RADIOLOGY IMAGE ANALYSIS AND REGISTRATION PROBLEMS

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Abstract

In this paper, a method for analyzing transversal plane images obtained by computer tomography scans is presented. A mathematical model that describes the ribs-bounded contour was created and the problem of approximation is solved by finding out the optimal parameters of the model in the least-squares sense. The paper discloses the problems that appear in building the proper model. Such a model would be useful in registration of images independently of the patient position on the bed and of the radiocontrast agent injection. We consider the slices, where ribs are visible, because many important internal organs are located here: liver, heart, stomach, pancreas, lungs, etc.

Keywords: Computer tomography; Mathematical modeling; Curve fitting; Optimization.
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1 Introduction

In medicine, many decisions on diagnostics and evaluation of effectiveness of the treatment are made by the analysis of images. Image data come from medical diagnostic techniques such as radiology, echoscopy, magnetic resonance, thermovision, tomography, etc.

Computed tomography (CT) is a technology allowing the inside of objects to be spatially viewed using computer-processed X-rays. It is very important in medical diagnostics because it shows human internal organs without cutting, e.g. brain, liver [1], prostate [2]. CT scans are 3D images, i.e. a collection of 2D images (slices), representing slices by the transversal plane. This paper deals with finding of the ribs-bounded contour. It is important for e.g. internal organ localization, because the ribs-bounded contour defines the region of location of internals in the slice. Defining the area of internal organs from the ribs-bounded contour restricts essentially the search area, where these organs are located, and may serve as the effective start for the detailed localization of particular organ. The rib anatomy is used as a reference point in CT scans analysis. In [3], an automated method is being developed in order to identify corresponding nodules in serial thoracic CT scans for interval change analysis. The problem of selection a proper function defining the ribs-bounded contour appears. In this paper, we suggest cardioid-type curve. However, it is not the only one possible. As alternative may serve snake-type curve [4]. The computing of such curve will face problems in the spine area.

The ribs-bounded contour may be important in the image registration. The image registration is a technique used to transform several images into one coordinate system. In the CT image analysis, registration would be useful e.g. in comparing slices from different CT scans of the same patient seeking to evaluate efficiency of a treatment or progress of the disease. The model of the ribs-bounded contour may be the basis of a criterion of similarity of images (slices). In this case, we will have a method of the feature-based registration. Image registration finds wide applications in medicine (eye fundus analysis [5], ultrasound [6], etc.) In the CT image analysis, an attempt to use the slice registration is done in [7]. Their comparison criteria is a vector made of white, gray and black pixels counts in a certain parts of an image. The drawbacks of this approach are insensitivity to body rotation and radio-contrast agent injection. The known model of the ribs-bounded contour would make comparison of two images easier and faster.

In this paper, a mathematical model that describes the ribs-bounded contour has been developed and the problem of approximation is solved. We restrict ourselves to the slices where ribs are visible. However, this fact does not lessen the significance of our work, because many important internal organs, such as liver, heart, stomach, pancreas, lungs, are located here. The paper is an essential extension of the primary ideas presented in [8], where the attempts to build a mathematical model of the ribs-bounded contour have been made.

2 Data to be analysed

Examples of CT scan slices are shown in Fig. 1. We investigate images of size 512 × 512, gathered by GE LightSpeed Pro 32 CT scanner1. 16-bit DICOM grayscale images were obtained using it. The images were automatically linearly normalized to

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the interval $[0; 255]$ by window level (center) 40 and window width 350 HU (Hounsfield units). The CT scanner uses a set of software algorithms to determine the amount of x-radiation absorbed by every element in a plane of tissue. Each of these elements is represented by a pixel on the video display, and the density (amount of x-radiation absorbed) is measured in Hounsfield units (HU). Fig. 2 details the possible content of particular scan slices. Depending on the slice, the heart, lungs, stomach, or liver can be seen. In all the slices of Fig. 2, the internal organs are bounded by ribs. Fig. 1 and 2 were obtained after the patient was given a radiocontrast agent injection. Therefore, the heart and aorta as well as all blood vessels are bright here.

