

Segmentation of Lung Images Using Textural Features

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Abstract. This paper proposes a technology for lung image segmentation using textural features. To analyze the informativeness of the features, the K-Means method was used. The segmentation result can be used to describe the characteristics of the patient: age, gender, physique, etc. The study was conducted on a large set of fragmented images. X-ray clustering errors for the 12x12, 24x24, and 36x36 fragmentation windows were presented. Pre-processing of images was also used to estimate the quality. The study showed that the technology provided key objects selecting error at little more than 25%. However, the alignment procedure reduced this error to 13%. When using the k-means method, a link was found between the segmentation error and the size of the fragmentation window. The selection of the range of interest on the lungs x-ray in accordance with the equalization was considered preferable. The high error of the first clustering method was associated with the choice of feature space; in our case, image processing was conducted for all features calculated using MaZda software.

1. Introduction

Lungs X-ray is used in pulmonology and this procedure is relatively fast and easy. It is particularly useful for screening respiratory diseases such as pneumonia and tuberculosis. According to medical studies, the mass of the lungs, being unevenly distributed in the chest, and has a higher density in the lower lobes. Many diseases can be distinguished at early stages due to the lung size screening and the ribs changes monitoring. In addition, the lung mass increases with a fibrosis degree because of conjunctive tissue diffusing [1]. Nowadays, there are no clinical methods to measure the density of the lungs directly. High-resolution computed tomography as the clinical standard in pulmonary fibrosis diagnostics, considers specific emission decreasing in lung tissue [2, 3]. These changes can be distinguished through the lungs x-ray image analysis. A technique based on textural features selection has been suggested for the x-ray image analysis. Earlier, textural features had shown good results for the recognition and further diagnostics of biomedical images [4-8]. Considering the relevance of the problem, the researchers have come up with a number of solutions based on feature generation via discriminative analysis [7], followed by image segmentation [9-11]. The well-known MaZda library [12-13] was used to calculate the textural features. The work [14] explores the detection of pathologies using blood cells images through textural characteristics of different classes of the source images in various colour subspaces; and as recent studies have shown, textural analysis is very well suited for highlighting the ranges of interest in medical pictures [4-9, 14].

A technology enhancing the ranges of interest, using the k-means classification methods has been proposed. The main benefit of the method is an opportunity to highlight the regions of interest by their textural features. The level of interaction between the signs, expressed by the value of correlation



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coefficients [7], may serve as additional information, which helps to improve the quality of the x-ray pictures of the lungs diagnosis. If the correlation between the signs is strong enough, the question arises about the appropriateness of using these signs and the possibility to reduce the dimension of feature space either by abandoning some of them and using only one of the associated signs or by identifying common properties. In the first case, we reduce the number of calculations, leaving the best feature values of any criterion. In the second case, the ability to obtain a new, more effective feature for classification appears. This technique was used in the work [15] and ensured high precision segmentation of fundus images. The presented results indicate that the proposed technology seems to be the most effective for x-ray image analysis.

2. Texture features

It is necessary to form such a set of features, on the basis of which it is possible to automatically conduct a more accurate classification of this image. As we mentioned above, texture features have shown themselves to be well-suited for biomedical image recognition and subsequent diagnostics. Consider some of the signs of texture, based on the statistical characteristics of the intensity levels of the elements of the decomposition. For the formation of these features, taking into account the mutual arrangement of pixels within a sliding window, there is an approach based on the use of an adjacency matrix [13, 8]. The software “MaZda” [8, 12, 13] utilized in this work is able to calculate the following groups of texture features: a) those based on statistical characteristics (histogram-based features); b) those based on gradient parameters; c) those based on the co-occurrence matrix; and d) those based on run-length matrix (see MaZda user manual, http://www.elel.p.lodz.pl/mazda/download/mazda_manual.pdf for further details) [13].

Let the analyzed image is rectangular and has N_x elements horizontally and N_y elements vertically. In this case, $G = \{1, 2, \dots, N\}$ - is the set of N quantized brightness values. Then the image is described by a function of brightness values from the set G , that is function $f : L_x \times L_y \rightarrow G$, where $L_x = \{1, 2, \dots, N_x\}$ and $L_y = \{1, 2, \dots, N_y\}$ - are horizontal and vertical spatial domains respectively. The set of N_x and N_y is a set of resolution elements in the bitmap.

