

Computed Tomography Image Analysis: The Model of Ribs-Bounded Contour

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ABSTRACT

In this paper, a method for analyzing transversal plane images from computer tomography scans is presented. This method allows not only the approximation of ribs-bounded contour but also the evaluation of patient rotation around the vertical axis during a scan. 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 mathematical model using least-squares.

Keywords

Ribs, ribs-bounded contour, mathematical model, computed tomography, cardioid, least squares, optimization.

1. INTRODUCTION

In medicine, more and more decisions are made via analysis of images. Image data comes 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 [Nug08], prostate [Che11]. CT scans are 3D images – a collection of 2D images (slices), representing slices by transversal plane. This paper deals with the finding the ribs-bounded contour. This is important for internal organ localization. In liver localization, the liver tissue looks very similar to intercostal muscles, which are separated by thin and almost invisible contours (where liver touches ribs). So, the ribs bounded contour restricts the region of location of internals in the slice. Internal organ localization is particularly important for the comparison of patient health state or to evaluate disease processes. Here the image registration problem arises (see e.g. [Tre08]).

CT scans show tissues of different electron density; bones have the highest density [Nug08] so bone tis-

sue has the highest intensity in the CT image. The goal of our paper is to define the ribs-bounded contour by some mathematical model and to propose a way to evaluate the parameters of this model from the CT image. In this paper, we are restricting the slices to ones where ribs are visible, but this does not lessen the significance of our work, because many important internal organs are located here: liver, heart, stomach, pancreas, lung, etc.

2. DATA TO BE ANALYZED

Example of CT scan slices is shown in Fig. 1. Depending on the slice, the heart, lungs, stomach, or liver can be seen. In all the cases of Fig. 1 internal organs are bounded by ribs. Fig. 1 was obtained after the patient was given a radiocontrast agent injection. In this image, the heart and aorta as well as all blood vessels are bright. We are investigating two dimensional images of size 512×512 .

3. METHOD

In this section a method of analysis of CT scan slice (through transversal plane) is proposed. This method allows us not only to find the ribs-bounded contour but also to evaluate patient rotation around the vertical axis during the scan.

We notice a symmetry of the ribs by the human sagittal plane, body rotation in respect to bed, aorta near spine, high grayscale intensity of bones, bed, heart and blood vessels (if the radiocontrast agent was injected to the patient). All these must be considered when building a method.

Our method consists of two steps: (a) extracting the bone tissue from image; (b) approximating the ribs-bounded contour with a mathematical function.

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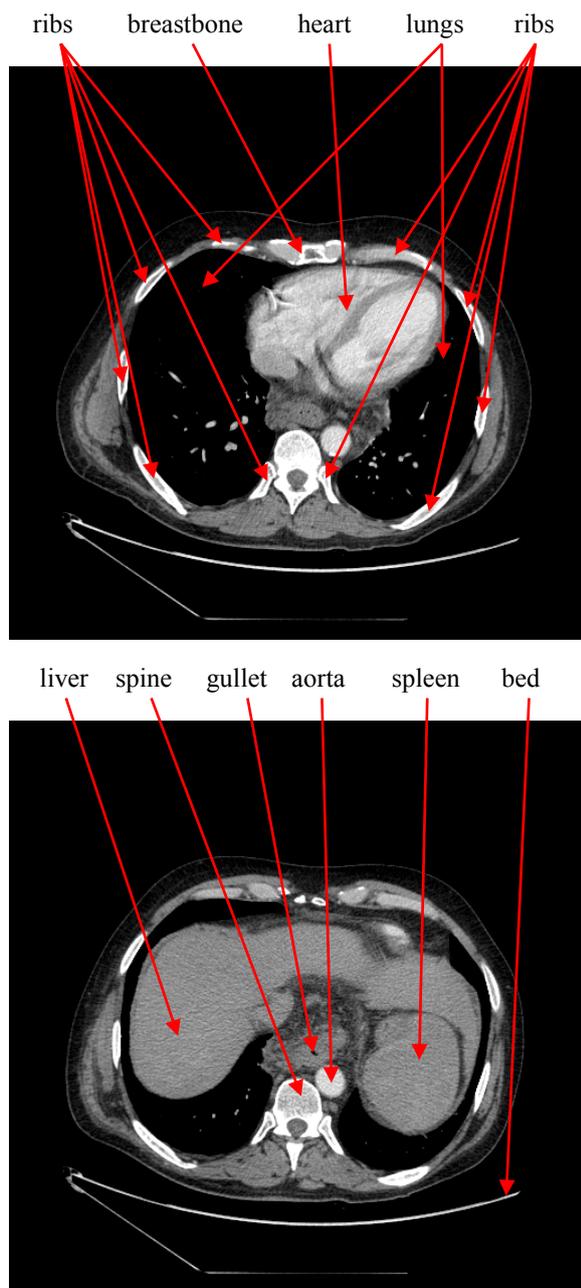


