Model-Based Interpretation using Anatomic Landmarks for Defining Shape Variations of the Lung and Heart

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Abstract
In this paper we review a PDM method for defining simple and flexible model of shape variations of the lung and heart anatomy in chest radiographs. Boundaries of these organs are represented by a set of landmark points and modes of variations are determined from ways which the landmark points tend to deform from a mean shape. The method has linear computational complexity. This model can be used as initial hypothesis in automatic image search, segmentation, and cancer detection algorithms. This method is shown to be an efficient method for refining initial hypothesis and has much less dimensions as compared to the original shape data.
Keywords: Landmarks, Mean Shape, Alignment, Boundary, Radiographs

1. Introduction

Organs among different people are varied in terms of size, shape, and appearance, and that is why it is very difficult to automatically identify, analyze, and segment a specific organ of body, such as lungs or the heart, in medical images using computer-aided diagnosis.

In order to overcome this problem, we can view variations in size, shape, and appearance through different methods. In references [1-3], some general methods for modeling these variations have been presented, but they are not applicable in medical studies, such as the present one. In [4-7] more specific methods have been presented, but, although they generally use a high level of applicability, again they are not applicable in other areas because the designer needs to define a distinct template for each application manually.

In this paper, the method of Point Distribution Models (PDM) has been utilized to model the variations in the size and appearance of the heart and lungs [8]. This method has complications in linear computations and works efficiently in medical applications. In this method, the boundaries of the target body part in the database are represented by a

number of landmarks. Then, the set of landmarks in all images are aligned with each other so that we can align similar landmarks of different images in a single coordinate.

In the end, the parameters of the model which include mean shape, landmarks, and vectors that describe mode of the variations will be calculated.

This model can be used in many segmentation methods, such as Active Shape Model, to determine organs and subsequently cancers detection [9-11].

2. Database

In order to have a sufficiently flexible method that can show different modes of variations, we need to use a sufficient database. Since every image in the database will have an effect in the final model, great care needs to be taken to choose images for the database.

In this paper, JSRT database, which includes 247 images of chest radiographs, has been used [12]. These images have been taken from thirteen institutes in Japan and one institute in the US. The size of the images is 2048*2048. Each pixel is 0.175 millimeters with a 12-bit gray scale. The images have been divided into two groups of normal and non-normal. 154 images have one nodule, while the other 93 images do not have any nodules. Figure 1 shows a sample image taken from our JSRT database.

Figure 1 – Image from JSRT database

3. Landmarks

In order to model the shape of a specific organ, such as lungs, its boundaries in each image are determined by a number of landmarks. Determining the number of landmarks and their labeling is of great significance. The number of the landmarks needs to be determined in a way that the whole shape with all its details is covered. The landmarks in each image need to be placed at the right place with great care. In addition, the order of

putting landmarks must be similar in all images. This is a very time-consuming task and need experts' supervision of the whole process.

In this paper, in order to determine the boundaries of lungs and the heart, we used SCR database [13]. This database has been divided into two groups of normal versus non-normal images, just like the images in JSRT database. SCR database has determined the boundaries of these body parts in all the images of JSRT database. This database has been developed by a radiologist and a computer software engineer. 50, 44, 26, 23, and 23 landmarks have been used for left lung, right lung, heart, left clavicle, and right clavicle respectively. Figure 2 shows the boundaries of the lungs, the heart, and the clavicles in a sample image of JSRT database [13].

Although locating landmarks in this database has been done manually, designing the final model and calculating the extent of variation dispersion are both automatic processes. The final model that is supposed to describe the variations of the shape will be formed based on the pose variations of the landmarks in the whole database. In other words, each landmark in all images has specific distribution. Since the final model is formed by these landmarks, it is called point distribution model.
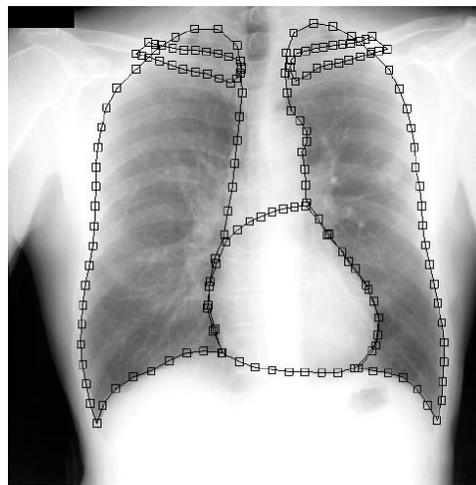

Figure 2 – Boundaries of the left and right lungs, heart, and left and right clavicles have been determined using 50, 44, 26, 23, and 23 landmarks respectively.

4. Modeling Shape Variations of the Heart and Lungs

4-1 Aligning images
In order to make similar landmarks in different images comparable, we need to align them in the same way with respect to a set of axes. If such alignments are not done, we cannot compare two different images. Such alignments are done through rotating, scaling, and translating. The aim of such alignments is to make different images as similar to each

other as possible. In addition, alignments minimize a weighted sum of squares of distances between equivalent points on different shapes [8].

