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Review Article

Comparative Analysis of Colon Cancer Classification Using RNN and CNN

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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 is done by recurrent neural network and CNN. 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. The obtained segments are forwarded for attribute selection module. Finally, the Comparison is done for CNN and RNN Results.

Keywords: Peritoneal Carcinomatosis; Colorectal Cancer (CRC); Deep Learning; Biomarkers

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 also 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 lymphocytesis 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.

Related work

Shafi, A.S.M., et al. [18] introduced a machine learning approach using the random forest classifier for analyzing 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" as the feature selection methods. 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 analyze 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 also 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 an 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 hyperspectral 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 detection of colon cancer from confocal laser microscopy (CLM) images. 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 immunoscores 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 lesional 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 not capable of assessing the effects of immunity in different cell types. 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 [20], IDSS approach was introduced for the classification of cancer. However, this method failed to perform the 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].

Proposed work

The goal of the work is to obtain a new method for colon cancer classification using RNN method and CNN.

RNN

Recurrent Neural network is a type of neural network whose last output is saved and fed as a input for the next step. It uses sequential or time series data. This type of network is used to model sequence of data. The following is the architecture of RNN.

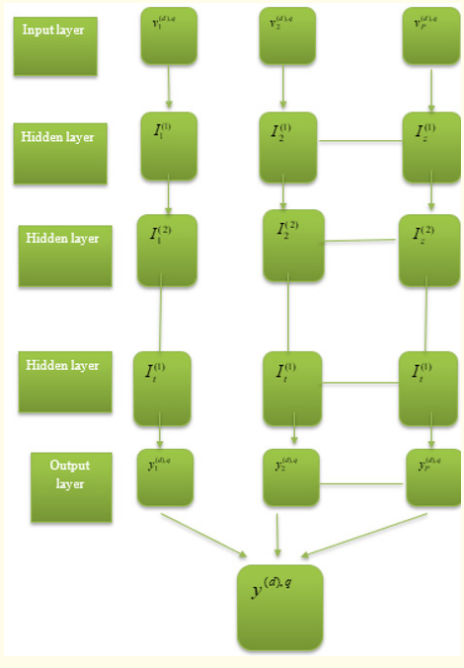


Figure 1: Construction of RNN.

For the d^{th} layer sum of units and arbitrary units are , P and p respectively. In the 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,

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

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,

$$y_p^{(d)\,q}=u^{(d)}(v_p^{(d)\,q}) \qquad (2)$$

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 $u(v)=\max(v,0)$. The biases are given as,

$$y^{(d)\,q}=u^{(d)}\left(E^{(d)}\,y^{(d-1)\,q}+F^{(d)}\,y^{(d)\,q-1}\right) \qquad (3)$$

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,

$$w^q=u^{(D)}(s^q)=u^{(D)}(E^{(D)}\,y^{(D-1)\,q}) \qquad (4)$$

CNN

CNN [11] is mainly comprised with multi-layers interconnected neurons especially trained effectively for classification and feature extraction. When compared with the existing classification algorithms, [5] CNN provides better classification results with minimum cost within a short time. CNN consists of 3 layers named Convolutional layer, pooling layer and Convolution Layer is the first layer of CNN network that decides the whole operation of the network. The performance of CNN is usually based on the utilization of learnable filters. The output of this layer is obtained by convolving each filter on the given image and the culmination will be a series of images where the number of images is similar to the amount of filters. Each filter in the convolution layer is a grid of discrete numbers and the procedure involves in initialization of weights randomly. For every convolution layer multiple kernels are defined and at each point underlying pixel values are multiplied and add them which give raise to corresponding output. In order to bring out the nonlinear property from CNN, activation function is used. The Rectified linear unit (ReLu) is used as activation functions in this work. ReLu removes the problem of over fitting and makes the model more adaptable to real world cases. Pooling Layer is also called as sub-sampling layer.

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.

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.

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.

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

$$Sensitivity=\frac{T^p}{F^n+T^p} \qquad (5)$$

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,

$$Accuracy=\frac{T^n+T^p}{F^p+F^n+T^p+T^n} \qquad (6)$$

Specificity

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

$$Specificity = \frac{T^n}{T^n + F^p} \quad (7)$$

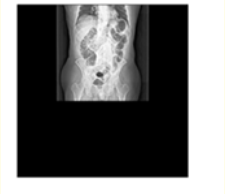
Where, T^p, F^p, T^n and F^n represents the true positive, false positive, true negative, false negative, and respectively. The competing method used in the proposed DWWO-based deepRNN method is, Convolutional Neural Network (CNN) [9]. The performance analysis of the proposed DWWO-based deepRNN method using the performance metrics, such as accuracy, specificity and sensitivity by varying the hidden layer.

Loss curves

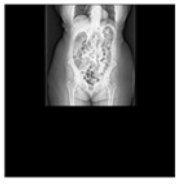
Loss curve is a graphical plot that depicts the training process of a neural network and it portrays the relation between the training loss or error and the number of epochs.

Experimental Results

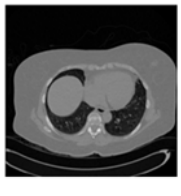
The experimental results that are performed considering cancer and non-cancer images. The quantity of images considered is 1000 out of which 700 images for training and 300 for testing phase Figure 2 demonstrate the input image 2(a) demonstrate the non-cancerous image, figure 2(b) represents the input image, figure 2(c) represents the segmented image, figure 2(d) represents the tumour image.



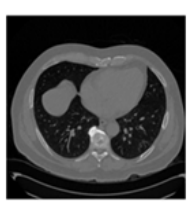
2(a)



2(b)



2(c)



2(d)

Figure 2

Segmentation Results

Table 2 describes the comparative discussion of the colon cancer detection methods. The values are shown corresponding to the 90% of training data.

Database	Metric	CNN	RNN
Using training percentage	Accuracy	89.4	90.1
	Sensitivity	93.9	92
	Specificity	79.4	83.2

Table 2: Comparative discussion of the colon cancer detection methods.

Conclusion

In this work a comparison is made between RNN and CNN in classifying the Colon Cancer and RNN is found to be better performed than CNN.

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