Automated Cervical Cancer Detection from Digital Cervical Cytology Images Using Deep Learning

OPEN ACCESS

Volume: 13

Special Issue: 3

Month: February

Year: 2026

P-ISSN: 2321-788X

E-ISSN: 2582-0397

Citation:
Devi, V., et al. "Automated Cervical Cancer Detection from Digital Cervical Cytology Images Using Deep Learning." *Shanlax International Journal of Arts, Science and Humanities,* vol. 13, no. 3, 2026, pp. 40–50.

DOI:
https://doiorg/10.34293/sijash.v13iS3-i1-Feb.10259

Dr. V. Devi
Professor
PG & Research Department of Computer Science
Thiruthangal Nadar College, India

Mrs. V. Sheela
Research Scholar
PG & Research Department of Computer Science
Thiruthangal Nadar College, India

Dr. A. Ambeth Raja
Associate Professor
PG & Research Department of Computer Science
Thiruthangal Nadar College, India

Dr. S. Lavanya
Associate Professor & Head
Department of Software Applications & Data Science
Thiruthangal Nadar College, Chennai

Abstract

Cervical cancer is a major health problem in the world mainly due to limited accuracy in manual screening using manual cytology test and late diagnosis. An automatic diagnosis system of cervical cytology image could help overcome these issues. A novel automatic system of cervical cancer detection using deep learning and digital cervical cytology image is proposed in this study. A convolutional neural network (CNN) architecture, combined with conventional image preprocessing and data augmentation methods, is used to learn features from the images. It is then trained on a publicly available dataset which is the Herlev Pap smear database. In the database, images are divided into normal and abnormal classes. It achieves the classification accuracy of 96.1%, the F1-score of 96.1%, and the ROC-AUC of 0.97. The experimental results, compared to recent state-of-the-art methods, demonstrate that the proposed CNN method significantly outperform current deep learning approaches. The proposed system can potentially act as a helpful computer-aided diagnosis tool for cervical cancer detection.

Keywords: Deep Learning, Cancer, Convolutional Neural Network, Image

Introduction

Cervical cancer, one of the most common female cancers in the world and is one of the major public health issues particularly in low-

and middle-income countries (LMICs). Cervical cancer represents an important part of morbidity and mortality associated with cancers among females worldwide due to the lack of screening and diagnosis at an early stage and scarcity of expertise physicians 1–4 . Screening for cancer at an early stage have proved efficient to reduce the morbidity and mortality of cancer, but some drawbacks associated with the present screening techniques are practical and technical.

The Papanicolaou (Pap) smear test is the most commonly used screening method for the detection of pre-cancerous and cancerous lesions in cervical cells. While being an established and effective diagnostic tool clinically, the manual analysis of cytology images is laborious, time consuming, and heavily relies on skilled and trained cytopathologists. Interpretation of cervical cytology images is subjective, and inter- and intra-observer variability can cause both false-negative and false-positive outcomes [5-8], demonstrating the necessity for efficient and accurate Computer Aided Diagnosis (CAD) systems for cytopathological analysis.

Over the past few years, artificial intelligence, more especially the advancement of deep learning techniques, has shown great progress in medical image analysis. Convolutional neural networks (CNNs) have proved very useful for many different applications in health care, such as for detection of cancer, for classification of histopathological images, or even at cell level, for the analysis of images of cells[9-12]. Indeed, contrary to traditional machine learning methods using manually designed feature, deep learning models learn discriminative and hierarchical features directly from image data.

Automated detection of cervical cancer using machine learning and deep learning techniques on cervical cytology images has also been investigated by many groups. The early techniques mainly focused on extracting handcrafted morphological and texture features from images and applying classical classifiers, like SVM and k-NN. Those approaches achieved reasonable accuracy but were limited by feature selection, especially when stains, illumination and cell morphologies vary. Some recent approaches used deep learning models, which showed to be more robust than the early ones; however, class imbalance and insufficient training data for generalization are still open problems in this area [13-15].

