Advanced Automation for Colorectal Tissue Classification in Histopathology

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***Abstract* - Colorectal cancer is one of the major global health issue due to it high death rate that requires an urgent need for its early detection that can improve patient outcomes. Previous and old methods for diagnosis of colorectal cancer included histopathological inspection, a method that was not only time consuming but highly relies on the medical professions judgment and opinions which would make it a long process. To tackle this problem, our research points out a very different and cutting-edge approach that includes multiple convolutional neural networks to automate the process of classification of histopathological images for multi-class colorectal tissue. An exceptional aspect of our research is the in-depth exploration of the computational time, a critical factor which is often ignored. In our research we found out that our proposed methodology not only improves the classification accuracy but also reduce the computational timing significantly, that makes our research more practical and implementational. Our study not only aims to improve advancement of automated histopathological image classification but also encourages the practical benefits of our model making it a valuable asset in the ongoing efforts to improve early detection and diagnosis of colorectal cancer.[20]**

Keywords—Machine Learning, Cancer Detection, CNN, VGG16, ResNet

I. INTRODUCTION

Colorectal cancer (CRC) is one of the major global health issues, ranking third as the cause of death according to recent global cancer survey. In 2022, the American Cancer Society predicted an astounding 1.55 million new cancer cases, resulting in approximately 53,000 deaths in the United States alone. This malice has its origin in the large intestine and is grown due to uncontrolled cell division triggered by genetic mutations. Also, The development of polyps noncancerous growths in the colon or rectum, is a primary fuel for CRC. Out of which adenomatous polyps has a higher chance developing into cancer, and those cells containing the cancerous element is called malignant polyps. CRC detection has always been a complex task for the clinicians and researchers. Old and conventional methods for diagnosis such as fecal occult blood and colonoscopy proves to be effective but they also lack precision and posed safety concerns due to natural differences.[20]

One of the emerging factors in the early diagnosis of CRC has been Medical imaging. But, despite the increasing availability of medical imaging data, the analysis has been proven to be consuming and challenging, which can lead to delay in early detection. Misinterpretation further has a negative impact on the accuracy, which requires need for real-time, precise, and objective diagnostic results. This paper introduces a methodology which include classification between four Convolutional Neural Network models that are InceptionResNetV2, Xception, VGG16, and DenseNet121 which compares the multi-class classification of CRC cancer tissue microscopic images to give the best and most accurate result in the most minimize time. Working on three different data sets NCT-CRC-HE-100K, CRC-VAL-HE-7K and Kather-texture-2016-image we have shown the effectiveness and accuracy of our methodology across diverse colorectal tissue histopathological images.

Major contribution of our work includes the proposal of our methodology, brief survey we performed to compare the effectiveness and efficiency of different proposed models and methodology, a brief introduction of all the dataset we have accessed for the effectiveness and robustness of our methodology. It also contains but is not limited to model, algorithms and architecture of our methodology. The presents result showcases the superiority of our model in terms of efficiency, sensitivity, precision, accuracy and F-1 score. Furthermore, we extend the robustness assessment of CRCCN-Net to lung cancer datasets, showcasing its versatility in classifying various tissues.[12]

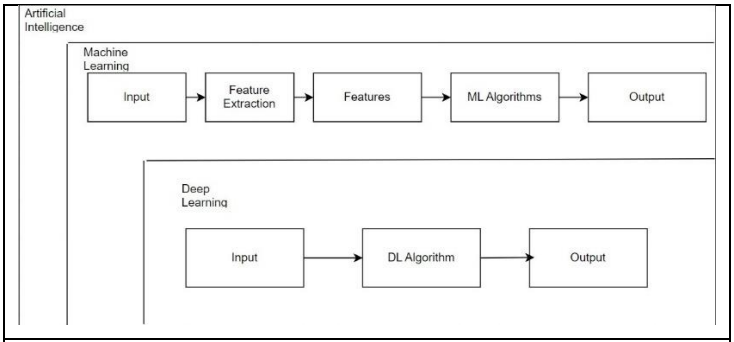

Figure 1. The Trends of Machine Learning

II. Literature Survey

Hiroshi Yoshida & Yoshiko Yamashita found in their studies that Colorectal cancer contributes as a major portion of death rate in Japan, Among women, it is a leading cause of death, and among men, it ranks as the third most common cause of death. To facilitate better and efficient diagnoses, a considerable number of specimens are routinely obtained through endoscopy. Moreover, there is a growing emphasis on pathologists double-checking slides to enhance diagnostic accuracy. However, despite the consistent number of pathologists, the growing number of cases has put more diagnostic workload on these professionals.[18]

DD Chlorogiannis & GI Verras research reached to the conclusion that Colorectal cancer stands as one of the most widespread cancer types across globe, and the common standard for diagnosis remains the histopathologic examination of the tissue samples. In recent years, artificial intelligence (AI) has made an integrated progress into the medical and pathology fields, particularly in the domain of whole slide imaging (WSI). The primary focus was on the composite balanced accuracy (ACC) and the F1 score. The collective findings from various studies indicated an average ACC of 95.8 ±4%. Notably, reported F1 scores reached up to 0.98, averaging 89.7 ±10%. This underscores the capability of existing deep learning algorithms to discern between malignant and benign conditions in silico. On the whole, the state-of-the-art algorithms has displayed its superiority to pathologists in image scrutiny and categorization tasks. Nevertheless, their universal applicability remains somewhat constrained due to their unique training characteristics and the absence of widely accepted external validation datasets.[1]

