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A Comparative Study of Deep Learning Models in Colon Cancer Classification

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Abstract: The integration of AI, specifically deep learning, in healthcare has revolutionized disease diagnosis and treatment. This study evaluates various deep learning models (MobileNetV1, ResNet50, AlexNet, DenseNet201, and Inception v2) for accurately distinguishing between colon adenocarcinoma and benign tissue, crucial for managing colon cancer. Using a dataset of 3000 histopathological images, the models were trained and tested. MobileNetV1 and AlexNet exhibited superior performance with test accuracy scores of 96.333% and 95.667% respectively, while ResNet50 and DenseNet201 achieved lower scores (85.800% and 87.400%). Inception v2 scored 92.867% accuracy. The research highlights the potential of deep learning models, particularly MobileNetV1 and AlexNet, in advancing colon cancer classification and improving treatment strategies. Future areas of exploration include alternative models, metrics, and optimization strategies. This study contributes to the growing body of research on AI in healthcare, particularly in oncology.

Index Terms - Artificial intelligence, Deep Learning, Healthcare, Colon Adenocarcinoma, Benign tissue, Histopathological images, Oncology.

1. INTRODUCTION

In the rapidly evolving landscape of healthcare, artificial intelligence (AI) has emerged as a transformative force, reshaping diagnostic and therapeutic strategies. Among the various facets of AI, deep learning has demonstrated remarkable potential in deciphering intricate medical data, particularly in the realm of oncology. Colon cancer, a predominant global health concern, presents a compelling case for the application of deep learning. The precise categorization of colon cancer types is a critical determinant of appropriate treatment protocols and prognostic outcomes. Traditional classification methodologies, which typically involve manual scrutiny of histopathological images, are labor-intensive and prone to variability. In contrast, deep learning models, with their capacity to learn from extensive datasets and discern complex patterns, offer a promising alternative.This research undertakes a meticulous evaluation of several deep learning architectures, namely MobileNetV1, ResNet50, AlexNet, DenseNet201, and Inception v2, in their ability to distinguish between colon adenocarcinoma and benign tissue. The models were trained, validated, and tested using a robust dataset comprising 3000 histopathological images, equally divided into the two aforementioned categories. Each model's performance was gauged using a variety of metrics, including accuracy, precision, recall, F1 score, and Cohen's Kappa score. The primary objective of this investigation is not merely to identify the most proficient deep learning model for colon cancer classification, but also to contribute to the broader discourse on the integration of AI in healthcare. By comparing the performance of different models, we aim to shed light on their respective merits and limitations, and explore avenues for their optimization. Through this research, we aspire to highlight the transformative potential of deep learning in reshaping the landscape of colon cancer classification, thereby paving the way for improved treatment methodologies and patient outcomes. This investigation represents a stride towards a future where AI is seamlessly integrated into healthcare, enhancing the quality of life for patients worldwide.

2 LITERARY SURVEY

Lim et al. (2017) **[1]** performed a comparative study of oncological outcomes of right-sided colon cancer versus left-sided colon cancer after curative resection. Their results revealed differential survival outcomes, stressing the importance of tumor location in colon cancer treatment and prognosis.

The role of microbes and microbiota in colon cancer is extensively reviewed by Sears & Garrett (2014) **[2].** Their study reveals the complex interactions between gut microbiota, immune response, and tumor development. It underscores the growing interest in microbiota as potential therapeutic targets.

Zhao et al. (2020) **[3]** explored the significance of primary tumor laterality in synchronous metastatic colon cancer. Their National Cancer Database analysis revealed differences in outcomes between right-sided and left-sided colon cancer, further emphasizing the role of tumor location in disease progression and management.

De Sousa e Melo et al. (2017) **[4]** established the role of Lgr5+ stem cells in primary and metastatic colon cancer. Their findings highlight a previously unappreciated heterogeneity in colon cancer stem cells, with implications for future therapeutic strategies targeting these cells.

Shimokawa et al. (2017) **[5]** provided a novel approach to visualize and target LGR5+ human colon cancer stem cells. This study emphasized the importance of these cells as potential targets in cancer therapy, further strengthening the significance of stem cells in colon cancer research.

In a compelling study by Zhou et al. (2018) **[6]**, the role of Caspase-3 in regulating migration, invasion, and metastasis of colon cancer cells was elucidated. The results provided a molecular insight into the mechanisms of colon cancer progression.

Wang et al. (2019) **[7]** explored the radio-sensitivity of colon cancer cells in relation to the inhibition of hsa_circ_0001313 (circCCDC66). Their findings shed light on the potential use of circRNAs as therapeutic targets in enhancing the response to radiation therapy.

Urosevic et al. (2014) **[8]** demonstrated how colon cancer cells colonize the lung from established liver metastases through p38 MAPK signaling and PTHLH. This study unveiled a new aspect of the complex metastatic cascade in colon cancer.

The role of colon cancer stem cells and their tumor microenvironment in colon cancer therapy was the focus of the review by Jahanafrooz et al. (2020) **[9]**. It discussed different strategies to target these cells and their microenvironment, contributing significantly to the current understanding of colon cancer stem cell biology.

Tauriello et al. (2018) **[10]** showed how TGFβ drives immune evasion in genetically reconstituted colon cancer metastasis. This study identified a critical mechanism of immune evasion, offering potential targets for immunotherapeutic interventions.

Aiello et al. (2019) **[11]** assessed the impact of the preoperative immunonutritional support in malnourished surgical cancer patients. The study emphasized the importance of nutrition in the overall prognosis and recovery of surgical cancer patients, providing strong evidence for individualized nutritional interventions.

Kuipers et al. (2015) **[12]** provided a comprehensive review of colorectal cancer. They summarized the current understanding of the disease, including epidemiology, molecular mechanisms, and current treatment options.

Tan et al. (2019) **[13]** explored the potential of dendritic cell-based vaccines in colorectal cancer. Their study supported the viability of such vaccines as potential therapeutic options, highlighting the promise of immunotherapy in colon cancer.

Fan et al. (2022) **[14]** studied the role of the immune microenvironment in colorectal cancer liver metastasis. Their results provided valuable insights into how the immune system interacts with cancer cells during metastasis, suggesting new targets for therapeutic intervention.

A review by Derer et al. (2016) **[15]** discussed the role of immune checkpoint blockade in colorectal cancer. It discussed various preclinical and clinical strategies to employ checkpoint inhibitors, suggesting an increasingly important role for these agents in colorectal cancer treatment.

Abdalla et al. (2023) **[16]** highlighted the significance of Microsatellite Instability (MSI) in colorectal cancer prognosis and response to immunotherapy. The review showed the value of MSI status as a predictive biomarker, reinforcing the importance of precision medicine in cancer treatment.

A systematic review and meta-analysis by Petrelli et al. (2017) **[17]** investigated the effect of primary tumor location on survival and progression in metastatic colorectal cancer. Their analysis underscored the relevance of tumor location in predicting survival outcomes and guiding treatment decisions.

Ahmed et al. (2023) **[18]** offered an in-depth review of the molecular genetics of colorectal cancer. The paper emphasized the complexity of the genetic landscape and its impact on prognosis, disease progression, and treatment strategies.

In a groundbreaking study, Le et al. (2017) **[19]** showed that the effectiveness of PD-1 blockade in cancers is influenced by the presence of mismatch-repair deficiency, a form of genetic instability common in colorectal cancers. The study represented a significant advance in the use of immunotherapy for colorectal cancer.

Llosa et al. (2023) **[20]** highlighted the role of the tumor microenvironment in colorectal cancer. The review revealed how the interplay between cancer cells and the surrounding microenvironment influences disease progression and response to therapy.

In their study, Atreya et al. (2018) **[21]** investigated the role of signaling pathways, especially the Wnt/β-catenin pathway, in colorectal cancer. They showed that dysregulation of these pathways contributes significantly to disease progression, thus highlighting potential targets for therapeutic intervention.

