Artificial Intelligence Methods Application in Liver Diseases Classification from CT Images

Daniel Smutek^{1,2}, Akinobu Shimizu¹, Ludvik Tesar¹, Hidefumi Kobatake¹ and Shigeru Nawano³

¹ Tokyo University of Agriculture and Technology, Koganei, 1848588 Tokyo, Japan
 ² 1st Medical Faculty, Charles University, Prague, Czech Republic
 ³ National Cancer Center Hospital East, Kashiwa, 2770882 Chiba, Japan

Abstract. An application of artificial intelligence in the field of automatization in medicine is described. A computer-aided diagnostic (CAD) system for focal liver lesions automatic classification in CT images is being developed. The texture analysis methods are used for the classification of hepatocellular cancer and liver cysts. CT contrast enhanced images of 20 adult subjects with hepatocellular carcinoma or with non-parasitic solitary liver cyst were used as entry data. A total number of 130 spatial and second-order probabilistic texture features were computed from the images. Ensemble of Bayes classifiers was used for the tissue classification. Classification success rate was as high as 100% when estimated by leave-one-out method. This high success rate was achieved with as few as one optimal descriptive feature representing the average deviation of horizontal curvature computed from original pixel gray levels. This promising result allows next amplification of this approach in distinguishing more types of liver diseases from CT images and its further integration to PACS and hospital information systems.

1 Introduction

The objective of this work is to develop a computer-aided diagnostic (CAD) system and validate texture analysis algorithms for classification of focal hypodense hepatic lesions.

Characterization of focal liver lesions on computed tomography (CT) depends on correct interpretation of morphology. The aim of this study is to develop a texture analysis concept for computer based interpretation of CT images. We concentrated on two very common focal liver lesions: hepatocellular cancer and liver cysts.

Hepatocellular carcinoma is common throughout the world. Its incidence is higher in cirrhotic patients. The overall survival rate ranges between 20 and 30 months, and is influenced by the local stage of the neoplasm and by the liver function. Successful long-term outcome is dependent on its early detection, as well as accurate delineation of the number and location of tumor nodules. Computed tomography is also outstandingly suitable for detecting cystic processes in the liver. The etiology of cysts is very wide, which means also large differences in their clinical relevance.

Similar works of classification of liver lesions such as tumors and their metastases, hepatic cysts, and hemangiomas, exist. They use mostly intensity-based histogram methods [1] or second-order texture features [2;3]. Our work differs from the previous ones by using an effective feature selection method and network (ensemble) of Bayes classifiers which already proved their clinical usability in texture analysis and classification of ultrasound images [4].

2 Methods

2.1 Images

Because most hepatocellular carcinoma receive equal or reduced blood supply from both portal and arterial flow compared with surrounding noncancerous parenchyma [5] late postcontrast enhancement images were used in our study. They were taken approximately 3 - 5 minutes after the bolus contrast administration. The voltage of Xray tube was 120 kV. The resolution of the CT image was 512x512 pixels with pixel size 0.625 mm. The slice thickness was 2 mm. Standard depth of 16 bits gray level was used.

The images were taken from 20 adult subjects: 15 subjects with hepatocellular carcinoma and 5 subjects with nonparasitic solitary liver cysts.

The total number of CT scans processed in this study was 535 (425 scans with hepatocellular carcinoma and 110 scans with cysts).

Regions of interest (ROI) with pathologic tissue (hepatocellular cancer or cyst) were interactively defined by a physician (see Figure 1).



Fig. 1. CT images of liver with segmented boundary of hepatic lesions. On the right manually drawn boundary (ROI) of hepatocellular cancer, on the left manually delineated cyst in liver parenchyma.

The maximum number of non-overlapping square windows within the boundaries was then automatically selected as the texture samples (see Figure 2). Each sample was assigned a label according to the patient diagnosis (hepatocellular cancer, cyst).



