Research article

DeepCyto: a hybrid framework for cervical cancer classification by using deep feature fusion of cytology images

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Abstract: Cervical cancer is the second most commonly seen cancer in women. It affects the cervix portion of the vagina. The most preferred diagnostic test required for screening cervical cancer is the pap smear test. Pap smear is a time-consuming test as it requires detailed analysis by expert cytologists. Cytologists can screen around 100 to 1000 slides depending upon the availability of advanced equipment. Due to this reason Artificial intelligence (AI) based computer-aided diagnosis system for the classification of pap smear images is needed. There are some AI-based solutions proposed in the literature, still an effective and accurate system is under research. In this paper, the deep learning-based hybrid methodology namely DeepCyto is proposed for the classification of pap smear cytology images. The DeepCyto extracts the feature fusion vectors from pre-trained models and passes these to two workflows. Workflow-1 applies principal component analysis and machine learning ensemble to classify the pap smear images. Workflow-2 takes feature fusion vectors as an input and applies an artificial neural network for classification. The experiments are performed on three benchmark datasets namely Herlev, SipakMed, and LBCs. The performance measures of accuracy, precision, recall and F1-score are used to evaluate the effectiveness of the DeepCyto. The experimental results depict that Workflow-2 has given the best performance on all three datasets even with a smaller number of epochs. Also, the performance of the DeepCyto Workflow 2 on multi-cell images of LBCs is better compared to single cell images of other datasets. Thus, DeepCyto is an efficient method for accurate feature extraction as well as pap smear image classification.

Keywords: cervical cancer; pap smear; artificial intelligence; deep features; PCA; artificial neural network

1. Introduction

Cervical cancer is one of the major cancer after breast cancer and others among women as the cause of death worldwide [1]. Most of the cases of cervical cancer are from low and middle-income countries which have a low standard of living and low hygienic conditions [2]. Healthcare infrastructure in low and middle-income countries is not too good, which compromises testing and diagnosing the potential patients of cervical cancer. Cervical cancer can be treated and cured if detected at an early stage but due to lack of infrastructure and cost for testing, low turnout is observed for testing. Pap smear test is currently used as a primary screening tool for finding the presence of precancerous cells [3]. However, the time required for getting the results of the pap smear test is long. Pathologists are required to classify each cell from the slide which contains thousands of cells. The slide with these many cells is viewed under a microscope and detection of precancerous or cancerous cells remains subjective to the expertise of pathologists.

Artificial Intelligent based medical imaging is being explored by researchers for diagnosing several diseases more accurately [4,5]. Advancement in artificial intelligence, machine learning, and deep learning technology in the area of healthcare and medical sciences provides assistance to pathologists for the task of classifying the cells [6]. The model constructed using these techniques gives a more accurate prediction based on the feature learning from a large amount of dataset. In this paper, we have developed an approach with two workflows where we utilize the deep learning-based features extraction using the pre-trained models and concatenate deep features to and apply Principal Component Analysis (PCA) for getting the most important features so that data is resolved without losing crucial traits of the dataset. The image feature obtained from PCA is then fed to multiple classifiers for classification and then voting is done on the prediction of the classifiers to get a collective decision for the classification of the data. In another workflow, we construct an artificial neural network with nodes containing dropout layer, batch normalization, and fully connected dense layer with softmax function, and then this model with concatenated deep features and artificial neural network is compiled and used for prediction of input image data. In this approach we leverage the deep features extracted from several pre-trained CNN models and flatten those deep features, keeping the relevant feature intact. Before getting the features from Deep learning CNN models we augmented the dataset to generate more images for better results, As the publicly available dataset for cervical cancer does not contain enough images we augmented those images using rotation, shifting, rescaling, shearing, flipping, and changing brightness. The deep features collected from pre-trained and penultimate layers of the CNN are passed to the machine learning classifiers for classification tasks and artificial neural network which is again trained.

The overall workflow of this paper can be summarized as follows:

1) A framework for optimal deep features selection of images using pre-trained Convolutional Neural Network (CNN) classifiers.

2) Deep features obtained from the penultimate layer of the convolutional neural network are passed through a dense layer so that dimension can be reduced. These reduced dimensional features of each convolutional neural network are concatenated to form a fusion of deep features to be called image features.

3) Since the deep features of the images extracted from the pre-trained CNN are large, principal component analysis is used for taking out crucial features without losing the traits of

features. The resultant features subset reduces computations required and time for execution thus ensuring faster convergence.

4) The features are then passed to the machine learning classifiers for enhanced classification of images in workflow 1. Scikit-learn, a popular python library is used for utilizing machine learning classifiers namely: Support Vector Machine, Random Forest Classifier, Neural Network Classifier. Comparative analysis of all the classifiers mentioned is done to find the best suitable classification technique for the datasets available.

5) The predictions obtained from the classifiers are then combined to take voting among them. The Maximum voted class is considered as the predicted class.