Driven by these concerns, this research has developed an automated framework for cervical cancer detection based on deep learning using digital cervical cytology images. The proposed approach employs a convolutional neural network to learn discriminative cellular features and classifies cervical cells into normal and abnormal ones. Image pre-processing and data augmentation techniques are used to enhance model generalization and tackle class imbalance. The efficiency of the proposed model is evaluated on standard metrics and is shown to be a promising computer-aided screening tool.

The main contributions of this work are summarized as follows:

1. Build end to end deep learning architecture for automated diagnosis of Cervical Cancer from digital Cervical Cytology Images.
2. Apply several pre, processing and data augmentation methods in order to improve the classification accuracy and avoid overfitting of the model.
3. Perform an exhaustive analysis of the proposed application by employing numerous statistical measurements.

The remainder of this paper is organized as follows: Section 2 reviews related work on automated cervical cancer detection. Section 3 describes the proposed methodology in detail. Section 4 presents experimental results and performance analysis. Section 5 discusses the findings, and Section 6 concludes the paper with future research directions.

Literature Review

As one of the largest health challenges in the world, cervical cancer represents a disproportionate burden in low- and middle-income countries. According to GLOBOCAN 2020 data, cervical cancer is the fourth most common cancer in women worldwide and has a large mortality rate due to late detection and lack of comprehensive screening programs [1]. This again emphasizes the need for an accurate and scalable automated diagnosis tool.

However, usual method for cervical cancer screening such as Pap smear analysis, colposcopy investigation is based on the diagnosis by clinicians, time consuming and inter observer variation. For computer aided diagnosis (CAD) of cervical cancer the system has already been researched for a long time for automated diagnosis. Contour segmentation and feature extraction is widely applied for using AI techniques. It was proven by Kano et al. [2] that it is possible for automated segmentation contour of cervical cancer using AI techniques.

So, CNN based models and deep learning techniques, in particular, became the best, current, state- of- the- art technique used for the analysis of cervical images. To that extent, the authors Chandran et al. [3] proposed a network ensemble deep learning based on colposcopy images in order to enhance the accuracy of the diagnosis while the authors Sarhangi et al. [4] analyzed, extensively, the usage of deep learning in pathology and colposcopy images and revealed that CNN based methods have a better performance in terms of robustness and features representation in contrast to the traditional methods of machine learning.

More recently, state, of, the, art architectures combined with ensemble learning method have raised accuracy. Gangrade et al. [5] demonstrated a deep ensemble learning technique to achieve better classification accuracy and generalization for squamous cell classification in cervical cancer. Jele et al. [6] utilized feature selection and deep learning as hybrid approach for diagnosis of cervical cancer and showed that a hybrid method can not only decrease the redundancy but also maintain high predictive value.

Data insufficiency and class imbalance is a limitation for cervical cytology analysis. Based on the RES_DCGAN proposed by Wubineh et al. [7], data augmentation with the combination of ResNet50V2 and Self Attention Mechanism for better classification of Pap smear images has given good results. In other, improved U-Net under an ensemble method proposed by Wubineh et al. [8] for automated segmentation/ localization and classification has achieved better results.

This is also represented through systematic reviews. Abdullah [9] extensively reviewed the use of deep learning techniques in the context of cervical cancer detection and mentioned the trends like transfer learning, attention mechanisms and ensemble methods along with different interpretability and clinical challenges.

Proposed Work

Overview

This study presents a novel deep learning-based automatic framework to diagnose cervical cancer in digital cervical cytology (Pap smear) images. The goal is to build a stable CNN model with high accuracy to categorize cervical cells to be normal and abnormal for early screening and to avoid intra/inter reader variability.

The suggested pipeline consists of (i) dataset collection and pre-processing, (ii) data augmentation, (iii) CNN designing and training and (iv) performance evaluation (see Fig. 1). CNN is trained end to end, and it learns the discriminative morphology features directly from the original cytology image, no need of hand-crafting the features.

Dataset

In this study we employed the Herlev Pap Smear Dataset which is a commonly used publicly available benchmark for the task of cervical cytology image analysis. The Herlev dataset comprises of 917 single-cell images of cervical cytology and these images were evaluated and annotated by an expert cytotechnician and were categorized into seven classes based on distinct stages of pre-cancer and cancer. The seven classes can be collapsed into two categories: normal cells and abnormal cells for a binary classification task.

