

Classifying Breast Cancer Using Deep Convolutional Neural Network Method

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Abstract. The efficacy of conventional classification systems is contingent upon the accurate representation of data and a substantial portion of the effort invested in feature engineering, which is a laborious and timeconsuming process requiring expert domain knowledge. In contrast, deep learning has the capacity to automatically identify and extract discriminative information from data without the need for manual feature creation by a domain expert. In particular, Convolutional Neural Networks (CNNs), a type of deep feedforward network, have garnered attention from researchers. This study conducts several preliminary experiments to classify breast cancer histopathology images using deep learning, given the small number and high resolution of training samples. The proposed approach is evaluated on the publicly available BreaKHis dataset, utilizing both a scratch model and transfer learning pre trained models. A comparison of the proposed scratch method to alternative techniques was carried out using a suite of performance evaluation metrics. The results indicate that the scratch model, with its independent magnification factor, achieved greater accuracy, with a binary classification accuracy of 99.5% and a multiclass classification accuracy of 96.1%.

Keywords: Transfer Learning, Convolutional Neural Network, Magnification Factor, Breast Cancer Classification

1 Introduction

Currently, one of the leading causes of human death is cancer which is cell growth of type abnormal that the invading body parts have high potential. Precancerous lesions give way to malignant tumors as part of the multi phase process by which cancer cells are transformed. Alcohol and cigarette use, physical inactivity, old age, pollution, and a few additional disorders like Hepatitis C, Hepatitis B and HIV are all risk factors for the development of cancer. World Health Organization (WHO) states that according to their estimation, here will be 10.6 million cancer related deaths and 19.3 million new cases worldwide in 2020 [1].

Any part of the human body can be affected by cancer cells including liver, lungs, breast etc. Among other types of cancer, breast cancer is one of the most common for women and the mortality of breast cancer is also very high, accounting for 1 in 4 new cases and 1 in 6 cancer related deaths worldwide in [1]. Breast cancer, which accounted for 35.3% of all fresh tumors of female and contributes 20.8% to cancer deaths in total in 2012, had the highest age standardized incidence of any female cancer, according to data from the International Agency for Research on Cancer (IARC) of the WHO states [1]. In 2020, study shows of 27 million fresh cases of cancer occurred [2]. Breast tissue cells proliferate out of control and infiltrate adjacent tissues via blood and lymphatic vessels to cause breast cancer. Breast cancer can also occur in fatty tissue. Breast discomfort, skin that is pitted and red or discolored on the breast, lumps or tissue thickening that feels different from surrounding tissue, and breasts that enlarge entirely or partially are typical symptoms of breast cancer. Breast tissue, which is detected by a breast lump, develops into breast cancer, along with other modifications to the usual environment [3]. Mammography, breast cancer screening and other clinical Ultrasound, biopsies and other techniques. Only a biopsy [4] can definitively verify whether

the suspicious region is malignant in terms of diagnosis. The pathologists make their diagnoses by looking at histology slides, which is regarded as the definitive gold standards. However, the traditional method requires a heavy burden from qualified experts. Pathologists who lack sufficient diagnostic experience are more likely to make errors in diagnosis.

Deep learning algorithms have obtained results on image classification and object detection tests that are on par with those of human experts [5]. The most popular deep learning framework for learning complicated discriminative characteristics between image classes is the convolutional neural network. Over the years, many CNN architectures have delivered outstanding results on the enormous ImageNet dataset. On medical images, CNNs are being used to produce state-of-the-art results. Patch wise classification is one of the existing deep learning methods for the task of classifying breast cancer (BC) histology images [6]. By doing this, CNN typically ignores the general properties of the entire tissue and only extracts local features near the nucleus. In addition to the drawback of patching, CNN's shallow architecture does not allow for the extraction of finer and more abstract features from patient breast histopathology images.

In order to gradually and reliably categorize the Breast Cancer pathological images, we developed a CNN model from scratch to extract characteristics from images and carry out the training which is end to end in nature. Hence, the following is a list of this paper's key contributions:

1. To increase classification performance, we developed a scratch CNN model.
2. Because of the independence of our developed model's accuracy against magnification factors, it can be used with different magnification factors.
3. To improve the quality of the breast histopathology images, we developed a histopathological image enhancement method.