6) In workflow 2, an ensemble of convolutional neural networks of pre-trained models is constructed and the features extracted from this ensemble model are passed to an artificial neural network with a dropout layer and batch normalization with a fully connected layer of softmax function. The artificial neural network model is compiled and trained to give predictions.

7) The framework is assessed on open-access datasets by converting them into two classes namely Normal and Abnormal cells. The dataset used is the Herlev Pap Smear cytology dataset, Sipakmed Pap smear cytology dataset, and Liquid Based Cytology (LBC) pap smear dataset by Guwahati Medical College and Hospital.

The rest of the paper covers the literature survey, proposed methodology, dataset, and performance evaluation of the proposed framework on the three mentioned datasets followed by the conclusion of the paper.

2. Literature survey

Previous studies show that feature extraction from images and choosing relevant features are important steps for image classification problems. These steps impact the classification performance significantly. There exist multiple methods for the extraction of handcrafted features from images [7]. But the handcrafted features cannot capture the spatial relationship among the pixels and researchers have to decide which features are better for the applications at hand based on the experimentation. This is because not all the feature extraction methods are well suited for all kinds of images. Also, the handcrafted features give less classification performances. Nowadays deep learning models of CNN are preferred as they are capable of feature extraction as well as classification. The drawback of these models is that they need more data and are complex in architecture. This limitation is taken care of by the transfer learning concept of deep learning, wherein the pre-trained models are made available to alleviate the limitation of limited datasets.

For cervical cancer classification, openly available datasets are limited in size. To overcome this problem, the proposed framework DeepCyto uses the pre-trained models and customizes the dataset into two classes to improve the quantity of per class samples. Table 1 refers to the authors and the approaches they used for the classification of cervical cancer.

The limitation of publicly available datasets related to pap smear images is addressed by using pre-trained models which are already trained on large ImageNet datasets [8], fine-tuned and widely used for different classification purposes. To increase the dataset, data augmentation is another approach where we increase the size of the dataset by using different operations. However, the features learned from similar-looking images would be similar to the original images. Therefore, we suggest an ensemble of convolutional neural networks deep features to increase the quality of features obtained

from different implemented convolutional neural networks and use robust machine learning classifiers for improving classification accuracy for our first approach and using newly constructed node of artificial neural network with normalization and softmax function to improve classification in our second approach.

Table 1. Literature survey.

Authors	Dataset	Method	Description
Md Mamunur Rahaman et al. [9]	Sipakmed pap smear	Hybrid deep feature fusion network	The author implemented an improved version of the late fusion technique where they combined multiple features into a single feature vector.
Hritam Basak et al. [10]	Herlev, Sipakmed and Mendeley dataset	Grey Wolf optimizer, PCA and SVM	The authors used a two-step feature reduction approach; PCA and Grey Wolf Optimizer and did multi-class classification gaining accuracy up to 97%.
Chankong et al. [11]	Langerhans cell histiocytosis (LCH)	Artificial Neural Network	They implemented different classifiers for two-class and multiclass classification.
William et al. [12]	Herlev Pap Smear	Fuzzy-C Means	After extracting features from the image they used enhanced fuzzy-c means for classification.
Byriel et al. [13]	Herlev Pap Smear	An adaptive network-based fuzzy inference system	The method used by the author performed good on binary classification but was not good enough for multi-class
Zhang et al. [14]	Medical Liquid Based Cytology	Fuzzy Clustering means	They used a dataset obtained from the hospital and got an accuracy of 72-77% on the 7-class problem
Marinakis et al. [15]	Herlev Pap Smear	Nearest neighbor classifier fusion with Genetic algorithm	They achieved the best accuracy of 98 on the first nearest neighbor classifier with 2 classes and 96 with 7 classes with the cross-validation technique.
Zhang et al. [16]	Herlev Pap Smear	Deep convolutional neural network	Using a Deep convolutional neural network the author suggested that they removed the need for segmentation and achieved an accuracy of around 98%