KS Wang, G Yu & C Xu while performing an analysis on pathological images for colorectal cancer (CRC) diagnosis found the analysis to be accurate and robust but it also proved to both time-consuming and information dependent, yet it proved to be critical for the treatment of the CRC patients. Due to the more workload on the pathologists in the clinics and hospitals has increased the risk of unintentional misdiagnosis in daily image analyses. To address this problem, they found and innovative solution which include the use of the deep convolutional neural network in artificial intelligence (AI) which also include a new approach of combining patches for the diagnosis of CRC in clinical environments. The following method uses feebly labelled pathological WSI(whole-slide images) patches which were trained and validated for an unparalleled and vast dataset consisting of 170,099 patches collected from more than 14,680 Whole Slide Images (WSIs) comprising of 9631 subjects. The dataset used was diverse and represented various clinical cases from China, the USA, and Germany. In testing, the AI model performed with an average Kappa statistic of 0.896 and performed at a par with the most experienced pathologists in diagnosing CRC WSIs. Also, the average area for the characteristics curve for AUC of their AI model was better than that of the pathologists(0.98 vs. 0.97),proving its superior efficiency and performance in comparison to other AI models for CRC diagnosis.[3]

III. Propropsed Methodology

The method proposed for this study mainly follows ML procedures. Machine learning is a field that instructs computers to emulate human learning processes through computational methods, allowing them to acquire knowledge from sample data. This technology finds widespread applications in challenging areas such as image processing, content recommendation, and computer vision, where traditional algorithms may struggle to address complex problems and fulfill specific tasks. Two fundamental techniques employed in machine learning are supervised learning, which focuses on mapping input to output, and unsupervised learning, centered around extracting relation within data. The primary objectives of machine learning comprises of feature extraction, selection, recognition and prediction. These goals drive the development and implementation of algorithms that enable computers to learn and adapt based on data patterns, enhancing their ability to perform various tasks effectively.

The deep learning methodology typically demands a substantial volume of data for effective training, implying that a larger dataset contributes to improved model performance. Nevertheless, the manual identification and labeling of histological images necessitate the expertise of individuals. This process is susceptible to potential challenges related to time consumption and high expenses.[11]

A. Dataset Description

For our research we are using the following data set.

NCT-CRC-HE-100K: This dataset comprises 100,000 distinct images patched with hematoxylin & eosin-stained histological images showcasing human colorectal cancer (CRC) and normal tissue. Each image is standardized to 224x224 pixels (px) at a resolution of 0.5 microns per pixel. Utilizing Macenko's method, color normalization has been applied to all images.

The images of 86 total H&E-stained slides of human cancer tissue were manually gathered. the NCT Biobank (National Center for Tumor Diseases, Heidelberg, Germany) and the UMM pathology archive (University Medical Center Mannheim, Mannheim, Germany) originated these slides from Formalin-fixed tissue(FFPE blocks). The sample collected mainly comprises of slides of primary tumors in colorectal cancer (CRC) and tissue from liver metastases in CRC. To enhance diversity, We combined regular tissue types with areas in the stomach surgery samples that weren't affected by tumors.[19]

CRC-VAL-HE-7K: The dataset comprises of 7,180 patched images of 50 patients diagnosed with colorectal adenocarcinoma. The most important feature of the NCT-CRC-HE-100K dataset is no patients feature overlaps. The NCT-CRC-HE-100K dataset was primarily designed for the validation of the model, but it shown promise for training of the model as well on more extensive dataset. Similar to the extensive dataset, we've standardized all images to a size of 224x224 pixels, maintaining a resolution of 0.5 microns per pixel (MPP).

All tissue samples were generously provided by the NCT tissue bank, and additional details, including ethical considerations, can be found in the information provided below.[19]

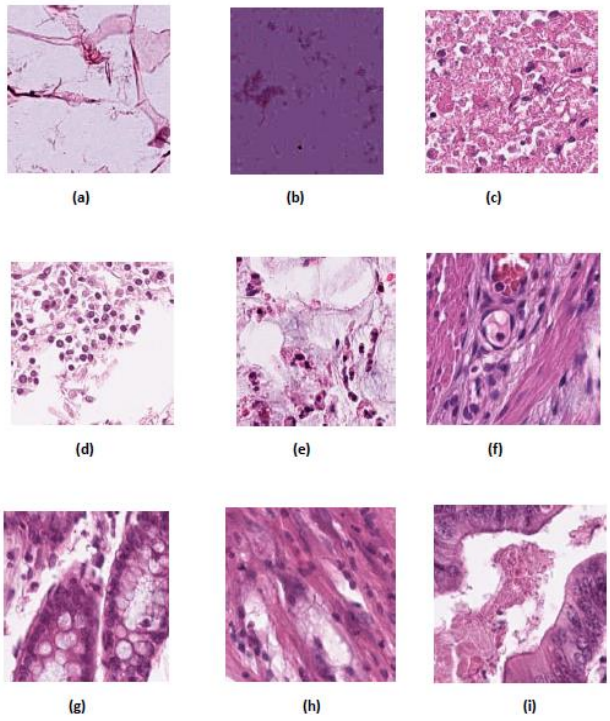

Figure 2. Sample pictures showcasing the nine types of tissues found in the NCT-CRC-HE-100K dataset.

Kather-texture-2016-image : The data contains RGB format 5000 images with a bit resolution of 0.495 µm. The digitalization of the images was done by an Aperio ScanScope(specifically the Aperio/Leica biosystems) with a amplification rate of 20x. These microscopic images were derived from human colorectal adenocarcinomas preserved through formalin fixation and paraffin embedding, specifically primary tumors and are represented as fully anonymized images. These images were sourced from the pathological record repository at the Institute of Pathology, University Medical Center Mannheim, affiliated with Heidelberg University in Mannheim, Germany.

