Clinical study of quantitative diagnosis of early cervical cancer based on the classification of acetowhiteness kinetics

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Abstract. A quantitative colposcopic imaging system for the diagnosis of early cervical cancer is evaluated in a clinical study. This imaging technology based on 3-D active stereo vision and motion tracking extracts diagnostic information from the kinetics of acetowhiteness measured from the cervix of human subjects in vivo. Acetowhiteness kinetics measured from 137 cervical sites of 57 subjects are analyzed and classified using multivariate statistical algorithms. Cross-validation methods are used to evaluate the performance of the diagnostic algorithms. The results show that an algorithm for screening precancer produced 95% sensitivity (SE) and 96% specificity (SP) for discriminating normal and human papillomavirus (HPV)-infected tissues from cervical intraepithelial neoplasia (CIN) lesions. For a diagnostic algorithm, 91% SE and 90% SP are achieved for discriminating normal tissue, HPV infected tissue, and low-grade CIN lesions from high-grade CIN lesions. The results demonstrate that the quantitative colposcopic imaging system could provide objective screening and diagnostic information for early detection of cervical cancer.

Keywords: acetowhiteness; cervical cancer; principal component analysis; support vector machine.

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1 Introduction

Cervical cancer is the second most common cancer in women worldwide. The major underlying cause of cervical cancer is the infection with certain types of human papillomavirus (HPV). After HPV infection, a small percentage of women will develop cervical intraepithelial neoplasia (CIN), which is graded into three classes (CIN 1, 2, and 3) based on changes in tissue morphology. The majority of cases with mild dysplasia, CIN 1, spontaneously regress to normal, but most cases with more severe lesions, CIN 2 and 3, will progress to invasive cervical cancer. It is therefore important to distinguish CIN 2 and 3 lesions from CIN 1 lesions, HPV-infected tissue, and normal tissue in the clinic to prevent cervical cancer progression. The Pap smear and colposcopy are the primary screening and diagnostic tests for the early detection of neoplastic growth in the cervix. Because the mean sensitivity of Pap smear is lower than 50%, further diagnosis by colposcopy is required to confirm the result of an abnormal Pap smear. In a meta-analysis of the performance of conventional diagnostic colposcopy for distinguishing high-grade CIN and cancerous tissue from the low-grade CIN and non-CIN tissue, the sensitivity was found to be high (64 to 99%) with a mean of 85%, whereas the specificity was lower (30 to 93%) with a mean of 69%.

The diagnostic information produced by colposcopy is based on the analysis of the acetic-acid-induced whitening or acetowhiteness effect in tissue. After applying 3 to 5% acetic acid to the cervix, abnormal cervical tissue turns white in a transient and delayed reaction, while normal epithelium maintains a pink translucent color. A contrast between precancerous lesions and normal tissues is therefore visible. The changes disappear when the acetic acid is completely neutralized, therefore making the effect temporary. Long-term experience has demonstrated that the dynamic changes of acetowhiteness, such as the maximum whiteness and duration, are statistically correlated with the histological grades of CIN. However, the traditional colposcopy procedure is subjective because the diagnostic accuracy very much depends on the experience of the individual physician. Therefore, an objective diagnostic procedure based on quantitative measurement of the kinetics of the acetowhiteness process could substantially improve the diagnostic accuracy in the detection of early cancer lesions.

Recently, we reported a new imaging technique that combines 3-D imaging and motion tracking to enable quantitative mapping of acetowhiteness kinetics over the cervical surface. Briefly, the system consists of a three-CCD color camera, a ring LED illuminator, and a structured laser light...
20 Attributed to the motion of the patient. In this paper, we develop multivariate classification algorithms to distinguish CIN lesions from non-CIN cervical tissues for screening purposes and to distinguish high-grade CIN lesions from low-grade CIN and non-CIN tissues for the diagnostic purposes, respectively. We investigate the potential to achieve objective and computer-aided colposcopy based on the classification of acetowhitening kinetics at the clinical level.

2 Materials and Methods

2.1 Clinical Procedure

The experimental 3-D colposcopic imaging system used for the data acquisition is described in detail elsewhere. Briefly, we developed an active stereo vision system to measure the 3-D topology of cervix surface. The system consists of an 8-bit three-CCD color camera, a ring illuminator of 30 blue-light LEDs, and a structured red laser (660-nm) light projector with a 33-stripes pattern. The field of view of the image is about 37.3 × 28 mm. The resolution of the imaging system is about 0.05 mm/pixel. To make sure that most of the laser stripes can be projected through the speculum used in colposcopy, the angle between the imaging channel and projection channel was set to about 5° and the spacing of the lines of the stripes projected at the cervix tissue is about 0.7 mm. The working distance of the imaging system is about 300 mm.

