

Transfer Learning Based Model for Colon Cancer Prediction Using VGG16

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Abstract— Colon cancer, or a colorectal cancer, is a malignant neoplasm that originates in the colon. It is one of the most prevalent forms of cancer globally, with significant impacts on morbidity and mortality rates. The essential task is to detect it and detect it at an initial phase for curing the patient precisely. The artificial intelligence plays important roles in the colon cancer prediction. The authors proposed various models on colon cancer prediction using ML and DL. The existing approaches are unable to achieve good accuracy for the colon cancer prediction. This research work suggests a transfer learning based framework for the colon cancer prediction. This framework is planned on the basis of VGG16 and CNN in colon cancer prediction. The proposed framework is implemented in python and results is analysed concerning accuracy, precision, recall.

Keywords— colon cancer, CNN, Transfer Learning, VGG16, Deep Learning

I. INTRODUCTION

In 2018, global cancer data indicated that CRC ranked as the second prevalent cancer all around the globe. It accounted for around 10% of all yearly cancer cases in people [1]. While CRC predominantly affected individuals aged 65 and older, younger patients also faced significant risks. The leading risk factor was heredity, contributing to 35% of cases, followed by other factors like obesity, unhealthy eating habits, and smoking. Unfortunately, there has been no downward trend in these rates, and projections suggest a concerning increase of more than 60% in the next decade. This surge could lead to over numerous fresh CRC cases and more than one billion mortality rate [2]. Consequently, there is an urgent requirement of constructing a promising technique in order to diagnose colorectal cancer patients accurately at premature phase. Predictable screening plays a pivotal role in reducing mortality rates, with colonoscopy being the primary and preferred clinical method for CRC diagnosis. This endoscopic procedure allows for effective detection. In addition to colonoscopy, other medical imaging techniques play a crucial role in detecting colorectal cancer (CRC). CT colonography is one such method, serving as a harmonizing imaging approach to detect polyp in colorectal cancer. Additionally, computing H&E slides histologically is quite a challenging task to examine colorectal cancer [3]. However, the traditional manual observation of these imaging modalities, which the doctors accomplished, is criticized as naive, burdensome, and laborious. Moreover, inter-observer variation leads to biased analysis in terms of cancer tumor typing and grading. To address these challenges, there is a

growing interest and demand for a more standardized and automated approach depending upon a CAD in recent times. These methods are widely used in conventional radiology, aiding doctors in various applications, such as better chest X-rays and mammography since the 1960s, and enabling cancer detection in advance in the 2000s [4]. Given the significant medicinal and financial burdens about predicting and curing the colorectal cancer, the development of Computer Aided Diagnosis systems is taken place to detect colorectal cancer at primary phase. The evolution of these method is traced from traditional frameworks which required composite mathematical a priori information [6–8] to recent ML-based mechanisms capable of surpassing human levels of accuracy. ML is a kind of AI which helps computers in learning tasks or predicting outcomes without explicit programming. Coined by Arthur Samuel in 1959, machine learning empowers computers to learn without being explicitly programmed [5]. It has proven effective in solving various problems, including classification tasks, such as determining whether a patient has colorectal cancer, as illustrated in Figure 1.

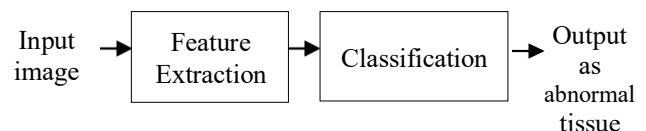


Figure 1. An example of colorectal cancer classification using ML.

To accomplish such a process, learning data from a dataset containing precise occurrences of cancerous and non-cancerous CRC cases is essential for computer program. Thus, a framework capable of generalizing afar this data is built. The efficacy of the model would be evaluated using quantitative performance metrics like accuracy, sensitivity, and specificity to ensure proper classification of previously unseen colorectal cancer cases. Machine learning approaches are categorized into supervised, unsupervised, and semi-supervised learning [6]. In initial one, the model improves its accuracy after the comparison of its output against the provided correct outputs after being trained on a collection of examples. This process is also known as learning from patterns or learning from instances. Supervised learning tasks

include classification and regression. DT and SVM are comprised in this category [7].

