

Texture Classification of Normal Tissues in Computed Tomography

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HYPOTHESIS

The hypothesis is that normal tissues can be automatically classified in high resolution computed tomography (CT) of the chest and abdomen. The tools proposed in this paper may also be used to assist segmentation, annotation and automatic selection of context sensitive tools for various tissues.

INTRODUCTION

Biomedical imaging is increasingly electronic in terms of image acquisition and display. Image detectors have become so sensitive that the amount of information acquired is greater than can be displayed at any one time without using special purpose hardware. Research in image processing methods is essential to fully exploit the information that has been acquired. Furthermore, the ability to extract quantitative information from images is becoming increasingly important, requiring algorithmic (as opposed to visual) processing. In medical image processing, texture is especially important, because it is difficult to classify human organ tissues using shape or gray level information. Some of the challenges are: 1) the shape of each organ is not consistent through out all slices of a 3D medical image and may change quickly where the inter-slice distance is large, and 2) the gray level intensities overlap considerably for soft tissues. On the other hand, organs are expected to have consistent and homogeneous textures within tissues.

The significance of the research presented in this paper lies in its contribution to the texture quantification and classification of normal tissue in Computed Tomography (CT) scans. The quantification will apply various texture analysis methods to the collection of data about the tissues. The classification step will involve the application of statistical categorization to learn numerical descriptions of the visual phenomena of texture in human tissue. The end product of this research will be a system that will classify automatically normal tissues in CT scans using texture information.

METHODS

Our preliminary results were implemented on 3D data extracted from two normal CT studies from Northwestern Memorial Hospital. The 3D image data consisted of 2D DICOM (Digital Imaging and Communications in Medicine) consecutive slices, each slice being of size 512 by 512 and having 12-bit gray level resolution. Using the Active Contour Models ("Snake") algorithm, we segmented five organs from 340 coronial slices: heart and great vessels, liver, renal and splenic parenchyma, and backbone. At this stage, in order to generate more organ data, each organ was then subdivided into 4 equal sized regions within the square convex hull of the organ; therefore, 1360 segmented regions were generated to be used for texture analysis and classification. We divided this dataset into a training set and a testing set. Figure 1 shows the diagram of the entire process performed in order to derive the presented results.

Our approach consisted of two steps: texture feature extraction and classifier creation. In the first step, a set of texture descriptors were calculated for each region of interest in the training and testing sets. We used two different texture models to generate these descriptors: the co-occurrence matrix model and the run-length encoding model. From the co-occurrence model, ten Haralick texture descriptors were calculated in order to quantify the spatial dependence of gray-level values; from the run-length model, eleven descriptors were calculated in order to quantify the differences between fine and coarse textures. In the second step, a decision tree classifier was built using the 21 texture descriptors calculated in the previous stage and the names of the tissues as class labels. There are many classifiers that can be used to discriminate among the

organ tissue classes in the feature space. In our preliminary work, we evaluated a decision tree classifier because: 1) it does not make any assumptions of the distribution of the data; 2) it has a relatively faster learning speed than other classification methods, while still producing classification accuracy comparable with those methods; and 3) it has a good ability to generate decision rules that can be easily understood, interpreted, and used to annotate different tissues in future CT scans. The implementation of our decision tree was based on the Classification and Regression Trees (C&RT) approach. From the decision tree, a set of the most important decision rules were generated to be used for classification of the regions, and to derive the most relevant texture descriptors for specific organs. To evaluate the performance of the classifier, we calculated four metrics on regions of interest in the testing set: sensitivity, specificity, precision, and accuracy.

RESULTS

For the training set, the overall performance for all four metrics was better than 89%. For the testing set, the overall performance for sensitivity and precision was above 80% and the performance for specificity and accuracy was above 90%. Table 1 shows the four performance metrics for each individual organ. Figure 2 shows a screenshot of the initial prototype used to classify one of the five organs.

DISCUSSION

The lowest sensitivity and precision values were recorded for spleen which was misclassified as liver most of the time; this indicates that either the used texture descriptors did not have enough discrimination power or another classifier might be needed to classify with higher accuracy the two organs. The classifier model obtained using decision tree approach generated a set of 21 rules: three rules for the heart, three rules for the kidneys, five rules for the spleen, eight rules for the liver, and two rules for the backbone. The fact that there are multiple rules to describe a single organ suggests that single classes (organs) may have multiple sub-classes (tissues). The decision tree and the rules also highlight the most discriminative descriptors that can be used to annotate different organ tissues in future CT images. Based on the analysis of our results, the most discriminative descriptor is High Gray-Level Run Emphasis (HGRE) descriptor (of the run-length texture model) which separates 94% of the backbone cases from all the other organs; the second most important is Cluster Tendency (of the co-occurrence texture model) which separates 85% of the hearts from the other three organs: liver, kidneys, and spleen. The analysis of the “goodness” of the descriptors shows texture information can be used for tissue texture classification and confirms our previous results (obtained using Latent Semantic Indexing technique) related to ‘goodness’ of the descriptors for different types of tissues.

