ULTRASONOGRAPHY DIAGNOSTICS USING GAUSSIAN MIXTURE MODEL

Ludvík Tesař[1]**, Daniel Smutek**[2]

[1] *Department of Adaptive Systems*
Institute of Information Theory and Automation
Academy of Sciences of the Czech Republic
Prague, Czech Republic

[2] *3rd Department of Medicine*
1st Medical Faculty, Charles University
Prague, Czech Republic

E-mail: tesar@utia.cas.cz

Abstract: The problem of diagnostics of diseases of thyroid gland is addressed, namely Hashimoto's Lymphotitic thyroiditis. Following statistical method is used for making diagnosis. Database of ultrasound images with known diagnosis is used for learning. Pattern features are calculated and Gaussian mixture model in the space of pattern features is used. In diagnostics stage, the sonogram of person with unknown diagnostics is taken and the most probable diagnosis is inferred using Bayesian inference with on Gaussian clusters of pattern features.

Keywords: Pattern recognition, medical image analysis, Bayesian system identification, Gaussian mixture modeling, Hashimoto's lymphocytic thyroiditis.

1. INTRODUCTION

We address the problem of diagnosing diseases of thyroid gland, as it can help in an early diagnosis, and immediate treatment improves the quality of lives of patients. The disease diagnosed is Hashimoto's lymphocytic thyroiditis (Wartfsky and Ingbar, 1991). It is possible to verify this disease reliably by invasive fine needle espiration biopsy or an expensive magnetic resonance imaging. Ultrasound image is cheaper, but harder to evaluate (Simeone *et al.*, 1985; Solbiati *et al.*, 1985). The inflammation in the gland changes the structure of the thyroid tissue. These changes are affecting the entire gland. Therefore it is likely to be detected by ultrasound imaging (Gooding, 1993; Loevner, 1996), using pattern recognition. Ultrasound imaging is the most widely used diagnostic and monitoring tool for thyroid gland (Gooding, 1993; Hopkins and Reading, 1995; Loevner, 1996). Developments in automatic texture analysis with computers give the possibility to use image texture analysis methods for medical diagnosis of various diseases.Examples of computer-based interpretation of ultrasound images are (Kimme-Smith and Jones, 1984; Mailloux *et al.*, 1986; Hirning *et al.*, 1989; Morifuji, 1989).

Quantitative analysis of diffuse changes in thyroid gland involving texture features other than first-order ones derived from gray-level histograms are not very widely used except for our own publications (Smutek *et al.*, 2003*a*; Smutek *et al.*, 2003*b*; Tesař *et al.*, 2005*b*; Tesař *et al.*, 2005*a*).

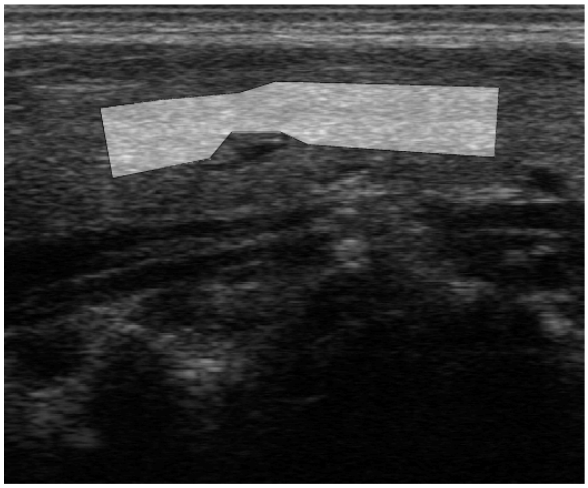

Fig. 1: Sonograph image with highlighted section of interior of thyroid gland

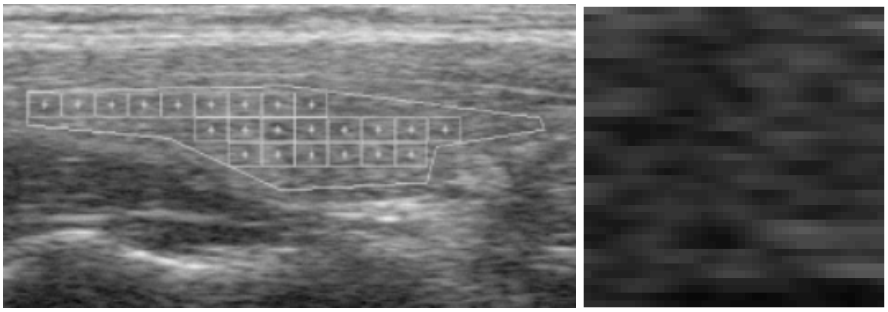

Fig. 2: Dividing interesting region of thyroid gland into squares, and example of one of these squares

2. DESCRIPTION OF THE METHOD FOR THYROID GLAND DISEASE DIAGNOSING

The statistical method used needs the set of data collected by experienced physician, with known diagnose found and verified by another methods. We denote this set of data as learning set. Learning set is used to construct model in learning stage (described in Section 2.1). The model constructed in learning stage is used for diagnosing of ultrasound image made for patient with unknown diagnose (described in Section 2.2), which is called inference step.

