a more detailed and detailed picture and produces a lower radiation load on the human body. This method is most often encountered in the human skeleton scan (Fig. 2), but also in the detection of teeth (teeth).



Fig. 2 X-ray images of the left foot

B. *Computer Tomography (CT)*

Computed tomography is a radiological examination method that displays the inside of the human body using X-rays. The device performing this examination is a computer tomograph (Fig. 3).



Fig. 3 CT snapshots

The mathematical procedure called tomographic reconstruction is used for recording. It uses inverse radon transformation.

It is a transformation that assigns the original function to Radon's image. The radon image is obtained by means of an integral transformation, which assigns to the real function f defined on the n -dimensional real space another function bearing information about the integrals of the function f through all the affine superficial spaces on which it is defined [4].

C. Magnetic Resonance Imaging (MRI)

Magnetic resonance imaging is a radiological imaging method that uses a strong and homogeneous magnetic field. Unlike CT, MRI does not use X-rays but ionizing radiation. Despite good X-ray control (the risk of exposure), MRI scanning is now seen as a better choice than CT.

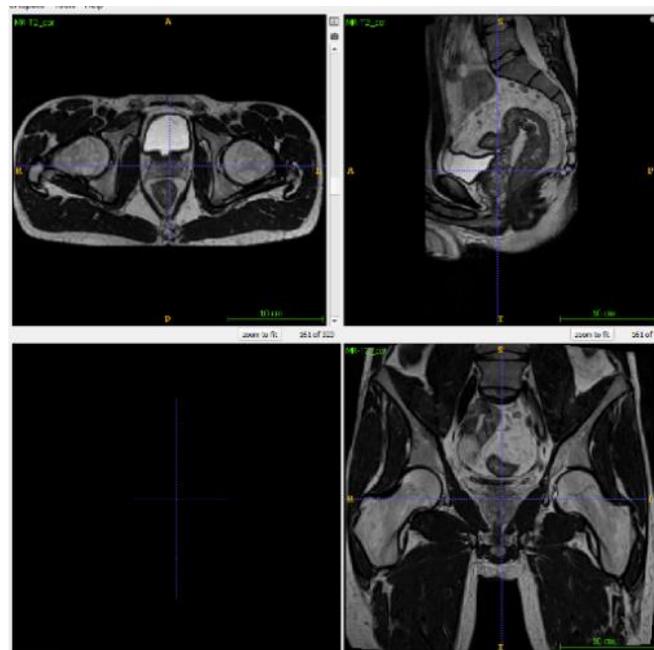


Fig. 4 MRI images

Unlike CT scanners, MR is noisier and can cause discomfort in patients because sensing is more time-consuming, is louder, and is usually inserted into a narrow tube. It is also not suitable for people who have a medical implant or other non-removable metal parts inside the body. MRI testing may not be safe for them if a high magnetic field device is used. At that time, the metal parts can be attracted by the magnet and can cause burns. This risk also arises when a

patient has a tattoo or permanent makeup that contains metal particles. Magnetic resonance imaging is suitable for recording changes and abnormalities in soft tissue, but it can also show the bone tissue of a patient well, see. Fig. 4 As with CT instruments, it has a high resolution and has no problem capturing small details [6].

D. Ultrasonography (USG)

Ultrasonography is a diagnostic imaging technique that uses ultrasound to visualize the human body. The ultrasonography sends high frequency ultrasound waves to the patient. Tissues in the body have different acoustic impedances, so the ultrasonic wave propagation rate is not the same in all tissues, and it is therefore possible to capture reflected waves. The ultrasound is transmitted in millisecond pulses and the instrument registers the intensity of the reflected signals and the time it takes to return the pulse to the sensor. Ultrasonic wave properties also include the fact that its intensity decreases exponentially, therefore the detected signal is further adjusted for good visualization. The adjustment consists in amplifying the signal in proportion to the time elapsed since the signal was transmitted. Ultrasonography can be performed differently. We know for example A mode, B mode, M mode, but also 2D and 3D mode. A mode is a one-dimensional view in which the amplitudes of the reflected signals are displayed on the screen and seen as a curve at the output. In this mode, distances are accurately measured. In medicine, a B mode is often used, which is a one-dimensional image in which the reflected signal pulses are displayed as different shades of gray. Then we can observe a line segment consisting of pixels with different degrees of brightness. This mode is the basis for other display modes. M mode represents the display of data from B mode in succession over time. It allows moving structures to be displayed and is most often used for cardiac examination. 2D mode is basic. One-dimensional images in mode A, B and M can also be obtained from this image. This image is obtained as a row next to one-dimensional lines of one-dimensional representation in B mode. It is used for the examination of human internal organs. The 3D mode is the latest kind of display that is created as a reconstruction of a series of two-dimensional cuts in a row. For this reconstruction information on the location of the cuts is needed. An example of images displayed in 2D and 3D mode can be seen in Fig. 5

