International Journal of Communication Networks and Information Security

ISSN: 2073-607X, 2076-0930

*Volume **14** Issue **1s Year 2022** Page **22:36***

An Optimized Deep Learning Based Optimization Algorithm for the Detection of Colon Cancer Using Deep Recurrent Neural Networks

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Article History

Received: 10 July 2022
Revised: 23 September 2022
Accepted: 16 October 2022

Abstract

Colon cancer is the second leading dreadful disease-causing death. The challenge in the colon cancer detection is the accurate identification of the lesion at the early stage such that mortality and morbidity can be reduced. In this work, a colon cancer classification method is identified out using Dragonfly-based water wave optimization (DWWO) based deep recurrent neural network. Initially, the input cancer images subjected to carry a pre-processing, in which outer artifacts are removed. The pre-processed image is forwarded for segmentation then the images are converted into segments using Generative adversarial networks (GAN). The obtained segments are forwarded for attribute selection module, where the statistical features like mean, variance, kurtosis, entropy, and textual features, like LOOP features are effectively extracted. Finally, the colon cancer classification is solved by using the deep RNN, which is trained by the proposed Dragonfly-based water wave optimization algorithm. The proposed DWWO algorithm is developed by integrating the Dragonfly algorithm and water wave optimization.

Keywords: Peritoneal carcinomatosis, colorectal cancer (CRC), deep learning, biomarkers.

1. Introduction

According to the WHO, the third most death causing death globally is the colorectal cancer (CRC) or the colon cancer. The CRC has high mortality rate in the countries with inadequate health infrastructure and limited resources. When compared to women, the men have higher CRC rates. The CRC is also developed due to the various environmental, genetic, and lifestyle-related factors. The peritoneal carcinomatosis occurs in the final stage because of the metastatic spread often leading to the short survival time. Thus, the detection of the metastases is important to prevent the spread. The intraoperative availability and the resolution required for the identification is not efficient in the typical imaging modalities, like computed tomography and magnetic resonance imaging. Now-a-days non-clinical approach is used for the detection of the cancer types. The non-clinical approach involves monitoring the biological samples using genes expression profiles. This advancement has made it possible to observe the gene expression in various gene chips concurrently by enhancing the

microarray technology. The development in the systemic treatments and the surgical techniques diagnosis the colon cancer at an early stage thus, improving the overall prognosis of patients. The conventional techniques, like blood tests, physical examination, colonoscopy [1], radiology, histopathology and PET-CT scan reduces the accuracy as they are evaluated based on the symptoms, which makes the diagnosis of CRC a challenging task. The methods double contrast barium enema requires well-trained experts and advanced instrumentation for the diagnosis and have complications, like bowel tears and bleeding. Thus, alternative user-friendly methods are developed for the diagnosis of CRC that is inexpensive and has high throughput screening. The tumour-infiltrating lymphocytes is extensively used for the studying the colon cancer and it is used as an important supplemental marker for the prediction of mortality and relapse in the TNM staging system. The image processing methods is used for further improving the CLM's intraoperative assessment and for the automatic and characterization of the fast tissue. For the classification of tasks and medical segmentation, the deep learning methods provided remarkable success in which human-level performance is achieved. Recently, the semantic segmentation and classification are done for the automatic tissue characterization using deep learning methods such as convolutional neural networks (CNNs). Deep learning methods are also widely applied to similar modalities and CLM. For instance, the motion correction with CLM and oral squalors cell carcinoma classification is done using CNN [2]. The risk of colon cancer is diminished in the patients using fluoxetine (FLX). The proliferation in hypoxic tumour that ranges within them and the improvement in the xenografts of the different colon tumor is decreased using the FLX. The hybrid feature set is obtained by considering the feature types, such as SIFT, morphological, texture features, EFDs along with the consolidation of the geometric features. The fluctuations in the biomarker level indicated the state of the disease. Cancer antigen like miRNA, carcinoembryonic antigen (CEA), cancer antigen 125 and ssDNA (colorectal cancer gene) are used for the detection of the colon cancer. The CA 19-9 is a poor diagnostic marker and less sensitive when compared to other CA. The use of miRNA as a biomarker in the detection of CRC is not well established. In the ssDNA, the dying tumor is released due to the high stability and they also remain during the circulation making it a drawback in the use of biomarker as a ssDNA [2]. The potential of new markers is explored due to the challenges posed by the existing biomarkers.

