CLASSIFICATION OF HISTOPATHOLOGICAL IMAGES USING DEEP LEARNING APPROACH

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Abstract: Deep learning-based computer-aided diagnosis (CAD) is gaining prominence, for interpreting histopathology pictures. However, there has been little research into reliably classifying breast biopsy tissue into different histological categories with hematoxylin and eosin stained images. Researchers and professionals aim to create a computer-aided diagnosis method for diagnosing breast cancer histopathology pictures. Using eosin stained and hematoxylin images, CAD has helped improve the diagnosis accuracy of biopsy tissue. Traditional methods for extracting handcrafted features have been employed by most CAD systems, which are inaccurate in diagnosis and are time-consuming. Both CAD and computational diagnostics are utilized to help pathologists work more efficiently and accurately. Different techniques that divide breast cancer histology images into benign and malignant categories have been proposed in this research. A custom CNN model and three pre-trained models for classification of histopathological images have been used with Resnet50 model yielding an accuracy of 96 percent.

Index Terms: **CAD, Histopathology, Classification,CNN**

I. INTRODUCTION

Cancer is a serious health problem that can cause a person's death. When a gene in a cell becomes aberrant, the cell begins to expand and divide uncontrollably, and cancer develops. Cancerous cells multiply at a significantly quicker rate than healthy cells. Tumors are formed when cells divide and grow, and they can be malignant or non-cancerous. Several biological processes appear to be linked to large changes in the cell and the nuclear shape. While viewing the image, human error can arise due to overlapping, blurriness, artifacts, weak border recognition, and uneven dying. Visualizing cells in particular entails analyzing minute structures, composition, functions, cell distribution, and regularities of cell shapes across the tissue, all of which aid the pathologist in determining if a cell is cancerous or not. This intricate and time-consuming technique necessitates a high level of competence. Pathologists examine histopathological pictures of cancer tissue samples on a regular basis for cancer type identification and prognosis. Pathologists have been using hematoxylin-eosin (H&E) stained slides for almost a century. Histopathological imaging is projected to remain in mainstream clinical practice in the future year, given its lengthy history and established relevance. To address these issues, CAD offers pathologists advice on the development of automation in biological imaging enhancement, feature extraction, and cancer classification. To aid pathology practice, automation overcomes over the constraints of manual microscopy-based detection methods. Deep learning-based image categorization systems have seen a lot of progress in recent years. Convolutional Neural Networks (CNNs) have been at the forefront of significant advances in computer vision, particularly in the field of image classification. All of these exciting methodological breakthroughs would be impossible to achieve without a large enough pool of training data to train accurate models. The Breast Cancer Histopathological Database, which has publicly available training data with annotated images, allows for algorithm benchmarking and evaluation, sparking new method development. A technique known as dropout has been proposed as a regularization method for CNNs. We present an accurate comprehensive framework for classifying histological imaging of breast cancer in this paper. To accomplish this, we train using a CNN model on the BreakHis dataset to classify breast cancer tissues as benign and malignant.

II. LITERATURE REVIEW

Using a deep convolution neural network model, some researchers[1] proposed "Multi-task deep learning for fine-grained classification and grading in breast cancer histopathological images," with the procedure divided into combining the representation of the learning process, multi-class recognition task, and image pair verification task, and with the prior knowledge that histopathological images with different magnification belong to the same subclass are embedded in the feature extraction process.

Filipczuk et al. [2] and George et al. [3] used fine needle biopsies to retrieve nuclei-based characteristics. The circular Hough transform was used to detect nucleus candidates first, followed by machine learning and Otsu thresholding to reduce false positives. Watershed is used to refine the nuclei segmentation in George et al. [3]. Shape and texture are prominent in both works. By majority voting over 11 photographs for each of the 67 patients, Filipczuk et al. [2] reached an accuracy of 98.51 percent, and George et al. [3] achieved between 71.9 percent and 97.15 percent in individual image categorization utilising 92 images. Belsare et al. [4] investigated tissue organisation for the binary classification of more complex pictures in addition to nuclei-related information. The authors looked at 70 photos from a private H&E breast histology dataset at a magnification of 40. The epithelial layer around the cell lumen was segmented using spatial-color-texture graphs, and statistical texture features were employed to train the final classifiers. The authors claim that their accuracy ranges from 70% to 100%.

