CHAPTER 4

AUTOMATED DIAGNOSIS OF CERVICAL CANCER USING TWBS AND RVDLNN IN PAP SMEAR IMAGE (CERVI-CYTO-NET)

4.1 Introduction

Cervical cancer is a major contributor to cancer-related fatalities among women worldwide. As reported by the World Health Organization, cervical cancer accounts for about 300,000 deaths annually, with the major part of these deaths occurring in developing countries. Detecting CC at an early stage is essential for successful treatment and better outcomes for patients. Some of the conventional techniques used to detect CC, like Pap smear examinations, have restrictions in terms of precision and effectiveness. Utilizing TWBS and RVDLNN is helpful in analyzing Pap smear images that aim at enhancing the effectiveness of cervical cancer diagnosis. Traditional Pap smear image analysis methods require skilled technicians and a longer processing time, which may delay the diagnosis and treatment. With automated diagnosis, the analysis can be done faster with less human effort, resulting in quicker and effective treatment. In a study conducted by researchers, this method achieves an accuracy of 95% in abnormal cell detection, outperforming other existing methods. The use of wavelets in the first step of the process allows for more accurate extraction of features. At the same time, RVDLNN improves the classification results by learning from the extracted features. This method is also time-efficient, which is crucial in areas where there is a shortage of trained pathologists. The automated analysis of Pap smear images can significantly reduce the time taken to diagnose cervical cancer, allowing for early detection and timely treatment. The major advantage of using this automated technique is that it is capable of reducing human error. Traditional methods of diagnosing cervical cancer depend on the pathologist, which is error prone. The automated analysis using TWBS and RVDLNN reduces the chances of misdiagnosis.

4.2 Methodology

4.2.1 Dataset Description

SIPaKMed dataset

SIPaKMed known as “Systematic Integration of Papanicolaou and Koss Meier datasets” is a computerized system that combines the results of both Pap smear and colposcopy (a procedure that examines the cervix with a magnifying instrument) to provide more accurate diagnosis. The SIPaKMed dataset is analyzed by assigning a score to each cell for determining the chance of the cells being normal or abnormal. This system is highly accurate in detecting cervical cancer and reduces the number of false negative results.

Herlev Dataset

The Herlev dataset contains single cell images which are 917 in number and are classified into seven classes by doctors and technicians. It has been widely used by various researchers for better understanding of CC cell classification.

4.2.2 Pre-processing

Pre-processing of Pap smear images of cervical cancer using DSF-CLAHE and Gabor gives a clear approach in enhancing the quality of the images. DSF-CLAHE helps to improve overall contrast and sharpness of the images. Gabor filter helps in identifying important features such as texture and edges. The proposed research applies DSF-CLAHE as pre-processing technique that combines two filters, Diffusion Stop Function and CLAHE, to enhance the contrast and sharpness of the images. Though, DSF-CLAHE refines the overall features of the images, there may be more useful techniques for detecting certain features, such as texture and edges, which are crucial in identifying cancerous cells.

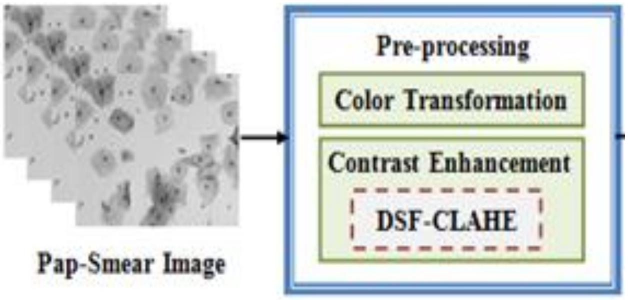

Figure 4.1 Illustration of Pap smear image to the phase of pre-processing

Figure 4.1 represents the information of Pap smear images of a person with cervical cancer. After collecting the Pap smear images, they undergo the pre-processing phase. During the pre-processing stage, color transformation and contrast enhancement are performed to achieve image clarity and enhanced color contrast in the image. DSF-CLAHE enhances contrast by dividing images into tiles and applying contrast to each tile for clearer images.

