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# HISTOPATHOLOGY IMAGE CLASSIFICATION USING HYBRID PARALLEL STRUCTURED DEEP-CNN MODELS

#### **Abstract**

The healthcare industry is one of the many out there that could majorly benefit from advancement in the technology it utilizes. Artificial intelligence (AI) technologies are especially integral and specifically deep learning (DL); a highly useful data-driven technology. It is applied in a variety of different methods but it mainly depends on the structure of the available data. However, with varying applications, this technology produces data in different contexts with particular connotations. Reports which are the images of scans play a great role in identifying the existence of the disease in a patient. Further, the automation in processing these images using technology like CNN-based models makes it highly efficient in reducing human errors otherwise resulting in large data. Hence this study presents a hybrid deep learning architecture to classify the histopathology images to identify the presence of cancer in a patient. Further, the proposed models are parallelized using the TensorFlow-GPU framework to accelerate the training of these deep CNN (Convolution Neural Networks) architectures. This study uses the transfer learning technique during training and early stopping criteria are used to avoid overfitting during the training phase. these models use LSTM parallel layer imposed in the model to experiment with four considered architectures such as MobileNet, VGG16, and ResNet with 101 and 152 layers. The experimental results produced by these hybrid models show that the capability of Hybrid ResNet101 and Hybrid ResNet152 architectures are highly suitable with an accuracy of 90% and 92%. Finally, this study concludes that the proposed Hybrid ResNet-152 architecture is highly efficient in classifying the histopathology images. The proposed study has conducted a well-focused and detailed experimental study which will further help researchers to understand the deep CNN architectures to be applied in application development.

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#### 1. INTRODUCTION

Medical technology professionals must work hard at developing durable and reliable classification techniques (Aziz, 2017). In the line of healthcare, data and image analysis must be a swift procedure to make sure that speedy diagnoses can ease the lives of numerous patients (Liang et al., 2021). Moreover, this would save the time of nurses and doctors when it comes to diagnosing minor diseases so as they can pay attention to more serious ones and investigate them. Progressive solutions for data and image analysis would also provide healthcare centers with the ability to generate treatment plans quickly. With instantaneous access to different databases and information sources, medical professionals are capable of raising success rates significantly as well as broadening the scope of available treatment options. By the means of advanced classification techniques for the analysis of healthcare data (Pramanik, Pal, Mukhopadhyay & Singh, 2021), professionals are capable of gaining insight into how they can generate precise and budget-friendly healthcare that is also of high caliber. It is with the assistance of such advanced artificial intelligence (Dwivedi et al., 2021) that early diagnosis can take place without leaving the patient unattended to and neglected until their symptoms worsen. High-tech classification techniques will also delve into meta-heuristic algorithms, learning schemes, mobile telemedicine clustering techniques, and brain-computer interfaces. These elements all group together to provide the highest quality patient care programs that are both cost and timeefficient for healthcare staff and customers. By creating a more responsive system of diagnosis and treatment solutions, the healthcare industry would reap the benefits of quick and easy healthcare delivered to all. Artificial intelligence (AI) (Dwivedi et al., 2021) technologies are especially integral and specifically deep learning (DL) (Djellali, Adda & Moutacalli, 2020) a highly useful data-driven technology. It is applied in a variety of different methods but it mainly depends on the structure of the available data. However, with varying applications, this technology produces data in different contexts with particular connotations. For instance, taking spatially correlated data as an example, it includes multiple imaging modalities that could range from radiology to pathology. Not just that but spatially correlated data exists in other forms such as patient monitoring systems that can be defined as electrocardiography (ECG) (Moon et al., 2004) or electroencephalography (EEG).

