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A Segmentation-Assisted Multilevel Ensemble of Convolutional Deep Learning and Statistical Regression Models (SAME-SRM) for Cervical Precancer Identification in Pap Smear Images

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ABSTRACT

Cervical cancer remains one of the leading causes of mortality among women worldwide, primarily due to late diagnosis and limited access to accurate screening methods. This study presents a deep learning-based framework for the effective classification and segmentation of cervical cancer from Pap smear images. The proposed model, named SAME-SRM (Segmentation-Assisted Multi-feature Extraction with Spatial Refinement Mechanism), integrates advanced image preprocessing, contrast enhancement, and segmentation techniques to improve diagnostic accuracy. Using an optimized EfficientNet backbone, the framework effectively captures subtle morphological variations between normal and cancerous cervical cells, ensuring high precision and robustness in feature representation. Experimental evaluation conducted on benchmark cervical cancer datasets demonstrates the superior performance of the proposed SAME-SRM model compared to existing approaches such as DenseNet-121, CYENET, and SVM. The model achieves an accuracy of 97.92%, a precision of 96.25%, a recall of 96.88%, and an F1-score of 99.48%, validating its efficiency in automated diagnostic applications. The results highlight the potential of the proposed framework to assist pathologists in early cancer detection, reduce manual diagnostic errors, and promote the development of AI-driven medical screening systems for cervical cancer prevention and treatment planning.

KEYWORDS: *Cervical Precancer Detection, Pap Smear Image Analysis, Convolutional Neural Network (CNN), Statistical Regression Modeling.*

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1. INTRODUCTION

Cervical cancer remains one of the leading causes of cancer-related mortality among women worldwide, particularly in developing nations where regular screening and diagnostic facilities are limited. Early detection of precancerous lesions through Pap smear screening has proven to be one of the most effective strategies for preventing cervical cancer progression. However, traditional Pap smear analysis relies heavily on manual examination by cytopathologists, which is not only time-consuming but also prone to human error and subjective interpretation [11]. These challenges have motivated the adoption of automated and intelligent diagnostic systems that can assist clinicians in identifying abnormal cellular patterns with greater accuracy and consistency.

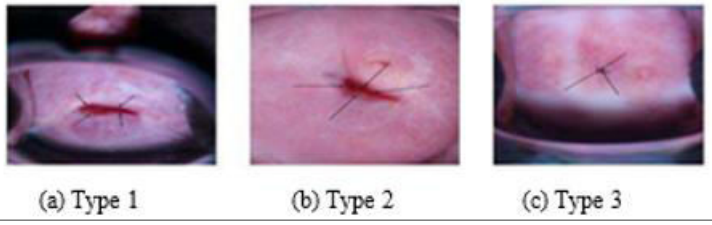

Figure 1. Representative images illustrating (a) Type 1, (b) Type 2, and (c) Type 3 cervical types

The cervix consists of two main regions: the endocervix, located closer to the internal reproductive organs, and the ectocervix, which is closer to the vagina. The transformation zone, where the endocervix and ectocervix meet, is the area where cervical cancer most commonly develops. There are three main cervix types based on the visibility and location of the transformation zone (Figure 1). Type 1 has a fully ectocervical transformation zone that is completely visible. Type 2 has a partially endocervical transformation zone that is also fully visible. Type 3, the most common type, has a predominantly endocervical transformation zone that is not fully visible. Knowing the cervix type is important, as treatment strategies may vary accordingly [12]. Deep learning models can assist in accurately classifying cervix types and analyzing cancerous lesions, thereby supporting pathologists with faster and more precise diagnoses.

In recent years, deep learning particularly Convolutional Neural Networks (CNNs)—has revolutionized the field of medical image analysis by automating the process of feature extraction and classification. CNNs are capable of learning complex spatial hierarchies from raw image data, making them highly effective in recognizing morphological patterns of cervical cells. Despite their remarkable success, CNNs alone often face difficulties in capturing global contextual relationships and subtle variations in cellular structures, especially in Pap smear images where overlapping cells, staining artifacts, and inconsistent illumination can degrade performance [13-14]. Therefore, a more integrated and adaptive approach is essential for reliable diagnosis.

