Automated Cell Nuclei Segmentation in Overlapping Cervical Images Using Deep Learning Model

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Abstract - Recently, an automated cell nuclei segmentation is an attractive research area in the cervical cancer image analysis with the overlapping cells. Due to the poor contrast, diverse cells and the occlusion, the segmentation suffers from several issues such as inaccurate region detection and the lack of boundary refinement. To alleviate such issues, this paper proposes the deep learning framework with the boundary refinement techniques. Prior to boundary refinement, this paper utilizes the noise removal technique called Neighborhood Concentric Filtering (NCF) based on connected component analysis. Then, the proposed work segments the cell nuclei and cytoplasm with clear boundary refinement. The proposed work utilizes the N-ary ternary-based texture pattern extraction to collect the features that describe the regions clearly. Then, this paper utilizes the fisher model to select the relevant features in order to reduce the dimensionality that directly reduces the time complexity. Finally, the Deep Learning (DL) models through the neural network approaches classifies the abnormal cells effectively. Besides, this paper investigates the effectiveness in terms of the various performance parameters over the existing methods in cervical cancer image analysis for earlier diagnosis applications.

Keywords: Cervical Cancer Image Analysis, Cytoplasm Segmentation, Deep Learning, Nuclei Segmentation, Overlapping cells.

1 Introduction

According to the Global cancer report, the cervical cancer is the third most cause of cancer-related deaths which is more than 80% in developing countries due to the lack of proper preventive policy. Hence, the researchers turn their attention into the development of suitable techniques that support the earlier diagnosis and provision of proper treatment[1]. Even though the cytology-based current standard care reduced the death rates due to the cervical cancer mortality, huge lesions are still missed that are referred for unnecessary biopsies. The gradual progression of cervical cancer for the long-period allows the screening procedures to detect the earlier neoplastic alterations that leads to different detection peaks. The lack of laborious infrastructure and the skilled cytopathologists initiates the active screening and timely treatment. The repetitive cytological examinations is the major requirement in the pathological examination to evaluate the tissue size variations and assist the directed biopsies. The major risk factor for the cervical cancer is the Human Papillomavirus (HPV) which is implicated in various sites such as vagina and penis. Hence, the novel diagnosis technique is required to screen the cancers caused due to the HPV. Biopsy and the evolution of cytological screening have the suspicious issues such as time consumption, laborious task and the costlier. The recent development of the optical imaging techniques[2] replaces the screening processes for high-sensitivity and specificity. The exceptional growth of the optical imaging techniques require the primary detection of the premalignant lesions which is more accessible in developing and developed countries. Fluorescent-based, amplification strategies and the nanoparticle-based detection techniques are available to meet the growth scenario. The primary deficiency of the optical-based methods is they are unsuitable to rapid and inexpensive testing for large size population groups. In the developing regions, the real-time amplification is unavailable that enable the sensitive, rapid and inexpensive assays to detect the HPV types. The Pap smear image analysis in HPV is governed by the wide research studies[3] that automatically segment the nuclei and cytoplasm. The segmentation of overlapping cells includes three major categories as follows: nuclei detection, cell clump detection and the segmentation of individual cell’s cytoplasm inside the cell clump. The improvement is required in the form of edge information inclusion and the reduction of false negative rate with the provision of ground truth. The issues affecting such segmentation and the overlapping cell segmentation processes are number of cells, variability, poor contrast and occlusion. The production of precise segmentation for the large number of isolated and overlapping cells available in the cytology images. The major issues observed from the review of cell segmentation methods[4] are automated cell nuclei detection and the cytoplasm
segmentation from clamps. The development of next-generation computer-aided diagnosis depends on the segmentation of individual cells from the overlapping clumps. An accurate detection and segmentation of both the nucleus and the cytoplasm with the partial occlusion is the difficult task. Due to the extensive shape, size and contrast variations, the boundary detection faced the issues.

