

Novel Approach of Simplification Detected Contours on X-Ray Medical Images

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Abstract

This paper gives description of a method for simplifying the number of points representing detected contours of the bones on digital X-ray images. Such simplification permits simplify way for correction the location of these points in the cases, if the analyzed image has poor quality, and to reduces the time of analysis it to get the reference lines and angles for diagnosis purposes of the area under investigation.

Key words: Object recognition, Digital X-ray image, reference lines and angles, contour simplification, Medicine diagnosis system.

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Introduction

X-ray diagnostics has a long history of development and is a field of medicine that has accumulated considerable experience, on the one hand, and on the other hand, developing as a result of new approaches and new technical means, including equipment for obtaining information, as well as algorithms and means for processing this information [1–5].

In [6–8], a method was developed for determining the boundaries of contours in medical radiographs using a complex of algorithms (Canny boundary detector, watershed algorithm, morphological operations, etc.).

These methods were used to detect deformities of human limbs by analyzing X-ray images using the so-called method of reference characteristics, anatomical and mechanical axes and angles, which allow the specialist to conclude that there are no deviations from the norm determined using expert estimates, or the presence of such deviations and in this case, suggest a treatment regimen [9–14].

Main part

The analysis scheme described in [6, 7] was used to create an application [15] that allows to obtain the above characteristics automatically. The selection of the bone contour to be analyzed is an important processing step. Here the result is previously obtained as a sequence of points representing the contour of the bone under analysis. The points are set by their coordinates on the lattice being the domain of definition of the image.

Experiments conducted using a large amount of real data have shown that in a relatively small number of cases it is impossible to obtain the reference characteristics in automatic mode. In all these cases, the reason was the poor quality of the original images due to the features of the diagnostic study or significant deviations in the analyzed areas.

To process images in such cases, the ability to manually adjust the contour was added to the software

product. The image of the automatically obtained boundaries of the contours on the screen is superimposed on the obtained radiograph in the form of a piecewise-linear contour determined by the found points, and the user, taking into account the radiograph itself, can move several of these points. (The user defines incorrect result of detected boundary, by visual way). It turned out that with a large number of points representing the contour, the correction mentioned above is very difficult or even impossible (see Fig. 1.).

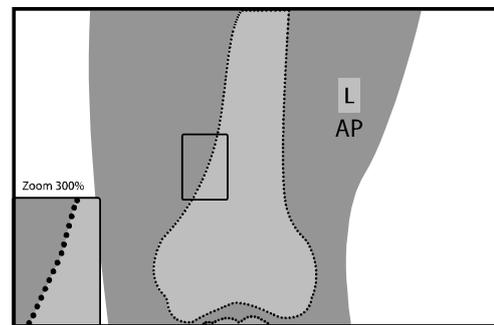


Fig. 1. The number of points on the border of bone

In connection with this problem, a method for reducing the number of points representing the contours of the bone was additionally developed and added to the software product. On the analyzed bone contour, sections that are approximately rectilinear are selected sequentially, and all points of each of these sections, except the extreme ones, are discarded. In this case, a natural restriction arises: simplification does not affect the quality of determining the reference characteristics.

To determine the possibility of replacing the image of a part of the bone contour with a segment, a numerical characteristic is used - the maximum deviation of this fragment from a straight line, allowing this operation to be performed. These characteristics were found for individual fragments of the contours of each of the bones under consideration as a result of experiments. In critical areas, which in some cases carry important information

for diagnostic purposes, additional analysis is carried out to prevent the loss of significant data.

We consider the coordinate plane and the discrete lattice of points with integer coordinates on which the contour points are plotted.

Let $M_0, M_1, \dots, M_k, M_0 \neq M_k$ be a sequence of points on the coordinate plane. We introduce the concept of deviation of this sequence from the segment: it is the largest of the distances of points M_1, M_2, \dots, M_{k-1} from segment M_0M_k . There is obtained a formula expressing this value using the coordinates of points.