2 Related Works

The original goal of the image analysis system was to categorize pathological images. For more than 40 years, this concept has been investigated in the context of automatic assistance cancer detection. The complexity of image analysis, however, made it difficult to deal with the inherent complexity of histological images [7]. The workload of pathologists can be reduced by modern deep learning method [8]. The absence of extensive datasets and class disparity are the key challenges in the field of breast cancer classification research. Since images have intrinsic problems including inadequate contrast, noise, and lack of visual acuity, models have been developed to build and improve image processing.

For the recognition of breast cancer histopathology images, several researchers apply customized features. BreakHis, dataset of breast available to public, was proposed by [9]. Six different features utilized the dataset's classification and accuracy ranged from percentage of 80 to 85. Phylogenetic diversity indexes were employed by Carvalho et al. In [10], to categorize the different forms of breast cancer. Three different features were combined by [11] for binary and eight class categorization of breast cancer histopathology images. Several researchers, notably CNNs, have become interested in deep learning as a result of its remarkable performance in image recognition in recent years.

Researchers created CNNs based CAD models based on these models and used them to diagnose cancers. There are two general categories of CNNs as pre trained CNNs [12] and CNNs which have been made from begin called scratch [13]. Additionally, deep networks can be created using transfer learning with samples which are few in number. Many researchers additionally employ CNN an extractor of features, which performs the task of extraction of features using various techniques.

For instance, in [14] employed 3-norm for feature fusion, ResNet50 for feature extraction from image patches of various sizes, and SVM for classification. On the basis of images produced from Haar wavelet decomposition, in [15] retrieved features using VGG16 and merged various properties of the next level layers for breast cancer identification. To assess the histopathology images and resolve the class imbalance issue. In [16], used ResNet50 and weighted learning machine. Using DenseNet121 [17] to extract overall features from slides. In order to diagnose breast and prostate cancer automatically, in [18] developed a 5-layered multi input CNN that took into account both RGB pictures and phase shearlet coefficients. This CNN achieved an amazing accuracy rate of 88% for a different dataset. In [19], a thorough analysis of the architecture and functioning of each network is performed and the performance of each network is then evaluated based on how accurately it diagnoses and classifies cancer causes in breast. CNN provide a little bit better precision than layer perceptron for the detection.

As a result, it can be concluded that the classification of cancer in breast has had a significant impact for a long time. Deep learning models combined with a wide range of configurations have recently exceeded current state-of-the-art methods, as well. There is a huge amount of scope for initiating innovation and development in this developing research field to overcome this.

3 Datasets

3.1 BreakHis

The images found from biopsy cancers in breast were gathered from January 2014 to December 2014 through clinical investigations and were included in the BreakHis dataset [20]. All patients with breast cancer clinical symptoms to take part in the trial over the time period. Hematoxylin and eosin staining was used after surgical open biopsy (SOB) sample collection. Pathologists working in the PD laboratory can mark these images and use them for histological investigations. Four sub classes are further separated into each kind. Adenosis (A), Fibroadenoma (F), Phyllodes Tumor (PT) and Tubular Adenoma (TA) are examples of Benign lesions, while Ductal Carcinoma (DC), Lobular Carcinoma (LC), Mucinous Carcinoma (MC) and Papillary Carcinoma (PC) are examples of Malignant lesions. The images are 700x460 pixels in size and were created in a three channel RGB (red, green, and blue) true color space with magnifications of 40X, 100X, 200X and 400X. The distribution of images is summarized in Table 1.

Table 1: BreakHis Dataset Summary

Magnification Factor	Benign	Malignant	Total
40X	625	1370	1995
100X	644	1437	2081
200X	623	1390	2013
400X	588	1232	1820
Total	2480	5429	7909

4 Methods

4.1 Preprocessing

Preprocessing is a necessary step in order to improve the performance for any type of breast cancer histopathological image classification model. In this work, a method was developed for improving histopathological images in low light.