2. Related Work

Shafi, A.S.M., *et al.* [18] introduced a machine learning approach using the random forest classifier for analysing and predicting the colon cancer. This approach reduced the issues caused by data with high dimensions, and permits efficient computations by integrating the "Mean Decrease Gini" and "Mean Decrease Accuracy". However, this method failed to improve the performance by solving the computational complexity issues. Baliarsingh, S.K., *et al*. [19] developed a gene selection approach using Enhanced Jaya Forest Optimization Algorithm (EJFOA) for classifying the cancer. At first, a statistical filter was utilized in order to sort the features, thereby generated the optimal feature subset. This method also employed the SVM classifier for categorizing the microarray data by choosing the optimal set of genes. However, this method does not minimize the computational cost problems. Fang, Z.*et al.* [20] designed a prognostic model in order to predict the colon cancer prognosis. The profile of the gene expression data was generated, and then the genes were utilized for screening the prognosis-associated differentially expressed genes (DEGs), thereby resulted in an effective construction of the prognostic system. However, this method failed to resolve the computational problems. Loey, M *et al*. [4] devised an Intelligent Decision Support System (IDSS) in order to analyse and diagnose the cancer with respect to the profiles of gene expression from the DNA microarray datasets. This approach was utilized to integrate the grey wolf optimization (GWO) and the information gain (IG), and SVM algorithm, whereas the IG was employed for selecting the gene features from the input structure. In addition, the GWO was employed for reduction in the feature, and the SVM classifier was utilized to diagnose the cancer. However, this method does not consider the other classifiers, namely neural network, decision tree, and KNN in order to enhance the performance results. Saroja, B. and SelwinMich Priyadharson [16] developed a clustering technique detection of colon cancer. The Lumen Circularity (LUC) based on the tree structure was calculated from the clustered region for classifying the samples as normal or malignant. The outliers were removed using the Mahalanobis distance and the score-based classification was used for the classification of the malignant colon biopsy samples. Gessert, N et al. [15]

designed a deep transfer learning method for the detection of colon cancer. In this method, the feasibility was investigated using the multiple transfer learning scenarios and CNN. Although this method detected the brain tumor effectively, it failed to provide optimal solution for the classification problems. Lall, M et al. [6] modelled a Fluorescence Excitation-Scanning hyper spectral Imaging for the classification of the colon tissue.

The fluorescence excitation-scanning hyperspectral Imaging measures the spectral changes for classifying the colon cancer. This method provided high accuracy along with high sensitivity and specificity. However, this method failed to provide faster acquisition time. Gessert, N et al. [14] developed a deep learning model for the identification of colon cancer. The learning process was complicated due to the similar appearance of the malignant and healthy tissue. However, this method was challenging for the learning process with large dataset size. Zhou, R et al.[13] designed a biomarker, known as immune cell infiltration for the detection of colon cancer. The immune scores were established for the diagnosis of the colon cancer that considered least absolute shrinkage, random forest method and selection operator model. This method provided higher net benefit, accuracy along with well-fitted calibration curves. However, this method was not used in the clinical application due to the diagnostic and prognostic immune risk score. Drouillard, A et al.[12] developed a color cancer detection based on Conditional net survival (CNS). This method proved that there was a dramatic increase in the CNS recurrence-free (RF) patients with time and these results provided reassuring information regarding the cancer patients. Although this method reduced the anxiety of the survivor, it failed to provide access to the insurance or credit and improve the quality of the survivors' life. Narayan, T et al.[11] developed a surface plasmon resonance (SPR) immunosensor for the detection of colon cancer. The monophasic model provided better result in evaluating the interaction within the antibody (anti-ET1) and antigen (ET-1) mechanism. The ET-1 based SPR sensor disk was characterized by the Fourier transform infrared (FT-IR), contact angle and atomic force microscopy (AFM) methods. This method provided effective detection as the SPR biomarker was used for the analysis. However, the SPR biosensor was not portable for the POC diagnostics. [3] Olaniran, O.R. and Abdullah, M.A.A designed a Bayesian model averaging for the classification of the colon cancer. In this method, the behaviours of the Quadratic Discriminant Analysis (QDA) and Linear Discriminant Analysis (LDA) were devised within the Bayesian averaging model. The problem of uncertainty was tackled by the discriminant analysis in the Bayesian averaging framework. However, the computational complexity was high in this Bayesian averaging model. The CNN addressee's the characterization of the tissue successfully for the semantic classification and segmentation.

The major concern in this approach is the insufficient data for optimal training that leads to limited generalization and over fitting problems [12]. In [6], spectral changes are measured using Fluorescence Excitation-Scanning Hyperspectral Imaging for the classification of the colon tissue into normal and lesion tissue. In the traditional method, the emission spectrum used for scanning the fluorescence hyperspectral imaging is weak as the emitted spectrum is filtered to narrow band before the detection. The limitation of this approach is that the diminished signal takes longer acquisition time for emission scanning. In [13], the immune landscape is systematically assessed for developing the immune model that detected the colon cancer patients who suffers from tumour transcriptomes of stage I–III. However, this method failed to show the discriminating power within the closely related cell populations and they are unable to access the immunity in cells. In the conventional techniques, like blood tests, physical examination, histopathology, colonoscopy, PET-CT scan and radiology, the accuracy is limited as the evaluation is based on the symptoms. Thus, the accuracy is the major concern diagnosis of CRC which should be improved by considering other parameters for the evaluation [10]. Machine learning approach was devised for improving the accuracy during cancer classification, but the major challenge lies in integrating this method with several other sophisticated techniques for the feature selection process in order to achieve efficient results [18].In [19], EJFOA was developed for the colon cancer classification. However, this method does not employ advanced machine learning approaches, such as reinforcement learning and deep learning in order to perform the gene selection and the classification process. In [21], IDSS approach was introduced for the identification of cancer but failed at testing process based on the other benchmarks, particularly binary-class datasets and also failed to test the reliability of analysis after frequent sampling of tissue from the same patient. A method was devised for improving the performance, challenge lies in improving this method by integrating other novel optimization algorithms [20].

