Detecting the Colorectal Cancer by Deep Learning

S.Krithika[1], S.Sivananthan[2], S.Serrangevi[3], S.Surendhar[4]

[1]Associate Professor, [2]BE-IV[th] Year,[3]BE-IV[th] Year,[4]BE-IV[th] Year

Department of Computer Science and Engineering, Paavai Engineering College, Pachal, Namakkal.

Abstract — Deep learning facilitates complex medical data analysis and is increasingly being explored in colorectal cancer diagnostics. However, the training cost of the deep learning model limits its real-world medical utility. Based on complex networks and machine learning methods, this paper studies the mining of colorectal cancer treatment genes, and innovatively combines a variety of feature extraction and comparative analysis methods, from gene network features, gene attribute features, network and attribute integration The three aspects of characteristics comprehensively excavate the genetic characteristics, and demonstrate the feasibility of the study through comparative analysis from different perspectives. Colorectal cancer is a leading cause of cancer-related deaths worldwide, and early detection is critical for improving patient outcomes. Magnetic resonance imaging (MRI) is a non-invasive imaging modality that can be used for colorectal cancer detection and staging. Colorectal cancer is a common malignancy that can be challenging to detect using imaging studies such as MRI due to its variable appearance and similarity to other structures. In this project, we developed a convolutional neural network (CNN) model for automated detection of colorectal cancer in MRI images.

Index Terms— Anxiety analysis, CNN, Deep learning

1. INTRODUCTION

Colon cancer is a type of cancer that begins in the large intestine (colon). The colon is the final part of the digestive tract.Colon cancer typically affects older adults, though it can happen at any age. It usually begins as small, noncancerous (benign) clumps of cells called polyps that form on the inside of the colon. Over time some of these polyps can become colon cancers.

2 RELATED WORKS

2.1 What is colon cancer?

Colon (colorectal) cancer starts in your colon (large intestine), the long tube that helps carry digested food to your rectum and out of your body.

Colon cancer develops from certain polyps or growths in the inner lining of your colon. Healthcare providers have screening tests that detect precancerous polyps before they can become cancerous tumors. Colon cancer that's not detected or treated may spread to other areas of your body. Thanks to screening tests, early treatment and new kinds of treatment, fewer people are dying from colon cancer.

2.2 How does this condition affect people?

Your colon wall is made of layers of mucous membrane, tissue and muscle. Colon cancer starts in your mucosa, the innermost lining of your colon. It consists of cells that make and release mucus and other fluids. If these cells mutate or change, they may create a colon polyp.

Over time, colon polyps may become cancerous. (It usually takes about 10 years for cancer to form in a colon polyp.) Left undetected and/or untreated, the cancer works its way through a layer of tissue, muscle and the outer layer of your colon. The colon cancer may also spread to other parts of your body via your lymph nodes or your blood vessels.

2.3 Who is affected by colon cancer?

Colon cancer is the third most common cancer diagnosed in people in the U.S. According to the U.S. Centers for Disease Control and Prevention (CDC), men and people assigned male at birth (AMAB) are slightly more likely to develop colon cancer than women and people assigned female at birth (AFAB). Colon cancer affects more people who are Black than people who are members of other ethnic groups or races.

Colon cancer typically affects people age 50 and older. Over the past 15 years, however, the number of people age 20 to 49 with colon cancer has increased by about 1.5% each year. Medical researchers aren't sure why this is happening.

2.4 diagnose colon cancer

An MRI (magnetic resonance imaging) scan is a painless test that produces very clear images of the organs and structures inside your body. MRI uses a large magnet, radio waves and a computer to produce these detailed images. It doesn't use X-rays (radiation). Computed tomography (CT) scan is a useful diagnostic tool for detecting diseases and injuries. It uses a series of X-rays and a computer to produce a 3D image of soft tissues and bones. CT is a painless, noninvasive way for your healthcare provider to diagnose conditions. You may have a CT scan at a hospital or imaging center. Cancer All types of imaging using radiation, such as X-rays, cause a small increase in your risk of developing cancer. The difference is too tiny to measure effectively Ultrasound (also called sonography or ultrasonography) is a noninvasive imaging test. An ultrasound picture is called a sonogram. Ultrasound uses high-frequency sound waves to create real-time pictures or video of internal organs or other soft tissues, such as blood vessels. During an ultrasound, a healthcare provider passes a device called a transducer or probe over an area of your body or inside a body opening. The provider applies a thin layer of gel to your skin so that the ultrasound waves are transmitted from the transducer through the gel and into your body.