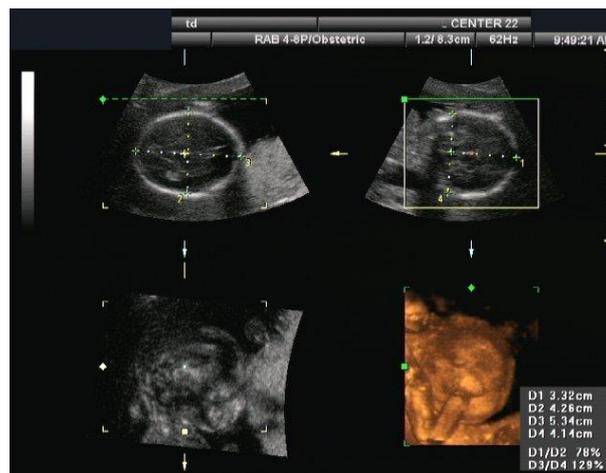


Fig. 5 Ultrasonograph images

E. Positive emission tomography

Positron-emission tomography (PET) belongs to imaging methods of nuclear medicine. It is based on the principle of annihilation, radiation detection and subsequent assembly of the cut in a given plane.

Annihilation is a process in elementary particle physics. This process can occur when a particle collides with its antiparticle, whereby the original particle disappears and its mass is transformed into some form of energy. In PET, this process is used to fuse the positron with the electron [7]. This device records inflammatory tissues very well and localizes tumor deposits. The most common use of this device is in collaboration with a CT device, when the light generated is precisely identified in the human body. On Fig. 6 we can see the difference between CT and PET images as well as the resulting image after joining these data [8].

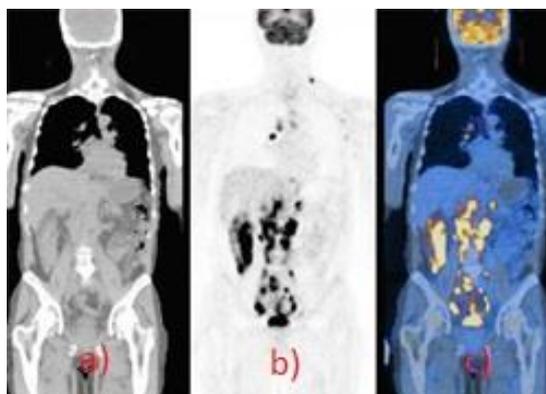


Fig. 6 a) CT scan b) PET scan c) CT + PET scan

IV. DATA RETENTION FORM

We need to keep the acquired data in some data form. The data we receive from medical devices is not effectively stored in basic formats (JPEG, PNG) because they contain additional information that cannot be written to them. Data standards and advanced file formats are used.

Data standards are important tools for maintaining information systems. This enables information and communication technologies to be used effectively across different health areas.

The standard is essentially a set of rules linked to the creation, development and use of information systems, which includes characteristics, methods, procedures and conditions, especially in terms of security and integrability with other systems. The issue of standards and standards for health care in Slovakia falls within the competence of the Ministry of Health of the Slovak Republic.

A. DICOM

DICOM [9] is an abbreviation of Digital Imaging and Communications in Medicine and is the communications standard for displaying, storing, distributing, and printing medical data worldwide. DICOM is used by all healthcare facilities, but each in a different range.

In particular, the standard was created to unify the transmission of image and data information between workplaces dealing with different diagnostic methods to display X-ray, MR, CT and PET. The need to standardize the creation and display of medical data has increased mainly due to the transfer of information and images when using devices from different manufacturers. The standard is very extensive.

In addition to data, the DICOM file format also includes a header with additional information describing not only the image itself, but also the patient information, type of examination, time, date of origin, and so on. Thus, the header ensures that the data cannot be exchanged and is uniquely identified. On a similar principle, JPEG also works, which can also store additional information. In each file, however, there is only one data object containing the pixels themselves.

