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Appendix L2

(Item No 5 of Check List) Details of Research Publications

S.No	Article	Journal	Other Details Vol/No/Page No/ Year	Published in UGC-CARE / Scopus Indexed/ Web of Science
1	A versatile Detection of Cervical Cancer with i-WFCM and Deep Learning based RBM classification.	Journal of Machine & Computing	Volume 3 Issue 3 Pages: 238-250 July 2023	Scopus
2	Novel Segmentation based Cervical Cancer Detection Using Deep Convolutional based Neural Network with RELU	Journal of Theoretical and Applied Information Technology	Volume: 102 No. 5 Pages: 1759 – 1772 March 2024	Scopus

*Proof of list of Journals from Internet to be attached along with copies of reprints.

Scholar : [signature]

Supervisor : T. [signature]

Checked By:

HoD/Dean of Respective School

The scholar miss. Soumya Haridas (17PHCSP010) has published her articles in the following journals:

1. Journal of machine and computing - indexed and active in Scopus from 2021 to present,
2. Journal of Theoretical and Applied Information Technology - is indexed and active in Scopus from 2008 to present.

This may be considered.

J. [signature]
27.04.24

A Versatile Detection of Cervical Cancer with i-WFCM and Deep Learning based RBM Classification

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Abstract—One of the most common and curable types of cancer in women is cervical cancer, a common chronic condition. Pap smear images is a common way for screening the cervical cancer. It does not present with symptoms until the disease has advanced stages, cervical cancer cannot be detected in its early stages. Because of this, accurate staging will make it easier to give the patient the right amount of treatment. In this paper proposes the Anisotropic Diffusion Filter has been used to improve the Pap smear image by removing noise and preserving the image's edges. The contrast of a Pap smear image has been enhanced using Histogram Equalization. The enhanced image has been segmented using Improved Weighted Fuzzy C-means clustering to make it easier to identify the effective features. As a result, the effective features are extracted from the segmented region and used by a Restricted Boltzmann Machine classifier based on Deep Learning to classify the cancer. The performance of the proposed cervical cancer detection system can be measured in terms of sensitivity, specificity, F-measure and accuracy. The performance measures for the proposed system can be achieves 95.3% accuracy, 88.6% specificity, 89.13% precision, 88.56% recall, and 89.7% F-measure respectively. Based on simulation results, the proposed method performs better than conventional methods such as RDVLNN, Random Forest (RF), Extreme Learning Machine (ELM), and Support Vector Machine (SVM) for detecting cervical cancer.

Keywords—Anisotropic Diffusion Filter, Histogram Equalization, Improved Weighted Fuzzy C-Means Clustering, RDVLNN, Random Forest (RF), Extreme Learning Machine (ELM), Support Vector Machine (SVM).

I. INTRODUCTION

Cervical cancer is the fourth most prevalent disease in women overall, as reported by the World Health Organization (WHO), with an anticipated 604,000 new cases and 342,000 fatalities in 2020. Almost 90% of all new cases and fatalities worldwide in 2020 took place in low- and middle-income nations [1, 2]. Early identification through routine examinations is crucial because cervical cancer has a long latency period and starts out without any obvious symptoms. Regardless of whether it spreads to other regions of the body, cancer is a condition in which the body's cells develop rapidly. It is typically named for the part of the body where it first appears [3-5]. Cancer that starts in the cervix is referred to as cervical cancer [6, 7].

According to estimates, more than 500,000 women had cervical cancer in the world in 2018, and more than 300,000 of those women passed away from the disease. Nearly all (99%) incidences of cervical cancer are linked to high-risk human papillomavirus (HPV) infection, an incredibly common virus transferred through sexual contact. As a result, screening tests and receiving an anti-HPV vaccine may help to prevent cervical cancer.

Moreover, a Pap smear test is typically used to identify cervical cancer. It is a quick, painless screening test for uterine cervix cancer or pre cancer. Moreover, the frequent Pap test procedure reduces the incidence rate of cervical cancer. An effective segmentation and classification technique is employed to determine the cervical cancer's real stage. Under a microscope, the extracted cervical cells are examined in order to manually classify the aberrant and normal cervical cells. However, this method is vulnerable to high percentages of false positives since cell sorting is sensitive to human error. Pathologists can only count 4 to 5 slides every day using this method, which is quite economical. It is challenging to carry out the process more quickly because of the cytoplasm and nucleus that are present in the cell structure. Two key procedures are used in every computer-aided cervical cancer screening system: segmentation and classification.

Motivation

The optimization algorithms and machine learning techniques are used in this study to produce superior solutions:

- Establishing a data validation mechanism to enhance cervical cancer prediction performance.
- To effectively locate the multiple cell nucleus rather than the single cell nucleus in an image of cervical cancer.
- How to identify key performance indicators for a classifier that outperforms other classifiers

Objective

Our study has the following objectives:

- Evaluate the performance of the developed system of our classifier.
- Explore and Compare different evaluation features for detecting the cervical cancer.
- Select the key performance indicators on the proposed model of cervical cancer identification and also measure the Accuracy, Specificity, Precision, Recall, and F-measure.

Contribution of the Proposed System

- To achieve precision, an Anisotropic Diffusion Filter with Histogram Equalization has been utilized which has used to remove the unwanted noises and preserve the edges of cells.
- The Improved Weighted FCM has been used to segment the area of interest in order to overcome histology images' composite nature and irregular forms.
- Feature extraction has been used to extract textural based features.
- A Restricted Boltzmann Machine has beenintroduced to classify cervical cancer and compare the accuracy with other existing classifiers.
- Standard benchmark measurements have been used in this research tomonitor the efficiency of an automated system in cervical cancer: Accuracy, Specificity, Precision, Recall, and F-measure.

This paper is organized as follows: section 2: Related Works; section 3: Proposed Methodology; section 4: Results and Discussion, and section 5: Conclusion and Future enhancements.

II. RELATED WORKS

Cervical cells have been studied extensively in this regard. A two-tier problem involves dividing cells into normal and defective cells, and a seven-tier problem is dividing cells into one of the seven groups. Nine features are used to depict the nucleus region, whereas eleven features are used to represent the cytoplasm.

To categorize cancer using Pap Smear Test images, Geetha and Suganya[8] suggested Elman Neural Network (ENN) working with the Teaching Learning Based Optimization (TLBO) algorithm. An input Pap smear image is first transformed from RGB to grey level. The grey level image is smoothed with the Kuan Filter during preprocessing in order to remove undesired noise created (KF). The detected cells from the Pap smear picture have been segmented using the Active Contour Method (ACM). To increase accuracy, features like GLCM, haralick, solidity, form, and other mathematical features are extracted. The ENN-TLBO classification algorithm was used. TLBO is used to obtain the best weights possible during the training period. Performance evaluation was carried out using experimental results, where ENN-TLBO produced good accuracy of 86.6%, outperforming other popular algorithms like SVM and RBF classifiers.

An Additional classification of cervical cells based on a multi-domain hybrid deep learning architecture was proposed by Chuanwang Zhang et al. [9]. By attempting for the first time to classify cervical cells using the multi-domain hybrid deep learning framework (MDHDN), they address the restrictions. The pretrained VGG-19 (Visual Geometry Group-19), a deep convolutional neural network (CNN) includes a hashing layer after the last fully connected layer, extracts cell deep features from multi-domain (time and frequency). Feature selection, clustering, and dimensionality reduction are used to process manually created features for the source photos. Following the output of the category results by the three sub channels of the proposed framework using the SVM classifier, the correlation analysis produces the final cell diagnosis. Findings indicate that the suggested method performs similarly to state-of-the-art models that employ novel structures and have accuracy, sensitivity, and specificity values in the Herlev dataset of 98.7%, 98.2%, and 98.9%, respectively.

Cervical cell multi-classification technique using global context information and attention mechanism was proposed by Jun Li et al. [10]. To categorize cervical cells, they created a convolutional neural network (L-PCNN) that combines information about the whole environment with an attention mechanism. To extract deep learning features, the cell image is forwarded to the upgraded ResNet-50 backbone network. Each convolution block adds a convolution block learning algorithm to instruct the network to concentrate on the cell area, improving the extraction of deep features. After that, the long short-term memory module (LSTM) and pyramid pooling layer are added at the end of the backbone network to combine picture features in various locations. The integration of low-level and high-level features allows the network as a whole to learn more about regional detail features and resolves the issue of network gradient vanishing. The SIPaKMeD open data set is used for the experiment. The experimental findings reveal that the suggested l-PCNN has accuracy in cervical cell classification of 98.89%, sensitivity of 99.9%, specificity of 99.8%, and F-measure of 99.89%, which is better than other cervical cell classification models, demonstrating the model's efficacy.

Several supervised machine learning methods were examined by Gaurav Kumavat et al. [11] in order to find cervical cancer in its earliest stages. A dataset on cervical cancer was taken from the UCI library and used to train the machine learning model. Using 36 risk indicators and one outcome variable, this dataset of 858 cervical cancer patients was used to compare the various approaches. In this study, six classification methods were used: a random tree, a logistic tree, an XG-boost tree, a Bayesian network, an SVM, and an artificial neural network. To assess the effectiveness and accuracy of the classifiers, all models were trained both with and without a feature selection technique. There were three feature selection techniques used: relief rank I wrapper method (ii), and LASSO regression (iii). With XG Boost's full feature set, the highest accuracy of 94.94% was noted. Also, it has been noted that the feature selection algorithm sometimes outperforms the dataset. However, the drawbacks of prediction studies and models, such as overfitting, lack of interpretability, and simplified, inadequate information, point to the need for additional work to increase the precision, dependability, and utility of clinical outcome prediction.

A unique method for the automatic identification of cervical cancer was presented by Lavanya and Thirumurugan[12] employing modified fuzzy C-means, textural and geometric feature extraction, Principal Component Analysis (PCA), and classification. Despite the uncertainty, modified fuzzy C-means segment the input image into useful sections with promising outcomes. By retaining only, the uncorrelated features, PCA is used to minimize the dimensionality of the data collection and shorten the algorithm's processing time. By using K Nearest Neighbor (KNN) classification with k-fold cross-validation, the images from pap smears are divided into normal and abnormal cells, and the results are compared with those from Fine Gaussian SVM, Linear Discriminant and Ensemble Bagged trees. By evaluating the minimum accuracy, average accuracy, sensitivity, specificity, maximum accuracy, F1-score, and precision, the effectiveness of the suggested approach is evaluated. With minimum accuracy of 94.15%, maximum accuracy of 96.28%, average accuracy of 94.86%, sensitivity of 97.96%, specificity of 83.65%, F1-score of 96.87%, and precision of 96.31% for threefold cross-validation, the experimental findings of the suggested technique demonstrate excellent results.

Research Gap

To automate the system to fill in a number of research gaps from the literature for the following reasons as

- Increase the sensitivity and specificity of the Pap smear test
- Reduce the workload of medical professionals and lab technicians;
- Make cervical cancer screening programs less expensive;
- Decrease the incidence of cervical cancer and mortality rates.