The prevention of cervical cancer requires the periodical screening tests in which the swipe of cervical regions using the cotton swab or the tissue sample handling. The problems observed in the periodical screening tests are time consuming, error prone and the abilities of doctors. The features such as the shape, texture and color are used to extract lot of details from the image. The Radiating Gradient Vector Flow (RGVF) snake model[5], the combination of low-intensity contrast with the nuclei loss result[6], clustering[7], contour detector are applied to segment the nuclei, cytoplasm effectively. The extraction of shape, texture and the image intensity efficient efficiently reduces the false positive edges. An automatic segmentation of nucleus and cytoplasm from the cervical images requires the proper distinguish between the background and the target region. With the diverse standard deviations or the classes the traditional threshold-based methods did not provide any proper threshold value. There are two phases in the Nucleus Cytoplasm Contour (NCC) detector detector[8]such as detection of nucleus and contour. On the basis of the gray-level differences between the nucleus and cytoplasm, the Adaptive Threshold Decision (ATD)-based methods are employed without proper initial contour. But, the major issues observed from these methods [9, 10] are inaccurate boundary detection, presence of noisy pixels, unclear image analysis, more false positive edges and misclassification. The novel technical contributions of proposed work are listed as follows:

- The integration of cell nuclei region of interest locating method with the segmentation methods helpful to extract the exact cell nuclei region in low-resolution cervical images
- The improvement in noise removal method through the connected components improves the splitting performance effectively.
- The employment of N-ary ternary-texture pattern-based methods extracted more accurate features which are helpful to improve the performance and accuracy
- The utilization of fisher model selects the relevant features which reduces the computational complexity and time complexity.
- The composition of multiple hidden units through the simple learning modules in deep learning enhances the classification performance effectively.

This paper is organized as follows: Section 2 describes the related works on cervical cancer image analysis with the overlapping cells. Section 3 discusses the implementation process of proposed Boundary Refinement-N-ary ternary Texture Pattern-based Deep Learning (BR-N-DL) to segment the nuclei, cytoplasm and the cell clump. Section 4 presents the performance analysis of BR-ATP-DL regarding the accuracy, precision, recall, sensitivity, specificity and the coefficient metrics for benchmark data. Finally, section 5 presents the conclusion and future work of proposed work.

2 Related Work

This section discusses major issues behind the existing cell / nuclei segmentation in overlapping cervical cells. Prior identification and quantification of shape irregularities and size variations are necessary to discriminate the normal and abnormal cells in the input images. Plissiti et al [11] presented the automated method for cell nuclei detection with the prior knowledge regarding the locations of nuclei centroids and their refining capabilities. The utilization of distance- dependent rule on the centroids provided better classification performance. Segmentation of large numbers of nuclei in isolated cells suffered from the problem under the different acquisition conditions in high-resolution scenarios.

Bergmeir et al [12] proposed the new segmentation algorithm to segment the nuclei with the adequate control of the expert user. The utilization of voting scheme with the prior knowledge regarding the cell nuclei shape localized the cell nuclei effectively. The removal of edges adjacent to the background was achieved by using the randomized Hough transform and the noise-free edges were processed by using the level set algorithm. An accurate boundary approximation suffered from the computational cost and the numerical instability. Lou et al [13] studied the problem of segmenting the multiple-cell nuclei from the stained microscope images with a shape prior. They proposed the novel extension to the graph cut approach which incorporated the blob-like shape prior. The structured learning was performed to identify the energy terms and parameterized them clearly. The lack of correct interpretation of the Pap smear images highly contributes to the accurate detection of nucleus shape. Plissiti et al [14] presented the overlapping cell segmentation in which local characteristics of boundary and the expected shape were combined together to form the deformable model. With the utilization of necessary weight parameters, the energy of the deformable model was controlled. The maximization of focus measure added the noise to the final result in energy maximization approaches and hence the attenuation of the effect of noises was the major requirement to remove the noise present in the images. Pertuz et al [15] proposed the approach that fused the different frames adaptively in order to reduce the noise effectively. The operating stages of the fused approach were focus measure, selectivity measure and the image fusion.