The image of reflection from cervix and the image of the structured light pattern projected on cervix were captured from blue and red channels of the three-CCD color camera, respectively. The time-sequenced images of the cervix were stored for the analysis of acetowhitenning kinetics over the cervix surface. The simultaneously captured images of the structured light pattern on the cervix were used for tracking the motion of the patient. In this paper, one reference image of the cervix was captured before the application of acetic acid. A total of 300 images were captured after the application of acetic acid with a 1-s time interval between two images. Therefore, the acetowhitenning kinetics over 300 s was measured. The 3-D surfaces of the cervix measured at different times are used to track the motion and to register the time-sequenced 2-D images. The acetowhitenning kinetics, the reflection from cervix as a function of time, could be measured from the intensity of the registered time-sequenced images.

Fifty-seven human subjects originally scheduled for colposcopy and a loop electrosurgical excision procedure (LEEP) were enrolled in the investigation of the imaging technique. To avoid interference from mucus discharge, the cervix was first cleaned with saline before applying 5% acetic acid. A routine colposcopy or LEEP was followed after the 3-D imaging. Tissue biopsies were taken from the subjects’ cervixes from the sites of the worst suspicious lesions, and from the most possible normal cervical squamous tissues for comparison. The histological analysis of tissue biopsies was performed by experienced pathologists and the histological reports were considered as the ground truth. This study was approved by the Ethical Committee of the Prince of Wales Hospital, the Chinese University of Hong Kong. Consent letters were obtained from all patients enrolled in this study.

2.2 Data Processing of Acetowhitenning Kinetics

A variety of multivariate statistical algorithms have been successfully utilized in the diagnosis of tissue. In this study, multivariate statistical algorithms based on principal component analysis (PCA) and a support vector machine (SVM) were investigated for the diagnosis of CIN lesions based on the classification of the kinetics of the acetowhitenning processes. Particularly, PCA was used to reduce the dimension of the acetowhitenning kinetics curves for visual separation of the different tissue types, such as CIN lesions and non-CIN tissues. The SVM algorithm was used to classify and grade the CIN lesions because it has been proved as a more effective method to classify multivariate signals when the separating boundaries between data measured from different types of tissues are nonlinear.

PCA is a method for analyzing the statistical characteristics of multidimensional data. In the application of the PCA method to processing acetowhitenning kinetics, the original time-resolved acetowhitenning signals were transformed into principal component (PC) scores, which indicated new sets of linear combinations of the informative orthogonal PCs. We first identified the diagnostic informative PCs and calculated the PC scores. The scores of informative PCs are used to illustrate the separation of normal and diseased tissue. The SVM is an effective algorithm for classifying multivariate data. After it was first induced by Vapnik, the SVM has been extensively used in the classification of data, particularly in the processing of biological and medical data. We used the nonlinear SVM [radial basis function (RBF) kernel] algorithm to classify tissue based on the correlation between the kinetics of in vivo acetowhitenning signals and the pathologic states of the tissue sites where the acetowhitenning signals were measured. In this work, SVMlight (version 6.02) was used for the development of classification algorithms. In the learning and testing procedures, each time-resolved acetowhitenning kinetics curve was labeled according to the result of histological examination. The kinetics curves of acetowhitenning were divided into categories of high-grade CIN, low-grade CIN, HPV, or normal tissue. Optimization of the
SVM algorithms via exhaustive search were performed to maximize the accuracy to distinguish CIN lesions from non-CIN cervical tissues for screening purposes and to distinguish high-grade CIN lesions from low-grade CIN and non-CIN tissues for diagnostic purposes, respectively. Details of the development of an SVM algorithm were described in our previous study. To evaluate the performance of the diagnostic algorithm, the leave-one-out cross-validation and k-fold cross-validation were used to calculate the sensitivity (SE) and specificity (SP) of the SVM algorithms. In each round of the leave-one-out cross-validation, one acetowhitening kinetics curve was held out from a total of 137 in vivo acetowhitening kinetics curves measured from all the cervical tissue samples. The remaining acetowhitening kinetics curves were used as a training set for construction and optimization of the SVM algorithm. The held-out acetowhitening kinetics curve was then classified by the optimized algorithm. This process was repeated until all the acetowhitening kinetics curves in the data set were classified. The criterion for optimizing the algorithms in the training set was to maximize the classification accuracy and the SE in the training set. The final SE and SP of a particular algorithm were calculated based on the classification of the held-out acetowhitening signal in the test set in each round of cross validation. In the k-fold cross-validation, the data set was randomly divided into k subsets. Then k-1 subsets were used for training, and the last subset was used for evaluation. This process was repeated k times, leaving a different subset for evaluation each time. The k cross-validation estimates were averaged to provide the aggregated classification accuracy of the SVM algorithms. The leave-one-out cross-validation is similar to the k-fold cross-validation where the value of k is set to the sample size.