Figure 1. Examples of the CT image slices.

Body tissue extraction

Because bone tissue is naturally brighter than any other tissue, an image can be thresholded – extracting pixels with a value higher than 150 if the whole CT scan is linearly normalized between 0 and 255. This threshold is chosen after the discussion below.

In [Hen02], the electron density of internal organs is evaluated. The densities are given in Table 1. We see that the maximal electron density is of bone, at $5.29 \cdot 10^{23}$, and the minimal electron density of bone is $3.72 \cdot 10^{23}$. The lung has the minimal possible density among internal organs with $0.83 \cdot 10^{23}$. In CT scan slices, lung tissue is purely black. Therefore, the

problem is to transform the interval $[0.83 \cdot 10^{23}; 5.29 \cdot 10^{23}]$ into the interval $[0; 255]$ and to find the point of the last interval corresponding to $3.72 \cdot 10^{23}$. After such conversion, we get the brightness 165 corresponding to the minimal electron density of the bone. Leaving some reserve, we fixed the threshold at 150.

Tissue	Electron Density (electrons/cm ³)
Water	$3.35 \cdot 10^{23}$
Bone	$3.72 - 5.29 \cdot 10^{23}$
Spleen	$3.52 \cdot 10^{23}$
Liver	$3.52 \cdot 10^{23}$
Heart	$3.46 \cdot 10^{23}$
Muscle	$3.44 \cdot 10^{23}$
Kidney	$3.42 \cdot 10^{23}$
Pancreas	$3.40 \cdot 10^{23}$
Fat	$3.07 \cdot 10^{23}$
Lung	$0.83 \cdot 10^{23}$

Table 1. Electron density of body area [Hen02]

After thresholding, undesirable regions can be selected: lateral objects like the bed or metal implants, and everything that contains blood with radiocontrast agent – heart and vessels. These regions can be removed with morphological operations [Rus11].

To extract the bone tissue, we suggest the algorithm:

```

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)-
   Rectangle(512,spine.GravityCenter.Y));
6. convexHullPoints={};
7. for each slice in image
   convexHullPoints=convexHullPoints U
   slice.ConvexHull;
8. image=
   image.FilterConnectedComponents
   (convexHullPoints);

```

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. `FillIsolatedBlobs` fills with white the isolated black blobs that are on larger white ones, `MorphologicalOpen(x)` and `Dilate(x)` are morphological open and dilate operators respectively with round kernel of diameter $2x + 1$. Function `Rectangle((x0, y0) - (x1, y1))` makes a binary image with a white filled rectangle at specified coordinates, and `&&` is pixel-wise binary AND operator. The binary image subtraction `X - Y` compares each pixel and returns the nonimplication. `GravityCenter` changes a binary blob to its center of gravity, `FilterConnectedComponents(seeds)` leaves bi-

nary blobs that are connected to seeds only. `ConvexHull` returns a set of points of the convex hull of all white pixels in the binary slice. A set `convexHullPoints` joins such convex hulls points of all slices of the CT scan. `FillIsolatedBlobs` is necessary because inner rib tissue may appear in black after the binarization using the threshold. `Spine[z].Dilate(4)-spine[z]` analyzes the slice z and gives the 4 pixels thickness ring around the spine. Its top part (intersection with rectangle) is subtracted from the image to separate aorta from spine where they touch each other. Then convex hull of slice is actually a convex hull of ribs – bone tissue is blobs that are connected to ribs.

