RESEARCH PAPER

TriCervix: Advanced Cervical Cancer Screening Using YOLO Detection and Sequential Texture-Based Hybrid Modeling

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ABSTRACT

Background: Cervical cancer (CC) is one of the most common malignancies affecting women worldwide, and early detection plays a crucial role in reducing morbidity and mortality. Traditional screening methods such as Pap smear examination rely heavily on manual interpretation, which can be time-consuming and prone to inter-observer variability. Recent advances in artificial intelligence (AI) and deep learning (DL) have enabled automated analysis of medical images, improving diagnostic accuracy and screening efficiency.

Objective: This study aims to develop a deep learning–based framework for the early detection and classification of cervical cancer using Pap smear and colposcopy images, and to evaluate the performance of a novel hybrid model for multi-class cervical intraepithelial neoplasia (CIN) prediction.

Methods: A DL-based pipeline was designed incorporating image pre-processing, lesion segmentation, region of interest (ROI) extraction, and data augmentation. Baseline classification models including VGG16, ResNet50, and DenseNet121 were evaluated. A novel hybrid architecture, TriCervix, was proposed, integrating YOLOv8 for lesion detection, EfficientNet-B3 for feature extraction, and Bi-LSTM for sequential texture learning. The model was trained and tested to classify different stages of cervical intraepithelial neoplasia (CIN1 and CIN2).

Results: The proposed TriCervix model demonstrated improved classification performance compared to conventional convolutional neural network (CNN) models such as VGG16, ResNet50, and DenseNet121. The hybrid architecture achieved higher accuracy, precision, and recall in detecting early-stage cervical lesions, particularly in distinguishing CIN1 and CIN2 stages.

Conclusion: The TriCervix hybrid deep learning framework provides an effective and accurate approach for early-stage cervical cancer detection using medical imaging data. Its improved performance highlights its potential as a low-cost automated screening tool, particularly beneficial for large-scale screening programs in resource-limited healthcare settings.

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INTRODUCTION

Cervical cancer (CC) represents the fourth most standard cancer in women and is responsible for the death of a significant proportion of cancer patients [1,2,3]. In 2020, CC is estimated to have caused more than 600,000 new cases and about 340,000 deaths [4,5,6]. The CC screening methods presently in use mostly entail cervical cytology and HPV testing. Cervical cytology consists of Pap smear and liquid-based cytology, while HPV testing uses immunological and nucleic acid level recognition methods [7]. According to a study conducted by Ubaid Mushtaq Naikoo et al [8], Traditional tests like Pap smears and HPV test are good but invasive, not very sensitive and dependent on clinical infrastructure. Modern imaging technology is being developed day by day. This has significantly improved the management of treatment of various neoplasms. In addition, it helps with decision-making. This also applies in the case of CC [9].

CC is one of the four most common disease in females across the global. Pap smear images used as a primary diagnostic technique to detect any precancerous and cancerous abnormalities in the cervix, vagina as well as vulva.

DL algorithms used to develop automated computer-aided diagnostic systems to solve the problems of manual assessment. The authors present a new hybrid method accurately classifying cervical cells. The model proposed uses a set of data enhancement methods. It includes resampling addressing class imbalance and augmentation to increase dataset diversity and improve generalization. The model becomes more versatile and trustworthy in real-world situations because of these techniques, which help it had better manage diverse data. Ashfaque Khowaja et al [10] use Vision Transformer's (ViT) linear projection and position embedding for transforming the input images into patches, which can feed into the transformer encoder. By adding additional layers, followed by a fully connected layer, they create a fusion architecture to enhance the model's extracted features. The ViT-based model allows fine-tuning and developed using retrained weights effectively address issues of CC classification. To improve the quality of these cell images, apply median smoothing followed by Gaussian filtering as a pre-processing step. Evidence from the experiment shows that the suggested approach can improve CC classification accuracy. This model showed remarkable accuracy on the 2-state classification on the Helve dataset and 3-state classification on the SIPaKMeD dataset at 98.07% and 98.08% respectively. The model's capacity to classify CC pictures is assessed by the accuracy of the different datasets. These illustrations that the model is robust and potentially useful for clinical applications.