4-1-1 Aligning a pair of images

In order to align two images of i and j with each other, let us assume that X_i is a vector with n landmarks that gives us the boundaries of these organs in the ith image of the database in the following way:

(1) $X_i = (x_{i0}, y_{i0}, x_{i1}, y_{i1}, \ldots, x_{ik}, y_{ik}, \ldots, x_{in-1}, y_{in-1})^{\mathrm{T}}$

Besides, $M_j[X_j]$ is X_j with θ_j rotation, S_j scale, and t_x and t_y translation to be aligned with X_i. Therefore, X_i will be obtained from equation (1), and $M_j[X_j]$ from equation (2):

(2) $M_j \begin{pmatrix} x_{jk} \\ y_{jk} \end{pmatrix} = \begin{pmatrix} (s_j \cos\theta) x_{jk} - (s_j \sin\theta) y_{jk} + t_{jx} \\ (s_j \sin\theta) x_{jk} + (s_j \cos\theta) y_{jk} + t_{jy} \end{pmatrix}$

E_j Will be minimized in equation (3) to align these two images:

(3) $E_j = (X_i - M_j(X_j))^T W (X_i - M_j(X_j))$

In the above equation, W is a diagonal matrix of weights for each point, which is obtainable for the Kth landmark from the following equation:

(4) $W_k = \left(\sum_{l=0}^{n-1} V_{R_{k,l}} \right)^{-1}$

In the above equation, $R_{k,l}$ is the distance between the landmarks k and l, and $V_{R_{k,l}}$ is the variance of this distance around all images. If a landmark is far from other landmarks, the total of variances will be great and thus lower weight will be obtained for that landmark. With the assumption of $a_x = s\cos\theta$ and $a_y = s\sin\theta$, then the least squares approach leads to a set of four linear:

(5) $\begin{pmatrix} U_2 & -V_2 & W & 0 \\ V_2 & U_2 & 0 & W \\ Z & 0 & U_2 & V_2 \\ 0 & Z & -V_2 & U_2 \end{pmatrix} \begin{pmatrix} a_x \\ a_y \\ t_x \\ t_y \end{pmatrix} = \begin{pmatrix} U_1 \\ V_1 \\ C_1 \\ C_2 \end{pmatrix}$

In the above equation, we will have:

(6) $V_1 = \sum_{k=0}^{n-1} W_k\, y_{ik}$ $\qquad\qquad$ $U_1 = \sum_{k=0}^{n-1} W_k\, x_{ik}$

(7) $V_2 = \sum_{k=0}^{n-1} W_k\, y_{jk}$ $\qquad\qquad$ $U_2 = \sum_{k=0}^{n-1} W_k\, x_{jk}$

(8) $Z = \sum_{k=0}^{n-1} W_k\, (x_{jk}^2 + y_{jk}^2)$

(9) $W = \sum_{k=0}^{n-1} w_k$

(10) $C_1 = \sum_{k=0}^{n-1} W_k\, (x_{ik}\, x_{jk} + y_{ik}\, y_{jk})$

(11) $C_2 = \sum_{k=0}^{n-1} W_k\, (y_{ik}\, x_{jk} - x_{ik}\, y_{jk})$

These can be solved for a_x, a_y, t_x and t_y using standard matrix methods [8].

4-1-2 Aligning all images

In order to align all the images in the database, we first align all images with the first image in the database. At the second stage, the mean of the aligned images is calculated. At the third stage, the calculated mean at the previous stage is changed into a default value. At the last stage, again all images are aligned with the mean of the images, and the algorithm back track to the second stage until the algorithm converges.

As it was stated before, the boundaries of the heart and lungs in the ith image of JSRT database is expressed through X_i vector. This vector is assigned a new size as a result of alignment with other images. Figures 3 and 4 show 247 vectors before and after alignment respectively.
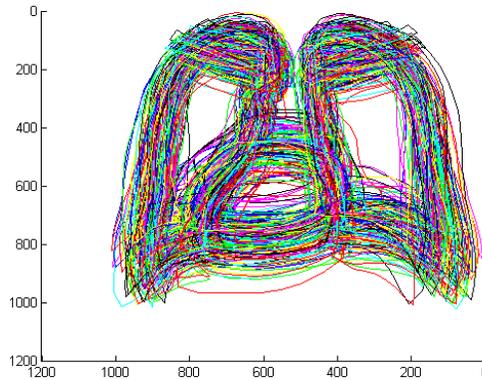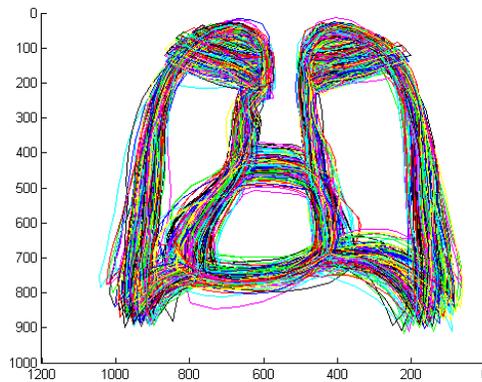
Figure 3 – 247 vectors before alignment