As a result of the bone tissue extraction above, we get binary images – see the example in Fig. 2.

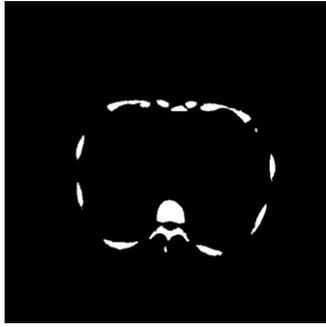


Figure 2. Pixels representing bone tissue.

Denote $B = \{(b_{1i}, b_{2i}), i = \overline{1, m}\}$ the set of coordinates of bone pixels obtained during analysis of CT image slices, m is the number of bone pixels.

Ribs-bounded contour approximation

The ribs form a shape similar to cardioid (see Fig. 1):

$$\rho = 1 + \cos(\varphi - \pi/2), \quad \varphi \in [-\pi/2; 3\pi/2] \quad (1)$$

Here ρ is the radius and φ is the polar angle. The shape of (1) is depicted in Fig. 3 (blue curve). It looks similar, because it features a cave which could be used to approximate ribs cave near spine. $\pi/2$ is introduced in (1) because the standard cardioid is rotated by 90° as compared with Fig. 3 and the ribs-bounded contour in the images should be oriented like ribs depicted in Fig. 1.

Our research showed that a ribs-bounded contour is more condensed vertically than the standard cardioid curve. Therefore, we suggest to add optimizable parameter – power s :

$$\rho = (1 + \cos(\varphi - \pi/2))^s \quad (2)$$

The (2) curve with different s is depicted in Fig. 3.

As we see in Fig. 1, the rib-bounded contour has some rotation in respect to the bed. Therefore, we should introduce the angle θ of such rotation. Parameter s influences not only the vertical scale of the curve (1), but the form of the curve, too (see Fig. 3 for curves with different values of s).

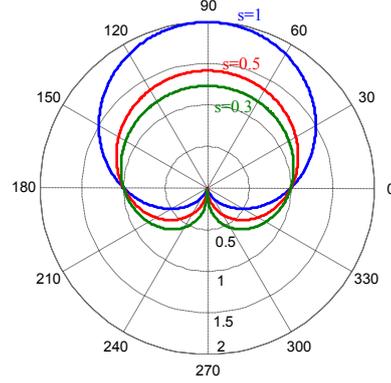


Figure 3. Blue – standard cardioid (1), red and green – (2) curve with $s = 0.5$ and $s = 0.3$.

In the CT scan slice (Figure 1), we see a cave influenced by the breastbone. Curve (2) is convex in this region. Therefore, we need to complement the model (2) redefining ρ with additional member ρ' whose form may vary depending on the cave:

$$\rho = (1 + \cos(\varphi - \pi/2))^s - \rho' \quad (3)$$

This member realizes the cave by subtraction of some value from the right side of (2) starting from $\varphi = \pi/2 - \beta$ till $\varphi = \pi/2 + \beta$. The member ρ' depends on φ and has special properties. It must (a) be unimodal non-negative function on φ , (b) achieve the maximal value as $\varphi = \pi/2$, (c) be symmetrical function in respect of $\varphi = \pi/2$, (d) be equal to 0 when $\varphi = \pi/2 - \beta$ and $\varphi = \pi/2 + \beta$, (e) have zero first and second derivatives on φ when $\varphi = \pi/2 - \beta$ and $\varphi = \pi/2 + \beta$. Function ρ' may be as follows:

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

In (4), we have three control parameters for which optimal values need to be found: β is an angle, defining the region of subtraction, c defines the maximal value of subtraction, l defines the steepness of curve describing the cave ($l \geq 2$). Example of ρ' is presented in Fig. 4 for different values of β , c , 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. The curve (3) should be fitted among ribs in the picture of bone tissue. For this reason, we need the optimal place of the point of (3) corresponding to $\rho = 0$ in the picture; denote coordinates of this point by (x_0, y_0) .

