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Artificial Intelligence Driven Colorectal Cancer Classification Via Deep Learning Technique

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Abstract: **Collateral cancer is a serious concern for patients with primary tumors, as the development of secondary tumors can significantly reduce survival rates and increase the complexity of treatment. Colon polyps are a common precursor to colorectal cancer, and early detection is essential for effective treatment. Traditional strategies for polyp detection include colonoscopy and biopsy, which can be invasive and time-consuming. In this work, we explore the use of convolutional neural networks (CNNs) to detect polyps in colonoscopy images, as machine learning methods have shown potential in this area. Improving patient outcomes requires early detection and prevention of collateral cancer. However, precisely predicting the probability of recurrent tumors can be challenging due to the complexity of cancer progression and the multiplicity of factors that may influence tumor formation. In this study, we examine the use of a CNN to forecast the likelihood that patients with primary tumors may develop collateral cancer. Machine learning algorithms have demonstrated potential in predicting cancer outcomes based on patient data. The study uses a dataset of colonoscopy images, including both positive and negative cases of polyps. A CNN model is developed using this dataset to classify images as either positive or negative for polyps. The model is trained using a supervised learning approach, where the network learns from labeled examples of images with and without polyps. The accuracy of the CNN model is compared to other polyp detection strategies, such as traditional image analysis techniques and other machine learning algorithms.**

Keywords: Colorectal Cancer, Medical Imaging, Machine Learning, Deep Learning, Neural Networks.

1. INTRODUCTION

Colorectal cancer (CRC) accounts for approximately 10% of all cancer cases worldwide, making it the third most common type of cancer after lung and breast cancers, according to the American Institute for Cancer Research [1]. Additionally, 9% of all cancer-related deaths are attributed to CRC. In the USA, the five-year survival rate for early-stage CRC (regionalized stage) can reach up to 70%, highlighting the importance of early and accurate detection. Globally, CRC ranks third in terms of cancer diagnoses and is the second leading cause of cancer-related deaths. CRC originates in the colon or rectum and is often associated with the formation of abnormal cells, which frequently begin as benign polyps but can develop into malignant tumors [2]. Early detection of CRC is crucial for improving survival rates, as localized tumors are often treatable. However, detecting CRC in its early stages remains challenging, particularly with traditional methods such as colonoscopies, biopsies, and histopathological analysis. These techniques are time-intensive and heavily reliant on the expertise of medical professionals. A comprehensive visual analysis of digital images is often required to detect CRC. With the advent of targeted therapies, many treatments now depend on molecular research, necessitating the sequencing of cancer tissue samples from paraffin blocks. Automated solutions have the potential to reduce the workload for pathologists by serving as screening tools and minimizing subjectivity in diagnosis [3]. Pathologists typically identify the stage of cancer by analyzing the quantity and size of tumors in

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relevant sections of digital images. However, this process is highly tedious and prone to errors, as tumor cells are often minute and easily overlooked. In many cases, identifying tumor cells requires significantly enlarging the images, further complicating the task. Colorectal cancer, sometimes referred to as "bowel cancer," poses a global threat to human life. A depiction of this is described in Figure 1.

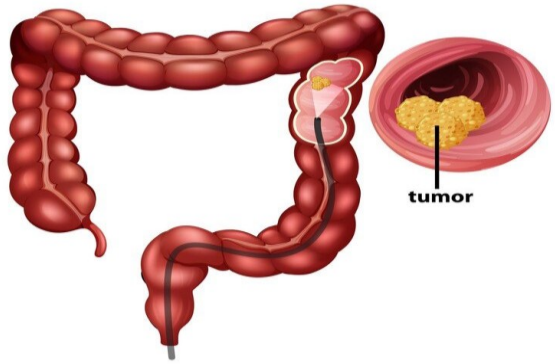

Fig. 1. Colarectal cancer (Refer: https://www.nanavatimaxhospital.org/blogs/advanced-treatment-measures-for-colorectal-cancer)