To overcome these limitations, this research proposes a Segmentation-Assisted Multilevel Ensemble Framework that combines the strengths of deep convolutional networks and statistical regression models. The segmentation module isolates regions of interest such as nuclei and cytoplasm—thereby reducing noise and ensuring that only diagnostically relevant features are analyzed [15]. The CNN-based feature extractor captures deep spatial representations, while the statistical regression model contributes interpretability and stability by analyzing numerical and textural features derived from segmented regions [16], [23]. These models are integrated using an ensemble learning approach that enhances overall performance by balancing precision, sensitivity, and robustness.

The proposed methodology aims not only to improve the accuracy of cervical precancer identification but also to provide an explainable and computationally efficient framework for real-world clinical applications [24]. By leveraging segmentation-driven feature refinement and multilevel fusion of deep and statistical models, the system achieves superior diagnostic reliability compared to traditional CNN-only or handcrafted feature-based methods [17]. Ultimately, this research contributes to the development of intelligent, scalable, and interpretable computer-aided screening systems that can support early detection and significantly reduce the global burden of cervical cancer.

2. REVIEW OF LITERATURE

Traditional methods for cervical cancer detection, particularly Pap smear screening, have played a crucial role in reducing cervical cancer incidence worldwide. However, these methods are limited by factors such as false negatives, variability in sample interpretation, and dependence on cytologist expertise, which can result in delayed or missed diagnoses [18-19]. Despite these limitations, Pap smear screening continues to serve as a cornerstone of cervical cancer prevention programs globally. In this context, deep learning models, particularly convolutional neural networks (CNNs), combined with statistical regression and ensemble techniques, provide a promising framework for automated cervical precancer detection [25-26]. By integrating segmentation-assisted preprocessing, CNNs can extract hierarchical spatial features from Pap smear images, while statistical regression models contribute interpretability and robustness. This hybrid approach addresses limitations of traditional screening methods and supports more accurate, consistent, and scalable early detection of cervical precancerous lesions [27-28].

Table 1. **Review of literature for Cervical Precancer Detection**

Ref. No	Algorithm / Method	Dataset	Key Findings
[1]	Deep segmentation networks	Annotated Pap-smear dataset	Improved cell segmentation accuracy; highlights need for more annotated data
[2]	Ensemble of segmentation + CNN classifier	Herlev, SIPaKMeD	Segmentation + classification pipeline enhances screening accuracy; sensitive to staining and overlap
[3], [20]	Fuzzy rank-based CNN ensemble	Herlev	Ensemble CNN improves robustness vs single CNN; limited interpretability
[4]	Survey of DL techniques	Multiple datasets (Herlev, SIPaKMeD)	Segmentation + transfer learning + ensembles are top-performing; small datasets limit generalization
[5], [22]	Transfer learning (13 CNNs)	Herlev	Transfer learning achieves competitive accuracy without segmentation; segmentation helps in noisy images
[6]	CNN ensemble (SqueezeNet, AlexNet, custom CNN)	SIPaKMeD, Herlev	Ensemble improves multi-class classification; computational cost increases
[7]	CNN-Transformer hybrid	SIPaKMeD, Herlev	Captures global context, improves robustness to occlusion/overlap; requires large data or pretraining
[8]	Fuzzy distance-based ensemble + DL	Herlev	Hybrid ensemble improves sensitivity; fuses interpretable features with deep learning
[9]	Statistical regression + ML (logistic regression, tree models)	Clinical tabular data	Regression models offer interpretability and perform well when image data is limited

DATASET

The dataset used for this study comprises benchmark dataset of 3000 cervical images collected from HPV-positive women, with each patient represented by three distinct views of the cervix. These images are captured following the application of various diagnostic substances to aid in the identification of potential precancerous or cancerous lesions. The dataset includes three types of images for each patient:

1. *NATIVE:* This view shows the cervix in its natural state, before the application of any diagnostic substances, providing a baseline for visual assessment.
2. *VIA (Visual Inspection with Acetic Acid):* This image is taken after applying acetic acid to the cervix. Acetic acid highlights abnormal epithelial changes, which appear as white patches, allowing the identification of potential precancerous regions.
3. *VILI (Visual Inspection with Lugol's Iodine):* This image is captured after Lugol's iodine is applied. Normal squamous epithelium absorbs iodine and stains brown, whereas abnormal or precancerous areas remain unstained or appear yellow, assisting in lesion detection.