Fig. 2. CT images of liver. On the right detail of hepatocellular cancer focus with fitted texture samples (windows of 9 x 9 pixels), on the left liver cyst with embedded texture samples with size 7 x 7 pixels.

2.2 Texture Features

Image texture features can be computed by combining pixel gray levels in many different ways [6]. By transforming the gray levels, it is possible to enhance some image characteristics that are specific to a particular type of texture. Since the current standard practice of diagnosing hepatic lesions is performed mainly subjectively, texture characteristics observable by the human visual system are considered adequate for an automatic computer analysis. We also note that psychophysical evidence has shown the human visual system is capable of pre-attentive texture discrimination from first-order to second-order properties, as defined by the moments of texture primitives [7].

In this paper 22 first-order features were investigated: gray level of pixel (feature called *raw*) and 21 spatial features based on the original gray levels of an image and based on four different gray-level transformations [8]. In addition to first-order features we also included second-order features in order to capture the spatial organization of texture primitives. Therefore, most of the further 108 features used are second-order statistical texture features based on co-occurrence matrices, which incorporate spatial organization of texture primitives.

Spatial features

Some of the 21 spatial features are based on the original pixel gray levels $p_{i,j}$, while others $p_{i,j}^m$, are based on transformations of the gray levels, where i,j denotes the image coordinates of a pixel and *m* denotes a transformation. These features were suggested by Muzzolini [8] and are summarized in this section. Four gray-level transformations obtained from each of *S* samples of *NxN* pixels were used and are defined as follows:

1) gradient magnitude

$$p_{i,j}^{(1)} = \left| p_{i,j} - p_{i+1,j} \right| + \left| p_{i,j} - p_{i,j+1} \right|$$

2) difference from sample mean

$$p_{i,j}^{(2)} = \left| p_{i,j} - \overline{p} \right|$$
 where $\overline{p} = \frac{1}{N^2} \sum_{i=1}^{N} \sum_{j=1}^{N} p_{i,j}$

3) horizontal curvature

$$p_{i,j}^{(3)} = p_{i,j} - \frac{p_{i-1,j} + p_{i+1,j}}{2}$$

4) vertical curvature

$$p_{i,j}^{(4)} = \left| p_{i,j} - \frac{p_{i,j-1} + p_{i,j+1}}{2} \right|$$

5) original pixel grey levels

$$p_{i,j}^{(\mathfrak{d})} = p_{i,j}$$

The Kolmogorov-Smirnov distance [9] between $H_i(p^{(m)})$ and $\overline{H}(p^{(m)})$ is used to derive features f_1, \dots, f_5 , from the transformations $p^{(m)}$. The $H_i(p^{(m)})$ is an estimate of the cumulative distribution function for $p^{(m)}$ computed from NxN sample *i* by histogramming and $\overline{H}(p^{(m)})$ is the robust estimate of the cumulative distribution function mean for $p^{(m)}$ computed from $H_i(p^{(m)})$ over all samples *i* as follows:

$$\overline{H}(p^{(m)}) = LMS \{ H_i(p^{(m)}), i = 1, 2, ..., S \}.$$

The *LMS*, Least Median of Squares, is used as a robust statistics instead of a nonrobust mean to suppress the influence of outlying values. *LMS* computes a value Mand a range m_T for a data set, such that $[M-m_T; M+m_T]$ is the shortest interval containing 50% of the original data. It is a common practice to set the estimate of standard deviation r to the value of 2.5 x 1.4826 m_T for the case of normal errors. Points in the range $M \pm r$ are called *inliers* and the remaining points are considered as *outliers*. Inliers fall within 98.7% of the samples in a Gaussian distribution.