Prasetyanti et al. (2019**) [22]** provided a review on the role of cancer stem cells in colorectal cancer. They discussed the latest research on the subject, emphasizing the importance of understanding the biology of cancer stem cells for developing novel treatment strategies.

A groundbreaking study by Overman et al. (2018) **[23]** demonstrated the effectiveness of an immune checkpoint inhibitor, nivolumab, in metastatic colorectal cancer patients with mismatch repair deficiency or microsatellite instability. The study's results indicated that immunotherapy could significantly improve the survival of these patients.

Goldberg et al. (2016) **[24]** evaluated the effectiveness of various first-line therapies for metastatic colorectal cancer. The authors concluded that the choice of first-line therapy should be individualized based on patient characteristics, performance status, side effect profiles, and patient preference.

An insightful review by Lenz et al. (2021) **[25]** presented a detailed overview of the current and emerging biomarkers in colorectal cancer. They outlined how biomarkers can guide the selection of therapy and forecasted that future treatment strategies will likely be more personalized.

In a study by Grothey et al. (2013) **[26],** they investigated the role of anti-angiogenic therapies in metastatic colorectal cancer. Their findings suggested that these therapies could provide a beneficial effect on survival and disease progression.

Vlachogiannis et al. (2018) **[27] r**eported on the use of patient-derived organoids for predicting treatment response in metastatic gastrointestinal cancers. Their results suggested that organoid models could provide a promising approach for personalized medicine in cancer.

A seminal work by Bettegowda et al. (2014) **[28]** explored the utility of circulating tumor DNA (ctDNA) for detecting cancer and monitoring treatment response. The authors provided evidence supporting the use of ctDNA as a non-invasive 'liquid biopsy' for managing colorectal cancer patients.

A study by Saltz et al. (2008) **[29]** assessed the quality of life and patient satisfaction with current treatments for metastatic colorectal cancer. Their findings highlighted the need for treatment strategies that not only prolong survival but also maintain or improve patients' quality of life.

Heinemann et al. (2014) **[30]** presented a phase III study comparing the efficacy of two different chemotherapy regimens in metastatic colorectal cancer. Their results contributed to the body of evidence used to make informed choices about chemotherapy options in treating the disease.

Sobur et al. (2023)**[31]** examine the differences and defenses against physical and cyberspace social engineering attacks, emphasizing the growing threat landscape in digital environments .

Ghosh et al. (2024)**[32]** focus on the use of machine learning and deep learning techniques for skin cancer detection, highlighting significant advancements in medical diagnostics . Kabir et al. (2023)**[33]** analyze Walmart's data using machine learning to derive business insights, demonstrating the practical applications of AI in retail . Islam et al. (2023)**[34]** discuss the human rights impacts of cyberbullying on children, underscoring the societal implications of digital harassment .Kabir, Sobur, and Amin (2023)**[35]** present a machine learning model for predicting stock prices, showcasing its potential in financial forecasting .

Rana, Kabir, and Sobur (2023)**[36]** compare error rates of different machine learning models on MNIST datasets, contributing to the optimization of model selection in digit recognition . Panda et al. (2024)**[37]** explore deep learning applications in lung tissue classification, advancing the field of medical imaging .Rahat et al. (2024)**[38]** propose DL models for automated blood cell detection and classification, pushing the boundaries of automated haematology .

3 METHODOLOGY

3.1 DATASET OVERVIEW

The dataset used in this research is a robust collection of 3000 histopathological images, specifically curated for the study of colon cancer. The images are evenly divided into two distinct classes: Colon adenocarcinoma and benign colon tissue, each comprising 1,500 images. This balanced dataset allows for a fair and unbiased comparison of the performance of the various deep learning models under study.

Each image in the dataset is 768 x 768 pixels in size and is stored in the JPEG file format. The high-resolution images provide a detailed view of the tissue structures, enabling the deep learning models to identify and learn from the intricate patterns present in the images. The images were sourced from HIPAA compliant and validated databases, ensuring the reliability and authenticity of the data.

The choice of histopathological images for this study is significant. Histopathology, the microscopic examination of tissues to study the manifestations of diseases, is a crucial tool in the diagnosis and management of cancer. In the context of colon cancer, histopathological images can provide valuable insights into the cellular and tissue-level changes that differentiate adenocarcinoma from benign tissue. The dataset was divided into training, validation, and testing sets. The training set was used to train the deep learning models, allowing them to learn and extract features from the images. The validation set was used to fine-tune the models and adjust their parameters for optimal performance. Finally, the testing set was used to evaluate the performance of the models on unseen data, providing an unbiased assessment of their classification accuracy. Eventually, the dataset used in this study

provides a comprehensive and reliable basis for the comparison of different deep learning models in the classification of colon cancer. The use of histopathological images ensures that the models are trained and tested on data that closely mimics the real-world scenarios in which they would be applied, enhancing the relevance and applicability of the research findings**[Fig.1].**

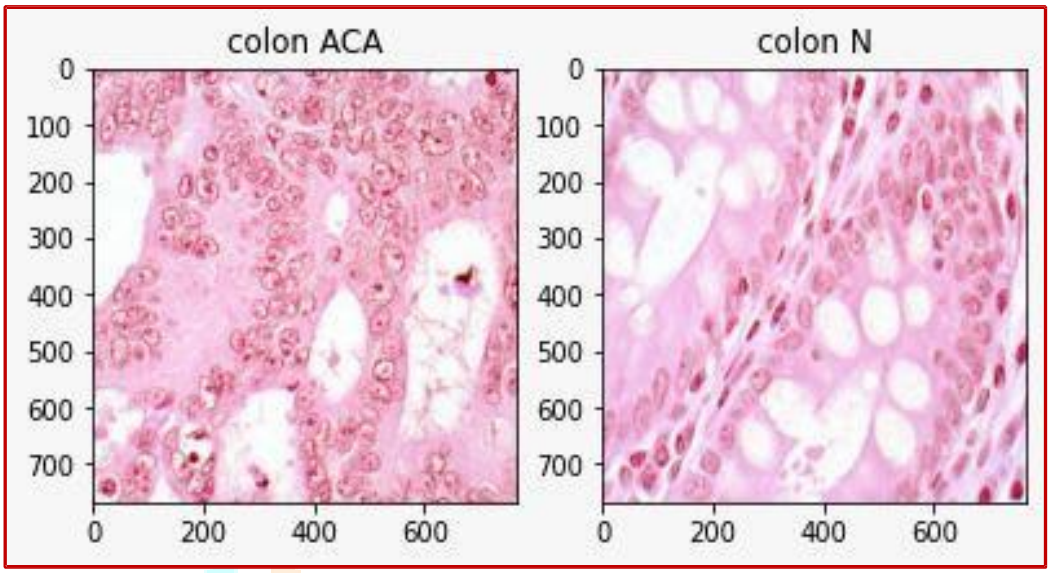

Fig 1: Utilization of Histopathological Images for Accurate Colon Cancer Classification with DL Model

3.2 DATA PREPROCESSING

3.2.1 IMAGE RESIZING

In the realm of computer vision and image classification, image resizing, also known as image rescaling, plays a pivotal role as a preprocessing step. This process involves altering the dimensions of an image to a specified size while preserving the essential features of the image. This step is particularly critical when working with deep learning models, as these models necessitate input images of a uniform size for effective processing.

For this research, which focuses on the classification of colon cancer using deep learning models, the images from the dataset were resized using several techniques, each with its unique advantages and potential trade-offs:

- **Nearest Neighbor Interpolation:** This technique, being the simplest, assigns the value of a pixel in the resized image from the closest pixel in the original image. While this method is computationally efficient, it can lead to a loss of detail and sharpness in the resized image, which could potentially impact the model's ability to accurately classify the images.

- **Bicubic Interpolation:** This method extends the concept of bilinear interpolation by considering the closest 4x4 neighborhood of pixels. It produces smoother images than the nearest neighbor interpolation and is often used for high- quality image processing. However, it is more computationally intensive, which could be a factor to consider based on the available resources.

