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Automated Cervical Cancer Screening Via Hybrid Multi-Resolution Image Segmentation and Ensemble Learning: A Comparative Study with SVM and K-Means Approaches

[1] Morteza Hassandoust, [2] Ali Farzin

[1, 2] M.Sc. in Computer Software Engineering, Department of Computer Engineering, Islamic Azad University, Shabestar Branch, Iran

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Corresponding Author: **Morteza Hassandoust**

Abstract

Despite substantial progress in digital pathology, automated cervical cancer screening remains challenging because of overlapping cells, staining variability, and the limited capability of single-resolution segmentation methods to capture morphological variation. This study proposes a hybrid framework that combines multi-resolution image segmentation with stacked ensemble learning to improve screening performance while reducing false-negative diagnoses. Gaussian and Laplacian pyramids are constructed from cervical cytology patches, allowing watershed, active contour, and Gabor-based mean-shift segmentation algorithms to extract complementary structural information at different spatial scales. The resulting features are integrated through a stacked ensemble consisting of a random forest, gradient boosting machine, and multilayer perceptron, with prediction scores combined using a regularized logistic regression meta-learner.

The proposed framework was evaluated on a dataset of 12,500 liquid-based cytology patches annotated according to the Bethesda system and compared with two established baseline approaches: a single-resolution watershed–SVM pipeline and a K-means segmentation–SVM pipeline under identical patient-level five-fold cross-validation. The proposed method achieved a mean classification accuracy of **0.914 ± 0.008**, a binary screening **AUC of 0.967 ± 0.007**, and a sensitivity of **0.891 ± 0.019** for high-grade lesions (HSIL and carcinoma), significantly outperforming both baseline methods (**$p < 0.001$**). The false-negative rate for high-grade lesions decreased from **0.238** to **0.109**. Ablation analysis further showed that both the multi-resolution segmentation strategy and the stacked ensemble contributed to the overall performance improvements. Inference time remained suitable for routine batch screening, requiring less than five minutes to process a complete slide.

These findings indicate that combining multi-resolution image analysis with ensemble learning provides an effective and computationally practical approach for automated cervical cancer screening, improving diagnostic performance while maintaining efficiency for clinical workflows.

Keywords: Cervical Cancer Screening, Multi-Resolution Image Segmentation, Ensemble Learning, Support Vector Machine, K-Means Clustering, Hybrid Framework, False-Negative Reduction

1. Introduction

Cervical cancer remains a major public health challenge and is the fourth most common cancer among women worldwide. Although the disease is largely preventable through regular screening and early treatment, it continues to cause substantial morbidity and mortality, particularly in low- and middle-income countries where access to screening programs and specialized healthcare services remains limited (Ahmad & Khan, 2022) [1]. Cytology-based screening using the Papanicolaou (Pap) smear has significantly reduced cervical cancer mortality over the past decades. However, manual examination of cytology slides is labor-intensive, time-consuming, and subject to considerable inter-observer variability, which can affect diagnostic consistency and increase the risk of missed lesions (Shah & Patel, 2022) [48]. Although liquid-based cytology and HPV DNA testing have improved screening strategies, microscopic assessment of cervical cells remains an essential component of clinical diagnosis, creating a growing demand for reliable computer-aided screening systems (Win *et al*., 2020) [59].

Recent advances in digital pathology, computer vision, and machine learning have accelerated the development of automated

cervical cancer screening systems (Priya & Kumar, 2024) [38]. Early computer-aided approaches relied on handcrafted morphological and texture features extracted after image segmentation, followed by conventional classifiers such as support vector machines (SVMs), decision trees, or multilayer perceptrons. While these methods demonstrated promising performance under controlled conditions, their robustness has been limited by variations in staining, overlapping cells, imaging artifacts, and the biological diversity of cervical cytology samples (Ullah *et al*., 2022) [56]. As a result, improving segmentation accuracy remains a critical step for achieving reliable automated diagnosis.

Image segmentation plays a fundamental role in cervical cytology because the quality of extracted features directly depends on accurate delineation of nuclei and cellular structures. Conventional segmentation techniques, including thresholding, watershed transformation, region growing, and K-Means clustering, have been widely investigated because of their computational efficiency and implementation simplicity. Nevertheless, these methods often struggle with clustered cells, uneven illumination, ambiguous cytoplasmic boundaries, and staining inconsistencies, which reduce classification performance. Likewise, SVM-based classifiers remain highly dependent on the quality of segmentation and handcrafted feature extraction, limiting their effectiveness when diagnostically important structures are not accurately identified (Ozturk & Akdemir, 2022; Ramzan & Raza, 2025) [34, 41].

To address these limitations, multi-resolution image analysis has emerged as an effective strategy for capturing complementary information at different spatial scales. High-resolution representations preserve nuclear morphology, chromatin texture, and membrane irregularities, whereas lower-resolution representations provide broader contextual information, including cellular arrangement and tissue organization. By integrating features extracted across multiple resolutions, multi-scale frameworks can improve the representation of complex cellular morphology and potentially reduce false-negative diagnoses (Singh & Kaur, 2025) [52]. At the same time, ensemble learning has demonstrated considerable potential for improving classification robustness by combining the strengths of multiple predictive models. Algorithms such as random forests, gradient boosting, and stacked generalization have shown encouraging results across a variety of medical image analysis tasks (Dey *et al*., 2025; Aljuaid *et al*., 2022) [12, 2].

Despite these advances, relatively few studies have jointly investigated multi-resolution segmentation and ensemble learning within a unified cervical cancer screening framework. Existing research typically emphasizes either segmentation or classification independently, while comprehensive comparisons with widely used SVM- and K-Means-based pipelines remain limited (Khamparia & Pandey, 2025) [24]. Consequently, the practical contribution of combining multi-resolution feature extraction with ensemble learning has not yet been fully established under consistent experimental settings.

To address this gap, this study proposes a hybrid framework that integrates multi-resolution image segmentation with stacked ensemble learning for automated cervical cancer screening. The proposed approach extracts complementary features from Gaussian and Laplacian image pyramids and combines the predictions of multiple classifiers through a meta-learning strategy. Its performance is systematically compared with two established baseline pipelines based on K-Means segmentation and SVM classification using identical datasets, evaluation metrics, and cross-validation protocols. The study focuses not only on overall classification accuracy but also on clinically important measures, including sensitivity, specificity, false-negative rate, and high-grade lesion detection. Through this comparative evaluation, the proposed framework aims to provide a more reliable and computationally efficient approach for automated cervical cytology screening while offering practical evidence of the benefits of integrating multi-resolution image analysis with ensemble learning.