The adjacency matrix contains the relative frequencies $p(i, j)$ of the presence of neighboring elements located at a distance d from each other, with brightness values $i, j \in G$. On the basis of adjacency matrices, texture features can be calculated. Below are some examples of it: 1) The second angular momentum - characterizes the degree of image homogeneity: $T_1 = \sum_{i=1}^N \sum_{j=1}^N p^2(i, j)$, where

$p(i, j) = P(i, j)/M$ - is the relative frequency of the presence in the image of neighboring elements located at a distance d from each other, with brightness values $i, j \in G$, $P(i, j)$ - is the frequency of appearance of two pixels in a sliding window with brightness i and j at an angle α at a distance d , M - is the total number of pairs of adjacent elements. 2) Contrast - describes the degree of contrast of the

image: $T_2 = \sum_{n=0}^{N-1} n^2 \sum_{i=1}^N \sum_{j=1}^N p(i, j), |i - j| = n$. 3) The correlation coefficient - serves as a measure of the

linearity of the regressive dependence of the brightness on the image:

$T_3 = \sigma_x^{-1} \sigma_y^{-1} \sum_{i=1}^N \sum_{j=1}^N [ijp(i, j) - m_x m_j]$, where $m_x, m_y, \sigma_x, \sigma_y$ - mean values and standard deviations for

$$p_x(i) = \sum_{j=1}^N p(i, j) \text{ and } p_y(j) = \sum_{i=1}^N p(i, j).$$

4) Dispersion - determines the brightness variations relative to the average value: $T_4 = \sum_{i=1}^N \sum_{j=1}^N (i-m)^2 p(i, j)$, where m – mean value. 5) The moment of the inverse difference is closely related to the contrast and reflects the degree of scatter of the elements of the matrix of gradients around the main diagonal $T_5 = \sum_{i=1}^N \sum_{j=1}^N \frac{1}{1+(i-j)^2} p(i, j)$. 6) The total entropy for the histogram of the sums of brightness values is determined by the classical measure of the statistical information theory and expresses the uneven distribution of the brightness properties of the image elements: $T_6 = \sum_{i=1}^N \sum_{j=1}^N p_+(n) \log p_+(n)$, where $p_+(n) = \sum_{i=1}^N \sum_{j=1}^N p(i, j), i+j=n, n=2,3,\dots,2N$ - histogram of sums of brightness values. 7) Entropy - is defined in the same way as total entropy, but only for the adjacency matrix. 8) Differential entropy - calculated as total entropy and entropy for the adjacency matrix, but for the histogram of differences in brightness values.

Now consider some of the features of texture, based on the description of structural elements. Below are features based on the length of the series. The length of a texture series is the number of raster line elements that have a constant brightness.

Let $C_\rho(i, j)$ denote the number of lines whose length is equal to j and which are oriented in the direction. The direction of the lines can be horizontal ($\alpha = 0^\circ$), vertical ($\alpha = 90^\circ$) and transverse-diagonal ($\alpha = 45^\circ, \alpha = 135^\circ$). Then we can distinguish the following features: 1) Moment:

$T_7 = \frac{1}{n_r} \sum_{i=1}^M \sum_{j=1}^N C(i, j) j^2$, where $n_r = \sum_{i=1}^M \sum_{j=1}^N C(i, j)$ – is the total number of lines, M – is the maximum

intensity level of this image, N – is the length of the longest line. This feature is characterized by the fact that for any gray level the weight of each line increases with increasing length. 2) Reverse

moment: $T_8 = \frac{1}{n_r} \sum_{i=1}^M \sum_{j=1}^N C(i, j) / j^2$. This feature is characterized by the fact that for any gray level the weight of each line decreases with increasing length. 3) Gray Level Distribution:

$T_9 = \frac{1}{n_r} \sum_{i=1}^M \left(\sum_{j=1}^N C(i, j) \right)^2$. This feature has a minimum in those cases when the number of lines of

constant optical density is uniformly distributed over gray levels. The distribution of the length of the

lines of constant optical density: $T_{10} = \frac{1}{n_r} \sum_{j=1}^N \left(\sum_{i=1}^M C(i, j) \right)^2$. 4) Relative number of constant optical

density lines: $T_{11} = n_r / n_p$ where $n_p = N_x N_y$ – is the total number of pixels in the image.

The features given above do not exhaust, all features on which classes for each pixel of the initial image were calculated.