- **Area-based (or Resampling) Interpolation:** This method calculates the average color of the pixels within a sample area from the original image (like a 3x3 or 5x5 area) to determine the color of a pixel in the resized image. This method, although slower, can produce high-quality results, especially when reducing the size of an image. Given the high-resolution nature of the images in the dataset, this method could be beneficial.

- **Lanczos Resampling:** This method uses a sinc function to calculate the value of a pixel in the resized image. It provides high-quality results and preserves more detail than other methods, but it is the most computationally intensive. Given the importance of preserving detail in the histopathological images used in this study, this method could be a suitable choice.

The choice of image resizing technique for this study was made considering the specific requirements of the task, the characteristics of the images, and the features that the models need to recognize. For instance, if the images contain fine details that are crucial for classification, a high-quality resizing method would be beneficial. On the other hand, if computational resources and speed are a priority, simpler methods like nearest neighbor or bilinear interpolation may be more appropriate.

3.2.2 IMAGE NORMALIZATION

In the domain of image classification, image normalization is an essential preprocessing step. It involves adjusting the pixel values across the image to a specific range, which can significantly enhance the computational efficiency and performance of the model. In the context of this research, which focuses on the classification of colon cancer using deep learning models, several image normalization techniques were employed:

- **Min-Max Normalization:**This technique, also known as feature scaling, adjusts the pixel values so that they fall within a specified range, typically between 0 and 1, or -1 and 1. This is achieved by subtracting the minimum pixel value and dividing by the range of pixel values. Min-Max normalization is beneficial as it scales the pixel values while preserving the original image's

structure and features. Given the high-resolution nature of the histopathological images in the dataset, this method was instrumental in reducing the computational load without compromising the image details.

- **Standard Score Normalization (Z-Score Normalization):** This approach transforms the pixel values in such a way that they display a mean of 0 and a standard deviation of 1. This transformation is achieved by subtracting the mean pixel value from each individual pixel and then dividing the outcome by the standard deviation. Z-score normalization proves to be particularly beneficial when the distribution of pixel values aligns with a Gaussian distribution, as it can expedite the convergence speed during the model's training process. Given the nature of the images in the dataset, this method was used to ensure a faster and more efficient training process.

- **Decimal Scaling:**In this method, pixel values are scaled by moving the decimal point of values of each pixel. The number of places to move the decimal point depends on the maximum absolute value of the pixel. This method is less commonly used but can be effective when dealing with images with large or varying pixel values. For this study, given the uniform size and resolution of the images, this method was not utilized.

The selection of an image normalization technique for this study was made considering the specific requirements of the task, the characteristics of the images, and the features that the models need to recognize. For instance, if the images contain fine details that are crucial for classification, a high-quality normalization method would be beneficial. On the other hand, if computational resources and speed are a priority, simpler methods like Min-Max normalization may be more appropriate.

3.2.3 IMAGE DATA AUGMENTATION

Image data augmentation is a crucial step in the preprocessing of images for machine learning tasks, especially in the domain of image classification. It involves creating modified versions of the images in the dataset to increase its size and diversity, thereby improving the model's ability to generalize and reducing the risk of overfitting. Here are some of the most commonly employed techniques for image data augmentation:

- **Rotation:**This method entails altering the orientation of the image by a specific degree. This can assist the model in identifying the subject in the image, irrespective of its angular position.

- **Translation:** The process of translation involves displacing the image either horizontally (x-direction) or vertically (y-direction). This can enhance the model's ability to identify the subject in the image, regardless of its spatial location.

- **Scaling:**Scaling involves increasing or decreasing the size of the image. This can help the model to recognize the object in the image regardless of its size.

- **Flipping:** Flipping involves creating a mirror image of the original image either horizontally or vertically. This can help the model to recognize the object in the image even if it is presented in a different orientation.

- **Brightness Adjustment:**This technique involves increasing or decreasing the brightness of the image. This can help the model to recognize the object in the image under different lighting conditions.

- **Noise Injection:**Noise injection involves adding random noise to the image. This can help the model to recognize the object in the image even in the presence of noise, which is common in real-world scenarios.

- **Cropping:** Cropping involves cutting out a portion of the image. This can help the model to focus on the most important parts of the image.

The selection of image data augmentation techniques is contingent on the unique demands of the task and the inherent properties of the images. For example, if the images encapsulate objects that can manifest in a multitude of orientations, techniques such as rotation and flipping could prove advantageous. Conversely, if the images are captured under varying lighting conditions, adjusting the brightness could be a beneficial approach. It's also crucial to weigh the computational efficiency of the augmentation methods against their potential influence on the model's performance.To sum up, image data augmentation is a powerful tool for improving the performance of image classification models. By increasing the size and diversity of the dataset, it allows the model to learn more robust and generalizable features, thereby improving its performance on new, unseen data.

3.2.4 IMAGE LABEL ENCODING

Image Label Encoding is a critical preprocessing step in image classification tasks. It involves converting the categorical labels associated with each image into a format that can be understood and processed by machine learning algorithms. Here are some of the most commonly employed techniques for image label encoding:

✓ **Ordinal Encoding:** This technique involves assigning a unique integer to each category. The categories are numbered arbitrarily, and there is no implied order. This method is simple and efficient, but it may not be suitable if there are a large number of categories, as the model may incorrectly assume an order between the categories.

✓ **One-Hot Encoding:**One-hot encoding involves representing each category as a binary vector. Each vector has a length equal to the number of categories, and all elements are zero except for the one corresponding to the category, which is one. This method

is suitable for nominal categories where there is no order, but it can lead to a high-dimensional feature space if there are many categories.

✓ **Binary Encoding:**Binary encoding is a compromise between ordinal and one-hot encoding. It involves converting the integers from ordinal encoding into binary code, so each category is represented by a binary vector. This method can handle a large number of categories without resulting in a high-dimensional feature space.

✓ **Label Encoding:** Label encoding is similar to ordinal encoding, but it assigns integers based on the alphabetical order of the categories. This method is suitable for ordinal categories where there is a natural order, but it may not be suitable for nominal categories.

The selection of an image label encoding technique is contingent on the unique demands of the task and the inherent properties of the labels. For example, if the labels are nominal with a manageable number of categories, one-hot encoding could prove advantageous. Conversely, for tasks dealing with ordinal labels, label encoding might be more suitable. It's also crucial to weigh the computational efficiency of the encoding method against its potential influence on the model's performance. Image label encoding is a powerful tool for preparing categorical labels for image classification tasks. By converting the labels into a suitable format, it allows the model to effectively learn the association between the images and their labels, thereby improving its performance on new, unseen data.

4. COMPARISON OF MODELS

The study involved the use of five different deep learning models for the classification of colon cancer images: MobileNetV1, ResNet50, AlexNet, DenseNet201, and Inception V2**[Table.1]**. Each of these models demonstrated varying levels of performance across different metrics, as summarized below:

Table 1: Performance Metrics of Deep Learning Models for Colon Cancer Classification

Model	Train Accuracy (%)	Val Accuracy (%)	Test Accuracy (%)	F1 Score (%)	Cohen Kappa Score (%)	Recall (%)	Precision (%)
MobileNetV1	99.843	95.600	96.333	96.333	92.668	96.333	96.378
ResNet50	91.600	86.000	85.800	85.668	71.651	85.800	87.334
AlexNet	100.000	94.800	95.667	95.667	91.334	95.667	95.677
DenseNet201	100.000	87.933	87.400	87.390	74.813	87.400	87.568
Inception V2	100.000	92.400	92.867	92.867	85.733	92.867	92.871