Histopathological image enhancement method Due to their poor visibility, low light images are not suitable for computer vision algorithms or human inspection. Image enhancement is the

process of focusing attention to details that are obscured in an image or enhancing contrast in low contrast images. To provide an accurate contrast enhancement, we developed an image contrast enhancement algorithm. To synthesize multi exposure images and determine the best exposure ratio, a weight matrix for image fusion using illumination estimation techniques is used first, followed by a response model and help to ensure that the synthetic image is properly exposed in the areas where the original image was underexposed. To produce the enhancement result, both types of images are finally fused in accordance with the weight matrix. The preprocessing method for enhancing the histopathological images are shown in Figure 1. Illumination estimation techniques to obtain the weight matrix for image fusion. Exposure ratio is used so that the synthetic image is well exposed in the regions where the original image is under exposed. The output for enhancing the histopathological images is shown in Figure 2. So, the it can be,

$$E = I \times W + I' \times (1 - W) \quad (1)$$

Where W indicates the weight matrix and I indicates real image and E indicates the enhanced image and then I' indicates the exposure image. For breast histopathology slides, MIRNet [21] was compared with our approach of histopathological image enhancement. Using the metrics for measuring the quality of an image.

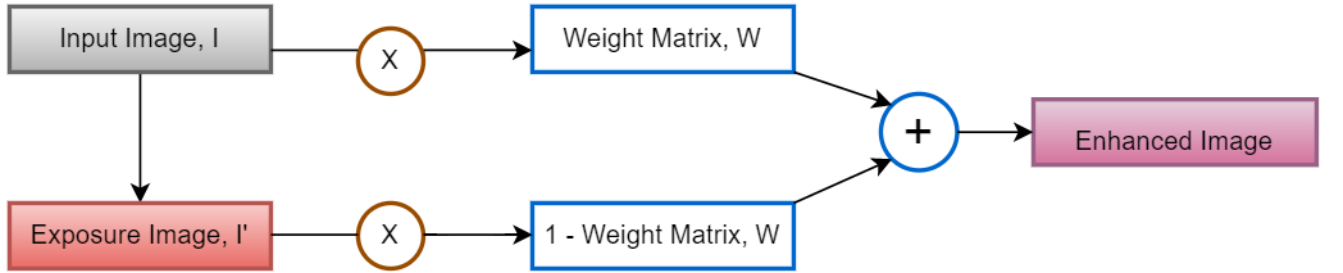


Fig. 1: Histopathological Image Enhancement Method.

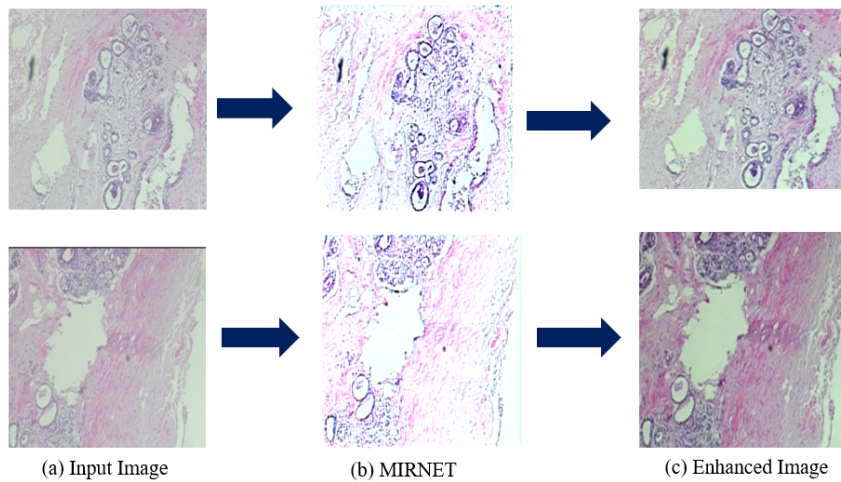


Fig. 2: Histopathological Image Enhancement Method output from. (a) Input Image. (b) MIRNET. (c) Enhanced Image.

Entropy measures an image's content and indicates how much uncertainty or randomness it has. Higher value of entropy indicates an image with higher details.

$$E(I) = - \sum_{k=0}^{L-1} p(k) \log_2(p(k)) \quad (2)$$

Peak Signal Noise Ratio (PSNR) affects how an image is represented, is the ratio between the maximum power and corrupting noise. The PSNR is frequently used to evaluate how well an image may be reconstructed. The original data in this case is the signal, while the introduced error is the noise.

$$PSNR = 10 \log_{10} \frac{MAX_i^2}{MSE} \quad (3)$$

$$PSNR = 20 \log_{10} \frac{MAX_i}{MSE} \quad (4)$$

$$PSNR = 20 \log_{10} MAX_i - 10 \log_{10} MSE \quad (5)$$

Where, MAX_i is the maximum possible pixel value of the image. MSE is Mean Square Error between the filtered image and the original image.