![Figure 1. Examples of the CT scan slices.](image1)

![Figure 2. Content of the scan slices.](image2)

3 Model approximating the ribs-bounded contour

In this section, an approach to find the ribs-bounded contour in the CT scan slice (through the transversal plane) is proposed. It produces a mathematical model approximating the contour. In addition, the approach allows us to evaluate patient rotation around the vertical axis during the scan.

In the particular scan slice, we may observe some consistent patterns:
- a symmetry of the ribs by the human sagittal plane,
- the cross-section of breast in the transversal plane is more condensed vertically than horizontally,
- body rotation with respect to bed,
- aorta near spine,
- high grayscale intensity of bones,
- bed,
- bright blood vessels (if the radiocontrast agent was injected to the patient).

All these patterns must be considered when building a model.

The approach below consists of two steps:

a) extracting the bone tissue from image;
b) approximating the ribs-bounded contour by a mathematical function.

### 3.1 Bone tissue extraction

Let us analyze a CT scan, consisting of some number of slices (images). In this paper, we restrict ourselves with the slices to that where ribs are visible.

The bone tissue is naturally brighter than any other tissue. Therefore, the bone tissue may be extracted from the whole CT scan via thresholding and removing undesirable regions. Let the CT scan be normalized linearly from 0 to 255, i.e. grayscale scanning (it is the usual case).

The bone tissue extraction algorithm is as follows:

1) thresholding – extracting pixels with a value higher than 150,
2) removing undesirable regions.

The internal organs contain mostly soft tissue, which is not dense. The densest organ is liver; it has up to 60 HU. Therefore, we choose threshold of 70 HU that corresponds to pixel brightness equal to 150.

After thresholding, some undesirable regions remain in the image: lateral objects like the bed or metal implants, and everything that contains blood with a radiocontrast agent – heart and vessels. These regions should be removed.

The bone tissue extraction algorithm using the morphological operations [9] looks as follows:

1. `image=CTScan.Threshold(150);`
2. `for each slice in image`
   `slice=slice.FillIsolatedBlobs;`
3. `image=image.MorphologicalOpen(2);`
4. `spine=image.MorphologicalOpen(14);`
5. `for z from 0 to image.SliceCount`
   `image[z]=image[z]-(spine[z].Dilate(4)-spine[z])&&Rectangle((0, 0)-(512,spine.MassCenter.Y));`
6. `points=;`
7. `for each slice in image`
   `points= points ∪ slice.ConvexHull;`
8. `image=image.FilterConnectedComponents (points);`

In the pseudo code, CTScan is the CT scan image, and the function Threshold (th) transforms the grayscale image into the binary one. image is the 3D binary image (Fig. 3a). The function FillIsolatedBlobs takes the isolated black blobs that are onto larger white ones (i.e. islands of white blobs) and fills them with white; blob is edge-connected group of pixels. MorphologicalOpen(x) and Dilate(x) are morphological open and dilate operators, respectively, with a round kernel of diameter
2x + 1. The function $\text{Rectangle}((x_0, y_0) - (x_1, y_1))$ makes a binary image with a white filled rectangle at specified coordinates, and $\& \&$ is pixel-wise binary AND operator – intersection of binary images. The binary image subtraction $X - Y$ compares each pixel and returns the nonimplication. $\text{MassCenter}$ changes a binary blob to its center of mass, i.e. an average of the coordinates of the pixels in the blob, $\text{FilterConnectedComponents}(\text{seeds})$ leaves binary blobs that are connected to seeds only. ConvexHull returns a set of points of the 2D convex hulls of all white pixels in the binary slice. A set points joins such convex hulls points of all slices of the CT scan.

$\text{FillIsolatedBlobs}$ is necessary because the inner rib tissue may appear in black after the binarization using the threshold. The morphological opening cleans the bed pixels and the noise (mostly produced by small vessels). Then only two 3D white objects have remained: bones and large vessels (Fig. 3b). They touch each other in one place only, aorta near spine.