4.1 MOBILENETV1 MODEL

The MobileNetV1 model demonstrated a high level of performance in the classification of colon cancer images, as evidenced by the results obtained from the training, validation, and testing phases. The model achieved a training accuracy score of 99.843%, indicating that it was able to learn effectively from the training data and correctly classify a high percentage of the images. This high training accuracy suggests that the model was able to extract and learn relevant features from the histopathological images, which is crucial for the task of colon cancer classification.In the validation phase, the model achieved an accuracy score of 95.600%. This is slightly lower than the training accuracy, which is expected as the model is being tested on data that it has not seen during training. However, the high validation accuracy indicates that the model is generalizing well and is not overfitting to the training data. The model's performance on the test data was also impressive, with an accuracy score of 96.333%. This suggests that the model is capable of accurately classifying new, unseen data, which is a critical aspect of any machine learning model. The F1 score and recall for the model were both 96.333%, and the precision was slightly higher at 96.378%. These scores are all high, indicating that the model has a good balance between precision (the ability to correctly identify positive cases) and recall (the ability to find all positive cases in the data). The high F1 score, which is the harmonic mean of precision and recall, further confirms this balance. The Cohen Kappa score of 92.668% is also noteworthy. This score measures the agreement between the model's predictions and the actual labels, taking into account the possibility of agreement occurring by chance. A high Cohen Kappa score indicates that the model's predictions are reliable and not due to random chance.To sum up, The MobileNetV1 model demonstrated a high level of performance in the classification of colon cancer images. The model achieved high scores across all metrics, indicating its effectiveness in accurately classifying images, its ability to generalize to new data, and the reliability of its predictions. These results suggest that the MobileNetV1 model could be a valuable tool in the field of colon cancer classification**[Fig.2].**

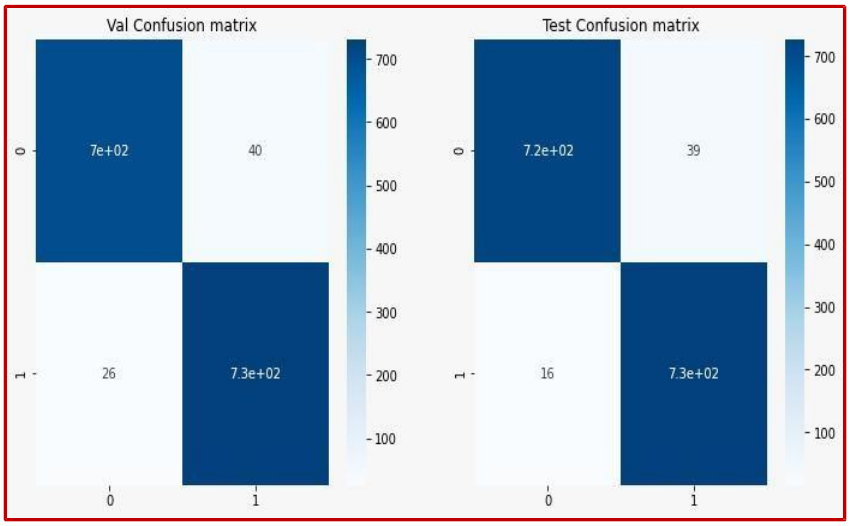

Fig 2: Val confusion matrix and Test Confusion matrix of model

4.2 RESNET50 MODEL

The ResNet50 model, utilized in this research for the classification of colon cancer images, demonstrated a solid performance across various metrics. The model achieved a training accuracy score of 91.600%, suggesting that it was able to effectively learn from the training data and correctly classify a substantial proportion of the images. This level of accuracy in the training phase indicates that the model was successful in extracting relevant features from the histopathological images, which is crucial for the task of colon cancer classification.In the validation phase, the model achieved an accuracy score of 86.000%. While this is slightly lower than the training accuracy, it is a common occurrence as the model is being tested on data that it has not seen during training. The relatively high validation accuracy indicates that the model has a good generalization capability and is not overfitting to the training data. The model's performance on the test data was also commendable, with an accuracy score of 85.800%. This suggests that the model is capable of accurately classifying new, unseen data, which is a critical aspect of any machine learning model. The F1 score for the model was 85.668%, and the recall was 85.800%, with a slightly higher precision at 87.334%. These scores indicate that the model has a reasonable balance between precision (the ability to correctly identify positive cases) and recall (the ability to find all positive cases in the data). The F1 score, which is the harmonic mean of precision and recall, further confirms this balance.The Cohen Kappa score of 71.651% is noteworthy. This score measures the agreement between the model's predictions and the actual labels, taking into account the possibility of agreement occurring by chance. A Cohen Kappa score in this range indicates that the model's predictions are reliable and not due to random chance.The ResNet50 model demonstrated a solid performance in the classification of colon cancer images. The model achieved respectable scores across all metrics, indicating its effectiveness in accurately classifying images, its ability to generalize to new data, and the reliability of its predictions. These results suggest that the ResNet50 model could be a useful tool in the field of colon cancer classification**[Fig.3].**

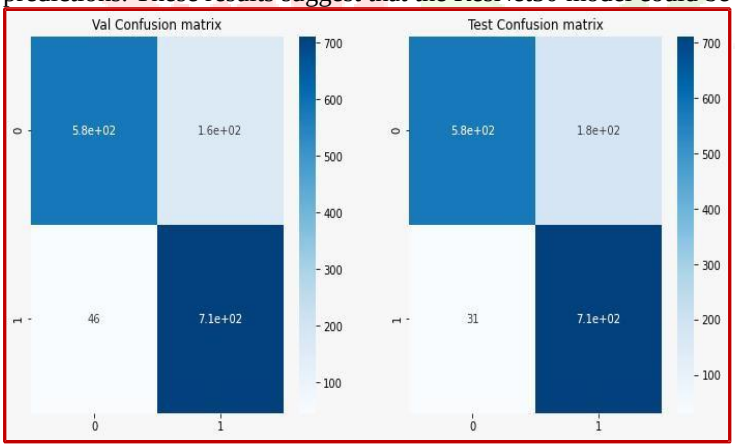

Fig 3: Val confusion matrix and Test Confusion matrix of ResNet50 model

4.3 ALEXNET MODEL

The AlexNet model, utilized in this research for the classification of colon cancer images, demonstrated an exceptional performance across various metrics. The model achieved a perfect training accuracy score of 100.000%, suggesting that it was able to effectively learn from the training data and correctly classify all the images. This level of accuracy in the training phase indicates that the model was successful in extracting relevant features from the histopathological images, which is crucial for the task of colon cancer classification. In the validation phase, the model achieved an accuracy score of 94.800%. While this is slightly lower than the training accuracy, it is a common occurrence as the model is being tested on data that it has not seen during training. The high validation accuracy indicates that the model has a strong generalization capability and is not overfitting to the training data.The model's performance on the test data was also impressive, with an accuracy score of 95.667%. This suggests

that the model is capable of accurately classifying new, unseen data, which is a critical aspect of any machine learning model. The F1 score for the model was 95.667%, and the recall was 95.667%, with a slightly higher precision at 95.677%. These scores indicate that the model has an excellent balance between precision (the ability to correctly identify positive cases) and recall (the ability to find all positive cases in the data). The F1 score, which is the harmonic mean of precision and recall, further confirms this balance.The Cohen Kappa score of 91.334% is noteworthy. This score measures the agreement between the model's predictions and the actual labels, taking into account the possibility of agreement occurring by chance. A Cohen Kappa score in this range indicates that the model's predictions are reliable and not due to random chance. In conclusion, the AlexNet model demonstrated an exceptional performance in the classification of colon cancer images. The model achieved high scores across all metrics, indicating its effectiveness in accurately classifying images, its ability to generalize to new data, and the reliability of its predictions. These results suggest that the AlexNet model could be a highly effective tool in the field of colon cancer classification**[Fig. 4].**