3. Proposed Work

The goal of the work is to obtain a new method for colon cancer identification using DWWO-based deep RNN method. In the first stage, the pre-processing is performed in the cancer images that are assembled by using dataset. Now, this image is forwarded to the segmentation component for the segmentation of the image using Generative adversarial networks (GAN). After the segmentation, the obtained Segments are fed to the feature extraction module for the extraction of the features, such as mean, variance, kurtosis, entropy and LOOP features. After the feature extraction, the colon cancer classification is performed by the method, which is instructed by proposed Dragonfly-based water wave optimization. The accurate detection of the region affected by the colon cancer for minimizing the mortality rate is an important issue faced in the existing colon cancer detection methods. Hence, in order to obtain the accurate results in the detection of tumorous images from the non-tumorous images, the proposed colon cancer detection method is developed. A DWWO-based deep RNN is developed for the detection of colon cancer. After the segmentation, the obtained segments are forwarded for feature extraction component for the extraction of the attributes, mean, variance, kurtosis, entropy and LOOP features. After the feature extraction, the work is performed by proposed RNN, instructed by proposed DWWO algorithm. DWWO method is obtained by combining DA and WWO. Proposed DWWO-based deep RNN method for the colon cancer detection: The proposed method is formed by combining the [5] Dragonfly algorithm (DA) and water wave optimization (WWO). Figure 1 shows the proposed block diagram for the detection of the colon cancer using the proposed DWWO-based deep RNN.

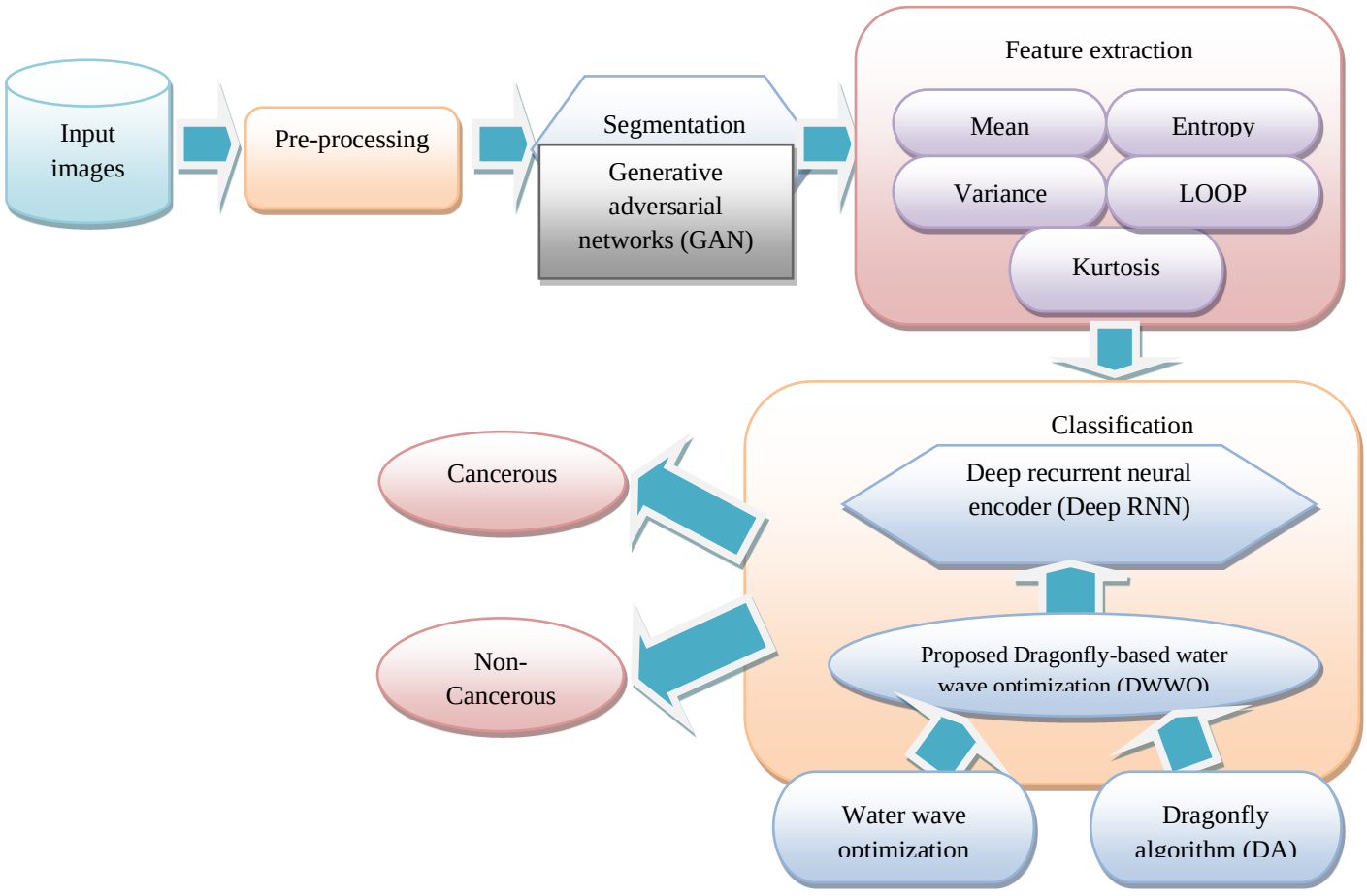

Figure 1. Proposed DWWO-Based Deep RNN For the Detection of Colon Cancer

From the Database G having various images termed as B,

$$G = \{B_1, B_2, \ldots, B_f, \ldots, B_h\} \tag{1}$$

Number of images is h, f^{th} image is given as, B_f .

