An Effective Approach for Detecting Colon Cancer Using Deep Convolutional Neural Network

Jamel Smida
College of Applied Science,
AlMaarefa University, Kingdom of Saudi Arabia
Microwave Electronics Research Laboratory,
Faculty of Sciences of Tunis,
University Tunis El Manar, Tunis, Tunisia
Email ID – jsmida@um.edu.sa

Anandh Sam Chandra Bose
College of Applied Sciences
AlMaarefa University, Kingdom of Saudi Arabia
Email ID – asam@um.edu.sa

Mohamed Karim Azizi
Microwave Electronics Research Laboratory,
Faculty of Sciences of Tunis,
University Tunis El Manar, Tunis, Tunisia
Email ID - medkarim.azizi@gmail.com

Amor Smida
Department of Medical Equipment Technology,
College of Applied Medical Sciences, Al-Majma'ah, Saudi Arabia
Microwave Electronics Research Laboratory,
Faculty of Sciences of Tunis,
University Tunis El Manar, Tunis, Tunisia
Email ID – a.smida@mu.edu.sa

2024 IEEE International Conference on Advanced Systems and Emergent Technologies (IC_ASET) | 979-8-3503-8489-5/24/$31.00 ©2024 IEEE | DOI: 10.1109/IC_ASET61847.2024.10596175

***Abstract*—One of the leading causes of sickness and mortality in the world is colon cancer, which is definitively diagnosed by histological investigation. While both conventional and current approaches may compare images that may cover cancer areas of different kinds after looking at a large number of images of colon cancer, it remains a major cause of cancer-related mortality. Diagnosing benign from malignant disorders to have several complex elements is the primary challenge for colon histopathologists. This is done by applying techniques from image processing and deep learning (DL). The utilisation of whole-slide photography and digital image processing has made it possible to analyse colon cancer using convolutional neural networks. Proficiency in analysis requires accurate classification of colon tumours. In this paper, an improved system for recognising and classifying colon adenocarcinomas by using an adaptive wiener filter to digital histopathology images and a deep convolutional neural network (DCNN) model shows 94.7% accuracy. In the following step, the image is routed to the areas for segmentation using K-means to accurately define the illness's size and shape. Grey level Concurrent Matric (GLCM) is used for feature extraction and by putting this strategy into practice, doctors can create an automated and best method for identifying different types of colon cancer. This work is implemented using MATLAB.**

Keywords—Deep Conventional Neural Network (DCNN), Colon Cancer, Adaptive Wiener filter, K-means clustering, Deep learning.

I. INTRODUCTION

The rectum, which is the colon's terminal segment, is where colon cancer usually begins to grow. Furthermore, the term "cancer" is wide and refers to a number of conditions where abnormal cells arise inside the body of a person as a result of chance changes. When these cells are created, they proliferate uncontrolled and spread through each organ. People can pass away from the majority of cancer types if they are not treated. It often begins developing tiny, benign clusters of cells termed polyps on the colon's inner lining. In the end, many of these polyps could develop into cancers of the colon. In most cases of colon cancer, an excessively large number of normal cells in the rectum or colon gives rise to a tumor. The big intestine's epithelial cells are the starting point for colon or rectum adenocarcinomas, which then migrate to the remaining layers. Over the years, factors including age, gender, ethnicity, habit of smoking, and financial standing can all affect how one's body develops. But if an individual has a rare genetic condition, changes may take place in a matter of months. Rarely, a person inherits the cancer-causing defective gene from parents who have the disease. People who are at risk of developing genetic cancers ought to have testing on a regular basis. Due to its high cost, many people have no way to afford these diagnostic tests. Approximately 70% of cancer deaths happen in countries with lower and medium incomes. Only 26% of countries with low incomes have the pathological resources needed to diagnose cancer available to the public, according to statistics from 2016; wealthy nations may offer cancer detection and evaluation to over ninety percent of their population [1-3].

Not only does inadequate medicine increase the risk of cancer, but it also makes people in underdeveloped and emerging countries more susceptible to a variety of ailments. These nations need to make significant investments in the health of their citizens, set up a number of labs and pathological centers with the necessary equipment, and hire more people to handle diagnostic procedures in order to solve this problem. They also need to make sure that those who are impoverished can afford the fees of these testing. To be honest, all of these goals are simple for any nation in the world to achieve, and even if they are, it won't happen quickly. It is needed to look at alternate diagnostic methods in order to keep cancer therapy relevant and provide those with cancer a reasonable chance of life [4-7].