Other researchers have concentrated on a more complicated three-class classification of breast cancer histology images. Brook et al. [5] and Zhang et al. [6], for example, divided breast cancer tissue pictures into three categories: normal, in situ carcinoma, and

invasive carcinoma. A dataset from the Israel Institute of Technology [7] was utilised for this. Brook et al. [5] binarized each image using different threshold values and trained a support vector machine (SVM) classifier using connected component statistics, reporting an average accuracy of 93.4 percent that could be raised to 96.4 percent by rejecting 20% of the photos. A cascade classification strategy was employed by Zhang et al. [6]. Images with a particular number of classifiers disagreeing were dismissed once again. With a rejection rate of 0.8 percent, our system achieved 97 percent accuracy.

Convolutional Neural Networks (CNNs) may now be used to solve image classification challenges because to recent increases in processing power and dataset sizes. Unlike classic feature extraction methods that need hand-crafting, CNNs discover relevant features directly from the training image patches by optimising the classification loss function. These deep learning models have excelled in picture classification difficulties in a variety of fields [8, 9], including medical image analysis [10], and specifically histopathology images [11].

CNNs make it possible to reduce the amount of field knowledge required to create a categorization system. As a result, the approaches' performance is less influenced by the dataset utilised, and similar network designs can obtain good results on a variety of tasks. As fact, utilising several magnifications, Spanhol et al. [12] used a CNN architecture inspired by the Imagenet network [8] to classify H&E breast tissue biopsy samples in benign and malignant cancers. Patches of 32 x 32 and 64 x 64 pixels were taken from the initial images and utilised to train the CNN in their study. The patch probabilities were combined with sum, product, or maximum rules to produce the final categorization. Sliding window and random patch extraction approaches were investigated. By reducing the amount of the input in succeeding layers, the extraction of patches allowed the model's complexity to be reduced. The scientists noticed a drop in accuracy as magnification increased, implying that their CNN design is unable to extract relevant characteristics at higher magnifications. In fact, as mentioned in the research, only nuclei edge-related features are retrieved at higher magnifications.

Some authors[13] suggested the "Locality Sensitive Deep Learning for Detection and Classification of Nuclei in Routine Colon Cancer Histology Images" evaluated on a large dataset of colorectal adenocarcinoma images, consisting of more than 20,000 annotated nuclei belonging to four different classes produced the highest average F1 score as compared to other approaches.In comparison to other recently published techniques, their results demonstrated that the suggested SC-CNN and NEP's joint detection and classification produces the highest average F1 score. In terms of quantitative analysis of tissue constituents in whole-slide images, the proposed methodologies could potentially assist pathology practise and lead to a better knowledge of cancer.

III. DATASET

Deep learning approaches are effective at identifying important characteristics and then attempting to classify them into multiple classes, such as benign and malignant, and then into different grades. The 400x zoomed images of benign and malignant tissues in our Breakhis dataset. The images of four benign tumours: adenosis, fibroadenoma, phyllodes tumour and tabular adenoma, and four malignant tumours carcinoma, lobular carcinoma, mucinous carcinoma and papillary carcinoma have been obtained. Sample images of benign and malignant tissues present in our folders are shown below:

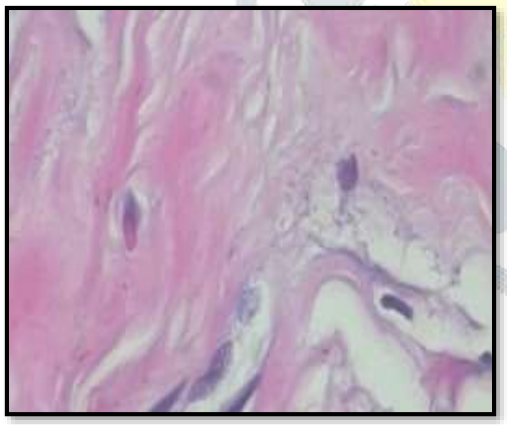


Fig-1: Benign

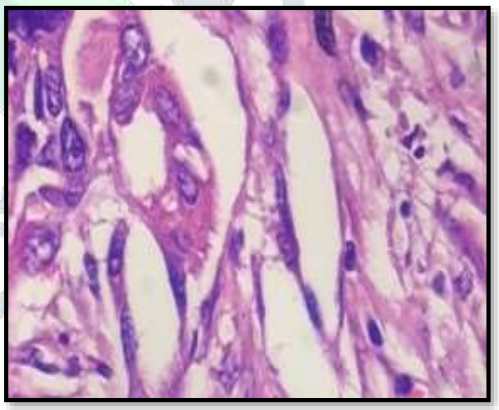


Fig-2: Malignant

There are 2149 images in total in the dataset. The entire dataset has been divided into three parts: train, test and validation. A total of 1148 images are available for training, 545 for validation and 456 for testing.