4.2.2.1. Color transformation

The colors are converted to the CIELAB format to obtain a better understanding of the input images. The CIELAB, also known as CIE L*a*b*, is a color space model that is not dependent on any particular device and allows for better assessment and evaluation of total visible colors. In this model, the assignment of statistical variations in color values with respect to how humans perceive color is accomplished.

The CIELAB is a model of color space consisting of three axes that are at right angles to each other. Figure 4.2 depicts the CIELAB model.

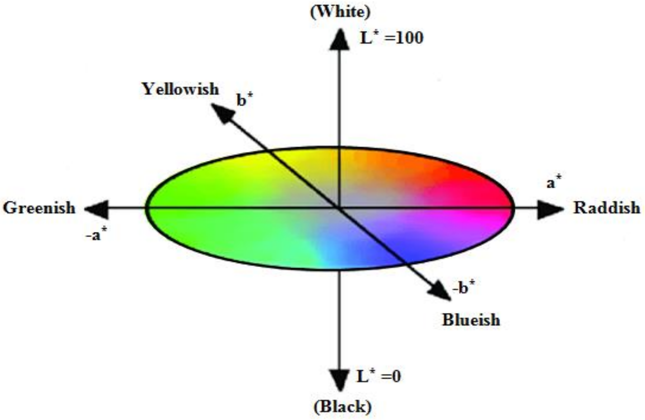

Figure 4.2 Pictorial description of the CIELAB model for the transformation of the color

Where L*-axis represents the brightness: A white object with brightness level of 100. A black object is with an L* value 0. Therefore, the neutral colors and the grey shades can be found along the L* axis. Chromatic ('real') colors are used to describe the two axes in the horizontal plane. The a*-axis represents the green-red axis, while the b*-axis ranges from blue (-b*) to yellow (+b*). A color point is used to show each color in the L*a*b* color space. The L*, a*, and b* values represent the color point's color coordinates.

4.2.2.2. Contrast enhancement

Inadequate visualization of images could impede the accurate diagnosis of CC. Therefore, contrast enhancement is required to increase the differences in images, allowing for a more effective analysis of details in the low dynamic range. Hence, the proposed work aims to enhance disparities in images by employing the DSF-CLAHE algorithm. Usually, the result is produced by adjusting the difference and modifying the clip limit. In addition, CLAHE needs help with too much improvement and more improvement. Hence, to tackle this problem, clip limit is accustomed according to DSF.

Contrast enhancement using DSF-CLAHE

The diffusion stop function (DSF) is developed as an innovative tool for controlling diffusion processes and has shown promising results in various applications. The DSF is a mathematical function that can be applied to a system to control the diffusion of particles. It works by creating a barrier that restricts the movement of particles, averting them from dispersing into or out of a specific area. This function is based on the principles of statistical mechanics, which describe the behavior of a large number of particles in a system. The significant advantage of the DSF is its ability to control diffusion in both time and space. The rate of diffusion can be enhanced by modifying the parameters of the function, such as the barrier height and width. This feature is predominantly beneficial in applications of slow or controlled diffusion process which is desired, such as in drugs delivery or the creation of microstructures.

CLAHE successfully resolves the problem of contrast enhancement being too exaggerated compared to Adaptive Histogram Equalization (AHE). CLAHE breaks down the image into sections, performs histogram equalization on each section, and merges adjacent sections with bilinear interpolation to get rid of fake edges. The DSF-CLAHE process is explained as follows.

Step 1: Initially, establish the dimensions of the tiles that require segmentation. The original image is segmented into several contextual regions of equal size that fails to overlap.

Step 2: Regulating the upper limit to clip the histogram of each tile is required to determine the threshold. i.e., the threshold value determines how much contrast enhancement is necessary; meanwhile, higher clip value provides greater level of enhancement. In this case, the clip limit value is modified using the Diffusion Stop Function, as shown in Eq. (4.1).

$$I_Q^{t+1} \approx I_Q^t + \frac{\delta}{\mathrm{I}\eta_{\mathrm{Q}}\mathrm{I}} \sum p \epsilon \eta_Q \, L\big(\mathrm{I}\nabla\mathrm{I}_{Q,P}^t\mathrm{I}\big), \mathfrak{I})\nabla\mathrm{I}_{Q,p}^t \tag{4.1}$$

Where I_Q^t is the amount of pixel Q from the image I at a prompt t, δ is a scalar connected to the dispersion rate, $\mathfrak{I}$ is an optimistic constant selected according to the chosen smoothing level, η_Q stands for fixed adjacent pixels of $Q, L(.)$ is ESF, and $\nabla I_{Q,p}^{t}$ is the degree of the image directional gradient from pixel Q to p an instant t.