DL for CC detection: Cancer diagnosis is rather subjective, relying very much on pathologists and gynaecologists. A good number of scientists are now using Artificial Intelligence (AI) especially DL. This has made diagnosis easier according to Akpudo et al [11]. The intricate extraction of features is automatic with DL; it identifies the existing features of an image, thus enhancing performance [12]. One of the preferred methods for classifying cancer is DL techniques that revolutionized image processing by removing the need for manual feature retrieval [5]. Existing DL models such as VGG16, ResNet50 and DenseNet121 have shown strong capability to classify medical images including CC detection. The architecture of VGG16 is simple and uniform, but it has a high computational cost, and it cannot extract features effectively to classify the complex pattern in cervical images. ResNet50 solves vanishing gradients using residual connections. However, these architectures often need many training data. Moreover, it misclassifies results sometimes as it learns from global features due to its deeper layers. DenseNet121 provides better performance than VGG16 and ResNet50 due to the improvement in feature reuse and gradient flow. However, it suffers from significant memory consumption and slow inference because of its dense connectivity. Due to this problem, it is difficult to perform real-time screening. Furthermore, all three models are affected by imbalanced medical datasets and difficulties in the identification of small or overlapping lesions. They are also sensitive to image quality differences and do not generalize across patients or imaging devices. According to these drawbacks, a domain-specific approach like TriCervix is required that can overcome these drawbacks and provide improved CC detection.

Motivation for a hybrid DL approach: Detecting CC is not easy because a lesion can look very different from device to device. Further, the device or camera used can also influence the quality of the image. Finally, specific texture patterns must be identified that are indicative of pre-cancerous changes. CNN models have good capabilities, but they fail to consider local details and global values together. Further, single-model architecture often struggles with more complex cervical structures, including mosaic patterns, acetowhite regions, and irregular vascular structures. The need for hybrid DL is motivated by this limitation in architecture. This hybrid DL will take strong points from the architecture mentioned. A hybrid system that combines object detection, deep feature extraction, and temporal textural learning can localize lesions, learn multi-scale representations, and model sequential feature patterns that may change across regions of interest. The multi-layer capability allows for the more accurate classification of CIN stages, particularly early lesions such as CIN1, CIN2 and CIN3that are misclassified by standard models. So, a hybrid technique would prove to be a more accurate, sensitive and flexible choice for an automated CC screening solution that will meet clinical needs for early and accurate diagnosis.

Objectives: Despite major advances in DL–based CC detection, existing literature has several important gaps. Most currently used models employ CNN classifiers with a single architecture, which cannot adequately represent the complex and heterogeneous characterizations of cervical lesions. Very often such models fail to effectively separate closely situated classes like CIN1, CIN2 and CIN3, as they have very subtle texture differences. It requires a multi-level feature understanding. The existing approaches do not have a strong lesion localization mechanism, and the ROI extraction is not accurate. Therefore, the classification is not reliable enough. Improper data sets used in many studies that lead to development of poor generalization for different patient populations, imaging modalities and clinical settings. In addition, sequential texture analysis is not applied; therefore, temporal correlation and spatial dependence in the lesion area have been ignored. Doctors have a hard time trusting AI to make decisions. The existing issues reveal the need for a hybrid, multi-stage DL model that involves detection, feature extraction and sequential learning for more precise and clinically relevant CC classification.

The key aim of this investigation is to design a hybrid DL model to detect and classify CC stages from images accurately. The second goal is to improve lesion localization by implementing an efficient region detection mechanism for relevant cervical lesions. The study also aims to enhance feature extraction using deep representations that capture global structures and fine texture patterns. The second goal is to integrate sequential texture learning to distinguish minor differences between the CIN stages, specifically early lesions. Lastly, the study assesses the proposed model against previous classifiers to demonstrate its superiority of accuracy, precision, and recall for reliable use of medicine.

MATERIALS AND METHODS

Dataset

This study used a combined dataset of Pap smear images and colposcopy images that included various cervical lesion categories, such as normal, CIN1, CIN2, and malignant cases. All images were standardized to a uniform resolution, anonymized, and curated to remove low-quality and duplicate samples.

Pre-processing

The raw images underwent several pre-processing steps to improve visual quality and standardize structure across samples:

Noise reduction:
Median and Gaussian filtering were applied to reduce imaging artifacts.

Color normalization:
Histogram equalization and contrast-limited adaptive histogram equalization (CLAHE) were used to improve the visibility of cervical epithelial regions.