The Euclidean distance from $(f_1, ..., f_5)$ to their mean and median, respectively, are used to compute features f_6 and f_7 as follows:

$$f_{6} = \sqrt{\frac{(\bar{f}_{1} - f_{1})^{2} + (\bar{f}_{2} - f_{2})^{2} + (\bar{f}_{3} - f_{3})^{2}}{+(\bar{f}_{4} - f_{4})^{2} + (\bar{f}_{5} - f_{5})^{2}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{2} - f_{2})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{4} - f_{4})^{2} + (\hat{f}_{5} - f_{5})^{2}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{2} - f_{2})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{5} - f_{5})^{2}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{2} - f_{2})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{5} - f_{5})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{2} - f_{2})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{5} - f_{5})^{2}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{2} - f_{2})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{3} - f_{3})^{2}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{2} - f_{2})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{2} - f_{2})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{1})^{2} + (\hat{f}_{3} - f_{3})^{2}}{+(\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{3})^{2} + (\hat{f}_{3} - f_{3})^{2}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{3})^{2} + (\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{3})^{2} + (\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{3})^{2} + (\hat{f}_{3} - f_{3})^{2}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{3})^{2} + (\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{3})^{2} + (\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_{1} - f_{3})^{2} + (\hat{f}_{3} - f_{3})^{2}}}}, f_{7} = \sqrt{\frac{(\hat{f}_$$

where \bar{f}_i is the mean of feature f_i for a sample, and \hat{f}_i is the median of feature f_i , i = 1, 2, ..., 5.

Features $f_{8,...,f_{12}}$ are derived from the transformations $p^{(m)}$ just like features $(f_{1,...,f_{5}})$ except that the average deviation (AD) of the pixel gray level $p^{(m)}_{i,j}$ is used as the measure, where

$$AD(p^{(m)}) = \frac{1}{N^2} \sum_{i} \sum_{j} \left| p_{i,j}^{(m)} - \overline{p}^{(m)} \right|, \quad m = 1, 2, \dots, 5.$$

Features f_{13} and f_{14} are based on the Euclidean distance from $(f_8,...,f_{12})$ to their mean and median, respectively. They are defined exactly the same way as the features f_6 and f_7 with the exception that the subscripts (1,...,5) are replaced with subscripts (8,...,12).

Features $f_{15,...,f_{19}}$ are based on the transformations $p^{(m)}$, just like features $(f_1,...,f_5)$, except that the standard deviation (SD) of the pixel gray level $p^{(m)}_{ij}$ is used as the measure, where

$$SD(p^{(m)}) = \sqrt{Var(p^{(m)})},$$

$$Var(p^{(m)}) = \frac{1}{N^2} \sum_{i} \sum_{j} \left(p_{i,j}^{(m)} - \overline{p}^{(m)} \right)^2$$

$$m = 1, 2, \dots, 5$$

Features f_{20} and f_{21} are based on the Euclidean distance from $(f_{15},...,f_{19})$ to the mean and median of $(f_{15},...,f_{19})$.

Co-occurrence matrix features. Co-occurrence matrices can be used to obtain texture features. For each *NxN* texture sample *W* taken from an image *I*, a set of gray level co-occurrence matrices $C_d(i,j)$ is calculated for a given separation vector \vec{d} as follows:

$$C_{\vec{d}}(i,j) = \frac{1}{(N-a)(N-b)} card \begin{cases} (\vec{r}, \vec{r} + \vec{d}) : \vec{r}, \vec{r} + \vec{d} \in W \\ and I(\vec{r}) = i \text{ and } I(\vec{r} + \vec{d}) = j \end{cases}$$

where d = (a,b), $I(\vec{r})$ is the gray level of pixel \vec{r} , from the interval of 0,1,..., G-1. The image resolution of G = 64 was used, and *card* X is the size of the set X.

The elements of C_d represent the frequencies of occurrence of different gray level combinations at a distance \vec{d} . In this paper, nine Haralick texture features [6] were investigated.