The future of cancer treatments would be completely revolutionized by the automated diagnosis that utilizes deep neural networks as classifier models as well as recursive feature elimination as a form of feature selection. The spatial-temporal features play a major role in the visual recognition task. CNN's are a very powerful source for the representation of classification results. These deep neural network models can directly extract the features from raw data. The convolution layers in CNN are designed with varying numbers of kernels and a well-suited stride to learn the features from the image. Further, the normalization layers improve data generalization and reduce overfitting. Activation function plays a significant role in classification task and pooling layers reduce the local convolution features complexity. Deep neural networks have a higher footing over other similar classification models such as SVM (Kaur, Singh & Kaur, 2019) since they work with multiple layers. Consequently, the multiple layers are administered to codify the breast cancer data and provide quick, automated, and correct results about it. Deep neural networks have previously been investigated in the Wisconsin Breast Cancer Dataset (UCI Machine Learning Repository, n.d.) from the UCI Machine Learning Repository

where the data was divided into distinct batches of a train-test split. Consequently, the system's functioning was measured upon the basis of precision, recall, specificity, sensitivity, and accuracy. However, deep neural networks are highly computation intensive, which require a lot of time in training depending on the complexity of the network and training data size (Eelbode, Sinonquel, Maes & Bisschops, 2021). By keeping these critical points in mind, the proposed research work uses different deep CNN architectures such as RESNET (Sarwinda, Paradisa, Bustamam & Anggia, 2021) with 50,101,152 layers, VGG16 (Guan et al., 2019), and Mobile Net to propose a hybrid model. While using this model we obtain feature output from the CNN model by removing the topmost classifying layer which provides the vector of features. The spatial features obtained are passed to the LSTM network for extracting the temporal features. LSTM as an advancement to the existing architecture makes it more suitable for the data with nature under consideration. With this set up this study aims to propose a transfer learning-based hybrid classification model which can work efficiently and effectively in the classification of cancer images. To accelerate the training time and computing power the proposed models utilize GPU computing using parallel computing library of tensorflow (TensorFlow Framework & GPU Acceleration. NVIDIA Data Center, n.d.) framework. The hybrid models presented here are evaluated for best performance and it is observed that ResNet152 surpasses the other model with the best performance. The model built here is developed in such a way that it can be trained for any type of microscopic cancer data set. Overall, the remainder of the paper is organized as follows: section 2 gives the brief methodology literature in constructing deep neural architectures. The proposed methodology and experimental results are presented in sections 3, 4, and 5 respectively. Finally, the last section concludes the study.

#### 2. LITERATURE SURVEY

In the recent era, breast cancer diagnosis from pathological images has got great attention from the research community. Kiranpreet Kaur et al (Kaur & Mittal, 2020) proposed the technique for extracting spatial-temporal features from the image for cancer detection. It is very important to understand which architecture may be suitable for data in consideration, before jumping to the conclusion. Hence this research work tried to understand the best deep CNN (Convolution Neural Networks) architectures for histopathological image classification. The mentioned work started with considering the pre-trained architectures such as ResNet, MobileNet, VGG16 and trained these models on the considered dataset. The design architecture generates multiple channels of data from input images and convolution is performed. The final feature representation is from all input data. The convolution architecture applied a group of hardware kernels to come up with feature information and encodes previous knowledge on features that results in high performance. The study about pre-trained CNN models proposed by Vijaya Gajanan et al. (Buddhavarapu & Jothi, 2020) proposes transfer learning techniques for architectures such as VGG Net, Inception Net, and ResNet to classify histopathology images. Convolutional neural networks are a class of feed-forward neural networks predominantly used for image processing. The CNN is a class of feed-forward networks with the input layer, convolution layer, pooling layer, fully connected layer, and output layer. The transfer learning technique uses the knowledge obtained by a deep learning model while solving the given