IV. METHODOLOGY

Classification of histopathological images is done using 4 models .A custom model is implemented followed by the implementation of classification using three pre-trained models: VGG-16, Inception and RESNET50.These models are trained on the Breakhis dataset and the results are obtained. The aim of these experiments is to classify the images in the dataset into benign and malignant. We have used 80 percent of the images for training and the rest 20 percent for validation.
The implementation of the code and the results of the experiments were produced using Python 3 and GPU runtime on Google Colab which is a research based jupyter notebook server provided by Google.

4.1 Custom CNN model

In this model, first a sequential model is instantiated and then the convolution layers are added. There are three Conv2D layers in total in our model. Following each convolution layer, there is a Maxpooling layer. The activation function used for the CNN layers is ReLu. A dropout layer is added after each Maxpooling layer. After that, a flatten layer is added, which flattens the layers into a 1-D array for usage in output layers. The final layers are dense layers, with the final output layer's activation set to sigmoid. The Adam optimizer was used to compile the model, and the function was set to binarycrossentropy for binary classification jobs. The model is run for a total of 20 epochs, yielding an accuracy of 87.42%.

4.2 VGG-16

The VGG-16 is one of the most often used pre-trained image classification models. The architecture of the model is as shown as follows:

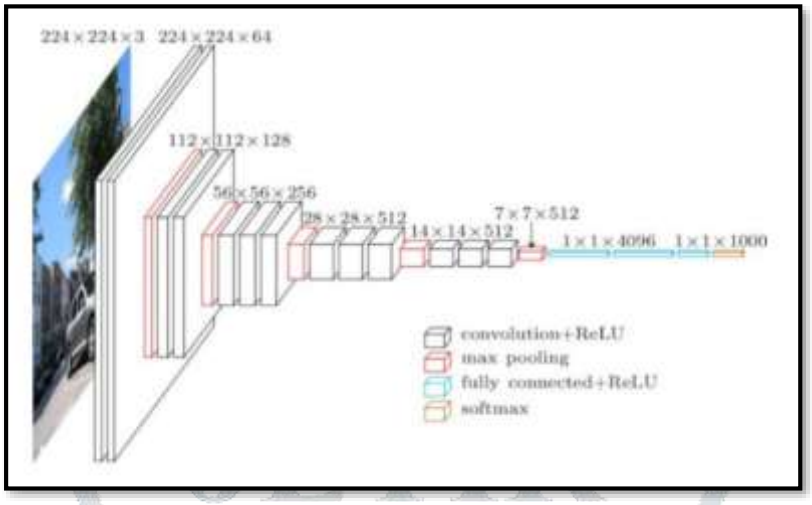


Fig-3: Architecture

There are 13 Convolution layers, 5 Pooling layers, and 5 dense layers in the pre-trained model. The basic model is used, with just the final layer being changed. This is due to the fact that our study is a binary classification problem, whereas these models are built to handle up to 1000 classes. Since all the layers need not be trained it is made as non trainable. The last fully connected layer is then built which consists of a global average pooling layer followed by dropout layer to reduce over-fitting. The batch normalization layer comes next, followed by a dense layer with two neurons for each of the two output classes, benign and malignant, with softmax as the activation function. The optimizer is Adam, and the function was set to 'binary-crossentropy' for binary classification jobs.

4.3 ResNet50 Model

Resnet50 model is one of the most efficient models for classification of images. The architecture of different versions of ResNet with respect to the layers used is shown below:

Fig-4:Different Versions of VGG-16 Architecture

layer name	output size	18-layer	34-layer	50-layer	101-layer	152-layer
conv1	112×112	7×7, 64, stride 2				
		3×3 max pool, stride 2				
conv2_x	56×56	[3×3, 64; 3×3, 64] ×2	[3×3, 64; 3×3, 64] ×3	[1×1, 64; 3×3, 64; 1×1, 256] ×3	[1×1, 64; 3×3, 64; 1×1, 256] ×3	[1×1, 64; 3×3, 64; 1×1, 256] ×3
conv3_x	28×28	[3×3, 128; 3×3, 128] ×2	[3×3, 128; 3×3, 128] ×4	[1×1, 128; 3×3, 128; 1×1, 512] ×4	[1×1, 128; 3×3, 128; 1×1, 512] ×4	[1×1, 128; 3×3, 128; 1×1, 512] ×8
conv4_x	14×14	[3×3, 256; 3×3, 256] ×2	[3×3, 256; 3×3, 256] ×6	[1×1, 256; 3×3, 256; 1×1, 1024] ×6	[1×1, 256; 3×3, 256; 1×1, 1024] ×23	[1×1, 256; 3×3, 256; 1×1, 1024] ×36
conv5_x	7×7	[3×3, 512; 3×3, 512] ×2	[3×3, 512; 3×3, 512] ×3	[1×1, 512; 3×3, 512; 1×1, 2048] ×3	[1×1, 512; 3×3, 512; 1×1, 2048] ×3	[1×1, 512; 3×3, 512; 1×1, 2048] ×3
	1×1	average pool, 1000-d fc, softmax				
FLOPs		1.8×10^9	3.6×10^9	3.8×10^9	7.6×10^9	11.3×10^9

After starting with a single Convolution layer and Max Pooling, it can be seen that there are four similar layers with only different filter sizes – all of which use the 3 * 3 convolution operation. After every two convolutions, the layer in between is skipped. These skipped connections use residual blocks:

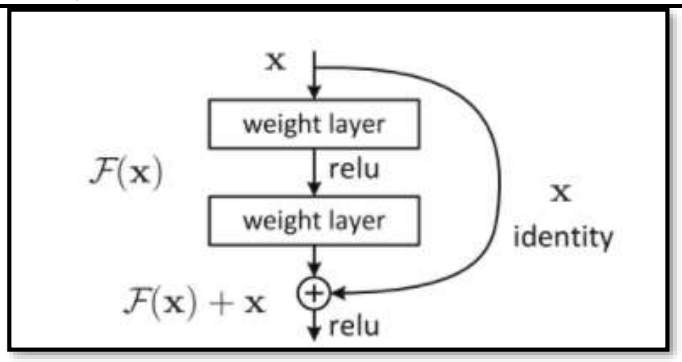


Fig-5: Blocks

Since all the layers need not be trained it is made as non-trainable. The last fully connected layer is then built which consists of a global average pooling layer followed by dropout layer to reduce over-fitting. The batch normalization layer comes next, followed by a dense layer with two neurons for each of the two output classes, benign and malignant, with softmax as the activation function. The optimizer is Adam, and the function was set to 'binarycrossentropy' for binary classification jobs.

4.4 Inception Model

The Inception model is also one of the most common models used for classification tasks. Over the years different versions of inception models where designed. InceptionV3 was introduced with major improvements including Introduction of Batch Normalization, More factorization and RMSProp Optimizer

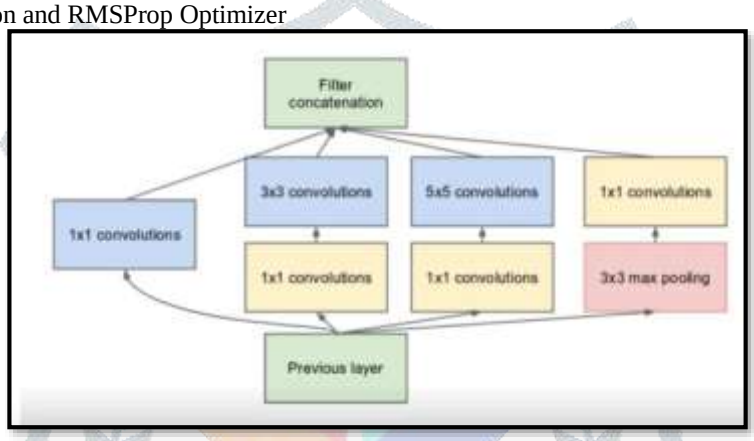


Fig-6: The dimensions are reduced

Since all the layers need not be trained, it is made as non-trainable. The last fully connected layer is then built which consists of a global average pooling layer followed by dropout layer to reduce over-fitting. The batch normalization layer comes next, followed by a dense layer with two neurons for each of the two output classes, benign and malignant, with softmax as the activation function. The optimizer is Adam, and the function was set to 'binarycrossentropy' for binary classification jobs.