Step 3: The mean number of pixels is determined to assign each gray level from every tile as per following Eq. (4.2).

$$\lambda_{avg} = \lambda_R * \frac{\lambda_C}{\lambda_{GY}} \qquad (4.2)$$

Step 4: Determine real clip limit by multiplying the average number of pixels of each gray level using Eq. (4.3).

$$\lambda_{cl} = \lambda_{clip} * \lambda_{avg} \qquad (4.3)$$

Step 5: This process includes cutting out pixels that have grayscale values above a set threshold, figuring out how many pixels to cut out, and finding the average number of pixels assigned to each grayscale level as in Eq. (4.4).

$$\lambda_{Acp} = \lambda_{SCp}/\lambda_{GY} \qquad (4.4)$$

Step 6: Modification of cut pixels. The quantity of pixels in the initial tile's histogram of each gray level is represented by G(i), including all gray levels found in the tile and this constitute the count of gray level pixels in the redistributed new tile post pixel redistribution, with clearly defined criteria for pixel assignment. This is shown in Eq. (4.5).

$$G(i) = \begin{cases} \lambda_{cl} & G(i) > \lambda_{cl} \\ \lambda_{cl} & G(i) + \lambda_{ACP} \geq \lambda_{cl} \\ G(i) + \lambda_{ACP} & else \end{cases} \qquad (4.5)$$

Step 7: It involves using the stated expression to determine the step size of the remaining distributed pixels following clipping using Eq. (4.6).

$$Step = \lambda_{GY}/\lambda_{lP} \qquad (4.6)$$

Initially, the process of selecting the optimal value from the lowest gray level and proceeding to the highest using the steps stated above. If the gray level has fewer pixels, it will be categorized under that gray level. After the search for pixels from the darkest to the lightest tones is finished and there are still pixels that have not been assigned, a new increment is determined, and this process continues until all pixels are assigned.

Step 8: Histogram equalization is applied with the aim of limiting contrast of tiles.

Step 9: Each tile is connected by using the center point of each tile as the point of reference for conducting bilinear interpolation to remove borders and generate the final processed image. It is depicted in Eq. (4.7).

$$\Pr(I) = \{pr1, pr2, pr3, \dots \dots \dots \dots \dots \dots ., pr_n\} \qquad (4.7)$$

Where, $\{pr1, pr2, pr3, \dots \dots \dots \dots \dots \dots ., pr_n\}$ are the pre-processed images.

4.2.3 Segmentation with proposed Topographic Weibull Bounding Segmentation

The suggested segmentation approach (TWBS) is splitted into three phases.

Stage 1: It involves recognition of the cell mass in the image by incorporating the enhanced SLIC algorithm.

A. **Step 1: Creation of super pixels.**

- The given image is pre-processed using the improved SLIC algorithm to segment it into superpixels. Let's label the group of superpixels as S.

B. Step 2: Determine Cell Perimeter

- For every superpixel in S, find the boundary pixels that are part of the superpixel's border. The boundary pixels for superpixels can be referred to as B_s.
- B_s is a binary mask for each superpixel and can be represented by B_s(x, y), where (x, y) are the pixel coordinates.

C. Step 3: Determine the average value of the boundary mask through the use of adaptive thresholding.

- Determine the average intensity value of the boundary for every pixel.
- Mean Boundary Intensity_s is calculated by adding the product of the intensity of each pixel in the boundary B_s and the intensity of the corresponding pixel in the image, divided by the total number of pixels in B_s.
- |B_s| represents the total count of pixels on the boundary within the superpixel s, with Image Intensity(x, y) denoting the brightness value of the image at the specific pixel (x, y).
- Th_s is the adaptive threshold value for superpixel s.