(i)Pre-processing of input images

The pre-processing is an important step in the colon cancer detection process that provides the smoothening of the input image to make it suitable for the detection. The antiquity and the disturbance in the image are eliminated in this step. The pre-processing also enhanced the contrast of the image.

(ii)Segmentation using Generative adversarial networks

The pre-processed image is divided into segments for efficient classification using GAN [8]. The GAN provided the statistical relationship between input images and the predicted masks. A strong correlation is provided with the input image in the GAN. The similar images are obtained using the GAN from the good mask. The input to the GAN is the round truth masks and the major concern is the minimization of the loss between the real images and the generated images. The segmentation model consists of three components, like generator, semantic segmentation model and discriminator. From the predicted masks, the images are generated using the generator, whereas the original images are differentiated from the images that are reconstructed by the generator using the discriminator. The relationship between the original image and the ground truth masks are provided to the generator and input to the generator is the ground-truth images. Based on the prediction of the segmentation model, the image is produced by the generator A During min-max optimization process, the supervisor of A is the discriminator network Y . The synthetical image in correspondence to the original one is generated by A , whereas the reconstructed image, T^R and the original image, T are differentiated using Y . In the GAN, the detail loss function is given as,

$$Loss\ function = \min_{\vartheta_A} \min_{\vartheta_Y} \log\left(Y\left(T\right)\right) + \log\left(1 - Y\left(T^R\right)\right) \tag{2}$$

The generator generates the image same as T by taking the prediction layer output, κ and T as input. This process is known as, $A(\kappa)$. 4 convolutional and de-convolutional layers are adopted in the A network, whereas 4-convolutional with the ReLU is adopted by the Y network as the activation function. In the Y network, the fake and the original images are sent concurrently. Finally, the segments obtained from the GAN is termed as,

$$X = \{X_1, X_2, ..., X_t\} \tag{3}$$

Here X_1,X_2, … respectively are segments in correspondence with the images obtained from GAN.

3.1 Feature Extraction Using the Texture and Statistical Features

Every segment is considered for removal. The extracted features provide the effective detection of the colon cancer. The texture features, like LOOP and the statistical features, like mean, variance, kurtosis, entropy.

a) Mean: The Salient Feature for classification is the mean parameter. Mean is defined as the average of pixels in the image. The mean is calculated as,

$$\partial = \frac{1}{\left|d\left(U_z\right)\right|} \times \sum_{z=1}^{\left|d\left(U_z\right)\right|} d\left(U_z\right) \tag{4}$$

individul pixels are represented as, $d(U_z)$ and $|d(U_z)|$, sum of segments is represented as, z .

b) Variance: The variance parameter is used in the feature extraction step for removing the features that failed to meet the threshold. The variance removes the feature that has the same value, which is also known as the zero-variance feature in the samples. The variance determined using the mean value is given as,

$$\alpha = \frac{\sum_{z=1}^{|d(U_z)|} |U_z - \partial|}{d(U_z)} \tag{5}$$

where, α denotes the variance feature.

c) Kurtosis: The smoothness describes the keenness of the peak is termed as, kurtosis. The probability distribution is the kurtosis. The appearance of the object is arithmetic rate using kurtosis and is represented as, λ .

d) LOOP: The LDP (Local Pattern Descriptor) and the LBP (Local Binary Pattern) are combined in a non-linear fashion to form LOOP descriptor [7]. The LBP is a descriptor that has improved discrimination characteristics and it catches the dissimilarities of image. The LDP is enhanced local pattern descriptor that is less vulnerable to noise. The directional component is induced by the LDP descriptor using the Kirsch compass kernels. The randomized sequence of binarization weights in both the LDP and LBP leads to adding dependency towards orientation. These drawbacks are addressed by the LOOP descriptor by providing the scale-independency. The LOOP feature is represented as,

$$O = LOOP(\hat{u}_o, \hat{v}_o) = \sum_{\hat{j}=0}^{7} \hat{g}(\hat{b}_j - \hat{b}_o) 2^{\omega_j} \tag{6}$$

$$\hat{g}(t) = \begin{cases} 1 & If \ \ t \geq 0 \\ 0 & Otherwise \end{cases} \tag{7}$$

e) ***Entropy***: The information content in the image is identified using the entropy feature. For the calculation of the entropy, the information from the corner and the edge pixels are considered.

The entropy is represented by the term, ρ

3.4 Formation of Feature Vector from The Extracted Features

The feature vector is formed by considering the texture features, like LOOP and the statistical features, like mean, variance, kurtosis, entropy, and the feature dimension is represented with v

$$Y = \{\lambda, O, v, \rho, \alpha, \partial\} \tag{8}$$

where, Y represents the feature vector calculated from each segment. The deep RNN classifies the input image as cancerous and non- cancerous image based on the feature vector.