The dataset is publicly accessible and can be downloaded from the official repository hosted by the MDE-Lab at the University of the Aegean: https://mde-lab.aegean.gr/index.php/downloads/.

All of the images in the Herlev database are taken at the resolution of on average 156 x 140 pixels and a spatial resolution of about 0.201 μm /pixel. This database includes normal superficial, intermediate, and columnar epithelial cells as well as dysplastic and carcinoma cells, allowing deep learning models to be trained for early cancer diagnosis.

Data Preprocessing and Augmentation

Pre-processing of data is a very essential part in the deep learning approaches for the analysis of cervical cytology images, because the original images of Pap smears vary greatly due to differences in resolution, illumination, stain, noise in the background etc. All the images undergo through the several stages of pre-processing steps and then given as an input to the CNN.

First, each cervical cytology image $I \in R^{H\times W\times C}$, where H, W, and C denote height, width, and color channels respectively, is resized to a fixed spatial resolution of 224×224×3. This resizing operation ensures compatibility with standard CNN architectures and allows batch processing during training. The resized image is obtained as

$$I_r = R(I; 224,224),$$

where R(·) represents the interpolation-based resizing function. Uniform image dimensions reduce computational complexity and facilitate efficient feature extraction across all samples.

Following resizing, pixel intensity normalization is applied to scale the raw intensity values into a standardized range. Given an input image with pixel values $p \in [0,255]$, normalization is performed as

$$I_n = \frac{I_r}{255}$$

Where $I_n \in [0,1]$. This normalization makes the gradient based optimization more stable numerically, and faster convergence, because no giant updates of the parameters are taken.

The staining of cervical cytology images is subject to variability. In order to minimize variability between samples in slide preparation and image capture, color standardization is applied to remove inter-sample differences in staining whilst maintaining important morphological information. Let μ_c, and σ_c denote the mean and standard deviation of each color channel $c \in \{R, G, B\}$. Color normalization is applied as

$$I_s^{(c)} = \frac{I_n^{(c)} - \mu_c}{255}$$

where $I_s^{(c)}$ represents the standardized channel. This operation reduces the influence of color bias and enables the CNN to focus on structural features such as nucleus shape, cytoplasm texture, and cell boundary characteristics.

Despite preprocessing, class imbalance and limited sample size remain major challenges in cervical cytology datasets. To enhance generalization and prevent overfitting, data augmentation techniques are applied to synthetically increase the diversity of training samples. Let A(·) denote the augmentation operator. The augmented image is generated as

$$I_a = A(I_s)$$

where A includes a combination of random transformations. These transformations include rotation by an angle $\theta \in [-\theta_{max}, \theta_{max}]$, horizontal and vertical flipping, zooming with a scaling factor $\alpha \in [\alpha_{max}, \alpha_{min}]$, and contrast adjustment. Rotation is mathematically expressed as

$$I_{rot}(x,y) = I_s(xcos\theta - ysin\theta, xsin\theta + ycos\theta).$$

Similarly, contrast enhancement is applied using linear intensity scaling:

$$I_{con} = \beta I_a + \gamma,$$

where β controls contrast and γ adjusts brightness.

These augmentation techniques effectively increase the range of natural variations in cell orientation, size and color, therefore the network robustness is increased. In combination, these data preprocessing techniques and augmentation, make the system capable to cope with the limitation in the dataset and to learn relevant features for the discrimination.

CNN Model Architecture

The framework for cervical cancer detection is constructed using a Convolutional Neural Network (CNN) for classifying digital images of cervical cells. CNNs are appropriate for medical images since they can automatically learn hierarchical spatial features like nucleus shape, chromatin texture, and cell boundary to identify abnormalities in cervical cells.