2. RELATED WORKS

Zi-Ning Lei et al. [1] proposed a system to examine the mechanism of collateral sensitivity (CS) in ABCB1-positive, multidrug-resistant (MDR) colorectal cancer cells using the survival inhibitor MX106–4C. ABCB1-positive colorectal cancer cells were entirely eradicated by MX106–4C, an effect that could be reversed through the use of an ABCB1 inhibitor, ABCB1 deletion, or loss-of-function mutations in ABCB1. This suggests an ABCB1 expression- and function-specific mechanism. The selective toxicity of MX106–4C was linked to cell cycle arrest and apoptosis via ABCB1-mediated survival inhibition and activation of the caspase-3/7 and p21-CDK4/6-pRb pathways. MX106–4C demonstrated high selectivity against colorectal cancer cells in multicellular tumor spheroids positive for ABCB1. Moreover, MX106–4C could desensitize ABCB1-positive cancer cells to doxorubicin or synergize with it to generate enhanced anticancer effects by reducing ABCB1 expression through prolonged exposure. Through a novel ABCB1-based survival inhibitory mechanism, MX106–4C selectively targets ABCB1-positive MDR colorectal cancer cells, offering a promising lead for developing CS drugs to combat ABCB1-mediated colorectal cancer resistance. The cytotoxic effects of MX106–4C may be attributed to its ABCB1-mediated inhibition of survival pathways, resulting in G0/G1 cell cycle arrest and apoptosis by modulating the p21-CDK4/6-pRb phosphorylation pathway and activating caspase-3/7. MX106–4C, a CS agent with strong selectivity for ABCB1-positive colorectal cancer cells compared to normal cells, shows potential as a treatment for colorectal cancer by desensitizing ABCB1-overexpressing cells to chemotherapeutic agents or acting synergistically with doxorubicin. Marcello Maida et al. [2] presented a comprehensive analysis of colorectal cancer (CRC) screening techniques, evaluating their efficacy, cost-effectiveness, and performance. The study identifies screening target populations and emphasizes the importance of personalized care for high-risk patients. Significant advancements in CRC screening have improved survival rates, but further improvements are needed. Health policies should focus on primary prevention by modifying behavioral risk factors in asymptomatic high-risk individuals and improving secondary prevention through enhanced understanding of risk factors and screening test performance. Future research is required to refine risk profiles for CRC and explore potential new target populations for screening programs, including those with comorbidities such as diabetes, thyroid disease, and metabolic syndrome. Athanasios G. Papavassiliou et al. [3] summarized innovative therapeutic strategies for colorectal cancer. The initiation, progression, and chemoresistance of CRC are attributed to mutations in multiple signaling pathways, notably the phosphoinositide 3-kinase (PI3K)/AKT/mTOR axis. While the efficacy of PI3K inhibitors in CRC is mixed, some studies have shown promising results, such as the use of the class I PI3K inhibitor pictilisib in slowing mucinous colorectal adenocarcinoma progression. However, resistance to these drugs limits their effectiveness as monotherapies. Cancer stem cells (CSCs) play a critical role in treatment resistance, tumor growth, and metastasis, underscoring the need for targeted therapies addressing these pathways.

D. Corrales et al. [4] developed a Bayesian network prediction model to characterize CRC risk groups and evaluate the impact of various risk factors. By integrating observational data and expert knowledge, the model uses structure learning techniques and local probability distributions to predict CRC risk and associated uncertainties. The network identifies key modifiable risk factors, such as alcohol and smoking, and non-modifiable factors, including age, genetics, and comorbidities like diabetes and hypertension. This approach helps design targeted screening and prevention programs tailored to high-risk populations.

Mustafa Gökhan Vural et al. [5] explored mechano-sensitive microRNAs (mechano-miRs) as potential

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prognostic biomarkers for collateral circulation in chronic total occlusion (CTO) patients. The study investigated the role of mechano-miRs in vascular collateralization and endothelial responses to mechanical stress, highlighting their potential as therapeutic targets. Larger cohort studies are needed to validate these findings for clinical application. Maxwell T. White et al. [6] reviewed research on the role of gut microbiota in CRC development and progression. They examined global disruptions in microbiota, correlations with CRC, and the mechanisms underlying microbial contributions to CRC pathogenesis. Current diagnostic methods, including colonoscopy and fecal tests, have limitations in detecting early-stage CRC. Emerging serum genetic tests may reduce diagnostic gaps. However, these methods are predominantly used for patients over 45 years old, while the incidence of CRC is increasing in younger populations, necessitating age-specific screening strategies.