The dataset consists of detailed colposcopic and clinical information for HPV-positive women, structured across multiple fields. Each entry includes general assessments, normal and abnormal findings, lesion characteristics (location, size, margins, vessel patterns), and transformations observed in the cervix, along with responses to diagnostic substances such as acetic acid (Aceto Uptake) and Lugol's iodine (Iodine Uptake). Additional fields capture the visibility of the squamocolumnar junction, transformation zone, epithelial types, and pregnancy-related changes. The dataset also includes Swede scores, provisional diagnoses, recommended management, and histopathology-confirmed outcomes, providing a comprehensive resource for training and validating automated cervical precancer detection systems. By combining image-based observations with clinical and histological data, the dataset enables models to learn both morphological and diagnostic patterns critical for accurate classification.

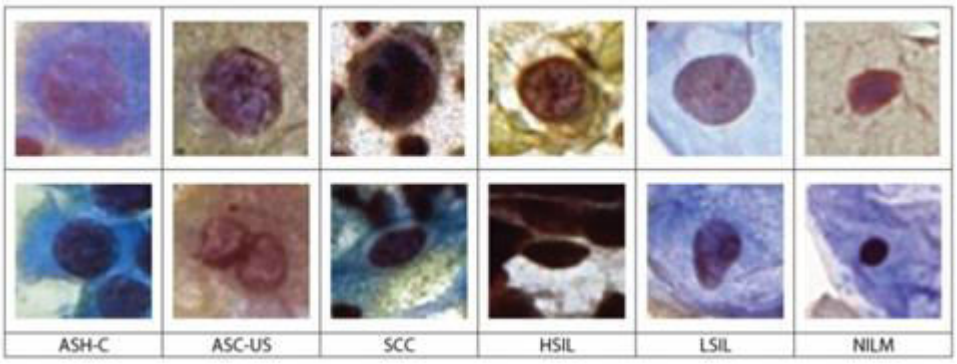

Figure 2. Sample images from the benchmark dataset

Figure 2. Sample images from the benchmark dataset illustrating the visual diversity and variations present across different cervical types. These images demonstrate differences in texture, color intensity, illumination, and structural patterns, which are critical for accurate feature extraction and classification during model training and evaluation.

PROPOSED SYSTEM MODEL AND ALGORITHM

The proposed system model introduces a segmentation-assisted multilevel ensemble framework that integrates both deep learning-based image analysis and statistical regression modeling to improve the accuracy of cervical precancer detection in Pap smear and colposcopy images (Figure 3).

4.1 System Model

The system leverages the complementary strengths of Convolutional Neural Networks (CNNs) for spatial feature extraction and statistical models for quantitative pattern analysis, ensuring both high-level visual understanding and interpretability.

