A Texture Dictionary for Human Organs Tissues' Classification

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ABSTRACT

The research presented in this paper is expected to aid the process of medical decision making by providing tools for automatic extraction of *the most discriminative features of regions of interest in medical images* produced by the Computerized Tomography (CT) modality. The regions of interest studied in this paper are the liver, heart, backbone, kidneys, and the spleen. To characterize the regions of interest, we use texture information as well as textual information. We capture the texture information of the regions of interest using the Haralick texture descriptors and the run-length encoding descriptors. The texture information is given by the keywords annotating the organs. We apply Latent Semantic Indexing (LSI) to find the relationships between the texture features and the header information; the motivation behind using LSI is the cross modality ability of the technique that allows the combination of different kinds of data in discovering the relationships. These relationships are stored in a *Texture Dictionary* that can be later used to automatically annotate new CT images with the appropriate organ names.

Keywords: Texture Classification, Computerized Tomography, Latent Semantic Indexing, Feature Selection

1. INTRODUCTION

Hospitals throughout the world are witnessing huge volumes of digital medical images and associated clinical data on a daily basis. The number of qualified personnel to inspect, analyze and make decisions is quickly being outnumbered in relation to the number of images needing their expertise. Better automated information systems have to be developed and our work presents the initial steps in a proof of concept of such a system.

The research presented in this paper is expected to aid the process of medical decision making by providing tools for automatic extraction of *the most discriminative features of regions of interest* in medical images produced by the Computerized Tomography (CT) modality. These tools would enable two functionalities: one is efficient retrieval of similar regions in large collections of images and the other is the discovery of associations between the low-level content of various types of regions of interest (representing human organs) and their high-level content (representing semantic meanings, such as organ names). Solving these problems will enable radiologists to integrate, manipulate and analyze large volumes of image data more efficiently and easily when compared to traditional manually annotated systems.

The regions of interest studied in this paper are the liver, heart, backbone, kidneys, and the spleen. To characterize these regions of interest, we use two types of information: texture information calculated from raw data (pixel data) and textual information assigned to each region by an expert using the anatomic information from the image. The reason of choosing texture to characterize different types of regions resides in the fact that different organ tissues present different textures in the CT images, and thus, we expect the texture descriptors will have enough discrimination power to distinguish among different types of regions. We capture the texture information of the regions of interest using two second-degree statistical models: the gray level co-occurrence matrices and gray level run length statistics; for each model, a set of texture descriptors was calculated. Therefore, each region of interest is encoded using a feature vector consisting of the combination of the texture descriptors of the two models and the keywords representing the names of the organs. The goal of the paper is to develop a strategy based on Latent Semantic Indexing (LSI) for selecting the *most discriminative texture features* conditioned on a set of training images containing examples of the regions of interest; the ultimate goal of the strategy is to *allow automatic classification/annotation of the regions in one of the classes denoted by the keyword descriptions*. The motivation behind using LSI is the cross modality ability of the technique (in addition to the dimensionality reduction property) that allows the combination of different kinds of data (in our case, numerical texture descriptors and textual annotations) in discovering the data relationships and patterns. Once these relationships are found, they are stored in a *texture dictionary for anatomical structures* that can be later used to automatically annotate new CT images with their appropriate organ names.

Our preliminary results obtained on a set of 340 chest and abdominal CT images show that, using only 5 texture descriptors out of 21 descriptors calculated from the two texture statistical models, one can differentiate among the five organs with good accuracy. Furthermore, the proposed approach can be incorporated into an efficient medical retrieval scheme whose indexing technique performs the best on a low dimensional feature set.

2. BACKGROUND & PREVIOUS WORK

Texture is a measure of the variation of the intensity of a surface, quantifying properties such as smoothness, coarseness, and regularity. It is often used as a region descriptor in image analysis and computer vision [1]. Several methods have been applied towards the analysis and characterization of texture within medical images including fractal dimension, run-length encoding, discrete wavelet transform, and two-dimensional co-occurrence matrices. Of these, we have implemented both co-occurrence matrices and run-length matrices in an attempt to classify the texture within the various organs of the human body.

Two-dimensional co-occurrence matrices are generally used in texture analysis because they are able to capture the spatial dependence of gray-level values within an image [4]. A 2D co-occurrence matrix, P, is an n x n matrix, where n is the number of gray-levels within an image. For reasons of computational efficiency, the number of gray levels can be reduced if one chooses to bin them, thus reducing the size of the co-occurrence matrix. The matrix acts as an accumulator so that P[*i* , *j*] counts the number of pixel pairs having the intensities *i* and *j*. Pixel pairs are defined by a distance and direction which can be represented by a displacement vector d = (*dx*,*dy*), where *dx* represents the number of pixels moved along the x-axis, and *dy* represents the number of pixels moved along the y-axis of the image slice. In order to quantify this spatial dependence of gray-level values, we calculate various textural features proposed by Haralick [3].