If the values of s , θ , a , b , x_0 , y_0 , β , c , l are fixed, we can draw some parametric curve $(x, y) = (x(\varphi), y(\varphi))$ approximating the rib-bounded contour:

$$\begin{aligned} x &= x_0 + a\rho \cos \varphi \cos \theta - b\rho \sin \varphi \sin \theta \\ y &= y_0 + a\rho \cos \varphi \sin \theta + b\rho \sin \varphi \cos \theta \end{aligned} \quad (5)$$

where ρ is defined by (3). If φ runs through the interval $[-\pi/2; 3\pi/2)$ with a step $2\pi/n$, we get from (5) a sequence of points $C_j = (x_j, y_j), j = \overline{1, n}$ of the curve. In our experiments, $n = 180$.

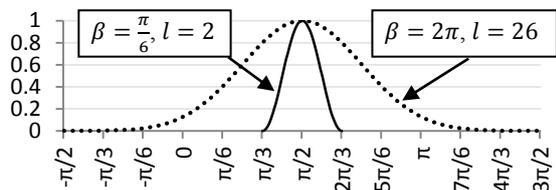


Figure 4. Dependencies of function ρ' on φ . $c = 1$.

Optimization problem

The model of ribs-bounded contour has nine parameters whose values can be varied seeking to find the best approximation of the contour: $s, \theta, a, b, x_0, y_0, \beta, c, l$. The optimal values of these parameters must be defined by the set B of coordinates of bone pixels obtained during the analysis of CT image slices. The optimization problem to find optimal $s, \theta, a, b, x_0, y_0, \beta, c, l$ is formulated as a least square one:

$$\min_{s, \theta, a, b, x_0, y_0, \beta, c, l} f(s, \theta, a, b, x_0, y_0, \beta, c, l) \quad (6)$$

$$f(\cdot) = \sum_i^m \|B_i - C_{k_i}\|^2, \quad k_i = \arg \min_j \|B_i - C_j\|$$

The optimization method to solve (6) may be any local minimization one. We use the Matlab realization of the quasi-Newton method [Unc15].

4. RESULTS

The performance and efficiency of the proposed method is illustrated in Figure 5. Approximation of the ribs-bounded contour is put on the image in red. The optimization results are as follows: $\min f(\cdot) = 212611$, $m = 5403$, $a = 160.51$, $b = 217.01$, $\theta = 0.076$, $s = 0.35$, $x_0 = 265.2$, $y_0 = 296.52$, $\beta = 6.25$, $c = 0.71$, and $l = 28.375$. The average distance from points from B to the curve approximating the ribs-bounded contour is 4.95 pixels. Both θ and β mean radians. Note, that the value of angle β is greater than π . This is acceptable because the values of function ρ' are close to zero at the boundaries of φ domain $[-\pi/2; 3\pi/2)$ when l is large (see Fig. 4).

5. CONCLUSIONS

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 vertical axis during scans.

The experiments showed that the number m of bone pixels depends on the CT scan slice and is large. The angle θ of patient rotation around vertical axis during the scan is about 4° in the analyzed data. This angle

is not large, but its optimal estimate allowed more precise approximation of the rib-bounded contour. Power s in (2) and (3) is less than 1. The angle β , defining the region of subtraction, is greater than π . This means that the subtraction is performed for all ρ in entire domain of φ . The steepness l of curve describing the cave is very large. The combination of values of angle β and steepness l allows us to describe various forms of cave influenced by the breastbone.

The proposed approximation defines the rib-bounded contour exactly. The model may be applied to any 2D slice where the ribs are visible. 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.

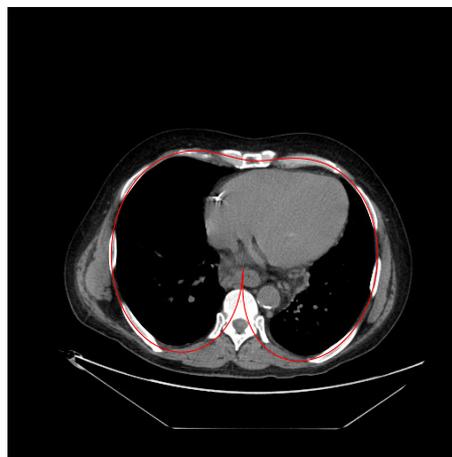


Figure 5. The ribs-bounded contour.

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