3. The technique for automatic highlighting the lungs on x-ray images based on images pre-processing and k-means clustering

We analyse the selection of the lungs at the chest x-ray images using automatic image segmentation. This method is widely used in the processing of biomedical images for various purposes, for example, for the detection of lung or liver cancer [16]. For the study, it was necessary to form a set of features that could provide the most accurate classification of x-ray images. There was a large number of textural features. Within this study, the “MaZda” program calculated 287 features [13, 17]. Figure 1 shows the scheme for highlighting the regions of interest using the k-means method; we will describe each point in detail.

To recognize the individual objects at the x-ray picture, the following steps were undertaken. The original image was preliminary processed (Figure 2a) as follows: the flare spots with inappropriate, informative part of the image were removed; then the image was fragmented for textural features by 12×12 , 24×24 , 36×36 windows; and a set of textural features of fragmented images and clustering images based on the generated informative features was formed. For enhancing the lungs area, the initial image was preliminarily equalized. After that, the threshold processing was performed at 160, the amount of the threshold being set up experimentally. For the resulting image, see Figure 2c. An assessment of the height and width of each lung was performed, and in accordance with the data obtained (Figure 2b), nonilluminated images were cropped to leave only the parts with the lungs images being in the range of interest of the physician (Figure 2d). Next, the image was fragmented and the textural properties were calculated for every pixel by the MaZda program.

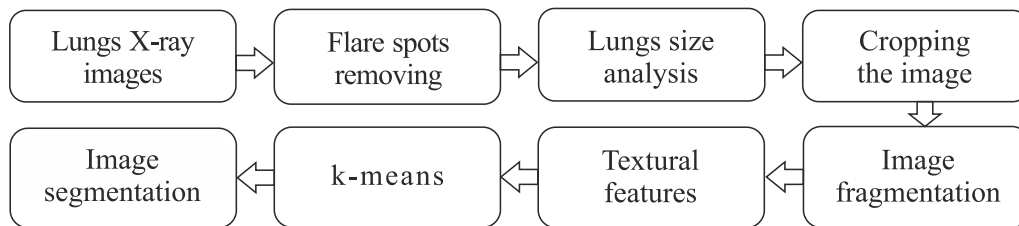


Figure 1. Technology for the regions of interest highlighting using the k-means method.

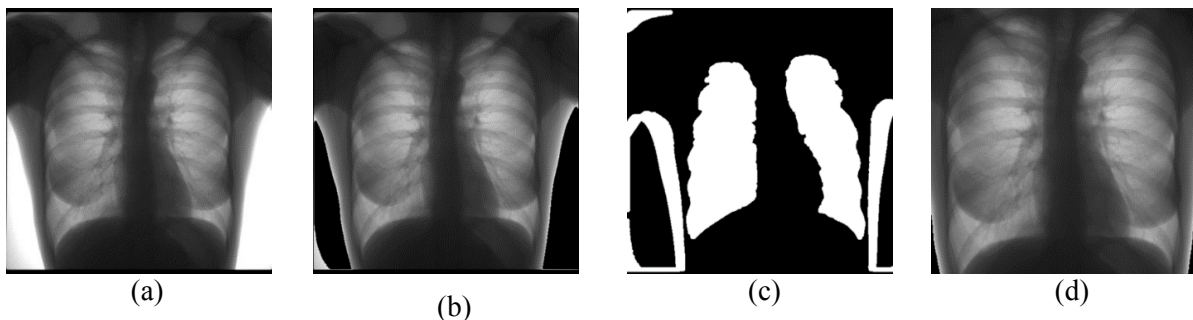


Figure 2. Image pre-processing results: (a) source image; (b) nonilluminated image; (c) equalized image with highlighted lungs and a flare spot; (d) image with the ranges of interest.

Having performed the space of features, clustering was performed based on the k-means method.

In the figure, the clustering of k-means on the lungs according to the textural attributes highlighted the ranges of interest incompletely. To improve the quality of the lung highlighting on X-ray pictures, the second technology based on morphological methods was considered. This technology is presented in Figure 3. A drawback of k-means is that it is not a deterministic algorithm. Typically, there are copious local minima; and the algorithm guarantees that it will converge to a local minimum rather than to a global one. Being an iterative algorithm (as the initial centers are not pre-set in advance), k-means starts with a random set of centers at the initial iteration and converges to a different local minimum in every run.