III. PROPOSED WORK

The research background demonstrates that Machine Learning and Deep Learning are increasingly being used to process medical images, particularly to diagnose Cervical Cancer. In order to achieve this goal with improved performance, the present study proposes an optimized cervical cancer segmentation method that makes use of Weighted FCM. The general method for the proposed strategy has been displayed in **Fig 1.**

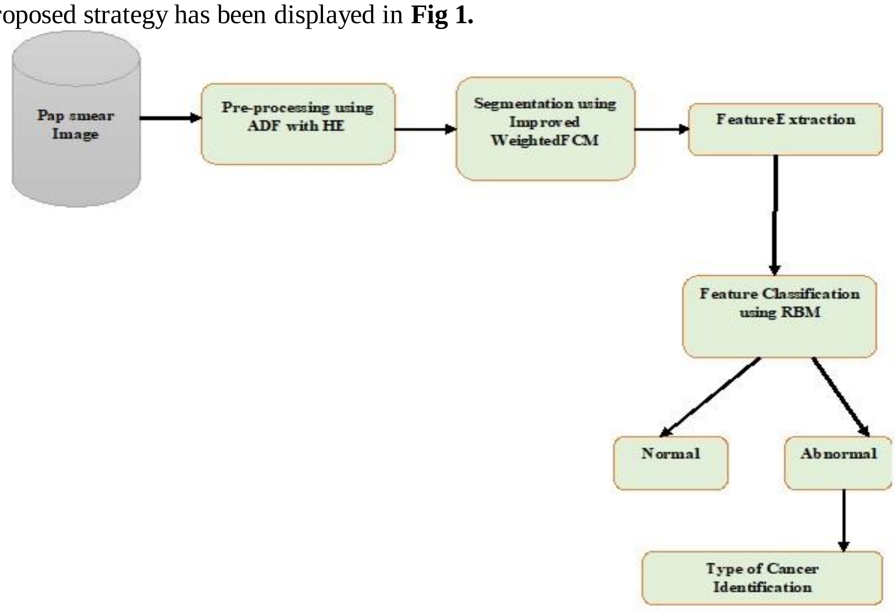

Fig 1. System Architecture of Cervical Cancer Detection

Pre-processing

Operations with images at the lowest level of abstraction are referred to as pre-processing because both the input and the output are intensity images. An intensity image is typically represented by a matrix of image function values (brightness), and these representative images are of the same kind as the original data which is captured by the sensor. The geometric transformations of images, such as rotation, scaling, and translation, are classified as pre-processing methods. The goal of pre-processing is an improvement of the image data that suppresses unwilling distortions or enhances some image features important for further processing.

The process of the Preprocessing in the proposed work is

- Converting the given color image of cervical cancer to Grayscale image transformation.
- Utilize the Anisotropic Diffusion Filter to eliminate any unnecessary noise from the image in order to achieve a high-quality result.

Adaptive Histogram Equalization has been used to make the more enhance image in a very effective manner. The Preprocessing Steps are depicted in **Fig 2.**

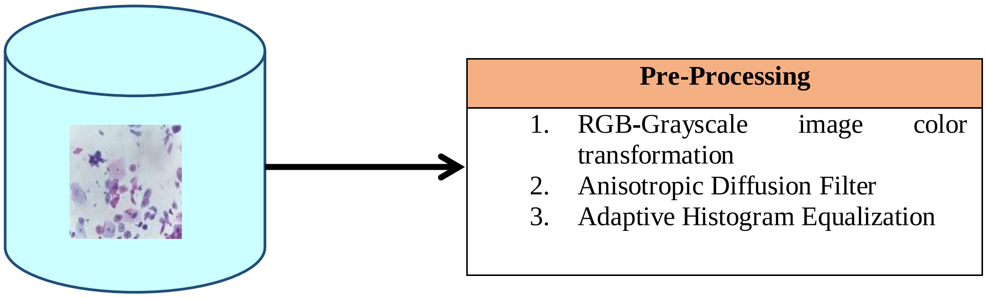

Fig 2. Preprocess

Anisotropic Diffusion Filter

The first and foremost step is to convert the Grayscale image of Pap smear image from the RGB image. In order to enhance the quality of an image, Anisotropic Diffusion Filter has been utilized by removing the noise in the image. Anisotropic diffusion, also known as Perona–Malik diffusion, is a method that aims to reduce image noise without removing significant parts of the image's content [12][13][14], typically edges, lines, or other important details for medical image interpretation. An image generates a parameterized family of successively more blurred images based on a similar process to anisotropic diffusion. Each of the images that come out of this family is a convolution of the image and a 2D Gaussian filter whose width grows as the parameter is changed [15][16].

The Partial Differential Equations (PDE) were used to design the anisotropic diffusion filter, which makes the image diffusion process simpler. This process of diffusion can be extended to include anisotropic diffusion; a collection of bound images is produced by the filter. The superposition of the input image and the filtered content of the input image are used to create the output image.A PDE, which is frequently utilized for noise removal, image edge detection, and detail preservation, is the source of the anisotropic diffusion equation.

The image's edge information can be preserved during denoising by the equation, which can adaptively alter the diffusion coefficient in response to the image's characteristics.

The expression for the diffusion model is

$$\frac{\partial I}{\partial t} = div(c(a,b,t)\nabla I) = \nabla c.\nabla I + c(a,b,t)\Delta I \tag{1}$$

Where,

{\displaystyle \Delta }Δ denotes the Laplacian, {\displaystyle \nabla }∇ denotes the gradient, $div(\dots)$ is the divergence operator and $c(a,b,t)\Delta${\displaystyle c(x,y,t)} is the diffusion coefficient.

For {\displaystyle t>0} $t > 0$the output image is available as$I(.,t)$ {\displaystyle I(\cdot,t)}, with larger {\displaystyle t}t producing blurrier images.

$c(a,b,t)$Controls the rate of diffusion and is usually chosen as a function of the image gradient so as to preserve edges in the image

$$c(\|\nabla I\|) = e^{-\left(\|\nabla I\|/K\right)^2} \tag{2}$$

Contrast Limited Adaptive Histogram Equalization

CLAHE [17] was a step up from AHE. An image is broken up using the CLAHE algorithm into contextual regions. Each contextual region's histogram is generated, and clipping is carried out at a predetermined value. The histogram bins are redistributed with the clipped amount. The problem of AHE's edge-shadowing and over-enhancement is reduced by this approach. CLAHE has demonstrated its effectiveness in enhancing medical images with low contrast. By redistributing the gray values used, this method makes the images hidden features more visible.

The intensity level of each pixel is compared to the intensity values of its adjacent pixels to determine its ranking. The pixel is then given a new intensity value that is proportional to its rank in the available range. The local area or contextual region, rather than the entire image, is what this method uses to boost contrast.

Segmentation Weighted FCM

Image segmentation is the most common method and analysis in Digital Image Processing, to divide an image into multiple regions based on the characteristics of the pixels [18]. It is the process of separating the foreground from the background, or clustering pixels into regions based on similarities in color or shape.Image segmentation can be used to filter noisy images, find objects in satellite images, perform object detection and recognition tasks, automate traffic control systems, and monitor video.[19][20]

Improved Weighted Fuzzy C-Means (IWFCM) algorithm

The fuzzy c-mean calculation is one of the normal calculations that used to divide the image into different group clusters based on image pixels values. Fuzzy clustering is the most appropriate type of clustering for segmenting medical images. The k-means algorithm can be thought of as the fuzzified version of the Fuzzy C-Means (FCM) algorithm. It is a clustering algorithm that allows data items to be classified according to their degree of membership in each cluster [21][22]. Even though this algorithm reduces the noise with less robust, it make the noisy data into separate cluster. This leads to the poor performance of the FCM.

In order to overcome this poor performance, modified FCM plays uniform contribution of Cluster analysis.

The objective function of FCM is defined as (3)

$$Y_l = \sum_{i=1}^{n} \sum_{j=1}^{c} b_{ij}^{l} \left\| x_i - c_j \right\|^2 \tag{3}$$

where$l$ represents the degree of fuzziness and is a real number greater than 1, bij is the membership degree of the ith datum in the jth cluster, x_i denotes the data points, and c_j is the cluster center. Also, $\|.\|$ represents the Euclidean distance, n is the number of data points, and c denotes the number of clusters. Determination of cluster center is not accurate. So, in order to find the weighting factor and improvement in cluster center, an Improved Weighted Fuzzy C-Means (IWFCM) algorithm is proposed. The proposed IWFCM clustering algorithm still works in the original data space, i.e. prototypes are located in data space, in contrast to the usual method used in FCM. IFCM is particularly well-suited for dealing with incomplete data because it is more resistant to outliers and noise than FCM.

Proposed Improved Weighted Fuzzy C-Means (IWFCM) Algorithm

The proposed IWFCM algorithm is to perform FCM in a higher-dimensional feature space after mapping the input data into it using a nonlinear transform. The objective function that follows is minimized by the Kernel Weighted Fuzzy C-Means. [23]

$$\mathrm{Y}\omega = \sum_{\mathrm{i}=1}^{\mathrm{k}} \sum_{\mathrm{j}=1}^{\mathrm{n}} \mathrm{b}_{\mathrm{ij}}^{\mathrm{l}} \left\| \omega(\mathrm{x_j}) - \omega(\mathrm{v_i}) \right\|^2 \tag{4}$$

Where, bij denotes the membership of x_j in cluster i, $\omega(v_i)$ is the center of cluster i in the feature space, and ω is the mapping from the input space X to the feature space F.

Algorithm

KFCM Algorithm

1. Select initial class prototype {Vi} c
2. Update all memberships bijusing the weighted average for cluster center by
3. $u_{ik} = \frac{(1-B(x_k,v_i))^{-\frac{1}{(m-1)}}}{\sum_{j=1}^{c}(1-B(x_k,x_j))^{-\frac{1}{(m-1)}}}$ (5)
4. Obtain the prototype of clusters in the forms of weighted average using the following
5. $v_i = \frac{\sum_{k=1}^{n} u_{ik}^{m} B(x_k,v_i) x_k}{\sum_{k=1}^{n} u_{ik}^{m} B(x_k,v_i)}$ (6)
6. Repeat step 2-3 till stopping criterion is met
7. The termination criterion is$|V_{new} - V_{old}| \leq \varepsilon$
8. Where $\|.\|$is the Euclidean norm. V is the vector of cluster centers ε is a small number that can be set by user (here ε=0.01)

Feature Extraction

The process of extracting more specific information from an image is called Feature Extraction. In this stage of the processing, the features extraction process is used to extract the most important features of the segmented cervical cancer area in order to make the diagnosis easier and more accurate. To characterize the cervical cancer and feed the classifier, Feature Extraction seeks to extract features from the Pap smear image. The most basic to the most advanced feature extraction algorithms for diagnosing cervical cancer from Pap smear images were presented in the recent research. Some of the features have been extracted for the identification of lesion image of skin is Geometrical features such as Asymmetry, Diameter, Concavity, Area, perimeter, eccentricity and other features such as Shape, Size, Texture identification [24] GLCM and Haralick Features.