3. Methodology

3.1. Augmentation

Image data augmentation is used to increase the image dataset by modifying and doing image processing operations. By using data augmentation we generated multiple images with the help of transformations and geometric operations, changing brightness and other augmentation techniques [17]. An input image is transferred to a data augmentation function where affine transformations [18] are applied to each image. A random number is selected between the range provided for rotation, scaling, translation, shearing, flipping horizontally as well as vertically. Rotation operation may rotate pixels out of the image frame and make some empty place which is to be filled. For filling empty areas we use padding. Along with these affine transformations, some Guassian blur is introduced [19]. Laplacian and Gaussian Noise are added to the input image and images are also generated by changing the contrast of the images. Other augmentation includes sharpening images by using canny filters. This new batch of images is used for training. Other parameters and their values used for augmentations are shown below in Table 2.
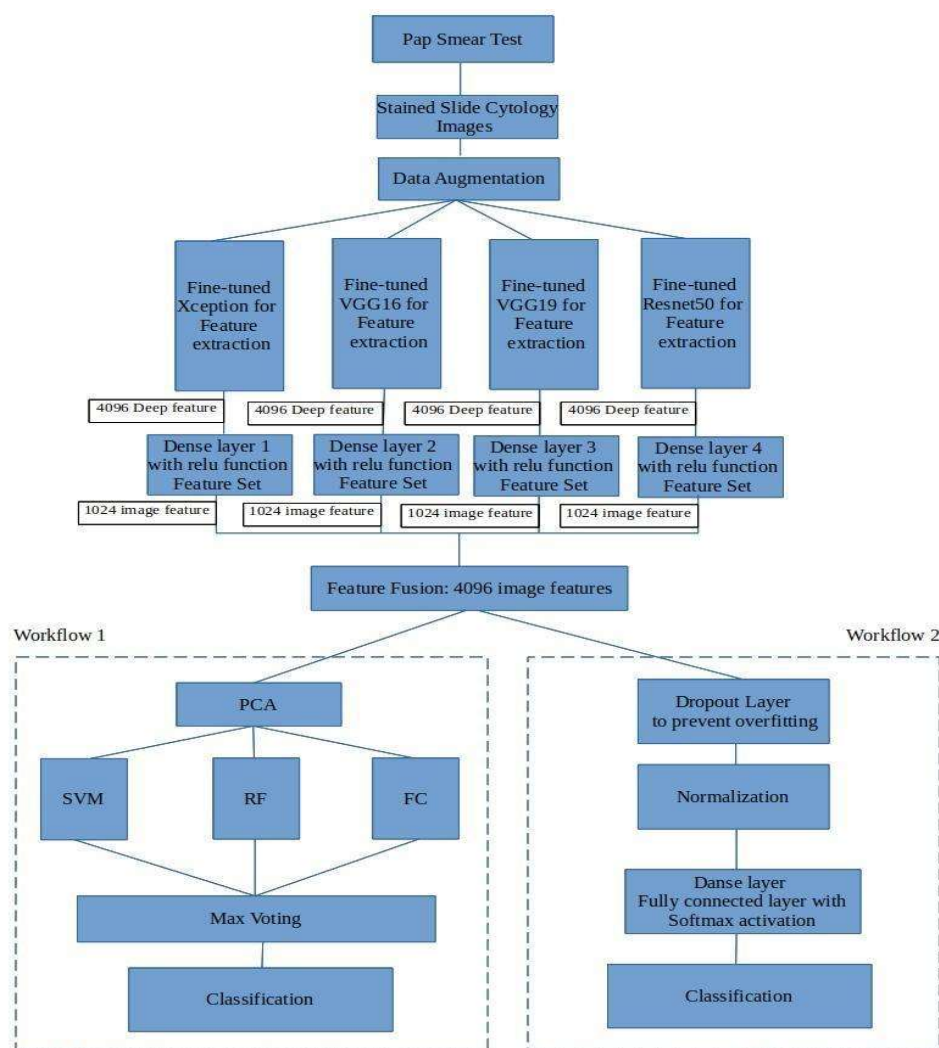

Figure 1. Proposed model framework with two workflows.

Table 2. Parameters of data augmentation.

Parameter of Image Augmentation	Values/Range
Rotation	−90 to 90 degree
Scaling	(0.5,0.9) on both axis
Shear	−2 to 2
Zooming	0.15
Horizontal Flip	True
Vertical Flip	True
Gaussian Blur	Sigma = 1.22
Hue and Saturation	0.5 to 1.5

3.2. Transfer learning

Convolutional Neural Network learns features from the input image and finds out features correlating with each other. Transfer learning is a technique where the pre-trained convolutional neural network is utilized for training on a new dataset [20]. Training CNN from scratch can be a tedious task where we need to have the high computational power and the time required to train on a new dataset is also high. To train from scratch we need a high amount of data so that model learns features that are important for prediction. But the amount of data available for cervical cancer pap smear images in open-access is not large. So to overcome this we used transfer learning where models are trained on the ImageNet dataset which consists of around 1.3 million images belonging to 1000 classes [16]. Some of the model layers are frozen while keeping some layers unfrozen. We train them on a new image dataset leveraging most of both ImageNet dataset learned features and our dataset learned features for making a pool of features powerful for more accurate prediction. We used four pre-trained models namely XceptionNet [21], VGG16 [22], VGG19 [22], ResNet50 [23] which were already trained on the ImageNet dataset. Most of the generic features that occur in most of the datasets are already learned by these pre-trained models and for specific features, we train the model again on the cervical cancer dataset. In this training, most of the layers are frozen and some layers are added for fine-tuning which include a convolutional block and a fully connected layer. This model is trained for learning new data-specific features with Adam optimizer [24].

3.2.1. XceptionNet

The xception model has 71 layers. It is based on depthwise separable convolution. It has three major parts namely Entry flow, Middle flow, and Exit flow. It is also termed as an extreme version of Inception. It involves convolution of 1×1 followed by spatial convolution of $n \times n$ [21].

