

# Image Segmentation of Uterine Cervix Images for Indexing in PACS

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## Abstract

*The National Cancer Institute has collected a large database of digitized 35mm slides of the uterine cervix, the idea being to build a system enabling to study the evolution of lesions related to cervical cancer. In taking the first few steps towards this goal, the objective of this work is to develop and evaluate methodologies required for visual-based (i.e. content-based) indexing and retrieval that substantially improve information management of such a database. In this paper we model the properties of three tissue types using color and texture features, and use these models for image segmentation. Statistical modeling and segmentation tools are used for the task.*

## 1 Introduction

Visual information management - be it image coding for efficient communication or storage, or image understanding for image database query and retrieval, is a topic of great value and research interest. The challenge for vision researchers and engineers is to develop tools for analyzing the content of images and represent it in a way that can be efficiently searched and compared. It is well acknowledged that medical image databases are key components in future diagnosis and preventive medicine which leads to an increasing trend towards the digitization of medical imagery and the formation of adequate archives.

This work is part of an on-going effort towards the creation of a content-based image retrieval (CBIR) system for cervicographic images. Cervical cancer, the second most common cancer affecting women worldwide and the most common in developing countries, can be cured in almost all patients, if detected by high quality repeated Pap screening, and treated. However, cervical cancer incidence and mortality remain high in resource-poor regions, where high-quality Pap screening programs often cannot be maintained because of inherent complexity and cost. An alternative method of cervical cancer screening, termed cervicography, uses visual testing based on color change of cervix tissues when exposed to acetic acid. The National Cancer Institute (NCI) has collected a vast amount of biomedical information related to the occurrence and evolution of uterine cervical cancer in a longitudinal multi-year study carried out in Guanacaste, Costa Rica. The data collected includes among other medical detail, 60,000 cervicographic images (“Cervigrams”) in the form of 35 mm color slides, as well as medical classifications for the Cervigrams into diagnostic

categories. A major long-term objective is to develop a unique Web-based database of the digitized cervix images for investigating the role of HPV in the development of cervical cancer and its intraepithelial precursor lesions in women.

## 2 Related work

Cervigrams contain complex and confusing lesion patterns. Correctly analyzing and classifying different types of tissues require substantial training, and the average physicians do not get to examine enough patients to maintain such expertise. The extreme data complexity motivates the need for additional tools, such as automated image processing and analysis tools, for a computer-aided cervicographic workstation that can help and guide the medical expert using cervicographic technology.

A small number of works can be found in this domain. Most of the works require the user to define regions of interest (ROI) on the various cervix tissues [2], [5], [4]. Features such as color [5] and texture [4] are then extracted automatically. Manual lesion segmentation enables the extraction of geometric features as well [2]. Based on these features the different regions are classified to different cervix tissue types using various classifiers, such as neural networks [2] or the minimum distance classifier [4]. In a more recent work, Van Raad [6] uses different tools for the segmentation of the Transformation Zone (TZ) based on the evaluation of the local frequency content within the TZ. A semi-automatic tool based on active contour model at multiple scales is used in [7]. The TZ is the most prominent area where cervical neoplasia can occur. This specific area within the normal cervix is frequently misclassified by the inexperienced physician and a segmentation procedure can guide and ensure that the test or the biopsy is taken from the right area of the cervix.

In this work we start with the first few steps towards the creation of a CBIR system for cervicographic images. We focus on the color and texture features and introduce initial efforts in cervigram image segmentation. In particular we focus on the segmentation of the following tissue types: The original squamous epithelium (SE), which is a featureless, smooth, pink epithelium; The columnar epithelium (CE) that extends between the endometrium and the squamous epithelium, and appears red and irregular with stromal papillae and clefts; and the acetowhite (AW) region which is a transient, white-appearing epithelium following the application of acetic acid. Areas of acetowhitening correlate with higher nuclear density and are of clinical significance.