Feature Classification using Restricted Boltzmann Machine (RBM)

A Neural Network known as the Restricted Boltzmann Machine (RBM) simulates a non-directed, symmetrical connection without any intra-layer connections between the visible and hidden nodes. When a set of patterns is given to the network as input, a RBM learns a probability distribution. A Deep Belief Network (DBN) is a deep neural network with many hidden unit layers. Each pair of connected layers in a DBN is a RBM. The data's input is set up in the input layer, and the abstract description of this input is characterized in the hidden layer.

A restricted Boltzmann machine has units connected across layers but no communication within layers. Based on the Hinton's contrastive divergence algorithm which is used to learn the weights of connections between visible and hidden nodes because there are no intra-layer connections [25].

In an RBM, an energy function is defined based on the visible-hidden arrangement of Gaussian neurons.

$$E(v,h) = \sum_i \frac{(v_i - a_i)^2}{2\sigma_i^2} - \sum_i \sum_j \frac{v_i}{\sigma_i^2} h_j w_{ij} - b'h \quad (7)$$

Where w is the visible –hidden weight matrix, and a and b are the bias vectors respectively.

To calculate the Joint Probability in RBM configuration, $p(v,h)$

$$P(v,h) = \frac{\exp^{-E(v,h)}}{K} \quad (8)$$

Where K is the Partition function can be expressed in

$$K = \sum_{v,h} \exp^{-E(v,h)} \quad (9)$$

Each vector in RBM can be assigned in the Probability as

$$P(v) = \frac{1}{K} \sum_h \exp^{-E(v,h)} \quad (10)$$

The conditional probabilities can be written based on the sigmoid function

$$P(h_j = 1|v) = \sigma(\sum_i \frac{v_i}{\sigma_i^2} w_{ij} + b_j) \quad (11)$$

$$\text{Where } \sigma(x) = \frac{1}{1+e^{-x}} \quad (12)$$

and

$$p(v_i = v|h) = \in (v| \sum_j h_j w_{ij} + a_i, \sigma_i^2 \quad (13)$$

Measuring Classification

To estimate the effectiveness of the RBM based cervical cancer detection method, appropriate metrics are utilized in this paper. The F-Measure, Recall, Sensitivity, Specificity, Accuracy, and Precision measures are utilized. For all images, let TP denote the value of the True Positive Rate, FP the value of the False Positive Rate, TN the value of the True Negative Rate, and FN the value of the False Negative Rate.

Precision = TP / (TP + FP) (14)
Recall = TP / (TP + FN) (15)
Specificity = TN / (TN + FP) (16)
Accuracy= (TP+TN)/ (TP+FN+TN+FP) (17)

F-Measure= 2*(Precision*Recall)/ (Precision+Recall) (18)

IV. RESULTS & DISCUSSION

Dataset Description

SIPaKMeD [26] and Herlev datasets [27] were the two datasets used in the proposed method. The Herlev dataset was utilized for single-cell classification, while the SIPaKMeD dataset was utilized for multi-cell classification. There were 917 images in the Herlev dataset. Classes 1 to 3 are cervical cells that are normal, while classes 4 to 7 are cervical cells that are abnormal. There were 966 images in the multi-cells dataset, and 4049 cells were cropped from these images. The normal, benign, and abnormal stages of the cell were separated.

Experimental Setup

The result of the systematic model is validated using Matlab 2022b simulation tool. The processor includes Intel (R) Core (TM) i5-3210M, CPU@2.5GHz, 2.0GB of RAM. A proposed RBM classification scheme has been evaluated and compared to the existing classification schemes like SVM, RF, ELM and RVDLNN in this section. Images from the MRI of Pap smear image database are initially tested before being trained. MATLAB is used to evaluate the results of the simulation. This evaluation takes into consideration an around 250 sample images. This consists of a training set of 150 images and a testing set of 100 images. The system processing times takes 10mins. **Fig 3** depicts the proposed RBM process in the Pap Smear Image Classification.

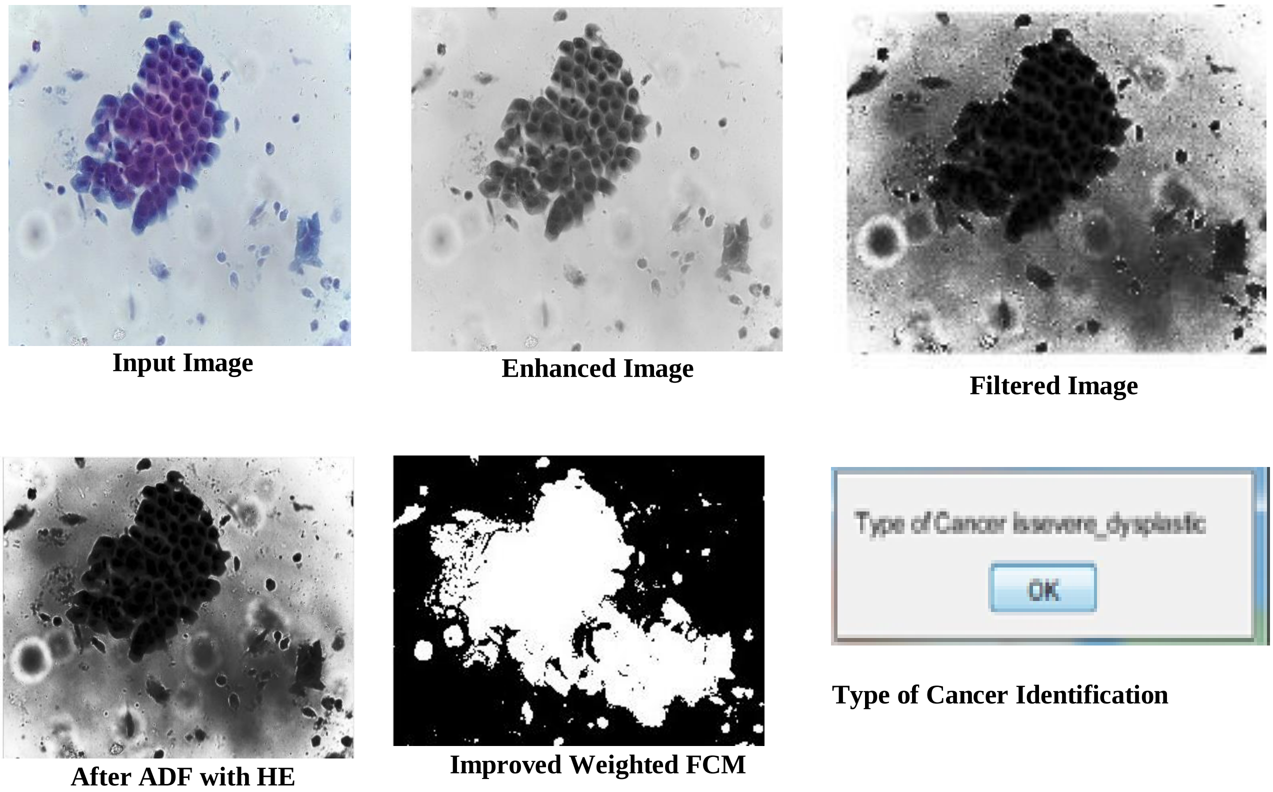

Fig 3. Proposed RBM Based Results for Input Pap Smear Cancer

Table 1. Training and Testing Accuracy

Classifier	Train Loss	Test Loss	Train Accuracy	Test Accuracy
Proposed RBN	0.125	0.126	0.921	0.946
RVDLNN	0.131	0.131	0.872	0.875
ELM	0.143	0.137	0.814	0.827
SVM	0.147	0.21	0.754	0.762
RF	0.162	0.152	0.781	0.782

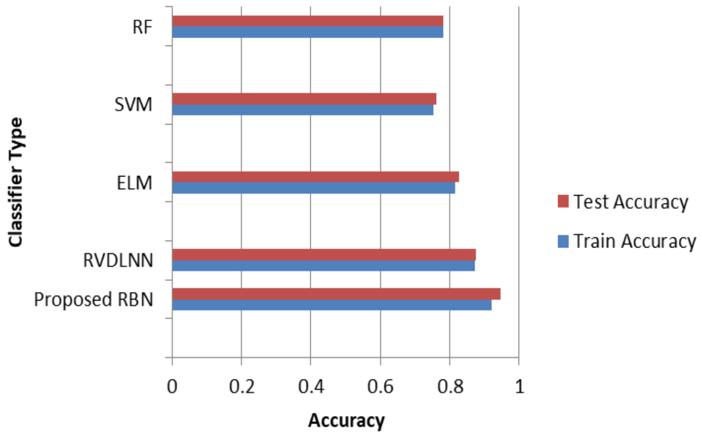

Fig 4. Training & Testing Accuracy results of Classifiers

Fig 4 depicts the Training and Testing accuracy of all classifiers implemented in cervical cancer Based on the improvement of weight vector calculation in our Proposed RBM, the true positive rate has been improved in **Table 2.**

Table 2. Specificity

Image Set	Proposed RBN	RVDLNN	ELM	SVM	RF
50	65.12	62.87	59.25	59.25	57.79
100	67.84	64.08	59.75	59.25	58.2
150	74.29	68.96	65.32	65.78	64.82
200	78.54	74.52	72.61	69.12	67.84
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

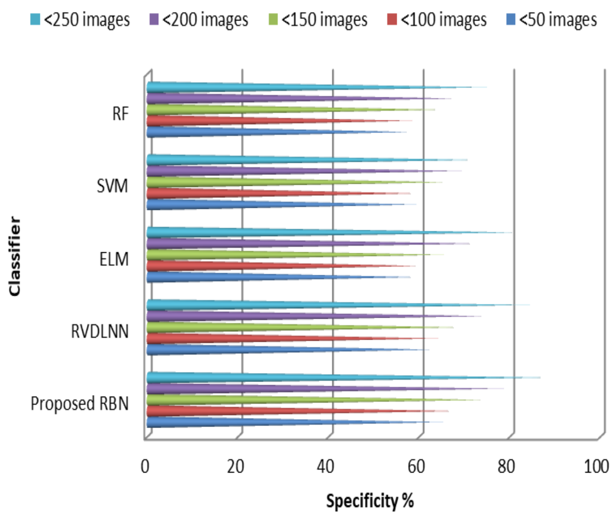

Fig 5. Specificity results of Classifiers

The Specificity execution of cervical malignant growth detection plans graphical depiction is showed up in **Fig 5**. It demonstrates that proposed RBM specificity is 4.43%, 7.35%, 16.41% and13.79% higher than that of RVDLNN, ELM, SVM and RF respectively for 250 image dataset. Inferable from true positive rate and true negative results, the specificity of proposed RBN is extended in **Table 3**.