The present cancer detection method requires a great deal of labour and time. To recognise colon pictures, pathologists need to get a thorough understanding of labelled histological images. This leads to a large waste of resources and labour-intensive tasks. Consequently, higher diagnostic precision and speed are required [8, 9].

The inherent benefits of computer technology, such as their speed, storage capacity, and processing power, have attracted a lot of interest. The goal of research now is to create an automated cancer detection device using computer-aided diagnostics. Due to its ability to gain knowledge from data and achieve human-like learning, deep learning represents one of the most interesting applications of computer-aided technologies. This is because it allows models to operate on their own better when making predictions. To present, a great deal of study has been done on colon cancer research with the use of computer technology. But in contrast, the specific systems are highly advanced [10, 11].

Authorized licensed use limited to: National Institute of Technology- Meghalaya. Downloaded on July 22,2025 at 02:59:57 UTC from IEEE Xplore. Restrictions apply.

Algorithms utilizing deep learning have demonstrated remarkable efficacy in picture recognition across a wide range of uses, often surpassing human capabilities. The main idea is that numerous labelled photos may be used to train an adaptive software network to recognize images by assigning values to its parameters. The network may be trained to identify the correct label for pictures that are not labelled [12-15].

The main goal of this research is to determine the impact of the proposed DCNN model and assess the use of deep learning for the histological investigation of colon cancer through the analysis of digital pathology pictures. With less preprocessing needed than other methods for classification, the algorithm's design has been influenced by the structures of neurons and their connections inside the human brain. The system has the capacity to learn properties that are superior to the crude method of filters. The proposed model can distinguish between input pictures that have weights given to several characteristics. Since the histopathology slide-making procedure maintains the underlying tissue construction, it offers a multidisciplinary picture of illness and its impact on tissues, which is choose it as our dataset. This work created a highly refined deep learning model that can identify organs and cancers in medical data. It has also been effectively used to categorize picture samples and diagnose disorders, revolutionizing the whole healthcare industry.

This paper's primary contribution is explained as follows:

a) An improved DL model that produces encouraging outcomes for colon cancer classification.
b) In a brief amount of time, the suggested DL model outperforms other comparable research in terms of accuracy.
c) Because the proposed model makes use of efficient data processing techniques, it might save space and time.

Finally, the structure of the paper is as follows: Introduction is discussed in section I and the proposed system in section II. Results are discussed in section III followed by conclusion in section IV.

II. Proposed System

Several image processing tasks are used in a pipeline to identify colon cancer. To diagnose colon cancer, a number of image processing tasks are completed before deep learning is used for classification. Fig. 1 depicts the generalized procedure for this investigation.