CONCLUSION

While there has been considerable work done for classification of normal and abnormal tissues within different organs (such as liver, lung, heart and brain), to our best knowledge, there is little research in regards to inter-organ classification. Our preliminary results show that using only 21 texture descriptors calculated from Hounsfield unit data, it is possible to automatically classify regions of interest representing different organs or tissues in CT images. Furthermore, the results lead us to the conclusion that the incorporation of some other texture models into our proposed approach will increase the performance of the classifier, and will also extend the classification functionality to other organs.

KEYWORDS: Texture, Classification, Decision Trees, Computed Tomography

FIGURES AND TABLES

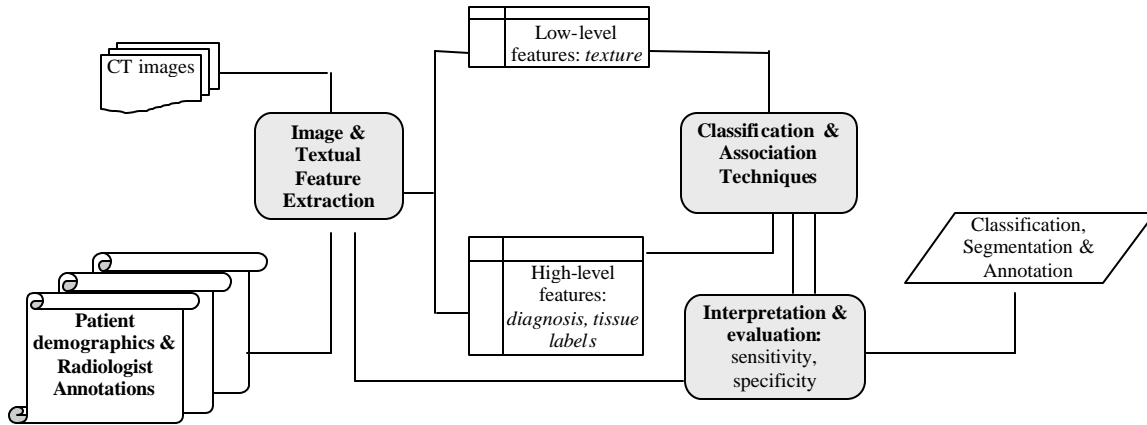


Figure 1: Steps performed to obtain the preliminary results

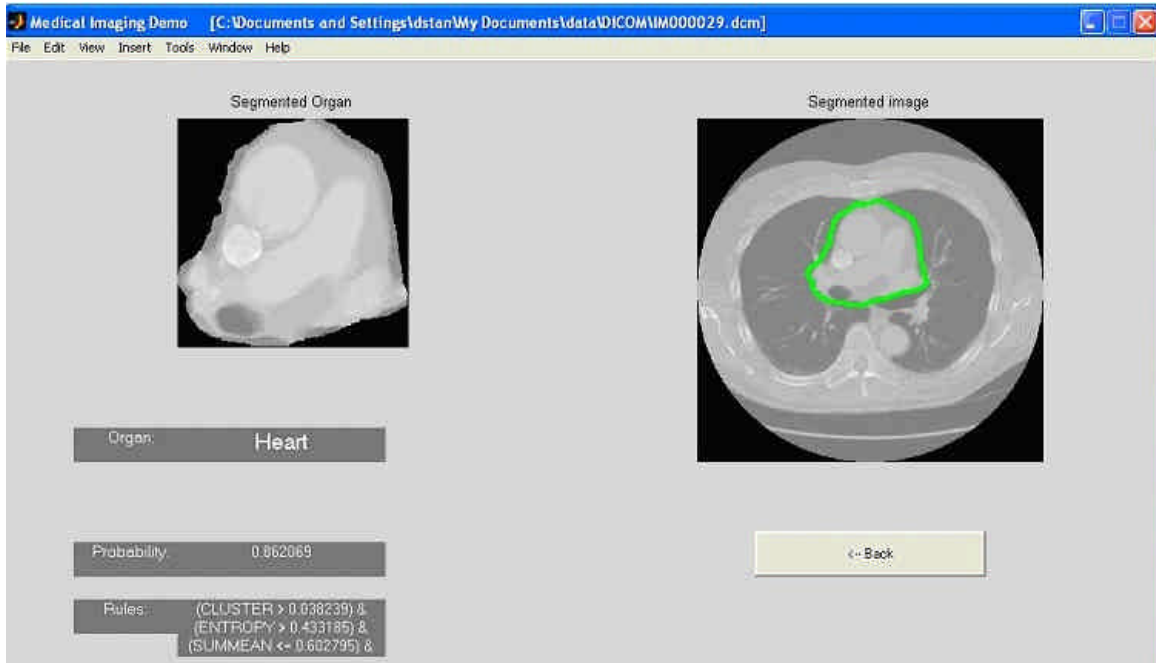


Figure 2: An example of heart classification in our proposed approach with a probability of 86.2%

Table 1: Classification performance on individual tissues of the testing set (decision tree parameters: number of parents = 28, number of children = 5, cross-validation fold =10)

	Backbone	Liver	Kidney	Heart	Spleen
Sensitivity	100.00%	73.85%	86.15%	73.61%	70.45%
Specificity	97.56%	95.88%	97.80%	97.20%	95.06%
Precision	96.83%	76.19%	87.50%	84.13%	62.00%
Accuracy	98.60%	92.54%	96.04%	93.24%	92.54%