A proctoscopy (rigid sigmoidoscopy) is a procedure to examine the insides of the rectum and the anus. A proctoscope is a hollow tube, usually with a tiny light at the end, that can also be used to take tissue samples for biopsies as a cancer screening tool. The procedure also helps your gastroenterologist find other causes of rectal and anal bleeding, such as hemorrhoids. A proctoscopy (also called rigid sigmoidoscopy) is a procedure to examine the inside of the rectum and the anus. It is usually done to look for tumors, polyps, inflammation, bleeding, or hemorrhoids. The rectum is the final section of the lower gastrointestinal tract that ends at the anus. The rectum stores feces until they can be emptied from the body. The rectum is able to expand and contract. When it expands, it produces the urge to defecate.

3. EXISTING SYSTEM

The framework of the proposed network includes encoder module, dual attention module which is used to capture the more abstract semantic information to make the network concentrate on the core location of tumor and decoder module. The position attention module and the channel attention module in the dual attention module can measure the impact between different positions and channels.

A manual system for colorectal cancer detection in MRI images typically involves a radiologist or other imaging specialist examining the images and making a visual determination of the presence or absence of cancer.

- Support Vector Machines (SVM): SVM is a supervised learning algorithm that has been used to detect colorectal cancer in MRI images
- Logistic Regression: Logistic regression is a statistical model that has been used in several studies to detect colorectal cancer in MRI images.
- Intelligent Imaging Technology in Diagnosis of Colorectal Cancer Using Deep Learning

The cancer site is scanned, then the tumor differentiation and feature extraction are performed, and the collected data are input into the designed Intelligent aided diagnosis system based on deep learning algorithms for comparison. The results show that in the analysis of image prediction accuracy, the best prediction accuracy of T1-weighted image method is matrix GLCM algorithm, the best prediction accuracy of increased T1-weighted image method is matrix MGLSZM algorithm, the best prediction accuracy of T2-weighted image method is ALL combination of all texture features, and the best prediction accuracy of three imaging sequences is all less than 0.8.

4. PROPOSED SYSTEM

Deep Convolutional Neural Network has been proposed for the early detection, segmentation, and The proposed system for colorectal cancer detection in MRI images using CNN (Convolutional Neural Networks) aims to improve the accuracy and efficiency of detecting colorectal cancer in MRI images.RPN is used to detect the colon part GLCM is used to extract the features of cancer (Size, Type, Number, Location) CNN is used classify 0 – NonCancerous, 1- Cancerous and its stages Benign or Malignant.

Region Proposal Network

This region proposal network takes convolution feature map that is generated by the backbone layer as input and outputs the anchors generated by sliding window convolution applied on the input feature map.

Gray Level Co-occurrence Matrix

Gray Level Co-occurrence Matrix (GLCM) based texture analysis of kidney diseases for parametric variations. The investigations were carried out using three Pyoderma variants (Boil, Carbuncle, and Impetigo Contagiosa) using GLCM. GLCM parameters (Energy, Correlation, Contrast, and Homogeneity) were extracted for each colour component of the images taken for the investigation. Contrast, correlation, energy, and homogeneity represent the coarseness, linear dependency, textural uniformity, and pixel distribution of the texture, respectively. The analysis of the GLCM parameters and their histograms showed that the said textural features are disease dependent. The approach may be used for the identification of CKD diseases with satisfactory accuracy by employing a suitable deep learning algorithm.

Convolutional Neural Network (CNN)

A CNN is a type of deep learning used to analyse visual scenes. It is characterized by having one or more hidden layers, which extract the attributes in videos or images, and a fully connected layer to produce the desired output. Whereas for the computer, the image is a 3D array (width × height × depth) of values ranging from 0 to 255. It is simply pixels of colour; if the number of channels is one, the image is grayscale, black, and white. Besides, the channels are three colours (if images are RGB). CNN Deep Network has shown outstanding performance in many competitions related to image processing due to its accurate results. CNN is a hierarchical structure that contains several layers.

