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# Effectiveness of Artificial Intelligence Assisted Methods in the Diagnosis and Screening of Cervical Cancer: Systematic Review

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## Abstract

**Background:** Prior research has demonstrated the exceptional diagnostic accuracy of artificial intelligence in cervical cytology and diagnosis of cervical cancer. Our goal was to investigate how well artificial intelligence-assisted cervical cytology screening work to detect cervical cancer.

**Method:** To locate every publication published between 2019 and 2024, we searched the MEDLINE, Cochrane, and Embase databases. Our work focused on AI-assisted cervical cytology diagnosis for the detection of cervical cancer. PRISMA reporting guidelines were used in the design of the review. A manual reference search of the included articles was also carried out to look for any more relevant studies. Research that developed and used machine learning or deep learning models for the categorization of cervical cancer lesions using medical imaging was taken into consideration.

**Result and Conclusion:** Four papers published between 2019 and 2024 were considered in this systematic review analysis. Alassisted models were helpful in the diagnosis of cervical lesions, but their effectiveness was limited by the models' intricacy and the caliber of the data. Shown the potential application of automated histopathology image analysis for early cervical cancer detection. In the categorization of cervical cancer, deep learning models outperformed traditional machine learning models by a significant margin, achieving high accuracy and precision. Deep learning based models were shown to be effective in classifying cervical images across a variety of cervical lesion classes.

Keywords: Artificial Intelligence; Diagnosis; Detection; Cervical Cancer

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#### Abbreviations

AI: Artificial Intelligence; CIN: Cervical Intraepithelial Neoplasia; CNN: Convolutional Neural Network; HPV: Human Papillomavirus; PRISMA: Preferred Reporting Items for Systematic Reviews and Meta-Analyses; ML: Machine Learning; SVM: Support Vector Machines; UNet: A Deep Learning Architecture Used for Image Segmentation; SE: Squeeze and Excitation; PCA: Principal Component Analysis; ARM: Association Rule Mining; CIN2/3+: Cervical Intraepithelial Neoplasia 2/3 and Higher-Grade Lesions; ASC-US: Atypical Squamous Cells of Undetermined Significance; ResNet: Residual Networks; VGG: Visual Geometry Group; DenseNet: Densely Connected Convolutional Networks; SIPaKMeD: A Publicly Available Dataset of Cervical Cell Images

#### Introduction

The development of malignant cells in cervical cancer (CC) is caused by human papillomavirus (HPV) [1]. Cancer may be treated when discovered early, but if left untreated, it can quickly spread and become lethal. CC is one of the main causes of death for women globally. The condition is more likely to strike women under 30 [2]. The Centers for disease Control and Prevention (CDC) estimate that the condition affects 13,000 women annually in the United States alone, leading to around 4,000 fatalities [3]. In 2020, 342 000 CC-related fatalities were recorded, and about 604 000 women globally received a CC diagnosis [4]. These concerning figures have brought attention to the urgent need to identify, diagnose, treat, and prevent the illness. The prognosis for the illness is favorable when it is discovered in its preinvasive stage. The PAP smear and HPV testing are two of the most widely used methods to identify the precursor for CC [5].

Since a radiologist must examine about 10,000 cells to find any abnormalities, a Pap smear test might take a long time [6]. Because of this, deep learning and artificial intelligence (AI) are now being used in modern healthcare to identify and diagnose CC. An automated procedure can provide accurate and objective findings in addition to detecting cancer cells in a quarter of the time. To find anomalies, researchers have classified pictures using Pap smear test data and examined the photos. Convolutional neural network (CNN) is frequently used to classify images. In order to identify if a cell in the picture is malignant or healthy, a CNN may automatically extract characteristics from the image. Using pictures of individual cervical cells, our suggested CNN model assigns each cell to one of the five categories. The form, color, and features of the nucleus of an infected cell vary. A fair estimate of the cytoplasm may also be obtained by accurately detecting the nuclei during segmentation [7]. Once these characteristics are retrieved, the CNN model may provide an accurate forecast. The intricacy and precision of the test are the largest obstacle to the use of Pap smear analysis for the identification of CC. There is considerable variation in the color, size, and form of cervical cells [8]. With the unaided eye, distinguishing between various cell types is challenging [9]. We aimed to examine the combined effectiveness of AI-assisted cervical cytology screening and colposcopy for CC screening.

Although prior reviews explored the role of artificial intelligence in cervical cancer detection, rapid technological advancements and the emergence of new deep learning models between 2019 and 2024 make it necessary to make an updated synthesis of evidence. Existing reviews have not addressed sufficiently the comparative performance of transfer learning approaches and the integration of multi-feature fusion techniques in cervical cytology. Therefore, our systematic review aims to fill this gap by focusing on recent innovations and evaluate their clinical relevance.