Run-length matrices capture the coarseness of texture in specified directions. A run-length matrix p(i, j, ?) stores the number of gray level runs with gray level i, length j, in ? direction. In our application we choose ? to be 0°, 45°, 90° and 135°. Eleven features are typically extracted from the run-length matrices: short run emphasis, long run emphasis, high grey emphasis, low grey emphasis, pairwise combinations of length and grey level emphases, run-length non-uniformity grey level non-uniformity, and run percentage. These texture features can then be used in a classification scheme to determine textures.

The features extracted using both co-occurrence and run-length matrices provide valuable information about the CT images that may not be visible to the human eye.

To implement co-occurrence and run-length matrices on Computerized Tomography (CT) images, organs must be segmented. We used active contours in order to segment out the organs that we wanted to analyze - kidneys, liver, spleen, backbone, and heart – from the CT images. An active contour [6][11] (snake) is a function that recreates a boundary. Given a user defined starting curve and parameters to determine smoothness and elasticity of the final curve, and a parameter to determine the effect of image intensities, the curve evolves to match the nearest internal boundary, typically based on gradient intensity measures. The resulting boundary curve can then be used to separate the object of interest from the background.

Snakes have some advantages that other segmenting algorithms do not have. One of these advantages is that they can segment objects in an image that look alike, or those that have the same texture. Also, they can segment areas that are not closed and objects that are generally difficult to segment due to irregularities in their shape.

After the feature extraction stage, the medical image database is transformed into a matrix W_0, whose rows correspond to the bins of the texture descriptors followed by the keywords annotating the anatomical structures, and columns correspond to the segmented regions from the CT images; each entry represents the weight of a given bin in a given image:

$$W_0 = \begin{bmatrix} \overbrace{w_{1,1}w_{1,2}\ldots w_{1,n}}^{\mathrm{Im}ag_1\,\mathrm{Im}ag_2\ldots\mathrm{Im}ag_n} & \left.\begin{matrix} \\ \\ \\ \\ \end{matrix}\right\} bin_1 \\ w_{2,1}w_{2,2}\ldots w_{2,n} & bin_2 \\ \vdots & \vdots \\ w_{m,1}w_{m,2}\ldots w_{m,n} & bin_m \\ w_{m+1,1}w_{m+1,2}\ldots w_{m+1,n} & organ_1 \\ \vdots & \vdots \\ w_{m+5,1}w_{m+5,2}\ldots w_{m+5,n} & organ_5 \end{bmatrix}$$

Singular Value Decomposition (SVD), the statistical method on which LSI [2] is based, is performed on the matrix W_0; by definition, the SVD of W_0 is any factorization of the form:

$$W_0 = T_0 \times \Sigma_0 \times D_0^{'}, \quad (1)$$

where T_0, D_0 are two $(m+5)\times(m+5)$ (m is the total number of bins) and $n\times n$ (n is the number of regions from database) orthonormal matrices, respectively. Σ_0 is a $(m+5)\times n$ diagonal matrix, $\Sigma_0 = diag(s_1, s_2, \ldots, s_p)$, $p = \min(m+5, n)$, with the diagonal elements having the property that $s_1 \geq s_2 \geq \ldots s_p \geq 0$ and being the singular values of W_0. The main idea behind SVD is that proper choice of T_0 and D_0 makes most of s_i zero; that is, most of the important information gets concentrated in a few dimensions. Let k, $k \leq p$, be the number of the first dimensions that contain this information; the remaining smaller singular values are set to zero. Since zeros were introduced into Σ_0, the representation can be simplified by deleting the rows and columns of Σ_0 to obtain a reduced diagonal matrix Σ, and then deleting the corresponding columns of T_0 and $D_0^{'}$ to obtain T and $D^{'}$, respectively. This results in a reduced model:

$$W = T \times \Sigma \times D^{'}, \quad (2)$$

which gives the rank-k model with the best possible least-squares-fit to W_0 [8].