D. Step 4: Identify superpixels that fall below a certain threshold value and classifying them as cell parts.

- For every superpixel s, assess MeanBoundaryIntensity_s in relation to threshold Th_s: If MeanBoundaryIntensity_s is less than Th_s, consider the complete superpixel s as a part of a cell.
- Exclude superpixel s from the cell portions if MeanBoundaryIntensity_s is greater than or equal to Th_s.

Stage 2: The nuclei from the image are detected using Local Threshold Topography.

A. **Step 1: Calculate the Standard Deviation and Mean of Neighborhood Pixels**

- For each pixel p(x,y) in the image, a local neighborhood is calculated around p(x,y).
- The mean (μp) and standard deviation (σp) of pixel intensities within the local neighborhood are calculated. This neighborhood defines the local characteristics around each pixel.

B. **Step 2: Find Nuclei Using Thresholding**

- Apply a thresholding method based on the mean and standard deviation values to segment potential nuclei.
- A common approach is to use a threshold value calculated as a function of the mean and standard deviation, for example:
    - Threshold = $\mu p+k\cdot\sigma p$, where k is a user-defined constant.
- Pixels with intensities above this threshold are considered potential nuclei candidates.

C. **Step 3: Calculate the Highest Intensity of Superpixels**

- The nuclei are segmented into clusters of pixels or super pixels, calculating the highest intensity within each cluster.
- For each cluster or superpixel, find the pixel with the highest intensity, which may correspond to the center or core of the nucleus.
- The highest intensity value can be utilized to characterize the feature of nucleus.

Stage 3: The cytoplasm is recognized and marked using Weibull Bounding Segmentation.

A. **Step 1: Cytoplasm Detection and Marking (Weibull Bounding Segmentation):**

- Let I represent the input image.
- After processing, a binary image B is obtained where $B(x,y)=1$ if (x,y) is related to the cytoplasm region, and otherwise $B(x,y)=0$.

B. **Step 2: Weibull Distribution function**

- ● The Weibull distribution function can be represented in the following equation: $f(x;\lambda,k)=\lambda k(\lambda x)k-1e-(x/\lambda)k$

  where, scale parameter (λ), and shape parameter (k) will be estimated from the data.

C. **Step 3: Fitting a Probability Distribution Object:**

- Estimate the Weibull distribution parameters λ and k that best fit the data from the cytoplasm regions.

D. **Step 4: Predicting the Probability of Occurrence of Nearest Nucleus:**

- Let D represent the distance from each pixel in the cytoplasm region to the nearest nucleus.
- Use the estimated Weibull distribution parameters λ and k to calculate the probability $P(D>d)$, where d is a given distance. This probability represents the likelihood that the nearest nucleus is at a distance greater than d from a point in the cytoplasm.

