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Ensemble and Transformer Encoder-based Models for the Cervical Cancer Classification Using Pap-smear Images

Abstract: - Cervical cancer poses a health concern for women globally ranking as the seventh most common disease and the fourth most frequent cancer among women. The classification of cytopathology images is utilized in diagnosing this condition with a focus on automating the process due to potential human errors in manual examinations. This study presents an approach that integrates transfer learning, ensemble learning and a transformer encoder to classify cervical cancer using pap-smear images from the SIPaKMeD dataset. By combining these methods human involvement in the classification task is minimized. Initially individual models based on transfer learning are. Their unique characteristics are combined to create an ensemble model. This ensemble model is then input into the proposed transformer encoder specifically utilizing the Vision Transformer (ViT) model. The results highlight the effectiveness of this methodology. The VGG16 model demonstrates accuracy of 97.04% and an F1 score of 97.06% when applied to classifying five categories using the SIPaKMeD dataset. However surpassing this performance is the learning model, with an accuracy of 97.37%. Notably outperforming all models is the transformer encoder model achieving an accuracy of 97.54%.Through the utilization of transfer learning, ensemble learning and the transformer encoder model this research introduces a method, for automating the classification of cervical cancer. The findings underscore the capability of the suggested approach to enhance the precision and effectiveness of diagnosing cancer.

Keywords: Cervical cancer, Pap-smear, hybrid CAD system, ensemble learning, transformer

I. INTRODUCTION

Cervical cancer is the most common and dangerous disease in women, as it is the fourth in the global prevalence level among the types of cancers for females, while it is considered the ninth in the Kingdom of Saudi Arabia [1, 2]. Since 1990, the number of new cases of cervical cancer in Saudi Arabia has climbed by more than 450%, with an average of 358 each year and 179 deaths. Cervical cancer is the most common and dangerous disease in women. Cervical cancer is more dangerous in developing countries. The primary causes of this disease are precocious sexual activity, smoking, sexual activity with multiple partners, early pregnancy, weak immunity, the use of oral anti pregnancy pills, and poor menstrual cycles [3, 4]. Abnor mal menstruation cycle and mild to moderate pain during sex are the most often reported signs of cervical cancer. Cervical cancers are often diagnosed using cytopathology screening, which involves placing cells on a glass slide and observing them under a microscope[5]. The manual examination is still insufficient, leading even specialists to make inaccurate diagnoses. Artificial intelligence (AI) helps diagnose this disease without any manual effort[6, 7]. as shown in the literature review section many researchers have used the Convolutional Neural Networks (CNNs) Deep Learning models along with Ensemble which is a machine learning technique that combines multiple models to improve model performance [8][9]. The Vision Transformer (ViT)has demonstrated the capacity of Transformer-based models as backbone networks in image synthesis and classification tasks, surpassing the performance of traditional pure CNN models [10] [11]. This study utilizes the capabilities of the ensemble learning algorithm and vision transformer encoder to evaluate pap smear images. The next few lines outline the primary contributions of the study:

• New hybrid transformer model is introduced for the prediction of cervical cancer using pap-smear images.

• Ensemble concatenated transfer learning is implemented using a Self-Attention transformer to decrease the computational complexity and prioritize the most important features.

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• A comprehensive empirical study is carried out on five sets of cancer cells utilizing cutting-edge machine learning (ML) and deep learning (DL) technologies. The paper is divided into several sections. Section 2 provides a summary of related works, while Section 3 introduces research techniques and materials used. The experimental results are presented in Section 4, Finally, the conclusion and findings are discussed in Section 5.