V. RESULTS AND DISCUSSION

5.1 Custom CNN Model

The custom model has fetched us an accuracy of 85%. The confusion matrix and the roc curve obtained are as shown below:

Fig-7: Confusion Matrix

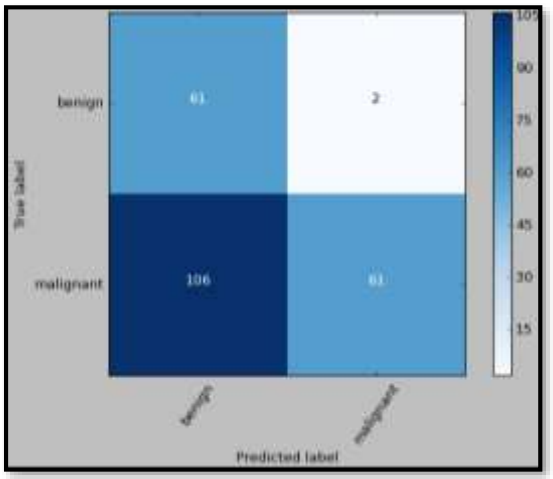
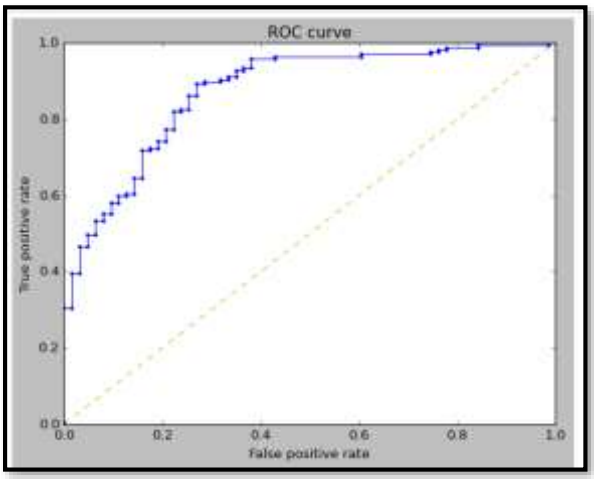


Fig-8: ROC Curve



5.2 VGG-16 MODEL

This VGG-16 model has fetched us an accuracy of 89%. The confusion matrix and the roc curve obtained are as shown below:

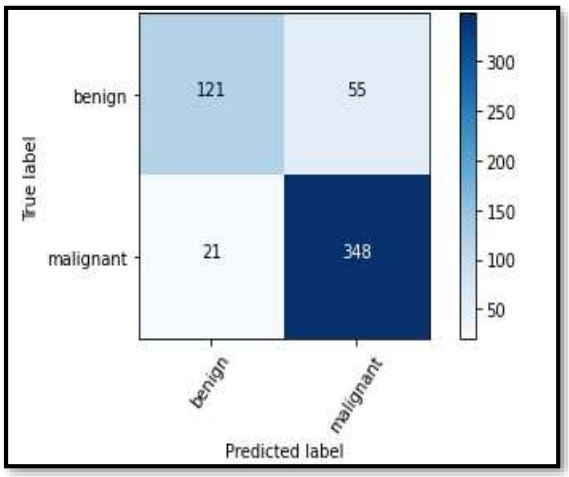


Fig-9: Confusion Matrix

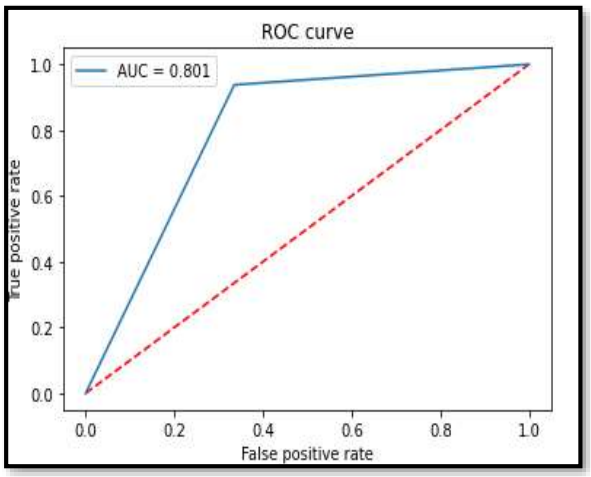


Fig-10: ROC Curve

5.3 Resnet50 Model

The Resnet50 model has fetched us an accuracy of 96%. The confusion matrix and the roc curve obtained are as shown below:

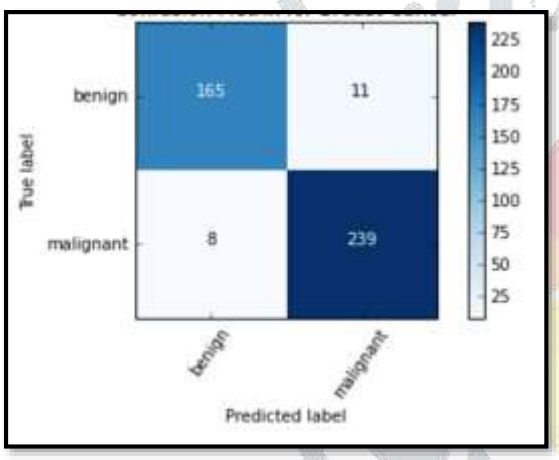


Fig-11: Confusion Matrix

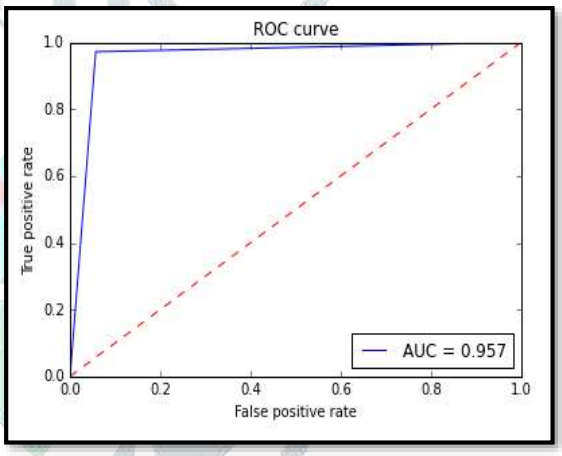


Fig-12: ROC Curve

5.4 InceptionV3 Model

The Inception model has fetched us an accuracy of 92%. The confusion matrix and the roc curve obtained are as shown below:

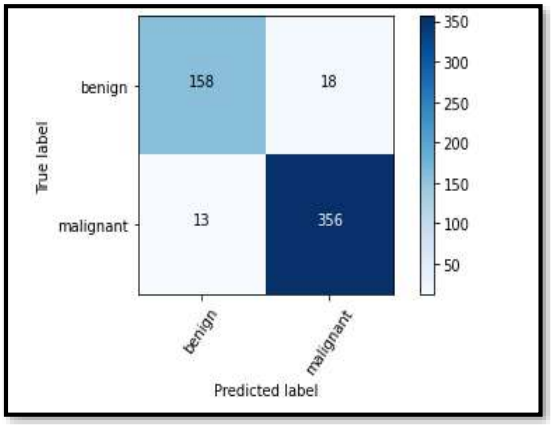


Fig-13: Confusion Matrix

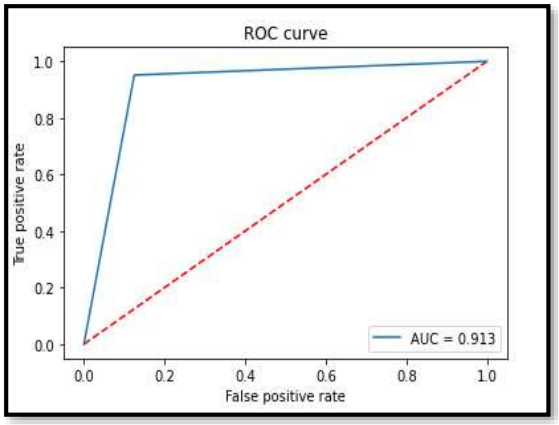


Fig-14: ROC Curve

5.5 Comparative analysis

When we compare the results, it can be seen that ResNet50 pre-trained model has provided us the highest accuracy that is 96 % which turns to be highly efficient in classification of images into benign and malignant.

VI. CONCLUSION

Cancer is a deadly disease which poses a threat to human existence. Detecting of cancer at an early stage is important for early treatment which aids the patient's recovery. Computer-assisted detection systems based on Convolutional neural networks (CNN) could aid in abnormality classification. Our research used a custom CNN model and three pre-trained models to classify cancer into malignant and benign categories, yielding accurate results, with the Resnet50 model yielding the highest accuracy of 96 percent.

VII. ACKNOWLEDGEMENT

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