problem, which is transferred to solve related target problems. Generally, the weight of the deep learning model is initialized randomly during training the network from scratch. The transfer learning technique is favorable in two forms. First, when transfer learning is used as a feature extractor, this will be used in solving the target problems with little modification to retain the convolution and pooling layers of the pre-trained model and remove the final fully connected layer and the classifier layer of the pre-trained model. The resultant is called the feature extractor model. The feature extracted here is then fed to any traditional classification. It is also possible to add new fully connected layers and classifier layers here. Further, the study from Said Boumaraf et al. (Boumaraf, Liu, Zheng, Ma & Ferkous, 2021) proposed a new transfer learning model for the classification of histopathological images. In this work, the researcher proposed a technique for intrinsic feature learning using ResNet with a total of 18 layers. This study utilized these pre-trained models to implement the ResNet (Sarwinda et al., 2021) with 52,101 and 152 architectures. Further, the arrangement of layers in other architectures such as VGG16 and MobileNet varies with the number of convolution layers and resultant parameters. We further investigated the structure of these models to be able to use them for the methodology performed in this work. Qian Xiang et al. (Xiang et al., 2019) proposed a classification model based on a lighter model using MobileNet architecture. In this work, a transfer learning technique was used for fruit image classification using the Imagenet dataset. This also discussed strategies to replace the top layer of the base network with the convolution layer and softmax classifier. Also, this work also presented scenario about adding drop out to the newly added conv2d to reduce the overfitting.

Further, it is also studied that the early stopping (Leen, Dietterich & Tresp, 2001) technique is highly useful to control the overfitting of the designed model. Research work VGG16 (Simonyan & Zisserman, 2015) claimed to use smaller 3X3 filters in each convolution layer and combining it in a sequence of convolution. In VGG the configuration in case of depth increases significantly from left to right as per the study stated by Karen Simonyan et al. (Simonyan & Zisserman, 2015) as more layers are added. Along with this the convolution layer parameters are denoted as Conv.

The table 3 below shows the overall comparison of the different architectures.

Tab. 3. Comparison of CNN Networks

Comparison					
Network	Year	Salient Feature	top5 accuracy	Parameters	FLOP
AlexNet	2012	Deeper	84.70%	62M	1.5B
VGGNet	2014	Fixed-size kernels	92.30%	138M	19.6B
Inception	2014	Wider – Parallel kernels	93.30%	6.4M	2B
ResNet-152	2015	Shortcut connections	95.51%	60.3M	11B

This study is motivated by aforesaid literature to propose a better deep neural network architecture that is hybrid in design. It also observed that objects in an image are often related to each other. Images are however not sequential but carry some dependencies which can helpful in modeling them as a sequence of occurrences of certain objects. So these latent semantic dependencies can be modeled as a sequence of occurrences using

the LSTM network. As added proof, the work presented by SuvidhaTripathi et al. (Tripathi, Singh & Lee, 2021) prosed a bi-LSTM model for the classification of breast tumors. It is also important to note the parameters that a network use and the time it takes to represent the training data from the computational point of view. The core computing jobs of deep learning are matrix operations, and hence it is possible to turn this into many simple computing jobs. GPU (Haghighat & Juanes, 2020) as they contain many cores have got greater attention in training the deep learning models. General-purpose processors like CPUs have complex instruction systems and execute the instructions in the sequence which is good at processing a small amount of data. High-density computing jobs like deep learning data are complex and as the training data increases the model accuracy can be improved. The work presented by Ehsan Haghighat et al. (Haghighat & Juanes, 2020) was highly motivational to use Tensorflow (TensorFlow Framework & GPU Acceleration. NVIDIA Data Center, n.d.) GPU framework (Deep Learning Frameworks. NVIDIA Developer, n.d.) in our work in implementing these models in our study.

#### 3. PROPOSED METHODOLOGY

This study proposes deep learning model for classifying the histopathological images using intrinsic feature learning techniques based on the Residual CNN, VGG16, and MobileNet architectures. These architectures are pre-trained on ImageNet and this Pre-trained knowledge is used as the backbone model in our approach. The proposed approach firstly normalizes the dataset images, followed by this a three-fold data augmentation is applied on the train set. Following this, we apply the transfer learning method based on the block-wise fine-tuning strategy to transfer the learned from the ImageNet dataset to the medical image data set used in this work. The research work presented here basically modifies the existing architecture by adding a parallel LSTM layer to build a hybrid network. This study Proposes hybrid LSTM model architectures for ResNet, MobileNet, and VGG16. Experimental setup and methodology used are brifly discussed in following sections.