II. RELATED WORK

Several research papers have delved into the classification of cancer through the application of deep learning methods. In an investigation led by [34] transfer learning was employed with established deep learning models, like InceptionResNetV2, VGG19 DenseNet201 and Xception to improve the precision of diagnosing cervical cancer. The study focused on the SIPaKMeD dataset for their analysis. Another research paper proposed by [35] suggests using an IDT framework that combines the strengths of deep learning and decision tree-based methods. This framework allowed Convolutional Neural Networks (CNNs) to understand novel categories better while maintaining high accuracy for previously learned categories. The framework was evaluated on different datasets, including MNIST, BreakHis, LBC, and SIPaKMeD, and demonstrated promising results with high accuracy rates ranging from 87% to 98%. In another study[36], researchers employed an ensemble strategy that utilized three pre-trained CNN architectures (Inception v3, Xception, and DenseNet-169) and considered the base classifiers' confidence when making final predic tions. The model proposed in this study demonstrated exceptional performance on both the Mendeley Liquid-Based Cytology (LBC) and SIPaKMeD datasets, achieving accuracy rates of 98.55% and 99.23% respectively. Moreover, the literature [37] uses the SIPaKMeD dataset and the adoption of ViT due to its competitive performance and low induc tive bias compared to CNNs. However, training large ViT networks can be computationally intensive. As an alterna tive, a transfer learning-based strategy is introduced, which leverages pre-trained CNN features and categorizes them using a resource-efficient LSTM network. The CNN-LSTM approach achieves a classification accuracy of 95.80% for 5-class classification. Finally,[38]is a recent research paper utilized state-of the-art such as Vision Transformers (ViTs) and, Convolutional Neural Networks (CNNs) are employed in this study to classify cervical cancer. The study also employed data augmentation techniques and improve the models accuracy by enhancing its learning capabilities. The research also used data augmentation techniques to enhance the dataset's and enhance the accuracy of the model through learning. The study demonstrated that newer ViT based models performed better than CNN models showing potential for application, in real world medical settings to improve cancer detection precision and speed. The study [39]utilized multiple individual models, namely GoogleNet, InceptionResNetV2, VGG16, ResNet50, and Xception. They optimized and froze specific layers as unmodifiable layers. They subsequently combined the high level characteristics to function as the backend of the convolutional network alongside the self-attention ViT. The model achieved an impressive accuracy of 97.87% when applied to INbreast mammograms.

III. METERIALS AND METHODS
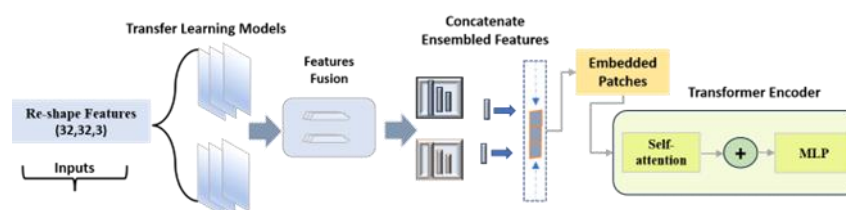
Figure 1 The proposed ensemble and transformer encoder-based models for cervical cancer classification.

The proposed model for cervical cancer classification is shown in Figure 1, including the ensemble and trans former encoder models, aim to obtain an accurate and effective diagnosis of cervical cancer malignancy. We utilize medical data collected from the SIPaKMeD. The primary steps of the suggested models include gathering medical pap-smear images , preprocessing it, separating the data, applying augmentations, and developing transfer learning models with fine-tuning. The models are then validated and evaluated, and the high-level features are fused. Finally, the models are evaluated again. Preprocessing is necessary to eliminate extraneous information and isolate the potential lesion region of interest (ROIs) or patches. The study uses ensemble transfer learning methodologies and the ViT model, which incorporates the self-attention mechanism.

1) SIPaKMeD Dataset

We utilized the SIPaKMeD dataset, which was produced by researchers associated with the University of Ioannina in Greece in 2018 [40]. This dataset contains 4049 images of women's cells that have been extracted from Pap smear slides. The dataset contains five categories for labeling cancer cells, such as Sup Intermediate, Parabasal, Koilocytotic, Dysketarotic and Metaplastic. To enhance the clarity and quality of images a preprocessing step was

carried out on the medical data. This involved adjusting intensities resizing images and eliminating unnecessary information to prepare them for machine learning algorithms [41]. The dataset was divided randomly into training, testing and validation sets. 70% of the images were allocated to the training set while 15% each went to the testing and validation sets. A special summary of the information acquired for this cervical cancerous dataset is furnished in Table1 .

Table 1 Types of cancerous cells in SIPaKMeD dataset

Cancer class	Cells per class	Number of images
Intermediate	813	126
Parabasal	787	108
Koilocytotic	825	238
Metaplastic	793	271
Dysketarotic	813	223
Total	**4049**	**966**

A. Preprocessing Medical data

 preprocessing is essential for adequately preparing trainable medical images. It involves removing unwanted or irrelevant information for AI classifiers, enhancing the spatial resolution and quality of the images, and normalizing and resizing the pixel intensities to ensure they fall within a consistent grayscale range for all images [41] . Moreover, skilled radiologists carefully establish the precise boundaries of the cancerous cell in each pap image, exclusively focusing on these specific areas rather than utilizing the entire image, for the purpose of training AI models. The patch images are retrieved by isolating only the regions of interest (ROIs) containing cervical malignant cells while ignoring the remaining information in the image. The retrieved image patches are scaled to dimensions of 256×256 pixels.