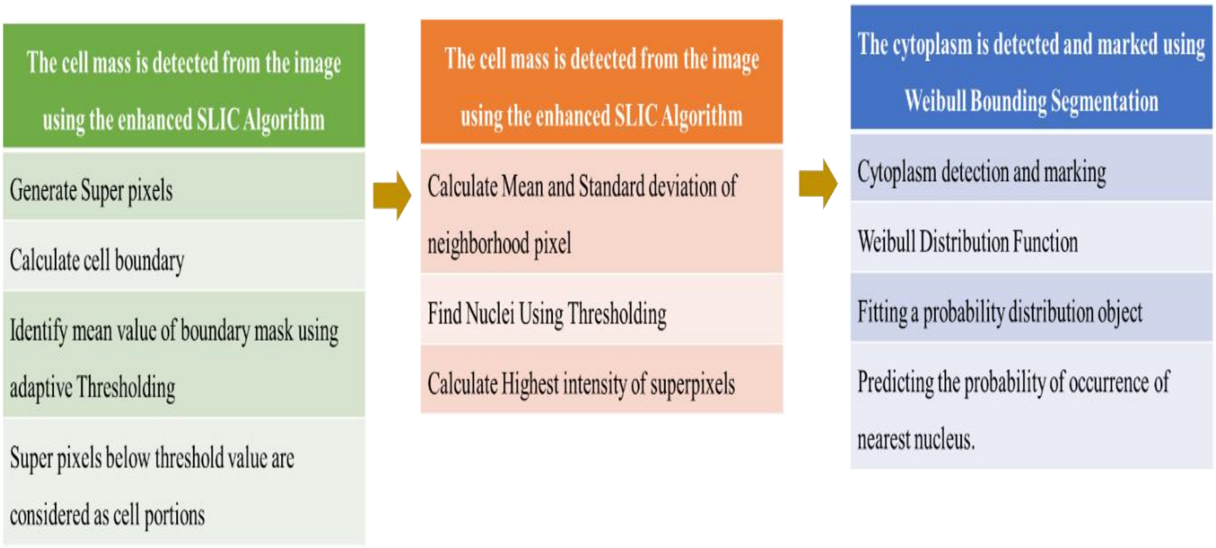

Figure 4.3 Segmentation of the cells with the aid of SLIC algorithm using TWBS

The process of cell segmentation is depicted in Figure 4.3. The implementation of an enhanced SLIC algorithm identifies the mass of the cells present in the image. It is calculated by generation of the superpixels, calculation of the cell boundary, and identification of the mean value of the boundary mask using adaptive thresholding. The superpixels that are below the threshold value are considered cell portions. Subsequently, using Local Threshold Topography, the nuclei of the images are identified using the calculation of the standard deviation and mean of neighborhood pixels. Nuclei is found using thresholding, and by the calculation of the highest intensity of superpixels. With the support of TWBS, the cytoplasm is detected and marked, fitting probability distribution of the object and predicting the probability of the occurrence of the nearest nucleus.

4.2.4 Feature Extraction and Selection

4.2.4.1 Feature Extraction

The selection of features in pap smear image classification comprises of diameter, area, perimeter, eccentricity, color intensity, Local Ternary Patterns (LTrP), Gray-Level Co-occurrence Matrix (GLCM), and Gabor filters is based on their ability to secure the prerequisite characteristics of cervical cells based on their state, whether normal or abnormal. The process of extricating features decreases the overall computational complexity of the classification. The features mentioned are shown in Figure 4.4.

Diameter, Area, and Perimeter: These geometric features are fundamental for capturing the shape and size of the cell nuclei and cytoplasm. Changes in these parameters can indicate cellular abnormalities.

Eccentricity: It is a valuable feature for classification that measures the deviation of the cell shape from a perfect circle that is different from abnormal cells which have irregular shapes.

Color Intensity: The color of the nucleus and cytoplasm can vary depending on the presence of abnormalities. Color intensity features help distinguish between different types of cellular changes.

LTrP: It is a texture descriptor that captures fine-grained patterns in the image, which can be altered in the presence of cervical abnormalities.

Gabor Filters: These are used to detect and represent local spatial frequency information and orientation, which are useful for capturing the texture and edge information that is often altered in abnormal cells.

At the initial stage, the above features are considered which can effectively represent the visual signs that pathologists look for when diagnosing CC from Pap smear images. They are quantifiable, allowing for objective analysis and comparison, and have been shown to contribute significantly to the performance of classification algorithms in distinguishing between normal and abnormal cells.

Features of GLCM: They characterize the image texture by counting the pixel pairs present in the image that makes the model 1 to be rationale. The different components of the GLCM characteristicsare given below.

1. Energy: energy is the capacity of a system to produce change or to cause movement. It is a crucial aspect of our daily lives, as it is responsible for powering everything from our cars

and homes to our own bodies. It is often defined as the ability to do work and can be calculated using various formulas, depending on the type of energy being considered as shown in Eq. (4.8).

$$En = \sum_{c1,c2=0}^{n-1} (Np(I)_{c1c2})^2 \quad (4.8)$$

2. Entropy: Entropy is a fundamental concept in physics and thermodynamics that regulates the intensity of disorder or randomness in a system. In thermodynamics, it is used to predict the direction of heat flow and the efficiency of energy conversion processes. A system with low entropy is considered to be in a highly ordered state, while a system with high entropy is considered to be in a highly disordered state. Entropy is calculated using the Eq. (4.9).

