



# Predicting p16 Immunohistochemical Staining in Cervical Biopsies on H&E Images using a Deep Learning Algorithm

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**Background:** Immunohistochemical staining for p16 protein is frequently used in cervical biopsies. Block positive p16 staining suggests prior infection with human papillomavirus (HPV) and precancerous potential. We sought to train a deep learning algorithm to predict p16 staining in cervical biopsies using H&E tiles extracted from digital whole slide images.

**Methods:** 44 slides were scanned at 40x magnification using an Aperio AT2 scanner. H&E and p16 whole slide images were aligned using QuPath software[1]. Epithelial regions on the H&E slides were correspondingly annotated as positive or negative with p16 immunostaining as ground-truth. 38 slides (73,817 image tiles) were used in the training and validation sets of a 10-layer neural network run for 50 epochs using GPUs in Google Colab [2]. 6 slides (11,217 tiles) were held out as a test set on original images. (Figure 1)

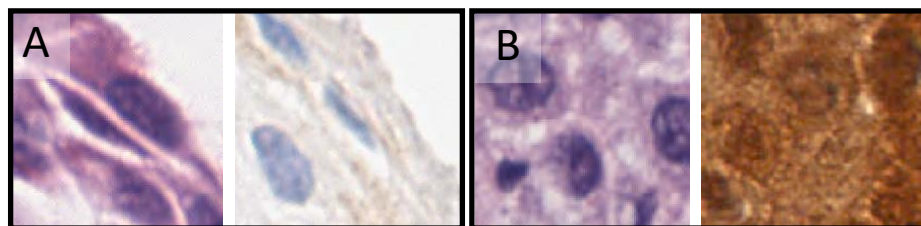
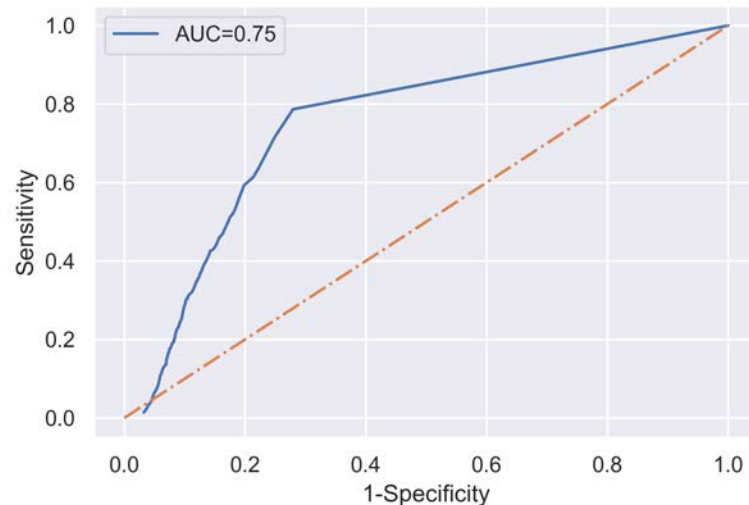


Figure 1. A. (left) squamous epithelium correctly predicted as negative. (right) Corresponding negative p16 stain. B. (left) H&E image correctly predicted as positive. (right) Corresponding positive p16 stain

Figure 2. H&E Prediction of p16 Positivity ROC Curve



**Results:** The model achieved 95.7% accuracy in the training set and 93.7% in the validation set. The testing set with 6 original images achieved an AUROC of 0.75 (Figure 2). The optimal threshold value was very low at 0.01 (out of 1). The test slide with the lowest accuracy (0% accuracy) was from a case of koilocytic atypia, and the highest accuracy (91% accuracy) was from a benign transformation zone.

**Conclusions:** The model performed decently on the test slide set. The optimal performance threshold was surprisingly low at 0.01. However, the testing set was limited by too few positive cases. Training the model on more images and using different model architectures would likely improve accuracy. This study explored the possibility of using a deep learning model to predict p16 immunohistochemical staining on digital H&E images.

## References:

1. Bankhead P et al. QuPath Open source software for digital pathology image analysis. Scientific Reports (2017)
2. Chollet F. Code examples/Computer Vision/ Image classification from scratch. Retrieved from: [https://keras.io/examples/vision/image\\_classification\\_from\\_scratch/](https://keras.io/examples/vision/image_classification_from_scratch/) Date last accessed: 9/29/2020