Table 3. Precision

Image Set	Proposed RBN	RVDLNN	ELM	SVM	RF
50	72.57	68.12	61.04	56.12	54.3
100	74.68	67.91	63.81	59.87	57.86
150	74.09	68.25	67.77	64.72	62.06
200	81.63	72.56	74.06	71.66	70.72
250	89.13	78.52	79.15	74.52	72.86

Fig 6. Precision results of Classifiers

Fig 6 depicts the precise execution of the graphical representation of plans for identifying the type of cervical cancer. It demonstrates that proposed RBM is 10.61%, 9.98%, 14.61% and 16.27% more precise than RVDLNN, ELM, SVM and RF classifier respectively for 250 image dataset. The proposed RBM precision is increased on the basis of its high specificity and True positive rate in **Table 4.**

Table 4. Recall

Image Set	Proposed RBN	RVDLNN	ELM	SVM	RF
50	78.14	70.15	64.76	69.15	60.88
100	78.14	72.54	69.01	72.14	61.46
150	84.34	73.33	69.45	73.41	64.15
200	86.15	74.74	71.36	76.11	68.67
250	88.56	76.48	73.44	78.61	71.11

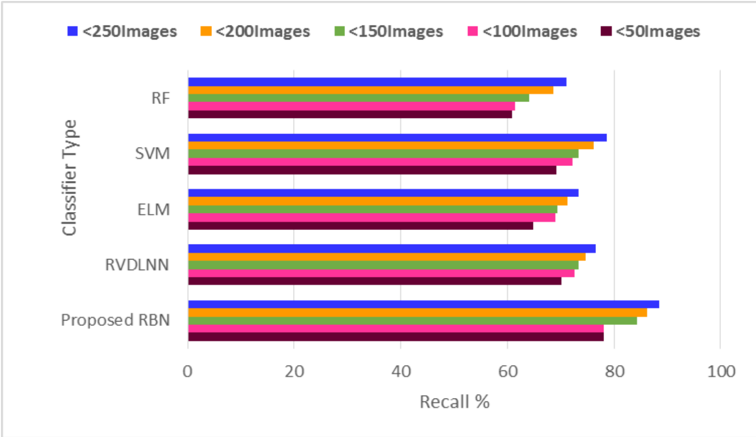

Fig 7. Recall results of Classifiers

Fig 7 depicts the graphical representation of the recall execution of recognition of the type of cervical cancer plans. It demonstrates that RBN outperforms RVDLNN, ELM, SVM and RF classifier respectively for 250 image dataset by 12.08%, 15.12%, 9.95% and 17.45%, respectively. Due to its low error rate and high specificity, RBN is the subject of numerous investigations in **Table 5**.

Table 5. F-measure

Image Set	Proposed RBN	RVDLNN	ELM	SVM	RF
50	71.11	62.33	58.4	57.85	54.31
100	75.36	64.21	61.78	60.57	62.36
150	79.19	68.89	65.12	67.54	69.34
200	84.25	70.11	69.44	71.19	72.13
250	89.7	73.8	72.51	75.4	74.58

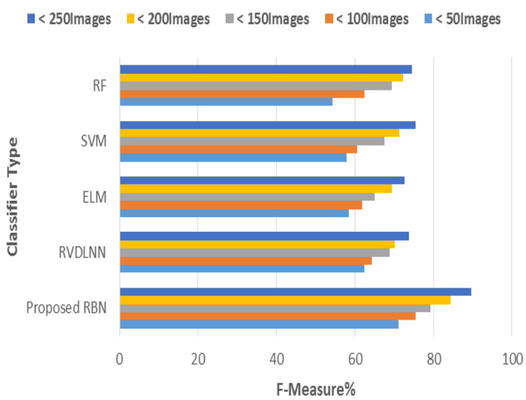

Fig 8. F-measure results of Classifier

The F-measure execution of cervical malignant growth acknowledgment plans graphicaldepiction is showed up in **Fig 8**. It demonstrates that proposed RBMreview is 15.9 %, 17.19%, 14.3%, and 15.12%RVDLNN, ELM, SVM and RF classifier respectively for 250 image dataset. Exhibitions of the proposed scheme have improved clustering's high positive rate and more positive rate.

After training, the generalization performance of the classifiers is evaluated with the test data. The performance measures of the classifiers have been shown in **Table 1-5** along with the graph **Fig 4-8**. From, each iteration, increasing the number of image dataset for testing to find the performance measures such as Testing accuracy, Specificity, Precision, Recall and F-measure. From the above **Table 1-5**, we analysed that our proposed system outperforms than the existing classifiers such as RVDLNN, ELM, SVM and RF.

Table 6. Overall performance numerical values for Pap Smear Cancer Identification

Performance Measures	Proposed RBN	RVDLNN	ELM	SVM	RF
Accuracy (%)	95.3	88.5	82.65	77.26	78.6
Specificity (%)	88.6	84.17	81.25	72.19	74.81
Precision (%)	89.13	78.52	79.15	74.52	72.86
Recall (%)	88.56	76.48	73.44	78.61	71.11
F-measure (%)	89.7	73.8	72.51	75.4	74.58

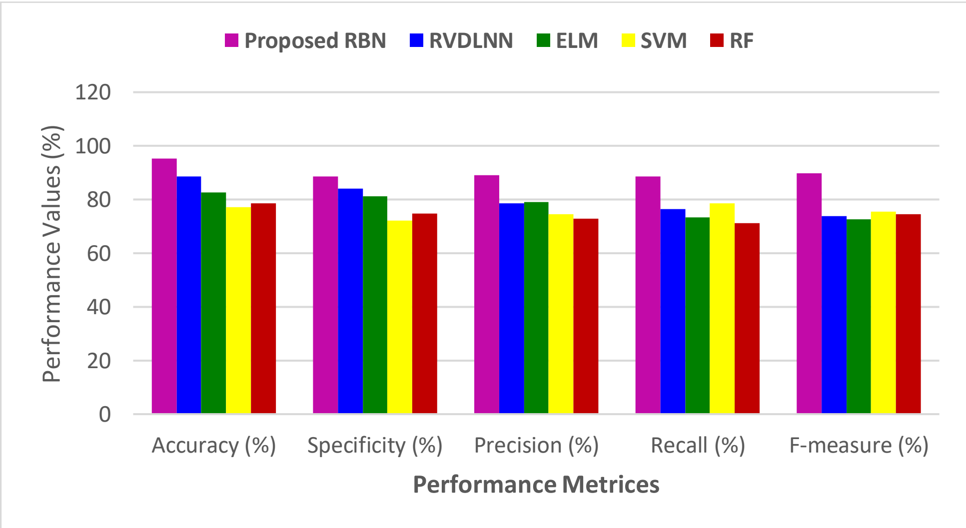

Fig 9. Prediction of overall performances for Pap Smear Cancer Classification schemes

The obtained results are significant when compared to all previous studies because the highest accuracy achieved with the same dataset is 95.3%. The RBM classifier was used to achieve this level of accuracy. This study used an existing structure and proposed a new structure to improve accuracy, sensitivity, and precision for all classes, despite the fact that the literature has focused on traditional methods. Additionally, the suggested approach is quick and precise. The proposed structure is straightforward, original, and precise, and the amount of time required to test a single new image does not exceed milliseconds, which is acceptable for use in medical applications**. Fig 9** shows Prediction of overall performances for Pap Smear Cancer Classification schemes. **Table 6** shows Overall performance numerical values for Pap Smear Cancer Identification.

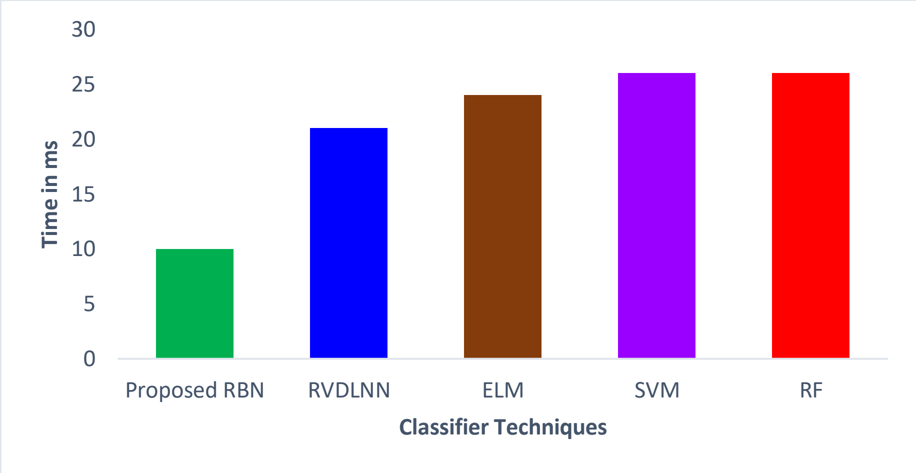

Fig 10. Computation Time

The computation time required by various algorithms, such as Proposed RBM, RVDLNN, ELM SVM, and RF, as well as the proposed work of RBM, is shown to be minimal in **Fig 10**. It is claimed in this paper that the proposed method is more accurate than other methods currently in use.

V. CONCLUSION

Based on Deep learning-based RBM classification, this study proposes Cervix Cancer Identification with the Pap Smear Test. Anisotropic Diffusion Filter with Histogram Equalization is used for reducing the commotion without eliminating the edges and by improving the contrast of image for better segmentation. An Improved Weighted FCM was utilized for determining the optimal cluster center of an image in the segmentation which leads to extract the features efficiently. The RBM classifier is utilized for classification. When compared to other classifiers like RVDLNN, ELM, SVM, and RF, the result of the proposed RBM achieved an accuracy of 95.3%. In the future, test the Pap smear image using a different algorithm that makes it easier and faster to find the cervical cancer earlier.

Data Availability
The data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interests
The author(s) declare(s) that they have no conflicts of interest.

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Ethics Approval and Consent to Participate
The research has consent for Ethical Approval and Consent to participate.

Competing Interests
There are no competing interests.

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NOVEL SEGMENTATION BASED CERVICAL CANCER DETECTION USING DEEP CONVOLUTIONAL BASED NEURAL NETWORK WITH RELU

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ABSTRACT

Malignant growth in the cervical area is the fourth most common cause of death in women worldwide. The global burden of cervical cancer has decreased as a result of early screening, which made the disease a preventable one. Early detection and treatment of this cancer may reduce its adverse effects. In this paper, a proposed Deep Convolution-based neural network is used to find cervical cancer. The cervical image is preprocessed utilizing the Anisotropic Diffusion Filter (ADF), in which the edges of the image get preserved. Dragonfly optimization (DA) is used to optimize the weights of ADF. The weighted Fuzzy C-Means (WFCM) clustering method is utilized for segmentation, and makes the weight as optimized in WFCM by using the Grasshopper Optimization Algorithm (GOA). Consequently, a Deep Convolutional Neural Network (Deep CNN) employing a Rectified Linear Unit (ReLU) as the activation function is utilized for the extraction and classification of features. The Deep CNN surpasses alternative classifiers, achieving an accuracy of 97.8% in identifying cervical cancer, as evidenced by the study's findings on the performance of the proposed method relative to existing classifiers.