Let us first consider a special case: $M_i(x_i, y_i), i=0, 1, \dots, k$, the start point M_0 and the end point M_k lie on the axis Ox , so $y_0=0, y_k=0$, let ρ denote the deviation of this sequence from the segment M_0M_k . It's obvious that $\rho = \max_{1 \leq i \leq k-1} |y_i|$ (see fig. 2.).

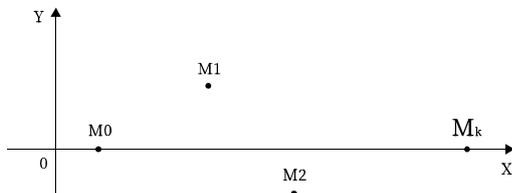


Fig. 2. Deviation from a segment in a particular case

The general case is reduced to the previous one. Suppose that the points have the coordinates: $M_i(x_i, y_i), i=0, 1, \dots, k, \varphi$ –the angle between the ray having the vertex at the point M_0 and passing through the point M_k and the axis Ox .

We consider the new coordinate system, taking the point M_0 as its origin and assuming that the new abscissa axis Ox' forms the angle φ with the original abscissa axis. Then the point M_k will also be on the axis Ox' (see fig. 3.).

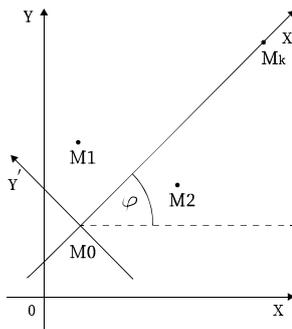


Fig. 3. Rotation of the plane.

Then:

$$\cos \varphi = \frac{x_k - x_0}{\sqrt{(x_k - x_0)^2 + (y_k - y_0)^2}} \tag{1}$$

$$\sin \varphi = \frac{y_k - y_0}{\sqrt{(x_k - x_0)^2 + (y_k - y_0)^2}} \tag{2}$$

Suppose that the points M in the original coordinate system had coordinates (x, y) , and in the new system it has the coordinates (x', y') , There hold the following relations:

$$\begin{cases} x' = (x - x_0) \cos \varphi + (y - y_0) \sin \varphi \\ y' = -(x - x_0) \sin \varphi + (y - y_0) \cos \varphi \end{cases} \tag{3}$$

Deviation of points from a segment does not change after transition to a new coordinate system. If $M_i(x_i, y_i)$, then for $i=1, 2, \dots, k-1$ we obtain:

$$y'_i = -(x_i - x_0) \sin \varphi + (y_i - y_0) \cos \varphi,$$

or:

$$y'_i = -x_i \sin \varphi + y_i \cos \varphi + (x_0 \sin \varphi - y_0 \cos \varphi).$$

Therefore the deviation ρ can be found by the following formula:

$$\rho = \max_{1 \leq i \leq k-1} ((-x_i \sin \varphi + y_i \cos \varphi) - (-x_0 \sin \varphi + y_0 \cos \varphi)). \tag{4}$$

Here the values $\cos \varphi$ and $\sin \varphi$ are defined above.

The algorithm of reducing the number of points works as follows.

In accordance with the location of the considered part of the contour, the value of the maximum deviation ρ_0 is selected.

Starting from point M_0 , the following contour points are added sequentially until the deviation ρ of these points from the line satisfies the inequality $\rho \leq \rho_0$.

When the last point M_k for which this condition is satisfied is found, the intermediate points M_1, \dots, M_{k-1} are discarded, and the process continues from the starting point M_k . The default value of ρ_0 is found as a result of experiments and can be changed in the settings of the software product.

The fig. 4 shows the result of detecting the boundary for the femur in the X-ray image after using the proposed algorithm with the value $\rho_0=3$. In this case, the number of points is reduced by about 13 times. After such simplification, the correction of borders becomes much simpler and more reliable.