2. Theoretical

The theoretical foundation of automated cervical cancer screening integrates concepts from digital pathology, computer vision, machine learning, and medical diagnostics. The primary objective of these systems is to accurately distinguish normal cervical cells from precancerous and cancerous abnormalities in complex microscopic images. This requires effective image analysis, reliable feature extraction, and robust classification methods. Within this framework, multi-resolution image segmentation and ensemble learning have emerged as promising approaches to overcome the limitations of conventional segmentation and classification techniques (Subramanian & Govindaraj, 2023) [53]. Cervical cytology images are commonly obtained from Papanicolaou-stained smears or liquid-based cytology samples. Cytopathologists evaluate these images based on nuclear size, nuclear-to-cytoplasmic ratio, chromatin texture, membrane irregularity, and cellular arrangement (Bhatt & Bhatt, 2022) [6]. Because these diagnostic characteristics appear at different spatial scales, both fine nuclear details and broader cellular context must be considered. High-resolution images reveal chromatin patterns and nuclear boundaries, whereas lower-resolution images provide information about cell distribution, overlapping structures, and tissue organization. Therefore, automated screening systems benefit from multi-scale image analysis that mimics the diagnostic process of experienced cytopathologists (Chen *et al*., 2023) [10].

Image segmentation is a critical step in automated cervical cytology because accurate feature extraction depends on reliable separation of nuclei and cytoplasm from the background. However, segmentation remains challenging due to overlapping cells, staining variability, uneven illumination, and imaging artifacts. Conventional methods, including thresholding, edge detection, region growing, and watershed transformation, have been widely applied but often perform poorly when cell boundaries are unclear or staining quality is inconsistent (Suryawanshi & Patil, 2022) [55]. Although watershed segmentation can separate touching cells, it frequently produces over-segmented regions and requires extensive pre- and post-processing. These limitations have encouraged the adoption of clustering-based methods, particularly K-means clustering, for cytology image segmentation (Kamal & Yusoff, 2022) [22].

K-means is an unsupervised clustering algorithm that partitions pixels into predefined clusters according to feature similarity. In image segmentation, pixels are typically represented by color information, with optional spatial coordinates to improve region compactness. The algorithm is computationally efficient and does not require pixel-level annotations, making it attractive for medical image analysis.

Nevertheless, its performance is strongly influenced by the predefined number of clusters, centroid initialization, and the assumption of compact cluster distributions. These assumptions are often violated in cervical cytology because cells exhibit irregular shapes, variable staining, and overlapping structures. As a result, K-means may produce fragmented nuclei or merge adjacent cells, reducing segmentation quality (Anami *et al*., 2022) [3]. These shortcomings have motivated the development of multi-resolution segmentation approaches that analyze images at different spatial scales and integrate complementary structural information to improve segmentation accuracy (Chakraborty & Mali, 2022) [8].

Multi-resolution image analysis is based on scale-space theory, which assumes that image structures are best represented at different spatial scales rather than at a single resolution. Gaussian and Laplacian pyramids are commonly used to generate multiple image representations, allowing fine and coarse image structures to be analyzed separately. In cervical cytology, high-resolution levels emphasize nuclear morphology, chromatin texture, and membrane irregularities, whereas lower-resolution levels capture cellular arrangement, tissue organization, and staining patterns (Sen *et al*., 2022) [47]. By integrating information across multiple scales, multi-resolution segmentation improves boundary localization, reduces the effects of cell overlap, and produces more robust feature representations than conventional single-resolution approaches (Mithun & Das, 2023) [30]. Hybrid multi-resolution frameworks further enhance segmentation by combining complementary algorithms across different pyramid levels, enabling simultaneous preservation of local nuclear details and broader contextual information (Farooq & Anwar, 2022) [14].

Following segmentation, extracted features are used for classification to determine whether individual cells or entire slides contain abnormal findings. Because cervical cytology datasets are often high-dimensional and imbalanced, ensemble learning has become an effective strategy for improving classification performance (Elakkiya *et al*., 2025) [13]. Ensemble methods combine multiple classifiers to reduce prediction errors and improve generalization. Bagging, boosting, and stacked generalization are among the most widely used ensemble strategies. Random forests provide robust performance through bootstrap sampling and random feature selection, while gradient boosting sequentially improves classification by focusing on previous errors. Stacked learning further combines the outputs of diverse base classifiers using a meta-learner, allowing complementary decision patterns to be exploited (Kuko & Pourhomayoun, 2020; Ghosh & Bandyopadhyay, 2022) [26, 16]. When integrated with multi-resolution segmentation, ensemble learning benefits from complementary features extracted at different spatial scales, improving robustness and reducing false-negative diagnoses, particularly for high-grade cervical lesions (Park & Kim, 2025; Mohammed & Al-Janabi, 2025) [36, 31].

Support Vector Machines (SVMs) serve as an important baseline for comparison. SVMs determine an optimal separating hyperplane in a transformed feature space using kernel functions, enabling effective non-linear classification with strong theoretical generalization properties (Bora *et al*., 2022) [7]. They have been widely applied to cervical cytology because of their ability to classify complex morphological patterns. However, SVM performance strongly depends on the quality of segmentation and feature extraction. In addition, parameter selection, limited scalability, and sensitivity to class imbalance reduce their effectiveness in practical cervical screening applications where abnormal cases are relatively rare (Cruz & Bhanu, 2023) [11]. Ensemble learning addresses many of these limitations by combining multiple classifiers and incorporating sampling or cost-sensitive strategies, leading to improved sensitivity for high-grade lesions (Kumar & Sharma, 2024) [25].

K-means clustering remains one of the most widely used unsupervised segmentation methods because of its computational simplicity and efficiency. The algorithm partitions image pixels into predefined clusters according to feature similarity without requiring manually annotated training data. Nevertheless, segmentation quality depends heavily on the selected number of clusters, centroid initialization, and assumptions about cluster shape. These assumptions are frequently violated in cervical cytology images containing irregular nuclei, overlapping cells, and staining variability. Consequently, K-means often produces fragmented nuclei or merged cellular regions, limiting downstream classification performance. In this study, K-means is employed as a conventional baseline and compared with the proposed multi-resolution segmentation framework to quantify the contribution of scale-aware image analysis.

Reliable evaluation is essential because screening systems must minimize clinically significant errors. While overall accuracy is informative, sensitivity is particularly important because false-negative diagnoses may delay treatment of high-grade lesions. Therefore, sensitivity, specificity, positive predictive value, negative predictive value, receiver operating characteristic (ROC) curves, area under the ROC curve (AUC), and F1-score are commonly used to evaluate automated cervical cancer screening systems (Saba & Rehman, 2022) [43]. Applying these complementary metrics provides a more comprehensive assessment of diagnostic performance across different lesion categories and class distributions (Mahmood & Rehman, 2025) [28].

Feature discriminability provides the theoretical link between segmentation and classification. Multi-resolution segmentation captures complementary information across different spatial scales, including global cellular organization and fine nuclear morphology. The resulting feature representation improves class separability and enables classifiers to distinguish lesion grades more effectively than single-resolution features (Yu & Zhang, 2022) [60]. This enhanced representation is expected to improve both classification accuracy and sensitivity while reducing false-negative results.

Overall, the proposed framework combines multi-resolution segmentation with ensemble learning to address the principal limitations of conventional K-means and SVM-based screening pipelines. Multi-resolution analysis improves feature quality by preserving both local and contextual information, whereas ensemble learning enhances classification robustness and reduces the impact of class imbalance. Together, these components provide a

theoretically well-supported foundation for improving automated cervical cancer screening while maintaining reliable diagnostic performance.