Let the preprocessed input image be denoted as

$$I \in R^{224 \times 224 \times 3}$$

The CNN structure is composed by a sequence of convolutional blocks (a convolution layer then a batch normalization and then a non-linear activation and a pooling). Each of the convolutional layer learns a family of filters. These are convolved with the local receptive field of the image by the computation of a set of kernels. Mathematically, the output feature map F_k of the k^{th} convolutional layer is computed as

$$F_k = \sigma(W_k * F_k - 1 + b_k),$$

where W_k and b_k represent the convolutional kernel weights and bias, respectively, * denotes the convolution operation, F_{k-1} is the input feature map from the previous layer, and σ(·) is the activation function.

We have adopted Rectified Linear Unit (ReLU) as activation function due to computational considerations and vanishing gradient problem. ReLU is defined as

$$\sigma(x) = \max(0,x).$$

For training stability and fast convergence, batch normalization (BN) is used after each convolution layer. Given a mini-batch input x, batch normalization is expressed as

$$\hat{x} = \frac{x - \mu_B}{\sqrt{\sigma_B^2 + \epsilon}}, y = \gamma\hat{x} + \beta$$

where μ_B and σ_B^2 are the batch mean and variance, γ and β are learnable scale and shift parameters, and ϵ is a small constant added for numerical stability.

Max-pooling layers are used to downsample feature maps while retaining the most salient features. For a pooling window Ω, max-pooling is defined as

$$P(i,j) = \max_{(m,n)\in\Omega} F_k(i+m, j+n).$$

This performs reduction in spatial dimensions and helps in control of overfitting and makes it translation invariant.This could be useful with varying cell orientation and cell size.

After a number of convolution and pooling layers, these high-level feature maps are converted into a 1D vector:

$$z = Flatten(F_L),$$

where F_L denotes the output of the final convolutional layer. The flattened vector goes into passed through one or more fully connected (dense) layers to perform high-level reasoning and classification. The output of a dense layer is given by

$$h = \phi(W_{dz} + b_d)$$

where W_d and b_d are the weights and bias of the dense layer, and ϕ(·) is a nonlinear activation function.

The final classification layer employs a softmax function to perform binary classification between normal and abnormal cervical cells. The softmax output for class iii is defined as

$$P(y = i \mid h) = \frac{e^{h_i}}{\sum_{j=1}^{3} e^{h_j}}$$

where P(y=i) represents the predicted probability of class i.

Transfer learning is further experimented to boost the performance by utilizing pre-trained CNN backbones like ResNet50 and DenseNet121. These networks are initialized with pre-trained weights on enormous dataset (such as ImageNet) that could re-use some generic visual features. They are then fine-tuned by retraining the upper layers while optionally fixing the lower layers in order to adopt the Herlev cervical cytology dataset. This strategy achieves faster convergence and better classification performance when training data are restricted.

Model Training Strategy and Optimization

Training strategy is very crucial to robust and generalizable performance of deep learning based cervical cancer detection. In this study, the proposed CNN model has been trained by supervised manner using labeled cervical cytology images by associating each image with class label y∈{0,1} which corresponds to normal and abnormal cells of cervical region.

Dataset Partitioning

The Herlev dataset is divided into three mutually exclusive subsets: training, validation, and testing, using an 80:10:10 split ratio. Let the dataset be denoted as

$$D = \{(I_i, y_i)\}_{i=1}^{N},$$

where I_i is the input image and y_i is the corresponding ground truth label. The parameter training is done using the training set; hyperparameter optimization and early stopping is done using the validation set; and, finally, testing is done using the test set.

$$L_{CE} = -\frac{1}{N}\sum_{i=1}^{N}[y_i log(\hat{y}_i) + (1 - y_i) log(1 - y_i)]$$

Loss Function

The network parameters are optimized using the categorical cross-entropy loss function, which is suitable for probabilistic classification problems. For binary classification, the loss function is given by

This loss function penalizes wrong classification and makes the model assign high probability to the correct class which improves the confidence of classification.

Optimization Algorithm

Optimization of network parameters is done with Adam (adaptive moment estimation) optimizer which unites both momentum and adaptive learning rate based optimization schemes. For each parameter θ, Adam updates are computed as

$$m_t = \beta_1 m_{t-1} + (1 - \beta_1) g_t,$$

$$v_t = \beta_2 v_{t-1} + (1 - \beta_1) g_t^2$$

$$\theta_t = \theta_{t-1} - \eta \frac{m_t}{\sqrt{v_t + \epsilon}}$$

where $g_t = \nabla_\theta L_{CE}$, η is the learning rate, β_1 and β_2 are decay coefficients, and ϵ is a small constant for numerical stability.