Images of Nine Tissue Classes: In our research, We utilized an accessible cellular dataset of NCT-CRC-HE-100K which include nine distinct tissue classes, for the training and testing of our model. These images are created by Kather which include 86 slides of tissue stained with hematoxylin and eosin. The information on these histological image labels in the provided data was retrieved from the NCT-UMM website. Figure 2 presents sample images representing the nine tissue classes. All these images are resized to a constant dimension of 224 x 224 pixels (112 x 112 µm) and were used for the training, validation, and testing of the model. [1]

Upon completing the training and testing phases with the "NCT-CRC-HE-100K" dataset, We conducted an assessment to determine the precision of tissue classification model through external validation set denoted as "CRC-VAL-HE-7K." This set comprised 7,180 image patches specifically intended for testing purposes. The nine classes were categorized as follows:

- ADI: Adipose tissue are connective tissue in the body mainly made of fat cells called adipocytes.
- BACK: Background for microscopic images.
- DEB: Debris, used mainly for the purpose of diagnosis in cancer treatment.
- LYM: Lymphocytes, are a type of white blood cell used by our immune system.
- MUC: Mucus, it is a viscous fluid produced by cell for protection and moistening the muscles.
- MUS: type of a muscle in our body which is very flexible.
- NORM TISSUE: a type of tissues found in colon mucosa.
- STR: Stroma, is a type of tissue in organs that used to support and connect tissues.
- TUM: Epithelial tissues one of the major kind of tissue

Images of Eight Tissue Classes: We used the Kather-texture-2016-image a free to use dataset clearly for only one purpose of assessing the accuracy and precision of our deep learning AI model on various tissue classes. The data set was accumulated at the Institute of Histological Images of Pathology of Human Colorectal Cancer and acquired from the pathology archive by Kather. The dataset contains 5000 unique microscopic images of CRC and normal tissue, employing hematoxylin and eosin staining. Every image in the dataset belongs to one of the eight distinct tissue texture features and are re-formatted to the dimensions of 150 x 150 pixels (74 x 74 µm) for each RGB color channel. The original tissue images within the dataset are sized at 5,000 pixels.[3]

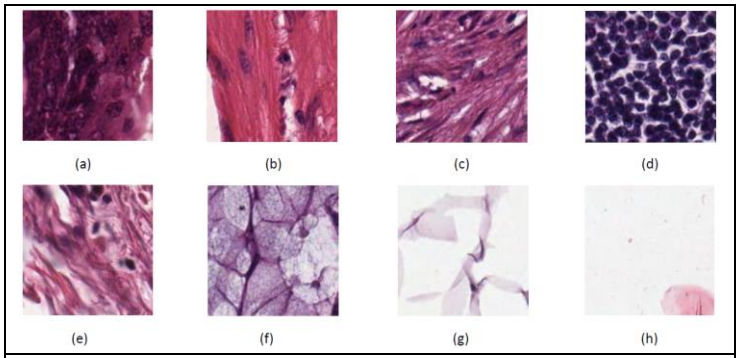

Figure 3. Sample pictures illustrating the eight types of tissues present in the Kather-texture-2016-image-5000 dataset.

The eight classes within this dataset are classified as follows:

- TUMOR: refers to an abnormal mass or lump of tissue.
- STROMA: it refers to the supportive and connective tissue withing an organ.
- COMPLEX: Stroma with a single tissue cell.
- LYMPHO: are a type of white blood cell that plays a crucial role in the immune system.
- DEBRIS: Remnants of tissues used mainly for the purpose of diagnosis in cancer treatment.
- MUCOSA: Layers of tissues used for providing protective force.
- ADIPOSE: refers to tissues or cells that are related to or composed of fat.
- EMPTY: Background for microscopic images.

Dataset	Diagnosis	Entire		Training	
		#WSI	(%)	#WSI	(%)
NCT-CRC-HE-100K	ADI	10,407	10.41	7285	10.41
	BACK	10,566	10.57	7396	10.57
	DEB	11,512	11.51	8058	11.51
	LYM	11,557	11.56	8090	11.56
	MUC	8896	8.90	6227	8.90
	MUS	13,536	13.54	9475	13.54
	NORM	8763	8.76	6134	8.76
	STR	10,446	10.45	7312	10.45
	TUM	14,317	14.32	10,022	14.32
CRC-VAL-HE-7K	ADI	1338	18.64	0	0
	BACK	847	11.80	0	0
	DEB	339	4.72	0	0
	LYM	634	8.83	0	0
	MUC	1035	14.42	0	0
	MUS	592	8.25	0	0
	NORM	741	10.32	0	0
	STR	421	5.86	0	0
	TUM	1233	17.17	0	0
Kather-texture-2016	TUMOR	625	78.125	468	12.48
	STORMA	625	78.125	468	12.48
	COMBLEX	625	78.125	468	12.48
	LYMPHO	625	78.125	468	12.48
	DEBRIS	625	78.125	468	12.48
	MUCOSA	625	78.125	468	12.48
	ADIPOSE	625	78.125	468	12.48
	EMPTY	625	78.125	468	12.48

Table 1. CRC dataset of histological images for Training.

Dataset	Diagnosis	Validate		Testing	
		#WSI	(%)	#WSI	(%)
NCT-CRC-HE-100K	ADI	1561	10.41	1561	10.41
	BACK	1585	10.57	1585	10.57
	DEB	1727	11.51	1727	11.51
	LYM	1734	11.56	1734	11.56
	MUC	1334	8.90	1334	8.90
	MUS	2030	13.54	2030	13.54
	NORM	1314	8.76	1314	8.76
	STR	1567	10.45	1567	10.45
	TUM	2148	14.32	2148	14.32
CRC-VAL-HE-7K	ADI	0	0	0	0
	BACK	0	0	0	0
	DEB	0	0	0	0
	LYM	0	0	0	0
	MUC	0	0	0	0
	MUS	0	0	0	0
	NORM	0	0	0	0
	STR	0	0	0	0
	TUM	0	0	0	0
Kather-texture-2016	TUMOR	93	12.48	93	12.48
	STORMA	93	12.48	93	12.48
	COMBLEX	93	12.48	93	12.48
	LYMPHO	93	12.48	93	12.48
	DEBRIS	93	12.48	93	12.48
	MUCOSA	93	12.48	93	12.48
	ADIPOSE	93	12.48	93	12.48
	EMPTY	93	12.48	93	12.48

Table 2. CRC dataset of histological images for Testing.