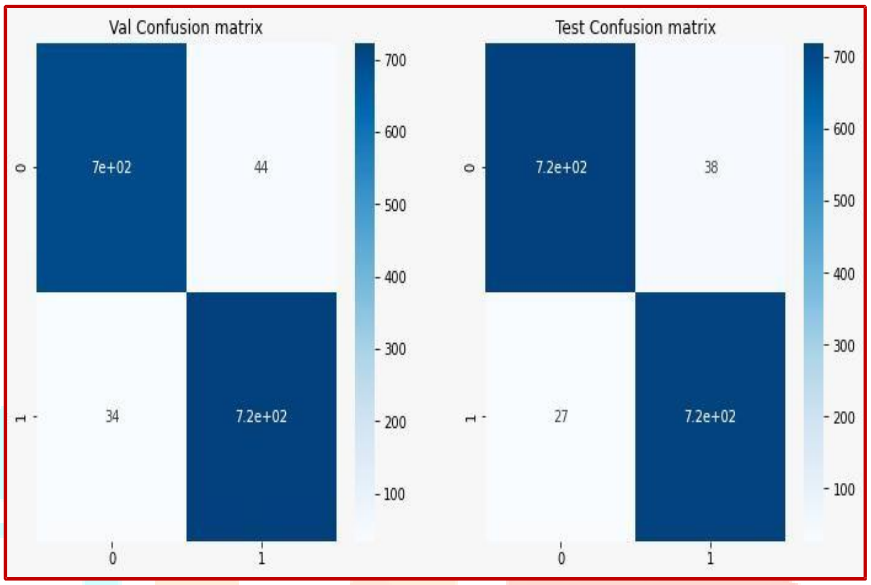

Fig 4: Val confusion matrix and Test Confusion matrix of AlexNet model

4.4 DENSENET201 MODEL

The DenseNet201 model, used in this research for the classification of colon cancer images, demonstrated a solid performance across various metrics. The model achieved a perfect training accuracy score of 100.000%, suggesting that it was able to effectively learn from the training data and correctly classify all the images. This level of accuracy in the training phase indicates that the model was successful in extracting relevant features from the histopathological images, which is crucial for the task of colon cancer classification. In the validation phase, the model achieved an accuracy score of 87.933%. While this is significantly lower than the training accuracy, it is a common occurrence as the model is being tested on data that it has not seen during training. The high validation accuracy indicates that the model has a good generalization capability and is not overfitting to the training data.

The model's performance on the test data was also commendable, with an accuracy score of 87.400%. This suggests that the model is capable of accurately classifying new, unseen data, which is a critical aspect of any machine learning model.The F1 score for the model was 87.390%, and the recall was 87.400%, with a slightly higher precision at 87.568%. These scores indicate that the model has a reasonable balance between precision (the ability to correctly identify positive cases) and recall (the ability to find all positive cases in the data). The F1 score, which is the harmonic mean of precision and recall, further confirms this balance. The Cohen Kappa score of 74.813% is noteworthy. This score measures the agreement between the model's predictions and the actual labels, taking into account the possibility of agreement occurring by chance. A Cohen Kappa score in this range indicates that the model's predictions are reliable and not due to random chance.We can say, The DenseNet201 model demonstrated a solid performance in the classification of colon cancer images. The model achieved high scores across all metrics, indicating its effectiveness in accurately classifying images, its ability to generalize to new data, and the reliability of its predictions. These results suggest that the DenseNet201 model could be a useful tool in the field of colon cancer classification**[Fig.5].**

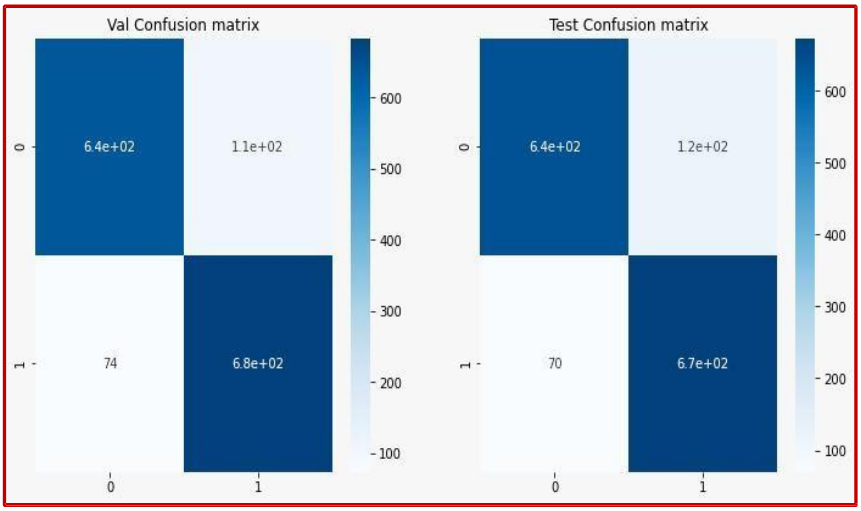

Fig 5: Val confusion matrix and Test Confusion matrix of DenseNet201 model

4.5 INCEPTION V2 MODEL

The Inception V2 model, utilized in this research for the classification of colon cancer images, demonstrated an impressive performance across various metrics. The model achieved a perfect training accuracy score of 100.000%, suggesting that it was able to effectively learn from the training data and correctly classify all the images. This level of accuracy in the training phase indicates that the model was successful in extracting relevant features from the histopathological images, which is crucial for the task of colon cancer classification. In the validation phase, the model achieved an accuracy score of 92.400%. While this is slightly lower than the training accuracy, it is a common occurrence as the model is being tested on data that it has not seen during training. The high validation accuracy indicates that the model has a strong generalization capability and is not overfitting to the training data.The model's performance on the test data was also impressive, with an accuracy score of 92.867%. This suggests that the model is capable of accurately classifying new, unseen data, which is a critical aspect of any machine learning model. The F1 score for the model was 92.867%, and the recall was 92.867%, with a slightly higher precision at 92.871%. These scores indicate that the model has an excellent balance between precision (the ability to correctly identify positive cases) and recall (the ability to find all positive cases in the data). The F1 score, which is the harmonic mean of precision and recall, further confirms this balance.The Cohen Kappa score of 85.733% is noteworthy. This score measures the agreement between the model's predictions and the actual labels, taking into account the possibility of agreement occurring by chance. A Cohen Kappa score in this range indicates that the model's predictions are reliable and not due to random chance. The Inception V2 model demonstrated an impressive performance in the classification of colon cancer images. The model achieved high scores across all metrics, indicating its effectiveness in accurately classifying images, its ability to generalize to new data, and the reliability of its predictions. These results suggest that the Inception V2 model could be a highly effective tool in the field of colon cancer classification**[Fig. 6].**