Although in the case of a successful boundary detection result, there is no need to adjust the boundary, such a fragment of the algorithm reduces the number of further calculations when searching for the required reference characteristics, which ultimately leads to program acceleration.

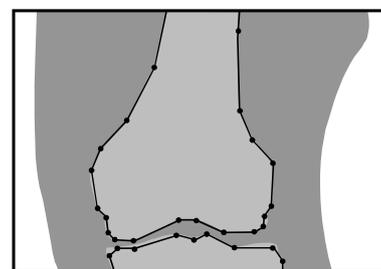


Fig. 4. Boundary detection by proposed algorithm

Experiments

The experiments were carried out on 20 images of the knee joint, in each of these attempts there were found two

contours, the upper of which was the femur, and the lower tibia. The data given in the table 1 allow us to compare the initial number of contour points and the results of applying the proposed contour simplification algorithm; the mentioned above $\rho_0=3$ was obtained as a default value after applying the new method on these images.

Table. 1 Data experiments.

No.	Before Simplification		After Simplification	
	No. points of femur	No. points of tibia	No. points of femur	No. points of tibia
1	324	358	26	19
2	348	345	21	21
3	308	357	25	20
4	352	426	24	25
5	311	331	24	24
6	339	418	26	23
7	261	378	23	19
8	299	368	26	25
9	407	422	26	33
10	336	411	26	23
11	432	493	31	21
12	351	377	26	24
13	446	449	22	22
14	361	451	27	21
15	387	409	26	21
16	323	376	27	22
17	235	256	19	20
18	337	379	25	22
19	298	383	27	23
20	319	373	23	23

The user can change the value of ρ_0 in software settings. We mentioned here that the threshold value of the maximum deviation ρ_0 was determined experimentally, and it is no more than five. (As not to influence on the result of diagnosis, which depends on the detected boundary of bone).

The experimental results show that in case of an error in determining the boundary of the contour, incorrectly found points are in a relatively small neighborhood of the boundary. Then, with manual adjustment, the user should only move points that are not on a visually defined border. This means that such a correction does not take much time to fix the boundary detection error. The fig. 5 shows the result of the detection of boundaries, the error region is represented by 4 points. In this case, the user must move these points to the correct places, which should lie on the boundary of the contour.

It should be noted that in the software product for greater flexibility of its use, functions for adding and deleting points are provided

Testing in medical institutions has shown the effectiveness of a software product developed using the pro-

posed algorithm, both in terms of the reliability of the results and in terms of processing speed (less than 0.4 seconds for a standard size image in cases where an additional setting is not used). Users also noted the simplicity of the additional settings required in a fairly small number of cases. Experiments confirm that the proposed simplification of contours doesn't effect on the diagnosis accuracy results.

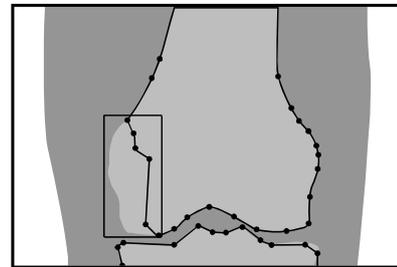


Fig. 5. The domain of the error region

Conclusion

Simplifying the contour using the proposed algorithm reduces the total amount of calculations, significantly reduces the time required for analyzing the x-ray image in most cases, when the analysis can be done in fully automatic mode, simplifies visual correction if necessary, allowing to get the desired result in this case, eliminating the need for repeated radiography.

This algorithm has significantly improved the performance of the software product in various cases, both in the case of analysis of individual x-ray images, and in the case of analysis for a series of the same type images.

The proposed and successfully tested algorithm makes it possible to significantly simplify information about the analyzed geometric objects in cases when eliminating redundant data allows to solve problems of saving memory, speeding up the program, and simplifying visual analysis. An insignificant modification allows to use the proposed method in the case of analyzing surfaces in three-dimensional space.

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