3.2.2. VGGNet

The model with both 16 layers and 19 layers achieves around 93% top 5 test accuracy in the ImageNet challenge. They have a large kernel with multiple 3×3 filters one after the other. In our work, we fine-tuned both our dataset using Adam optimizer and Rectified Linear Unit (ReLU) activation function. VGG19 has three additional convolutional layers than VGG16. Since they use

ReLU, both do not use Local Response Normalization (LRN) as it might increase training time making it slow and also increasing memory consumption [22].

3.2.3. ResNet50

It is 50 layers deep with 48 convolutional layers and 1 max pool and average pool layer each. ResNet overcomes the problem of saturation and degrading of accuracy due to a large number of layers additionally added. Authors of ResNet addressed this issue by deep residual learning technique referred to as skip connection [23].

3.3. Deep feature extraction

Feature extraction plays an important part in the classification of images since it helps the model to predict output class [25]. Concatenating features obtained from the mentioned models and utilizing them is an efficient approach. Concatenating features will help to make use of information gained through multiple models and will contribute more to prediction than initial individual features. There can be multiple ways to concatenate features obtained from the model like serially adding features with respect to the vector dimension or parallel concatenating using some imaginary component. But the shortcoming of such techniques is that the features obtained after concatenating like this lead to loss of old feature values as new features are being created. In our approach, we concatenate the 1024 features from the dense layer of each model and pass it to the concatenate layer where it forms a vector of 4096 dimensions. This 4096 dimension vector is extracted in the form of vectors as deep features to be used on various classifiers like support vector machine, random forest classifier and fully connected neural network classifier.

3.4. Workflow 1

As shown in Figure 1, two approaches for prediction on the image are given. In the first approach labeled as workflow 1 following steps are performed:

(1) Passing the deep feature vector to Principal Component Analysis for reducing the number of features without losing their prominence of the features. The reduced feature vector obtained after principal component analysis helps in faster execution and less memory consumption [26].

(2) The output of PCA is given to three classifiers namely Support Vector Machine [27], Random Forest [28] and Fully connected Neural Network [29].

(3) The classifier's predictions are then passed to the voter. The output of maximum voting is the predicted class of the image.

3.5. Principal component analysis (PCA)

PCA is used to reduce dimensions by projecting the data points into a few principal components by keeping as much of the variation of the data as possible [30]. For implementing principal component analysis scikit-learn python library is used [31]. PCA in scikit-learn does linear dimension reduction by utilizing singular value decomposition [32] to project the data onto a lower-dimensional space. The data passed to PCA is centered for each of the feature values before singular value decomposition can

be applied. PCA in scikit-learn uses the method proposed by Halko et al. in 2009 [33]. It uses the linear algebra package LAPACK for a randomized truncated singular value decomposition. The Singular Value Decomposition (SVD) solver parameter we used depended on the input shape and number of components passed. To run full singular value decomposition we selected components by post-processing from the standard LAPACK solver [34]. In PCA covariance matrix is calculated from the input feature data as in Eq (1). Then an eigenvector is computed which has eigenvalues. Eigenvalues of the vector have the biggest say in the making of a new feature vector of reduced dimensionality. To avoid loss of important features we use the eigenvalues to preserve 95% of the variance. In scikit-learn the number of components are estimated from the input data based on the threshold between 0 and 1 is passed for the variance among the features.

$$\text{covariance matrix} = \frac{1}{n}\sum_{i=1}^{n} \quad x^a \times (x^a)^Y \tag{1}$$

If p^{th} completed principal component of the vector x^a which is the processed coordinates which can be allocated a score $y^p = x^a \times z^p$ where z^p is the pth eigenvector of the matrix of covariance then PCA can be formulated as $T = Z\ x\ Q$ where Z is vector and Q is the eigenvalues of the matrix of covariance.

3.6. Ensemble of classifiers

The information-rich features obtained from PCA are then passed through classifiers for prediction. For classification of pap smear images, the ensemble of classifiers consisting of Support Vector Machine (SVM) classifier with linear kernel [27], Random Forest classifier with tree size of 1500 [28] and a Fully connected neural network with dense layer and softmax activation function [29] are used.

Support Vector Machine (SVM) algorithm is one of the popular supervised learning algorithms which can be used for both classifications as well as regression. It separates classes in the pattern space using hyperplanes. SVM selects points in this space that give maximum margin from the line dividing two classes. Such extreme points are termed as support vectors and thus the algorithm is known as a Support Vector Machine.

In addition to SVM, we also have used the Random Forest (RF) classifier which is an ensemble model that makes decision trees based on a subset of features. Multiple random trees are made and thus a stable and more accurate prediction is obtained in RF classifiers. RF itself uses a majority ranking method to prevent possible overfitting. Both SVM and RF classifiers were implemented using the scikit-learn library. In a random forest, we used 1500 trees. Higher the trees mean that we will get better results but this can make computation utilization more and slow the process. So we decided to have a stable number after experimentation that will provide enough stability to the prediction.