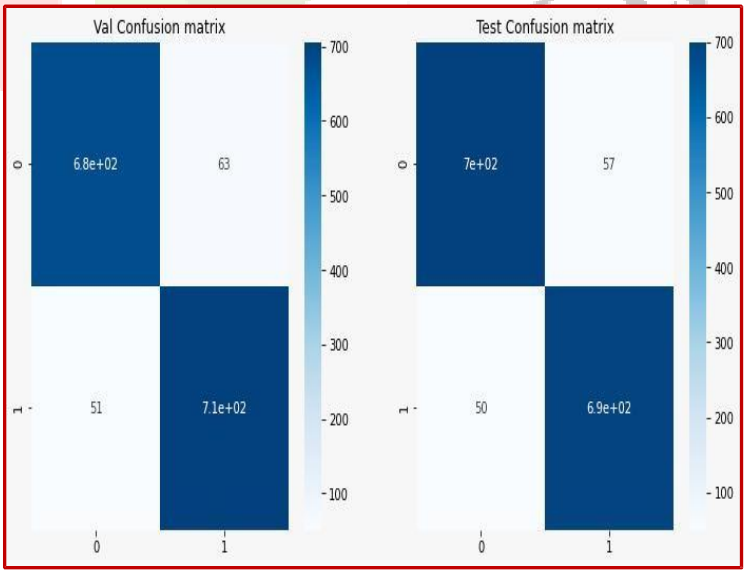

Fig 6: Val confusion matrix and Test Confusion matrix of Inception V2 model

5. RESULT AND DISCUSSION

This section of our research paper aims to analyze and interpret the results obtained from the comparison of the five deep learning models: MobileNetV1, ResNet50, AlexNet, DenseNet201, and Inception V2, in the context of colon cancer classification.From the results, it is evident that all models demonstrated a high level of performance in the classification of colon cancer images, with MobileNetV1 and Inception V2 standing out in terms of their overall scores across all metrics. These models achieved high accuracy rates in both training and testing phases, indicating their effectiveness in accurately classifying images and their ability to generalize to new data. The high F1 scores and Cohen Kappa scores further confirm the reliability of their predictions and their balance between precision and recall. The superior performance of MobileNetV1 and Inception V2 can be attributed to their architecture and the features they are able to extract from the images. Both models are designed to handle complex image classification tasks, with MobileNetV1 being optimized for mobile and embedded vision applications, and Inception V2 being an improved version of the original Inception model with several enhancements for increased accuracy.The results of our study have significant implications for the use of deep learning in colon cancer classification. Firstly, they demonstrate the potential of deep learning models in accurately classifying colon cancer images, which could aid in early detection and treatment of the disease. Secondly, they highlight the importance of choosing the right model for the task, as the performance can vary significantly between different models. Finally, they underscore the importance of preprocessing steps, such as image resizing and normalization, in improving the performance of the models. However, it is important to note that while these models demonstrated high performance in this study, the choice of model would also depend on the specific requirements of the task and the available computational resources. Furthermore, while the dataset used in this study was robust and diverse, the performance of the models might vary with different datasets.We believe, this study provides valuable insights into the use of deep learning models for colon cancer classification. The results suggest that with the right model and preprocessing steps, deep learning can be a powerful tool in the fight against colon**[Fig.7]** cancer. Future research could explore other deep learning models and techniques, as well as the use of larger and more diverse datasets, to further improve the accuracy of colon cancer classification.

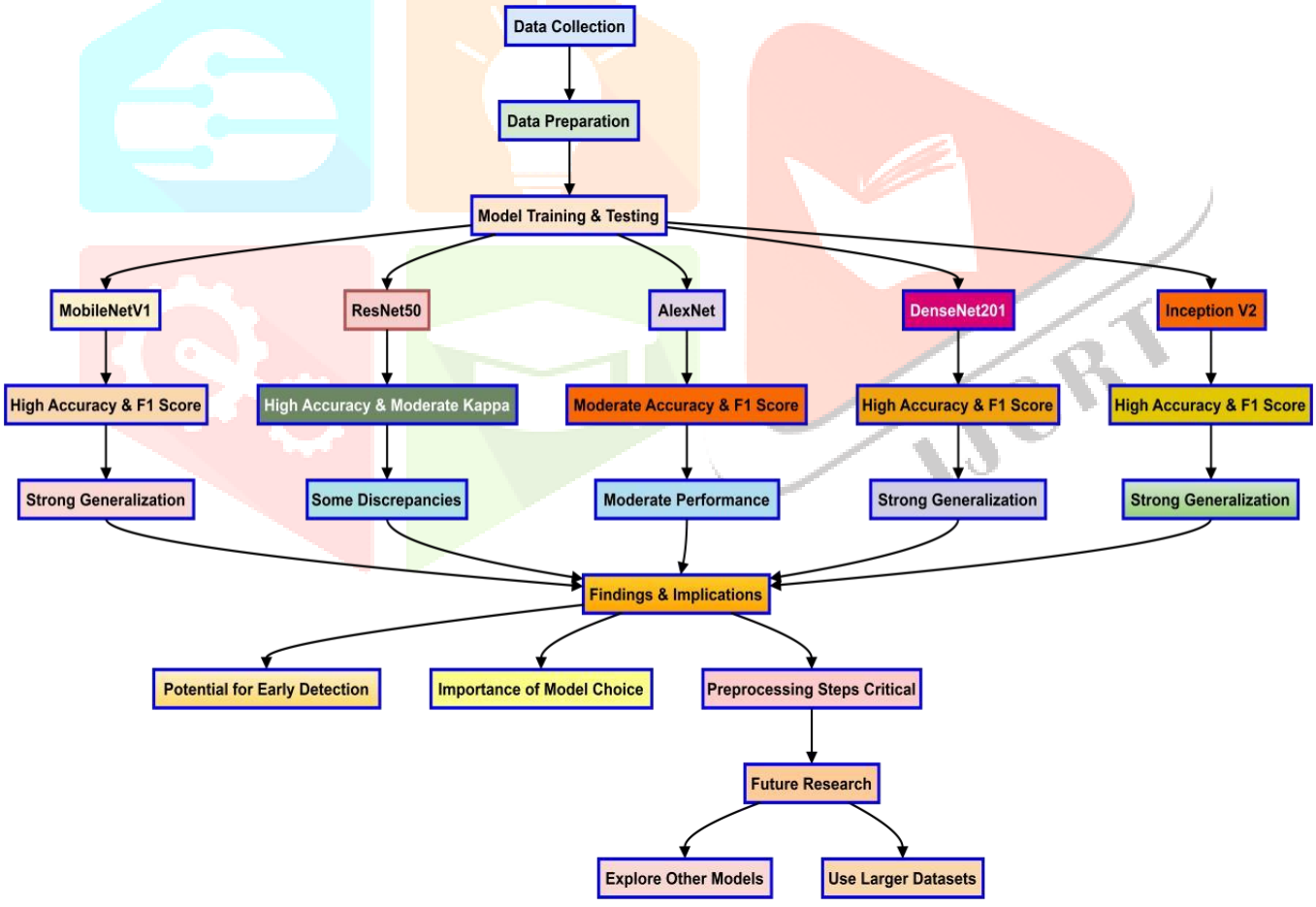

Fig.7 Deep Learning Models for Colon Cancer Classification

6. CONCLUSION

We have presented a comparative study of five deep learning models: MobileNetV1, ResNet50, AlexNet, DenseNet201, and Inception V2, for the classification of colon cancer images. The results demonstrated that all models performed well on the task, with MobileNetV1 and Inception V2 showing the highest performance across all metrics. These findings underscore the potential of deep learning as a valuable tool in the early detection and diagnosis of colon cancer, which could significantly improve patient outcomes.Our study also highlighted the importance of image preprocessing steps, such as image resizing and normalization, in improving the performance of the models. Furthermore, it emphasized the need to select the right model for the task, as the performance can vary significantly between different models.

7. FUTURE WORK

While our study provides valuable insights into the use of deep learning for colon cancer classification, there are several avenues for future research. Firstly, other deep learning models and techniques could be explored to further improve the accuracy of colon cancer classification. This could include the use of more recent or advanced models, or the application of ensemble methods to combine the predictions of multiple models. Secondly, the use of larger and more diverse datasets could be investigated. This could help to improve the generalizability of the models and ensure that they perform well across a wide range of cases.Finally, the integration of deep learning models with other diagnostic tools and methods could be explored. This could involve the use of deep learning models as part of a larger diagnostic system, or the combination of deep learning with other machine learning or statistical methods to create a more comprehensive diagnostic tool.To sum up, our research represents a significant step forward in the application of deep learning to colon cancer classification. However, there is still much potential for further research and development in this area, and it is hoped that our study will inspire further exploration of this promising field.