B. Architecture of the Project

1. Image Acquisition and Preprocessing:

- **Image Collection:** Gather a diverse dataset of high-resolution histopathology images of colorectal tissue samples covering various conditions (normal, adenoma, carcinoma, etc.).
- **Preprocessing Techniques:**
- **Color Normalization:** Ensure uniformity in color spaces across images.
- **Noise Reduction:** Apply filters (e.g., Gaussian, median) to eliminate noise.
- **Contrast Enhancement:** Techniques like histogram equalization to improve contrast.[5]

2. Feature Extraction:

- **Morphological Features:** Extract shape-related features (area, perimeter, eccentricity) of tissue structures.
- **Texture Analysis**: Uses methods such as GLCM(gray-level co-occurrence matrices) or LBP(local binary patterns) to capture textural details.
- **Deep Learning-Based Features:** Use pre-trained CNNs (like ResNet, Inception, or custom architectures) to extract features via transfer learning.[5]

3. Dataset Preparation and Annotation:

- **Annotation Process:** Expert pathologists annotate images to create ground truth labels (normal, adenoma, carcinoma).
- Ensure sufficient and balanced representation of each class to prevent bias.[6]

4. Model Development:

- **Traditional Machine Learning Models**: Start with classifiers like SVM, Random Forest, or k-Nearest Neighbors using extracted features.
- **Deep Learning Models**: Develop CNN architectures for end-to-end learning from raw images, considering:
- Multiple layers, possibly with residual connections for deeper networks.
- Regularization techniques (dropout, batch normalization) to prevent overfitting.
- Loss functions suitable for multi-class classification (e.g., categorical cross-entropy).[6]

5. **Validation and Evaluation:**

- **Cross-Validation:** Use k-fold cross-validation to perform model assessment on various data splits.
- **Evaluation Metrics:** Calculate accuracy, precision, true positive rate, F1-score, ROC curves, and confusion matrices to measure model performance.
- **External Validation:** Validate models on unseen datasets to ensure generalizability.[6]

6. **Interpretability and Explainability:**

- **Model Interpretability:** Utilize techniques such as Grad-CAM, SHAP values, or attention mechanisms to interpret model decisions and highlight important regions in images.
- **Visualizations:** Create visualizations to aid pathologists in understanding the basis of the model's classifications.[5]

7. **Optimization and Deployment:**

- **Model Optimization:** Optimize models for inference speed, memory efficiency, and accuracy.
- **User Interface:** Create a user-friendly interface that will helps pathologists to use the system and provide explanation for predictions.
- **Deployment:** Deploy the model in safe and scalable environment make sure it follows healthcare rules like HIPAA for security.[5]

8. **Continual Improvement:**

- **Feedback Loop:** Gather feedback from pathologists to improve and update the model over time.
- **Data Augmentation and Re-training:** Continuously adding new data to improve the accuracy of the model so that it can adapt or keep up with changing patterns.
- **Ethical and Regulatory Compliance:** Make sure to keep the patient information private and follow the rules like GDPR in Europe and HIPAA in US.
- **Collaboration with Domain Experts:** Involve pathologists throughout the process to make sure that model is useful and make sense in real world medical situations.[6]

This detailed methodology aims to cover everything from gathering and preparing data and preprocessing to model development ,evaluation and continually improving a model. Adjustment may be needed based on the dataset, available resources and advancement in technology.

C. Algorithms Used

In the context of classifying colorectal tissue histological images for diagnosing colorectal cancer (CRC), the mentioned pre-trained model VGG16, Xception, DenseNet121 and InceptionResNetV2, ,—serve as powerful tools for feature extraction and image classification. Here's a general explanation of how these algorithms can be applied in this context:

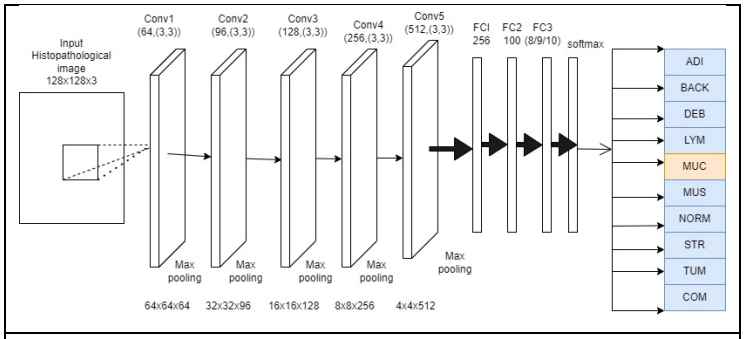

Figure 4. Basic CNN model

- **Xception:** Xception, with its depth-wise separable convolutions, can capture detailed feature in histological images. In the contest of CRC classification, it might excel in spotting strongest subtle in how cell nuclei look, crypto plasm characteristics and tissue structure. The picture below shows what the model looks like.