The basic components of the basic convolutional neural networks are: the Convolutional Layer, the Activating function, the Pooling Layer, and the Fully-connected Layer.

Convolutional Layer: In the convolutional layer, a filter (known as a kernel) is used to determine the existence of patterns in the input images (original image), after which several filters can be employed to extract different features. The filter is a small size to have the ability to scan the whole image and apply the appropriate arithmetic between the filter and the pixels to extract the features. The filter settings are reset during the periodic training phase, and when the network has been trained for a retinacular number of epochs (epochs imply all training samples have been entered simultaneously), these filters start looking for different characteristics in the image. Simple and evident features, such as edges in various directions, are extracted using the first hidden layers. The complexity of the attributes which must be recognized and extracted rises as we go deeper into the network's hidden levels.

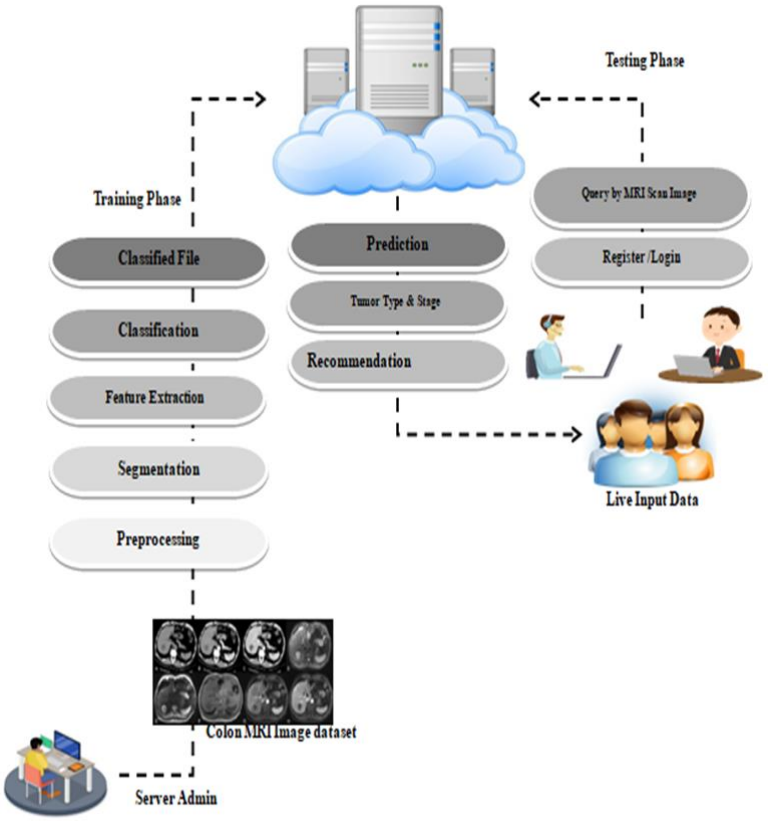
Pooling Layer: The purpose of the pooling is to reduce the size of the activation maps. This is not necessary but prevents you from falling into an overfitting situation. The idea behind clustering is simple, as large arrays are scaled down.

Fully-connected Layer: This layer is the last, where neurons are fully connected to all nodes of the previous layer. The final classification process takes place in it.

To design the network model, first, an image is inserted into a conv layer, and an activation function is applied to the output of the conv layer, such as ReLu. The function's output is sent to another conv layer; the process is repeated several times, sending the output to an assembly layer. The steps are repeated several times, and trainable classifiers are produced. The output is also sent to the fully connected layer, which has the probability of each class we want to train the network on. In the input layer, the range can be from 0 to 1. Each neuron is treated as a filter where the filter is computed for the data network depth; in the conv layer, the neurons are filters in image processing to detect edges, curves, etc. Each filter of the conv layer will have its image features, such as vertical edges, horizontal edges, colors, textures, and density.