3.5. Proposed DWWO-Based Method for The Identifying Colon Cancer

The attribute vector formed by classification of the image. The method recognizes the abnormality with high precision and its highly preferable as deep networks holds effective performance compared with any other types of classifiers. Thus, this method is designed for the categorizing of the image. It is integrated using proposed

DWWO which is the integration of DA and WWO [4]. In DA, the location of the dragonfly depends on the factors, such as alignment, separation, attraction towards food source, Cohesion, and distraction from enemy. The factor varies with the velocity and it influences the survival of dragonfly. The WWO algorithm is inspired from shallow water wave models. For the high-dimensional global optimization problems, the search mechanism is designed by considering the wave–current–bottom interactions that controls the wave motion. The DA method enhanced the convergence factor by employing the weight parameters that ranges from [0-1], whereas the WWO algorithm is a simple framework with few control parameters. In order to obtain better optimization solution with improved performance, both the DA and WWO algorithms are combined. The DWWO for training the deep RNN are described below.

(i)Construction of Deep RNN

With D layers, the input and output vector of the d^{th} layer at time q is,

$v^{(d),g} = [v_1^{(d),q} v_2^{(d),q} \ldots . v_p^{(d),q} \ldots v_P^{(d),q}]^M$ and $y^{(d),g} = [y_1^{(d),q} y_2^{(d),q} \ldots . y_p^{(d),q} \ldots y_P^{(d),q}]^M$.

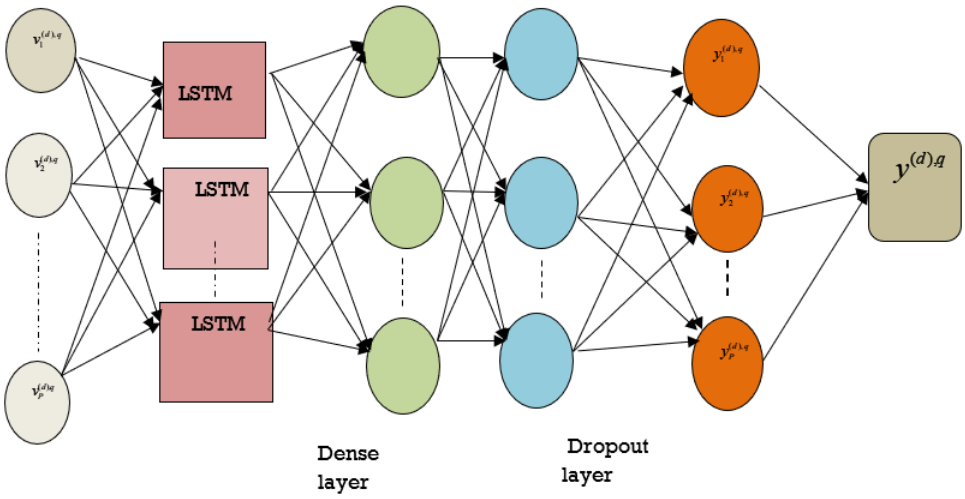

Figure 2. Construction of the Deep RNN

For the d^{th} layer sum of units and arbitrary units are, P and p sequentially. For output layer, the term $w^q = y_P^{(D),q}$ and $s^q = v_P^{(D),q}$, whereas in the input layer, the term $g^q = y^{(d),q}$. For the $(d-1)^{th}$ layer, the total number of units and arbitrary unit number is represented as, K and k respectively. The recurrent weight and the weight of the input propagation from the $(d-1)^{th}$ to the d^{th} layer is denoted as, $E^{(d)} (\in H^{P \times I})$ and $F^{(d)} (\in H^{P \times P})$. Before one unit time, the random unit is denoted by, p' and the components of $y^{(d),q}$ are denoted as,

$$v_p^{(d),q} = \sum_k^K a_{kp}^{(d)} \, y_k^{(d-1),q} + \sum_{p'}^P c_{pp'}^{(d)} \, y_{p'}^{(d),q-1} \tag{9}$$

The element of $F^{(d)}$ and $E^{(d)}$ are represented as, $c_{pp'}^{(d)}$ and $a_{kp}^{(d)}$, respectively. The d^{th} layer's output vector element is represented as,

$$y_p^{(d),q} = u^{(d)} (v_p^{(d),q}) \tag{10}$$

where, activation function is denoted as, $u^{(d)}(.)$. Other frequently used functions are logistic sigmoid $u(v)=1/(1+e^{-v})$, sigmoid function $u(v)=\tanh(v)$, and rectified linear unit (ReLU) function $u(v)=\max(v,0)$.