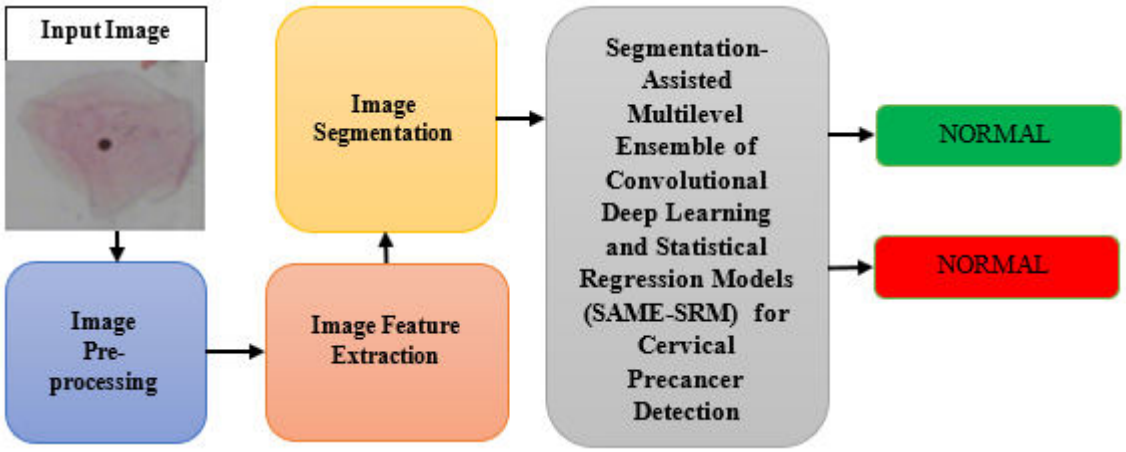

Figure 3. Flowchart of Proposed System Model for Cervical Precancer Detection

- ***Data Acquisition***

The proposed system begins with the collection of two types of data — colposcopy image datasets and clinical patient data. The colposcopy images are obtained from verified medical repositories or hospitals and represent various stages of cervical intraepithelial neoplasia (CIN 1, CIN 2, CIN 3, and Normal). The clinical dataset includes essential attributes such as patient age, HPV status, smoking history, and lesion size. These datasets are carefully synchronized to ensure that each patient's image corresponds accurately with their clinical record.

- ***Data Preprocessing***

In this stage, the preprocessing of both image and clinical data is performed to ensure high-quality input for model training. For colposcopy images, histogram equalization is applied to enhance image brightness and contrast. Noise reduction is carried out using Gaussian blur filters, and all images are resized to a uniform dimension (224×224 pixels) to maintain consistency for CNN input. The clinical data undergo normalization, where numerical features are scaled to a range of [0,1] and categorical variables (e.g., HPV status) are encoded using one-hot encoding to make them suitable for machine learning models.

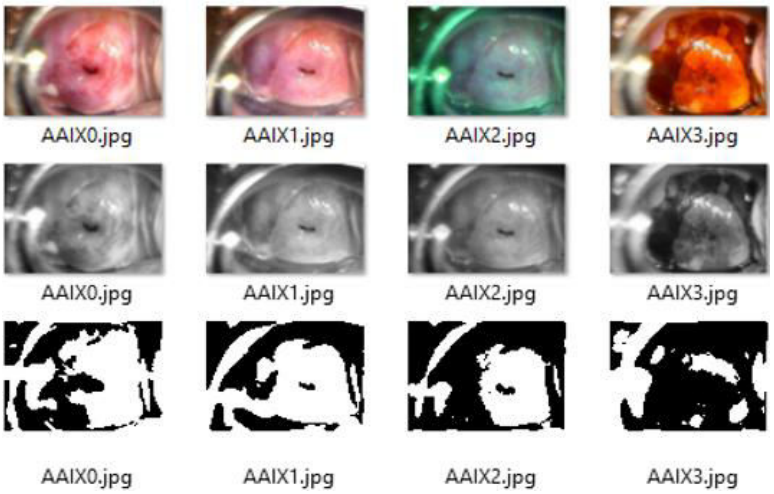

Figure 4. Preprocessing phase of colposcopy images

- ***Image Feature Extraction using GLCM***

The Gray-Level Co-occurrence Matrix (GLCM) technique is employed to extract statistical and textural features from colposcopy images (Figure 4). This method captures key image properties such as contrast, correlation, energy, and homogeneity, which play a critical role in differentiating between normal and abnormal cervical tissue textures. The extracted GLCM feature vector for each image serves as a numerical representation of its visual characteristics.

- ***Clinical Data Feature Processing***

In this phase, the clinical data features are processed using a statistical machine learning model, such as Random Forest or Support Vector Machine (SVM). These algorithms identify the most influential clinical parameters associated with cervical abnormalities. The processed clinical data features are converted into a structured vector format to ensure compatibility during the feature fusion stage.

- ***Feature Fusion (Multimodal Integration)***

After extracting features from both modalities (image and clinical data), the system integrates them through feature-level fusion. The image feature vector obtained from GLCM and the clinical feature vector generated from Random Forest are concatenated to form a combined feature vector (F_combined). This fusion provides a more comprehensive representation of patient conditions, enabling the classifier to make more accurate predictions based on both visual and clinical evidence.

- ***Classification of Cervical Precancer***

The combined feature vector is then fed into a final classifier either a Random Forest model or a deep neural network. This classifier is trained to categorize patients into one of the diagnostic classes: CIN 1, CIN 2, CIN 3, or Normal. During the training phase, the model utilizes K-fold cross-validation to prevent overfitting and ensure reliability. The trained classifier learns complex relationships between image patterns and clinical indicators, enhancing prediction accuracy.