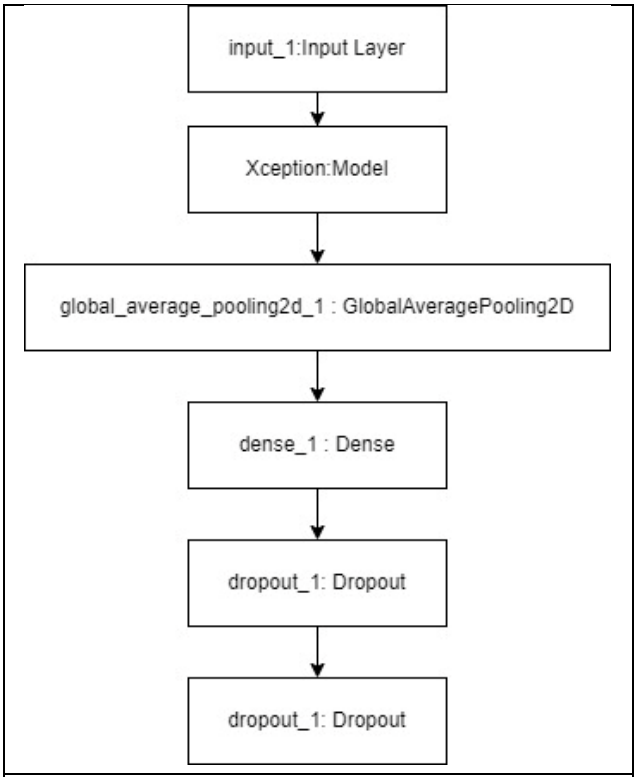

Figure 5. Xception

- **InceptionResNetV2:** : InceptionResNetV2 with its combination of inception blocks and residual connection is effective at capturing both small and large to features. In the context of CRC classification ,this model , might be well suited to analyze the nucleus cytoplasm ratio and recognize complex pattern in cyst geometry. The architecture of the following model is shown in figure 6.

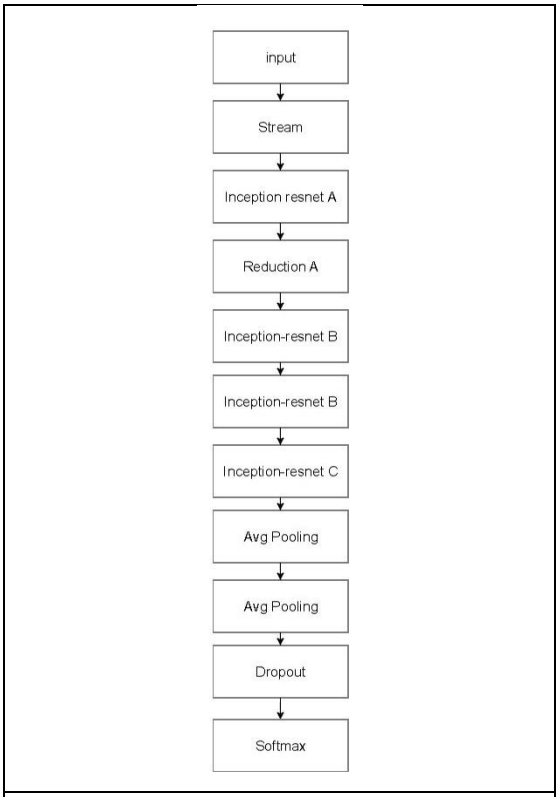

Figure 6. InceptionResNetV2

- **DenseNet121:** DenseNet121 is dense connectivity means directly connected with each and every layer allows for efficient information flow across layers, which can be beneficial for capturing features related to the nucleus to cytoplasm ratio and tissue appearance .Its features reuse mechanism makes it easier to see how different parts of image depend on each other. The architecture of the following model is shown in figure 7.

- **VGG16:** VGG16, with its simple and uniform architecture, might be useful for capturing basic features in histological images. It could be applied to analyze overall tissue appearance and may perform well if the distinguishing characteristics are relatively straightforward. The architecture of the following model is shown in figure 8.