Poor contrast directly affects the quality of segmentation of overlapping cells. Happy et al [16] presented the unsupervised cell segmentation on the basis of the Extended Depth of Field (EDF) created under the different focal planes. They proposed the Otsu method and the level set method on the basis of the prior class weights to segment the nuclei and cytoplasm respectively. The optimization of energy function dependent on the various terms such as
regularization, shape prior, intensity ratio and overlap ratio. Due to the inefficient elliptical shape, the segmentation problem was not declared accurately. Nosrati and Hamarneh [17] proposed the new continuous variational segmentation according to the prior star-shape. The segmentation of overlapping cervical cells in the Pap smear images was achieved by using the directional derivatives. The threshold-based, morphological-based and the front propagation-based methods were available for cervical cell segmentation. Ushizima et al [18] proposed the computer vision algorithm to detect and distinguish the subcellular components from the cervical images by using three steps such as cellular mass estimation, nuclei through the super-pixel representation and cytoplasm detection through the nuclear narrow-band seeding and Voronoi diagrams. An automated segmentation of overlapping cells and the reduction of cell overlap were the major issues in traditional approaches. Lu et al [19] performed the cell segmentation based on the integration of level set methods with the optimization methods. They presented the quantitative results related to the nuclei detection and segmentation. The reasonable relationship management of irregular super-pixels was the major requirement to reduce the computational complexity effectively. Zhao et al [20] proposed the novel superpixel-based methods such as Markov Random Field (MRF) and the composition of superpixels with the connecting edges. The gap search algorithm was designed to enhance the model efficiency in fast manner. The occlusion, staining variation and the cell diversity were the major challenges in automated cervical cytology. Ramalho et al [21] tackled the various issues through the rough segmentation of sub-cellular compartments, structural refinement of cytoplasm boundary and the morphological reconstruction. However, the multiple-touching cell splitting was the challenging issue under dust impurities, uneven illumination and the irregular leucocytes. Hence, Song et al [22] proposed the Multi-Scale Convolution Network (MSCN) and graph-partitioning-based methods to extract the scale invariant features which refined the coarse segmentation. With this framework, the computational complexity was reduced effectively. An approximate representation of overlapping cell contour points as either strong points or weak points was modelled as the contour locating problem in Gradient Vector Flow Snake model [23]. The presence of inflammatory cells, poor contrast of the cell cytoplasm and the degree of overlap made the segmentation process as the difficult issue. Lu et al [24] presented the improved segmentation algorithm by using the joint optimization of multiple level set formulations. Sharma and Mangat [25] presented the brief review of existing methods to detect, segment and discriminate the boundaries between the cell nuclei and cytoplasm segmentation. They highlighted that some of the research studies did not consider the presence of unwanted components and the inconsistent staining in cervical cancer image analysis. The fixed number of clusters led to the accuracy and performance degradation. The clustering uncertain data was the major issue in traditional methods. With these factors, this paper proposes the new boundary refinement model through the Deep Learning (DL) framework to improve the accuracy and performance.

3 Boundary Refinement-based Deep Learning Model

An efficient cell nuclei segmentation and the boundary discrimination through the DL framework is discussed in detail in this section. The proposed work comprises various successive processes such as Neighborhood Concentric Filtering (NCF), Multi-level set segmentation for nuclei, cytoplasm, N-ary ternary-based texture feature extraction, feature selection and the Neural Network (NN) based DL as shown in Fig. 1. Initially, Neighborhood Concentric Filtering (NCF) removes the noise present in the images through the connected component analysis. The extraction of information present in the images is the major requirement for segmentation. The enhanced image is the prerequisite for the segmentation process. Hence, the NCF is integrated with the Gaussian model to enhance the image quality effectively. Then, the identification of cell nuclei boundary and the isolation of nuclei with the cytoplasm through the level set formulation are performed. An N-ary ternary-based texture pattern is applied to extract the features for clear image analysis. With the increase in dimensionality of features, the time required for classification is more. Hence, the fisher model-based feature selection process is applied to select the relevant features corresponding to classification. Finally, the DL model is used to classify the normal and abnormal samples in the images.

3.1 Neighborhood Concentric Filtering

Prior to the segmentation of cell nuclei regions, the quality of the images is to be improved with the suitable noise removal techniques. Here, the NCF and the Gaussian enhancement are integrated to remove the noise and enhance the quality of images effectively. The matrix window with the size 3 X 3 is projected over the input image. From the matrix, the maximum Connected Components (CC) is extracted and it replaces the original pixels of the matrix. Then, the center...
pixel is extracted from the matrix and it is compared with the neighboring pixels. If the difference between the center pixel with the neighboring pixel is greater than the center pixel, then the cell is replaced with the average value otherwise it is replaced with the median value effectively. Once the noisy pixels are removed, the quality of the image is enhanced with the Gaussian model of standard deviation ($\sigma$) which is calculated in equation (1). The enhanced image ($I_e$) is expressed as follows:

$$ \sigma = \sqrt{\frac{1}{N \cdot M} \sum_{i=1}^{N} \left( I_g(i) - \frac{1}{N} \sum I_g \right)^2} $$  \hspace{1cm} (1)

$$ I_e = \frac{I_g}{\max \left( I_g - \sigma \right)} $$  \hspace{1cm} (2)

Where, $M, N$ - Row and column size of the image. Fig. 2 (a), (b) and (c) show the input, filtered and enhanced images.