A Fully Connected Neural Network (FCNN) created from scratch is also used for the classification of pap smear images. Here a neural network with a dropout rate of 50%, batch normalization and a dense layer with a softmax activation function is used. The newly constructed neural network is compiled with Adam optimizer at a learning rate of 10^{-3}. This FCNN is then trained and used for prediction, hyperparameters used for neural network classifiers are as shown in Table 3.

Table 3. Hyperparameter values of fully connected neural network classifier.

Hyperparameter	Value
Input shape	As per PCA (number of components)
Optimizer	Adam
Learning Rate	10^{-3}
Dropout Rate	50%
Loss Function	Mean squared error
Number of epochs	5 or 20
Batch size	32

3.7. Maximum voting and classification

To predict the final prediction of the ensemble classifier, the maximum voting approach is used [35]. The ensemble of the three classifiers using maximum voting is independent of bias and is more stable. The misclassification of individual classifiers is normalized and the accuracy of prediction is improved. The final prediction of the model is done by estimating the mode of the set of individual predictions.
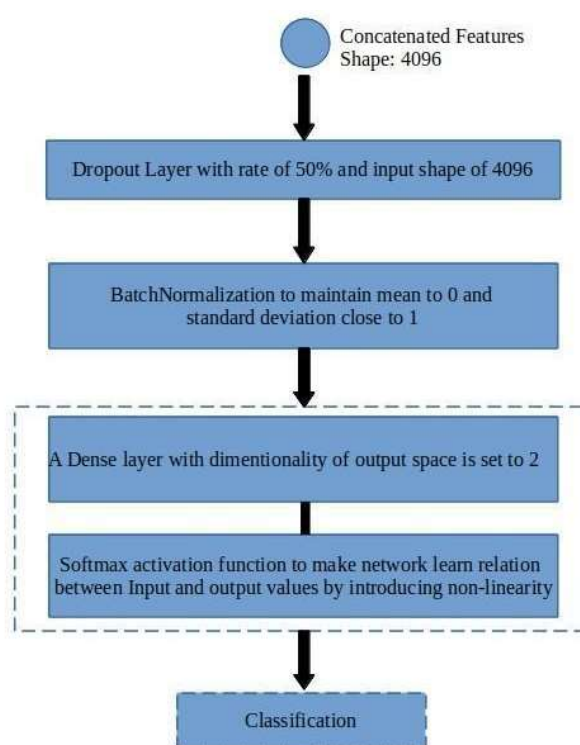
Figure 2. Workflow-2 of the proposed model framework.

3.8. Workflow 2

In workflow 2 as shown in Figure 2, the deep features extracted from the pap smear images from four pre-trained CNN models using transfer learning are used. The features are extracted as mentioned in the subsection on Deep Feature Extraction given earlier. The 4,096 image features obtained are passed to a sequential model of a traditional fully connected artificial neural network (ANN). A dropout layer with an input shape of 4,096 features and a rate of 50% is added and a batch normalization layer that maintains the mean and standard deviation of features to 0 and 1 respectively. After normalization, a dense layer with an output shape of 2 and softmax activation function is added. This model is compiled with the features obtained from frozen layers of pre-trained models. Additional parameters include the Adam optimizer and categorical cross-entropy loss function and trained with backpropagation to learn and predict the class of test images. The hyperparameters used in the different pre-trained models and ANN trained on deep features are as shown below in Table 4. The model is trained on the feature fusion vector obtained from pre-trained models and then predictions are done based on the output probabilities estimated by the output layer of ANN.

Table 4. Hyperparameters used in ANN.

Hyperparameter	XceptionNet	VGG16	VGG19	Resnet50	Newly added layers (ANN)
Optimizer	Adam	Adam	Adam	Adam	Adam
Loss function	Categorical cross-entropy	Categorical cross-entropy	Categorical cross-entropy	Categorical cross-entropy	Categorical cross entropy
Learning rate	10^{-4}	10^{-4}	10^{-4}	10^{-4}	10^{-3}
Batch size	32	32	32	32	32
Layers	71	16	19	50	Ensemble + 3
Pooling	3 × 3 max pool	2 × 2 max pool	2 × 2 max pool	3 × 3 max pool	Ensemble
Activation	ReLU	ReLU	ReLU	ReLU	softmax
Epochs	5 or 20	5 or 20	5 or 20	5 or 20	5 or 20

4. Dataset

The dataset is made ready for implementation in two steps- (1) Data acquisition from publicly available sources, (2) Data Pre-processing which includes converting varying class datasets into 2 classes namely Normal and Abnormal cells denoting non-cancerous and cancerous lesion presence respectively. To have uniformity for comparison among the datasets, the multi-class dataset is converted into a binary class. The datasets used for the experimentation on the proposed model framework are (a) Herlev Pap Smear cytology dataset [36,37], (b) Sipakmed Pap Smear dataset [38,39] and (c) LBC dataset of pap smear [40,41].