Segmentation and ROIeExtraction:
YOLOv8 was used to detect and locate lesion areas. Detected bounding boxes helped extract the Region of Interest (ROI), ensuring the model focuses on clinically relevant areas.

Data augmentation

To increase variability in the dataset and reduce overfitting, we applied the following augmentation strategies: Rotation (±15°–30°), Horizontal/vertical flipping, Zoom and random cropping, Brightness and contrast adjustments, Augmentation ensured robust generalization to changes in lighting, orientation, and texture.

Baseline models

To compare the performance of the proposed method, we trained three popular CNN architectures: VGG16, ResNet50, and DenseNet121 on the same pre-processed dataset. Their performance serves as the baseline for evaluation.

Proposed TriCervix model

The proposed TriCervix architecture combines detection, feature extraction, and sequential texture modeling: YOLOv8 detector: Identifies lesion areas and extracts ROI patches with high accuracy. EfficientNet-B3 backbone: Creates multi-scale deep feature maps from the extracted ROIs. Bi-LSTM Sequential Texture Module: Captures dependencies and texture transitions across feature sequences, allowing for better distinction between CIN1 and CIN2. This hybrid approach supports both spatial and sequential texture learning, improving classification reliability.

Classification and training protocol

Task: Multi-class classification of cervical abnormalities (Normal, CIN1, CIN2, etc.). Loss Function: Categorical cross-entropy. Optimizer: Adam with an initial learning rate of 0.0001. Batch Size: 16. Epochs: 50–100 based on early stopping. Hardware: A GPU-enabled environment that supports efficient training and inference.

Evaluation Metrics

We assessed model performance using: Accuracy, precision, recall (sensitivity) These metrics focus on reducing false positives (FPs) and false negatives (FNs), which are important in medical screening.

Statistical and comparative analysis

All models were tested on an independent test set. TriCervix showed better performance than VGG16, ResNet50, and DenseNet121 across all evaluation metrics. Its higher recall indicates fewer missed precancerous lesions, while better precision reduces unnecessary follow-up procedures.

Proposed model

This study begins with a collection of cervical images from different sources like Pap smear, VIA/VILI, and colposcopy. Each image annotated by expert into categories like Normal, CIN1, CIN2, CIN3, and Cancer. To improve the image quality and make it consistent, various pre-processing steps applied such as resizing, noise removal, CLAHE enhancement, and normalization. Segmentation methods used to extract the lesion regions that include the nucleus and abnormal regions of the tissue from the healthy region so that the model emphases important clinical attributes. In the end, a multiclass CIN classification takes place and features extracted by NNs and explanations provided to make it interpretable.

Working procedure of TriCervix

The initial stage collects cervical images from different clinical sources like Pap smear slides, VIA–VILI examinations, and digital colposcopy. Each test can tell you something unique: Pap smear images talk about the cytology, VIA–VILI highlights the abnormal epithelium with color changes, and colposcopy gives a magnified view of the lesion. Having a variety of data helps the model learn a wide representation of cervical abnormalities across different populations and conditions for the imaging system to ensure robustness and generalizability.

Let an input cervical image be$I \in R^{H \times W \times 3}$

Index training examples by k, so $I^{(k)}$ indicate the k^{th} image.

ROI Detection using YOLOv8

The main goal of ROI detections is to detect candidate lesion bounding boxes and objectless scores. YOLOv8 predicts for each grid cell a set of bounding box attributes and class scorevalues. For detection output of the image I:

$$B = \{B_i\}_{i=1}^{N}, b_i = (x_i, w_i, y_i, h_i, o_i, p_i) - - - (1)$$

Wherex_i,y_i denotes the box center coordinates,$w_i h_i$ defines width and height, oi∈ [0, 1] is objectness confidence, and p_i is the class probabilities vector. After non-maximum suppression (NMS) retain boxes with $o_i > \tau_{obj}$. In **ROI, extraction phase images are** crop and optionally pad each box to obtain ROIs:

$$ROI_i = crop(I, b_i) - - - (2)$$

YOLO loss is assessed using combined localization, confidence and classification loss. $L_{YOLO} = \lambda_{loc} \sum_i 1_i^{obj} \left\| b_i - \hat{b}_i \right\|_2^2 + \lambda_{conf} \sum_i (o_i - \hat{o}_i)^2 + \lambda_{cls} \sum_i 1_i^{obj} CE(p_i, \hat{p}_i) - - - (3)$

Where illustrates ground truth, 1_i^{obj}defines positive box, and CE represents cross entropy.

