Multi-Stage CNN with Minimum Duplication Maximum Correlation Method for Pap Smear Images Classification

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KEYWORDS

CNN, Cervical Cancer Classification, Feature selection, Pap smear image analysis, Pap smear image segmentation

ABSTRACT:

Cervical cancer is a fatal disease that threatens women's lives. It is frequently discovered in an advanced stage and cannot be cured. Cervical cancer is a preventable disease, and one of the most effective methods of prevention is to get regular pap tests. Pap tests detect pre-cancerous cells, which can be treated before they turn into cancer. Generally, a cytopathologist uses a microscope to do Pap smear image analysis. Pap smear images are likely to contain thousands of normal and malignant cells. Due to the cytopathologist's error, the pre-cancerous stages of mild to moderate dysplasia and moderate dysplasia cells are frequently overlooked. In recent times, advanced technology such as automated computer-assisted image analysis (ACIA) has been used to improve the accuracy and efficiency of Pap smear image analysis. The design of ACIA for Pap smear image analysis is mostly based on CNN. In the existing studies based on CNN, emphasis has been placed primarily on accuracy. As a result, increasingly complex CNN architectures with high computational costs for Pap smear image analysis have been developed. The primary goal of this study is to create a CNN model that is both lightweight and computationally efficient for intelligent Pap smear image analysis. The proposed multi-stage CNN architecture utilizes two CNN models. In Pap smear images, the initial CNN model efficiently separates complex cells from the background. The creation of a second CNN model for the extraction of Pap smear image features. This study introduces the Minimum Duplication Maximum Correlation (MDMC) method to reduce redundant and undesired features. This significantly reduces the processing resources that the classification models usually require. Finally, multiclass SVM is used to separate the seven types of normal and abnormal cells from Pap smear images. To achieve a precise accuracy analysis, training efficiency analysis, and computational efficiency analysis of the proposed method, the model is trained and validated using various data set combinations. The experimental results demonstrate that the proposed method is more accurate at classifying seven types of normal and abnormal cells, has very little training loss, and consumes fewer computational resources for classification and model training.

1. Introduction

Cancer is a devastating disease that affects millions of people around the world each year, and there is still much research being done to find more effective treatments and cures [1]. Cancer is the uncontrollable proliferation of malignant cells within the body. This uncontrolled growth can lead to the destruction of normal tissue and can potentially spread to other parts of the body through a process known as metastasis [2]. Scientists and medical professionals have worked tirelessly to develop treatments that can limit the progression of cancer, such as chemotherapy and radiation, but there is still much work to be done in order to find a cure [3]. Cervical cancer is the most prevalent form of cervix cancer, and it is caused by the human papillomavirus (HPV). Every year, more than 604,100 women worldwide are diagnosed with cervical cancer, and over 341,831 women die from the disease. Cervical cancer can be diagnosed and treated early, before it advances to malignancy [4]. Diagnosis and treatment of cervical cancer before it advances to malignancy can

result in a complete cure [5]. To diagnose cervical cancer, doctors utilize imaging tests such as X-rays, ultrasounds, and magnetic resonance imaging (MRI) scans to view the inside of the patient's body and detect any abnormalities [6][7]. The Pap smear test has been an effective diagnostic test in detecting pre-cancerous changes and has helped to reduce the rates of cervical cancer mortality worldwide [8]. This method involves taking a sample of cells from the cervix and analysing them for abnormal changes, allowing for early diagnosis and treatment. A cytological sample is collected from the cervical region and spread onto a thin microscope slide using a soft brush, cotton stick, or wooden stick. The slide is then stained and examined under a microscope for any precancerous changes [9]. The stained slide is then examined by a trained laboratory technician to identify any abnormal cell changes that may indicate cervical cancer or precancerous conditions. The cell's central nucleus is typically difficult to view with the naked eye, making it difficult for doctors to diagnose cancer cells. The nucleus of a normal cell is smaller than the nucleus of an aberrant cell. Therefore, they rely on a microscope and other advanced computer aided technology to make sure they have identified the cancer cell correctly. Cervical screening is the process of detecting changes in the cells of the cervix that could potentially lead to cervical cancer.

In recent years, CNN models have been extensively studied and developed to address the increasingly challenging tasks in computer vision [10]. In addition to the advantages of CNN models are popular due to their ability to capture hierarchical and spatial information, as well as their capacity to leverage both labelled and unlabelled data. In most cases, CNN will automatically perform the process of feature extraction and selection [11]. However, in certain cases, a specialized method is required to perform feature selection in order to obtain the best results. Good feature extraction methods examine the data to identify which variables are most influential in determining the outcome and then select a subset of those variables to use in the model [12][13][14]. This can be done by looking at the correlation between the variables and the outcome, as well as by exploring non-linear relationships among variables. Furthermore, feature selection can also be done by examining the underlying patterns within the data.

Recently, academic researchers and medical experts have successfully developed CNN for cervical cancer screening [15][16][17][18]. However, the research objectives of the existing methodologies primarily focus only on classification accuracy. In addition, the architectures of the existing approaches for cervical cancer screening are composed of a high number of parameters and require a huge dataset for training the network and prevent over fitting. In some studies, the accuracy of CNN for cervical cancer screening has been improved through hybridization. In this study, a multi-stage CNN architecture and an innovative feature selection strategy is invented in order to create a cervical cancer detection system with high accuracy, low computational cost, and a limited data set.

Figure 1 illustrates the overall structure of the proposed cervical cancer detection system. Five significant image processing modules incorporate it. These five modules include pre-processing, feature extraction, feature selection, training and classification

Following is a discussion of the pros and cons of recently developed Pap smear image analysis and classification approaches. Section 3 explains the image processing steps and the proposed feature selection method for Pap smear image cell classification. Section 4 discusses the performance of Pap smear image classification using the proposed feature selection technique. In Section 5, the advantages and disadvantages of the proposed approach are discussed in detail. Section 6 concludes with a summary of the research findings and suggestions for future research.

2 Related works

Ankur Manna et al [19]. proposed a fuzzy rank-based ensemble of CNN models for cervical cytology classification. Three Convolutional Neural Network (CNN) architectures, Xception, DenseNet-169, and Inception v3, are utilised to build ensemble-based classification. On the ImageNet dataset, DenseNet-169 is trained to classify Pap stained single cell and whole-slide images. This method employs fuzzy rank-

based fusion of classifiers by considering two nonlinear functions on the decision scores created based on the response of said base learners. The final decision is depending on the forecast confidence level of the base classifiers. On the Mendeley Liquid Based Cytology (LBC) and SIPKMeD Pap Smear datasets, the model is assessed using a 5-fold cross-validation approach. This model achieves a precision of 99.55 percent. Some preprocessing procedures must be applied to the model so that the categorization of cells is unaffected by low picture contrast and overlapping cells.

Xiangyu Tan et al [20]. introduced a convolutional neural network-based Automatic model for cervical cancer screening. This screening technique could extract the distinctive characteristics of TCT pictures. Creating a model begins with diagnosing the pathological condition of glass slides. This diagnosis involves separating the scanned images into several single visual field images using glass slides. The results of processing the visual field are then integrated. This model could distinguish between positive and negative cells with a 99.6% degree of accuracy. The model has a minimal computational cost and demonstrates high robustness and objectivity.

The downsides of this strategy for using TCT images are that it is difficult to acquire TCT images, and it is also difficult to compare such images. The resulting TCT pictures contain considerable overlap and are difficult to compare. Aziz-ur –Rehman et al [21]. suggested a solution for automated screening utilising a convolutional neural network. This convolutional neural network is trained using a database of cervical cells. This network is trained using the transfer learning approach. ImageNet provides the weights required for initialization during the training phase. The network is then fine-tuned using a database of cervical cells. The feature vector is then extracted from the last layer that is fully connected. The cell samples are then classified or screened with the use of three classifiers: GentleBoost ensemble of decision trees (GEDT), Softmax reregression (SR), and Support vector machine (SVM). The system's performance is evaluated using 2-class and 7-class problems on the Herley database.

Using an attention feature pyramid network, Lei Cao et al [22]. proposed a method for detecting aberrant cervical cells in cervical cytology pictures. Two components comprise the method: an attention module and a multi-scale region-based feature fusion network module. Attention module interprets cervical cytology images similarly to pathologists. This module first determines whether extracted features should be emphasized or suppressed during the refinement process. The clinical information guides the second module. In this module, the improved characteristics used to identify aberrant cervical cells at many scales are merged. The model utilized clinical knowledge of actual aberrant cells, including their size and morphology. The model is validated using the 7030 standard. The model's shortcomings include the study's reliance on a restricted number of photos and the unexplored fact that there are numerous kinds of aberrant cells in the cervical abnormality condition.

Xia Li et al [23]. proposed a framework for the detection of aberrant cervical cells in the cytology pictures generated by the cancer screening test. For this objective, the suggested framework employs RCNN-FPN architecture. The model's scalability is improved by adding deformable convolution layers to the feature pyramid network (FPN). The geographical link between the foreground and background is enhanced by incorporating a contextually aware global module into the Region Proposal Network (RPN). The RCNN-FPN model is implemented in the Python environment using PyTorch (version 1.8.1). (version 3.5). The investigation utilised 20 WSI pictures.