Similarity Index (SI) is ratio of pixels in the enhanced image that coincide with pixels in original image is known as the similarity index. When the this is larger than 40 percent when represented in percent or greater than 0.4 when expressed in ones, it is suggested that an improved image be regarded as being comparable to the original image. Lower value (less than 40 percent) of SI indicates good measure. It's measurement is given by-

$$SI = \frac{m_{ab} 2xy 2m_a m_b}{m_a m_b x^2 + y^2 m_a^2 + m_b^2} \quad (6)$$

Image Quality Index (IQI) is a common metric for comparing the number of pixels that separate two images. The quality of the converted image is considered to be good if the IQI is less than but close to 1 (for example 0.8704). Higher value of IQI indicates good measure. It can be concluded that the proposed histopathological image enhancement method provides high percentage values than MIRNet for the quality image measurement metrics.

$$IQI = 1 - SI \quad (7)$$

Table 2: Enhancement Comparison between MIRNet and Proposed method

Performance Metrics	Input Image	MIRNet	Ours
Entropy	6.004	4.0417	6.7127
PSNR		14.1574	14.6509
SI		67.3573	29.7719
IQI		95.3723	96.7513

4.2 Proposed CNN Architecture

One of the most effective architectures for the problem of image classification is CNNs. CNNs use filtering techniques to extract the most innovative features from an image's pixels. Deep neural networks are used in images as they extract characteristics features from images, as opposed to classic ML algorithms that pick up engineered features for detection of cancer in breast. Machine learning neural networks (ML-NNs) are a type of learning and they typically require a training stage to determine the optimal weights.

CNNs are used to analyze patterns in an image. In the few early layers of CNNs, the network can identify lines and corners. However, as go deeper, these patterns may transfer via neural network and start to recognize more complicated features. CNNs are exceptionally good at identifying objects in images because of this feature. The suggested approach analyzes histopathologic images using CNNs for classification of breast cancer. The convolutional layer, pooling layer, batch normalization layer, and fully connected layer were just a few of the layers that constitute a CNN's architecture, as depicted in Figure 3.

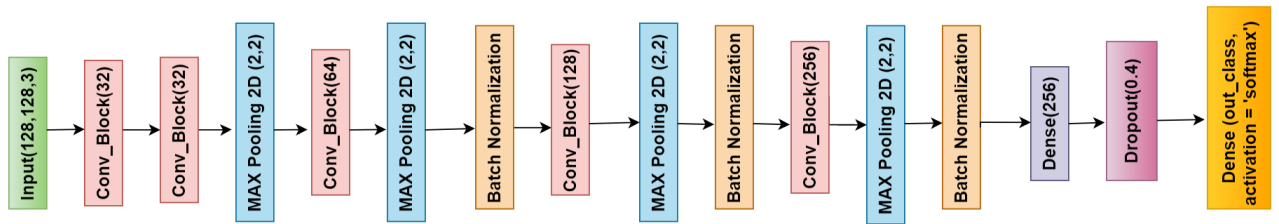


Fig. 3: Proposed Convolutional Neural Network Architecture.

The convolution layer utilizes filters that carry out convolution operations while dimensionally scanning the input image. Convolution is a linear procedure where a set of weights are multiplied and the input images are represented by metrics resembling those of conventional neural networks. All of the features were computed using the input layers and filters and are included in the output, which is known as the feature map or activation map. Here, used RGB images with a size of 128x128 pixels when using this layer. 3x3 kernel size convolutional layers with successive use of 32, 32, 64, 128 and 256 filters. As the activation function, ReLU was employed. The rectifier function was being used to increase the non linearity of the images.

The Convolved Feature's spatial size is decreased by the Pooling layer. By lowering the dimensions, this will decrease the total power required to process the slides. Max Pooling determines a pixel's maximum value from a portion of the image that the kernel has processed. By choosing the maximum value for each input channel over a pool size (2,2) input window, down sampled the input along its spatial dimensions are performed.

In Normalization, the input layers are scaled. Learning becomes more effective when batch normalization is utilized. Thus, batch normalization as regularization to prevent model overfitting is used here. A layer that is densely connected to the layer above it means that every neuron in the layer is attached to every neuron in the layer above it. A typical layer having many connections called dense layer after performing the operation on input returns the result. To do the activation (dot (input, kernel) + bias) operation, this formula is applied in it.