$$Et = \sum_{c1,c2=0}^{n-1} -Ln(Np\big(I_{C1,C2}\big))Np(I_{c1,c2}) \quad (4.9)$$

3. Correlation: Correlation is a statistical measure utilized to evaluate the relationship between two variables. It is a technique for gauging the degree of correlation between two variables. In other words, correlation evaluates the degree of relationship between two variables. The correlation coefficient, denoted as 'r', is a numerical value ranging from -1 to 1 that demonstrates the strength and direction of the relationship between the two variables and is calculated using the following Eq. (4.10).

$$Cr = \sum_{c1,c2}^{n-1} Np(I_{C1,C2})(\frac{(C1-\mu)(C2-\mu)}{\sigma^2}) \quad (4.10)$$

4. Homogeneity: Homogeneity refers to the even distribution of components within a mixture or formula. This means that every part of the mixture has the same composition and properties as the whole. In contrast, heterogeneity refers to a mixture with uneven distribution and varying properties in different parts. Homogeneity can be calculated using the following equation 4.11.

$$Hm = \sum_{c1,c2}^{n-1} \frac{Np(I_{c1,c2})}{1+(c1-c2)^2} \quad (4.11)$$

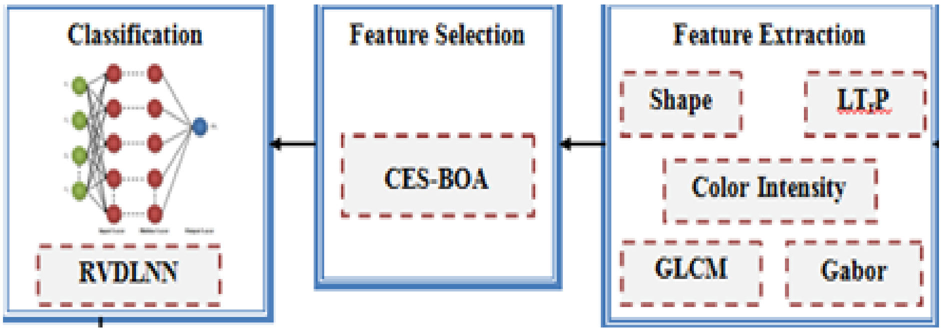

Figure 4.4 Feature extraction and selection of the Pap smear cervical cancer images

4.2.4.2 Feature Selection

Following the extraction of features, the procedure is to select the most impactful features. This process eliminates irrelevant data and reduces the resources needed for computation. Therefore, improving accuracy can be achieved with minimal time and expense. It is carried out with CES-BOA. Typically, population initialization in BOA is carried out randomly which could deteriorate the performance of algorithm. In order to address this issue, the suggested approach utilizes the chaos function (C) for initializing the population.

Moreover, the BOA offers improved optimal outcomes for features with low dimensions. If the dimensions of the features are large, it could result in an inferior ability to search effectively. The BOA utilizes the exponential scale function (ES) to address this issue with the aim of enhancing the BOA's search functionality.

Feature selection using CES-BOA

BOA is an evolutionary algorithm inspired by the natural process of evolution. It uses a probabilistic model to estimate the relationships between features and the target variable and then uses this model to select the most relevant features for a given problem. Unlike traditional methods, BOA does not require any prior knowledge or assumptions about the data, making it suitable for a wide range of applications. BOA uses a probabilistic model to learn the relationships between features and fitness values. This model generates the new subsets by sampling from the probability distribution. These recently formed subsets are assessed, and the cycle continues until a stopping condition is reached, such as reaching the maximum number of iterations or achieving a specific performance level. BOA's strength lies in its capacity to manage nonlinear connections between features and the target variable. Traditional feature selection methods are based on linear models, and it can fail to capture the datas’ complex relationships. BOA, on the other hand, can handle non-linear relationships by using a probabilistic model to capture the underlying distribution of the data.