Chen Zhao et al [24]. proposed a model for improving the categorization of cervical cancer from disparate data sets. The model generates images of cervical cells by utilizing taming transformers. It tends to give high-quality, adequate samples with balanced weights for cervical cancer datasets. The inclusion of MultiRes-block improves the model's extraction capability. The SE block is introduced to enhance the model's encoder structure. Incorporating the Normalization layer standardizes the data. The data is normalized to make linear processing via ReLU activation function in feed-forward more convenient. Using SMOTE-Tomek Links, a balance is achieved between the quantity of samples and weights of the photos and the source dataset. The combination of Tokens-to-Token Vision Transformers (T2T-ViT) and transfer learning improves the categorization of cervical cancer from the smear cell image dataset. On three publicly available cervical cancer datasets, the model's accuracy is evaluated. In rare instances, two types of cervical cancer cells may overlap on the same picture, making the classification of cervical cancer

cells more challenging. Consequently, the classification issue must be investigated further.
Yao Xiang et al [25]. proposed a segmentation-free and effective approach for the automatic screening of cervical cells. For the identification of cells or lumps, this method employs a contemporary object detector. In this investigation, the basis model is YOLOv3. YOLOv3 is a Convolutional Neural Network-based object detection algorithm. The classification phase is improved by cascading it with an extra classifier tailored to a given task. The smoothing procedure dealt with the presence of superfluous annotations. The procedure can be improved by providing computer-assisted primary screening and clinical diagnosis.
Dongyao Jia et al [26]. proposed a framework for the classification of cervical cells that includes the strong features of both Convolutional Neural Networks (CNN) and Support Vector Machine (SVM). GLCM (Gray-Level Co-occurrence Matrix) and Gabor were used to extract robust features. These retrieved features were then combined and provided as classification input to SVM. Using an efficient dataset amplification technique, the method's resilience was improved. Optimizing the feature extraction in both the strong features and the neural network can improve the model. The size of the dataset can be increased by allowing other researchers to access it.

3. Methods

The main objective of this research article is to effectively and automatically classify different types of cells in Pap smear images using a light weight deep learning architecture. After analysing the recently published methods in this area in terms of accuracy and runtime, a new cervical cancer classification method is proposed in this paper. Its process flow is explained through figure 2. According to this architecture, there are five important Pap smear image analysis modules namely image pre-processing, image segmentation, feature extraction, feature selection and classification. Feature selection plays an important role in this architecture. Feature selection is an important part of this architecture, as it helps to eliminate features that are irrelevant and add those that are most relevant to the model. Accuracy and computational complexity vary depending on the efficiency of feature selection. The efficiency of feature selection can help improve model accuracy while reducing computational complexity. Additionally, this architecture consists of two CNN models, the first of which is utilised to extract cells from background images. A second CNN model is utilised to extract texture features from segmented images in an efficient manner. Finally, a support vector machine is used to classify the different types of cells in Pap smear images.

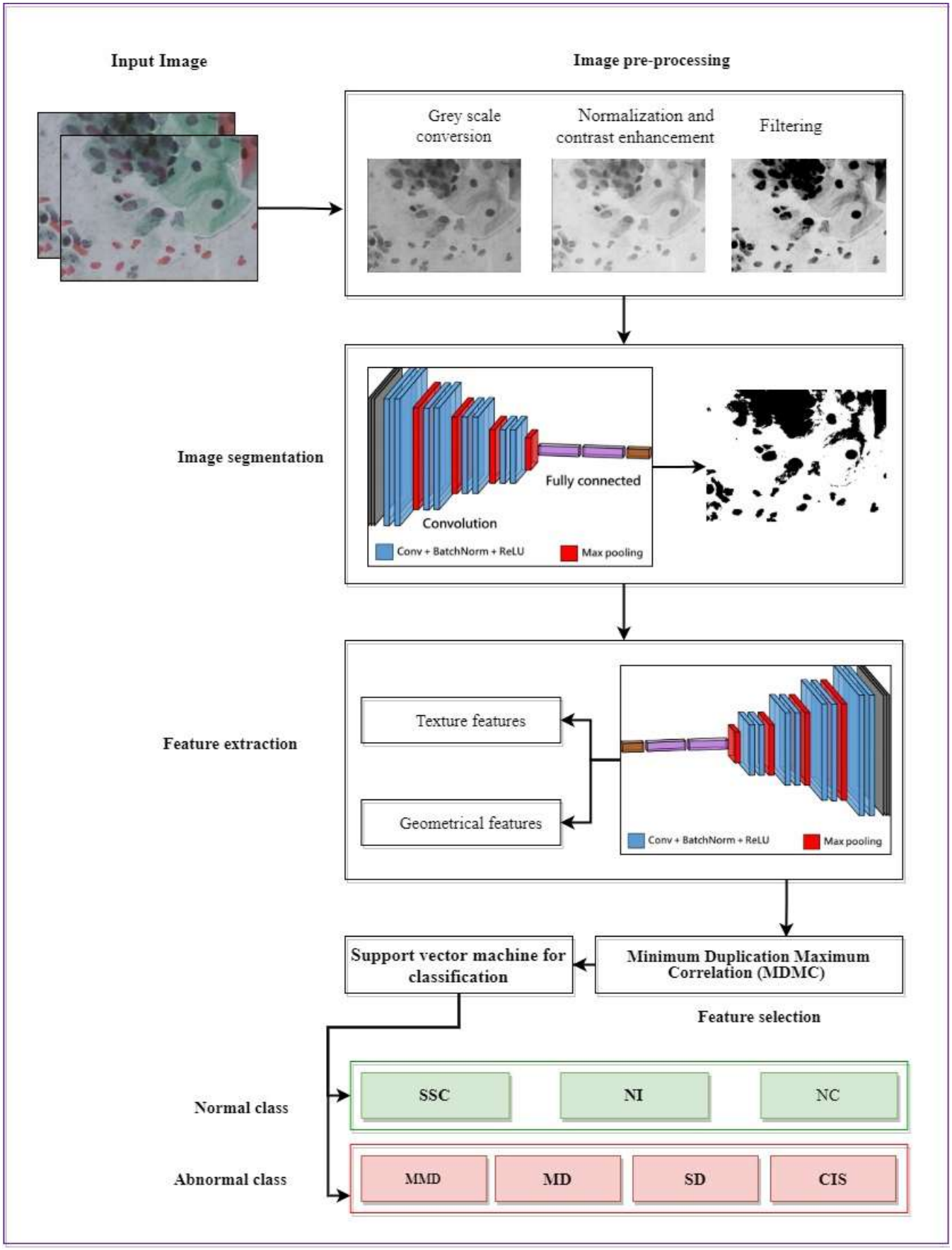


Figure 2 process flow of multi-stage CNN

3.1 Image pre-processing

Pap smear images contain a great deal of noise, which can make it difficult to diagnose and identify abnormal cells. To aid in this process, in this research, digital image processing techniques such as image normalization and adaptive Wiener filtering are used to reduce the amount of noise present in the images and make it easier to identify any abnormalities.

3.1.1 Image normalization

Normalizing Pap smear images can help improve the accuracy of computer-aided diagnosis and reduce errors caused by the low resolution and cellular structure of tissue samples. Generally, all Pap smear images are in RGB format. These images have different color combinations. To normalize these images, they must be converted to grayscale and then filtered with a contrast-limited adaptive histogram (CLAE) technique to create more uniform color distributions across the image. Following steps are used to improve the contrast of Pap smear images.

Step 1: Divide Pap smear images into a set of non-overlapping contextual regions of 8x8 blocks, with each region containing 64 pixels.

Step 2: For each contextual region, calculate the intensity histogram by dividing the range of pixel intensities into a predetermined number of intervals and counting the number of pixels in each interval.

Step 3: Once the histogram of intensity is found, the clip limit is found by measuring the distance from the histogram's first peak to a certain threshold value. After the clip limit is determined, each pixel's intensity is multiplied by a transformation function that adjusts the contrast of the image.

Step 4: The transformed pixel intensities are then placed in a new histogram, which is used to determine the optimal threshold value for the image.

Step 5: Each histogram is modified such that its height does not beyond the clip limit.

Step 6: The clip limit is used to determine how much the contrast of the image is adjusted, while the optimal threshold value is used to determine which pixels are lightened or darkened. For the standard CLAHE method with Uniform Distribution, the mathematical expression for changed grey levels is as follows.

$$g = [g_{max} - g_{min}] * p(f) + g_{min} \qquad [1]$$

g_{max} *is the maximum pixel value of* Pap smear*image*
g_{min} *is the minimum pixel value of* Pap smear*image*
g_{min} *is the computed pixel value of* Pap smear*image*

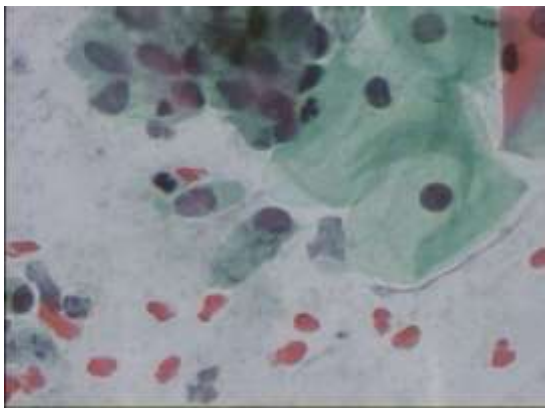
Regarding the exponential distribution the grey level can be changed as needed.

$$g = g_{min} - \left(\frac{1}{\propto}\right) * In[1 - p(f)] \qquad [2]$$

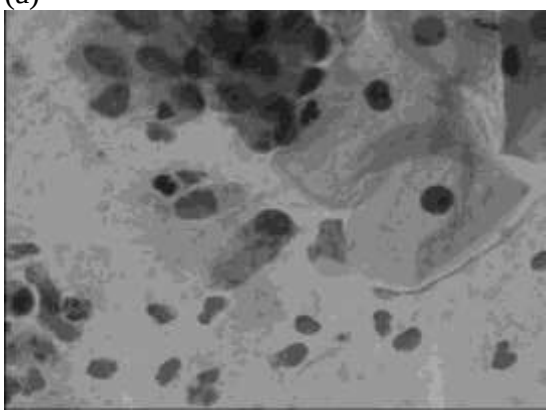
The CLAHE approach works on small areas of a picture called "tiles" rather than the complete image. The contrast of each tile is increased so that the histogram of the output region closely matches the histogram defined by the Distribution type. Rayleigh distribution CDF is given as;

$$y = p\left(f\frac{x}{b}\right) = \int_0^x \frac{x}{b^2} e^{\frac{-x^2}{2b^2}} \qquad [3]$$

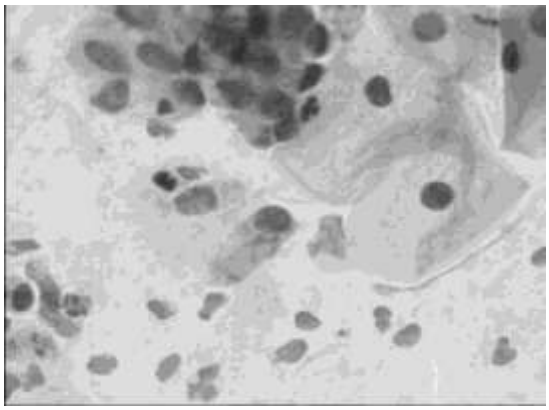
Step 6: Bilinear interpolation was used to mix neighboring tiles, and the picture grayscale values were adjusted based on the updated histograms.