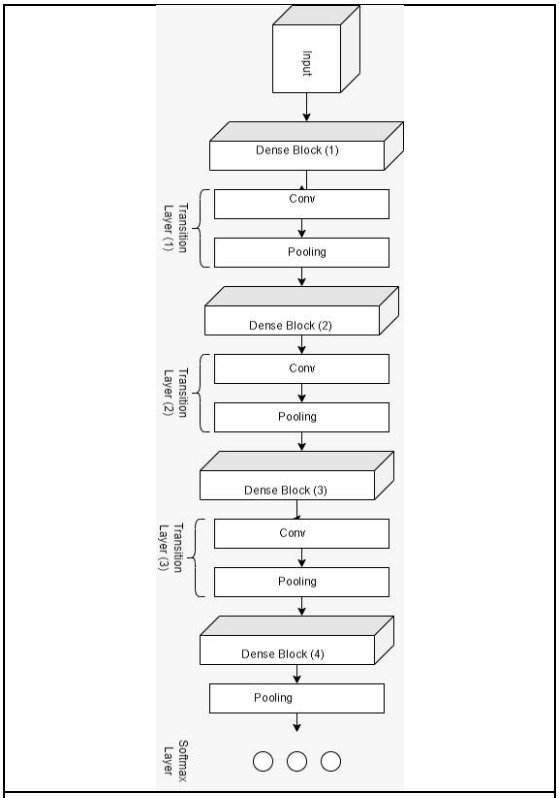

Figure 7. DenseNet 121

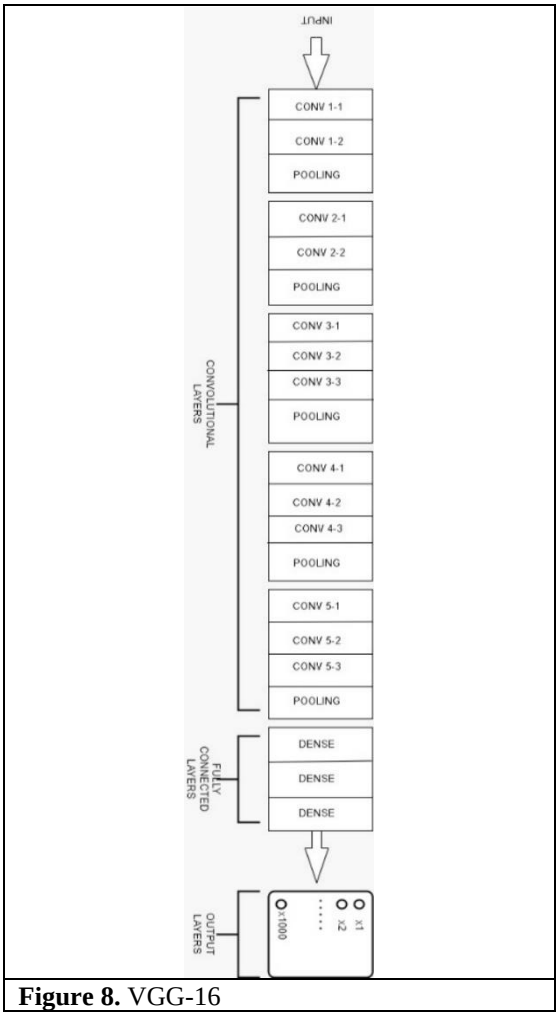

Figure 8. VGG-16

D. Model Used

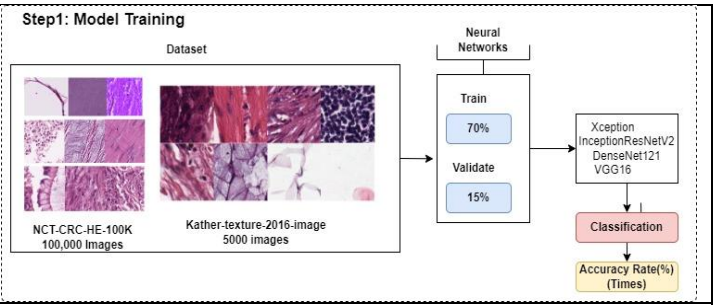

Figure 9. Step 1 – Model Training

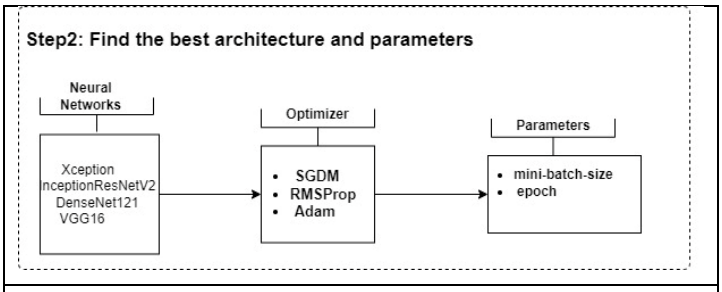

Figure 10. Step 2 – Finding the Best architecture and parameters

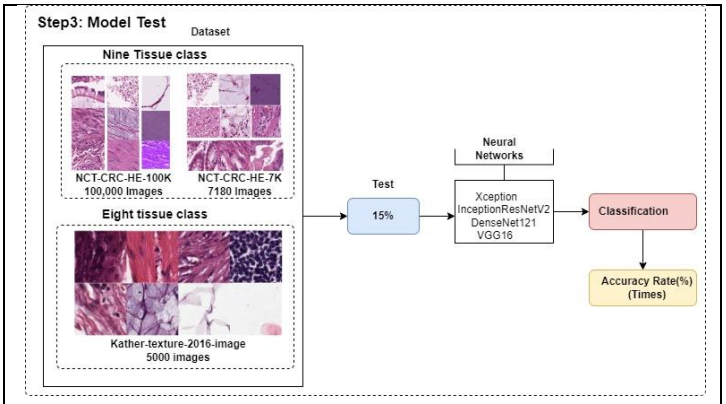

Figure 11. Step 3 – Model Test

IV. Result and Analysis

A. Evaluation

Performance parameters:

- **Performance Metrics:** Accuracy, precision, true positive rate, F1 score, and AUC curve are commonly used metrics to evaluate classification models. These metrics help assess how well each model distinguishes between different classes, such as normal tissue and CRC-affected tissue.
- **Dataset Considerations:** The choice of dataset is critical. Histological images can vary significantly, and the models' performance may be influenced by the diversity and size of the dataset. A well-balanced and representative dataset is crucial for unbiased evaluation.
- **Computational Efficiency:** Training and iinference times and training and the computational resources that are required should be reviewed. Models with low computational requirements and comparably high performance are usually adopted in practical applications.
- **Robustness:** It is essential to evaluate the robustness of the models through techniques like cross validation as it makes sure that models generalize well to unseen data and also prevent overfitting.
- **Interpretability:** Interpretability of a model is an important factor to be considered as it is crucial to understand how and why models make a particular classification decision which is essential in comprehending the diagnostic features it identifies.[8]

In the end, the efficiency of these models in classifying colorectal tissues is dependent on the specified characters of the histological images and also the capability of these models to accurately capture and leverage relevant features for precise diagnosis.

Confusion Matrix: Confusion Matrix is as an major method for evaluation of the performance of an algorithm used for classification when the true values are known for a particular dataset. It is widely used in machine learning and statistics as it provide understanding of how effectively a model classifies instances into different categories. The key components included in a confusion matrix are as follows:

• True Positive (TP): these are the values which are noted as positive(+).

• True Negative (TN): These are the values which are notes as negative(-).

• False Positive (FP): these are a type of error in which the values are notes as positive(+) when they are actually negative(-).