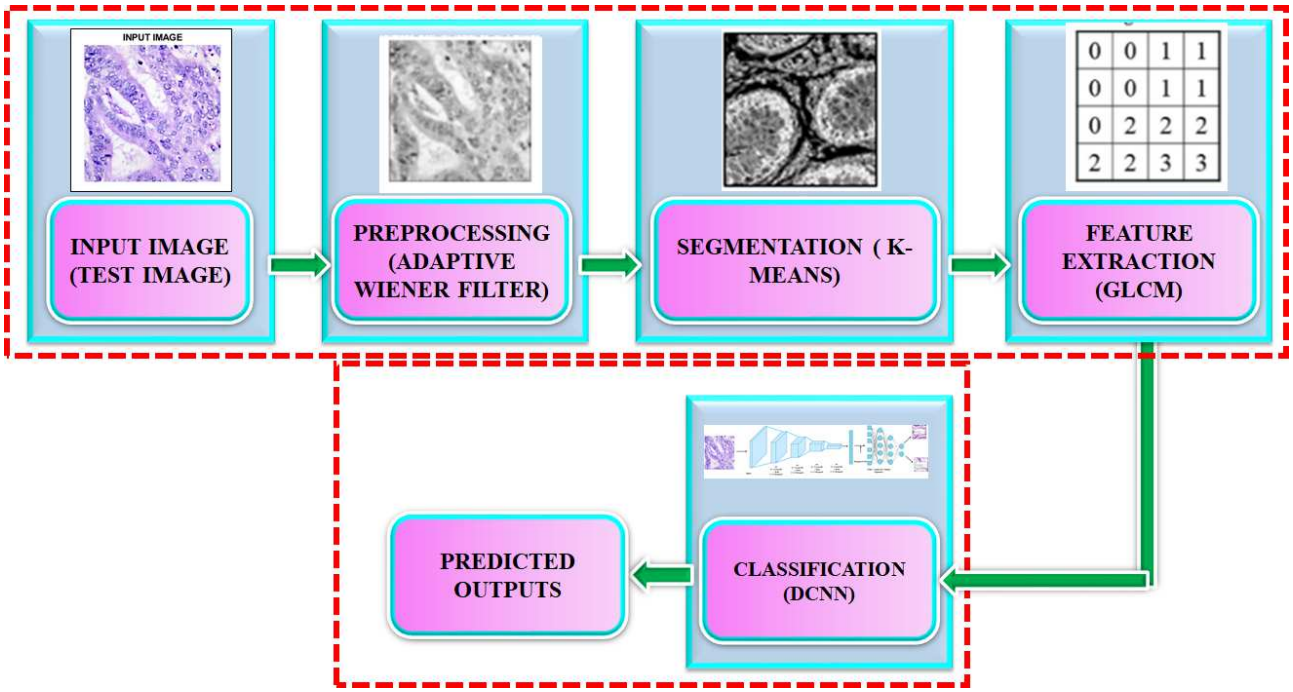

Fig. 1. Proposed Block Diagram

A suggested technique for detecting colon cancer employing image processing is depicted in Fig. 1. An image of the colon that is deemed infectious is sent into the system. Then, pre-processing by wiener filter enhances the visual attractiveness of this image. The noise and artefacts are removed from the photos in order to get a high classification rate. It initially boost the brightness of the input picture before using k-means segmentation to divide it in order to identify cancer. Using k-means clustering, which divides a particular set of information into k number of groups, an assortment of data is divided into a group of k numbers. Classifying lesions requires determining a number of characteristics, such as colour, texture, and the most common features determined by entropy. Feature extraction classifies data using an object-based method. A group of pixels with similar spectral, spatial, and/or textural properties is called a segment. In this case, the features are extracted using GLCM. It produces a classification result that predicts the output and indicates whether the appearance of the brain is typical or atypical. Following acquisition, the data is analyzed in DCNN utilizing a specific framework tailored to the patient's characteristics. Preprocessing the GLCM data into a CNN-compatible format is usually required before integrating GLCM features with CNN. For CNN input, the GLCM feature matrix is reshaped into multi-dimensional arrays. The original picture data is merged with the altered GLCM features. The CNN receives extra texture information from this combined input, which consists of both raw pixel values and GLCM features, to enhance performance.

Authorized licensed use limited to: National Institute of Technology- Meghalaya. Downloaded on July 22,2025 at 02:59:57 UTC from IEEE Xplore. Restrictions apply.

A. *Pre-processing By Adaptive Wiener filter*

Making pictures appropriate for the next stage of the detecting system is the aim in preprocessing. The initial and most significant phase in getting data ready to be utilized with a model that uses machine learning is preprocessing it. The noise and artefacts are removed from the photos in the proposed study to get a high categorization rate. It also performed feature extraction, data reduction, and data normalization before converting the label string information into numerical information. Mapping a space with high dimensions to a more relevant lower-dimensional space is called reduction. It is sometimes an essential step before creating models. Think about filtering pictures that have been tainted by zero-mean white Gaussian noise that is independent of signal. One way to model the issue is as

$$y(i,j) = x(i,j) + n(i,j) \quad (1)$$

where $y(i,j)$ is the noisy evaluation, $x(i,j)$ is the noise free picture and $n(i,j)$ is incremental Gaussian noise. The objective is to minimize the mean squared error (MSE) by obtaining a linear approximation of $x(i,j)$ by "denoising" (or removing) noise from $y(i,j)$

$$MSE(\hat{x}) = \frac{1}{N}\sum_{i,j=1}^{N}(\hat{x}\,(i,j) - x(i,j))^2 \quad (2)$$

where N is the total number of items in $x(i,j)$.