The disadvantage of leave-one-out cross-validation is that the results could be biased because of overtraining of the algorithm. The k-fold cross-validation can reduce the bias caused by overtraining and the variance associated with the validation process. The empirical studies indicated that the optimal number of folds for k-fold cross-validation is 10. However, because the sample size of normal tissue and CIN 1 lesions in this work were relatively small, the sample number in each subset would be too small if the samples are divided into 10 subsets. We compromised to choose the number of folds as five, as the previously reported studies with relatively small sample volumes. To further reduce the bias, we randomly divided the samples in each category into five subsets and performed the fivefold cross-validation. The random division of samples and fivefold cross-validation were repeated by a large number of rounds (>10^4). This helped us to determine the lower boundary of the algorithm performance with the worst subdivision.

A receiver operating characteristics (ROC) curve is used in this study to visualize and to select different classifiers based on their performance. Areas under the ROC curve (AUC) can be used to quantify the performance of the classifier. Moreover, the optimal cutoff points can be determined from the ROC curve to best balance the SE and SP, where the optimal SE and SP are defined as those producing the minimal value for (1-SE)^2+(1-SP)^2. In this study, we used this method to evaluate the SE and SP of the ROC curves.

### 3 Results and Discussion

#### 3.1 Measurement of Acetowhitening Kinetics in Vivo

The 3-D colposcopic imaging system was evaluated in vivo. A representative result of image registration on a tissue sample without treatment with acetic acid is shown in Fig. 1. A reference image and an unregistered target image captured with a 35-s interval are shown in Figs. 1(a) and 1(b), respectively. To evaluate the performance of the diagnostic algorithm, the leave-one-out cross-validation and k-fold cross-validation were used to calculate the sensitivity (SE) and specificity (SP) of the SVM algorithms in each round of the leave-one-out cross-validation, one acetowhitening kinetics curve was held out from a total of 137 in vivo acetowhitening kinetics curves measured from all the cervical tissue samples. The remaining acetowhitening kinetics curves were used as a training set for construction and optimization of the SVM algorithm. The held-out acetowhitening kinetics curve was then classified by the optimized algorithm. This process was repeated until all the acetowhitening kinetics curves in the data set were classified. The criterion for optimizing the algorithms in the training set was to maximize the classification accuracy and the SE in the training set. The final SE and SP of a particular algorithm were calculated based on the classification of the held-out acetowhitening signal in the test set in each round of cross validation. In the k-fold cross-validation, the data set was randomly divided into k subsets. Then k-1 subsets were used for training, and the last subset was used for evaluation. This process was repeated k times, leaving a different subset for evaluation each time. The k cross-validation estimates were averaged to provide the aggregated classification accuracy of the SVM algorithms. The leave-one-out cross-validation is similar to the k-fold cross-validation where the value of k is set to the sample size.

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tured for acetowhiteness measurements. We identified the corresponding site in the images for acetowhiteness measurements where the biopsy was taken. The difference in locations between the exact biopsy site and the optical measurement site was sufficiently small compared with the CIN lesion size (normally a few millimeters). The statistical results are presented in Fig. 2. As we can see, the kinetics of acetowhiteness measured from different types of tissues are distinct.

Note that the representative results in Fig. 2 are slightly different from the results shown in Fig. 6 of the previous study in Ref. 9, though the tendencies in the two figures are the same. There may be a few factors that caused the difference. The kinetics curves of acetowhiteness signals vary from patient to patient and even from tissue site to site in the same patient. Only 10 patients were enrolled in the previous clinical pilot study. The results based on such a small sample volume do not produce a high statistical significance and may deviate from the results obtained in this study with a much longer enrolment of human subjects. Furthermore, the results shown in the previous study were based on colposcopy diagnosis and were not based on pathological analysis, the gold standard of diagnosis, as used in this study. The diagnostic error made by the colposcopist could lead to the corresponding kinetics curves of acetowhiteness being labeled with the wrong pathological status.