### Method

We looked through the MEDLINE, Cochrane, and Embase databases to find every paper published between 2019 and 2024. AI-assisted cervical cytology screening for CC diagnosis was the subject of our study. The review was designed using the Preferred Reporting Items for Systematic Reviews and Meta-analyses (PRISMA) reporting criteria. To find any more pertinent papers, a manual reference search of the contained articles was also conducted. Studies that created and used deep learning or machine learning (ML) models for CC lesion classification using medical imaging were considered.

All observational studies that were published only in English and related to AI-assisted cervical cytology screening for the identification of cervical Intraepithelial Neoplasia (CIN) and CC were included. Two independent reviewers screened the research based on abstracts and titles; disagreements were settled by consulting a third reviewer. After abstract screening, three reviewers independently determined eligibility for inclusion

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based on the inclusion and exclusion criteria. When there was disagreement, the three reviewers reached a consensus to make decisions. Two reviewers separately retrieved pertinent data from eligible full-text publications using a template data extraction form; disagreements were settled by adding a third reviewer.

First author, year of publication, country of data collection, validation and testing, study type, number of training images, type of AI algorithm, database used, data availability, and number of patients who underwent both a clinician reference test and an AI screening trial were all taken from studies that met the eligibility requirements.

#### **Results and Discussion**

In this systematic review study we included 4 articles (Figure 1) published in the period from 2019 to 2024. Alsubai., *et al.* (2023) [10] classified cervical cell pictures using extracted characteristics using conventional ML techniques, such as Random Forest and Support Vector Machines (SVM).centered on classifying photos by extracting features. Chowdary., *et al.* (2023) [11] detected CC using the Herlev dataset by CNN with transfer learning.used pre-trained models for classification, such as DenseNet, ResNet, VGG16, and VGG19. Tan., *et al.* (2024) [12] concentrated on transfer learning for the seven-class categorization of CC cells using pre-trained CNN models (such as DenseNet and ResNet).placed a strong emphasis on transfer learning, adapting CNN models that had previously been trained on big datasets for the Herlev dataset with the goal of increasing model accuracy in spite of the scarcity of data. The purpose of the Wong., *et al.* (2019) [13] study was to assess the

presence of hrHPV types and their correlation with CIN2/3+ lesions by HPV testing utilizing the Onclarity and Cobas platforms. Constructed classifiers utilizing various models, such as SVM, random forest, and decision tree, and carried out association rule mining (ARM) (Table 1).



Figure 1: PRISMA consort chart of studies selection.

Citation	Study method	Objective
Alsubai., <i>et al</i> .	Study tested applied ML method that uses a CNN to	The main objective is to develop a CNN model to classify
2023	classify images. A flatten layer is used to transform 3D	cervical cell images from Pap smears into five categories:
	input to 1D, three fully connected layers are used for	dyskeratotic, koilocytotic, metaplastic, parabasal, and
	classification, four convolutional layers are used for	superficial-intermediate. This classification aims to detect
	feature extraction, and three max-pooling layers are	cell abnormalities that could indicate the presence of pre-
	used for dimensionality reduction.	cancerous cells, aiding in early diagnosis and the manage-
	Accuracy is used to gauge how accurate the predic-	ment of disease progression.
	tions are, while log loss is used to account for forecast	
	uncertainty.	

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**Table 1:** Study method and objective of the included articles.

The Alsubai., *et al.* (2023) study discovered that while ML models might be useful for diagnosing cervical lesions, their performance was constrained by the complexity of the models and the quality of the data. Shown how automated histopathology image analysis may be used to detect CC early. According to the Chowdary., *et al.* (2023) study, deep learning models achieved great accuracy and precision in CC classification, outperforming conventional ML models by a large margin. It was demonstrated that CNN-based models performed well in categorizing cervical pictures across a range of cervical lesion classifications. Tan., *et al.* (2024) study despite having little data, pre-trained CNN models were able to

get good accuracy (over 80%) on the Herlev dataset thanks to transfer learning approaches, issues such as class imbalance, where certain classes were more challenging to categorize. In seven-class classification, DenseNet-201 and ResNet models performed especially well. According to the Wong., *et al.* (2019) study, Onclarity and Cobas both did a comparable job of identifying CIN2/3+ lesions. While the two tests' sensitivity and specificity for identifying high-grade lesions were almost the same, there were variations in the HPV genotyping findings. Association rule mining (ARM) assisted in determining which HPV genotypes were most predictive of high-grade lesions, and HPV16 and HPV33/58 had a greater relative risk (RR) for developing CIN2/3+ (Table 2).