DICOM has expanded over the years to include several guidelines and standards that describe not only image data, but also the transmission, printing and reporting of these data, as unambiguous information objects, among which it also defines interconnections. Supports network operations using TCP / IP protocol. Works with offline media that use industry standards such as CD-R or MOD. It also determines the match level, t. j. declares to the standard implementer the exact structure of the compliance document where it describes each applied function, as well as the properties of the objects. DICOM also specifies the semantics of commands and associated data. It also uses logical file systems FAT 16, ISO 9660, etc. [9].

DICOM consists of services that allow data transmission over network channels. Basic services include: Store - Send object to PACS, Storage Commitment - Retention certificate, Query / Retrieve - Search, Modality Worklist - List of scheduled tasks (examination) with object, Print - Print X-ray image, Off-line media how to store on removable media and more [2].

B. RAW

Raw Image File RAW is a "raw" image file from the camera, with only minimal data from the image sensor. These data are not yet ready for printing or editing with the bitmap graphics editor. Normally, the image is processed by a converter in a wide-range internal color space, where precise adjustments can be made before converting to a "positive" format such as JPEG, which is suitable for storage, printing or other manipulation. This color space is often dependent on the device being used.

They are often attributed to the term "digital negatives", although they are not negative images, but perform the same role as negatives from a film camera. The essence is that the negative is not directly usable as an image, but has all the information needed to create the image.

Their task is to capture the best possible radiometric characteristics of the scene (light intensity information and scene color) in the best possible sensor performance. Most often, this information is stored in pixels.

Raw format has several advantages compared to compressed format. For intensity, they have 12 or 14 channels, giving 4096 to 16384 shades compared to 8 bits that use compressed formats. It is because of this feature that they are also very often used to store medical data, as imaging devices provide shades of gray, so multiple objects in the image can be distinguished. This format also provides data transformation, e.g. increase exposure. An important feature of the RAW format is that the changes that are made to the file are non-destructive, that is, only the metadata that controls the rendering changes to different output versions, leaving the original unchanged [10].

V. SEGMENTATION

When data is processed in certain formats, segmentation algorithms are run on them. These will create 3D images from 2D images so that the Z-axis is also appended to the points on the X-axis and Y-axis, so that the individual frames are stacked on each other to obtain a spatial view. The snapshot order defines the process by which the data was collected. They are stored according to the scan direction of the device. Here's some basic approaches to image data segmentation.

According to [11], the main task of segmentation is to divide the image into parts or categories. We know complete and partial segmentation. When fully segmented, the image is divided into disjoint parts that have a high correlation with real world objects or regions

displayed in the image. They are only partially responsible for partial segmentation. In this kind of segmentation, we divide the image into homogeneous parts in terms of the property we have chosen, e.g. brightness, reflectance, texture, and so on. Most often, we will see segmentation in solving the problem of background image separation from the foreground. If the object being scanned is not on the entire frame, we say that we will focus segmentation on the area of interest. In doing so, the target objects may not always be clear, and the individual types of segmentation must also take into account undesirable effects such as, for example, bugs in the form of noise that we were unable to remove when preparing images before segmentation or parts (e.g., other objects) that are not in the interest of our investigation.

In segmentation, the individual exploration areas can be represented by a closed boundary, and each boundary that is enclosed describes an area. Segmentation methods can be categorized by segmentation method:

A. *Thresholding Segmentation*

Thresholding is the basis for a number of segmentation methods, mainly for its simple implementation and computational simplicity. The basic step in thresholding is to choose the right threshold. Later, the image is divided into two groups. The first group contains pixels whose degree of brightness is greater than the threshold value and the second one whose degree is less than or equal to the threshold value. Subsequently, the image is converted into binary form, i.e. black and white image.