2.1 Modeling

In every image produced by sonograph, the region with interior of the thyroid gland is outlined by physician, and only this region is considered. As an example of interior of thyroid gland, see Figure 1, where interior is highlighted. After that outlined interior of thyroid gland is automatically divided into non-overlapping squares of the size 41×41, as illustrated in the Figure 2. Feature vectors are calculated from every little square of the size 41×41. Feature vector is the vector of numbers which characterize some aspect of the pattern which is present on given image. In our case the most interesting property, which likely changes in inflamed tissue is the contrast. Therefore Haralick's co-occurance and Muzzolini's spatial features were used. Similar set of features is used as in (Smutek *et al.*, 2003*a*; Smutek *et al.*, 2003*b*; Šára *et al.*, 2001). The assumption concerning feature vector, is that features contained in this vector carry substantial information about texture in the original image. This assumption is justified due to the fact, that presence of Hashimoto's lymphotitic thyroiditis changes consistence of the thyroid gland and this difference should be detectable by change in pattern in the sonograph

scan.

Feature vectors consist of features, that are calculated from co-occurance matrices. Number of colors in gray scale is reduced from 256 to 64. Haralick features are calculated from 12 different co-occurance matrices (4 horizontally, 4 vertically, 4 diagonally). Nine types of Haralick features for every spatial vector were used. Also, we used 21 Muzzolini spatial features. Whole feature vector consist of 129 features.

The idea behind the method is that feature vectors of inflamed and healthy tissue should form different clusters in the multidimensional feature space (In this case 129-dimensional space). For modeling in the space of feature vectors we use Gaussian Mixture Model. Features calculated for each small image cut are fitted to the Mixture. Two models are to be constructed. Data obtained from the healthy tissue are used to construct the model number 1 and data from the tissue with inflammation are used for constructing the model number 2.

For modeling of feature vector Y, we use Gaussian mixture model:

$$p(Y) = \sum_{i=1}^{n} \frac{\alpha_i \exp\left[-\frac{1}{2}(Y - Y_i)^T C_i^{-1}(Y - Y_i)\right]}{(2\pi)^{\frac{d}{2}}|C_i|^{\frac{1}{2}}} \tag{1}$$

Where n is order of the mixture, d dimension of vector Y, $|\cdot|$ denotes determinant of matrix, symbol $()^T$ denotes transposition. Probability density function $p(Y)$ is thus characterized by scalar parameters α_i (called weights), vectors Y_i (called centers) and positive definite matrices C_i, called covariance matrices, each defined for $i = 1, \ldots, n$. Another condition is, that $\sum_{i=1}^{n} \alpha_i = 1$. Such model is rich enough to represent data even if it is unevenly clustered.

The method used for estimating parameters was standard Expectation Maximization (EM) algorithm (Dempster *et al.*, 1977). Learning set of feature vectors $Y^{(h)}(1), Y^{(h)}(2) \ldots, Y^{(h)}(t)$ was taken and estimates $\hat{\alpha}_i^{(h)}$, $\hat{Y}_i^{(h)}$ and $\hat{C}_i^{(h)}$ are calculated by the iterative process (upper index $.^{(h)}$ denotes healthy data or parameters). Strictly speaking, resulting probability density function from (1) is now conditioned by data, therefore the model: $p^{(h)}(Y|Y^{(h)}(1), Y^{(h)}(2), \ldots, Y^{(h)}(t))$ describes healthy data. Analogically data with Hashimoto's lymphocytic thyroiditis are described by probability density function $p^{(f)}(Y|Y^{(f)}(1), Y^{(f)}(2), \ldots, Y^{(f)}(t))$ with parameter estimates $\hat{\alpha}_i^{(f)}$, $\hat{Y}_i^{(f)}$ and $\hat{C}_i^{(f)}$. Symbolically we can write $p(Y|\mathcal{H})$ as model for healthy and $p(Y|\mathcal{F})$ for tissue sample with inflammation.

Estimation of optimal number of clusters is an interesting question of parameter estimation of Gaussian mixture (1). The more clusters (and bigger n) we have, the more accurately are data modeled. Some kind of Occam's razor should be used if this decision is important. We did not perform any estimation of n, we just manually set this parameter to a few different values and compared performance. As an optimal compromise between accuracy of modeling and speed of estimation we decided to use $n = 8$.