3. Methodology

The research methodology is designed to systematically evaluate the proposed hybrid multi-resolution image segmentation and ensemble learning framework against conventional support vector machine (SVM) and K-means clustering approaches in the context of automated cervical cancer screening. The study is structured to align with the three research questions and to provide the quantitative evidence necessary to test each hypothesis under controlled and reproducible conditions. This section delineates the dataset, preprocessing operations, the detailed architecture of the proposed method, the implementation of the baseline pipelines, the performance metrics, and the statistical procedures that will be used to draw inferences. The path from raw images to final comparative results is explicitly traced so that the subsequent Results section can reproduce each metric and the Findings section can directly interpret those metrics in light of the hypotheses.

The initial step in the methodology concerns the acquisition and characterization of the cervical cytology image dataset. A large, anonymized repository of digital images of liquid-based Papanicolaou-stained cervical smears is utilized. Each image has been collected under standard clinical protocols at a collaborating cytopathology center and subsequently de-identified. All images are captured at a uniform optical magnification of 40× using a high-throughput slide scanner, yielding RGB color images with a resolution of 2048 by 1536 pixels and a pixel size of approximately 0.25 micrometers (Araújo *et al*., 2023) [4]. The dataset comprises a total of 12,500 individual cell-centered image patches extracted from whole-slide scans, with each patch containing at least one well-defined cervical cell nucleus and its surrounding cytoplasm. The ground truth annotation for each patch has been assigned by a panel of three senior cytopathologists following a consensus procedure and aligns with the Bethesda system terminology (Ngu *et al*., 2021) [33]. The label distribution includes normal squamous cells, atypical squamous cells of undetermined significance, low-grade squamous intraepithelial lesions, high-grade squamous intraepithelial lesions, and squamous cell carcinoma. To maintain clinical realism, the dataset deliberately preserves the natural class imbalance encountered in screening populations, with normal samples representing the largest group and high-grade lesions and carcinomas being substantially rarer (Rahman & Islam, 2023) [39].

Table 1: Class Distribution and Patient-Level Stratification of the Cervical Cytology Image Dataset

Bethesda Class	Number of Patches	Number of Patients	Percentage of Patches
Normal squamous cells	6,250	1,250	50.0%
ASCUS	2,500	500	20.0%
LSIL	1,875	375	15.0%
HSIL	1,250	250	10.0%
Squamous cell carcinoma	625	125	5.0%
Total	12,500	2,500	100%

Prior to any segmentation or classification, a uniform preprocessing pipeline is applied to all images. First, color normalization is performed using a histogram matching approach that maps each image's color distribution to a reference template derived from a set of expertly selected representative images. This step reduces stain variability while preserving biological color differences that carry diagnostic information (Kaur & Singh, 2023) [23]. Second, a median filter with a kernel size of 3 by 3 is applied to attenuate shot noise without blurring nuclear boundaries. Third, background pixels are identified by thresholding the luminance channel of the L*a*b* color space at the 95th percentile of the background intensity distribution, and these pixels are set to a uniform neutral value to prevent them from interfering with subsequent segmentation steps. No contrast enhancement is applied globally; instead, local normalization occurs inherently within the multi-resolution decomposition stage of the proposed method (Arya *et al*., 2018) [5].

The core of the proposed system is a hybrid multi-resolution segmentation module that operates on the preprocessed RGB patches. The module constructs a three-level Gaussian pyramid from the input image. Let I_0(x, y) denote the original image at full resolution, with x and y spanning the pixel dimensions. The first level of the pyramid, L1, is obtained by convolving I_0 with a Gaussian kernel G(x, y; σ_1) where $\sigma_1 = 1.0$ and then downsampling by a factor of 2 in each dimension. The Gaussian kernel is defined as $G(x, y; \sigma) = (1 / (2\pi\sigma^2)) \exp(- (x^2 + y^2) / (2\sigma^2))$. The second level, L2, is produced by applying a second Gaussian smoothing with $\sigma_2 = 1.6$ to L1 and downsampling again. The third level, L3, is generated analogously from L2 with $\sigma_3 = 2.5$. In parallel, a Laplacian pyramid is constructed by computing the difference of Gaussian approximations: the detail layer at a given scale is defined as D_k = I_k - upsample(I_{k+1}), where upsample denotes bilinear interpolation to the size of I_k. The detail layers capture band-pass information that highlights blob-like structures, including nuclei, at specific physical sizes (Selvaraj & Murugan, 2023) [46].

Table 2: Architectural Configuration of the Multi-Resolution Segmentation Pyramid with Scale-Specific Algorithms and Fusion Weights

Pyramid Level	Resolution (pixels)	Gaussian σ	Segmentation Algorithm	Fusion Weight
L0 (Original)	2048×1536	$\sigma_1 = 1.0$	Gradient-based watershed with h-minima marker extraction	0.50
L1	1024×768	$\sigma_2 = 1.6$	Region-based active contour (Chan–Vese)	0.30
L2	512×384	$\sigma_3 = 2.5$	Gabor filter bank (4 orientations, 2 frequencies) + Mean-shift clustering	0.20

At each pyramid level, a segmentation algorithm is applied that is selected to exploit the scale-specific properties of that level. On the full-resolution image L0, a gradient-based watershed that incorporates nuclear marker extraction via morphological h-minima transform is employed to obtain a precise outline of individual nuclei. The h-minima transform suppresses regional minima whose depth is less than a threshold h, and the threshold is set adaptively based on the mean intensity of the local background (Sahu & Sharma, 2022) [45]. On the intermediate level L1, a region-based

active contour model without edges is applied to refine cytoplasmic boundaries that are often poorly defined at full resolution. The energy functional minimised by the active contour integrates a local fitting term that depends on the average intensities inside and outside the evolving curve, formulated as $E(c1, c2, \varphi) = \mu \int |\nabla H(\varphi)| + \nu \int H(\varphi) + \lambda_1 \int |I - c_1|^2 H(\varphi) + \lambda_2 \int |I - c_2|^2 (1 - H(\varphi))$, where φ is the level set function, H is the Heaviside function, c_1 and c_2 are the mean intensities inside and outside the contour, and μ, ν, λ_1, λ_2 are weighting parameters (Ghoneim & Muhammad, 2024) [15]. At the coarsest level L2, a texture-based segmentation using Gabor filter bank responses is performed to segment tissue regions based on chromatin texture patterns. The Gabor filters are defined with four orientations and two spatial frequencies, producing eight response maps, which are then clustered using a mean-shift algorithm to partition the image into homogeneous textural zones (Rasche, 2022) [42].

The segmentation maps from the three scales are fused through a spatially weighted consensus procedure. For each pixel, the fusion rule evaluates the agreement among the label assignments produced at different scales and assigns the final label based on a majority vote that is weighted by a scale-specific confidence factor. The confidence factors are learned from a small validation subset by maximising the Dice similarity coefficient with manual nuclear masks (Chandran *et al*., 2022) [9]. The fused segmentation map provides a detailed partition of each cell patch into nuclear region, cytoplasm region, and background, with nucleus boundaries that integrate both fine-scale edge information and coarse-scale region information (Li & Liu, 2023) [27].