B. Data splitting, Training, and testing

 The data splitting for both datasets includes assigning 70% of SIPaKMeD Pap- smear images from each class to the training set, 15% to the testing set, and 15% to the validation set in random allocation. . The distribution of the SIPaKMeD dataset for five classes is depicted in Table 2.

Table 2. Data splitting for training, validating, and testing, for SIPaKMeD dataset.

Class	Records	Training	Validation	Testing
Intermediate	831	578	128	125
Parabasal	787	547	121	119
Koilocytotic	825	574	127	124
Metaplastic	813	566	125	122
Dysketarotic	793	552	122	119
Total	4049	2817	623	609

C. Augmentation of data training

The data augmentation task is executed with the machine learning imgaug library, which offers a wide range of augmentation approaches. The freshly generated images are stored together with the training images, resulting in a six-fold increase in the quantity of the training data. This leads to improved outcomes. Augmentation is achieved by applying Affine transformations to an image, which include rotation, scaling, translation, shearing, and horizontal and vertical flip operations [42] . CLAHE, or contrast-limited adaptive histogram equalization, improves image contrast by partitioning images into smaller blocks and applying histogram equalization to each block. The image involves modifications in contrast and brightness to accomplish edge identification, Canny edge detection, photometric transfor mations (Pms), and contrast adaptation

D. AI MODELS

a) InceptionResNetV2

 While InceptionResNetV1 serves as a model for the network design, InceptionV4 forms the basis of the stem [43] . A quick link is located on the far left of every module. It enhances classification results by combining inception architecture with residual connections. For the inception modules convolutional operation to work, both the input and the output must be similar to the inception convolutional operation.

b) VGG16

VGG16 is a convolutional neural network (CNN) that is widely regarded as one of the top-performing models for computer vision tasks[44]. The developers of this model assessed the networks and enhanced the depth by employing an architecture which includes extremely small (3×3) convolution filters. This modification resulted in a notable enhancement compared to the previous configurations used in the field. The depth was increased to 16–19 weight layers, resulting in roughly 138 trainable parameters. It can accurately classify 1000 photos over 1000 distinct categories for image classification tasks. Additionally, it offers the advantage of being user-friendly and compatible with transfer learning techniques [45] .

c) ResNet50

ResNet50 is a convolutional neural network that consists of 50 layers and is specifically optimized for tasks related to image recognition. The model underwent training using the ImageNet dataset in order to classify over one thousand categories, similar to the pre-trained VGG16 model. More over, the classification the classification layers have been removed. The process of adding new layers for multiple classifications to the model after freezing. Optimized setups are implemented for the ResNet50 model by freezing 123 layers [46] .

d) ResNet50-V2

The ResNet50 v2 model uses pre activation of weight layers of post activation. The latest update removed the non linearity and added Batch Normalization and ReLU activation to the input before multiplying it with the weight matrix (convolution operation).

e) Xception

Xception is a neural network design comprising layers of convolution organized in a straightforward manner, with each layer distinguished by its depth. It features 36 layers grouped into 14 modules with residual connections forming the core structure for feature extraction, around each module

f) Transformer Encoder Model

The primary utility of the vision transformer lies in its ability to effectively recognize objects by leveraging carefully extracted and significant observable features. Furthermore, the self-attention mechanism is employed to achieve remarkable performance while minimizing the reliance on vision-specific assumptions. Unlike traditional CNN models, transformers utilize self-attention to assign varying weights to evaluate the importance of each input data point in an encoder-decoder configuration. In contrast, CNN models primarily analyze the correlations among neighboring pixels within the receptive area defined by the f ilter size. Therefore, these models are unable to process pixels that are far away. Consequently, in order to tackle this problem, a novel approach was adopted that relied on the attention process. The attention strategy relies on identifying and analyzing the most significant components of the images while disregarding redundant elements [48] . This approach helps to minimize false negative outcomes. The study utilized and refined the vision transformer through the use of an encoder as calculated by equation:

$$\text{Attention}(Q, KV), = \ \text{Softmax}(\frac{Qkt}{dk} \ )^v$$

E. Evaluation Strategy

(1) The performance of this approach is evaluated using common metrics such as accuracy, precision, recall, F1 score, and AUC and compared to other existing cervical cancer detection methods.