Pre-processing and normalization

Resize each ROIto fixed input size S×S (e.g., 224×224), utilize color normalization and optional contrast enhancement. Denote preprocessed ROI as:

$$X_i = \tau(ROI_i), X_i \in R^{S \times S \times 3} - - - (4)$$

Normalization employed each channel:

$$X_i \leftarrow \frac{X_i - \mu_{chan}}{\sigma_{chan}} - - - (5)$$

With μ_{chan},σ_{chan} measured on training set.

Feature Extraction using EfficientNet-B3

Efficient Net turns as a mapping $f_E : R^{S \times S \times 3} \rightarrow R^{d \times T}$. Extract a sequence of T vectors of dimension d:

$$F = f_E(X) = [f_1, f_2, \ldots\ldots, f_T], f_t \in R^d - - - (6)$$

Efficient Net yields a final convolutional feature map of shape (h×w×d). Flatten spatial locations into a sequence of length T=h·w so each f_t encodes a localized texture descriptor useful for sequential modeling. If a single vector is preferred instead, use global average pooling:

$$f_G = \frac{1}{T}\sum_{t=1}^{T} f_t \in R^d - - - (7)$$

Sequential texture modeling with Bi-LSTM

TriCervix forces a bidirectional LSTM to capture ordered texture patterns across the spatial sequence. For each time step t:

Forward Based LSTM is: $\vec{h}_t = LSTM_f(f_t, \vec{h}_{t-1})$

Backward Based LSTM is : $\overleftarrow{h}_t = LSTM_b(f_t, \overleftarrow{h}_{t+1})$

Concatenate to form Bi-LSTM state:

$$h_t = \vec{h}_t |x| \overleftarrow{h}_t \in R^{2u} - - - (8)$$

Where u is the hidden size of individual LSTM direction. Aggregate sequence into a fixed representation (options):

Last state pooling: $H = h_T$

Global average pooling: $H = \frac{1}{T}\sum_{t=1}^{T} h_t$

Attention-weighted pooling (preferred for focusing on important patches):

$$\alpha_t = \frac{\exp(w^T h_t)}{\sum_j exp(w^T h_j)}, H = \sum_t \alpha_t h_t - - - (9)$$

With learnable vector w. Bi-LSTM models are directional based on relations among local textures (e.g., nucleus border → chromatin pattern), refining discrimination between subtle CIN stages.

Classification head

Map representation H to logits z∈$R^C$for C classes (here C=5: Normal, CIN1, CIN2, CIN3, and Cancer):

$$z = WH + b, W \in R^{C \times m}, b \in R^C - - - (10)$$

Convert logits to class probabilities with SoftMax:

$$\hat{y}_c = P(y - c|X) = \frac{\exp(z_c)}{\sum_{j=1}^{C} \exp(z_j)} - - - (11)$$

Predicted class represented as: $\hat{y} = \arg\max_c \hat{y}_c$

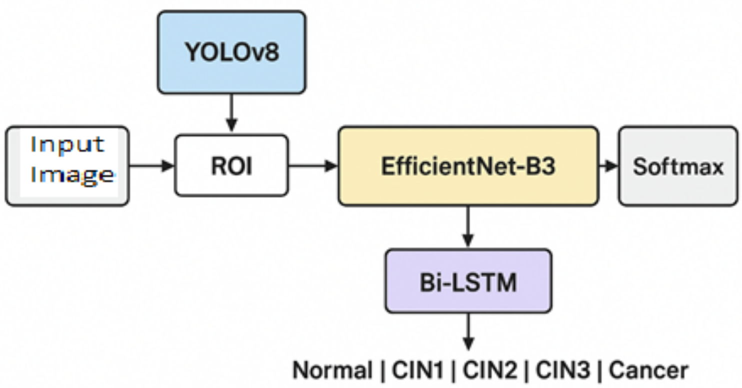

Fig. 1 Architecture of **TriCervix**

Figure 1 shows how to manage the system of CC classification. Initially, YOLOv8 takes the input cervical image and processes it to identify the ROI that may contain the lesion. The ROI passed to EfficientNet-B3 to generate rich and discriminative feature representations. The Bi-LSTM network further analyzed these features to capture temporal texture variations and structural changes in the cervical tissues. In the end, it can classify the image as one of the categories- Normal, CIN1, CIN2, CIN3, or Cancer.