(a) Herlev Pap Smear dataset is collected from Herlev University Hospital, Denmark. The dataset has multiple versions and here is the improved version which was formed in 2005 is used. It is a seven-

class dataset and it is converted into two classes of normal and abnormal. Seven classes are Normal, Intermediate squamous, Columnar, Mild dysplasia, Moderate dysplasia, Severe dysplasia and Carcinoma in situ [36].

(b) Sipakmed Pap Smear dataset is a five-class dataset of isolated cells. These cells are classified as superficial-intermediate cells, parabasal cells, koilocytotic cells, Dysketarotic cells and Metaplastic cells depending upon the morphological properties of the cells [38]

(c) Liquid-Based Cytology (LBC) Dataset is made available by the Institute of Advanced Study in Science and Technology, Guwahati and Guwahati Medical College and Hospital. The dataset is a multi-cell dataset where images contain frames from the microscopic slide, whereas the Herlev and Sipakmed dataset we used contains single-cell images. The dataset is classified into four classes namely Negative for Intraepithelial Lesion or Malignancy (NILM), Low-grade squamous intraepithelial lesion (LSIL), High grade squamous intraepithelial lesion (HSIL) and Squamous cell carcinoma (SCC) [40].

Table 5. Distribution of dataset of the three datasets used in our experimentation.

Dataset	Category	Class	Number of images
Herlev	Normal squamous	Normal	74
	Intermediate squamous		70
	Columnar		98
	Mild dysplasia		182
	Moderate dysplasia	Abnormal	146
	Severe dysplasia		197
	Carcinoma in situ		150
SipakMed	Superficial	Normal	831
	Parabasal		787
	Koilocytotic		825
	Dyskeratotic	Abnormal	813
	Metaplastic		793
LBC	NILM	Normal	613
	LSIL	Abnormal	163
	HSIL		113
	SCC		74

As all the datasets are converted into two classes, distribution on the dataset is given in Table 5 for Herlev, Sipakmed and LBC datasets.
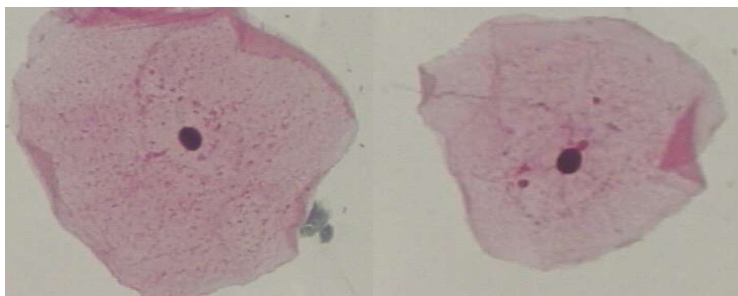

Figure 3. Normal class sample images from Herlev dataset.

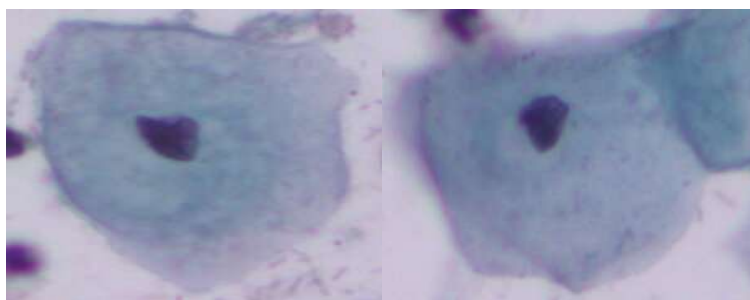**Figure 4.** Abnormal class sample images from Herlev dataset.

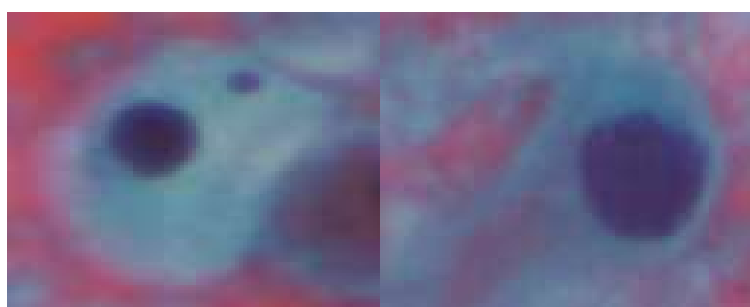**Figure 5.** Normal class sample images from Sipakmed dataset.