According to the number of thresholds per image, we divide the threshold into global and local. Global thresholding is the easiest and most convenient to use when the background image brightness and foreground object intensity is vastly different. At that time, a single threshold is sufficient to divide all the points in the image. The threshold value is obtained from a histogram in which the brightness of each pixel is recorded. This may be automatic or manual. If the contrast between background and objects is low, local thresholding is used. In doing so, the image is divided into smaller parts based on the width of the surroundings we want to work with and the threshold is determined separately for each area depending on the surroundings. Local thresholding is mainly used for images that contain noise. Noise can be created especially when the object is not evenly distributed

B. *Area-based segmentation*

Area-based segmentation method must ensure that the criterion for full segmentation is met:

$$R = \bigcup_{i=1}^S R_i \quad R_i \cap R_j = 0 \quad i \neq j \quad (2.1)$$

and conditions of maximum homogeneity:

$$H(R_i) = \text{TRUE}, \quad \text{pre } i = 1, 2, \dots, S \quad (2.2)$$

$$H(R_i \cap R_j) = \text{FALSE} \quad \text{pre } i \neq j \text{ a } R_i \text{ is adjacent to } R_j \quad (2.3)$$

where R is the region designation, H is the homogeneity mark and S is the number of all regions. This method uses 3 basic approaches:

1. Connecting areas
2. Partitioning
3. Partitioning and joining areas

C. Edge-based segmentation

The basic principle of segmentation based on edge detection is the discontinuity of image data. Subsequently, borders are detected between regions. In this method, it is important to distinguish two basic terms, which are edge and boundary. An edge is only a property of a pixel that represents its degree (brightness, gradient). Unlike the boundary that is already the result of segmentation, it shows the contour of the segmented area. The boundaries are detected by gradient operators (1st and 2nd derivatives). In places where the level of brightness, color or texture is changed, a local edge is created. The drawback of this method is that it cannot work with noise. This causes detection of local edges even where there is no global boundary and vice versa, sometimes they are missing where the global boundary exists. An important factor is therefore the choice of the threshold height for the local edges, provided that the thicker edges are part of the boundary. In particular, the method achieves valid results when the contrast between the subject and the background is large enough. But this may not apply to local edges, which gives us incomplete boundaries [11].

D. Clustering Segmentation

The clustering method is characterized in that the objects are placed in clusters based on the similarity of data properties. The basic clustering algorithms include K-means and K-medoids.

K-means is a two-step method. In the first step, the centroids are created. These are assigned at random positions. The number of centroids created is the same as the resulting number of clusters we require. This point can be moved, unlike a data point that is static. The data point is assigned to the cluster, based on the distance from the centroid. When the assignment of data points to clusters is complete, the second point continues to calculate the centroid distances and they move to the center of the cluster to which they are assigned. This process of assigning data points to clusters and recalculating centroid coordinates is repeated until their position is stable (Fig. 7). The centroids are then removed and only clusters with data points whose properties are similar remain [12].

K-medoids is a method that is an enhancement of K-means. Compared to the previous one, it has less sensitivity to disturbing and inappropriate data that a dataset may contain. Also, the distance is not calculated with respect to the average value, but to the median (nearest value to average value). In the first step, like K-means, we determine the random objects, that is, the number of resulting clusters. We assign data points to clusters based on the smallest distance. In the second step we then select a random median and try to replace it with the current one. The method is similar to the first method, until the median position is stabilized [12].

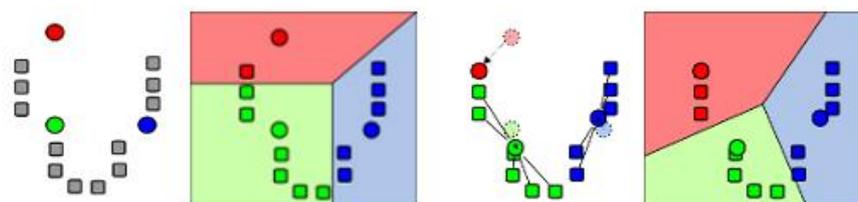


Fig. 7 Method of K-means Method

E. Livewire Segmentation

Livewire [13] (magnetic lasso) is a kind of segmentation that anchors segmentation points to edges in the input image. The algorithm works with volume data in sections. The segmentation area of interest is bounded by a boundary. In determining a boundary, a price function is used that describes the two adjacent pixels the price of the edge between them. Segmentation begins by setting the starting point so that the user clicks on the image pixel. We consider this pixel an anchor. Subsequent movement of the mouse creates the smallest path to the pixel where the

current mouse is located. If a user wants to select the path that this movement has to show, the user will click the image again. For a more accurate object contour, it is possible to add another control vertex (another anchor). After joining all the anchors with the edges, an image contour is created that resembles a magnetic lasso (Fig. 8).