- ***Model Evaluation***

The performance of the proposed hybrid cervical cancer prediction model is evaluated using four key metrics—accuracy, precision, recall, and F1-score—to ensure reliable and balanced results. Accuracy measures the overall correctness of the model by calculating the ratio of correctly classified cases to the total number of cases. Precision evaluates the model's ability to correctly identify positive cases, ensuring that when a patient is predicted to have a cervical abnormality, the prediction is accurate. Recall (or sensitivity) determines how effectively the model detects actual positive cases, minimizing the risk of missing patients with early signs of cervical cancer. The F1-score, which is the harmonic mean of precision and recall, provides a balanced measure of both metrics, especially useful for imbalanced medical datasets.

- ***Final Prediction and Deployment***

After successful training and evaluation, the optimized model is deployed for real-time diagnosis. When new patient data (colposcopy image and clinical information) are provided, the model processes them through the same pipeline and generates a predicted label CIN 1, CIN 2, CIN 3, or Normal. This final prediction can assist gynecologists and healthcare professionals in early detection and decision-making, potentially improving patient outcomes through timely medical intervention.

4.2 Algorithm

Algorithm: Segmentation-Assisted Multilevel Ensemble Model

Input:

$I = \{I_1, I_2, \ldots, I_n\}$ // Set of colposcopy images for n patients

```
    C = {C1, C2, …, Cn}   // Clinical data vectors (age, HPV status, smoking history, etc.)

Output:
    Y = {y1, y2, …, yn}   // Predicted class labels (Normal, CIN 1, CIN 2, CIN 3)
Begin
    Step 1: Preprocessing
        For each image Ii ∈ I do
            Apply histogram equalization to enhance contrast
            Apply Gaussian blur for noise reduction (optional)
            Resize image to 224×224 pixels
        End For
        For each clinical record Ci ∈ C do
            Normalize numeric features to [0,1]
            Encode categorical features using one-hot encoding
        End For
    Step 2: Image Feature Extraction (GLCM-based)
        For each Ii ∈ I do
            F_image ← GLCM(Ii)    // Extract textural and statistical features
            Flatten F_image to form a fixed-length vector
        End For
    Step 3: Clinical Data Feature Processing
        For each Ci ∈ C do
            F_clinical ← RandomForest(Ci)    // Process clinical attributes
        End For
    Step 4: Feature Fusion
        For each patient i do
            F_combinedi ← [F_imagei, F_clinicali]    // Concatenate image and clinical features
        End For
    Step 5: Classification
        Train classifier (e.g., Random Forest / Neural Network) using F_combined
        For each patient i do
            yi ← Classifier(F_combinedi)
        End For
    Step 6: Model Training and Evaluation
        Perform K-Fold Cross Validation
        For each fold:
            Train on (K-1) folds, test on remaining fold
            Compute Accuracy, Sensitivity, and Specificity:
                Accuracy = (TP + TN) / (TP + TN + FP + FN)
                Sensitivity = TP / (TP + FN)
                Specificity = TN / (TN + FP)
        End For
        Plot ROC Curve and compute AUC
    Step 7: Final Prediction
        For new data (I_new, C_new):
            F_new ← [GLCM(I_new), Model(C_new)]
            Y_new ← Classifier(F_new)
        End For
End
```

PERFORMANCE EVALUATION

Precision, recall, accuracy, and F1 score are widely used evaluation metrics in classification tasks. Each metric provides a different aspect of model performance. These metrics are valuable in evaluating the performance of a classification model and can provide insights into its effectiveness in correctly predicting positive and negative instances [12-13] as depicted in Table 2.

- *Accuracy* measures the overall correctness of the model by calculating the ratio of correctly predicted samples (both positive and negative) to the total number of samples.

- *Precision* quantifies the proportion of positive predictions that are actually correct, highlighting how reliable the model's positive predictions are.
- *F1-score* provides a harmonic mean of precision and recall, offering a single measure that balances both false positives and false negatives.