## 3.1. Transfer Learning

This study uses Transfer Learning (TL) (Zhuang et al., 2021) technique to address the challenge of requiring millions of images to train a deep learning model. In TL technique a network is trained on a base dataset to learn general features of image. The learned features are then transferred to another network to train the network on a target cancer dataset (Figure 2). In this phase the weights of pre-trained networks are transferred to the network to fine-tune it for a complex dataset of histopathological images. The approach is utilized by fine-tuning the layers of the network. All the layers are retrained on the target dataset and the initialization of weights has been carried out from the pre-trained weights in fine-tuning. Using this technique the proposed work handle the scarcity of the dataset and high computational cost (Boumaraf et al., 2021). The layer specialization, size, and complexity of the dataset are some factors that need to be considered while implementing transfer learning (Sertolli, Ren, Schuller & Cummins, 2021) which carefully considered in this phase.

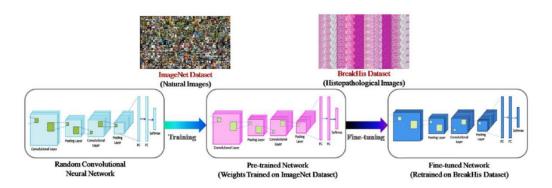


Fig. 2. Illustration of the transfer learning (TL) approach

The complexity of the dataset is a major concern as it affects the generalization of acquired information during the training process. The influence of layer-wise fine-tuning of a pre-trained network on the performance of the model on BC histopathological images has been demonstrated using the proposed approach. The experiment is performed by employing VGG16+LSTM, Mobilenet+LSTM, and Resnet152+LSTM using the BreakHis dataset. It is important to emphasize that the aim is not to achieve state-of-the-art performance but to explore the influence of knowledge transfer from natural images (simpler dataset) to histopathological images (complex dataset). Moreover, this work is based on an assumption that the transferring of weights from natural images to histopathological images would lead to better performance, irrespective of their domain.

#### 3.2. Training Protocol

The network is trained using a backpropagation algorithm (Improving the convergence of back-propagation learning with second-order methods – NYU Scholars, n.d.) to minimize the cost function (C) concerning the weights (W), defined as:

$$c = -\frac{1}{|m|} \sum_{i}^{|m|} \ln(p\left(\frac{n^{i}}{m^{i}}\right)) \tag{1}$$

Where |m| implies the number of images in the training set,  $n^i$  represents the label correspond to the i<sup>th</sup> image of the training set and  $p(n^i/m^i)$  denotes the probability of  $m^i$  to be classified correctly. The cost function is optimized by the stochastic gradient descent (SGD) method which is a powerful tool of optimization in machine learning. SGD considers only a few training samples to follow either the negative or positive gradient of the cost instead of the entire training set and leads to fast convergence at a minimum cost. Consider, C as the cost over a mini-batch of size X and  $W_{je}$  as the weights in the jth convolutional layer at e epoch (iteration). The updated weights in the next epoch are computed as:

$$\gamma^e = \gamma^{\left[\frac{e^N}{|m|}\right]} \tag{2}$$

$$V_e^{e+1} = \mu V_j^e - V^t \alpha_j \frac{\partial \hat{c}}{\partial W_j}$$

$$W_j^{e+1} = W_j^e + V_j^{e+1}$$
(3)

where  $\gamma$  represents the scheduling rate,  $\mu$  denotes the momentum, and  $\alpha_j$  represents the learning rate of the jth layer. The scheduling rate is used to reduce the learning rate according to a pre-defined schedule with the progression of training, while momentum is a moving average of gradients and is used to update the weights in the network. The value of all these parameters are adjusted during the experiment by an extensive set of trial and found 0.001, 0.9, and 0.95 as a reasonable choice for the learning rate, momentum, and scheduling rate, respectively. A batch of size 500 along with 75,150,200 numbers of epochs per layer is considered for the training process.

## 3.3. Proposed framework

The proposed models are developed using the pre-trained CNN with LSTM layers for feature vector extraction on medical dataset. Objective of combining LSTM is to sustain sequence prediction as presented in Figure 3.