(a)



(b)



(c)

Figure 3(a) Input image, (b) After grey scale conversion. 3(c) contrast enhanced image.

3.1.2 Adaptive Wiener filtering

Adaptive Wiener filtering is an effective method for restoring degraded images that have been corrupted by noise and blur [27] [28]. This filtering method provides a great degree of control over the image restoration process. This allows to effectively reduce noise in low contrast regions while still preserving edges in high contrast regions. The primary objective is to reduce the mean square error between the restored and original images. To accomplish this, Adaptive Wiener filtering works by analysing the local variance of an image in order to determine the degree of restoration needed. The goal of Adaptive Wiener filtering is to recover the clean, noise-free image, x (a, b), from the given noisy measurement, y (a, b). It can be represented by the following formula.

$x(a,b) = y(a,b) + n(a,b)$[4]

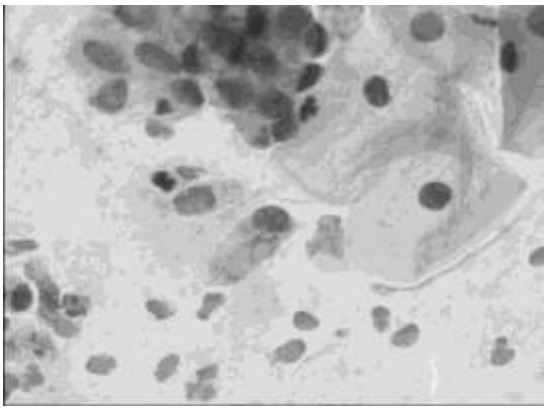
$n(a,b)$ is the noise in the Pap smear images (speckle noise, which can reduce image contrast and blur fine structures). By comparing the mean and variance of a pixel in different window sizes, such as (3 + 2i)2, where i is equal to 0, 1, 2, or 3, the best-suited window size can be determined. The window with the lowest average value is then selected as the final processing window. The filter template can be chosen based on the region's characteristics. For example, if there is a high amount of contrast or noise present in an image, a larger window size should be selected for that region. The large window filter is applied to the smooth portion of the image, while the small window filter is applied to the detail portion. By selecting the appropriate filter template for different regions of an image, it is possible to effectively reduce noise and maintain the integrity of more complex details. This can boost efficiency and preserve edges and texture. The following equation is utilized to filter pixels and obtain the noise free image.

$$r(a,b) = \mu + 1 - q + \Delta) * (s(a,b)) - \mu) \quad [5]$$

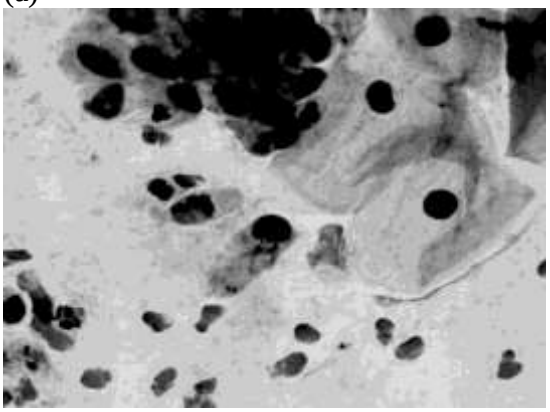
$$q = \frac{\sigma_{avg}}{\sigma_{var}+1} \quad [6]$$

$$\Delta = \frac{\sigma_{avg}}{\sigma_{min}+\sigma_{max}+1} \quad [7]$$

$s(a,b)$ represent the actual pixel of Pap smear images, $r(a,b)$ represents the processed pixel, parameters σmin which represents the minimum variance of all pixels in the image, σvar which is used to calculate the variance of a particular window in an image, and σmax which is used to calculate the maximum intensity value of a particular window in an image. This helps to ensure that the pixel values of the image are processed in the most accurate and efficient manner possible, resulting in a higher quality image. The output of adaptive wiener filtering is shown in figure 4.



(a)



(b)

Figure 4 (a) After normalization. (b) After adaptive wiener filtering

3.3 Feature details

In this research, two types of features are extracted from the Pap smear images after segmentation: texture features and geometrical features. Texture features, such as variance and skewness, measure the spatial arrangement of pixels, while geometrical features characterize the shape of nuclei. Texture features are used to detect the changes in texture in Pap smear images and identify regions where cancerous or precancerous cells exist. Geometrical features, such as cell intensity, average cell size, total cell area, and maximum cell intensity, are used to describe the shape of cells and identify abnormal cells. The combination of these two types of features can provide more information about the cells present in Pap smear images, leading to improved accuracy in automated screening. Features details are explained in the following tables 1 and 2.

In this study, CNN is used to extract four significant geometrical features: Average Cell Intensity, Average Cell Size, Total Cell Area, and Maximum Cell Intensity. All of these terms are related to cell morphology. Following formulas determine these geometrical features.

Table 1 texture features extracted by the CNN model.

Feature name	Equations	
Autocorrelation	$\mathrm{T_{AC}} = \sum_i \sum_j (i,j)p(i,j)$	[8]
Contrast	$T_T = \sum_{n=0}^{N_e-1} n^2 \sum_{n=i}^{N_e} \sum_{n=j}^{N_e} \{p(i,j)\}$	[9]
Correlation	$T_C = \frac{\sum_i \sum_j (i,j)p(i,j) - \mu_x \mu_y}{\sigma_x \sigma_y}$	[10]
Energy	$= \sum_i \sum_j p(i,j)$	[11]
Dissimilarity	$T_D = \sum_i \sum_j \lvert i-j \rvert * p(i,j)$	[12]
Entropy	$T_E = \sum_i \sum_j p(i,j) \log\big(p(i,j)\big)$	[13]
Homogeneity	$T_H = \sum_i \sum_j \frac{1}{1+(i-j)^2} p(i,j)$	[14]
Variance	$T_V = \sum_i \sum_j (i-\mu)^2 p(i,j)$	[15]
Cluster shade	$T_{CS} = \sum_i \sum_j (i+j-\mu_x-\mu_y)^2 p(i,j)$	[16]
Cluster Prominence	$\sum_{i=0}^{n-1} \sum_{b=0}^{n-1} \{i+j-\mu_x-\mu_y\}^4 p(i,j)$	[17]
Average Skewness	$T_{AS} = \sum \frac{1}{\sigma^3} \sum_i^i \sum_j^j \big((a*b)-\mu\big) \frac{3\big(p(i,j)\big)}{n}$	[18]

Average Kurtosis	$T_{AK} = \sum \frac{1}{\sigma^4} \sum_i^i \sum_j^j \big((a * b) - \mu\big) \frac{4\big(p(i,j)\big)^{-3}}{n}$	[19]
Maximum probability	$T_{MP} = \max_{i,j} P_D[i,j]$	[20]
Homop	$T_{HP} = \sum_i \sum_j \frac{1}{1 + abs(i-j)} P_{dij}$	[21]
Cluster Homogeneity	$T_{CH} = \sum_i \sum_j \frac{P_D[i,j]}{1 + (i-j)}$	[22]

Table 2 geometrical features extracted by the CNN model.

Feature name	Equations	
Average Cell Intensity (ACI)	$ACI = \frac{Sum\ of\ total\ intensities}{Number\ of\ segmented\ pixels}$	[23]
Average Cell Size (ACS)	$ACS = Total\ lengthe\ and\ total\ breadth\ of\ cells$	[24]
Total Cell Area (TCA)	$TCA = The\ total\ number\ of\ cells\ in\ the\ segmented\ image$	[25]
Maximum Cell Intensity (MCI)	$MCI = Maximum\ value\ of\ intensity$	[26]

3.3 Multistage CNN

In this study, a CNN with multiple stages is proposed. In previous studies, a single CNN architecture was used to extract the feature of Pap smear images. This makes the process of extracting features from Pap smear images more difficult. In order to address this issue, stage 1 CNN and stage 2 CNN are introduced in this study. The stage 1 CNN locates complex cell structure from Pap smear images. The stage 2 CNN extract textural and geometrical features from the localized cell structure, which are then sent to the feature extraction layer.

3.3.1 Stage 1 CNN

Stage 1 CNN architecture is used to efficiently localize the cell structure of Pap smear images. The segmentation network differs from the common CNN structure in several ways. Firstly, it replaces the traditional fully-connected layer with a fully convolutional layer. This is beneficial because a convolutional layer allows for features to be detected in any region of an image, regardless of size. Additionally, a segmentation network reduces the number of parameters in the model, making it more efficient and easier to optimize. Moreover, a segmentation network offers more precise results than a regular CNN because it produces feature maps that indicate the exact location of specific objects.

In this paper, the 2D U-Net architecture is used to extract complex cell structure from Pap smear images. The 2D U-Net architecture is well suited for segmenting cell structures due to its efficient use of both the contracting and expansive paths. Further, the 2D U-Net architecture has the advantage of having a contracting path, which allows for feature extraction at multiple resolutions. The convolutional path of the 2D U-Net architecture consists of a series of convolutional layers, each of which has an increasing number of filters and decreasing resolution. The contracting path of the 2D U-Net architecture is able to extract increasingly complex features from the image, which allows for the extraction of more intricate cell structures. Meanwhile, the expansive path of the 2D U-Net architecture is composed of convolutional layers, pooling layers, and up sampling layers, which allow for efficient feature mapping and pixel-wise segmentation. By using both the contracting and expansive paths, the 2D U-Net architecture is able to take advantage of the feature extraction of the contracting path, as well as the pixel-wise segmentation of the expansive path. Through the integration of the contracting and expansive paths, the 2D U-Net architecture

is able to provide accurate and efficient segmentation of cell structures. This makes the 2D U-Net architecture a powerful tool for segmenting and analysing cell structures. Figure 5 shows the 2D U-Net architecture for Pap smear images cells localization.