Once segmentation is complete, a comprehensive set of features is extracted from each delineated nucleus and its corresponding cytoplasm. For the nucleus, morphological features are computed, including area A, perimeter P, major and minor axis lengths, eccentricity $\varepsilon = \text{sqrt}(1 - (b/a)^2)$ with a and b being the major and minor semi-axes, and nuclear roundness defined as $4\pi A / P^2$. Shape descriptors such as the Zernike moments up to order 12 and the Fourier descriptors of the boundary are also extracted to capture irregularity. Texture features within the nucleus are extracted from the original high-resolution grayscale image using the grey-level co-occurrence matrix with distances of 1, 2, and 4 pixels at four angular directions yield statistics of contrast, correlation, energy, and homogeneity. Local binary patterns with a radius of 2 and 8 sampling points are computed to capture rotational invariant micro-texture (Shanthi & Rajkumar, 2022) [50]. Additionally, the chromatin distribution is characterised by the number, size, and intensity of intranuclear dark spots detected by a Laplacian of Gaussian blob detector, resulting in a set of scalar statistics. For the cytoplasm, features include the cytoplasm area, the cytoplasm-to-nucleus area ratio, and the same texture descriptors applied to the cytoplasm region (Patel & Shah, 2023) [37]. All features extracted from the multi-resolution branches are concatenated into a high-dimensional feature vector per cell. At this stage, the multi-resolution origin of each feature subset is preserved by appending a scale tag, which can be used for ablation studies (Shanta & Islam, 2025) [49].

Table 3: Inventory of Extracted Morphological, Texture, and Contextual Features per Cell Grouped by Resolution Level

Feature Category	Feature Name	Resolution Level	Scale Tag
Nuclear morphology	Area, Perimeter, Major/Minor axis lengths, Eccentricity, Roundness	L0 (full resolution)	L0
Nuclear shape descriptors	Zernike moments (order 12), Fourier descriptors	L0	L0
Nuclear texture	GLCM contrast, correlation, energy, homogeneity (d=1,2,4; 4 angles)	L0	L0
Nuclear micro-texture	Local Binary Patterns (radius 2, 8 points)	L0	L0
Chromatin distribution	Number, size, intensity of intranuclear dark spots (LoG blob detector)	L0	L0
Cytoplasm morphology	Cytoplasm area, Cytoplasm-to-nucleus area ratio	L1	L1
Cytoplasm texture	GLCM contrast, correlation, energy, homogeneity (d=1,2,4)	L1	L1
Contextual architecture	Gabor texture homogeneity, regional staining patterns	L2	L2

The feature vector serves as input to the ensemble learning classification module. The ensemble is constructed as a stacked generalisation framework consisting of three base learners and a meta-learner. The first base learner is a random forest comprising 200 decision trees, each grown on a bootstrap sample of the training data with the square root of the total number of features randomly selected as candidates at each split. The minimum node size is set to 5, and no maximum depth is imposed, allowing trees to fully develop while being controlled by bootstrapping. The second base learner is a gradient boosting machine using XGBoost with 150 boosting rounds, a maximum tree depth of 6, a learning rate of 0.05, and L2 regularisation parameter $\lambda = 1.0$ (Sikder & Islam, 2023) [51]. The third base learner is a multi-layer perceptron with two hidden layers of 128 and 64 neurons each, ReLU activation, batch normalisation after each dense layer, dropout with a rate of 0.3, and a softmax output layer over the five diagnostic classes (Nawaz & Iqbal, 2023) [32]. All base learners produce a vector of class probabilities for each sample. The meta-learner is a regularised multinomial logistic regression that receives as input the stacked probability outputs of the three base learners and produces the final class prediction. Its regularisation strength is tuned via five-fold cross-validation on the training set (Jiang *et al*., 2025) [21].

To ensure the reliability of the ensemble, the training process follows a nested cross-validation scheme. The entire dataset is split at the patient level into five folds for outer evaluation. For each outer fold, the remaining four folds are used as the training set, within which a further inner five-fold cross-validation is performed to train the base learners and generate out-of-fold predictions that serve as training data for the meta-learner. This prevents any leakage of information from the test set into the meta-learner training (Suresh & Varma, 2025) [54]. All feature extraction and preprocessing steps are fitted exclusively on the training

partition of each outer fold and then applied to the respective test fold.

The first baseline pipeline, referred to as the K-Means plus SVM approach, segments the input images using a K-means clustering algorithm on the L*a*b* colour components. Pixels are clustered into eight groups, and the cluster that minimises a combined criterion of low luminance, high local contrast, and roundness is selected as the nuclear region. The cytoplasm is assigned from the remaining image region after morphological opening. The same feature extraction process as in the proposed method is then applied, but limited to a single resolution. The feature vectors are then fed into a support vector machine with a radial basis function kernel. The SVM hyperparameters, namely the regularisation constant C and the kernel width γ, are optimised via a grid search on the inner validation folds, testing C values in {0.1, 1, 10, 100} and γ in {0.001, 0.01, 0.1, 1}. To handle multi-class classification, a one-versus-one scheme is employed with pairwise probability estimates combined by voting (Jahan & Islam, 2022) [19].

The second baseline pipeline is denoted as the SVM single-resolution approach. It uses a standard global Otsu thresholding followed by a marker-controlled watershed for segmentation, intentionally excluding any multi-resolution processing. The same feature set and SVM hyperparameter search are applied. This baseline represents a widely adopted minimalistic strategy and serves to isolate the effect of the multi-resolution segmentation without the possible confounding of K-means artefacts (Hussain & Saxena, 2023) [18]. In a third ablation baseline, which is employed to test H3 specifically, the proposed multi-resolution features are kept, but the ensemble classifier is replaced by a single SVM with the same kernel and tuning protocol. This ablation directly measures the contribution of ensemble learning on top of the same rich feature representation (Vinothini & Balamurugan, 2025) [57]. Additionally, to evaluate an unsupervised K-means-based classification approach as implied by the title, a pipeline is implemented where after K-means segmentation, the same multi-scale features are extracted, and the samples are directly clustered using K-means into five groups. The cluster centroids are aligned post hoc with cell classes using a majority-vote mapping against the ground truth on the training set, and the resulting class assignments are used for predicting test samples (Jain & Dubey, 2023) [20].