Since the spine is a large continuous object, it can be extracted using the morphological opening with a very large kernel (the result is presented in Fig. 3c). $\text{spine}[z].\text{Dilate}(4) - \text{spine}[z]$ analyses the slice $z$ and gives a ring of 4 pixels thickness around the spine (Fig. 3d). Its intersection with $\text{Rectangle}((0, 0) - (512, \text{spine.GravityCenter.Y}))$ is a cap above the spine (Fig. 3e), which is removed from the image using non-implication in order to separate aorta from the spine where they touch each other (Fig. 3f). Now we need to take a connected component representing bones. Since large blood vessels never appear outside the ribs-bounded contour, bone is a component connected with a 2D convex hull of the image (an example of one slice is presented in Fig. 3g). Convex hulls off all slices are used, because if CT scan does not include all the lungs, some ribs can be left unselected.

As a result of the bone tissue extraction above, we get binary images, see the example in Fig. 3h.

For simplicity, let us skip the order number of slices in the CT scan and denote by $B = \{B_i = (b_{1i}, b_{2i}), i = 1, m\}$ the set of coordinates of bone pixels, obtained during the analysis of some particular CT image slice, and $m$ is the number of bone pixels in this slice. This set of coordinates serves as numerical data to develop a mathematical model of the ribs-bounded contour for a particular slice.

![Figure 3. Bone tissue extraction](image-url)
3.2 Ribs-bounded contour approximation

The ribs form a shape similar to cardioid (see Fig. 2):
\[
\rho(\phi) = 1 + \cos(\phi - \pi/2), \quad \phi \in [-\pi/2; 3\pi/2]
\]  

(1)

Here \( \rho \) is the radius and \( \theta \) is the polar angle. The shape of (1) is depicted in Fig. 4 (blue curve). It looks similarly, because it features a cave that could be used to approximate the ribs cave near the spine. \( \pi/2 \) is introduced in (1) because the standard cardioid is rotated by (1) as compared with Fig. 4 and the ribs-bounded contour in the images should be oriented just like the ribs depicted in Fig. 2.

Fig. 4 indicates that a ribs-bounded contour is more condensed vertically than the standard cardioid curve. Therefore, we suggest to add an optimizable parameter – power \( s \):
\[
\rho(\phi) = \left( 1 + \cos \left( \phi - \frac{\pi}{2} \right) \right)^s
\]  

(2)

The parameter \( s \) influences not only the vertical scale of the curve (1), but also the form of the curve (see Fig. 4 for curves with different values of \( s \)).

![Figure 4. Blue – standard cardioid (1), red and green – (2) curve with \( s = 0.5 \) and \( s = 0.3 \).](image)

In the CT scan slice (Fig. 2), we see a cave influenced by the breastbone. Curve (11) is convex in this region. Therefore, we need to complement model (11) redefining \( \rho \) with an additional member \( \rho^+ \) the form of which may vary depending on the cave:
\[
\rho(\phi) = \left( 1 + \cos \left( \phi - \frac{\pi}{2} \right) \right)^s - c \rho^+(\phi)
\]  

(3)

This member realizes the cave by subtracting some value from the right side of (2) starting from \( \phi = \pi/2 - \beta \) to \( \phi = \pi/2 + \beta \) is an angle, defining the region of subtraction. A non-negative multiplier \( c \) defines the scale of subtraction, if \( c = 0 \), we get the case with no subtraction.

The member \( \rho^+(\phi) \) depends on \( \phi \) with domain \([-\pi/2; 3\pi/2]\) and has special properties. It must:
1. be unimodal non-negative function on \( \phi \) and achieve the maximal value as \( \phi = \pi/2 \),
2. be symmetrical function in respect of \( \phi = \pi/2 \),
3. be equal to 0 when \( \phi = \pi/2 - \beta \) and \( \phi = \pi/2 + \beta \),

![Figure 5. Dependencies of function \( \rho^+ \) on \( \phi \in \left[-\frac{\pi}{2}, \frac{3\pi}{2}\right] \).](image)
have zero first and second derivatives on $\varphi$ when $\varphi = \frac{\pi}{2} - \beta$ and $\varphi = \frac{\pi}{2} + \beta$.

Properties 1-3 show that the subtraction is applied in the interval $\beta > |\varphi - \pi/2|$, and $\rho^+(\pi/2 - \beta) = \rho^+(\pi/2 + \beta) = 0$.