Philip D. Dunne et al. [7] proposed updates to the molecular pathological classification of CRC, focusing on intra- and inter-tumor heterogeneity. Recent transcriptional analyses have highlighted the role of the tumor microenvironment (TME) in prognosis and led to the identification of CRC intrinsic subtypes (CRIS). Advances in digital pathology and immunohistochemistry are enhancing the understanding of transcriptional signals and improving classification methods. Further transcriptomic analyses are needed to refine CRC subtype classification and guide personalized treatment strategies. Laura Andersen et al. [8] conducted a study involving 747 individuals with stage I–III CRC, assessing clinical data, ctDNA measurements, and tumor RNA sequencing. Tumor size and proliferative capacity were identified as key factors influencing ctDNA shedding, with subtype-specific differences observed. Insights from this study provide a better understanding of ctDNA biology and its potential as a diagnostic and monitoring tool across CRC subtypes. Gholamreza Roshandel et al. [9] emphasized the importance of CRC prevention through primary and secondary prophylaxis. Randomized controlled trials are needed to evaluate the impact of protective factors, such as aspirin use and physical activity, and to identify modifiable risk factors like smoking, alcohol, and diet. Screening programs should consider patient preferences, accessibility, and cost-effectiveness to optimize early detection and prevention efforts. William H. Gmeiner et al. [10] highlighted the role of biomarker-based classification in targeting mutational patterns for precision medicine in metastatic colorectal cancer (mCRC). Advances in targeting RAS/RAF/MAPK pathways, along with anti-RAS/RAF therapies, have improved survival rates in specific mCRC subtypes. Future research should focus on integrating these advancements with emerging next-generation sequencing technologies to identify novel therapeutic targets and improve patient outcomes.

3. EXISTING WORK

Recent studies utilizing deep learning (DL) models to identify colorectal polyps have demonstrated promising performance with large datasets. However, the effectiveness of these models for detecting nonpolypoid lesions remains uncertain. This is clinically significant, as nonpolypoid lesion identification is typically a straightforward task for an endoscopist, and the goal of the developed AI system is to accurately detect these lesions. Moreover, a user-independent AI system that minimizes missed lesions and achieves higher sensitivity and specificity would be highly beneficial in clinical trials. Such a system could offer two key advantages: reducing inter-server variability and enhancing reliability.

To achieve this, there is a pressing need to develop or curate large, high-quality, and diverse clinical imaging datasets that encompass various stages of colorectal disease, complete with expert annotations. Additionally, techniques such as semi-supervised learning or active learning could be explored to address the challenges posed by smaller labeled datasets. The DL techniques discussed in the following sections can be applied to colon screening and diagnostic tasks using various image formats. These methods were originally developed with specific objectives in mind. Figure 2 outlines the approaches used for colon detection.