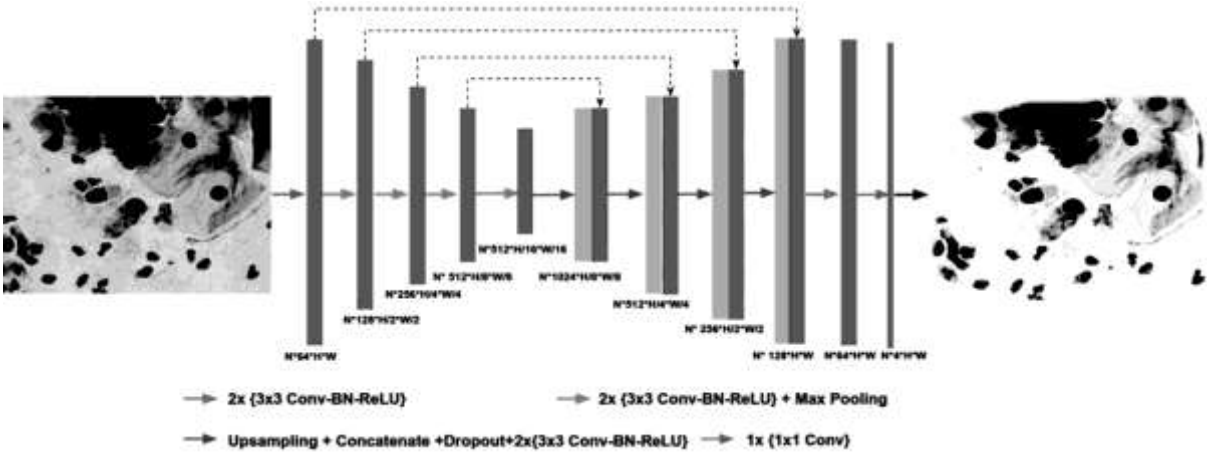


Figure 5 the 2D U-Net architecture for Pap smear images cells localization.

3.3.2 Stage 2 CNN

Stage 2 CNN is used in this paper to extract texture and geometrical features from segmented Pap smear images. Unlike shallow neural networks, CNNs are capable of capturing complex patterns in large images by making use of convolutional layers that perform feature extraction. This extraction of features is further enhanced by pooling layers, which reduces the resolution of the images and helps to reduce over fitting. The structure of the CNN includes convolutional layers for feature extraction and pooling layers for resolution reduction. Figure 6 shows the outline of the feature extraction process. After segmentation, numerous superfluous Pap smear image components are eliminated. For feature extraction, a relatively simple CNN architecture is adequate. In this research, two convolution and pooling layers are employed. These two convolution layers are comprised of convolution kernels, with the first layer being responsible for initial feature detection. The two convolution and pooling layers extract features from the Pap smear images, allowing for efficient computation and improved accuracy of results. These extracted features are then used to train a Support Vector Machine (SVM) model, which is then used to classify the images into different classes.

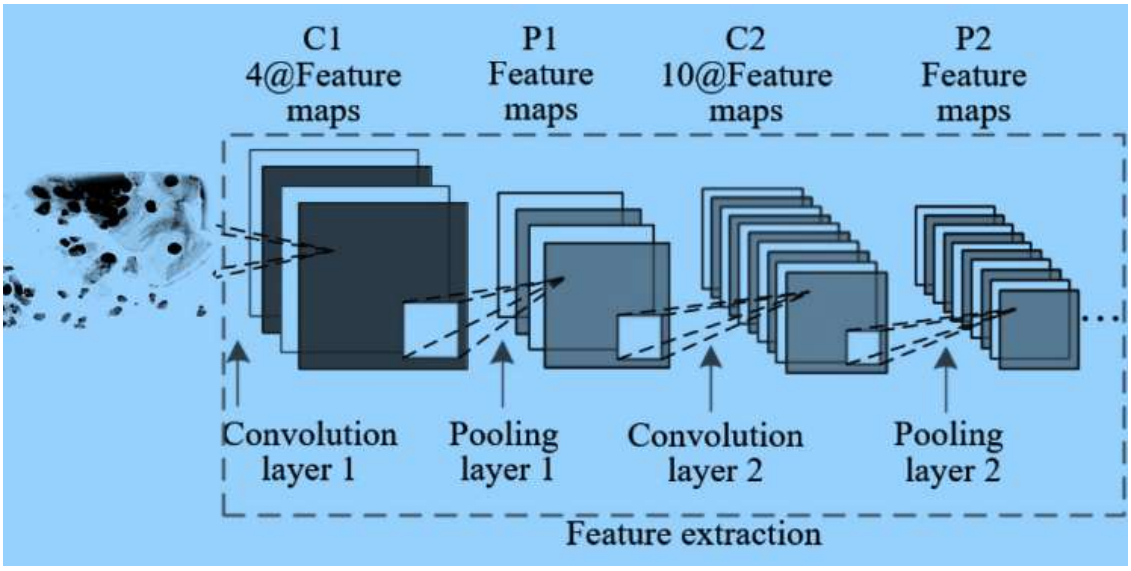


Figure 6 CNN architecture for feature extraction process.

3.4 Feature selection (Minimum Duplication Maximum Correlation)

In most cases, CNN will automatically perform the processes of feature extraction and selection. In general, the features extracted using CNN will be highly redundant, with a large number of features that are unrelated to the classification results. CNN's efficiency can be increased if these two issues are resolved effectively. In this study, the Minimum Duplication Maximum Correlation (MDMC) method is developed to improve the efficiency of CNN's feature selection. There are two different kinds of algorithms in this proposed MDMC feature selection technique. Initially, redundant features are deleted from the features extracted by a multi-tier CNN. Second, MDMC eliminates features with no correlation to the classification results. The MDMC algorithm selects a set of features that have the highest correlation with the final output result. Following formula 27 is used to determine the maximum correlation features.

$$Max(F,y), C = \frac{1}{|F|}\sum_{x_i \in F} I(x_i; y) \quad [27]$$

The features set F contains n number of texture and geometrical features. The relationship between the features and the target class is represented by $Max(F,y)$, where y is the target class. If the relationship between the (F,y) high it returns 1, otherwise the value is close to 0. In the above equation, select the highly correlated texture and geometrical features, but also the features that contain a significant number of redundant features. This can lead to a decrease in accuracy due to an increase in false positive detections and other issues. To effectively solve this problem, we introduced a minimum duplication approach by using the following formula:

$$Min_D, D = \frac{1}{|s|^2}\sum_{x_i \in F} I(x_i, x_j) \quad [28]$$

By combining a minimum duplication maximum correlation.

$$Max\phi(C,D), \phi = C \quad [29]$$

The MDMC algorithm has the capability to reduce redundancy in feature sets, resulting in improved prediction accuracy and reduced computational cost. This algorithm allows for a simplified selection process, as it minimizes the redundancy of features while maximizing the correlation of features to the final output. The MDMC method's process flow is described in algorithm 1.

Algorithm 1: MDMC Algorithm

Input: $(T_{f1}, T_{f2}, T_{f3}, \_\_\_\_\_ T_{fn})$
Output: $F_{Bestfeatures}$
Begin
For $i = 1$ *to n texture and geometrical featu*
    $Max(F,y) = (T_{fi})$// *determine the maximum correlation features using formula 27*
    Set $\tau = 0.7$ // τ *is the threshold value*
    If $(Max(F,y) < \tau)$
        There is no significant correlation
    Else
        $F_{List} \leftarrow Add(T_{fi})$
    End If
Minimum duplication approach by using the formula (28)
Combining a minimum duplication maximum correlation

12 ***End For***
13 $F_{Bestfeatures} \leftarrow F_{List}$
14 ***Return*** $F_{Bestfeatures}$

3.4 Classification

The SVM method works by finding an optimal hyperplane in an N-dimensional space that best separates the data into two classes [29]. The hyperplane can then be used to identify lesions of the same type in new images, allowing for an accurate and fast diagnosis. SVM is used in this study to classify the seven types of lesions from Pap smear images. By using a data set of Pap smear images and labelling them according to their respective lesion types, SVM can be used to find an optimal hyperplane that correctly classifies these images. The goal of equation (31) is to make the classification process as simple as possible. The optimal hyperplane can be determined by solving the optimization problem defined in equation 32 and 33.

$$U = \vec{w}.\vec{x} - b \quad [31]$$

$$\frac{1}{2}||\vec{w}||^2 \quad [33]$$

$$y_i(\vec{w}.\vec{x} - b) \geq 1 \forall i \quad [33]$$

4. Results

4.1 System setup

The potential of the proposed computer-based cervical cancer system has been thoroughly examined in this section. In this section, the experiment's software tools, system specifications, datasets, and performance measures are explained in detail.

4.1 System specifications

Table 3 describes the hardware required in the development of the proposed cervical cancer classification system. The operating system and software tools used to develop this model are detailed in Table 4.

Table 3 System details

Device name	Configuration
Processor	12th Gen Intel Core i7-12100
SSD	500 GB-7200 RPM
GPU processor	NVIDIA GTX 1660 SUPER
Memory	2 x 16 GB, DDR5

Table 4 Software tools and system details

Software details	Version
Operating system	Windows 11 Pro
Matlab version	2019
Deep Learning Toolbox	2019

4.2 Dataset details

In this study, two types of data sets were employed to train and evaluate the classification performance of the proposed multi-stage CNN. DTU/Herlev, a widely used Pap smear data set, is first used to train a multi-stage CNN [30]. It includes single cell and multi cell images. All of the Pap smear images in the DTU/Herlev data set were captured by cytopathologists with a microscope equipped with a frame grabber. Additionally, these Pap smear images were captured with a pixel resolution of 0.201 m/pixels. In this data set, single cells were isolated from multi-cell images using the CHAMP commercial tool developed by

DIMAC Imaging systems. All these extracted cells are divided into seven classes. Its details are explained in detail in the following table.