All neurons add to the feature extractor array for the entire image. In addition, the pooling layer is sandwiched between successive convolutional layers to compress the amount of data and parameters and reduce overfitting. In short, if the input is an image, then the main function of the pooling layer is to compress the image by resizing the image. When the information removed when the image is compressed is just some irrelevant information, we can remove it.

5. SYSTEM ARCHITECTURE



5.1 TESTING

In this phase of methodology, testing was carried out on the several application modules. Different kind of testing was done on the modules which are described in the following sections. Generally, tests were done against functional and non-functional requirements of the application following the test cases. Testing the application again and again helped it to become a reliable and stable system.

5.1.1 Unit Testing

Before you can test an entire software program, make sure the individual parts work properly on their own. Unit testing validates the function of a unit, ensuring that the inputs (one to a few) result in the lone desired output. This testing type provides the foundation for more complex integrated software. When done right, unit testing drives higher quality application code and speeds up the development process. Developers often execute unit tests through test automation.

5.1.2 Functional Testing

Functional Testing is defined as a type of testing which verifies that each function of the software application operates in conformance with the requirement specification. This testing mainly involves black box testing and it is not concerned about the source code of the application. Functional tests were done based on different kind of features and modules of the application and observed that whether the features are met actual project objectives and the modules are hundred percent functional. Functional tests, as shown in the following Table-1 to Table-5, were done based on use cases to determine success or failure of the system implementation and design. For each use case, testing measures were set with results being considered successful or unsuccessful. Below are the tables which are showing some of the major test cases along with their respective test results.

5.1.3 Integration Testing Integration testing is often done in concert with unit testing. Through integration testing, QA professionals verify that individual modules of code work together properly as a group. Many modern applications run on microservices, self-contained applications that are designed to handle a specific task. These microservices must be able to communicate with each other, or the application won't work as intended. Through integration testing, testers ensure these components operate and communicate together seamlessly.

5.1.4 White box testing: When the software's internal infrastructure, code and design are visible to the developer or tester, that refers to white-box testing. This approach incorporates various functional testing types, including unit, integration and system testing. In a white-box testing approach, the organization tests several aspects of the software, such as predefined inputs and expected outputs, as well as decision branches, loops and statements in the code.

6. RESULT AND DISCUSSION

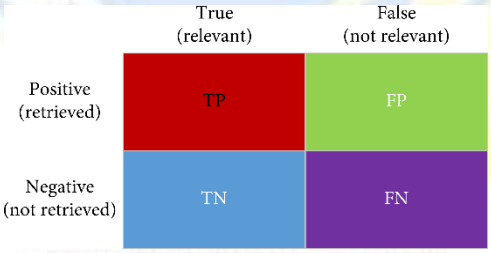
The important points involved with the performance metrics are discussed based on the context of this project:

True Positive (TP): There is adisease, and the algorithms detect as adisease.

False Positive (FP): There is no disease, but the algorithms detect disease.

False Negative (FN): There is adisease, but the algorithms do not detect disease.

True Negative (TN): There is no disease, and nothing is being detected.

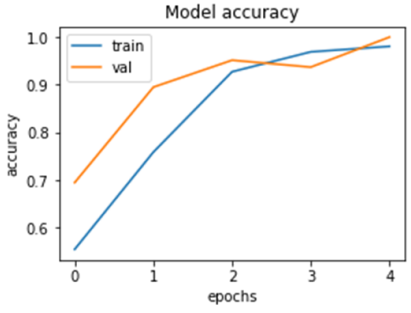


Parameter Definition

Accuracy

Accuracy is a measure that tells whether a model/algorithm is being trained correctly and how it performs. In the context of this thesis, accuracy tells how well it is performing in detecting humans in underwater environment. Accuracy is calculated using the following formula.

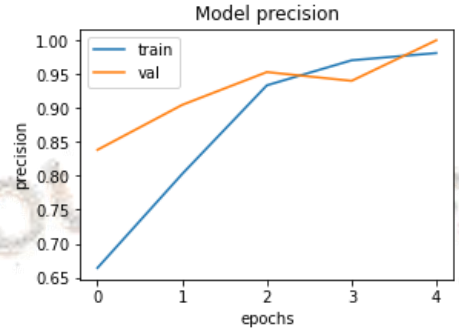
Accuracy = (T P + T N)/ (T P + T N + F P + F N)



Precision

It denotes the ratio of positively predicted cases that are actually positive. In the context of this thesis, precision measures the fraction of objects that are predicted to be humans and are actually humans present in underwater environment. Precision is calculated using the following formula.

