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| 28 | DEEP LEARNING BASED CYTOLOGY NEGATIVE SAMPLE SCREENING METHOD |

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Objectives We show that deep learning can be used to create high accuracy cells classifiers that can support cytologists in their work.

Two deep learning models are presented. The first model is used for cervical cancer cytology negative/positive prescreening and we show its high specificity at 100% Negative Predict Value (NPV). The second model is used to predict among 15 categories common to cervical analysis, as listed in figure 1(b).

Our classifiers include Grad-Cam visualizations that show both models concentrate on relevant areas of images.

Methods Classifiers are based on deep convolutional networks. The crucial aspects in achieving high accuracy are data augmentation and focal loss.
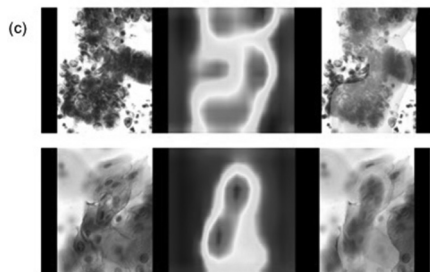
Grad-Cam visualizations are used to explain models' reasoning.

Abstract 28 Figure 1 (a) Confusion matrix of prescreening model; (b) Accuracy of 15 categories classification model; (c) Grad-Cam visualizations

Results Prescreening model, based on 2700 samples, achieves 95.89% overall accuracy and 91.62% specificity at 100% NPV (figure 1(a)) ; second stage screening model, based on approximately 9500 samples, achieves 92.03% overall accuracy (figure. 1(b)). Grad-Cam visualizations show that both models concentrate on relevant areas of the image when making predictions (figure 1(c)).

Conclusions We show that deep learning based classifiers can be useful in supporting cytologist in their work. Approximately 92% of samples that cytologist screen for cervical cancer are negative. With our model cytologists can concentrate their efforts on only positive samples and a small number of false positives predictions.

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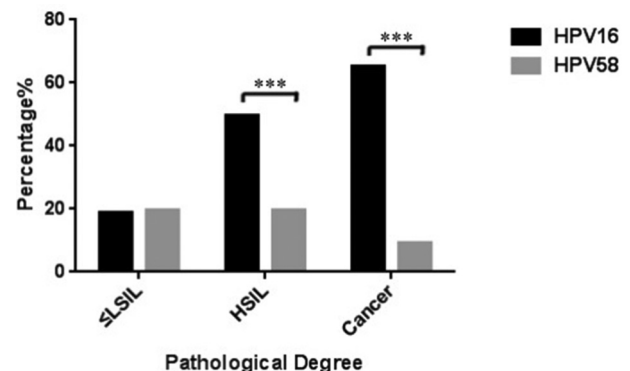| 29 | E6-P53 AND E7-RB CO-MEDIATED HIGHER CARCINOGENIC ABILITY OF HPV16 THAN HPV58 IN CERVICAL CANCER |

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Objectives HPV16 presents most frequent infection and most powerful carcinogenic capacity in human cervix. HPV58 is more common in Asian women. The mechanism of HPV16 gaining higher carcinogenic ability than HPV58 is still unknown.

Methods We collected 4030 cervical exfoliated cell samples in our hospital. All the samples did HPV genotyping using HybriBio's proprietary flow-through hybridization technique and liquid-based cytology (LBC), and if necessary colposcopy-guided quadrant biopsies. Four plasmids containing E6 and E7 of HPV 16 and 58 were constructed and transfected into 293T and U2OS cells, respectively. Cell cycle, apoptosis, proliferation and invasion were detected by FCM, CCK8 detection and transwell assay, respectively. E6-P53 and E7-pRB co-expression and co-localization were detected by western blot and confocal immunofluorescence.

Results We found that the percentage of HPV16 in ≤LSIL group was 18.9% while HPV58 was 19.7%; HPV16 in HSIL group was 49.5% while HPV58 was 19.6%; HPV16 in cancer group was 65.3% while HPV58 was 9.0%. The proportion of early apoptosis in 293T cells with HPV58 E6/E7

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