1) Accuracy(ACC) = $\dfrac{(TP+TN)}{(TP+TN+FP+FN)}$

2) Specificity(SPE)= $\dfrac{TN}{TN+FP}$

3) Sensitivity(SEN)= $\dfrac{TP}{TP+FN}$

4) F1- score=2 $* \dfrac{(\text{precision}\times \text{Sensitivity})}{(\text{precision}+\text{Sensitivity})}$

IV. RESULTS

A. Individuals Transfer Learning Models

The SIPaKMeD database involved the implementation and comparison of five different pre-trained transfer learning models: InceptionResNetV2, ResNet50, ResNet50-V2, VGG16, and Xception. All layers of the InceptionResNetV2 model were frozen and unable to be trained. However, in the Xception, VGG16, ResNet50, and ResNet50-v2 models, we expect that specific layers will be trainable. Specifically, for the Xception model, we expect training to start at layer 106, and for the VGG16 model, training will begin from layer 17. The training process for ResNet50 and ResNet50-v2 begins at the 143rd layer and continues until the classification layers. The ultimate outcomes include the individual transfer learning models, the fine-tuning of models, and the addition of new hidden layers with varying units. In addition, the Adam optimizer was employed, with a learning rate of 0.001 and a total of 50 epochs for all models. The evaluation predictions for each transfer models on this dataset are displayed in Table 3 . The VGG16 model demonstrates superior classification performance, as shown by its outstanding results across all evaluation measures. Specifically, it achieves an overall accuracy of 97.04% and an F1-score of 97.06%. ResNet50 achieves superior prediction performance, with an overall accuracy and F1 score of 96.05% and 96.06%, respectively. Conversely, the InceptionResNetV2 demonstrated a third-order accuracy performance of 94.75% and an F1-score of 94.73%. The Xception model showed the lowest accuracy rate of 83.25% when compared to other transfer models. According to the confusion matrix evaluation, the VGG16 model demonstrated the highest prediction accuracy, with only 18 cases misclassified out of a total of 609 occurrences across all 5 classes. Out of the entire test set including all classes, the ResNet50 model made incorrect classifications for 28 occurrences. The Xception model showed a higher number of misclassified cases, specifically 94 cases across all classes, with a special focus on the koilocytotic class, which accounted for 41 cases. Figure 2 displays the confusion matrices of each individual transfer learning model conducted in the study.

Table 3 Performance evaluation of individual transfer learning models, for the SIPaKMeD dataset.

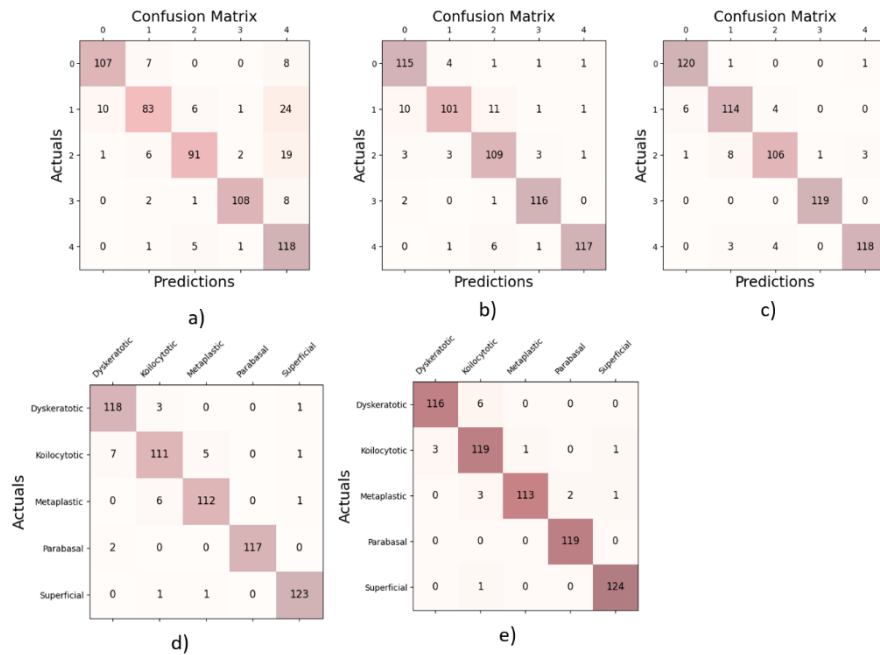| The Model	Accuracy	Sensitivity	Specificity	F1-Score	AUC
InceptionResNetV2	0.9475	0.9475	0.9475	0.9473	0.967
ResNet50	0.9606	0.9606	0.9609	0.9605	0.975
ResNet50-V2	0.9163	0.9163	0.9182	0.9160	0.948
VGG16	0.9704	0.9704	0.9710	0.9706	0.982
Xception	0.8325	0.8325	0.8503	0.8335	0.895

Figure 2The confusion matrices of for individual transfer learning models: (a) Xception, (b)ResNet50-vV2, (c) InceptionResNetV2, (d) ResNet50, and (e) VGG16 for the SIPaKMeD dataset.

