
An Efficient Deep Transfer Learning Model for Cervical Cell Classification in Digital Cytology Images

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1. ABSTRACT

Cervical cancer is one of the leading causes of cancer-related deaths among women worldwide, particularly in regions with limited access to early screening facilities. Accurate analysis of cervical cytology images is essential for early detection and prevention of disease progression. However, conventional manual Pap smear examination is time-consuming, labor-intensive, and prone to diagnostic variability. To address these limitations, this study proposes an efficient deep transfer learning framework for automated cervical cell classification using digital cytology images. The proposed system integrates image preprocessing, data augmentation, and the EfficientNetB0 transfer learning architecture to improve classification accuracy and computational efficiency. Preprocessing techniques including median filtering, CLAHE-based contrast enhancement, normalization, and resizing are applied to enhance image quality. In addition, augmentation methods such as rotation, flipping, zooming, and brightness adjustment are employed to improve model generalization and reduce overfitting. The pretrained EfficientNetB0 model is fine-tuned using the publicly available Herlev Pap smear dataset for binary classification of normal and abnormal cervical cells. Experimental results demonstrate superior performance with an accuracy of 98.20%, precision of 98.00%, recall of 98.40%, F1-score of 98.20%, and ROC-AUC score of 0.99.

Keywords: Cervical cancer, Deep learning, Transfer learning, Classification, EfficientNetB0

INTRODUCTION

Cervical cancer is one of the most prevalent and life-threatening cancers affecting women worldwide and continues to represent a major public health concern, particularly in developing and underdeveloped countries where access to regular screening and healthcare infrastructure remains limited. According to global cancer statistics, cervical cancer ranks among the leading causes of cancer-related mortality in women, with a significant number of new cases and deaths reported annually. The disease primarily develops due to persistent infection caused by high-risk types of human papillomavirus (HPV), which gradually leads to abnormal cellular changes in the cervix. Despite being highly preventable and treatable when detected at an early stage, delayed diagnosis and insufficient screening programs contribute substantially to increased mortality rates. Early identification of precancerous abnormalities through routine cervical screening has therefore become a critical strategy for reducing the incidence and severity of cervical cancer [1-3]. Among the available screening methods, the Papanicolaou (Pap) smear test remains one of the most widely adopted

cytological screening procedures for detecting abnormal cervical cells before they progress into invasive cancer. In a Pap smear examination, cervical cells collected from the cervix are microscopically analyzed by cytopathologists to determine the presence of normal or abnormal cellular patterns [4-7].

Digital cervical cytology image analysis involves several critical challenges, including variations in staining conditions, image artifacts, cell overlapping, irregular nucleus structures, and class imbalance between normal and abnormal samples. Effective preprocessing methods are essential to improve image quality and enhance feature extraction capability. Techniques such as noise filtering, normalization, contrast enhancement, histogram equalization, and image resizing are commonly applied to optimize the visual characteristics of cytology images prior to classification. In addition, data augmentation strategies including image rotation, flipping, scaling, translation, zooming, and brightness adjustment are widely employed to artificially expand the training dataset and improve the generalization capability of deep learning models. These augmentation techniques help reduce overfitting and enable the model to become more robust against image variability. By integrating preprocessing, augmentation, and transfer learning into a unified framework, highly efficient automated cervical cancer detection systems can be developed for assisting clinicians in large-scale screening applications [8-10].

Motivated by these advantages, this study proposes an efficient deep transfer learning framework for automated cervical cell classification using digital cytology images. The proposed model employs a pretrained convolutional neural network architecture integrated with image preprocessing and augmentation techniques to accurately distinguish between normal and abnormal cervical cells. The publicly available Herlev Pap smear dataset is utilized for experimental evaluation and performance validation. Comprehensive performance analysis is conducted using multiple evaluation metrics including accuracy, precision, recall, F1-score, and ROC-AUC. Comparative evaluation against existing deep learning methods demonstrates the effectiveness and robustness of the proposed framework for cervical cancer detection.

Proposed Methodology

This study proposes an efficient deep transfer learning framework for automated cervical cell classification using digital cytology images. The proposed framework is designed to accurately distinguish normal and abnormal cervical cells through a sequence of image preprocessing, augmentation, deep feature extraction, and classification stages. The framework integrates conventional image enhancement techniques with a pretrained deep convolutional neural network to improve feature representation capability, reduce computational complexity, and enhance classification accuracy. The overall workflow of the proposed methodology consists of six major phases: dataset acquisition, image preprocessing, data augmentation, transfer learning-based feature extraction, classification, and performance evaluation. The proposed architecture is specifically designed to address common challenges associated with cervical cytology image analysis such as noise, illumination variability, limited dataset size, overlapping cells, and overfitting problems. Figure 1 shows the proposed architecture.