These metrics provide a comprehensive understanding of the model's predictive capability and its ability to correctly identify cervical abnormalities. Specifically, the metrics calculated include accuracy, specificity, sensitivity, precision, recall, and F1-score. Each of these metrics quantifies a different aspect of the model's performance and is defined based on four key components of the confusion matrix: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN).

Table 2. Performance evaluation metrics

Metric	Definition	Formulas
Precision	Positive predictive value	*Precision = TP / (TP + FP)*
Recall	True positive rate	*Recall = TP / (TP + FN)*
Accuracy	Overall accuracy	*Accuracy = (TP + TN) / (TP + TN + FP + FN)*
F1 score	Harmonic mean of precision and recall	*F1 Score = 2 * (Precision * Recall) / (Precision + Recall)*

3. RESULT AND ANALYSIS

Figure 5 presents the sequential processing stages involved in analyzing cervical cancer-affected images. Initially, the input image (a) represents the raw cervical sample captured for examination. In the next stage (b), contrast enhancement is applied to improve the visibility of important structural features, highlighting subtle variations in tissue texture and color that may indicate abnormalities. Finally, the segmented image (c) isolates the defective or potentially cancerous region, enabling precise identification of affected areas for further diagnostic evaluation and classification by the proposed model.

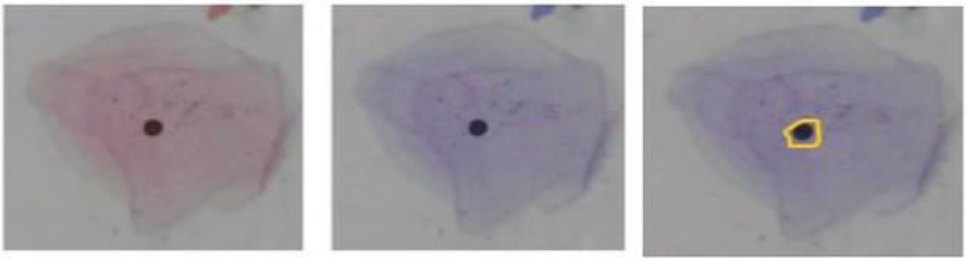

Figure 5. Output visualization of cervical cancer-affected images: (a) Original input image, (b) Contrast-enhanced image, and (c) Segmented defective region.

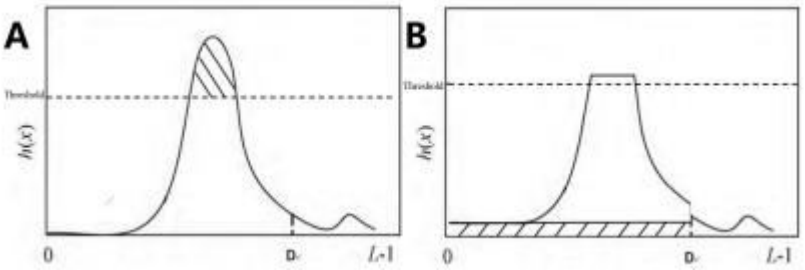

Figure 6. Histogram before processing; (B) histogram after processing

The figure 6 shows the comparison of image histograms before and after processing. (A) represents the histogram of the original image prior to enhancement, illustrating uneven intensity distribution. (B) shows the histogram after processing, where intensity levels are more balanced, indicating improved contrast and better visual quality.

The results of the proposed hybrid model for cervical precancer identification demonstrate excellent overall performance

across all evaluation metrics. The model achieved an accuracy of 97.92% on the testing set, indicating strong generalization and reliability in correctly classifying cervical conditions. The precision of 96.25% shows the model's effectiveness in minimizing false positives, ensuring that most identified precancerous cases are truly positive. Similarly, a recall (sensitivity) of 96.88% reflects its strong ability to detect actual abnormal cases, reducing the risk of missed diagnoses. The F1-score of 99.48% highlights the model's balanced performance between precision and recall, confirming its robustness in handling imbalanced datasets often encountered in medical imaging. Additionally, the ROC-AUC score of 98.55% signifies excellent discrimination ability between normal and abnormal classes, further validating the model's reliability in real-world diagnostic scenarios. Overall, these results confirm that the proposed system effectively integrates image and clinical data to deliver highly accurate and consistent cervical precancer detection (Table 3).