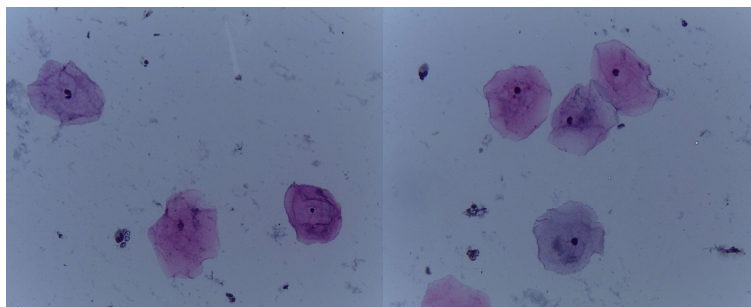**Figure 6.** Abnormal class sample images from Sipakmed dataset.

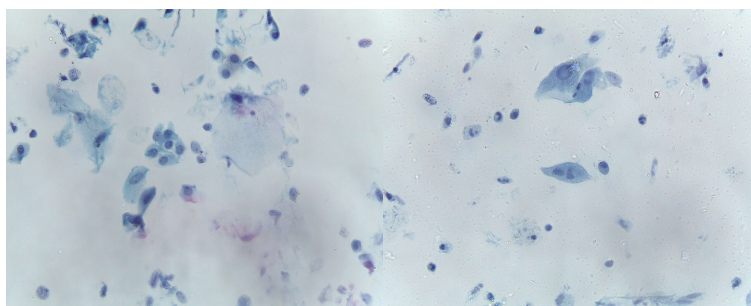**Figure 7.** Normal class sample images from LBC dataset.

Figure 8. Abnormal class sample images from LBC dataset.

Few sample images from the adopted datasets are as shown. Figures 3 and 4 show images from Herlev dataset with normal and abnormal class respectively [37]. Figures 5 and 6 show images from Sipakmed dataset with normal and abnormal class respectively [39] and Figures 7 and 8 show images from LBC dataset with normal and abnormal class respectively [41].

5. Experimental setup

For experimentation, online available Google colaboratory is used, which is a cloud-based service used here to train and test on the proposed model framework. In Google colaboratory, python 3 along with supported libraries like Tensorflow, Keras, Opencv are used. It provides a runtime GPU hardware accelerator to execute deep learning [42].

6. Results and discussion

The dataset used for experimentation is partitioned into 75% as training and 25% as testing images data. For evaluating the performance of the DeepCyto, different performance measures including accuracy, precision, recall and F-1 score are used [43]. The definition of the assessment metrics used is listed in Table 6.

Table 6. Evaluation metrics and their definition and formula.

Evaluation Metric	Definition and Formula
Accuracy (A)	It is correctly classified images from the total number of images $\dfrac{TP + TN}{TP + TN + FP + FN}$, where TP is True Positive and FP is False Positive
Precision (P)	It is the total number of True Positive (TP) divided by the total number of positive prediction $\dfrac{TP}{TP + FP}$
Recall (R)	It is the total number of Positive images correctly classified as Positive divided by the total number of Positive images $\dfrac{TP}{TP + FN}$
F-1 score (F1)	It is a weighted average of Precision and Recall $2 \times \dfrac{P \times R}{P + R}$

In experimentation of the DeepCyto model with both the workflows, feature fusion vectors are extracted by using stated pre-trained models. These vectors are given as input to both workflows.

Table 7. Performance of DeepCyto with 5 epochs.

Dataset ⇒	Herlev				Sipakmed				LBC			
Classifier/Model	A	P	R	F1	A	P	R	F1	A	P	R	F1
SVM	76.63	75	77	76	96.91	97	97	97	59.58	61	60	60
RF	87.50	89	88	86	96.35	96	96	96	60.58	57	60	57
FCNN	79.89	80	80	77	71.56	72	72	71	61.13	58	61	58
Voting-Ensemble	87.09	99	85	91	96.92	98	98	97	60.79	56	44	40
ANN	97.23	97	94	95	99.71	99	99	99	100	100	100	100

The results of these are given in Tables 7–10. Tables 7 and 8 depict the classification performance of individual classifiers, their ensemble, and ANN with 5 epochs and 20 epochs respectively. Tables 9,10 depicts the confusion matrices of the ensembles with 5 and 20 epochs respectively. Table 11 and 12 depict the confusion matrices of the ANN with 5 and 10 epochs respectively.

Table 8. Performance of DeepCyto with 20 epochs.

Dataset ⇒	Herlev				Sipakmed				LBC			
Classifier/ Model	A	P	R	F1	A	P	R	F1	A	P	R	F1
SVM	79.89	79	80	79	89.75	99	99	99	94.30	99	99	99
RF	86.41	86	86	86	99.57	96	96	96	98.48	92	92	91
FCNN	87.50	89	88	86	80.67	85	81	79	78.23	78	78	77
Voting-Ensemble	87.90	99	86	92	88.95	99	84	90	92.26	82	98	89
ANN	97.95	98	97	97	99.71	99	99	99	100	100	100	100

From Tables 7 and 8, it can be observed that among the three ML classifiers of Workflow-I, namely SVM, RF and FCNN, RF has given the better performance for almost all the datasets. Also, the Voting ensemble has given a better performance than each of the individual Workflow-I machine learning models for all the datasets.