Twelve separation vectors d = (1,0); (2,0); (3,0); (4,0); (1,1); (2,2); (3,3); (4,4); (0,1); (0,2); (0,3); (0,4) were used in the experiments, resulting in twelve different gray level co-occurrence matrices for each size of texture sample. Thus *D* co-occurrence matrix features (*f111-f1129*) were generated for each of the sample size. These are denoted according to the following notation: "*f1dh*", where *d* is the index of a separation vector (of a possible twelve) and *h* is the number of a Haralick feature (of a possible nine) giving D=108. For example, f195 is texture homogeneity for vector $\vec{d} = (0,1)$.

To achieve uniform scale, all features were normalized by their standard deviation from zero.

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2.3 Diagnosing

Bayes classifier [10] was selected for its best possible ability to distinguish classes that overlap in feature space. The classifier uses the decision function $d_i(\vec{v})$ over *M* classes

 $d_i(\vec{v}) = p(\vec{v} | C_i) p(C_i), \quad i = 1, 2, ..., M$

to assign a feature vector \vec{v} to class _______ if for that vector $d_i(\vec{v}) > d_j(\vec{v})$ for all $j \neq i$, where $p(C_i)$ is the *a priori* probability of class C_i (i.e., the probability of occurrence of class C_i) and $p(\vec{v} | C_i)$ is the probability that \vec{v} comes from C_i (this as the model probability function and it must be learned from a training set). A priori probabilities of 0.5 for both classes (since hepatocellular cancer and cysts are evenly included in our experiment) were used for estimating $J(\vec{v})$.

The choice of model probability function $p(\vec{v} | C_i)$ is determined by discrete quantization of the feature space.

2.4 Feature Selection Learning Method

The purpose of feature selection is to reduce the texture description from D to d dimensions, where $d \le D$. Each sample of the classes (hepatocelullar carcinoma, cyst) can be represented in terms of d features and be viewed as a vector in d-dimensional space. From the statistical point of view, reduction of feature vector dimension is important to determine classifier parameters reliably from a limited amount of data, i.e., to limit the expected bias and variance of the classifier.

The goal in our approach for feature selection is to select a subset of features that minimize the expected classification error. It is based on a direct classification error minimization and requires a specific choice of classifier. Since the data is sufficient to estimate probability density of a feature vector even in high dimension, Bayes classifier is used in this approach.

We successively search for the optimal feature vector \vec{v} of length k+1 by adding a new feature in a locally optimal way to the best existing feature vector candidate of length k. The quality $J(\vec{v})$ of a feature vector \vec{v} (computed as above) initially increases with increasing length of the vector and then starts to decrease due to data over-fitting [10]. Therefore, a simple depth-first search for the optimal feature vector cannot be used. Our algorithm therefore performs the search for optimal solutions by a modified branch-and-bound algorithm [10].

The classifier is trained by estimating the conditional probability density for each class by optimal histogramming. Optimal histogram resolution according to Scott's rule was used for the corresponding feature vector dimension and the number of samples [11]. Our data collection mechanism produces a sufficiently large number of samples to obtain statistically meaningful estimates this way.

2.5 Subject Classification

The subject classifier then works in two stages (see Figure 3): In the first stage, individual texture samples (e.g., from 7x7 windows) from all images from a single subject are classified independently. In the second stage the classifier outputs are combined using majority voting to determine the class label for the given subject. The reason for using a two-stage classifier is that the primary features exhibit a large overlap between the classes. It is well known [12] that classifier combination can lead to increased performance even if the individual classifiers are weak. Of the known combination methods [13] the best performance was achieved by majority voting in our data.

The subject is thus assigned the label C (hepatocellular cancer, cyst), which corresponds to the class of most of its samples. For more detailed description see Figure 3.



Fig. 3. The classifier works in two stages: In the first stage, individual texture samples from all images of the given scan type from a single subject are classified independently using Bayes classifier. In the second stage, the classifier outputs are combined using majority vote to determine the class label for the given subject.

2.6 Evaluation of the Success Rate

Finally classification success rates were estimated by leave-one-out method for all optimal feature vectors found by selection scheme Bayes classifier. Leave-one-out means that 1. all images of one subject are removed from training set, 2. classifier is learned on the remaining images, and 3. the images that were left out are classified using the classifier. The three steps are repeated for all subjects. This method provides good estimate of classifier generalization accuracy.