The function $\rho^+$ may be as follows:

$$\rho^+(\varphi) = \begin{cases} \sin\left(\frac{\pi(\varphi - \pi/2 + \beta)}{2\beta}\right), & \text{if } \beta \geq |\varphi - \pi/2| \\ 0, & \text{otherwise} \end{cases} \quad (4)$$

In (3) and (11), we have three control parameters characterizing the breastbone cave for which the optimal values need to be found: $\beta$ is an angle, defining the region of subtraction, $l$ defines the steepness of a curve describing the cave, $c$ is the scale of subtraction. The example of $\rho^+$ is presented in Fig. 5 for different values of $\beta$ and $l$.

Moreover, we need some additional parameters $a$ and $b$ that define the horizontal and vertical scales of the curve that approximates the rib-bounded contour, respectively. Curve (3) should be fitted to ribs in the picture of bone tissue. For this reason, we need the optimal place for the point of (3) corresponding to $\varphi = 0$ in the picture; denote the coordinates of this point by $(x_0; y_0)$.

As we see in Fig. 2, the rib-bounded contour has some rotation in respect of the bed. Therefore, we should introduce the angle $\theta$ of such rotation. If the values of $s$, $\theta$, $a$, $b$, $x_0$, $y_0$, $\beta$, $c$, $l$ are fixed, we can draw some parametric curve $(x, y) = (x(\varphi), y(\varphi))$ approximating the rib-bounded contour:

$$x(\varphi) = x_0 + a \rho(\varphi) \cos \varphi \cos \theta - b \rho(\varphi) \sin \varphi \sin \theta$$

$$y(\varphi) = y_0 + a \rho(\varphi) \cos \varphi \sin \theta + b \rho(\varphi) \sin \varphi \cos \theta \quad (5)$$

While the ribs are symmetric, their cross-section may appear asymmetric due to the position of the patient on the bed. Even more, the spine is a very large white blob in the image of bone tissue, so it can attract one side of the curve. Moreover, we observe a spinous process in the spine bone tissue (see Fig. 2 and Fig. 3h). This spinous process influences the shape of the model as well. The notices above lead to the addition of a line segment parallel to the sagittal axis in the model. This line segment must include at least the whole spine in the slice: from $(x_0; y_0)$ to the bottom of the unrotated model (case $\theta = 0$). Formally, the line segment is a part of a line that is bounded by two distinct end points (Fig. 6):

a) $(x_0; y_0)$

b) $(x_0 + (y_0 - \min_y) \sin \theta; y_0 - (y_0 - \min_y) \cos \theta)$

where $\min_y$ is the minimal value of $y$ defined by (5) in case of $\theta = 0$:

$$\min_y = \min_{\varphi} (y_0 + b \rho(\varphi) \sin \varphi) = y_0 + b \min_{\varphi} (\rho(\varphi) \sin \varphi) \quad (7)$$

Figure 6. Example of CT scan slice and a desired model
3.3 Realization of the model

If $\varphi$ runs through the interval $[-\pi/2; 3\pi/2]$ with a step $2\pi/n$, we get sequence $C' = (C'_i = (x_i, y_i), i = 0, n-1)$ of the curve points, where $x_i, y_i$ are defined by (5), $x_i = x\left(\frac{2\pi}{n}i\right)$ and $y_i = y\left(\frac{2\pi}{n}i\right)$. The line segment (6) is sampled by sequence of $n_i$ points $C'' = (C''_i = (x_0 + \frac{(y_0 - \min y)\sin \theta}{n_i}i, y_0 - \frac{(y_0 - \min y)\sin \theta}{n_i}i), i = 1, n_i)$. Both the sequences together form the sequence $C = (C', C'')$ of the length $n + n_i$. In our experiments, $n = 180$ and $n_i = 10$.

$\min y$ is approximated by $\min_{i=0,n-1}(y_0 + b\rho\left(\frac{2\pi}{n}i\right)\sin\left(\frac{2\pi}{n}i\right))$ to avoid the analytical solving of equation $\frac{d\rho}{d\varphi} = 0$.