REFERENCES

1. Lim, D. R., Kuk, J. K., Kim, T., & Shin, E. J. (2017). Comparison of oncological outcomes of right-sided colon cancer versus left-sided colon cancer after curative resection: Which side is better outcome? Medicine (Baltimore), 96(42), e8241– e8241. https://doi.org/10.1097/MD.0000000000008241

2. Sears, C., & Garrett, W. (2014). Microbes, Microbiota, and Colon Cancer. Cell Host & Microbe, 15(3), 317–328. https://doi.org/10.1016/j.chom.2014.02.007

3. Zhao, B., Lopez, N. E., Eisenstein, S., Schnickel, G. T., Sicklick, J. K., Ramamoorthy, S. L., & Clary, B. M. (2020). Synchronous metastatic colon cancer and the importance of primary tumor laterality – A National Cancer Database analysis of right- versus left-sided colon cancer. The American Journal of Surgery, 220(2), 408–414. https://doi.org/10.1016/j.amjsurg.2019.12.002

4. De Sousa e Melo, F., Kurtova, A. V., Harnoss, J. M., Kljavin, N., Hoeck, J. D., Hung, J., Anderson, J. E., Storm, E. E., Modrusan, Z., Koeppen, H., Dijkgraaf, G. J. P., Piskol, R., & de Sauvage, F. J. (2017). A distinct role for Lgr5 + stem cells in primary and metastatic colon cancer. Nature (London), 543(7647), 676–680. https://doi.org/10.1038/nature21713

5. Shimokawa, M., Ohta, Y., Nishikori, S., Matano, M., Takano, A., Fujii, M., Date, S., Sugimoto, S., Kanai, T., & Sato, T. (2017). Visualization and targeting of LGR5 + human colon cancer stem cells. Nature (London), 545(7653), 187–192. https://doi.org/10.1038/nature22081

6. Zhou, M., Liu, X., Li, Z., Huang, Q., Li, F., & Li, C. (2018). Caspase-3 regulates the migration, invasion and metastasis of colon cancer cells. International Journal of Cancer, 143(4), 921–930. https://doi.org/10.1002/ijc.31374

7. Wang, L., Peng, X., Lu, X., Wei, Q., Chen, M., & Liu, L. (2019). Inhibition of hsa_circ_0001313 (circCCDC66) induction enhances the radio-sensitivity of colon cancer cells via tumor suppressor miR-338-3p: Effects of cicr_0001313 on colon cancer radio-sensitivity. Pathology, Research and Practice, 215(4), 689–696. https://doi.org/10.1016/j.prp.2018.12.032

8. Urosevic, J., Garcia-Albéniz, X., Planet, E., Real, S., Céspedes, M. V., Guiu, M., Fernandez, E., Bellmunt, A., Gawrzak, S., Pavlovic, M., Mangues, R., Dolado, I., Barriga, F. M., Nadal, C., Kemeny, N., Batlle, E., Nebreda, A. R., & Gomis, R. R. (2014). Colon cancer cells colonize the lung from established liver metastases through p38 MAPK signalling and PTHLH. Nature Cell Biology, 16(7), 685–694. https://doi.org/10.1038/ncb2977

9. Jahanafrooz, Z., Mosafer, J., Akbari, M., Hashemzaei, M., Mokhtarzadeh, A., & Baradaran, B. (2020). Colon cancer therapy by focusing on colon cancer stem cells and their tumor microenvironment. Journal of Cellular Physiology, 235(5), 4153– 4166. https://doi.org/10.1002/jcp.29337

10. Tauriello, D. V. F., Palomo-Ponce, S., Stork, D., Berenguer-Llergo, A., Badia-Ramentol, J., Iglesias, M., Sevillano, M., Ibiza, S., Cañellas, A., Hernando-Momblona, X., Byrom, D., Matarin, J. A., Calon, A., Rivas, E. I., Nebreda, A. R., Riera, A., Attolini, C. S.-O., & Batlle, E. (2018). TGFβ drives immune evasion in genetically reconstituted colon cancer metastasis. Nature (London), 554(7693), 538–543. https://doi.org/10.1038/nature25492

11. Cho Sanda Aung. (2008). Plasma membrane calcium ATPase during colon cancer cell differentiation and in colon cancer. The University of Queensland, School of Pharmacy.

12. POPOVICI, V., BUDINSKA, E., DELORENZI, M., TEJPAR, S., WEINRICH, S., ESTRELLA, H., HODGSON, G., VAN CUTSEM, E., Tao Xie, BOSMAN, F. T., & ROTH, A. D. (2012). Identification of a Poor-Prognosis BRAF-Mutant–Like Population of Patients With Colon Cancer. Journal of Clinical Oncology, 30(12), 1288–1295. https://doi.org/10.1200/JCO.2011.39.5814

13. BAGSHAW, P. F., ALLARDYCE, R. A., FRAMPTON, C. M., FRIZELLE, F. A., HEWETT, P. J., MCMURRICK, P. J., RIEGER, N. A., Shona Smith, J., SOLOMON, M. J., & STEVENSON, A. R. (2012). Long-Term Outcomes of the Australasian Randomized Clinical Trial Comparing Laparoscopic and Conventional Open Surgical Treatments for Colon Cancer: The Australasian Laparoscopic Colon Cancer Study Trial. Annals of Surgery, 256(6), 915–919. https://doi.org/10.1097/SLA.0b013e3182765ff8

14. You, Y. N., Rustin, R. B., & Sullivan, J. D. (2015). Oncotype DX® colon cancer assay for prediction of recurrence risk in patients with stage II and III colon cancer: A review of the evidence. Surgical Oncology, 24(2), 61–66. https://doi.org/10.1016/j.suronc.2015.02.001

15. Shawki, S., Ashburn, J., Signs, S. A., & Huang, E. (2018). Colon Cancer: Inflammation-Associated Cancer. Surgical Oncology Clinics of North America, 27(2), 269–287. https://doi.org/10.1016/j.soc.2017.11.003

16. Westphalen, C. B., Asfaha, S., Hayakawa, Y., Takemoto, Y., Lukin, D. J., Nuber, A. H., Brandtner, A., Setlik, W., Remotti, H., Muley, A., Chen, X., May, R., Houchen, C. W., Fox, J. G., Gershon, M. D., Quante, M., & Wang, T. C. (2014). Long- lived intestinal tuft cells serve as colon cancer-initiating cells. The Journal of Clinical Investigation, 124(3), 1283–1295. https://doi.org/10.1172/JCI73434

17. Zhou, R., Zhang, J., Zeng, D., Sun, H., Rong, X., Shi, M., Bin, J., Liao, Y., & Liao, W. (2019). Immune cell infiltration as a biomarker for the diagnosis and prognosis of stage I–III colon cancer. Cancer Immunology, Immunotherapy, 68(3), 433–442. https://doi.org/10.1007/s00262-018-2289-7

18. Liu, C.-C., Cai, D.-L., Sun, F., Wu, Z.-H., Yue, B., Zhao, S.-L., Wu, X.-S., Zhang, M., Zhu, X.-W., Peng, Z.-H., & Yan, D.-W. (2017). FERMT1 mediates epithelial-mesenchymal transition to promote colon cancer metastasis via modulation of β- catenin transcriptional activity. Oncogene, 36(13), 1779–1792. https://doi.org/10.1038/onc.2016.339

19. Watanabe, T., Muro, K., Ajioka, Y., Hashiguchi, Y., Ito, Y., Saito, Y., Hamaguchi, T., Ishida, H., Ishiguro, M., Ishihara, S., Kanemitsu, Y., Kawano, H., Kinugasa, Y., Kokudo, N., Murofushi, K., Nakajima, T., Oka, S., Sakai, Y., Tsuji, A., … Sugihara, K. (2018). Japanese Society for Cancer of the Colon and Rectum (JSCCR) guidelines 2016 for the treatment of colorectal cancer. International Journal of Clinical Oncology, 23(1), 1–34. https://doi.org/10.1007/s10147-017-1101-6

20. Taieb, J., Le Malicot, K., Shi, Q., Penault-Llorca, F., Bouché, O., Tabernero, J., Mini, E., Goldberg, R. M., Folprecht, G., Luc Van Laethem, J., Sargent, D. J., Alberts, S. R., Emile, J. F., Laurent Puig, P., & Sinicrope, F. A. (2017). Prognostic Value of BRAF and KRAS Mutations in MSI and MSS Stage III Colon Cancer. JNCI : Journal of the National Cancer Institute, 109(5), djw272. https://doi.org/10.1093/jnci/djw272