Keywords: *Cervical Cancer, Anisotropic Diffusion Filter (ADF), Dragonfly optimization (DA), weighted Fuzzy C-Means (WFCM), Grasshopper Optimization Algorithm (GOA), Deep Convolutional Neural Network (Deep CNN), Rectified Linear Unit (Relu).*

1. INTRODUCTION

The uterine cervix, a vital region of a woman's reproductive system, is susceptible to irregular cell proliferation leading to cervical cancer. Second only to breast cancer, cervical cancer stands as a prevalent threat to women's health. Early detection of cervical cell abnormalities carries significant clinical implications, particularly in the context of early-stage cervical cancer screening. Various screening techniques, such as Pap smear, colposcopy, and HPV testing, play pivotal roles in identifying and diagnosing cervical cancer. Among these methods, Pap smear cell classification holds promise for precise and automated early diagnosis. Accurate classification of Pap smear cell images not only aids in early identification but also streamlines the diagnostic process for cervical cancer. It is impossible to understate the importance of accurate Pap smear image screening in assisting to identify and diagnose cervical cancer early on. While traditional screening methods like visual examination of the cervix (VIA), cytology through the Pap smear test, colposcopy, biopsy, and HPV-DNA detection involve skilled medical professionals, the subjective nature of cancer diagnosis emphasizes the importance of a pathologist's expertise and experience.

The integration of automated and intelligent screening technologies becomes important in this case. Such technologies can provide valuable support by enhancing the accuracy and efficiency of the screening process,

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reducing subjective assessments, and potentially improving early diagnosis outcomes. In the coming sections of this article, we look into the advancements and applications of automated cervical cancer classification techniques, particularly focusing on the utilization of intelligent technologies to augment the traditional screening methods. These advancements aim to contribute to the development of more effective and accessible approaches for early detection and diagnosis of cervical cancer.

2. LITERATURE SURVEY

With the advent of computer-based solution for early prediction of cervical cancer, numerous methods were proposed. The freshly released researches indicate that they can be used to determine the stages of various cancer kinds. The conventional approach for early detection of cervical cancer involves a cytology-based screening procedure [1]. However, a significant drawback of this method is its time-consuming nature and the need for specialized knowledge [2]. Hence, it increases the demand for computer-based algorithms to serve the general community.

Lu et al. [3] compared various methods for enhancing the image quality. Methods from the domains such as spatial, frequency, and fuzzy were used during this study. Histogram-based methods along with fuzzy logic-based methods have been proven to be successful. According to the study the author suggests ant colony optimization to automate the assessment of the enhancement factor based on fuzzy-logic, giving a more precise description of the image.

As stated by Deepa and Rao [4], the quasi distribution of photons causes the Poisson noise to be injected into cell pictures. The study's conclusions indicate that an adaptable Wiener filter may be able to successfully reduce Poisson noise. An adaptable Wiener filter can be used to denoise photos even if the image quality varies from one area to another.

By using a technique called bi-histogram equalization, Tang and Isa [5] were able to improve the calibre of grayscale images. A total of two sub-histograms are generated from the input histogram. Clipping the histogram was used to reduce the picture's oversaturation, and the output that was produced was then equalised and combined to create the final product. A comparison with existing histogram-based enhancement algorithms demonstrates that, on average, the efficiency of the authors' technique is better.

Sharma and Mangat [6], improved the research, by improving the "fuzzy c-means (FCM)" clustering technique. They handled many clusters instead of just one, to strengthen the data clustering. The author proposed integrating segmentation techniques to improve the segmentation accuracy with methods for identifying areas of interest. The Herlev dataset's current accuracy might be enhanced through different feature modifications, enhanced noise reduction, and segmentation (93.7 percent).

In order to improve the boundary of the nucleus, Saha et al. [7] developed a function with a circular shape that restricted the cluster's shape. This was done to give the nucleus a fuller appearance. Extreme learning machine with crow search optimization [ELMCSO] classification was the method for cervical cancer diagnosis proposed by Geetha and Suganya [8]. This study's major goal is to prevent failures by detecting the cervical cell using computerized techniques. Here, the Pap smear image is enhanced using Kaun Filter. The Bayesian Optimization Algorithm is an optimization method used to determine the weight in the kaun filter. It is typically an enhanced KF as a result. Active Contour model was used to segment the rebuilt image. This uses the Analytic Hierarchy Process optimization technique to address the weight upgrade issue. Later, from the segmented region, the solid characteristics are removed which is most important for diagnosing the malignancy.

Devi et al. [9] tested different neural network designs for the goal of diagnosing diseases. In terms of accelerating the detection process, ANN designs like the multilayered perception may indeed be useful. A knowledge-based network and a feed forward network were used here. It helps in mapping the input images with the rules and also to extract the classification features. The network's classification results were excellent, and its accuracy rate was respectable. Using the artificial neural network (ANN) for classification yields more accurate and improved results.

By examining pictures from Pap smears, Athinarayanan et al. [10] created cervical disease classification system. We used the concatenated feature extraction method (CFE), the ERSTCM and CABS descriptors, and the rough set text on co-occurrence matrix to improve it. The effectiveness of the retrieved characteristics can be evaluated using a classifier by correlating them to statistical standards like sensitivity, accuracy and specificity by using classification algorithm (FL-HKSVM). The CFE method outperformed the other two classifiers in terms of performance. By preserving the qualities of the original dataset, feature extraction coverts raw information into quantitative attributes that can be managed. Comparatively, it yields superior outcomes when contrasted with applying machine learning directly to raw data. CNNs are frequently used in healthcare applications. It has the capability to autonomously extract features from both time series data and images represented in the frequency domain. These features are then used by a classifier network to perform classification and regression. Deep learning networks are characterized by a substantial number of hidden layers within the neural network. This type of network may accurately predict outcomes by capturing the nonlinear relationship between complex patterns. Deep neural network structures like convolution neural network (CNN) are frequently implemented for image recognition and analysis [11]. To be able to learn any imaginable attribute, a machine will inevitably learn features at numerous levels of abstraction. To enable the system to learn everything, this is required.

The effectiveness of classical machine learning techniques depends heavily on how precisely cells are segmented. Taha et al. [12] suggested a method for classifying cells without segmentation. They used a deep feature learning CNN as part of their strategy. With a rate of 98 percent accuracy, they were able to successfully categorize the Herlev dataset.

Hyeon et al. [13] formulated a prototype proficient in distinguishing healthy and unhealthy cervical cells. The model utilizes a convolutional neural network (CNN) to generate feature vectors from images depicting cervical cells. An SVM classifier was used to train on these collected characteristics, and the overall success rate was 78%. In this paper, a classification model for prostate cancer is proposed. The model uses deep learning techniques, achieving accuracy rates of 78.1% and 80.1% on testing sets and training sets, respectively.

Manik Sharma et al. provide a robust analysis of diabetes and cancer detection using five distinct insect-based methodologies in their work [14]. Ant Colony Optimization (ACO), Glow Worm Swarm Optimization (GSO), Firefly Algorithm (FA), Artificial Bee Colony (ABC) and Ant Lion Optimization are these five insect-based approaches (ALO). Their research shows that a neural network using an ACO optimization strategy can produce predictions with a higher degree of accuracy.

3. PROPOSED METHODOLOGY

The proposed approach to cervical cancer screening is a computer-aided automatic detection system. The general strategy for the discovery component is outlined in Figure 1. The initial cervical image is preprocessed using the Anisotropic Diffusion Filter. Dragonfly optimization can be utilized to improve the ADF's weight in order to reduce the noise and also preserve the edges. The preprocessed image is then used to segment the affected cell by using the Weighted FCM with Grasshopper Enhancement Algorithm (GOA) for productively distinguishing the features such as shape, GLCM highlights and other geometrical features. Comparing the pap smear image with the trained features, these features are used to train the Deep CNN with Relu as an activation function to classify it as benign or malignant. Accuracy, Recall, and Specificity are the performance measurement parameters used to evaluate performance of the cervical image classification.

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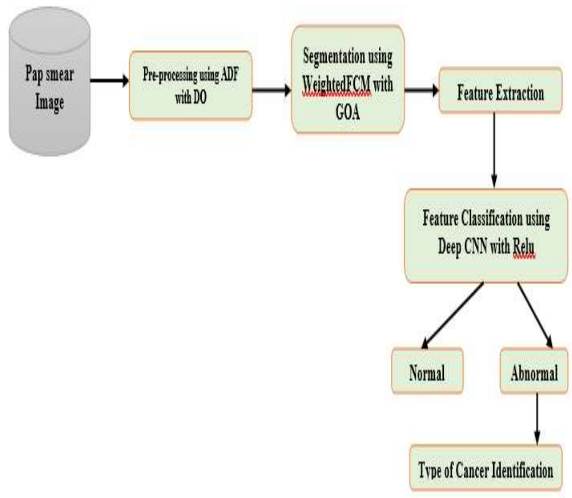

Figure 1: System Architecture of Cervical Cancer Detection

3.1. Preprocessing

In many image applications, pre-processing is an essential step because it reduces the input image distortions and eliminates the noise and also improves the quality of an image. Preprocessing functions are typically categorized as radiometric or geometric corrections and are typically performed prior to the primary data analysis and information extraction [18]. Image resizing, Noise Removal, Image Quality, and RGB to gray scale conversion techniques have been used in this paper.

In this proposed work, the process of Preprocessing is as:

1. The pap-smear colour image is converted to a grayscale image.
2. To preserving the edges and reducing the noise in an image by applying the Anisotropic Diffusion Filter.
3. The best weights for the ADF filter were found using Dragonfly Optimization, which effectively preprocess the image. The preprocessing process are shown in figure 2.

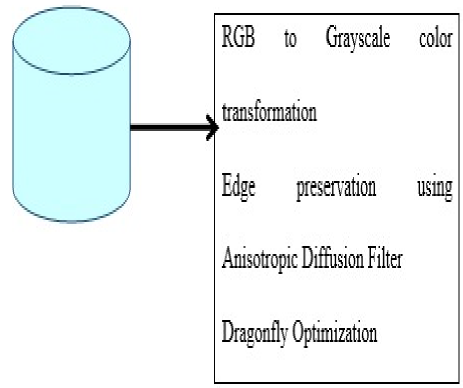

Figure 2: Pre-process

3.1.1 Anisotropic Diffusion Filter

Anisotropic diffusion is a technique that constructs a scale-space by introducing an image into a set of progressively blurred images with varying parameters, employing a diffusion process. In fact, the generalized diffusion equation is approximated and is used to implement anisotropic diffusion, and the equation is applied on the previous image to determine each new image in the group. As a result, the anisotropic diffusion process proceeds iteratively until a sufficient level of smoothing is achieved [15, 16]. The original image is qualitatively smoothed while brightness discontinuities are preserved by anisotropic diffusion [17].