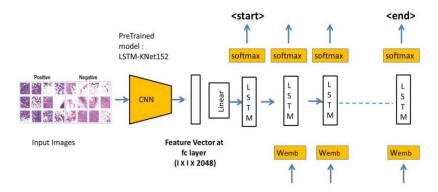


Fig. 3. Illustration of the overall design of proposed models using parallel LSTM layer

The pre-trained models specifically VGG 16, MobileNet, ResNet152, Resnet101, and Resnet50 are used for feature vector extraction. They were trained by quite 1.3 million images obtained from the ImageNet (Deng et al., 2010) database. ImageNet is one of the highest datasets in DL and is right to be used within the pre-training part of the model, due to its popularity and data diversity. Here the feature yield from the CNN model is obtained by removing the topmost classifying layer which supplies a vector of features. Here the feature yield from the CNN model is first obtained by removing the topmost layer which provides a vector of features. The spatial features we obtained from the CNN model are passed to the LSTM architecture for extracting temporal features to pass to the trained model for action classification. At Last, a softmax classifier is added to construct the prediction of those high-level features.

The proposed hybrid models are tested for best suited deep learning architecture to classify the histopathology images. The following section will reflect a detailed experimental setup used to evaluate the performance of the model. As it is evident from the results the proposed resnet152 architecture with LSTM network outperformed among other models and hence it is proposed with the name LSTM-KNet152 architecture from this study.

### 3.4. Model parallelism using TensorFlow

Long Short-Term Memory is a powerful network to solve the problem of long-term dependence in the recurrent neural network. This has got attention because of its ability to refine internal processing units to store and update context information efficiently. At each time LSTM takes the input value $X_t$ ,  $h_{t-1}$  at the previous time and a value  $C_{t-1}$  at the final time. Here the output is the current time  $h_t$  with current state  $C_t$  respectively. Therefore the forget gate  $f_t$  will determine the information that cell discards using the equation:

$$f_t = \sigma(W_f[h_{t-1}, x_t] + b_f) \tag{4}$$

Here  $\sigma$  represents activation function, W and b are weight and bias respectively. The forget gate  $f_t$  outputs the value '0' or '1' by taking  $x_t$  and the cell state  $h_{t-1}$  of the previous moment. Here '1' means TRUE and '0' means FALS. Then the cell will predict the value to be updated using:

$$i_t = (W_i[h_{t-1}, x_t] + b_i) (5)$$

$$C_t^{\sim} = \tanh(W_c[h_{t-1}, x_t] + b_c) \tag{6}$$

The sigmoid layer determines the value to be updated. A tanh layer will create a new candidate value vector. The status is then updated by cell from  $C_{t-1}$  to  $C_t$  thereby the output  $h_t$ :

$$C_t = f_t * C_{t-1} + i_t * C_t^{\sim} \tag{7}$$

$$h_t = o_t * \tanh(C_t) \tag{8}$$

The expanded LSTM model can obtain repetitive network structure and share parameters among each network, the parameters of training are relatively reduced and the model can be extended to different length sequences. Therefore this allows the LSTM model to be used for sequences of varying length.

The network structure proposed in this study is described in Figure 4. The main objective is to improve the convergence speed of the model. The network presented here is designed to have a parallel LSTM module to improve the learning thereby promising to produce better performance. In this study, we first normalize the input images. Followed by this we extract two different feature representations using these two parallel modules. First, the CNN module is employed to learn the details of features in histopathology cancer images. To get a better training effect we make use of pre-trained CNN architectures such as MobileNet, VGG-16, ResNet-101, and ResNet-152. Further from which we feature the

Resnet with 150 layers with the power LSTM module outperforms all the remaining architectures. Hence from this study developed a hybrid model we term LSTM-KNet152. The model structure of CNN is shown in Figure 4.