3 Results

For practical experiments only the faster feature selection learning method was used.

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A total of 6,239,480 feature values (130 features for each of 47,996 samples) were computed and the different combinations of them were used for classification. The best value of $J(\vec{v}) = 100$ was achieved for several texture sample sizes and several features.

All the features suitable for classification (which gave results with leave-one-out error less than 0.1) and the corresponding sample sizes are shown in Table 1.

Originally, also slower Mixture model method was considered, because it should give better results. Because even feature selection method provided right diagnosis for every patient, we decided not to do so.

	Size of	LOO	Features used for classification
	sample	Error	
	7x7	0.056	f10, f11, f15, f186, f2, f8, f9, raw
	9x9	0	f10, f15, f20

f10, f11, f129, f13, f132, f157, f16, f172, f187, f2, f20,

f10, f11, f1117, f1127, f117, f119, f12, f127, f13, f157,

f10, f11, f1107, f1117, f117, f12, f13, f16, f197, f2,

f10, f11, f117, f12, f13, f147, f157, f197, f2, f20, f8, f9,

f16, f167, f172, f177, f197, f2, f20, f8, f9, raw

f10, f129, f16, f20, f8, f9

 Table 1. Size of texture samples, leave-one-out classification error and the features used for the classification.

4 Discussion and Conclusion

0

0

0.071

0.071

0.077

f8. f9

raw

f20, f8, f9, raw

11x11

13x13

15x15

17x17

19x19

The results show the excellent discrimination between hepatocellular carcinoma and liver cysts can be established on the basis as few as one optimal feature among the 130 texture characteristics tested.

From these results the principal descriptive feature can be identified: f10. Feature f10, which was chosen among other 130 features, represents the average deviation of horizontal curvature computed from original pixel gray levels. This feature gave 100% classification success rate in all texture samples size (from 7x7 to 19x19 pixels).

Also the most effective size of texture sample was determined. We computed features for samples from the tiny squares of size 7x7 pixels up to large squares with side of 41 pixels. The maximum success of 100% correct classification was achieved for texture samples with size 9x9 to 13x13 pixels. Then with the increasing size of side the error also increased (for 41x41 samples the total error was 0.25). The failure of the large squares can be contributed to the fact that they do not cover the area of ROI sufficiently and thus it results in an information wasting (a considerable big

amount of the tissue, near to the border of segmentation boundaries is not used for computing texture features in such case).

On the other hand it can be seen that there are considerably more texture features which are useful for successful classification in larger samples. E.g., three possible features in 9x9 samples, six features in 11x11 samples, and thirteen texture features in samples of 13x13 pixels. We attribute it to the fact that there is more information about spatial organization of texture primitives available in the larger samples.

We infer that in future research the texture samples with the size 13x13 pixels and texture feature f10 (the average deviation of horizontal curvature) will be the most useful.

As the next step it is desirable to include more classes (diagnoses) in the classification process. The most important which should be comprised in the very next step are hepatic hemangiomas, focuses of liver cirrhosis and various tumor metastases.

On the assumption that the majority of used features were higher order texture features (and thus independent on the gray level histograms of the image but dependent on spatial organization of texture primitives) we did not perform any image preprocessing. Nevertheless the normalization of the images prior to computing the texture features (e.g., by comparison with other organs in abdominal cavity or the diaphragm) in our future experiments might get even better results.

Also the other important step, which is necessary to undertake, is to utilize all information which is available from 3D CT images and thus using texture features which comprise this data. The usability of non enhanced CT images and images in earlier stages of contrast enhancement or their combination should be also explored.

Finally we can conclude that initial implementation of our CAD system is promising for automating liver lesion classification and that it may be integrated to Picture Archiving & Communications Systems (PACS) and to hospital information systems.

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