B. *Segmentation by K Means*

One ML method for partitioning data is k-means clustering. With k-means clustering, you may divide your data into k groups based on a similarity criterion if there are n observations in total. Applying clustering is one approach of partitioning a set of data into a certain amount of categories. K-means clustering constitutes a widely used technique. It divides a batch of information into k number collections of data using k-means clustering. With this method, a given collection of data is split up into k distinct clusters. The method known as K-means involves two distinct stages. It locates the *k* center in the first phase. Each point is moved to the cluster that is nearest to the corresponding data point during the subsequent stage. The distance determined by Euclid represents one of the more frequently employed techniques for calculating a distance to the closest centroid. Following categorization, each group's new center is computed and the cluster points having the least distance from Euclid are assigned. Furthermore, this process calculates a new Euclidean distance between the center and every point of data based on the centroid. The centroid and member items of every partition serve as markers for its cluster. The point where the overall distances to all the items in a cluster are the least is known as the cluster center. Consequently, K-means is an iterative approach that reduces the overall distances among each cluster center and every single item. Consider an image that has to be resolved to $x \times y$ and clustered into k distinct clusters. Let c_k represent the cluster centers and $p(x,y)$ represent the input pixels to be clustered. The following is the k-means clustering method,

a) Set the cluster k and center numbers to zero.
b) By applying the relationship shown below, determine the Euclidean distance, or d, for each pixel in a picture between its center and each pixel.

$$d = \|p(x,y) - c_k\| \quad (3)$$

c) Based on distance d, assign each and every pixel to the closest center.
d) Applying the relation shown below, compute the new center position after all pixels have been allocated.

$$c_k = \frac{1}{k}\sum_{y \in c_k}\sum_{x \in c_k} p(x,y) \quad (4)$$

e) Continue doing so until the tolerance or error value is met.
f) Reconstruct the picture from the cluster pixels.

Despite its significant benefit of being simple to apply, k-means has a few shortcomings. The arbitrary selection of the starting centroid determines the level of accuracy of the final clustering outcomes. Therefore, various beginning centres will provide different results if the first centroid is selected at random. Thus, much care will be used in selecting the starting centre to ensure the desired segmentation. Additionally, it must take computing cost into account while creating the K-means clustering. It is dependent upon the quantity of data items, clusters, and iterations. The square root of N, where N is the total number of samples, is typically determined to be the ideal K value. An accuracy or error plot can be used to determine the optimal K value.

C. *Proposed DCNN Model*

A DCNN algorithm is proposed that distinguished between colon cancer and normal colon tissue using two categories. The updated weights can be adjusted further using the back-propagation algorithm. The proposed DCNN model uses the Adam optimizer. Lastly, the labelled image limitations in the dataset are circumvented using augmentation. Figure 2 shows the structure of the proposed DCNN model.

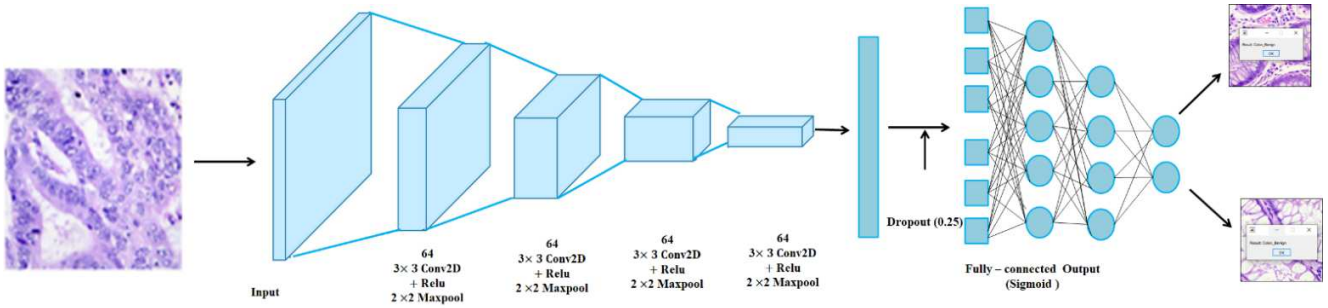

Fig. 2. DCNN model's architecture.

Input layer- The first convolution layer receives the data that is loaded in this layer. In this instance, the input consists of a 128 by 128 pixel picture with three colour channels, or RGB = 3.

Authorized licensed use limited to: National Institute of Technology- Meghalaya. Downloaded on July 22,2025 at 02:59:57 UTC from IEEE Xplore. Restrictions apply.

Pooling layer- The output pictures of the convolution layer are down sampled using the pooling procedure. It is employed to reduce the input photo size in order to make training easier. The most popular max pooling technique is employed by all pooling layers.

Optimizer (Adam)-Adam is an exchange optimisation method based on stochastic gradient descent that minimises the loss function involved in training deep learning models. For the purpose of this research, the conventional gradient descent technique is selected with a learning rate of 0.001 and a momentum of 0.999.

Flatten layer- This layer joins a dense or completely connected layer by transforming the convolution layer's output into a 1D tensor.