Since the columns $t^j, j = 1\ldots k$, of T form a basis for the space spanned by W's columns, they can be considered the axis of the rearranged space. First axis, t^1, reflects the first major pattern, named $pattern_1$, present in the medical image database: t_1^1 shows the contribution of bin_1 in $pattern_1$, t_2^1 shows the contribution of bin_2 in $pattern_1$ and so on up to

the last t_m^1 that shows the contribution of bin_m in the first pattern. Second axis, t^2, reflects the second major pattern in the data, named $pattern_2$, and so on up to axis t^k corresponding to $pattern_k$ [6].

3. METHODOLOGY

The first step in the textural analysis was the segmentation and isolation of the organs of interest. We used CT images from two patients and segmented the backbone, kidneys, liver, spleen and heart from all of the slices in which we could be sure of a reliable segmentation. We used an active contour algorithm [10] to segment the organs from 340 coronal slices over the two patients. To isolate the organs for texture analysis, we created separate images containing only the segmented organ on a black background (Figure 1). Finally, we derived the rectilinear convex hull for each organ and split it in half both vertically and horizontally to create four sub-images for each organ/slice image in order to generate more data points for the LSI analysis. The result was 1360 separate images of organ tissue on a black background (the black background acts as a flag when calculating our co-occurrence and run-length matrices so that we only take into account the actual segmented organ).

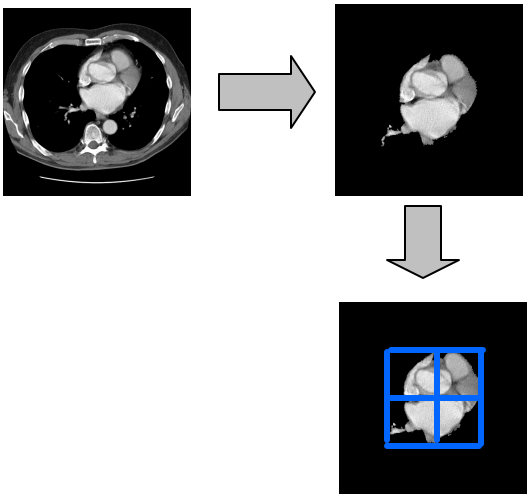

Figure 1: Generating Data

We then calculated 10 texture descriptors from the Haralick co-occurrence matrices, using 4 directions (0°, 45°, 90° and 135°) and 5 distances (1 to 5 pixels), resulting in 200 co-occurrence features for each image. We used intensity binning to reduce the size of the co-occurrence matrices so as to increase the efficiency of the program. Thus, sixteen levels of intensity in the organ sub-image were mapped to a single intensity level in the co-occurrence matrix. In addition, we calculated 11 run-length descriptors using the same four directions mentioned above, resulting in 44 run-length features for each image. For the run-length matrices, intensity was binned by a factor of 128 to 1 and run-length indices based on the base-2 logarithm of the actual length of the run. These decisions are fairly standard and represent the relative scarcity of runs of similar intensity and the general rarity of long runs in non-homogenous regions [5][8]. Finally, each sub-image was assigned an organ label based on the anatomic knowledge of the segmented organ.

Since LSI technique takes as input the counts of different values for each descriptor and each region, and the texture descriptors are just real valued data, we could not perform LSI directly on the calculated feature values. As a preprocessing step, we had to preprocess the data by first normalizing each descriptor, and second by binning the values in 10 intervals. As a result, the number of columns in the input matrix for LSI increased from 26 to 216 as follows:

1. 100 co-occurrence features corresponding to 10 bins for each of 10 co-occurrence descriptors,
2. 110 run-length features corresponding to 10 bins for each of 11 run-length descriptors,
3. 5 binary features for organs.

Each input in the new input matrix represents the number of values falling into that range. Since for each co-occurrence descriptor there might be maximum 20 values falling into the same range, and for the run-length descriptors there might be maximum 4 values falling into the same range, we normalize the frequency or count matrix by descriptors.

The resulting feature matrix (1360 sub-images/documents by 215 features/terms for each sub-image) was analyzed using Singular Value Decomposition (SVD) in order to determine the most relevant terms for each sub-image (Figure 2).