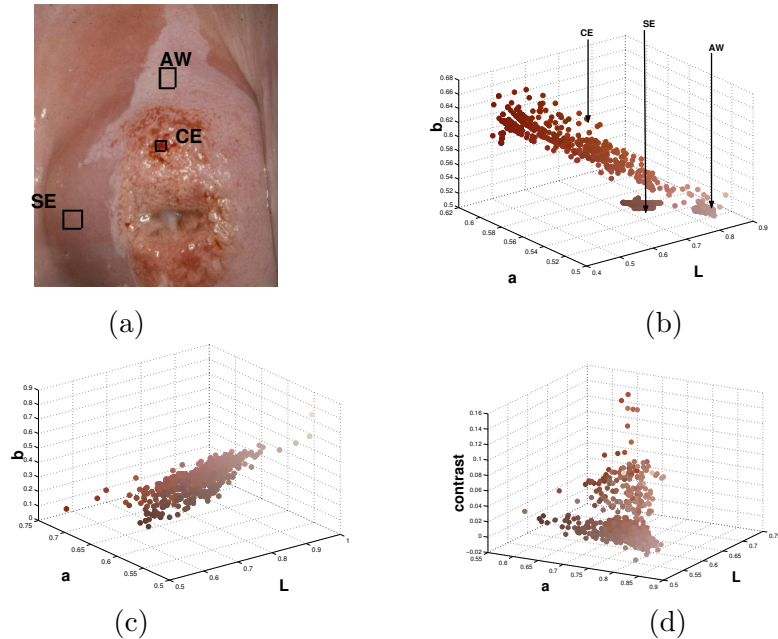
## 3 Cervigram segmentation

A recently proposed continuous image representation scheme is utilized for the cervicographic image modeling and segmentation [3]. Each image is modeled as a mixture of Gaussians in a color-texture feature space. Following the model generation, probabilistic image segmentation is enabled.

### 3.1 Feature selection and extraction

A properly chosen feature-space provides for a good separation between the various tissues of interest. As an important first step we explore color and texture feature spaces for the task.

Former works (mentioned above) used color information from a one-dimensional color feature space in order to analyze the cervix images. Gray-level images are used in [4] and [6]. *RGB* color channels are used separately in [5] and a weighted single combination of the *RGB* channels is used in [7]. In our work color features are extracted by representing each pixel with a three-dimensional color descriptor in the *Lab* color space which was shown to be approximately perceptually uniform [3]. Figure 1(a) shows manually marked patches of the three tissues of interest. Looking at the distribution of the pixel colors within the selected patches (Figure 1(b)) shows an apparent separation between the different tissues, which illustrates the importance of color in the cervigram analysis task. The clusters within the tissue color distribution can be modeled with Gaussian or Gaussian mixture models (GMM). The CE patch is less clustered as the CE tissue is very inhomogeneous in color. Looking at the distribution of the entire image pixel-set (Figure 1(c)) presents a much more complex scenario, thus implying that additional features are needed in order to distinguish between the tissues.



**Figure 1. Pixels scatter in the feature-space. (a) Cervigram image, with manually selected patches from each tissue; (b) Pixels from each patch in Lab color-space; (c) Pixels from entire image in Lab color-space; (d) Pixels from entire image in La-contrast color-texture space.**

We investigate next the relevance of texture features for the task. The texture features used describe both the underlying texture parameters and the adequate texture scale [1]. The scale is defined as the width of the Gaussian window within which gradient vectors of the image are pooled. The second moment matrix for the vectors within this window, computed about each pixel in the image, can be approximated using Equation 1:

$$M_{\sigma}(x, y) = G_{\sigma}(x, y) * (\nabla I)(\nabla I)^T \quad (1)$$

where  $G_{\sigma}$  is a separable binomial approximation to a Gaussian smoothing kernel with variance  $\sigma^2$ , and  $(\nabla I)$  is the gradient of the image intensity. Two texture descriptors are