Furthermore, to evaluate the real time classification efficiency of the proposed model, 3600 Pap smear images were collected from the cancer research laboratory at the NIMS Medicine and Research Center in Thiruvananthapuram, Kerala. This includes 1029 normal cells images and 2571 malignancy cells images. All these images were captured at 0.25 µm pixel size. All of these were selected with the assistance of knowledgeable cytopathologists from the NIMS medical centre. All of the test images were obtained with a microscope (Olympus BX51 bright-field microscope) and camera (Hamamatsu ORCA-05G 1.4 Mpx monochrome camera) that had a different configuration than the training images.

4.3 Cell structure

In general, normal cell structure can vary greatly depending on the type of cell, but all cells contain the same core components: the nucleus, cytoplasm, and organelles, as shown in figure 7. The nucleus contains chromosomal material and has a number of specialized organelles, like the nucleolus, the endoplasmic reticulum, and ribosomes. The cytoplasm surrounds the nucleus and contains other organelles like mitochondria, lysosomes, and vacuoles.

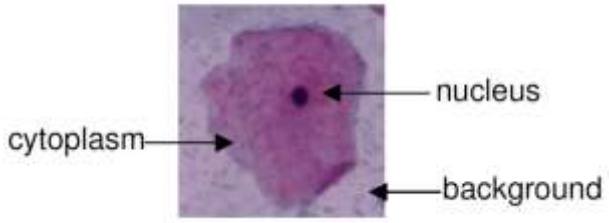
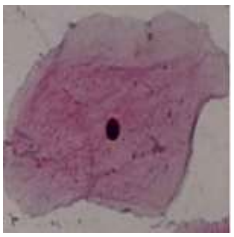
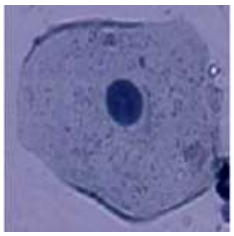
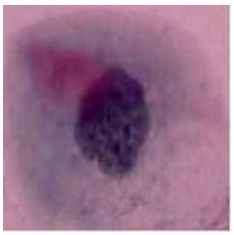


Figure 7 cell structure.

Table 5 Normal and abnormal cells in the DTU/Herlev dataset.

Cell name	Definition	Class name	Cell type	Image
Superficial squamous cells	The superficial squamous cells are the most abundant type of epithelial cells found in the body and line many of its surfaces, such as the skin, esophagus, trachea, and other organs. These cells have a diameter of approximately 45 to 50 µm and are composed of two layers that form a protective barrier [31].	SSC	Normal	
Normal Intermediate	This intermediate cell typically contains coarsely granular chromatin with one or two nucleoli and a single nucleolar organizing region. These cells have a diameter of 35 to 40 µm, and their cytoplasm contains ribosomes and small granules [32].	NI	Normal	
Normal Columnar	This type of epithelium is found in parts of the body such as the stomach and small intestine, where they play an important role in absorption and secretion. These cells have a diameter of approximately 120-180 µm and are specialized for absorption and secretion.	NC	Normal	

Mild to moderate dysplasia	"Mild to moderate dysplasia" is a term used to describe an abnormality of the cells in a given area. This indicates that the cells are dividing at an increased rate, which suggests that it may be a pre-cancerous condition. Their nuclei have an irregular shape [33].	MMD	Abnormal	
Moderate Dysplasia	Dysplasia Moderate dysplasia is a pre-cancerous condition that is characterized by abnormally dividing cells that have nuclei of an irregular shape.	MD	Abnormal	
Severe Dysplasia	Severe dysplasia is a pre-cancerous condition in which the abnormal cells are even larger, and they have nuclei that are even more irregularly shaped than those seen with moderate dysplasia [34].	SD	Abnormal	
Carcinoma In Situ	Carcinoma in situ is a more advanced form of dysplasia and can be identified by atypical cells that have nuclei with an irregular shape [35].	CIS	Abnormal	

4.3 Experiment details

The experiment is split up into four sections, with the first section evaluating the segmentation effectiveness of the recommended method. Second, the proposed method's cancer classification accuracy has been assessed utilising important accuracy measures. Thirdly, the proposed method's training effectiveness has been examined. Finally, the proposed method's computing efficiency has been evaluated. In addition, the comparison is performed using the following most prevalent deep learning models: CNN, AlexNet and GoogleNet

4.3.1 Classification accuracy analysis

This section explains the experimental results obtained using the proposed multistage CNN for cervical cancer classification system. Accuracy is an important criterion to use to evaluate the performance of the proposed algorithms since misclassification of benign cells as malignant can lead to false diagnoses and mistreatment, while misclassification of malignant cells as benign can lead to neglecting serious medical conditions. Thus, the evaluation of accuracy in this study focuses on the ability of algorithms to correctly identify benign and malignant cells from Pap smear images. The accuracy of the proposed model is evaluated by measuring the true positive rate (TPR) and true negative rate (TNR), which are defined as the number of true positives and true negatives divided by the total number of samples in the dataset. True positives (TP) refer to cases where the cervical cancer cells have been correctly identified, while true negatives (TN) refer to cases where the cervical cancer cells have been correctly identified as not being present. False positive (FP) cases refer to those where cervical cancer cells have been incorrectly identified and false negatives (FN) refer to cases where normal tissue has been incorrectly identified as cervical cancer cells. Accuracy can be expressed mathematically by the formula 36.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad [36]$$

Sensitivity being a measure of how well a screening test identifies the presence of a condition or disease. A higher proportion of true positives indicates higher sensitivity in the classification system, which can help reduce mortality rates for cervical cancer patients. According to the classification of cervical cancer, sensitivity entails the precise identification of the various stages of cervical cancer cells from Pap smear images. Following formula is used to calculate the sensitivity of proposed cervical cancer classification system.

$$\text{Sensitivity (Recall)} = \frac{TP}{TP+FN} \quad [37]$$

According to the classification of cervical cancer cells, specificity determines the reliability of non-cancer cells' classification results. High specificity (low false positives) indicates that the model is able to correctly identify non-cancer cells, while high sensitivity (low false negatives) indicates that the model is able to correctly identify cancer cells. The following formula is used to calculate the specificity of a model.

$$\text{Specificity} = \frac{TN}{TN+FP} \quad [38]$$

Precision is an important metric for evaluating a cervical cancer detection system, since it provides an indication of how well the system is able to distinguish between true positive and true negative results. Precision is calculated by the following formula.

$$Precision = \frac{TP}{TP+FP} \quad [39]$$

The F1-score is a metric used to evaluate a model's performance, based on its precision and recall. Formula for calculating the F1-score is as follows.

$$F1 - score = \frac{2(Recall \times Precision)}{Recall+Precision} \quad [40]$$

This section examines the classification accuracy of the suggested technique while classifying MMD, MD, SD, and CIS abnormal classes in Pap smear images, as well as the classification accuracy of CNN, AlexNet, and GoogleNet.

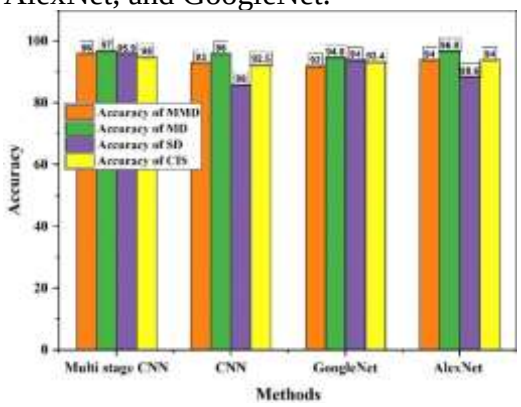


Figure 5(a) accuracy comparison results.

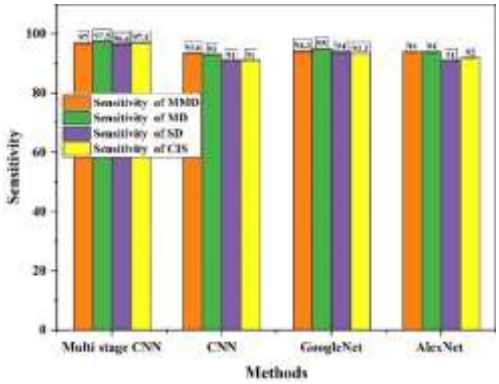


Figure 5(b) accuracy sensitivity results.

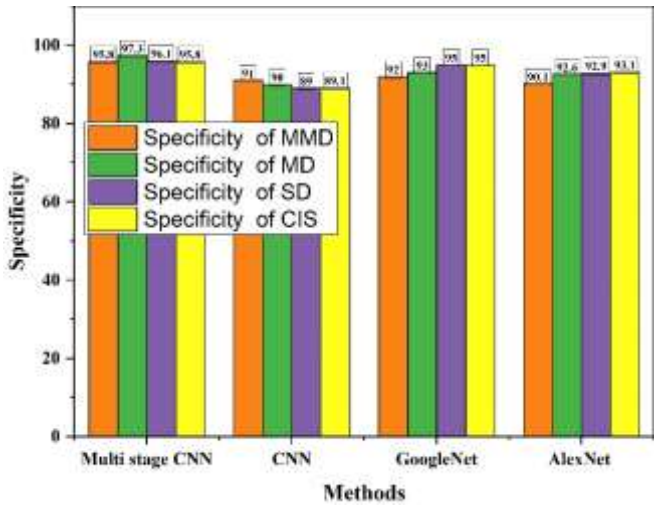


Figure 5(c) specificity comparison results.