(a) (b) (c)  
Fig. 2. (a) Input image, (b) Filtered image and (c) Enhanced image

Once the quality of the images is enhanced, the boundaries of nuclei, cell and cytoplasm are refined which is considered as the consecutive stage in proposed model.

### 3.2 Multi-level set formulation for boundary refinement

The boundary refinement comprises the two different steps such as nuclei and cell clamp segmentation. In this section, the multi-level set formulation is employed to segment the nucleus from the cervical images effectively. The boundary refinement consists of two stages such as nuclei detection and cell clamp detection.

**Nucleus Detection**

The major characteristics used in nucleus segmentation are area, average intensity, solidity and circularity. On the basis of the changes of the threshold values from highest to lowest, the darker sub-regions of the images are regarded as the nucleus part in the cervical images. A contour of interest ($\varphi$) is identified using the level set formulation with the desirable properties. Here, the energy function is integrated with the distance regularization framework which is expressed as follows:

$$ R(\varphi) = \int p(|\nabla \varphi|)dx $$  \hspace{1cm} (3)

Where, $p$ – Potential energy. The steady state solution to the regularization term through the gradient flow equations as follows:

$$ \frac{\partial \varphi}{\partial t} = -\frac{\partial F}{\partial \varphi} $$  \hspace{1cm} (4)

Where, $F$ – Energy functional. This equation is regarded as the evolution equation of the time-dependent function of $\varphi(x,t)$ ($x$ – spatial variable and $t$ – temporal variable).

The overall derivative is called as Gateaux derivative which is applied to the regularization as follows:

$$ \frac{\partial \varphi}{\partial t} = -d \text{div}(d_p |\nabla \varphi| \nabla \varphi) $$  \hspace{1cm} (5)

With these formulations, the level set formulations performed to detect the nucleus effectively. The DRLSE framework does not require any reinitialization set-up. The binary step function to initialize the level set formula to identify the nucleus as shown in Fig. 3 is expressed as

$$ \varphi_0 = \begin{cases} 1, & \text{if } x \in R_0 \\ 0, & \text{otherwise} \end{cases} $$  \hspace{1cm} (7)

Fig. 3. Nucleus detected output

With this initialization, the number of iterations to segment the nucleus region are less and hence the trade-off between accurate segmentation ($I_n$) and minimum steps is achieved.

**Clump and Cell Detection**

To form the active contour over the region, the energy, weight and the direction are updated iteratively for clump and cytoplasm detection. The algorithm to detect the nuclei is expressed as follows:

<table>
<thead>
<tr>
<th>Multi-level set segmentation</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Input</strong> – Enhanced image, $I_e$’, ROI Mask, $R_{out}$’</td>
</tr>
<tr>
<td><strong>Output</strong> – Cytoplasm detected output $I_{cy}$’</td>
</tr>
</tbody>
</table>

**Step 1:** Initial Masking

$$ M = \sqrt{(R_{out}(x))^2 - (R_{out}(y))^2} $$

$$ \sqrt{(1 - R_{out}(x))^2 - (1 - R_{out}(y))^2} + R_{out} - \frac{1}{2} $$

**Step 2:** For iteration = 1 to $N$

**Step 3:** $Idx = Index(M)$

**Step 4:** Curvature, $\frac{\partial^2 u}{\partial t} = \nabla u M (Idx) + k$

**Step 5:** Energy Update,

$$ I_p = \begin{cases} M, & \text{if } (M \leq 0) \\ 0, & \text{else} \end{cases} $$  Internal Energy
Step 6: Difference in energy update,
\[
\frac{\partial I_E}{\partial t} = \frac{I_E(t + \Delta t) - I_E(t)}{\Delta t}
\]