Decision Tree is a versatile ML method used to classify data and regression tasks, with a stronger preference for solving classification problems. The core idea behind Decision Trees is to use features from the dataset to create yes/no questions and iteratively split the data until each class is isolated. On the other hand, SVM is an algorithm which starts by identifying a hyperplane and then classifies the classes accordingly [8]. SVM is widely used in classification analysis due to its higher accuracy and quick speed, especially for relatively minor data sets. It effectively enhances generalization by minimizing the structural risk of the learning machine. As a result, SVM has proven to be efficient and effective for various classification tasks, ensuring optimal risk management and maximizing generalizability [9].

In general, the second category is implemented for detecting the anonymous patterns in the data and deploying them for concluding rules. This category performs well in case of unclear kinds of data. no label is assigned to the data used to train model. this approach is a kind of challenge to recognize unseen structures in unlabeled data and is called statistic-based method to perform learning. KMC method is executed to cluster an unlabeled dataset into distinct clusters [10]. The primary goal of clustering is to divide the data points into clusters, ensuring the similarity among points within every group and different from those in other groups. Moreover, the grouping data is contained on the basis of their factors without relying on predefined labels or classes. The K-Means algorithm works by identifying optimal cluster centers (centroids) and assigning data points to the nearest centroid based on their feature space distances. As a result, it facilitates the creation of groups of data points that share common characteristics within each cluster, making it a valuable method for various data exploration and pattern recognition tasks [11]. Semi-supervised learning represents a valuable approach that combines the characteristics of both supervised and unsupervised methods. In supervised learning, every observation is provided with labels, while in unsupervised learning, no labels are available for the observations. However, there are situations where only a few observations have labels due to the high cost and specialized human expertise required for labeling. In such cases, semi-supervised algorithms offer a suitable solution for building models. They can effectively handle classification, regression, and prediction tasks even when only a portion of the data is labelled [12].

Deep learning, a subset of machine learning, empowers computers for learning from their practices and represent the world in a hierarchical manner, with every concept built upon simpler ones. In healthcare radiology, cancer diagnosis using DL is garnered significant interest. However, inclusive analysis focusing on diverse factors of detecting and predicting colorectal cancer based on Deep Learning approaches are scarce [13]. DL reduces the reliance on explicit human input for providing the computer with knowledge, as it learns from accumulated experience. The

hierarchical structure of concepts allows computers to grasp complex ideas by building upon simpler ones. Despite the relatively recent terminology "deep learning," the field has roots dating back to the 1950s. Figure 2 showcases how DL classifies the colorectal region as either normal or abnormal.

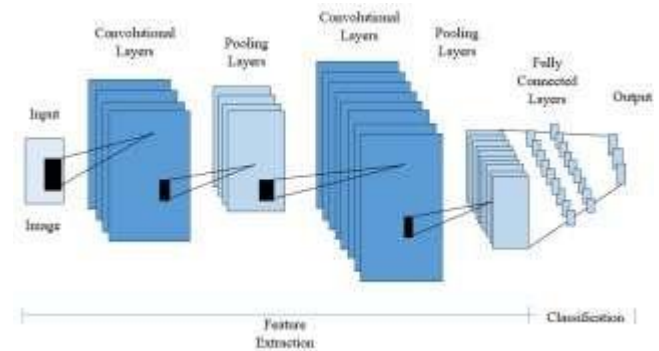


Figure 2. Classification of colorectal cancer using Deep Learning

There are three main categories of deep learning architectures, each serving different types of applications: supervised, unsupervised, and ensemble DNs [14]. The initial one involves training a model using labeled data to improve its performance. In the context of analysing clinical images, CNNs are widely used as a popular supervised learning architecture. Unsupervised learning, on the other hand, enables a computer in recognizing patterns and features from input data with no use of labeled data. Autoencoders are a type of unsupervised learning technique commonly utilized for this purpose [15]. Both CNNs and AEs are robust and effectual deep learning algorithms applied to tasks related to colorectal cancer detection and analysis. The last kind of algorithms are created with an integration of numerous deep learning models to achieve enhanced and more powerful results for specific applications. These networks leverage the strengths of different models to improve overall performance and outcomes [16].

II. LITERATURE REVIEW

Sakr, et.al (2022) suggested a novel lightweight CNN-based DL framework with the purpose of detecting colon cancer [17]. The initial task of this framework was to normalize the input histopathological images. Thereafter, the suggested framework employed these images in order to detect colon cancer. A public dataset consisted of histopathological images was executed for analyzing this framework against the traditional methods while diagnosing colon cancer. The experimental outcomes indicated that the suggested framework was effective for detecting colon cancer and yielded an accuracy up to 99.50%. Moreover, this framework worked more successfully in contrast to others.