The equation has the potential to modify the diffusion coefficient based on the properties of the image, and it maintains the edge details of the image during denoising.
The diffusion model is expressed as

$$\frac{\partial P}{\partial t} = div(c(x,y,t)\nabla P) = \nabla c.\nabla P + c(x,y,t)\Delta P \quad (1)$$

Where,
Δ - Laplacian, ∇ - the gradient, $div(\ldots)$ – the divergence operator and $c(x,y,t)\Delta$ - the diffusion coefficient.
For $t > 0$ the output is given as $P(.,t)$, with larger t produce images with blur effect.
$c(x,y,t)$ regulates the diffusion rate. It is considered as an image gradient function to preserve edges.

$$c(\|\nabla P\|) = e^{-\left(\|\nabla I\|/K\right)^2} \quad (2)$$

Based on the discrete sampled image, the equation made by Perona and Malik [19] [20] as follows:

$$P_{t+1}^{s} = IP_{t}^{s} + \frac{\lambda}{|\eta^{s}|} \sum_{p \in \eta} g\left(\left|\nabla P_{s,p}(t)\right|\right) \nabla P_{s,p}(t) \qquad (3)$$

Where, t represents the discrete time, I_t^s is the discrete image sample. η^s is neighbourhood pixel s, $|\eta^s|$ gives the count of neighbouring pixels. The image gradient magnitude for the given direction is described by the given formula as:

$$\nabla I_{s,p}(t) = I_t^p - I_t^s, p \in \eta^s \qquad (4)$$

3.1.2 Dragonfly Optimization:

The natural behaviour of dragonflies served as inspiration for the development of the Dragonfly Algorithm (DA). The natural swarming patterns of dragonflies, as both static and dynamic, served as the basis for this algorithm. The static along with dynamic swarming are two imperative periods of advancement: (1) Exploration is employed to identify promising regions within the search space and (2) Exploitation that contributes to the convergence of the global optimum. Flowchart for Dragonfly Algorithm is shown in Figure 3.

The cycle begins with an introduction stage, followed by N emphases to recognize the neighbouring pixels of an image and it performs the exploration and the exploitation repeatedly. A decision process is carried out at the end to identify the optimal image edges.

During the exploration and exploitation, the dragonflies are guided by five factors: specifically, the food factor, the enemy factor, separation, alignment, and cohesion. The factors are regulated by the following components: (i) separation weight denoted as "s," (ii) alignment weight represented by "a," (iii) cohesion weight indicated as "c," (iv) food factor labeled as "f," (v) enemy factor denoted by "e," and (vi) inertia weight identified as "w". To ensure the swarm's survival, the objective is to attract it towards food sources and divert it away from potential threats. In each iteration, the weakest solution is identified as the enemy, while the best solution serves as the food source. During the exploration phase, weight adjustments promote strong alignment and discourage cohesion. In the exploitation phase, there is an emphasis on high alignment but low cohesion. To enable the algorithm to move from exploration to exploitation phase, the weights are altered.

The collision of one dragonfly with the other in the neighbouring pixels is avoided by calculating the separation factor as

$$Sf^{i} = -\sum_{j=1}^{N} X^{i} - X^{j} \qquad (5)$$

Where $X^i - the$ current position, X^j - the position of neighbour, N - number of adjacent dragonflies.

To match the speed of one dragonfly to another the alignment weight Aw^i is computed as

$$Aw^{i} = \frac{\sum_{j=1}^{N} V^{j}}{N} \qquad (6)$$

Where V^j is the speed of the jth neighbour of dragonfly.

The Cohesion factor is calculated based on the affinity of a single dragonfly towards the neighbourhood's mass centre as:

$$Cf^{i} = \frac{\sum_{j=1}^{N} X^{j}}{N} - X^{i} \qquad (7)$$

The Food factor is calculated based on the dragonfly's affinity towards the food source

$$Ff^{i} = X_{f} - X^{i} \qquad (8)$$

Where X_f represents the food source location.
The computation of the Enemy factor is determined by the deviation of a dragonfly from a designated enemy

$$Ef^{i} = X_{e} + X^{i} \qquad (9)$$

Where, X_e is the enemy position.
The step vector ΔX_{t+1}^{i} can be calculated to imitate the movements thus updating the location of the dragonflies within the search space.

$$\Delta X_{t+1}^{i} = (swSf^{i} + awAw^{i} + cwCf^{i} + fwFf^{i} + ewEf^{i}) + \omega \Delta X_{t}^{i} \qquad (10)$$

Here, the symbols represent specific weights and parameters: sw for separation weight, aw for alignment weight, cw for cohesion weight, fw for the weight of the food factor, ew for the weight of the enemy factor, ω for inertia weight, and t for the counter. The dragonflies' positions can be updated following the calculation of the step vector ΔX_{t+1}^{i} using

$$X_{t+1}^{i} = X_{t}^{i} + \Delta X_{t+1}^{i} \qquad (11)$$

All of the dragonflies will unite into a single dynamic swarm during the final optimization stage, moving toward the global optimal solution. When no other artificial dragonflies left in the search space, they use the Lévy flight mechanism [21] to move around. Dragonflies

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without neighbors are given a random position by performing a random walk. The position can be updated using the

$$X_{t+1}^{i} = X_{t}^{i} + Levy(d) \times X_{t}^{i} \quad (12)$$

Here, the symbol t signifies the current iteration count, while d is used to denote the dimensionality of the position vectors. At last the optimum pixel intensity value can be found to identify the optimized edges of an image from the enhanced image using anisotropic diffusion Filter.

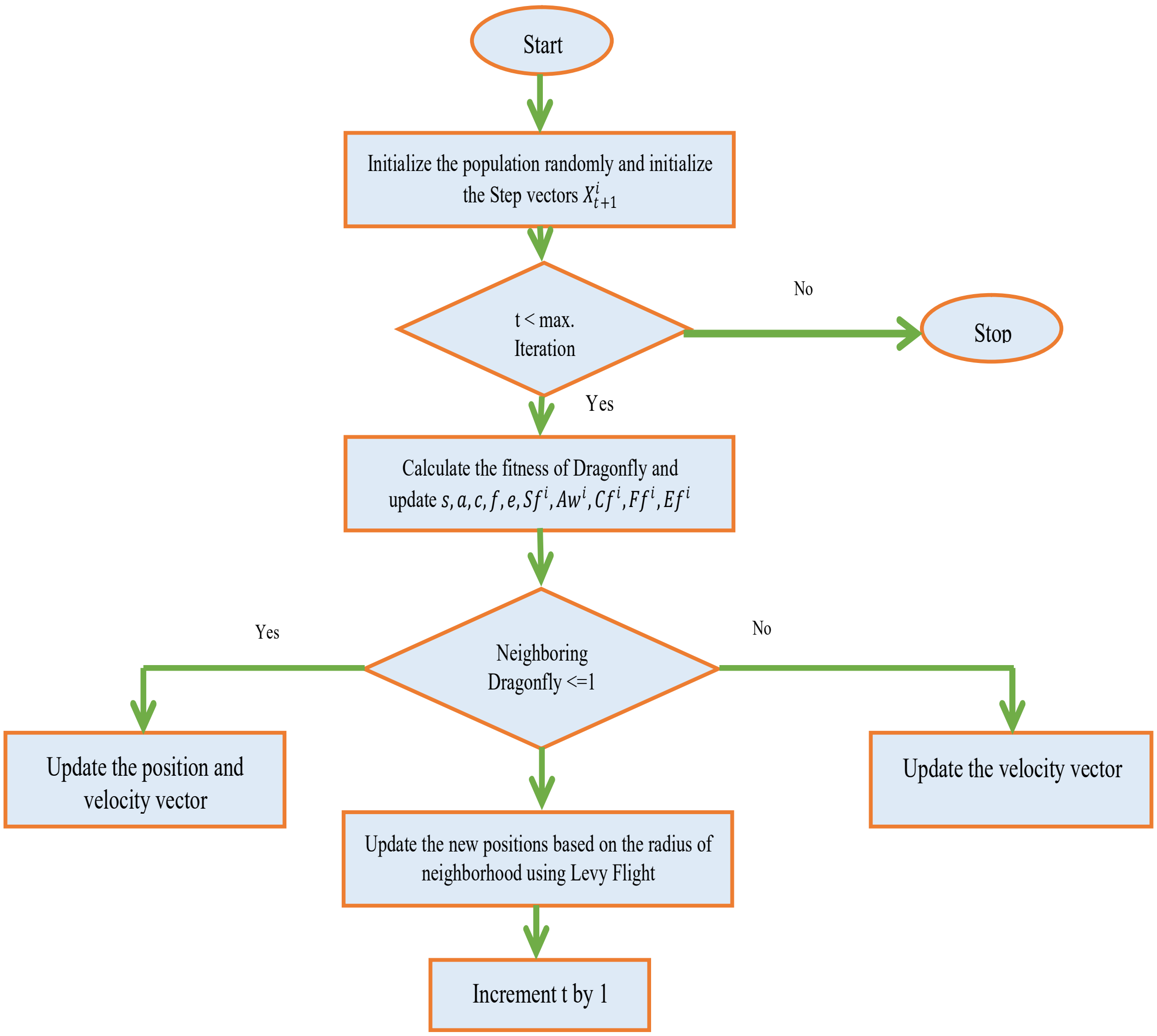

Figure 3: Flowchart for Dragonfly Algorithm

3.2 Segmentation Weighted FCM

In computer vision, image segmentation can be used in a variety of real-world System. Medical imaging, image retrieval with content, video surveillance, object detection and recognition, and Automatic Traffic Control systems are all important applications of image segmentation. In order to facilitate with diagnosis and treatment planning, segmentation algorithms have lately been applied in the medical industry to extract relevant information from medical images.

Segmentation is the process of splitting an image into different parts by grouping together pixels of the same type based on factors such as color, intensity, texture, or volume. During the past ten years, numerous approaches to segmentation have been proposed in an effort to raise the precision level and to improve the efficiency of the results. Image segmentation techniques for medical images are widely used to separate input images and to get important information about the area of interest. The ROI can be lesions, cancerous cells, or tumour tissues. The effects of division are exceptionally vital and significant and requests high accuracy level for all intents and purposes based on these outcomes that the specialist recommends finding to their patients.

3.3 Weighted Fuzzy C-Means (WFCM) algorithm with Grasshopper Optimization Algorithm:

In the weighted FCM, the weighting factor has been utilized to improve the cluster center for the FCM. This was proposed in the previous work. In order to improve the weight in WFCM and made as an optimal weight has been proposed through the Grasshopper Optimization Algorithm (GOA).