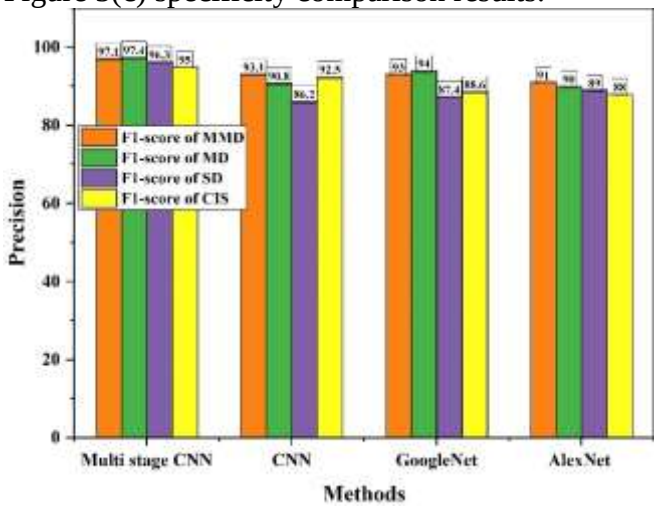


Figure 5(d) accuracy precision results.

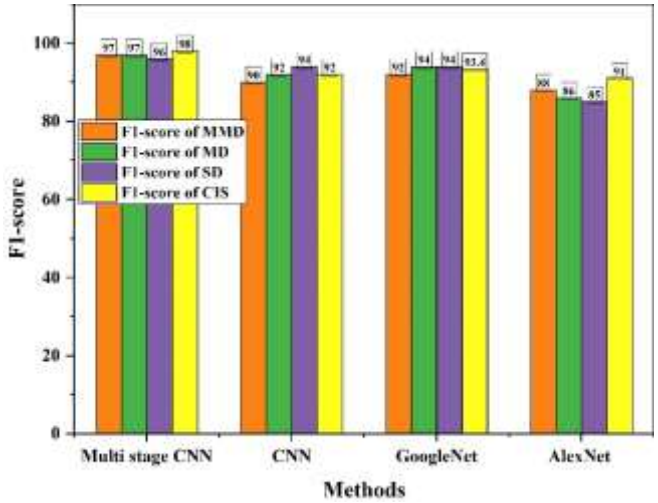


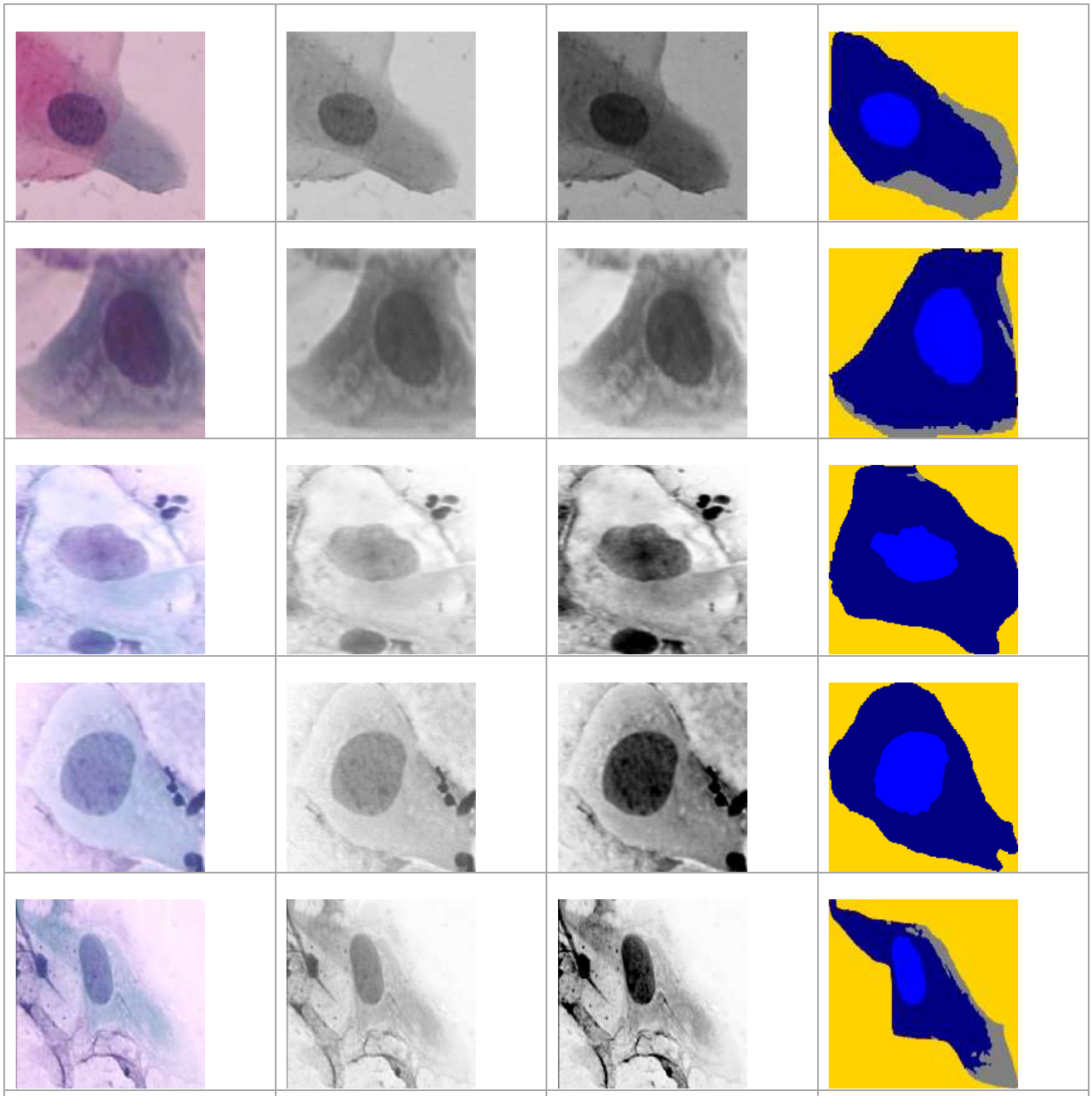
Figure 5(e) F1-score comparison results.

The experimental results show that the proposed multi stage CNN architecture can achieve high classification accuracy in identifying cervical cancer from Pap smear images. The results obtained were promising, with accuracy values of MMD with 96 %, MD with 97 %, SD with 95.9 % and CIS with 95 % for malignant and pre-malignant classifications respectively. Figure 5(a) shows that the proposed multi-stage CNN outperforms existing deep learning methods in terms of accuracy. By leveraging the ability of the multi-stage CNN to accurately identify complex features, the MDMC feature selection technique is able to significantly reduce the total number of input features used by traditional deep learning methods while still maintaining a high level of accuracy. This suggests that the proposed MDMC feature selection is a promising approach to feature selection, as it can effectively identify relevant features while avoiding over fitting or redundancy in the input data. Additionally, the accuracy values for classifying individual types (MMD, MD, SD, and CIS) of lesions were also high.

Furthermore, the sensitivity of our multi-stage CNN model is 97% for MMD classification, 97.5% for MD classification, 96.6% for SD classification, and 97.1% for CIS classification, which is significantly higher than models such as GoogleNet and AlexNet. As shown in Figure 7(b), the multi-stage CNN has higher sensitivity than existing deep learning methods, which can detect abnormal cells with greater accuracy. This implies that the multi-stage CNN can detect abnormal cells in Pap smear images more effectively. The high sensitivity of the multi-stage CNN suggests that it has the potential to improve cervical cancer screening.

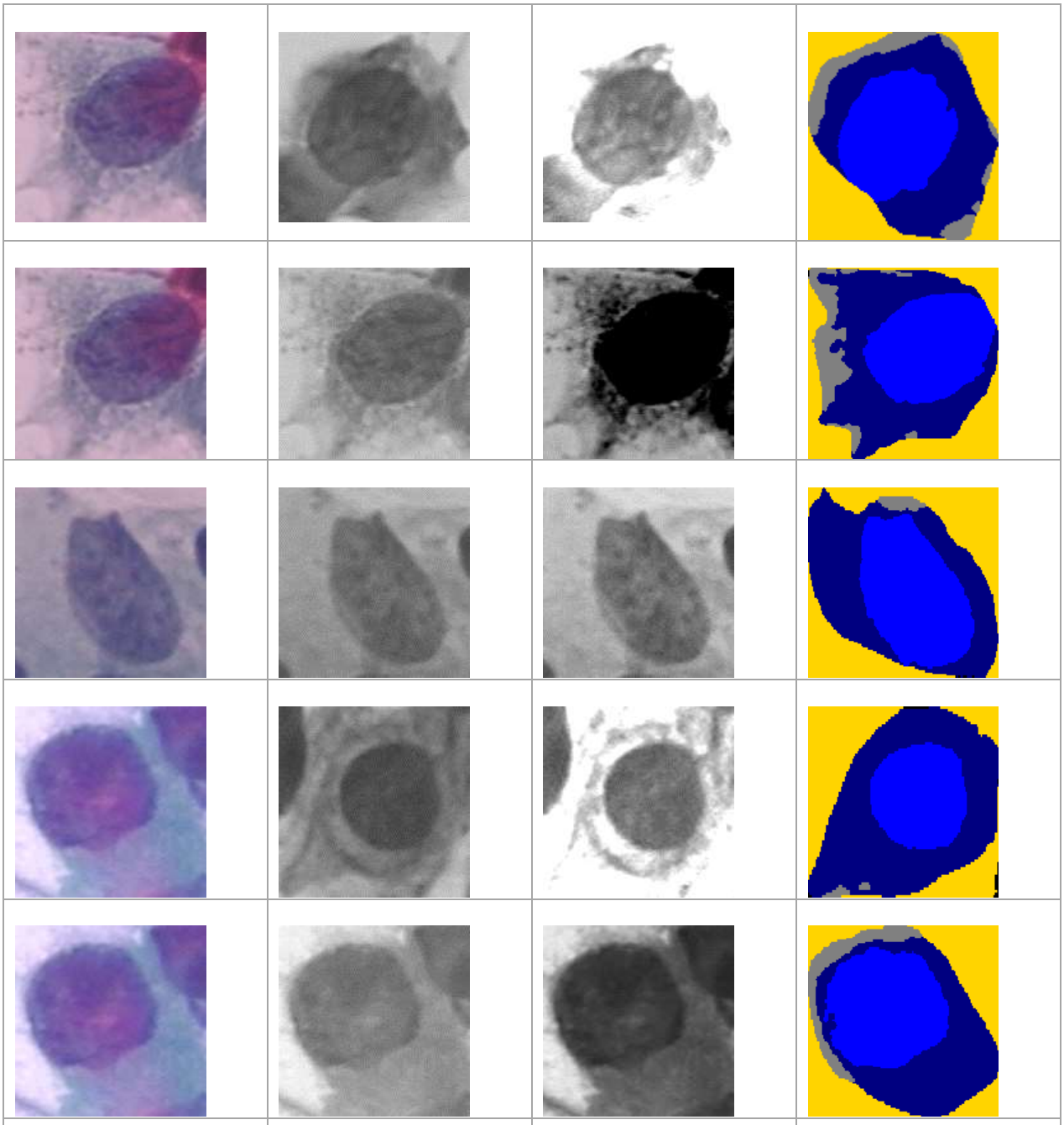
As shown in Figure 5(c), the multi-stage CNN has a higher specificity rate for cervical cancer screening than existing deep learning methods. This increased specificity results in fewer false positives. The higher specificity rate of the multi-stage CNN leads to a more accurate and efficient screening process, reducing unnecessary costs associated with false positive results. The benefits of using a multi-stage CNN are clear from figures 5(d) and 5(e): it achieves higher precision and an F1 score than existing deep learning methods. The experimental results indicate that the combination of the multi-stage CNN model with the MDMC feature selection technique and preprocessing techniques can greatly improve the accuracy of cervical cancer diagnosis. These results also indicate that the proposed method is capable of accurately predicting cervical cancer at earlier stages, making it a valuable tool for cancer screening.