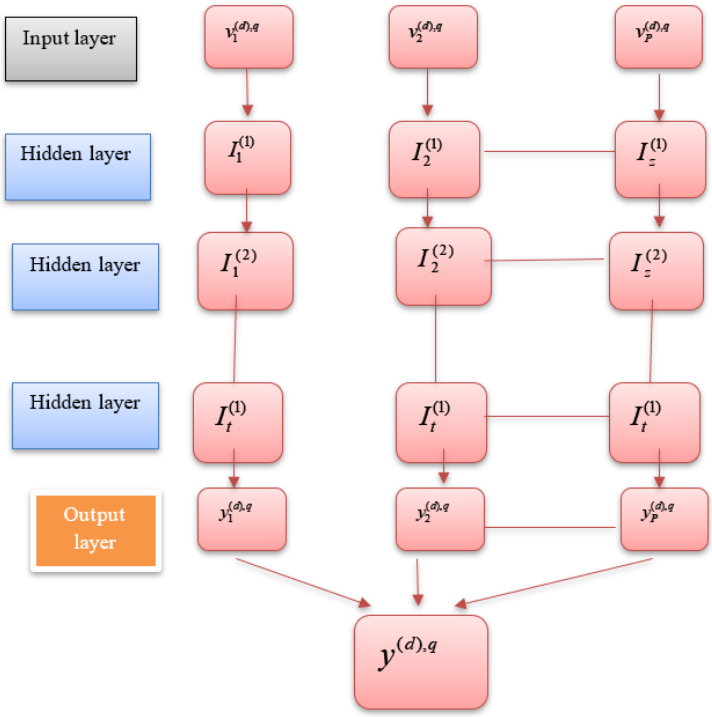

Figure 3. Construction Of RNN

The biases are given as,

$$y^{(d),q}=u^{(d)}\left(E^{(d)}\,y^{(d-1),q}+F^{(d)}\,y^{(d),q-1}\right) \tag{11}$$

where, 0-th unit and the 0-th weight is given as, $y_{p0}^{(d)}=1$, $a_0^{(d-1),q}$ and $u(e)=[u(e_1)u(e_2)..u(e_N)]^M$. The output vector w is expressed as,

$$w^q=u^{(D)}(s^q)=u^{(D)}(E^{(D)}\,y^{(D-1),q}) \tag{12}$$

3.5.1 Deep RNN For Classification of Colon Cancer

The deep RNN is trained using the proposed algorithm. The steps of the proposed DWWO based deep RNN is as follows,

Step 1: Initialization of the population: The population of the dragonflies are initialized for determining the best solution, which is represented as

$$V=\{V_1,V_2,\ldots,V_x,\ldots,V_n\} \tag{13}$$

where, the location of the x^{th} dragonfly in the solution is represented as, V_x . The step vectors are also initialized as, $\Delta V_i\,(i=1,2,...,n)$.

Step 2: Calculation of the objective function*:* After the initialization, the objective function is determined for each solution. The optimal position is determined at the end of every iteration.

Step 3: Update the source of the food and the enemy*:* From the whole swarm, the food source and the enemy are determined.

Step 4: Position update of the individuals in swarm*:* The factors, such as alignment, separation, cohesion, appeal towards the food origin and the diversion outwards an enemy influence the value is update for individual dragonfly. The matching of velocity from one individual to the other individual in the neighbourhood is defined as, alignment. The alignment is determined by the following equation as,

$$C_i = \frac{\sum_{j=1}^{W} Q_j}{W} \tag{14}$$

where, the j^{th} neighbouring individual's velocity is represented as, Q_j and W is the number of neighbouring individuals. The static collision avoidance from one individual to the other neighbourhood individual is defined as, Separation. The separation is determined as,

$$J_i = -\sum_{j=1}^{W} V - V_j \tag{15}$$

where, the position of the j^{th} neighbouring individual and the current individual is denoted as, V_j and V . The individual's tendency towards the centre of the neighbourhood mass is defined as, cohesion. The cohesion is determined as follows

$$S_i = \frac{\sum_{j=1}^{W} V_j}{W} - V \tag{16}$$

The attraction of the swarm towards the food source is calculated as,

$$L_i = V^+ - V \tag{17}$$

where, the position of the food source is represented as, V^+ . The distraction of the dragonfly swarm outwards an enemy is determined as,

$$R_i = V^- + V \tag{18}$$

where, the enemy's position is represented as, V^-. Thus, these five patterns influence the behaviour of the dragonfly

Step 5: Update the neighbouring radius*:* Place of the artificial dragonflies in the search area is updated, the motions are simulated by collecting two vectors, position vector (V) and the step vector (ΔV). Direction of the dragonfly's is indicated by the step vector. The step vector is calculated as,

$$\Delta V_{t+1} = \left(\tilde{j} J_i + \tilde{c} C_i + \tilde{s} S_i + \tilde{l} L_i + \tilde{r} R_i\right) + \tilde{w} \Delta V_t \tag{19}$$

where, the i^{th} individual's separation and the separation weight is indicated as, J_i and $\tilde{j}$, i^{th} individual's alignment and the alignment weight is indicated as, C_i and $\tilde{c}$, the i^{th} individual's cohesion and the cohesion weight is indicated as, S_i and $\tilde{s}$, i^{th} individual's food source and the food factor is indicated as, L_i and $\tilde{l}$, i^{th}

individual's position of the enemy and the enemy factor is indicated as, R_i and $\tilde{r}$, the iteration counter and the inertia weight are represented as, t and $\tilde{w}$. The position vectors are calculated followed by the calculation of the step vector. The position vector is determined as,

$$V_{t+1} = V_t + \Delta V_{t+1} \tag{20}$$

where, the current iteration is represented as, t. When there is no neighbouring solution (neighbouring dragonfly) then, the position is updated using the Levy flight method for improving the stochastic behaviour, randomness, and the exploration of the artificial dragonfly. The position of the dragonfly updated using the Levy flight is given as,

$$V_{t+1} = V_t + Levy(m) \times V_t \tag{21}$$

where, the dimension of the position vector is given as, m.