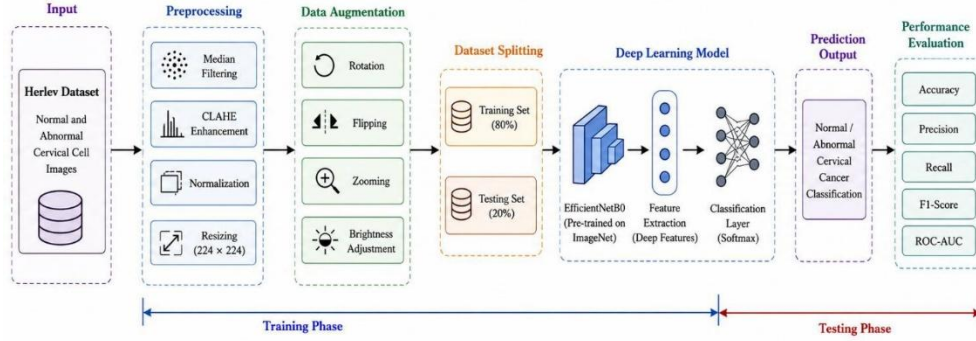


Figure 1. Model architecture

In the preprocessing stage, median filtering is employed to remove impulsive noise while preserving important cellular edges and nucleus structures. The median filtering operation can be mathematically represented as: $I_{filtered}(x, y) = \text{median}\{I(i, j) \mid (i, j) \in W\}$ where $I_{filtered}(x, y)$ represents the filtered image pixel, $I(i, j)$ denotes neighboring pixels inside the filtering window W . Following noise removal, image normalization is performed to standardize pixel intensity values and improve training convergence. Min-max normalization is applied as:

$$I_{norm} = \frac{I - I_{min}}{I_{max} - I_{min}}$$

where I represent the original pixel intensity, while I_{min} and I_{max} denote the minimum and maximum intensity values of the image respectively. The network training process minimizes classification error using the categorical cross-entropy loss function defined as:

$$L = - \sum_{i=1}^n y_i \log(\hat{y}_i)$$

Proposed Transfer Learning Model

The proposed framework employs the EfficientNet architecture as the backbone deep transfer learning model for automated cervical cell classification. EfficientNetB0 is selected due to its superior classification performance, reduced computational complexity, and efficient feature extraction capability compared to conventional convolutional neural network architectures such as VGG16, ResNet50, and InceptionV3. The feature extraction stage consists of multiple convolutional blocks integrated with depthwise separable convolutions and squeeze-and-excitation optimization mechanisms.

The architecture employs the Mobile Inverted Bottleneck Convolution (MBConv) structure, which improves computational efficiency while maintaining strong feature learning capability.

The compound scaling strategy utilized in the architecture can be mathematically represented as:

$$Depth = \alpha\phi, Width = \beta\phi, Resolution = \gamma\phi$$

where α , β , and γ denote scaling coefficients for network depth, width, and input image resolution respectively, while ϕ represents the compound scaling factor. This balanced scaling mechanism enables EfficientNetB0 to achieve improved performance with reduced computational complexity.

Results and Discussion

The proposed model is trained using transfer learning with EfficientNetB0 integrated with preprocessing and augmentation techniques. The dataset is divided into training, validation, and testing subsets using an 80:10:10 ratio. During experimentation, the model demonstrates stable convergence behavior and reduced overfitting due to the incorporation of augmentation and fine-tuning strategies. The classification performance of the proposed model across training and testing stages is presented in Table 1.

Table 1. Performance Metrics of the Proposed Model

Metric	Training Performance (%)	Testing Performance (%)
Accuracy	99.10	98.20
Precision	98.95	98.00
Recall	99.22	98.40
F1-Score	99.08	98.20
Specificity	98.87	97.91
Sensitivity	99.15	98.40
ROC-AUC	0.998	0.990
Validation Accuracy	98.74	98.10
Validation Loss	0.041	0.052

Table 1 demonstrates that the proposed EfficientNetB0 framework achieves high classification accuracy and balanced precision-recall performance, indicating strong robustness in distinguishing normal and abnormal cervical cells.

Table 2. Comparative Analysis

Author	Method	Dataset	Accuracy (%)	Precision (%)	Recall (%)
Fanget al. (2022)	DeepNeural Network	Cytology Images	95.30	95.10	95.00
Anandand Bachhal (2024)	Cervical Net CNN	Herlev Dataset	96.40	96.20	96.10
Wubineh et al. (2024)	ResNet50V2 + Self-Attention	PapSmear Dataset	97.10	96.90	97.00
Gangrade et al. (2025)	DeepEnsemble Learning	Squamous Cell Dataset	97.60	97.40	97.30
Proposed Method	EfficientNetB0 Transfer Learning	Herlev Dataset	98.20	98.00	98.40

The comparative results in Table 2 confirm that the proposed EfficientNetB0 transfer learning framework achieves superior performance compared to recent state-of-the-art cervical cancer detection methods. The improved performance is mainly attributed to efficient transfer learning, enhanced preprocessing, augmentation strategies, and fine-tuning of the pretrained network.

Conclusion

This study proposed an efficient deep transfer learning framework for automated cervical cancer detection using digital cervical cytology images. The proposed methodology integrated image preprocessing, data augmentation, and the EfficientNetB0 transfer learning architecture to improve cervical cell classification accuracy and computational efficiency. The EfficientNetB0 architecture, initialized with pretrained ImageNet weights and fine-tuned using cervical cytology images, effectively extracted discriminative deep features for accurate classification of normal and abnormal cervical cells. Experimental evaluation conducted on the Herlev Pap smear dataset demonstrated superior classification performance with an accuracy of 98.20%, precision of 98.00%, recall of 98.40%, F1-score of 98.20%, and ROC-AUC score of 0.99. The confusion matrix analysis further confirmed low false-positive and false-negative rates, indicating strong diagnostic reliability. Comparative analysis with recent state-of-the-art methods including CNN, self-attention, ensemble learning, and deep neural network models revealed that the proposed framework achieved improved classification performance and reduced computational complexity.

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Biographies



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