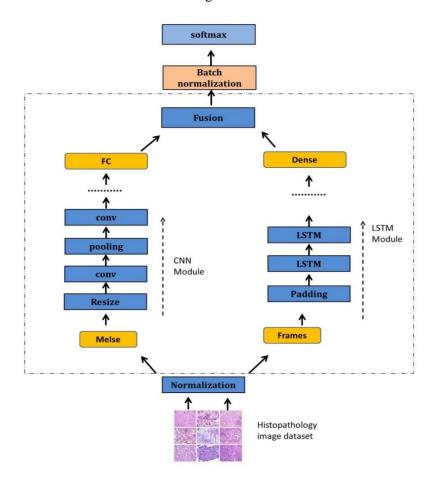


Fig. 4. Proposed parallel model structure

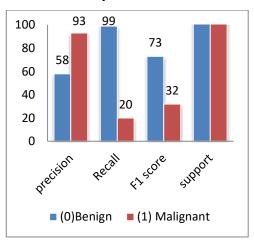
There are five convolution layers, three pooling layers, and two fully connected layers in all proposed model structures. Since most convolutional neural networks need fixed inputs size, in this work we will resize images  $Mels \in R$   $^{TXFXC}$  into  $227 \times 227 \times 3$ . Here the resize operation is performed using bilinear interpolation. During the same time model uses LSTM to learn the temporal changes of cancer images. LSTM model can handle variable length features by feeding it image features. To accomplish the requirement of the model, these features should be zero-padded into the same dimension. When the time steps are outside the range of actual data length, the LSTM internal parameters stop updating. The model structure of LSTM is shown in Figure 4. Followed by this, we integrate two different types of high-level features. To maximize the convergence speed and avoid gradient diffusion of training, the output was normalized by batch normalization. Finally, a softmax classifier is used to classify histopathology images into benign or malignant.

#### 4. PERFORMANCE EVALUATION

The experiment in this study is conducted by using Breast Cancer Histopathological Database (BreakHis) (Spanhol, Oliveira, Petitjean & Heutte, 2016). This database consists of 9,109 microscopic images of breast tumor tissue collected from 82 patients using different magnifying factors (40X, 100X, 200X, and 400X). As per the present update, this database contains 2,480 benign and 5,429 malignant samples (700X460 pixels, 3-channel RGB, 8-bit depth in each channel, PNG format). The proposed methodology in our experiment is evaluated based on transfer learning techniques applied to popular architecture such as MobileNet with LSTM, VGG-16 with LSTM, ResNet-101 with LSTM, and ResNet-152 with LSTM. This study is conducted to evaluate the best architecture model to be proposed for histopathology cancer image classification. The performance of the classifier for the transfer learning approach is examined using accuracy, precision, recall, F1-score, and support. Further, to make the model learn the input information over sufficient large iterations of the epoch, model performance is evaluated for a set of 150, 200 epochs. Further, to address the overfitting issue we have implemented early stopping criteria where all considered models produced the best performance. For each set of the experiment, the considered dataset is divided into 90%:10% for training and testing respectively, and the training set is further divided into 80% for training purposes and 20% for validation purposes. The splitting of the dataset is done in a manner that the patients involved in the building of the training set are not included in the testing set. In this study, we use a parallel computing framework to address the computational complexity imposed by these deep CNN architectures. We use NVIDIA RTX2060 GPU combined with the power of the TensorFlow-GPU framework to accelerate the training speed. This GPU has 1,920 CUDA cores with 240 tensors that can deliver 52 teraflops of deep learning horsepower. This is a powerful addition to our developed network to make it further trained in parallel using these multiple cores. Our effort in this study at the same time lies in proposing a highly parallel training technique applied to accelerate the training time of this deep architecture on a single GPU. This highly favorable in the cost of resources required to implement these deep architectures.