$$V_{t+1} = V_t + 0.01 \frac{l_1 \beta}{|l_2|^{1/\alpha}} \times V_t \tag{22}$$

where, l_1 and l_2 are the random numbers. In the proposed DWWO-based deep RNN method, the arbitrary number, l_1 is in the range $[0,1]$, it is equated to the update equation of the WWO. Thus, the random variable l_1 calculated using the WWO is given as,

$$l_1 = Gaussian\left(\frac{V_{best,m} + V_t}{2}, \frac{V_{best,m} - V_t}{2}\right) \tag{23}$$

$$l_1 = V_{t+1} \tag{24}$$

$$V_{t+1} = V_t + 0.01 \frac{V_{t+1} \beta}{|l_2|^{1/\alpha}} V_t \tag{25}$$

$$V_{t+1} - 0.01 \frac{V_{t+1} \beta}{|l_2|^{1/\alpha}} V_t = V_t \tag{26}$$

$$V_{t+1}\left(1 - \frac{\beta 0.01}{|l_2|^{1/\alpha}} V_t\right) = V_t \tag{27}$$

$$V_{t+1}\left(\frac{|l_2|^{1/\alpha} - \beta 0.01}{|l_2|^{1/\alpha}} V_t\right) = V_t \tag{28}$$

$$V_{t+1} = \frac{|l_2|^{1/\alpha} V_t}{|l_2|^{1/\alpha} - 0.01 \beta V_t} \tag{29}$$

where, $\alpha = 1.5$, l_2 ranges from $[0,1]$, $\beta = \left(\frac{\Gamma(1+\alpha) * \sin\left(\frac{\pi\alpha}{2}\right)}{\Gamma(\frac{1+\alpha}{2}) * \alpha * 2^{\left(\frac{\alpha-1}{2}\right)}}\right)^{\frac{1}{\alpha}}$, and $\Gamma(x) = (x-1)!$. Thus, the equation

(29) is used for updating the position of the dragonfly. The effective update of the dragonfly helps in the determination of the location of the minimum fitness.

Step 6: Checking the feasibility of the solution: After updating the location of the dragonflies, the feasibility of the solution is checked. The best solution for location is low fitness. The older solution is replaced with the optimal solution.

Step 7: Termination*:* Until the best solution is obtained the above process is repeated. Below is the pseudo code.

Input: Features Y
Output: Best optimal solution
Initialization of the dragonfly's population V
Initialization of the step vectors
While no satisfaction in the end condition
Calculate the objective function
Update the enemy and the food source
Update the position of the individual dragonfly
Update the neighbouring radius
If there is at least one neighbouring dragonfly
Update the velocity vector using eqn. (14)
Update the position vector using eqn. (20)
else
Update the position vector using eqn. (29)
end if
Update the new positions based on the variable boundaries
end while

Algorithm. Pseudo code of the proposed DWWO-based deep RNN method

3.6 Database Description

The dataset used for colon cancer classification is CT (Computed Tomography) colonography. The total number of images considered is 1000 in that 700 images are used for training and 300 images are used for testing phase and the modalities which have been used for this data are CT. [17] The 825 cases provide the polyp description and their locations. A polyp is a little clump of cells which forms the lining of the colon that can develop into colon cancer. In 825 cases, 582 are positive cases and 243 are negative cases. The descriptions of the polyp and the location of the polyp in the colon segments are provided in the XLS sheet. The supine and prone DICOM (Digital Imaging and Communication in Medicine) images can be downloaded from the CT Colonography collection.

3.7 Performance Metrics

The performance of DWWO-based deep RNN is analysed with respect to evaluation metrics, such as Confusion Matrix, accuracy, sensitivity, specificity, and Loss curves

(i)Confusion Matrix.

A confusion matrix depicts the predicted and the actual classification produced by any classifier. A classifier utilized in classifying n classes will have a size $n \times n$.

	Predicted Positive	**Predicted negative**
Actual Positive	T^n	F^p
Actual negative	F^n	T^p

Table 1. Confusion matrix

(ii)Sensitivity:

The sensitivity is the positive cancerous cells identified in the colon cancer detection as positive. The sensitivity in the colon cancer detection is represented as

$$Sensitivity = \frac{T^p}{F^n + T^p}$$

(iii)Accuracy:

The level of closeness in the detection process between the original and the estimated value is the accuracy. The accuracy in the colon cancer detection method is represented as,

$$Accuracy = \frac{T^n + T^p}{F^p + F^n + T^p + T^n}$$

(iv)Specificity:

It is negative cancerous cells identified in the colon cancer detection as negative. The specificity in the colon cancer detection is represented as,

$$Specificity = \frac{T^n}{T^n + F^p}$$

where, T^p, F^p, T^n and F^n represents the true positive, false positive, true negative, false negative, and respectively. The competing method used in the proposed DWWO-based deep RNN method is, Convolutional Neural Network (CNN)[9]. The performance is measured with metrics by varying the hidden layer.

(v)Loss curves

Loss curve is a graphical plot that depicts the training process of a neural network and it portrays the relation between the training loss or error and the number of epochs.

4. Experimental Results

The experimental results that are performed considering cancer and non-cancer images. The quantity of images considered is 1000 out of which 700 images for training and 300 for testing phase Figure 4 demonstrate the input image 4(a) demonstrate the non-cancerous image, figure 4(b) represents the input image, figure4(c) represents the segmented image, figure 4(d) represents the tumour image.