extracted for each pixel: polarity and texture contrast. Polarity is a measure of the extent to which the gradient vectors in a certain neighborhood all point in the same direction, as defined in Equation 2:

$$p_\sigma = \frac{E_+ - E_-}{E_+ + E_-} \quad (2)$$

where  $\sigma$  is the scale. The definitions of  $E_+$  and  $E_-$  are:

$$E_+ = \sum_{x,y} G_\sigma(x,y)[\nabla I \cdot \hat{n}]_+ ; E_- = \sum_{x,y} G_\sigma(x,y)[\nabla I \cdot \hat{n}]_- \quad (3)$$

where  $[\cdot]_+$  and  $[\cdot]_-$  are the rectified positive and negative parts of their argument and  $\hat{n}$  is a unit vector perpendicular to  $\phi$  (the direction of principal eigenvector of the second moment matrix, as defined in Equation 1. This feature is used later for the selection of an appropriate texture scale for each pixel in the image. The contrast relates to the energy of the gradients in the vicinity of each pixel as given by Equation 4, where  $\lambda_1$  and  $\lambda_2$  are eigenvalues of  $M_\sigma$  ( $\lambda_1 \geq \lambda_2$ ) at each location:

$$contrast = 2\sqrt{\lambda_1 + \lambda_2} \quad (4)$$

The process of selecting an appropriate scale is based on the derivative of the polarity with respect to the scale. For each pixel  $(x,y)$  the scale is selected as the first value for which the difference between values of polarity at successive scales is less than 2%. The contrast feature of the appropriate scale is extracted and used during the segmentation process. Figure 1(d) shows the distribution of pixels in the combined color-texture space. A separation between textured and non-textured clusters can be seen on the contrast axis.

### 3.2 Statistical modeling and segmentation

Following the feature extraction stage, each pixel is represented with a four-dimensional feature vector,  $[L,a,b,C]$ , and the image as a whole is represented by a collection of feature vectors in the four-dimensional space. Pixels are grouped into homogeneous regions by grouping the feature vectors in the selected feature space. The underlying assumption is that the image colors and texture are generated by a mixture of Gaussians. Each homogeneous region in the image plane is thus represented by a Gaussian distribution, and the set of regions in the image is represented by a Gaussian mixture model.

The distribution of a d-dimensional random variable is a mixture of  $k$  Gaussians if its density function is :

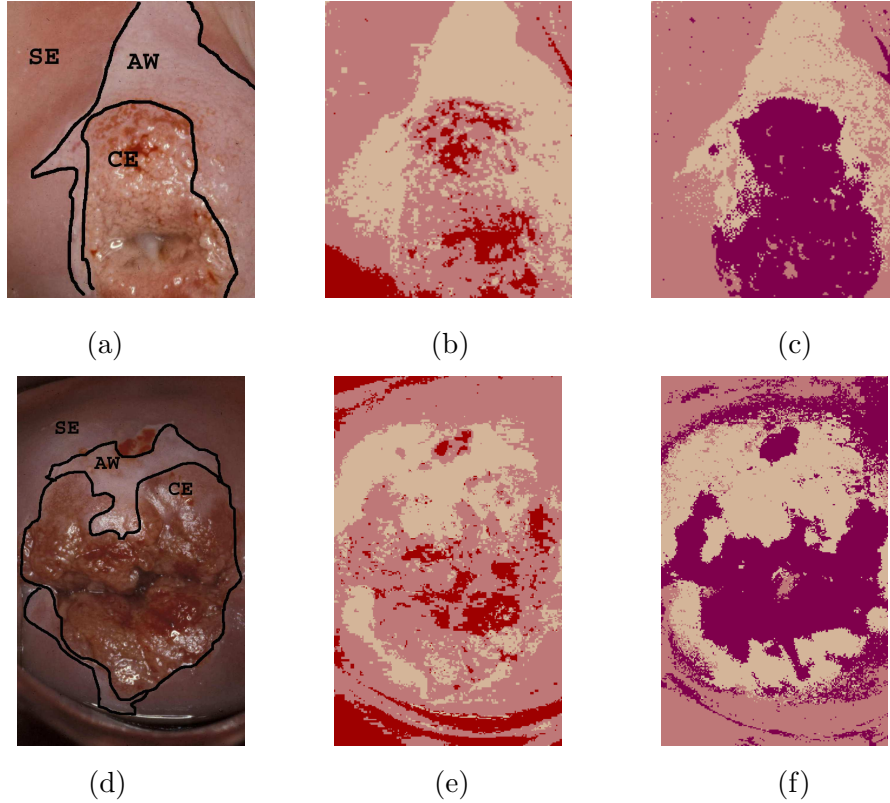
$$f(y) = \sum_{j=1}^k \alpha_j \frac{1}{\sqrt{(2\pi)^d |\Sigma_j|}} \exp\left\{-\frac{1}{2}(y - \mu_j)^T \Sigma_j^{-1} (y - \mu_j)\right\}, \quad (5)$$