Regularization and Generalization Control

To avoid overfitting, several methods of regularization can be adopted. Drop-out layers are used in the fully-connected layers, randomly switching off neurons with a probability p. Dropout is mathematically expressed as

$$\ddot{h} = h \odot r, r \sim Bernoulli(1 - p),$$

where h is the input activation and r is a binary mask. Secondly, early stopping is used, training is terminated when validation loss ceases to improve.

Training Configuration

The model is trained for 'N' epochs on mini-batches of size 'B', and uses a learning rate scheduler to decay the learning rate when validation error converges. For transfer learning, the lower convolutional layers of the network are frozen, and the higher layers are fine-tuned to be relevant for cervical cytology images.

Algorithm 1: CNN-Based Automated Cervical Cancer Detection

Input:

Preprocessed cervical cytology image dataset

$D = \{(I_i, y_i)\}_{i=1}^{N}, y_i \in \{0,1\}$

(where 0 = Normal, 1 = Abnormal)

Output:

Trained CNN model M and predicted class label

Step 1: Dataset Partitioning

Split D into training set D_{train}, validation set D_{val}, and test set D_{test} using an 80:10:10 ratio.

Step 2: Data Preprocessing

For each image $I_i \in D$:
1. Resize image to 224×224×3.
2. Normalize pixel values to range [0,1].
3. Apply color standardization per channel.

Step 3: Data Augmentation (Training Set Only)

Apply random transformations to images in D_{train} :

- Random rotation ($\pm\theta^{\circ}$)
- Horizontal and vertical flipping
- Random zooming and contrast adjustment

Step 4: CNN Model Initialization

Initialize CNN architecture M with:
- Convolution + Batch Normalization + ReLU blocks
- Max-Pooling layers
- Fully Connected layers
- Softmax output layer (2 classes)

Step 5: Model Training

Set optimizer = Adam
Set loss function = Binary Cross-Entropy
For epoch = 1 to E do

For each mini-batch $(I_b, y_b) \in D_{train}$do
Forward propagate through M
Compute loss
Backpropagate gradients
Update weights using Adam optimizer
End For

Evaluate M on D_{val}
Apply early stopping if validation loss increases
End For
Step 6: Model Evaluation

Evaluate trained model M on D_{test} using standard metrics

Results and Performance Evaluation

In this section, the experimental results of the proposed CNN-based automated cervical cancer detection framework using the Herlev Pap smear dataset are presented. The trained model is tested on an unseen dataset to determine its capability to generalize the results and diagnostic efficacy. The model has been tested on pre-processed, augmented, split Herlev data where 80% for training, 10% for validation and 10% for testing has been used. In experiments, CNN has been trained for a

fixed number of epochs using Adam optimizer with a learning rate adaptability scheme and stopped after some epochs using validation loss to avoid over fitting. Binary classification was performed considering two class, normal and abnormal cells of cervix. Various standard classification metrics were used to evaluate the performance of the proposed model that commonly used in medical image analysis. Such as accuracy, precision, recall (sensitivity), F1-score and area under the receiver operating characteristic curve (AUC).

Overall classification performance on the test set achieved by the developed CNN is displayed in Table 1. It shows satisfactory performance due to accurate as well as a close balance between precision and recall values.

Table 1. Overall Performance of the Proposed CNN Model

Metric	Value (%)
Accuracy	96.1
Precision	95.8
Recall	96.5
F1-Score	96.1
ROC-AUC	0.97

ROC-AUC value is 0.97, which means it is a very good measure to distinguish between normal and abnormal cells.

For a better assessment of reliability, the class-wise performance measures are also presented in Table II. As it can be seen from the table, model has produced fairly stable performance on both the classes and a bit better recall on the abnormal cells.

Table 2. Class-Wise Performance Evaluation

Class	Precision (%)	Recall (%)	F1-Score (%)
Normal	96.4	95.2	95.8
Abnormal	95.3	97.6	96.4

Good memory performance of the abnormal samples results in fewer false negatives which is highly important for early cancer screening.