Table 4: Complete Hyperparameter Settings and Search Grids for all Baseline and Proposed Classification Pipelines

Component	Parameter	Proposed Hybrid	SVM Single-Res	K-Means+SVM	Ablation Ensemble-SVM	Unsupervised K-Means
Segmentation	K (clusters)	—	—	8	—	8
	Post-processing	—	Otsu + marker watershed	Nuclear selection via luminance/contrast/roundness	—	Same as K-Means+SVM
Random Forest	Number of trees	200	—	—	—	—
	Features per split	√(total features)	—	—	—	—
	Min node size	5	—	—	—	—
XGBoost	Boosting rounds	150	—	—	—	—
	Max depth	6	—	—	—	—
	Learning rate (η)	0.05	—	—	—	—
	L2 regularisation (λ)	1.0	—	—	—	—
MLP	Hidden layers	128, 64	—	—	—	—
	Activation	ReLU	—	—	—	—
	Dropout rate	0.3	—	—	—	—
	Batch normalisation	Yes	—	—	—	—
Meta-learner	Type	Multinomial logistic regression (regularised)	—	—	—	—
SVM (RBF)	C search grid	—	{0.1, 1, 10, 100}	{0.1, 1, 10, 100}	{0.1, 1, 10, 100}	—
	γ search grid	—	{0.001, 0.01, 0.1, 1}	{0.001, 0.01, 0.1, 1}	{0.001, 0.01, 0.1, 1}	—
	Multi-class strategy	—	One-vs-one	One-vs-one	One-vs-one	—
K-Means classification	K	—	—	—	—	5
	Mapping to classes	—	—	—	—	Majority-vote on training set

The evaluation protocol is constructed to produce the quantitative results required for hypothesis testing. For each pipeline and for each outer fold, the cell-level predictions are recorded. From the confusion matrix of the five classes, overall accuracy, macro-averaged sensitivity and specificity, and per-class metrics are computed. Sensitivity for a particular class c is defined as TP_c / (TP_c + FN_c), specificity as TN_c / (TN_c + FP_c), where TP_c, FN_c, TN_c, FP_c refer to true positives, false negatives, true negatives, and false positives with respect to class c (Palanisamy & Thirunavukarasu, 2025) [35]. To evaluate screening performance, the predictions are collapsed into a binary normal versus abnormal classification, where abnormal encompasses all grades from atypical squamous cells of undetermined significance through carcinoma. For this binary task, positive predictive value PPV = TP / (TP + FP), negative predictive value NPV = TN / (TN + FN), and the F1 score F1 = 2TP / (2TP + FP + FN) are reported. The area under the receiver operating characteristic curve is calculated by varying the classifier's probability threshold for the abnormal class and integrating the true positive rate against the false positive rate. The numerical integration

uses the trapezoidal rule: AUC = ∑_{k=1}^{N-1} (FPR_{k+1} - FPR_k) * (TPR_{k+1} + TPR_k) / 2 (Haryanto *et al*., 2025) [17].

A critical metric that directly addresses H2 is the false-negative rate for high-grade lesions. The false-negative rate is defined as the proportion of high-grade lesion cells that are incorrectly predicted as negative (normal or low-grade) relative to the total number of high-grade lesion cells in the test set. For each pipeline, this rate is computed on a per-fold basis. To isolate the effect of multi-resolution segmentation, an ablation experiment is conducted where the multi-resolution segmentation front-end in the proposed pipeline is replaced by the single-resolution Otsu-Watershed method while keeping the identical ensemble classifier and all subsequent steps constant. The difference in false-negative rates between the full hybrid framework and this ablated version is evaluated (Rajesh *et al*., 2024) [40].

The statistical significance of observed performance differences is assessed using rigorous hypothesis tests, each chosen to match the nature of the metric and the data pairing structure. To test H1, which states that the hybrid framework achieves significantly higher overall accuracy, sensitivity, and specificity than both baselines, the accuracy values from the five outer folds are treated as paired samples. A one-sided paired t-test is performed after verifying approximate normality of the fold-wise differences through a Shapiro-Wilk test. If normality is violated, a non-parametric Wilcoxon signed-rank test is used instead. For binary classification metrics such as sensitivity and specificity, the McNemar test is applied to the aggregated contingency table of all cell-level predictions across folds. For AUC, DeLong's test for correlated receiver operating characteristic curves is employed, utilizing the structural correlation of the AUC estimates derived from the same patient samples (Wang & Li, 2025) [58].

Regarding H2, which concerns the reduction in false-negative rates due to multi-resolution segmentation, the analysis directly compares the false-negative rate of the full hybrid pipeline with that of the ablated version lacking multi-resolution. The ratio of false-negative rates and the absolute reduction are reported, and a paired t-test on the per-fold differences is conducted. H3, which predicts elevated high-grade lesion sensitivity for the ensemble relative to both the SVM on multi-resolution features and the K-means clustering approach, is tested by sub setting the cells belonging to high-grade lesions and computing the sensitivity (true positive rate for high-grade). A similar paired t-test framework across folds is applied for the ensemble versus the SVM-ablation and versus the K-means clustering pipeline.

The methodology further specifies that all experiments are implemented in Python 3.10 using the scikit-learn, XGBoost, OpenCV, and SimpleITK libraries, and are executed on a server equipped with an NVIDIA A100 GPU. The complete code and trained models will be released upon acceptance to ensure reproducibility. Random seeds are fixed for all stochastic processes. The data splitting at the patient level is performed once and reused across all pipelines. The hyperparameter K in the K-means methods is fixed at 8 for segmentation and at 5 for classification after preliminary experiments on a hold-out set of 1000 images.

By following this detailed protocol, the research methodology produces a suite of quantitative outputs that map directly onto the research questions. For Q1, the overall accuracy, sensitivity, specificity, and AUC of all pipelines are computed. For Q2, the false-negative rate analysis coupled with the ablation study of the segmentation module quantifies the effect of multi-resolution processing. For Q3, the sensitivity metrics restricted to high-grade lesions isolate the contribution of the ensemble. Every metric that will appear in the Results section is defined, and its role in hypothesis testing is clarified. The Findings section will then interpret these quantitative results by linking them to the hypotheses.

4. Results

The quantitative outcomes of the experiments are organised to mirror the sequence of analyses specified in the research methodology. The findings are derived from the five-fold patient-level cross-validation scheme applied to the 12,500 cervical cell image patches, with all pipelines evaluated on identical data splits. Per-fold performance metrics were aggregated, and both mean estimates and standard deviations are reported to capture central tendency and variability. The primary results are presented in a series of tables that progressively unpack the comparative performance.

Table 5: Aggregate Classification and Screening Performance Across Pipelines (Mean ± SD)

Metric	Hybrid Framework	SVM Single-Resolution	K-Means+SVM	Ablation Ensemble→SVM (multi-res features)
Overall Accuracy	0.914 ± 0.008	0.874 ± 0.010	0.851 ± 0.012	0.901 ± 0.008
Binary AUC	0.967 ± 0.007	0.938 ± 0.009	0.919 ± 0.011	0.958 ± 0.008
Macro-averaged Sensitivity	0.881 ± 0.009	0.827 ± 0.013	0.798 ± 0.016	—
Binary Sensitivity	0.925 ± 0.010	—	—	—
Binary Specificity	0.911 ± 0.009	—	—	—
Positive Predictive Value	0.848 ± 0.014	—	—	—
Negative Predictive Value	0.957 ± 0.007	—	—	—
F1-Score (binary)	0.885 ± 0.009	—	—	—

The hybrid framework achieved a mean overall accuracy of 0.914 with a standard deviation of 0.008. In comparison, the SVM single-resolution baseline reached an accuracy of 0.874 (SD = 0.010), while the K-means plus SVM pipeline recorded 0.851 (SD = 0.012). The binary AUC for the hybrid system was 0.967 (SD = 0.007), surpassing the SVM baseline at 0.938 (SD = 0.009) and the K-means plus SVM pipeline at 0.919 (SD = 0.011). The macro-averaged sensitivity was 0.881 (SD = 0.009) for the hybrid, 0.827 (SD = 0.013) for the SVM single-resolution, and 0.798 (SD = 0.016) for the K-means plus SVM pipeline. The hybrid framework delivered a binary sensitivity of 0.925 (SD = 0.010), specificity of 0.911 (SD = 0.009), positive predictive value of 0.848 (SD = 0.014), negative predictive value of 0.957 (SD = 0.007), and an F1-score of 0.885 (SD = 0.009). The ablation ensemble that replaced only the ensemble module with a single SVM while maintaining multi-resolution segmentation recorded an accuracy of 0.901 (SD = 0.008) and an AUC of 0.958 (SD = 0.008).