RESULT AND DISCUSSION

Finding CC early is very important. It helps to reduce death when finding precancerous lesions before they become invasive cancer. CC takes time to develop, so the opportunity to diagnosis it early. When effective screening is done, it can help prevent late-stage disease. It also lowers treatment costs, enhances quality of life, and reduces clinical burden. In low-resource areas where screening is difficult, detection methods should be reliable and automated so that diagnosis and early intervention can be helped in saving lives. The disease categorizes into three stages: CIN1, CIN2, and CIN3, which are slightly moderate severe phases respectively [13].

Evaluation metrics

Evaluation scales play a vital role in measuring the reliability of the model and its performance. In simple words, accuracy, precision, and recall measures how well the system detects normal and abnormal cases, reduces false prediction and detects true lesion. They give numbers about how well the models work, allowing fair comparison between different models. These measures ensure that the created system is clinically reliable, minimize diagnosis errors and the essential norms needed for real-world medical screening applications.

Accuracy

In detecting CC, accuracy measures the extent to which the DL system correctly classifies cervical images into their corresponding categories like Normal, CIN1, CIN2, CIN3, or Cancer. It shows how many of all cases, health and diseases alike, the system rates as correct. A high value means that the model successfully differentiates normal cervical tissue from the various stages of cervical intraepithelial neoplasia or CIN. In clinical language, improved accuracy signifies a lower misclassification of patients. This indicates that patients at risk of missing an early precancerous lesion are misclassified less often. Similarly, patients who are healthy are less likely to be misclassified as diseased. Accuracy summarizes how the model performs regarding automated cervical screening.

$$Accuracy = \frac{1}{N}\sum_{k=1}^{N} 1\left(\hat{y}^{(k)} = y^{(k)}\right) - - - (12)$$

In this equation of accuracy, N is the quantity of samples in the total dataset, and it acts as a denominator to normalize the correct predictions. For every sample k, denote the predicted label of the model as $\hat{y}^{(k)}$, and the actual ground-truth label as $y^{(k)}$. The function $1\left(\hat{y}^{(k)} = y^{(k)}\right)$is called the indicator function and checks if the expected label is equal to the true label. If the prediction is correct, the function returns one; otherwise, zero. All indicator values across all samples are summed, in effect counting the number of correct samples. Finally, divide the sum by N for the proportion of predictions that the model classified correctly, which is overall accuracy.

Precision

When a model predicts a certain CC stage (like CIN1, CIN2, CIN3 or Cancer) based on a cervical smear, precision indicates how many of these images are correct. It is the percentage of true positive type predictions relating to all the instances that are predicted positive for that stage. An accurate system will cause very few false alarms. For instance, it will not mislabel healthy-looking cervical cells or mildly abnormal cells such as high-grade CIN or cancer. When the operational precision of the tests increases, then the patient does not have to go through unnecessary follow-up procedures, biopsies, or anxiety due to false positive (FP) predictions.

$$Precision_c = \frac{TP_c}{TP_c + FP_c} - - - (13)$$

In this formula, $Precision_c$ represents the precision score for a specific CC class *c* (such as Normal, CIN1, CIN2, CIN3, or Cancer). The term TP_c stands for *True Positives* for class *c*, which refers to the number of cervical images that truly belong to class *c* and correctly predicted by the model. The term FP_c stands for *FPs* for class *c*, representing the number of images incorrectly predicted as class *c* even though they belong to another class. The denominator, $TP_c + FP_c$, therefore indicates all samples the model predicted as class *c*. The resulting precision value expresses how reliably the model avoids misclassifying other cervical lesion stages as class *c*, making it particularly significant in clinical uses where minimizing false alarms is crucial.