The regularization method used to avoid model overfitting is called dropouts. Dropouts are added to the network's neurons, which are changed at random in some proportion. The connections to the neurons' incoming and outgoing neurons are likewise broken off when they are turned off. To improve the model's learning, this is done. After that, turned off 40 percent of the neurons and utilized dropouts after the network's dense layers. After building the model, classification of the breast histopathology images using the Softmax activation function.

5 Result Analysis

The model configurations are described in this section. There are several accuracy metrics that stand out, including precision, recall and the f1-score of the best model. The classification report, confusion matrix and performance graphs are examined for additional analysis of the best model. The method which down samples the image size to 128x128 so that higher accuracy using 24 sized each batch. However, applied different pretrained transfer learning model in the dataset. The accuracy comparison chart for different transfer learning model and the proposed model as follows:

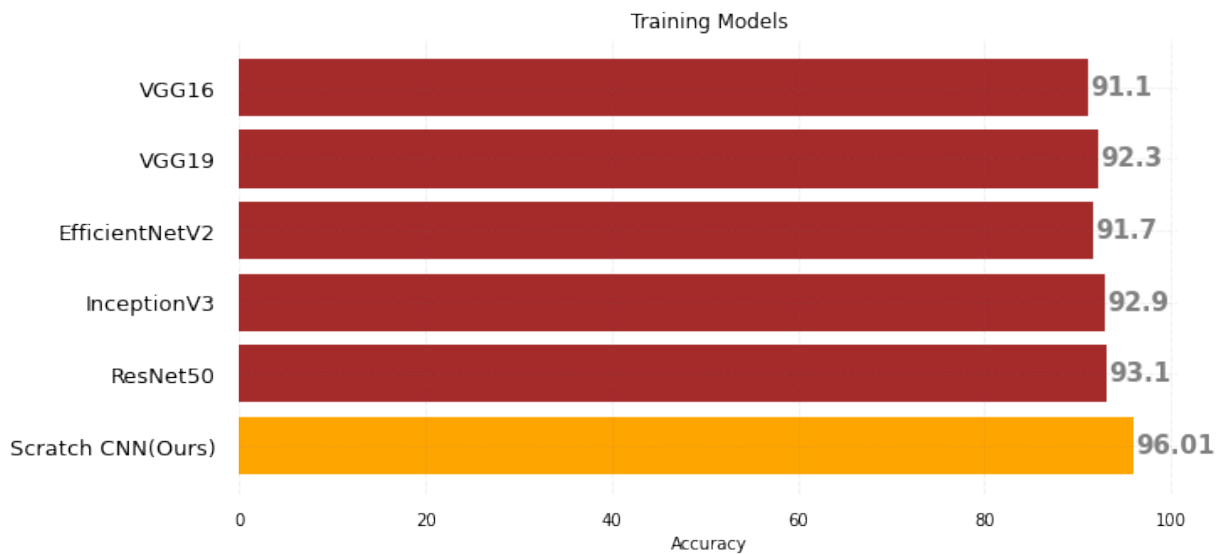


Fig. 4: Accuracy Comparison of Different Models.

An optimizer is a technique that modifies the properties of a neural network, such as a function or algorithm. Accuracy is improved and there is decreased overall loss. Thus, utilizing the following three optimizers in figure 5, Adam, SGD and RMSProp are illustrated. Adam's accuracy in the proposed model was the highest according to the following figure.