Figures 6, 7, 8, and 9 show the implemented findings of this research. This section provides the segmentation results for mild to moderate dysplasia (MMD), moderate dysplasia (MD), severe dysplasia (SD), and carcinoma in situ (CIS). Three distinct colours are used to differentiate the nucleus, cytoplasm, and background region of cells. Accordingly, light blue symbolizes the nucleus, dark blue represents the cytoplasm, and yellow represents the cell's background. Through these findings, it is possible to accurately assess the different types of dysplasia and to visually observe their differences. The three distinct colors help to easily distinguish the various components of the cell, making it much easier to accurately train a classification model. Through the use of these three distinct colors, a physician can quickly and easily identify various components of a cell and detect any abnormalities that may be present. Overall, the MMD segmentation result shows that the presence of light blue is less than dark blue, while in the MD and SD segmentation results, the presence of light blue is slightly more and dark blue is slightly less. CIS reveals a similar pattern, where the light blue region is more dense than the dark blue region. This is an important distinction, as it allows physicians to easily and quickly distinguish between healthy cells and cells affected by dysplasia.



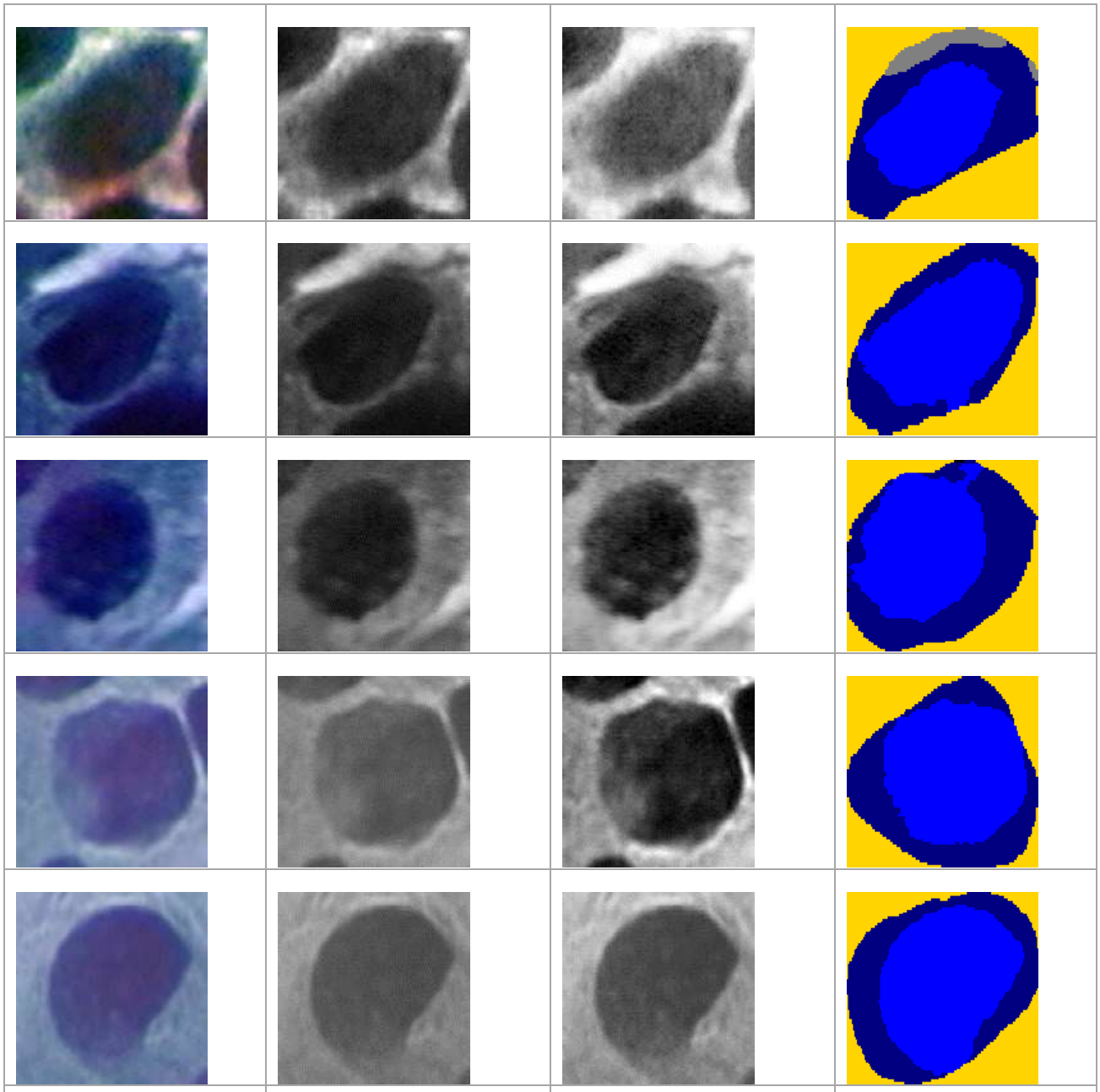
6 (a) MD input images	6 (b) MD gray scale images	6 (c) MD contrast enhanced images	6 (d) MD Segmented images

Figure 6 proposed image processing steps for MD classification



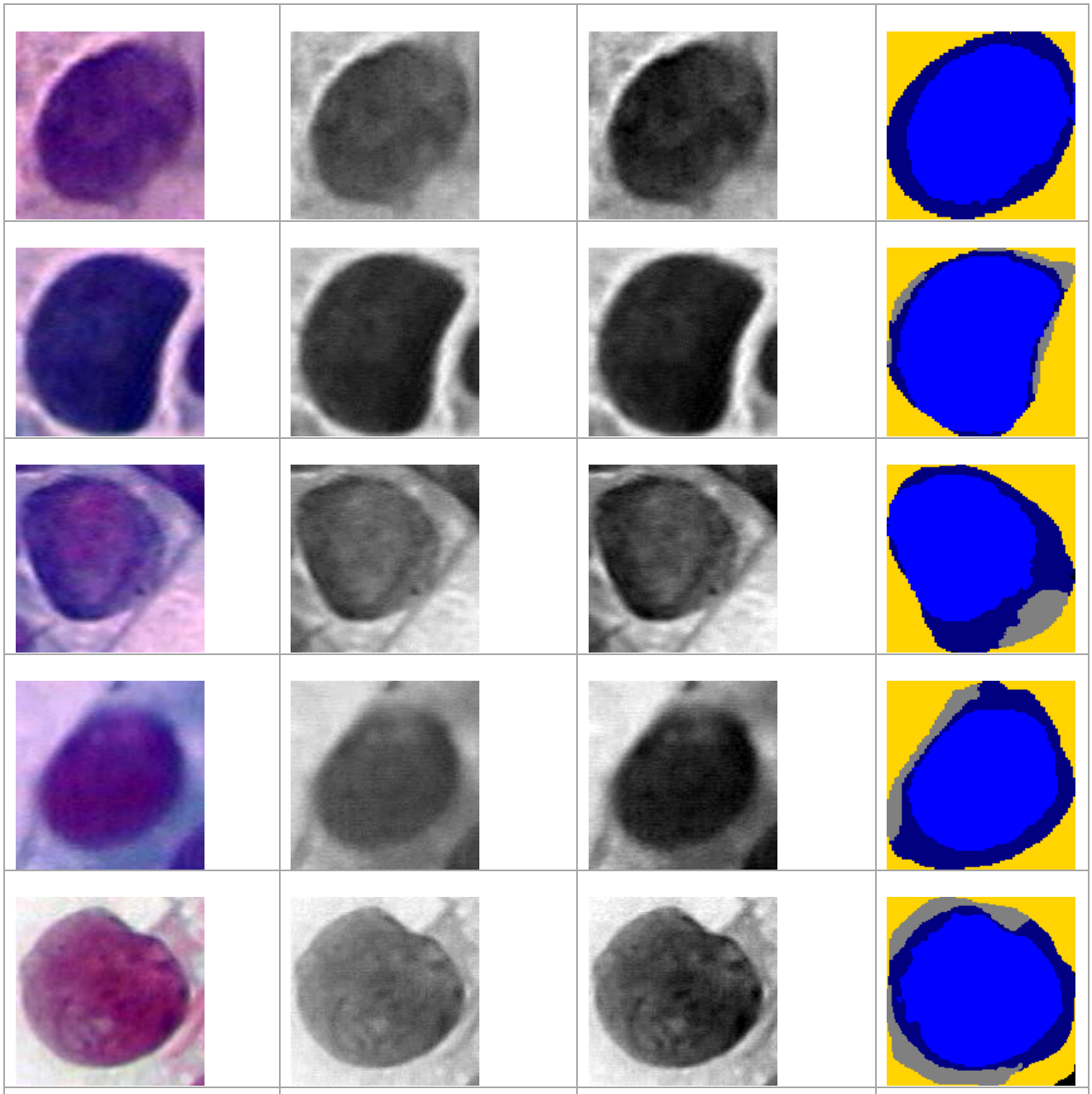
7 (a) MMD input images	7 (b) MMD gray scale images	7 (c) MMD contrast enhanced images	7 (d) MMD Segmented images