Citation	Main findings
Alsubai., et al.	The study used a CNN model to categorize pictures into five categories using the SIPaKMeD dataset, a publi-
2023	cally available cervical cell imaging collection. The CNN model with its eleven layers, classifies cervical cells, identify aberrant and normal cells, and forecast precancerous abnormalities effectively.
Chowdary., et al.	Based on the popular UNet design, the segmentation network incorporates Residual SE modules to extract
2023	features efficiently. By taking the role of the convolutional layers in the conventional UNet, the residual SE
	modules improve the capacity to retrieve pertinent features for segmentation. The segmented nuclei are used
	to extract two sets of hand-crafted features and three sets of deep features. These characteristics are first re-
	duced in dimensionality using Principal Component Analysis (PCA). In segmentation and classification tasks,
	the suggested approaches produce more accurate results than previously reported in the literature.

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Tan., <i>et al</i> . 2024	Except for ResNets, every pre-trained CNN model generate higher the 80 percent accuracy values. The trans- fer learning approach addressed the limited data and a lack of high-quality medical data, allowing the models to be trained in less than six minutes. The models performed well for Class 2 and Class 5. No model was able to accurately classify all seven CC types.
Wong., et al. 2019	There were variations in Onclarity and Cobas genotyping (particularly for HPV16 and HPV18) although perform similarly for primary screening. The findings of HPV16 and HPV18 genotyping varied, however both tests were shown to be useful for identifying CIN2/3+ lesions and classifying ASC-US patients. The ARM method shown that specific HPV genotypes, including HPV16 and HPV33/58, are highly predictive of the occurrence of CIN2/3+ lesions, giving important new information for future studies on HPV-based risk assessment and CC screening decision-making.

Table 2: Main finding of the included studies.

Large-scale CC diagnosis using pap smear slides requires laborious and time-consuming hand morphological examination of cellular pictures. Furthermore, human error frequently occurs during a manual review of these slides [14,15] leading to falsepositive or false-negative results. Compared to the manual process, automated nuclei segmentation and categorization will enable quick, large-scale pap smear slide evaluation with no human error and reduced diagnostic time.

Certain HPV genotype combinations may impose greater risks, and some HPV types are more carcinogenic than others [16,17], which may contribute to the increased specificity in the Wong., *et al.* research. Additionally, there is proof that the risk of developing CC is influenced by the co-occurrence of many HPV strains. Coinfection with numerous  $\alpha$ 9 species, for example, was linked to a considerably higher risk of CIN2+ or HSIL+, according to genotyping analysis of the Costa Rica HPV Vaccine Trial, which was supported by the National Cancer Institute [18].

A South American investigation found that the incidence of CIN2-3+ is higher when HPV68 and HPV16 are coinfected than when either virus is present alone [19]. Similarly, a Brazilian study found that multiple HPV genotype infection was linked to a worse survival rate for invasive CC [20]. However, women who have both high-risk and low-risk HPV infections are said to have a decreased chance of CIN2 development [21]. It has been demonstrated that numerous HPV infections increase the likelihood of carcinogenic E6/E7 mRNA expression compared to single infections, while the biological impact of many infections is unknown. Thus, even in low-grade lesions, multiple infection may be a clinically significant finding [22].

Future research should focus on developing standardized datasets and multicenter studies to validate AI models in different populations. Integration of AI-assisted screening into routine clinical practice improve early detection rates, mainly in lowresource settings where access to expert cytologists is limited. Refining AI algorithms to address class imbalance and improve interpretability is crucial to gain wider clinical acceptance and regulatory approval.

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#### Conclusion

The included articles discussed how ML techniques enhance early detection and categorization of CC. One research examined the effectiveness of pre-trained CNN models in classifying CC from sparse data using transfer learning, while two studies foucused on applying sophisticated segmentation networks and multi-feature fusion techniques to improve cervical cell picture segmentation and classification. Furthermore one research examined how well HPV genotyping assays (Onclarity vs. Cobas) identified highgrade lesions, showing encouraging outcomes for CIN2/3+ lesion prediction and patient triage. The included studies discussed the effectiveness of combining ML techniques with existing clinical diagnostic methods for CC diagnosis, offering information for improving diagnostic accuracy, addressing data limitations, and enabling more efficient triaging of cases. The use of deep learning and advanced algorithms is paving the way for more reliable, faster, and cost-effective solutions for CC screening and diagnosis, especially when integrated with molecular testing such as HPV genotyping.

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