Yang, et.al (2023) introduced a technique to detect and segment the colon polyp on the basis of MRCNN with PrROI [18]. There were two stages in this technique. Initially, the primary image was filtered using an image filter when the image data of lower level was filtered out. The next stage

focused on splitting the screened pictures into several groups in accordance with patients and transmitting them into the enhanced MRCNN to train the data. Hence, the consistent private framework of every patient was generated. The introduced technique was quantified on the datasets taken from an open source and a Chinese hospital. According to experimental results, the introduced technique was applicable for detecting colon cancer at average-precision (AP) up to 76% and segmenting the colon polyps at IOU around 0.8687. This technique was useful for doctors to diagnose and segment the polyps during colonoscopy.

Hasan, et.al (2022) investigated a mechanism to detect and classify the colon adenocarcinomas for which a DCNN algorithm was exploited with some preprocessing methods on digital histopathology pictures [19]. The colon adenocarcinomas were the major reason behind the life loss in the colon cancer. Thus, the major task was to distinguish the images as benign and malignant illnesses. Artificial Intelligence (AI) was an effective method for detecting colon cancer automatically at initial stage and it consumed lower cost. MDL and DIP methods were adopted for this purpose. The experimental outcomes revealed that the investigated mechanism had performed well for analyzing the cancer tissues at an accuracy of 99.80%. Additionally, this mechanism was helpful for generating an automated and reliable system which were efficiently detected several kinds of colon cancer.

Javed, et.al (2020) formulated a new MCC-based mechanism to phenotype the tissue when the cell-level attributes were incorporated in a graph-based hierarchical model to diagnose colon cancer [20]. Unlike the traditional techniques, this approach was capable of detecting colon cancer. Afterward, the texture, alpha diversity and multi-resolution deep attributes were utilized for developing the cell-level graphs. These graphs were emphasized on evaluating the cellular connectivity attributes and a patch-level multiplex network was built on the basis of these features. In addition, a new objective function (OF) was deployed for evaluating the multiplex cellular communities and a subspace of lower dimensionality from every cellular network. The Grassmann manifold was implemented to exploit the given subspace. Three public datasets were executed for conducting experiments. The results exhibited the supremacy of the formulated algorithm over the conventional methods.

Radhakrishnan, et.al (2023) developed an effective method to detect the colon cancer [21]. This method had diverse stages in which various histopathological pictures of the colon were collected, features were extracted, filtered, and the images were classified for distinguishing the healthy images from the cancerous ones. The image was transformed into grayscale. The filters were adopted for mitigating the image noise. The K-Mean (K-Mean), Fuzzy C-Means (FCM), and Fast Fourier Transform (FFT) methods were assisted in extracting the features. The values were recorded and stored after normalization. This method focused on evaluating diverse factors for every calculation. Furthermore, a classification method was executed for converting the nonlinear data into linear data. The developed method was useful for doctors to analyze higher volume of tissue samples consuming least

time every day and make the decision after diagnosis of colon cancer.

Nayagam et.al (2022) designed an effectual scheme for diagnosing colon cancer in advance and providing considerable treatment for alleviating the death rates [22]. The histopathological images were deployed for classifying the images. A Convolutional Neural Networks(CNN) based technique was employed for detecting the colon cancer. After that, the deep learning (DL) method was implemented for differentiating amid the normal and unhealthy large intestine tissues. The CNN technique was trained on the basis of ten thousand images. In addition, this scheme aimed to illustrate the total metrics of employed technique. This process resulted in performing epoch/iteration and offering accuracy and the loss as output. The designed scheme yielded 99.7% accuracy for detecting and classifying colon cancer and lessening the efforts of pathologists while diagnosing the colon cancer.

Sarwinda, et.al (2021) intended a DL technique in classifying and detecting the images of colon cancer based on ResNet model [23]. This technique was effective for classifying the cancer from medicinal images of colon. The images of colon glands were utilized for training ResNet-18 and ResNet-50 algorithms so that the colorectal cancer was classified benign and malignant. According to the experimental outcomes, the higher reliability was obtained from the latter algorithm over the initial one concerning accuracy, sensitivity, and specificity. The analysis depicted that the utilized algorithms were robust for detecting colon cancer at an accuracy within 73% -88% and sensitivity 64%-96% for classifying the colon cancer as benign and malignant. The intended technique worked reliably and generated optimal results for analyzing the biomedical image.