The proposed IWFCM technique involves mapping input data into a higher-dimensional feature space through a nonlinear transformation. Subsequently, Fuzzy C-Means (FCM) is applied within this feature space. The Kernel Weighted Fuzzy C-Means method is employed to minimize the resulting objective function, as discussed in reference [23].

$$Y\omega = \sum_{i=1}^{k}\sum_{j=1}^{n} b_{ij}^{l}\left\|\omega(x_j) - \omega(v_i)\right\|^2 \quad (13)$$

Where ω(v_i) is the feature space centre of cluster i, bij indicates if x_j is a member of cluster i, and ω is used to map input space X to feature space F.

3.3.1 Grasshopper Optimization Algorithm

The natural swarming behavior of grasshoppers serves as inspiration for the grasshopper optimization algorithm. Saremi et al. first proposed to decide the ideal state of systematic structures [22]. The grasshopper's individual movement is influenced by three main factors: social relationship, force of gravity, and wind advection [24, 25]. Below is a mathematical depiction of their swarm activity.:

$$X^i = r_1S^i + r_2G^i + r_3A^i \quad (14)$$

where r_1, r_2 and r_3 are the random numbers, S^i, G^i, A^i are social relationship, gravity force and wind advection respectively.
To improve the version of equation (14), in order to solve the best optimization problems using the equation (15)

$$X_d^i = c\left(\sum_{j=1, j\neq i}^{n} c\frac{UB_d - L\_d}{2} S\left(\left|x_d^j - x_d^i\right|\right)\frac{x^j - x^i}{d^{ij}}\right) + \text{best}, \quad (15)$$

The upper bound (UB_d) and lower bound (LB_d) represent the limits in the d^th dimension, while "best" denotes the current optimal value in that specific dimension within the solution space $d^{ij} = \left|x^j - x^i\right|$ shows the distance between the ith and jth grasshoppers (r) is calculated using $s(r) = fe^{-r/l} - e^{-r}$, where fe and l are two constants.
c is a parameter in GOA which is used to balance the exploration and exploitation. The coefficient of c decreases according to the number of iterations. The value of c can be computed as follows:

$$c = c^{max} - u\frac{c^{max} - c^{min}}{u^{max}}, \quad (16)$$

Where, c^{min} and c^{max} are the minimum and maximum values of c respectively. u^{max} is the maximum number of iterations, u is the current iteration.

Algorithm:

Weighted FCM with Grasshopper Optimization Algorithm (WFCM-GOA)

1. *Initial class prototype $\{V_i\}^c$ is selected.*
2. *All memberships b_{ij} is updated using the cluster center's weighted average by*

$$u_{ik} = \frac{(1 - B(x_k, v_i))^{-\frac{1}{(m-1)}}}{\sum_{j=1}^{c}(1 - B(x_k, x_j))^{-\frac{1}{(m-1)}}} \quad (17)$$

3. *The clusters prototype is obtained as weighted average using*

$$v_i = \frac{\sum_{k=1}^{n} u_{ik}^m B(x_k, v_i)x_k}{\sum_{k=1}^{n} u_{ik}^m B(x_k, v_i)} \quad (18)$$

4. *Initialize the parameters c^{min}, c^{max}, u, f and l*
5. *Initialize the random population in the search space where X^j,{j=1,2,3…N} and initialize the search agent "best"*
6. *while $u < u^{max}$*
   a. *Evaluate c using Equation (16)*
   b. *For i=1: n begin*
      i. *Update best*
      ii. *Normalize the distance between the grasshopper in the range [1,4]*
      iii. *Update the position of grasshopper X_d^i using the equation (15)*
      iv. *Check the current grasshopper position if it goes over the boundaries*
      v. *End for*

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c. $u = u + 1;$
7. End while
8. Return the best solution for updating the weights in WFCM in equation (17) and (18)
9. Continue steps 2-3 until the stopping requirement is satisfied.
10. The criterion for termination is $|V_{new} - V_{old}| \leq \varepsilon$
11. The Euclidean norm is ‖.‖. The cluster centre vector is denoted by V. ε is a user-adjustable small number (in this case, ε=0.01).
12.

The WFCM-GOA algorithm is used in the proposed method to raise the weighted factor for the clustering center without making computation more difficult. Typically, a population aims to evaluate the collective performance of search agents within the current generation. An individual's fitness function value should be lower than the average for a problem to be minimized. As a result, a plan to improve local search should be implemented. Additionally, the population is distributed more randomly. Especially during the later stages of evolution, this property can help population maintain their diversity more effectively.

3.4 Feature Extraction

The most crucial method in image processing is image feature extraction. It assumes a significant part in the recognition of malignant growth. To detect cancer, image features are extracted from the image following segmentation. An essential step in the process of predicting cancer and non-cancer in an image is feature extraction. It is the process of identifying and representing particular image features of interest for further processing.

To illustrate the condition and facilitate classifier training, Feature Extraction eliminates specific details from Pap smear images. Recent studies have concentrated on incorporating state-of-the-art feature extraction algorithms for the detection of cervical cancer in Pap smear images. Geometric properties, encompassing asymmetry, diameter, concavity, area, perimeter, and eccentricity, are among the extracted attributes. Additionally, characteristics like shape, size, and texture identification are also considered using GLCM and Haralick features. This approach has previously been applied in the identification of skin lesion images [26].

The calculation of asymmetry is determined by the following equation:

$$A_I = \frac{\Delta A}{A} X\ 100 \qquad (19)$$

a. Eccentricity is calculated using the below equation:

$$Eccen = \frac{Length_{(Major)}}{Lengt\ _{(Minor)}} \qquad (20)$$

b. Area of the nucleus can be calculated as:

$$Area_N = \sum_{i=1}^{n} \sum_{j=1}^{m} I(i,j) \qquad (21)$$

c. Perimeter can be computed using the formula:

$$Perimeter_N = Even_{Count} + \sqrt{2}(odd_{Count}) \qquad (22)$$

Nucleus Diameter can be calculated by the distance between the two points on both the major and minor axis.

3.5 Feature Classification using ReLu

The features classification is performed with the Deep Convolutional Network (Deep CNN) with Relu. Here Relu is used as an activation function. In the Deep CNN, organise the network comprises of input layer followed by 2X2 Convolution layers, Pooling layer and 2X2 Convolution layer which is used for the learning step of features. Deep CNN uses the fully connected and softmax layers for its classification stage and is shown in Figure 4.

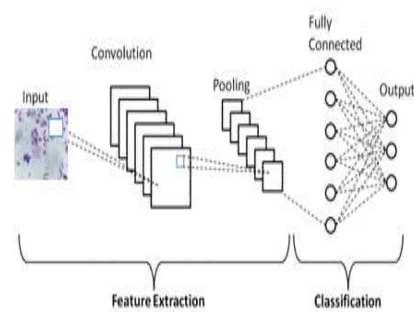

Figure 4: Architecture of Deep CNN with Relu for Detection of Cervical Cancer

3.5.1 Convolutional layer

Each neuron serves as one of the convolutional kernels that make up the convolutional layer. The way a convolutional kernel operates is by slicing the image into tiny segments, which are called receptive fields. The extraction of features is made easier by breaking up an image into smaller pieces. Kernel multiplies its elements with the corresponding receptive field elements to interact with the images using a particular set of weights. The efficiency of CNN parameters surpasses that of fully connected networks due to the weight-sharing capability of convolutional operations. This enables the extraction of distinct feature sets from an image by sliding a kernel with the same weights across the image.

The Rectified Linear Activation Function, known as ReLU, is a piecewise linear function that directly produces the input if it is positive; otherwise, it returns zero. The utilization of ReLU in a model simplifies the training process and often leads to enhanced performance.

The ReLU function is calculated as

$$R_f = \max(0.0, y) \tag{23}$$

When the value of R_f reaches to zero, the gradient descent method stops its learning.

3.5.2 Pooling Layer:

A Pooling Layer comes next to a Convolution Layer. It works upon each component map independently to make another arrangement of a similar number of pooled include maps. This layer's primary objective is to cut down on computational costs by making the convolved feature map smaller. This is accomplished independently on each feature map by reducing the connections between layers. Here, max pooling has been chosen because it provides the better results than the other pooling methods.

3.5.3 Fully connected Layer:

At the network's end, the fully connected layer is typically used for classification. It is a global operation, in contrast to pooling and convolution. Selected features are combined in a non-linear way for the purpose of classifying data. It receives input from the feature extraction phases and performs a global analysis of all previous layers' output.

3.5.4 Softmax Layer:

The concluding layer in a Deep Convolutional Neural Network (CNN) is commonly the Softmax layer. Softmax serves as an activation function, transforming numerical values into probabilities. It generates a vector presenting the probabilities of each potential outcome, ensuring that the probabilities of all classes in the vector collectively sum up to one.

4. RESULTS & DISCUSSION

4.1 Dataset Description

Multicell nucleus of cervical cancer image were collected from SIPaKMeD [28] and Herlev datasets [27] which is utilized in the proposed method. The Herlev dataset, consisting of 917 images, includes cells categorized into classes 1 through 3 representing usual phases, and classes 4 through 7 representing abnormal stages. 4049 cells were cropped from the 966 images that made up the multicell dataset. Here the cells were separated based on benign, normal and abnormal.

4.2 Experimental Setup:

Utilising the Matlab 2022b simulation tool, the results were verified. Matlab's Deep Neural Network tool can be used for categorization. The CPU is an Intel (R) Core (TM) i5-3210M with a 2.5GHz CPU and 2.0GB of RAM. Here the proposed Deep CNN with Relu as an activation function is used for feature classification. About 250 sample images are taken into consideration for evaluation. For improved accuracy results, a testing set of 100 sample images and a training set of 150 sample images were used. For validation process, 30% of sample images were used.The trained image size is 250 x 250 pixels which is determined by simulation results of the analysis of MATLAB. Based on the features, the class labels are assigned to values in the hidden nodes, and the relevant values are mapped with the cervical cancer class label. Figure 5 depicts the proposed Deep CNN with Reluclassifier in the Pap Smear Image Classification.

4.3 Performance Metrics:

The efficiency of the method Deep CNN with Relu as an activation function is evaluated and compared with other classifiers such as RBM, SVM, RF, ELM and RVDLNN. Accuracy, Recall, and Specificity are the

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performance criteria used to inspect these methods.

4.3.1 Accuracy:

An estimate of the cervical cancer image's classification accuracy can be calculated by dividing the total number of instances by the number of correctly identified class labels. The accuracy value determines the efficiency of the classification model. The accuracy is measured using the cervical cancer's true positive (TP) and true negative (TN) values. The accuracy is computed by

$$Accuracy = \frac{TP + T}{TP+TN+FP+FN} \quad (24)$$

4.3.2 Recall:

The proportion of positive or correctly categorised values across all instances is referred to as Recall, which is expressed as the rate of TP. It shows the values that were correctly identified after the test, with higher sensitivity indicating lower specificity rates and lower Recall indicating higher specificity rates. The TP value determines the performance of proper identification, and the following evaluation of Recall is provided:

$$Recall = \frac{TP}{TP+FN} \quad (25)$$

4.3.3 Specificity:

The proportion of incorrectly classified values among all cases is referred to as specificity, or the rate of TN, in the medical field. The following is the assessment of specificity, which helps determine whether the classification sample as a whole is correct.