Dropout layer- A dropout layer is used between fully connected layers that regularly removes neurons from both obvious and hidden layers in order to prevent the model layers from being over fit.

III. Results And Discussions

The suggested model's main goal is to use DCNN to categorize colon cancer tissue that has been recovered and distinguish between benign and adenocarcinoma. The processing of medical images may be assessed using two different measures. It is investigated that the level of individual photos by determining the proportion of accurately recognized cancer images. Nearly all of the PLCO study data that are accessible for studies of colon cancer screening, incidence, and death are included in the extensive Colon dataset. Each of the roughly 155,000 participants in the PLCO study has a record in this dataset. Fig.3 shows the input image to the proposed model.

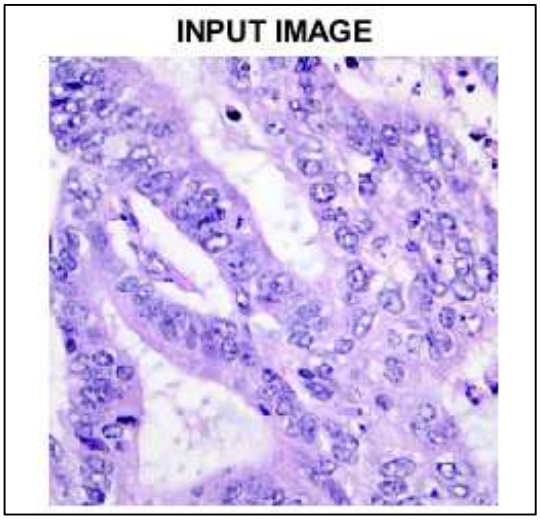

Fig.3. Input image

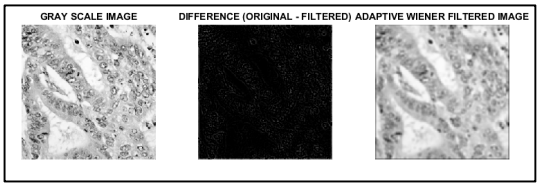

Fig.4. Filtered image

Unwanted data are removed using adaptive wiener filter is seen to be present in the retrieved frames and the resultant pictures as shown in Fig.4. The input image is enhanced, Segmented and classified as shown in Fig. 5 – 7.

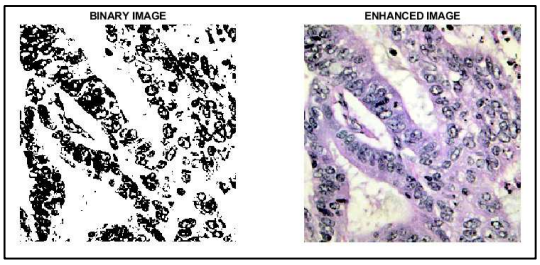

Fig.5. Binary and enhanced image

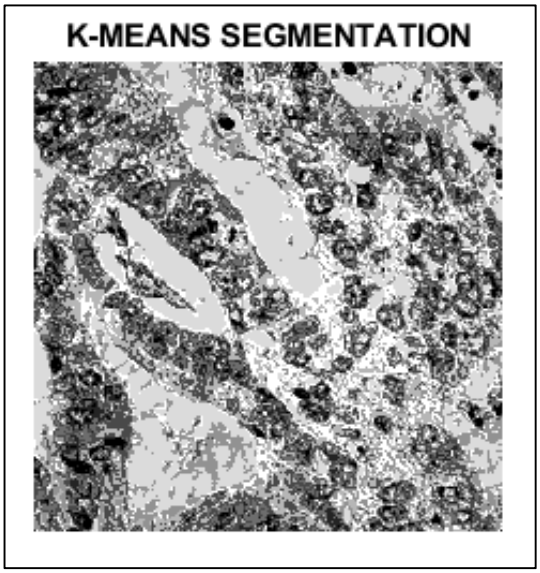

Fig.6. Segmented image

TABLE 1. EXTRACTED FEATURES

Correlation	0.020000
Contrast	0.000000
Energy	1.000000
Homogeneity	1.000000
Mean	5.125916
Standard Deviation	2.006197
Entropy	-0.000000
RMS	5.485971
Variance	3.797639
Smoothness	0.999997
Kurtosis	1.907464
Skewness	-0.255161

Fig.7. Output image

Authorized licensed use limited to: National Institute of Technology- Meghalaya. Downloaded on July 22,2025 at 02:59:57 UTC from IEEE Xplore. Restrictions apply.