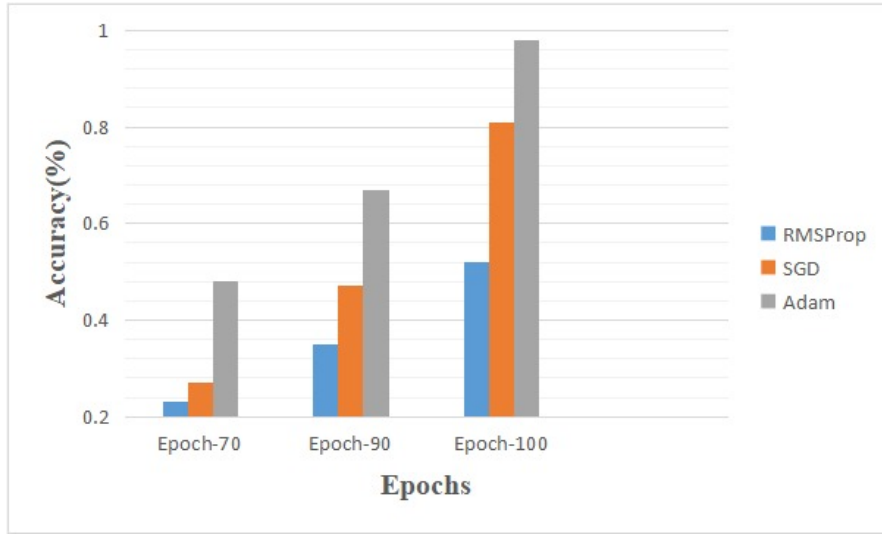


Fig. 5: Optimizer's Accuracy Comparison

The batch size is the quantity of samples processed before to a model modification. The number of epochs is the total number of complete iterations through the training dataset. The minimum and maximum sizes of a batch must be one and the number of samples in the training dataset, respectively. The batch sizes that used for this classification are depicted in figure 6. From the comparison curve, batch size 24 provide highest accuracy among others.

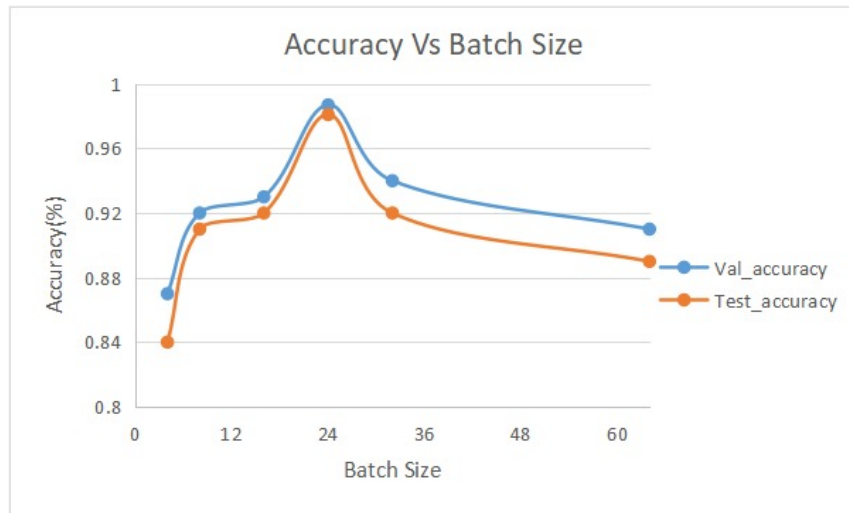


Fig. 6: Accuracy versus Batch Size.

Prior research endeavors were found to be inadequate in their implementation of batch normalization, a technique that accelerates the learning rate of neural networks while simultaneously offering regularization benefits to counteract overfitting. Despite this, subsequent authors opted to utilize hashing in [22], a decision that was made to prevent precision loss, however this approach has not

been implemented. The utilization of a model comprising EfficientNetB2 and RestNet50, as documented in [23], was already implemented in our research however the accuracy achieved was only 93.1 % which was not satisfactory. The implementation of batch normalization in the proposed model was aimed at optimizing the velocity and stability of the training process of artificial neural networks through normalization of the inputs at each layer by rescaling them. Hence, developed a new CNN model from scratch, resulting in a marked improvement in the performance of training data, exhibiting a two times increase in efficiency as compared to the previous efforts documented in [24]. The comparative analysis of the outcome of the classification procedure is presented in the following manner.

For binary classification:

The experiment's accuracy for binary classification was tested by comparing it to the findings of other authors, which are displayed in Table 3. The classification accuracy is 99.10%, 99.15%, 99.22%, and 98.99% respectively for the independence of a very crucial factor called magnification of images by 40, 100, 200 and 400 respectively. The classification result, independent of the magnification factor achieved accuracy of 99.5%.

Table 3: Classification Accuracy Comparison for Binary Class

Author	Model	40X	100X	200X	400X
Pratiher et al., [22]	L-Isomap and SSAEm	96.8	98.1	98.2	97
Bardou et al., [24]	CNN	94.65	98.33	94.07	97.12
	Ensemble CNN model	94.54	97.85	93.77	96.15
Yun Jianget al., [13]	BHCNet-3 + Exp	98.12	98.80	98.88	98.21
	BHCNet-3 + Cos	98.75	98.88	99.17	98.76
Proposed Method	CNN (Scratch)	99.10	99.15	99.22	98.99

For multiclass classification:

The experiment's results for multiclass classification accuracy were measured and compared to those of other authors, as shown in Table 4.