B. Ensemble learning vs transformer encoder model

Utilizing the outcomes of the individual transfer models, we combined the vgg16 and resnet50 models to construct the ensemble backbone network for classification. Within this area, we conduct performance assessments through a two-step process. Firstly the ensemble learning model is constructed, trained and assessed independently before in corporating the ViT. Subsequently we establish the encoder model by integrating the ViT to produce the prediction based on the amalgamated high level deep features derived from merging two distinct CNN models. The evaluation performance findings of cervical cancer, obtained by the utilization of ensemble learning and the transformer encoder, are succinctly presented in Table 4. The experimental proof shows the transformer encoder model yields the most optimal assessment outcomes when employed in conjunction with the ensemble learning model and others models with 97.54% accuracy and F1-score. Figure 3 illustrates the confusion matrices produced by the ensemble learning and transformer encoder models on the SIPaKMeD dataset. While the Parabasal class remained error-free, the rest of the classes made fifteen and sixteen wrong predictions, respectively, for the ensemble and transformer encoder models, for the SIPaKMeD dataset Figure 4 illustrates the comparative performance results of the prediction error for each individual transfer learning model in contrast to the proposed ensemble and transformer encoder models. The VGG16 model has a prediction error of 0.029, which is the closest to the proposed models that have prediction errors of 0.026 and 0.024, respectively. Conversely, the Xception model has the largest degree of error variation in terms of accuracy, with a prediction error of 0.16.

Table 4. The evaluation performance results of ensemble CNN fusion and Transformer encoder models for SIPaKMeD dataset.

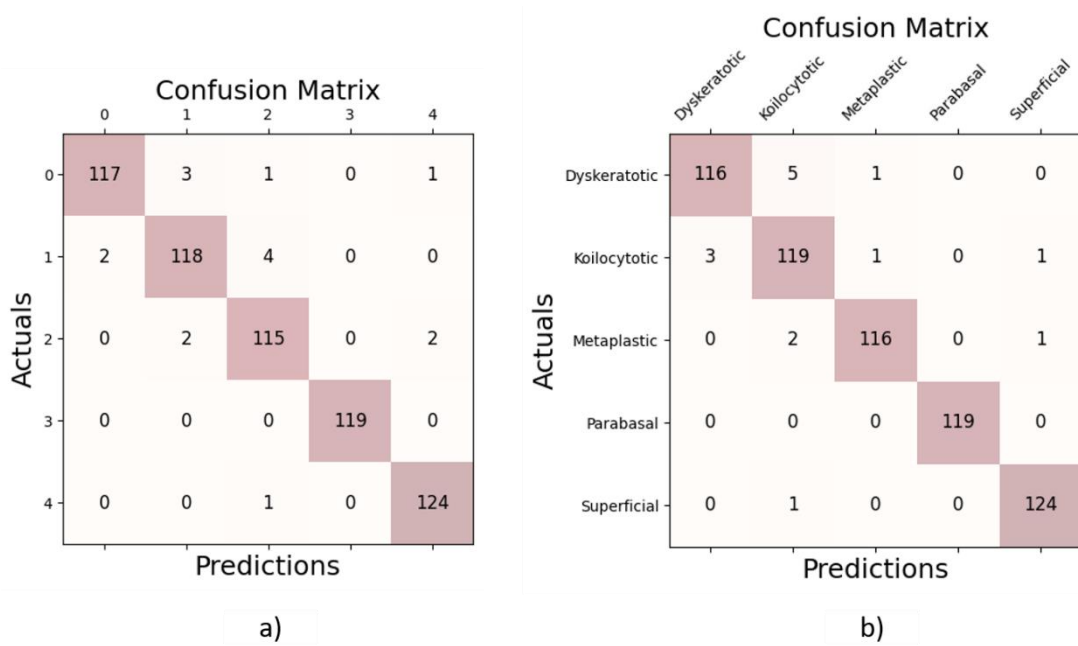| The Model	Accuracy	Sensitivity	Specificity	F1-Score	AUC
Ensemble Learning Model	0.9737	0.9737	0.9738	0.9737	0.984
Transformer Encoder Model	0.9754	0.9754	0.9756	0.9754	0.985