3.4 Constraints on parameters

Model (3) has several parameters the values of which should be defined analyzing a particular image. The values of these parameters are constrained. The suppositional constraints are presented below:

1. $0 < s \leq 1$
2. $-\pi/6 < \theta < \pi/6$
3. $a > 0$,
4. $b > 0$,
5. $0 \leq \min_{\varphi \in [-\frac{\pi}{2}; \frac{\pi}{2}]}(x_0 + a\rho(\varphi)\cos \varphi \cos \theta - b\rho(\varphi)\sin \varphi \sin \theta) < \max_{\varphi \in [-\frac{\pi}{2}; \frac{\pi}{2}]}(x_0 + a\rho(\varphi)\cos \varphi \cos \theta - b\rho(\varphi)\sin \varphi \sin \theta) < 512$
6. $0 \leq \min_{\varphi \in [-\frac{\pi}{2}; \frac{\pi}{2}]}(y_0 + a\rho(\varphi)\cos \varphi \sin \theta + b\rho(\varphi)\sin \varphi \cos \theta) < \max_{\varphi \in [-\frac{\pi}{2}; \frac{\pi}{2}]}(y_0 + a\rho(\varphi)\cos \varphi \sin \theta + b\rho(\varphi)\sin \varphi \cos \theta) < 512$
7. $0 \leq \beta \leq \pi$
8. $0 \leq c < 1$
9. $l \geq 2$,
10. $\max_{\varphi}(2a\rho(\varphi)\cos \varphi) > \max_{\varphi}(b\rho(\varphi)\sin \varphi) - \min_{\varphi}(b\rho(\varphi)\sin \varphi)$

Optimization of an unconstrained model could result in strange shapes such as in Fig. 7a – that occurs as $c \geq 2^s$. In fact, $c$ should not approach to $2^s$ (Fig. 7b), so we restrict it to be less than 1. Approximation of the ribs-bounded contour is shown in the image in red.

![Figure 7. The shape of the model as (a) $c > 2^s$, (b) $c = 2^s$, (c) constraint 10 is violated, (d) constraint 2 is violated.](image-url)
Constraint 10 describes the relation between the width and height of breast. It means that we require the cross-section of breast in the transversal plane to be more condensed vertically than horizontally. Experiments have showed that the optimization algorithm can find strange local minima (see Fig. 7c), if this constraint is violated.

The model may be flipped over, if the constraint 2 is violated (see Fig. 7d).

4 Fitting the model: optimization problems

Optimization in the image analysis becomes an usual practices [10, 11, 12]. The model of the ribs-bounded contour of a particular slice of CT scan has nine parameters the values of them can be varied seeking to find the best approximation of the contour: \( s, \theta, a, b, x_0, y_0, \beta, c, \) and \( l \). The optimal values of these parameters must be defined by the set \( B = \{ B_i = (b_{1i}, b_{2i}), i = 1, m \} \) of coordinates of bone pixels, obtained during the analysis of CT image slices. The optimization problem to find optimal \( s, \theta, a, b, x_0, y_0, \beta, c, \) and \( l \) is formulated as the least-squares one:

\[
\min_{s, \theta, a, b, x_0, y_0, \beta, c, l} f(s, \theta, a, b, x_0, y_0, \beta, c, l)
\]

\[
f(\cdot) = \sum_i^m \| B_i - C_{k_i} \|^2, \quad k_i = \min_{j=0, n+1} \| B_i - C_j \|\]  

The least-squares functions are used usually in approximation problems. Non-linear least squares is used to fit a set of \( m \) observations with a model that is non-linear in some number of parameters. In case of problem above, the number of such parameters is 9. Such problem of data fitting bridges many disciplines, especially those traditionally dealing with statistics like physics, mathematics, engineering, biology, economy, or psychology, but also more recent fields like computer vision [13, 14].

Function (11) is rather computational expensive. For example, computation of its value takes 0.6 seconds in the case \( m = 6097 \) and 0.4 seconds in the case \( m = 4486 \).

The optimization method to solve (11) can be any local minimization one. We use the Matlab realization of the quasi-Newton method [15]. Constraints 2, 7, 8, and 10 are applied only. As a result, other constraints were not violated during optimization process.