This study proposes the novel deep learning architecture using well-known existing architecture like VGG-16, Mobile Net, ResNet-101, and ResNet-152. Existing architecture are reused by combining them with LSTM network to form a hybrid model. The contribution of this work is to present the best-suited hybrid architecture for the classification of pathology cancer images. Even though the model is pre-trained using the Imagenet database, in order to make model to learn cancer image features the network is fine-tuned using the BreakHis data set. Further, it also noted that the developed model is efficient to classify any random new microscopic image provided related features are modeled in advance. During initial trial, experiment utilizes 2000 images for validation. The deep learning model is trained for different values of epoch and the performance of the model is recorded. The following tables depict the overall performance of the models for different epoch values; it is evident that the early stopping technique is significant in solving the overfitting problem. Hence the models produce the best performance with the learning rate noted.

## **Hybrid MobileNet Model Performance Comparision**



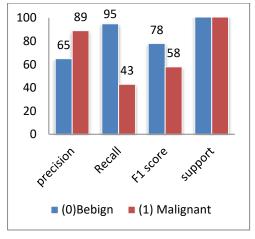
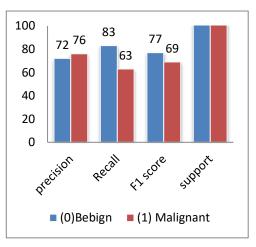


Fig. 5. model Performance for epoch 100

Fig. 6. model performance for epoch 200



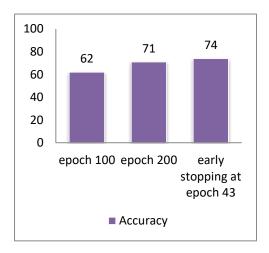
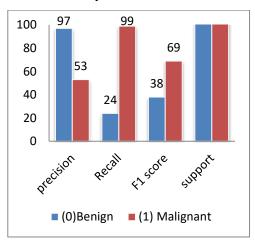


Fig. 7. early stopping at epoch 43

Fig. 8. Accuracy of model

To follow the best practice of training the model, experiments are conducted for epoch trials 100 and 200. To avoid overfitting, early stopping criteria is employed to get the best performance from the model. The rest of all models follow the same procedure where every model's performance comparison is done using the same technique. Initially, trials run the model for these epoch values and compare the training, validation loss and finally early stopping criteria is used. In connection with the mobile net model architecture, MobileNet is the lightweight model in deep neural network architecture as it consists of fewer parameters in the case of depth-wise layers. In our experiment, Mobile net showed its best performance with maximum accuracy of 74% being received using the early stopping criteria. It is worth visualizing the model performance to understand the model performance as shown in Figure 5, Figure 6, and Figure 7, and finally, Figure 8 shows the overall accuracy of the hybrid MobileNet model.

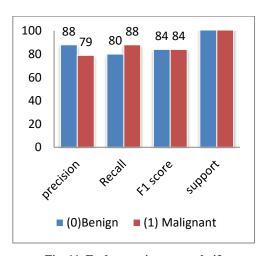
# **Hybrid VGG16 Model Performance Comparision based**



100 96 99 80 68 68 60 40 27 39 68 27 20 0 Parecision Recall Figure Support

Fig. 9. Model Performance for epoch 100





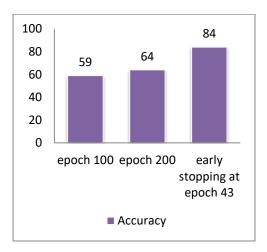
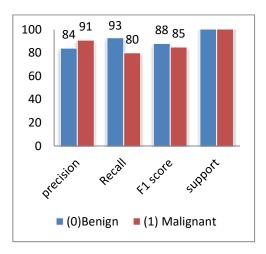


Fig. 11. Early stopping at epoch 43

Fig. 12. Accuracy of the model

Results obtained for hybrid VGG16 model architecture using the same experimental criteria are discussed further. VGG16 model improves AlexNet by replacing large kernel-sized filters with multiple 3×3 kernel-sized filters one after another. This is being the heavier model in terms of number of parameters , consumes more time during the training. The following graphs in figure 9, Figure 10, Figure 11, and Figure 12 visualize the overall results.