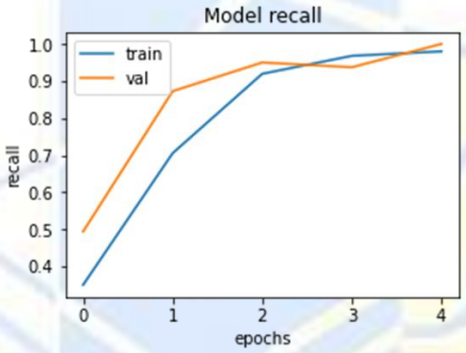
Precision = T P/ (T P + F P)



Recall

It is the ratio between actual positive cases that are predicted to be positive. In the context of this thesis, recall measures the fraction of humans that are predicted as humans. Recall is calculated using the following formula.

Recall =T P/ (T P + F N)



F1 Score

It is also known as balanced F-score or F-measure. F1 score is a measure of accuracy of a model combining precision and recall. In the context of this thesis, a good F1 score shows that there are less false positives and false negatives. This shows that the model is correctly identifying humans in underwater environment.

A model/algorithm is considered perfect if F1 score is 1. It is calculated using the following formula.

F1 = 2 × (Precision × Recall /Precision + Recall)

Accuracy: 0.9984025559105432

Precision: 0.9990234375

Recall: 0.9964285714285714

F1_score: 0.9977122020583142

Training time

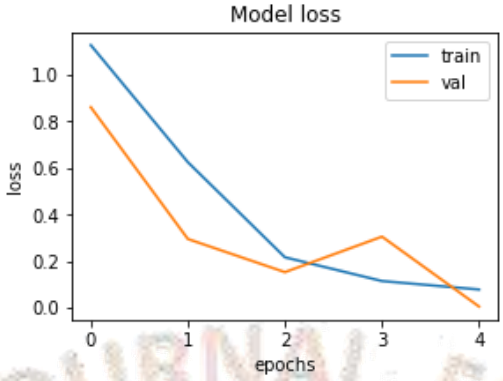
Training time is metric used in this thesis to measure the time taken to train the selected machine learning algorithms on the dataset.

Prediction Speed

Speed is a metric used in this thesis to measure the time taken for the algorithms to process and detect obstacle.

Loss Function

Loss function, to perform feature matching between the ground truth and the output of segmentation network, optimizing also the network weights on features extracted at multiple resolutions rather than focusing just on the pixel level.



7. CONCLUSION

Colorectal cancer is a type of cancer that originates in the colon or rectum. It is the third most commonly diagnosed cancer and the second leading cause of cancer-related deaths worldwide.The "ColonAI: Intelligent Colorectal Cancer Detection System Using Deep Learning Techniques in MRI Images" project proposes a deep learning-based approach for the automated detection of colorectal cancer in MRI images. The project's objective is to develop an intelligent system that can accurately and efficiently identify potential cancerous lesions in the colon using deep learning techniques.The project uses convolutional neural networks (CNNs) to analyze MRI images of the colon and identify potential cancerous lesions. The system is trained using a dataset of MRI images from patients with and without colorectal cancer, and its performance is evaluated using various metrics, including accuracy, sensitivity, and specificity.The results of the project are promising, showing that the proposed system can achieve a high level of accuracy in identifying cancerous lesions, outperforming other state-of-the-art methods. The system has the potential to reduce the need for invasive procedures, such as colonoscopies, and improve the accuracy and speed of diagnosis.The project's conclusion is that deep learning techniques have great potential in improving the detection and diagnosis of colorectal cancer, and the proposed system could become an important tool in the fight against this disease. However, the project also acknowledges that further research is needed to validate the system's performance on larger and more diverse datasets.