In Table 7, for LBC datasets, all the Workflow-I ML classifiers and even the ensemble have given significantly less results for 5 epochs. This is due to the fact that, for multi-cell images of LBCs, five epochs are not enough for extracting informative feature vectors. This is improved in Table 8 with 20 epochs. In this case, performance on LBCs is improved than in Table 8. For other than LBCs, both tables show the most similar performance of ML classifiers and their ensemble.

ANN Classifier of Workflow-2 has given the best performances for 5 epochs as well as for 20 epochs on all three datasets. In summary, the combination of pre-trained models for feature fusion followed by the ANN classifiers is the best modality for the classification of pap smear cytology images. Also, it is just a two-step process consisting of feature extraction and training the ANN classifier. Moreover, it is best suited for single as well as multi-cell images. It is applicable for both conventional pap smear images as well as LBC images.

To illustrate the performance of our models following confusion matrices of the test data are as shown below.

Among the two workflows, higher accuracy is achieved in the second workflow where ANN is used. From the confusion matrices, we observe that the ANN model performed best for LBC where the normal class is in majority over the abnormal class. In Herlev and Sipakmed abnormal class is in majority and it is classified with accuracy above 97 and 99% respectively for both 5 and 20 epochs.

Table 9. Confusion matrices of the workflow-1. Voting ensemble classifier on test data with 5 epochs: a. Herlev, b. Sipakmed, c. LBC.

	a			b			c	
	Abnormal	Normal		Abnormal	Normal		Abnormal	Normal
Abnormal	134	22	Abnormal	420	11	Abnormal	24	31
Normal	1	27	Normal	10	273	Normal	46	92

Table 10. Confusion matrices of the workflow-1. Voting ensemble classifier on test data with 20 epochs: a. Herlev, b. Sipakmed, c. LBC.

a	Abnormal	Normal	b	Abnormal	Normal	c	Abnormal	Normal
Abnormal	135	23	Abnormal	429	77	Abnormal	57	1
Normal	0	26	Normal	1	207	Normal	13	122

Table 11. Confusion matrices of the workflow-2. Artificial neural network classifier on test data with 5 epochs: a. Herlev, b. Sipakmed, c. LBC.

a	Abnormal	Normal	b	Abnormal	Normal	c	Abnormal	Normal
Abnormal	134	4	Abnormal	429	1	Abnormal	70	0
Normal	1	45	Normal	1	283	Normal	0	123

Table 12. Confusion matrices of the workflow-2. Artificial neural network classifier on test data with 20 epochs: a. Herlev, b. Sipakmed, c. LBC.

a	Abnormal	Normal	b	Abnormal	Normal	c	Abnormal	Normal
Abnormal	133	2	Abnormal	429	1	Abnormal	70	0
Normal	2	47	Normal	1	283	Normal	0	123

The comparative analysis of the voting ensemble model and the Artificial Neural Network approach is given in Table 13. For both 5 and 20 epochs, the ANN model has outperformed the rest of the individual as well as voting ensemble classifiers.

Table 13. Accuracy on a test set using both approaches on all three datasets.

Dataset ⇓	Voting Ensemble Model		Artificial Neural Network	
	5 epochs	20 epochs	5 epochs	20 epochs
Herlev	87.09	87.90	97.23	97.95
Sipakmed	96.92	88.95	99.71	99.71
LBC	60.79	92.26	100	100

5. Conclusions and future work

The proposed framework DeepCyto presented in this paper has two workflows for the classification of pap smear images. Both of these workflows classify the pap smear images based on the feature fusion vectors extracted by a set of pre-trained models. The strength of the DeepCyto lies in the informative features extraction and is followed by accurate classification. The best accuracy achieved is 97% on the Herlev dataset, 99% on the Sipakmed dataset and 100% on the LBC dataset. The reason behind a high accuracy for Sipkamed is also due to the even distribution of images in the two classes. ANN has achieved the highest accuracy on Liquid-Based Cytology. The highest accuracies are given by the ANN trained on feature fusion vectors extracted by a set of pre-trained

models. By considering the overall performance on all datasets together, DeepCyto has given better performance as compared to the existing methods found in the literature. Additionally, the DeepCyto works evenly on single-cell as well as multi-cell images. Even with fewer epochs, workflow-2 has outperformed on LBC multi-cell images. In summary, the DeepCyto is an effective, accurate and two-step simple methodology consisting of extraction of feature fusion vectors and classification of single as well as multi-cell pap smear images even with a lesser number of epochs. One of the future works on this framework is tuning the machine learning ensemble models to provide higher accuracy. The limitations of this work include the computation cost and the ability of the model to handle overlapping multi-cell images. So our proposed framework can be generalized for overlapping cell prediction. Along with this, pap smear images contain a lot of distortion in image quality. Improving image quality without losing morphological information can be implemented to improve the accuracy of the models.

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Conflict of interest

All authors declare no conflicts of interest in this paper.

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