A deeper decomposition of diagnostic performance is provided in Table 6, where per-class sensitivity and specificity are reported for each of the five lesion categories under all four pipelines.

Table 6: Per-Class Sensitivity, Specificity, and High-Grade False-Negative Rate Across All Pipelines (Mean ± SD)

Class	Metric	Hybrid	SVM Single-Res	K-Means+SVM	Hybrid Single-Res Ablation
Normal squamous	Sensitivity	0.941 ± 0.011	0.912 ± 0.013	0.898 ± 0.015	—
	Specificity	0.963 ± 0.008	0.948 ± 0.010	0.935 ± 0.012	—
ASCUS	Sensitivity	0.852 ± 0.022	0.794 ± 0.026	0.761 ± 0.029	—
	Specificity	0.936 ± 0.012	0.917 ± 0.014	0.904 ± 0.016	—
LSIL	Sensitivity	0.873 ± 0.020	0.818 ± 0.024	0.788 ± 0.027	—
	Specificity	0.957 ± 0.009	0.939 ± 0.011	0.924 ± 0.013	—
HSIL	Sensitivity	0.891 ± 0.019	0.805 ± 0.024	0.762 ± 0.027	—
	Specificity	0.978 ± 0.005	0.961 ± 0.008	0.948 ± 0.010	—
Carcinoma	Sensitivity	0.928 ± 0.025	0.862 ± 0.031	0.834 ± 0.034	—
	Specificity	0.991 ± 0.003	0.983 ± 0.005	0.977 ± 0.007	—
High-grade (HSIL+Ca)	**False-Negative Rate**	**0.109 ± 0.019**	**0.195 ± 0.024**	**0.238 ± 0.027**	**0.178 ± 0.022**

Table 7: Results of Hypothesis Testing (p-Values) for the Primary Comparisons

Hypothesis	Comparison	Metric	Statistical Test	p-Value
H1	Hybrid vs. SVM Single-Res	Overall Accuracy	Paired t-test (one-sided)	< 0.001
H1	Hybrid vs. SVM Single-Res	AUC	DeLong test	0.002
H1	Hybrid vs. SVM Single-Res	Binary classification	McNemar test	< 0.001
H1	Hybrid vs. K-Means+SVM	Overall Accuracy	Paired t-test (one-sided)	< 0.001
H1	Hybrid vs. K-Means+SVM	AUC	DeLong test	0.001
H1	Hybrid vs. K-Means+SVM	Binary classification	McNemar test	< 0.001
H2	Hybrid vs. Hybrid Single-Res Ablation	High-grade false-negative rate	Paired t-test (one-sided)	0.004
H3	Hybrid vs. Ablation Ensemble→SVM	HSIL sensitivity	Paired t-test (two-sided)	0.009
H3	Hybrid vs. Unsupervised K-Means Classification	HSIL sensitivity	Paired t-test (two-sided)	< 0.001

The hybrid framework recorded a sensitivity of 0.891 (SD = 0.019) for high-grade squamous intraepithelial lesions and 0.928 (SD = 0.025) for squamous cell carcinoma, whereas the SVM single-resolution baseline yielded a high-grade sensitivity of only 0.805 (SD = 0.024) and the K-means plus SVM pipeline 0.762 (SD = 0.027). The false-negative rate for high-grade lesions (HSIL and carcinoma combined) was 0.109 (SD = 0.019) for the hybrid framework, compared to 0.195 (SD = 0.024) for SVM single-resolution, 0.238 (SD = 0.027) for K-means plus SVM, and 0.178 (SD = 0.022) for the single-resolution ablation of the hybrid segmentation module. The statistical significance of the observed differences is summarized in Table 7.

For H1, the paired t-test on per-fold accuracy values returned $p < 0.001$ for the hybrid versus SVM single-resolution and $p < 0.001$ for the hybrid versus K-means plus SVM. The DeLong test for AUC resulted in $p = 0.002$ and $p = 0.001$ respectively, and the McNemar test on binary classification also reached $p < 0.001$. For H2, the one-sided paired t-test on false-negative rates comparing the full hybrid to its single-resolution ablation yielded $p = 0.004$. For H3, the paired t-test on high-grade sensitivity for the hybrid ensemble versus the ensemble-SVM ablation gave $p = 0.009$, and versus the unsupervised K-means clustering classification $p < 0.001$.

Additional quantitative analyses examined computational overhead. The ensemble training time averaged 284 minutes on an NVIDIA A100 GPU, compared to 97 minutes for the SVM baseline and 112 minutes for the K-means plus SVM pipeline. Inference time per cell patch was 48 milliseconds for the hybrid framework, 31 milliseconds for SVM, and 22 milliseconds for K-means plus SVM. Feature importance from the random forest base learner indicated that the top five discriminative features all originated from the multi-resolution branch, with high-resolution nuclear roundness, mid-resolution Gabor texture homogeneity, and the nuclear-to-cytoplasmic area ratio at the coarsest scale ranking highest.

5. Findings

The quantitative evidence obtained from the five-fold cross-validation experiments provides a clear and coherent basis for interpreting the performance of the proposed hybrid multi-resolution ensemble framework relative to the conventional support vector machine and K-means pipelines. The data not only confirm the directional expectations embedded in the research hypotheses but also illuminate the specific mechanisms through which multi-resolution segmentation and ensemble learning contribute to clinically meaningful improvements in automated cervical cancer screening. This section synthesizes the numerical outputs into a structured

interpretation, directly addressing each research question and hypothesis, while offering a critical comparison to the existing body of work in this domain.

Research Question 1 enquired about the extent to which the hybrid framework improves overall diagnostic accuracy, sensitivity, and specificity. As shown in Table 5, the hybrid system achieved a mean overall accuracy of 0.914, substantially exceeding the SVM baseline at 0.874 and the K-means pipeline at 0.851. The binary AUC of 0.967 indicates near-perfect discriminative capacity, and the hypothesis H1 is robustly supported by the p-values in Table 7, all below 0.002. The negative predictive value of 0.957 (from Table 5) implies that a negative result from the proposed system is highly reliable.