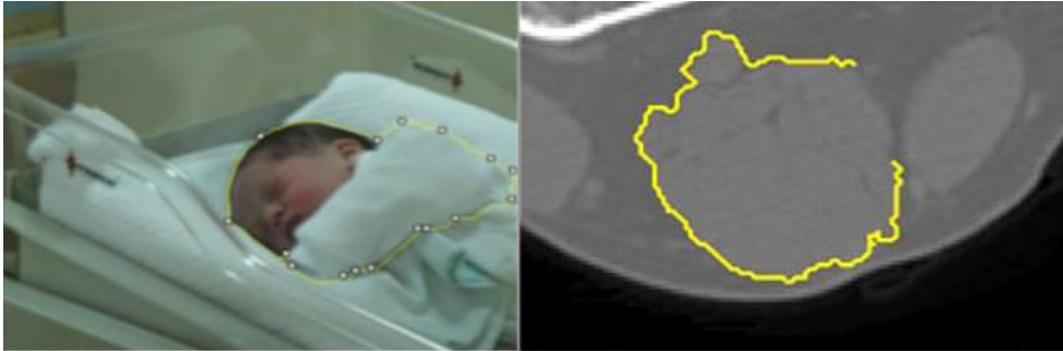


Fig. 8 Livewire selection

VI. METHODOLOGY OF SEGMENTATION ALGORITHMS EVALUATION

For the segmentation of image data, not only medical ones, there are several basic approaches that we have described in the previous chapter. By implementing these approaches, it is possible to obtain specific algorithms that exhibit different properties when segmented. In this work we focus on evaluation of properties of these algorithms. To this end, it is necessary to design a methodology that will allow us to do so.

Medical image data segmentation algorithms are implemented in multiple successful software tools, and therefore their implementation would be rather unnecessary. We prefer to focus on existing software and explore the algorithms implemented in it. We will evaluate the work with existing software as well as the resulting segmentation images of individual algorithms on different data.

For tools, we will first monitor whether the tool is free or is paid for. Another aspect will be open-source code, number of implemented segmentation algorithms, support for input / output formats, availability and dossier development, and finally the complexity of tooling.

In segmentation algorithms, we will evaluate the rate of segmentation and the resulting 3D model, using the algorithm. Our goal will be to segment the support system. We will observe whether the resulting segmentation contains other human tissues, but also whether the segmentation has captured the entire area of the support system shown in the images (empty bones). Based on this, we will evaluate the individual algorithms according to Tab. I.

TABLE I
METHODOLOGY OF SEGMENTATION ALGORITHMS EVALUATION

Good	The 3D model does not contain any (or very few) tissues other than the tissues of the support system. Object contours are clear and objects in the image are easily recognizable. The algorithm speed is appropriate to the results.
Average	The 3D model contains tissues other than the support system tissue, but the contours of the objects are not quite clear and the objects in the image are more difficult to recognize. Segmentation required more time with respect to the result.
Poor	The 3D model contains other tissues, such as tissue of the support system. Object contours are not clear and objects in the image are difficult to recognize. Segmentation required too much time due to the result.

VII. SOFTWARE TOOLS FOR MEDICAL DATA SEGMENTATION

The implementation of segmentation algorithms is dealt with by several companies or institutions. It has been found that effective segmentation of image data can greatly aid in the treatment of the patient, therefore the emphasis is on the most confidential display of reality. This largely affects the correct selection of the algorithm. In larger projects, several methods are used simultaneously for segmentation to achieve the best result. The 3D models thus obtained are often more sophisticated than models that were created using only one segmentation method. Many tools that implement visualization and segmentation algorithms are freely accessible. The best known are Medviso [14], 3D Slicer [15], ITK-SNAP [16], MeVisLab [17], TurtleSeg [18], ImageJ [19]. However, there are many tools using different combinations of algorithms. In this work, we focused on 2 tools, namely ITK-SNAP and MeVisLab, where ITK-SNAP is a tool that is also suitable for a user who does not have great knowledge of advanced data preparation and subsequent segmentation. MeVisLab is a representative of an advanced tool and some knowledge is needed to work with it.

A. ITK-SNAP

ITK-SNAP [16] is a software application that is used to segment structures in 3D medical images. It was created in collaboration with the University of Pennsylvania, Utah University and Paul Yushkevich. This tool is multi-platform and free. ITK-SNAP provides semi-automatic segmentation using active contour methods as well as manual delimitation and image navigation. In addition to basic features, it also offers other support tools.