Table 4: Classification Accuracy Comparison for Multi Class

Author	Model	40X	100X	200X	400X
Bardou et al., [24]	CNN	86.34	84.00	79.93	79.74
	Ensemble CNN model	88.23	84.64	83.31	83.98
Yun Jianget al., [13]	BHCNet-3 + Exp	94.43	94.45	92.27	91.15
Abhijeet Patil et al., [25]	A-MIL	82.95	86.45	86.56	84.43
Richa Upadhyay et al., [23]	MPCS-OP (RN-50)	93.00	93.26	92.28	88.74
Proposed Method	CNN (Scratch)	96.36	96.43	96.12	95.91

As seen in the table, the proposed model's accuracy variance for various magnification factors is significantly less than that of other authors and also outperformed them in terms of accuracy. The experiment's results for the independent magnification factor are represented by the classification report in table 5 and confusion matrix and accuracy curve in figure 7, 8.

Table 5: Classification report for multi class

Author	Precision	Recall	F1-score	Support
adenosis	0.94	0.94	0.94	18
ductal carcinoma	0.85	1.00	0.92	22
fibroadenoma	1.00	0.93	0.96	28
lobular carcinoma	1.00	0.90	0.95	20
mucinous carcinoma	0.92	1.00	0.96	24
papillary carcinoma	1.00	0.93	0.97	15
phyllodes tumor	1.00	0.95	0.98	22
tubular adenoma	1.00	1.00	1.00	19

		Confusion Matrix							
Actual	adenosis	17	1	0	0	0	0	0	0
	ductal_carcinoma	0	22	0	0	0	0	0	0
	fibroadenoma	0	1	26	0	1	0	0	0
	lobular_carcinoma	1	1	0	18	0	0	0	0
	mucinous_carcinoma	0	0	0	0	24	0	0	0
	papillary_carcinoma	0	0	0	0	1	14	0	0
	phyllodes_tumor	0	1	0	0	0	0	21	0
	tubular_adenoma	0	0	0	0	0	0	0	19
		adenosis	ductal_carcinoma	fibroadenoma	lobular_carcinoma	mucinous_carcinoma	papillary_carcinoma	phyllodes_tumor	tubular_adenoma
		Predicted							

Fig. 7: Confusion Matrix of multi class classification.

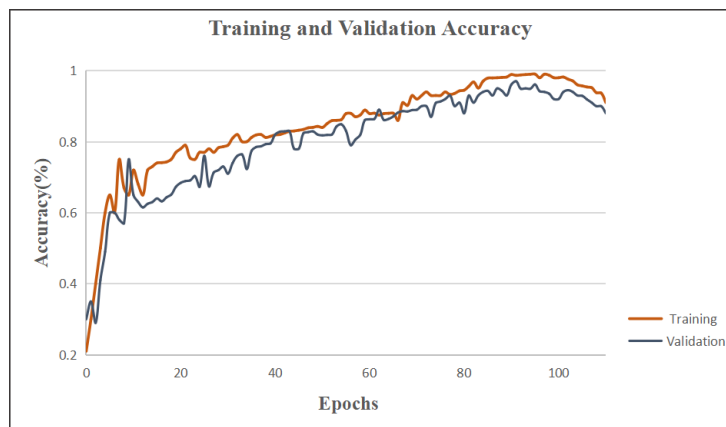


Fig. 8: Accuracy Curve of multi class classification.

The approach suggested in this work is reliable to the problems of classification, according to experimental outcomes. The comparison findings with various baseline models identifies that the strategy proposed in the model performs better.

6 Conclusion

This study posits the deployment of a deep learning based network, constructed entirely from scratch, that boasts dense layers in higher level representation, resulting in a marked improvement over conventional classification systems. The proposed scratch method has been subjected to numerous performance evaluations, comparing it with existing technique. It has been found that the model enhance the generalizability and robustness of classification in dealing with imbalanced dataset of breast cancer histopathology images. The deep scratch network exhibits higher accuracy 96.1 % compared to transfer learning models and has the potential to effectively classify both majority and minority classes. Despite the challenges posed by the BreakHis dataset, including low light images and varying magnification factors, there is a need for continuous improvement of histopathology images for better accuracy. The proposed future implementation of attention in the scratch model is aimed at further increasing classification precision and providing a more nuanced classification of histopathology images.

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