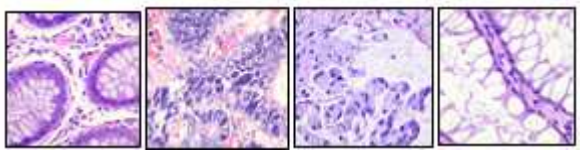

Fig. 8. Input image

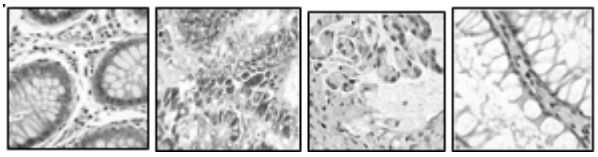

Fig. 9. Gray scale

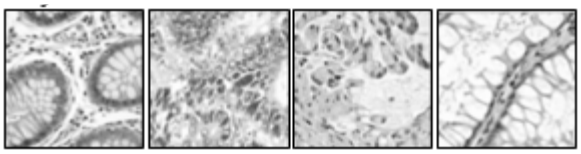

Fig. 10. Adaptive Wiener filter

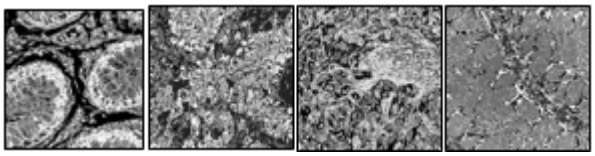

Fig. 11. Segmentation by K-means

The proposed model reduces computations considerably by using dimension reduction and parameter sharing. The fundamental idea is that knowledge from one region of a picture may be transferred to another, leading to enhanced functionality. A system can effectively classify colon cancer at an early stage by using the proposed DCNN model as shown in Fig. 8 – 12. Additionally, early discovery of colon cancerous development might significantly increase the propensity for survivors to seek treatment, especially for those without access to medical care.

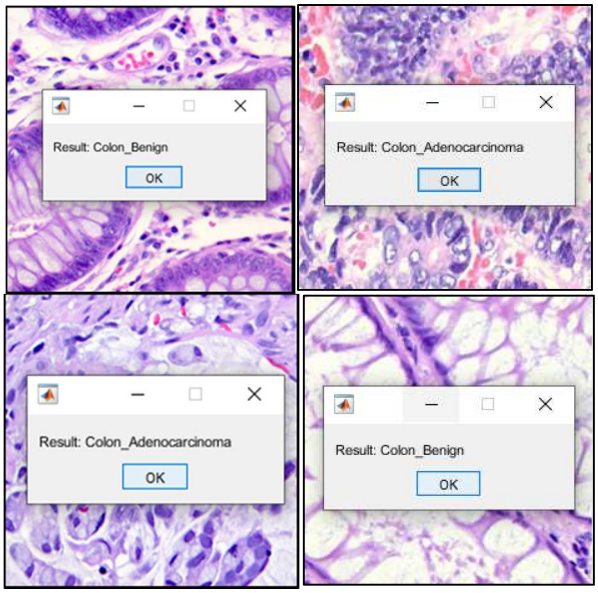

Fig. 12. Predicted output.

It is evident that the performance is uniform over all databases, supporting the assertion. Compared to all the techniques, the DCNN model may be applied to polyp classification with good results.

TABLE 2. EXTRACTED FEATURES BY GLCM

	Image1	Image 2	Image 3	Image 4
Correlation	0.020000	0.020000	0.020000	0.020000
Contrast	0.000000	0.000000	0.000000	0.000000
Energy	1.000000	1.000000	1.000000	1.000000
Homogeneity	1.000000	1.000000	1.000000	1.000000
Mean	4.305206	4.364944	4.504562	4.517715
Standard Deviation	2.426128	2.392209	2.408945	1.989019
Entropy	-0.00000	-0.00000	-0.00000	-0.00000
RMS	4.928439	4.961876	5.101058	4.932137
Variance	5.731338	5.572884	5.708437	4.932137
Smoothness	0.999996	0.999997	0.999997	0.999997
Kurtosis	1.725484	1.640055	1.577829	2.315972
Skewness	0.064024	0.072388	-0.02057	0.177099