Manual segmentation provides three orthogonal planes at a time. It also supports various input formats (DICOM - image series, DICOM - single image, GE, GIPL, MetaImage, NIfTI, Raw, Siemens Vision, VoxBo CUB, VTK Image), but also outputs (JPEG, PNG, TIFF, VTK Image etc) . The app contains a linked cursor that makes 3D navigation easier. 3D images can be color coded and explored using a function that can cut a plane. The graphical interface preview of this tool is shown in Fig. 9.

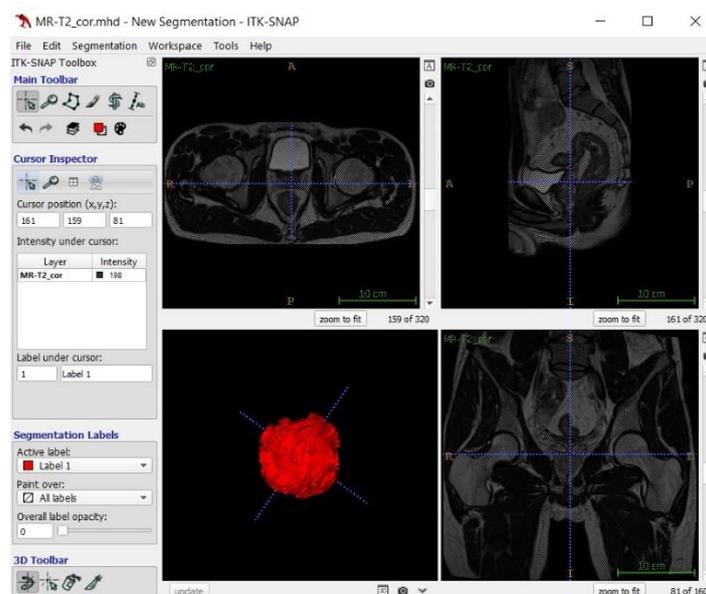


Fig. 9 ITK-SNAP tool

ITK-SNAP has implemented 4 kinds of segmentation algorithms that can be used for semi-automatic as well as manual segmentation.

The segmentation methods they use are:

1. Thresholding - Provides two-page thresholding (Segmentation Threshold is closed from top and bottom) or only from one side (Top / Bottom Threshold setting only)
2. Clustering - ability to determine the number of resulting clusters (parameter k)
3. Edge Based Segmentation - Edge smoothing parameter
4. Classification

ITK-SNAP developers focused primarily on image segmentation. The other unrelated functions are developed only minimally. Application orientation is intuitive, also provides training videos for easier work and user experience. It also offers a variety of color options to display the segmentation area.

B. MeVisLab

MeVisLab [17] is developed by MeVis Medical Solutions AG in collaboration with Fraunhofer MEVIS. The application is a powerful research and development tool for image processing with a special focus on medical imaging. Enables rapid integration and testing of new algorithms. It is also used to develop clinical applications prototypes.

The application includes advanced modules for segmentation, registration, volumetry, as well as quantitative morphological and functional analysis. It is often used for neuro-imaging, dynamic image analysis, operation planning as well as cardiovascular analysis.