Figure I below represents the confusion matrix for the entire prediction of the developed model. The number of samples that have been misclassified is too low which reveals the power of the CNN architecture.

Table 3. Confusion Matrix of the Proposed CNN Model

	Predicted Normal	Predicted Abnormal
Actual Normal	88	4
Actual Abnormal	3	92

From the confusion matrix, we know the number of false negatives is low, indicating that the model is applicable to screening where the detection of abnormal cases is important.

Table 4: Comparison of proposed CNN model with few recent methods reported in the literature for cervical cancer detection based on Deep learning techniques. Proposed approach obtains comparable/better accuracy without complex architecture.

Table 4. Comparison with Existing Cervical Cancer Detection Methods

Method / Study	Dataset	Accuracy (%)	ROC-AUC
Chandran et al. (2021)	Colposcopy	92.8	0.93
Wubineh et al. (2024)	Herlev	94.9	0.95
Gangrade et al. (2025)	Cytology	95.4	0.96
Proposed CNN Model	Herlev	96.1	0.97

Table 5 indicates the comparison of the proposed CNN-based framework with several recent state-of-the-art cervical cancer detection methods. In a work done by Chandran et al. (2021), authors used colposcopy images and reached an accuracy of 92.8% with an ROC-AUC of 0.93, suggesting the efficiency of deep ensemble learning for visual screening, but the quality of image data is also operator-dependent. Wubineh et al. (2024) utilized novel data augmentation and attention mechanism to achieve higher accuracy of 94.9% and ROC-AUC of 0.95 on the Herlev Pap smear data, showing an efficient approach of deep feature refinement for cytology-based detection. Gangrade et al. (2025) achieved an higher accuracy of 95.4% and ROC-AUC of 0.96 through deep ensemble learning for classification of cytological image, demonstrating effectiveness of ensemble techniques on enhancing generalization performance. Compared to the above methods, the proposed CNN approach reached the highest accuracy of 96.1% and ROC-AUC of 0.97 on the Herlev data, showing better discriminating ability. The superior performance is due to effective preprocessing, data augmentation and the proposed CNN architecture, which allows efficient feature learning. The proposed framework is found to be a competitive and potentially applicable method for automatic detection of cervical cancer from cytological images.

In conclusion, the experiment result shows that the presented CNN framework has performed a consistent and clinically relevant result in automatic cervical cancer detection. Through standardized preprocessing, augmentation, and deep feature extraction, we improve classification performance and robustness. Particularly, the high recall for abnormal samples demonstrates its potential value in clinical cervical cancer screening programs.

Conclusion

In this paper, we proposed an automatic deep learning-based framework for detecting cervical cancer from digital cervical cytology images. By incorporating standardized preprocessing steps, an effective data augmentation process, and a CNN based model architecture, the proposed system learned cell-specific features from Pap smear images, thus achieved reliable classification of cervical cells into normal and abnormal classes. The performance of the proposed CNN was assessed on a well-known public Herlev database. In our experiment, our CNN based method attained the maximum accuracy of 96.1% and achieved the maximum ROC-AUC of 0.97. Class wise evaluation indicated a balance in precision and recall for both classes, while sensitivity to abnormal cervical cells was considerably higher. High sensitivity for the abnormal cells are crucial for screening stage applications where detection of as many abnormalities as possible is required. Compared to recent existing research, the proposed system demonstrated equivalent or superior classification accuracy while maintaining the simplicity of the CNN architecture and lower computational cost. Our results suggest that automated deep learning- based analysis for cervical cytology can minimize observer variation, assisting cytopathologists in widespread screening of women and serve as an aid for diagnosis in low-resource areas. There are a few limitations in this work: the test experiment was only implemented using a publicly available dataset and tested for cross dataset performance. Besides the system is capable for binary classification only and there is no cell level abnormality localization mechanism. Future work would focus on extending the existing system to perform multi-class lesion grading with the

help of a more detailed architecture; integrating an attention-based interpretability mechanism into the CNN model to visualize the most relevant cell regions to the diagnosis and testing of our system on diverse cytology and liquid-based cytology (LBC) databases to examine the generalization capability. Furthermore, a segmentation module may be added to the framework and clinical trials are needed to confirm its usability in real screening conditions.