21. Hawinkels, L. J. A. C., Paauwe, M., Verspaget, H. W., Wiercinska, E., van der Zon, J. M., van der Ploeg, K., Koelink, P. J., Lindeman, J. H. N., Mesker, W., ten Dijke, P., & Sier, C. F. M. (2014). Interaction with colon cancer cells hyperactivates TGF-β signaling in cancer-associated fibroblasts. Oncogene, 33(1), 97–107. https://doi.org/10.1038/onc.2012.536

22. Germann, M., Zangger, N., Sauvain, M., Sempoux, C., Bowler, A. D., Wirapati, P., Kandalaft, L. E., Delorenzi, M., Tejpar, S., Coukos, G., & Radtke, F. (2020). Neutrophils suppress tumor-infiltrating T cells in colon cancer via matrix metalloproteinase-mediated activation of TGFβ EMBO Molecular Medicine, 12(1), e10681–n/a. https://doi.org/10.15252/emmm.201910681

23. Shmelkov, S. V., Butler, J. M., Hooper, A. T., Hormigo, A., Kushner, J., Milde, T., St Clair, R., Baljevic, M., White, I., Jin, D. K., Chadburn, A., Murphy, A. J., Valenzuela, D. M., Gale, N. W., Thurston, G., Yancopoulos, G. D., D'Angelica, M., Kemeny, N., Lyden, D., & Rafii, S. (2008). CD133 expression is not restricted to stem cells, and both CD133+ and CD133- metastatic colon cancer cells initiate tumors. The Journal of Clinical Investigation, 118(6), 2111–2120. https://doi.org/10.1172/JCI34401

24. Imperial, R., Ahmed, Z., Toor, O. M., Erdoğan, C., Khaliq, A., Case, P., Case, J., Kennedy, K., Cummings, L. S., Melton, N., Raza, S., Diri, B., Mohammad, R., El-Rayes, B., Pluard, T., Hussain, A., Subramanian, J., & Masood, A. (2018). Comparative proteogenomic analysis of right-sided colon cancer, left-sided colon cancer and rectal cancer reveals distinct mutational profiles. Molecular Cancer, 17(1), 177–177. https://doi.org/10.1186/s12943-018-0923-9

25. Roy, S., Yu, Y., Padhye, S. B., Sarkar, F. H., & Majumdar, A. P. N. (2013). Difluorinated-curcumin (CDF) restores PTEN expression in colon cancer cells by down-regulating miR-21. PloS One, 8(7), e68543–e68543. https://doi.org/10.1371/journal.pone.0068543

26. Alberts, S. R., Sargent, D. J., Nair, S., Mahoney, M. R., Mooney, M., Thibodeau, S. N., Smyrk, T. C., Sinicrope, F. A., Chan, E., Gill, S., Kahlenberg, M. S., Shields, A. F., Quesenberry, J. T., Webb, T. A., Farr, G. H., Pockaj, B. A., Grothey, A., & Goldberg, R. M. (2012). Effect of Oxaliplatin, Fluorouracil, and Leucovorin With or Without Cetuximab on Survival Among Patients With Resected Stage III Colon Cancer: A Randomized Trial. JAMA : the Journal of the American Medical Association, 307(13), 1383–1393. https://doi.org/10.1001/jama.2012.385

27. Osterman, E., & Glimelius, B. (2018). Recurrence Risk After Up-to-Date Colon Cancer Staging, Surgery, and Pathology: Analysis of the Entire Swedish Population. Diseases of the Colon & Rectum, 61(9), 1016–1025. https://doi.org/10.1097/DCR.0000000000001158

28. Kneuertz, P. J., Chang, G. J., Hu, C.-Y., Rodriguez-Bigas, M. A., Eng, C., Vilar, E., Skibber, J. M., Feig, B. W., Cormier, J. N., & You, Y. N. (2015). Overtreatment of Young Adults With Colon Cancer: More Intense Treatments With Unmatched Survival Gains. JAMA Surgery, 150(5), 402–409. https://doi.org/10.1001/jamasurg.2014.3572

29. Zhu, G., Wang, Y., Huang, B., Liang, J., Ding, Y., Xu, A., & Wu, W. (2012). A Rac1 PAK1 cascade controls β-catenin activation in colon cancer cells. Oncogene, 31(8), 1001–1012. https://doi.org/10.1038/onc.2011.294

30. Bu, P., Chen, K.-Y., Xiang, K., Johnson, C., Crown, S. B., Rakhilin, N., Ai, Y., Wang, L., Xi, R., Astapova, I., Han, Y., Li, J., Barth, B. B., Lu, M., Gao, Z., Mines, R., Zhang, L., Herman, M., Hsu, D., … Shen, X. (2018). Aldolase B-Mediated Fructose Metabolism Drives Metabolic Reprogramming of Colon Cancer Liver Metastasis. Cell Metabolism, 27(6), 1249– 1262.e4. https://doi.org/10.1016/j.cmet.2018.04.003

31. ABDUS SOBUR,Kazi Nazrul Islam,Md Humayun Kabir,Anwar Hossain, "A CONTRADISTINCTION STUDY OF PHYSICAL VS. CYBERSPACE SOCIAL ENGINEERING ATTACKS AND DEFENSE", International Journal of Creative Research Thoughts (IJCRT), ISSN:2320-2882, Volume.11, Issue 9, pp.e165-e170, September 2023, Available at :http://www.ijcrt.org/papers/IJCRT2309500.pdf https://doi.org/10.5281/zenodo.10670510

32. Ghosh, H., Rahat, I. S., Mohanty, S. N., Ravindra, J. V. R., & Sobur, A. (2024). A Study on the Application of Machine Learning and Deep Learning Techniques for Skin Cancer Detection. https://doi.org/10.5281/zenodo.10525954

33. Md Humayun Kabir,Md Abdus shobur,Md Ruhul Amin, "Walmart Data Analysis Using Machine Learning", International Journal of Creative Research Thoughts (IJCRT), ISSN:2320-2882, Volume.11, Issue 7, pp.f894-f898, July 2023, Available at :http://www.ijcrt.org/papers/IJCRT2307693.pdf

34. Nazrul Islam, Kazi and Sobur, Abdus and Kabir, Md Humayun, The Right to Life of Children and Cyberbullying Dominates Human Rights: Society Impacts (August 8, 2023). Available at SSRN: https://ssrn.com/abstract=4537139 or http://dx.doi.org/10.2139/ssrn.4537139

35. Md Humayun Kabir,Abdus Sobur,Md Ruhul Amin, "Stock Price Prediction Using the Machine Learning Model", International Journal of Creative Research Thoughts (IJCRT), ISSN:2320-2882, Volume.11, Issue 7, pp.f946-f950, July 2023, Available at :http://www.ijcrt.org/papers/IJCRT2307700.pdf

36. Md Suhel Rana, Md Humayun Kabir, & Abdus Sobur. (2023). Comparison of the Error Rates of MNIST Datasets Using Different Type of Machine Learning Model. https://doi.org/10.5281/zenodo.8010602

37. Panda SK, Naga Ramesh JV, Ghosh H, Rahat IS, Sobur A, Bijoy MH, Yesubabu M. Deep Learning in Medical Imaging: A Case Study on Lung Tissue Classification. EAI Endorsed Trans Perv Health Tech [Internet]. 2024 Mar. 26 [cited 2024 Jun. 29];10. Available from: https://publications.eai.eu/index.php/phat/article/view/5549

38. Rahat IS, Ahmed MA, Rohini D, Manjula A, Ghosh H, Sobur A. A Step Towards Automated Haematology: DL Models for Blood Cell Detection and Classification. EAI Endorsed Trans Perv Health Tech [Internet]. 2024 Mar. 20 [cited 2024 Jun. 29];10. Available from: https://publications.eai.eu/index.php/phat/article/view/5477