Sharma, et.al (2020) constructed a two-phase approach for diagnosing the colorectal cancer [24]. The initial phase was emphasized on extracting the frames of colonoscopy video and rating them as considerable in case of presence of a polyp. The subsequent phase was executed for aggregating these outcomes so that a decision was taken for classifying the frame into cancerous and normal. An evaluation was conducted on diverse deep learning (DL) methods, such as VGG16, VGG19, Inception V3, Xception, GoogLeNet, ResNet50, ResNet100, DenseNet, NASNetMobile, MobilenetV2, InceptionResNetV2 for executing this process. The outcomes demonstrated that the constructed approach performed well with VGG19, and offered an accuracy of 95.75% for diagnosing colon cancer.

Babu, et.al (2022) suggested a methodology for detecting colon cancer on histopathological colon images [25]. First of all, this methodology aimed to normalize the images in a color stain way and improve the contrast of the picture. Thereafter, the largest connected component was discovered after segmenting the images. This segmented region was assisted in extracting DDDT-DWT coefficients through which the details regarding the structure and boundary of the colon cells were obtained. FCM algorithm was further put forward in mitigating extracted attributes. The artificial neural network (ANN) algorithm, whose optimization was done with salp swarm optimization (SSO), was adopted for

classifying the images as healthy and cancerous. The experimental results confirmed that the suggested methodology was robust for detecting colon cancer and offered an accuracy of 95% on utilized datasets.

III. DESIGN AND IMPLEMENTATION

Following are the various phases of proposed model:

Input image colon cancer detection: Around 20280 pictures are included in the dataset whose classification is done into tumorous or non- tumorous. The labels are assigned to only 10284 pictures for cell-type namely fibroblast, inflammatory, epithelial, and others and no label is assigned to rest of the images for cell kind.

Classification: The transfer learning model is applied for diagnosing colon cancer. TL is the combination of VGG16 and CNN. The VGG16 is used as the base model over which CNN model is used for the training. The structure of this algorithm is depicted in given figure 3.

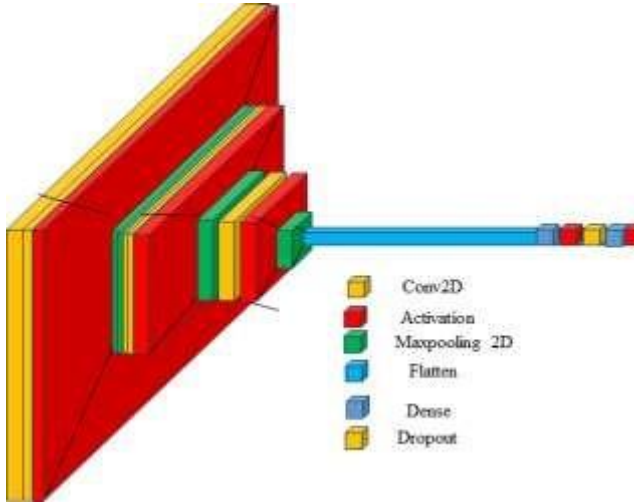


Figure 3: VGG16 Model Architecture

Following are the various specifications of VGG16 Model:

- Sixteen layers having weights are utilized in this model. This model is composed of twenty-one layers: 13 conv. layers, 5 MP layers and 3 dense layers. However, 16 weight layers are from weight layers i.e., learnable parameters layer.
- The tensor size of 224, 244 with 3 RGB channel is deployed for input.
- Rather than the deployment of huge amount of hyper-parameters, this model focuses on convolution layers with 3x3 filter with stride 1. Most unique thing about VGG16 is that instead of having a large number of hyper-parameters they focused on having convolution layers of 3x3 filter having stride 1, and the same padding and maxpool layer with 2x2 filter of stride 2.
- The entire structure aims to arrange both layers

- Around 64 filters are comprised in Conv-1 Layer, 128 in Conv-2, 256 filters in Conv-3, 512 filters in Conv-4 and Conv-5.
- A stack of conv layers is composed in 3 FC layers in which 4096 channels are comprised in first 2 layer each, the third leads to classify data in 1000-way ILSVRC way and therefore one channels (one for each class) are contained. The last layer is called softmax layer.