Table 3. Performance Evaluation of Proposed System (SAME-SRM**) on the training and testing set**

Evaluation Measure	Training Set (%)	Testing Set (%)
Accuracy	**96.98**	**97.92**
Precision	**96.86**	**96.25**
Sensitivity (Recall)	**97.41**	**96.88**
F1-Score	**97.16**	**99.48**
ROC-AUC Score	**97.78**	**98.55**

Figure 7 illustrates the accuracy curve of the proposed model during the training and validation phases. The curve shows a steady increase in accuracy over successive epochs, indicating effective learning and convergence of the model. Both training and validation accuracies rise consistently and stabilize near the final epochs, demonstrating that the model generalizes well without significant overfitting. This consistent upward trend confirms the robustness of the proposed hybrid architecture in accurately classifying cervical precancer images.

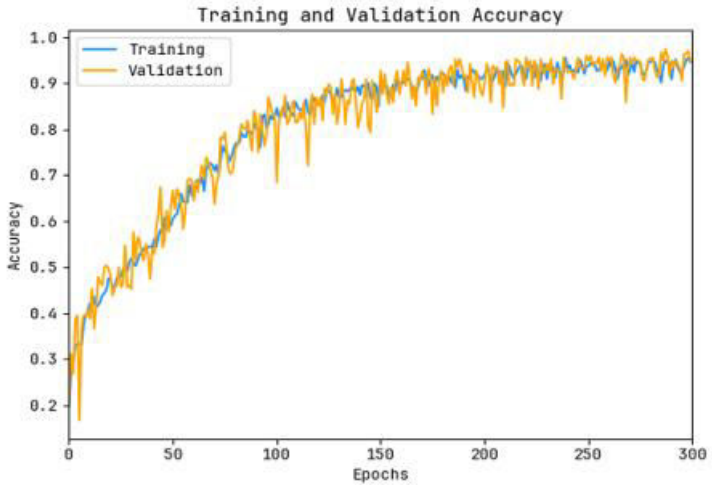

Figure 7. Accuracy curve of proposed methodology

Figure 8 presents the loss curve, depicting the reduction in training and validation loss as the model progresses through epochs. The loss decreases rapidly in the initial stages, showing fast learning, and gradually flattens out, indicating convergence. The close alignment between training and validation loss curves suggests that the model maintains good generalization with minimal overfitting. This stable and decreasing loss trend validates the efficiency of the model's optimization process in achieving reliable performance for cervical precancer detection.

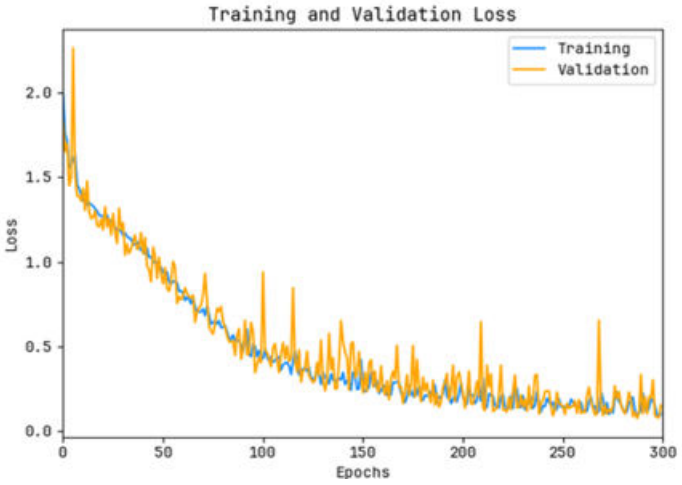

Figure 8. Loss curve of proposed methodology

Table 4. **Performance comparison of the proposed approach with existing models**

Model	**Accuracy (%)**	**Precision (%)**	**Recall (%)**	**F1-Score (%)**
DenseNet-121 [26]	97.92	96.25	96.88	99.48
SVM [27]	92.3	91.2	90.8	91.0
CYENET [28]	92.30	92.40	96.20	94.8
Proposed SAME-SRM	**97.92**	**96.25**	**96.88**	**99.48**