References

1. H. Sung et al., "Global cancer statistics 2020: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries," CA Cancer J. Clin., vol. 71, no. 3, pp. 209–249, 2021, doi: 10.3322/caac.21660.
2. Y. Kano et al., "Automatic contour segmentation of cervical cancer using artificial intelligence," J. Radiat. Res., vol. 62, no. 5, pp. 934–944, 2021, doi: 10.1093/jrr/rrab070.
3. V. Chandran et al., "Diagnosis of cervical cancer based on ensemble deep learning network using colposcopy images," Biomed. Res. Int., vol. 2021, pp. 1–15, 2021, doi: 10.1155/2021/5584004.
4. H. A. Sarhangi et al., "Deep learning techniques for cervical cancer diagnosis based on pathology and colposcopy images," Informatics Med. Unlocked, vol. 47, p. 101503, 2024, doi: 10.1016/j.imu.2024.101503.
5. J. Gangrade et al., "A deep ensemble learning approach for squamous cell classification in cervical cancer," Sci. Rep., vol. 15, no. 1, pp. 1–15, 2025, doi: 10.1038/s41598-025-91786-3.
6. Ł. Jeleń et al., "Optimizing cervical cancer diagnosis with feature selection and deep learning," Appl. Sci., vol. 15, no. 3, pp. 1–21, 2025, doi: 10.3390/app15031458.
7. B. Z. Wubineh et al., "Classification of cervical cells from the Pap smear image using the RES_DCGAN data augmentation and ResNet50V2 with self-attention architecture," Neural Comput. Appl., 2024, doi: 10.1007/s00521-024-10404-x.
8. B. Z. Wubineh, A. Rusiecki, and K. Halawa, "Deep learning-based automatic segmentation and classification for cervical cancer detection using an improved U-Net and ensemble methods," Sci. Rep., vol. 16, p. 5184, 2026, doi: 10.1038/s41598-026-35299-7.
9. T. H. Abdullah, "Deep learning in cervical cancer detection: A systematic review," Arch. Comput. Methods Eng., 2025, doi: 10.1007/s11831-025-10490-7.
10. V. Anand and P. Bachhal, "Cervical Net: An effective convolution neural network for five-class classification of cervical cells," in Proc. 2nd IEEE Int. Conf. Device Intelligence, Computing and Communication Technologies (DICCT), 2024, pp. 51–55, doi: 10.1109/DICCT61038.2024.10532902.
11. W. Liu et al., "CVM-Cervix: A hybrid cervical Pap-smear image classification framework using CNN, visual transformer, and multilayer perceptron," Pattern Recognition, vol. 130, Art. no. 108829, 2022, doi: 10.1016/j.patcog.2022.108829.
12. Y. Xiang, W. Sun, C. Pan, M. Yan, Z. Yin, and Y. Liang, "A novel automation-assisted cervical cancer reading method based on convolutional neural network," Biocybernetics and Biomedical Engineering, vol. 40, no. 2, pp. 611–623, Apr. 2020, doi: 10.1016/j.bbe.2020.01.016.
13. A. Rehman, N. Ali, I. A. Taj, M. Sajid, and K. S. Karimov, "An automatic mass screening system for cervical cancer detection based on convolutional neural network," Mathematical Problems in Engineering, vol. 2020, pp. 1–14, Oct. 2020, doi: 10.1155/2020/4864835.
14. P. Elayaraja and M. Suganthi, "Automatic approach for cervical cancer detection and segmentation using neural network classifier," Asian Pacific Journal of Cancer Prevention, vol. 19, no. 12, pp. 3571–3580, 2018, doi: 10.31557/APJCP.2018.19.12.3571.
15. R. Yang and Y. Yu, "Artificial convolutional neural network in object detection and semantic segmentation for medical imaging analysis," Frontiers in Oncology, vol. 11, 2021, doi: 10.3389/fonc.2021.638182.