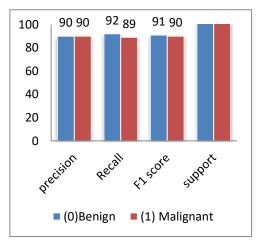
## **Hybrid ResNet 101 Model Performance Comparision**



100 84 91 93 88 85 80 60 40 20 0 Precision Recall F. Score Support.

Fig. 13. Model Performance for epoch 100

Fig. 14. Model performance for epoch 200



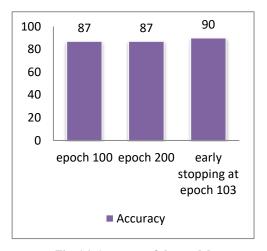


Fig. 15. Early stopping at epoch 103

Fig. 16. Accuracy of the model

Figure 13, Figure 14, Figure 15, and Figure 16 compare the experimental comparison of ResNet101 model using different epoch values.

From these results, it is also noted that the ResNet 101 model shows highly favorable results intern showing its better suitability in classifying the histopathology images. It is worth noting that the number of parameters used by ResNet architecture is lighter compared to VGG16 architecture and hence it reduces the overhead of increased training time and computational complexity. Further work implemented the Hybrid ResNet 152 model with increased layers to demonstrate the model's capability to classify the given training data. Performence of these models is shown in the Figure 17, Figure 18, Figure 19 and Figure 20.

# **Hybrid ResNet152 Model Performance Comparison**

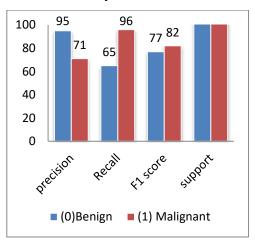
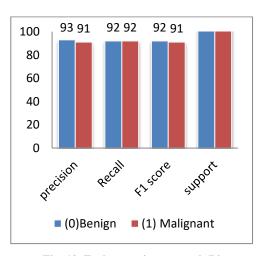


Fig. 17. Model Performance for epoch 100





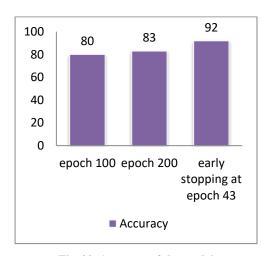


Fig. 19. Early stopping at epoch 74

Fig. 20. Accuracy of the model

It is evident from these results that the Hybrid ResNet 152 model is highly suitable for the classification of given data and adopts comparatively most suitable learning accuracy. Further, we claim that out of all proposed variants of models the Hybrid ResNet 152 model is well suited for the classification of histopathology cancer images. The following Figure 21 visualize the comparison of all models' accuracy in one chart.

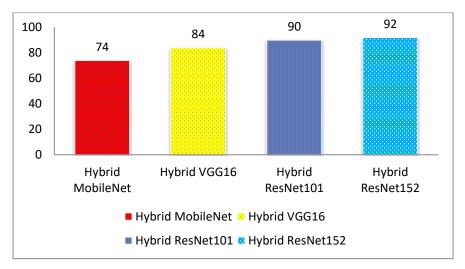


Fig. 21. Accuracy of Hybrid models

Figure 21 summarize the overall accuracy of models, in which Hybrid ResNet152 has surpassed the other model with 92% of accuracy. Hence it is justified that developed hybrid deep learning architecture is highly suitable and capable of classifying the cancer images efficiently.

#### 5. CONCLUSION

This study proposed Hybrid deep CNN-based architectures for the classification of histopathology cancer images. This study presents techniques to reuse the existing deep CNN architectures for Histopathology image classification. In order to improve the performance of existing architecture LSTM network used to retain and learn relationship between features across multiple layers. The proposed hybrid architectures use parallel LSTM network layers. Implemented models use TensorFlow-GPU combined with CUDA libraries to accelerate the training time required to train these complex architectures. Out of proposed Hybrid models, the Hybrid ResNet-based architectures with 101 and 152 layers have shown high accuracy of 90% and 92% and hence it is to justified that these models are well suited for the given problem. The developed architectures can be extended with any histopathology image dataset using transfer learning technique, which remains one of the advantages in reusing these models.

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