where  $\alpha_j$  are the probabilities of the occurrence of each Gaussian, and  $\mu_j$ ,  $\Sigma_j$  are the mean and the covariance matrix of each Gaussian cluster respectively.

The Expectation-Maximization (EM) algorithm is used to determine the maximum likelihood parameters of a mixture of three Gaussians in the feature space (representing the three tissue types of interest) [3]. An immediate transition is possible between the image representation using the GMM, and probabilistic image segmentation. Each pixel of the

original image can be affiliated with the most probable Gaussian cluster (Equation 6). The labeling of a pixel related to the feature vector  $x$  is chosen as the maximum *a posteriori* probability, as follows::

$$label(x) = \arg \max_j \alpha_j f(x | \mu_j, \Sigma_j) \quad (6)$$



**Figure 2. Segmentation examples. Unsupervised clustering into three classes: (a),(d) - manually segmented images; (b),(e) - images segmented in Lab color feature space; (c),(f) - images segmented in color-texture feature space.**

## 4 Results

Unsupervised image segmentation using the described procedure was performed on cervix images. Figure 2 presents two segmentation examples. Original images with approximate region boundaries drawn manually, are shown in Figure 2(a) and Figure 2(d). Segmentation results in Lab color space are shown in Figure 2(b) and Figure 2(e) and results of segmentation in Lab-contrast feature space are displayed in Figure 2(c) and Figure 2(f).

Figures 2 (b) and (e) show a good separation of the AW regions, in the color-space segmentation. Portions of CE, and various strongly lit regions are incorrectly identified as AW as well. Increasing the representation space to include the texture feature, helps to identify the CE tissue region as a homogeneous entity and prevents the over segmentation of the CE tissue. In Figure 2(c) all the pixels belonging to CE tissue were labelled as

belonging to the same class. Using color only, pixels in that region were identified as belonging to three different clusters, as seen in Figure 2(b). Further improvement of the segmentation results may be achieved by eliminating specular reflections, which contribute a certain amount of misclassifications, as can be seen in Figure 2(f).

## 5 Discussion

In this work we display initial segmentation results for cervigrams. We have used GMM modeling per input image. Preliminary experiments that were conducted on large sets of data lead us to the conclusion that the color-features alone do not suffice for an adequate description of the data-set thus motivating the investigation of texture features. The results, although preliminary, look promising for the differentiation of the three examined tissue types: the squamous epithelium (SE), the columnar epithelium (CE) and the acetowhite lesions (AW). The AW regions are of particular interest since estimates of their size are of clinical significance. We are currently working on improving the initial results by investigating additional features and improving the segmentation scheme. Attention should be given to the specular reflections which currently interfere with the image segmentation task. Future work entails the merging of different regions related to the same tissue, by utilizing higher-level knowledge. The segmentation results should be further analyzed and evaluated by medical experts.

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