Step 7: Direction Update

\[
D_{\text{Pos}} = \sqrt{\max(ap^2, bn^2) + \max(cp^2, dp^2)}
\]

\[
D_{\text{Neg}} = \sqrt{\max(an^2, bp^2) + \max(cn^2, dp^2)}
\]

Step 8: Contour Weight Update

\[
\varnothing_{i+1} = \varnothing_i - dt \cdot \frac{\partial E_p}{\partial I_E} = (M + dt \cdot I_E) - \varnothing_i
\]

3.3 N-ary Ternary Pattern (NTP)-based feature extraction

The N-ary pattern discussed in [27] is regarded as the base for the proposed feature extraction process. The pixel value selection for comparison is the major difference between the proposed and traditional work. The median value is selected value for the comparison of pixel value with the neighboring pixels which is the basic difference in proposed work. Then, the row (R) and column (C) values corresponding to the pixel values of (3, 4), (2, 4), (2, 3), (2, 2), (3, 2), (4, 2), (4, 3) and (4, 4) are updated by subtracting the median value (med) in proposed N-ary Ternary-based feature extraction as shown in Fig. 5.

The replacement of pixel values by the binary values such as 0 and 1 based on the comparison of each pixel with the neighboring pixels provides the diverse direction analysis that helpful to the clear image analysis. The steps to extract the features through the NTP-based method are listed as follows:

NTP-based features

Input: Enhanced image \( I_E \)

Output: Feature set \( F \)

Step 1: Apply the NTP to extract the lower and upper patterns from the \( I_E \)

Step 2: Initialize the no of images train the machine (R), temporary variable K=0

Step 3: For each image

Step 4: Create the temporary list (templist) of extracted patterns

Step 5: Extract the minimum value in temporary list
Step 6: Extract the maximum value of the temporary list.
Step 7: Compute the mean and standard deviation of the values in the list.
Step 8: Update the feature matrix with the following formula:

$$ F = \sqrt{\frac{\text{std}}{\text{length (template)}}} $$

Once the features from the N-ary ternary patterns are extracted, more, the dimensionality of the feature set will increase the computational time. Hence, the relevant feature that describe the better classification performance are selected to reduce the dimensionality.

### 3.4 Fisher Model-based feature selection

The utilization of statistical and discrimination methods select the best features to describe the normal and abnormal levels clearly. Here, the Fisher score-based feature selection is used to identify the relevant features from the extracted feature-set. The operating principle to select the relevant features is the distance between the data points is small if they lie in same class and it is large if they lie in different class. Let us consider the set of features $F = (F_1, F_2, \ldots, F_n) \in \mathbb{R}^{d \times n} - 1$ is regarded as the vector of all ones and it is zero for all zero values. The mathematical formulation of fisher score is expressed as follows:

$$ f(z) = \text{tr}((\overline{s}_a)(\overline{s}_b + yI) - 1) $$  \hspace{1cm} (12)

Where, $\gamma$ - positive regularization parameter

$$ \overline{s}_a = \sum_{k=1}^{n} n_k (\overline{\mu}_k - \overline{\mu})(\overline{\mu}_k - \overline{\mu})^T $$  \hspace{1cm} (13)

$$ \overline{s}_b = \sum_{i=1}^{n} (\overline{z}_i - \overline{\mu})(\overline{z}_i - \overline{\mu})^T $$  \hspace{1cm} (14)

Where, $\overline{\mu}_k$ – mean vector of $k$ – th class
$\overline{z}_i$ – Subset of features

The features with the top score $f(z)$ are regarded as the relevant features to classify the normal and abnormal levels in the cervical images with the overlapping cells.

### 3.5 Deep Learning for classification

The classification of normal and abnormal cells in the cervical images is modelled as the deep learning problem with the back propagation algorithm in this paper. The formulation of back propagation algorithm with the single input and output is expressed as follows:

Feed forward: Input feature set is feed forward to the network.
The primitive computations of functions and associated derivatives are evaluated and stored on the node in the neurons.

Back propagation: The total network is run backwards with the constant value-1. The incoming information to a node is added which is multiplied together with the value stored in the left part of the unit.