Figure 4 – 247 vectors after alignment

4-2 Parameters of the Model

After a set of aligned images is ready, we can calculate the mean shape and mode of the variations. For each X_i, the distance from the mean shape is calculated and labeled dX_i :

(12) $\bar{X} = \dfrac{1}{N} \sum\limits_{i=1}^{N} X_i$

(13) $dX_i = X_i - \bar{X}$

Now covariance matrix S is shown in equation (14):

(14) $S = \dfrac{1}{N} \sum\limits_{i=1}^{N} dX_i dX_i^{\mathrm{T}}$

Eigenvectors of this matrix describe the mode of variations. The mode of variation that each vector represents is determined by its similar eigenvalue. A large section of the variations are described with a limited number (t) of eigenvectors. Equation (15) can be used to find this limited number. The size of M is chosen arbitrarily, which is 0.9 in this research.

$$(15) \quad \sum_{i=1}^{t} \lambda_i \geq M \sum_{i=1}^{2n} \lambda_i$$

The covariance matrix for 247 aligned images of JSRT database has been calculated. Table 1 shows the most important eigenvalues obtained from this matrix. In this table, λ_T has been calculated from equation (16):

$$(16) \quad \lambda_T = \sum_{i=1}^{2n} \lambda_i$$

As Table 1 shows, almost 84% of these variations have been described by only 5 eigenvectors.

Table 1. eigenvalues obtained from covariance matrix of JSRT database

λ_i	eigenvalue	$\dfrac{\lambda_i}{\lambda_T} \times (\% \, 100)$
λ_1	8.41	41%
λ_2	4.55	21%
λ_3	2.91	11%
λ_4	1.12	7%
λ_5	0.69	4%

As the ith eigenvector has affects landmark k in the model by moving it along a vector parallel to (dx_{ik}, dy_{ik}), each shape in each image (X) can be approximated using the mean shape $(\bar{X})$ [8].

This is the geometrical interpretation of equation (17) in which $P = (p_1, p_2,...,p_t)$ is a t-dimensional matrix of eigenvectors, and $b = (b_1, b_2,...b_t)$ is also a t-dimensional vector of weights for each eigenvector. Vector b determines which landmarks from the mean shape $(\bar{X})$ need to be translated to produce a shape (X).

(17) $X = \bar{X} + Pb$

On the other hand, in equation (17), P and $\bar{X}$ have been calculated with respect to the images of the database and are thus fixed. In addition, as it was mentioned earlier, SCR database determines X for each image of JSRT database. Therefore, vector b for each X from the images of JSRT database is obtainable from equation (18):

(18) $b = P^{\mathrm{T}}(X - \bar{X})$

Table 2 shows the minimum and maximum of the 5 elements of vector b among 247 images of JSRT database.

Table 2. Minimum and maximum of vector b

b_i	maximum	minimum
b_1	796.451	-704.8542
b_2	576.3457	-581.6490
b_3	392.7548	-422.7600
b_4	241.6581	-350.2037
b_5	126.8534	-172.4689

Figure 6 shows the mean shape obtained from 247 images of JSRT database.

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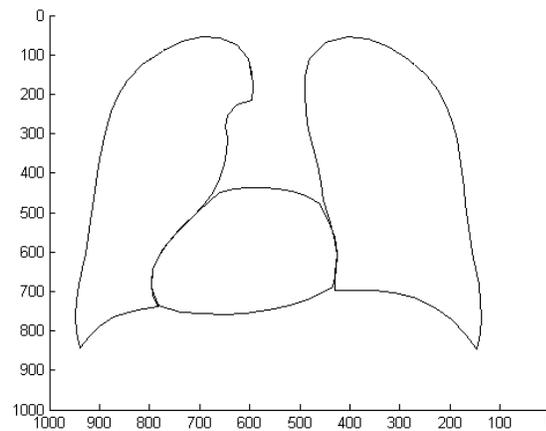**Special Issue on Computer Science**

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Figure 6 – The mean shape obtained from JSRT database

5. Conclusion

The method for modeling variations in the shape of the heart and lungs introduced in this paper is simple, efficient, and yet flexible. A relatively large group of chest radiograph images has been modeled using mean shape, a set of landmarks, and the mode of variations around this mean.

In the presented model, changing each parameter (b_i) results in the translation of the landmarks of the model in a straight line. That is why this model does not work well with non-linear variations, such as bends or rotations of two sub-components. However, as it is self-evident, the shape of the heart, lungs does not have any sub-components, and a simple linear model is sufficient to represent them, so there is no need to design more complicated models.

This model can also be used in classifiers. If we take a radiographic image of the chest radiograph of a new patient as the input, it will be easy to calculate how similar our input is to the images of JSRT database. In order to do this, as it was discussed in the method in section 4-1-1, we need to align the landmarks representing the boundaries of the organ in the new image with the mean shape of images. Then, using equation (18), the required parameters for producing the new image are calculated. The probability of having such parameters can be calculated from the distribution of the parameters of the database. This way, the degree of similarity of the new image with the images of the database is obtained.

Acknowledgments

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