3.2 Multivariate Statistical Classification

As shown in Fig. 2, tissues in different pathological categories could be roughly separated based on their kinetics curves of

![Fig. 1](https://www.spiedigitallibrary.org/journals/Journal-of-Biomedical-Optics March/April 2010)

![Fig. 2](https://www.spiedigitallibrary.org/journals/Journal-of-Biomedical-Optics March/April 2010)

### Table 1

<table>
<thead>
<tr>
<th>Normal</th>
<th>HPV</th>
<th>CIN 1</th>
<th>CIN 2 and 3</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Subjects</td>
<td>12</td>
<td>36</td>
<td>12</td>
<td>23</td>
</tr>
<tr>
<td>Number of biopsy</td>
<td>12</td>
<td>66</td>
<td>15</td>
<td>44</td>
</tr>
</tbody>
</table>

Fig. 2 Kinetics of acetowhiteness for each type of tissues measured from 57 subjects over 300 s after the application of acetic acid.
acetowhitenning. To create a clear and simple visualization of tissue classification, we used a PCA algorithm to calculate the PCs from the 137 acetowhitenning kinetics curves and to identify their diagnostic relevance. In the PC-score-based method, the proportion of variations explained by the PCs determines the number of informative PCs. We found that the first two PCs accounted for 93% of the data variation, while each higher order PC then accounted for less than 4%, suggesting that the higher order PCs were not significant to present the data. This indicates that use of the first two PCs could be adequate to extract significant data variation for diagnosis. The scatter plot of the first two PC scores is shown in Fig.3. As we can see in the figure, the difference in PC scores between CIN lesions and non-CIN tissues are statistically significant. The p values from a t test are $2.28 \times 10^{-22}$ and 0.006 for the PC1 and PC2 scores, respectively. Therefore, the classification of samples could be based on the PC1 and PC2 score values. The classification using PC scores also shows that the boundary between different tissue types, especially between high-grade CIN lesions and the rest, are not linear. In this work, a nonlinear SVM method that can effectively classify data with a nonlinear boundary was used to develop algorithms for screening and diagnostic purposes. We compared the difference in performance between the SVM algorithm based on the first two PCs and the algorithm using the whole kinetics curve without a reduction of data dimension.

In the first trial, we used the nonlinear SVM algorithm to classify CIN lesions and non-CIN tissues for the purposes of screening for CIN lesions. In the leave-one-out cross-validation, the optimized parameters of the SVM algorithm developed from the training set were used to classify the held-out acetowhitenning kinetics curves. The results of the classifications using the first two PC scores and whole kinetics curve of the acetowhitenning signals are summarized in Table 2. With the SVM algorithm, we were able to identify 56 of 59 CIN lesions and 75 of 78 non-CIN tissue samples correctly. Thus, the CIN lesions could be distinguished with an SE of 95% and an SP of 96%. In detail, all of the samples diagnosed as normal tissue and CIN 1 lesions were identified correctly. Three of 66 HPV-infected samples were misdiagnosed, as well as 3 of 44 CIN 2 and 3 lesions. Compared to the Pap smear screening method with less than 50% SE, the SVM algorithm can improve the SE to a great extent while maintaining high SP. The results in the table show that the accuracy of the nonlinear SVM algorithm using only two PC scores and the whole acetowhitenning signals are identical, demonstrating again that the first two PCs carry the most diagnostic information to separate CIN tissue from non-CIN tissue.

In the second trial, we used the SVM algorithm to classify high-grade CIN lesions (CIN 2 and 3) from low-grade lesions (CIN 1) and non-CIN tissue for diagnostic purposes. The results of the nonlinear SVM classifications using the first two PC scores and the whole acetowhitenning signals based on leave-one-out cross-validation are summarized in Table 3. With a nonlinear SVM algorithm based on the first two PCs, we could obtain an SE of 91% and an SP 87% for the separation of CIN 2 and 3 lesions from other tissue types. When using the whole acetowhitenning kinetics signals, the nonlinear SVM algorithm could generate a slightly higher accuracy than only using the first two PC scores. The SE and SP are 91 and 90%, respectively. This may be caused by the fact that when projecting the acetowhitenning kinetics signals only to the space of the first two PC scores, some information useful for the classification of the high-grade CIN lesions from other types of tissues was lost.