• False Negative (FN): these are an another type of error in which the values are noted as negative(-) when they are actually positive.(+)

Various performance matrix can be calculated such as accuracy, precision , true positive rate, specificity, and F1 score by utilizing information from confusion matrix. These metrics offer various insights into the classification model's performance, disclosing its strengths and weaknesses.

Few common metrices derived from the confusion matrix includes:

Accuracy: (TP + TN) / (TP + TN + FP + FN)

Precision: TP / (TP + FP)

Recall (Sensitivity): TP / (TP + FN)

Specificity: TN / (TN + FP)

F1 Score: 2 * (Precision * Recall) / (Precision + Recall)

These metrics play a crucial role in evaluating the model's effectiveness, and the selection of a specific metric depends on the particular goals and requirements of the task at hand.[8]

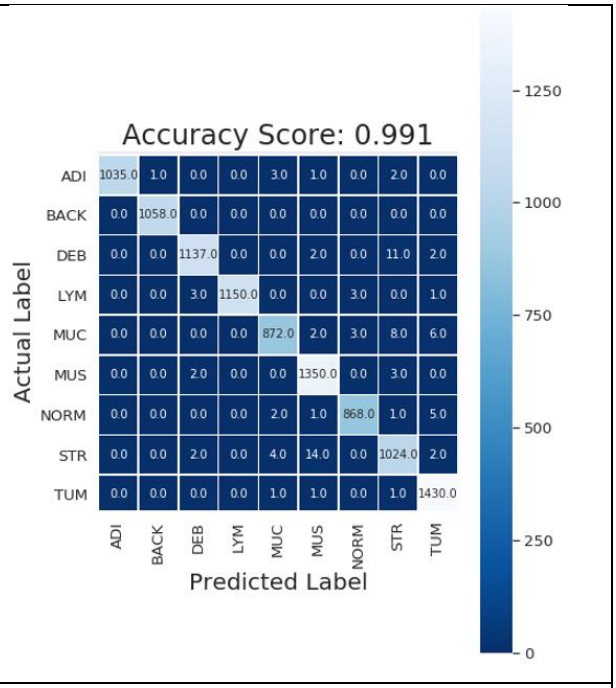

Figure 12. Confusion Matrix: VGG-16

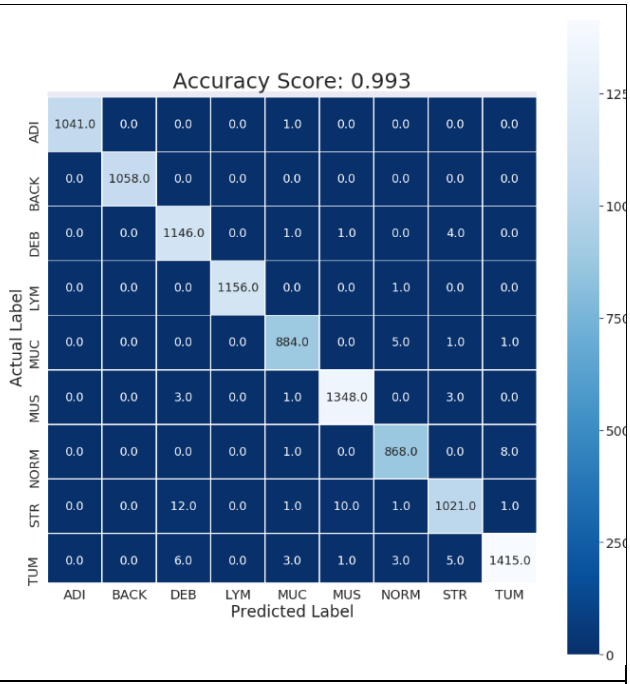

Figure 14. Confusion Matrix: Inception ResNet V2

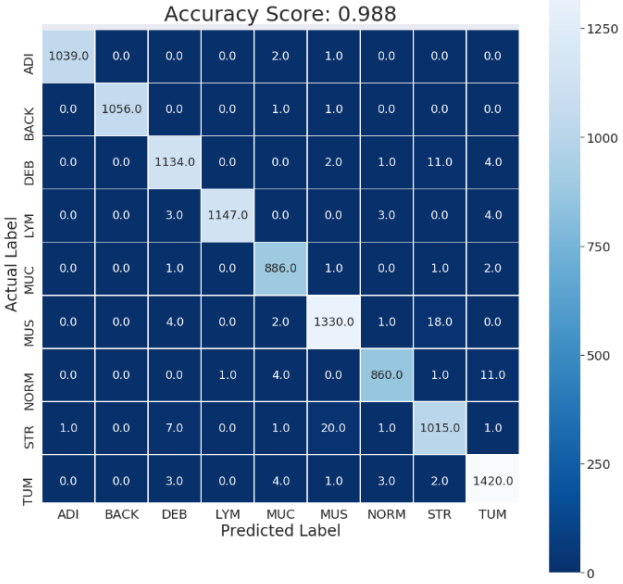

Figure 13. Confusion Matrix: Xception

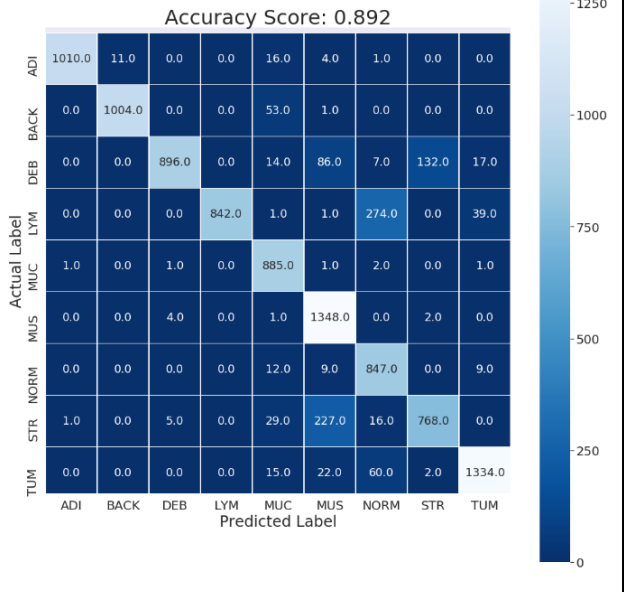

Figure 15. Confusion Matrix: DenseNet 121

B. Results

In this section, we present the experimental result and analysis of our model for the classification of colorectal tissue using 3 datasets namely Kather-texture-2016-image, CRC-VAL-HE-7K and NCT-CRC-HE-100K and it perform a comparison between four pre-trained models i.e. DenseNet121, Xception, VGG16 and InceptionResNetV2, , and. We present our evaluation using various performance factors. The information provided contains details about the essential layers and the total number of trainable parameters for each layer in the network.

Epoch: An epoch signifies a complete cycle through the entire training dataset during the model training process. The training phase is segmented into epochs, wherein the model processes the entire training dataset, and its weights are adjusted based on the calculated error or loss from the training data.

The number of epochs is a configurable hyperparameter in machine learning model training, allowing the selection of how many times the learning algorithm iterates through the entire training dataset. Insufficient epochs may lead to underfitting, indicating the model hasn't captured the data patterns adequately. On the contrary, a huge number of epochs

leads to overfitting, where the model becomes excessively specialized to data on which it was trained on, it tends to struggle when confronted with unseen data.

To reduce these issues, it is common to evaluate the model's performance on a different validation Dataset during training. The process of training may be stop when the model's performance on the validation data shows signs of degradation, by a method known as early stopping. This technique helps in preventing overfitting, which in result enhances the model's generalization capabilities to perform good on new and unseen datasets.[19]