4.1 One-step optimization

The approximation of the ribs-bounded contour via solving the optimization problem (11) with all nine variables \( s, \theta, a, b, x_0, y_0, \beta, c \) and \( l \) is illustrated bellow.

Usually, the local optimization starts from some initial values of variables. These values influence the optimization result depending on properties of the function \( f(s, \theta, a, b, x_0, y_0, \beta, c, l) \). Specific knowledge (e.g. on the anatomy of the ribs, etc.) leads to the idea that the initial values of \( s, \theta, a, b, x_0, y_0, \beta, c \) and \( l \) in problem (11) can be set to form a shape slightly smaller than the ribs-bounded contour. Further optimization would expand the model area to the proper size.

![Figure 8. Examples of optimization; slices No. 1, 36, 71, 106.](image-url)
In Error! Not a valid bookmark self-reference., we present several examples of optimization results (both $\theta$ and $\beta$ mean radians). The respective graphical results are presented in Fig. 8 (the approximating curve is in red).

**Table 1. Examples of optimization results.**

<table>
<thead>
<tr>
<th>Slice</th>
<th>$m$</th>
<th>$a$</th>
<th>$b$</th>
<th>$\theta$</th>
<th>$s$</th>
<th>$x_0$</th>
<th>$y_0$</th>
<th>$\beta$</th>
<th>$c$</th>
<th>$l$</th>
<th>$\min f(\cdot)$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>6097</td>
<td>169</td>
<td>253</td>
<td>-0.05</td>
<td>0.684</td>
<td>257</td>
<td>187</td>
<td>3.14</td>
<td>1</td>
<td>6.94</td>
<td>24.35</td>
</tr>
<tr>
<td>36</td>
<td>6561</td>
<td>210</td>
<td>287</td>
<td>-0.07</td>
<td>0.36</td>
<td>261</td>
<td>238</td>
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<td>0.9</td>
<td>4.36</td>
<td>28.87</td>
</tr>
<tr>
<td>71</td>
<td>5686</td>
<td>208</td>
<td>290</td>
<td>-0.08</td>
<td>0.644</td>
<td>258</td>
<td>212</td>
<td>2.73</td>
<td>1</td>
<td>3.64</td>
<td>32.88</td>
</tr>
<tr>
<td>106</td>
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<td>207</td>
<td>270</td>
<td>-0.08</td>
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<td>258</td>
<td>214</td>
<td>2.36</td>
<td>1</td>
<td>2.6</td>
<td>58.5</td>
</tr>
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</table>

### 4.2 Two-step optimization

Knowledge on the specific nature of the problem domain renders a possibility to simplify and/or to stabilize the process of optimization by dividing the main problem (11) into a certain sequence of problems. The sequence can contain e.g. several simpler independent problems or the problems in the sequence are dependent and supplement one another. Function (5) is not separable from different variables or their groups. However, the approximation of the ribs-bounded contour can be divided into two subproblems:

- the model is fitted without breastbone cave (variables are $s$, $\theta$, $a$, $b$, $x_0$, $y_0$ only, and $\beta$, $c$, and $l$ values are fixed),
- the correction of the model taking into account the breastbone cave (variables are $s$, $\theta$, $a$, $b$, $x_0$, $y_0$, $\beta$, $c$, and $l$).

The first subproblem is simpler as compared to (5), with a smaller number of variables:

$$\min_{s, a, b, \theta, x_0, y_0} f(s, \theta, a, b, x_0, y_0, \pi, 0, 2) \tag{9}$$

As a result, the optimal values of $s$, $\theta$, $a$, $b$, $x_0$, $y_0$ in the sense of problem (11) are obtained. The six values serve as the starting ones for variables $s$, $\theta$, $a$, $b$, $x_0$, and $y_0$ in the second subproblem that is defined by (8). The subproblem has three new variables $\beta$, $c$, and $l$. Their values were fixed in the first subproblem to be equal to $\beta = \pi$, $c = 0$ and $l = 2$. These values were set as the initial ones for variables $\beta$, $c$, and $l$ of the second subproblem.

In Table 2 we present several examples of two-step optimization results.