Feature selection using BOA offers a more efficient, effective, and interpretable approach compared to traditional methods. It can handle high-dimensional data, noisy and redundant features, and non-linear relationships, making it suitable for data analysis using machine learning. The primary goal of employing BOA in feature selection is to enhance the effectiveness of machine learning models by decreasing the dataset's dimensionality. It can be achieved by choosing a subset of most relevant features to the problem at hand. By reducing the count of features, the model becomes less complex, more interpretable, and less prone to overfitting. Moreover, feature selection using BOA can also help in reducing the computational time and cost of training the model.

Initialization

The butterfly population is set at the initial stage. Typically, the BOA starts the population with a random initialization. This arbitrary starting point could lower the algorithm's effectiveness. Therefore, in this suggested system, the initialization is performed using a chaos function that can significantly enhance the butterfly search efficiency.

Fragrance refreshment.

Each butterfly in BOA has its own distinct scent and character. Fragrance is characterized by the strength of the stimulus and can be identified.

Movement of Butterflies

During the second phase, butterflies change their position same number of times as the number of iterations. In this room, every butterfly changes its position. Next, the fitness of every butterfly is assessed. Each round involves updating the fitness values of every butterfly. Moreover, the butterflies emit scent from their precise location. BOA is comprised of two stages: the worldwide search stage and the nearby search stage. In global search, one butterfly will approach anotherwith the best solution. The global search for butterflies is illustrated in this way.

Termination

The butterflies will remain still until the specified requirements are met. The highest number of iterations reached serves as the stopping criteria are utilized. By tracking the butterflies' actions, the algorithm gives the best solution up on the fitness values.

Pseudo-code 1: CES-BOA algorithm

```
Input: Number of extracted features
Output: Selection of optimal features
Begin
    Generate initial population of butterflies $X_i$= (i=1,2,3,….n)
    Determine stimulus intensity $v_{zi}$ at $X_i$
    Describe sensor modality S, power exponent m and switch probability
    While ending criteria not met do,
    For each butterfly do
            Calculate fragrance for by computing,
                    $F_g = S.v_{si}^m$
Conclusion for
Invention best $X_i$
Aimed at each $X_i$
        Compute the best move by computing global search and local search by using,
                $X_V^{T-1} = X_i^T + (R^2 * X_j^T - X_v^T)Fg_i * e^{SF}$
                $X_V^{T-1} = X_i^T + (R^2 * G^* - X_i^T)Fg_i$
            Expiration for
            Apprise the value of m
            End while
            Return the best solution
End
```

4.2.5 Classification with proposed RVDLNN

RVDLNN is a state-of-the-art technology that becomes popular in the artificial intelligence field and has demonstrated promising outcomes in different areas such as image recognition, speech recognition, time series prediction and processes like natural language processing. RVDLNN is a type of generative model that learns to generate new data by understanding the underlying patterns and relationships in a given dataset. It works by using a combination of RNNs and VAEs to capture both short-term and long-term dependencies in the data, which will result in a more robust and accurate model.

A key feature of RVDLNN is its capability to handle sequential data, which is common in many real-world situations. The RNN component allows the model to process sequential data by taking into account the previous inputs and using them to make predictions for the next step. This is especially beneficial in natural language processing, where the implication of a sentence relies on preceding words. RVDLNN has demonstrated encouraging outcomes in forecasting time series, showcasing its efficacy in capturing extended dependencies and managing absent data.

The RVDLNN model has been emerged as a powerful technique in the fight against cervical cancer due to its ability to accurately classify Pap smear images. It can help in early detection and treatment of the disease, ultimately saving lives.