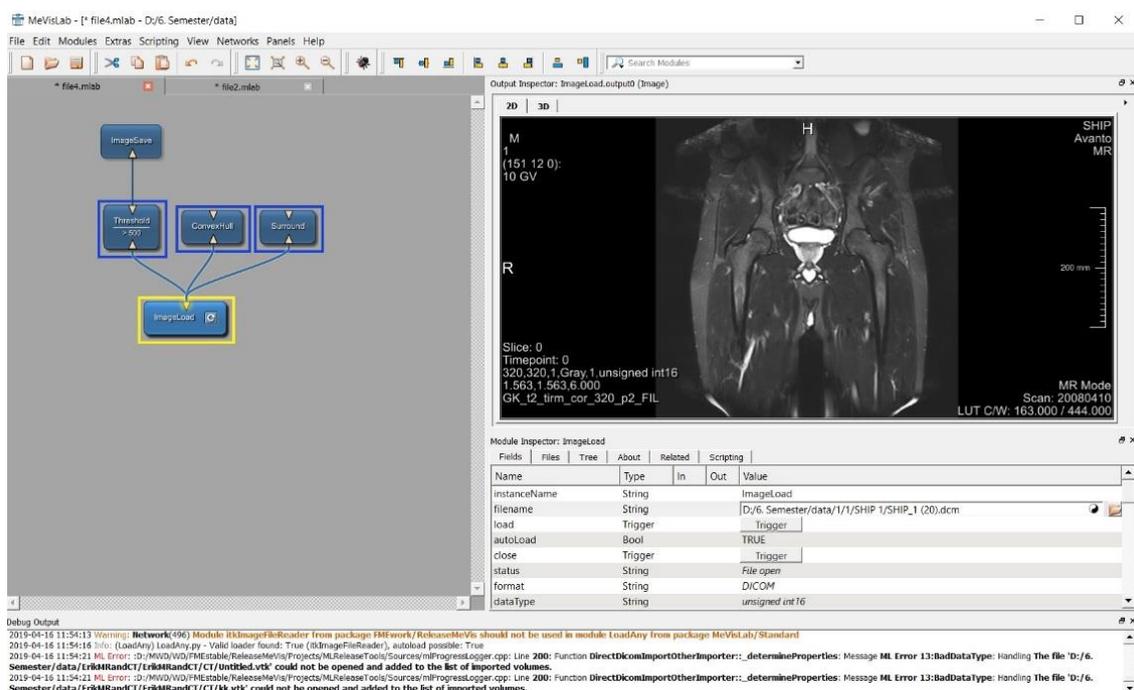


Fig. 10 MeVisLab tool

MeVisLab (Fig. 10) uses known libraries as well as third party technologies. It uses the QT library, OpenGL standard, for the graphical interface and data visualization.

The core component of MeVisLab is the object-oriented MeVis Image Processing Library (ML), which provides general image processing support. A distinctive feature of ML is demand-based image processing control, which is based on multiple multithreaded pages. It uses priority site management to avoid unnecessary data recalculation.

It currently has more than 5000 image processing modules, including image filtering, segmentation, and statistical analysis. They can be divided into 5 main groups: Filters, Segmentation, Transformation, Statistics, and more. Each group contains several hundred

modules. It supports various input data formats (DICOM, TIFF, RAW, JPG, BMP).

Segmentation offers the following implemented methods:

1. Thresholding
2. Segmentation based on areas
3. Livewire segmentation
4. Manual Contours

In this work we used modules mainly from segmentation. Tab. II shows an overview of implemented segmentation algorithms in individual tools.

TABLE II
OVERVIEW OF SEGMENTATION ALGORITHM USAGE

	MeVisLab	ITK-SNAP
Thresholding	✓	✓
Area-based segmentation	✓	✗
Edge-based segmentation	✗	✓
Clustering	✗	✓
LiveWire	✓	✗
Classification	✗	✓

VIII. PRACTICAL TESTING OF SEGMENTATION ALGORITHMS

We used CT and MRI data to test algorithms and compare their properties. The CT of the device shows images of the left knee and pelvic area. The knee images consist of 26 and 28 frames (different viewing angles) where the distance of each frame is 4.4 and 3.9 mm. The pelvic imagery consists of 40 images that are 6mm apart. The frame distance determines the width of the cut. MRI images of the pelvic area. These images are 160 (front-to-back view) and 320 (side-to-side and top-down view) The images we use are DICOM or RAW.

The first tool for segmentation in which we performed semgneting was ITK-SNAP. Navigation in it is very simple and intuitive. At least minimal knowledge of the English language is assumed when using this tool. The calculations themselves were quite fast, but this depends on the segmentation method used and the number of iterations triggered. In this case, the iterations are considered to be a sequence of steps, that is, how many times the given algorithm is run at a certain parameter setting over the data. This means that we can combine segmentation algorithms and run them on the same data several times, while the individual segmentation algorithms can be re-calculated multiple times on a single run. In general, the more iterations we run, the more accurate segmentation is. The resulting evaluation of segmentation algorithms is recorded in Tab. III.

From the table we can see that the tools that were selected to compare segmentation algorithms were representatives of two groups. ITK-SNAP was a tool that is simple for a user who does not have a deeper knowledge of segmentation. Best results were obtained with CT images using a threshold algorithm where the threshold was set manually. Comparable results were also observed when using the clustering and classification algorithm in MRI images.