2.2 Inference Step

The task of inference step is to perform classification of any new sonographic image taken from patient, and infer whether the thyroid gland is healthy or it is not, based on model parameters estimated in learning step. For a new sonographic image we calculate the probability that the image belongs to the class of healthy images and probability that it belongs to the class of inflamed images. Using Bayes theorem, we can calculate posterior probabilities of both cases.

Information obtained from different images for the same patient can be easily combined giving probability of inflamed thyroid gland for one patient.

During inference step, we are going to tell whether an image represented by its feature vector Y^{new} belongs to the class of healthy or inflamed tissue. We are going to judge this image based on probability densities $p(Y|\mathcal{H})$ and $p(Y|\mathcal{F})$ learned in Section 2.1. Probability density functions $p(Y|\mathcal{H})$ and $p(Y|\mathcal{F})$ can be easily evaluated for Y^{new}. Using Bayes rule we obtain:

$$\begin{aligned} \Pr(\mathcal{H}|Y^{\mathrm{new}}) = & \\ = & \frac{\Pr(\mathcal{H}|Y_0)p(Y^{\mathrm{new}}|\mathcal{H})}{\Pr(\mathcal{H}|Y_0)p(Y^{\mathrm{new}}|\mathcal{H}) + \Pr(\mathcal{F}|Y_0)p(Y^{\mathrm{new}}|\mathcal{F})} \end{aligned} \tag{2}$$

We assume prior information $\Pr(\mathcal{H}|Y_0) = \frac{1}{2}$ and $\Pr(\mathcal{F}|Y_0) = \frac{1}{2}$. Expression $\Pr(\mathcal{H}|Y^{\mathrm{new}})$ is probability that tested sample Y^{new} belongs to healthy class of images.

Bayes rule (2) allows to classify one image based on learned models. We have group of feature vectors based on several different images from the same patient (denoted as $Y^{\mathrm{new}}(1)$, $Y^{\mathrm{new}}(2)$, ..., $Y^{\mathrm{new}}(n)$). We will put them together by calculating joint probability density function for one patient:

$$\begin{aligned} p(\mathbf{Y}|\mathcal{H}) = & \\ = & \; p(Y^{\mathrm{new}}(1), Y^{\mathrm{new}}(2), \ldots, Y^{\mathrm{new}}(n)|\mathcal{H}) = \\ = & \prod_{k=1}^{n} p(Y^{\mathrm{new}}(k)|\mathcal{H}) \end{aligned} \tag{3}$$

Analogically we can obtain $p(\mathbf{Y}|\mathcal{H})$.

We can make similar formula as (2) for the series of images:

$$\begin{aligned} \Pr(\mathcal{H}|\mathbf{Y}) = & \\ = & \frac{\Pr(\mathcal{H}|Y_0)p(\mathbf{Y}|\mathcal{H})}{\Pr(\mathcal{H}|Y_0)p(\mathbf{Y}|\mathcal{H}) + \Pr(\mathcal{F}|Y_0)p(\mathbf{Y}|\mathcal{F})} \end{aligned} \tag{4}$$

Formula (4) gives the probability that given patient has healthy or inflamed gland.

3. EXAMPLE

To test the method, we used a set of sonograms from 81 patients, from which 30 were healthy and 51 had Hashimoto's lymphocytic thyroiditis. From each patient we had between 100 to 1000 images. Total number of feature vectors was approximately 34000. We used leave-one-out method to ensure that method was trained with different data than tested. Leave-one-out method also avoids the possible bias introduced by relying on any one particular division into test and train data sets. We performed 81 experiments, in each of them we removed one patient, tried to learn from the rest, and tried to diagnose removed patient. Results are in table below. Column "total" denote total number of patients, "diag=" denotes diagnosis from the algorithm.

patients	total	diag=non-healthy	diag=healthy
non-healthy	30	30	0
healthy	51	1	50

One patient from healthy-group was incorrectly diagnosed as non-healthy, which might be border-case. This patient had 40% of feature vectors diagnosed correctly. There is also one patient diagnosed correctly with only 60% of feature vectors diagnosed correctly. All other patients have more than 95% of feature vectors diagnosed correctly.

4. CONCLUSION

On the example of Hashimoto's lymphocytic thyroiditis it was shown that some diseases are possible to be diagnosed using feature vectors. For inference and statistical processing of data we used Gaussian Mixture modeling with Bayesian decision-making. We are able to tell the probability, that the set of images from given patient or just the single image belong to the class of healthy images or images with inflammation. The method was tested on practical example with real data. Using leave-one-out method all tested patients except for one healthy patient were diagnosed correctly.

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