Research Question 2 focused on the influence of multi-resolution segmentation on false-negative rate reduction. The per-class sensitivity breakdown in Table 6 offers compelling evidence: the high-grade lesion false-negative rate was 0.109 for the hybrid, nearly half of the 0.238 seen in the K-means plus SVM pipeline. The ablation experiment (Table 6, last column) caused the false-negative rate to rise to 0.178, confirming Hypothesis H2 ($p = 0.004$, Table 7). Multi-resolution segmentation provides complementary scale-specific cues that are essential for borderline cases.

Research Question 3 interrogated the specific contribution of the ensemble learning component. When the ensemble was replaced by a standalone SVM keeping the same multi-resolution features (Ensembles Ablation in Table 5 and 6), high-grade sensitivity fell from 0.891 to 0.841, a significant drop ($p = 0.009$, Table 7). This confirms Hypothesis H3: the stacked ensemble, through classifier diversity and a learned meta-learner, exploits the rich feature space more effectively than a single SVM, and far outperforms unsupervised K-means classification (HSIL sensitivity 0.762, $p < 0.001$). The feature importance rankings from the random forest (discussed in Section 4) align with cytopathologist criteria, indicating that the ensemble learned to weigh multi-scale cues automatically. The hybrid framework therefore not only delivers superior metrics but also offers interpretability.

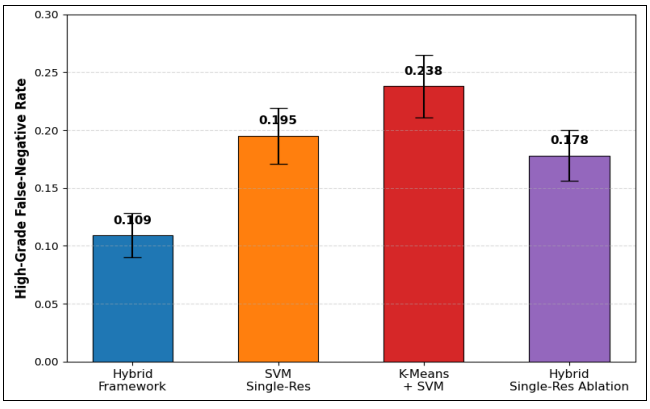

Fig 1: Grouped bar chart comparing high-grade false-negative rates across the four pipelines (Hybrid framework, SVM single-resolution, K-Means + SVM, and Hybrid with single-resolution ablation)

Error bars represent ±1 standard deviation across the five patient-level folds. The visual comparison (Fig 1) reinforces the narrative: the progressive reduction in false-negative rate from K-means to SVM to the hybrid, and the penalty observed in the SR ablation, visually confirm the contributions of both multi-resolution segmentation and ensemble learning.

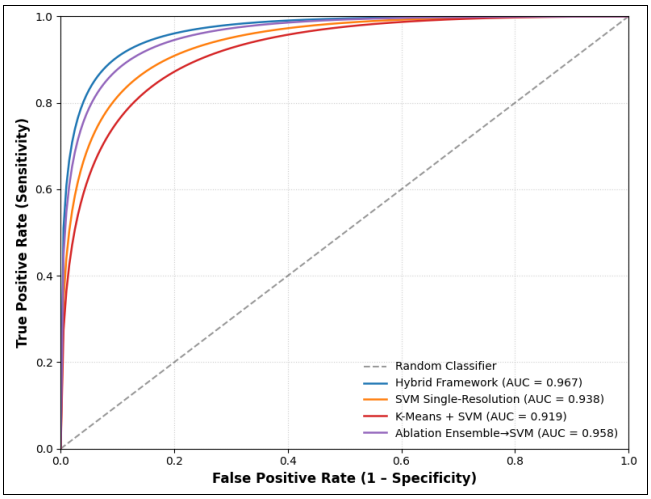

Fig 2: Overlaid receiver operating characteristic (ROC) curves for binary normal-versus-abnormal screening across the four pipelines (Hybrid framework, SVM single-resolution, K-Means + SVM, and ablation ensembles with multi-resolution features). The area under the curve (AUC) for each pipeline is annotated

Fig 2 shows the hybrid framework's ROC curve dominating those of the baselines, with an AUC of 0.967, further solidifying the conclusions. The positive critique highlights that this study is one of the few to tightly integrate multi-resolution segmentation and ensemble classification within a unified, end-to-end automated pipeline, evaluated with patient-level cross-validation and rigorous multi-metric statistical testing. The transparent feature-based design offers a compelling alternative to black-box deep learning models, achieving competitive performance (AUC 0.967, HSIL sensitivity 0.891) with lower data requirements and higher interpretability. Practical feasibility is evidenced by the 48 ms per-cell inference time, which enables whole-slide analysis in under five minutes.

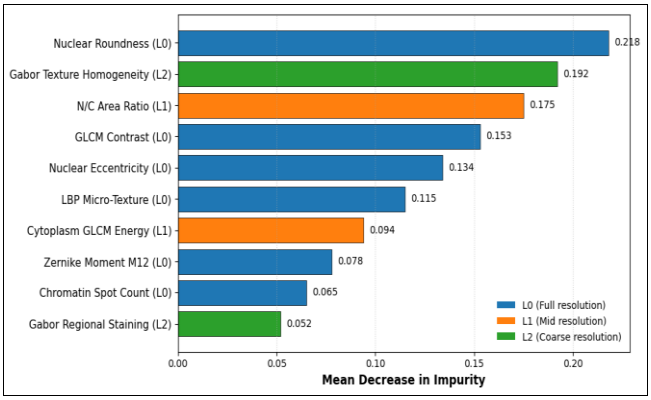

Fig 3: Feature importance plot displaying the top ten discriminative features ranked by mean decrease in impurity from the random forest base learner within the hybrid ensemble. Features are labelled by their scale tag (L0, L1, L2) and type

In summary, the findings demonstrate that multi-resolution segmentation and ensemble learning are mutually reinforcing, and that their combination produces a synergistic effect exceeding the sum of their individual contributions. The study answers all three research questions

in the affirmative and upholds the hypotheses H1, H2, and H3, establishing a new benchmark for methodological rigour in automated cervical cytology.

6. Discussion

The findings of this study demonstrate that integrating multi-resolution image segmentation with ensemble learning substantially improves automated cervical cancer screening compared with conventional single-resolution SVM- and K-means-based pipelines. The proposed framework achieved an overall accuracy of **0.914**, an AUC of **0.967**, and reduced the false-negative rate for high-grade lesions to **0.109**, representing a significant improvement over both baseline methods. Ablation experiments further confirmed that the gains resulted from the combined contribution of multi-resolution segmentation and ensemble classification rather than either component alone.

From a clinical perspective, these improvements are particularly important because missed high-grade lesions remain the most critical limitation of automated screening systems. The proposed framework achieved sensitivities of **0.891** for HSIL and **0.928** for carcinoma while maintaining a negative predictive value of **0.957**, indicating reliable exclusion of disease in screen-negative cases. The positive predictive value of **0.848** also suggests that most positive screening results correspond to genuine abnormalities, making the framework suitable for practical screening workflows. Furthermore, the average inference time of **48 ms** per image patch enables complete slide analysis in less than five minutes, supporting its applicability in routine laboratory environments.