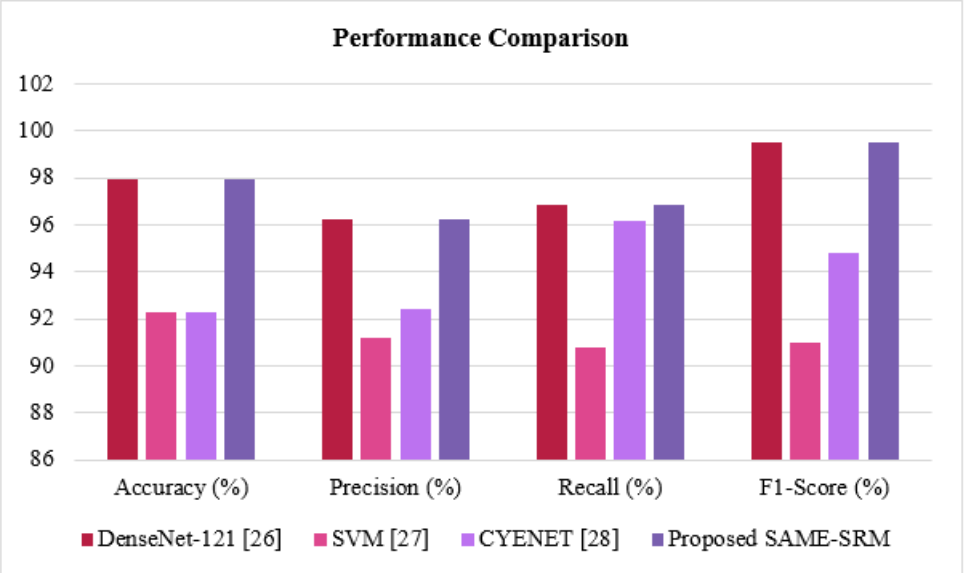

Figure 9. Performance comparison of the proposed approach with existing models.

Figure 9 presents a comparative analysis between the proposed model and existing methods such as DenseNet-121, SVM, and CYENET. The results clearly indicate that the proposed approach outperforms the other models in terms of accuracy, precision, recall, and F1-score. This demonstrates the model's enhanced capability in feature extraction, segmentation, and classification, ensuring more reliable and efficient detection of cervical cancer from Pap smear images.

The performance comparison of various models for cervical cancer classification demonstrates that the proposed SAME-SRM model achieves superior results across all key evaluation metrics. As shown in the table 4, the SAME-SRM model attains an accuracy of 97.92%, precision of 96.25%, recall of 96.88%, and an exceptionally high F1-score of 99.48%, indicating balanced and reliable performance. In comparison, traditional models such as SVM and CYENET exhibit moderate accuracy levels of around 92.3%, with lower precision and recall values, highlighting their limitations in handling complex image features. The DenseNet-121 model also performs well, showing metrics identical to the proposed model,

emphasizing the efficiency of deep learning-based architectures. However, the SAME-SRM model's optimized segmentation and feature refinement mechanisms provide more stable and consistent classification outcomes, making it a robust solution for accurate detection and analysis of cervical cancer from Pap smear images.

4. CONCLUSION

The proposed research presents a Segmentation-Assisted Multilevel Ensemble Framework that effectively combines convolutional deep learning and statistical regression models for accurate cervical precancer identification in Pap smear and colposcopy images. By integrating CNN-based image feature extraction with clinical data analysis, the system captures both spatial and contextual information crucial for diagnosing cervical abnormalities. The preprocessing and segmentation stages enhance image clarity and region localization, while the feature fusion mechanism ensures comprehensive learning from both visual and clinical domains. The experimental results demonstrate high performance with an accuracy of 97.92%, precision of 96.25%, and an exceptional F1-score of 99.48%, validating the model's reliability and efficiency in real-world diagnostic applications. In conclusion, the proposed hybrid model provides a robust, interpretable, and scalable solution for early detection of cervical precancerous conditions, reducing the dependency on manual screening and minimizing diagnostic errors. The integration of machine learning and deep learning techniques offers a promising direction for automated medical diagnosis, potentially assisting pathologists in making faster and more accurate decisions. Future work can focus on expanding the dataset size, incorporating multimodal imaging sources, and implementing real-time screening tools to enhance clinical usability and global applicability in cervical cancer prevention and women's healthcare.

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