As shown in Fig. 3, it is not possible to discriminate high-grade CIN lesions from other types of tissue with a single linear boundary. However, the nonlinear SVM algorithm can generate a nonlinear boundary in the space of the first two PC scores to differentiate the CIN 2 and 3 lesions from other tissue types. When we compare the algorithm for diagnostic purposes with the accuracy of the algorithm for screening CIN lesions, the performance of diagnostic algorithm is poorer. This was mainly caused by the fact that part of the acetowhitenning kinetics curves of CIN 1 lesions were highly overlapped with the acetowhitenning kinetics curves measured from CIN 2 and 3 lesions. In addition, there were only 15 CIN 1 lesions out of 137 cases in this study. When the sample size of CIN 1 lesions was small, one or two misclassifications of

### Table 2: Classification of acetowhitenning kinetics with the algorithms for screening purpose.

<table>
<thead>
<tr>
<th>Algorithms</th>
<th>SE (%)</th>
<th>SP (%)</th>
<th>Accuracy (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2 PC scores + SVM</td>
<td>94.9</td>
<td>96.2</td>
<td>95.6</td>
</tr>
<tr>
<td>SVM (RBF)</td>
<td>94.9</td>
<td>96.2</td>
<td>95.6</td>
</tr>
</tbody>
</table>

### Table 3: Classification of acetowhitenning kinetics with the algorithms for diagnostic purpose.

<table>
<thead>
<tr>
<th>Algorithms</th>
<th>SE (%)</th>
<th>SP (%)</th>
<th>Accuracy (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2 PC scores + SVM</td>
<td>90.9</td>
<td>87.1</td>
<td>88.3</td>
</tr>
<tr>
<td>SVM (RBF)</td>
<td>90.9</td>
<td>90.3</td>
<td>90.5</td>
</tr>
</tbody>
</table>
CIN 1 lesions could reduce the SP significantly. In future work, it is necessary to increase the sample number of CIN 1 lesions to make the classification algorithms more robust.

To reduce the possible bias caused by overtraining in the leave-one-out cross-validation, we evaluated the nonlinear SVM algorithms for screening and diagnostic purposes by using $k$-fold cross-validation and setting $k=5$ (Refs. 18–20). Compared with the leave-one-out cross-validation, this validation is closer to a clinical condition. To avoid any loss of diagnostic information, we developed the nonlinear SVM algorithms using the whole acetowhiteness signals instead of the first two PC scores. As described in Sec. 2, the fivefold cross-validations with random division of samples in each pathological category were repeated over $10^4$ rounds. The corresponding mean and the worst ROC curves of diagnostic accuracy for screening and diagnostic purposes were determined and are presented in Figs. 4 and 5, respectively. As shown in Fig. 4, the mean and the worst AUC for fivefold cross-validation of the SVM algorithm for screening purposes were 0.98 and 0.84, respectively. The evaluations of the algorithm for the diagnostic purposes in Fig. 5 show that the mean and the worst AUC for fivefold cross-validation were 0.94 and 0.69, respectively. After the cut-off points were determined, the balanced SE and SP can be calculated. We found that the worst performances in the fivefold cross-validation still could achieve 82% SE and 87% SP for screening purposes and 78% SE and 61% SP for the diagnostic purposes. These results determined the low boundary of the classification algorithm in the worst situation. However, the averaged performance over $10^4$ rounds of fivefold cross-validation could achieve 93% SE and 96% SP for screening purposes and was 89% SE and 89% SP for diagnostic purposes. Note that leave-one-out cross-validation and $k$-fold cross-validation produced similar results, indicating that based on the data in this study, the disadvantage of overtraining with leave-one-out cross-validation was not being realized. Overall, the classification results from using nonlinear SVM algorithms demonstrate that our colposcopy technique based on 3-D imaging and motion tracking has the potential to make colposcopic diagnosis objective and quantitative. The screening accuracy in discriminating CIN lesions from normal and HPV-infected tissues and the diagnostic accuracy in discriminating high-grade CIN lesions from low-grade CIN lesions, HPV, and normal tissue are significantly higher than the reported SE and SP of conventional methods such as Pap smear and colposcopy.12

4 Conclusion

We described a novel optical imaging method to make colposcopic diagnosis objective for the early detection of cervical cancer. It provides quantitative diagnostic information and can potentially lead to a development of a fully automated colposcope system. This technology could impact significantly on cervical cancer prevention and management in regions where screening/diagnostic equipment and professional colposcopists are in short supply. In our future work, we plan to integrate the classification algorithms with the 3-D colposcopic imaging of acetowhiteness kinetics of cervical tissue and to create an automated instrument for the diagnosis of precancerous lesions in the cervix. Finally, note that this technique can not totally replace conventional colposcopy. In some of these cases, the entire transformation zone of the cervix cannot be seen in one view or identified in the field of view, which limits the application of this imaging technique.

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