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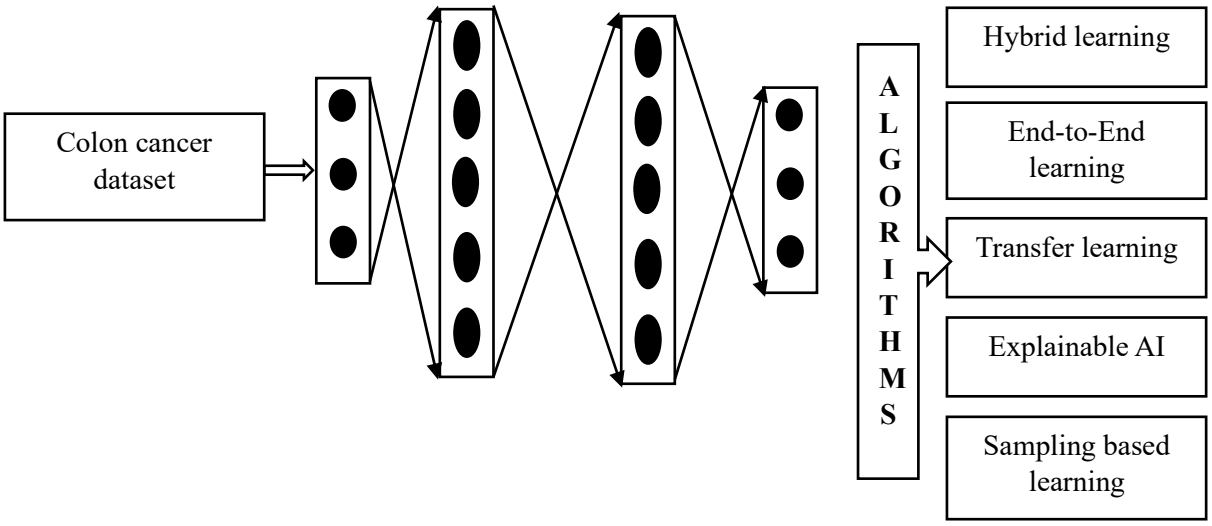

Fig. 2. COLON DETECTION USING ADVANCED APPROACHES

4. PROPOSED FRAMEWORK

A proposed system for colon cancer detection using the Convolutional Neural Network (CNN) algorithm involves training a neural network on a dataset of colon cancer patients to identify patterns indicative of cancer. The neural network would be trained using scan image data to recognize these patterns. CNN is a computational technique that mimics the brain's problem-solving mechanism by using large clusters of artificial neurons interconnected through simulated axons [19][20]. Neural networks achieve this through numerous interconnected neural units. These connections may either enhance (excitatory) or inhibit (inhibitory) the activity of associated neural units. The network employs a summing mechanism that aggregates input values from each neural unit. A limiting or threshold function determines whether the signal surpasses a specified threshold, enabling it to propagate to other neurons. CNN systems are well-suited for domains where feature detection or solution formulation is challenging to explicitly encode in conventional computer programs, as they are self-learning and trainable rather than hard-coded. A neural network is composed of interconnected neurons through links, forming either a single-layered or multi-layered network. A multilayer CNN typically consists of three layers: an input layer, an output layer, and one or more hidden layers. Hidden layers perform intermediate computations before mapping inputs to the output layer. When designing a CNN model for a specific application, the model is trained using inputs and corresponding targets until it learns to associate a given input with its desired output. During training, the network adjusts its weights iteratively until weight changes reach a minimal value.

Model validation ensures the trained model generates accurate results. Multi-layered networks are effective because they possess a large number of adjustable synaptic weights, allowing them to memorize and generalize patterns. Neurons in the output layer may use a threshold function to qualify their outputs. Although artificial neurons differ from biological ones, they are modeled as nodes connected by weighted edges in a directed graph.

The process of building a CNN model involves five sequential steps:

- Collection of input and output data: Collect data for supervised learning.
- Normalization: Normalize input and output data to ensure consistent scaling.
- Training: Train the normalized data using neural network learning algorithms.
- Validation: Test the model's accuracy to ensure a good fit.
- Comparison: Compare the predicted outputs with the expected outcomes.

A layered feedforward neural network comprises layers of processing units. Each layer performs independent computations on the input it receives and passes the results to the subsequent layer. Successive layers execute their computations and relay outputs further until the network produces a final result.

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The first layer in a CNN is the input layer, which processes raw data. The last layer is the output layer, which produces the final predictions. Layers between the input and output are called hidden layers, where intermediate computations occur. The processing units in these layers, often called artificial neurons, nodes, or cells, function analogously to neurons in the human brain.

This concept serves as the backbone of a CNN's learning process.

Steps in a neural network algorithm:

Step-1 Random initialization: Initialize the weights and biases randomly.

Step-2 Input data: Feed the training data into the network.