There is no magic bullet in practical applications, typically, trying to guess the location of initial centers is not easier as guessing where, for example, the global minimum is. The idea behind k-means, which essentially achieves determinism statistically, is simple. If we run k-means with the input number of clusters k but initially unspecified centers, every run will generally produce a new local optimum. k-means reduces and in fact essentially eliminates this indeterminism via two levels. This problem can be solved as follows. At level 1 it takes clusterings obtained via M independent runs or samplings. However, by aggregating a large number M of samplings, the degree of nondeterminism is greatly reduced. The “catch” is that sometimes this aggregation yields a clustering with $K' < K$ clusters, but this does not pose an issue. Thus, at level 2, we take a large number P of such

aggregations (each based on M samplings). The occurrence counts of aggregated clusterings are not uniform but typically have a (sharply) peaked distribution around a few (or manageable) number of aggregated clusterings. So this way we can pinpoint the “ultimate” clustering, which is simply the aggregated clustering with the highest occurrence count [16].

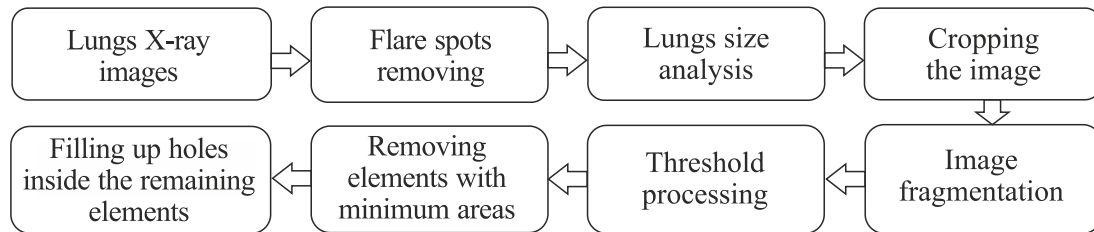


Figure 3. Technology for the selection of the ranges of interest according to the morphological methods.

In fact, it is acceptable in many applications. However, in the context of extracting of lungs signatures it might result in an exercise in futility. We need a way to eliminate or greatly reduce indeterminism, so we propose the second technique.

At the first step, similar to the technology based on the k-means method, the original image was cropped to avoid processing fragments that were out of interest. This method contained the following steps: equalization of the original image; removing the elements with the smallest areas (while two elements, i.e. the lungs, remain); filling in holes inside the remaining elements.

A comparative analysis of the results of the research methods was carried out and the corresponding errors were calculated, i.e. the k-means clustering error and the segmentation error of the equalization method. To analyze the obtained results, the image of the lungs highlighted by the expert was considered a reference. The clustering errors were calculated separately for each class, i.e. for the lungs and for the background; in case of the lungs, the error was calculated as a ratio of the number of incorrectly classified image fragments to the total number entering the region of the lungs. For the results of the analysis, see Table 1.

Table 1. Clustering error.

	1 class (lungs)	2 class (background)	Total error
Segmentation errors 1nd method (12×12, %)	29.16	56.70	38.49
Segmentation errors 1nd method (24×24, %)	33.2	27.83	30.61
Segmentation errors 1nd method (36×36, %)	40.93	17.69	28.06
Segmentation errors 2nd method (%)	24.26	0	13.20

The total clustering error with the k-means method was 38.49% for 12×12 fragmentation, 30.61% and 28.06% for fragmentation 24×24 and 36×36 respectively. For the equalization, the error was noticeably smaller and amounted to 13.2%, and all the pixels corresponding to the segmentation error were located at the boundaries of the range of interest; that fact simplified further improvement of the algorithm.

4. Conclusion

The present study considers the application of the k-means method for the detection of images of individual objects, such as the lungs and background. The information technology for automatic highlighting the ranges of interest on lung X-rays has been proposed. The article presents the relationship between the segmentation error and the fragmentation window size. The analysis of the obtained images was carried out, and the clustering error was found. Regarding the first method of lung X-ray, the result was less effective and revealed the objects of certain classes with an error of

28.06%, whereas technology based on the morphological methods highlighted lungs with an error of 13.90%. The clustering error of the x-ray image for the fragmentation windows of 12×12 , 24×24 and 36×36 has also been found. The selection of the range of interest on the lungs x-ray in accordance with the equalization was considered preferable. The high error of the first clustering method was associated with the choice of feature space; in our case, image processing was conducted for all features calculated using MaZda software. In the future, we are planning to improve the results by the use of discriminant analysis for texture features.

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