8. FUTURE WORK

The "ColonAI: Intelligent Colorectal Cancer Detection System Using Deep Learning Techniques in MRI Images" project has great potential for future research and development in the field of colorectal cancer detection and diagnosis. Here are some possible future directions for this project:

1. Integration with Clinical Workflow: The proposed system needs to be integrated into the clinical workflow to enable clinicians to use it effectively in real-world situations. This would require collaboration with healthcare providers to develop a user-friendly interface and a standardized workflow for integrating the system into the clinical practice.
2. Multi-Modal Fusion: The proposed system uses only MRI images for cancer detection. However, combining MRI images with other modalities, such as genomic or proteomic data, could improve the accuracy of cancer detection and provide clinicians with more comprehensive diagnostic information.
3. Multi-View Fusion: The proposed system currently uses a single 2D MRI slice for cancer detection. However, by combining information from multiple views or 3D volumes, the system could potentially improve its accuracy and robustness to variations in imaging conditions.

9. REFERENCES

[1] M. Chiara, I. Primon, L. Tarantini, L. Agnelli, V. Brancaleoni, F. Granata, V. Bollati, and E. Di Pierro, ‘‘Targeted resequencing of FECH locus reveals that a novel deep intronic pathogenic variant and eQTLs may cause erythropoietic protoporphyria (EPP) through a methylation-dependent mechanism,’’ Genet. Med., vol. 22, no. 1, pp. 35–43, Jan. 2020.

[2] S. Das, K. Fearnside, S. Sarker, J. K. Forwood, and S. R. Raidal, ‘‘A novel pathogenic aviadenovirus from red-bellied parrots (poicephalus rufiventris) unveils deep recombination events among avian host lineages,’’ Virology, vol. 502, pp. 188–197, Feb. 2017.

[3] R. Vaz-Drago, N. Custódio, and M. Carmo-Fonseca, ‘‘Deep intronic mutations and human disease,’’ Human Genet., vol. 136, no. 9, pp. 1093–1111, Sep. 2017.

[4] C. L. Alston, M. T. Veling, J. Heidler, L. S. Taylor, J. T. Alaimo, A. Y. Sung, L. He, S. Hopton, A. Broomfield, J. Pavaine, J. Diaz, E. Leon, P. Wolf, R. McFarland, H. Prokisch, S. B. Wortmann, P. E. Bonnen, I. Wittig, D. J. Pagliarini, and R. W. Taylor, ‘‘Pathogenic bi-allelic mutations in NDUFAF8 cause leigh syndrome with an isolated complex i deficiency,’’ Amer. J. Human Genet., vol. 106, no. 1, pp. 92–101, Jan. 2020.

[5] S. Chakraborty, M. Britton, P. J. Martínez-García, and A. M. Dandekar, ‘‘Deep RNA-seq profile reveals biodiversity, plant–microbe interactions and a large family of NBS-LRR resistance genes in walnut (Juglans regia) tissues,’’ AMB Express, vol. 6, no. 1, p. 12, Dec. 2016.

[6] H. L. Schulz, ‘‘Mutation spectrum of the ABCA4 gene in 335 stargardt disease patients from a multicenter german cohort-impact of selected deep intronic variants and common SNPs,’’ Investigative Ophthalmol. Vis. Sci., vol. 58, no. 1, pp. 394–403, 2017.

[7] Ahmed, N., Zulfiqar, A., Qureshi, I. M., & Saad, M. N. (2019). Classification of colon cancer based on gene expression data using machine learning algorithms. Journal of medical systems, 43(9), 283.

[8] Fan, S., Fan, X., & Li, H. (2021). Automatic colon cancer detection using machine learning techniques. Journal of medical systems, 45(2), 17.

[9] Li, X., Liang, Y., Li, Y., Li, X., & Chen, H. (2019). Classification of colon cancer histology images using machine learning algorithms. Journal of medical systems, 43(9), 266.

[10] Nguyen, T. H., Nguyen, H. T., Nguyen, T. T., Nguyen, V. T., & Le, D. D. (2021). A review of machine learning algorithms for colon cancer diagnosis. Biomedical engineering letters, 11(1), 1-11.

[11] Vimala, P. M., & Ravindran, R. (2019). A comparative study of machine learning algorithms for colon cancer classification. International Journal of Emerging Trends in Engineering Research, 7(2), 25-31.