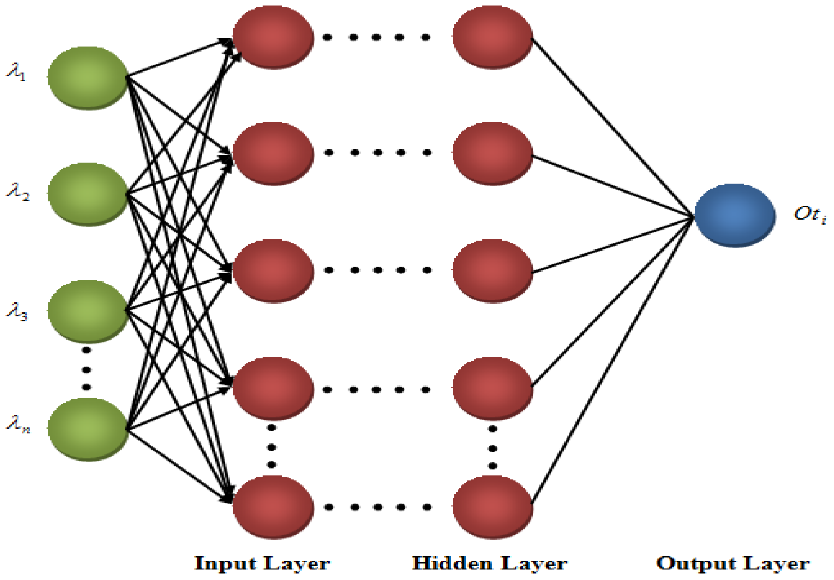

Figure 4.5 DLNN classifier diagrammatically represents the input, hidden, and output layers.

The steps required for proposed RVDLNN classifier outlined in Figure 4.5 are as follows.

Input layer: The classifier receives the particular features through the input layer, following a specific mathematical formulation as shown in Eq. (4.12).

$$\lambda_i = \{\lambda_{1,}\lambda_{2,}\lambda_{3,\ldots\ldots\ldots\ldots\ldots\ldots\ldots,}\lambda_{n}\} \quad (4.12)$$

Next, the weight values are set up accordingly. In the proposed study, the weight values are chosen based on variance calculation instead of random initialization. By doing this, the error values can be greatly reduced, leading to achieve the best results. The adjustment is determined by following revised weight values and is shown below in Eq. (4.13).

$$wg_i = (wg_1, wg_{2,}wg_{3,\ldots\ldots\ldots\ldots\ldots\ldots}wg_n) \quad (4.13)$$

Subsequently, the provided inputs are increased by weight vectors, and randomly chosen bias values are collected. Input layer is mathematically represented as in2 Eq. (4.14).

$$IN_i = \sum_{i=1}^{n} \lambda_i \, wg_i + \, Bais_i \quad (4.14)$$

Hidden layer: Input layer's output is then passed to hidden layer. Its result is combined with activation function. The hidden layer is mathematically represented as following Eq. (4.15).

$$Hd_i = f_r \, (IN_i wg_i + \, Bais_i) \quad (4.15)$$

Where $f(.)$ signifies activation function.

Output layer: Ultimately, output unit is specified by summing weights of input characteristics to effectively perceive severity of the cervical cancer. Output layer is described below in Eq. (4.16).

$$Ot_i = \, f_R(\sum Hd_i \, wg_i + \, Bais_i) \quad (4.16)$$

Finally, network output is evaluated against desired output value. The loss function or error value demonstrates the discrepancy between these two values. The mathematical representation of the loss function is given by Eq. (4.17).

$$L_s = (Tg_i - Ot_i) \quad (4.17)$$

If the loss function values are known, the model will provide the correct solution. If there is a loss, the weights are updated through back-propagation. Ultimately, the categorization stage precisely recognizes the stage and severity of cervical cancer in individuals.

The input images of the Pap smear are pre-processed with the aid of Diffusion Stop Function-based CLAHE. After the pre-processing phase, the data are segmented using Topographic Weibull Bounding Segmentation. Segmented images are selected by feature extraction, and they are chosen with CES-BOA. The selected features are classified by various methods, which comprise ResNet50V2, AlexNet, DLNN, and Radiance and Variance Enabled Deep Learning Neural Networks.

4.3 Summary

Chapter 4 delves into the automated detection of cervical cancer. The SIPaKMed and Herlev datasets are utilized and the data is chosen. The DSF-CLAHE preprocesses the data and the TWBS process segments it. Butterfly Optimization Algorithm processes the characteristics of the extracted and chosen data and categorizes it within the RVDLNN framework. Thus, by undergoing this process, cervical cancer cells can be classified effectively.