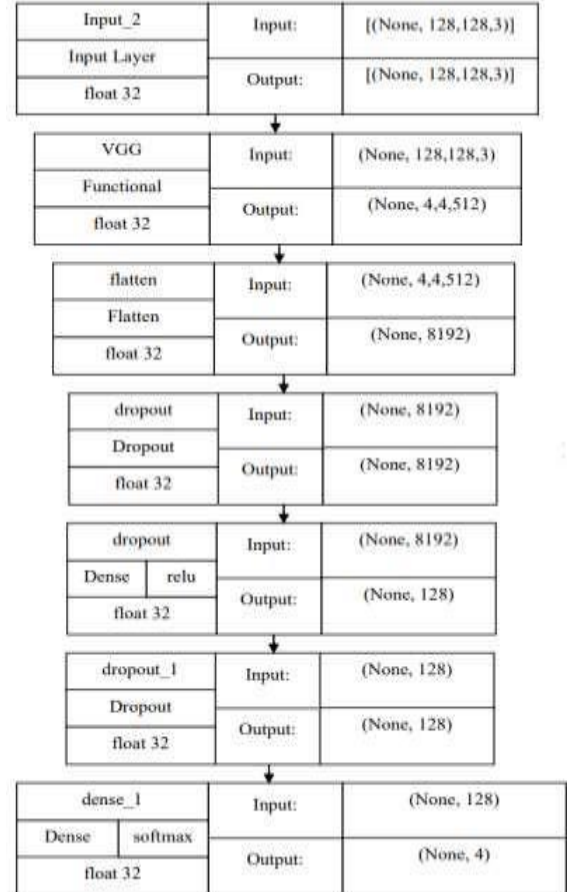


Figure 4: Proposed Model

IV. RESULT AND DISCUSSIONS

The dataset comprises 20,280 images, with 10,284 of them having labels for specific cell types such as fibroblast, inflammatory, epithelial, and others. The remaining 9,996 images lack cell type labels. The distribution of cell types in the labelled subset shows that epithelial constitutes 42%, inflammatory comprises 26%, fibroblast represents 18%, and others account for 14% of the labelled images. The images are categorized into two classes: "Cancerous" and "Non-Cancerous." Approximately 33% of the images belong to the "Cancerous" category, while the remaining 67% are labelled as "Non-Cancerous." This dataset could be valuable for various tasks, including image classification and recognition, as well as potentially exploring the relationship between different cell types and cancerous conditions. However, it's worth noting that the percentage of cancerous images is

relatively low, which might impact the efficacy of certain ML algorithms.

As shown in figure 5, the dataset images have two classes which is having cancer and not. The cancerous and non-cancerous images are presented in classification.

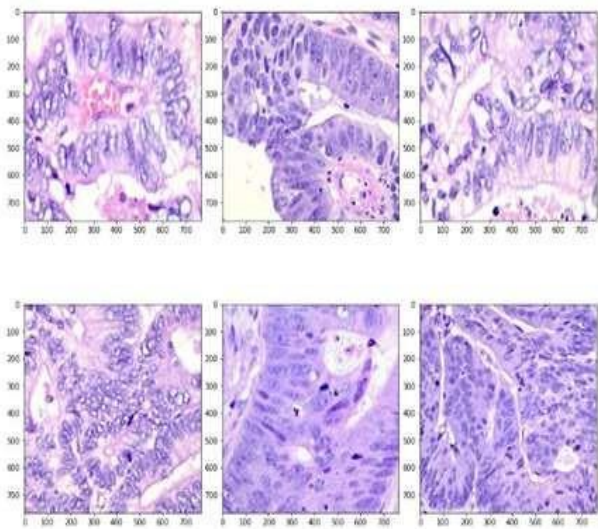


Figure 5: Dataset Images

As shown in figure 6, the dataset images have cancerous and non-cancerous cells. The non-cancerous cells images is 60% of the whole dataset and rest 40% is cancerous cell images.

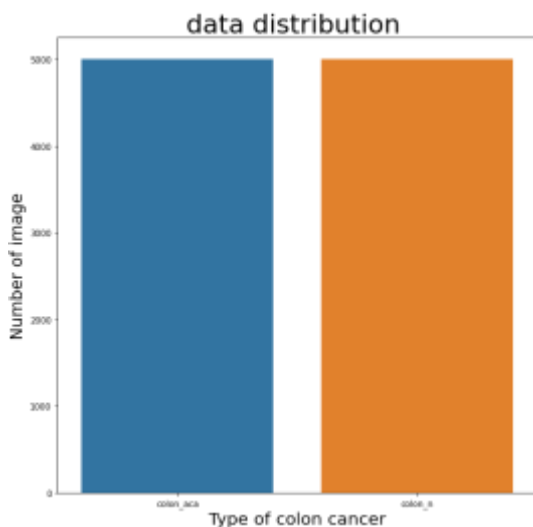


Figure 6: Dataset Distribution

As shown in figure 7, graph represents the proposed model loss in training and validation set. The proposed model has high model loss in validation set as compared to initial one. The x-axis is used to denote the epoch and y-axis for loss.