Step-3 Forward propagation: Pass the inputs through the network, calculating the net input and output for each unit in the hidden and output layers.

Step-4 Error backpropagation: Backpropagate the error from the output layer to the hidden layer.

Step-5 Weight and bias updates: Adjust the weights and biases using mathematical processes known as training and learning functions to reflect the propagated errors.

Step-6 Termination: Conclude the process when a predefined stopping criterion is met, such as minimal error or maximum iterations.

Neural network techniques outperform conventional machine learning algorithms due to these principles.

The proposed framework is illustrated in Fig. 3.

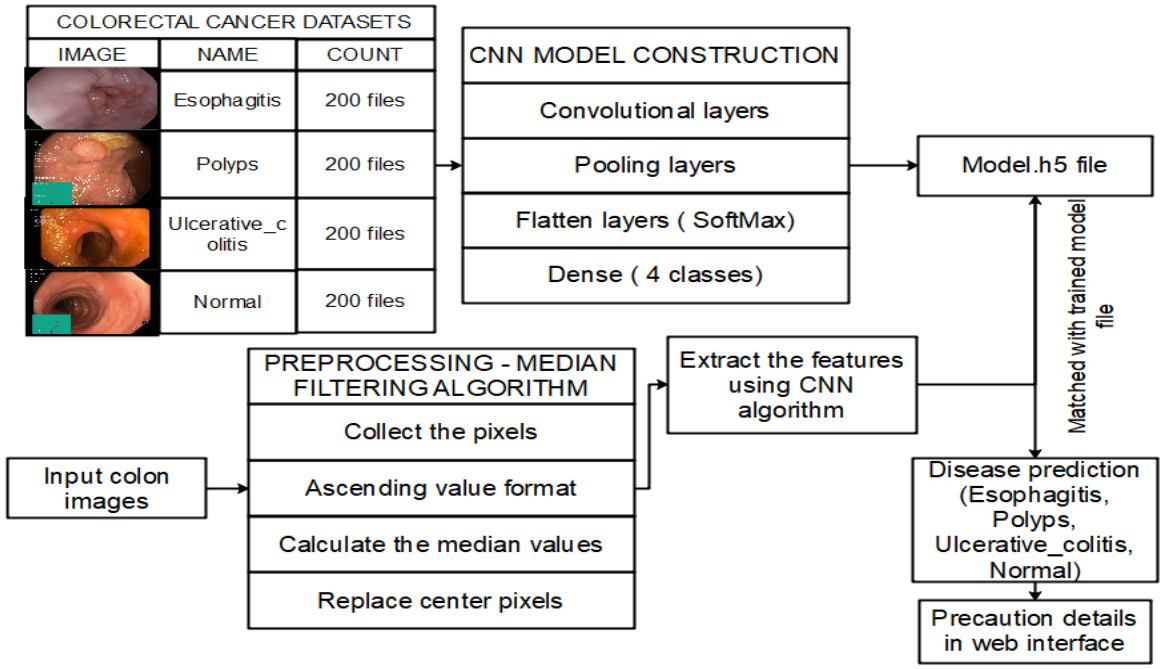

Fig. 3. Proposed Architecture

5. EXPERIMENTAL RESULTS

Colon images are collected from KAGGLE datasets the dataset links as

(https://www.kaggle.com/datasets/francismon/curated-colon-dataset).

The model performance is then evaluated with different measures such as accuracy. Table 1 provides detailed description about performance measures.

True Positive (TP): The number of actual positives correctly predicted as positive.

False Positive (FP): The number of incorrect positive predictions, i.e., false positives.

True Negative (TN): The number of actual negatives correctly predicted as negative.

False Negative (FN): The number of actual positives incorrectly predicted as negative.