During the learning process, the error function depends on the weight parameter is minimum in order to deal with all weights to the neurons. The back propagation computes the error function and brings all the neuron’s attention to one of the weight parameter called $w_{ij}$ with the edge points $(i, j)$. The information necessary to the classification is fed to the sub-network during the feed forward step as $\omega_j$. Then the gradient of error function $E$ with respect to the given input and the weight as $\frac{\partial E}{\partial \omega \partial w_{ij}}$. The back propagated error to the node $j$ is represented as $\theta_j$. Then, the partial derivative of the error $E$ is expressed as

$$ \frac{\partial E}{\partial w_{ij}} = \omega_j \theta_j $$  \hspace{1cm} (15)

With the addition of each weight to the increment, the gradient value of descent is formulated as

$$ \Delta w_{ij} = -\gamma \omega_j \theta_j $$  \hspace{1cm} (16)

This correction step is required to make the back propagation as the learning model for neural network. Finally, the deep learning model through the back propagation algorithm classifies the normal and abnormal effectively.

### 4 Performance Analysis

Table 1 presents the comparative analysis proposed BR-N-DL with the SVM on the basic performance parameters for cervical cancer image analysis.

<table>
<thead>
<tr>
<th>Parameters</th>
<th>BR-N-DL</th>
<th>SVM</th>
</tr>
</thead>
<tbody>
<tr>
<td>TP</td>
<td>11</td>
<td>7</td>
</tr>
<tr>
<td>TN</td>
<td>0</td>
<td>3</td>
</tr>
<tr>
<td>FP</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>FN</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Sensitivity (%)</td>
<td>98.6</td>
<td>95.4</td>
</tr>
<tr>
<td>Specificity (%)</td>
<td>100</td>
<td>98.1</td>
</tr>
<tr>
<td>Precision (%)</td>
<td>96.1</td>
<td>94.1</td>
</tr>
<tr>
<td>Recall (%)</td>
<td>98.6</td>
<td>95.4</td>
</tr>
<tr>
<td>Jaccard Coeff.</td>
<td>91.6</td>
<td>90.3</td>
</tr>
<tr>
<td>Dice Overlap</td>
<td>95.65</td>
<td>90.3</td>
</tr>
<tr>
<td>Kappa Coeff.</td>
<td>67</td>
<td>50</td>
</tr>
<tr>
<td>Accuracy (%)</td>
<td>91.6</td>
<td>83.3</td>
</tr>
</tbody>
</table>

Fig. 6 shows the comparative analysis of sensitivity, specificity measures for BT-N-DL and SVM. The optimal weight update by the multi-level set formulation and the NTP improves both the sensitivity and specificity values. Compared to SVM, the BT-N-DL offers 3.24 and 1.9 % better in sensitivity and specificity values.
Fig. 6. Sensitivity and specificity analysis

Fig. 7 shows the comparative analysis of accuracy, precision and recall values for BT-N-DL and SVM formulation. The SVM offers 83.3, 94.4 and 95.4% and the BT-N-DL offers 91.6, 96.1 and 98.6%. The ML formulation and the integrated feature extraction improves the accuracy, precision and recall by 9.06, 1.77 and 3.25% respectively.

Fig. 8. Coefficient analysis

Fig. 8 shows the comparative analysis of coefficient metrics (Jaccard, Dice, and Kappa) for proposed BT-N-DL and the existing SVM formulation. The SVM offers 90.3, 90.3 and 51.24% and the BT-N-DL offers 91.6, 95.6 and 67.25%. The ML formulation and the extended features improves the coefficient metrics by 1.42, 5.59 and 23.81% for overlapping cervical images.

5 Conclusion and Future Work

This paper discussed the issues such as inaccurate region detection and the lack of boundary refinement due to the factors such as dimensionality and the poor contrast. In this paper, the DL models integrated with the novel N-ary ternary texture pattern-based and the boundary refinement-based methods to alleviate the issues observed in the existing models. This paper utilized the noise removal technique called NCF based on connected component analysis. Then, the proposed work segmented the cell, nuclei and cytoplasm with clear boundary refinement technique. The proposed work utilized the N-ary ternary-based texture pattern extraction to collect the features that described the regions clearly. Then, this paper utilized the fisher model and DL model to select the relevant features and classify the abnormality levels in cervical images. Finally, the performance of proposed work is investigated with the various performance parameters over the existing methods to assure the applicability in earlier diagnosis applications.

6 References