Recall

In CC detection, recall refers to how well the model identifies all instances of a given stage of cervical lesion, such as CIN1, CIN2, CIN3 or Cancer. It shows how many real positive cases were detected as true cases of that stage. A high recall value means that the application will capture most/all patients that have a cervical abnormality thus reducing the chances of missing a diagnosis. Clinically, high recall is important because a false negative (FN) may delay treatment of a precancerous lesion and increase disease progression.

$$Recall_c = \frac{TP_c}{TP_c + FN_c} - - - (14)$$

The formula $Recall_c$denotes the recall value for the class c of a cervical lesion, which could be Normal, CIN1, CIN2, CIN3, or Cancer. TP_c is True Positives for class c, which means the number of cervical images that truly belong to class c and which are predicted correctly by the model. FN_c refers to FNs – these occur when an image belongs to class c, but the model does not identify it as such and instead incorrectly labels it as belonging to some other class. The denominator TP_c plus FN_c equals all the real samples of CC in the dataset. Therefore, recall helps you understand how effectively the model can correctly identify all the true cases of a given cervical lesion stage. This is especially true during the early detection of precancerous conditions.

Table 1 compares the accuracy, precision, and recall of four different DL models, VGG16, ResNet50, and DenseNet121, with the proposed TriCervix model. The results indicate that conventional models perform well and that DenseNet121 achieved the highest scores of all existing models. The proposed model, TriCervix, outperforms all the baseline classifiers with the highest values of all metrics. TriCervix is better at detecting cervical abnormality and classifying them correctly as compared to the other competitor. Moreover, it also generates lesser FPs. In general, the table illustrates the robustness and clinical applicability of the hybrid DL framework.

Table 1. Comparing DL models performance with TriCervix model.

DL Model	Accuracy (%)	Precision (%)	Recall (%)
VGG16	88.12	86.34	85.09
ResNet50	90.74	89.29	88.64
DenseNet121	92.39	91.09	89.79
TriCervix	95.74	94.89	95.39

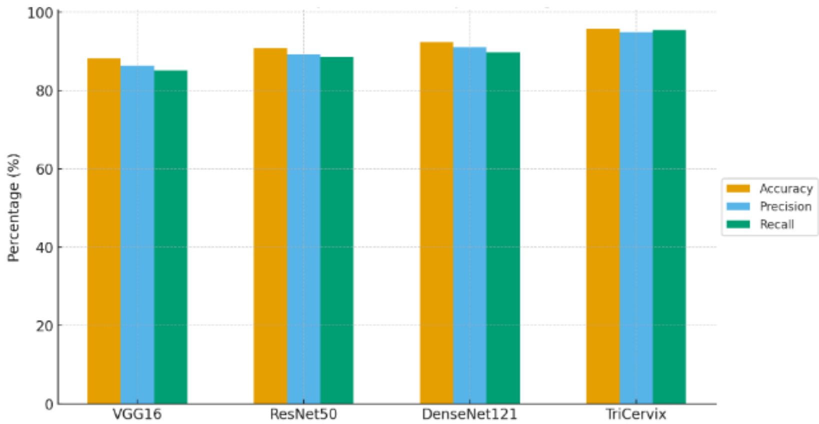

Fig 2. Performance comparison of DL models

The bar graph shows the accuracy, precision and recall of four DL models VGG16, ResNet50, and DenseNet121 and TriCervix. The three bars of each model respectively represent accuracy in yellow, precision in blue and recall in green. The charts show that TriCervix beats all the existing models in each metric and Tricervix has the highest accuracy (95.74%), precision (94.89%) and recall (95.39%). The proposed TriCervix algorithm performs better in terms of classification performance, as illustrated by the graph.

CONCLUSIONS

This study has shown that the proposed TriCervix DL model has made considerable progress in detecting century CC. TriCervix outperforms established architectures like VGG16, ResNet50, and DenseNet121. The evidence shows TriCervix achieves superior accuracy, precision, and recall scores than these architectures. The metrics reveal that the proposed model does a better job in identifying cervical abnormalities with lesser FPs and FNs that are critical in medical diagnosis. TriCervix outperforms other state-of-the-art solutions in all evaluation metrics, demonstrating robustness to variations in the feature of the dataset. It ensures quicker diagnosis, screening and improved clinical decision support therefore enhancing detection time. By improving recall, only few FNs would be there in detection of cervical abnormalities. This is beneficial for early detection as timely diagnosis is essential to cancer prevention. The study confirms that TriCervix is an efficient and reliable solution that outperforms many existing deep-learning classifiers. When incorporated into healthcare systems, it can enhance women’s health by timely, accurately, and automatically assisting CC screening.

Conflict of Interest
Authors do not express any conflict of interest.

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