(i)Segmentation Results

Table.2 provides the relative discussion for colon cancer detection technique. The values are shown corresponding to the 90% of training data

Database	Metric	CNN	Proposed DWWO-based deep RNN
Using training percentage	**Accuracy**	89.4	**96**
	Sensitivity	93.9	**96**
	Specificity	79.4	**94.9**
Using K-Fold	**Accuracy**	80.9	**96**
	Sensitivity	90.1	**96**
	Specificity	79.1	**95**

Table 2. Comparative Discussion of The Colon Cancer Detection Methods

(ii)Classifier Results for Analysis using Confusion matrix and loss curve

Table 3. illustrates the confusion matrix of the devised DWWO-based deep RNN approach. The classifier performs exceptionally well while detecting colon cancer. Out of the 288 outcomes, the classifier predicted 281 outcomes perfectly. Figure 4 illustrates the loss and accuracy curve of the DWWO-based deep RNN approach. The deep RNN based approach is shown to have fast learning capability and produces a significant decrease in training loss as the number of epochs is varied from 0 to 200.

Table 3. Confusion Matrix of The Devised DWWO-Based Deep RNN Method

Outcomes		**Predicted Output**	
		No	Yes
Actual Output	No	$T^n = 288$	$F^p = 32$
	Yes	$F^n = 2$	$T^p = 281$

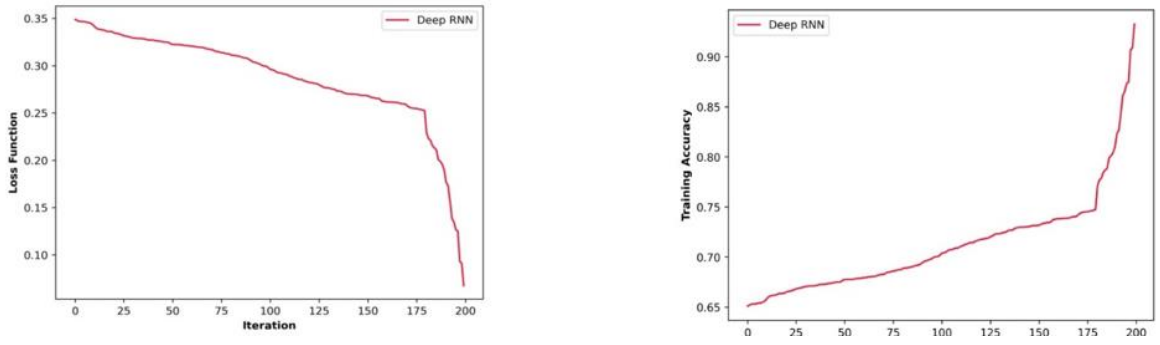

Figure 4. Shows The Loss Curve and Accuracy Curve of The Deep RNN Classifier Used in The Introduced DWWO-Based Deep RNN Approach Method

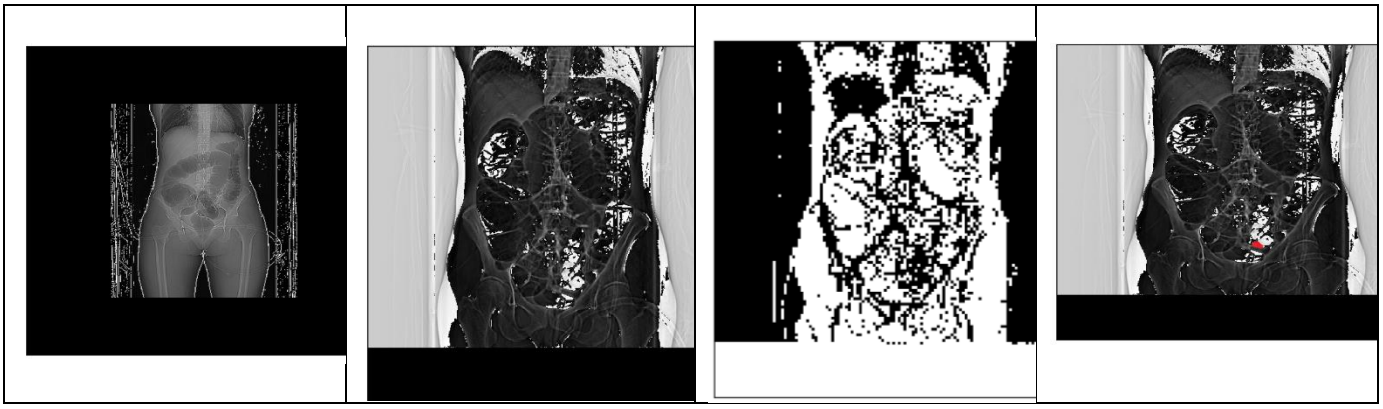

Figure 4. Experimental Results (A) Input Without Cancer Image, (B) Input Image, (C) Segmented Image, (D) Tumour Image

5. Conclusion

A deep learning-based hybrid optimization namely, DWWO-based deep RNN method is developed for the detection of colon cancer. After pre-processing, the segments are provided to the segmentation module for segmentation using GAN. The extracted features are used for the colon cancer detection mechanism with the proposed optimization algorithm. At last, the deep RNN is trained using the proposed method. The analysis of the proposed DWWO-based deep RNN method is carried out using the performance metrics, like sensitivity, accuracy, and specificity. The further enhancement in the proposed colon cancer detection can be done using more advanced segmentation and optimization methods.

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