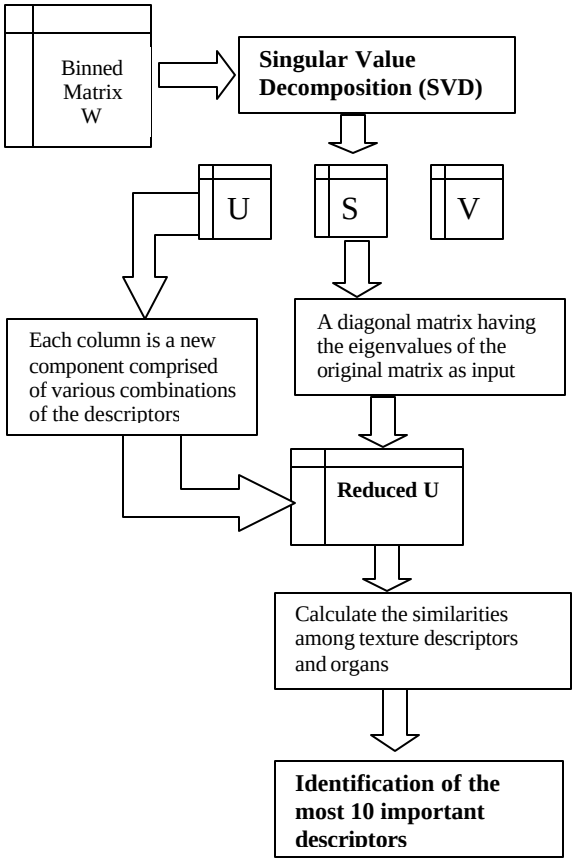

Figure 2: The feature discrimination identification process

The output of the SVD technique will give us three matrices, named U, S, and V in the diagram from Figure 2. Since the

goal of the paper is to find the similarity among the features, we will focus only on the matrix U whose rows give the representation of the descriptors with respect to the new features (the combinations of the most important descriptors). The most important combinations are given by the first columns of U; trying different number of most important combinations, we noticed that keeping the most important 20 components will be enough to discriminate among the descriptors with respect to their power in classifying the organs. Therefore, we ended up with a reduced matrix U having 215 rows and 20 columns.

The reduced matrix U was used in the next stage for comparing each of the 210 texture features with each of five organ labels; the dot product was used as a similarity metric. Similarity values closer to 1 will indicate those texture features that correspond best with each organ label. The 10 closest values to 1 indicated the most important 10 descriptors for a certain organ.

4. RESULTS

By looking at the most relevant descriptors for each organ, our initial results show that using only the 10 most relevant features out of the 210 will still give us enough power to differentiate among the organs. One can analyze the top 15 or 20 most relevant features per organ; however, the additional features only provide redundant information. We then used these most relevant features to create our *texture dictionary* (Table 1) by listing the 10 most relevant texture descriptors for each organ and their associated ranges.

Table 1: Texture Dictionary: most important descriptors

	Kidney	Liver	Spleen	Backbone	Heart
Entropy	.4-.5			.6-.7	
Energy	0-.1		.2-.3		0-.1
Contrast		0-.1			0-.1
Homogeneity	.4-.5				
SumMean	.5-.6	.5-.6	.4-.5	.6-.7 .7-.8	
Variance					.3-.4
Correlation		.2-.3			.3-.4
Max Prob	0-.1		.2-.3	0-.1	.1-.2
IDM		.7-.8			
Cluster Tend					
SRE	.2-.3				
LRE			.2-.3	0-.1	
LGRE					
HGRE	.3-.4	.1-.2 .4-.5	.2-.3	.4-.5	.2-.3
SRLGE		.1-.2	.1-.2		
SRHGE		0-.1	0-.1	.2-.3	.1-.2
LRHGE	.3-.4		.1-.2		.2-.3
LRLGE		.2-.3		0-.1	.1-.2
GLNU			0-.1	0-.1	
RLNU	0-.1		.1-.2		.2-.3
RPC	.1-.2	0-.1		.5-.6	

We also looked at the features across organs and determined that HGRE (high grey run emphasis) and SumMean were the most important features. In fact, through the combination of these two, one can differentiate between the kidney, liver, backbone, heart vs. backbone, and spleen vs. kidney and liver.

5. FUTURE WORK

Our current work uses texture information encoding only the spatial distribution of the gray levels and the length of the texture primitives; as future work, we are going to incorporate other texture models in order to capture additional properties of the texture present in the regions. At the high-level description of the regions, we will be exploring the role of other patient information (sex, age, diagnosis) in the labeling of tissue textures and expect that it will lead to increased discriminatory power. Some of the textual information we are going to incorporate into our approach already resides in the header of the DICOM images used to implement the proposed approach.

Further, CT is a true three dimensional modality, and the use of two dimensional co-occurrence matrices cannot capture the volumetric texture of human organ tissue. We will therefore apply volumetric texture analysis to the problem as well.

Finally, we are going to use the low-level and high-level texture descriptors presented in this paper in different classification techniques. We have begun comparing the LSI results with decision tree results and will investigate the effectiveness of neural networks as well. We eventually will compare each of these three methods against each other to determine which is most effective.

6. REFERENCES

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