MeVisLab is an advanced tool for image data segmentation and visualization that is very comprehensive and provides a large number of modules that offer data pre-processing, data processing and data editing. Some knowledge of medical image segmentation is needed to work with it. Just because of this, it is already suitable for an advanced user. In MeVisLab, we investigated the threshold method and the effect of threshold value on each frame type. The 3D model, which was very close to reality, came from images created by a CT machine. The threshold value was set to 450.

The segmentation algorithms used showed different results using different data. The main

factors that influence the resulting 3D model include the quality of data collected from medical imaging devices. With CT knee shots, we can observe poor results even with manual but also automatic threshold values. This is probably due to the low number of frames, because using both the CT threshold method and the MRI in the ITK-SNAP tool, we achieved average and good segmentation model results, with the aforementioned CT and MRI data being known to be of higher quality and greater as knee images.

TABLE III
SEGMENTATION PERFORMED STATS

Segmentation order	Tool	Segmentation algorithm	Data	Iteration count	Rating
1.	ITK-SNAP	Thresholding	MRI	4x150	Average
2.	ITK-SNAP	Thresholding	MRI	4x150	Poor
3.	ITK-SNAP	Zhlukovanie	MRI	4x1500	Good
4.	ITK-SNAP	Edge Segmentation	MRI	4x150	Poor
5.	ITK-SNAP	Classification	MRI	4x3500	Good
6.	ITK-SNAP	Thresholding	CT	2x150	Poor
7.	ITK-SNAP	Thresholding	CT	5x900	Good
8.	ITK-SNAP	Thresholding	CT	4x200	Poor
9.	MeVisLab	Thresholding	MRI	1	Poor
10.	MeVisLab	Thresholding	MRI	1	Average
11.	MeVisLab	Thresholding	MRI	1	Average
12.	MeVisLab	Thresholding	MRI	1	Poor
13.	MeVisLab	Thresholding	CT	1	Poor
14.	MeVisLab	Thresholding	CT	1	Average
15.	MeVisLab	Thresholding	CT	1	Good
16.	MeVisLab	Thresholding	CT	1	Good
17.	MeVisLab	Thresholding	CT	1	Average
18.	MeVisLab	Thresholding	CT	1	Good
19.	MeVisLab	Thresholding	CT	1	Good
20.	MeVisLab	Thresholding	CT	1	Good

In MeVisLab, we can also see that thresholding achieves different results with the same data (CT images of knee and CT scan of pelvis and chest). These differences can be attributed to data quality (number of frames, accuracy of the device). After the experiments performed, it cannot be stated that CT scan images are more suited to segmenting 3D models than images from an MRI instrument because we achieved good results for both CT and MRI images.

Segmentation algorithms achieved different results, but none of the algorithms used created a 100% 3D model of the human body support system. This problem could be solved by a combination of individual segmentation algorithms that would be used sequentially for different segmentation regions.

IX. CONCLUSION

The aim of this work was to investigate and compare selected algorithms for medical image data segmentation. In the work we are familiar with the procedure for creating a 3D model of the human body.

The first step is to obtain data from medical devices. We described the scanning procedure of X-ray apparatus, computed tomography, magnetic resonance, ultrasonograph and positron emission tomography. The data produced by these devices is stored in different formats. In addition, we have described the basic medical data storage formats. Most of this data is in the DICOM standard, which also makes data transfer easier. The acquired data is recorded in 2D images from which a 3D model is created using segmentation algorithms. There are several

basic principles for creating a segmentation algorithm. These include thresholding, edge-based segmentation, area-based segmentation, clustering segmentation, and modern livewire segmentation. The described principles implement various software tools. We chose ITK-SNAP and MeVisLab for our research. ITK-SNAP is a segment-oriented tool that is also suitable for users with minimal knowledge of image data segmentation. MeVisLab is an advanced tool that allows you to work more with your data. I.e. not just segmentation but also visualization, transformation, various statistics and others. Both tools have shown good and bad results. These arose depending on different data and setting of input parameters of individual segmentation algorithms. In ITK-SNAP, the manual thresholding algorithm for CT scans, but also the MRI image clustering algorithm, yielded the best results. In MeVisLab, a similar thresholding algorithm with a manually set threshold using CT scan images also achieved similar results. In general, it cannot be argued that the device from which we obtained the data affects the resulting segmentation because we have achieved good results in both CT and MRI images. The implemented segmentation algorithms achieved good results, but this does not mean that they did not have minor deficiencies. These deficiencies could be eliminated by using multiple segmentation methods on a single 3D model.

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