Accuracy (ACC): The ratio of the total number of correct predictions to the total number of test data points. The highest possible accuracy is 1.0, while the lowest is 0.0.

$$ACC = \frac{TP+TN}{TP+TN+FN+FP} \text{ x } 100$$

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ALGORITHM	ACCURACY
ARTIFICIAL NEURAL NETWORK (ANN)	50%
BACK PROPOGATION NEURAL NETWORK (BPNN)	65%
CONVOLUTIONAL NEURAL NETWORK (CNN)	80%

TABLE 1. PEFORMANCE TABLE

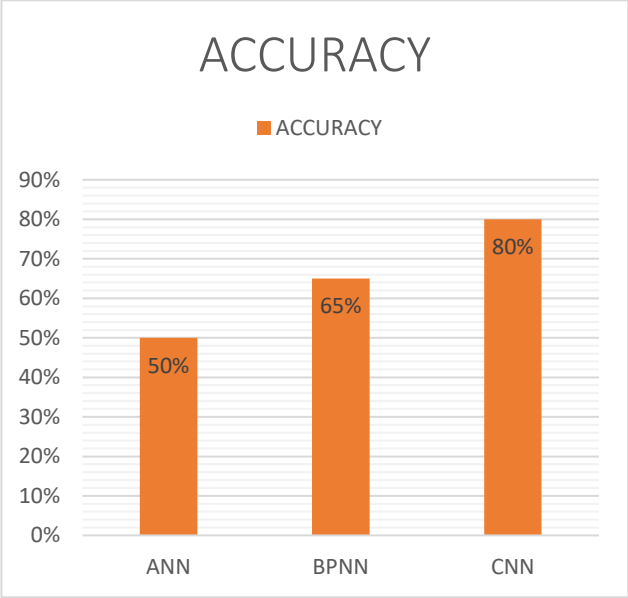

Fig. 4. Performance Comparison

6. CONCLUSION

The overall results indicate that AI performs well in terms of accuracy when it comes to colorectal cancer diagnosis. The reason for the limited use of this approach in clinical practice is the complexity and opacity of user-dependent deep network models, which do not provide sufficient evidence for the fundamental principles of categorization. Most AI systems that predict cancer are prone to over-detection. This highlights the importance of using unbiased data in AI-based colorectal cancer detection to ensure the optimization of the model and justification of the training level. From this survey, we can conclude that the proposed computer vision technique using Convolutional Neural Networks offers improved efficiency compared to existing algorithms.

REFERENCES

[1] Lei, Zi-Ning, et al. "ABCB1-dependent collateral sensitivity of multidrug-resistant colorectal cancer cells to the survivin inhibitor MX106-4C." Drug Resistance Updates 73 (2024): 101065.

[2] Maida, Marcello, et al. "Screening and Surveillance of Colorectal Cancer: A Review of the Literature." Cancers 16.15 (2024): 2746.

[3] Papavassiliou, Athanasios G., and Donatella Delle Cave. "Novel Therapeutic Approaches for Colorectal Cancer Treatment." International Journal of Molecular Sciences 25.4 (2024): 2228.

[4] Corrales, Daniel, et al. "Colorectal cancer risk mapping through Bayesian networks." Computer Methods and Programs in Biomedicine (2024): 108407.

[5] Vural, Mustafa Gökhan, et al. "Transcoronary Gradients of Mechanosensitive MicroRNAs as Predictors of Collateral Development in Chronic Total Occlusion." Medicina 60.4 (2024): 590.

[6] White, Maxwell T., and Cynthia L. Sears. "The microbial landscape of colorectal cancer." Nature Reviews Microbiology 22.4 (2024): 240-254.

[7] Dunne, Philip D., and Mark J. Arends. "Molecular pathological classification of colorectal cancer—an update." Virchows Archiv 484.2 (2024): 273-285.

[8] Andersen, Laura, et al. "Exploring the biology of ctDNA release in colorectal cancer." European Journal of Cancer 207 (2024): 114186.

[9] Roshandel, Gholamreza, Fatemeh Ghasemi-Kebria, and Reza Malekzadeh. "Colorectal Cancer: Epidemiology, Risk Factors, and Prevention." Cancers 16.8 (2024): 1530

[10] Gmeiner, William H. "Recent Advances in Therapeutic Strategies to Improve Colorectal Cancer Treatment." Cancers 16.5 (2024): 1029.

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