Epoch of the four pre-trained models are as follows:

A. VGG 16

B. Xception

C. InceptionResNetV2

D. DenseNet 121

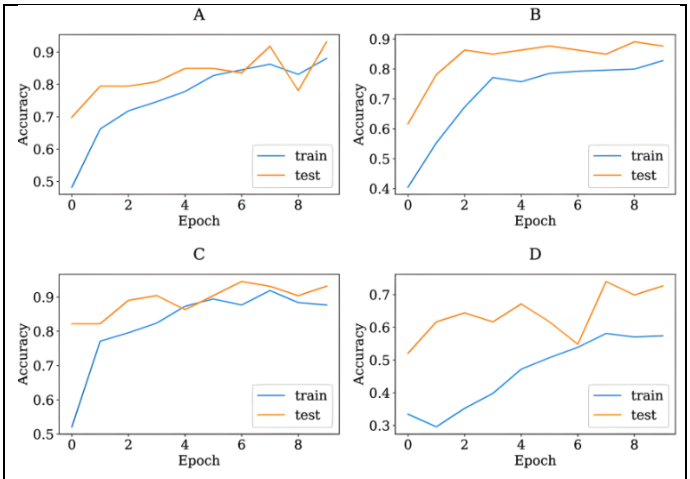

Figure 16. Epochs of the four pre-trained model

Final Accuracy:

Parameters	Xception	Inception ResNet 2	DenseNet121	VGG16
Acc (%)	95.2	94.2	87.2	97.6
F-1 Score	0.95	0.94	0.85	0.96
Spe(%)	97.4	93.8	86.8	98.4
AUC	0.96	0.95	0.89	0.97
Sen (%)	95.4	95.7	85.6	96.8
FPR(%)	5.4	7.6	10.8	2.0
FNR(%)	5.1	4.2	10.3	3.7
Pre (%)	95.2	92.5	84.7	96.1

Table 3. Final Accuracy of the 4 pre-trained models

V. CONCLUSION

Our research shows different models used to automate the classification of colorectal tissue in histopathology. By using new and emerging technologies like ML , image processing and some advance deep learning algorithms, we tried to make a significant approach to classify the colorectal tissue samples. Our work highlights the following main points:

- **Improved Accuracy:** We made our methodology such that it increases and enhances the accuracy to classify the colorectal tissues by making to attempt to reduce the number of wrong diagnosed image to minimum.
- **Time Efficiency:** We tried to made our models more efficient and accurate such that it reduces the time and workload for diagnoses on the pathologists.
- **Consistency:** By the making the classification process automate we tried to produce consistent and more accurate results by modifying the pre-trained models.
- **Challenges:** Even though our results are promising, there are still many challenges that occurs including bad quality images in the data, non-predictable behavior of our deep learning models and the in-hand requirement of good and diverse datasets.

Future Directions:

Our research has made good and significant progress in in automated colorectal tissue classification but it has more scope for improvement so we propose few changes for future:

- **Data Augmentation and Diversity:** We can concentrate on gathering more accurate and diverse datasets with larger range of images that can improve the overall performance of the models. We can also explore more advance models to further improve the performance of our model.
- **Interpretable Models:** We can develop models with more understandability which can help in gaining trust among healthcare professionals and make further research to offer explanations for their predictions.
- **Integration with Clinical Workflows:** We should make efforts to collaborate with the clinical workplaces and laboratory for the effective use of our research by the doctors as well as pathologists.
- **Transfer Learning and Ensemble Methods:** Applying transfer learning and ensemble methods that can be used to improve pre-trained models for colorectal tissue classification.
- **Validation and Clinical Trials:** Clinical trials should be made for the models to judge the real-time efficiency of the model for the diagnosis and detection of colorectal cancer tissues.

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