**Table 2. Examples of two-step optimization results.**

<table>
<thead>
<tr>
<th>Slice</th>
<th>$m$</th>
<th>$a$</th>
<th>$b$</th>
<th>$\theta$</th>
<th>$s$</th>
<th>$x_0$</th>
<th>$y_0$</th>
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<td>213</td>
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<td>1</td>
<td>2</td>
<td>55.92</td>
</tr>
</tbody>
</table>

### 4.3 Simplification of the model

The experiments show that optimal values of the parameter $\beta$ are close to $\pi$. Therefore, $\beta$ can be fixed at $\pi$, i.e. it may be set as a non-optimizable parameter. This means that:

- subtraction for breastbone is applied for all $\phi \in [-\pi/2; 3\pi/2]$ in $\rho(\phi)$,
- the shape of the breastbone cave is controlled by the scale $c$ and power $l$. 

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Now, as shown in (11), only 8 parameters are optimized instead of 9 parameters in (8).

\[
\min_{s, \theta, a, b, x_0, y_0, \pi, c, l} f(s, \theta, a, b, x_0, y_0, \pi, c, l)
\]

(10)

Model (3) in polar coordinates becomes

\[
\rho(\varphi) = (1 + \cos(\varphi - \pi/2))^s - c \sin^l((\varphi + \pi/2)/2)
\]

(11)

Examples of two-step optimization results of simplified model are presented in Table 3. The optimization results of a simplified model as compared to that in Table 2 are slightly worse than in Table 3. However, less number of variables ensures faster optimization.

Table 3. Examples of optimization results of simplified model (two-step optimization).

<table>
<thead>
<tr>
<th>Slice</th>
<th>m</th>
<th>a</th>
<th>b</th>
<th>\theta</th>
<th>s</th>
<th>x_0</th>
<th>y_0</th>
<th>\beta</th>
<th>c</th>
<th>l</th>
<th>\min f(\cdot)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>6097</td>
<td>169</td>
<td>253</td>
<td>0.05</td>
<td>0.63</td>
<td>257</td>
<td>187</td>
<td>3.14</td>
<td>1</td>
<td>6.94</td>
<td>24.35</td>
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<tr>
<td>36</td>
<td>6561</td>
<td>210</td>
<td>287</td>
<td>0.07</td>
<td>0.36</td>
<td>261</td>
<td>239</td>
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<td>0.89</td>
<td>4.36</td>
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<tr>
<td>71</td>
<td>5686</td>
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<td>295</td>
<td>0.08</td>
<td>0.64</td>
<td>258</td>
<td>212</td>
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<tr>
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<td>215</td>
<td>3.14</td>
<td>1</td>
<td>3.45</td>
<td>58.21</td>
</tr>
</tbody>
</table>

5 Conclusions and Discussions

In this paper, a method for the analysis of transversal plane images of computer tomography scans is presented. This method allows us not only to find the approximation of the ribs-bounded contour, but also to evaluate the patient rotation around the vertical axis during scans.

The experiments have shown that the number m of bone pixels depends on the CT scan slice and is large. Among the pixels of the images of size 512 × 512, the bone pixels take about 2%.

The angle \( \theta \) of patient rotation around the vertical axis during the scan is about 6° in the analyzed data. The angle is not large, but its optimal estimate allowed a more precise approximation of the rib-bounded contour.

The proposed approximation defines the rib-bounded contour exactly. The average distance between the model the bone-tissue pixels is about 4.94, it is about 7.3 mm (one pixel represents 0.916016 mm × 0.916016 mm area in the investigated CT data). The model can be applied to any 2D slice, where the ribs are visible. Definition of the area of internal organs from the ribs-bounded contour essentially restricts the search area, where these organs are located and may serve as an effective start for a detailed localization of a particular organ.

Further research can be directed at the CT scan image registration. When evaluating the effectiveness of the treatment, pre- and post-treatment CT scans must be made (for the same patient) and compared by aligning (registering) these two (or more) scans [7]. The model of the ribs-bounded contour can serve as the basis of a criterion of similarity of images (slices). In this case, we would have a method of the feature-based registration. Moreover, some mixture of feature-based and region-based registration may be developed seeking to strengthen accuracy of registration and to compensate the disadvantages of both methods.
6 References