As shown in figure 8, The F1 score of proposed model is shown in training and validation set. The x-axis shows the epoch and y-axis shows F1-score. The F1 score of training is high as compared to validation set.

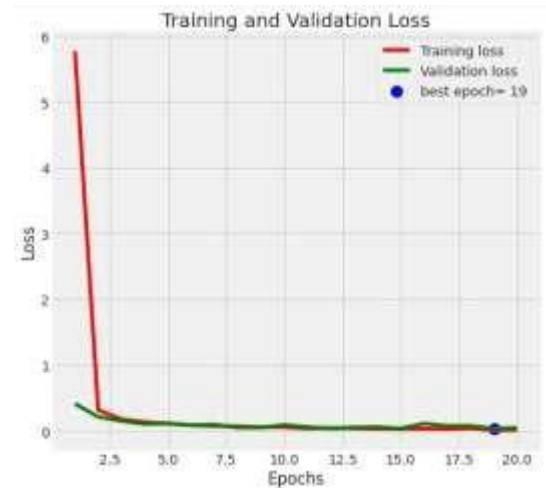


Figure 7: Model Loss

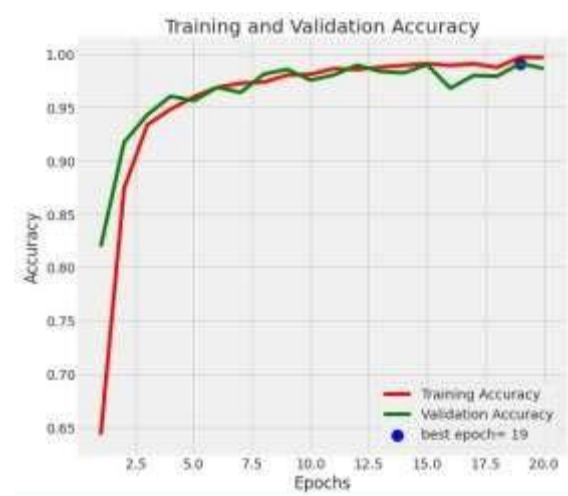


Figure 8: F1 Score of Proposed Model

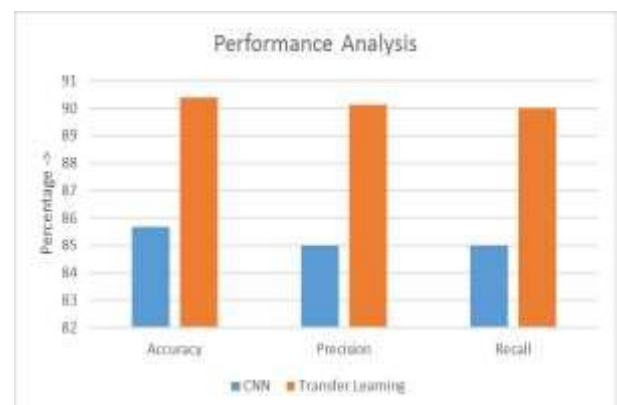


Figure 9: Performance Analysis

As shown in figure 9, the comparison of suggested framework is done against CNN. The suggested framework is transfer learning model along with VGG16 and Convolutional Neural Network. The suggested framework has high accuracy, precision and recall than transfer learning for colon cancer prediction.

V. CONCLUSIONS

In this paper, it is concluded that artificial intelligence has proven valuable in diagnosing colon cancer at initial phase through the analysis of clinical imaging and clinical data. CAD are useful for doctors for identifying suspicious lesions in colonoscopy or CT scans, potentially increasing the detection rate of early-stage tumors. The machine learning algorithms are proposed in the previous years for the colon cancer detection. It is analysed that algorithms which are already been proposed is unable to achieve good accuracy. In this research work, transfer learning based model is proposed for colon cancer prediction. The colon cancer prediction model is the combination of CNN and VGG16. The VGG16 is the based model and convolution layer will extract features for the classification. The proposed model is implemented in python and results is compared with CNN. It is analysed that proposed model achieve approx. 6 percent high accuracy in comparison with others. The future work will implement other TL models on place of VGG16.

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