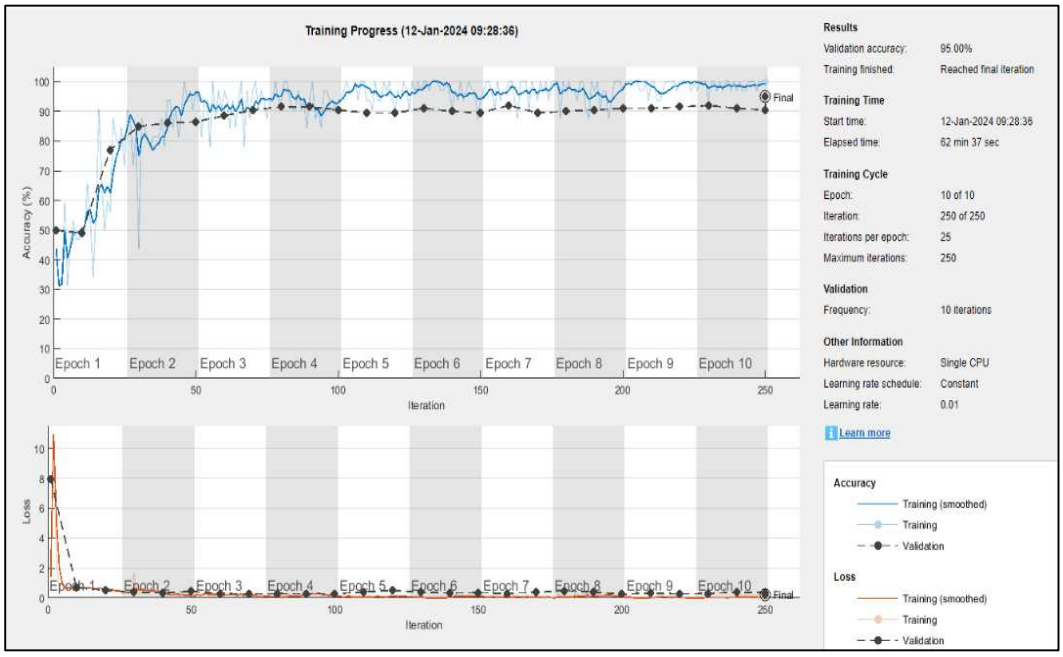

Fig. 13. Training and testing accuracy

Authorized licensed use limited to: National Institute of Technology- Meghalaya. Downloaded on July 22,2025 at 02:59:57 UTC from IEEE Xplore. Restrictions apply.

Using the train-test approach, the dataset is divided into training, validation, and test datasets. For training and validation, two thousand sample photos are utilized, and 400 unique images are used for testing every model. After every epoch, the validation loss and accuracy are assessed in accordance with early-stopping criteria, and training is terminated if the validation loss rises above a certain epoch. The training and the testing accuracy with samples is shown in Fig. 13. This method aids in preventing over-fitting.

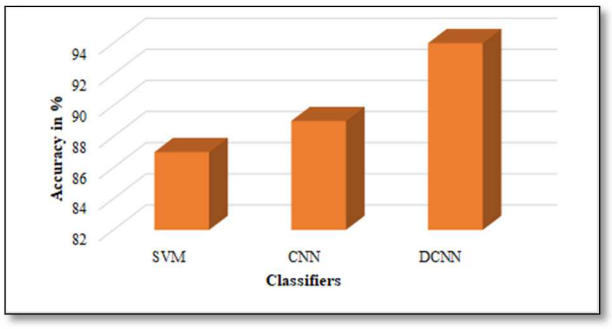

Fig.14. Accuracy Comparison

Figure 14 compares the accuracy of many classifiers, with DCNN displaying the best accuracy of 94.7%.

IV. Conclusion

The suggested DCNN model in this study replaces binary categorization in the output activating layer to enhance earlier transfer learning methods with the sigmoid function that could identify colon tissues free of cancer and colon cancer. In order to teach the DCNN architecture to produce high-resolution textured pictures without converting them into low-resolution images, a training and assessment method is suggested. The utilisation of whole-slide photography and digital image processing has made it possible to analyse colon cancer using convolutional neural networks. Proficiency in analysis requires accurate classification of colon tumours. By using a DCNN model along with an image pre-processing techniques to digital histopathology pictures using an adaptive wiener filter, the goal is to advance a system for identifying and categorising colon adenocarcinomas. In the following step, the image is routed to the areas for segmentation using K-means segmentation may be used to accurately define the illness's size and shape. GLCM is used for feature extraction and by putting this strategy into practice, doctors can create an automated and best method for identifying different types of colon cancer. Furthermore, the suggested approach was compared with previous models in terms accuracy in which it shows highest accuracy of 94.7%.