Figure 7 proposed image processing steps for MMD classification



8 (a) MMD input images	8 (b) MMD gray scale images	8 (c) MMD contrast enhanced images	8 (d) MMD Segmented images

Figure 8 proposed image processing steps for MMD classification



9 (a) CIS input images	9 (b) CIS gray scale images	9 (c) CIS contrast enhanced images	9 (d) CIS Segmented images

Figure 9 proposed image processing steps for CIS classification

4.3.2 Training efficiency evaluation

Training efficiency evaluation in deep learning means making sure the model is able to accurately predict the desired output with a minimal amount of error, as this is critical for successful deployment. When training the model, it is important to compare the model's performance on both the training set and a separate testing set. MAE (mean absolute error), MSE (mean square error), and RMSE (Root Mean Square Error) provide a powerful way to assess how well deep learning models are being trained, as they measure the gap between predicted output and desired output. If the MAE, MSE and RMSE values are

both low, this indicates that the model is performing well, making accurate predictions, and minimizing the gap between its predicted output and the desired output.

The mean absolute error (MAE) is a measure of prediction accuracy, calculated by taking the average absolute difference between predicted and observed values. The formula for calculating MAE is as follows.

$$MAE = \frac{1}{N}\sum_{i=1}^{N}|yi - \hat{y}\imath|$$

Where n is the number of observations and yi and yi represent the actual and predicted values, respectively. The Root Mean Square Error (RMSE) is a measure of the magnitude of differences between values predicted by a model and observed values.

$$RSME = \sqrt{\frac{1}{N}\sum_{i=1}^{N}|yi - \hat{y}\imath|^2}$$

The mean square error (MSE) is a measure of the average of the squares of errors between a given estimation and its actual value.

$$MSE = \frac{1}{N}\sum_{i=1}^{N}|yi - \hat{y}\imath|^2$$

Table 6 the comparison results of MAE, MSE, and RMSE.

Models	**MAE**	**MSE**	**MSE**
Multi stage CNN	1	1.1	1.05
CNN	2.1	4.2	2.05
GoogleNet	2.2	2.4	1.55
AlexNet	3.12	6.25	2.5

The MAE, MSE, and RMSE comparisons are summarized in Table 2, and it is clear that the model is performing very well on the training set, as the values are both low. The model is also performing well on the testing set, as evidenced by its low MAE, MSE, and RMSE values.

4.3.3 Computational effectiveness analysis

In general, CNN models require a huge amount of training data, high computer resources, and extensive training time to construct a classification or prediction model. As a result, they are often complex and expensive to construct. It varies according to the feature selection algorithm, training algorithm, CNN architecture, image type (JPEG, PNG, grayscale, etc.) and size (bit size of the image), as well as the computational resources needed to construct the model (memory size, graphical processor configuration, CPU clock speed). Through the use of training and testing images, the computational efficiency of a multi-stage CNN architecture has been investigated in this study. To provide a reliable training time evaluation, three random sets of images from the data set have been used. The first data set includes 600 RGB Pap smear images, the second data set contains 1200 RGB Pap smear images, and the third data set includes 1800 RGB Pap smear images. In addition, training is conducted via a personal computer (PC) with three distinct configurations. The configuration details of the system are detailed in the table below.

Table 7 system configuration for computational effectiveness analysis.

Computational resources	**PC 1**	**PC 2**	**PC 3**
Memory	8 GB	16 GB	32 GB
CPU clock speed	12th Gen Intel i3	12th Gen Intel i5	12th Gen Intel i7
GPU processor	NVIDIA GTX 660 2gb	NVIDIA GTX 660 4gb	NVIDIA GTX 660 6gb

Table 8 training time of proposed model (in minutes).

System details	**Data set 1**	**Data set 2**	**Data set 3**	**Average**
PC 1	13	19	24	18.6
PC 2	11	17	22	16.6
PC 3	10	15	20	15
Average	11.33	17	22	16.73

Table 9 training time of CNN model (in minutes).

System details	**Dataset 1**	**Data set 2**	**Data set 3**	**Average**
PC 1	21	36	42	33
PC 2	15	25	30	23
PC 3	12	17	25	18
Average	16	26	32	24.66

Table 9 training time of GooleNet model (in minutes).

System details	**Data set 1**	**Data set 2**	**Data set 3**	**Average**
PC 1	28	58	68	51.33
PC 2	20	40	51	37
PC 3	18	36	43	32.33
Average	22	44.66	54	40.22

Table 10 training time of AlexNet model (in minutes).

System details	**Data set 1**	**Data set 2**	**Data set 3**	**Average**
PC 1	25	41	53	39.66
PC 2	23	36	44	34.33
PC 3	18	31	38	29
Average	22	36	45	34.33

The training time comparisons of the existing and suggested approaches are depicted in the tables 7, 8, 9 and 10. According to the findings of the training time, the recommended multi-stage CNN requires 16,73 minutes to gain intelligence from the given data set. Conversely, existing deep learning models CNN demands 24.66 minutes, GoogleNet demands 40.22 minutes, and AlexNet demands 34.33 minutes to train on the data set, which is considerably long when compared to multi stage CNN. This training time results of the multi stage CNN and the deep learning models demonstrates that the suggested MDMC feature selection method makes the complex featureselection process extremely effective.

In the medical field, time is of the essence; if a disease is diagnosed a second earlier, it plays a major role in saving lives. Thus, medical professionals must act quickly to diagnose and treat any ailment. The classification in this research is to analyses the Pap smear images by the proposed method and present the possibility of cervical cancer to a medical professional. The classification time of the model is critical, as it determines how long it takes for the medical professional to receive accurate results. Three Pap smear images of varying sizes are picked from the data set to provide a reliable classification time evaluation. The first image is 2244 kb in size, the second image is 1444 kb in size, and the third image is 3014 kb in size. Classification is conducted via an above-mentioned PC.

Table 11 classification time of proposed model (in seconds).

System details	Image 1	Image 2	Image 3	Average
PC 1	0.23	0.24	0.28	0.25
PC 2	0.21	0.23	0.25	0.23
PC 3	0.19	0.21	0.21	0.2
Average	0.21	0.22	0.24	0.22

Table 12 classification time of CNN model (in seconds).

System details	Image 1	Image 2	Image 3	Average
PC 1	0.33	0.38	0.41	0.37
PC 2	0.3	0.34	0.35	0.33
PC 3	0.28	0.2	0.31	0.26
Average	0.3	0.3	0.35	0.32

Table 13 classification time of GoogleNet model (in seconds).

System details	Image 1	Image 2	Image 3	Average
PC 1	0.45	0.49	0.51	0.48
PC 2	0.42	0.45	0.5	0.45
PC 3	0.4	0.42	0.48	0.43
Average	0.42	0.45	0.49	0.45

Table 14 classification time of AlexNet model (in seconds).

System details	Image 1	Image 2	Image 3	Average
PC 1	0.32	0.36	0.41	0.36
PC 2	0.28	0.33	0.37	0.32
PC 3	0.25	0.3	0.35	0.3
Average	0.28	0.33	0.37	0.32

The classification time of the model is an important factor, as it helps make sure that a medical professional is able to diagnose cervical cancer quickly and accurately. To achieve this, the proposed model has been designed to be computationally efficient, so that the classification time is fast enough to meet the desired requirements. Tables 11, 12, 13, and 14 detail the classification times for Pap smear images of various sizes using multi-stage CNN and existing deep learning models. According to the results, the multi-stage CNN requires an average of 0.22 seconds to classify various cell types from the Pap smear image, which is more than fifty percent less time than other deep learning models.

4.3.4 Discussion

Cervical cancer is preventable, however, the initial symptoms can be difficult to detect, and, if left untreated, the cancer can spread and become more difficult to treat. Pap tests can detect abnormal cells in the cervix before they become cancerous, allowing for early intervention and more successful treatment outcomes. However, a manual error during the Pap smear image analysis can lead to an incorrect diagnosis and delayed or missed treatment. In an effort to improve the accuracy of cervical cancer screening, medical and academic researchers have developed various types of computer-aided diagnosing tools for Pap smear images. Most of the developed systems are based on deep learning algorithms. Unfortunately, due to the complexity of image structure, the created models are computationally intensive. To solve this problem efficiently, this study proposed a multistage CNN architecture for Pap smear image segmentation and classification, as well as a Minimum Duplication Maximum Correlation (MDMC) method for efficient feature selection.

5. Conclusion

Cervical cancer is a serious health concern that affects women around the world. So early diagnosis of cervical cancer is the key to reducing the morbidity and mortality associated with the disease. This study presented an efficient method for analyzing Pap smear images for the early diagnosis of cervical cancer, based on a proposed multi-tier CNN and MDMC. This architecture consists of two CNN models, the first of which is utilized to extract cells from background images. A second CNN model is utilized to extract texture features from segmented images in an efficient manner. Finally, a support vector machine is used to classify the different types of cells in Pap smear images. The redundancy of CNN's features map has been considerably decreased by the incorporation of the MDMC approach for cervical cancer diagnosis. According to the experimental results, the MDMC technique efficiently eliminates uncorrelated features. This will make the overall accuracy about 3–4% better. Also, experimental results show that the proposed method takes less time for training and classifying.

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