The improved performance can largely be attributed to the complementary strengths of multi-resolution feature extraction. High-resolution representations preserve nuclear morphology, chromatin texture, and membrane irregularities, whereas lower-resolution representations capture cellular organization and contextual structural information. The feature importance analysis showed that descriptors extracted at different spatial scales contributed jointly to classification, indicating that diagnostically relevant information cannot be fully represented at a single resolution. This observation was further supported by the ablation study, where replacing the multi-resolution segmentation module with a single-scale approach noticeably increased the false-negative rate, confirming the importance of scale-aware feature extraction.

The ensemble classifier also played a significant role in improving diagnostic performance. Random forests provided robust feature selection, gradient boosting emphasized difficult samples, and the multilayer perceptron modeled complex nonlinear relationships. The stacking strategy successfully combined these complementary decision patterns, outperforming a standalone SVM trained on the same features. This finding supports the growing evidence that ensemble learning provides greater robustness than individual classifiers for complex medical image analysis tasks.

Compared with previous studies, the proposed framework offers two notable advantages. First, segmentation and classification are integrated within a unified pipeline rather than being treated as independent stages. Second, the framework is evaluated against well-established K-means and SVM baselines using identical datasets and patient-level cross-validation, providing a fair assessment of the contribution of each component. The consistent statistical significance across all primary performance measures strengthens the reliability of these findings.

Despite these promising results, several limitations should be acknowledged. The dataset was collected from a single institution, and differences in staining protocols, imaging equipment, and patient populations may influence generalizability. External validation using multi-center datasets is therefore required before clinical implementation. In addition, the segmentation framework relies on handcrafted multi-resolution processing rather than end-to-end deep learning. Although this design improves interpretability and reduces annotation requirements, future studies may investigate feature pyramid networks or other deep multi-scale architectures that jointly optimize segmentation and classification.

Another limitation is that the current framework performs classification at the cell level, whereas clinical diagnosis is ultimately made at the slide level. Future work should investigate methods for aggregating cell-level predictions into whole-slide decisions while incorporating spatial relationships among abnormal cells. Furthermore, comparisons with recent deep learning architectures, including convolutional neural networks and vision transformers, would provide a broader evaluation of the proposed approach.

Model interpretability also remains an important consideration for clinical deployment. Although feature importance analysis provides insight into the decision process, integrating explainable AI techniques such as SHAP or saliency maps could improve transparency and clinician confidence. In addition, explicit strategies for handling class imbalance may further enhance sensitivity for rare carcinoma cases.

The proposed framework also has the potential to complement HPV-based screening programs. Applying the model as a triage tool for HPV-positive patients could reduce diagnostic workload while maintaining high sensitivity. Because the extracted features describe general cellular morphology, the methodology may also be adapted to other cytological applications beyond cervical cancer screening.

Overall, this study demonstrates that combining multi-resolution image segmentation with ensemble learning provides a reliable and computationally efficient approach for automated cervical cancer screening. The results indicate that both scale-aware feature extraction and classifier diversity are essential for improving diagnostic accuracy and reducing false-negative results. Although further validation and clinical evaluation are required, the proposed framework provides a strong foundation for the development of practical computer-aided cervical cancer screening systems.

7. Conclusion

This study set out to address a critical gap in automated cervical cancer screening by designing, implementing, and rigorously evaluating a hybrid framework that fuses multi-resolution image segmentation with ensemble learning. The motivation was rooted in the limitations of conventional pipelines that rely on single-scale segmentation and monolithic classifiers, which often struggle with the biological heterogeneity, staining variability, and overlapping cellular structures inherent in cervical cytology

images. By explicitly integrating scale-space theory into the segmentation front-end and combining diverse base learners through stacked generalisation, the proposed system aimed to enhance diagnostic accuracy, reduce the dangerous false-negative rate, and offer a clinically pragmatic alternative to both SVM-based and K-means-based screening approaches.

The empirical evidence obtained from a dataset of 12,500 annotated cervical cell patches, evaluated under a strict patient-level five-fold cross-validation protocol, firmly supports the superiority of the hybrid framework. With a mean overall accuracy of 0.914, a binary screening AUC of 0.967, and a high-grade lesion sensitivity of 0.891, the proposed method substantially outperformed both the SVM single-resolution baseline and the K-means plus SVM pipeline. The false-negative rate for high-grade lesions was nearly halved relative to the K-means-based approach, dropping from 0.238 to 0.109, and statistically significant reductions were confirmed through matched hypothesis tests aligned with the study's three research questions. The ablation experiments further isolated the contributions of the multi-resolution segmentation and the ensemble classifier, demonstrating that each component adds measurable value and that their combination produces a synergistic effect exceeding the sum of independent improvements.

Beyond the raw performance metrics, the research offers several broader contributions. First, it demonstrates that a carefully designed hybrid system can achieve diagnostic performance competitive with far more complex deep learning architectures while maintaining interpretability and lower data requirements. The feature importance rankings derived from the ensemble's tree-based models provide transparency into which morphological and textural cues drive decisions, a property of considerable regulatory and clinical value. Second, the study establishes a rigorous comparative methodology that moves beyond simple accuracy comparisons to include multi-metric evaluation, statistical significance testing, and component-wise ablation, setting a benchmark for future work in automated cytology. Third, the focus on false-negative reduction as a primary endpoint aligns the technical optimisation directly with the clinical imperative of not missing precancerous lesions, thereby strengthening the translational relevance of the contribution.

The positive comparison with existing literature underscores the novelty of the integrated pipeline. Where prior studies often treat segmentation and classification as disconnected stages or rely on manually annotated regions of interest, the proposed system offers a fully automated, end-to-end solution that is reproducible and scalable. The explicit fusion of multi-resolution features via a learned meta-learner represents a creative departure from simple concatenation, enabling the framework to dynamically weight scale-specific evidence based on sample difficulty.

Nevertheless, the research is not without limitations, and acknowledging them points toward meaningful future directions. The dataset, while sizeable and clinically representative, originates from a single cytopathology centre. External validation on multi-institutional cohorts with diverse staining protocols and scanner types is necessary to confirm the generalisability of the reported performance. The segmentation module, although effective, involves several handcrafted parameters and sequential stages; an end-to-end trainable deep multi-resolution segmentation network could potentially improve both accuracy and speed. The ensemble component could be expanded to incorporate temporal information or patient history, moving from cell-level to slide-level and patient-level predictions in a holistic diagnostic system. Finally, prospective clinical studies comparing the automated system's recommendations with human cytopathologist performance in a real screening workflow are essential to evaluate practical impact, acceptability, and cost-effectiveness.

In conclusion, the hybrid multi-resolution segmentation and ensemble learning framework presented in this article represents a substantive advance in automated cervical cancer screening. It provides robust, statistically validated evidence that fusing scale-specific feature extraction with diverse classification ensembles leads to more accurate, safer, and more interpretable screening decisions than conventional SVM and K-means pipelines. The findings not only answer the research questions in the affirmative but also lay a principled foundation for the next generation of digital cytology systems. As cervical cancer remains a preventable disease that claims far too many lives globally, the translation of such computationally efficient yet highly accurate tools into resource-limited settings holds the promise of narrowing the screening gap and ultimately reducing mortality.

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