References

[1] S. Mehmood et al., "Malignancy Detection in Lung and Colon Histopathology Images Using Transfer Learning With Class Selective Image Processing," in IEEE Access, vol. 10, pp. 25657-25668, 2022.

[2] Y. Li, F. Zhang and C. Xing, "Screening of Pathogenic Genes for Colorectal Cancer and Deep Learning in the Diagnosis of Colorectal Cancer," in IEEE Access, vol. 8, pp. 114916-114929, 2020.

[3] C. T. Sari and C. Gunduz-Demir, "Unsupervised Feature Extraction via Deep Learning for Histopathological Classification of Colon Tissue Images," in IEEE Transactions on Medical Imaging, vol. 38, no. 5, pp. 1139-1149, May 2019.

[4] M. M. Fadel, N. G. Elseddeq, R. Arnous, Z. H. Ali and A. I. Eldesouky, "A Fast Accurate Deep Learning Framework for Prediction of All Cancer Types," in IEEE Access, vol. 10, pp. 122586-122600, 2022.

[5] M. Liang, Z. Ren, J. Yang, W. Feng and B. Li, "Identification of Colon Cancer Using Multi-Scale Feature Fusion Convolutional Neural Network Based on Shearlet Transform," in IEEE Access, vol. 8, pp. 208969-208977, 2020.

[6] R. Feng, X. Liu, J. Chen, D. Z. Chen, H. Gao and J. Wu, "A Deep Learning Approach for Colonoscopy Pathology WSI Analysis: Accurate Segmentation and Classification," in IEEE Journal of Biomedical and Health Informatics, vol. 25, no. 10, pp. 3700-3708, Oct. 2021.

[7] X. Yang, Q. Wei, C. Zhang, K. Zhou, L. Kong and W. Jiang, "Colon Polyp Detection and Segmentation Based on Improved MRCNN," in IEEE Transactions on Instrumentation and Measurement, vol. 70, pp. 1-10, 2021, Art no. 4501710.

[8] S. Poudel, Y. J. Kim, D. M. Vo and S. -W. Lee, "Colorectal Disease Classification Using Efficiently Scaled Dilation in Convolutional Neural Network," in IEEE Access, vol. 8, pp. 99227-99238, 2020.

[9] M. Liu, J. Jiang and Z. Wang, "Colonic Polyp Detection in Endoscopic Videos With Single Shot Detection Based Deep Convolutional Neural Network," in IEEE Access, vol. 7, pp. 75058-75066, 2019.

[10] D. Banik, K. Roy, D. Bhattacharjee, M. Nasipuri and O. Krejcar, "Polyp-Net: A Multimodel Fusion Network for Polyp Segmentation," in IEEE Transactions on Instrumentation and Measurement, vol. 70, pp. 1-12, 2021.

[11] M. Obayya, M. A. Arasi, N. Alruwais, R. Alsini, A. Mohamed and I. Yaseen, "Biomedical Image Analysis for Colon and Lung Cancer Detection Using Tuna Swarm Algorithm With Deep Learning Model," in IEEE Access, vol. 11, pp. 94705-94712, 2023.

[12] T. Thakur, I. Batra, A. Malik, D. Ghimire, S. -H. Kim and A. S. M. Sanwar Hosen, "RNN-CNN Based Cancer Prediction Model for Gene Expression," in IEEE Access, vol. 11, pp. 131024-131044, 2023.

[13] Z. Qian et al., "A New Approach to Polyp Detection by Pre-Processing of Images and Enhanced Faster R-CNN," in IEEE Sensors Journal, vol. 21, no. 10, pp. 11374-11381, 15 May15, 2021.

[14] K. Sirinukunwattana, S. E. A. Raza, Y. -W. Tsang, D. R. J. Snead, I. A. Cree and N. M. Rajpoot, "Locality Sensitive Deep Learning for Detection and Classification of Nuclei in Routine Colon Cancer Histology Images," in IEEE Transactions on Medical Imaging, vol. 35, no. 5, pp. 1196-1206, May 2016.

[15] H. A. Qadir, I. Balasingham, J. Solhusvik, J. Bergsland, L. Aabakken and Y. Shin, "Improving Automatic Polyp Detection Using CNN by Exploiting Temporal Dependency in Colonoscopy Video," in IEEE Journal of Biomedical and Health Informatics, vol. 24, no. 1, pp. 180-193, Jan. 2020.

Authorized licensed use limited to: National Institute of Technology- Meghalaya. Downloaded on July 22,2025 at 02:59:57 UTC from IEEE Xplore. Restrictions apply.