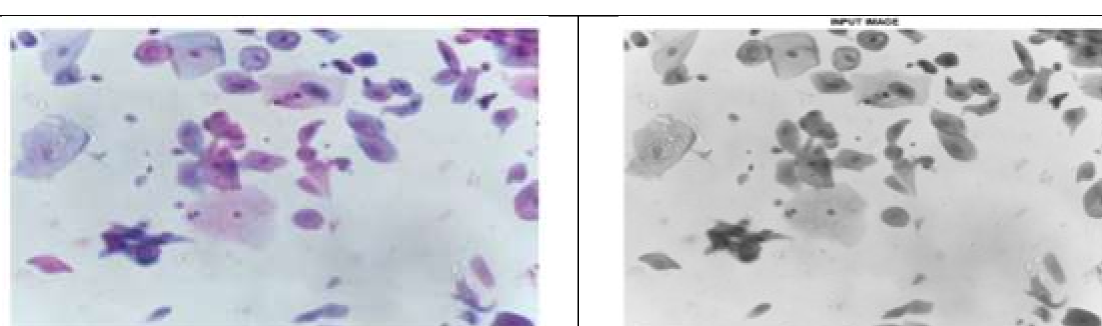
$$Specificity = \frac{TN}{TN+F} \quad (26)$$

4.4 Performance Evaluation:

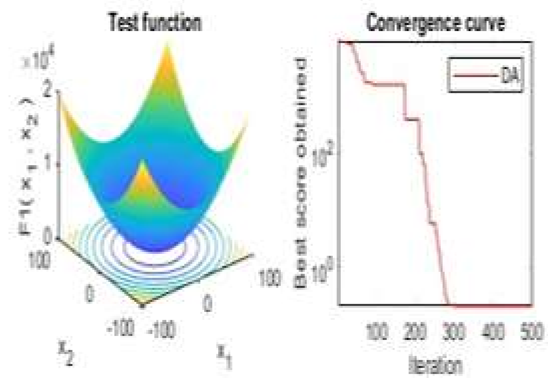
The performance of the Deep Convolutional Neural Network (CNN) in classifying data is contrasted with the performance of the existing method. Image preprocessing enhances the images, and the optimal segmentation, along with feature selection, is employed to retrieve essential features. The acquired information is then forwarded to the classification phase. A learning rate of 0.001 is utilized in this process. The fully connected layer involves 7 classes, and the batch normalized layer employs 4 channels. These layers encapsulate the extracted features along with their corresponding class labels.

The figure 5.a shows the result of input image that is retrieved from the dataset. Then the image is converted to grayscale image which displays in the figure 5.b. By applying the Dragonfly optimization (DO) in ADF, the test function and result of the preprocessed image shown in figure 5.b and 5.c respectively.

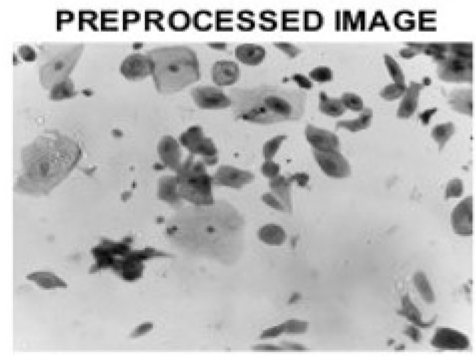
The weighted FCM is used to perform image segmentation on cervical cancer image. In order to optimize the weights, Grasshopper optimization algorithm (GOA) is employed to generate the optimal values of weight in WFCM. This will be very useful for further feature classification by Deep CNN using Relu. From the GOA, optimal score of 0.318 is retrieved. Based on the optimized segmentation results, the network get trained to classify the cervical cancer effectively. The figure 5.e. and 5.f shows the results of GOA convergence of the segmented image and optimized segmented image of cervical cancer image respectively. The figure 5.g. shows the classification of the cervical cancer image.



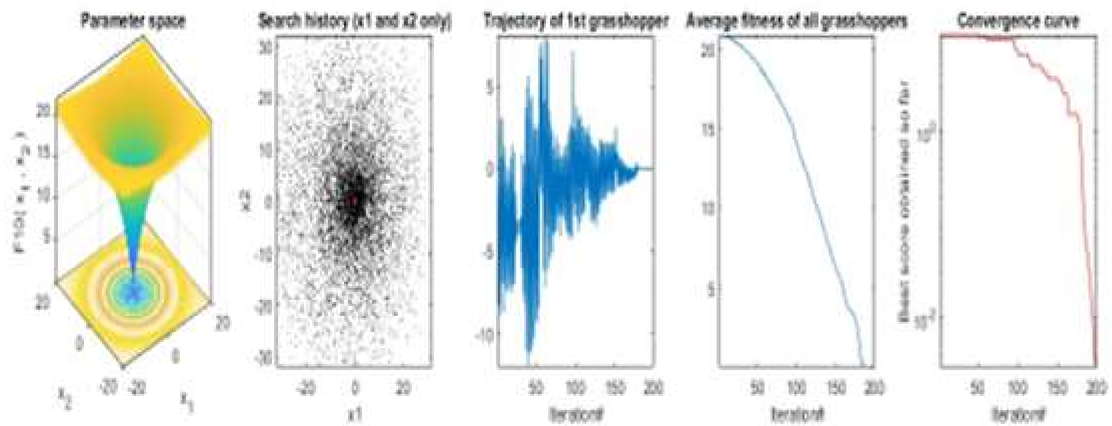
a. Input Image *b. Conversion of RGB to Gray Scale*



c. Preprocessing using Dragonfly Optimization

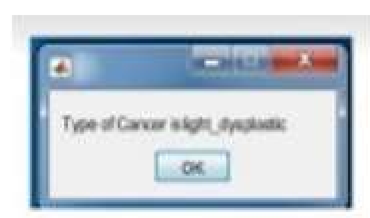


d. Preprocessed using ADF with DA optimization



e.Grasshopper Optimization Algorithm for Segmentation of cervical cancer image

F. Weighted FCM with GOA forSegmentation of cervical cancer image



G. Cervical Cancer Classification

Figure 5: Proposed Deep CNN with Relu based results for detecting Cervical Cancer

4.5 Classification of Cervical Cancer:

With the support of feature selection, the preprocessed and segmented cervical image is categorised to determine the cervical cancer. Table 1 and Figure 6 show the DCNN classification performance

Table 1: *Comparison of Cervical cancer classification Performance*

Performance Rates	DCNN	RBN	RVDLNN	ELM	SVM	RF
Accuracy (%)	97.8	95.3	88.5	82.65	77.26	78.6
Specificity (%)	91.3	88.6	84.17	81.25	72.19	74.81
Recall (%)	89.8	88.56	76.48	73.44	78.61	71.11

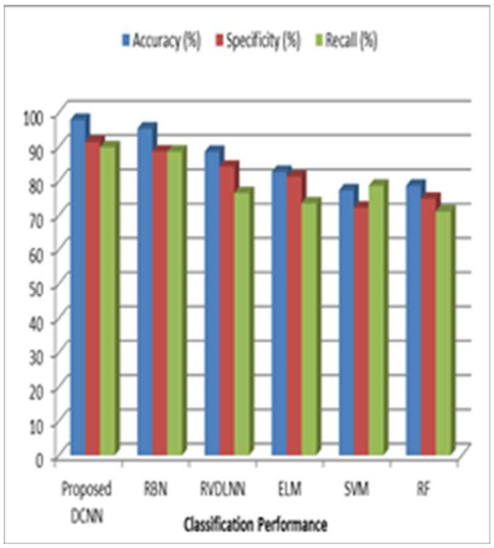


Figure 6: Comparison of Cervical Cancer Performance

The effectiveness of the proposed Deep CNN with Relu and the current method for classifying cervical cancer is shown in Figure 6. Deep CNN outperforms RBN, RVDLNN, ELM, SVM, and RF by 2.5%, 9.3%, 15.15%, 20.6 %, and 19.2%, respectively, in terms of classification accuracy. The classification specificity of Deep CNN outperforms other existing classifiers, including RBN, RVDLNN, ELM, SVM, and RF, by 2.7%, 7.13%, 10.1%, 19.1%, and 16.5%, respectively. Deep CNN is higher than RBN, RVDLNN, ELM, SVM, and RF in terms of classification recall by 1.2%, 13.4%, 16.36%, 11.19%, and 18.69%, respectively. In terms of classification performance, the proposed DCNN performs better than the current method.

The accuracy rate as well as the frequency of error or loss throughout the Deep CNN routine for each iteration is depicted in Figure 7. The pace of exactness increments at cycle 4, and loss diminishes at iteration 2. The reduction of the loss function enhances the performance of Deep CNN. The classifier's performance is typically assessed using accuracy, while the loss function is employed to enhance and optimize overall performance. As accuracy and iteration increase in Deep CNN, the loss function gets decreases.

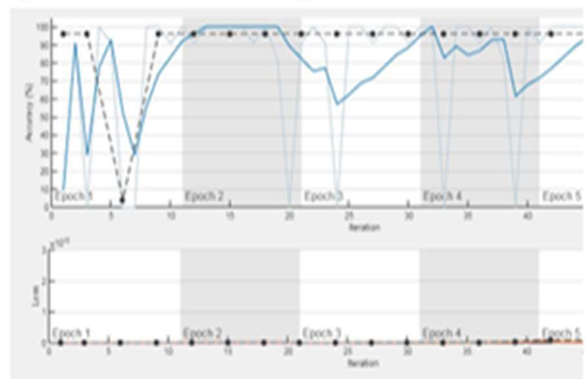


Figure 7: Accuracy and Loss function of Deep CNN with Relu

5 CONCLUSION

This article outlines an effective cervical cancer classification technique. In this proposed work mainly focuses on the detection of cervical cancer at earlier stage. The noise in the cervical image is preprocessed using Anisotropic Diffusion filter. The weights of the filter have been optimized through the Dragonfly optimization (DA). So the edges are preserved and also noise gets reduced. Based on the preprocessed image, Weighted FCM with Grasshopper optimization algorithm has been utilized. The needed parts of the segmented image of cervical cancer have been taken out and optimized the features for the phase of feature classification. With the aid of Deep CNN with Relu as an activation function, the features are classified and identify the classification label of cervical cancer effectively. Here, the proposed Deep CNN achieves97.8% of accuracy than other existing classifiers for cervical cancer classification. Few images are examined through

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this classifier and investigation of more images through other novel classifier can be done in the future.

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