Figure 3 The confusion matrices of ensemble CNN fusion and Transformer encoder models: (a) Ensemble learning model, and (b) Transformer encoder model using the SIPaKMeD dataset.
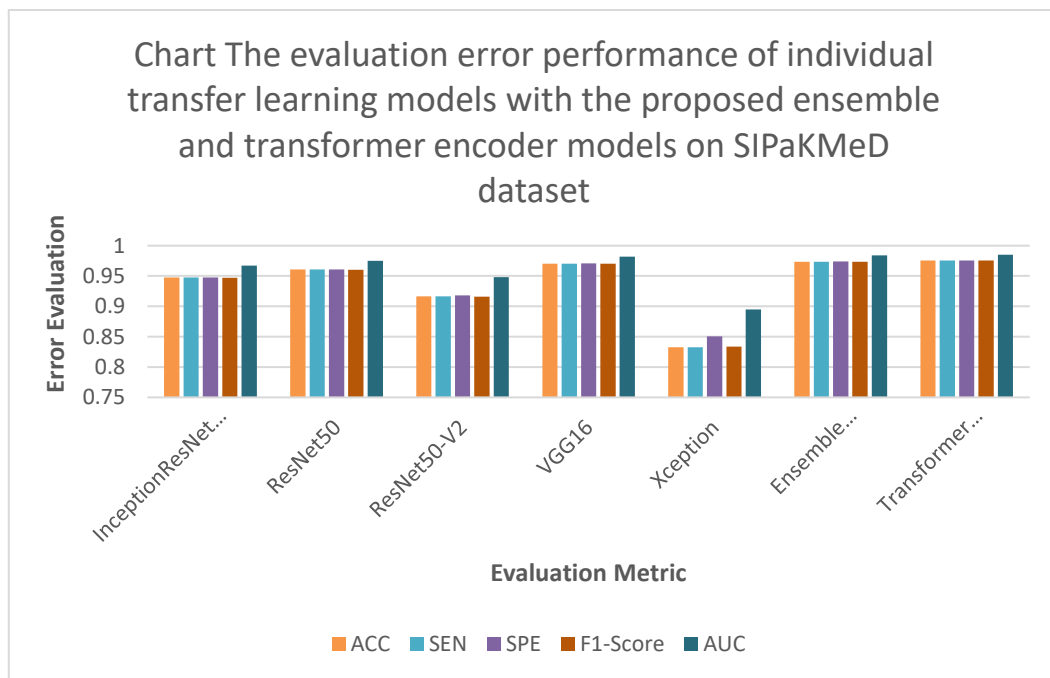

Figure 4 The evaluation error performance of individual transfer learning models with the proposed ensemble and transformer encoder models on SIPaKMeD dataset.

V. CONCLUSIONS AND FUTURE WORK

The study presents an approach that use deep learn ing to classify cervical cells. The pre-trained transfer learning models, including InceptionResNetV2, ResNet50, ResNet50-V2, VGG16, and Xception, are utilized with fine tuned and frozen layers. The high-level characteristics of these models are then fused to create an ensemble model, which is subsequently input into the proposed transformer encoder ViT model. The SIPaKMeD were utilized for models training with 5 cervical cancer classes for model training. Based on the performance metrics, it is evident that the suggested transformer encoder ViT model outperforms both the ensemble learning and pre-trained models in terms of classification accuracy. The VGG16 model achieved the highest accuracy of 97.04% and an F1-score of 97.06% for 5-class classification problems in the SIPaKMeD dataset. Nevertheless, the ensemble learning model attained an accuracy of 97.37%, while the transformer encoder model surpassed all other models with an accuracy

of 97.54%.And to compare the results obtained here with those of other methods found in the literature, Table 5 shows that the proposed method achieved the highest accuracy for 5 classes compared with the literature.
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Table 5 Comparison with previous work

Refrence	Accurecy %	classes	Dataset/s	Model
[34]	96.63	5	SIPaKMeD	DenseNet201
[35]	93	5	SIPaKMeD	IDT framework
[36]	95.43	5	SIPaKMeD	ensemble
[37]	95.8	5	SIPaKMeD	ViT-CNN
[38]	92.04	2	SIPaKMeD	Rd
proposed model	97.37	5	SIPaKMeD	Ensemble Learning Model
proposed model	97.54	5	SIPaKMeD	Transformer Encoder Model

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